

# frmaTools

October 25, 2011

---

`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)
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 `makeVectorsExonFeatureSet` instead.

## Usage

```
makeVectorPackage(files, batch.id, version, maintainer, species,
annotation, packageName, background="rma", normalize="quantile", normVec=NULL,
type="AffyBatch", target=NULL, file.dir=".", output.dir=".", unlink=TRUE, verbose=
  makeVectorsAffyBatch(files, batch.id, background="rma",
normalize="quantile", normVec=NULL, cdfname=NULL, file.dir=".", verbose=TRUE)
  makeVectorsExonFeatureSet(files, batch.id, target, pkgname,
background="rma", normalize="quantile", normVec=NULL, file.dir=".", verbose=TRUE)
```

## Arguments

<code>files</code>	the CEL file names from which to create the vectors
<code>batch.id</code>	a vector of batch ids used to compute within and between batch variances
<code>background</code>	type of background correction to perform: either "none" or "rma".
<code>normalize</code>	type of normalization to perform: either "none" or "quantile".
<code>normVec</code>	normalization vector. If NULL, a normalization vector is created based on the given CEL files. Ignored if <code>normalize</code> is "none".
<code>annotation</code>	the "cdfname" or "pkgname" to be passed to either <code>makeVectorsAffyBatch</code> or <code>makeVectorsExonExpressionSet</code> depending on the value of "type".
<code>cdfname</code>	used to specify the name of an alternative cdf package. Passed to the <code>ReadAffy</code> function. If set to "NULL", then the usual cdf package based on Affymetrix's mappings will be used.
<code>pkgname</code>	alternative data package to be loaded. Passed to the <code>read.celfiles</code> function. If set to "NULL", then the default package will be used.
<code>target</code>	summarization level for exon arrays. Must be one of: <code>probeset</code> , <code>core</code> , <code>full</code> , <code>extended</code> .
<code>packageName</code>	name of the package to be created
<code>version</code>	the version number of the package to be created
<code>maintainer</code>	typically your name
<code>species</code>	species of samples in object
<code>type</code>	the type of data object to be loaded. Must be one of: <code>AffyBatch</code> , <code>ExonFeatureSet</code> .
<code>file.dir</code>	directory in which the CEL files are located
<code>output.dir</code>	directory in which to create the package
<code>unlink</code>	logical value. If TRUE and <code>output.dir</code> already contains a file or directory with the same name as the package being generated, then try to unlink (remove) it.
<code>verbose</code>	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 hgu133afmavecs.

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

## \*Topic **manip**

- convertPlatform, [1](#)
- makeVectorPackage, [2](#)

convertPlatform, [1](#)

makeVectorPackage, [2](#)  
makeVectorsAffyBatch  
    (*makeVectorPackage*), [2](#)  
makeVectorsExonFeatureSet  
    (*makeVectorPackage*), [2](#)