

Package ‘aroma.core’

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Title Core methods and classes used by aroma.* packages part of The Aroma Framework

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Description This package contains core methods and classes used by higher-level aroma.* packages part of the Aroma Project, e.g. aroma.affymetrix and aroma.cn. Its API should be considered to be in alpha and beta versions, and is mostly of interest to developers.

License LGPL (>= 2.1)

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

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

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Description

This package contains core methods and classes used by higher-level *aroma.** packages part of the Aroma Project, e.g. *aroma.affymetrix* and *aroma.cn*. Its API should be considered to be in alpha and beta versions, and is mostly of interest to developers.

This package is a support package for ***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. Consider this package a private package.

Installation and updates

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

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.

References

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

[1] 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/>

AromaCellCpgFile *A binary file holding local CpG density for each cell (probe/feature)*

Description

A binary file holding local CpG density for each cell (probe/feature).

Usage

```
AromaCellCpgFile(...)
```

Arguments

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

Details

Note that this class does *not* assume a rectangular chip layout. In other words, there is no concept of mapping a *spatial* location on the array to a cell index and vice versa. The reason for this to be able to use this class also for non-rectangular chip types.

Author(s)

Mark Robinson

AromaCellPositionFile *A binary file holding chromosome/position for each cell*

Description

A binary file holding chromosome/position for each cell.

Usage

```
AromaCellPositionFile(...)
```

Arguments

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

Details

Note that this class does *not* assume a rectangular chip layout. In other words, there is no concept of mapping a *spatial* location on the array to a cell index and vice versa. The reason for this to be able to use this class also for non-rectangular chip types.

Author(s)

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

AromaCellTabularBinaryFile

The AromaCellTabularBinaryFile class

Description

Package: aroma.core

Class AromaCellTabularBinaryFile**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaMicroarrayTabularBinaryFile
~~~~~|
~~~~~+--AromaCellTabularBinaryFile

```

Directly known subclasses:

[AromaCellCpgFile](#), [AromaCellPositionFile](#), [AromaCellSequenceFile](#)

public abstract static class **AromaCellTabularBinaryFile**

extends [AromaMicroarrayTabularBinaryFile](#)

An AromaCellTabularBinaryFile is an [AromaTabularBinaryFile](#) with the constraint that the rows map one-to-one to the cells (features) of a microarray.

Usage

```
AromaCellTabularBinaryFile(...)
```

Arguments

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

Fields and Methods**Methods:**

nrOfCells -

Methods inherited from AromaMicroarrayTabularBinaryFile:

allocate, as.character, byChipType, findByChipType, getChipType, getFilenameExtension, getPlatform

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, nrOfColumns, nrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from GenericTabularFile:

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nrOfColumns, nrOfRows, 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/>)

See Also

[AromaUnitTabularBinaryFile](#).

AromaGenomeTextFile *The AromaGenomeTextFile class*

Description

Package: aroma.core

Class AromaGenomeTextFile**Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---GenericTabularFile
~~~~~|
~~~~~+---TabularTextFile
~~~~~|
~~~~~+---AromaGenomeTextFile

```

Directly known subclasses:

[AromaUcscGenomeTextFile](#)

public abstract static class **AromaGenomeTextFile**
 extends [TabularTextFile](#)

An AromaGenomeTextFile represents a annotation tabular text file that specifies the number of bases (nucleotides) per chromosome for a particular genome/organism.

Usage

```
AromaGenomeTextFile(...)
```

Arguments

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

Details

An AromaGenomeTextFile is a tab-delimited text file with a header containing (at least) column names 'chromosome' and 'nbrOfBases'. The 'chromosome' column specifies the chromosomes (character strings) and the 'nbrOfBases' column specifies the lengths (integer) of the chromosomes in number of bases (nucleotides).

The filename of an AromaGenomeTextFile should have format "<genome>,chromosomes(<tag>)*.txt", and be located in annotationData/genomes/<genome>/, e.g. annotationData/genomes/Human/Human,chromosomes,max,200

Fields and Methods

Methods:

```
byGenome      -
findByGenome  -
readDataFrame -
```

Methods inherited from TabularTextFile:

[, as.character, getColumnNames, getCommentChar, getHeader, getReadArguments, hasColumnHeader, nbrOfLines, nbrOfRows, readColumnNames, readColumns, readDataFrame, readLines, readRawHeader, setCommentChar, writeColumnsToFiles

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/>)

Examples

```
# Locate a Human,chromosomes(,.*).txt file
```

```

db <- AromaGenomeTextFile$byGenome("Human");
print(db);

# Read the data
df <- readDataFrame(db);
print(df);
str(df);

# Details on the file format
oopts <- options(width=40);
print(readLines(db));
options(oopts);

```

AromaMicroarrayDataFile

The abstract AromaMicroarrayDataFile class

Description

Package: aroma.core

Class AromaMicroarrayDataFile

Object

```

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

```

Directly known subclasses:

public abstract static class **AromaMicroarrayDataFile**

extends *GenericDataFile*

An AromaMicroarrayDataFile object represents a single microarray data file. Each such file originates from a specific chip type on a given platform.

Usage

```
AromaMicroarrayDataFile(...)
```

Arguments

... Arguments passed to *GenericDataFile*.

Fields and Methods**Methods:**

```

getChipType      -
getPlatform      -
getXAM           -
isAverageFile    -

```

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 [AromaMicroarrayDataSet](#).

AromaMicroarrayDataSet

The AromaMicroarrayDataSet class

Description

Package: aroma.core

Class AromaMicroarrayDataSet**Object**

```

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

```

Directly known subclasses:

public abstract static class **AromaMicroarrayDataSet**
 extends [GenericDataFileSet](#)

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

Usage

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

Arguments

files A [list](#) of [AromaMicroarrayDataFile](#)s.
 ... Arguments passed to [GenericDataFileSet](#).

Fields and Methods**Methods:**

```

as.AromaMicroarrayDataSetList -
as.AromaMicroarrayDataSetTuple -
getAromaFullNameTranslatorSet -
getAverageFile                 -
getChipType                    -
getDefaultFullName             -
getPlatform                    -
nbrOfArrays                    -

```

Methods inherited from GenericDataFileSet:

getFullNameTranslatorSet, getParentName, append, appendFiles, appendFullNamesTranslator, ap-

pendFullNamesTranslatorBydata.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/>)

AromaMicroarrayDataSetTuple

The AromaMicroarrayDataSetTuple class

Description

Package: aroma.core

Class AromaMicroarrayDataSetTuple

Object

~~|

~~+---FullNameInterface

~~~~~|

~~~~~+---GenericDataFileSetList

~~~~~|

~~~~~+---AromaMicroarrayDataSetTuple

Directly known subclasses:

AromaUnitTotalCnBinarySetTuple

```
public abstract static class AromaMicroarrayDataSetTuple
  extends GenericDataFileSetList
```

Usage

```
AromaMicroarrayDataSetTuple(..., .setClass="AromaMicroarrayDataSet")
```

Arguments

```
...           Arguments passed to GenericDataFileSetList.
.setClass     The name of the class of the input set.
```

Fields and Methods

Methods:

| | |
|--------------------------------|--------------------------------|
| as | - |
| as.AromaMicroarrayDataSetTuple | - |
| byPath | - |
| getChipTypes | - |
| getFullNames | - |
| getSets | - |
| getTags | - |
| indexOf | - |
| nrOfArrays | - |
| nrOfChipTypes | Gets the number of chip types. |

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, nrOfFiles, nrOfSets, 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/>)

AromaMicroarrayTabularBinaryFile

The AromaMicroarrayTabularBinaryFile class

Description

Package: aroma.core

Class AromaMicroarrayTabularBinaryFile**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaMicroarrayTabularBinaryFile

```

Directly known subclasses:

[AromaCellCpgFile](#), [AromaCellPositionFile](#), [AromaCellSequenceFile](#), [AromaCellTabularBinaryFile](#), [AromaUflFile](#), [AromaUgpFile](#), [AromaUnitChromosomeTabularBinaryFile](#), [AromaUnitTabularBinaryFile](#)

public abstract static class **AromaMicroarrayTabularBinaryFile**

extends [AromaPlatformInterface](#)

An AromaMicroarrayTabularBinaryFile is an abstract [AromaTabularBinaryFile](#).

Usage

