

Package ‘aroma.affymetrix’

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Title Analysis of large Affymetrix microarray data sets

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Depends

R (>= 2.12.0), R.utils (>= 1.9.9), R.filesets (>= 1.1.4), aroma.core (>= 2.4.0), aroma.light (>= 1.22.0), aroma.apd (>= 0.2.0), R.rsp (>= 0.7.1), affxparser (>= 1.22.0)

Imports MASS, methods, splines, matrixStats (>= 0.4.3)

Suggests RColorBrewer (>= 1.0-5), preprocessCore (>= 1.8.0), affyPLM (>= 1.22.0), affy (>= 1.24.0), limma (>= 3.2.0), gcrma (>= 2.10.0), gsmoothr (>= 0.1.5), dChipIO (>= 0.1.0), oligo (>= 1.12.0), oligoClasses (>= 1.10.0), DBI (>= 0.2-5), pdInfoBuilder (>= 1.12.0), Biobase (>= 2.9.0), AffymetrixDataTestFiles

Description This package implements classes for files and sets of files for various Affymetrix file formats, e.g. AffymetrixCdfFile, AffymetrixCelFile, and AffymetrixCelSet. These are designed to be memory efficient but still being fast. The idea is to keep all data on file and only read data into memory when needed. Clever caching mechanisms are used to minimize the overhead of data IO. All of the above is hidden in the package API and for the developer (and the end user), the data is queried as if it lives in memory. With this design it is only the disk space that limits the number of arrays that can be analyzed. To install, do: `source("http://www.aroma-project.org/hbLite.R"); hbInstall("aroma.affymetrix")`.

License LGPL (>= 2.1)

URL <http://www.aroma-project.org/>

PatchURL <http://www.braju.com/R/>

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aroma.affymetrix-package

Package aroma.affymetrix

Description

This package implements classes for files and sets of files for various Affymetrix file formats, e.g. AffymetrixCdfFile, AffymetrixCelFile, and AffymetrixCelSet. These are designed to be memory efficient but still being fast. The idea is to keep all data on file and only read data into memory when needed. Clever caching mechanisms are used to minimize the overhead of data IO. All of the above is hidden in the package API and for the developer (and the end user), the data is queried as if it lives in memory. With this design it is only the disk space that limits the number of arrays that can be analyzed. To install, do: `source("http://www.aroma-project.org/hbLite.R"); hbInstall("aroma.affymetrix")`.

This package should be considered to be in an alpha or beta phase. You should expect the API to be changing over time.

Requirements

This package requires several packages from CRAN, Bioconductor, R-forge and our local braju.com repository. We are moving more and more of the package to CRAN and Bioconductor.

Installation and updates

To install this package, see instructions at <http://www.aroma-project.org/>.

To get started

To get started, see the online user guides and the vignettes <http://www.aroma-project.org/>.

How to cite this package

Please cite references [1] and [2] when using this package.

License

The releases of this package is licensed under LGPL version 2.1 or newer.

The development code of the packages is under a private licence (where applicable) and patches sent to the author fall under the latter license, but will be, if incorporated, released under the "release" license above.

Author(s)

Henrik Bengtsson with great contributions from Ken Simpson, Elizabeth Purdom, and Mark Robinson.

References

Some of the reference below can be found at <http://www.maths.lth.se/bioinformatics/publications/>.

[1] H. Bengtsson, K. Simpson, J. Bullard, and K. Hansen, *aroma.affymetrix: A generic framework in R for analyzing small to very large Affymetrix data sets in bounded memory*, Tech Report \#745, Department of Statistics, University of California, Berkeley, February 2008.

[2] H. Bengtsson, R. Irizarry, B. Carvalho, and T. Speed, *Estimation and assessment of raw copy numbers at the single locus level*, Bioinformatics, 2008.

[3] H. Bengtsson, *The R.oo package - Object-Oriented Programming with References Using Standard R Code*, In Kurt Hornik, Friedrich Leisch and Achim Zeileis, editors, Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), March 20-22, Vienna, Austria. <http://www.ci.tuwien.ac.at/Conferences/DSC-2003/Proceedings/>

AbstractProbeSequenceNormalization

The AbstractProbeSequenceNormalization class

Description

Package: aroma.affymetrix

Class AbstractProbeSequenceNormalization

Object

~~|

~~+--AromaTransform

```

~~~~~|
~~~~~+---Transform
~~~~~|
~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---ProbeLevelTransform3
~~~~~|
~~~~~+---AbstractProbeSequenceNormalization

```

Directly known subclasses:

[BaseCountNormalization](#), [BasePositionNormalization](#), [LinearModelProbeSequenceNormalization](#), [MatNormalization](#)

```

public abstract static class AbstractProbeSequenceNormalization
extends ProbeLevelTransform3

```

This abstract class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in probe sequences.

Usage

```

AbstractProbeSequenceNormalization(..., target=NULL)

```

Arguments

...	Arguments passed to the constructor of ProbeLevelTransform3 .
target	A character string specifying type of "target" used. If "zero", all arrays are normalized to have no effects. If <code>NULL</code> , all arrays a normalized to have the same effect as the average array has.

Fields and Methods**Methods:**

getTargetFile	-
process	Normalizes the data set.

Methods inherited from [ProbeLevelTransform3](#):

[clearCache](#), [getCellsTo](#), [getCellsToFit](#), [getCellsToUpdate](#), [getUnitsTo](#), [getUnitsToFit](#), [getUnitsToUpdate](#), [writeSignals](#)

Methods inherited from [Transform](#):

[getOutputDataSet](#), [getOutputDataSetOLD20090509](#), [getOutputFiles](#)

Methods inherited from [AromaTransform](#):

[getExpectedOutputFiles](#), [getExpectedOutputFullnames](#), [getFullName](#), [getInputDataSet](#), [getName](#), [getOutputDataSet](#), [getOutputDataSet0](#), [getOutputFiles](#), [getPath](#), [getTags](#), [isDone](#), [process](#), [setTags](#)

Methods inherited from Object:

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

Requirements

This class requires that an [AromaCellSequenceFile](#) is available for the chip type.

Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

AdditiveCovariatesNormalization

The AdditiveCovariatesNormalization class

Description

Package: aroma.affymetrix

Class AdditiveCovariatesNormalization**Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--AdditiveCovariatesNormalization

```

Directly known subclasses:

[GcContentNormalization2](#)

```
public abstract class AdditiveCovariatesNormalization
```

```
extends ChipEffectTransform
```

This class represents a normalization method that corrects for GC-content effects on copy-number chip-effect estimates.

Usage

```
AdditiveCovariatesNormalization(dataSet=NULL, ..., target=NULL, subsetToFit="-XY", shift=0, onMissing
```

Arguments

dataSet	A SnpChipEffectSet .
...	Additional arguments passed to the constructor of ChipEffectTransform .
target	(Optional) A character string or a function specifying what to normalize toward.
subsetToFit	The units from which the normalization curve should be estimated. If <code>NULL</code> , all are considered.
onMissing	Specifies how to normalize units for which the GC contents are unknown.
shift	An optional amount the data points should be shifted (translated).

Details

For SNPs, the normalization function is estimated based on the total chip effects, i.e. the sum of the allele signals. The normalizing is done by rescale the chip effects on the intensity scale such that the mean of the total chip effects are the same across samples for any given GC content. For allele-specific estimates, both alleles are always rescaled by the same amount. Thus, when normalizing allele-specific chip effects, the total chip effects is change, but not the relative allele signal, e.g. the allele B frequency.

Fields and Methods**Methods:**

<code>clearCache</code>	-
<code>getCdf</code>	-
<code>getCovariates</code>	-
<code>getOutputDataSet00</code>	-
<code>process</code>	Normalizes the data set.

Methods inherited from Transform:

`getOutputDataSet`, `getOutputDataSetOLD20090509`, `getOutputFiles`

Methods inherited from AromaTransform:

`getExpectedOutputFiles`, `getExpectedOutputFullNames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getTags`, `isDone`, `process`, `setTags`

Methods inherited from Object:

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

AffineCnPlm

*The AffineCnPlm class***Description**

Package: aroma.affymetrix

Class AffineCnPlm**Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AffinePlm
~~~~~|
~~~~~+--AffineSnpPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--CnPlm
~~~~~|
~~~~~+--AffineCnPlm

```

Directly known subclasses:public static class **AffineCnPlm**extends [CnPlm](#)**Usage**

AffineCnPlm(..., combineAlleles=FALSE)

Arguments... Arguments passed to [AffineSnpPlm](#).combineAlleles If **FALSE**, allele A and allele B are treated seperately, otherwise together.

Fields and Methods

Methods:

No methods defined.

Methods inherited from CnPlm:

getCellIndices, getChipEffectSet, getCombineAlleles, getProbeAffinityFile, setCombineAlleles

Methods inherited from SnpPlm:

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

Methods inherited from AffineSnpPlm:

getAsteriskTags

Methods inherited from AffinePlm:

getAsteriskTags, getProbeAffinityFile

Methods inherited from ProbeLevelModel:

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

Methods inherited from MultiArrayUnitModel:

getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

Methods inherited from Model:

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from Object:

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

AffinePlm

The AffinePlm class

Description

Package: aroma.affymetrix

Class AffinePlm

Object

~~|

~~+--Model

~~~~~|

```

~~~~~+---UnitModel
~~~~~|
~~~~~+---MultiArrayUnitModel
~~~~~|
~~~~~+---ProbeLevelModel
~~~~~|
~~~~~+---AffinePlm

```

**Directly known subclasses:**

[AffineCnPlm](#), [AffineSnpPlm](#)

```

public static class AffinePlm
extends ProbeLevelModel

```

This class represents affine model in Bengtsson & Hössjer (2006).

**Usage**

```
AffinePlm(..., background=TRUE)
```

**Arguments**

... Arguments passed to [ProbeLevelModel](#).

background If [TRUE](#), background is estimate for each unit group, otherwise not. That is, if [FALSE](#), a *linear* (proportional) model without offset is fitted, resulting in very similar results as obtained by the [MbeiPlm](#).

**Fields and Methods****Methods:**

```

getAsteriskTags -
getProbeAffinityFile -

```

**Methods inherited from [ProbeLevelModel](#):**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from [MultiArrayUnitModel](#):**

getListOfPriors, setListOfPriors, validate

**Methods inherited from [UnitModel](#):**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from [Model](#):**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Model**

For a single unit group, the affine model is:

$$y_{ik} = a + \theta_i \phi_k + \varepsilon_{ik}$$

where  $a$  is an offset common to all probe signals,  $\theta_i$  are the chip effects for arrays  $i = 1, \dots, I$ , and  $\phi_k$  are the probe affinities for probes  $k = 1, \dots, K$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance. The model is constrained such that  $\prod_k \phi_k = 1$ .

Note that with the additional constraint  $a = 0$  (see arguments above), the above model is very similar to [MbeiPlm](#). The differences in parameter estimates is due to difference in assumptions about the error structure, which in turn affects how the model is estimated.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

Bengtsson & Hössjer (2006).

---

AffineSnpPlm

*The AffineSnpPlm class*

---

**Description**

Package: aroma.affymetrix

**Class AffineSnpPlm****Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|

```

```

~~~~~+--AffinePlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--AffineSnpPlm

```

**Directly known subclasses:**[AffineCnPlm](#)

```

public static class AffineSnpPlm
 extends SnpPlm

```

**Usage**

```
AffineSnpPlm(..., mergeStrands=FALSE)
```

**Arguments**

```

... Arguments passed to AffinePlm.
mergeStrands If TRUE, the sense and the anti-sense strands are fitted together, otherwise separately.

```

**Fields and Methods****Methods:***No methods defined.***Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

**Methods inherited from AffinePlm:**

getAsteriskTags, getProbeAffinityFile

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$&lt;-, [, [ [&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AffymetrixCdfFile      *The AffymetrixCdfFile class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCdfFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AromaChipTypeAnnotationFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--UnitAnnotationDataFile
~~~~~|
~~~~~+--UnitTypesFile
~~~~~|
~~~~~+--UnitNamesFile
~~~~~|
~~~~~+--AffymetrixCdfFile

```

**Directly known subclasses:**

```

public abstract static class AffymetrixCdfFile
extends UnitNamesFile

```

An AffymetrixCdfFile object represents a generic Affymetrix CDF file.

**Usage**

```
AffymetrixCdfFile(...)
```

**Arguments**

... Arguments passed to [AromaChipTypeAnnotationFile](#).

**Fields and Methods****Methods:**

|                                             |                                                           |
|---------------------------------------------|-----------------------------------------------------------|
| <a href="#">convert</a>                     | Converts a CDF into the same CDF but with another format. |
| <a href="#">createExonByTranscriptCdf</a>   | Creates an exon-by-transcript CDF.                        |
| <a href="#">createMonoCell</a>              | -                                                         |
| <a href="#">getACSFile</a>                  | -                                                         |
| <a href="#">getAromaCellSequenceFile</a>    | -                                                         |
| <a href="#">getCellIndices</a>              | Gets the cell indices unit by unit.                       |
| <a href="#">getChipType</a>                 | -                                                         |
| <a href="#">getDimension</a>                | -                                                         |
| <a href="#">getFileFormat</a>               | -                                                         |
| <a href="#">getGenomeInformation</a>        | Gets genome information for this chip type.               |
| <a href="#">getImage</a>                    | -                                                         |
| <a href="#">getMonoCell</a>                 | -                                                         |
| <a href="#">getPlatform</a>                 | -                                                         |
| <a href="#">getUnitGroupNamesFromUgcMap</a> | -                                                         |
| <a href="#">getUnitNames</a>                | Gets the names of each unit.                              |
| <a href="#">getUnitTypes</a>                | Gets the types of a set of units.                         |
| <a href="#">hasUnitTypes</a>                | -                                                         |
| <a href="#">isMonocellCdf</a>               | -                                                         |
| <a href="#">isPm</a>                        | Checks which cells (probes) are PMs and not.              |
| <a href="#">isUniqueCdf</a>                 | -                                                         |
| <a href="#">nbrOfCells</a>                  | -                                                         |
| <a href="#">nbrOfColumns</a>                | -                                                         |
| <a href="#">nbrOfQcUnits</a>                | -                                                         |
| <a href="#">nbrOfRows</a>                   | -                                                         |
| <a href="#">nbrOfUnits</a>                  | -                                                         |
| <a href="#">readDataFrame</a>               | -                                                         |
| <a href="#">readUnits</a>                   | Reads CDF data unit by unit.                              |
| <a href="#">setGenomeInformation</a>        | -                                                         |
| <a href="#">setSnPInformation</a>           | -                                                         |

**Methods inherited from UnitNamesFile:**

[getUnitNames](#), [indexOf](#), [nbrOfUnits](#)

**Methods inherited from UnitTypesFile:**

[getUnitTypes](#), [nbrOfUnits](#)

**Methods inherited from UnitAnnotationDataFile:**

[byChipType](#), [getAromaUflFile](#), [getAromaUgpFile](#), [getChipType](#), [getPlatform](#), [nbrOfUnits](#)

**Methods inherited from AromaPlatformInterface:**

[getAromaPlatform](#), [getAromaUgpFile](#), [getPlatform](#), [getUnitAnnotationDataFile](#), [getUnitNamesFile](#),

getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaChipTypeAnnotationFile:**

byChipType, byName, findByChipType, fromFile, getChipType, getHeader, getPlatform

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [, [ [<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AffymetrixCelFile

*The AffymetrixCelFile class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCelFile**

**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|

```

```

~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---AffymetrixCelFile

```

**Directly known subclasses:**

*ChipEffectFile, CnChipEffectFile, CnProbeAffinityFile, ExonChipEffectFile, ExonProbeAffinityFile, FirmaFile, ParameterCelFile, ProbeAffinityFile, QualityAssessmentFile, ResidualFile, SnpChipEffectFile, SnpProbeAffinityFile, WeightsFile*

```

public abstract static class AffymetrixCelFile
extends AffymetrixFile

```

An AffymetrixCelFile object represents a single Affymetrix CEL file.

**Usage**

```
AffymetrixCelFile(..., cdf=NULL)
```

**Arguments**

|     |                                                                                                                                                                                                                                                                                                                                      |
|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ... | Arguments passed to <a href="#">AromaMicroarrayDataFile</a> .                                                                                                                                                                                                                                                                        |
| cdf | An optional <a href="#">AffymetrixCdfFile</a> making it possible to override the default CDF file as specified by the CEL file header. The requirement is that its number of cells must match that of the CEL file. If <code>NULL</code> , the CDF structure is inferred from the the chip type as specified in the CEL file header. |

**Fields and Methods****Methods:**

|                          |                                                      |
|--------------------------|------------------------------------------------------|
| [                        | -                                                    |
| [[                       | -                                                    |
| clone                    | -                                                    |
| extractMatrix            | -                                                    |
| <a href="#">fromFile</a> | Defines an AffymetrixCelFile object from a CEL file. |
| getAm                    | -                                                    |
| <a href="#">getCdf</a>   | Gets the CDF structure for this CEL file.            |
| getFileFormat            | -                                                    |
| <a href="#">getImage</a> | Creates an RGB Image object from a CEL file.         |
| getUnitNamesFile         | -                                                    |
| getUnitTypesFile         | -                                                    |
| highlight                | -                                                    |
| <a href="#">image270</a> | Displays all or a subset of the data spatially.      |

|                                |                                                                |
|--------------------------------|----------------------------------------------------------------|
| <code>nbrOfCells</code>        | -                                                              |
| <code>plotDensity</code>       | Plots the density of the probe signals on the array.           |
| <code>plotImage</code>         | Displays a spatial plot of a CEL file.                         |
| <code>plotMvsA</code>          | Plots log-ratio versus log-intensity in a scatter plot.        |
| <code>plotMvsX</code>          | Plots log-ratio versus another variable in a scatter plot.     |
| <code>setCdf</code>            | Sets the CDF structure for this CEL file.                      |
| <code>smoothScatterMvsA</code> | Plots log-ratio versus log-intensity in a smooth scatter plot. |
| <code>writeImage</code>        | Writes a spatial image of the signals in the CEL file.         |

#### Methods inherited from AromaPlatformInterface:

`getAromaPlatform`, `getAromaUgpFile`, `getPlatform`, `getUnitAnnotationDataFile`, `getUnitNamesFile`, `getUnitTypesFile`, `isCompatibleWith`

#### Methods inherited from AromaMicroarrayDataFile:

`getAttributeXY`, `getChipType`, `getPlatform`, `getPloidy`, `getXAM`, `hasAttributeXY`, `isAverageFile`, `setAttributeByTags`, `setAttributeXY`

#### Methods inherited from GenericDataFile:

`getParentName`, `compareChecksum`, `copyTo`, `equals`, `fromFile`, `getAlias`, `getAttribute`, `getAttributes`, `getChecksum`, `getCreatedOn`, `getDefaultFullName`, `getExtension`, `getExtensionPattern`, `getFilename`, `getFilenameExtension`, `getFileSize`, `getFileType`, `getLastAccessedOn`, `getLastModifiedOn`, `getOutputExtension`, `getPath`, `getPathname`, `gunzip`, `gzip`, `hasBeenModified`, `isFile`, `readChecksum`, `renameTo`, `renameToUpperCaseExt`, `setAlias`, `setAttribute`, `setAttributes`, `setAttributesBy`, `setAttributesByTags`, `setExtensionPattern`, `testAttributes`, `validateChecksum`, `writeChecksum`

#### Methods inherited from FullNameInterface:

`appendFullNameTranslator`, `appendFullNameTranslatorBycharacter`, `appendFullNameTranslatorBydata.frame`, `appendFullNameTranslatorByfunction`, `appendFullNameTranslatorBylist`, `appendFullNameTranslatorByNULL`, `appendFullNameTranslatorByTabularTextFile`, `appendFullNameTranslatorByTabularTextFileSet`, `clearFullNameTranslator`, `clearListOfFullNameTranslators`, `getDefaultFullName`, `getFullName`, `getFullNameTranslator`, `getListOfFullNameTranslators`, `getName`, `getTags`, `hasTag`, `hasTags`, `setFullName`, `setFullNameTranslator`, `setListOfFullNameTranslators`, `setName`, `setTags`, `updateFullName`

#### Methods inherited from Object:

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

### For developers

If you subclass this class, please make sure to query the `AffymetrixCdfFile` object (see `*getCdf()`) whenever querying CDF information. Do not use the CDF file inferred from the chip type in CEL header, unless you really want it to be hardwired that way, otherwise you will break to possibility to override the CDF structure.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically part of an [AffymetrixCelSet](#).

---

|                  |                                   |
|------------------|-----------------------------------|
| AffymetrixCelSet | The <i>AffymetrixCelSet</i> class |
|------------------|-----------------------------------|

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCelSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet

```

**Directly known subclasses:**

[ChipEffectSet](#), [CnChipEffectSet](#), [ExonChipEffectSet](#), [FirmaSet](#), [ParameterCelSet](#), [QualityAssessmentSet](#), [ResidualSet](#), [SnpChipEffectSet](#), [WeightsSet](#)

```

public static class AffymetrixCelSet
extends AffymetrixFileSet

```

An AffymetrixCelSet object represents a set of Affymetrix CEL files with *identical* chip types.

