Package ‘aroma.core’

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Depends R (>= 3.2.1), R.utils (>= 2.10.1), R.filesets (>= 2.14.0), R.devices (>= 2.16.1)

DependsNote BioC (>= 3.2)

Imports stats, tools, utils, R.methodsS3 (>= 1.8.1), R.oo (>= 1.24.0), R.cache (>= 0.14.0), R.rsp (>= 0.44.0), matrixStats (>= 0.57.0), RColorBrewer (>= 1.1-2), PSCBS (>= 0.65.0), listenv, future, BiocManager

Suggests KernSmooth, png (>= 0.1-7), Cairo (>= 1.5-9), EBImage (>= 4.8.3), preprocessCore (>= 1.28.0), aroma.light (>= 2.2.1), DNAcopy (>= 1.40.0), GLAD (>= 2.30.0), sfit (>= 0.1.8), expectile (>= 0.2.5), HaarSeg (>= 0.0.2), mpcbs (>= 1.1.1)

SuggestsNote BioC (>= 3.0), Recommended: aroma.light, DNAcopy, png, preprocessCore, sfit

Additional_repositories `https://henrikbengtsson.r-universe.dev`, `https://r-forge.r-project.org`

Title Core Methods and Classes Used by 'aroma.*' Packages Part of the Aroma Framework

Description Core methods and classes used by higher-level 'aroma.*' packages part of the Aroma Project, e.g. 'aroma.affymetrix' and 'aroma.cn'.

License LGPL (>= 2.1)

URL `https://github.com/HenrikBengtsson/aroma.core`, `https://www.aroma-project.org/`

BugReports `https://github.com/HenrikBengtsson/aroma.core/issues`

LazyLoad TRUE

biocViews Microarray, OneChannel, TwoChannel, MultiChannel, DataImport, DataRepresentation, GUI, Visualization, Preprocessing, QualityControl, aCGH, CopyNumberVariants

NeedsCompilation no

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Repository CRAN

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R topics documented:

`aroma.core-package` *Package aroma.core*

Description

Core methods and classes used by higher-level 'aroma.*' packages part of the Aroma Project, e.g. 'aroma.affymetrix' and 'aroma.cn'.

This package is a support package for **aroma.affymetrix**. This package should be considered to be in an alpha or beta phase. You should expect the API to be changing over time. For practical purposes, consider this package a private package.

Installation and updates

This package is available on CRAN, i.e. to install do `install.packages("aroma.core")`.

License

The releases of this package is licensed under LGPL version 2.1 or newer.

The development code of the packages is under a private licence (where applicable) and patches sent to the author fall under the latter license, but will be, if incorporated, released under the "release" license above.

Author(s)

Henrik Bengtsson

References

[1] H. Bengtsson, *The R.oo package - Object-Oriented Programming with References Using Standard R Code*, In Kurt Hornik, Friedrich Leisch and Achim Zeileis, editors, Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), March 20-22, Vienna, Austria. `https://www.r-project.org/conferences/DSC-2003/Proceedings/`

`AbstractCNData` *The AbstractCNData class*

Description

Package: aroma.core
Class AbstractCNData

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AbstractCNData
```

Directly known subclasses:
AbstractPSCNData, NonPairedPSCNData, PairedPSCNData

public class **AbstractCNData**
extends RawGenomicSignals

An AbstractCNData object holds copy number data.

Usage

```
AbstractCNData(chromosome=NULL, x=NULL, y=NULL, ..., name=NULL, .virtuals=NULL)
```

Arguments

`chromosome`	(Optional) An `integer` scalar (or a `vector` of length J), which can be used to specify which chromosome each locus belongs to in case multiple chromosomes are segments. This argument is also used for annotation purposes.
`x`	Optional `numeric` `vector` of J genomic locations. If `NULL`, index locations `1:J` are used.
`y`	Optional `numeric` `vector` of J genomic locations.
`...`	Optional named locus-specific signal `vector`s of length J.
`name`	Optional `character` string.
`.virtuals`	(Internal) a `list` with virtual column name `function`s.

Fields and Methods

Methods:

`findLargeGaps`	-
`getChipType`	-
`getLocusData`	-
`getPlatform`	-
`setChipType`	-
`setPlatform`	-

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`AbstractPSCNData` *The AbstractPSCNData class*

Description

Package: aroma.core
Class AbstractPSCNData

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AbstractCNData
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AbstractPSCNData
```

Directly known subclasses:
NonPairedPSCNData, PairedPSCNData

public class **AbstractPSCNData**
extends AbstractCNData

A AbstractPSCNData object holds parent-specific copy number data.

Usage

```
AbstractPSCNData(chromosome=NULL, x=NULL, isSNP=NULL, mu=NULL, ...)
```

Arguments

`chromosome`	(Optional) An `integer` scalar (or a `vector` of length J), which can be used to specify which chromosome each locus belongs to in case multiple chromosomes are segments. This argument is also used for annotation purposes.
`x`	Optional `numeric` `vector` of J genomic locations. If `NULL`, index locations `1:J` are used.
`isSNP`	An optional `logical` `vector` of length J specifying whether each locus is a SNP or not (non-polymorphic loci).
`mu`	An optional `numeric` `vector` of J genotype calls in {0,1/2,1} for AA, AB, and BB, respectively, and `NA` for non-polymorphic loci.
`...`	Optional named locus-specific signal `vector`s of length J.

Fields and Methods

Methods:
No methods defined.

Methods inherited from AbstractCNData:
findLargeGaps, getChipType, getLocusData, getPlatform, hasKnownPositions, orderAlongGenome, setChipType, setPlatform

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`AromaCellCpgFile` *A binary file holding local CpG density for each cell (probe/feature)*

Description

A binary file holding local CpG density for each cell (probe/feature).

Usage

```
AromaCellCpgFile(...)
```

Arguments

`...`	Arguments passed to constructor of `AromaCellTabularBinaryFile`.

Details

Note that this class does *not* assume a rectangular chip layout. In other words, there is no concept of mapping a *spatial* location on the array to a cell index and vice versa. The reason for this to be able to use this class also for non-rectangular chip types.

Author(s)

Mark Robinson

`AromaCellPositionFile` *A binary file holding chromosome/position for each cell*

Description

A binary file holding chromosome/position for each cell.

Usage

```
AromaCellPositionFile(...)
```

Arguments

`...`	Arguments passed to constructor of `AromaCellTabularBinaryFile`.

Details

Note that this class does *not* assume a rectangular chip layout. In other words, there is no concept of mapping a *spatial* location on the array to a cell index and vice versa. The reason for this to be able to use this class also for non-rectangular chip types.

Author(s)

Henrik Bengtsson

`AromaCellTabularBinaryFile`

The AromaCellTabularBinaryFile class

Description

Package: aroma.core
Class AromaCellTabularBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaCellTabularBinaryFile
```

Directly known subclasses:
AromaCellCpgFile, AromaCellPositionFile, AromaCellSequenceFile

public abstract static class **AromaCellTabularBinaryFile**
extends *AromaMicroarrayTabularBinaryFile*

An AromaCellTabularBinaryFile is an `AromaTabularBinaryFile` with the constraint that the rows map one-to-one to the cells (features) of a microarray.

Usage

```
AromaCellTabularBinaryFile(...)
```

Arguments

`...`	Arguments passed to `AromaTabularBinaryFile`.

Fields and Methods

Methods:

`byChipType`	-
`nbrOfCells`	-

Methods inherited from AromaMicroarrayTabularBinaryFile:
allocate, as.character, byChipType, findByChipType, getChipType, getFilenameExtension, getPlatform

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

See Also

`AromaUnitTabularBinaryFile`.

`AromaGenomeTextFile` *The AromaGenomeTextFile class*

Description

Package: aroma.core
Class AromaGenomeTextFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--TabularTextFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaGenomeTextFile
```

Directly known subclasses:
AromaUcscGenomeTextFile

public abstract static class **AromaGenomeTextFile**
extends FileCacheKeyInterface

An AromaGenomeTextFile represents a annotation tabular text file that specifies the number of bases (nucleotides) per chromosome for a particular genome/organism.

Usage

```
AromaGenomeTextFile(...)
```

Arguments

`...`	Arguments passed to `TabularTextFile`.

Details

An AromaGenomeTextFile is a tab-delimited text file with a header containing (at least) column names 'chromosome' and 'nbrOfBases'. The 'chromosome' column specifies the chromosomes (character strings) and the 'nbrOfBases' column specifies the lengths (integer) of the chromosomes in number of bases (nucleotides).

The filename of an AromaGenomeTextFile should have format "<genome>,chromosomes(,<tag>)*.txt", and be located in annotationData/genomes/<genome>/, e.g. annotationData/genomes/Human/Human,chromosomes,max,200

Fields and Methods

Methods:

`byGenome`	-
`readDataFrame`	-

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from TabularTextFile:
as.character, getCommentChar, getDefaultColumnClassPatterns, getDefaultColumnClasses, getDefaultColumnNames, getHeader, getReadArguments, hasColumnHeader, nbrOfLines, nbrOfRows, readColumnNames, readColumns, readDataFrame, readLines, readRawHeader, setCommentChar

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:

appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

Examples

```
# Locate a Human,chromosomes(,.*)*.txt file
db <- AromaGenomeTextFile$byGenome("Human")
print(db)

# Read the data
df <- readDataFrame(db)
print(df)
str(df)

# Details on the file format
oopts <- options(width=40)
print(readLines(db))
options(oopts)
```

`AromaMicroarrayDataFile` *The abstract AromaMicroarrayDataFile class*

Description

Package: aroma.core
Class AromaMicroarrayDataFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
```

Directly known subclasses:

public abstract static class **AromaMicroarrayDataFile**
extends FileCacheKeyInterface

An AromaMicroarrayDataFile object represents a single microarray data file. Each such file originates from a specific chip type on a given platform.

Usage

```
AromaMicroarrayDataFile(...)
```

Arguments

`...`	Arguments passed to `GenericDataFile`.

Fields and Methods

Methods:

`getChipType`	-
`getPlatform`	-
`isAverageFile`	-

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

See Also

An object of this class is typically part of an `AromaMicroarrayDataSet`.

`AromaMicroarrayDataSet`

The AromaMicroarrayDataSet class

Description

Package: aroma.core
Class AromaMicroarrayDataSet

```
Object
~~|
~~+--FullNameInterface
```

```
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
```

Directly known subclasses:

public abstract static class **AromaMicroarrayDataSet**
extends GenericDataFileSet

An AromaMicroarrayDataSet object represents a set of `AromaMicroarrayDataFile`s with *identical* chip types.

Usage

```
AromaMicroarrayDataSet(files=NULL, ...)
```

Arguments

`files`	A `list` of `AromaMicroarrayDataFile`:s.
`...`	Arguments passed to `GenericDataFileSet`.

Fields and Methods

Methods:

`as.AromaMicroarrayDataSetList`	-
`as.AromaMicroarrayDataSetTuple`	-
`getAverageFile`	-
`getChipType`	-
`getPlatform`	-

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaMicroarrayDataSetTuple`

The AromaMicroarrayDataSetTuple class

Description

Package: aroma.core
Class AromaMicroarrayDataSetTuple

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSetList
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSetTuple
```

Directly known subclasses:
AromaUnitTotalCnBinarySetTuple

public abstract static class **AromaMicroarrayDataSetTuple**
extends GenericDataFileSetList

Usage

```
AromaMicroarrayDataSetTuple(..., .setClass="AromaMicroarrayDataSet")
```

Arguments

`...`	Arguments passed to `GenericDataFileSetList`.
`.setClass`	The name of the class of the input set.

