

# RMAGEML

April 19, 2009

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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>

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MEXP14

*Example dataset in MAGEML-format*

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## 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

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

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### Description

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

### Usage

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

### Arguments

data	Numeric vector or matrix in which the columns correspond 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	Description 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, Stoekert 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 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

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	Description 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/~jallemeee>.

**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/~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 present
  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 present
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/~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")
#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)  
}
```

---

 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
derivQTD	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 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:
}
```



---

makeMarrayRaw	<i>Creation of a marrayRaw object</i>
---------------	---------------------------------------

---

## 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

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")
}

```

---

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**

<code>mageOM</code>	Reference to MAGE Object Model
<code>directory</code>	Directory to which the MAGEML file should be written to
<code>file</code>	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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