

# pdInfoBuilder

April 19, 2009

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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  
**csvAnnoFile:** CSV annotation file  
**tabSeqFile:** TAB sequence file  
**chipName:** NA  
**manufacturer:** Affymetrix  
**genomebuild:** Genome Build  
**pdInfoObjectName:** NA  
**geometry:** Array's geometry  
**name:** name  
**version:** version  
**license:** license  
**author:** author  
**email:** email  
**url:** url  
**biocViews:** biocViews

## Extends

Class "**PDInfoPkgSeed**", directly. Class "**PkgSeed**", by class "**PDInfoPkgSeed**", distance 2.

**Methods**

**chipName** chipName  
**initialize** initialize  
**makePdInfoPackage** package creator

**Examples**

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

---

```
AffyGenePDInfoPkgSeed-class
```

```
Class "AffyGenePDInfoPkgSeed" for the Sense Target gene-level array
```

---

**Description**

container for parameters related to pdmapping package construction for ST gene level array

**Objects from the Class**

Objects can be created by calls of the form `new("AffyGenePDInfoPkgSeed", 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" ~~  
**transFile:** Object of class "ScalarCharacter" ~~  
**chipName:** Object of class "character" ~~  
**manufacturer:** Object of class "character" ~~  
**genomebuild:** Object of class "character" ~~  
**pdInfoObjectName:** Object of class "character" ~~  
**geometry:** Object of class "integer" ~~  
**name:** Object of class "character" ~~  
**version:** Object of class "character" ~~  
**license:** Object of class "character" ~~  
**author:** Object of class "character" ~~  
**email:** Object of class "character" ~~  
**url:** Object of class "character" ~~  
**biocViews:** Object of class "character" ~~

**Extends**

Class "**PDInfoPkgSeed**", directly. Class "**PkgSeed**", by class "PDInfoPkgSeed", distance 2.

**Methods**

**chipName** signature(object = "AffyGenePDInfoPkgSeed"): ...  
**initialize** signature(.Object = "AffyGenePDInfoPkgSeed"): ...  
**makePdInfoPackage** signature(object = "AffyGenePDInfoPkgSeed"): ...

**Author(s)**

B. Carvalho

**Examples**

```
showClass("AffyGenePDInfoPkgSeed")
```

---

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

---

**Description**

This class represents Platform Design (PD) packages for Affymetrix genomewide (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  
**genomebuild:** The genome build this platform is based upon.  
**pdInfoObjectName:** Name of the R object that will be made available in a generated pdInfo package.  
**geometry:** Used to describe the geometry of the platform.  
**name:** The name of the package.

**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  
**url:** URL  
**biocViews:** Character data for the biocViews field of the DESCRIPTION file

### Extends

Class "[PDInfoPkgSeed](#)", directly. Class "[PkgSeed](#)", by class "PDInfoPkgSeed", distance 2.

### Methods

**chipName** signature(object = "AffySNPCNVPDInfoPkgSeed"): ...  
**initialize** signature(.Object = "AffySNPCNVPDInfoPkgSeed"): ...  
**makePdInfoPackage** signature(object = "AffySNPCNVPDInfoPkgSeed"): ...

### Notes

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](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")
```

---

```
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", ...)`.

**Slots**

**cdfFile:** Path to the CDF file for this platform. Example: "files/Mapping250K\_Nsp.cdf"

**csvAnnoFile:** Path to the Affymetrix CSV annotation file. Example: "files/Mapping250K\_Nsp\_annot.csv"

**csvSeqFile:** Path to the Affymetrix probe sequence file. Example: Mapping250K\_Nsp\_probe\_tab

**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

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

**pdInfoObjectName:** Name of the R object that will be made available in a generated `pdInfo` package.

**geometry:** Used to describe the geometry of the platform.

**name:** The name of the package.

**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

**url:** URL

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

**Extends**

Class "`PDInfoPkgSeed`", directly. Class "`PkgSeed`", by class "`PDInfoPkgSeed`", distance 2.

**Methods**

See `showMethods(classes="AffySNPPDInfoPkgSeed")`

**Notes**

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](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)**

Seth Falcon

**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))
```

---

```
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  
**cifFile:** CIF File - provided by Affymetrix  
**chipName:** Automatically determined.  
**manufacturer:** Automatically determined.  
**genomebuild:** Genome Build.  
**pdInfoObjectName:** Automatically determined.  
**geometry:** Automatically determined.  
**name:** Automatically determined.  
**version:** Version  
**license:** License  
**author:** Author  
**email:** Email  
**url:** URL  
**biocViews:** biocViews

**Extends**

Class "[PDInfoPkgSeed](#)", directly. Class "[PkgSeed](#)", by class "PDInfoPkgSeed", distance 2.