Fields and Methods

Methods:

`as`	-
`as.AromaMicroarrayDataSetTuple`	-
`getChipTypes`	-
`getFullNames`	-
`getSets`	-
`getTags`	-
`nbrOfChipTypes`	Gets the number of chip types.

Methods inherited from GenericDataFileSetList:
as, as.GenericDataFileSetList, as.character, as.data.frame, as.list, assertDuplicates, clone, extract, getAsteriskTags, getDefaultFullName, getFileList, getFileListClass, getFullNames, getNames, getSet, getSets, getTags, indexOf, length, nbrOfFiles, nbrOfSets, setTags

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaMicroarrayTabularBinaryFile`

The AromaMicroarrayTabularBinaryFile class

Description

Package: aroma.core
Class AromaMicroarrayTabularBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayTabularBinaryFile
```

Directly known subclasses:
AromaCellCpgFile, AromaCellPositionFile, AromaCellSequenceFile, *AromaCellTabularBinaryFile*, AromaUflFile, AromaUgcFile, AromaUgpFile, *AromaUnitChromosomeTabularBinaryFile*, AromaUnitGcContentFile, *AromaUnitTabularBinaryFile*

public abstract static class **AromaMicroarrayTabularBinaryFile**
extends *AromaPlatformInterface*

An AromaMicroarrayTabularBinaryFile is an abstract `AromaTabularBinaryFile`.

Usage

```
AromaMicroarrayTabularBinaryFile(...)
```

Arguments

`...`	Arguments passed to `AromaTabularBinaryFile`.

Fields and Methods

Methods:

`byChipType`	-

`getChipType`	-
`getFilenameExtension`	-
`getPlatform`	-

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

See Also

`AromaTabularBinaryFile`.

`AromaPlatform` *The AromaPlatform class*

Description

Package: aroma.core
Class AromaPlatform

```
Object
~~|
~~+--AromaPlatform
```

Directly known subclasses:

public abstract static class **AromaPlatform**
extends Object

An AromaPlatform provides methods for a given platform, e.g. Affymetrix, Agilent, Illumina.

Usage

```
AromaPlatform(...)
```

Arguments

`...`	Not used.

Methods

Methods:

`byName`	-
`equals`	-
`getAromaUgpFile`	-

```
getName           -
getUnitNamesFile  -
getUnitTypesFile  -
```

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

Examples

```
## Not run:
 library("aroma.affymetrix")
platform <- AromaPlatform$byName("Affymetrix")
print(platform)
stopifnot(getName(platform) == "Affymetrix")


## End(Not run)
```

`AromaPlatformInterface`

The AromaPlatformInterface class

Description

Package: aroma.core
Class AromaPlatformInterface

```
Interface
~~|
~~+--AromaPlatformInterface
```

Directly known subclasses:
AromaCellCpgFile, AromaCellPositionFile, AromaCellSequenceFile, *AromaCellTabularBinaryFile*, *AromaMicroarrayTabularBinaryFile*, AromaUflFile, AromaUgcFile, AromaUgpFile, AromaUnitCallFile, *AromaUnitChromosomeTabularBinaryFile*, AromaUnitFracBCnBinaryFile, AromaUnitGcContentFile, AromaUnitGenotypeCallFile, *AromaUnitPscnBinaryFile*, AromaUnitSignalBinaryFile, *AromaUnitTabularBinaryFile*, *AromaUnitTotalCnBinaryFile*, AromaUnitTypesFile

public abstract class **AromaPlatformInterface**
extends Interface

An AromaPlatformInterface provides methods for a given platform, e.g. Affymetrix, Agilent, Illumina.

Usage

```
AromaPlatformInterface(...)
```

Arguments

`...`	Not used.

Methods

Methods:

`getAromaPlatform`	Gets the platform.
`getAromaUflFile`	-
`getAromaUgpFile`	-
`getChipType`	Gets the chip type.
`getPlatform`	Gets the platform.
`getUnitNamesFile`	-
`getUnitTypesFile`	-

Methods inherited from Interface:
extend, print, uses

Author(s)

Henrik Bengtsson

`AromaRepository` *The AromaRepository class*

Description

Package: aroma.core
Class AromaRepository

```
Object
~~|
~~+--AromaRepository
```

Directly known subclasses:

public static class **AromaRepository**
extends Object

An AromaRepository object provides methods for downloading annotation data from the Aroma repository.

Usage

```
AromaRepository(urlPath="https://www.aroma-project.org/data", verbose=FALSE, ...)
```

Arguments

`urlPath`	The URL to the Aroma repository.
`verbose`	The `Verbose` to be used during processing.
`...`	Not used.

Methods

Methods:

`downloadACC`	-
`downloadACM`	-
`downloadACP`	-
`downloadACS`	-
`downloadAll`	-
`downloadCDF`	-
`downloadChipTypeFile`	Download a particular chip type annotation file.
`downloadProbeSeqsTXT`	-
`downloadTXT`	-
`downloadUFL`	-
`downloadUGC`	-
`downloadUGP`	-

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

`AromaTabularBinaryFile` *The AromaTabularBinaryFile class*

Description

Package: aroma.core
Class AromaTabularBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
```

Directly known subclasses:
AromaCellCpgFile, AromaCellPositionFile, AromaCellSequenceFile, *AromaCellTabularBinaryFile*, *AromaMicroarrayTabularBinaryFile*, AromaUflFile, AromaUgcFile, AromaUgpFile, AromaUnitCallFile, *AromaUnitChromosomeTabularBinaryFile*, AromaUnitFracBCnBinaryFile, AromaUnitGcContentFile, AromaUnitGenotypeCallFile, *AromaUnitPscnBinaryFile*, AromaUnitSignalBinaryFile, *AromaUnitTabularBinaryFile*, *AromaUnitTotalCnBinaryFile*, AromaUnitTypesFile

public abstract static class **AromaTabularBinaryFile**
extends FileCacheKeyInterface

A AromaTabularBinaryFile represents a file with a binary format. It has a well defined header, a data section, and a footer.

Usage

```
AromaTabularBinaryFile(...)
```

Arguments

`...`	Arguments passed to `GenericTabularFile`.

Fields and Methods

Methods:

`[`	-
`[<-`	-
`colMeans`	-
`colSums`	-
`getBytesPerColumn`	-
`getColClasses`	-
`importFrom`	-
`nbrOfColumns`	-
`nbrOfRows`	-
`readColumns`	-
`readFooter`	Reads the file footer in XML format into a named nested list.
`subset`	-
`summary`	-
`writeFooter`	Writes a named nested list to the file footer in XML format.

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFull-

NameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

See Also

`GenericDataFile`.

`AromaTabularBinarySet` *The AromaTabularBinarySet class*

Description

Package: aroma.core
Class AromaTabularBinarySet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
```

Directly known subclasses:
AromaUnitCallSet, AromaUnitFracBCnBinarySet, AromaUnitGenotypeCallSet, AromaUnitPscnBinarySet, AromaUnitSignalBinarySet, AromaUnitTotalCnBinarySet

public static class **AromaTabularBinarySet**
extends GenericTabularFileSet

An AromaTabularBinarySet object represents a set of `AromaTabularBinaryFile`s with *identical* chip types.

Usage

```
AromaTabularBinarySet(files=NULL, ...)
```

Arguments

`files`	A `list` of `AromaTabularBinaryFile`:s.
`...`	Arguments passed to `GenericDataFileSet`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaTransform` *The AromaTransform class*

Description

Package: aroma.core
Class AromaTransform

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
```

Directly known subclasses:

public abstract static class **AromaTransform**
extends ParametersInterface

This abstract class represents a transform (algorithm/operator) that transforms data. A transform has an input data set, which is transformed into an output data set.

Usage

```
AromaTransform(dataSet=NULL, tags="*", ..., .reqSetClass="AromaMicroarrayDataSet")
```

Arguments

`dataSet`	The input data set as an `AromaMicroarrayDataSet`.
`tags`	A `character vector` of tags to be appended to the tags of the input data set.
`...`	Not used.
`.reqSetClass`	Internal argument.

Details

Subclasses must implement the `process()` method.

Fields and Methods

Methods:

`getFullName`	Gets the full name of the output data set.
`getInputDataSet`	Gets the input data set.

`getName`	Gets the name of the output data set.
`getOutputDataSet`	Gets the transformed data set.
`getPath`	Gets the path of the output directory.
`getRootPath`	Gets the root path of the output directory.
`getTags`	Gets the tags of the output data set.
`isDone`	Checks if the data set is processed or not.
`process`	Processes the data set.
`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

`AromaUnitCallFile` *The AromaUnitCallFile class*

Description

Package: aroma.core
Class AromaUnitCallFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitCallFile
```

Directly known subclasses:
AromaUnitGenotypeCallFile

public static class **AromaUnitCallFile**
extends AromaUnitSignalBinaryFile

An AromaUnitCallFile is a `AromaUnitSignalBinaryFile`.

Usage

```
AromaUnitCallFile(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinaryFile`.

Fields and Methods

Methods:

`extractCallArray`	-
`extractCalls`	-
`extractMatrix`	-
`findUnitsTodo`	-

Methods inherited from AromaUnitSignalBinaryFile:
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitCallSet` *The AromaUnitCallSet class*

Description

Package: aroma.core
Class AromaUnitCallSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinarySet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitCallSet
```

Directly known subclasses:
AromaUnitGenotypeCallSet

public static class **AromaUnitCallSet**
extends AromaUnitSignalBinarySet

An AromaUnitCallSet object represents a set of `AromaUnitCallFile`s with *identical* chip types.

Usage

```
AromaUnitCallSet(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinarySet`.

