Package 'frmaTools'

November 10, 2026

Version 1.65.0

Date 2015-07-08

Title Frozen RMA Tools

Description Tools for advanced use of the frma package.

Author Matthew N. McCall <mccallm@gmail.com>, Rafael A. Irizarry <rafa@jhu.edu>

Maintainer Matthew N. McCall <mccallm@gmail.com>

Depends R (>= 2.10.0), affy

Imports Biobase, DBI, methods, preprocessCore, stats, utils

Suggests oligo, pd.huex.1.0.st.v2, pd.hugene.1.0.st.v1, frma, affyPLM, hgu133aprobe, hgu133atagprobe, hgu133plus2probe, hgu133acdf, hgu133atagcdf, hgu133plus2cdf, hgu133afrmavecs, frmaExampleData

biocViews Software, Microarray, Preprocessing

License GPL (>= 2)

URL http://bioconductor.org

git_url https://git.bioconductor.org/packages/frmaTools

git_branch devel

git_last_commit 571bff3

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-11-09

Contents

convertPlatform 2
makeVectorPackage 2

Index **5**

convertPlatform *convertPlatform*

Description

Convert an AffyBatch object from one platform to another where the new platform is a subset of the original (i.e. hgu133atag to hgu133a).

Usage

```
convertPlatform(object, new.platform)
```

Arguments

object	an AffyBatch object to be converted
new.platform	the name of the platform to be converted to

Value

An AffyBatch object containing the data from the original object that could be mapped to the new platform.

Author(s)

Matthew N. McCall

Examples

```
library(frmaExampleData)
data(AffyBatch133atag)
require(hgu133aprobe)
require(hgu133atagprobe)
require(hgu133acdf)
require(hgu133atagcdf)
object <- convertPlatform(AffyBatch133atag, "hgu133a")
```

makeVectorPackage *makeVectorPackage*

Description

Make a package containing the vectors used by the frma package. If you don't plan to distribute and maintain this set of vectors, consider using either makeVectorsAffyBatch or makeVectorsFeatureSet instead.

Usage

```
makeVectorPackage(files, batch.id, version, maintainer, species, annotation, packageName, backgro
makeVectorsAffyBatch(files, batch.id, background="rma", normalize="quantile", normVec=NULL, cdfn
makeVectorsFeatureSet(files, batch.id, pkgname, background="rma", normalize="quantile", normVec=
```

Arguments

files	the CEL file names from which to create the vectors
batch.id	a vector of batch ids used to compute within and between batch variances
background	type of background correction to perform: either "none" or "rma".
normalize	type of normalization to perform: either "none" or "quantile".
normVec	normalization vector. If NULL, a normalization vector is created based on the given CEL files. Ignored if normalize is "none".
annotation	the "cdfname" or "pkgname" to be passed to either makeVectorsAffyBatch or makeVectorsFeatureSet depending on the value of "type".
cdfname	used to specify the name of an alternative cdf package. Passed to the ReadAffy function. If set to "NULL", then the usual cdf package based on Affymetrix's mappings will be used.
pkgname	alternative data package to be loaded. Passed to the read.celfiles function. If set to "NULL", then the default package will be used.
packageName	name of the package to be created
version	the version number of the package to be created
maintainer	typically your name
species	species of samples in object
type	the type of data object to be loaded. Must be one of: AffyBatch, FeatureSet.
file.dir	directory in which the CEL files are located
output.dir	directory in which to create the package
unlink	logical value. If TRUE and output.dir already contains a file or directory with the same name as the package being generated, then try to unlink (remove) it.
verbose	logical value. If TRUE then some messages are displayed while the function runs

Value

The makeVectorPackage function creates a package with the name <array platform>frmavecs. For example if the files are HGU133a arrays, the package would be called hgu133afrmavecs.

The makeVectors functions create a list with 6 elements:

normVec	normalization vector
probeVec	probe effect vector
probeVarWithin	within batch probe variance
probeVarBetween	between batch probe variance
probesetSD	within probeset standard deviation
medianSE	median standard errors

Author(s)

Matthew N. McCall

Examples

```
## assuming the celfiledir points to a directory with 9 CEL files
## this takes a long time
## Not run:
  vecs <- makeVectorsAffyBatch(celfiledir, batch.id=rep(1:3, each=3))

## End(Not run)
```

Index

∗ **manip**
convertPlatform, 2
makeVectorPackage, 2

convertPlatform, 2

makeVectorPackage, 2
makeVectorsAffyBatch
(makeVectorPackage), 2
makeVectorsFeatureSet
(makeVectorPackage), 2