AffyGenePDInfo-class

Class AffyGenePDInfo

Description

Short description

Objects from the Class

Objects can be created by calls of the form `new("AffyGenePDInfo", ...)`. 

Slots

- `getdb`: Object of class "function"
- `tableInfo`: Object of class "data.frame"
- `geometry`: Object of class "integer"
- `manufacturer`: Object of class "character"
- `genomebuild`: Object of class "character"

Extends


Methods

No methods defined with class "AffyGenePDInfo" in the signature.

Author(s)

RS

Examples

```
showClass("AffyGenePDInfo")
```
DBPDIInfo-class  Class “DBPDIInfo”

Description
A class for Platform Design Information objects, stored using a database approach

Objects from the Class
Objects can be created by calls of the form `new("DBPDIInfo", ...)`.

Slots
- `getdb`: Object of class "function"
- `tableInfo`: Object of class "data.frame"
- `manufacturer`: Object of class "character"
- `genomebuild`: Object of class "character"
- `geometry`: Object of class "integer" with length 2 (rows x columns)

Extends
Class "PDInfo", directly.

Methods
No methods defined with class "DBPDIInfo" in the signature.

Examples
```r
##---- Should be DIRECTLY executable !! ----
```

FeatureSet-class  Classes for Feature level data

Description
Virtual class to store feature level data.

Objects from the Class
This is a VIRTUAL class.
Slots

- **manufacturer**: Object of class "character"
- **platform**: Object of class "character"
- **assayData**: Object of class "AssayData"
- **phenoData**: Object of class "AnnotatedDataFrame"
- **featureData**: Object of class "AnnotatedDataFrame"
- **experimentData**: Object of class "MIAME"
- **annotation**: Object of class "character"
- **.__classVersion__**: Object of class "Versions"

Extends

Class **class.eSet**, directly. Class **class.VersionedBiobase**, by class "eSet", distance 2. Class **class.Versioned**, by class "eSet", distance 3.

Methods

No methods defined with class "FeatureSet" in the signature.

Author(s)

Benilton Carvalho

See Also

eSet, VersionedBiobase, Versioned

Description

Classes to store data from Expression/Exon/SNP/Tiling arrays at the feature level.

Objects from the Class

Objects can be created by calls of the form `new("ExonFeatureSet", assayData, manufacturer, platform, exprs, phenoData, featureData, experimentData, annotation, ...).`

Slots

- **manufacturer**: Object of class "character"
- **platform**: Object of class "character"
- **assayData**: Object of class "AssayData"
- **phenoData**: Object of class "AnnotatedDataFrame"
- **featureData**: Object of class "AnnotatedDataFrame"
- **experimentData**: Object of class "MIAME"
- **annotation**: Object of class "character"
- **.__classVersion__**: Object of class "Versions"
GeneFeatureSet-class

Extends


Methods

No methods defined with class "ExonFeatureSet" in the signature.

Author(s)

Benilton Carvalho

See Also

eSet, VersionedBiobase, Versioned

Examples

```r
set.seed(1)
tmp <- 2^matrix(rnorm(100), ncol=4)
rownames(tmp) <- 1:25
colnames(tmp) <- paste("sample", 1:4, sep="")
efs <- new("ExpressionFeatureSet", exprs=tmp)
```

GeneFeatureSet-class

Class GeneFeatureSet

Description

A short description

Objects from the Class

Objects can be created by calls of the form `new("GeneFeatureSet", assayData, phenoData, featureData, experimentData, annotation, ...)`.

Slots

- `manufacturer`: Object of class "character"
- `platform`: Object of class "character"
- `assayData`: Object of class "AssayData"
- `phenoData`: Object of class "AnnotatedDataFrame"
- `featureData`: Object of class "AnnotatedDataFrame"
- `experimentData`: Object of class "MIAME"
- `annotation`: Object of class "character"
- `__classVersion__`: Object of class "Versions"
PDInfo-class

Extends


Methods

No methods defined with class "GeneFeatureSet" in the signature.

Author(s)

RS

Examples

```
showClass("GeneFeatureSet")
```

---

PDInfo-class

Classes "PDInfo" and "SNPPDInfo"

Description

Containers for chip information

Slots

- **manufacturer**: Object of class "character"
- **genomebuild**: Object of class "character"
- **geometry**: Object of class "integer" with length 2 (rows x columns)

Methods

No methods defined with class "PDInfo" in the signature.

