

# Package ‘aroma.core’

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**Description** This package is a private support package for aroma.affymetrix et al. The methods and classes of this package are independent of platform. Its API is in alpha and beta stage.

**License** LGPL (>= 2.1)

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aroma.core-package *Package aroma.core*

---

## Description

This package is a private support package for aroma.affymetrix et al. The methods and classes of this package are independent of platform. Its API is in alpha and beta stage.

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. Consider this package a private package.

## Installation and updates

To install this package, see instructions at <http://www.braju.com/R/>.

## 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

Some of the reference below can be found at <http://www.maths.lth.se/bioinformatics/publications/>.

[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. <http://www.ci.tuwien.ac.at/Conferences/DSC-2003/Proceedings/>

---

AromaCellTabularBinaryFile

*The AromaCellTabularBinaryFile class*


---

## Description

Package: aroma.core

### Class AromaCellTabularBinaryFile

#### Object

~~ |

~~+--FullNameInterface

~~~~~ |

~~~~~+--GenericDataFile

~~~~~ |

~~~~~+--GenericTabularFile

~~~~~ |

~~~~~+--AromaTabularBinaryFile

~~~~~ |

~~~~~+--AromaPlatformInterface

~~~~~ |

~~~~~+--AromaMicroarrayTabularBinaryFile

~~~~~ |

~~~~~+--AromaCellTabularBinaryFile

#### Directly known subclasses:

[AromaCellPositionFile](#), [AromaCellSequenceFile](#)

public abstract static class **AromaCellTabularBinaryFile**

extends [AromaMicroarrayTabularBinaryFile](#)

A [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:

nbrOfCells -

**Methods inherited from AromaMicroarrayTabularBinaryFile:**

allocate, as.character, byChipType, findByChipType, getChipType, getFilenameExtension, getPlatform

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

**Methods inherited from AromaTabularBinaryFile:**

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[AromaUnitTabularBinaryFile.](#)

---

AromaMicroarrayDataFile

*The abstract AromaMicroarrayDataFile class*


---

## Description

Package: aroma.core

### Class AromaMicroarrayDataFile

Object

~~ |

~~+--FullNameInterface

~~~~~ |

~~~~~+--GenericDataFile

~~~~~ |

~~~~~+--AromaMicroarrayDataFile

### Directly known subclasses:

public abstract static class **AromaMicroarrayDataFile**

extends *GenericDataFile*

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 -
```

### Methods inherited from GenericDataFile:

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension,

getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [], [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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 static class AromaMicroarrayDataSet
extends GenericDataFileSet
```

An AromaMicroarrayDataSet object represents a set of [AromaMicroarrayDataFiles](#) with *identical* chip types.

**Usage**

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

**Arguments**

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

**Fields and Methods****Methods:**

```
getChipType -
getPlatform -
nbrOfArrays -
```

**Methods inherited from GenericDataFileSet:**

append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, fromFiles, getAlias, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaMicroarrayDataSetTuple

*The AromaMicroarrayDataSetTuple class*

---

**Description**

Package: aroma.core

**Class AromaMicroarrayDataSetTuple**

Object

~~|

~~+--AromaMicroarrayDataSetTuple

**Directly known subclasses:**

public abstract static class **AromaMicroarrayDataSetTuple**  
 extends [Object](#)

**Usage**

```
AromaMicroarrayDataSetTuple (csList=NULL, tags="*", ..., .setClass="AromaMicroarrayD
```

**Arguments**

|           |  |
|-----------|--|
| csList    | A single or <a href="#">list</a> of <a href="#">AromaMicroarrayDataSet:s</a> . |
| tags      | A <a href="#">character vector</a> of tags.                                    |
| ...       | Not used.  |
| .setClass | The name of the class of the input set.  |

**Fields and Methods****Methods:**

|                                |  |
|--------------------------------|--|
| byPath                         | -  |
| <a href="#">extract</a>        | Extracts a subset AromaMicroarrayDataSetTuple. |
| getAlias                       | -  |
| <a href="#">getArrays</a>      | Gets the names of the arrays.                  |
| <a href="#">getArrayTuple</a>  | Gets arrays across chip types for one sample.  |
| getChipTypes                   | -  |
| getFullName                    | -  |
| getFullNames                   | -  |
| getListOfSets                  | -  |
| getName                        | -  |
| getNames                       | -  |
| getTags                        | -  |
| <a href="#">nbrOfArrays</a>    | Gets the number of arrays.                     |
| <a href="#">nbrOfChipTypes</a> | Gets the number of chip types.                 |
| setAlias                       | -  |
| setTags                        | -  |

**Methods inherited from Object:**

asThis, <-, [], [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaMicroarrayTabularBinaryFile

*The AromaMicroarrayTabularBinaryFile class*

---

**Description**

Package: aroma.core

**Class AromaMicroarrayTabularBinaryFile**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFile

~~~~~|

~~~~~+--GenericTabularFile

~~~~~|

~~~~~+--AromaTabularBinaryFile

~~~~~|

~~~~~+--AromaPlatformInterface

~~~~~|

~~~~~+--AromaMicroarrayTabularBinaryFile

**Directly known subclasses:**

*AromaCellPositionFile, AromaCellSequenceFile, AromaCellTabularBinaryFile, AromaUgpFile, AromaUnitChromosomeTabularBinaryFile, 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:**

|                      |   |
|----------------------|---|
| allocate             | - |
| as.character         | - |
| byChipType           | - |
| getChipType          | - |
| getFilenameExtension | - |
| getPlatform          | - |