```
AromaMicroarrayTabularBinaryFile(...)
```

Arguments

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

Fields and Methods**Methods:**

| | |
|----------------------|---|
| allocate | - |
| as.character | - |
| byChipType | - |
| getChipType | - |
| getFilenameExtension | - |
| getPlatform | - |

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/>)

See Also

[AromaTabularBinaryFile](#).

AromaPlatform

The AromaPlatform class

Description

Package: aroma.core

Class AromaPlatform

[Object](#)

~~|

~~+--AromaPlatform

Directly known subclasses:

public abstract static class **AromaPlatform**

extends [Object](#)

An AromaPlatform provides methods for a given platform, e.g. Affymetrix, Agilent, Illumina.

Usage

AromaPlatform(...)

Arguments

... Not used.

Methods**Methods:**

| | |
|-------------------|---|
| byName | - |
| findUnitNamesFile | - |
| findUnitTypesFile | - |
| getAromaUgpFile | - |
| getName | - |
| getUnitNamesFile | - |
| getUnitTypesFile | - |

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/>)

AromaTabularBinaryFile

The AromaTabularBinaryFile class

Description

Package: aroma.core

Class AromaTabularBinaryFile**Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---GenericTabularFile
~~~~~|
~~~~~+---AromaTabularBinaryFile

```

Directly known subclasses:

[AromaCellCpgFile](#), [AromaCellPositionFile](#), [AromaCellSequenceFile](#), [AromaCellTabularBinaryFile](#), [AromaMicroarrayTabularBinaryFile](#), [AromaUflFile](#), [AromaUgpFile](#), [AromaUnitCallFile](#), [AromaUnitChromosomeTabularBinaryFile](#), [AromaUnitFracBCnBinaryFile](#), [AromaUnitGenotypeCallFile](#), [AromaUnitSignalBinaryFile](#), [AromaUnitTabularBinaryFile](#), [AromaUnitTotalCnBinaryFile](#), [AromaUnitTypesFile](#)

```

public abstract static class AromaTabularBinaryFile
extends GenericTabularFile

```

A AromaTabularBinaryFile represents a file with a binary format. It has a well defined header, a data section, and a footer.

Usage

```
AromaTabularBinaryFile(...)
```

Arguments

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

Fields and Methods**Methods:**

| | |
|-----------------------------|---|
| [| - |
| [[| - |
| [<- | - |
| allocate | Creates an AromaTabularBinaryFile. |
| as.character | - |
| colMeans | - |
| colMedians | - |
| colStats | - |
| colSums | - |
| dimnames<- | - |
| getBytesPerColumn | - |
| getColClasses | - |
| getColumnNames | - |
| importFrom | - |
| lapply | - |
| nrOfColumns | - |
| nrOfRows | - |
| readColumns | - |
| readFooter | Reads the file footer in XML format into a named nested list. |
| subset | - |
| summary | - |
| writeFooter | Writes a named nested list to the file footer in XML format. |

Methods inherited from GenericTabularFile:

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nrOfColumns, nrOfRows, 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, getDefault-

FullName, 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

[GenericDataFile](#).

AromaTabularBinarySet *The AromaTabularBinarySet class*

Description

Package: aroma.core

Class AromaTabularBinarySet

Object

```

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

```

Directly known subclasses:

[AromaUnitCallSet](#), [AromaUnitFracBCnBinarySet](#), [AromaUnitGenotypeCallSet](#), [AromaUnitSignalBinarySet](#), [AromaUnitTotalCnBinarySet](#)

```

public static class AromaTabularBinarySet
extends GenericTabularFileSet

```

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

Usage

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

Arguments

```
files      A list of AromaTabularBinaryFile:s.
...        Arguments passed to GenericDataFileSet.
```

Fields and Methods**Methods:**

```
getDefaultFullName -
```

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/>)

AromaTransform *The AromaTransform class*

Description

Package: aroma.core

Class AromaTransform

[Object](#)

~~|

~~+--AromaTransform

Directly known subclasses:

```
public abstract static class AromaTransform
extends Object
```

This abstract class represents a transform (algorithm/operator) that transforms data. A transform has an input data set, which is transformed into an output data set.

Usage

```
AromaTransform(dataSet=NULL, tags="*", ..., .reqSetClass="AromaMicroarrayDataSet")
```

Arguments

| | |
|--------------|--|
| dataSet | The input data set as an AromaMicroarrayDataSet . |
| tags | A character vector of tags to be appended to the tags of the input data set. |
| ... | Not used. |
| .reqSetClass | Internal argument. |

Details

Subclasses must implement the process() method.

Fields and Methods

Methods:

| | |
|----------------------------------|--|
| getFullName | Gets the full name of the output data set. |
| getInputDataSet | Gets the input data set. |
| getName | Gets the name of the output data set. |
| getOutputDataSet | Gets the transformed data set. |

| | |
|-------------------------|---|
| getPath | Gets the path of the output data set. |
| getTags | Gets the tags of the output data set. |
| isDone | Checks if the data set is processed or not. |
| process | Processes the data set. |
| 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/>)

AromaUnitCallFile *The AromaUnitCallFile class*

Description

Package: aroma.core

Class AromaUnitCallFile**Object**

```

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

```

Directly known subclasses:

[AromaUnitGenotypeCallFile](#)

```
public static class AromaUnitCallFile
  extends AromaUnitSignalBinaryFile
```

An AromaUnitCallFile is a [AromaUnitSignalBinaryFile](#).

Usage

```
AromaUnitCallFile(...)
```

Arguments

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

Fields and Methods

Methods:

```
allocate -
extractCallArray -
extractCalls -
extractMatrix -
findUnitsTodo -
```

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/>)

AromaUnitCallSet *The AromaUnitCallSet class*

Description

Package: aroma.core

Class AromaUnitCallSet**Object**

```

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

```

Directly known subclasses:

[AromaUnitGenotypeCallSet](#)

public static class **AromaUnitCallSet**

extends [AromaUnitSignalBinarySet](#)

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

Usage

```
AromaUnitCallSet(...)
```

Arguments

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

Fields and Methods**Methods:**

```

byPath -
extractCallArray -
extractCalls -
extractGenotypeMatrix -
findByName -
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, 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/>)

AromaUnitFracBCnBinaryFile

The AromaUnitFracBCnBinaryFile class

Description

Package: aroma.core

Class AromaUnitFracBCnBinaryFile

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFile

~~~~~|

~~~~~+--GenericTabularFile

~~~~~|

~~~~~+--AromaTabularBinaryFile

~~~~~|

~~~~~+--AromaPlatformInterface

~~~~~|

~~~~~+--AromaUnitSignalBinaryFile

~~~~~|

~~~~~+--AromaUnitFracBCnBinaryFile

Directly known subclasses:

public static class **AromaUnitFracBCnBinaryFile**

extends [AromaUnitSignalBinaryFile](#)

An AromaUnitFracBCnBinaryFile is a [AromaUnitTabularBinaryFile](#).

Usage

AromaUnitFracBCnBinaryFile(...)

Arguments

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

Fields and Methods**Methods:**

extractRawAlleleBFractions -

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, getColumnNameTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnNameTranslator, 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/>)

AromaUnitFracBCnBinarySet

The AromaUnitFracBCnBinarySet class

Description

Package: aroma.core

Class AromaUnitFracBCnBinarySet

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFileSet

~~~~~|

~~~~~+--GenericTabularFileSet

~~~~~|

~~~~~+--AromaTabularBinarySet

~~~~~|

~~~~~+--AromaUnitSignalBinarySet

~~~~~|

~~~~~+--AromaUnitFracBCnBinarySet

Directly known subclasses:

public static class **AromaUnitFracBCnBinarySet**

extends [AromaUnitSignalBinarySet](#)

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

Usage

AromaUnitFracBCnBinarySet(...)

Arguments

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

Details

The term "allele B fraction" is also known as "allele B frequency", which was coined by Peiffer et al. (2006). Note that the term "frequency" is a bit misleading since it is not a frequency in neither the statistical nor the population sense, but rather only proportion relative to the total amount of allele A and allele B signals, which is calculated for each sample independently.

Fields and Methods**Methods:**

```

byName          -
exportFracBDiffSet -
writeDataFrame  -

```

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/>)

References

[1] Peiffer et al., *High-resolution genomic profiling of chromosomal aberrations using Infinium whole-genome genotyping*, Genome Res, 2006.

AromaUnitGenotypeCallFile

The AromaUnitGenotypeCallFile class

Description

Package: aroma.core

Class AromaUnitGenotypeCallFile

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaUnitSignalBinaryFile
~~~~~|
~~~~~+--AromaUnitCallFile
~~~~~|
~~~~~+--AromaUnitGenotypeCallFile

```

Directly known subclasses:

```

public static class AromaUnitGenotypeCallFile
extends AromaUnitCallFile

```

An AromaUnitGenotypeCallFile is a [AromaUnitTabularBinaryFile](#).

