RMAGEML

October 25, 2011

JavaVMRef-class   *JavaVMRef*

Description

Represents a pointer to the Java Virtual Machine

Details

This Class is used to represent a pointer to the Java Vitrual Machine

Author(s)

Steffen Durinck, <http://www.esat.kuleuven.ac.be/~sdurinck>

MEXP14   *Example dataset in MAGEML-format*

Description

This dataset is available from ArrayExpress(http://www.ebi.ac.uk/arrayexpress/) as E-MEXP-14 and contains data from a study for comparison of environmentally sampled flounder from the Tyne and Alde estuaries.

Details

See ArrayExpress

Source

ArrayExpress, http://www.ebi.ac.uk/arrayexpress/

References

Timothy Williams, Karl Gensberg, Steven Minchin and James Chipman (2003). A DNA expression array to detect toxic stress response in European flounder (Platichthys flesus). Aquatic Toxicology, 65, 141-157

1

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addDerivedData *Adding a derived dataset to an existing MAGEML document*

Description

This function adds a derived dataset to an existing MAGEML document.

Usage

```
addDerivedData(mageOM = NULL, data = NULL, outputDirectory = ".", externalDataFi
```

Arguments

data
: Numeric vector or martix in which the columns corresepond to the derived data one wants to add and the rows correspond to one DesignElementDimension present in the original MAGEML document

mageOM
: Reference to MAGE Object Model, generated by importMAGEOM() method.

outputDirectory
: Directory where updated MAGEML document will be written to

externalDataFile
: Name for external data file associated with a DerivedBioAssayData object. the filename should end with .txt as this is the standard output file format

protocolID
: ID you want to give to the protocol, e.g. P-normalised-1

protocol
: Describiption of the used protocol

date
: Date when protocol was applied

qtIDs
: List of identifiers used for the QuantitationTypes. Order should be the same as the columns of the data matrix

qtNames
: List of names for the QuantitationTypes. Order should be the same as in the qtIDs list and as the columns of the data matrix.

qtScales
: Scales of the QuantitationType, e.g. linear. Order should be the same as in the qtIDs list and as the columns of the data matrix.

qtDescriptions
: Description of the QuantitationType. Order should be the same as in the qtIDs list and as the columns of the data matrix.

qtDataTypes
: DataTypes of the QuantitationType e.g. scalar. Order should be the same as in the qtIDs list and as the columns of the data matrix.

qtTypes
: Type of QuantitationType e.g. specialized or derived. length should be the same as in the qtIDs list and as the columns of the data matrix.

qtDimID
: A new QuantitationTypeDimension will be generated you'll have to specify it's identifier

transformationID
: Identifier for the applied transformation e.g. TFM:1

arrayID
: Array identifier

DED
: DesignElementDimension selected during MAGEML import. If only one dimension present in original MAGEML file then this parameter should not be specified

BAD	BioAssayData identifier
derivedBioAssayID	
	Identifier for the DerivedBioAssay e.g. DBA-1
derivedBioAssayDataID	
	Identifier for the DerivedBioAssayData
rawDataFiles	filenames of the MeasuredBioAssays used to generate the DerivedBioAssay-Data as present in the raw object created by import from a MAGEML document.

