R topics documented:

affyPlatforms ........................................ 2
chromosome ........................................ 2
efsExample ........................................ 3
sqsExample ........................................ 3
sfsExample ........................................ 4
sqsExample ........................................ 4
DBPDInfo-class ..................................... 5
db ..................................................... 5
exprs-methods ...................................... 6
FeatureSet-class ..................................... 6
genomeBuild ......................................... 7
getPlatformDesign ................................... 7
mmindex .............................................. 8
kind .................................................... 9
length-methods ..................................... 9
manufacturer-methods .............................. 9
oligoSnpSet-methods .............................. 10
geometry ............................................. 10
platform-methods ................................... 10
pmAllele ............................................. 11
pmFragmentLength-methods ....................... 11
pmPosition .......................................... 11
pm Strand ........................................... 12
position ............................................. 12
probeNames ......................................... 13
QuantificationSet-class ............................ 13
sampleNames-methods ............................ 14
mmSequence .......................................... 14
calls ............................................... 15
SnpCallSetPlus-class .............................. 15
SnpCnvQSet-class ................................... 16
cnfConfidence ....................................... 17
SnpLevelSet-class ................................... 17
SnpQSet-class ....................................... 18
cfA ................................................... 19
antisenseThetaA .................................... 20
SnpCallSet-class .................................... 21
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()

---

chromosome  

Accessor for chromosome information

Description

Returns chromosome information.

Usage

pmChr(object)

Arguments

object TilingFeatureSet or SnpCallSet object

Details

chromosome() returns the chromosomal information for all probes and pmChr() subsets the output to the PM probes only (if a TilingFeatureSet object).

Value

Vector with chromosome information.
**efsExample**

**ExpressionFeatureSet Object**

**Description**
Example of ExpressionFeatureSet Object.

**Usage**
```
data(efsExample)
```

**Format**
Object belongs to ExpressionFeatureSet class.

**Examples**
```
data(efsExample)
class(efsExample)
```

---

**scqsExample**

**SnpCnvQSet Example**

**Description**
Example of SnpCnvQSet object.

**Usage**
```
data(scqsExample)
```

**Format**
Object belongs to SnpCnvQSet class.

**Examples**
```
data(scqsExample)
class(scqsExample)
```
**sfsExample**  
*SnpFeatureSet Example*

**Description**  
Example of SnpFeatureSet object.

**Usage**  
`data(sfsExample)`

**Format**  
Object belongs to SnpFeatureSet class

**Examples**  
`data(sfsExample)`  
`class(sfsExample)`

---

**sqsExample**  
*SnpQSet Example*

**Description**  
Example of SnpQSet instance.

**Usage**  
`data(sqsExample)`

**Format**  
Belongs to SnpQSet class.

**Examples**  
`data(sqsExample)`  
`class(sqsExample)`
**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)

**Methods**

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

---

**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 = "FeatureSet"` object of class FeatureSet
- `object = "SnpCallSet"` object of class SnpCallSet
- `object = "DBPDInfo"` object of class DBPDInfo
- `object = "SnpLevelSet"` object of class SnpLevelSet
FeatureSet-class

Author(s)
Benilton Carvalho

Examples

## db(object)

### exprs-methods

**Accessor for the ’exprs’ slot**

**Description**

Accessor for the ’exprs’/’se.exprs’ slot of FeatureSet-like objects

**Methods**

object = "ExpressionSet"  Expression matrix for objects of this class. Usually results of preprocessing algorithms, like RMA.
object = "FeatureSet"  General container ’exprs’ inherited from eSet
object = "SnpSet"  General container ’exprs’ inherited from eSet, not yet used.

**FeatureSet-class  "FeatureSet" and "FeatureSet" Extensions**

**Description**

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

**Objects from the Class**

The FeatureSet class is VIRTUAL. Therefore users are not able to create instances of such class.

Objects for FeatureSet-like classes can be created by calls of the form: new(CLASSNAME, assayData, manufacturer, platform, exprs, phenoData, featureData, experimentData, annotation, ...). But the preferred way is using parsers like read.celfiles and read.xysfiles.

**Slots**

manufacturer: 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"
Methods

show signature(.Object = "FeatureSet"): show object contents

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)

genomeBuild

Genome Build Information

Description

Returns the genome build information. This information comes from the annotation package and is given as an argument during the package creation process.

Usage

geneBuild(object)

Arguments

object PDInfo or FeatureSet object.

getPlatformDesign

Retrieve Platform Design object

Description

Retrieve platform design object.

Usage

getPlatformDesign(object)
getPD(object)

Arguments

object FeatureSet object
**Details**

Retrieve platform design object.

