

# oligoClasses

April 19, 2009

---

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

Class "[AffyExpressionPDInfo](#)", directly. Class "[ExpressionPDInfo](#)", by class "Affy-ExpressionPDInfo", distance 2. Class "[DBPDInfo](#)", by class "AffyExpressionPDInfo", distance 3. Class "[PDInfo](#)", by class "AffyExpressionPDInfo", distance 4.

## Methods

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

## Author(s)

RS

## Examples

```
showClass("AffyGenePDInfo")
```

---

DBPDInfo-class      *Class "DBPDInfo"*

---

### 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("DBPDInfo", ...)`.

### 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 "DBPDInfo" in the signature.

### Examples

```
##---- 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](#)

---

ExonFeatureSet-class

*"FeatureSet" Extensions*

---

**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"

**Extends**

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

**Methods**

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

**Author(s)**

Benilton Carvalho

**See Also**

`eSet`, `VersionedBiobase`, `Versioned`

**Examples**

```
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"

**Extends**

Class "[FeatureSet](#)", directly. Class [eSet](#), by class "FeatureSet", distance 2. Class [VersionedBiobase](#), by class "FeatureSet", distance 3. Class [Versioned](#), by class "FeatureSet", distance 4.

**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 !! ----
```

QuantificationSet-class  
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

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

### Arguments

object	SnpCallSet object.
value	matrix

### 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"

**Extends**

Class "SnpQSet", directly. Class "SnpCnvQSet", directly. Class "SnpCallSet", directly. Class "QuantificationSet", by class "SnpQSet", distance 2. Class eSet, by class "SnpQSet", distance 3. Class VersionedBiobase, by class "SnpQSet", distance 4. Class Versioned, by class "SnpQSet", distance 5. Class "QuantificationSet", by class "SnpCnvQSet", distance 2. Class eSet, by class "SnpCnvQSet", distance 3. Class VersionedBiobase, by class "SnpCnvQSet", distance 4. Class Versioned, by class "SnpCnvQSet", distance 5. Class "SnpLevelSet", by class "SnpCallSet", distance 2. Class eSet, by class "SnpCallSet", distance 3. Class VersionedBiobase, by class "SnpCallSet", distance 4. Class Versioned, by class "SnpCallSet", distance 5.

**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**

Class "SnpFeatureSet", directly. Class "FeatureSet", by class "SnpFeatureSet", distance 2. Class eSet, by class "SnpFeatureSet", distance 3. Class VersionedBiobase, by class "SnpFeatureSet", distance 4. Class Versioned, by class "SnpFeatureSet", distance 5.



## 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 confidences.

---

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
- chromosome** signature(object = "SnpLevelSet"): See also [chromosome](#)
- chromosome<-** 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](#)
- position** 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**

```
##----- 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"

**Extends**

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

**Methods**

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

**See Also**

`eSet`, `VersionedBiobase`, `Versioned`

**Examples**

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

---

TilingQSet-class    *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**

<code>object</code>	an instance of SnpCallSetPlus
<code>...</code>	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](#)

---

chromosome

*Accessor for chromosome information*

---

**Description**

Returns chromosome information.

**Usage**

```
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

---

`db`*Get the connection to the SQLite Database*

---

**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)
```

---

`oligoSnpSet-methods`*Methods for oligoSnpSet class*

---

**Description**

Methods for oligoSnpSet



---

```
platformDesign-class
  Class "platformDesign"
```

---

### Description

Container for chip information, this is environment-based and is being replaced by [DBPDInfo](#).

### 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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