

RMAGEML

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addDerivedData	<i>Adding a derived dataset to an existing MAGEML document</i>
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Description

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

Usage

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

Arguments

<code>data</code>	Numeric vector or matrix in which the columns correspond to the derived data one wants to add and the rows correspond to one <code>DesignElementDimension</code> present in the original MAGEML document
<code>mageOM</code>	Reference to MAGE Object Model, generated by <code>importMAGEOM()</code> method.
<code>outputDirectory</code>	Directory where updated MAGEML document will be written to
<code>externalDataFile</code>	Name for external data file associated with a <code>DerivedBioAssayData</code> object. the filename should end with <code>.txt</code> as this is the standard output file format
<code>protocolID</code>	ID you want to give to the protocol, e.g. P-normalised-1
<code>protocol</code>	Description of the used protocol
<code>date</code>	Date when protocol was applied
<code>qtIDs</code>	List of identifiers used for the <code>QuantitationTypes</code> . Order should be the same as the columns of the data matrix
<code>qtNames</code>	List of names for the <code>QuantitationTypes</code> . Order should be the same as in the <code>qtIDs</code> list and as the columns of the data matrix.
<code>qtScales</code>	Scales of the <code>QuantitationType</code> , e.g. linear. Order should be the same as in the <code>qtIDs</code> list and as the columns of the data matrix.
<code>qtDescriptions</code>	Description of the <code>QuantitationType</code> . Order should be the same as in the <code>qtIDs</code> list and as the columns of the data matrix.
<code>qtDataTypes</code>	<code>DataTypes</code> of the <code>QuantitationType</code> e.g. scalar. Order should be the same as in the <code>qtIDs</code> list and as the columns of the data matrix.
<code>qtTypes</code>	Type of <code>QuantitationType</code> e.g. specialized or derived. length should be the same as in the <code>qtIDs</code> list and as the columns of the data matrix.
<code>qtDimID</code>	A new <code>QuantitationTypeDimension</code> will be generated you'll have to specify its identifier
<code>transformationID</code>	Identifier for the applied transformation e.g. TFM:1
<code>arrayID</code>	Array identifier
<code>DED</code>	<code>DesignElementDimension</code> selected during MAGEML import. If only one dimension present in original MAGEML file then this parameter should not be specified
<code>BAD</code>	<code>BioAssayData</code> identifier
<code>derivedBioAssayID</code>	Identifier for the <code>DerivedBioAssay</code> e.g. DBA-1
<code>derivedBioAssayDataID</code>	Identifier for the <code>DerivedBioAssayData</code>
<code>rawDataFiles</code>	filenames of the <code>MeasuredBioAssays</code> used to generate the <code>DerivedBioAssayData</code> as present in the raw object created by import from a MAGEML document.

Author(s)

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 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 (MAGEML). *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 intensities. 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

<code>norm</code>	Normalised limma (MAList) or marray (marrayNorm) object
<code>mageOM</code>	Reference to MAGE Object Model, generated by importMAGEOM() method.
<code>outputDirectory</code>	Directory where updated MAGEML document will be written to
<code>externalDataFiles</code>	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
<code>protocolID</code>	ID you want to give to the protocol, e.g. P-normalised-1
<code>protocol</code>	Description of the used protocol
<code>date</code>	Date when protocol was applied
<code>qtID</code>	Identifier used for the QuantitationType (the normalised value)
<code>qtName</code>	Name for the QuantitationType
<code>qtDescription</code>	Description of the QuantitationType
<code>qtScale</code>	Scale of the QuantitationType, e.g. linear
<code>qtDataType</code>	DataType of the QuantitationType e.g. scalar
<code>qtDimID</code>	A new QuantitationTypeDimension will be generated you'll have to specify it's identifier
<code>transformationID</code>	Identifier for the applied transformation e.g. TFM:1
<code>arrayID</code>	Array Identifier
<code>DED</code>	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
<code>BADIDs</code>	List of BioAssayData identifier
<code>derivedBioAssayIDs</code>	List of identifiers for the DerivedBioAssay e.g. DBA-1
<code>derivedBioAssayDataIDs</code>	List of identifiers for the DerivedBioAssayData
<code>rawDataFiles</code>	raw data filenames

Author(s)

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 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-test2")
#tfm<-"TFM-1"
#addNormToMAGEML(mageOM = mageom, norm = norm, outputDirectory = outputDirectory, externalDataFile = externalDataFile)
```

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/~jallemeesch>

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 )  
}
```

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 present
  mageom<-importMAGEOM(directory=data)
  getArrayLayoutLimma(mageom, arrayID="A-MEXP-14", DED="DED:707")
}
```

getArrayLayout	<i>Creation of a marrayLayout object</i>
----------------	--

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>
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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 present
  mageom<-importMAGEOM(directory=data)
  getArrayLayout(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

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

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 present  
  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/~jallemeesch>.

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 (MAGEML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

[getNames](#), [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	<i>import MAGEOM of MAGEML documents</i>
--------------	--

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)  
}
```

JavaVMRef-class *JavaVMRef*

Description

Represents a pointer to the Java Virtual Machine

Details

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

Author(s)

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

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/~jalleme>.

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 present
  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:707")
}
```

makeMarrayRaw

Creation of a marrayRaw object

Description

This function creates a marrayRaw object.

Usage

```
makeMarrayRaw(mageOM, layout, gnames, directory = ".", arrayID = "none", DED = "DED:707")
```

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/~jallemeesch>

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](#), [getArrayLayout](#)

Examples

```
if(interactive()){
  data<-system.file("MAGEMLdata", package="RMAGEML")
  #To obtain a marrayInfo object containing the database identifiers of the features present
  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

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](#), [getArrayLayoutLimma](#)

Examples

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

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

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

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 )
  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

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 (MAGEML). Genome Biol. 2002 Aug 23;3(9):RESEARCH0046.

See Also

[importMAGEOM](#), [writeMAGEML](#), [addDerivedData](#), [addNormToMAGEML](#)

Examples

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

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