Package 'ACNE'

January 20, 2025

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

NeedsCompilation no

Author Maria Ortiz [aut],
Henrik Bengtsson [aut, cre, cph],
Angel Rubio [aut]

Maintainer Henrik Bengtsson `<henrikb@braju.com>`

Repository CRAN

Date/Publication 2024-02-17 21:10:22 UTC

Contents

`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 `NmfPlm` 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 `TRUE`, CRMAv2-style PCR fragment-length normalization is performed, otherwise not.
`drop`	If `TRUE`, the RMA summaries are returned, otherwise a named `list` of all intermediate and final results.
`verbose`	See `Verbose`.
`...`	Additional arguments used to set up `AffymetrixCelSet` (when argument `dataSet` 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, 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