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM,writeMAGEML

Examples

```
#library(RMAGEML)
#mageom <- importMAGEOM(directory = "/home/steffen/data/MEXP-14")
#data1 <- rep(1, 960); #dummy dataset
#data <- cbind(data1, data1) #dummy dataset
#outputDirectory <- "/home/steffen/XMLout"
#magemlFile <- "RMAGEMLtest.xml"
#derivedFile <- "deriv_test.txt"
#protocolID <- "P-CAGE-test"
#protocol <- "This is a test protocol! Applied Anova to the raw signal intesities. Flags
#qtIDs <- c("esat.kuleuven.ac.be:quantT-1-test", "esat.kuleuven.ac.be:quantT-2-test")
#qtNames <- c("quantitation Name 1", "quantitation Name 2")
#qtDescriptions <- c("description of first QType","description of second QType")
#qtScales <- c("linear","linear")
#qtDataTypes <- c("scalar","scalar")
#qtDimID <- "esat.kuleuven.ac.be:QTD-test"
#BAD <- "esat.kuleuven.ac.be:BAD-test"
#tfm <- transformationID
#derivedBioAssayID <- "esat.kuleuven.ac.be:DBA-test"
#derivedBioAssayDataID <- "esat.kuleuven.ac.be:DBD-test"
#rawDataFiles <- c("","")
#addDerivedData(mageOM = mageom, data = data, outputDirectory = outputDirectory, external
```

---

addNormToMAGEML   *Adding a norm object to an existing MAGEML document*

Description

This function adds normalised data object obtained with limma or marray package to a MAGEML document.

Usage

```
addNormToMAGEML(mageOM = NULL, norm = NULL, outputDirectory = ".",
externalDataFiles = NULL, protocolID = NULL, protocol = "none", date="NA", qtID
NULL, qtName = NULL, qtDescription = NULL, qtScale = NULL, qtDataType = NULL, qt
NULL,transformationID = NULL, arrayID = "none", DED = "none", BADIDs = NULL, der
```

Arguments

norm	Normalised limma (MAList) or marray (marrayNorm) object
mageOM	Reference to MAGE Object Model, generated by importMAGEOM() method.
outputDirectory	
	Directory where updated MAGEML document will be written to
externalDataFiles	
	List of names for external data files associated with a DerivedBioAssayData object. Each filename should end with .txt as this is the standard output file format
protocolID	ID you want to give to the protocol, e.g. P-normalised-1
protocol	Describiption of the used protocol
date	Date when protocol was applied
qtID	Identifier used for the QuantitationType (the normalised value)
qtName	Name for the QuantitationType
qtDescription	
	Description of the QuantitationType
qtScale	Scale of the QuantitationType, e.g. linear
qtDataType	DataType of the QuantitationType e.g. scalar
qtDimID	A new QuantitationTypeDimension will be generated you'll have to specify it's identifier
transformationID	
	Identifier for the applied transformation e.g. TFM:1
arrayID	Array Identifier
DED	DesignElementDimension corresponding to the features that are present in the normalised object, if only one dimension present in original MAGEML file then this parameter should not be specified
BADIDs	List of BioAssayData identifier
derivedBioAssayIDs	
	List of identifiers for the DerivedBioAssay e.g. DBA-1
derivedBioAssayDataIDs	
	List of identifiers for the DerivedBioAssayData
rawDataFiles	raw data filenames

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM,writeMAGEML

Examples

```
#library(RMAGEML)
#raw<- importMAGEML(directory = "/home/steffen/data/MEXP-14")
#norm<-maNorm(raw)
#mageom <- importMAGEOM(directory = "/home/steffen/data/MEXP-14")
#outputDirectory <- "/home/steffen/XMLout"
#externalDataFile <- "deriv_test.txt"
#protocolID <- "P-CAGE-test"
#protocol <- "This is a test protocol! Applied maNorm."
#qtID <- c("esat.kuleuven.ac.be:quantT-1-test", "esat.kuleuven.ac.be:quantT-2-test")
#qtName <- c("quantitation Name 1", "quantitation Name 2")
#qtScale <- c("linear","linear")
#
#qtDataType <- c("scalar","scalar")
#qtDimID <- "esat.kuleuven.ac.be:QTD-test"
#BADIDs <- c("esat.kuleuven.ac.be:BAD-test1","esat.kuleuven.ac.be:BAD-test2")
#derivedBioAssayIDs <- c("esat.kuleuven.ac.be:DBA-test1","esat.kuleuven.ac.be:DBA-test2")
#derivedBioAssayDataIDs <- c("esat.kuleuven.ac.be:DBD-test1", "esat.kuleuven.ac.be:DBD-te
#tfm<-"TFM-1"
#addNormToMAGEML(mageOM = mageom, norm = norm, outputDirectory = outputDirectory, externa
```

---

getArrayID   *Get ArrayID's*

Description

This function retrieves a list of ID's of the arrays that were used in the experiment.