**Usage**

```
AffymetrixCelSet(files=NULL, ...)
```

**Arguments**

|       |                                                                |
|-------|----------------------------------------------------------------|
| files | A <a href="#">list</a> of <a href="#">AffymetrixCelFile</a> s. |
| ...   | Not used.                                                      |

**Fields and Methods**

**Methods:**

|                                     |                                                                                                    |
|-------------------------------------|----------------------------------------------------------------------------------------------------|
| [                                   | -                                                                                                  |
| [[                                  | -                                                                                                  |
| append                              | -                                                                                                  |
| as                                  | -                                                                                                  |
| <a href="#">as.AffymetrixCelSet</a> | Coerce an object to an AffymetrixCelSet object.                                                    |
| byName                              | -                                                                                                  |
| convertToUnique                     | -                                                                                                  |
| doCRMAv1                            | -                                                                                                  |
| doCRMAv2                            | -                                                                                                  |
| <a href="#">doFIRMA</a>             | Finding Isoforms using Robust Multichip Analysis (FIRMA).                                          |
| doGCRMA                             | -                                                                                                  |
| doRMA                               | -                                                                                                  |
| <a href="#">extractAffyBatch</a>    | Extracts an in-memory AffyBatch object from the CEL set.                                           |
| <a href="#">extractMatrix</a>       | Extract data as a matrix for a set of arrays.                                                      |
| extractSnpFeatureSet                | -                                                                                                  |
| findByName                          | -                                                                                                  |
| getAverage                          | -                                                                                                  |
| getAverageAsinh                     | -                                                                                                  |
| <a href="#">getAverageFile</a>      | Calculates the mean and the standard deviation of the cell signal (intensity, standard deviation e |
| getAverageLog                       | -                                                                                                  |
| <a href="#">getCdf</a>              | Gets the CDF structure for this CEL set.                                                           |
| <a href="#">getChipType</a>         | Gets the chip type for this CEL set.                                                               |
| getData                             | -                                                                                                  |
| <a href="#">getIntensities</a>      | Gets cell intensities from a set of cells and a set of arrays.                                     |
| getPlatform                         | -                                                                                                  |
| getTimestamps                       | -                                                                                                  |
| getUnitGroupCellMap                 | -                                                                                                  |
| <a href="#">getUnitIntensities</a>  | Gets cell signals for a subset of units and a subset of arrays.                                    |
| getUnitNamesFile                    | -                                                                                                  |
| getUnitTypesFile                    | -                                                                                                  |
| <a href="#">isDuplicated</a>        | Identifies duplicated CEL files.                                                                   |
| justSNPRMA                          | -                                                                                                  |
| <a href="#">nbrOfArrays</a>         | Gets the number of arrays in the file set.                                                         |
| <a href="#">plotDensity</a>         | Plots the densities of all samples.                                                                |
| range                               | -                                                                                                  |
| readUnits                           | -                                                                                                  |
| <a href="#">setCdf</a>              | Sets the CDF structure for this CEL set.                                                           |
| writeSgr                            | -                                                                                                  |

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTransla-

torSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [, [[:<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[AffymetrixCelFile](#).

**Examples**

```
Not run:
 for (zzz in 0) {

Find any dataset
path <- NULL
if (is.null(path))
 break

Define a dataset object based on all CEL files in a directory

ds <- AffymetrixCelSet$fromFiles(path)
print(ds)
```

```

Keep at most three arrays for this example
ds <- extract(ds, 1:min(3,nbrOfArrays(ds)))
print(ds)

} # for (zzz in 0)
rm(zzz)

End(Not run)

```

---

AffymetrixCelSetReporter

*The AffymetrixCelSetReporter class*

---

## Description

Package: aroma.affymetrix

### Class AffymetrixCelSetReporter

#### Object

```

~~|
~~+--GenericReporter
~~~~~|
~~~~~+--AffymetrixFileSetReporter
~~~~~|
~~~~~+--AffymetrixCelSetReporter

```

#### Directly known subclasses:

*SpatialReporter*

public abstract static class **AffymetrixCelSetReporter**

extends *AffymetrixFileSetReporter*

## Usage

```
AffymetrixCelSetReporter(..., .setClass="AffymetrixCelSet")
```

## Arguments

... Arguments passed to *AffymetrixFileSetReporter*.  
.setClass The name of the class of the input set.

## Fields and Methods

### Methods:

`getDataSet` Gets the data set.

**Methods inherited from AffymetrixFileSetReporter:**

`getFileSet`, `getInputName`, `getInputTags`

**Methods inherited from GenericReporter:**

`getAlias`, `getAsteriskTags`, `getFullName`, `getInputName`, `getInputTags`, `getMainPath`, `getName`, `getPath`, `getReportSet`, `getTags`, `process`, `setAlias`, `setup`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[]`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AffymetrixCelSetTuple *The AffymetrixCelSetTuple class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCelSetTuple**

**Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFileSetList
~~~~~|
~~~~~+---AromaMicroarrayDataSetTuple
~~~~~|
~~~~~+---AffymetrixCelSetTuple

```

**Directly known subclasses:**

`ChipEffectSetTuple`, `CnChipEffectSetTuple`

public static class **AffymetrixCelSetTuple**

extends *AromaMicroarrayDataSetTuple*

**Usage**

```
AffymetrixCelSetTuple(..., .setClass="AffymetrixCelSet")
```

**Arguments**

... Arguments passed to the constructor of [AromaMicroarrayDataSetTuple](#).  
 .setClass The name of the class of the input set.

**Fields and Methods****Methods:**

byPath -

**Methods inherited from AromaMicroarrayDataSetTuple:**

as, as.AromaMicroarrayDataSetTuple, byPath, getAsteriskTags, getChipTypes, getFullNames, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes

**Methods inherited from GenericDataFileSetList:**

as.character, as.data.frame, as, as.GenericDataFileSetList, as.list, assertDuplicates, clone, extract, getAsteriskTags, getDefaultFullName, getFileList, getFileListClass, getFullNames, getNames, getSet, getSets, getTags, indexOf, length, nbrOfFiles, nbrOfSets, setTags

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AffymetrixCnChpSet      *The AffymetrixCnChpSet class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCnChpSet**

```

Object
~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFileSet
~~~~~|
~~~~~+---AromaMicroarrayDataSet
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFileSet
~~~~~|
~~~~~+---AffymetrixCnChpSet

```

### Directly known subclasses:

```

public abstract static class AffymetrixCnChpSet
extends AffymetrixFileSet

```

A `AffymetrixCnChpSet` object represents a set of `AffymetrixCnChpFile`:s with *identical* chip types.

### Usage

```
AffymetrixCnChpSet(files=NULL, ...)
```

### Arguments

|                    |                                                                |
|--------------------|----------------------------------------------------------------|
| <code>files</code> | A <a href="#">list</a> of <code>AffymetrixCnChpFile</code> :s. |
| <code>...</code>   | Not used.                                                      |

### Fields and Methods

#### Methods:

|                                    |                                                                |
|------------------------------------|----------------------------------------------------------------|
| <code>as</code>                    | -                                                              |
| <code>as.AffymetrixCnChpSet</code> | Coerce an object to an <code>AffymetrixCnChpSet</code> object. |
| <code>byName</code>                | -                                                              |
| <code>byPath</code>                | -                                                              |
| <code>exportTotalCnRatioSet</code> | -                                                              |
| <code>extractLogRatios</code>      | -                                                              |
| <code>findByName</code>            | -                                                              |
| <code>getCdf</code>                | -                                                              |
| <code>nbrOfArrays</code>           | Gets the number of arrays in the file set.                     |
| <code>setCdf</code>                | -                                                              |

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[AffymetrixCnChpFile](#).

**Description**

Package: aroma.affymetrix

**Class AffymetrixFile****Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile

```

**Directly known subclasses:**

*AffymetrixCdfFile, AffymetrixCelFile, AffymetrixCnChpFile, AffymetrixTsvFile, AromaChipTypeAnnotationFile, ChipEffectFile, CnagCfhFile, CnChipEffectFile, CnProbeAffinityFile, DChipCdfBinFile, DChipDcpFile, ExonChipEffectFile, ExonProbeAffinityFile, FirmaFile, ParameterCelFile, ProbeAffinityFile, QualityAssessmentFile, ResidualFile, SnpChipEffectFile, SnpProbeAffinityFile, WeightsFile*

public abstract static class **AffymetrixFile**

extends *AromaPlatformInterface*

An AffymetrixFile object represents a single Affymetrix file, e.g. an Affymetrix CEL file or an Affymetrix CDF file. Note that this class is abstract and can not be instantiated, but instead you have to use one of the subclasses or the generic fromFile() method.

**Usage**

```
AffymetrixFile(...)
```

**Arguments**

... Arguments passed to *GenericDataFile*.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically part of an [AffymetrixFileSet](#).

---

AffymetrixFileSet      *The AffymetrixFileSet class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixFileSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface

```

```
~~~~~|
~~~~~+--AffymetrixFileSet
```

**Directly known subclasses:**

[AffymetrixCelSet](#), [AffymetrixCnChpSet](#), [ChipEffectSet](#), [CnChipEffectSet](#), [DChipDcpSet](#), [ExonChipEffectSet](#), [FirmaSet](#), [ParameterCelSet](#), [QualityAssessmentSet](#), [ResidualSet](#), [SnpChipEffectSet](#), [WeightsSet](#)

```
public abstract static class AffymetrixFileSet
 extends AromaPlatformInterface
```

An [AffymetrixFileSet](#) object represents a set of [AffymetrixFiles](#) with *identical* chip types.

**Usage**

```
AffymetrixFileSet(files=NULL, ...)
```

**Arguments**

|       |                                                              |
|-------|--------------------------------------------------------------|
| files | A <a href="#">list</a> of <a href="#">AffymetrixFile</a> :s. |
| ...   | Arguments passed to <a href="#">GenericDataFileSet</a> .     |

**Fields and Methods****Methods:**

|                                      |                                                                                                        |
|--------------------------------------|--------------------------------------------------------------------------------------------------------|
| as                                   | -                                                                                                      |
| <a href="#">as.AffymetrixFileSet</a> | Coerce an object to an <a href="#">AffymetrixFileSet</a> object.                                       |
| <a href="#">byPath</a>               | Defines an <a href="#">AffymetrixFileSet</a> object by searching for <a href="#">Affymetrix</a> files. |
| <a href="#">getDefaultFullName</a>   | -                                                                                                      |

**Methods inherited from [AromaPlatformInterface](#):**

[getAromaPlatform](#), [getAromaUgpFile](#), [getPlatform](#), [getUnitAnnotationDataFile](#), [getUnitNamesFile](#), [getUnitTypesFile](#), [isCompatibleWith](#)

**Methods inherited from [AromaMicroarrayDataSet](#):**

[as.AromaMicroarrayDataSetList](#), [as.AromaMicroarrayDataSetTuple](#), [getAromaFullNameTranslatorSet](#), [getAverageFile](#), [getChipType](#), [getDefaultFullName](#), [getPlatform](#), [nbrOfArrays](#), [setAttributesBy](#), [setAttributesBySampleAnnotationFile](#), [setAttributesBySampleAnnotationSet](#), [validate](#)

**Methods inherited from [GenericDataFileSet](#):**

[getFullNameTranslatorSet](#), [getParentName](#), [append](#), [appendFiles](#), [appendFullNamesTranslator](#), [appendFullNamesTranslatorBydata.frame](#), [appendFullNamesTranslatorByfunction](#), [appendFullNamesTranslatorBylist](#), [appendFullNamesTranslatorByNULL](#), [appendFullNamesTranslatorByTabularTextFile](#), [appendFullNamesTranslatorByTabularTextFileSet](#), [as.list](#), [byName](#), [byPath](#), [clearCache](#), [clearFullNamesTranslator](#), [copyTo](#), [equals](#), [extract](#), [findByName](#), [getAlias](#), [getChecksum](#), [getChecksumObjects](#), [getDefaultFullName](#), [getFile](#), [getFileClass](#), [getFileSize](#), [getFullNames](#), [getNames](#), [getPath](#),

getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

AffymetrixFileSetReporter

*The AffymetrixFileSetReporter class*

**Description**

Package: aroma.affymetrix

**Class AffymetrixFileSetReporter**

**Object**

```

~~|
~~+---GenericReporter
~~~~~|
~~~~~+---AffymetrixFileSetReporter

```

**Directly known subclasses:**

*AffymetrixCelSetReporter, SpatialReporter*

```

public abstract static class AffymetrixFileSetReporter
extends GenericReporter

```

**Usage**

```
AffymetrixFileSetReporter(set=NULL, ..., .setClass="AffymetrixFileSet")
```

**Arguments**

set            An `AffymetrixFileSet` object.  
 ...            Arguments passed to `GenericReporter`.  
 .setClass     The name of the class of the input set.

**Fields and Methods****Methods:**

getInputName -  
 getInputTags -

**Methods inherited from GenericReporter:**

getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getTags, process, setAlias, setup

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

 AlleleSummation

*The AlleleSummation class*


---

**Description**

Package: aroma.affymetrix

**Class AlleleSummation****Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--AlleleSummation

```

**Directly known subclasses:**

public abstract static class **AlleleSummation**  
 extends *UnitModel*

This class takes allele-specific chip effect estimates of a *SnpcChipEffectSet* and returns a *CnChipEffectSet* holding the summed allele estimates.

### Usage

```
AlleleSummation(dataSet=NULL, ignoreNAs=TRUE, ...)
```

### Arguments

|           |                                                                                             |
|-----------|---------------------------------------------------------------------------------------------|
| dataSet   | A <i>SnpcChipEffectSet</i> .                                                                |
| ignoreNAs | If <b>TRUE</b> , missing values are excluded when summing the signals from the two alleles. |
| ...       | Arguments passed to <i>UnitModel</i> .                                                      |

### Fields and Methods

#### Methods:

|                         |                                              |
|-------------------------|----------------------------------------------|
| findUnitsTodo           | -                                            |
| getAsteriskTags         | -                                            |
| <i>getChipEffectSet</i> | Gets the set of chip effects for this model. |
| process                 | -                                            |

#### Methods inherited from *UnitModel*:

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

#### Methods inherited from *Model*:

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

#### Methods inherited from *Object*:

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AllelicCrosstalkCalibration

*The AllelicCrosstalkCalibration class*


---

## Description

Package: aroma.affymetrix

### Class AllelicCrosstalkCalibration

#### Object

```

~~|
~~+---AromaTransform
~~~~~|
~~~~~+---Transform
~~~~~|
~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---AllelicCrosstalkCalibration

```

#### Directly known subclasses:

```

public static class AllelicCrosstalkCalibration
extends ProbeLevelTransform

```

This class represents a calibration function that transforms the probe-level signals such that the signals from the two alleles are orthogonal. The method fits and calibrates PM signals only. MM signals will not affect the model fitting and are unaffected.

## Usage

```
AllelicCrosstalkCalibration(dataSet=NULL, ..., model=c("asis", "auto", "CRMA", "CRMAv2"), rescaleBy=c
```

## Arguments

|           |                                                                                                                                                                                                      |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataSet   | An <i>AffymetrixCelSet</i> .                                                                                                                                                                         |
| ...       | Arguments passed to the constructor of <i>ProbeLevelTransform</i> .                                                                                                                                  |
| model     | A <i>character</i> string for quickly specifying default parameter settings.                                                                                                                         |
| rescaleBy | A <i>character</i> string specifying what sets of cells should be rescaled towards a target average, if any. Default is to rescale all cells together. If "none", no rescaling is done.              |
| targetAvg | The signal(s) that either the average of the sum (if one target value) or the average of each of the alleles (if two target values) should have after calibration. Only used if rescaleBy != "none". |

|                     |                                                                                                                                                                                              |
|---------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| subsetToAvg         | The indices of the cells (taken as the intersect of existing indices) used to calculate average in order to rescale to the target average. If <code>NULL</code> , all probes are considered. |
| mergeShifts         | If <code>TRUE</code> , the shift of the probe sequence relative to the SNP position is ignored, otherwise not.                                                                               |
| B                   | An <code>integer</code> specifying by how many nucleotides the allelic groups should be stratified by. If zero, all SNPs are put in one group.                                               |
| flavor              | A <code>character</code> string specifying what algorithm is used to fit the crosstalk calibration.                                                                                          |
| alpha, q, Q, lambda | Model fitting parameters.                                                                                                                                                                    |
| pairBy              | A <code>character</code> string specifying how allele probe pairs are identified.                                                                                                            |

### What probe signals are updated?

Calibration for crosstalk between allele signals applies by definition only SNP units. Furthermore, it is only SNP units with two or four unit groups that are calibrated. For instance, in at least on custom SNP CDFs we know of, there is a small number of SNP units that have six groups. *Currently these units are not calibrated (at all)*. It is only PM probes that will be calibrated. Note that, non-calibrated signals will be saved in the output files.

### What probe signals are used to fit model?

All PM probe pairs are used to fit the crosstalk model. In the second step where signals are rescaled to a target average, it is possible to specify the set of cells that should be included when estimating the target average.

### Important about rescaling towards target average

Rescaling each allele-pair group (e.g. AC, AG, AT, CG, CT, GC) towards a target average (`rescaleBy="groups"`) *must not* be used for multi-enzyme chip types, e.g. GenomeWideSNP\_6. If still done, due to confounded effects of non-perfect enzyme mixtures etc, there will be a significant bias between raw CNs for SNPs and CN probes. Instead, for such chip types *all probe signals* should be rescale together towards the target average (`rescaleBy="all"`).

## Fields and Methods

### Methods:

```
clearCache -
process Calibrates the data set.
```

### Methods inherited from Transform:

```
getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles
```

### Methods inherited from AromaTransform:

```
getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName,
```

getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaChipTypeAnnotationFile

*The AromaChipTypeAnnotationFile class*

---

**Description**

Package: aroma.affymetrix

**Class AromaChipTypeAnnotationFile**

**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AromaChipTypeAnnotationFile

```

**Directly known subclasses:**

*AffymetrixCdfFile*

public abstract static class **AromaChipTypeAnnotationFile**

extends *AffymetrixFile*

An AromaChipTypeAnnotationFile object represents an annotation file for a specific chip type.

**Usage**

AromaChipTypeAnnotationFile(...)

**Arguments**

... Arguments passed to [AffymetrixFile](#).

**Fields and Methods****Methods:**

|                                |                                                             |
|--------------------------------|-------------------------------------------------------------|
| <a href="#">byChipType</a>     | Defines an AromaChipTypeAnnotationFile object by chip type. |
| <a href="#">findByChipType</a> | Locates an annotation file by its chip type.                |
| <a href="#">getChipType</a>    | -                                                           |
| <a href="#">getHeader</a>      | Gets the header of the annotation file.                     |
| <a href="#">getPlatform</a>    | -                                                           |

**Methods inherited from AromaPlatformInterface:**

[getAromaPlatform](#), [getAromaUgpFile](#), [getPlatform](#), [getUnitAnnotationDataFile](#), [getUnitNamesFile](#), [getUnitTypesFile](#), [isCompatibleWith](#)

**Methods inherited from AromaMicroarrayDataFile:**

[getAttributeXY](#), [getChipType](#), [getPlatform](#), [getPloidy](#), [getXAM](#), [hasAttributeXY](#), [isAverageFile](#), [setAttributesByTags](#), [setAttributeXY](#)

**Methods inherited from GenericDataFile:**

[getParentName](#), [compareChecksum](#), [copyTo](#), [equals](#), [fromFile](#), [getAlias](#), [getAttribute](#), [getAttributes](#), [getChecksum](#), [getCreatedOn](#), [getDefaultFullName](#), [getExtension](#), [getExtensionPattern](#), [getFilename](#), [getFilenameExtension](#), [getFileSize](#), [getFileType](#), [getLastAccessedOn](#), [getLastModifiedOn](#), [getOutputExtension](#), [getPath](#), [getPathname](#), [gunzip](#), [gzip](#), [hasBeenModified](#), [isFile](#), [readChecksum](#), [renameTo](#), [renameToUpperCaseExt](#), [setAlias](#), [setAttribute](#), [setAttributes](#), [setAttributesBy](#), [setAttributesByTags](#), [setExtensionPattern](#), [testAttributes](#), [validateChecksum](#), [writeChecksum](#)

**Methods inherited from FullNameInterface:**

[appendFullNameTranslator](#), [appendFullNameTranslatorBycharacter](#), [appendFullNameTranslatorBydata.frame](#), [appendFullNameTranslatorByfunction](#), [appendFullNameTranslatorBylist](#), [appendFullNameTranslatorByNULL](#), [appendFullNameTranslatorByTabularTextFile](#), [appendFullNameTranslatorByTabularTextFileSet](#), [clearFullNameTranslator](#), [clearListOfFullNameTranslators](#), [getDefaultFullName](#), [getFullName](#), [getFullNameTranslator](#), [getListOfFullNameTranslators](#), [getName](#), [getTags](#), [hasTag](#), [hasTags](#), [setFullName](#), [setFullNameTranslator](#), [setListOfFullNameTranslators](#), [setName](#), [setTags](#), [updateFullName](#)

**Methods inherited from Object:**

[asThis](#), [getChecksum](#), [\\$](#), [\\$<-](#), [\[\[](#), [\[\[<-](#), [as.character](#), [attach](#), [attachLocally](#), [clearCache](#), [clearLookupCache](#), [clone](#), [detach](#), [equals](#), [extend](#), [finalize](#), [gc](#), [getEnvironment](#), [getFieldModifier](#), [getFieldModifiers](#), [getFields](#), [getInstantiationTime](#), [getStaticInstance](#), [hasField](#), [hashCode](#), [ll](#), [load](#), [objectSize](#), [print](#), [registerFinalizer](#), [save](#)

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ArrayExplorer      *The ArrayExplorer class*

---

## Description

Package: aroma.affymetrix

### Class ArrayExplorer

Object

~~|

~~+--Explorer

~~~~~|

~~~~~+--ArrayExplorer

### Directly known subclasses:

public abstract static class **ArrayExplorer**

extends *Explorer*

## Usage

```
ArrayExplorer(csTuple=NULL, ...)
```

## Arguments

csTuple      An *AffymetrixCelSet* object.

...          Not used.