Fields and Methods

Methods:

`extractCallArray`	-
`extractCalls`	-
`extractGenotypeMatrix`	-
`findUnitsTodo`	-

Methods inherited from AromaUnitSignalBinarySet:
byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

Methods inherited from AromaTabularBinarySet:
getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitFracBCnBinaryFile`

The AromaUnitFracBCnBinaryFile class

Description

Package: aroma.core
Class AromaUnitFracBCnBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
```

```
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitFracBCnBinaryFile
```

Directly known subclasses:

public static class **AromaUnitFracBCnBinaryFile**
extends AromaUnitSignalBinaryFile

An AromaUnitFracBCnBinaryFile is a `AromaUnitTabularBinaryFile`.

Usage

```
AromaUnitFracBCnBinaryFile(...)
```

Arguments

`...`	Arguments passed to `AromaUnitTabularBinaryFile`.

Fields and Methods

Methods:

`extractRawAlleleBFractions` -

Methods inherited from AromaUnitSignalBinaryFile:
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitFracBCnBinarySet` *The AromaUnitFracBCnBinarySet class*

Description

Package: aroma.core
Class AromaUnitFracBCnBinarySet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinarySet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitFracBCnBinarySet
```

Directly known subclasses:

public static class **AromaUnitFracBCnBinarySet**
extends AromaUnitSignalBinarySet

An AromaUnitFracBCnBinarySet object represents a set of `AromaUnitFracBCnBinaryFile`s with *identical* chip types.

Usage

```
AromaUnitFracBCnBinarySet(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinarySet`.

Details

The term "allele B fraction" is also know as "allele B frequency", which was coined by Peiffer et al. (2006). Note that the term "frequency" is a bit misleading since it is not a frequency in neither the statistical nor the population sense, but rather only proportion relative to the total amount of allele A and allele B signals, which is calculated for each sample independently.

Fields and Methods

Methods:

`byName`	-
`writeDataFrame`	-

Methods inherited from AromaUnitSignalBinarySet:
byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

Methods inherited from AromaTabularBinarySet:
getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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] Peiffer et al., *High-resolution genomic profiling of chromosomal aberrations using Infinium whole-genome genotyping*, Genome Res, 2006.

`AromaUnitGenotypeCallFile`

The AromaUnitGenotypeCallFile class

Description

Package: aroma.core
Class AromaUnitGenotypeCallFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitCallFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitGenotypeCallFile
```

Directly known subclasses:

public static class **AromaUnitGenotypeCallFile**
extends AromaUnitCallFile

An AromaUnitGenotypeCallFile is a `AromaUnitTabularBinaryFile`.

Usage

```
AromaUnitGenotypeCallFile(...)
```

Arguments

`...`	Arguments passed to `AromaUnitTabularBinaryFile`.

Fields and Methods

Methods:

`extractGenotypeMatrix`	-
`extractGenotypes`	-
`isHeterozygous`	-
`isHomozygous`	-
`updateGenotypes`	-

Methods inherited from AromaUnitCallFile:
allocate, extractCallArray, extractCalls, extractMatrix, findUnitsTodo

Methods inherited from AromaUnitSignalBinaryFile:
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames,

getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitGenotypeCallSet`

The AromaUnitGenotypeCallSet class

Description

Package: aroma.core
Class AromaUnitGenotypeCallSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
```

```
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinarySet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitCallSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitGenotypeCallSet
```

Directly known subclasses:

public static class **AromaUnitGenotypeCallSet**
extends AromaUnitCallSet

An AromaUnitGenotypeCallSet object represents a set of `AromaUnitGenotypeCallFile`s with *identical* chip types.

Usage

```
AromaUnitGenotypeCallSet(...)
```

Arguments

`...`	Arguments passed to `AromaUnitCallSet`.

Fields and Methods

Methods:

`byName`	-	
`extractGenotypes`	-	

Methods inherited from AromaUnitCallSet:
byPath, extractCallArray, extractCalls, extractGenotypeMatrix, findByName, findUnitsTodo

Methods inherited from AromaUnitSignalBinarySet:
byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

Methods inherited from AromaTabularBinarySet:
getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorBy-

function, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitPscnBinaryFile`

The AromaUnitPscnBinaryFile class

Description

Package: aroma.core
Class AromaUnitPscnBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CopyNumberDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitPscnBinaryFile
```

Directly known subclasses:

public abstract static class **AromaUnitPscnBinaryFile**
extends *CopyNumberDataFile*

An AromaUnitPscnBinaryFile is a `AromaUnitSignalBinaryFile` that holds total copy number signals (TCNs) and allele B fractions (BAFs). The TCNs can either be on an unknown scale or ratios relative to a reference. The signals are always stored on the original scale, i.e. they are never stored on the logaritmic scale. The BAFs are always on a [0-eps,1+eps] scale, where eps >= 0.

Usage

```
AromaUnitPscnBinaryFile(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinaryFile`.

Fields and Methods

Methods:

`extractRawCopyNumbers` -
`hasAlleleBFractions` -
`hasStrandiness` -
`hasTotalCopyNumberRatios` -

Methods inherited from CopyNumberDataFile:
as, as.CopyNumberDataFile, getNumberOfFilesAveraged, hasAlleleBFractions, hasStrandiness

Methods inherited from AromaUnitSignalBinaryFile:
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitPscnBinarySet`

The AromaUnitPscnBinarySet class

Description

Package: aroma.core
Class AromaUnitPscnBinarySet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinarySet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CopyNumberDataSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitPscnBinarySet
```

Directly known subclasses:

public static class **AromaUnitPscnBinarySet**
extends CopyNumberDataSet

An AromaUnitPscnBinarySet object represents a set of `AromaUnitPscnBinaryFile`s with *identical* chip types.

Usage

```
AromaUnitPscnBinarySet(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinarySet`.

Fields and Methods

Methods:

`byName`	-
`getAverageFile`	-
`writeDataFrame`	-

Methods inherited from CopyNumberDataSet:
as, as.CopyNumberDataSet, doCBS, hasAlleleBFractions, hasStrandiness

Methods inherited from AromaUnitSignalBinarySet:
byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

Methods inherited from AromaTabularBinarySet:
getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitSignalBinaryFile` *The AromaUnitSignalBinaryFile class*

Description

Package: aroma.core
Class AromaUnitSignalBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
```

Directly known subclasses:
AromaUnitCallFile, AromaUnitFracBCnBinaryFile, AromaUnitGenotypeCallFile, *AromaUnitPscnBinaryFile*, *AromaUnitTotalCnBinaryFile*, AromaUnitTypesFile

public static class **AromaUnitSignalBinaryFile**
extends *AromaPlatformInterface*

An AromaUnitSignalBinaryFile is a `AromaTabularBinaryFile`.

Usage

```
AromaUnitSignalBinaryFile(...)
```

Arguments

`...`	Arguments passed to `AromaTabularBinaryFile`.

Fields and Methods

Methods:

`extractMatrix`	-
`getChipType`	-
`getNumberOfFilesAveraged`	-
`getPlatform`	-
`isAverageFile`	-
`nbrOfUnits`	-
`readDataFrame`	-
`writeDataFrame`	Writes the data file as a tab-delimited text file.

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTab-

ularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

See Also

`AromaTabularBinaryFile`.

`AromaUnitSignalBinarySet`

The AromaUnitSignalBinarySet class

Description

Package: aroma.core
Class AromaUnitSignalBinarySet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinarySet
```

Directly known subclasses:
AromaUnitCallSet, AromaUnitFracBCnBinarySet, AromaUnitGenotypeCallSet, AromaUnitPscnBinarySet, AromaUnitTotalCnBinarySet

public static class **AromaUnitSignalBinarySet**
extends AromaTabularBinarySet

An AromaUnitSignalBinarySet object represents a set of `AromaUnitSignalBinaryFile`s with *identical* chip types.

Usage

```
AromaUnitSignalBinarySet(...)
```

Arguments

`...`	Arguments passed to `AromaTabularBinarySet`.

Fields and Methods

Methods:

`byName`	-
`getAromaUgpFile`	-
`getChipType`	-
`getPlatform`	-
`writeDataFrame`	Writes the data set as a tab-delimited text file.

Methods inherited from AromaTabularBinarySet:
getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitTabularBinaryFile`

The AromaUnitTabularBinaryFile class

Description

Package: aroma.core
Class AromaUnitTabularBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitAnnotationDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitTabularBinaryFile
```

Directly known subclasses:
AromaUflFile, AromaUgcFile, AromaUgpFile, *AromaUnitChromosomeTabularBinaryFile*, AromaUnitGcContentFile

public abstract static class **AromaUnitTabularBinaryFile**
extends UnitAnnotationDataFile

A AromaUnitTabularBinaryFile is an `AromaTabularBinaryFile` with the constraint that the rows map one-to-one to, and in the same order as, the units in a annotation chip type file (e.g. CDF file). The (full) chip type of the annotation chip type file is given by the mandatory file footer `chipType`.

Usage

```
AromaUnitTabularBinaryFile(...)
```

Arguments

`...`	Arguments passed to `AromaTabularBinaryFile`.

Fields and Methods

Methods:

`byChipType`	-
`nbrOfUnits`	-
`writeDataFrame`	Writes the data file as a tab-delimited text file.

Methods inherited from UnitAnnotationDataFile:
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from AromaMicroarrayTabularBinaryFile:
allocate, as.character, byChipType, findByChipType, getChipType, getFilenameExtension, getPlatform

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitTotalCnBinaryFile`

The AromaUnitTotalCnBinaryFile class

Description

Package: aroma.core
Class AromaUnitTotalCnBinaryFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
```

```
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CopyNumberDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitTotalCnBinaryFile
```

Directly known subclasses:

public abstract static class **AromaUnitTotalCnBinaryFile**
extends *CopyNumberDataFile*

An AromaUnitTotalCnBinaryFile is a `AromaUnitSignalBinaryFile`.

Usage

```
AromaUnitTotalCnBinaryFile(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinaryFile`.