**Value**

platformDesign or PDInfo object.

---

**Description**

Extracts the indexes for PM, MM or background probes.

**Usage**

```r
mmindex(object, ...)  
pmindex(object, ...)  
bgindex(object, ...)
```

**Arguments**

- **object**: FeatureSet or DBPDInfo object
- **...**: Extra arguments, not yet implemented

**Details**

The indices are ordered by ‘fid’, i.e. they follow the order that the probes appear in the CEL/XYS files.

**Value**

A vector of integers representing the rows of the intensity matrix that correspond to PM, MM or background probes.

**Examples**

```r
## How pm() works  
## Not run:  
x <- read.celfiles(list.celfiles())  
pms0 <- pm(x)  
pmi <- pmindex(x)  
pms1 <- exprs(x)[pmi,]  
identical(pms0, pms1)  
## End(Not run)
```
**kind**

**Array type**

**Description**
Retrieves the array type.

**Usage**

```r
t = last<-
```

**Arguments**

- `object`: FeatureSet or DBPDInfo object

**Value**
String: "Expression", "Exon", "SNP" or "Tiling"

**Examples**

```r
if (require(pd.mapping50k.xba240)){
data(sfsExample)
annotation(sfsExample) <- "pd.mapping50k.xba240"
kind(sfsExample)
}
```

---

**length-methods**

**Number of samples for FeatureSet-like objects.**

**Description**
Number of samples for FeatureSet-like objects.

**Methods**

- `x = "FeatureSet"` Number of samples

---

**manufacturer-methods**

**Manufacturer ID for FeatureSet-like objects.**

**Description**
Manufacturer ID for FeatureSet-like and DBPDInfo-like objects.

**Methods**

- `object = "FeatureSet"` Manufacturer ID
- `object = "PDInfo"` Manufacturer ID
Description

Methods for oligoSnpSet

geometry

Array Geometry Information

Description

For a given array, geometry returns the physical geometry of it.

Usage

geometry(object)

Arguments

object PDInfo object

Examples

if (require(pd.mapping50k.xba240))
  geometry(pd.mapping50k.xba240)

Description

Platform Information

Methods

object = "FeatureSet" platform information
pmAllele

Access the allele information for PM probes.

Description
Accessor to the allelic information for PM probes.

Usage
pmAllele(object)

Arguments
object SnpFeatureSet or PDInfo object.

pmFragmentLength-methods

Information on Fragment Length

Description
This method will return the fragment length for PM probes.

Methods
object = "AffySNPPDInfo" On AffySNPPDInfo objects, it will return the fragment length that contains the SNP in question.

pmPosition

Accessor to position information

Description
pmPosition will return the genomic position for the (PM) probes.

Usage
pmPosition(object)

Arguments
object AffySNPPDInfo, TilingFeatureSet or SnpCallSet object

Details
pmPosition will return genomic position for PM probes on a tiling array.

pmOffset will return the offset information for PM probes on SNP arrays.
pmStrand

Accessor to the strand information

Description
Returns the strand information on SNP arrays for PM probes (0 - sense / 1 - antisense).

Usage
pmStrand(object)

Arguments
object AffySNPPDInfo object

position

Accessory 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
**probeNames**

*Accessor to feature names*

**Description**

Accessor to PM feature names.

**Usage**

```r
probeNames(object, subset = NULL)
```

**Arguments**

- `object`: FeatureSet or DBPDInfo
- `subset`: not implemented yet.

---

**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")

---

**Sample names for FeatureSet-like objects**

**Description**

Returns sample names for FeatureSet-like objects.

**Methods**

- **object** = "FeatureSet"  
  Sample names

---

**Probe Sequences**

**Description**

Accessor to the (PM/MM/background) probe sequences.

**Usage**

- `mmSequence(object)`
- `pmSequence(object, ...)`
- `bgSequence(object, ...)`

**Arguments**

- **object**  
  FeatureSet, AffySNPPDInfo or DBPDInfo object
- **...**  
  additional arguments

**Value**

A DNAStringSet containing the PM/MM/background probe sequence associated to the array.
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**

- `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**

cr1mm

---

**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"
SnpCnvQSet-class

Extends


Methods

\( \text{db signature(object="SnpCallSetPlus")} \)

Examples

\( \text{showClass("SnpCallSetPlus")} \)

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 \( \text{new("SnpCnvQSet", assayData, phenoData, featureData, experimentData, annotation, \ldots).} \)

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

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

#### Arguments

- **object**: SnpCopyNumberSet
- **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"
SnpQSet-class

Class \texttt{SnpQSet} extends \texttt{Class eSet}, directly. Class \texttt{VersionedBiobase}, by class \texttt{eSet}, distance 2. Class \texttt{Versioned}, by class \texttt{eSet}, distance 3.