Examples

```
## Should be DIRECTLY executable !! ----
```
Class "QuantificationSet"

Description

A virtual class to store summarized measures.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

- **assayData**: Object of class "AssayData"
- **phenoData**: Object of class "AnnotatedDataFrame"
- **featureData**: Object of class "AnnotatedDataFrame"
- **experimentData**: Object of class "MIAME"
- **annotation**: Object of class "character"
- **.\_classVersion\_**: Object of class "Versions"

Extends

Class eSet, directly. Class VersionedBiobase, by class "eSet", distance 2. Class Versioned, by class "eSet", distance 3.

Methods

No methods defined with class "QuantificationSet" in the signature.

See Also

SnpQSet, SnpCnvQSet

Examples

showClass("QuantificationSet")
**calls**

*Accessors for SnpCallSet*

**Description**

Accessors and replacement methods for genotype calls and associated confidences.

**Usage**

```r
calls(object)
callsConfidence(object)
calls(object) <- value
callsConfidence(object) <- value
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>SnpCallSet object.</td>
</tr>
<tr>
<td>value</td>
<td>matrix</td>
</tr>
</tbody>
</table>

**Value**

Matrix with R rows (SNP’s) and C columns (Samples) with genotype calls (1 - AA; 2 - AB; 3 - BB) or confidences.

**See Also**

crlmm

---

**SnpCallSetPlus-class**

*Class "SnpCallSetPlus"*

**Description**

Description for Genotyping

**Objects from the Class**

Objects of this class are unions of Quantification and Calls.

**Slots**

- **assayData**: Object of class "AssayData"
- **phenoData**: Object of class "AnnotatedDataFrame"
- **featureData**: Object of class "AnnotatedDataFrame"
- **experimentData**: Object of class "MIAME"
- **annotation**: Object of class "character"
- **__classVersion__**: Object of class "Versions"
SnpCnvFeatureSet-class

Extends

Methods

calculateCopyNumber signature(object="SnpCallSetPlus") See calculateCopyNumber
db signature(object="SnpCallSetPlus")

Examples

showClass("SnpCallSetPlus")

SnpCnvFeatureSet-class

Class "SnpCnvFeatureSet"

Description
A class to store feature-level intensities from arrays that contain both SNP and CNV probes.

Objects from the Class

Objects can be created by calls of the form new("SnpCnvFeatureSet", assayData, phenoData, featureData, experimentData, annotation, ...).

Slots

manufacturer: Object of class "character"
platform: Object of class "character"
assayData: Object of class "AssayData"
phenoData: Object of class "AnnotatedDataFrame"
featureData: Object of class "AnnotatedDataFrame"
experimentData: Object of class "MIAME"
annotation: Object of class "character"
__.classVersion__: Object of class "Versions"

Extends
SnpCnvQSet-class

Methods

No methods defined with class "SnpCnvFeatureSet" in the signature.

Examples

showClass("SnpCnvFeatureSet")

SnpCnvQSet-class  Class "SnpCnvQSet"

Description

A class to store summarized measures from SnpCnvFeatureSet objects

Objects from the Class

Objects can be created by calls of the form new("SnpCnvQSet", assayData, phenoData, featureData, experimentData, annotation, ...).

Slots

assayData: Object of class "AssayData"
phenoData: Object of class "AnnotatedDataFrame"
featureData: Object of class "AnnotatedDataFrame"
experimentData: Object of class "MIAME"
annotation: Object of class "character"
__classVersion__: Object of class "Versions"

Extends

Class QuantificationSet, directly. Class eSet, by class "QuantificationSet", distance 2. Class VersionedBiobase, by class "QuantificationSet", distance 3. Class Versioned, by class "QuantificationSet", distance 4.

Methods

No methods defined with class "SnpCnvQSet" in the signature.

Examples

showClass("SnpCnvQSet")
cnConfidence  Accessors for SnpCopyNumberSet objects

Description
Accessors and replacement methods for SnpCopyNumberSet objects.

Usage

copyNumber(object)
cnConfidence(object)
copyNumber(object)<-value
cnConfidence(object)<-value

Arguments

  object SnpCopyNumberSet object