Usage

```
AromaUnitGenotypeCallFile(...)
```

Arguments

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

Fields and Methods**Methods:**

| | |
|-----------------------|---|
| allocate | - |
| extractGenotypeMatrix | - |
| extractGenotypes | - |
| isHeterozygous | - |
| isHomozygous | - |
| updateGenotypes | - |

Methods inherited from AromaUnitCallFile:

allocate, extractCallArray, extractCalls, extractMatrix, findUnitsTodo

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, getColumnNameTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnNameTranslator, 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, 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/>)

AromaUnitGenotypeCallSet

The AromaUnitGenotypeCallSet class

Description

Package: aroma.core

Class AromaUnitGenotypeCallSet

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--GenericTabularFileSet
~~~~~|
~~~~~+--AromaTabularBinarySet
~~~~~|
~~~~~+--AromaUnitSignalBinarySet
~~~~~|
~~~~~+--AromaUnitCallSet
~~~~~|
~~~~~+--AromaUnitGenotypeCallSet

```

Directly known subclasses:

```
public static class AromaUnitGenotypeCallSet
  extends AromaUnitCallSet
```

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

Usage

```
AromaUnitGenotypeCallSet(...)
```

Arguments

```
... Arguments passed to AromaUnitCallSet.
```

Fields and Methods

Methods:

```
byName -
byPath -
extractGenotypes -
```

Methods inherited from [AromaUnitCallSet](#):

```
byPath, extractCallArray, extractCalls, extractGenotypeMatrix, findByName, 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, 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

Author(s)

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

AromaUnitSignalBinaryFile

The AromaUnitSignalBinaryFile class

Description

Package: aroma.core

Class AromaUnitSignalBinaryFile

Object

```

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

```

Directly known subclasses:

[AromaUnitCallFile](#), [AromaUnitFracBCnBinaryFile](#), [AromaUnitGenotypeCallFile](#), [AromaUnitTotalCnBinaryFile](#), [AromaUnitTypesFile](#)

public static class **AromaUnitSignalBinaryFile**
 extends [AromaPlatformInterface](#)

An AromaUnitSignalBinaryFile is a [AromaTabularBinaryFile](#).

Usage

```
AromaUnitSignalBinaryFile(...)
```

Arguments

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

Fields and Methods**Methods:**

| | |
|------------------------------------|--|
| allocate | - |
| allocateFromUnitAnnotationDataFile | - |
| allocateFromUnitNamesFile | - |
| as.character | - |
| extractMatrix | - |
| fromFile | - |
| getAromaUgpFile | - |
| getChipType | - |
| getPlatform | - |
| isAverageFile | - |
| nrOfUnits | - |
| readDataFrame | - |
| writeDataFrame | Writes the data file as a tab-delimited text file. |

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, nrOfColumns, nrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from GenericTabularFile:

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nrOfColumns, nrOfRows, 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, 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/>)

See Also

[AromaTabularBinaryFile](#).

AromaUnitSignalBinarySet

The AromaUnitSignalBinarySet class

Description

Package: aroma.core

Class AromaUnitSignalBinarySet

Object

```

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

```

Directly known subclasses:

[AromaUnitCallSet](#), [AromaUnitFracBCnBinarySet](#), [AromaUnitGenotypeCallSet](#), [AromaUnitTotalCnBinarySet](#)

```
public static class AromaUnitSignalBinarySet
  extends AromaTabularBinarySet
```

An `AromaUnitSignalBinarySet` object represents a set of `AromaUnitSignalBinaryFiles` with *identical* chip types.

Usage

```
AromaUnitSignalBinarySet(...)
```

Arguments

... Arguments passed to `AromaTabularBinarySet`.

Fields and Methods

Methods:

| | |
|--|---|
| <code>byName</code> | - |
| <code>findByName</code> | - |
| <code>getAromaFullNameTranslatorSet</code> | - |
| <code>getAromaUgpFile</code> | - |
| <code>getChipType</code> | - |
| <code>getPlatform</code> | - |
| <code>writeDataFrame</code> | Writes the data set as a tab-delimited text file. |

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`, `get-`

Tags, 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/>)

AromaUnitTabularBinaryFile

The AromaUnitTabularBinaryFile class

Description

Package: aroma.core

Class AromaUnitTabularBinaryFile

Object

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---GenericTabularFile
~~~~~|
~~~~~+---AromaTabularBinaryFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AromaMicroarrayTabularBinaryFile
~~~~~|
~~~~~+---UnitAnnotationDataFile
~~~~~|
~~~~~+---AromaUnitTabularBinaryFile

```

Directly known subclasses:

[AromaUfflFile](#), [AromaUgpFile](#), [AromaUnitChromosomeTabularBinaryFile](#)

```

public abstract static class AromaUnitTabularBinaryFile
extends UnitAnnotationDataFile

```

A `AromaUnitTabularBinaryFile` is an `AromaTabularBinaryFile` with the constraint that the rows map one-to-one to, and in the same order as, the units in an annotation chip type file (e.g. CDF file). The (full) chip type of the annotation chip type file is given by the mandatory file footer `chipType`.

Usage

```
AromaUnitTabularBinaryFile(...)
```

Arguments

... Arguments passed to `AromaTabularBinaryFile`.

Fields and Methods

Methods:

| | |
|---|--|
| <code>allocateFromUnitAnnotationDataFile</code> | - |
| <code>allocateFromUnitNamesFile</code> | - |
| <code>byChipType</code> | - |
| <code>nbrOfUnits</code> | - |
| <code>writeDataFrame</code> | Writes the data file as a tab-delimited text file. |

Methods inherited from `UnitAnnotationDataFile`:

`byChipType`, `getAromaUflFile`, `getAromaUgpFile`, `getChipType`, `getDefaultExtension`, `getPlatform`, `nbrOfUnits`

Methods inherited from `AromaMicroarrayTabularBinaryFile`:

`allocate`, `as.character`, `byChipType`, `findByChipType`, `getChipType`, `getFilenameExtension`, `getPlatform`

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`, `getColumnNameTranslator`, `nbrOfColumns`, `nbrOfRows`, `readColumns`, `readDataFrame`, `setColumnNameTranslator`, `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, 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/>)

AromaUnitTotalCnBinaryFile

The AromaUnitTotalCnBinaryFile class

Description

Package: aroma.core

Class AromaUnitTotalCnBinaryFile

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaUnitSignalBinaryFile
~~~~~|
~~~~~+--CopyNumberDataFile
~~~~~|
~~~~~+--AromaUnitTotalCnBinaryFile

```

Directly known subclasses:

public static class **AromaUnitTotalCnBinaryFile**
 extends *CopyNumberDataFile*

An AromaUnitTotalCnBinaryFile is a [AromaUnitSignalBinaryFile](#).

Usage

```
AromaUnitTotalCnBinaryFile(...)
```

Arguments

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

Fields and Methods**Methods:**

| | |
|--------------------------|---|
| extractPSCNArray | - |
| extractPSCNMatrix | - |
| extractRawCopyNumbers | - |
| getAM | - |
| getNumberOfFilesAveraged | - |
| getXAM | - |
| hasAlleleBFractions | - |
| hasStrandiness | - |

Methods inherited from CopyNumberDataFile:

as, as.CopyNumberDataFile, getNumberOfFilesAveraged, hasAlleleBFractions, hasStrandiness

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, getColumnNameTranslator, nbrOfColumns,

nbrOfRows, readColumns, readDataFrame, setColumnNameTranslator, 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/>)

AromaUnitTotalCnBinarySet

The AromaUnitTotalCnBinarySet class

Description

Package: aroma.core

Class AromaUnitTotalCnBinarySet

Object

```

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

```

```

~~~~~|
~~~~~+--CopyNumberDataSet
~~~~~|
~~~~~+--AromaUnitTotalCnBinarySet

```

Directly known subclasses:

```

public static class AromaUnitTotalCnBinarySet
extends CopyNumberDataSet

```

An `AromaUnitTotalCnBinarySet` object represents a set of `AromaUnitTotalCnBinaryFiles` with *identical* chip types.

Usage

```
AromaUnitTotalCnBinarySet(...)
```

Arguments

... Arguments passed to `AromaUnitSignalBinarySet`.