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

**Methods inherited from AromaTabularBinaryFile:**

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnNameTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnNameTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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                    -
findUnitNamesFile        -
findUnitTypesFile        -
getAromaUgpFile          -
getName                   -
getUnitNamesFile         -
getUnitTypesFile         -

```

**Methods inherited from Object:**

asThis, <-, [], [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaTabularBinaryFile

*The AromaTabularBinaryFile class*

---

### Description

Package: aroma.core

#### Class AromaTabularBinaryFile

Object

~~ |

~~+--FullNameInterface

~~~~~ |

~~~~~+--GenericDataFile

~~~~~ |

~~~~~+--GenericTabularFile

~~~~~ |

~~~~~+--AromaTabularBinaryFile

#### Directly known subclasses:

[AromaCellPositionFile](#), [AromaCellSequenceFile](#), [AromaCellTabularBinaryFile](#), [AromaMicroarrayTabularBinaryFile](#), [AromaUgpFile](#), [AromaUnitCallFile](#), [AromaUnitChromosomeTabularBinaryFile](#), [AromaUnitFracBCnBinaryFile](#), [AromaUnitGenotypeCallFile](#), [AromaUnitSignalBinaryFile](#), [AromaUnitTabularBinaryFile](#), [AromaUnitTotalCnBinaryFile](#), [AromaUnitTypesFile](#)

public abstract static class **AromaTabularBinaryFile**

extends [GenericTabularFile](#)

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:**

|                                |   |
|--------------------------------|---|
| [                              | -   |
| [[                             | -   |
| [<-                            | -   |
| <code>allocate</code>          | Creates an AromaTabularBinaryFile.                            |
| <code>as.character</code>      | -   |
| <code>colMeans</code>          | -   |
| <code>colMedians</code>        | -   |
| <code>colStats</code>          | -   |
| <code>colSums</code>           | -   |
| <code>dimnames&lt;-</code>     | -   |
| <code>getBytesPerColumn</code> | -   |
| <code>getColClasses</code>     | -   |
| <code>getColumnNames</code>    | -   |
| <code>importFrom</code>        | -   |
| <code>lapply</code>            | -   |
| <code>nrOfColumns</code>       | -   |
| <code>nrOfRows</code>          | -   |
| <code>readColumns</code>       | -   |
| <code>readFooter</code>        | Reads the file footer in XML format into a named nested list. |
| <code>subset</code>            | -   |
| <code>summary</code>           | -   |
| <code>writeFooter</code>       | Writes a named nested list to the file footer in XML format.  |

**Methods inherited from GenericTabularFile:**

`as.character`, `dim`, `extractMatrix`, `getColumnNames`, `getColumnNameTranslator`, `nrOfColumns`, `nrOfRows`, `readColumns`, `readDataFrame`, `setColumnNameTranslator`, `translateColumnNames`

**Methods inherited from GenericDataFile:**

`compareChecksum`, `copyTo`, `equals`, `fromFile`, `getAlias`, `getAttribute`, `getAttributes`, `getChecksum`, `getCreatedOn`, `getDefaultFullName`, `getExtension`, `getExtensionPattern`, `getFilename`, `getFilenameExtension`, `getFileSize`, `getFileType`, `getLastAccessedOn`, `getLastModifiedOn`, `getOutputExtension`, `getPath`, `getPathname`, `gunzip`, `gzip`, `hasBeenModified`, `isFile`, `readChecksum`, `renameTo`, `renameToUpperCaseExt`, `setAlias`, `setAttribute`, `setAttributes`, `setAttributesBy`, `setAttributesByTags`, `setExtensionPattern`, `testAttributes`, `validateChecksum`, `writeChecksum`

**Methods inherited from FullNameInterface:**

`appendFullNameTranslator`, `appendFullNameTranslatorBycharacter`, `appendFullNameTranslatorByfunction`, `appendFullNameTranslatorBylist`, `appendFullNameTranslatorByNULL`, `clearFullNameTranslator`, `clearListOfFullNameTranslators`, `getDefaultFullName`, `getFullName`, `getFullNameTranslator`, `getListOfFullNameTranslators`, `getName`, `getTags`, `hasTag`, `hasTags`, `setFullName`, `setFullNameTranslator`, `setListOfFullNameTranslators`, `setName`, `setTags`, `updateFullName`

**Methods inherited from Object:**

`asThis`, `<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[GenericDataFile](#).

---

AromaTabularBinarySet

*The AromaTabularBinarySet class*

---

**Description**

Package: aroma.core

**Class AromaTabularBinarySet**

Object

```

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

```

**Directly known subclasses:**

[AromaUnitCallSet](#), [AromaUnitFracBCnBinarySet](#), [AromaUnitGenotypeCallSet](#), [AromaUnitSignalBinarySet](#), [AromaUnitTotalCnBinarySet](#)

```

public static class AromaTabularBinarySet
extends GenericTabularFileSet

```

An AromaTabularBinarySet object represents a set of [AromaTabularBinaryFiles](#) with *identical* chip types.

**Usage**

