

Package ‘ACNE’

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Version 0.8.1

Depends R (>= 3.0.0), aroma.affymetrix (>= 2.14.0)

Imports MASS, R.methodsS3 (>= 1.7.0), R.oo (>= 1.19.0), R.utils (>= 2.1.0), matrixStats (>= 0.14.2), R.filesets (>= 2.9.0),
aroma.core (>= 2.14.0)

Suggests DNACopy

Date 2015-10-26

Title Affymetrix SNP Probe-Summarization using Non-Negative Matrix
Factorization

Description A summarization method to estimate allele-
specific copy number signals for Affymetrix SNP microarrays using non-
negative matrix factorization (NMF).

License LGPL (>= 2.1)

URL <https://github.com/HenrikBengtsson/ACNE>

BugReports <https://github.com/HenrikBengtsson/ACNE/issues>

LazyLoad TRUE

biocViews aCGH, CopyNumberVariants, SNP, Microarray, OneChannel,
TwoChannel, Genetics

NeedsCompilation no

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ACNE-package *Package ACNE*

Description

A summarization method to estimate allele-specific copy number signals for Affymetrix SNP microarrays using non-negative matrix factorization (NMF).

Installation and updates

This package requires the **aroma.affymetrix** package. To install this package, do: `install.packages("ACNE")`

To get started

1. For a one-command pipeline, see the `doACNE()` method.
2. For other usages, see the `NmfP1m` class.

License

LGPL (>= 2.1)

Author(s)

Maria Ortiz, Henrik Bengtsson, Angel Rubio

References

[1] M. Ortiz-Estevez, H. Bengtsson, A. Rubio, *ACNE: a summarization method to estimate allele-specific copy numbers for Affymetrix SNP arrays*, *Bioinformatics*, 2010 [PMC2913655].

doACNE (*ACNE*)

Description

(ACNE) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems.

Usage

```
## S3 method for class 'AffymetrixCelSet'
doACNE(csR, fln=FALSE, drop=TRUE, verbose=FALSE, ...)
## Default S3 method:
doACNE(dataSet, ..., verbose=FALSE)
```

Arguments

csR, dataSet	An AffymetrixCelSet (or the name of an AffymetrixCelSet).
fln	If <code>TRUE</code> , CRMAv2-style PCR fragment-length normalization is performed, otherwise not.
drop	If <code>TRUE</code> , the RMA summaries are returned, otherwise a named <code>list</code> of all intermediate and final results.
verbose	See Verbose .
...	Additional arguments used to set up AffymetrixCelSet (when argument <code>dataSet</code> is specified).

Value

Returns a named `list`, iff `drop == FALSE`, otherwise a named `list` of [AromaUnitTotalCnBinarySet](#) and [AromaUnitFracBCnBinarySet](#).

Author(s)

Henrik Bengtsson

References

[1] M. Ortiz-Estevez, H. Bengtsson, A. Rubio, *ACNE: a summarization method to estimate allele-specific copy numbers for Affymetrix SNP arrays*, *Bioinformatics*, 2010 [PMC2913655].

NmfPlm

The NmfPlm class

Description

Package: ACNE

Class NmfPlm

[Object](#)

```

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

```

```
~~~~~+--NmfPlm
```

Directly known subclasses:

[NmfSnpPlm](#)

```
public abstract static class NmfPlm
extends ProbeLevelModel
```

This class represents the NMF model of [REF].

Usage

```
NmfPlm(..., maxIter=10L, maxIterRlm=20L, refs=NULL, flavor=c("v4", "v3", "v2", "v1"))
```

Arguments

...	Arguments passed to ProbeLevelModel .
maxIter	The maximum number of iteration in the NMF step.
maxIterRlm	A positive integer specifying the maximum number of iterations used in rlm.
refs	An index vector (integer or logical) specifying the reference samples. If NULL , all samples are used as a reference.
flavor	(Internal/developmental only) A character string specifying which algorithm to use.

Fields and Methods

Methods:

```
getAsteriskTags -
```

Methods inherited from [ProbeLevelModel](#):

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

Methods inherited from [MultiArrayUnitModel](#):

getListOfPriors, setListOfPriors, validate

Methods inherited from [UnitModel](#):

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from [Model](#):

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

Methods inherited from [ParametersInterface](#):

getParameterSets, getParameters, getParametersAsString

Methods inherited from [Object](#):

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,

equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

References

[1] M. Ortiz-Estevez, H. Bengtsson, A. Rubio, *ACNE: a summarization method to estimate allele-specific copy numbers for Affymetrix SNP arrays*, Bioinformatics, 2010 [PMC2913655].

See Also

Internally, for each SNP the NMF model is fitted using the [fitSnpNmf\(\)](#) function.

NmfSnpPlm

The NmfSnpPlm class

Description

Package: ACNE

Class NmfSnpPlm

Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--NmfPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--NmfSnpPlm

```

Directly known subclasses:

```
public abstract static class NmfSnpPlm
  extends SnpPlm
```

Usage

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

Arguments

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

Fields and Methods

Methods:

No methods defined.

Methods inherited from SnpPlm:

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from NmfPlm:

getAsteriskTags

Methods inherited from ProbeLevelModel:

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

Methods inherited from MultiArrayUnitModel:

getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:

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

Methods inherited from ParametersInterface:

getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:

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

Author(s)

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