

# Package ‘ACNE’

October 27, 2015

**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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**Repository** CRAN

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## R topics documented:

|                        |   |
|------------------------|---|
| ACNE-package . . . . . | 2 |
| doACNE . . . . .       | 2 |
| NmfPlm . . . . .       | 3 |
| NmfSnpPlm . . . . .    | 5 |

**Index****7**


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ACNE-package                      *Package ACNE*

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**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].

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doACNE                                      (*ACNE*)

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**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 <a href="#">AffymetrixCelSet</a> (or the name of an <a href="#">AffymetrixCelSet</a> ).  |
| 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 <a href="#">Verbose</a> .   |
| ...          | Additional arguments used to set up <a href="#">AffymetrixCelSet</a> (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].

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NmfPlm

*The NmfPlm class*

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**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, 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.

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NmfSnpPlm

*The NmfSnpPlm class*

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### 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)

Henrik Bengtsson

# Index

## \*Topic **classes**

NmfPlm, [3](#)

NmfSnpPlm, [5](#)

## \*Topic **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](#)