pdInfoBuilder

March 24, 2012

AffyExpressionPDInfoPkgSeed-class

Class "AffyExpressionPDInfoPkgSeed"

Description

PD Info Package Seed for Affymetrix Expression Arrays

Objects from the Class

Objects can be created by calls of the form `new("AffyExpressionPDInfoPkgSeed", cdfFile, csvAnnoFile, tabSeqFile, ...)`.

Slots

`cdfFile`: CDF filename

`celFile`: CEL filename

`tabSeqFile`: TAB sequence file

`chipName`: Name of the chip or platform

`manufacturer`: chip/platform manufacturer

`url`: chip URL

`genomebuild`: The genome build this platform is based upon.

`organism`: organism for chip.

`species`: species for chip.

`version`: A character vector giving the version number of the package.

`license`: The license of the package

`author`: Author of the package

`email`: An email address to use in the Maintainer field

`biocViews`: Character data for the biocViews field of the DESCRIPTION file

Methods

chipName chipName
getGeometry initialize
makePdInfoPackage package creator

Examples

```
showClass("AffyExpressionPDInfoPkgSeed")
```

```
AffySNPCNVPDInfoPkgSeed-class
```
Class "AffySNPCNVPDInfoPkgSeed"

Description

This class represents Platform Design (PD) packages for Affymetrix genomewide (SNP 5.0 and SNP 6.0) arrays.

Objects from the Class

Objects can be created by calls of the form `new("AffySNPCNVPDInfoPkgSeed", cdfFile, csvAnnoFile, csvSeqFile, csvAnnoFileCnv, csvSeqFileCnv, splineParamFile, crlmmInfoFile, referenceDistFile, ...)`.

Slots

`cdfFile`: Path to the CDF file for this.

`csvAnnoFile`: Path to the Affymetrix CSV annotation for the SNP probes.

`csvSeqFile`: Path to the (SNP) probe sequence file.

`csvAnnoFileCnv`: Path to the Affymetrix CSV annotation for the CNV probes.

`csvSeqFileCnv`: Path to the (CNV) probe sequence file.

`splineParamFile`: Path to the spline parameters file used to compute the predicted accuracy of the the genotype calls. Used internally in `.predictAccuracy`.

`crlmmInfoFile`: Path to is data file containing regions data used by the `crlmm` function.

`referenceDistFile`: Path to a reference distribution file used in the normalization step. This is the reference used in `snprma`.

`chipName`: Name of the chip or platform

`manufacturer`: chip/platform manufacturer

`url`: chip URL

`genomebuild`: The genome build this platform is based upon.

`organism`: organism for chip.

`species`: species for chip.

`version`: A character vector giving the version number of the package.

`license`: The license of the package

`author`: Author of the package

`email`: An email address to use in the Maintainer field

`biocViews`: Character data for the biocViews field of the DESCRIPTION file

Methods

chipName `signature(object = "AffySNPCNVPDInfoPkgSeed")`: ...

getGeometry `signature(object = "AffySNPCNVPDInfoPkgSeed")`: ...

makePdInfoPackage `signature(object = "AffySNPCNVPDInfoPkgSeed")`: ...

Notes

IMPORTANT Users are strongly advised to download Affymetrix SNP packages from BioConductor.

The files used for slots `splineParamFile`, `crlmmInfoFile`, and `referenceDistFile` are generated by the Bioconductor project for each chip/platform and are hosted in our svn data repository at https://hedgehog.fhcrc.org/bioc-data/trunk/annotation/parms_store. When `makePdInfoPackage` is run, these files are simply copied to the `inst/extdata` directory of the generated package.

Author(s)

Benilton Carvalho

Examples

```
showClass("AffySNPCNVPDInfoPkgSeed")
```

AffySNPCNVPDInfoPkgSeed2-class
Class "AffySNPCNVPDInfoPkgSeed2"

Description

A generic annotation package builder for Affymetrix SNP/CNV arrays. This is a simplified version of the annotation package and `crlmm` will *NOT* work for them.

Objects from the Class

Objects can be created by calls of the form `new("AffySNPCNVPDInfoPkgSeed2", csvAnnoFileCnv, csvSeqFileCnv, ...)`.

Slots

`cdfFile`: Path to the CDF file for this.

`csvAnnoFile`: Path to the Affymetrix CSV annotation for the SNP probes.

`csvSeqFile`: Path to the (SNP) probe sequence file.

`csvAnnoFileCnv`: Path to the Affymetrix CSV annotation for the CNV probes.

`csvSeqFileCnv`: Path to the (CNV) probe sequence file.