**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  
**pairFile:** PAIR (pair) file - used as template  
**xysFile:** XYS File - used as template  
**ngdFile:** NGD File - annotation data  
**chipName:** Design identifier  
**manufacturer:** Manufacturer: Affymetrix/NimbleGen  
**genomebuild:** Genome Build  
**pdInfoObjectName:** object name  
**geometry:** array dimensions  
**name:** name  
**version:** Version  
**license:** License  
**author:** Author  
**email:** Author's email  
**url:** website  
**biocViews:** biocViews

**Extends**

Class "[PDInfoPkgSeed](#)", directly. Class "[PkgSeed](#)", by class "PDInfoPkgSeed", distance 2.

**Methods**

**chipName** signature(object = "NgsPDInfoPkgSeed"): ...  
**initialize** signature(.Object = "NgsPDInfoPkgSeed"): ...

**Examples**

```
showClass("NgsExpressionPDInfoPkgSeed")
```

---

```
NgsPDInfoPkgSeed-class
      Class "NgsPDInfoPkgSeed"
```

---

**Description**

PDInfo package Seed for NimbleGen arrays

**Objects from the Class**

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

**Slots**

**ndfFile:** NDF (NimbleGen Design) file  
**chipName:** Design identifier  
**manufacturer:** Manufacturer: Affymetrix/NimbleGen  
**genomebuild:** Genome Build  
**pdInfoObjectName:** object name  
**geometry:** array dimensions  
**name:** name  
**version:** Version  
**license:** License  
**author:** Author  
**email:** Author's email  
**url:** website  
**biocViews:** biocViews

**Extends**

Class "[PDInfoPkgSeed](#)", directly. Class "[PkgSeed](#)", by class "PDInfoPkgSeed", distance 2.

**Methods**

**chipName** signature(object = "NgsPDInfoPkgSeed"): ...  
**initialize** signature(.Object = "NgsPDInfoPkgSeed"): ...

**Examples**

```
showClass("NgsPDInfoPkgSeed")
```



---

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, posFile, pairFile, ...)`.

### Slots

**ndfFile:** NDF (NimbleGen Design) file  
**posFile:** POS (Positions) file  
**pairFile:** XYS File - used as template  
**chipName:** Design identifier  
**manufacturer:** Manufacturer: Affymetrix/NimbleGen  
**genomebuild:** Genome Build  
**pdInfoObjectName:** object name  
**geometry:** array dimensions  
**name:** name  
**version:** Version  
**license:** License  
**author:** Author  
**email:** Author's email  
**url:** website  
**biocViews:** biocViews

### Extends

Class "[PDInfoPkgSeed](#)", directly. Class "[PkgSeed](#)", by class "[PDInfoPkgSeed](#)", distance 2.

### Methods

**chipName** signature(object = "NgsPDInfoPkgSeed"): ...  
**initialize** signature(.Object = "NgsPDInfoPkgSeed"): ...

### Examples

```
showClass("NgsTilingPDInfoPkgSeed")
```

---

```
PDInfoPkgSeed-class  
  Class "PDInfoPkgSeed"
```

---

### Description

This class represents platform design (PD) packages.

### Objects from the Class

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

### Slots

**chipName:** Name of the chip or platform  
**manufacturer:** chip/platform manufacturer  
**genomebuild:** The genome build this platform is based upon.  
**pdInfoObjectName:** Name of the R object that will be made available in a generated pdInfo package.  
**geometry:** Used to describe the geometry of the platform.  
**name:** The name of the package.  
**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  
**url:** URL  
**biocViews:** Character data for the biocViews field of the DESCRIPTION file

### Extends

Class "[PkgSeed](#)", directly.

### Methods

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

### Author(s)

Seth Falcon

### Examples

```
showClass("PDInfoPkgSeed")
```

---

PkgSeed-class	<i>Class "PkgSeed"</i>
---------------	------------------------

---

**Description**

This class represents R package details. It is intended to provide a base upon which package generating methods can be built.

**Objects from the Class**

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

**Slots**

**name:** The name of the package.

**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

**url:** URL

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

**Methods**

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

**Author(s)**

Seth Falcon

**Examples**

```
showClass("PkgSeed")
```

---

chipName	<i>Return an Official Chip/Platform Name</i>
----------	--

---

**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

---

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)
```

**Arguments**

<code>object</code>	See <code>showMethods("makePdInfoPackage")</code> to see available methods.
<code>destDir</code>	Path where the resulting <code>pdInfo</code> package source directory will be written.
<code>batch_size</code>	An integer controlling the size of batches processed when reading the flatfiles and loading the DB. In general, larger values of <code>batch_size</code> will use more memory and less time (unless you exceed physical memory, in which case more time will be used as well).
<code>quiet</code>	A logical value. When <code>TRUE</code> , diagnostic and status messages are not printed.

**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"

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)

## Not run:
makePdInfoPackage(pkg, destDir=".")
## End(Not run)
```

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