Usage

```
getArrayID( mageOM = NULL )
```

Arguments

mageOM   R reference to MAGE Object Model

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
getArrayID( mageOM = mageom )
}
```

---

getArrayLayout   *Creation of a marrayLayout object*

Description

This function creates a marrayLayout object.

Usage

```
getArrayLayout( mageOM, arrayID = "none", DED = "none")
```

Arguments

mageOM	Reference to MAGE Object Model
arrayID	Array identifier
DED	Design Element Dimension

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#To obtain a marrayInfo object containing the database identifiers of the features preser
mageom<-importMAGEOM(directory=data)
getArrayLayout(mageom, arrayID="A-MEXP-14", DED="DED:707")
}
```

---

getArrayLayoutLimma

Get layout for limma

Description

This function gets the genes dataframe.

Usage

```
getArrayLayoutLimma( mageOM, arrayID = "none", DED = "none", db = "none")
```

Arguments

mageOM	Reference to MAGE Object Model
arrayID	Array identifier
DED	The DesignElement Dimension
db	database identifier to be retrieved

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#To obtain a marrayInfo object containing the database identifiers of the features presen
mageom<-importMAGEOM(directory=data)
getArrayLayoutLimma(mageom, arrayID="A-MEXP-14",DED="DED:707")
}
```

---

getGnames   *Creation of a Gnames marrayInfo object*

Description

This function creates a marrayInfo object containing the database identifiers of the features present
on the array.

Usage

```
getGnames( mageOM, arrayID = "none", DED = "none", db = "none", package = NULL )
```

Arguments

mageOM	Reference to MAGE Object Model
arrayID	Array identifier
DED	the DesignElement Dimension
db	database from which identifiers should be retrieved
package	the package to which you want to export to, either limma, marray or eset

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball
C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A,
White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and
Brazma A. Design and implementation of microarray gene expression markup language (MAGE-
ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#To obtain a marrayInfo object containing the database identifiers of the features presen
mageom<-importMAGEOM(directory=data)
getGnames(mageom, DED="DED:707", package = "marray")
}
```

```
getNumberOfFeatures
```
Retrieves number of features

Description

Retrieves number of features from an experiment for a given DesignElementDimension

Usage

```
getNumberOfFeatures( mageOM = NULL , DED = "none" )
```

Arguments

`mageOM`	R reference to MAGE object model
`DED`	DesignElementDimension: If not specified and there is more than one DED present, selection pop-up menus will appear.

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
getNumberOfFeatures( mageOM = mageom )
}
```

---

getOrganization   *Retrieves Organization who did experiment*

Description

This function function retrieves Organization who did experiment.

Usage

```
getOrganization( mageOM = NULL )
```

Arguments

mageOM   R reference to MAGE Object Model

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball
C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A,
White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and
Brazma A. Design and implementation of microarray gene expression markup language (MAGE-
ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
getOrganization( mageOM = mageom )
}
```

---

getQTDimensions   *Retrieves QuantitationType Dimensions*

Description

This function function retrieves QuantitationType Dimensions.