## Fields and Methods

### Methods:

|                 |                                                                    |
|-----------------|--------------------------------------------------------------------|
| addColorMap     | -                                                                  |
| getAlias        | -                                                                  |
| getAsteriskTags | -                                                                  |
| getColorMaps    | -                                                                  |
| getDataSet      | Gets the data set.                                                 |
| getSetTuple     | -                                                                  |
| nbrOfChipTypes  | -                                                                  |
| process         | Generates image files, scripts and dynamic pages for the explorer. |
| setAlias        | -                                                                  |
| setArrays       | Sets the arrays.                                                   |
| setColorMaps    | -                                                                  |

**Methods inherited from Explorer:**

addIncludes, addIndexFile, display, getAlias, getArraysOfInput, getAsteriskTags, getFullName, getIncludePath, getMainPath, getName, getNameOfInput, getNames, getParallelSafe, getPath, getReportPathPattern, getSampleLayerPrefix, getSubname, getTags, getTagsOfInput, getTemplatePath, nbrOfArrays, process, setAlias, setArrays, setParallelSafe, setReportPathPattern, setSubname, setup, splitByReportPathPattern

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AvgCnPlm

*The AvgCnPlm class*

---

**Description**

Package: aroma.affymetrix

**Class AvgCnPlm****Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AvgPlm
~~~~~|
~~~~~+--AvgSnpPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--CnPlm
~~~~~|
~~~~~+--AvgCnPlm

```

**Directly known subclasses:**

```
public static class AvgCnPlm
 extends CnPlm
```

## Usage

```
AvgCnPlm(..., combineAlleles=FALSE)
```

## Arguments

```
... Arguments passed to AvgSnpPlm.
combineAlleles If FALSE, allele A and allele B are treated seperately, otherwise together.
```

## Fields and Methods

### Methods:

*No methods defined.*

### Methods inherited from CnPlm:

getCellIndices, getChipEffectSet, getCombineAlleles, getProbeAffinityFile, setCombineAlleles

### Methods inherited from SnpPlm:

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

### Methods inherited from AvgSnpPlm:

getAsteriskTags

### Methods inherited from AvgPlm:

getAsteriskTags, getCalculateResidualsFunction, validate

### Methods inherited from ProbeLevelModel:

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

### Methods inherited from MultiArrayUnitModel:

getListOfPriors, setListOfPriors, validate

### Methods inherited from UnitModel:

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

### Methods inherited from Model:

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

### Methods inherited from Object:

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

AvgPlm

*The AvgPlm class***Description**

Package: aroma.affymetrix

**Class AvgPlm****Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AvgPlm

```

**Directly known subclasses:**[AvgCnPlm](#), [AvgSnpPlm](#)

```

public static class AvgPlm
extends ProbeLevelModel

```

This class represents a PLM where the probe intensities are averaged assuming identical probe affinities. For instance, one may assume that replicated probes with identical sequences have the same probe affinities, cf. the GenomeWideSNP\6 chip type.

**Usage**

```

AvgPlm(..., flavor=c("median", "mean"))

```

**Arguments**

|        |                                                                                                                                                             |
|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...    | Arguments passed to <a href="#">ProbeLevelModel</a> .                                                                                                       |
| flavor | A <a href="#">character</a> string specifying what model fitting algorithm to be used. This makes it possible to get identical estimates as other packages. |

**Fields and Methods****Methods:**

```

getAsteriskTags -

```

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Model**

For a single unit group, the averaging PLM of K probes is:

$$y_{ik} = \theta_i + \varepsilon_{ik}$$

where  $\theta_i$  are the chip effects for arrays  $i = 1, \dots, I$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance.

**Different flavors of model fitting**

The above model can be fitted in two ways, either robustly or non-robustly. Use argument `flavor="mean"` to fit the model non-robustly, i.e.

$$\hat{\theta}_i = 1/K \sum_k y_{ik}$$

.

Use argument `flavor="median"` to fit the model robustly, i.e.

$$\hat{\theta}_i = \text{median}_k y_{ik}$$

.

Missing values are always excluded.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

AvgSnpPlm

*The AvgSnpPlm class***Description**

Package: aroma.affymetrix

**Class AvgSnpPlm****Object**

```

~|
~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AvgPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--AvgSnpPlm

```

**Directly known subclasses:**[AvgCnPlm](#)public static class **AvgSnpPlm**extends [SnpPlm](#)**Usage**

AvgSnpPlm(..., mergeStrands=FALSE)

**Arguments**

|              |                                                                                                  |
|--------------|--------------------------------------------------------------------------------------------------|
| ...          | Arguments passed to <a href="#">AvgPlm</a> .                                                     |
| mergeStrands | If <b>TRUE</b> , the sense and the anti-sense strands are fitted together, otherwise separately. |

**Fields and Methods****Methods:***No methods defined.*

**Methods inherited from SnpPIm:**

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

**Methods inherited from AvgPIm:**

getAsteriskTags, getCalculateResidualsFunction, validate

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

BackgroundCorrection *The BackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class BackgroundCorrection****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection

```

**Directly known subclasses:**

GcRmaBackgroundCorrection, LimmaBackgroundCorrection, NormExpBackgroundCorrection, OpticalBackgroundCorrection, RmaBackgroundCorrection

public abstract static class **BackgroundCorrection**  
 extends *ProbeLevelTransform*

This class represents a background adjustment function.

**Usage**

```
BackgroundCorrection(..., subsetToUpdate=NULL, typesToUpdate=NULL)
```

**Arguments**

... Arguments passed to the constructor of *ProbeLevelTransform*.  
 subsetToUpdate The probes to be updated. If *NULL*, all probes are updated.  
 typesToUpdate Types of probes to be updated.

**Fields and Methods****Methods:**

*process* Processes the data set.

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

**Description**

Package: aroma.affymetrix

**Class BaseCountNormalization****Object**

```

~|
~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--BaseCountNormalization

```

**Directly known subclasses:**

```

public static class BaseCountNormalization
extends AbstractProbeSequenceNormalization

```

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in the number of A, C, G, and T:s in the probe sequences.

**Usage**

```
BaseCountNormalization(..., model=c("robustSmoothSpline", "lm"), bootstrap=FALSE)
```

**Arguments**

|           |                                                                                    |
|-----------|------------------------------------------------------------------------------------|
| ...       | Arguments passed to the constructor of <i>AbstractProbeSequenceNormalization</i> . |
| model     | A <b>character</b> string specifying the model used to fit the base-count effects. |
| bootstrap | If <b>TRUE</b> , the model fitting is done by bootstrap in order to save memory.   |

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from AbstractProbeSequenceNormalization:**

fitOne, getAromaCellSequenceFile, getTargetFile, indexOfMissingSequences, predictOne, process

**Methods inherited from ProbeLevelTransform3:**

clearCache, getCellsTo, getCellsToFit, getCellsToUpdate, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullNames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Requirements**

This class requires that an aroma probe sequence file is available for the chip type.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

BasePositionNormalization

*The BasePositionNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class BasePositionNormalization****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--LinearModelProbeSequenceNormalization
~~~~~|
~~~~~+--BasePositionNormalization

```

**Directly known subclasses:**

```
public static class BasePositionNormalization
 extends LinearModelProbeSequenceNormalization
```

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in positioning of A, C, G, and T:s in the probe sequences.

### Usage

```
BasePositionNormalization(..., model=c("smooth.spline"), df=5)
```

### Arguments

|       |                                                                                       |
|-------|---------------------------------------------------------------------------------------|
| ...   | Arguments passed to the constructor of <i>LinearModelProbeSequenceNormalization</i> . |
| model | A <i>character</i> string specifying the model used to fit the base-count effects.    |
| df    | The degrees of freedom of the model.                                                  |

### Fields and Methods

#### Methods:

*No methods defined.*

#### Methods inherited from *LinearModelProbeSequenceNormalization*:

fitOne, getDesignMatrix, getNormalEquations, getSignalTransform, predictOne

#### Methods inherited from *AbstractProbeSequenceNormalization*:

fitOne, getAromaCellSequenceFile, getTargetFile, indexOfMissingSequences, predictOne, process

#### Methods inherited from *ProbeLevelTransform3*:

clearCache, getCellsTo, getCellsToFit, getCellsToUpdate, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

#### Methods inherited from *Transform*:

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

#### Methods inherited from *AromaTransform*:

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

#### Methods inherited from *Object*:

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ChipEffectFile      *The ChipEffectFile class*

---

## Description

Package: aroma.affymetrix

### Class **ChipEffectFile**

#### Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ChipEffectFile

```

#### Directly known subclasses:

*CnChipEffectFile*, *ExonChipEffectFile*, *SnpChipEffectFile*

```

public abstract static class ChipEffectFile
extends ParameterCelFile

```

This class represents estimates of chip effects in the probe-level models.

## Usage

```
ChipEffectFile(..., probeModel=c("pm"))
```

## Arguments

```

... Arguments passed to ParameterCelFile.
probeModel The specific type of model, e.g. "pm".

```

**Fields and Methods**

**Methods:**

|                                       |                                                                                |
|---------------------------------------|--------------------------------------------------------------------------------|
| extractChromosomalDataFrame           | -                                                                              |
| extractMatrix                         | -                                                                              |
| extractTheta                          | -                                                                              |
| findUnitsTodo                         | -                                                                              |
| getAM                                 | Gets the log-intensities and log-ratios of chip effects for two arrays.        |
| getCellIndices                        | -                                                                              |
| getCellMapForMainCdf                  | -                                                                              |
| getExpandedCellMap                    | -                                                                              |
| getParameters                         | -                                                                              |
| getUnitGroupCellChromosomePositionMap | -                                                                              |
| getXAM                                | Gets the physical position, log-intensities and log-ratios of chip effects for |
| readUnits                             | -                                                                              |

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, getParameters, readUnits

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically obtained through the `getChipEffectSet()` method for the [ProbeLevelModel](#) class. An object of this class is typically part of a [ChipEffectSet](#).

---

ChipEffectSet

*The ChipEffectSet class*

---

**Description**

Package: aroma.affymetrix

**Class ChipEffectSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParameterCelSet
~~~~~|
~~~~~+--ChipEffectSet

```

**Directly known subclasses:**

[CnChipEffectSet](#), [ExonChipEffectSet](#), [SnpChipEffectSet](#)

```

public static class ChipEffectSet
extends ParameterCelSet

```

This class represents estimates of chip effects in the probe-level models.

**Usage**

```

ChipEffectSet(..., probeModel=c("pm"))

```

**Arguments**

... Arguments passed to [AffymetrixCelSet](#).  
 probeModel The specific type of model, e.g. "pm".

**Fields and Methods****Methods:**

|                                      |                                                                                            |
|--------------------------------------|--------------------------------------------------------------------------------------------|
| boxplotStats                         | -                                                                                          |
| <a href="#">calculateBaseline</a>    | Estimates the baseline signal chromosome by chromosome.                                    |
| calculateFieldBoxplotStats           | -                                                                                          |
| calculateNuseBoxplotStats            | -                                                                                          |
| calculateRleBoxplotStats             | -                                                                                          |
| extractChromosomalDataFrame          | -                                                                                          |
| <a href="#">extractExpressionSet</a> | Extracts an in-memory ExpressionSet object.                                                |
| extractMatrix                        | -                                                                                          |
| extractTheta                         | -                                                                                          |
| findByName                           | -                                                                                          |
| findUnitsTodo                        | -                                                                                          |
| fromDataSet                          | -                                                                                          |
| <a href="#">getAM</a>                | Gets the log-intensities and log-ratios of chip effects of the set relative to a reference |
| getAverageFile                       | -                                                                                          |
| <a href="#">getBaseline</a>          | Gets the baseline signals across chromosomes.                                              |
| getCellIndices                       | -                                                                                          |
| getParameters                        | -                                                                                          |
| <a href="#">getXAM</a>               | Gets the physical position, log-intensities and log-ratios of chip effects for two arrays. |
| plotBoxplot                          | -                                                                                          |
| readUnits                            | -                                                                                          |

**Methods inherited from ParameterCelSet:**

extractDataFrame, extractMatrix

**Methods inherited from AffymetrixCelSet:**

[, [, append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTransla-

torSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically obtained through the `getChipEffectSet()` method for the [ProbeLevelModel](#) class.

---

ChipEffectTransform    *The ChipEffectTransform class*

---

**Description**

Package: aroma.affymetrix  
**Class ChipEffectTransform**

```
Object
~~|
~~+--AromaTransform
~~~~~|
```

```

~~~~~+---Transform
~~~~~|
~~~~~+---ChipEffectTransform

```

**Directly known subclasses:**

*AdditiveCovariatesNormalization*, *ChipEffectGroupMerge*, *FragmentEquivalentClassNormalization*, *FragmentLengthNormalization*, *GcContentNormalization*, *GcContentNormalization2*, *SnpChipEffectGroupMerge*

public abstract static class **ChipEffectTransform**

extends *Transform*

This abstract class represents a transform that transforms chip-effect estimates obtained from probe-level modelling.

**Usage**

```
ChipEffectTransform(dataSet=NULL, ...)
```

**Arguments**

`dataSet`            The input data set as an *ChipEffectSet*.  
`...`                Arguments passed to the constructor of *Transform*.

**Details**

Subclasses must implement the `process()` method.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from Transform:**

`getOutputDataSet`, `getOutputDataSetOLD20090509`, `getOutputFiles`

**Methods inherited from AromaTransform:**

`getExpectedOutputFiles`, `getExpectedOutputFullnames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getTags`, `isDone`, `process`, `setTags`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

CnagCfhFile

*The CnagCfhFile class***Description**

Package: aroma.affymetrix

**Class CnagCfhFile**

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--CnagCfhFile

```

**Directly known subclasses:**

```

public abstract static class CnagCfhFile
extends AffymetrixFile

```

A CnagCfhFile object represents a single CNAG CFH file.

**Usage**

```
CnagCfhFile(..., cdf=NULL)
```

**Arguments**

```

... Arguments passed to AromaMicroarrayDataFile.
cdf An optional AffymetrixCdfFile

```

**Fields and Methods****Methods:**

```

[-
[[-

```

|            |                                                |
|------------|------------------------------------------------|
| clone      | -                                              |
| fromFile   | Defines an CnagCfhFile object from a CFH file. |
| getCdf     | Gets the CDF structure for this CEL file.      |
| nbrOfCells | -                                              |
| nbrOfSnps  | -                                              |
| setCdf     | Sets the CDF structure for this CEL file.      |

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically part of an [CnagCfhSet](#).

CnagCfhSet

*The CnagCfhSet class***Description**

Package: aroma.affymetrix

**Class CnagCfhSet**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFileSet

~~~~~|

~~~~~+--CnagCfhSet

**Directly known subclasses:**public static class **CnagCfhSet**extends [GenericDataFileSet](#)

An CnagCfhSet object represents a set of CNAG CFH files with *identical* chip types.

**Usage**

CnagCfhSet(files=NULL, ...)

**Arguments**files            A *list* of [CnagCfhFile](#)s.

...              Not used.

**Fields and Methods****Methods:**

|                               |                                           |
|-------------------------------|-------------------------------------------|
| [                             | -                                         |
| [[                            | -                                         |
| append                        | -                                         |
| as                            | -                                         |
| <a href="#">as.CnagCfhSet</a> | Coerce an object to an CnagCfhSet object. |
| byName                        | -                                         |
| byPath                        | -                                         |
| findByName                    | -                                         |

|                                 |                                                                                                       |
|---------------------------------|-------------------------------------------------------------------------------------------------------|
| <code>getAverage</code>         | -                                                                                                     |
| <code>getAverageAsinh</code>    | -                                                                                                     |
| <code>getAverageFile</code>     | Calculates the mean and the standard deviation of the cell signal (intensity, standard deviation etc. |
| <code>getAverageLog</code>      | -                                                                                                     |
| <code>getCdf</code>             | Gets the CDF structure for this CFH set.                                                              |
| <code>getData</code>            | -                                                                                                     |
| <code>getDefaultFullName</code> | -                                                                                                     |
| <code>getTimestamps</code>      | -                                                                                                     |
| <code>isDuplicated</code>       | Identifies duplicated CFH files.                                                                      |
| <code>nbrOfArrays</code>        | Gets the number of arrays in the file set.                                                            |
| <code>range</code>              | -                                                                                                     |
| <code>readUnits</code>          | -                                                                                                     |
| <code>setCdf</code>             | Sets the CDF structure for this CFH set.                                                              |

**Methods inherited from GenericDataFileSet:**

`getFullNameTranslatorSet`, `getParentName`, `append`, `appendFiles`, `appendFullNamesTranslator`, `appendFullNamesTranslatorBydata.frame`, `appendFullNamesTranslatorByfunction`, `appendFullNamesTranslatorBylist`, `appendFullNamesTranslatorByNULL`, `appendFullNamesTranslatorByTabularTextFile`, `appendFullNamesTranslatorByTabularTextFileSet`, `as.list`, `byName`, `byPath`, `clearCache`, `clearFullNamesTranslator`, `copyTo`, `equals`, `extract`, `findByName`, `getAlias`, `getChecksum`, `getChecksumObjects`, `getDefaultFullName`, `getFile`, `getFileClass`, `getFileSize`, `getFullNames`, `getNames`, `getPath`, `getPathnames`, `getSubdirs`, `hasFile`, `indexOf`, `lapply`, `nbrOfFiles`, `sapply`, `seq`, `setAlias`, `setFullNamesTranslator`, `sortBy`, `update2`, `updateFullName`, `updateFullNames`, `validate`

**Methods inherited from FullNameInterface:**

`appendFullNameTranslator`, `appendFullNameTranslatorBycharacter`, `appendFullNameTranslatorBydata.frame`, `appendFullNameTranslatorByfunction`, `appendFullNameTranslatorBylist`, `appendFullNameTranslatorByNULL`, `appendFullNameTranslatorByTabularTextFile`, `appendFullNameTranslatorByTabularTextFileSet`, `clearFullNameTranslator`, `clearListOfFullNameTranslators`, `getDefaultFullName`, `getFullName`, `getFullNameTranslator`, `getListOfFullNameTranslators`, `getName`, `getTags`, `hasTag`, `hasTags`, `setFullName`, `setFullNameTranslator`, `setListOfFullNameTranslators`, `setName`, `setTags`, `updateFullName`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[CnagCfhFile](#).

---

CnChipEffectFile      *The CnChipEffectFile class*

---

## Description

Package: aroma.affymetrix

### Class CnChipEffectFile

#### Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ChipEffectFile
~~~~~|
~~~~~+--SnpChipEffectFile
~~~~~|
~~~~~+--CopyNumberDataFile
~~~~~|
~~~~~+--CnChipEffectFile

```

#### Directly known subclasses:

```

public abstract static class CnChipEffectFile
extends CopyNumberDataFile

```

This class represents estimates of chip effects in a copy-number probe-level models.

## Usage

```
CnChipEffectFile(..., combineAlleles=FALSE)
```

**Arguments**

... Arguments passed to [SnpChipEffectFile](#).  
 combineAlleles A **logical** indicating if the signals from allele A and allele B are combined or not.

**Fields and Methods****Methods:**

```
exportAromaSignalBinaryFileList -
exportTotalAndFracB -
extractTheta -
extractTotalAndFreqB -
getCellIndices -
getExpandedCellMap -
getParameters -
hasAlleleBFractions -
hasStrandiness -
mergeStrands -
readUnits -
```

**Methods inherited from CopyNumberDataFile:**

as, as.CopyNumberDataFile, getNumberOfFilesAveraged, hasAlleleBFractions, hasStrandiness

**Methods inherited from SnpChipEffectFile:**

exportTotalAndFracB, extractCNT, extractTheta, extractTotalAndFracB, getCellIndices, getExpandedCellMap, getParameters, mergeStrands, readUnits, writeCNT

**Methods inherited from ChipEffectFile:**

extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters, getUnitGroupCellArrayMap, getUnitGroupCellChromosomePositionMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCelFile

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, getParameters, readUnits

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically part of a [CnChipEffectSet](#).

---

CnChipEffectSet

*The CnChipEffectSet class*

---

**Description**

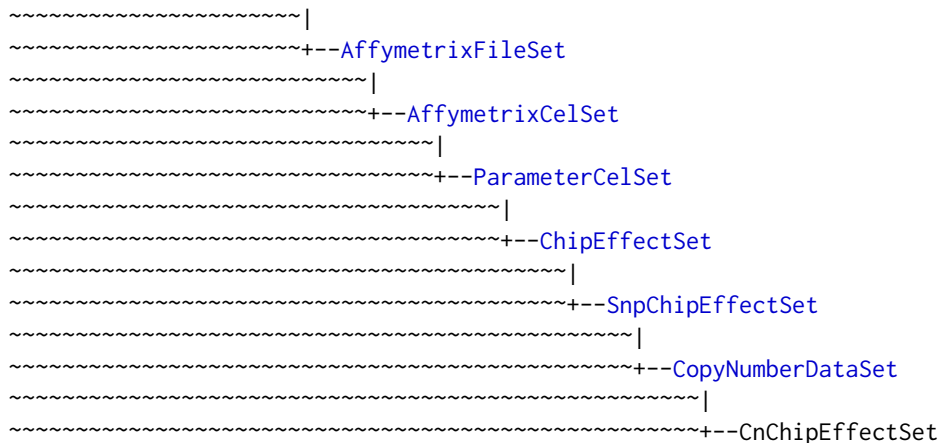
Package: aroma.affymetrix

**Class CnChipEffectSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface

```



**Directly known subclasses:**

```

public static class CnChipEffectSet
extends CopyNumberDataSet

```

This class represents estimates of chip effects in the probe-level models.

**Usage**

```

CnChipEffectSet(..., combineAlleles="byFirstFile")

```

**Arguments**

- ... Arguments passed to [SnpChipEffectSet](#).
- combineAlleles A [logical](#) indicating if the signals from allele A and allele B are combined or not.

**Fields and Methods**

**Methods:**

- as.CopyNumberDataSetTuple -
- exportTotalAndFracB -
- extractTheta -
- extractTotalAndFreqB -
- getAverageFile -
- getBaseline -
- getCombineAlleles -
- hasAlleleBFractions -
- hasStrandiness -
- setCombineAlleles -

writeWig

**Methods inherited from CopyNumberDataSet:**

as, as.CopyNumberDataSet, doCBS, hasAlleleBFractions, hasStrandiness

**Methods inherited from SnpChipEffectSet:**

byPath, exportTotalAndFracB, extractAlleleSet, extractCNT, extractSnpCnvQSet, extractSnpQSet, extractTheta, extractTotalAndFreqB, getAverageFile, getBaseline, getMergeStrands, setMergeStrands, writeCNT

**Methods inherited from ChipEffectSet:**

boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getParameters, getXAM, plotBoxplot, readUnits, updateUnits

**Methods inherited from ParameterCelSet:**

extractDataFrame, extractMatrix

**Methods inherited from AffymetrixCelSet:**

[, [[, append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFull-

NameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

CnPlm

*The CnPlm class*

---

**Description**

Package: aroma.affymetrix

**Class CnPlm**

**Interface**

```

~|
~+--SnpPlm
~~~~~|
~~~~~+--CnPlm

```

**Directly known subclasses:**

[AffineCnPlm](#), [AvgCnPlm](#), [HetLogAddCnPlm](#), [MbeiCnPlm](#), [RmaCnPlm](#)

```

public class CnPlm
 extends SnpPlm

```

This support class represents a [SnpPlm](#) specially designed for copy-number analysis.

**Usage**

```
CnPlm(...)
```

**Arguments**

... Arguments passed to [SnpPlm](#).

## Details

Models implementing this copy-number PLM, provides either allele-specific or total copy-number estimates. For allele-specific CNs the underlying [SnpPlm](#) model is fitted as is, i.e. for each allele separately with or without the strands first being merged.

For total CNs the probe signals for the two alleles are combined (=summed; not averaged) on the intensity scale before fitting underlying [SnpPlm](#) model, again with or without the strands first being merged.

## Methods

### Methods:

|                      |   |
|----------------------|---|
| getCellIndices       | - |
| getChipEffectSet     | - |
| getCombineAlleles    | - |
| getProbeAffinityFile | - |
| setCombineAlleles    | - |

### Methods inherited from SnpPlm:

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

### Methods inherited from Interface:

extend, print, uses

## Requirements

Classes inheriting from this [Interface](#) must provide the following fields, in addition to the ones according to [SnpPlm](#):

- combineAllelesA [logical](#) indicating if total or allele-specific copy numbers should be estimated according to the above averaging.

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

CnProbeAffinityFile    *The CnProbeAffinityFile class*

---

## Description

Package: aroma.affymetrix

**Class CnProbeAffinityFile**

```

Object
~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---AffymetrixCelFile
~~~~~|
~~~~~+---ParameterCelFile
~~~~~|
~~~~~+---ProbeAffinityFile
~~~~~|
~~~~~+---SnpProbeAffinityFile
~~~~~|
~~~~~+---CnProbeAffinityFile

```

#### Directly known subclasses:

```

public abstract static class CnProbeAffinityFile
extends SnpProbeAffinityFile

```

This class represents estimates of probe affinities in SNP probe-level models.

#### Usage

```
CnProbeAffinityFile(..., combineAlleles=FALSE)
```

#### Arguments

```

... Arguments passed to SnpProbeAffinityFile.
combineAlleles If FALSE, allele A and allele B are treated separately, otherwise together.

```

#### Fields and Methods

##### Methods:

```

getCellIndices -
setCombineAlleles -

```

**Methods inherited from SnpProbeAffinityFile:**

getCellIndices, setMergeStrands

**Methods inherited from ProbeAffinityFile:**

getCellIndices, getParameters, readUnits

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, getParameters, readUnits

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

CrlmmParametersFile    *The CrlmmParametersFile class*

---

## Description

Package: aroma.affymetrix

### Class CrlmmParametersFile

#### Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaUnitSignalBinaryFile
~~~~~|
~~~~~+--CrlmmParametersFile

```

#### Directly known subclasses:

```

public static class CrlmmParametersFile
extends AromaUnitSignalBinaryFile

```

An CrlmmParametersFile is a [AromaUnitSignalBinaryFile](#).

