

Package: ACNE (via r-universe)

October 14, 2024

Version 0.9.1

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

Imports MASS, R.methodsS3 (>= 1.7.0), R.oo (>= 1.23.0), R.utils (>= 2.1.0), matrixStats (>= 0.50.0), R.filesets (>= 2.9.0),
aroma.core (>= 2.14.0)

Suggests DNACopy

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

Repository <https://henrikbengtsson.r-universe.dev>

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

RemoteRef master

RemoteSha 7f31698ad03921f03eb33497f6054a78f89695bd

Contents

ACNE-package	2
doACNE	2
NmfPlm	3
NmfSnpPlm	5
Index	7

 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).
f1n	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 <a href="#">ProbeLevelModel</a> .                                                                                                                                   |
| maxIter    | The maximum number of iteration in the NMF step.                                                                                                                                        |
| maxIterRlm | A positive <a href="#">integer</a> specifying the maximum number of iterations used in rlm.                                                                                             |
| refs       | An index <a href="#">vector</a> ( <a href="#">integer</a> or <a href="#">logical</a> ) specifying the reference samples. If <a href="#">NULL</a> , all samples are used as a reference. |
| flavor     | (Internal/developmental only) A <a href="#">character</a> 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, names, 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, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

# Index

## \* classes

NmfPlm, 3

NmfSnpPlm, 5

## \* package

ACNE-package, 2

ACNE (ACNE-package), 2

ACNE-package, 2

AffymetrixCelSet, 3

AromaUnitFracBCnBinarySet, 3

AromaUnitTotalCnBinarySet, 3

character, 4

doACNE, 2, 2

fitSnpNmf, 5

integer, 4

list, 3

logical, 4

Model, 3, 5

MultiArrayUnitModel, 3, 5

NmfPlm, 2, 3, 5, 6

NmfSnpPlm, 4, 5

NULL, 4

Object, 3, 5

ParametersInterface, 3, 5

ProbeLevelModel, 3–5

SnpPlm, 5, 6

TRUE, 3, 6

UnitModel, 3, 5

vector, 4

Verbose, 3