Fields and Methods

Methods:

```

as.AromaUnitTotalCnBinarySetTuple -
as.CopyNumberDataSetTuple -
byName -
exportTotalCnRatioSet -
extractPSCNArray -
getAverageFile -
getUnitNamesFile -
nbrOfArrays -
writeDataFrame -

```

Methods inherited from `CopyNumberDataSet`:

as, as.CopyNumberDataSet, doCBS, hasAlleleBFractions, hasStrandiness

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/>)

AromaUnitTypesFile *The AromaUnitTypesFile class*

Description

Package: aroma.core

Class AromaUnitTypesFile

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|

```

```

~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaUnitSignalBinaryFile
~~~~~|
~~~~~+--UnitAnnotationDataFile
~~~~~|
~~~~~+--UnitTypesFile
~~~~~|
~~~~~+--AromaUnitTypesFile

```

Directly known subclasses:

```

public static class AromaUnitTypesFile
extends UnitTypesFile

```

Usage

```
AromaUnitTypesFile(...)
```

Arguments

```
... Arguments passed to AromaUnitTabularBinaryFile.
```

Fields and Methods

Methods:

```

allocate -
getChipType -
getPlatform -
getUnitTypes -
importFromUnitTypesFile -

```

Methods inherited from [UnitTypesFile](#):

```
getUnitTypes, nbrOfUnits
```

Methods inherited from [UnitAnnotationDataFile](#):

```
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform,
nbrOfUnits
```

Methods inherited from [AromaUnitSignalBinaryFile](#):

```
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extract-
Matrix, extractRawGenomicSignals, fromFile, getAromaUgpFile, getChipType, getExtensionPat-
tern, 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/>)

as.GrayscaleImage.matrix

Creates a Grayscale (TrueColor) Image from a matrix file

Description

Creates a Grayscale (TrueColor) Image from a matrix file.

Usage

```
## S3 method for class 'matrix'
as.GrayscaleImage(z, transforms=NULL, interleaved=c("none", "h", "v", "auto"), scale=1, ..., verbose=F
```

Arguments

| | |
|-------------|---|
| z | A KxN matrix . |
| transforms | A list of transform functions . |
| interleaved | A character string specifying how the image data should be interleaved, if at all. |
| scale | A numeric scale factor in (0,+Inf) for resizing the imaging. If 1, no resizing is done. |
| ... | Passed to colorize() for the object created. |
| verbose | A logical or a Verbose object. |

Value

Returns a bitmap image object.

Author(s)

Henrik Bengtsson and Ken Simpson.

See Also

For more information see [matrix](#).

BinnedScatter

The BinnedScatter class

Description

Package: aroma.core

Class BinnedScatter

list

~~|

~~+--BinnedScatter

Directly known subclasses:

public class **BinnedScatter**

extends list

Usage

BinnedScatter(data=NULL, density=NULL, map=NULL, params=NULL)

Arguments

| | |
|---------|--------------------------------|
| data | A Nx2 @numeric <i>matrix</i> . |
| density | ... |
| map | ... |
| params | A <i>list</i> of parameters. |
| ... | Not used. |

Fields and Methods**Methods:**

| | |
|-----------|---|
| plot | - |
| points | - |
| reorder | - |
| subsample | - |
| subset | - |

Methods inherited from list:

all.equal, as.CopyNumberDataSetTuple, as.data.frame, attachLocally, averageQuantile, callHooks, listToXml, mergeBoxplotStats, normalizeAverage, normalizeDifferencesToAverage, normalizeQuantileRank, normalizeQuantileSpline, plotDensity, relist, within

Author(s)

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

See Also

The spatial density is estimated by internal functions of the **smoothScatter** package.

Examples

```
# Sample scatter data
n <- 10e3
x <- rnorm(n=n)
y <- rnorm(n=n)
xy <- cbind(x=x, y=sin(x)+y/5)

# Bin data and estimate densities
xyd <- binScatter(xy)

layout(matrix(1:4, nrow=2))
par(mar=c(5,4,2,1))

# Plot data
plot(xyd, pch=1)
```

```

# Thin scatter data by subsampling
rhos <- c(1/3, 1/4, 1/6)
for (kk in seq(along=rhos)) {
  xyd2 <- subsample(xyd, size=rhos[kk])
  points(xyd2, pch=1, col=kk+1)
}

for (kk in seq(along=rhos)) {
  xyd2 <- subsample(xyd, size=rhos[kk])
  plot(xyd2, pch=1, col=kk+1)
  mtext(side=3, line=0, sprintf("Density: %.1f%%", 100*rhos[kk]))
}

```

CbsModel

The CbsModel class

Description

Package: aroma.core

Class CbsModel

Object

```

~~|
~~+---ChromosomalModel
~~~~~|
~~~~~+---CopyNumberChromosomalModel
~~~~~|
~~~~~+---CopyNumberSegmentationModel
~~~~~|
~~~~~+---CbsModel

```

Directly known subclasses:

```

public static class CbsModel
extends CopyNumberSegmentationModel

```

This class represents the Circular Binary Segmentation (CBS) model [1].

Usage

```
CbsModel(cesTuple=NULL, ..., seed=NULL)
```

Arguments

| | |
|----------|---|
| cesTuple | A CopyNumberDataSetTuple . |
| ... | Arguments passed to the constructor of CopyNumberSegmentationModel . |
| seed | An (optional) integer that if specified will (temporarily) set the random seed each time before calling the segmentation method. For more information, see segmentByCBS() . |

Fields and Methods**Methods:**

getFitFunction -

Methods inherited from CopyNumberSegmentationModel:

fit, getAsteriskTags, getFitFunction, getFullNames, getRegions, getTags, plot, plotCopyNumberRegionLayers, writeRegions

Methods inherited from CopyNumberChromosomalModel:

as.character, calculateChromosomeStatistics, calculateRatios, clearCache, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getNames, getOptionalArguments, getPairedNames, getReferenceSetTuple, getRefSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers

Methods inherited from ChromosomalModel:

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/>)

References

- [1] Olshen, A. B., Venkatraman, E. S., Lucito, R., Wigler, M. *Circular binary segmentation for the analysis of array-based DNA copy number data*. *Biostatistics* 5: 557-572, 2004.
- [2] Venkatraman, E. S. & Olshen, A. B. *A faster circular binary segmentation algorithm for the analysis of array CGH data*. *Bioinformatics*, 2007.

See Also

[CopyNumberSegmentationModel](#).

ChromosomalModel *The ChromosomalModel class*

Description

Package: aroma.core

Class ChromosomalModel

[Object](#)

~~|

~~+--ChromosomalModel

Directly known subclasses:

[CbsModel](#), [CopyNumberChromosomalModel](#), [CopyNumberSegmentationModel](#), [GladModel](#), [HaarSeg-Model](#), [RawCopyNumberModel](#)

public abstract static class **ChromosomalModel**

extends [Object](#)

This *abstract* class represents a chromosomal model.

Usage

```
ChromosomalModel(cesTuple=NULL, tags="*", genome="Human", ...)
```

Arguments

| | |
|----------|---|
| cesTuple | A AromaMicroarrayDataSetTuple . |
| tags | A character vector of tags. |
| genome | A character string specifying what genome is process. |
| ... | Not used. |

Fields and Methods**Methods:**

| | |
|-----------------------------|---|
| clearCache | - |
| fit | - |
| getAlias | - |
| getChipType | Gets a label for all chip types merged. |
| getChipTypes | - |

| | |
|--|---------------------------------|
| getChromosomes | Gets the chromosomes available. |
| getFullName | - |
| getFullNames | - |
| getGenome | - |
| getListOfAromaUgpFiles | - |
| getName | - |
| getNames | Gets the names of the arrays. |
| getParentPath | - |
| getPath | - |
| getRootPath | - |
| getSets | - |
| getTags | - |
| indexOf | - |
| nbrOfArrays | Gets the number of arrays. |
| nbrOfChipTypes | Gets the number of chip types. |
| 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

Requirements

This class requires genome information annotation files for every chip type.

Author(s)

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

ChromosomeExplorer *The ChromosomeExplorer class*

Description

Package: aroma.core

Class ChromosomeExplorer

[Object](#)

~~|

~~+--[Explorer](#)

~~~~~|

~~~~~+--ChromosomeExplorer

Directly known subclasses:

public static class **ChromosomeExplorer**
 extends *Explorer*

Usage

ChromosomeExplorer(model=NULL, zooms=2^(0:6), ..., version=c("3"))

Arguments

| | |
|---------|--|
| model | A <i>CopyNumberChromosomalModel</i> object. |
| zooms | An positive <i>integer vector</i> specifying for which zoom levels the graphics should be generated. |
| ... | Not used. |
| version | The version of the Explorer HTML/Javascript generated/used. |

Fields and Methods**Methods:**

| | |
|-----------------------|--|
| display | - |
| getChromosomeLabels | - |
| <i>getChromosomes</i> | Gets the chromosomes available. |
| getFullNames | - |
| <i>getModel</i> | Gets the model. |
| getNames | - |
| getPath | - |
| getSampleLabels | - |
| getZooms | - |
| indexOf | - |
| <i>process</i> | Generates image files, scripts and dynamic pages for the explorer. |
| <i>setArrays</i> | Sets the arrays. |
| setCytoband | - |
| setZooms | - |

Methods inherited from Explorer:

addIncludes, addIndexFile, display, getAlias, getArrayOfInput, 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

Generating PNG images

In order to get better looking graphs, but also to be able to generate bitmap images on systems without direct bitmap support, which is the case when running R in batch mode or on Unix without X11 support, images are created using the `png2` device (a wrapper for `bitmap()` immitating `png()`). The `png()` is only used if `png2()`, which requires Ghostscript, does not. Note, when images are created using `png2()`, the images does not appear immediately, although the function call is completed, so be patient.