## Usage

```
CrlmmParametersFile(...)
```

## Arguments

...                    Arguments passed to [AromaUnitSignalBinaryFile](#).

## Fields and Methods

### Methods:

allocate                -

```

findUnitsTodo -
readParameter -
updateParameter -

```

**Methods inherited from AromaUnitSignalBinaryFile:**

allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getAromaUgpFile, getChipType, getExtensionPattern, getFilenameExtension, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaTabularBinaryFile:**

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, getRootName, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

CrlmmParametersSet      *The CrlmmParametersSet class*


---

**Description**

Package: aroma.affymetrix

**Class CrlmmParametersSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--GenericTabularFileSet
~~~~~|
~~~~~+--AromaTabularBinarySet
~~~~~|
~~~~~+--AromaUnitSignalBinarySet
~~~~~|
~~~~~+--CrlmmParametersSet

```

**Directly known subclasses:**

```

public static class CrlmmParametersSet
extends AromaUnitSignalBinarySet

```

An CrlmmParametersSet object represents a set of [CrlmmParametersFiles](#) with *identical* chip types.

**Usage**

```
CrlmmParametersSet(...)
```

**Arguments**

```
... Arguments passed to AromaUnitSignalBinarySet.
```

**Fields and Methods****Methods:**

```

byName -
byPath -
findUnitsTodo -

```

**Methods inherited from AromaUnitSignalBinarySet:**

byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

**Methods inherited from AromaTabularBinarySet:**

getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

**Methods inherited from GenericTabularFileSet:**

calculateAverageColumnAcrossFiles, extractMatrix

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

DChipCdfBinFile

*The DChipCdfBinFile class*

---

**Description**

Package: aroma.affymetrix

**Class DChipCdfBinFile**

[Object](#)

~~|

```

~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---UnitAnnotationDataFile
~~~~~|
~~~~~+---UnitNamesFile
~~~~~|
~~~~~+---DChipCdfBinFile

```

**Directly known subclasses:**

```

public abstract static class DChipCdfBinFile
extends UnitNamesFile

```

A DChipCdfBinFile object represents a DChip CDF.bin file.

**Usage**

```

DChipCdfBinFile(...)

```

**Arguments**

```

... Arguments passed to AffymetrixFile.

```

**Fields and Methods**

**Methods:**

```

byChipType -
findByChipType -
fromFile -
getChipType -
getFileFormat -
getHeader -
getPlatform -
getUnitNames -
getUnitSizes -
nbrOfCells -
nbrOfUnits -
readDataFrame -

```

**Methods inherited from UnitNamesFile:**

getUnitNames, indexOf, nbrOfUnits

**Methods inherited from UnitAnnotationDataFile:**

byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, nbrOfUnits

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**Description**

Package: aroma.affymetrix

**Class DChipDcpFile****Object**

```

~|
~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--DChipDcpFile

```

**Directly known subclasses:**

```

public abstract static class DChipDcpFile
extends AffymetrixFile

```

A DChipDcpFile object represents a DChip DCP file.

**Usage**

```
DChipDcpFile(...)
```

**Arguments**

... Arguments passed to [AffymetrixFile](#).

**Fields and Methods****Methods:**

```

dim -
extractTheta -
fromFile -
getCalls -
getExcludes -
getFileFormat -
getHeader -
getNormalizedIntensities -
getRawIntensities -

```

|                   |   |
|-------------------|---|
| getThetas         | - |
| getThetasAB       | - |
| getThetaStds      | - |
| hasMbeiData       | - |
| hasNormalizedData | - |
| nbrOfCells        | - |
| nbrOfUnits        | - |

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[DChipDcpSet](#).

DChipDcpSet

*The DChipDcpSet class***Description**

Package: aroma.affymetrix

**Class DChipDcpSet**

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--DChipDcpSet

```

**Directly known subclasses:**

```

public abstract static class DChipDcpSet
extends AffymetrixFileSet

```

A DChipDcpSet object represents a set of DChip DCP files for *identical* chip types.

**Usage**

```
DChipDcpSet(files=NULL, ...)
```

**Arguments**

|       |                                  |
|-------|----------------------------------|
| files | A <i>list</i> of DChipDcpFile:s. |
| ...   | Not used.                        |

**Fields and Methods****Methods:**

|                             |                                            |
|-----------------------------|--------------------------------------------|
| as                          | -                                          |
| <code>as.DChipDcpSet</code> | Coerce an object to an DChipDcpSet object. |

|                     |                                            |
|---------------------|--------------------------------------------|
| byName              | -                                          |
| byPath              | -                                          |
| exportTotalAndFracB | -                                          |
| extractTheta        | -                                          |
| findByName          | -                                          |
| getCdfBin           | -                                          |
| getChipType         | -                                          |
| nbrOfArrays         | Gets the number of arrays in the file set. |

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[DChipDcpFile](#).

---

DChipGenomeInformation

*The DChipGenomeInformation class*

---

**Description**

Package: aroma.affymetrix

**Class DChipGenomeInformation****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenomeInformation
~~~~~|
~~~~~+--DChipGenomeInformation

```

**Directly known subclasses:**

public abstract static class **DChipGenomeInformation**  
 extends [GenomeInformation](#)

This class represents dChip genome information files, which typically contains information about chromosomal locations of the units.

**Usage**

```
DChipGenomeInformation(...)
```

**Arguments**

... Arguments passed to [GenomeInformation](#).

**Details**

The dChip genome information files for various chip types can be downloaded from <http://www.dchip.org/>. Put each file in a directory named identically as the corresponding chip type under the *annotations/* directory, e.g. *annotations/Mapping50K\_Hind240/50k hind genome info AfAm june 05 hg17.xls*. Note that dChip changes the filename and file format slightly between chip types, but

currently the `*byChipType()` basically searches for files with names consisting of "genome info" or "genome\_info". At least for the most common chip types, there is no need to rename the files in order for this class to recognize them.

## Fields and Methods

### Methods:

`byChipType` Defines a DChipGenomeInformation object by chip type.  
`readDataFrame` -

### Methods inherited from GenomeInformation:

`byChipType`, `fromCdf`, `fromDataSet`, `getChipType`, `getChromosomes`, `getChromosomeStats`, `getData`, `getPositions`, `getUnitIndices`, `getUnitsOnChromosome`, `getUnitsOnChromosomes`, `isCompatibleWithCdf`, `nbrOfUnits`, `plotDensity`, `readDataFrame`

### Methods inherited from GenericDataFile:

`getParentName`, `compareChecksum`, `copyTo`, `equals`, `fromFile`, `getAlias`, `getAttribute`, `getAttributes`, `getChecksum`, `getCreatedOn`, `getDefaultFullName`, `getExtension`, `getExtensionPattern`, `getFilename`, `getFilenameExtension`, `getFileSize`, `getFileType`, `getLastAccessedOn`, `getLastModifiedOn`, `getOutputExtension`, `getPath`, `getPathname`, `gunzip`, `gzip`, `hasBeenModified`, `isFile`, `readChecksum`, `renameTo`, `renameToUpperCaseExt`, `setAlias`, `setAttribute`, `setAttributes`, `setAttributesBy`, `setAttributesByTags`, `setExtensionPattern`, `testAttributes`, `validateChecksum`, `writeChecksum`

### Methods inherited from FullNameInterface:

`appendFullNameTranslator`, `appendFullNameTranslatorBycharacter`, `appendFullNameTranslatorBydata.frame`, `appendFullNameTranslatorByfunction`, `appendFullNameTranslatorBylist`, `appendFullNameTranslatorByNULL`, `appendFullNameTranslatorByTabularTextFile`, `appendFullNameTranslatorByTabularTextFileSet`, `clearFullNameTranslator`, `clearListOfFullNameTranslators`, `getDefaultFullName`, `getFullName`, `getFullNameTranslator`, `getListOfFullNameTranslators`, `getName`, `getTags`, `hasTag`, `hasTags`, `setFullName`, `setFullNameTranslator`, `setListOfFullNameTranslators`, `setName`, `setTags`, `updateFullName`

### Methods inherited from Object:

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

**Description**

Package: aroma.affymetrix

**Class DChipQuantileNormalization****Object**

```

~|
~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--QuantileNormalization
~~~~~|
~~~~~+--DChipQuantileNormalization

```

**Directly known subclasses:**

```

public static class DChipQuantileNormalization
extends QuantileNormalization

```

This class represents a special [QuantileNormalization](#) using smooth-splines.

**Usage**

```
DChipQuantileNormalization(..., robust=FALSE)
```

**Arguments**

|        |                                                                                         |
|--------|-----------------------------------------------------------------------------------------|
| ...    | Arguments passed to the constructor of <a href="#">QuantileNormalization</a> .          |
| robust | If <code>TRUE</code> , the normalization function is estimated robustly, otherwise not. |

**Details**

This normalization method implements the two-pass algorithm described in Bengtsson et al. (2008).

**Fields and Methods****Methods:**

[process](#) Normalizes the data set.

**Methods inherited from [QuantileNormalization](#):**

clearCache, findTargetDistributionFile, process

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullNames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

[1] H. Bengtsson, R. Irizarry, B. Carvalho, & T.P. Speed. Estimation and assessment of raw copy numbers at the single locus level, *Bioinformatics*, 2008.

---

DChipSnpInformation    *The DChipSnpInformation class*

---

**Description**

Package: aroma.affymetrix

**Class DChipSnpInformation****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--SnpInformation
~~~~~|
~~~~~+--DChipSnpInformation

```

**Directly known subclasses:**

```

public abstract static class DChipSnpInformation
extends SnpInformation

```

This class represents dChip genome information files, which typically contains information on nucleotide sequences and fragment lengths of the units.

**Usage**

```
DChipSnpInformation(...)
```

**Arguments**

```
... Arguments passed to SnpInformation.
```

**Details**

The dChip SNP information files for various chip types can be downloaded from <http://www.dchip.org/>. Put each file in a directory named identically as the corresponding chip type under the *annotations/* directory, e.g. *annotations/Mapping50K\_Hind240/50k hind snp info AfAm june 05 hg17.xls*. Note that dChip changes the filename and file format slightly between chip types, but currently the `*byChipType()` basically searches for files with names consisting of "snp info" or "snp\_info". At least for the most common chip types, there is no need to rename the files in order for this class to recognize them.

**Fields and Methods****Methods:**

```
byChipType Defines a DChipSnpInformation object by chip type.
readDataFrame -
```

**Methods inherited from SnpInformation:**

```
byChipType, fromCdf, fromDataSet, getChipType, getData, getFields, getFragmentLengths, getFragmentStarts, getFragmentStops, isCompatibleWithCdf, nbrOfEnzymes, nbrOfUnits, readDataFrame
```

**Methods inherited from GenericDataFile:**

```
getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum
```

**Methods inherited from FullNameInterface:**

```
appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName
```

**Methods inherited from Object:**

```
asThis, getChecksum, $, $<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldMod-
```

ifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ExonChipEffectFile      *The ExonChipEffectFile class*

---

### Description

Package: aroma.affymetrix

#### Class ExonChipEffectFile

##### Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ChipEffectFile
~~~~~|
~~~~~+--ExonChipEffectFile

```

#### Directly known subclasses:

```

public abstract static class ExonChipEffectFile
extends ChipEffectFile

```

This class represents estimates of chip effects in the probe-level models.

### Usage

```

ExonChipEffectFile(..., mergeGroups=FALSE)

```

**Arguments**

... Arguments passed to [ChipEffectFile](#).  
 mergeGroups Specifies if the groups are merged or not for these estimates.

**Fields and Methods****Methods:**

```
getCellIndices -
getParameters -
readUnits -
```

**Methods inherited from ChipEffectFile:**

extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCellFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters, getUnitGroupCellArrayMap, getUnitGroupCellChromosomePositionMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCellFile

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, getParameters, readUnits

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically part of a [ExonChipEffectSet](#).

---

ExonChipEffectSet      *The ExonChipEffectSet class*

---

**Description**

Package: aroma.affymetrix

**Class ExonChipEffectSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParameterCelSet
~~~~~|
~~~~~+--ChipEffectSet
~~~~~|
~~~~~+--ExonChipEffectSet

```

**Directly known subclasses:**

```
public static class ExonChipEffectSet
 extends ChipEffectSet
```

This class represents estimates of chip effects in the probe-level models.

### Usage

```
ExonChipEffectSet(..., mergeGroups=TRUE)
```

### Arguments

|             |                                                                                                                                                          |
|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...         | Arguments passed to <a href="#">ChipEffectSet</a> .                                                                                                      |
| mergeGroups | Specifies if groups (individual exons in a CDF file) are merged or not for these estimates, i.e. whether transcript-level expression is to be estimated. |

### Fields and Methods

#### Methods:

|                            |   |
|----------------------------|---|
| findUnitsTodo              | - |
| getAverageFile             | - |
| getFirstCellPerUnitIndices | - |
| getMergeGroups             | - |
| setMergeGroups             | - |

#### Methods inherited from [ChipEffectSet](#):

boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getParameters, getXAM, plotBoxplot, readUnits, updateUnits

#### Methods inherited from [ParameterCelSet](#):

extractDataFrame, extractMatrix

#### Methods inherited from [AffymetrixCelSet](#):

[, [[, append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

#### Methods inherited from [AffymetrixFileSet](#):

as, as.AffymetrixFileSet, byPath, getDefaultFullName

#### Methods inherited from [AromaPlatformInterface](#):

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ExonProbeAffinityFile *The ExonProbeAffinityFile class*

---

**Description**

Package: aroma.affymetrix

**Class ExonProbeAffinityFile**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFile

~~~~~|

~~~~~+--AromaMicroarrayDataFile

```

~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---AffymetrixCelFile
~~~~~|
~~~~~+---ParameterCelFile
~~~~~|
~~~~~+---ProbeAffinityFile
~~~~~|
~~~~~+---ExonProbeAffinityFile

```

### Directly known subclasses:

```

public abstract static class ExonProbeAffinityFile
extends ProbeAffinityFile

```

This class represents estimates of probe affinities in exon array probe-level models.

### Usage

```
ExonProbeAffinityFile(..., mergeGroups=FALSE)
```

### Arguments

```

... Arguments passed to ProbeAffinityFile.
mergeGroups Specifies if the groups (exons) are merged or not for these estimates.

```

### Fields and Methods

#### Methods:

```

getCellIndices -
setMergeGroups -

```

#### Methods inherited from *ProbeAffinityFile*:

```
getCellIndices, getParameters, readUnits
```

#### Methods inherited from *ParameterCelFile*:

```
extractDataFrame, extractMatrix, getParameters, readUnits
```

#### Methods inherited from *AffymetrixCelFile*:

```
[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtension-
Pattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOf-
Cells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage
```

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ExonRmaPlm

*The ExonRmaPlm class*

---

**Description**

Package: aroma.affymetrix

**Class ExonRmaPlm**

Object

~~|

~~+--Model

~~~~~|

~~~~~+--UnitModel

~~~~~|

```

~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--ExonRmaPlm

```

### Directly known subclasses:

```

public static class ExonRmaPlm
extends RmaPlm

```

This class represents the log-additive model part of the Robust Multichip Analysis (RMA) method described in Irizarry et al (2003), as implemented for exon arrays. The model may be fitted with exons merged into transcripts (all probes fitted together) or on an individual exon basis (probes within an exon treated as a group, but exons fitted separately).

### Usage

```
ExonRmaPlm(..., mergeGroups=TRUE)
```

### Arguments

```

...           Arguments passed to RmaPlm.
mergeGroups   A logical flag specifying whether to merge exons into transcripts.

```

### Fields and Methods

#### Methods:

```

calculateWeights -
getCellIndices  -
getChipEffects  -
getChipEffectSet -
getProbeAffinities -
getProbeAffinityFile -
setMergeGroups -

```

#### Methods inherited from [RmaPlm](#):

```
getAsteriskTags, getCalculateResidualsFunction, getRlmFitFunctions
```

#### Methods inherited from [ProbeLevelModel](#):

```
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChip-EffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet
```

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Model**

[RmaPlm](#).

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

**References**

Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

---

FirmaFile

*The FirmaFile class*

---

**Description**

Package: aroma.affymetrix

**Class FirmaFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|

```

```

~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--FirmaFile

```

### Directly known subclasses:

```

public abstract static class FirmaFile
extends ParameterCelFile

```

This class represents scores calculated by the FIRMA algorithm.

### Usage

```
FirmaFile(...)
```

### Arguments

... Arguments passed to *AffymetrixCelFile*.

### Fields and Methods

#### Methods:

```

extractMatrix -
findUnitsTodo -
getCellIndices -
readUnits -

```

#### Methods inherited from *ParameterCelFile*:

extractDataFrame, extractMatrix, getParameters, readUnits

#### Methods inherited from *AffymetrixCelFile*:

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

#### Methods inherited from *AromaPlatformInterface*:

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

#### Methods inherited from *AromaMicroarrayDataFile*:

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

#### Methods inherited from *GenericDataFile*:

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes,

getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

**See Also**

An object of this class is typically part of a [FirmaSet](#).

---

FirmaModel

*The FirmaModel class*

---

**Description**

Package: aroma.affymetrix

**Class FirmaModel**

```
Object
~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--FirmaModel
```

**Directly known subclasses:**

```
public static class FirmaModel
  extends UnitModel
```

This class represents the FIRMA (Finding Isoforms using RMA) alternative splicing model.

### Usage

```
FirmaModel(rmaPlm=NULL, summaryMethod=c("median", "upperQuartile", "max"), operateOn=c("residuals", "
```

### Arguments

|               |                                                                                  |
|---------------|----------------------------------------------------------------------------------|
| rmaPlm        | An @RmaPlm object.                                                               |
| summaryMethod | A <a href="#">character</a> specifying what summarization method should be used. |
| operateOn     | A <a href="#">character</a> specifying what statistic to operate on.             |
| ...           | Arguments passed to constructor of <a href="#">UnitModel</a> .                   |

### Fields and Methods

#### Methods:

|                                         |                                                                |
|-----------------------------------------|----------------------------------------------------------------|
| <a href="#">calculateResidualSet</a>    | Gets the set of residuals corresponding to the PLM.            |
| <a href="#">calculateWeights</a>        | -                                                              |
| <a href="#">fit</a>                     | Estimates the model parameters.                                |
| <a href="#">getAsteriskTags</a>         | -                                                              |
| <a href="#">getCdf</a>                  | -                                                              |
| <a href="#">getDataSet</a>              | -                                                              |
| <a href="#">getFirmaScores</a>          | -                                                              |
| <a href="#">getFirmaSet</a>             | Gets the set of FIRMA results for this model.                  |
| <a href="#">getFitUnitGroupFunction</a> | Static method to get the low-level function that fits the PLM. |
| <a href="#">getName</a>                 | -                                                              |
| <a href="#">getPlm</a>                  | -                                                              |
| <a href="#">getTags</a>                 | -                                                              |

#### Methods inherited from UnitModel:

[findUnitsTodo](#), [getAsteriskTags](#), [getFitSingleCellUnitFunction](#)

#### Methods inherited from Model:

[fit](#), [getAlias](#), [getAsteriskTags](#), [getDataSet](#), [getFullName](#), [getName](#), [getPath](#), [getRootPath](#), [getTags](#), [setAlias](#), [setTags](#)

#### Methods inherited from Object:

[asThis](#), [getChecksum](#), [\\$](#), [\\$<-](#), [\[\[](#), [\[\[<-](#), [as.character](#), [attach](#), [attachLocally](#), [clearCache](#), [clearLookupCache](#), [clone](#), [detach](#), [equals](#), [extend](#), [finalize](#), [gc](#), [getEnvironment](#), [getFieldModifier](#), [getFieldModifiers](#), [getFields](#), [getInstantiationTime](#), [getStaticInstance](#), [hasField](#), [hashCode](#), [ll](#), [load](#), [objectSize](#), [print](#), [registerFinalizer](#), [save](#)

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

---

FirmaSet

*The FirmaSet class*

---

**Description**

Package: aroma.affymetrix

**Class FirmaSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParameterCelSet
~~~~~|
~~~~~+--FirmaSet

```

**Directly known subclasses:**

```

public static class FirmaSet
extends ParameterCelSet

```

**Usage**

```
FirmaSet(...)
```

**Arguments**

... Arguments passed to constructor of [AffymetrixCelSet](#).

**Fields and Methods**

**Methods:**

```

extractMatrix -
findUnitsTodo -
fromDataSet -
getCellIndices -
readUnits -

```

**Methods inherited from ParameterCelSet:**

extractDataFrame, extractMatrix

**Methods inherited from AffymetrixCelSet:**

[, [[, append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldMod-

ifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Ken Simpson (ksimpson[at]wehi.edu.au).

---

FragmentEquivalentClassNormalization

*The FragmentEquivalentClassNormalization class*

---

### Description

Package: aroma.affymetrix

#### Class **FragmentEquivalentClassNormalization**

##### Object

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--FragmentEquivalentClassNormalization

```

#### Directly known subclasses:

```

public static class FragmentEquivalentClassNormalization
extends ChipEffectTransform

```

This class represents a normalization method that corrects for systematic effects between loci of different equivalent classes of pairs of sequences that are recognized by the restriction enzymes that cut the DNA studies.