Usage

```
getQTDimensions( mageOM = NULL )
```

Arguments

mageOM   R reference to MAGE Object Model

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball
C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A,
White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and
Brazma A. Design and implementation of microarray gene expression markup language (MAGE-
ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
getQTDimensions( mageOM = mageom )
}
```

---

getQTypeDescription

Retrieves description of a QuantitationType

Description

This function retrieves the description of a QuantitationType.

Usage

```
getQTypeDescription( mageOM = NULL, QTypeID = "" )
```

Arguments

mageOM   R reference to MAGE Object Model

QTypeID   ID of QuantitationType

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM,getQuantitationTypes

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
QTypes <- getQuantitationTypes( mageOM = mageom )
getQTypeDescription( mageOM = mageom , QTypeID = QTypes[1] )
}
```

---

getQuantitationTypes

Retrieves QuantitationTypes from an experiment

Description

This function function retrieves QuantitationTypes from an experiment.

Usage

```
getQuantitationTypes( mageOM = NULL , QTD = "none" )
```

Arguments

mageOM	R reference to MAGE object model
QTD	QuantitationTypeDimension: If not specified and there is more than one QTD present, selection pop-up menus will appear.

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
getQuantitationTypes( mageOM = mageom , QTD = "none")
}
```

---

getSubmitterAddress

Retrieves address of the data submitter

Description

This function retrieves the address of the submitter

Usage

getSubmitterAddress(mageOM = NULL)

Arguments

mageOM   R reference to MAGE Object Model

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
getSubmitterAddress( mageOM = mageom )
}
```

---

importMAGEML *import MAGEML documents*

Description

This function imports MAGEML documents and creates a marrayRaw object.

Usage

```
importMAGEML(directory = ".", package = "marray", arrayID = "none", DED = "none"
"none", derivQT = "none", db = "none")
```

Arguments

directory   Directory which contains the MAGEML files that need to be imported

package   name of package to which the MAGEML should be imported

arrayID   Array identifier

DED   the DesignElement Dimension

QTD   the Quantitation Type Dimension

name.Rf   the name of the red foreground intensity

name.Rb   the name of the red background intensity

name.Gf   the name of the green foreground intensity

name.Gb   the name of the green background intensity

derivQT   the name of the derived QuantitationType

db   database identifier which should be retrieved

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

getGnames, getArrayLayout, makeMarrayRaw

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#will return marrayRaw object.#
importMAGEML(directory = data, package = "marray", arrayID = "A-MEXP-14", DED = "DED:707"
}
```

---

importMAGEOM   *import MAGEOM of MAGEML documents*

Description

This function imports the MAGE Object Model MAGEML documents and creates a reference to this object.

Usage

```
importMAGEOM(directory = ".")
```

Arguments

directory   Directory which contains the MAGEML files that need to be imported

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

getGnames,getArrayLayout

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#will return a reference to the MAGE Object Model.#
importMAGEOM(directory=data)
}
```

---

makeEset   *Creation of a ExpressionSet object*

Description

This function creates a ExpressionSet object.

Usage

```
makeEset(mageOM, genes, directory = ".", QTD = "none", arrayID = "none", DED = "
```

Arguments

mageOM	Reference to MAGE Object Model
directory	Directory which contains the MAGEML files that need to be imported
genes	the Gnames marrayInfo object e.g. created by getGnames
QTD	the Quantitation Type Dimension
arrayID	Array identifier
DED	the Design Element Dimension
derivQT	the name of the QuantitationType you want to import

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

Spellman PT, Miller M, Stewart J, Troup C, Sarkans U, Chervitz S, Bernhart D, Sherlock G, Ball C, Lepage M, Swiatek M, Marks WL, Goncalves J, Markel S, Iordan D, Shojatalab M, Pizarro A, White J, Hubley R, Deutsch E, Senger M, Aronow BJ, Robinson A, Bassett D, Stoeckert CJ Jr and Brazma A. Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

importMAGEOM, getGnames

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#To obtain a marrayInfo object containing the database identifiers of the features presen
mageom<-importMAGEOM(directory=data)
genes<-getGnames(mageom, arrayID = "A-MEXP-14", DED = "DED:707", package ="marray")
makeEset(mageOM=mageom, genes = genes, directory=data, arrayID = "A-MEXP-14", DED = "DED:
}
```

---

makeMarrayRaw *Creation of a marrayRaw object*

Description

This function creates a marrayRaw object.

Usage

