

Package ‘ACNE’

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Version 0.7.0

Depends R (>= 2.15.0), aroma.affymetrix (>= 2.11.0)

Imports MASS, R.methodsS3 (>= 1.5.2), R.oo (>= 1.15.8), R.utils (>= 1.27.1), matrixStats (>= 0.8.12), R.filesets (>= 2.3.0)

Date 2013-10-17

Title Affymetrix SNP probe-summarization using non-negative matrix factorization

Description Package for NMF summarization of SNP probes.

License LGPL (>= 2.1)

URL <http://r-forge.r-project.org/projects/snpsprocessing/>

LazyLoad TRUE

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 ACNE-package

Package ACNE

Description

Package for NMF summarization of SNP probes.

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, getParameterSet, 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, gc, 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	<i>The NmfSnpPlm class</i>
-----------	----------------------------

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, getParameterSet, 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, gc, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

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