### Usage

```

FragmentEquivalentClassNormalization(dataSet=NULL, ..., targetAvgs=NULL, subsetToFit="-XY")

```

### Arguments

|            |                                                                                                                                           |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------|
| dataSet    | A <a href="#">CnChipEffectSet</a> .                                                                                                       |
| ...        | Additional arguments passed to the constructor of <a href="#">ChipEffectTransform</a> .                                                   |
| targetAvgs | An optional list of <a href="#">functions</a> . For each enzyme there is one target averages to which all arrays should be normalized to. |

subsetToFit      The units from which the normalization curve should be estimated. If `NULL`, all are considered.

## Fields and Methods

### Methods:

|                                 |                          |
|---------------------------------|--------------------------|
| <code>clearCache</code>         | -                        |
| <code>getAromaUfcFile</code>    | -                        |
| <code>getCdf</code>             | -                        |
| <code>getOutputDataSet00</code> | -                        |
| <code>process</code>            | Normalizes the data set. |

### Methods inherited from Transform:

`getOutputDataSet`, `getOutputDataSetOLD20090509`, `getOutputFiles`

### Methods inherited from AromaTransform:

`getExpectedOutputFiles`, `getExpectedOutputFullNames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getTags`, `isDone`, `process`, `setTags`

### Methods inherited from Object:

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

## Requirements

This class requires an UFC (Unit Fragment Class) annotation file.

## Acknowledgments

The idea of normalization signals stratified on enzyme recognition sequences is credited to Jim Veitch and Ben Bolstad at Affymetrix Inc. (2008) who have designed a similar method for copy number estimation in the Affymetrix' Genotype Console v2.

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

**Description**

Package: aroma.affymetrix

**Class FragmentLengthNormalization****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--FragmentLengthNormalization

```

**Directly known subclasses:**

public static class **FragmentLengthNormalization**  
 extends *ChipEffectTransform*

This class represents a normalization method that corrects for PCR fragment length effects on copy-number chip-effect estimates.

**Usage**

```
FragmentLengthNormalization(dataSet=NULL, ..., target=targetFunctions, subsetToFit="-XY", lengthRange
```

**Arguments**

|                 |                                                                                                                                                                                                   |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataSet         | A <i>SnpcChipEffectSet</i> .                                                                                                                                                                      |
| ...             | Additional arguments passed to the constructor of <i>ChipEffectTransform</i> .                                                                                                                    |
| target          | (Optional) A <i>character</i> string or a list of <i>functions</i> specifying what to normalize toward. For each enzyme there is one target function to which all arrays should be normalized to. |
| subsetToFit     | The units from which the normalization curve should be estimated. If <i>NULL</i> , all are considered.                                                                                            |
| lengthRange     | If given, a <i>numeric vector</i> of length 2 specifying the range of fragment lengths considered. All fragments with lengths outside this range are treated as if they were missing.             |
| onMissing       | Specifies how to normalize units for which the fragment lengths are unknown.                                                                                                                      |
| shift           | An optional amount the data points should be shifted (translated).                                                                                                                                |
| targetFunctions | Deprecated.                                                                                                                                                                                       |

**Details**

For SNPs, the normalization function is estimated based on the total chip effects, i.e. the sum of the allele signals. The normalizing is done by rescale the chip effects on the intensity scale such that the mean of the total chip effects are the same across samples for any given fragment length. For allele-specific estimates, both alleles are always rescaled by the same amount. Thus, when normalizing allele-specific chip effects, the total chip effects is change, but not the relative allele signal, e.g. the allele B frequency.

**Fields and Methods****Methods:**

|                                 |                          |
|---------------------------------|--------------------------|
| <code>clearCache</code>         | -                        |
| <code>getCdf</code>             | -                        |
| <code>getOutputDataSet00</code> | -                        |
| <code>process</code>            | Normalizes the data set. |

**Methods inherited from Transform:**

`getOutputDataSet`, `getOutputDataSetOLD20090509`, `getOutputFiles`

**Methods inherited from AromaTransform:**

`getExpectedOutputFiles`, `getExpectedOutputFullnames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getTags`, `isDone`, `process`, `setTags`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Requirements**

This class requires a SNP information annotation file for the chip type to be normalized.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

GcContentNormalization

*The GcContentNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class GcContentNormalization****Object**

```

~|
~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--GcContentNormalization

```

**Directly known subclasses:**

```

public static class GcContentNormalization
extends ChipEffectTransform

```

**Usage**

```
GcContentNormalization(dataSet=NULL, ..., targetFunction=NULL, subsetToFit=NULL)
```

**Arguments**

|                |                                                                                                        |
|----------------|--------------------------------------------------------------------------------------------------------|
| dataSet        | A <i>CnChipEffectSet</i> .                                                                             |
| ...            | Additional arguments passed to the constructor of <i>ChipEffectTransform</i> .                         |
| targetFunction | A <i>function</i> . The target function to which all arrays should be normalized to.                   |
| subsetToFit    | The units from which the normalization curve should be estimated. If <i>NULL</i> , all are considered. |

**Fields and Methods****Methods:**

|                    |                          |
|--------------------|--------------------------|
| getCdf             | -                        |
| getOutputDataSet00 | -                        |
| <i>process</i>     | Normalizes the data set. |

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Requirements**

This class requires an Aroma unit GC-content (UGC) file.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

GcContentNormalization2

*The GcContentNormalization2 class*

---

**Description**

Package: aroma.affymetrix

**Class GcContentNormalization2**

**Object**

```

~|
~+---AromaTransform
~~~~~|
~~~~~+---Transform
~~~~~|
~~~~~+---ChipEffectTransform
~~~~~|
~~~~~+---AdditiveCovariatesNormalization
~~~~~|
~~~~~+---GcContentNormalization2

```

**Directly known subclasses:**

```

public static class GcContentNormalization2
extends AdditiveCovariatesNormalization

```

This class represents a normalization method that corrects for annotation-data covariate effects on copy-number chip-effect estimates.

**Usage**

```
GcContentNormalization2(...)
```

**Arguments**

... Arguments passed to the constructor of [AdditiveCovariatesNormalization](#).

**Fields and Methods****Methods:**

```
plotCovariateEffects -
```

**Methods inherited from AdditiveCovariatesNormalization:**

```
clearCache, getCdf, getCovariates, getOutputDataSet00, process
```

**Methods inherited from Transform:**

```
getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles
```

**Methods inherited from AromaTransform:**

```
getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName,
getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags
```

**Methods inherited from Object:**

```
asThis, getChecksum, $, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookup-
Cache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldMod-
ifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize,
print, registerFinalizer, save
```

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

GcRmaBackgroundCorrection

*The GcRmaBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class GcRmaBackgroundCorrection**

```
Object
```

```
~~|
```

```
~~+--AromaTransform
```

```
~~~~~|
```

```

~~~~~+---Transform
~~~~~|
~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---BackgroundCorrection
~~~~~|
~~~~~+---GcRmaBackgroundCorrection

```

### Directly known subclasses:

```

public static class GcRmaBackgroundCorrection
extends BackgroundCorrection

```

This class represents the GCRMA background adjustment function.

### Usage

```
GcRmaBackgroundCorrection(..., indicesNegativeControl=NULL, affinities=NULL, type=c("fullmodel", "affinities"))
```

### Arguments

|                        |                                                                                                                                                                                                                            |
|------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...                    | Arguments passed to the constructor of <a href="#">ProbeLevelTransform</a> .                                                                                                                                               |
| indicesNegativeControl | Locations of any negative control probes (e.g., the anti-genomic controls on the human exon array). If <code>NULL</code> and <code>type == "affinities"</code> , then all non-PM probes are used as the negative controls. |
| affinities             | A <a href="#">numeric vector</a> of probe affinities, usually as calculated by <code>computeAffinities()</code> of the <a href="#">AffymetrixCdfFile</a> class.                                                            |
| type                   | Type (flavor) of background correction, which can be either "fullmodel" (uses MMs; requires that the chip type has PM/MM pairs) or "affinities" (uses probe sequence only).                                                |
| gsbAdjust              | If <code>TRUE</code> , adjustment for specific binding is done, otherwise not.                                                                                                                                             |
| opticalAdjust          | If <code>TRUE</code> , correction for optical effect is done first, utilizing <a href="#">OpticalBackgroundCorrection</a> .                                                                                                |
| gsbParameters          | Additional argument passed to the internal <code>bgAdjustGcrma()</code> method.                                                                                                                                            |

### Fields and Methods

#### Methods:

[process](#) Performs background correction.

#### Methods inherited from [BackgroundCorrection](#):

[process](#)

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

---

GenericReporter

*The GenericReporter class*

---

**Description**

Package: aroma.affymetrix

**Class GenericReporter****Object**

~~|

~~+--GenericReporter

**Directly known subclasses:**

*AffymetrixCelSetReporter, AffymetrixFileSetReporter, SpatialReporter*

```
public abstract static class GenericReporter
  extends Object
```

**Usage**

```
GenericReporter(tags="*", ...)
```

**Arguments**

|      |                                                                            |
|------|----------------------------------------------------------------------------|
| tags | A <a href="#">character vector</a> of tags to be added to the output path. |
| ...  | Not used.                                                                  |

**Fields and Methods****Methods:**

|                                 |                                |
|---------------------------------|--------------------------------|
| <a href="#">getAlias</a>        | Gets the alias of the report.  |
| <a href="#">getAsteriskTags</a> | -                              |
| <a href="#">getFullName</a>     | -                              |
| <a href="#">getInputName</a>    | -                              |
| <a href="#">getInputTags</a>    | -                              |
| <a href="#">getName</a>         | Gets the name of the explorer. |
| <a href="#">getPath</a>         | -                              |
| <a href="#">getTags</a>         | Gets the tags of the reporter. |
| <a href="#">process</a>         | Generates report.              |
| <a href="#">setAlias</a>        | Sets the alias of the report.  |
| <a href="#">setup</a>           | -                              |

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

GenomeInformation      *The GenomeInformation class*

---

**Description**

Package: aroma.affymetrix

**Class GenomeInformation****Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---GenomeInformation

```

**Directly known subclasses:**

*AffymetrixCsvGenomeInformation, DChipGenomeInformation, UgpGenomeInformation*

```

public abstract static class GenomeInformation
extends GenericDataFile

```

**Usage**

```
GenomeInformation(..., .verify=TRUE)
```

**Arguments**

```
...           Arguments passed to GenericDataFile.
.verify       For internal use only.
```

**Fields and Methods****Methods:**

|                                       |                                                                |
|---------------------------------------|----------------------------------------------------------------|
| <a href="#">byChipType</a>            | Static method to define a genome information set by chip type. |
| <a href="#">fromCdf</a>               | Static method to define a genome information set from a CDF.   |
| <a href="#">fromDataSet</a>           | -                                                              |
| <a href="#">getChipType</a>           | Gets the chip type of this genome information set.             |
| <a href="#">getChromosomes</a>        | -                                                              |
| <a href="#">getChromosomeStats</a>    | -                                                              |
| <a href="#">getData</a>               | Gets all or a subset of the genome information data.           |
| <a href="#">getPositions</a>          | Gets the physical positions for a set of units.                |
| <a href="#">getUnitsOnChromosome</a>  | -                                                              |
| <a href="#">getUnitsOnChromosomes</a> | -                                                              |
| <a href="#">nbrOfUnits</a>            | -                                                              |
| <a href="#">plotDensity</a>           | Plots the density of SNPs for a given chromosome.              |

**Methods inherited from [GenericDataFile](#):**

[getParentName](#), [compareChecksum](#), [copyTo](#), [equals](#), [fromFile](#), [getAlias](#), [getAttribute](#), [getAttributes](#), [getChecksum](#), [getCreatedOn](#), [getDefaultFullName](#), [getExtension](#), [getExtensionPattern](#), [getFilename](#), [getFilenameExtension](#), [getFileSize](#), [getFileType](#), [getLastAccessedOn](#), [getLastModifiedOn](#), [getOutputExtension](#), [getPath](#), [getPathname](#), [gunzip](#), [gzip](#), [hasBeenModified](#), [isFile](#), [readChecksum](#), [renameTo](#), [renameToUpperCaseExt](#), [setAlias](#), [setAttribute](#), [setAttributes](#), [setAttributesBy](#), [setAttributesByTags](#), [setExtensionPattern](#), [testAttributes](#), [validateChecksum](#), [writeChecksum](#)

**Methods inherited from [FullNameInterface](#):**

[appendFullNameTranslator](#), [appendFullNameTranslatorBycharacter](#), [appendFullNameTranslatorBydata.frame](#), [appendFullNameTranslatorByfunction](#), [appendFullNameTranslatorBylist](#), [appendFullNameTranslatorByNULL](#), [appendFullNameTranslatorByTabularTextFile](#), [appendFullNameTranslatorByTabularTextFileSet](#), [clearFullNameTranslator](#), [clearListOfFullNameTranslators](#), [getDefaultFullName](#), [getFullName](#), [getFullNameTranslator](#), [getListOfFullNameTranslators](#), [getName](#), [getTags](#), [hasTag](#), [hasTags](#), [setFullName](#), [setFullNameTranslator](#), [setListOfFullNameTranslators](#), [setName](#), [setTags](#), [updateFullName](#)

**Methods inherited from [Object](#):**

[asThis](#), [getChecksum](#), [\\$](#), [\\$<-](#), [\[\[](#), [\[\[<-](#), [as.character](#), [attach](#), [attachLocally](#), [clearCache](#), [clearLookupCache](#), [clone](#), [detach](#), [equals](#), [extend](#), [finalize](#), [gc](#), [getEnvironment](#), [getFieldModifier](#), [getFieldModifiers](#), [getFields](#), [getInstantiationTime](#), [getStaticInstance](#), [hasField](#), [hashCode](#), [ll](#), [load](#), [objectSize](#), [print](#), [registerFinalizer](#), [save](#)

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

HetLogAddCnPlm

*The HetLogAddCnPlm class*

---

**Description**

Package: aroma.affymetrix

**Class HetLogAddCnPlm**

**Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--HetLogAddPlm
~~~~~|
~~~~~+--HetLogAddSnpPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--CnPlm
~~~~~|
~~~~~+--HetLogAddCnPlm

```

**Directly known subclasses:**

```

public static class HetLogAddCnPlm
extends CnPlm

```

**Usage**

```

HetLogAddCnPlm(..., combineAlleles=FALSE)

```

**Arguments**

... Arguments passed to [HetLogAddCnPlm](#).  
 combineAlleles If `FALSE`, allele A and allele B are treated separately, otherwise together.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from CnPlm:**

getCellIndices, getChipEffectSet, getCombineAlleles, getProbeAffinityFile, setCombineAlleles

**Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

**Methods inherited from HetLogAddSnpPlm:**

getAsteriskTags

**Methods inherited from HetLogAddPlm:**

getAsteriskTags

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Model**

TO DO.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

HetLogAddPlm

*The HetLogAddPlm class***Description**

Package: aroma.affymetrix

**Class HetLogAddPlm****Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--HetLogAddPlm

```

**Directly known subclasses:**[HetLogAddCnPlm](#), [HetLogAddSnpPlm](#)

```

public static class HetLogAddPlm
extends RmaPlm

```

This class represents a log-additive model similar to the one described in Irizarry et al (2003), except that the errors may have different variances for different probes.

**Usage**

```
HetLogAddPlm(...)
```

**Arguments**

```
... Arguments passed to RmaPlm.
```

**Fields and Methods****Methods:**

```
getAsteriskTags -
```

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[RmaPlm](#).

---

HetLogAddSnpPlm

*The HetLogAddSnpPlm class*

---

**Description**

Package: aroma.affymetrix

**Class HetLogAddSnpPlm**

**Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm

```

```

~~~~~|
~~~~~+--HetLogAddPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--HetLogAddSnpPlm

```

**Directly known subclasses:**[HetLogAddCnPlm](#)

```

public static class HetLogAddSnpPlm
extends SnpPlm

```

**Usage**

```
HetLogAddSnpPlm(..., mergeStrands=FALSE)
```

**Arguments**

```

...           Arguments passed to HetLogAddPlm.
mergeStrands  If TRUE, the sense and the anti-sense strands are fitted together, otherwise separately.

```

**Fields and Methods****Methods:***No methods defined.***Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

**Methods inherited from HetLogAddPlm:**

getAsteriskTags

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

LimmaBackgroundCorrection

*The LimmaBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class LimmaBackgroundCorrection****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--LimmaBackgroundCorrection

```

**Directly known subclasses:**

[NormExpBackgroundCorrection](#)

```

public static class LimmaBackgroundCorrection
  extends BackgroundCorrection

```

This class represents the various "background" correction methods implemented in the **limma** package.

**Usage**

```

LimmaBackgroundCorrection(..., args=NULL, addJitter=FALSE, jitterSd=0.2)

```

**Arguments**

|           |                                                                                                               |
|-----------|---------------------------------------------------------------------------------------------------------------|
| ...       | Arguments passed to the constructor of <a href="#">BackgroundCorrection</a> .                                 |
| args      | A <a href="#">list</a> of additional arguments passed to the correction algorithm.                            |
| addJitter | If <a href="#">TRUE</a> , Zero-mean gaussian noise is added to the signals before being background corrected. |
| jitterSd  | Standard deviation of the jitter noise added.                                                                 |

**Details**

By default, only PM signals are background corrected and MMs are left unchanged.

**Fields and Methods****Methods:**

[process](#) Performs background correction.

**Methods inherited from BackgroundCorrection:**

[process](#)

**Methods inherited from Transform:**

[getOutputDataSet](#), [getOutputDataSetOLD20090509](#), [getOutputFiles](#)

**Methods inherited from AromaTransform:**

[getExpectedOutputFiles](#), [getExpectedOutputFullnames](#), [getFullName](#), [getInputDataSet](#), [getName](#), [getOutputDataSet](#), [getOutputDataSet0](#), [getOutputFiles](#), [getPath](#), [getTags](#), [isDone](#), [process](#), [setTags](#)

**Methods inherited from Object:**

[asThis](#), [getChecksum](#), [\\$](#), [\\$<-](#), [\[\[](#), [\[\[<-](#), [as.character](#), [attach](#), [attachLocally](#), [clearCache](#), [clearLookupCache](#), [clone](#), [detach](#), [equals](#), [extend](#), [finalize](#), [gc](#), [getEnvironment](#), [getFieldModifier](#), [getFieldModifiers](#), [getFields](#), [getInstantiationTime](#), [getStaticInstance](#), [hasField](#), [hashCode](#), [ll](#), [load](#), [objectSize](#), [print](#), [registerFinalizer](#), [save](#)

**Jitter noise**

The fitting algorithm of the normal+exponential background correction model may not converge if there too many small and discrete signals. To overcome this problem, a small amount of noise may be added to the signals before fitting the model. This is an ad hoc solution that seems to work. However, adding Gaussian noise may generate non-positive signals.

**Author(s)**

Henrik Bengtsson. Adopted from RmaBackgroundCorrection by Ken Simpson.

**See Also**

Internally, [backgroundCorrect](#) is used.

---

 LinearModelProbeSequenceNormalization

*The LinearModelProbeSequenceNormalization class*


---

## Description

Package: aroma.affymetrix

### Class LinearModelProbeSequenceNormalization

#### Object

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--LinearModelProbeSequenceNormalization
  
```

#### Directly known subclasses:

[BasePositionNormalization](#)

```

public abstract static class LinearModelProbeSequenceNormalization
  extends AbstractProbeSequenceNormalization
  
```

This abstract class represents a normalization method that corrects for systematic effects in the probe intensities due to probe-sequence dependent effects that can be modelled using a linear model.

## Usage

```
LinearModelProbeSequenceNormalization(...)
```

## Arguments

... Arguments passed to the constructor of [AbstractProbeSequenceNormalization](#).

## Fields and Methods

### Methods:

*No methods defined.*

### Methods inherited from AbstractProbeSequenceNormalization:

fitOne, getAromaCellSequenceFile, getTargetFile, indexOfMissingSequences, predictOne, process

**Methods inherited from ProbeLevelTransform3:**

clearCache, getCellsTo, getCellsToFit, getCellsToUpdate, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Requirements**

This class requires that an aroma probe sequence file is available for the chip type.