Fields and Methods

Methods:

`extractPSCNArray`	-
`extractPSCNMatrix`	-
`extractRawCopyNumbers`	-
`getAM`	-
`hasAlleleBFractions`	-
`hasStrandiness`	-

Methods inherited from CopyNumberDataFile:
as, as.CopyNumberDataFile, getNumberOfFilesAveraged, hasAlleleBFractions, hasStrandiness

Methods inherited from AromaUnitSignalBinaryFile:
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitTotalCnBinarySet`

The AromaUnitTotalCnBinarySet class

Description

Package: aroma.core
Class AromaUnitTotalCnBinarySet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinarySet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CopyNumberDataSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitTotalCnBinarySet
```

Directly known subclasses:

public static class **AromaUnitTotalCnBinarySet**
extends CopyNumberDataSet

An AromaUnitTotalCnBinarySet object represents a set of `AromaUnitTotalCnBinaryFile`s with *identical* chip types.

Usage

```
AromaUnitTotalCnBinarySet(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinarySet`.

Fields and Methods

Methods:

`as.AromaUnitTotalCnBinarySetTuple`	-
`as.CopyNumberDataSetTuple`	-
`byName`	-
`exportAromaUnitPscnBinarySet`	-
`exportTotalCnRatioSet`	-
`extractPSCNArray`	-
`getAverageFile`	-
`getUnitNamesFile`	-
`writeDataFrame`	-

Methods inherited from CopyNumberDataSet:
as, as.CopyNumberDataSet, doCBS, hasAlleleBFractions, hasStrandiness

Methods inherited from AromaUnitSignalBinarySet:
byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

Methods inherited from AromaTabularBinarySet:
getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags,

hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`AromaUnitTypesFile` *The AromaUnitTypesFile class*

Description

Package: aroma.core
Class AromaUnitTypesFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitAnnotationDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitTypesFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitTypesFile
```

Directly known subclasses:

public static class **AromaUnitTypesFile**
extends *UnitTypesFile*

Usage

```
AromaUnitTypesFile(...)
```

Arguments

`...`	Arguments passed to `AromaUnitTabularBinaryFile`.

Fields and Methods

Methods:

`getChipType`	-
`getPlatform`	-
`getUnitTypes`	-
`importFromUnitTypesFile`	-

Methods inherited from UnitTypesFile:
getUnitTypes, nbrOfUnits

Methods inherited from UnitAnnotationDataFile:
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from AromaUnitSignalBinaryFile:
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

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

`BinnedScatter` *The BinnedScatter class*

Description

Package: aroma.core
Class BinnedScatter

```
list
~~|
~~+--BinnedScatter
```

Directly known subclasses:

public class **BinnedScatter**
extends list

Usage

```
BinnedScatter(data=NULL, density=NULL, map=NULL, params=NULL)
```

Arguments

`data`	A Nx2 `numeric` `matrix`.
`density`	...
`map`	...
`params`	A `list` of parameters.

Fields and Methods

Methods:

```
plot       -
points     -
reorder    -
subsample  -
subset     -
```

Methods inherited from list:
Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, all.equal, as.CopyNumberDataSetTuple, as.data.frame, attachLocally, callHooks, coerce,ANY,list-method, exportAromaUnitPscnBinarySet, listToXml, mergeBoxplotStats, relist, type.convert, within

Author(s)

Henrik Bengtsson

See Also

The spatial density is estimated by internal functions of the **smoothScatter** package.

Examples

```
# Sample scatter data
n <- 10e3
x <- rnorm(n=n)
y <- rnorm(n=n)
xy <- cbind(x=x, y=sin(x)+y/5)

# Bin data and estimate densities
xyd <- binScatter(xy)

layout(matrix(1:4, nrow=2))
par(mar=c(5,4,2,1))

# Plot data
plot(xyd, pch=1)

# Thin scatter data by subsampling
rhos <- c(1/3, 1/4, 1/6)
for (kk in seq_along(rhos)) {
  xyd2 <- subsample(xyd, size=rhos[kk])
  points(xyd2, pch=1, col=kk+1)
}

for (kk in seq_along(rhos)) {
  xyd2 <- subsample(xyd, size=rhos[kk])
  plot(xyd2, pch=1, col=kk+1)
  mtext(side=3, line=0, sprintf("Density: %.1f%%", 100*rhos[kk]))
}
```

`CbsModel` *The CbsModel class*

Description

Package: aroma.core
Class CbsModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--CopyNumberChromosomalModel
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CopyNumberSegmentationModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--CbsModel
```

Directly known subclasses:

public static class **CbsModel**
extends *CopyNumberSegmentationModel*

This class represents the Circular Binary Segmentation (CBS) model [1].

Usage

```
CbsModel(cesTuple=NULL, ..., seed=NULL)
```

Arguments

`cesTuple`	A `CopyNumberDataSetTuple`.
`...`	Arguments passed to the constructor of `CopyNumberSegmentationModel`.
`seed`	An (optional) `integer` that if specified will (temporarily) set the random seed each time before calling the segmentation method. For more information, see `segmentByCBS`().

Fields and Methods

Methods:
No methods defined.

Methods inherited from CopyNumberSegmentationModel:
fit, getAsteriskTags, getFitFunction, getFullNames, getRegions, getTags, plot, plotCopyNumberRegionLayers, writeRegions

Methods inherited from CopyNumberChromosomalModel:
as.character, calculateChromosomeStatistics, calculateRatios, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getMaxNAFraction, getNames, getOptionalArguments, getPairedNames, getRefSetTuple, getReference, getReferenceSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers, setReference

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome

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] Olshen, A. B., Venkatraman, E. S., Lucito, R., Wigler, M. *Circular binary segmentation for the analysis of array-based DNA copy number data. Biostatistics 5: 557-572, 2004.*
[2] Venkatraman, E. S. & Olshen, A. B. *A faster circular binary segmentation algorithm for the analysis of array CGH data*. Bioinformatics, 2007.

See Also

`CopyNumberSegmentationModel`.

`ChromosomalModel` *The ChromosomalModel class*

Description

Package: aroma.core
Class ChromosomalModel

```
Object
~~|
~~+--ChromosomalModel
```

Directly known subclasses:
CbsModel, *CopyNumberChromosomalModel*, *CopyNumberSegmentationModel*, GladModel, HaarSegModel, *RawCopyNumberModel*

public abstract static class **ChromosomalModel**
extends Object

This *abstract* class represents a chromosomal model.

Usage

```
ChromosomalModel(cesTuple=NULL, tags="*", genome="Human", chromosomes=NULL, ...)
```

Arguments

`cesTuple`	A `AromaMicroarrayDataSetTuple`.
`tags`	A `character vector` of tags.
`genome`	A `character` string specifying what genome is process.
`chromosomes`	(optional) A `vector` specifying which chromosomes to process.
`...`	Not used.

Fields and Methods

Methods:

`fit`	-
`getChipType`	Gets a label for all chip types merged.
`getChipTypes`	-
`getChromosomes`	Gets the chromosomes to be processed.
`getFullName`	-
`getFullNames`	-
`getGenome`	-
`getName`	-
`getNames`	Gets the names of the arrays.
`getPath`	-
`getSets`	-
`getTags`	-
`indexOf`	-
`nbrOfArrays`	Gets the number of arrays.
`nbrOfChipTypes`	Gets the number of chip types.
`setChromosomes`	-
`setGenome`	-

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

Requirements

This class requires genome information annotation files for every chip type.

Author(s)

Henrik Bengtsson

`ChromosomeExplorer` *The ChromosomeExplorer class*

Description

Package: aroma.core
Class ChromosomeExplorer

```
Object
~~|
```

```
~~+--Explorer
~~~~~~~|
~~~~~~~+--ChromosomeExplorer
```

Directly known subclasses:

public static class **ChromosomeExplorer**
extends *Explorer*

Usage

```
ChromosomeExplorer(model=NULL, zooms=2^(0:6), ...)
```

Arguments

`model`	A `CopyNumberChromosomalModel` object.
`zooms`	An positive `integer vector` specifying for which zoom levels the graphics should be generated.
`...`	Not used.

Fields and Methods

Methods:

`display`	-
`getChromosomes`	Gets the chromosomes available.
`getFullNames`	-
`getModel`	Gets the model.
`getNames`	-
`getPath`	-
`getZooms`	-
`indexOf`	-
`process`	Generates image files, scripts and dynamic pages for the explorer.
`setArrays`	Sets the arrays.
`setCytoband`	-
`setZooms`	-

Methods inherited from Explorer:
addIncludes, addIndexFile, as.character, display, getAlias, getArraysOfInput, getAsteriskTags, getFullName, getIncludePath, getMainPath, getName, getNameOfInput, getNames, getPath, getReportPathPattern, getRootPath, getSampleLayerPrefix, getSubname, getTags, getTagsOfInput, getTemplatePath, getVersion, nbrOfArrays, process, setAlias, setArrays, setReportPathPattern, setSubname, setup, splitByReportPathPattern, updateSetupExplorerFile

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

Generating PNG images

In order to get better looking graphs, but also to be able to generate bitmap images on systems without direct bitmap support, which is the case when running R in batch mode or on Unix without X11 support, images are created using the `png2` device (a wrapper for `bitmap()` imitating `png()`). The `png()` is only used if `png2()`, which requires Ghostscript, does not. Note, when images are created using `png2()`, the images does not appear immediately, although the function call is completed, so be patient.

Author(s)

Henrik Bengtsson

See Also

`CopyNumberChromosomalModel`.

`colBinnedSmoothing.matrix`

Binned smoothing of a matrix column by column

Description

Binned smoothing of a matrix column by column.

Usage

```
## S3 method for class 'matrix'
colBinnedSmoothing(Y, x=seq_len(nrow(Y)), w=NULL, xOut=NULL, xOutRange=NULL,
 from=min(x, na.rm = TRUE), to=max(x, na.rm = TRUE), by=NULL, length.out=length(x),
  na.rm=TRUE, FUN="median", ..., verbose=FALSE)
```

Arguments

`Y`	A `numeric` JxI `matrix` (or a `vector` of length J.)
`x`	A (optional) `numeric` `vector` specifying the positions of the J entries. The default is to assume uniformly distributed positions.
`w`	A optional `numeric` `vector` of prior weights for each of the J entries.
`xOut`	Optional `numeric` `vector` of K bin center locations.
`xOutRange`	Optional Kx2 `matrix` specifying the boundary locations for K bins, where each row represents a bin $[x0, x1)$. If not specified, the boundaries are set to be the midpoints of the bin centers, such that the bins have maximum lengths without overlapping. Vice verse, if `xOut` is not specified, then `xOut` is set to be the mid points of the `xOutRange` boundaries.