```

AromaTabularBinarySet (files=NULL, ...)

```

**Arguments**

```

files      A list of AromaTabularBinaryFiles.
...       Arguments passed to GenericDataFileSet.

```

## Fields and Methods

### Methods:

*No methods defined.*

### Methods inherited from GenericTabularFileSet:

calculateAverageColumnAcrossFiles, extractMatrix

### Methods inherited from GenericDataFileSet:

append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, fromFiles, getAlias, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, update2, updateFullName, updateFullNames, validate

### Methods inherited from FullNameInterface:

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

### Methods inherited from Object:

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaTransform

*The AromaTransform class*

---

## Description

Package: aroma.core

### Class AromaTransform

[Object](#)

~~ |

~~+--AromaTransform

### Directly known subclasses:

public abstract static class **AromaTransform**  
 extends [Object](#)

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

|                           |  |
|---------------------------|--|
| <code>dataSet</code>      | The input data set as an <a href="#">AromaMicroarrayDataSet</a> .                            |
| <code>tags</code>         | A <a href="#">character vector</a> of tags to be appended to the tags of the input data set. |
| <code>...</code>          | Not used.  |
| <code>.reqSetClass</code> | Internal argument.   |

### Details

Subclasses must implement the `process()` method.

### Fields and Methods

#### Methods:

|                                  |   |
|----------------------------------|---|
| <a href="#">getFullName</a>      | Gets the full name of the output data set.  |
| <a href="#">getInputDataSet</a>  | Gets the input data set.                    |
| <a href="#">getName</a>          | Gets the name of the output data set.       |
| <a href="#">getOutputDataSet</a> | Gets the transformed data set.              |
| <a href="#">getPath</a>          | Gets the path of the output data set.       |
| <a href="#">getTags</a>          | Gets the tags of the output data set.       |
| <a href="#">isDone</a>           | Checks if the data set is processed or not. |
| <a href="#">process</a>          | Processes the data set.                     |
| <a href="#">setTags</a>          | -   |

#### Methods inherited from Object:

`asThis`, `<-`, `[[`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `gc`, `getEnvironment`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `objectSize`, `print`, `registerFinalizer`, `save`

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

**Description**

Package: aroma.core

**Class AromaUnitCallFile**

Object

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---GenericTabularFile
~~~~~|
~~~~~+---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:**

```

allocate -
extractCallArray -
extractCalls -
extractMatrix -
findUnitsTodo -

```

**Methods inherited from AromaUnitSignalBinaryFile:**

allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getAromaUgpFile, getChipType, getExtensionPattern, getFilenameExtension, getPlatform, nbrOfUnits, readDataFrame

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

**Methods inherited from AromaTabularBinaryFile:**

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

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 [AromaUnitCallFiles](#) with *identical* chip types.

**Usage**

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

**Arguments**

... Arguments passed to [AromaUnitSignalBinarySet](#).

**Fields and Methods****Methods:**

|                       |   |
|-----------------------|---|
| byPath                | - |
| extractCallArray      | - |
| extractCalls          | - |
| extractGenotypeMatrix | - |
| findByName            | - |
| findUnitsTodo         | - |

**Methods inherited from [AromaUnitSignalBinarySet](#):**

byName, findByName, getAromaUgpFile, getChipType, getPlatform, validate

**Methods inherited from [GenericTabularFileSet](#):**

calculateAverageColumnAcrossFiles, extractMatrix

**Methods inherited from GenericDataFileSet:**

append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, fromFiles, getAlias, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaUnitFracBCnBinaryFile

*The AromaUnitFracBCnBinaryFile class*

---

**Description**

Package: aroma.core

**Class AromaUnitFracBCnBinaryFile**

Object

~~ |

~~+--FullNameInterface

~~~~~ |

~~~~~+--GenericDataFile

~~~~~ |

~~~~~+--GenericTabularFile

~~~~~ |

~~~~~+--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, getAromaUgpFile, getChipType, getExtensionPattern, getFilenameExtension, getPlatform, nbrOfUnits, readDataFrame

#### Methods inherited from [AromaPlatformInterface](#):

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

#### Methods inherited from [AromaTabularBinaryFile](#):

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

#### Methods inherited from [GenericTabularFile](#):

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnTranslator, translateColumnNames

#### Methods inherited from [GenericDataFile](#):

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [], [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

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 [AromaUnitFracBCnBinaryFiles](#) with *identical* chip types.

**Usage**

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

**Arguments**

... Arguments passed to [AromaUnitSignalBinarySet](#).

**Details**

The term "allele B fraction" is also known 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 -
exportFracBDiffSet -
```

**Methods inherited from AromaUnitSignalBinarySet:**

byName, findByName, getAromaUgpFile, getChipType, getPlatform, validate

**Methods inherited from GenericTabularFileSet:**

calculateAverageColumnAcrossFiles, extractMatrix

**Methods inherited from GenericDataFileSet:**

append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, fromFiles, getAlias, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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
~~~~~ |
~~~~~+--GenericTabularFile
~~~~~ |
~~~~~+--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:**

|                       |   |
|-----------------------|---|
| allocate              | - |
| 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, getAromaUgpFile, getChipType, getExtensionPattern, getFilenameExtension, getPlatform, nbrOfUnits, readDataFrame

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

**Methods inherited from AromaTabularBinaryFile:**

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, fi-

nalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

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 [AromaUnitGenotypeCallFiles](#) with *identical* chip types.

