# Package: frmaTools (via r-universe)

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**Title** Frozen RMA Tools

**Description** Tools for advanced use of the frma package.

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**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)

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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, background
makeVectorsAffyBatch(files, batch.id, background="rma", normalize="quantile", normVec=NULL, cdfname=
makeVectorsFeatureSet(files, batch.id, pkgname, background="rma", normalize="quantile", normVec=NULL
```

## 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)
```

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