  value    matrix

Value
Matrix with R rows (SNP’s) and C columns (Samples) containing copy number estimates and con-
fidences.

SnpLevelSet-class  Class "SnpLevelSet"

Description
Virtual class for SNP-level data

Objects from the Class
A virtual Class: No objects may be created from it.

Slots

  assayData: The usual restrictions on assayData: contains matrices with equal dimensions,
             and with column number equal to nrow(phenoData). Class: class.AssayData
  phenoData: See class.eSet
  featureData: See class.eSet
  experimentData: See class.eSet
  annotation: See class.eSet
  __classVersion__: Object of class "Versions"

Extends
Class eSet, directly. Class VersionedBiobase, by class "eSet", distance 2. Class Versioned, by class "eSet", distance 3.
Methods

calls signature(object = "SnpLevelSet"): Accessor for matrix of genotype calls
calls<- signature(object = "SnpLevelSet", value = "matrix"): Replacement method for genotype calls.
callsConfidence signature(object = "SnpLevelSet"): Accessor for matrix of confidence scores for the genotype calls
callsConfidence<- signature(object = "SnpLevelSet", value = "matrix"): Replacement method
cromosome signature(object = "SnpLevelSet"): See also chromosome
cromosome<- signature(object = "SnpLevelSet", value = "character"): See also chromosome
cnConfidence signature(object = "SnpLevelSet"): Accessor for matrix of confidence scores for the copy number estimates.
cnConfidence<- signature(object = "SnpLevelSet", value = "matrix"): Replacement method for confidence scores of copy number estimates.
combine signature(x = "SnpLevelSet", y = "SnpLevelSet"): Useful for combining two objects with the same phenoData. For instance, combine an object created from the Hind 50k chip and an object created from the Xba 50k chip.
copyNumber signature(object = "SnpLevelSet"): Accessor for matrix of copy numbers.
copyNumber<- signature(object = "SnpLevelSet", value = "matrix"): Replacement method for copy number matrices
db signature(object = "SnpLevelSet"): See also db
db signature(object = "SnpLevelSet"): See also position

Author(s)
RS

Examples

showClass("SnpLevelSet")

---

SnpQSet-class

Class “SnpQSet”

Description

Class to store Snp (Quantifications) Summaries

Objects from the Class

Objects can be created by calls of the form new("SnpQSet", assayData, senseThetaA, senseThetaB, antisenseThetaA, antisenseThetaB, phenoData, featureData, experimentData, annotation).
Slots

- **assayData**: Object of class "AssayData"
- **phenoData**: Object of class "AnnotatedDataFrame"
- **featureData**: Object of class "AnnotatedDataFrame"
- **experimentData**: Object of class "MIAME"
- **annotation**: Object of class "character"
- **__classVersion__**: Object of class "Versions"

Extends

Class **eSet**, directly. Class **VersionedBiobase**, by class "eSet", distance 2. Class **Versioned**, by class "eSet", distance 3.

Methods

No methods defined with class "SnpQSet" in the signature.

See Also

**eSet, VersionedBiobase, Versioned**

Examples

```r
##---- Should be DIRECTLY executable !! ----
SnpCallSet-class
"SnpSet" Extensions

Description

Class to store genotype calls / copy number estimates (and confidences) obtained via SNP arrays.

Objects from the Class

Objects can be created by calls of the form `new("SnpCallSet", assayData, featureData, phenoData, experimentData, annotation, calls, callsConfidence, ...)`.

Slots

- **assayData**: Object of class "AssayData"
- **phenoData**: Object of class "AnnotatedDataFrame"
- **featureData**: Object of class "AnnotatedDataFrame"
- **experimentData**: Object of class "MIAME"
- **annotation**: Object of class "character"
- **__classVersion__**: Object of class "Versions"
Class `TilingQSet`:

**Description**

A place-holder for future uses of Quantification on Tiling Arrays.

**Objects from the Class**

Objects can be created by calls of the form `new("TilingQSet", assayData, M, phenoData, featureData, experimentalData, annotation)`.