`chipName`: Name of the chip or platform

`manufacturer`: chip/platform manufacturer

`url`: chip URL

`genomebuild`: The genome build this platform is based upon.

`organism`: organism for chip.

`species`: species for chip.

`version`: A character vector giving the version number of the package.

`license`: The license of the package

`author`: Author of the package

`email`: An email address to use in the Maintainer field

`biocViews`: Character data for the biocViews field of the DESCRIPTION file

Methods

chipName signature(object = "AffySNPCNVPDInfoPkgSeed2"): ...

makePdInfoPackage signature(object = "AffySNPCNVPDInfoPkgSeed2"): ...

Note

This is a simplified annotation package. CRLMM won't work for these objects.

The user may need to rename the columns or even add column names to the annotation and sequence files. In case problems are found, column names are suggested.

Author(s)

Benilton Carvalho

Examples

```
showClass("AffySNPCNVPDInfoPkgSeed2")
```

AffySNPPDInfoPkgSeed–class
                    Class "AffySNPPDInfoPkgSeed"

Description

This class represents Platform Design (PD) packages for Affymetrix mapping (SNP chip) arrays.

Objects from the Class

Objects can be created by calls of the form new("AffySNPPDInfoPkgSeed", splineParamFile, crlmmInfoFile, referenceDistFile, ...).

Slots

splineParamFile: Spline parameters file used to compute the predicted accuracy of the genotype calls.

crlmmInfoFile: Data file containing regions data used by the crlmm function.

referenceDistFile: Reference distribution file used in the normalization step by snprma.

cdfFile: CDF file for the design.

csvAnnoFile: Affymetrix CSV Annotation file.

csvSeqFile: Affymetrix Probe Sequence file.

chipName: Name of the chip or platform

manufacturer: chip/platform manufacturer

url: chip URL

genomebuild: The genome build this platform is based upon.

organism: organism for chip.

species: species for chip.

version: A character vector giving the version number of the package.

license: The license of the package

author: Author of the package

email: An email address to use in the Maintainer field

biocViews: Character data for the biocViews field of the DESCRIPTION file

Methods

chipName signature(object = "AffySNPPDInfoPkgSeed"): ...

getGeometry signature(object = "AffySNPPDInfoPkgSeed"): ...

makePdInfoPackage signature(object = "AffySNPPDInfoPkgSeed"): ...

Note

IMPORTANT The user is strongly advised to download Affymetrix SNP packages from BioConductor.

The files used for slots splineParamFile, crlmmInfoFile, and referenceDistFile are generated by the Bioconductor project for each chip/platform and are hosted in our svn data repository at https://hedgehog.fhcrc.org/bioc-data/trunk/annotation/parms_store. When makePdInfoPackage is run, these files are simply copied to the inst/extdata directory of the generated package.

Examples

```
showClass("AffySNPPDInfoPkgSeed")

cdfFile <- "Mapping250K_Nsp.cdf"
csvAnno <- "Mapping250K_Nsp_annot.csv"
csvSeq <- "Mapping250K_Nsp_probe_tab"

spline <- "pd.mapping250k.nsp.spline.params.rda"
refd <- "pd.mapping250k.nspRef.rda"
crlmmInf <- "pd.mapping250k.nspCrlmmInfo.rda"

pkg <- new("AffySNPPDInfoPkgSeed",
           version="0.1.5",
           author="A. U. Thor", email="au@thor.net",
           biocViews="AnnotationData",
           genomebuild="NCBI Build 35, May 2004",
           cdfFile=cdfFile, csvAnnoFile=csvAnno, csvSeqFile=csvSeq,
           splineParamFile=spline, crlmmInfoFile=crlmmInf,
           referenceDistFile=refd)

showMethods(classes=class(pkg))
```

AffySNPPDInfoPkgSeed2-class

Class "AffySNPPDInfoPkgSeed2"

Description

A generic annotation package builder for Affymetrix SNP arrays. This is a simplified version of the annotation package and crlmm will *not* work for them.

Objects from the Class

Objects can be created by calls of the form `new("AffySNPPDInfoPkgSeed2", cdfFile,`
`csvAnnoFile, csvSeqFile, ...)`.

Slots

`axiom`: Logical flag for experimental build of annotation packages for Axiom arrays.

`cdfFile`: CDF file for the design.

`csvAnnoFile`: Affymetrix CSV Annotation file.

`csvSeqFile`: Affymetrix Probe Sequence file.

`chipName`: Name of the chip or platform

`manufacturer`: chip/platform manufacturer

`url`: chip URL

`genomebuild`: The genome build this platform is based upon.

`organism`: organism for chip.

`species`: species for chip.