### Usage

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

**Arguments**

... Arguments passed to [AromaUnitCallSet](#).

**Fields and Methods****Methods:**

```

byName          -
byPath          -
extractGenotypes -

```

**Methods inherited from AromaUnitCallSet:**

byPath, extractCallArray, extractCalls, extractGenotypeMatrix, findByName, findUnitsTodo

**Methods inherited from AromaUnitSignalBinarySet:**

byName, findByName, getAromaUgpFile, getChipType, getPlatform, validate

**Methods inherited from GenericTabularFileSet:**

calculateAverageColumnAcrossFiles, extractMatrix

**Methods inherited from GenericDataFileSet:**

append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, fromFiles, getAlias, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaUnitSignalBinaryFile

*The AromaUnitSignalBinaryFile class*

---

**Description**

Package: aroma.core

**Class AromaUnitSignalBinaryFile**

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaUnitSignalBinaryFile

```

**Directly known subclasses:**

[AromaUnitCallFile](#), [AromaUnitFracBCnBinaryFile](#), [AromaUnitGenotypeCallFile](#), [AromaUnitTotalCnBinaryFile](#), [AromaUnitTypesFile](#)

```

public static class AromaUnitSignalBinaryFile
  extends AromaPlatformInterface

```

An [AromaUnitSignalBinaryFile](#) is a [AromaTabularBinaryFile](#).

**Usage**

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

**Arguments**

... Arguments passed to [AromaTabularBinaryFile](#).

**Fields and Methods****Methods:**

```

allocate -
allocateFromUnitAnnotationDataFile -
allocateFromUnitNamesFile -
as.character -
extractMatrix -
fromFile -
getAromaUgpFile -
getChipType -

```

```

getPlatform          -
nbrOfUnits          -
readDataFrame       -

```

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

**Methods inherited from AromaTabularBinaryFile:**

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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](#), [AromaUnitTotalCnBinarySet](#)

```

public static class AromaUnitSignalBinarySet
    extends AromaTabularBinarySet

```

An [AromaUnitSignalBinarySet](#) object represents a set of [AromaUnitSignalBinaryFiles](#) with *identical* chip types.

## Usage

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

## Arguments

... Arguments passed to [AromaTabularBinarySet](#).

## Fields and Methods

### Methods:

```

    byName          -
    findByName      -

```

```

getAromaUgpFile -
getChipType     -
getPlatform     -

```

**Methods inherited from GenericTabularFileSet:**

calculateAverageColumnAcrossFiles, extractMatrix

**Methods inherited from GenericDataFileSet:**

append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, fromFiles, getAlias, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, update2, updateFullName, updateFullNames, validate

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaUnitTabularBinaryFile

*The AromaUnitTabularBinaryFile class*

---

**Description**

Package: aroma.core

**Class AromaUnitTabularBinaryFile**

Object

~~ |

~~+--FullNameInterface

~~~~~ |

~~~~~+--GenericDataFile

~~~~~ |

~~~~~+--GenericTabularFile

~~~~~ |

```

~~~~~+---AromaTabularBinaryFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AromaMicroarrayTabularBinaryFile
~~~~~|
~~~~~+---AromaUnitTabularBinaryFile

```

**Directly known subclasses:**

[AromaUgpFile](#), [AromaUnitChromosomeTabularBinaryFile](#)

public abstract static class **AromaUnitTabularBinaryFile**

extends [AromaMicroarrayTabularBinaryFile](#)

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:**

```

allocateFromUnitAnnotationDataFile -
allocateFromUnitNamesFile         -
byChipType                         -
nbrOfUnits                         -

```

**Methods inherited from [AromaMicroarrayTabularBinaryFile](#):**

`allocate`, `as.character`, `byChipType`, `findByChipType`, `getChipType`, `getFilenameExtension`, `getPlatform`

**Methods inherited from [AromaPlatformInterface](#):**

`getAromaPlatform`, `getPlatform`, `getUnitAnnotationDataFile`, `getUnitNamesFile`, `getUnitTypesFile`

**Methods inherited from [AromaTabularBinaryFile](#):**

`[`, `[[`, `[<-`, `allocate`, `as.character`, `colMeans`, `colMedians`, `colStats`, `colSums`, `dimnames<-`, `getBytesPerColumn`, `getColClasses`, `getColumnNames`, `importFrom`, `lapply`, `nbrOfColumns`, `nbrOfRows`, `readColumns`, `readDataFrame`, `readFooter`, `readHeader`, `readRawFooter`, `setAttributesByTags`, `subset`, `summary`, `updateData`, `updateDataColumn`, `writeFooter`, `writeRawFooter`

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnNameTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnNameTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaUnitTotalCnBinaryFile

*The AromaUnitTotalCnBinaryFile class*

---

**Description**

Package: aroma.core

**Class AromaUnitTotalCnBinaryFile**

```
Object
~~ |
~~+--FullNameInterface
~~~~~ |
~~~~~+--GenericDataFile
~~~~~ |
~~~~~+--GenericTabularFile
~~~~~ |
~~~~~+--AromaTabularBinaryFile
~~~~~ |
~~~~~+--AromaPlatformInterface
~~~~~ |
```

```