Author(s)

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

See Also

[CopyNumberChromosomalModel](#).

colBinnedSmoothing.matrix

Binned smoothing of a matrix column by column

Description

Binned smoothing of a matrix column by column.

Usage

```
## S3 method for class 'matrix'
colBinnedSmoothing(Y, x=seq(length = ncol(Y)), w=NULL, xOut=NULL, xOutRange=NULL, from=min(x, na.rm = T
```

Arguments

| | |
|-----------|---|
| Y | A numeric JxI matrix (or a vector of length J.) |
| x | A (optional) numeric vector specifying the positions of the J entries. The default is to assume uniformly distributed positions. |
| w | A optional numeric vector of prior weights for each of the J entries. |
| xOut | Optional numeric vector of K bin center locations. |
| xOutRange | Optional Kx2 matrix specifying the boundary locations for bins. If not specified, the boundaries are set to be the midpoints of the bin centers, such that the bins have maximum lengths without overlapping. Also, if xOut is not specified, then it is set to be the mid points of these boundaries. |

| | |
|--------------------------|--|
| from, to, by, length.out | If neither xOut nor xOutRange is specified, the xOut is generated uniformly from these arguments, which specify the center location of the first and the last bin, and the distance between the center locations, utilizing the <code>seq()</code> function. Argument length.out can be used as an alternative to by, in case it specifies the total number of bins instead. |
| FUN | A function . |
| na.rm | If <code>TRUE</code> , missing values are excluded, otherwise not. |
| ... | Not used. |
| verbose | See Verbose . |

Value

Returns a [numeric](#) KxI [matrix](#) (or a [vector](#) of length K) where K is the total number of bins. The following attributes are also returned:

- xOutThe center locations of each bin.
- xOutRangeThe bin boundaries.
- countThe number of data points within each bin (based solely on argument x).
- binWidthThe *average* bin width.

Author(s)

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

See Also

[*colKernelSmoothing\(\)](#).

Examples

```
# Number of tracks
I <- 4

# Number of data points per track
J <- 100

# Simulate data with a gain in track 2 and 3
x <- 1:J
Y <- matrix(rnorm(I*J, sd=1/2), ncol=I)
Y[30:50,2:3] <- Y[30:50,2:3] + 3

# Uniformly distributed equal-sized bins
Ys3 <- colBinnedSmoothing(Y, x=x, from=2, by=3)
Ys5 <- colBinnedSmoothing(Y, x=x, from=3, by=5)

# Custom bins
xOutRange <- t(matrix(c(
  1, 11,
```

```

11, 31,
31, 41,
41, 51,
51, 81,
81, 91,
91,101
), nrow=2))
YsC <- colBinnedSmoothing(Y, x=x, xOutRange=xOutRange)

# Custom bins specified by center locations with
# maximized width relative to the neighboring bins.
xOut <- c(6, 21, 36, 46, 66, 86, 96)
YsD <- colBinnedSmoothing(Y, x=x, xOut=xOut)

xlim <- range(x)
ylim <- c(-3,5)
layout(matrix(1:I, ncol=1))
par(mar=c(3,3,1,1)+0.1, pch=19)
for (ii in 1:I) {
  plot(NA, xlim=xlim, ylim=ylim)
  points(x, Y[,ii], col="#999999")

  xOut <- attr(Ys3, "xOut");
  lines(xOut, Ys3[,ii], col=2)
  points(xOut, Ys3[,ii], col=2)

  xOut <- attr(Ys5, "xOut");
  lines(xOut, Ys5[,ii], col=3)
  points(xOut, Ys5[,ii], col=3)

  xOut <- attr(YsC, "xOut");
  lines(xOut, YsC[,ii], col=4)
  points(xOut, YsC[,ii], col=4, pch=15)

  xOut <- attr(YsD, "xOut");
  lines(xOut, YsD[,ii], col=5)
  points(xOut, YsD[,ii], col=5, pch=15)

  if (ii == 1) {
    legend("topright", pch=c(19,19,15,15), col=c(2,3,4,5),
          c("by=3", "by=5", "Custom #1", "Custom #2"), horiz=TRUE, bty="n");
  }
}

# Sanity checks
xOut <- x
YsT <- colBinnedSmoothing(Y, x=x, xOut=xOut)
stopifnot(all(YsT == Y))
stopifnot(all(attr(YsT, "counts") == 1))

xOut <- x[seq(from=2, to=J, by=3)]
YsT <- colBinnedSmoothing(Y, x=x, xOut=xOut)

```

```

stopifnot(all(YsT == Ys3))
stopifnot(all(attr(YsT, "counts") == 3))

xOut <- x[seq(from=3, to=J, by=5)]
YsT <- colBinnedSmoothing(Y, x=x, xOut=xOut)
stopifnot(all(YsT == Ys5))
stopifnot(all(attr(YsT, "counts") == 5))

```

colKernelSmoothing.matrix

Kernel smoothing of a matrix column by column

Description

Kernel smoothing of a matrix column by column.

Usage

```

## S3 method for class 'matrix'
colKernelSmoothing(Y, x=seq(length = nrow(Y)), w=NULL, xOut=x, kernel=c("gaussian", "uniform"), h, cen

```

Arguments

| | |
|---------|---|
| Y | A numeric JxI matrix (or a vector of length J.) |
| x | A (optional) numeric vector specifying the positions of the J entries. The default is to assume uniformly distributed positions. |
| w | A optional numeric vector of prior weights for each of the J entries. |
| xOut | A numeric vector specifying K target positions where the kernel is applied. |
| kernel | A character string or a function specifying the kernel used. |
| h | A single positive numeric specifying the bandwidth of the kernel. |
| tensorH | A single positive numeric specifying the where to truncate the kernel. If Inf , no truncation is done. |
| na.rm | If TRUE , missing values are excluded, otherwise not. |
| robust | If TRUE , robust estimators are used, otherwise not. |
| ... | Not used. |
| verbose | See Verbose . |

Value

Returns a **numeric** KxI **matrix** (or a **vector** of length K).

Author(s)

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

See Also

[*colBinnedSmoothing\(\)](#).

Examples

```
J <- 100
I <- 4
Y <- matrix(rnorm(I*J, sd=1/2), ncol=I)
# Introduce a gain in column 2 and 3
Y[30:50,2:3] <- Y[30:50,2:3] + 3
x <- 1:J

xOut <- x
Ys1 <- colKernelSmoothing(Y, x=x, xOut=xOut, kernel="gaussian", h=1)
Ys5 <- colKernelSmoothing(Y, x=x, xOut=xOut, kernel="gaussian", h=5)

xlim <- range(c(x,xOut))
ylim <- c(-3,5)
layout(matrix(1:I, ncol=1))
par(mar=c(3,3,1,1)+0.1, pch=19)
for (ii in 1:I) {
  plot(NA, xlim=xlim, ylim=ylim)
  points(x, Y[,ii], col="#999999")
  lines(xOut, Ys1[,ii], col=2)
  points(xOut, Ys1[,ii], col=2)
  lines(xOut, Ys5[,ii], col=3)
  points(xOut, Ys5[,ii], col=3)
}
```

CopyNumberChromosomalModel

The CopyNumberChromosomalModel class

Description

Package: aroma.core

Class CopyNumberChromosomalModel

Object

~~|

~~+--ChromosomalModel

~~~~~|

~~~~~+--CopyNumberChromosomalModel

Directly known subclasses:

[CbsModel](#), [CopyNumberSegmentationModel](#), [GladModel](#), [HaarSegModel](#), [RawCopyNumberModel](#)

```
public abstract static class CopyNumberChromosomalModel
  extends ChromosomalModel
```

This *abstract* class represents a copy-number model.

Usage

```
CopyNumberChromosomalModel(cesTuple=NULL, refTuple=NULL, tags="*", genome="Human", ...)
```

Arguments

| | |
|----------|---|
| cesTuple | A CopyNumberDataSetTuple . |
| refTuple | An optional CopyNumberDataFile , or CopyNumberDataSet or CopyNumberDataSetTuple for pairwise comparisons. |
| tags | A character vector of tags. |
| genome | A character string specifying what genome is process. |
| ... | Optional arguments that may be used by some of the subclass models. |

Fields and Methods

Methods:

| | |
|---------------------------------------|---------------------------------|
| clearCache | - |
| extractRawCopyNumbers | Extracts relative copy numbers. |
| fit | Fits the model. |
| getChromosomeLength | - |
| getNames | - |
| getReferenceSetTuple | - |
| isPaired | - |
| plotAxesLayers | - |
| plotChromosomesLayers | - |
| plotCytobandLayers | - |
| plotFitLayers | - |
| plotGridHorizontalLayers | - |
| plotRawCopyNumbers | - |
| plotSampleLayers | - |

Methods inherited from ChromosomalModel:

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, getFieldMod-

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

Requirements

This class requires genome information annotation files for every chip type.