**Memory usage**

The model fitting methods of this class are bounded in memory. This is done by first building up the normal equations incrementally in chunks of cells. The generation of normal equations is otherwise the step that consumes the most memory. When the normal equations are available, the `solve()` method is used to solve the equations. Note that this algorithm is still exact.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

MatNormalization

*The MatNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class MatNormalization****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3

```

```

~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--MatNormalization

```

### Directly known subclasses:

```

public static class MatNormalization
extends AbstractProbeSequenceNormalization

```

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in the number of A, C, G, and T:s and the match scores according to MAT [1].

### Usage

```
MatNormalization(..., unitsToFit=NULL, model=c("lm"), nbrOfBins=200)
```

### Arguments

|            |                                                                                                              |
|------------|--------------------------------------------------------------------------------------------------------------|
| ...        | Arguments passed to the constructor of <a href="#">AbstractProbeSequenceNormalization</a> .                  |
| unitsToFit | The units from which the normalization curve should be estimated. If <code>NULL</code> , all are considered. |
| model      | A <a href="#">character</a> string specifying the model used to fit the base-count effects.                  |
| nbrOfBins  | The number of bins to use for the variance smoothing step.                                                   |

### Fields and Methods

#### Methods:

[process](#) Normalizes the data set.

#### Methods inherited from [AbstractProbeSequenceNormalization](#):

[fitOne](#), [getAromaCellSequenceFile](#), [getTargetFile](#), [indexOfMissingSequences](#), [predictOne](#), [process](#)

#### Methods inherited from [ProbeLevelTransform3](#):

[clearCache](#), [getCellsTo](#), [getCellsToFit](#), [getCellsToUpdate](#), [getUnitsTo](#), [getUnitsToFit](#), [getUnitsToUpdate](#), [writeSignals](#)

#### Methods inherited from [Transform](#):

[getOutputDataSet](#), [getOutputDataSetOLD20090509](#), [getOutputFiles](#)

#### Methods inherited from [AromaTransform](#):

[getExpectedOutputFiles](#), [getExpectedOutputFullNames](#), [getFullName](#), [getInputDataSet](#), [getName](#), [getOutputDataSet](#), [getOutputDataSet0](#), [getOutputFiles](#), [getPath](#), [getTags](#), [isDone](#), [process](#), [setTags](#)

#### Methods inherited from [Object](#):

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Requirements

This class requires that an aroma probe sequence file and aroma match scores file is available for the chip type.

### Author(s)

Mark Robinson, WEHI.

### References

[1] Johnson WE, Li W, Meyer CA, Gottardo R, Carroll JS, Brown M, Liu XS. *Model-based analysis of tiling-arrays for ChIP-chip*, PNAS, 2006.

---

MatSmoothing

*The MatSmoothing class*

---

### Description

Package: aroma.affymetrix

#### Class MatSmoothing

#### Object

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--MatSmoothing

```

#### Directly known subclasses:

```

public static class MatSmoothing
extends ProbeLevelTransform

```

This class represents a function for smoothing data with a trimmed mean.

**Usage**

```
MatSmoothing(..., design=NULL, probeWindow=300, nProbes=10, meanTrim=0.1)
```

**Arguments**

|             |                                                                                                                |
|-------------|----------------------------------------------------------------------------------------------------------------|
| ...         | Arguments passed to <a href="#">ProbeLevelTransform</a> .                                                      |
| design      | A design <a href="#">matrix</a> .                                                                              |
| probeWindow | Bandwidth to use. Effectively the width is 2*probeWindow since it looks probeWindow bases in either direction. |
| nProbes     | The minimum number of probes to calculate a MAT score for.                                                     |
| meanTrim    | The amount of trimming of the mean in [0,0.5].                                                                 |

**Fields and Methods****Methods:**

[process](#) Processes the data set.

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Mark Robinson (mrobinson[at]wehi.edu.au).

---

MbeiCnPlm

*The MbeiCnPlm class*

---

**Description**

Package: aroma.affymetrix

**Class MbeiCnPlm**

[Object](#)

~~|

```

~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--MbeiPlm
~~~~~|
~~~~~+--MbeiSnPm
~~~~~|
~~~~~+--SnPm
~~~~~|
~~~~~+--CnPm
~~~~~|
~~~~~+--MbeiCnPm

```

### Directly known subclasses:

```

public static class MbeiCnPm
extends CnPm

```

### Usage

```
MbeiCnPm(..., combineAlleles=FALSE)
```

### Arguments

... Arguments passed to [MbeiSnPm](#).

combineAlleles If [FALSE](#), allele A and allele B are treated seperately, otherwise together.

### Fields and Methods

#### Methods:

*No methods defined.*

#### Methods inherited from CnPm:

getCellIndices, getChipEffectSet, getCombineAlleles, getProbeAffinityFile, setCombineAlleles

#### Methods inherited from SnPm:

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

#### Methods inherited from MbeiSnPm:

getAsteriskTags

#### Methods inherited from MbeiPlm:

getAsteriskTags

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], []<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

MbeiPlm

*The MbeiPlm class*


---

**Description**

Package: aroma.affymetrix

**Class MbeiPlm****Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--MbeiPlm

```

**Directly known subclasses:**

[MbeiCnPlm](#), [MbeiSnpPlm](#)

```

public static class MbeiPlm
extends ProbeLevelModel

```

This class represents the *model-based expression indexes* (MBEI) multiplicative model in Li & Wong (2001).

### Usage

```
MbeiPlm(...)
```

### Arguments

... Arguments passed to [ProbeLevelModel](#).

### Fields and Methods

#### Methods:

```
getAsteriskTags -
```

#### Methods inherited from [ProbeLevelModel](#):

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

#### Methods inherited from [MultiArrayUnitModel](#):

getListOfPriors, setListOfPriors, validate

#### Methods inherited from [UnitModel](#):

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

#### Methods inherited from [Model](#):

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

#### Methods inherited from [Object](#):

asThis, getChecksum, \$, \$<-, [], [ [<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Model

For a single unit group, the multiplicative model is:

$$y_{ik} = \theta_i \phi_k + \varepsilon_{ik}$$

where  $\theta_i$  are the chip effects for arrays  $i = 1, \dots, I$ , and  $\phi_k$  are the probe affinities for probes  $k = 1, \dots, K$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance. To make to parameters identifiable, the constraint  $\prod_k \phi_k = 1$  is added.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

- Li, C. and Wong, W.H. (2001), Genome Biology 2, 1-11.  
 Li, C. and Wong, W.H. (2001), Proc. Natl. Acad. Sci USA 98, 31-36.

**See Also**

Internally [fit.li.wong](#) is used.

---

|            |                             |
|------------|-----------------------------|
| MbeiSnpPlm | <i>The MbeiSnpPlm class</i> |
|------------|-----------------------------|

---

**Description**

Package: aroma.affymetrix

**Class MbeiSnpPlm****Object**

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--MbeiPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--MbeiSnpPlm

```

**Directly known subclasses:**

[MbeiCnPlm](#)

```

public static class MbeiSnpPlm
  extends SnpPlm

```

**Usage**

```

MbeiSnpPlm(..., mergeStrands=FALSE)

```

**Arguments**

- ... Arguments passed to `MbeiPlm`.
- `mergeStrands` If `TRUE`, the sense and the anti-sense strands are fitted together, otherwise separately.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from SnpPlm:**

`getCellIndices`, `getChipEffectSet`, `getMergeStrands`, `getProbeAffinityFile`, `setMergeStrands`

**Methods inherited from MbeiPlm:**

`getAsteriskTags`

**Methods inherited from ProbeLevelModel:**

`calculateResidualSet`, `calculateWeights`, `fit`, `getAsteriskTags`, `getCalculateResidualsFunction`, `getChipEffectSet`, `getProbeAffinityFile`, `getResidualSet`, `getWeightsSet`

**Methods inherited from MultiArrayUnitModel:**

`getListOfPriors`, `setListOfPriors`, `validate`

**Methods inherited from UnitModel:**

`findUnitsToDo`, `getAsteriskTags`, `getFitSingleCellUnitFunction`

**Methods inherited from Model:**

`fit`, `getAlias`, `getAsteriskTags`, `getDataSet`, `getFullName`, `getName`, `getPath`, `getRootPath`, `getTags`, `setAlias`, `setTags`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

Model

*The Model class*

---

**Description**

Package: `aroma.affymetrix`

**Class Model**

`Object`

~~|

```
~~+--Model
```

**Directly known subclasses:**

[AffineCnPlm](#), [AffinePlm](#), [AffineSnpPlm](#), [AlleleSummation](#), [AvgCnPlm](#), [AvgPlm](#), [AvgSnpPlm](#), [CrlmModel](#), [ExonRmaPlm](#), [FirmaModel](#), [HetLogAddCnPlm](#), [HetLogAddPlm](#), [HetLogAddSnpPlm](#), [MbeiCnPlm](#), [MbeiPlm](#), [MbeiSnpPlm](#), [MultiArrayUnitModel](#), [ProbeLevelModel](#), [RmaCnPlm](#), [RmaPlm](#), [RmaSnpPlm](#), [SingleArrayUnitModel](#), [UnitModel](#)

```
public abstract static class Model
extends Object
```

This class is abstract and represents a generic model that applies to a data set.

**Usage**

```
Model(dataSet=NULL, tags="*", ...)
```

**Arguments**

|         |                                                                                              |
|---------|----------------------------------------------------------------------------------------------|
| dataSet | The data set to which this model should be fitted.                                           |
| tags    | A <a href="#">character vector</a> of tags to be appended to the tags of the input data set. |
| ...     | Not used.                                                                                    |

**Fields and Methods**

**Methods:**

|                                 |                                         |
|---------------------------------|-----------------------------------------|
| <a href="#">fit</a>             | Estimates the model parameters.         |
| <a href="#">getAlias</a>        | Gets the name alias for the model.      |
| <a href="#">getAsteriskTags</a> | -                                       |
| <a href="#">getDataSet</a>      | Gets the input data set for this model. |
| <a href="#">getFullName</a>     | Gets the full name of the output set.   |
| <a href="#">getName</a>         | Gets the name of the output data set.   |
| <a href="#">getPath</a>         | Gets the path of this model.            |
| <a href="#">getRootPath</a>     | Gets the root path of this model.       |
| <a href="#">getTags</a>         | Gets the tags of the output data set.   |
| <a href="#">setAlias</a>        | Sets the name alias for the model.      |
| <a href="#">setTags</a>         | Sets the tags to be appended.           |

**Methods inherited from Object:**

[asThis](#), [getChecksum](#), [\\$](#), [\\$<-](#), [\[\[](#), [\[\[<-](#), [as.character](#), [attach](#), [attachLocally](#), [clearCache](#), [clearLookupCache](#), [clone](#), [detach](#), [equals](#), [extend](#), [finalize](#), [gc](#), [getEnvironment](#), [getFieldModifier](#), [getFieldModifiers](#), [getFields](#), [getInstantiationTime](#), [getStaticInstance](#), [hasField](#), [hashCode](#), [ll](#), [load](#), [objectSize](#), [print](#), [registerFinalizer](#), [save](#)

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

MultiArrayUnitModel    *The MultiArrayUnitModel class*

---

**Description**

Package: aroma.affymetrix

**Class MultiArrayUnitModel**

Object

```

~|
~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel

```

**Directly known subclasses:**

[AffineCnPlm](#), [AffinePlm](#), [AffineSnpPlm](#), [AvgCnPlm](#), [AvgPlm](#), [AvgSnpPlm](#), [ExonRmaPlm](#), [HetLogAddCnPlm](#), [HetLogAddPlm](#), [HetLogAddSnpPlm](#), [MbeiCnPlm](#), [MbeiPlm](#), [MbeiSnpPlm](#), [ProbeLevelModel](#), [RmaCnPlm](#), [RmaPlm](#), [RmaSnpPlm](#)

public abstract static class **MultiArrayUnitModel**

extends [UnitModel](#)

This abstract class represents a unit model that fits one model per unit based on signals for all arrays in the data set. The nature of a multi-array unit model is that all arrays must be available at the time of the fit and the estimated parameters will depend on the data from all arrays. Thus, if the signals in one array changes the model has to be refitted.

**Usage**

```
MultiArrayUnitModel(...)
```

**Arguments**

...                    Arguments passed to [UnitModel](#).

**Fields and Methods****Methods:**

```

getListOfPriors    -
setListOfPriors    -

```

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$&lt;-, [], [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**Henrik Bengtsson (<http://www.braju.com/R/>)

---

NormExpBackgroundCorrection*The NormExpBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class NormExpBackgroundCorrection****Object**

```

~|
~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--LimmaBackgroundCorrection
~~~~~|
~~~~~+--NormExpBackgroundCorrection

```

**Directly known subclasses:**

```

public static class NormExpBackgroundCorrection
extends LimmaBackgroundCorrection

```

This class represents the normal exponential background correction model. Estimators of the **limma** package is used.

**Usage**

```
NormExpBackgroundCorrection(..., method=c("rma", "saddle", "mle"))
```

**Arguments**

... Arguments passed to the constructor of [LimmaBackgroundCorrection](#).

method The estimator used, cf. argument normexp.method of [backgroundCorrect](#) in **limma** for more details.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from LimmaBackgroundCorrection:**

process

**Methods inherited from BackgroundCorrection:**

process

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson

**See Also**

Internally, [backgroundCorrect](#) is used.

---

OpticalBackgroundCorrection

*The OpticalBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class OpticalBackgroundCorrection****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--OpticalBackgroundCorrection

```

**Directly known subclasses:**

public static class **OpticalBackgroundCorrection**  
 extends *BackgroundCorrection*

This class represents "optical" background adjustment.

**Usage**

```
OpticalBackgroundCorrection(..., minimum=1)
```

**Arguments**

|         |                                                                     |
|---------|---------------------------------------------------------------------|
| ...     | Arguments passed to the constructor of <i>ProbeLevelTransform</i> . |
| minimum | The minimum signal allowed after adjustment.                        |

**Fields and Methods****Methods:**

[process](#) Performs background correction.

**Methods inherited from BackgroundCorrection:**

[process](#)

**Methods inherited from Transform:**

[getOutputDataSet](#), [getOutputDataSetOLD20090509](#), [getOutputFiles](#)

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

---

ParameterCelFile      *The ParameterCelFile class*

---

**Description**

Package: aroma.affymetrix

**Class ParameterCelFile**

```
Object
~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
```

**Directly known subclasses:**

*ChipEffectFile, CnChipEffectFile, CnProbeAffinityFile, ExonChipEffectFile, ExonProbeAffinityFile, FirmaFile, ProbeAffinityFile, ResidualFile, SnpChipEffectFile, SnpProbeAffinityFile, WeightsFile*

```
public abstract static class ParameterCelFile
extends AffymetrixCelFile
```

A ParameterCelFile object represents parameter estimates.

**Usage**

```
ParameterCelFile(..., encodeFunction=NULL, decodeFunction=NULL)
```

**Arguments**

... Arguments passed to [AffymetrixCelFile](#).

encodeFunction A [function](#) taking a single [list](#) structure as its argument.

decodeFunction A [function](#) taking a single [list](#) structure as its argument.

**Fields and Methods****Methods:**

```
extractDataFrame -
extractMatrix -
readUnits -
```

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookup-

Cache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### File format

The idea behind this class is store data fields which by nature have one value per probe (per field) in CEL files. A perfect example is to store probe-affinity estimates and their standard deviations. There is one probe affinity per probe so the structure of a CEL file (and its coupled CDF file) is well suited to read/write such information.

Consider a unit group with L probes. A CEL file stores intensities (L floats), stdvs (L floats), and pixels (L integers). Thus, for each probe  $l=1,\dots,L$ , a (float, float, integer) tuple is stored. We can use this for any information we want. If we want a slightly different structure, we can choose to encode/decode our structure/information to fit the structure of the CEL file. This abstract class provides transparent methods for encoding and decoding such information through methods `encodeUnitGroup()` and `decodeUnitGroup()`. By subclassing you can implement different types of data structures.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ParameterCelSet

*The ParameterCelSet class*

---

### Description

Package: aroma.affymetrix

#### Class ParameterCelSet

##### Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParameterCelSet

```

**Directly known subclasses:**

[ChipEffectSet](#), [CnChipEffectSet](#), [ExonChipEffectSet](#), [FirmaSet](#), [SnpChipEffectSet](#)

```
public static class ParameterCelSet
  extends AffymetrixCelSet
```

A ParameterCelSet object represents a set of [ParameterCelFile](#):s.

**Usage**

```
ParameterCelSet(...)
```

**Arguments**

... Arguments passed to [AffymetrixCelSet](#).

**Fields and Methods****Methods:**

```
extractDataFrame  Extract data as a data.frame for a set of arrays.
extractMatrix    Extract data as a matrix for a set of arrays.
```

**Methods inherited from AffymetrixCelSet:**

[, [[, append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumOb-

jects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ProbeAffinityFile      *The ProbeAffinityFile class*

---

**Description**

Package: aroma.affymetrix

**Class ProbeAffinityFile**

**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|

```

```
~~~~~+--ProbeAffinityFile
```

**Directly known subclasses:**

*CnProbeAffinityFile*, *ExonProbeAffinityFile*, *SnpProbeAffinityFile*

```
public abstract static class ProbeAffinityFile
extends ParameterCelFile
```

This class represents estimates of probe affinities in probe-level models.

**Usage**

```
ProbeAffinityFile(..., probeModel=c("pm", "mm", "pm-mm", "min1(pm-mm)", "pm+mm"))
```

**Arguments**

```
...           Arguments passed to ParameterCelFile.
probeModel    The specific type of probe model.
```

**Fields and Methods****Methods:**

```
getCellIndices -
getParameters  -
readUnits      -
```

**Methods inherited from *ParameterCelFile*:**

extractDataFrame, extractMatrix, getParameters, readUnits

**Methods inherited from *AffymetrixCelFile*:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from *AromaPlatformInterface*:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from *AromaMicroarrayDataFile*:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from *GenericDataFile*:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, re-

nameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically obtained through the `getProbeAffinityFile()` method for the [ProbeLevelModel](#) class.

---

|                 |                                  |
|-----------------|----------------------------------|
| ProbeLevelModel | <i>The ProbeLevelModel class</i> |
|-----------------|----------------------------------|

---

**Description**

Package: aroma.affymetrix

**Class ProbeLevelModel**

```
Object
~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
```

**Directly known subclasses:**

[AffineCnPlm](#), [AffinePlm](#), [AffineSnpPlm](#), [AvgCnPlm](#), [AvgPlm](#), [AvgSnpPlm](#), [ExonRmaPlm](#), [HetLogAddCnPlm](#), [HetLogAddPlm](#), [HetLogAddSnpPlm](#), [MbeiCnPlm](#), [MbeiPlm](#), [MbeiSnpPlm](#), [RmaCnPlm](#), [RmaPlm](#), [RmaSnpPlm](#)

```
public static class ProbeLevelModel
extends MultiArrayUnitModel
```

This abstract class represents a probe-level model (PLM) as defined by the **affyPLM** package: "A [...] PLM is a model that is fit to probe-intensity data. More specifically, it is where we fit a model with probe level and chip level parameters on a probeset by probeset basis", where the more general case for a probeset is a *unit group* in Affymetrix CDF terms.

**Usage**

```
ProbeLevelModel(..., standardize=TRUE)
```

**Arguments**

|             |                                                                                                                                    |
|-------------|------------------------------------------------------------------------------------------------------------------------------------|
| ...         | Arguments passed to <a href="#">MultiArrayUnitModel</a> .                                                                          |
| standardize | If <code>TRUE</code> , chip-effect and probe-affinity estimates are rescaled such that the product of the probe affinities is one. |

**Details**

In order to minimize the risk for mistakes, but also to be able compare results from different PLMs, all PLM subclasses must meet the following criteria:

1. All parameter estimates must be (stored and returned) on the intensity scale, e.g. log-additive models such as [RmaPlm](#) have to transform the parameters on the log-scale to the intensity scale.
2. The probe-affinity estimates  $\phi_k$  for a unit group must be constrained such that  $\prod_k \phi_k = 1$ , or equivalently if  $\phi_k > 0, \sum_k \log(\phi_k) = 0$ .

Note that the above probe-affinity constraint guarantees that the estimated chip effects across models are on the same scale.

**Fields and Methods****Methods:**

|                                   |                                              |
|-----------------------------------|----------------------------------------------|
| <code>calculateResidualSet</code> | -                                            |
| <code>calculateWeights</code>     | -                                            |
| <code>fit</code>                  | Estimates the model parameters.              |
| <code>getChipEffectSet</code>     | Gets the set of chip effects for this model. |
| <code>getProbeAffinityFile</code> | Gets the probe affinities for this model.    |
| <code>getResidualSet</code>       | -                                            |
| <code>getWeightsSet</code>        | -                                            |

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

For more details on probe-level models, please see the **affyPLM** package.

---

ProbeLevelTransform    *The ProbeLevelTransform class*

---

**Description**

Package: aroma.affymetrix

**Class ProbeLevelTransform****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform

```

**Directly known subclasses:**

*AbstractProbeSequenceNormalization*, *AllelicCrosstalkCalibration*, *BackgroundCorrection*, *BaseCountNormalization*, *BasePositionNormalization*, *DChipQuantileNormalization*, *GcRmaBackgroundCorrection*, *LimmaBackgroundCorrection*, *LinearModelProbeSequenceNormalization*, *MatNormalization*, *MatSmoothing*, *NormExpBackgroundCorrection*, *OpticalBackgroundCorrection*, *ProbeLevelTransform3*, *QuantileNormalization*, *ReseqCrosstalkCalibration*, *RmaBackgroundCorrection*, *ScaleNormalization*, *ScaleNormalization3*, *SpatialRowColumnNormalization*, *UnitTypeScaleNormalization*

```
public abstract static class ProbeLevelTransform  
extends Transform
```

This abstract class represents a transformation methods that transforms probe-level signals, typically intensities.

### Usage

```
ProbeLevelTransform(...)
```

### Arguments

... Arguments passed to the constructor of *Transform*.

### Details

Subclasses must implement the `process()` method.

### Fields and Methods

#### Methods:

*No methods defined.*

#### Methods inherited from *Transform*:

`getOutputDataSet`, `getOutputDataSetOLD20090509`, `getOutputFiles`

#### Methods inherited from *AromaTransform*:

`getExpectedOutputFiles`, `getExpectedOutputFullNames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getTags`, `isDone`, `process`, `setTags`

#### Methods inherited from *Object*:

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

**Description**

Package: aroma.affymetrix

**Class ProbeLevelTransform3****Object**

```

~|
~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3

```

**Directly known subclasses:**

*AbstractProbeSequenceNormalization*, *BaseCountNormalization*, *BasePositionNormalization*, *LinearModelProbeSequenceNormalization*, *MatNormalization*, *ScaleNormalization3*, *UnitTypeScaleNormalization*

```

public abstract static class ProbeLevelTransform3
extends ProbeLevelTransform

```

This abstract class is specialized from *ProbeLevelTransform* and provides methods to identify subsets and types of probes that are used for fitting and/or updating the signals.

**Usage**

```

ProbeLevelTransform3(dataSet=NULL, ..., unitsToFit="-XY", typesToFit=typesToUpdate, unitsToUpdate=NULL)

```

**Arguments**

|               |                                                                                                        |
|---------------|--------------------------------------------------------------------------------------------------------|
| dataSet       | A <i>AffymetrixCelSet</i> .                                                                            |
| ...           | Arguments passed to the constructor of <i>ProbeLevelTransform</i> .                                    |
| unitsToFit    | The units from which the normalization curve should be estimated. If <i>NULL</i> , all are considered. |
| typesToFit    | Types of probes to be used when fitting the model.                                                     |
| unitsToUpdate | The units to be updated. If <i>NULL</i> , all are considered.                                          |
| typesToUpdate | Types of probes to be updated.                                                                         |
| shift         | An optional amount to shift data before fitting and updating.                                          |

**Fields and Methods****Methods:**

clearCache -

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

QualityAssessmentFile *The QualityAssessmentFile class*

---

**Description**

Package: aroma.affymetrix

**Class QualityAssessmentFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--QualityAssessmentFile

```

**Directly known subclasses:**

```

public abstract static class QualityAssessmentFile
extends AffymetrixCelFile

```

This class represents probe-level QC information (residuals, weights, etc.)