Methods

- \texttt{calls} \Signature{object = "SnpLevelSet"}: Accessor for matrix of genotype calls
- \texttt{calls<-} \Signature{object = "SnpLevelSet", value = "matrix"}: Replacement method for genotype calls.
- \texttt{callsConfidence} \Signature{object = "SnpLevelSet"}: Accessor for matrix of confidence scores for the genotype calls
- \texttt{callsConfidence<-} \Signature{object = "SnpLevelSet", value = "matrix"}: Replacement method
- \texttt{chromosome} \Signature{object = "SnpLevelSet"}: See also \texttt{chromosome}
- \texttt{chromosome<-} \Signature{object = "SnpLevelSet", value = "character"}: See also \texttt{chromosome}
- \texttt{cnConfidence} \Signature{object = "SnpLevelSet"}: Accessor for matrix of confidence scores for the copy number estimates.
- \texttt{cnConfidence<-} \Signature{object = "SnpLevelSet", value = "matrix"}: Replacement method for confidence scores of copy number estimates.
- \texttt{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.
- \texttt{copyNumber} \Signature{object = "SnpLevelSet"}: Accessor for matrix of copy numbers.
- \texttt{copyNumber<-} \Signature{object = "SnpLevelSet", value = "matrix"}: Replacement method for copy number matrices
- \texttt{db} \Signature{object = "SnpLevelSet"}: See also \texttt{db}
- \texttt{position} \Signature{object = "SnpLevelSet"}: See also \texttt{position}

Author(s)

RS

Examples

\texttt{showClass("SnpLevelSet")}

---

\texttt{SnpQSet-class} \texttt{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

---

getA

*Compute average log-intensities / log-ratios*

Description

Methods to compute average log-intensities and log-ratios across alleles, within strand.

Usage

```
getA(object)
gem(object)
```

Arguments

- `object` SnpQSet, SnpCnvQSet or TilingFeatureSet2 object.
For SNP data, SNPRMA summarizes the SNP information into 4 quantities (log2-scale):

antisenseThetaA  antisense allele A
antisenseThetaB  antisense allele B
senseThetaA  sense allele A
senseThetaB  sense allele B

The average log-intensities are given by: (antisenseThetaA + antisenseThetaB) / 2 and (senseThetaA + senseThetaB) / 2.

The average log-ratios are given by: antisenseThetaA - antisenseThetaB and senseThetaA - senseThetaB.

For Tiling data, getM and getA return the log-ratio and average log-intensities computed across channels: M = \log_2(\text{channel1}) - \log_2(\text{channel2}) A = (\log_2(\text{channel1}) + \log_2(\text{channel2})) / 2

Value

A 3-dimensional array (SNP’s x Samples x Strand) with the requested measure, when the input SNP data (50K, 250K).
A 2-dimensional array (SNP’s x Samples), when the input is from SNP 5.0 and SNP 6.0 arrays.
A 2-dimensional array if the input is from Tiling arrays.

See Also

snprma

antisenseThetaA  Summarized Measures for SNP

Description

SNPRMA summarizes the intensities for each SNP into 4 quantities. These measures are at the log2 scale and are used to create log-ratios and log-averages, which are used by the genotype algorithm and copy number tool.

Usage

antisenseThetaA(object)
antisenseThetaB(object)
senseThetaA(object)
senseThetaB(object)
thetaA(object)
thetaB(object)

Arguments

object   SnpQSet object
Details
For a given SNP, an Affymetrix SNP array usually contains multiple features for each combination allele x strand, on which the summaries are computed.

Value
A matrix with R rows (SNP’s) x C columns (Samples).

See Also
snprma, crlmm

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
Index

*Topic classes
  DBPDInfo-class, 4
  FeatureSet-class, 5
  QuantificationSet-class, 12
  SnpCallSet-class, 20
  SnpCallSetPlus-class, 14
  SnpCnvQSet-class, 15
  SnpLevelSet-class, 16
  SnpQSet-class, 17

*Topic datasets
  efsExample, 2
  scqsExample, 2
  sfsExample, 3
  sqsExample, 3

*Topic list
  affyPlatforms, 1

*Topic manip
  antisenseThetaA, 19
  chromosome, 1
  cnConfidence, 16
  genomeBuild, 6
  geometry, 9
  getA, 18
  getPlatformDesign, 6
  kind, 8
  mmindex, 7
  mmSequence, 13
  pmAllele, 10
  pmPosition, 10
  pmStrand, 11
  position, 11
  probeNames, 12