`from, to, by, length.out`	If neither `xOut` nor `xOutRange` is specified, the `xOut` is generated uniformly from these arguments, which specify the center location of the first and the last bin, and the distance between the center locations, utilizing the `seq`() function. Argument `length.out` can be used as an alternative to `by`, in case it specifies the total number of bins instead.
`FUN`	A `function`.
`na.rm`	If `TRUE`, missing values are excluded, otherwise not.
`...`	Not used.
`verbose`	See `Verbose`.

Details

Note that all zero-length bins $[x0, x1)$ will get result in an `NA` value, because such bins contain no data points. This also means that `colBinnedSmoothing(Y, x=x, xOut=xOut)` where `xOut` contains duplicated values, will result in some zero-length bins and hence `NA` values.

Value

Returns a `numeric` KxI `matrix` (or a `vector` of length K) where K is the total number of bins. The following attributes are also returned:

`xOut` The center locations of each bin.

`xOutRange` The bin boundaries.

`count` The number of data points within each bin (based solely on argument `x`).

`binWidth` The *average* bin width.

Author(s)

Henrik Bengtsson

See Also

`*colKernelSmoothing`().

Examples

```
# Number of tracks
I <- 4

# Number of data points per track
J <- 100

# Simulate data with a gain in track 2 and 3
x <- 1:J
Y <- matrix(rnorm(I*J, sd=1/2), ncol=I)
Y[30:50,2:3] <- Y[30:50,2:3] + 3

# Uniformly distributed equal-sized bins
```

```
Ys3 <- colBinnedSmoothing(Y, x=x, from=2, by=3)
Ys5 <- colBinnedSmoothing(Y, x=x, from=3, by=5)

# Custom bins
xOutRange <- t(matrix(c(
  1, 11,
 11, 31,
 31, 41,
 41, 51,
 51, 81,
 81, 91,
 91,101
), nrow=2))
YsC <- colBinnedSmoothing(Y, x=x, xOutRange=xOutRange)

# Custom bins specified by center locations with
# maximized width relative to the neighboring bins.
xOut <- c(6, 21, 36, 46, 66, 86, 96)
YsD <- colBinnedSmoothing(Y, x=x, xOut=xOut)

xlim <- range(x)
ylim <- c(-3,5)
layout(matrix(1:I, ncol=1))
par(mar=c(3,3,1,1)+0.1, pch=19)
for (ii in 1:I) {
  plot(NA, xlim=xlim, ylim=ylim)
  points(x, Y[,ii], col="#999999")

  xOut <- attr(Ys3, "xOut")
  lines(xOut, Ys3[,ii], col=2)
  points(xOut, Ys3[,ii], col=2)

  xOut <- attr(Ys5, "xOut")
  lines(xOut, Ys5[,ii], col=3)
  points(xOut, Ys5[,ii], col=3)

  xOut <- attr(YsC, "xOut")
  lines(xOut, YsC[,ii], col=4)
  points(xOut, YsC[,ii], col=4, pch=15)

  xOut <- attr(YsD, "xOut")
  lines(xOut, YsD[,ii], col=5)
  points(xOut, YsD[,ii], col=5, pch=15)

  if (ii == 1) {
    legend("topright", pch=c(19,19,15,15), col=c(2,3,4,5),
           c("by=3", "by=5", "Custom #1", "Custom #2"), horiz=TRUE, bty="n")
  }
}


# Sanity checks
xOut <- x
```

```
YsT <- colBinnedSmoothing(Y, x=x, xOut=xOut)
stopifnot(all(YsT == Y))
stopifnot(all(attr(YsT, "counts") == 1))

xOut <- attr(YsD, "xOut")
YsE <- colBinnedSmoothing(YsD, x=xOut, xOut=xOut)
stopifnot(all(YsE == YsD))
stopifnot(all(attr(YsE, "xOutRange") == attr(YsD, "xOutRange")))
stopifnot(all(attr(YsE, "counts") == 1))

# Scramble ordering of loci
idxs <- sample(x)
x2 <- x[idxs]
Y2 <- Y[idxs,,drop=FALSE]
Y2s <- colBinnedSmoothing(Y2, x=x2, xOut=x2)
stopifnot(all(attr(Y2s, "xOut") == x2))
stopifnot(all(attr(Y2s, "counts") == 1))
stopifnot(all(Y2s == Y2))

xOut <- x[seq(from=2, to=J, by=3)]
YsT <- colBinnedSmoothing(Y, x=x, xOut=xOut)
stopifnot(all(YsT == Ys3))
stopifnot(all(attr(YsT, "counts") == 3))

xOut <- x[seq(from=3, to=J, by=5)]
YsT <- colBinnedSmoothing(Y, x=x, xOut=xOut)
stopifnot(all(YsT == Ys5))
stopifnot(all(attr(YsT, "counts") == 5))
```

`colKernelSmoothing.matrix`

Kernel smoothing of a matrix column by column

Description

Kernel smoothing of a matrix column by column.

Usage

```
## S3 method for class 'matrix'
colKernelSmoothing(Y, x=seq_len(nrow(Y)), w=NULL, xOut=x,
  kernel=c("gaussian", "uniform"), h, censorH=3, na.rm=TRUE, robust=FALSE, ...,
  verbose=FALSE)
```

Arguments

`Y`	A `numeric` JxI `matrix` (or a `vector` of length J.)
`x`	A (optional) `numeric` `vector` specifying the positions of the J entries. The default is to assume uniformly distributed positions.

`w`	A optional `numeric` `vector` of prior weights for each of the J entries.
`xOut`	A `numeric` `vector` specifying K target positions where the kernel is applied.
`kernel`	A `character` string or a `function` specifying the kernel used.
`h`	A single positive `numeric` specifying the bandwidth of the kernel.
`censorH`	A single positive `numeric` specifying the where to truncate the kernel. If `Inf`, no truncation is done.
`na.rm`	If `TRUE`, missing values are excluded, otherwise not.
`robust`	If `TRUE`, robust estimators are used, otherwise not.
`...`	Not used.
`verbose`	See `Verbose`.

Value

Returns a `numeric` KxI `matrix` (or a `vector` of length K).

Author(s)

Henrik Bengtsson

See Also

`*colBinnedSmoothing`().

Examples

```
J <- 100
I <- 4
Y <- matrix(rnorm(I*J, sd=1/2), ncol=I)
# Introduce a gain in column 2 and 3
Y[30:50,2:3] <- Y[30:50,2:3] + 3
x <- 1:J

xOut <- x
Ys1 <- colKernelSmoothing(Y, x=x, xOut=xOut, kernel="gaussian", h=1)
Ys5 <- colKernelSmoothing(Y, x=x, xOut=xOut, kernel="gaussian", h=5)

xlim <- range(c(x,xOut))
ylim <- c(-3,5)
layout(matrix(1:I, ncol=1))
par(mar=c(3,3,1,1)+0.1, pch=19)
for (ii in 1:I) {
  plot(NA, xlim=xlim, ylim=ylim)
  points(x, Y[,ii], col="#999999")
  lines(xOut, Ys1[,ii], col=2)
  points(xOut, Ys1[,ii], col=2)
  lines(xOut, Ys5[,ii], col=3)
  points(xOut, Ys5[,ii], col=3)
}
```

`CopyNumberChromosomalModel` *The CopyNumberChromosomalModel class*

Description

Package: aroma.core
Class CopyNumberChromosomalModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--CopyNumberChromosomalModel
```

Directly known subclasses:
CbsModel, *CopyNumberSegmentationModel*, GladModel, HaarSegModel, *RawCopyNumberModel*

public abstract static class **CopyNumberChromosomalModel**
extends *ChromosomalModel*

This *abstract* class represents a copy-number model.

Usage

```
CopyNumberChromosomalModel(cesTuple=NULL, refTuple=NULL, calculateRatios=TRUE, tags="*",
  genome="Human", chromosomes=NULL, maxNAFraction=1/5, ...)
```

Arguments

`cesTuple`	A `CopyNumberDataSetTuple`.
`refTuple`	An optional `CopyNumberDataFile`, or `CopyNumberDataSet` or `CopyNumberDataSetTuple` for pairwise comparisons.
`calculateRatios`	A `logical` specifying whether ratios should be calculated relative to the reference. If `FALSE`, argument `refTuple` is ignored.
`tags`	A `character` `vector` of tags.
`genome`	A `character` string specifying what genome is process.
`chromosomes`	(optional) A `vector` specifying which chromosomes to process.
`maxNAFraction`	A `double` in [0,1] indicating how many non-finite signals are allowed in the sanity checks of the data.
`...`	Optional arguments that may be used by some of the subclass models.

Fields and Methods

Methods:

`extractRawCopyNumbers`	Extracts relative copy numbers.
`fit`	Fits the model.
`getChromosomeLength`	-
`getNames`	-
`getReference`	-
`isPaired`	-

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome

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

Requirements

This class requires genome information annotation files for every chip type.

Author(s)

Henrik Bengtsson

`CopyNumberSegmentationModel`

The CopyNumberSegmentationModel class

Description

Package: aroma.core
Class CopyNumberSegmentationModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--CopyNumberChromosomalModel
~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~+--CopyNumberSegmentationModel
```

Directly known subclasses:
CbsModel, GladModel, HaarSegModel

public abstract static class **CopyNumberSegmentationModel**
extends *CopyNumberChromosomalModel*

This *abstract* class represents a copy-number segmentation model.

Usage

```
CopyNumberSegmentationModel(...)
```

Arguments

`...`	Arguments passed to constructor `CopyNumberChromosomalModel`.

Fields and Methods

Methods:

`fit`	Fits the model.
`getFullNames`	-
`getRegions`	-
`getTags`	-
`plot`	-
`writeRegions`	-

Methods inherited from CopyNumberChromosomalModel:
as.character, calculateChromosomeStatistics, calculateRatios, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getMaxNAFraction, getNames, getOptionalArguments, getPairedNames, getRefSetTuple, getReference, getReferenceSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers, setReference

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome

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

`doCBS` *Performs Circular Binary Segmentation (CBS) on a data set*

Description

Performs Circular Binary Segmentation (CBS) on a data set for one or more chip types.