`version`: A character vector giving the version number of the package.

`license`: The license of the package

`author`: Author of the package

`email`: An email address to use in the Maintainer field

`biocViews`: Character data for the biocViews field of the DESCRIPTION file

Methods

chipName `signature(object = "AffySNPPDInfoPkgSeed2")`: ...

Note

This is a simplified annotation package. CRLMM won't work for these objects.

The user may need to rename the columns or even add column names to the annotation and sequence
files. In case problems are found, column names are suggested.

Examples

```
showClass("AffySNPPDInfoPkgSeed2")
```

`AffySTPDInfoPkgSeed-class`
                    Class "AffySTPDInfoPkgSeed" for the Sense Target gene-level array

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Description

container for parameters related to pdmapping package construction for ST type arrays

Objects from the Class

Objects can be created by calls of the form `new("AffySTPDInfoPkgSeed", pgfFile,`
`clfFile, probeFile, transFile, ...)`.

Slots

pgfFile: Object of class "ScalarCharacter" path to pgf

clfFile: Object of class "ScalarCharacter" path to clf

probeFile: Object of class "ScalarCharacter", path to probe sequence file (Optional)

transFile: Object of class "ScalarCharacter", path to trans file (Optional)

chipName: Name of the chip or platform

manufacturer: chip/platform manufacturer

url: chip URL

genomebuild: The genome build this platform is based upon.

organism: organism for chip.

species: species for chip.

version: A character vector giving the version number of the package.

license: The license of the package

author: Author of the package

email: An email address to use in the Maintainer field

biocViews: Character data for the biocViews field of the DESCRIPTION file

Methods

chipName signature(object = "AffySTPDInfoPkgSeed"): ...

getGeometry signature(object = "AffySTPDInfoPkgSeed"): ...

makePdInfoPackage signature(object = "AffySTPDInfoPkgSeed"): ...

Author(s)

B. Carvalho

Examples

```
showClass("AffySTPDInfoPkgSeed")
```

AffyTilingPDInfoPkgSeed-class

Class "AffyTilingPDInfoPkgSeed"

Description

PD Info Package Seed for Affymetrix Tiling Arrays

Objects from the Class

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

Slots

    `bpmapFile`: BPMAP File - provided by Affymetrix

    `celFile`: CEL File - provided by Affymetrix

    `chipName`: Name of the chip or platform

    `manufacturer`: chip/platform manufacturer

    `url`: chip URL

    `genomebuild`: The genome build this platform is based upon.

    `organism`: organism for chip.

    `species`: species for chip.

    `version`: A character vector giving the version number of the package.

    `license`: The license of the package

    `author`: Author of the package

    `email`: An email address to use in the Maintainer field

    `biocViews`: Character data for the biocViews field of the DESCRIPTION file

Methods

    makePdInfoPackage `signature(object = "AffyTilingPDInfoPkgSeed")`: ...

    chipName `signature(object = "AffyTilingPDInfoPkgSeed")`: ...

Examples

    `showClass("AffyTilingPDInfoPkgSeed")`

`NgsExpressionPDInfoPkgSeed-class`
Class "NgsExpressionPDInfoPkgSeed"

Description

    PDInfo package Seed for NimbleGen Expression arrays

Objects from the Class

    Objects can be created by calls of the form `new("NgsExpressionPDInfoPkgSeed", ndfFile, pairFile, xysFile, ngdFile ...)`.

Slots

    `ndfFile`: NDF (NimbleGen Design) file

    `xysFile`: XYS File - used as template

    `chipName`: Name of the chip or platform

    `manufacturer`: chip/platform manufacturer

    `url`: chip URL

    `genomebuild`: The genome build this platform is based upon.

organism: organism for chip.

species: species for chip.

version: A character vector giving the version number of the package.

license: The license of the package

author: Author of the package

email: An email address to use in the Maintainer field

biocViews: Character data for the biocViews field of the DESCRIPTION file

Methods

makePdInfoPackage signature(.Object = "NgsExpressionPDInfoPkgSeed"): ...

chipName signature(object = "NimbleGenPDInfoPkgSeed"): ...

getGeometry signature(.Object = "NimbleGenPDInfoPkgSeed"): ...

Examples

showClass("NgsExpressionPDInfoPkgSeed")

NgsTilingPDInfoPkgSeed-class
Class "NgsTilingPDInfoPkgSeed"

Description

PDInfo package Seed for NimbleGen Tiling arrays

Objects from the Class

Objects can be created by calls of the form new("NgsTilingPDInfoPkgSeed", ndfFile, xysFile, pairFile, posFile ...).