~~~~~+---AromaUnitSignalBinaryFile
~~~~~|
~~~~~+---AromaUnitTotalCnBinaryFile

```

### Directly known subclasses:

```

public static class AromaUnitTotalCnBinaryFile
  extends AromaUnitSignalBinaryFile

```

An `AromaUnitTotalCnBinaryFile` is a `AromaUnitSignalBinaryFile`.

### Usage

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

### Arguments

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

### Fields and Methods

#### Methods:

```
extractRawCopyNumbers -
```

#### Methods inherited from `AromaUnitSignalBinaryFile`:

allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getAromaUgpFile, getChipType, getExtensionPattern, getFilenameExtension, getPlatform, nbrOfUnits, readDataFrame

#### Methods inherited from `AromaPlatformInterface`:

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

#### Methods inherited from `AromaTabularBinaryFile`:

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

#### Methods inherited from `GenericTabularFile`:

as.character, dim, extractMatrix, getColumnNames, getColumnNameTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnNameTranslator, translateColumnNames

#### Methods inherited from `GenericDataFile`:

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, rename-

ToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [], [<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaUnitTotalCnBinarySet

*The AromaUnitTotalCnBinarySet class*

---

**Description**

Package: aroma.core

**Class AromaUnitTotalCnBinarySet**

**Object**

```

~~ |
~~+--FullNameInterface
~~~~~ |
~~~~~+--GenericDataFileSet
~~~~~ |
~~~~~+--GenericTabularFileSet
~~~~~ |
~~~~~+--AromaTabularBinarySet
~~~~~ |
~~~~~+--AromaUnitSignalBinarySet
~~~~~ |
~~~~~+--AromaUnitTotalCnBinarySet

```

**Directly known subclasses:**

```

public static class AromaUnitTotalCnBinarySet
extends AromaUnitSignalBinarySet

```

An AromaUnitTotalCnBinarySet object represents a set of [AromaUnitTotalCnBinaryFiles](#) with *identical* chip types.

### Usage

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

### Arguments

... Arguments passed to [AromaUnitSignalBinarySet](#).

### Fields and Methods

#### Methods:

```
byName -
exportTotalCnRatioSet -
```

#### Methods inherited from AromaUnitSignalBinarySet:

byName, findByName, getAromaUgpFile, getChipType, getPlatform, validate

#### Methods inherited from GenericTabularFileSet:

calculateAverageColumnAcrossFiles, extractMatrix

#### Methods inherited from GenericDataFileSet:

append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, appendFullNamesTranslatorByNULL, as.list, byName, byPath, clearCache, clearFullNamesTranslator, copyTo, equals, extract, findByName, fromFiles, getAlias, getDefaultFullName, getFile, getFileClass, getFileSize, getFullNames, getNames, getPath, getPathnames, hasFile, indexOf, lapply, nbrOfFiles, sapply, seq, setAlias, setFullNamesTranslator, update2, updateFullName, updateFullNames, validate

#### Methods inherited from FullNameInterface:

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

#### Methods inherited from Object:

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

AromaUnitTypesFile *The AromaUnitTypesFile class*

---

## Description

Package: aroma.core

### Class AromaUnitTypesFile

Object

```

~~ |
~~+--FullNameInterface
~~~~~ |
~~~~~+--GenericDataFile
~~~~~ |
~~~~~+--GenericTabularFile
~~~~~ |
~~~~~+--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:**

```

allocate -
getChipType -
getPlatform -
getUnitTypes -
importFromUnitTypesFile -

```

**Methods inherited from UnitTypesFile:**

getUnitTypes, nbrOfUnits

**Methods inherited from UnitAnnotationDataFile:**

byChipType, getAromaUgpFile, getChipType, getPlatform, nbrOfUnits

**Methods inherited from AromaUnitSignalBinaryFile:**

allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getAromaUgpFile, getChipType, getExtensionPattern, getFilenameExtension, getPlatform, nbrOfUnits, readDataFrame

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile

**Methods inherited from AromaTabularBinaryFile:**

[, [[, [<-, allocate, as.character, colMeans, colMedians, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getColumnNames, importFrom, lapply, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from GenericTabularFile:**

as.character, dim, extractMatrix, getColumnNames, getColumnTranslator, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, setColumnTranslator, translateColumnNames

**Methods inherited from GenericDataFile:**

compareChecksum, copyTo, equals, fromFile, getAlias, getAttribute, getAttributes, getChecksum, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFilename, getFilenameExtension, getFileSize, getFileType, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, isFile, readChecksum, renameTo, renameToUpperCaseExt, setAlias, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validateChecksum, writeChecksum

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorBycharacter, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, appendFullNameTranslatorByNULL, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

```
as.GrayscaleImage.matrix
```

*Creates a Grayscale (TrueColor) Image from a matrix file*

---

## Description

Creates a Grayscale (TrueColor) Image from a matrix file.