Usage

```
  ## Default S3 method:
doCBS(dataSet, tags=NULL, chipTypes, arrays=NULL, ..., verbose=FALSE)
  ## S3 method for class 'CopyNumberDataSet'
doCBS(ds, arrays=NULL, ...)
  ## S3 method for class 'CopyNumberDataSetTuple'
doCBS(dsTuple, arrays=NULL, ..., verbose=FALSE)
```

Arguments

`ds, dsTuple, dataSet`	A `CopyNumberDataSet`, a `CopyNumberDataSetTuple` or a `character` string with the name of one of them.
`tags`	An optional `character` `vector` of data set tags (only when `dataSet` is specified).
`chipTypes`	A `character` `vector` specifying the chip types for the different data sets (only when `dataSet` is specified).
`arrays`	An optional `vector` specifying the subset of arrays to process.
`...`	Additional arguments passed to `CbsModel` and its `fit()` method.
`verbose`	A `logical` or `Verbose`.

Value

Returns the output dataset of `CbsModel`.

Author(s)

Henrik Bengtsson

Examples

```
## Not run:

dataSet <- "GSE20939"
tags <- "ACC,-XY,BPN,-XY,RMA,FLN,-XY"
chipTypes <- c("Mapping250K_Nsp", "Mapping250K_Sty")
fit <- doCBS(dataSet, tags=tags, chipTypes=chipTypes, verbose=-10)
print(fit)


## End(Not run)
```

`Explorer` *The Explorer class*

Description

Package: aroma.core
Class Explorer

```
Object
~~|
~~+--Explorer
```

Directly known subclasses:
ChromosomeExplorer

public abstract static class **Explorer**
extends Object

Usage

```
Explorer(tags="*", version="0", ...)
```

Arguments

`tags`	A `character` `vector` of tags to be added to the output path.
`version`	An optional `character` string.
`...`	Not used.

Fields and Methods

Methods:

`display`	Displays the explorer in the default browser.
`getFullName`	-
`getName`	Gets the name of the explorer.
`getNames`	Gets the names of the input samples.
`getPath`	Gets the path of the output directory.
`getRootPath`	Gets the root path of the output directory.
`getTags`	Gets the tags of the explorer.
`getVersion`	-
`nbrOfArrays`	Gets the total number of arrays.
`process`	Generates image files, scripts and dynamic pages for the explorer.
`setArrays`	Sets the arrays.

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

Output directory structure

The *main directory* of an Explorer report is `reports/<name>/<subname>/`. The `<name>` is typically the same as the name of the input data set, and the `<subname>` is typically the tags of ditto. This main directory is where main HTML document is stored.

For each chip type, real or "virtual" (combined), there is a subdirectory with the same name as the chip type, i.e. `reports/<name>/<subname>/<chiptype>/`.

For each chip type directory, there are set of subdirectories each specifying a so called *image layer*, e.g. an image layer showing the raw data, another containing the estimates of a model fit and so on. Path format: `reports/<name>/<subname>/<chiptype>/<image layer>/`. In this directory all image files are stored, e.g. PNG files.

In some cases one do not want to all input tags to become part of the subname, but instead for instance use those to name the image layer(s). In such cases one has to override the default names.

Author(s)

Henrik Bengtsson

`GladModel` *The GladModel class*

Description

Package: aroma.core
Class GladModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--CopyNumberChromosomalModel
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CopyNumberSegmentationModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GladModel
```

Directly known subclasses:

public static class **GladModel**
extends *CopyNumberSegmentationModel*

This class represents the Gain and Loss Analysis of DNA regions (GLAD) model [1]. This class can model chip-effect estimates obtained from multiple chip types, and not all samples have to be available on all chip types.

Usage

```
GladModel(cesTuple=NULL, ...)
```

Arguments

`cesTuple`	A `CopyNumberDataSetTuple`.
`...`	Arguments passed to the constructor of `CopyNumberSegmentationModel`.

Details

Data from multiple chip types are combined "as is". This is based on the assumption that the relative chip effect estimates are non-biased (or at the equally biased across chip types). Note that in GLAD there is no way to down weight certain data points, which is why we can control for differences in variance across chip types.

Fields and Methods

Methods:

`writeRegions` -

Methods inherited from CopyNumberSegmentationModel:
fit, getAsteriskTags, getFitFunction, getFullNames, getRegions, getTags, plot, plotCopyNumberRegionLayers, writeRegions

Methods inherited from CopyNumberChromosomalModel:
as.character, calculateChromosomeStatistics, calculateRatios, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getMaxNAFraction, getNames, getOptionalArguments, getPairedNames, getRefSetTuple, getReference, getReferenceSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers, setReference

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome

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

Benchmarking

In high-density copy numbers analysis, the most time consuming step is fitting the GLAD model. The complexity of the model grows more than linearly (squared? exponentially?) with the number of data points in the chromosome and sample being fitted. This is why it take much more than twice the time to fit two chip types together than separately.

Author(s)

Henrik Bengtsson

References

[1] Hupe P et al. *Analysis of array CGH data: from signal ratio to gain and loss of DNA regions*. Bioinformatics, 2004, 20, 3413-3422.

See Also

`CopyNumberSegmentationModel`.

`HaarSegModel` *The HaarSegModel class*

Description

Package: aroma.core
Class HaarSegModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--CopyNumberChromosomalModel
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CopyNumberSegmentationModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--HaarSegModel
```

Directly known subclasses:

public static class **HaarSegModel**
extends *CopyNumberSegmentationModel*

This class represents the Haar wavelet-based segmentation (HaarSeg) model [1].

Usage

```
HaarSegModel(cesTuple=NULL, ..., breaksFdrQ=1e-04)
```

Arguments

`cesTuple`	A `CopyNumberDataSetTuple`.
`breaksFdrQ`	Default tuning parameters specific to the HaarSeg algorithm.
`...`	Arguments passed to the constructor of `CopyNumberSegmentationModel`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from CopyNumberSegmentationModel:
fit, getAsteriskTags, getFitFunction, getFullNames, getRegions, getTags, plot, plotCopyNumberRegionLayers, writeRegions

Methods inherited from CopyNumberChromosomalModel:
as.character, calculateChromosomeStatistics, calculateRatios, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getMaxNAFraction, getNames, getOptionalArguments, getPairedNames, getRefSetTuple, getReference, getReferenceSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers, setReference

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome

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] Ben-Yaacov E. and Eldar YC. *A fast and flexible method for the segmentation of aCGH data*, Bioinformatics, 2008. `https://www.weizmann.ac.il/math/yonina/software-hardware/software/haarseg-fast-and-flexible-microarray-segmentation`

See Also

`CopyNumberSegmentationModel`.

`NonPairedPSCNData` *The NonPairedPSCNData class*

Description

Package: aroma.core
Class NonPairedPSCNData

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AbstractCNData
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AbstractPSCNData
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--NonPairedPSCNData
```

Directly known subclasses:

public class **NonPairedPSCNData**
extends AbstractPSCNData

A NonPairedPSCNData object holds parent-specific copy number data. Two NonPairedPSCNData objects for a matched tumor-normal pair can be combined into a `PairedPSCNData` object.

Usage

```
NonPairedPSCNData(chromosome=NULL, x=NULL, isSNP=NULL, mu=NULL, C=NULL, beta=NULL, ...)
```

Arguments

`C`	A `numeric` `vector` of J tumor total copy number (TCN) ratios in [0,+`Inf`) (due to noise, small negative values are also allowed). The TCN ratios are typically scaled such that copy-neutral diploid loci have a mean of two.
`beta`	A `numeric` `vector` of J tumor allele B fractions (BAFs) in [0,1] (due to noise, values may be slightly outside as well) or `NA` for non-polymorphic loci.
`mu`	An optional `numeric` `vector` of J genotype calls in {0,1/2,1} for AA, AB, and BB, respectively, and `NA` for non-polymorphic loci. If not given, they are estimated from the normal BAFs using `callNaiveGenotypes` as described in [2].
`isSNP`	An optional `logical` `vector` of length J specifying whether each locus is a SNP or not (non-polymorphic loci).
`chromosome`	(Optional) An `integer` scalar (or a `vector` of length J), which can be used to specify which chromosome each locus belongs to in case multiple chromosomes are segments. This argument is also used for annotation purposes.
`x`	Optional `numeric` `vector` of J genomic locations. If `NULL`, index locations `1:J` are used.
`...`	Optional named locus-specific signal `vector`s of length J.

Fields and Methods

Methods:

`as`	-
`as.NonPairedPSCNData`	-
`as.PairedPSCNData`	-
`callNaiveGenotypes`	-
`callSegmentationOutliers`	-
`dropSegmentationOutliers`	-
`getSignalColumnNames`	-
`segmentByCBS`	-

Methods inherited from AbstractPSCNData:
callSNPs, getSNPFields

Methods inherited from AbstractCNData:

findLargeGaps, getChipType, getLocusData, getPlatform, hasKnownPositions, orderAlongGenome, setChipType, setPlatform

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`PairedPSCNData` *The PairedPSCNData class*

Description

Package: aroma.core
Class PairedPSCNData

```
data.frame
~~|
~~+--RichDataFrame
```

```
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AbstractCNData
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AbstractPSCNData
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--PairedPSCNData
```

Directly known subclasses:

public class **PairedPSCNData**
extends AbstractPSCNData

A PairedPSCNData object holds paired tumor-normal parent-specific copy number data.

Usage

```
PairedPSCNData(chromosome=NULL, x=NULL, isSNP=NULL, muN=NULL, CT=NULL, betaT=NULL,
  CN=NULL, betaN=NULL, ...)
```

Arguments

`CT`	A `numeric` `vector` of J tumor total copy number (TCN) ratios in [0,+`Inf`) (due to noise, small negative values are also allowed). The TCN ratios are typically scaled such that copy-neutral diploid loci have a mean of two.
`CN`	An optional `numeric` `vector` of J normal TCN ratios.
`betaT`	A `numeric` `vector` of J tumor allele B fractions (BAFs) in [0,1] (due to noise, values may be slightly outside as well) or `NA` for non-polymorphic loci.
`betaN`	A `numeric` `vector` of J matched normal BAFs in [0,1] (due to noise, values may be slightly outside as well) or `NA` for non-polymorphic loci.
`muN`	An optional `numeric` `vector` of J genotype calls in {0,1/2,1} for AA, AB, and BB, respectively, and `NA` for non-polymorphic loci. If not given, they are estimated from the normal BAFs using `callNaiveGenotypes` as described in [2].
`isSNP`	An optional `logical` `vector` of length J specifying whether each locus is a SNP or not (non-polymorphic loci).
`chromosome`	(Optional) An `integer` scalar (or a `vector` of length J), which can be used to specify which chromosome each locus belongs to in case multiple chromosomes are segments. This argument is also used for annotation purposes.
`x`	Optional `numeric` `vector` of J genomic locations. If `NULL`, index locations `1:J` are used.
`...`	Optional named locus-specific signal `vector`s of length J.

Fields and Methods

Methods:

`as`	-
`as.PairedPSCNData`	-
`callNaiveGenotypes`	-
`callSegmentationOutliers`	-
`dropSegmentationOutliers`	-
`getSignalColumnNames`	-
`getTCNs`	-
`getTotalCopyNumbers`	-
`normalizeTumorBoost`	-
`plotTracks`	-
`segmentByCBS`	-
`segmentByPairedPSCBS`	-

Methods inherited from AbstractPSCNData:
callSNPs, getSNPFields

Methods inherited from AbstractCNData:
findLargeGaps, getChipType, getLocusData, getPlatform, hasKnownPositions, orderAlongGenome, setChipType, setPlatform

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head,

initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`ParametersInterface` *The ParametersInterface class interface*

Description

Package: aroma.core
Class ParametersInterface