*Topic methods
  db, 4
  exprs-methods, 5
  length-methods, 8
  manufacturer-methods, 8
  oligoSnpSet-methods, 9
  platform-methods, 9
  pmFragmentLength-methods, 10
  sampleNames-methods, 13
  SnpCallSet-class, 20

*Topic misc
  affyPlatforms, 1
  AffyExonPDInfo-class
    (DBPDInfo-class), 4
  AffyExpressionPDInfo-class
    (DBPDInfo-class), 4
  AffyGenePDInfo-class
    (DBPDInfo-class), 4
  affyPlatforms, 1
  AffySNPCNVPDInfo-class
    (DBPDInfo-class), 4
  AffySNPPDInfo-class
    (DBPDInfo-class), 4
  AffySTPDInfo-class
    (DBPDInfo-class), 4
  AffyTilingPDInfo-class
    (DBPDInfo-class), 4
  antisenseThetaA, 19
  antisenseThetaA, SnpQSet-method
    (antisenseThetaA), 19
  antisenseThetaB, 19
  antisenseThetaB, SnpQSet-method
    (antisenseThetaA), 19
  bgindex
    (mmindex), 7
  bgindex, DBPDInfo-method
    (mmindex), 7
  bgindex, FeatureSet-method
    (mmindex), 7
  bgSequence
    (mmSequence), 13
  bgSequence, DBPDInfo-method
    (mmSequence), 13
  bgSequence, FeatureSet-method
    (mmSequence), 13
  calls, 14
  calls, oligoSnpSet-method
    (oligoSnpSet-methods), 9
  calls, SnpCallSet-method(calls), 14
  calls, SnpLevelSet-method
    (SnpLevelSet-class), 16
calls<-(calls), 14
calls<-, oligoSnpSet, matrix-method (oligoSnpSet-methods), 9
calls<-, SnpCallSet, matrix-method (calls), 14
calls<-, SnpLevelSet, matrix-method (SnpLevelSet-class), 16
callsConfidence(calls), 14
callsConfidence, oligoSnpSet-method (oligoSnpSet-methods), 9
callsConfidence, SnpCallSet-method (calls), 14
callsConfidence, SnpLevelSet-method (SnpLevelSet-class), 16
callsConfidence<-(cnConfidence), 16
callsConfidence<-, oligoSnpSet, matrix-method (oligoSnpSet-methods), 9
callsConfidence<-, SnpCopyNumberSet, matrix-method (SnpCopyNumberSet-class), 16
callsConfidence<-, SnpLevelSet, matrix-method (SnpLevelSet-class), 16
crllm, 14, 17
db<-, db, DBPDInfo-method (db), 4
db<-, db, FeatureSet-method (db), 4
db<-, db, SnpCopyNumberSet-method (db), 4
db<-, db, SnpLevelSet-method (SnpLevelSet-class), 16
db<-, db, SnpQSet-method (SnpLevelSet-class), 16
db<-, db-methods (db), 4
db<-, DBPDInfo-class, 4
db<-, eSet, 6, 12, 15, 17, 18, 20
eSet-methods (eSet-methods), 5
ExpressionFeatureSet-class (FeatureSet-class), 5
ExpressionPDInfo-class (DBPDInfo-class), 4
exprs<-, exprs-method (exprs-methods), 5
eSet-class, 5
GeneFeatureSet-class (FeatureSet-class), 5
genomeBuild, 6
genomeBuild, DBPDInfo-method (genomeBuild), 6
genomeBuild, FeatureSet-method (genomeBuild), 6
gene, 9
gene<-, geometry, DBPDInfo-method (geometry), 9
gene<-, getA, 18
gene<-, SnpCopyNumberSet-method (getA), 18
genomeBuild, 6
getA, TilingFeatureSet2-method (getA), 18
getM(getA), 18
getM, SnpCnvQSet-method (getA), 18
getM, SnpQSet-method (getA), 18
getM, TilingFeatureSet2-method (getA), 18
getPD(getPlatformDesign), 6
getPlatformDesign, 6
getPlatformDesign, FeatureSet-method (getPlatformDesign), 6
initialize, DBPDInfo-method (DBPDInfo-class), 4
initialize, FeatureSet-method (FeatureSet-class), 5
initialize, oligoSnpSet-method (oligoSnpSet-methods), 9
initialize, SnpCallSet-method (SnpCallSet-class), 20
initialize, SnpCallSetPlus-method (SnpCallSetPlus-class), 14
initialize, SnpCnvCallSetPlus-method (SnpCallSetPlus-class), 14
initialize, SnpCopyNumberSet-method (SnpCallSet-class), 20
initialize, SnpQSet-method (SnpQSet-class), 17