## Usage

```
## S3 method for class 'matrix':  
as.GrayscaleImage(z, transforms=NULL, interleaved=c("none", "h", "v", "auto"), scale=1, ...)
```

## Arguments

|                          |                                                                                                            |
|--------------------------|------------------------------------------------------------------------------------------------------------|
| <code>z</code>           | A <code>KxN matrix</code> .                                                                                |
| <code>transforms</code>  | A <code>list</code> of transform <code>functions</code> .                                                  |
| <code>interleaved</code> | A <code>character</code> string specifying how the image data should be interleaved, if at all.            |
| <code>scale</code>       | A <code>numeric</code> scale factor in $(0, +\infty)$ for resizing the imaging. If 1, no resizing is done. |
| <code>...</code>         | Passed to <code>colorize()</code> of <code>Image</code> .                                                  |
| <code>verbose</code>     | A <code>logical</code> or a <code>Verbose</code> object.                                                   |

## Value

Returns an `Image` object.

## Author(s)

Henrik Bengtsson and Ken Simpson.

## See Also

`Image`. For more information see `matrix`.

---

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.  |
| ...     | Not used.              |

### Fields and Methods

#### Methods:

|           |   |
|-----------|---|
| plot      | - |
| points    | - |
| reorder   | - |
| subsample | - |
| subset    | - |

#### Methods inherited from list:

all.equal, as.data.frame, attachLocally, averageQuantile, callHooks, listToXml, mergeBoxplotStats, normalizeAverage, normalizeQuantileRank, normalizeQuantileSpline, plotDensity, relist, within

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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]))
}
```

---

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(length = ncol(Y)), w=NULL, from=min(x, na.rm = TRUE), t
```

**Arguments**

|            |                                                                                                                                         |
|------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| Y          | A <b>numeric JxI matrix</b> (or a <b>vector</b> of length J.)                                                                           |
| x          | A (optional) <b>numeric vector</b> specifying the positions of the J entries. The default is to assume uniformly distributed positions. |
| w          | A optional <b>numeric vector</b> of prior weights for each of the J entries.                                                            |
| from,to    | The center location of the first and the last bin.                                                                                      |
| by         | The distance between the center locations of each bin.                                                                                  |
| length.out | The number of bins.                                                                                                                     |
| xOut       | Prespecified center locations.                                                                                                          |
| na.rm      | If <b>TRUE</b> , missing values are excluded, otherwise not.                                                                            |
| FUN        | A <b>function</b> .                                                                                                                     |
| ...        | Not used.                                                                                                                               |
| verbose    | See <b>Verbose</b> .                                                                                                                    |

**Value**

Returns a **numeric KxI matrix** (or a **vector** of length K) where K is the total number of bins. Attribute 'xOut' specifies the center locations of each bin. The center locations are always uniformly distributed. Attribute 'binWidth' specifies the width of the bins. The width of the bins are always the same and identical to the distance between two adjacent bin centers.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

`*colKernelSmoothing()`.

**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

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

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)
}

```

---

```
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(length = nrow(Y)), w=NULL, xOut=x, kernel=c("gaussian",

```

## Arguments

|         |                                                                                                                                         |
|---------|-----------------------------------------------------------------------------------------------------------------------------------------|
| Y       | A <b>numeric</b> JxI <b>matrix</b> (or a <b>vector</b> of length J.)                                                                    |
| x       | A (optional) <b>numeric vector</b> specifying the positions of the J entries. The default is to assume uniformly distributed positions. |
| w       | A optional <b>numeric vector</b> of prior weights for each of the J entries.                                                            |
| xOut    | A <b>numeric vector</b> specifying K target positions where the kernel is applied.                                                      |
| kernel  | A <b>character</b> string or a <b>function</b> specifying the kernel used.                                                              |
| h       | A single positive <b>numeric</b> specifying the bandwidth of the kernel.                                                                |
| tensorH | A single positive <b>numeric</b> specifying the where to truncate the kernel. If <b>Inf</b> , no truncation is done.                    |
| na.rm   | If <b>TRUE</b> , missing values are excluded, otherwise not.                                                                            |
| robust  | If <b>TRUE</b> , robust estimators are used, otherwise not.                                                                             |
| ...     | Not used.                                                                                                                               |
| verbose | See <b>Verbose</b> .                                                                                                                    |

## Value

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

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

**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)
}
```

---

Explorer

*The Explorer class*

---

**Description**

Package: aroma.core

**Class Explorer****Object**

~~|

~~+--*Explorer*

**Directly known subclasses:**

public abstract static class **Explorer**  
 extends [Object](#)

**Usage**

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

**Arguments**

|      |                                                                            |
|------|----------------------------------------------------------------------------|
| tags | A <a href="#">character vector</a> of tags to be added to the output path. |
| ...  | Not used.                                                                  |

**Fields and Methods****Methods:**

|                             |                                                                    |
|-----------------------------|--------------------------------------------------------------------|
| addIncludes                 | -                                                                  |
| <a href="#">display</a>     | Displays the explorer in the default browser.                      |
| <a href="#">getAlias</a>    | Gets the alias of the output set.                                  |
| <a href="#">getArrays</a>   | Gets the names of the arrays.                                      |
| getAsteriskTags             | -                                                                  |
| getFullName                 | -                                                                  |
| <a href="#">getName</a>     | Gets the name of the explorer.                                     |
| getPath                     | -                                                                  |
| getReportPathPattern        | -                                                                  |
| <a href="#">getTags</a>     | Gets the tags of the explorer.                                     |
| getTagsOfInput              | -                                                                  |
| <a href="#">nbrOfArrays</a> | Gets the total number of arrays.                                   |
| <a href="#">process</a>     | Generates image files, scripts and dynamic pages for the explorer. |
| <a href="#">setAlias</a>    | Sets the alias of the output set.                                  |
| <a href="#">setArrays</a>   | Sets the arrays.                                                   |
| setReportPathPattern        | -                                                                  |
| setSubname                  | -                                                                  |
| setup                       | -                                                                  |
| splitByReportPathPattern    | -                                                                  |