```
Interface
~~|
~~+--ParametersInterface
```

Directly known subclasses:
AromaTransform

public class **ParametersInterface**
extends Interface

Usage

```
ParametersInterface(...)
```

Arguments

`...`	Not used.

Fields and Methods

Methods:

`getParameters`	-
`getParametersAsString`	-

Methods inherited from Interface:

extend, print, uses

Author(s)

Henrik Bengtsson

`RawAlleleBFractions` *The RawAlleleBFractions class*

Description

Package: aroma.core
Class RawAlleleBFractions

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--RawAlleleBFractions
```

Directly known subclasses:
RawMirroredAlleleBFractions, SegmentedAlleleBFractions

public class **RawAlleleBFractions**
extends RawGenomicSignals

Usage

```
RawAlleleBFractions(...)
```

Arguments

`...`	Arguments passed to `RawGenomicSignals`.

Fields and Methods

Methods:

`extractRawMirroredAlleleBFractions`	-
`plot`	-

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`RawCopyNumberModel` *The RawCopyNumberModel class*

Description

Package: aroma.core
Class RawCopyNumberModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--CopyNumberChromosomalModel
```

```
~~~~~~~~~~~~|
~~~~~~~~~~~~+--RawCopyNumberModel
```

Directly known subclasses:

public abstract static class **RawCopyNumberModel**
extends *CopyNumberChromosomalModel*

This class represents an identity copy-number model which returns the input as is.

Usage

```
RawCopyNumberModel(...)
```

Arguments

`...`	Passed to the constructor of the superclass.

Fields and Methods

Methods:
No methods defined.

Methods inherited from CopyNumberChromosomalModel:
as.character, calculateChromosomeStatistics, calculateRatios, estimateSds, extractRawCopyNumbers, fit, getChromosomeLength, getDataFileMatrix, getMaxNAFraction, getNames, getOptionalArguments, getPairedNames, getRefSetTuple, getReference, getReferenceSetTuple, isPaired, newPlot, plotAxesLayers, plotChromosomesLayers, plotCytobandLayers, plotFitLayers, plotGridHorizontalLayers, plotRawCopyNumbers, plotSampleLayers, setReference

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome

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

`RawCopyNumbers` *The RawCopyNumbers class*

Description

Package: aroma.core
Class RawCopyNumbers

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--RawCopyNumbers
```

Directly known subclasses:
SegmentedCopyNumbers

public class **RawCopyNumbers**
extends RawGenomicSignals

Usage

```
RawCopyNumbers(cn=NULL, ...)
```

Arguments

`cn`	A `numeric` `vector` of length J specifying the copy number at each loci.
`...`	Arguments passed to `RawGenomicSignals`.

Fields and Methods

Methods:

`cnRange`	-
`extractRawCopyNumbers`	-
`getSignals`	-
`plot`	-

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimat-

eStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

Examples

```
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Simulating copy-number data
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Number of loci
J <- 1000

mu <- double(J)
mu[200:300] <- mu[200:300] + 1
mu[650:800] <- mu[650:800] - 1
eps <- rnorm(J, sd=1/2)
y <- mu + eps
x <- sort(runif(length(y), max=length(y)))


cn <- RawCopyNumbers(y, x)
print(cn)

cn2 <- extractSubset(cn, subset=xSeq(cn, by=5))
```

```
print(cn2)

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Plot along genome
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
plot(cn, ylim=c(-3,3))
title(main="Complete and subsetted loci")
points(cn2, col="red", pch=176, cex=2)

legend("topright", pch=c(19,176), col=c("#999999", "red"),
       sprintf(c("raw [n=%d]", "every 5th [n=%d]"),
               c(nbrOfLoci(cn), nbrOfLoci(cn2))), bty="n")


# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Binned smoothing
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Binned smoothing")

cnSa <- binnedSmoothing(cn, by=3)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- binnedSmoothing(cn, by=9)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"),
       sprintf(c("raw [n=%d]", "Bin(w=3) [n=%d]", "Bin(w=9) [n=%d]"),
       c(nbrOfLoci(cn), nbrOfLoci(cnSa), nbrOfLoci(cnSb))), bty="n")


# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Binned smoothing (by count)
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Binned smoothing (by count)")

cnSa <- binnedSmoothing(cn, by=3, byCount=TRUE)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- binnedSmoothing(cn, by=9, byCount=TRUE)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"),
       sprintf(c("raw [n=%d]", "BinO(w=3) [n=%d]", "BinO(w=9) [n=%d]"),
       c(nbrOfLoci(cn), nbrOfLoci(cnSa), nbrOfLoci(cnSb))), bty="n")


# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

```
# Kernel smoothing (default is Gaussian)
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Kernel smoothing w/ Gaussian kernel")

cnSa <- kernelSmoothing(cn, h=2)
points(cnSa, col="blue")

cnSb <- kernelSmoothing(cn, h=5)
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"),
       sprintf(c("raw [n=%d]", "N(.,sd=2) [n=%d]", "N(.,sd=5) [n=%d]"),
       c(nbrOfLoci(cn), nbrOfLoci(cnSa), nbrOfLoci(cnSb))), bty="n")


# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Kernel smoothing
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Kernel smoothing w/ uniform kernel")

xOut <- xSeq(cn, by=10)
cnSa <- kernelSmoothing(cn, xOut=xOut, kernel="uniform", h=2)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- kernelSmoothing(cn, xOut=xOut, kernel="uniform", h=5)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"),
       sprintf(c("raw [n=%d]", "U(w=2) [n=%d]", "U(w=5) [n=%d]"),
       c(nbrOfLoci(cn), nbrOfLoci(cnSa), nbrOfLoci(cnSb))), bty="n")
```

`RawGenomicSignals` *The RawGenomicSignals class*

Description

Package: aroma.core
Class RawGenomicSignals

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
```

Directly known subclasses:
AbstractCNData, AbstractPSCNData, NonPairedPSCNData, PairedPSCNData, RawAlleleBFractions, RawCopyNumbers, RawMirroredAlleleBFractions, RawSequenceReads, SegmentedAlleleBFractions, SegmentedCopyNumbers

public class **RawGenomicSignals**
extends RichDataFrame

Usage

```
RawGenomicSignals(y=NULL, x=NULL, w=NULL, chromosome=0L, name=NULL, ...)
```

Arguments

`y`	A `numeric` `vector` of length J specifying the signal at each locus.
`x`	A (optional) `numeric` `vector` of length J specifying the position of each locus.
`w`	A (optional) non-negative `numeric` `vector` of length J specifying a weight of each locus.
`chromosome`	An (optional) `integer` specifying the chromosome for these genomic signals.
`name`	An (optional) `character` string specifying the sample name.
`...`	Not used.

Fields and Methods

Methods:

`*`	-
`+`	-
`-`	-
`addBy`	-
`append`	-
`as.data.frame`	-
`binnedSmoothing`	-
`divideBy`	-
`drawDensity`	-
`estimateStandardDeviation`	-
`gaussianSmoothing`	-
`getChromosome`	-
`getChromosomes`	-
`getPositions`	-
`getSigma`	-
`getSignals`	-
`getWeights`	-
`getXScale`	-
`getYScale`	-
`hasWeights`	-

`kernelSmoothing`	-
`lines`	-
`multiplyBy`	-
`nbrOfChromosomes`	-
`nbrOfLoci`	-
`plot`	-
`points`	-
`segmentByCBS`	-
`segmentByGLAD`	-
`segmentByHaarSeg`	-
`segmentByMPCBS`	-
`setSigma`	-
`setSignals`	-
`setWeights`	-
`setXScale`	-
`setYScale`	-
`signalRange`	-
`sort`	-
`subtractBy`	-
`xMax`	-
`xMin`	-
`xRange`	-
`xSeq`	-
`yMax`	-
`yMin`	-
`yRange`	-

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`RawMirroredAlleleBFractions`

The RawMirroredAlleleBFractions class

Description

Package: aroma.core
Class RawMirroredAlleleBFractions

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--RawAlleleBFractions
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--RawMirroredAlleleBFractions
```

Directly known subclasses:

public class **RawMirroredAlleleBFractions**
extends RawAlleleBFractions

Usage

```
RawMirroredAlleleBFractions(...)
```

Arguments

`...`	Arguments passed to `RawAlleleBFractions`.

Fields and Methods

Methods:

`plot` -

Methods inherited from RawAlleleBFractions:

extractRawMirroredAlleleBFractions, plot

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`RawSequenceReads` *The RawSequenceReads class*

Description

Package: aroma.core
Class RawSequenceReads

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
```

```
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--RawSequenceReads
```

Directly known subclasses:

public class **RawSequenceReads**
extends RawGenomicSignals

Usage

```
RawSequenceReads(x=NULL, y=rep(1L, length(x)), ...)
```

Arguments

`x`	An `integer` `vector` of length J specifying the read positions.
`y`	An (optional) `integer` `vector` of length J specifying the number of reads at each position. Default is one read per position.
`...`	Arguments passed to `RawGenomicSignals`.