**Usage**

```
QualityAssessmentFile(...)
```

**Arguments**

```
... Arguments passed to AffymetrixCelFile.
```

**Fields and Methods****Methods:**

```
findUnitsTodo -
```

**Methods inherited from AffymetrixCelFile:**

```
[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage
```

**Methods inherited from AromaPlatformInterface:**

```
getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith
```

**Methods inherited from AromaMicroarrayDataFile:**

```
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY
```

**Methods inherited from GenericDataFile:**

```
getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum
```

**Methods inherited from FullNameInterface:**

```
appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName
```

**Methods inherited from Object:**

```
asThis, getChecksum, $, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save
```

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

**See Also**

An object of this class is typically part of a [QualityAssessmentSet](#).

---

QualityAssessmentModel

*The QualityAssessmentModel class*

---

**Description**

Package: aroma.affymetrix

**Class QualityAssessmentModel**

[Object](#)

~~|

~~+--QualityAssessmentModel

**Directly known subclasses:**

```
public static class QualityAssessmentModel
  extends Object
```

**Usage**

```
QualityAssessmentModel(plm=NULL, tags="*", ...)
```

**Arguments**

|      |                                             |
|------|---------------------------------------------|
| plm  | A <a href="#">ProbeLevelModel</a> .         |
| tags | A <a href="#">character vector</a> of tags. |
| ...  | Not used.                                   |

**Fields and Methods****Methods:**

|                  |   |
|------------------|---|
| getAsteriskTags  | - |
| getChipEffectSet | - |
| getDataSet       | - |
| getFullName      | - |

```

getName          -
getPath          -
getPlm          -
getResiduals    Calculates the residuals from a probe-level model.
getRootPath      -
getTags         -
getWeights      Calculates the weights from the robust fit to a probe-level model.
nbrOfArrays     -
plotNuse        -
plotRle         -

```

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

---

QualityAssessmentSet    *The QualityAssessmentSet class*

---

**Description**

Package: aroma.affymetrix  
**Class QualityAssessmentSet**

**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--QualityAssessmentSet

```

**Directly known subclasses:**

```
public static class QualityAssessmentSet
extends AffymetrixCelSet
```

**Usage**

```
QualityAssessmentSet(...)
```

**Arguments**

```
... Arguments passed to constructor of AffymetrixCelSet.
```

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from AffymetrixCelSet:**

[, [[, append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFull-

NameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Ken Simpson (ksimpson[at]wehi.edu.au).

---

QuantileNormalization *The QuantileNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class QuantileNormalization**

**Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--QuantileNormalization

```

**Directly known subclasses:**

[DChipQuantileNormalization](#)

```
public static class QuantileNormalization
```

```
extends ProbeLevelTransform
```

This class represents a normalization function that transforms the probe-level signals towards the same empirical distribution.

**Usage**

```
QuantileNormalization(..., subsetToUpdate=NULL, typesToUpdate=NULL, targetDistribution=NULL, subsetTo
```

**Arguments**

|                                 |                                                                                                                                                                                                          |
|---------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...                             | Arguments passed to the constructor of <code>ProbeLevelTransform</code> .                                                                                                                                |
| <code>subsetToUpdate</code>     | The probes to be updated. If <code>NULL</code> , all probes are updated.                                                                                                                                 |
| <code>typesToUpdate</code>      | Types of probes to be updated.                                                                                                                                                                           |
| <code>targetDistribution</code> | A <code>numeric vector</code> . The empirical distribution to which all arrays should be normalized to.                                                                                                  |
| <code>subsetToAvg</code>        | The probes to calculate average empirical distribution over. If a single <code>numeric</code> in (0,1), then this fraction of all probes will be used. If <code>NULL</code> , all probes are considered. |
| <code>typesToAvg</code>         | Types of probes to be used when calculating the average empirical distribution. If "pm" and "mm" only perfect-match and mismatch probes are used, respectively. If "pmmm" both types are used.           |

**Fields and Methods****Methods:**

`clearCache` -  
`process` Normalizes the data set.

**Methods inherited from Transform:**

`getOutputDataSet`, `getOutputDataSetOLD20090509`, `getOutputFiles`

**Methods inherited from AromaTransform:**

`getExpectedOutputFiles`, `getExpectedOutputFullNames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getTags`, `isDone`, `process`, `setTags`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**Examples**

```
## Not run:
  for (zzz in 0) {

# Setup verbose output
verbose <- Arguments$getVerbose(-2)
timestampOn(verbose)
```

```

# -----
# Define an example dataset
# -----
# Find any dataset
path <- NULL
if (is.null(path))
  break

ds <- AffymetrixCelSet$fromFiles(path)
print(ds)

# -----
# Normalization
# -----
norm <- QuantileNormalization(ds, subsetToAvg=1/3)
dsQN <- process(norm, verbose=verbose)
print(dsQN)

} # for (zzz in 0)
rm(zzz)

## End(Not run)

```

---

ReseqCrosstalkCalibration

*The ReseqCrosstalkCalibration class*

---

## Description

Package: aroma.affymetrix

### Class ReseqCrosstalkCalibration

#### Object

```

~~|
~~+---AromaTransform
~~~~~|
~~~~~+---Transform
~~~~~|
~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---ReseqCrosstalkCalibration

```

#### Directly known subclasses:

public static class **ReseqCrosstalkCalibration**  
 extends *ProbeLevelTransform*

This class represents a calibration function that transforms the probe-level signals such that the signals from the four nucleotides (A, C, G, T) are orthogonal.

### Usage

```
ReseqCrosstalkCalibration(dataSet=NULL, ..., targetAvg=2200, subsetToAvg=NULL, mergeGroups=FALSE, fla
```

### Arguments

|             |                                                                                                                                                                                        |
|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataSet     | An <i>AffymetrixCelSet</i> .                                                                                                                                                           |
| ...         | Arguments passed to the constructor of <i>ProbeLevelTransform</i> .                                                                                                                    |
| targetAvg   | The signal(s) that the average of the sum of the probe quartets should have after calibration.                                                                                         |
| subsetToAvg | The indices of the cells (taken as the intersect of existing indices) used to calculate average in order to rescale to the target average. If <i>NULL</i> , all probes are considered. |
| mergeGroups | A <i>logical</i> ...                                                                                                                                                                   |
| flavor      | A <i>character</i> string specifying what algorithm is used to fit the crosstalk calibration.                                                                                          |
| alpha, q, Q | Additional arguments passed to <i>fitMultiDimensionalCone()</i> .                                                                                                                      |

### Fields and Methods

#### Methods:

|                   |                          |
|-------------------|--------------------------|
| <i>clearCache</i> | -                        |
| <i>process</i>    | Calibrates the data set. |

#### Methods inherited from Transform:

*getOutputDataSet*, *getOutputDataSetOLD20090509*, *getOutputFiles*

#### Methods inherited from AromaTransform:

*getExpectedOutputFiles*, *getExpectedOutputFullnames*, *getFullName*, *getInputDataSet*, *getName*, *getOutputDataSet*, *getOutputDataSet0*, *getOutputFiles*, *getPath*, *getTags*, *isDone*, *process*, *setTags*

#### Methods inherited from Object:

*asThis*, *getChecksum*, *\$*, *\$<-*, *[[*, *[[<-*, *as.character*, *attach*, *attachLocally*, *clearCache*, *clearLookupCache*, *clone*, *detach*, *equals*, *extend*, *finalize*, *gc*, *getEnvironment*, *getFieldModifier*, *getFieldModifiers*, *getFields*, *getInstantiationTime*, *getStaticInstance*, *hasField*, *hashCode*, *ll*, *load*, *objectSize*, *print*, *registerFinalizer*, *save*

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

ResidualFile

*The ResidualFile class***Description**

Package: aroma.affymetrix

**Class ResidualFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ResidualFile

```

**Directly known subclasses:**

```

public abstract static class ResidualFile
extends ParameterCelFile

```

This class represents estimates of residuals in the probe-level models.

**Usage**

```

ResidualFile(..., probeModel=c("pm"))

```

**Arguments**

```

...           Arguments passed to ParameterCelFile.
probeModel   The specific type of model, e.g. "pm".

```

**Fields and Methods**

**Methods:**

```

findUnitsTodo -
getCellIndices -
getImage -
getParameters -
readUnits -
writeImage -

```

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, getParameters, readUnits

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically obtained through the `getResidualSet()` method for the [ProbeLevelModel](#) class. An object of this class is typically part of a [ResidualSet](#).

---

|             |                              |
|-------------|------------------------------|
| ResidualSet | <i>The ResidualSet class</i> |
|-------------|------------------------------|

---

**Description**

Package: aroma.affymetrix

**Class ResidualSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ResidualSet

```

**Directly known subclasses:**

```

public static class ResidualSet
extends AffymetrixCelSet

```

This class represents probe-level residuals from probe-level models.

**Usage**

```
ResidualSet(..., probeModel=c("pm"))
```

**Arguments**

```

...           Arguments passed to AffymetrixCelSet.
probeModel   The specific type of model, e.g. "pm".

```

**Fields and Methods****Methods:**

```

findUnitsTodo -
fromDataSet -
getAverageFile -
getCellIndices -
getParameters -
readUnits -

```

**Methods inherited from AffymetrixCelSet:**

[, [], append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically obtained through the `getResidualSet()` method for the [ProbeLevelModel](#) class.

---

RmaBackgroundCorrection

*The RmaBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class RmaBackgroundCorrection****Object**

```

~|
~+---AromaTransform
~~~~~|
~~~~~+---Transform
~~~~~|
~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---BackgroundCorrection
~~~~~|
~~~~~+---RmaBackgroundCorrection

```

**Directly known subclasses:**

```

public static class RmaBackgroundCorrection
  extends BackgroundCorrection

```

This class represents the RMA background adjustment function.

**Usage**

```
RmaBackgroundCorrection(..., addJitter=FALSE, jitterSd=0.2)
```

**Arguments**

|           |                                                                                                            |
|-----------|------------------------------------------------------------------------------------------------------------|
| ...       | Arguments passed to the constructor of <a href="#">BackgroundCorrection</a> .                              |
| addJitter | If <code>TRUE</code> , Zero-mean gaussian noise is added to the signals before being background corrected. |
| jitterSd  | Standard deviation of the jitter noise added.                                                              |

**Details**

Internally `bg.adjust` is used to background correct the probe signals. The default is to background correct PM signals only.

**Fields and Methods****Methods:**

`process` Performs background correction.

**Methods inherited from BackgroundCorrection:**

`process`

**Methods inherited from Transform:**

`getOutputDataSet`, `getOutputDataSetOLD20090509`, `getOutputFiles`

**Methods inherited from AromaTransform:**

`getExpectedOutputFiles`, `getExpectedOutputFullnames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getTags`, `isDone`, `process`, `setTags`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Jitter noise**

The fitting algorithm of the RMA background correction model may not converge if there too many small and discrete signals. To overcome this problem, a small amount of noise may be added to the signals before fitting the model. This is an ad hoc solution that seems to work. However, add Gaussian noise may generate non-positive signals.

**Author(s)**

Ken Simpson ([ksimpson\[at\]wehi.edu.au](mailto:ksimpson[at]wehi.edu.au)).

RmaCnPlm

*The RmaCnPlm class***Description**

Package: aroma.affymetrix

**Class RmaCnPlm****Object**

```

~|
~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--RmaSnpPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--CnPlm
~~~~~|
~~~~~+--RmaCnPlm

```

**Directly known subclasses:**

```

public static class RmaCnPlm
extends CnPlm

```

**Usage**

```
RmaCnPlm(..., combineAlleles=FALSE)
```

**Arguments**

```

...           Arguments passed to RmaSnpPlm.
combineAlleles If FALSE, allele A and allele B are treated seperately, otherwise together.

```

**Fields and Methods****Methods:***No methods defined.***Methods inherited from CnPlm:**

getCellIndices, getChipEffectSet, getCombineAlleles, getProbeAffinityFile, setCombineAlleles

**Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

**Methods inherited from RmaSnpPlm:**

getAsteriskTags

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$&lt;-, [[, [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Model**

TO DO.

**Author(s)**Henrik Bengtsson (<http://www.braju.com/R/>)

**Description**

Package: aroma.affymetrix

**Class RmaPlm****Object**

```

~|
~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm

```

**Directly known subclasses:**

[ExonRmaPlm](#), [HetLogAddCnPlm](#), [HetLogAddPlm](#), [HetLogAddSnpPlm](#), [RmaCnPlm](#), [RmaSnpPlm](#)

public static class **RmaPlm**

extends [ProbeLevelModel](#)

This class represents the log-additive model part of the Robust Multichip Analysis (RMA) method described in Irizarry et al (2003).

**Usage**

```
RmaPlm(..., flavor=c("affyPLM", "affyPLMold", "oligo"))
```

**Arguments**

... Arguments passed to [ProbeLevelModel](#).

flavor A [character](#) string specifying what model fitting algorithm to be used. This makes it possible to get identical estimates as other packages.

**Fields and Methods****Methods:**

getAsteriskTags -

**Methods inherited from [ProbeLevelModel](#):**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from [MultiArrayUnitModel](#):**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

## Model

For a single unit group, the log-additive model of RMA is:

$$\log_2(y_{ik}) = \beta_i + \alpha_k + \varepsilon_{ik}$$

where  $\beta_i$  are the chip effects for arrays  $i = 1, \dots, I$ , and  $\alpha_k$  are the probe affinities for probes  $k = 1, \dots, K$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance. The model is constrained such that  $\sum_k \alpha_k = 0$ .

Note that all PLM classes must return parameters on the intensity scale. For this class that means that  $\theta_i = 2_i^\beta$  and  $\phi_k = 2_k^\alpha$  are returned.

## Different flavors of model fitting

There are a few differ algorithms available for fitting the same probe-level model. The default and recommended method (`flavor="affyPLM"`) uses the implementation in the **preprocessCore** package which fits the model parameters robustly using an M-estimator (the method used to be in **affyPLM**).

Alternatively, other model-fitting algorithms are available. The algorithm (`flavor="oligo"`) used by the **oligo** package, which originates from the **affy** packages, fits the model using median polish, which is a non-robust estimator. Note that this algorithm does not constraint the probe-effect parameters to multiply to one on the intensity scale. Since the internal function does not return these estimates, we can neither rescale them.

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

## References

Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

RmaSnpP1m

*The RmaSnpP1m class***Description**

Package: aroma.affymetrix

**Class RmaSnpP1m****Object**

```

~|
~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaP1m
~~~~~|
~~~~~+--SnpP1m
~~~~~|
~~~~~+--RmaSnpP1m

```

**Directly known subclasses:**[RmaCnP1m](#)public static class **RmaSnpP1m**extends [SnpP1m](#)**Usage**

RmaSnpP1m(..., mergeStrands=FALSE)

**Arguments**

|              |                                                                                                  |
|--------------|--------------------------------------------------------------------------------------------------|
| ...          | Arguments passed to <a href="#">RmaP1m</a> .                                                     |
| mergeStrands | If <b>TRUE</b> , the sense and the anti-sense strands are fitted together, otherwise separately. |

**Fields and Methods****Methods:***No methods defined.*

**Methods inherited from SnpPIm:**

getCellIndices, getChipEffectSet, getMergeStrands, getProbeAffinityFile, setMergeStrands

**Methods inherited from RmaPIm:**

getAsteriskTags, getCalculateResidualsFunction, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ScaleNormalization      *The ScaleNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class ScaleNormalization****Object**

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ScaleNormalization

```

**Directly known subclasses:**

```
public static class ScaleNormalization
  extends ProbeLevelTransform
```

This class represents a normalization function that transforms the probe-level signals towards the same scale.

### Usage

```
ScaleNormalization(dataSet=NULL, ..., targetAvg=4400, subsetToUpdate=NULL, typesToUpdate=NULL, subset
```

### Arguments

|                |                                                                                                                                                                                |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataSet        | <i>AffymetrixCelSet</i> to be normalized.                                                                                                                                      |
| ...            | Arguments passed to the constructor of <i>ProbeLevelTransform</i> .                                                                                                            |
| targetAvg      | A <i>numeric</i> value.                                                                                                                                                        |
| subsetToUpdate | The probes to be updated. If <i>NULL</i> , all probes are updated.                                                                                                             |
| typesToUpdate  | Types of probes to be updated.                                                                                                                                                 |
| subsetToAvg    | The probes to calculate average signal over. If a single <i>numeric</i> in (0,1), then this fraction of all probes will be used. If <i>NULL</i> , all probes are considered.   |
| typesToAvg     | Types of probes to be used when calculating the average signal. If "pm" and "mm" only perfect-match and mismatch probes are used, respectively. If "pmmm" both types are used. |
| shift          | Optional amount of shift if data before fitting/normalizing.                                                                                                                   |

### Fields and Methods

#### Methods:

*process* Normalizes the data set.

#### Methods inherited from Transform:

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

#### Methods inherited from AromaTransform:

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

#### Methods inherited from Object:

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

ScaleNormalization3    *The ScaleNormalization3 class*

---

## Description

Package: aroma.affymetrix

### Class ScaleNormalization3

#### Object

```

~~|
~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--ScaleNormalization3

```

#### Directly known subclasses:

```

public static class ScaleNormalization3
extends ProbeLevelTransform3

```

This class represents a normalization function that transforms the probe-level signals towards the same scale.

## Usage

```
ScaleNormalization3(..., targetAvg=4400)
```

## Arguments

|           |                                                                               |
|-----------|-------------------------------------------------------------------------------|
| ...       | Arguments passed to the constructor of <a href="#">ProbeLevelTransform3</a> . |
| targetAvg | A <a href="#">numeric</a> value.                                              |

## Fields and Methods

### Methods:

[process](#)    Normalizes the data set.

**Methods inherited from ProbeLevelTransform3:**

clearCache, getCellsTo, getCellsToFit, getCellsToUpdate, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from Transform:**

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

**Methods inherited from AromaTransform:**

getExpectedOutputFiles, getExpectedOutputFullNames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

SingleArrayUnitModel    *The SingleArrayUnitModel class*

---

**Description**

Package: aroma.affymetrix

**Class SingleArrayUnitModel**

Object

~~|

~~+---Model

~~~~~|

~~~~~+---UnitModel

~~~~~|

~~~~~+---SingleArrayUnitModel

**Directly known subclasses:**

public abstract static class **SingleArrayUnitModel**

extends *UnitModel*

This abstract class represents a unit model that fits one model per unit based on signals from a single arrays. The nature of a single-array unit model is that each array can be fitted independently of the others.

**Usage**

```
SingleArrayUnitModel(...)
```

**Arguments**

```
... Arguments passed to UnitModel.
```

**Fields and Methods****Methods:**

```
fit Estimates the model parameters.
```

**Methods inherited from UnitModel:**

```
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction
```

**Methods inherited from Model:**

```
fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags
```

**Methods inherited from Object:**

```
asThis, getChecksum, $, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save
```

**Author(s)**

```
Henrik Bengtsson (http://www.braju.com/R/)
```

---

```
SmoothMultiarrayModel The SmoothMultiarrayModel class
```

---

**Description**

```
Package: aroma.affymetrix
```

```
Class SmoothMultiarrayModel
```

```
Object
```

```
~~|
```

```
~~+--ChromosomalModel
```

```
~~~~~|
```

```
~~~~~+--SmoothMultiarrayModel
```

**Directly known subclasses:**

[SmoothRmaModel](#), [SmoothSaModel](#)

public abstract static class **SmoothMultiarrayModel**  
 extends [ChromosomalModel](#)

This abstract class represents a chromosomal smoothing method done chromosome by chromosome.

**Usage**

```
SmoothMultiarrayModel(..., typOfWeights=c("none", "1/s2"), bandwidth=10000, tags="*")
```

**Arguments**

... Arguments passed to the constructor of [ChromosomalModel](#).  
 typOfWeights A [character](#) string.  
 bandwidth A single [numeric](#) specifying the smoothing bandwidth in units of nucleotides.  
 tags A [character vector](#) of tags to be added.

**Fields and Methods****Methods:**

|                         |   |
|-------------------------|---|
| clearCache              | - |
| createOutputTuple       | - |
| fitOneChromosome        | - |
| getBandwidth            | - |
| getFitUnitGroupFunction | - |
| getOutputTuple          | - |
| getRootPath             | - |
| setBandwidth            | - |

**Methods inherited from ChromosomalModel:**

getListOfGenomeInformations, getPcuTheta, getPositionChipTypeUnit, as.character, clearCache, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSets, getSetTuple, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setGenome

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [, [ [<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[CopyNumberSegmentationModel](#).

---

SmoothRmaModel

*The SmoothRmaModel class*

---

**Description**

Package: aroma.affymetrix

**Class SmoothRmaModel****Object**

```

~|
~+--ChromosomalModel
~~~~~|
~~~~~+--SmoothMultiarrayModel
~~~~~|
~~~~~+--SmoothRmaModel

```

**Directly known subclasses:**

```

public static class SmoothRmaModel
extends SmoothMultiarrayModel

```

This class represents the Chromosomal Smoothing Robust Multichip Analysis method.

**Usage**

```
SmoothRmaModel(...)
```

**Arguments**

... Arguments passed to the constructor of [SmoothMultiarrayModel](#).

**Fields and Methods****Methods:**

```

getFitUnitGroupFunction -
getRootPath -

```

**Methods inherited from SmoothMultiarrayModel:**

as.character, clearCache, createOutputTuple, fitOneChromosome, getAsteriskTags, getBandwidth, getFitUnitGroupFunction, getOutputTuple, getRootPath, setBandwidth

**Methods inherited from ChromosomalModel:**

getListOfGenomeInformations, getPcuTheta, getPositionChipTypeUnit, as.character, clearCache, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSets, getSetTuple, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setGenome

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

SnpChipEffectFile      *The SnpChipEffectFile class*

---

**Description**

Package: aroma.affymetrix

**Class SnpChipEffectFile**

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ChipEffectFile
~~~~~|

```

~~~~~+--SnpChipEffectFile

### Directly known subclasses:

[CnChipEffectFile](#)

public abstract static class **SnpChipEffectFile**  
 extends [ChipEffectFile](#)

This class represents estimates of chip effects in the probe-level models.