**Methods inherited from Object:**

asThis, <-, [], [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**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 (<http://www.braju.com/R/>)

---

RawAlleleBFractions

*The RawAlleleBFractions class*

---

### Description

Package: aroma.core

#### Class RawAlleleBFractions

Object

~~ |

~~+--RawGenomicSignals

~~~~~ |

~~~~~+--RawAlleleBFractions

#### Directly known subclasses:

[RawMirroredAlleleBFractions](#), [SegmentedAlleleBFractions](#)

public static class **RawAlleleBFractions**

extends [RawGenomicSignals](#)

### Usage

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

### Arguments

... Arguments passed to [RawGenomicSignals](#).

### Fields and Methods

#### Methods:

```
extractRawMirroredAlleleBFractions -
plot -
```

**Methods inherited from RawGenomicSignals:**

addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

RawCopyNumbers      *The RawCopyNumbers class*

---

**Description**

Package: aroma.core

**Class RawCopyNumbers**

```
Object
~~ |
~~+--RawGenomicSignals
~~~~~ |
~~~~~+--RawCopyNumbers
```

**Directly known subclasses:**

[SegmentedCopyNumbers](#)

```
public static 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:**

```
as.data.frame -
cnRange      -
plot         -
```

**Methods inherited from RawGenomicSignals:**

addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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 5t

# - - - - -
# 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

# - - - - -
# 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=

# - - - - -
# 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=

# - - - - -
# 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)"),

```

---

RawGenomicSignals *The RawGenomicSignals class*

---

## Description

Package: aroma.core

### Class RawGenomicSignals

#### Object

~~|

~~+--RawGenomicSignals

#### Directly known subclasses:

[RawAlleleBFractions](#), [RawCopyNumbers](#), [RawMirroredAlleleBFractions](#), [RawSequenceReads](#), [SegmentedAlleleBFractions](#), [SegmentedCopyNumbers](#)

public static class **RawGenomicSignals**

extends [Object](#)

## Usage

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

## Arguments

|            |                                                                                                         |
|------------|---------------------------------------------------------------------------------------------------------|
| y          | A <a href="#">numeric vector</a> of length J specifying the signal at each locus.                       |
| x          | A (optional) <a href="#">numeric vector</a> of length J specifying the position of each locus.          |
| w          | A (optional) non-negative <a href="#">numeric vector</a> of length J specifying a weight of each locus. |
| chromosome | An (optional) <a href="#">integer</a> specifying the chromosome for these genomic signals.              |
| name       | An (optional) @character string specifying the sample name.                                             |
| ...        | Not used.                                                                                               |

**Fields and Methods****Methods:**

|                                           |                                                 |
|-------------------------------------------|-------------------------------------------------|
| addBy                                     | -                                               |
| addLocusFields                            | -                                               |
| append                                    | -                                               |
| as.data.frame                             | -                                               |
| binnedSmoothing                           | -                                               |
| divideBy                                  | -                                               |
| <a href="#">estimateStandardDeviation</a> | Estimates the standard deviation of the raw Ys. |
| extractRegion                             | -                                               |
| extractSubset                             | -                                               |
| gaussianSmoothing                         | -                                               |
| getChromosome                             | -                                               |
| getLocusFields                            | -                                               |
| getName                                   | -                                               |
| getPositions                              | -                                               |
| getSigma                                  | -                                               |
| getSignals                                | -                                               |
| getWeights                                | -                                               |
| getXScale                                 | -                                               |
| getXY                                     | -                                               |
| getYScale                                 | -                                               |
| hasWeights                                | -                                               |
| kernelSmoothing                           | -                                               |
| lines                                     | -                                               |
| multiplyBy                                | -                                               |
| nbrOfLoci                                 | -                                               |
| plot                                      | -                                               |
| points                                    | -                                               |
| setLocusFields                            | -                                               |
| setName                                   | -                                               |
| setSigma                                  | -                                               |
| setWeights                                | -                                               |
| setXScale                                 | -                                               |
| setYScale                                 | -                                               |
| signalRange                               | -                                               |
| sort                                      | -                                               |
| subtractBy                                | -                                               |
| summary                                   | -                                               |
| xMax                                      | -                                               |
| xMin                                      | -                                               |
| xRange                                    | -                                               |
| xSeq                                      | -                                               |
| yMax                                      | -                                               |
| yMin                                      | -                                               |
| yRange                                    | -                                               |

**Methods inherited from Object:**

asThis, <-, [], [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

RawMirroredAlleleBFractions

*The RawMirroredAlleleBFractions class*

---

**Description**

Package: aroma.core

**Class RawMirroredAlleleBFractions**

Object

~~|

~~+--RawGenomicSignals

~~~~~|

~~~~~+--RawAlleleBFractions

~~~~~|

~~~~~+--RawMirroredAlleleBFractions

**Directly known subclasses:**

public static 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, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