```
makeMarrayRaw(mageOM, layout, gnames, directory = ".", arrayID = "none", DED = "
```

Arguments

mageOM	Reference to MAGE Object Model
directory	Directory which contains the MAGEML files that need to be imported
gnames	the Gnames marrayInfo object e.g. created by getGnames
layout	the marrayLayout object e.g. created by getLayout
QTD	the Quantitation Type Dimension
arrayID	Array identifier
DED	the Design Element Dimension
name.Rf	the name of the red foreground intensity
name.Rb	the name of the red background intensity
name.Gf	the name of the green foreground intensity
name.Gb	the name of the green background intensity

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

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See Also

importMAGEOM, getGnames, getArrayLayout

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#To obtain a marrayInfo object containing the database identifiers of the features presen
mageom<-importMAGEOM(directory=data)
gnames<-getGnames(mageom, arrayID = "A-MEXP-14", DED = "DED:707", package = "marray")
layout<-getArrayLayout(mageom, arrayID = "A-MEXP-14", DED = "DED:707")
makeMarrayRaw(mageOM=mageom, layout = layout, gnames = gnames, directory = data, arrayID
}
```

---

makeRG   *Creation of a RGList object*

Description

This function creates a RGList object.

Usage

```
makeRG(mageOM, genes, directory = ".", QTD = "none", arrayID = "none", DED = "no
```

Arguments

mageOM	Reference to MAGE Object Model
directory	Directory which contains the MAGEML files that need to be imported
genes	the Gnames marrayInfo object e.g. created by getGnames
QTD	the Quantitation Type Dimension
arrayID	Array identifier
DED	the Design Element Dimension
name.Rf	the name of the red foreground intensity
name.Rb	the name of the red background intensity
name.Gf	the name of the green foreground intensity
name.Gb	the name of the green background intensity

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

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See Also

importMAGEOM, getArrayLayoutLimma

Examples

```
if(interactive()){
data<-system.file("MAGEMLdata", package="RMAGEML")
#To obtain a marrayInfo object containing the database identifiers of the features presen
mageom<-importMAGEOM(directory=data)
genes<-getArrayLayoutLimma(mageom, arrayID="A-MEXP-14", DED = "DED:707")
makeRG(mageOM=mageom, genes = genes, directory=data, arrayID = "A-MEXP-14", DED = "DED:70
}
```

---

reset	*reset*

Description

This function resets previous selections which were stored internally and is used when for example a MAGE-ML document contains more than one array design and one wants to write MAGEML after adding normalized data to this document

Usage

```
reset( mageOM = NULL)
```

Arguments

mageOM   R reference to MAGE Object Model

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

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See Also

importMAGEOM

Examples

```
if(interactive()){
data <- system.file( "MAGEMLdata", package = "RMAGEML" )
mageom <- importMAGEOM( directory = data )
reset( mageOM = mageom )
}
```

---

writeMAGEML   *write MAGEML documents*

Description

This function writes MAGEML documents from MAGE Object references.

Usage

```
writeMAGEML( mageOM = NULL, directory = ".", file = NULL)
```

Arguments

mageOM	Reference to MAGE Object Model
directory	Directory to which the MAGEML file should be written to
file	Filename. Note should have extension xml e.g. update.xml

Author(s)

Steffen Durinck, http://www.esat.kuleuven.ac.be/~sdurinck
Joke Allemeersch, http://www.esat.kuleuven.ac.be/~jallemee.

References

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See Also

importMAGEOM,writeMAGEML,addDerivedData,addNormToMAGEML

Examples

```
#data<-system.file("MAGEMLdata", package="RMAGEML")
#mageom<-importMAGEOM(directory = data)
#writeMAGEML(mageOM = mageom, directory = ".", file = "updatedMAGEML.xml")
```

Index