Author(s)

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

CopyNumberSegmentationModel

The CopyNumberSegmentationModel class

Description

Package: aroma.core

Class CopyNumberSegmentationModel

Object

~~|

~~+--ChromosomalModel

~~~~~|

~~~~~+--CopyNumberChromosomalModel

~~~~~|

~~~~~+--CopyNumberSegmentationModel

Directly known subclasses:

[CbsModel](#), [GladModel](#), [HaarSegModel](#)

public abstract static class **CopyNumberSegmentationModel**

extends [CopyNumberChromosomalModel](#)

This *abstract* class represents a copy-number segmentation model.

Usage

CopyNumberSegmentationModel(...)

Arguments

... Arguments passed to constructor [CopyNumberChromosomalModel](#).

Fields and Methods

Methods:

| | |
|---|-----------------|
| <code>fit</code> | Fits the model. |
| <code>getFullNames</code> | - |
| <code>getRegions</code> | - |
| <code>getTags</code> | - |
| <code>plot</code> | - |
| <code>plotCopyNumberRegionLayers</code> | - |
| <code>writeRegions</code> | - |

Methods inherited from CopyNumberChromosomalModel:

as.character, calculateChromosomeStatistics, calculateRatios, clearCache, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getNames, getOptionalArguments, getPairedNames, getReferenceSetTuple, getRefSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers

Methods inherited from ChromosomalModel:

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/>)

doCBS.character

Performs CBS segmentation on a data set

Description

Performs CBS segmentation on a data set for one or more chip types.

Usage

```
## S3 method for class 'character'
doCBS(dataSets, tags=NULL, chipTypes, ..., verbose=FALSE)
```

Arguments

| | |
|-----------|---|
| dataSets | A character string specifying the data set(s). |
| tags | And optional character vector of data set tags. |
| chipTypes | A character vector specifying the chip types to be used and merged. |
| ... | Additional arguments passed to ... |
| verbose | A logical or Verbose . |

Value

Returns a ...

Author(s)

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

See Also

For more information see [character](#).

Examples

```
## Not run:
  library("aroma.cn");
  verbose <- Arguments$getVerbose(-8, timestamp=TRUE);

  dataSet <- "GSE20939";
  tags <- "ACC,-XY,BPN,-XY,RMA,FLN,-XY";
  chipTypes <- c("Mapping250K_Nsp", "Mapping250K_Sty");
  fit <- doCBS(dataSet, tags=tags, chipTypes=chipTypes, verbose=verbose);
  print(fit);

## End(Not run)
```

Explorer

The Explorer class

Description

Package: aroma.core

Class Explorer**Object**

~~|

~~+--Explorer

Directly known subclasses:[ChromosomeExplorer](#)

```
public abstract static class Explorer
extends Object
```

Usage

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

Arguments

| | |
|------|--|
| tags | A character vector of tags to be added to the output path. |
| ... | Not used. |

Fields and Methods**Methods:**

| | |
|--|--|
| addIncludes | - |
| display | Displays the explorer in the default browser. |
| getAlias | Gets the alias of the output set. |
| getAsteriskTags | - |
| getFullName | - |
| getName | Gets the name of the explorer. |
| getNames | Gets the names of the input samples. |
| getPath | - |
| getReportPathPattern | - |
| getTags | Gets the tags of the explorer. |
| getTagsOfInput | - |
| nbrOfArrays | Gets the total number of arrays. |
| process | Generates image files, scripts and dynamic pages for the explorer. |
| setAlias | Sets the alias of the output set. |
| setArrays | Sets the arrays. |
| 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

Output directory structure

The *main directory* of an Explorer report is `reports/<name>/<subname>/`. The `<name>` is typically the same as the name of the input data set, and the `<subname>` is typically the tags of ditto. This main directory is where main HTML document is stored.

For each chip type, real or "virtual" (combined), there is a subdirectory with the same name as the chip type, i.e. `reports/<name>/<subname>/<chiptype>/`.

For each chip type directory, there are set of subdirectories each specifying a so called *image layer*, e.g. an image layer showing the raw data, another containing the estimates of a model fit and so on. Path format: `reports/<name>/<subname>/<chiptype>/<image layer>/`. In this directory all image files are stored, e.g. PNG files.

In some cases one do not want to all input tags to become part of the subname, but instead for instance use those to name the image layer(s). In such cases one has to override the default names.

Author(s)

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

GladModel

The GladModel class

Description

Package: aroma.core

Class GladModel

Object

```

~~|
~~+--ChromosomalModel
~~~~~|
~~~~~+--CopyNumberChromosomalModel
~~~~~|
~~~~~+--CopyNumberSegmentationModel
~~~~~|
~~~~~+--GladModel

```

Directly known subclasses:

```

public static class GladModel
extends CopyNumberSegmentationModel

```

This class represents the Gain and Loss Analysis of DNA regions (GLAD) model [1]. This class can model chip-effect estimates obtained from multiple chip types, and not all samples have to be available on all chip types.

Usage

```
GladModel(cesTuple=NULL, ...)
```

Arguments

```
cesTuple      A CopyNumberDataSetTuple.
...           Arguments passed to the constructor of CopyNumberSegmentationModel.
```

Details

Data from multiple chip types are combined "as is". This is based on the assumption that the relative chip effect estimates are non-biased (or at the equally biased across chip types). Note that in GLAD there is no way to down weight certain data points, which is why we can control for differences in variance across chip types.

Fields and Methods**Methods:**

```
getFitFunction -
writeRegions   -
```

Methods inherited from CopyNumberSegmentationModel:

```
fit, getAsteriskTags, getFitFunction, getFullNames, getRegions, getTags, plot, plotCopyNumber-
RegionLayers, writeRegions
```

Methods inherited from CopyNumberChromosomalModel:

```
as.character, calculateChromosomeStatistics, calculateRatios, clearCache, estimateSds, extractRaw-
CopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getNames, getOptionalArguments,
getPairedNames, getReferenceSetTuple, getRefSetTuple, isPaired, newPlot, plotAxesLayers, plotChro-
mosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNum-
bers, plotSampleLayers
```

Methods inherited from ChromosomalModel:

```
as.character, clearCache, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType,
getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenome-
File, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, get-
RootPath, getSets, getSetTuple, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setGenome
```

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
```

Benchmarking

In high-density copy numbers analysis, the most time consuming step is fitting the GLAD model. The complexity of the model grows more than linearly (squared? exponentially?) with the number

of data points in the chromosome and sample being fitted. This is why it take much more than twice the time to fit two chip types together than separately.

Author(s)

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

References

[1] Hupe P et al. *Analysis of array CGH data: from signal ratio to gain and loss of DNA regions*. *Bioinformatics*, 2004, 20, 3413-3422.

See Also

[CopyNumberSegmentationModel](#).

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

Description

Package: aroma.core

Class HaarSegModel

Object

```

~~|
~~+--ChromosomalModel
~~~~~|
~~~~~+--CopyNumberChromosomalModel
~~~~~|
~~~~~+--CopyNumberSegmentationModel
~~~~~|
~~~~~+--HaarSegModel

```

Directly known subclasses:

```

public static class HaarSegModel
extends CopyNumberSegmentationModel

```

This class represents the Haar wavelet-based segmentation (HaarSeg) model [1].

Usage

```
HaarSegModel(cesTuple=NULL, ..., breaksFdrQ=1e-04)
```

Arguments

| | |
|------------|--|
| cesTuple | A CopyNumberDataSetTuple . |
| breaksFdrQ | Default tuning parameters specific to the HaarSeg algorithm. |
| ... | Arguments passed to the constructor of CopyNumberSegmentationModel . |

Fields and Methods**Methods:**

getFitFunction -

Methods inherited from CopyNumberSegmentationModel:

fit, getAsteriskTags, getFitFunction, getFullNames, getRegions, getTags, plot, plotCopyNumberRegionLayers, writeRegions

Methods inherited from CopyNumberChromosomalModel:

as.character, calculateChromosomeStatistics, calculateRatios, clearCache, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getNames, getOptionalArguments, getPairedNames, getReferenceSetTuple, getRefSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers

Methods inherited from ChromosomalModel:

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/>)

References

[1] Ben-Yaacov E. and Eldar YC. *A fast and flexible method for the segmentation of aCGH data*, Bioinformatics, 2008. <http://www.ee.technion.ac.il/Sites/People/YoninaEldar/Info/software/HaarSeg.htm>

See Also

[CopyNumberSegmentationModel](#).

RawAlleleBFractions *The RawAlleleBFractions class*

Description

Package: aroma.core

Class RawAlleleBFractions

Object

