Package 'pdInfoBuilder'

November 12, 2026

Title Platform Design Information Package Builder

Description Builds platform design information packages.
These consist of a SQLite database containing feature-level
data such as x, y position on chip and
featureSet ID. The database also incorporates featureSet-level
annotation data. The products of this packages are used by the oligo pkg.

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Author Seth Falcon, Vince Carey, Matt Settles, Kristof de Beuf, Benilton Carvalho

Maintainer Benilton Carvalho <benilton@unicamp.br>

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Collate AllClasses.R AllGenerics.R initialize-methods.R utils.R schema.R initDb.R initDb.snp6.R pmmmBlockToMat.R loaders.R loaders.snp6.R makePdInfoPackage-methods.R chipName-methods.R getGeometry-methods.R pdBuilderV2TiledRegion.R pdBuilderV2ExonTranscription.R pdBuilderV2Gene.R pdBuilderV2HTA2.R pdBuilderV2AffyTiling.R pdBuilderV2NgsExpression.R pdBuilderV2AffyExpressionHT.R pdBuilderV2AffySNP.R pdBuilderV2AffySNPCNV.R pdBuilderV2miRNA.R pdBuilderV3GenericArray.R pdBuilderV2Clariom.R

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`AffyClariomSPDInfoPkgSeed`
Class "AffyClariomSPDInfoPkgSeed"

Description

PD Info Package Seed for Affymetrix Clariom S Arrays

Objects from the Class

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

Slots

`pgfFile`: PGF filename

`clfFile`: CLF filename

`coreMps`: MPS filename

`transFile`: Transcript annotation CSV 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("AffyClariomSPDInfoPkgSeed")
```

`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")
```

---

cdf2table *Helper functions to assist the creation of an annotation package for a generic array*

Description

Helper functions to assist the creation of an annotation package for a generic array. This includes converting CDF files into flat tables and parsing probe sequence files.

Usage

```
cdf2table(cdfFile)
sequenceParser(seqFile)
```

Arguments

cdfFile	name of the CDF file to be used
seqFile	name of the probe sequence file

Details

`cdf2table` will convert a CDF to a flat table.

`seqFile` will extract a flat table containing physical location and probe sequences.

`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 subclass 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

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 = FALSE)
```

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)
```

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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