kind, 8
kind, AffyExonPDInfo-method (kind), 8
kind, AffyExpressionPDInfo-method (kind), 8
kind, AffyGenePDInfo-method (kind), 8
kind, AffySNPCNVPDInfo-method (kind), 8
kind, AffySNPPDInfo-method (kind), 8
kind, ExpressionPDInfo-method (kind), 8
kind, FeatureSet-method (kind), 8
kind, TilingPDInfo-method (kind), 8

length, FeatureSet-method (length-methods), 8
length-methods, 8

manufacturer, FeatureSet-method (manufacturer-methods), 8
manufacturer-methods, 8
manufacturer-methods (manufacturer-methods), 8

mmindex, 7
mmindex, DBPDInfo-method (mmindex), 7
mmindex, FeatureSet-method (mmindex), 7

mmSequence, 13
mmSequence, DBPDInfo-method (mmSequence), 13

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

NgsExpressionPDInfo-class (DBPDInfo-class), 4
NgsTilingPDInfo-class (DBPDInfo-class), 4

pmAllele, 10
pmAllele, AffySNPPDInfo-method (pmAllele), 10
pmAllele, SnpFeatureSet-method (pmAllele), 10

pmChr (chromosome), 1
pmChr, FeatureSet-method (chromosome), 1

pmFragmentLength (pmFragmentLength-methods), 10
pmFragmentLength, AffySNPPDInfo-method (pmFragmentLength-methods), 10

pmFragmentLength-methods, 10
pmindex (mmindex), 7
pmindex, DBPDInfo-method (mmindex), 7

pmindex, FeatureSet-method (mmindex), 7
pmOffset (pmPosition), 10
pmOffset, AffySNPPDInfo-method (pmPosition), 10

pmPosition, 10
pmPosition, ExpressionPDInfo-method (pmPosition), 10
pmPosition, TilingFeatureSet-method (pmPosition), 10
pmPosition, TilingPDInfo-method (pmPosition), 10
pmSequence (mmSequence), 13
pmSequence, AffySNPPDInfo-method (mmSequence), 13
pmSequence, DBPDInfo-method (mmSequence), 13
pmSequence, FeatureSet-method (mmSequence), 13
pmStrand, 11
pmStrand, AffySNPPDInfo-method (pmStrand), 11
position, 11, 17
position, SnpLevelSet-method (SnpLevelSet-class), 16
probeNames, 12
probeNames, DBPDInfo-method (probeNames), 12
probeNames, FeatureSet-method (probeNames), 12
QuantificationSet, 15
QuantificationSet-class, 12
read.celfiles, 5
read.xysfiles, 5
sampleNames, FeatureSet-method (sampleNames-methods), 13
sampleNames-methods, 13
scqsExample, 2
se.exprs, FeatureSet-method (exprs-methods), 5
senseThetaA (antisenseThetaA), 19
senseThetaA, SnpQSet-method (antisenseThetaA), 19
senseThetaB (antisenseThetaA), 19
senseThetaB, SnpQSet-method (antisenseThetaA), 19
sfsExample, 3
show, DBPDInfo-method (DBPDInfo-class), 4
show, FeatureSet-method (FeatureSet-class), 5
SnpCallSet, 15
SnpCallSet-class, 20
SnpCallSet-methods (SnpCallSet-class), 20
SnpCallSetPlus-class, 14
SnpCnvCallSetPlus-class (SnpCallSetPlus-class), 14
SnpCnvFeatureSet-class (FeatureSet-class), 5
SNPCNVDPDInfo-class (DBPDInfo-class), 4
SnpCnvQSet, 12, 15
SnpCnvQSet-class, 15
SnpCopyNumberSet-class (SnpCallSet-class), 20
SnpCopyNumberSet-methods (SnpCallSet-class), 20
SnpFeatureSet-class (FeatureSet-class), 5
SnpLevelSet, 15
SnpLevelSet-class, 16
SNPPDInfo-class (DBPDInfo-class), 4
SnpQSet, 12, 15
SnpQSet-class, 17
snprma, 19, 20
sqsExample, 3
thetaA (antisenseThetaA), 19
thetaA, SnpCnvQSet-method (antisenseThetaA), 19
thetaB (antisenseThetaA), 19
thetaB, SnpCnvQSet-method (antisenseThetaA), 19
TilingFeatureSet-class (FeatureSet-class), 5
TilingPDInfo-class (DBPDInfo-class), 4
Versioned, 6, 12, 15, 17, 18, 20
VersionedBiobase, 6, 12, 15, 17, 18, 20