Slots

ndfFile: NDF (NimbleGen Design) file

xysFile: XYS File - used as template

posFile: POS (Positions) file

chipName: Name of the chip or platform

manufacturer: chip/platform manufacturer

url: chip URL

genomebuild: The genome build this platform is based upon.

organism: organism for chip.

species: species for chip.

version: A character vector giving the version number of the package.

license: The license of the package

author: Author of the package

email: An email address to use in the Maintainer field

biocViews: Character data for the biocViews field of the DESCRIPTION file

Methods

    makePdInfoPackage `signature(.Object = "NgsTilingPDInfoPkgSeed"):` ...

    chipName `signature(object = "NimbleGenPDInfoPkgSeed"):` ...

    getGeometry `signature(object = "NimbleGenPDInfoPkgSeed"):` ...

Examples

    `showClass("NgsTilingPDInfoPkgSeed")`

`NimbleGenPDInfoPkgSeed-class`
Class "NimbleGenPDInfoPkgSeed"

Description

    PDInfo package Seed for all NimbleGen arrays

Objects from the Class

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

Slots

    `manufacturer`: Manufacturer = NimbleGen

    `chipName`: Name of the chip or platform

    `url`: chip URL

    `genomebuild`: The genome build this platform is based upon.

    `organism`: organism for chip.

    `species`: species for chip.

    `version`: A character vector giving the version number of the package.

    `license`: The license of the package

    `author`: Author of the package

    `email`: An email address to use in the Maintainer field

    `biocViews`: Character data for the biocViews field of the DESCRIPTION file

Methods

    chipName `signature(object = "NimbleGenPDInfoPkgSeed"):` ...

    getGeometry `signature(object = "NimbleGenPDInfoPkgSeed"):` ...

Examples

    `showClass("NimbleGenPDInfoPkgSeed")`

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chipName   *Return an Official Chip/Platform Name*

Description

This generic function returns an official or standard chip/platform name.

Usage

```
chipName(object)
```

Arguments

object   See `showMethods("chipName")`, but generally `object` will be a sub-
                class of `PkgSeed`.

Details

The idea is that the input files can be used to determine a standard name for each platform. For
example, the method for `AffySNPPDInfoPkgSeed` objects reads the header of the CDF file to
extract a name.

Value

A character vector of length one giving a standard name for the platform.

Author(s)

Seth Falcon

---

getGeometry   *Return the Chip/Platform geometry*

Description

This generic function returns the geometry for a chip/platform.

Usage

```
getGeometry(object)
```

Arguments

object   See `showMethods("getGeometry")`, but generally `object` will be a
                subclass of `PkgSeed`.

Details

The idea is that the input files can be used to determine the geometry for each platform. For example,
the method for `AffySNPPDInfoPkgSeed` objects reads the header of the CDF file to extract the
geometry.

Value

A list with two elements nrows and ncols

Author(s)

Matt Settles

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makePdInfoPackage   *Create a Platform Design Info Package*

Description

This generic function create a platform design info package based on the parameters contained in `object` which will generally be an instance of a subclass of `PkgSeed`. The result is a new directory on the filesystem containing the source for the generated pdInfo package.

Usage

```
makePdInfoPackage(object, destDir, batch_size = 10000, quiet = FALSE, unlink = F
```

Arguments

`object`	See `showMethods("makePdInfoPackage")` to see available methods.
`destDir`	Path where the resulting pdInfo package source directory will be written.
`batch_size`	An integer controlling the size of batches processed when reading the flatfiles and loading the DB. In general, larger values of `batch_size` will use more memory and less time (unless you exceed physical memory, in which case more time will be used as well).
`quiet`	A logical value. When `TRUE`, diagnostic and status messages are not printed.
`unlink`	A logical value. If 'TRUE', and 'destDir' already contains a file or directory with the name 'pkgname', try to unlink (remove) it.

Details

In general, creating the SQLite database will be a time and memory intensive task.

Value

This function is called for its side-effect of producing a pdInfo source package directory.

Author(s)

Seth Falcon

Examples

```
cdfFile <- "Mapping250K_Nsp.cdf"
csvAnno <- "Mapping250K_Nsp_annot.csv"
csvSeq <- "Mapping250K_Nsp_probe_tab"

## Not run:
pkg <- new("AffySNPPDInfoPkgSeed",
           version="0.1.5",
           author="A.U. Thor", email="au@thor.net",
           biocViews="AnnotationData",
           genomebuild="NCBI Build 35, May 2004",
           cdfFile=cdfFile, csvAnnoFile=csvAnno, csvSeqFile=csvSeq)

makePdInfoPackage(pkg, destDir=".")

## End(Not run)
```

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