**Slots**

- `assayData`: Object of class "AssayData"
- `phenoData`: Object of class "AnnotatedDataFrame"
- `featureData`: Object of class "AnnotatedDataFrame"
- `experimentData`: Object of class "MIAME"
- `annotation`: Object of class "character"
- `__classVersion__`: Object of class "Versions"

**Extends**

Class "QuantificationSet", directly. Class "class.eSet", by class "QuantificationSet", distance 2. Class "class.VersionedBiobase", by class "QuantificationSet", distance 3. Class "class.Versioned", by class "QuantificationSet", distance 4.

**Methods**

- `initialize` signature(.Object = "TilingQSet"):.........

**Note**

Alpha-version
Author(s)

Benilton Carvalho

Examples

showClass("TilingQSet")

affyPlatforms  Available Affymetrix platforms for SNP arrays

Description

Provides a listing of available Affymetrix platforms currently supported by the R package oligo

Usage

affyPlatforms()

Value

A vector of class character.

Author(s)

R. Scharpf

Examples

affyPlatforms()

calculateCopyNumber  Calculates copy number as the average of SNP-level summaries from the A and B alleles

Description

Calculates copy number as the average of SNP-level summaries from the A and B alleles from an object of class SnpCallSetPlus

Usage

calculateCopyNumber(object, ...)

Arguments

object  an instance of SnpCallSetPlus

...  Not implemented
**Details**

The average A (and B) allele intensities for each SNP is centered by the median intensity across samples (should have a reasonable (e.g., > 10) samples). Additionally, we assume that the median intensity across all samples for autosomes should be the same for homozygous genotypes and heterozygous genotypes. The resulting intensities are then recentered at 2 copies (for autosomes), 1 for the male X chromosome, 2 for the female X, etc. We assume that for a given SNP, the median copy number is normal. If this is not likely to be the case, alternative approaches should be explored.

**Value**

A matrix of copy number intensities.

**Author(s)**

R. Scharpf

**See Also**

*SnpCallSetPlus-class*

---

**Description**

Returns chromosome information.

**Usage**

```r
chromosome(object)
chromosome(object) <- value
```

**Arguments**

- `object`: object inheriting from `SnpLevelSet`
- `value`: vector of class `character`

**Value**

Vector with chromosome information. Chromosomes are recorded as character strings (e.g., "1", "2", "X", ...)

**Author(s)**

R. Scharpf
Description

This function will return the SQLite connection to the database associated to objects used in oligo.

Usage

db(object)

Arguments

object Object of valid class. See methods.

Value

SQLite connection.

Methods

object = "SnpCallSet" object of class SnpCallSet
object = "DBPDInfo" object of class DBPDInfo
object = "SnpLevelSet" object of class SnpLevelSet

Author(s)

Benilton Carvalho

Examples

## db(object)

---

Methods for oligoSnpSet method

Description

Methods for oligoSnpSet
### platformDesign-class

**Class** "platformDesign"

#### Description

Container for chip information, this is environment-based and is being replaced by DBPDIinfo.

#### Objects from the Class

Objects can be created by calls of the form `new("platformDesign", ...)`.

#### Slots

- **featureInfo**: Object of class "environment" containing vectors describing the array.
- **featureTypeDescription**: Object of class "list"
- **type**: Object of class "character" describing the type of the array ("expression", "exon", "SNP", "tiling"
- **nrow**: Object of class "numeric" providing the number of rows.
- **ncol**: Object of class "numeric" providing the number of columns
- **nwells**: Object of class "numeric" providing the number of wells - NimbleGen specific.
- **lookup**: Object of class "data.frame": a lookup table for complex designs by NimbleGen.
- **indexes**: Object of class "list" ~~
- **platforms**: Object of class "character" ~~
- **manufacturer**: Object of class "character" ~~
- **genomebuild**: Object of class "character" ~~

#### Extends

Class "PDInfo", directly.

#### Methods

No methods defined with class "platformDesign" in the signature.

#### Examples

`##---- Should be DIRECTLY executable !! ----`
position  

Accessor to position information

Description

position will return the genomic position of a SNP.

Usage

position(object)

Arguments

object  

object inheriting from SnpLevelSet

Details

position will return genomic position of a SNP (number of basepairs from the 5-prime chromosomal end)

Value

an integer

Author(s)

R. Scharpf
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