Fields and Methods

Methods:

```
binnedSums              -
extractRawCopyNumbers   -
nbrOfReads              -
plot                    -
```

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction,

getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`SegmentedAlleleBFractions`

The SegmentedAlleleBFractions class

Description

Package: aroma.core
Class SegmentedAlleleBFractions

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--RawAlleleBFractions
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--SegmentedGenomicSignalsInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--SegmentedAlleleBFractions
```

Directly known subclasses:

public class **SegmentedAlleleBFractions**
extends SegmentedGenomicSignalsInterface

Usage

```
SegmentedAlleleBFractions(..., states=NULL)
```

Arguments

`...`	Arguments passed to `RawAlleleBFractions`.
`states`	A `function` returning the copy-number states given a `vector` of locus positions.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SegmentedGenomicSignalsInterface:
as.data.frame, binnedSmoothingByState, extractSubsetByState, findChangePointsByState, getStateColorMap, getStateColors, getStates, getUniqueStates, getVirtualField, getVirtualLocusFields, kernelSmoothingByState, plot, points, setStateColorMap, setStates

Methods inherited from RawAlleleBFractions:
extractRawMirroredAlleleBFractions, plot

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

`SegmentedCopyNumbers` *The SegmentedCopyNumbers class*

Description

Package: aroma.core
Class SegmentedCopyNumbers

```
data.frame
~~|
~~+--RichDataFrame
~~~~~~~|
~~~~~~~+--RawGenomicSignals
~~~~~~~~~~~~|
~~~~~~~~~~~~+--RawCopyNumbers
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--SegmentedGenomicSignalsInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--SegmentedCopyNumbers
```

Directly known subclasses:

public class **SegmentedCopyNumbers**
extends SegmentedGenomicSignalsInterface

Usage

```
SegmentedCopyNumbers(..., states=NULL)
```

Arguments

`...`	Arguments passed to `RawCopyNumbers`.
`states`	A `function` returning the copy-number states given a `vector` of locus positions.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SegmentedGenomicSignalsInterface:
as.data.frame, binnedSmoothingByState, extractSubsetByState, findChangePointsByState, getStateColorMap, getStateColors, getStates, getUniqueStates, getVirtualField, getVirtualLocusFields, kernelSmoothingByState, plot, points, setStateColorMap, setStates

Methods inherited from RawCopyNumbers:
cnRange, extractRawCopyNumbers, getCNs, getCn, getSignals, plot

Methods inherited from RawGenomicSignals:
*, +, -, addBy, append, applyBinaryOperator, as.character, as.data.frame, assertOneChromosome, binnedSmoothing, binnedSmoothingByField, clearCache, clone, divideBy, drawDensity, estimateStandardDeviation, extractChromosome, extractChromosomes, extractDataForSegmentation, extractRegion, extractRegions, extractSubset, gaussianSmoothing, getBasicField, getCXY, getChromosome, getChromosomes, getDefaultLocusFields, getLocusFields, getPositions, getSigma, getSignalColumnName, getSignalColumnNames, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfChromosomes, nbrOfLoci, plot, points, print, segmentByCBS, segmentByGLAD, segmentByHaarSeg, segmentByMPCBS, setBasicField, setSigma, setSignals, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

Methods inherited from RichDataFrame:
$, $<-, [, [[, [[<-, as.data.frame, as.list, dim, dropVirtualColumn, getColumnNames, getColumnNamesTranslator, getFullName, getName, getTags, getVirtualColumn, getVirtualColumnFunction, getVirtualColumnNames, hasColumn, hasColumns, hasVirtualColumn, hasVirtualColumns, length, names, newInstance, print, rbind, setAttributes, setColumnNamesMap, setColumnNamesTranslator, setName, setTags, setVirtualColumn, subset, translateColumnNames

Methods inherited from data.frame:
$<-,data.frame-method, $<-, Math, Ops,nonStructure,vector-method, Ops,structure,vector-method, Ops,vector,nonStructure-method, Ops,vector,structure-method, Ops, Summary, [, [<-,data.frame-method, [<-, [[, [[<-,data.frame-method, [[<-, aggregate, anyDuplicated, anyNA, as.NonPairedPSCNData, as.PairedPSCNData, as.data.frame, as.list, as.matrix, as.vector, attachLocally, by, callSegmentationOutliers, cbind, coerce,ANY,list-method, coerce,oldClass,S3-method, dim, dimnames, dimnames<-, dropSegmentationOutliers, droplevels, duplicated, edit, findLargeGaps, format, formula, head, initialize,oldClass-method, is.na, merge, na.exclude, na.omit, plot, plotDensity, print, prompt, rbind, row.names, row.names<-, rowsum, segmentByCBS, segmentByPairedPSCBS, show,oldClass-method, slotsFromS3,data.frame-method, split, split<-, stack, str, subset, summary, t, tail, transform, type.convert, unique, unstack, unwrap, within, wrap, writeDataFrame, xtfrm

Author(s)

Henrik Bengtsson

Examples

```
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Simulating copy-number data
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# True CN states
stateFcn <- function(x, ...) {
  states <- integer(length(x))
  states[200 <=x & x <= 300] <- -1L
```

```
  states[650 <=x & x <= 800] <- +1L
  states
}

# Number of loci
J <- 1000

y <- rnorm(J, sd=1/2)
x <- 1:length(y)
for (state in c(-1,+1)) {
  idxs <- (stateFcn(x) == state)
  y[idxs] <- y[idxs] + state
}


cn <- SegmentedCopyNumbers(y, x, states=stateFcn)
print(cn)

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Subsetting
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
plot(cn, ylim=c(-4,4))
title("Copy numbers annotated by state (and subset by state)")

cnS <- extractSubsetByState(cn, states=c(0,+1L))
print(cnS)
points(cnS, pch=21, cex=1.2, lwd=2, col="purple")

legend("topright", pch=c(19, 21), col=c("#999999", "purple"),
       sprintf(c("raw [n=%d]", "CN in {0,1} [n=%d]"),
       c(nbrOfLoci(cn), nbrOfLoci(cnS))), bty="n")


# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Kernel smoothing stratified by state
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Kernel smoothing stratified by state w/ Gaussian kernel")

cnSa <- kernelSmoothingByState(cn, h=2)
points(cnSa, col="blue")

cnSb <- kernelSmoothingByState(cn, h=5)
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"),
       sprintf(c("raw [n=%d]", "N(.,sd=2) [n=%d]", "N(.,sd=5) [n=%d]"),
       c(nbrOfLoci(cn), nbrOfLoci(cnSa), nbrOfLoci(cnSb))), bty="n")


# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Binned smoothing stratified by state
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

```
plot(cn, col="#999999", ylim=c(-3,3))
title(main="Binned smoothing stratified by state")

cnSa <- binnedSmoothingByState(cn, by=3, verbose=-1)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- binnedSmoothingByState(cn, by=9, verbose=-1)
lines(cnSb, col="red")
points(cnSb, col="red")

legend("topright", pch=19, col=c("#999999", "blue", "red"),
       sprintf(c("raw [n=%d]", "Bin(w=3) [n=%d]", "Bin(w=9) [n=%d]"),
       c(nbrOfLoci(cn), nbrOfLoci(cnSa), nbrOfLoci(cnSb))), bty="n")
```

`SegmentedGenomicSignalsInterface`

The SegmentedGenomicSignalsInterface class interface

Description

Package: aroma.core
Class SegmentedGenomicSignalsInterface

```
Interface
~~|
~~+--SegmentedGenomicSignalsInterface
```

Directly known subclasses:
SegmentedAlleleBFractions, SegmentedCopyNumbers

public class **SegmentedGenomicSignalsInterface**
extends Interface

Usage

```
SegmentedGenomicSignalsInterface(...)
```

Arguments

`...`	Not used.

Fields and Methods

Methods:

`as.data.frame`	-
`binnedSmoothingByState`	-
`extractSubsetByState`	-
`findChangePointsByState`	-
`getStateColorMap`	-
`getStateColors`	-
`getStates`	-
`getUniqueStates`	-
`kernelSmoothingByState`	-
`plot`	-
`points`	-
`setStateColorMap`	-
`setStates`	-

Methods inherited from Interface:
extend, print, uses

Author(s)

Henrik Bengtsson

`UnitAnnotationDataFile`

The UnitAnnotationDataFile interface class

Description

Package: aroma.core
Class UnitAnnotationDataFile

```
Interface
~~|
~~+--UnitAnnotationDataFile
```

Directly known subclasses:
AromaUflFile, AromaUgcFile, AromaUgpFile, *AromaUnitChromosomeTabularBinaryFile*, AromaUnitGcContentFile, *AromaUnitTabularBinaryFile*, AromaUnitTypesFile, TextUnitNamesFile, *UnitNamesFile*, *UnitTypesFile*

public static class **UnitAnnotationDataFile**
extends Interface

A UnitAnnotationDataFile provides methods for querying certain types of chip type annotation data by units.

Usage

```
UnitAnnotationDataFile(...)
```

Arguments

`...`	Arguments passed to `Interface`.

Methods

Methods:

`byChipType`	-
`getAromaUflFile`	-
`getAromaUgpFile`	-
`getChipType`	-
`getPlatform`	-
`nbrOfUnits`	-

Methods inherited from Interface:
extend, print, uses

Author(s)

Henrik Bengtsson

`UnitNamesFile` *The UnitNamesFile interface class*

Description

Package: aroma.core
Class UnitNamesFile

```
Interface
~~|
~~+--UnitAnnotationDataFile
~~~~~~~|
~~~~~~~+--UnitNamesFile
```

Directly known subclasses:
TextUnitNamesFile

public abstract static class **UnitNamesFile**
extends UnitAnnotationDataFile

A UnitNamesFile provides methods for querying the unit names of a given chip type.

Usage

```
UnitNamesFile(...)
```

Arguments

`...`	Arguments passed to `UnitAnnotationDataFile`.

Methods

Methods:

`getUnitNames`	-
`indexOf`	-
`nbrOfUnits`	-

Methods inherited from UnitAnnotationDataFile:
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from Interface:
extend, print, uses

Author(s)

Henrik Bengtsson

`UnitTypesFile` *The UnitTypesFile interface class*

Description

Package: aroma.core
Class UnitTypesFile

```
Interface
~~|
~~+--UnitAnnotationDataFile
~~~~~~~|
~~~~~~~+--UnitTypesFile
```

Directly known subclasses:
AromaUnitTypesFile

public abstract static class **UnitTypesFile**
extends UnitAnnotationDataFile

A UnitTypesFile provides methods for querying the unit types of a given chip type, e.g. genotyping or copy-number unit, exon unit etc.

Usage

```
UnitTypesFile(...)
```

Arguments

`...`	Arguments passed to `UnitAnnotationDataFile`.

Methods

Methods:

```
getUnitTypes  -
nbrOfUnits    -
```

Methods inherited from UnitAnnotationDataFile:
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from Interface:
extend, print, uses

The aroma unit-type map

unknown=0, expression=1, genotyping=2, resequencing=3, tag=4, copynumber=5, genotypingcontrol=6, expressioncontrol=7

Author(s)

Henrik Bengtsson

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