**Methods inherited from Object:**

asThis, &lt;-, [[, [[&lt;-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**Henrik Bengtsson (<http://www.braju.com/R/>)

---

 RawSequenceReads     *The RawSequenceReads class*


---

**Description**

Package: aroma.core

**Class RawSequenceReads**

Object

~~|

~~+--RawGenomicSignals

~~~~~|

~~~~~+--RawSequenceReads

**Directly known subclasses:**public static class **RawSequenceReads**extends [RawGenomicSignals](#)**Usage**

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

**Arguments**

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

**Fields and Methods****Methods:**

|                       |   |
|-----------------------|---|
| binnedSums            | - |
| extractRawCopyNumbers | - |
| nbrOfReads            | - |
| plot                  | - |

**Methods inherited from RawGenomicSignals:**

addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

SegmentedAlleleBFractions

*The SegmentedAlleleBFractions class*

---

**Description**

Package: aroma.core

**Class SegmentedAlleleBFractions**

Object

~~ |

~~+--RawGenomicSignals

~~~~~ |

```
~~~~~+--RawAlleleBFractions
~~~~~|
~~~~~+--SegmentedGenomicSignalsInterface
~~~~~|
~~~~~+--SegmentedAlleleBFractions
```

### Directly known subclasses:

```
public static 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, getStateColorMap, getStateColors, getStates, getUniqueStates, kernelSmoothingByState, plot, points, setStateColorMap, setStates

#### Methods inherited from [RawAlleleBFractions](#):

extractRawMirroredAlleleBFractions, plot

#### Methods inherited from [RawGenomicSignals](#):

addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXy, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

#### Methods inherited from [Object](#):

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

 SegmentedCopyNumbers

*The SegmentedCopyNumbers class*


---

## Description

Package: aroma.core

**Class SegmentedCopyNumbers**

Object

~~ |

~~+---RawGenomicSignals

~~~~~ |

~~~~~+---RawCopyNumbers

~~~~~ |

~~~~~+---SegmentedGenomicSignalsInterface

~~~~~ |

~~~~~+---SegmentedCopyNumbers

**Directly known subclasses:**

public static class **SegmentedCopyNumbers**

extends [SegmentedGenomicSignalsInterface](#)

## Usage

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

## Arguments

|        |  |
|--------|--|
| ...    | Arguments passed to <a href="#">RawCopyNumbers</a> .   |
| states | A <a href="#">function</a> returning the copy-number states given a <a href="#">vector</a> of locus positions. |

## Fields and Methods

**Methods:**

*No methods defined.*

**Methods inherited from [SegmentedGenomicSignalsInterface](#):**

as.data.frame, binnedSmoothingByState, extractSubsetByState, getStateColorMap, getStateColors, getStates, getUniqueStates, kernelSmoothingByState, plot, points, setStateColorMap, setStates

**Methods inherited from [RawCopyNumbers](#):**

as.data.frame, cnRange, getCn, getCNs, plot

**Methods inherited from RawGenomicSignals:**

addBy, addLocusFields, append, applyBinaryOperator, as.data.frame, binnedSmoothing, divideBy, estimateStandardDeviation, extractDataForSegmentation, extractRegion, extractSubset, gaussianSmoothing, getChromosome, getLocusFields, getName, getPositions, getSigma, getSignals, getWeights, getXScale, getXY, getYScale, hasWeights, kernelSmoothing, lines, multiplyBy, nbrOfLoci, plot, points, setLocusFields, setName, setSigma, setWeights, setXScale, setYScale, signalRange, sort, subtractBy, summary, xMax, xMin, xRange, xSeq, yMax, yMin, yRange

**Methods inherited from Object:**

asThis, <-, [[, [[<-, as.character, attach, attachLocally, clearCache, clone, detach, equals, extend, finalize, gc, getEnvironment, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, objectSize, print, registerFinalizer, save

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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

# - - - - -
# 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=

# - - - - -
# 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)
lines(cnSa, col="blue")
points(cnSa, col="blue")

cnSb <- binnedSmoothingByState(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

```

---

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  -
getStateColorMap      -
getStateColors        -
getStates              -
getUniqueStates       -
kernelSmoothingByState -
plot                  -
points                -
setStateColorMap      -
setStates              -
```

#### Methods inherited from Interface:

```
extend, print, uses
```

### Author(s)

```
Henrik Bengtsson (http://www.braju.com/R/)
```

---

```
UnitAnnotationDataFile
```

```
The UnitAnnotationDataFile interface class
```

---

### Description

```
Package: aroma.core
```

```
Class UnitAnnotationDataFile
```

**Interface**

~~|

~~+--*UnitAnnotationDataFile***Directly known subclasses:**[AromaUnitTypesFile](#), [TextUnitNamesFile](#), [UnitNamesFile](#), [UnitTypesFile](#)

public abstract 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           -
getAromaUgpFile     -
getChipType         -
getPlatform         -
nbrOfUnits          -
```

**Methods inherited from Interface:**

extend, print, uses

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

 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      Gets the indices of units by their names.
nbrOfUnits  -

```

**Methods inherited from UnitAnnotationDataFile:**

byChipType, getAromaUgpFile, getChipType, getPlatform, nbrOfUnits

**Methods inherited from Interface:**

extend, print, uses

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**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, getAromaUgpFile, getChipType, 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 (<http://www.braju.com/R/>)

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