```

~~|
~~+--RawGenomicSignals
~~~~~|
~~~~~+--RawAlleleBFractions

```

Directly known subclasses:

[RawMirroredAlleleBFractions](#), [SegmentedAlleleBFractions](#)

public static class **RawAlleleBFractions**

extends [RawGenomicSignals](#)

Usage

```
RawAlleleBFractions(...)
```

Arguments

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

Fields and Methods

Methods:

```

extractRawMirroredAlleleBFractions -
plot -

```

Methods inherited from RawGenomicSignals:

-, *, +, addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, drawDensity, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getX, getY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

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/>)

RawCopyNumberModel *The RawCopyNumberModel class*

Description

Package: aroma.core

Class RawCopyNumberModel**Object**

```

~~|
~~+---ChromosomalModel
~~~~~|
~~~~~+---CopyNumberChromosomalModel
~~~~~|
~~~~~+---RawCopyNumberModel

```

Directly known subclasses:

```

public abstract static class RawCopyNumberModel
extends CopyNumberChromosomalModel

```

This class represents an identity copy-number model which returns the input as is.

Usage

```
RawCopyNumberModel(...)
```

Arguments

... Passed to the constructor of the superclass.

Fields and Methods**Methods:**

```
getAsteriskTags -
getSetTag      -
```

Methods inherited from CopyNumberChromosomalModel:

as.character, calculateChromosomeStatistics, calculateRatios, clearCache, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getNames, getOptionalArguments, getPairedNames, getReferenceSetTuple, getRefSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers

Methods inherited from ChromosomalModel:

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/>)

RawCopyNumbers

The RawCopyNumbers class

Description

Package: aroma.core

Class RawCopyNumbers**Object**

```
~~|
~~+--RawGenomicSignals
~~~~~|
~~~~~+--RawCopyNumbers
```

Directly known subclasses:

[SegmentedCopyNumbers](#)

```
public static class RawCopyNumbers
  extends RawGenomicSignals
```

Usage

```
RawCopyNumbers(cn=NULL, ...)
```

Arguments

`cn` A **numeric vector** of length J specifying the copy number at each loci.
`...` Arguments passed to `RawGenomicSignals`.

Fields and Methods**Methods:**

```
as.data.frame      -
cnRange            -
extractRawCopyNumbers -
plot              -
```

Methods inherited from RawGenomicSignals:

-, *, +, addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, drawDensity, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

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

```
# -----
# Simulating copy-number data
# -----
# Number of loci
J <- 1000

mu <- double(J)
mu[200:300] <- mu[200:300] + 1
mu[650:800] <- mu[650:800] - 1
eps <- rnorm(J, sd=1/2)
```

```

y <- mu + eps
x <- sort(runif(length(y), max=length(y)))

cn <- RawCopyNumbers(y, x)
print(cn)

cn2 <- extractSubset(cn, subset=xSeq(cn, by=5))
print(cn2)

# -----
# Plot along genome
# -----
plot(cn, ylim=c(-3,3))
title(main="Complete and subsetted loci")
points(cn2, col="red", pch=176, cex=2)

legend("topright", pch=c(19,176), col=c("#999999", "red"), sprintf(c("raw [n=%d]", "every 5th [n=%d]"), c(nbrOfLo

# -----
# Binned smoothing
# -----
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Binned smoothing")

cnSa <- binnedSmoothing(cn, by=3)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- binnedSmoothing(cn, by=9)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"), sprintf(c("raw [n=%d]", "Bin(w=3) [n=%d]", "Bin(w=9)

# -----
# Binned smoothing (by count)
# -----
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Binned smoothing (by count)")

cnSa <- binnedSmoothing(cn, by=3, byCount=TRUE)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- binnedSmoothing(cn, by=9, byCount=TRUE)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"), sprintf(c("raw [n=%d]", "Bin0(w=3) [n=%d]", "Bin0(w=9)

```

```

# -----
# Kernel smoothing (default is Gaussian)
# -----
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Kernel smoothing w/ Gaussian kernel")

cnSa <- kernelSmoothing(cn, h=2)
points(cnSa, col="blue")

cnSb <- kernelSmoothing(cn, h=5)
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"), sprintf(c("raw [n=%d]", "N(.,sd=2) [n=%d]", "N(.,sd=5) [n=%d]"), n, n, n))

# -----
# Kernel smoothing
# -----
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Kernel smoothing w/ uniform kernel")

xOut <- xSeq(cn, by=10)
cnSa <- kernelSmoothing(cn, xOut=xOut, kernel="uniform", h=2)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- kernelSmoothing(cn, xOut=xOut, kernel="uniform", h=5)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"), sprintf(c("raw [n=%d]", "U(w=2) [n=%d]", "U(w=5) [n=%d]"), n, n, n))

```

RawGenomicSignals *The RawGenomicSignals class*

Description

Package: aroma.core

Class RawGenomicSignals

Object

~~|

~~+--RawGenomicSignals

Directly known subclasses:

[RawAlleleBFractions](#), [RawCopyNumbers](#), [RawMirroredAlleleBFractions](#), [RawSequenceReads](#), [SegmentedAlleleBFractions](#), [SegmentedCopyNumbers](#)

```
public static class RawGenomicSignals
  extends Object
```

Usage

```
RawGenomicSignals(y=NULL, x=NULL, w=NULL, chromosome=NA, name=NULL, ...)
```

Arguments

| | |
|------------|---|
| y | A numeric vector of length J specifying the signal at each locus. |
| x | A (optional) numeric vector of length J specifying the position of each locus. |
| w | A (optional) non-negative numeric vector of length J specifying a weight of each locus. |
| chromosome | An (optional) integer specifying the chromosome for these genomic signals. |
| name | An (optional) character string specifying the sample name. |
| ... | Not used. |

Fields and Methods

Methods:

| | |
|---|---|
| - | - |
| * | - |
| + | - |
| addBy | - |
| addLocusFields | - |
| append | - |
| as.data.frame | - |
| binnedSmoothing | - |
| divideBy | - |
| drawDensity | - |
| estimateStandardDeviation | Estimates the standard deviation of the raw Ys. |
| extractRegion | - |
| extractRegions | - |
| extractSubset | - |
| gaussianSmoothing | - |
| getChromosome | - |
| getLocusFields | - |
| getName | - |
| getPositions | - |
| getSigma | - |
| getSignals | - |
| getWeights | - |
| getXScale | - |
| getXY | - |
| getYScale | - |

| | |
|------------------|---|
| hasWeights | - |
| kernelSmoothing | - |
| lines | - |
| multiplyBy | - |
| nbrOfLoci | - |
| plot | - |
| points | - |
| segmentByCBS | Segment copy numbers using the CBS method. |
| segmentByGLAD | Segment copy numbers using the GLAD method. |
| segmentByHaarSeg | Segment copy numbers using the HaarSeg method. |
| segmentByMPCBS | Segment copy numbers using the multi-platform CBS (mpCBS) method. |
| setLocusFields | - |
| setName | - |
| setSigma | - |
| setWeights | - |
| setXScale | - |
| setYScale | - |
| signalRange | - |
| sort | - |
| subtractBy | - |
| summary | - |
| xMax | - |
| xMin | - |
| xRange | - |
| xSeq | - |
| yMax | - |
| yMin | - |
| yRange | - |

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/>)

RawMirroredAlleleBFractions

The RawMirroredAlleleBFractions class

Description

Package: aroma.core

Class RawMirroredAlleleBFractions**Object**

```

~~|
~~+--RawGenomicSignals
~~~~~|
~~~~~+--RawAlleleBFractions
~~~~~|
~~~~~+--RawMirroredAlleleBFractions

```

Directly known subclasses:

public static class **RawMirroredAlleleBFractions**
 extends [RawAlleleBFractions](#)

Usage

```
RawMirroredAlleleBFractions(...)
```

Arguments

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

Fields and Methods**Methods:**

plot -

Methods inherited from RawAlleleBFractions:

extractRawMirroredAlleleBFractions, plot

Methods inherited from RawGenomicSignals:

-, *, +, addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, drawDensity, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getX, getY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

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/>)

RawSequenceReads *The RawSequenceReads class*

Description

Package: aroma.core

Class RawSequenceReads

Object

```

~~|
~~+--RawGenomicSignals
~~~~~|
~~~~~+--RawSequenceReads

```

Directly known subclasses:

```

public static class RawSequenceReads
extends RawGenomicSignals

```

Usage

```
RawSequenceReads(x=NULL, y=rep(1, length(x)), ...)
```

Arguments

| | |
|-----|---|
| x | An integer vector of length J specifying the read positions. |
| y | An (optional) integer vector of length J specifying the number of reads at each position. Default is one read per position. |
| ... | Arguments passed to RawGenomicSignals . |

Fields and Methods**Methods:**

```

binnedSums          -
extractRawCopyNumbers -
nbrOfReads          -
plot                -

```

Methods inherited from RawGenomicSignals:

-, *, +, addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, drawDensity, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getX, getY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

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/>)

SegmentedAlleleBFractions

The SegmentedAlleleBFractions class

Description

Package: aroma.core

Class SegmentedAlleleBFractions

Object

```

~~|
~~+--RawGenomicSignals
~~~~~|
~~~~~+--RawAlleleBFractions
~~~~~|
~~~~~+--SegmentedGenomicSignalsInterface
~~~~~|

```

```
~~~~~+---SegmentedAlleleBFractions
```

Directly known subclasses:

```
public static class SegmentedAlleleBFractions
  extends SegmentedGenomicSignalsInterface
```

Usage

```
SegmentedAlleleBFractions(..., states=NULL)
```

Arguments

```
...           Arguments passed to RawAlleleBFractions.
states       A function returning the copy-number states given a vector of locus positions.
```

Fields and Methods

Methods:

No methods defined.

Methods inherited from [SegmentedGenomicSignalsInterface](#):

as.data.frame, binnedSmoothingByState, extractSubsetByState, getStateColorMap, getStateColors, getStates, getUniqueStates, kernelSmoothingByState, plot, points, setStateColorMap, setStates

Methods inherited from [RawAlleleBFractions](#):

extractRawMirroredAlleleBFractions, plot

Methods inherited from [RawGenomicSignals](#):

-, *, +, addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, drawDensity, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXy, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

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/>)

SegmentedCopyNumbers *The SegmentedCopyNumbers class*

Description

Package: aroma.core

Class SegmentedCopyNumbers

Object

```

~|
~+--RawGenomicSignals
~~~~~|
~~~~~+--RawCopyNumbers
~~~~~|
~~~~~+--SegmentedGenomicSignalsInterface
~~~~~|
~~~~~+--SegmentedCopyNumbers

```

Directly known subclasses:

```

public static class SegmentedCopyNumbers
extends SegmentedGenomicSignalsInterface

```

Usage

```
SegmentedCopyNumbers(..., states=NULL)
```

Arguments

```

...           Arguments passed to RawCopyNumbers.
states       A function returning the copy-number states given a vector of locus positions.

```

Fields and Methods

Methods:

No methods defined.

Methods inherited from SegmentedGenomicSignalsInterface:

as.data.frame, binnedSmoothingByState, extractSubsetByState, getStateColorMap, getStateColors, getStates, getUniqueStates, kernelSmoothingByState, plot, points, setStateColorMap, setStates

Methods inherited from RawCopyNumbers:

as.data.frame, cnRange, extractRawCopyNumbers, getCn, getCNs, plot

Methods inherited from RawGenomicSignals:

-, *, +, addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, drawDensity, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

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

```
# -----
# Simulating copy-number data
# -----
# True CN states
stateFcn <- function(x, ...) {
  states <- integer(length(x))
  states[200 <= x & x <= 300] <- -1L
  states[650 <= x & x <= 800] <- +1L
  states
}

# Number of loci
J <- 1000

y <- rnorm(J, sd=1/2)
x <- 1:length(y)
for (state in c(-1,+1)) {
  idxs <- (stateFcn(x) == state)
  y[idxs] <- y[idxs] + state
}

cn <- SegmentedCopyNumbers(y, x, states=stateFcn)
print(cn)

# -----
# Subsetting
# -----
plot(cn, ylim=c(-4,4))
title("Copy numbers annotated by state (and subset by state)")
```

```

cnS <- extractSubsetByState(cn, states=c(0,+1L))
print(cnS)
points(cnS, pch=21, cex=1.2, lwd=2, col="purple")

legend("topright", pch=c(19, 21), col=c("#999999", "purple"), sprintf(c("raw [n=%d]", "CN in {0,1} [n=%d]"), c(nbr

# - - - - -
# Kernel smoothing stratified by state
# - - - - -
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Kernel smoothing stratified by state w/ Gaussian kernel")

cnSa <- kernelSmoothingByState(cn, h=2)
points(cnSa, col="blue")

cnSb <- kernelSmoothingByState(cn, h=5)
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"), sprintf(c("raw [n=%d]", "N(.,sd=2) [n=%d]", "N(.,sd=5

# - - - - -
# Binned smoothing stratified by state
# - - - - -
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Binned smoothing stratified by state")

cnSa <- binnedSmoothingByState(cn, by=3)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- binnedSmoothingByState(cn, by=9)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"), sprintf(c("raw [n=%d]", "Bin(w=3) [n=%d]", "Bin(w=9) [

```

SegmentedGenomicSignalsInterface

The SegmentedGenomicSignalsInterface class interface

Description

Package: aroma.core

Class SegmentedGenomicSignalsInterface

[Interface](#)

~~|

~+--SegmentedGenomicSignalsInterface

Directly known subclasses:

[SegmentedAlleleBFractions](#), [SegmentedCopyNumbers](#)

public class **SegmentedGenomicSignalsInterface**
 extends [Interface](#)

Usage

SegmentedGenomicSignalsInterface(...)

Arguments

... Not used.

Fields and Methods

Methods:

| | |
|------------------------|---|
| as.data.frame | - |
| binnedSmoothingByState | - |
| extractSubsetByState | - |
| getStateColorMap | - |
| getStateColors | - |
| getStates | - |
| getUniqueStates | - |
| kernelSmoothingByState | - |
| plot | - |
| points | - |
| setStateColorMap | - |
| setStates | - |

Methods inherited from Interface:

extend, print, uses

Author(s)

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

UnitAnnotationDataFile

The UnitAnnotationDataFile interface class

Description

Package: aroma.core

Class UnitAnnotationDataFile**Interface**

~~|

~~+--UnitAnnotationDataFile

Directly known subclasses:

[AromaUflFile](#), [AromaUgpFile](#), [AromaUnitChromosomeTabularBinaryFile](#), [AromaUnitTabularBinaryFile](#), [AromaUnitTypesFile](#), [TextUnitNamesFile](#), [UnitNamesFile](#), [UnitTypesFile](#)

public static class **UnitAnnotationDataFile**

extends [Interface](#)

A UnitAnnotationDataFile provides methods for querying certain types of chip type annotation data by units.

Usage

```
UnitAnnotationDataFile(...)
```

Arguments

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

Methods**Methods:**

| | |
|-----------------|---|
| byChipType | - |
| getAromaUflFile | - |
| getAromaUgpFile | - |
| getChipType | - |
| getPlatform | - |
| nbrOfUnits | - |

Methods inherited from Interface:

extend, print, uses

Author(s)

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

UnitNamesFile *The UnitNamesFile interface class*

Description

Package: aroma.core

Class UnitNamesFile[Interface](#)

~~|

~~+--[UnitAnnotationDataFile](#)

~~~~~|

~~~~~+--UnitNamesFile

Directly known subclasses:[TextUnitNamesFile](#)public abstract static class **UnitNamesFile**extends [UnitAnnotationDataFile](#)

A UnitNamesFile provides methods for querying the unit names of a given chip type.

Usage

UnitNamesFile(...)

Arguments... Arguments passed to [UnitAnnotationDataFile](#).**Methods****Methods:**

```

getUnitNames -
indexOf      Gets the indices of units by their names.
nbrOfUnits  -

```

Methods inherited from UnitAnnotationDataFile:

byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from Interface:

extend, print, uses

Author(s)

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

UnitTypesFile

The UnitTypesFile interface class

Description

Package: aroma.core

Class UnitTypesFile

Interface

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~~+--UnitAnnotationDataFile

~~~~~|

~~~~~+--UnitTypesFile

Directly known subclasses:

[AromaUnitTypesFile](#)

public abstract static class **UnitTypesFile**

extends [UnitAnnotationDataFile](#)

A UnitTypesFile provides methods for querying the unit types of a given chip type, e.g. genotyping or copy-number unit, exon unit etc.

Usage

UnitTypesFile(...)

Arguments

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

Methods

Methods:

getUnitTypes -

nbrOfUnits -

Methods inherited from UnitAnnotationDataFile:

byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform,

nbrOfUnits

Methods inherited from Interface:

extend, print, uses

The aroma unit-type map

unknown=0, expression=1, genotyping=2, resequencing=3, tag=4, copynumber=5, genotypingcontrol=6, expressioncontrol=7

Author(s)

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

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