### Usage

SnpChipEffectFile(..., mergeStrands=FALSE)

### Arguments

... Arguments passed to [ChipEffectFile](#).  
 mergeStrands Specifies if the strands are merged or not for these estimates.

### Fields and Methods

#### Methods:

|                      |   |
|----------------------|---|
| extractCNT           | - |
| extractTheta         | - |
| extractTotalAndFracB | - |
| getCellIndices       | - |
| getExpandedCellMap   | - |
| getParameters        | - |
| readUnits            | - |
| writeCNT             | - |

#### Methods inherited from [ChipEffectFile](#):

extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFull-  
 CelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters, getUnit-  
 GroupCellArrayMap, getUnitGroupCellChromosomePositionMap, getUnitGroupCellMatrixMap,  
 getXAM, mergeGroups, readUnits, writeAsFullCelFile

#### Methods inherited from [ParameterCelFile](#):

extractDataFrame, extractMatrix, getParameters, readUnits

#### Methods inherited from [AffymetrixCelFile](#):

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtension-  
 Pattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOf-  
 Cells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

#### Methods inherited from [AromaPlatformInterface](#):

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile,

getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically part of a [SnpChipEffectSet](#).

SnpChipEffectSet      *The SnpChipEffectSet class*

**Description**

Package: aroma.affymetrix

**Class SnpChipEffectSet**

```
Object
~~|
~~+--FullNameInterface
~~~~~|
```

```

~~~~~+---GenericDataFileSet
~~~~~|
~~~~~+---AromaMicroarrayDataSet
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFileSet
~~~~~|
~~~~~+---AffymetrixCelSet
~~~~~|
~~~~~+---ParameterCelSet
~~~~~|
~~~~~+---ChipEffectSet
~~~~~|
~~~~~+---SnpChipEffectSet

```

**Directly known subclasses:**[CnChipEffectSet](#)

```

public static class SnpChipEffectSet
extends ChipEffectSet

```

This class represents estimates of chip effects in the probe-level models.

**Usage**

```
SnpChipEffectSet(..., mergeStrands="byFirstFile")
```

**Arguments**

|              |                                                                 |
|--------------|-----------------------------------------------------------------|
| ...          | Arguments passed to <a href="#">ChipEffectSet</a> .             |
| mergeStrands | Specifies if the strands are merged or not for these estimates. |

**Fields and Methods****Methods:**

|                      |   |
|----------------------|---|
| extractAlleleSet     | - |
| extractCNT           | - |
| extractSnpCnvQSet    | - |
| extractSnpQSet       | - |
| extractTheta         | - |
| extractTotalAndFreqB | - |
| getAverageFile       | - |
| getBaseline          | - |
| getMergeStrands      | - |
| setMergeStrands      | - |

writeCNT

**Methods inherited from ChipEffectSet:**

boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getParameters, getXAM, plotBoxplot, readUnits, updateUnits

**Methods inherited from ParameterCelSet:**

extractDataFrame, extractMatrix

**Methods inherited from AffymetrixCelSet:**

[, [[, append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpcFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<, [[, [[<, as.character, attach, attachLocally, clearCache, clearLookup-

Cache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

SnpInformation      *The SnpInformation class*

---

### Description

Package: aroma.affymetrix

#### Class SnpInformation

##### Object

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---SnpInformation

```

#### Directly known subclasses:

*DChipSnpInformation, UflSnpInformation*

public abstract static class **SnpInformation**  
 extends *GenericDataFile*

### Usage

```
SnpInformation(...)
```

### Arguments

...                    Arguments passed to *GenericDataFile*.

### Fields and Methods

#### Methods:

|                             |                                                                |
|-----------------------------|----------------------------------------------------------------|
| <a href="#">byChipType</a>  | Static method to define a genome information set by chip type. |
| <a href="#">fromCdf</a>     | Static method to define a genome information set from a CDF.   |
| <a href="#">fromDataSet</a> | -                                                              |

|                                 |                                                      |
|---------------------------------|------------------------------------------------------|
| <code>getChipType</code>        | Gets the chip type of this genome information set.   |
| <code>getData</code>            | Gets all or a subset of the genome information data. |
| <code>getFields</code>          | -                                                    |
| <code>getFragmentLengths</code> | -                                                    |
| <code>getFragmentStarts</code>  | -                                                    |
| <code>getFragmentStops</code>   | -                                                    |
| <code>nbrOfEnzymes</code>       | -                                                    |
| <code>nbrOfUnits</code>         | -                                                    |
| <code>readDataFrame</code>      | -                                                    |

**Methods inherited from GenericDataFile:**

`getParentName`, `compareChecksum`, `copyTo`, `equals`, `fromFile`, `getAlias`, `getAttribute`, `getAttributes`, `getChecksum`, `getCreatedOn`, `getDefaultFullName`, `getExtension`, `getExtensionPattern`, `getFilename`, `getFilenameExtension`, `getFileSize`, `getFileType`, `getLastAccessedOn`, `getLastModifiedOn`, `getOutputExtension`, `getPath`, `getPathname`, `gunzip`, `gzip`, `hasBeenModified`, `isFile`, `readChecksum`, `renameTo`, `renameToUpperCaseExt`, `setAlias`, `setAttribute`, `setAttributes`, `setAttributesBy`, `setAttributesByTags`, `setExtensionPattern`, `testAttributes`, `validateChecksum`, `writeChecksum`

**Methods inherited from FullNameInterface:**

`appendFullNameTranslator`, `appendFullNameTranslatorBycharacter`, `appendFullNameTranslatorBydata.frame`, `appendFullNameTranslatorByfunction`, `appendFullNameTranslatorBylist`, `appendFullNameTranslatorByNULL`, `appendFullNameTranslatorByTabularTextFile`, `appendFullNameTranslatorByTabularTextFileSet`, `clearFullNameTranslator`, `clearListOfFullNameTranslators`, `getDefaultFullName`, `getFullName`, `getFullNameTranslator`, `getListOfFullNameTranslators`, `getName`, `getTags`, `hasTag`, `hasTags`, `setFullName`, `setFullNameTranslator`, `setListOfFullNameTranslators`, `setName`, `setTags`, `updateFullName`

**Methods inherited from Object:**

`asThis`, `getChecksum`, `$`, `$<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

SnpPlm

*The SnpPlm interface class*

---

**Description**

Package: aroma.affymetrix

**Class SnpPlm****Interface**

~~|

```
~+--SnpPlm
```

**Directly known subclasses:**

[AffineCnPlm](#), [AffineSnpPlm](#), [AvgCnPlm](#), [AvgSnpPlm](#), [CnPlm](#), [HetLogAddCnPlm](#), [HetLogAddSnpPlm](#), [MbeiCnPlm](#), [MbeiSnpPlm](#), [RmaCnPlm](#), [RmaSnpPlm](#)

```
public class SnpPlm
 extends Interface
```

An [Interface](#) implementing methods special for [ProbeLevelModels](#) specific to SNP arrays.

**Usage**

```
SnpPlm(...)
```

**Arguments**

```
... Not used.
```

**Methods**

**Methods:**

```
getCellIndices -
getChipEffectSet -
getMergeStrands -
getProbeAffinityFile -
setMergeStrands -
```

**Methods inherited from Interface:**

extend, print, uses

**Requirements**

Classes inheriting from this [Interface](#) must provide the following fields:

- mergeStrandsA [logical](#) value indicating if strands should be merged or not.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**Examples**

```
for (zzz in 0) {
 # Setup verbose output
```

```

verbose <- Arguments$getVerbose(-2)
timestampOn(verbose)

Define an example dataset using this path

Find any SNP dataset
path <- NULL
if (is.null(path))
 break

if (!exists("ds")) {
 ds <- AffymetrixCelSet$fromFiles(path)
}
print(ds)

Create a set of various PLMs for this dataset

if (!exists("models", mode="list")) {
 mergeStrands <- TRUE
 models <- list(
 rma = RmaSnpPlm(ds, mergeStrands=mergeStrands),
 mbei = MbeiSnpPlm(ds, mergeStrands=mergeStrands)
 # affine = AffineSnpPlm(ds, background=FALSE, mergeStrands=mergeStrands)
)
}
print(models)

For each model, fit a few units
#
Note, by fitting the same set of units across models, the internal
caching mechanisms of aroma.affymetrix makes sure that the data is
only read into memory once. See log for reading speed.

units <- 55+1:100

for (model in models) {
 ruler(verbose)
 fit(model, units=units, force=TRUE, verbose=verbose)
}

For each unit, plot the estimated (thetaB,thetaA) for all models

Should we plot the on the log scale?
log <- TRUE

Do only user to press ENTER if more than one unit is plotted
opar <- par(ask=(length(units) > 1))

```

```

Alab <- expression(theta[A])
Blab <- expression(theta[B])
if (log) {
 lim <- c(6, 16)
} else {
 lim <- c(0, 2^15)
}

For each unit...
for (unit in units) {
 # For all models...
 for (kk in seq(along=models)) {
 ces <- getChipEffects(models[[kk]])
 ceUnit <- ces[unit]
 snpName <- names(ceUnit)[1]
 theta <- ceUnit[[1]]
 thetaA <- theta[[1]]$theta
 thetaB <- theta[[2]]$theta
 if (log) {
 thetaA <- log(thetaA, base=2)
 thetaB <- log(thetaB, base=2)
 }

 # Create the plot?
 if (kk == 1) {
 plot(NA, xlim=lim, ylim=lim, xlab=Blab, ylab=Alab, main=snpName)
 abline(a=0, b=1, lty=2)
 }

 # Plot the estimated parameters
 points(thetaB, thetaA, col=kk, pch=19)
 }
} # for (unit ...)

Reset graphical parameter settings
par(opar)

} # for (zzz in 0)
rm(zzz)

```

---

SnpProbeAffinityFile *The SnpProbeAffinityFile class*

---

## Description

Package: aroma.affymetrix  
**Class SnpProbeAffinityFile**

## Object

~~|

```

~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---AffymetrixCelFile
~~~~~|
~~~~~+---ParameterCelFile
~~~~~|
~~~~~+---ProbeAffinityFile
~~~~~|
~~~~~+---SnpProbeAffinityFile

```

**Directly known subclasses:***CnProbeAffinityFile*

```

public abstract static class SnpProbeAffinityFile
extends ProbeAffinityFile

```

This class represents estimates of probe affinities in SNP probe-level models.

**Usage**

```
SnpProbeAffinityFile(..., mergeStrands=FALSE)
```

**Arguments**

```

... Arguments passed to ProbeAffinityFile.
mergeStrands Specifies if the strands are merged or not for these estimates.

```

**Fields and Methods****Methods:**

```

getCellIndices -
setMergeStrands -

```

**Methods inherited from *ProbeAffinityFile*:**

```
getCellIndices, getParameters, readUnits
```

**Methods inherited from *ParameterCelFile*:**

```
extractDataFrame, extractMatrix, getParameters, readUnits
```

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

SpatialReporter

*The SpatialReporter class*

---

**Description**

Package: aroma.affymetrix

**Class SpatialReporter****Object**

~~|

```

~+--GenericReporter
~~~~~|
~~~~~+--AffymetrixFileSetReporter
~~~~~|
~~~~~+--AffymetrixCelSetReporter
~~~~~|
~~~~~+--SpatialReporter

```

### Directly known subclasses:

public abstract static class **SpatialReporter**  
 extends [AffymetrixCelSetReporter](#)

A SpatialReporter generates image files of spatial representations of cell signals for each of the arrays in the input set.

### Usage

```
SpatialReporter(..., reference=NULL)
```

### Arguments

... Arguments passed to [AffymetrixCelSetReporter](#).  
 reference An optional reference [AffymetrixCelFile](#).

### Fields and Methods

#### Methods:

|                         |                                                                    |
|-------------------------|--------------------------------------------------------------------|
| addColorMap             | -                                                                  |
| calculateMargins        | -                                                                  |
| getColorMaps            | -                                                                  |
| plotMargins             | -                                                                  |
| <a href="#">process</a> | Generates image files, scripts and dynamic pages for the explorer. |
| readRawDataRectangle    | -                                                                  |
| setColorMaps            | -                                                                  |

#### Methods inherited from [AffymetrixCelSetReporter](#):

getChipType, getDataSet, getPath, nbrOfArrays

#### Methods inherited from [AffymetrixFileSetReporter](#):

getFileSet, getInputName, getInputTags

#### Methods inherited from [GenericReporter](#):

getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getTags, process, setAlias, setup

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

TransformReport      *The TransformReport class*

---

**Description**

Package: aroma.affymetrix

**Class TransformReport****Object**

~~|

~~+--TransformReport

**Directly known subclasses:**

```
public static class TransformReport
 extends Object
```

**Usage**

```
TransformReport(inSet=NULL, outSet=NULL, ...)
```

**Arguments**

|        |                                                              |
|--------|--------------------------------------------------------------|
| inSet  | The input data set as an <a href="#">AffymetrixCelSet</a> .  |
| outSet | The output data set as an <a href="#">AffymetrixCelSet</a> . |
| ...    | Not used.                                                    |

**Fields and Methods****Methods:**

|          |   |
|----------|---|
| getAlias | - |
| getCdf   | - |

|                                    |                                            |
|------------------------------------|--------------------------------------------|
| <a href="#">getFullName</a>        | Gets the full name of the output data set. |
| <a href="#">getInputDataSet</a>    | Gets the source data set.                  |
| <a href="#">getName</a>            | Gets the name of the output data set.      |
| <a href="#">getOutputDataSet</a>   | Gets the transformed data set.             |
| <a href="#">getPath</a>            | Gets the path of the output data set.      |
| <a href="#">getTags</a>            | Gets the tags of the output data set.      |
| <a href="#">getUnitNamesFile</a>   | -                                          |
| <a href="#">getUnitTypesFile</a>   | -                                          |
| <a href="#">getY</a>               | -                                          |
| <a href="#">nbrOfArrays</a>        | -                                          |
| <a href="#">plotXYCurve</a>        | -                                          |
| <a href="#">plotXYCurveLog2</a>    | -                                          |
| <a href="#">seq</a>                | -                                          |
| <a href="#">setAlias</a>           | -                                          |
| <a href="#">writeImageCombined</a> | -                                          |
| <a href="#">writeImages</a>        | -                                          |

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

UgpGenomeInformation    *The UgpGenomeInformation class*

---

**Description**

Package: aroma.affymetrix

**Class UgpGenomeInformation****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenomeInformation
~~~~~|
~~~~~+--UgpGenomeInformation

```

**Directly known subclasses:**

public abstract static class **UgpGenomeInformation**  
 extends *GenomeInformation*

This class represents Aroma UGP genome information files.

**Usage**

```
UgpGenomeInformation(..., .ugp=NULL, .verify=TRUE)
```

**Arguments**

|         |                                                |
|---------|------------------------------------------------|
| ...     | Arguments passed to <i>GenomeInformation</i> . |
| .ugp    | For internal use only.                         |
| .verify | For internal use only.                         |

**Fields and Methods****Methods:**

|                      |                                                     |
|----------------------|-----------------------------------------------------|
| <i>byChipType</i>    | Defines a UgpGenomeInformation object by chip type. |
| clearCache           | -                                                   |
| getChipType          | -                                                   |
| getChromosomes       | -                                                   |
| getData              | -                                                   |
| getUnitsOnChromosome | -                                                   |
| isCompatibleWithCdf  | -                                                   |
| nbrOfUnits           | -                                                   |
| readDataFrame        | -                                                   |

**Methods inherited from GenomeInformation:**

byChipType, fromCdf, fromDataSet, getChipType, getChromosomes, getChromosomeStats, getData, getPositions, getUnitIndices, getUnitsOnChromosome, getUnitsOnChromosomes, isCompatibleWithCdf, nbrOfUnits, plotDensity, readDataFrame

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBy-

data.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

#### Methods inherited from Object:

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

#### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

UnitModel

*The UnitModel class*

---

#### Description

Package: aroma.affymetrix

#### Class UnitModel

#### Object

```

~~|
~~+--Model
~~~~~|
~~~~~+--UnitModel

```

#### Directly known subclasses:

[AffineCnPlm](#), [AffinePlm](#), [AffineSnpPlm](#), [AlleleSummation](#), [AvgCnPlm](#), [AvgPlm](#), [AvgSnpPlm](#), [ExonRmaPlm](#), [FirmaModel](#), [HetLogAddCnPlm](#), [HetLogAddPlm](#), [HetLogAddSnpPlm](#), [MbeiCnPlm](#), [MbeiPlm](#), [MbeiSnpPlm](#), [MultiArrayUnitModel](#), [ProbeLevelModel](#), [RmaCnPlm](#), [RmaPlm](#), [RmaSnpPlm](#), [SingleArrayUnitModel](#)

```
public abstract static class UnitModel
```

```
extends Model
```

This class is abstract and represents a generic unit model, i.e. a model that is applied to each unit separately.

#### Usage

```
UnitModel(dataSet=NULL, probeModel=c("pm", "mm", "pm-mm", "min1(pm-mm)", "pm+mm"), shift=0, ...)
```

**Arguments**

|            |                                                                                                                             |
|------------|-----------------------------------------------------------------------------------------------------------------------------|
| dataSet    | An <a href="#">AffymetrixCelSet</a> to which this model should be fitted.                                                   |
| probeModel | A <a href="#">character</a> string specifying how PM and MM values should be modelled. By default only PM signals are used. |
| shift      | An optional amount the signals should be shifted (translated) before fitting the model.                                     |
| ...        | Arguments passed to the constructor of <a href="#">Model</a> .                                                              |

**Fields and Methods****Methods:**

|                                              |                              |
|----------------------------------------------|------------------------------|
| <a href="#">findUnitsTodo</a>                | Identifies non-fitted units. |
| <a href="#">getFitSingleCellUnitFunction</a> | -                            |

**Methods inherited from Model:**

fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

UnitTypeScaleNormalization

*The UnitTypeScaleNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class UnitTypeScaleNormalization**

[Object](#)

~~|

~~+--[AromaTransform](#)

~~~~~|

~~~~~+--[Transform](#)

~~~~~|

```

~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---ProbeLevelTransform3
~~~~~|
~~~~~+---UnitTypeScaleNormalization

```

### Directly known subclasses:

```

public static class UnitTypeScaleNormalization
extends ProbeLevelTransform3

```

This class represents a normalization function that transforms the probe signals such that each unit type gets the same average.

### Usage

```
UnitTypeScaleNormalization(..., targetAvg=4400)
```

### Arguments

```

...           Arguments passed to the constructor of ProbeLevelTransform3.
targetAvg    A numeric value.

```

### Fields and Methods

#### Methods:

```

process    Normalizes the data set.

```

#### Methods inherited from *ProbeLevelTransform3*:

```

clearCache, getCellsTo, getCellsToFit, getCellsToUpdate, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

```

#### Methods inherited from *Transform*:

```

getOutputDataSet, getOutputDataSetOLD20090509, getOutputFiles

```

#### Methods inherited from *AromaTransform*:

```

getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getTags, isDone, process, setTags

```

#### Methods inherited from *Object*:

```

asThis, getChecksum, $, $<-, [, [ [<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

```

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

 WeightsFile

*The WeightsFile class*


---

**Description**

Package: aroma.affymetrix

**Class WeightsFile****Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---AffymetrixCelFile
~~~~~|
~~~~~+---ParameterCelFile
~~~~~|
~~~~~+---WeightsFile
  
```

**Directly known subclasses:**

```

public abstract static class WeightsFile
  extends ParameterCelFile
  
```

This class represents weights calculated from residuals of probe-level models.

**Usage**

```
WeightsFile(..., probeModel=c("pm"))
```

**Arguments**

```

...           Arguments passed to ParameterCelFile.
probeModel   The specific type of model, e.g. "pm".
  
```

**Fields and Methods****Methods:**

```

findUnitsTodo -
getCellIndices -
getImage -
getParameters -
readUnits -
writeImage -

```

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, getParameters, readUnits

**Methods inherited from AffymetrixCelFile:**

[, [[, allocateFromCdf, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributesByTags, setAttributeXY

**Methods inherited from GenericDataFile:**

getParentName, compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

An object of this class is typically obtained through the `getWeightsSet()` method for the `ProbeLevelModel` class. An object of this class is typically part of a `WeightsSet`.

---

 WeightsSet

*The WeightsSet class*


---

**Description**

Package: aroma.affymetrix

**Class WeightsSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--WeightsSet
  
```

**Directly known subclasses:**

```

public static class WeightsSet
  extends AffymetrixCelSet
  
```

This class represents probe-level weights.

**Usage**

```
WeightsSet(..., probeModel=c("pm"))
```

**Arguments**

... Arguments passed to [AffymetrixCelSet](#).  
 probeModel The specific type of model, e.g. "pm".

**Fields and Methods****Methods:**

```

findUnitsTodo -
fromDataSet -
getAverageFile -
getCellIndices -
getParameters -
readUnits -

```

**Methods inherited from AffymetrixCelSet:**

[, [], append, as, as.AffymetrixCelSet, averageQuantile, byName, byPath, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUgpFile, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, nbrOfArrays, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, getAlias, getChecksum, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, getSubdirs, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, sortBy, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTrans-

latorByTabularTextFileSet, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, getChecksum, \$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

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**See Also**

An object of this class is typically obtained through the `getWeightsSet()` method for the `ProbeLevelModel` class.

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