

# Package ‘biomaRt’

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**Title** Interface to BioMart databases (e.g. Ensembl, COSMIC ,Wormbase and Gramene)

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**Depends** methods

**Imports** utils, XML, RCurl, AnnotationDbi

**Suggests** annotate

**biocViews** Annotation

**Description** In recent years a wealth of biological data has become available in public data repositories. Easy access to these valuable data resources and firm integration with data analysis is needed for comprehensive bioinformatics data analysis. biomaRt provides an interface to a growing collection of databases implementing the BioMart software suite (<http://www.biomart.org>). The package enables retrieval of large amounts of data in a uniform way without the need to know the underlying database schemas or write complex SQL queries. Examples of BioMart databases are Ensembl, COSMIC, Uniprot, HGNC, Gramene, Wormbase and dbSNP mapped to Ensembl. These major databases give biomaRt users direct access to a diverse set of data and enable a wide range of powerful online queries from gene annotation to database mining.

**License** Artistic-2.0

**LazyLoad** yes

**NeedsCompilation** no

## R topics documented:

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|                |   |
|----------------|---|
| attributePages | <i>Gives a summary of the attribute pages</i> |
|----------------|---|

---

## Description

Attributes in BioMart databases are grouped together in attribute pages. The `attributePages` function gives a summary of the attribute categories and groups present in the BioMart. These page names can be used to display only a subset of the available attributes in the `listAttributes` function.

## Usage

```
attributePages(mart)
```

## Arguments

`mart`                    object of class `Mart`, created with the `useMart` function.

## Author(s)

Steffen Durinck

## Examples

```
if(interactive()){
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")
  attributeSummary(mart)
}
```

---

|             |  |
|-------------|--|
| exportFASTA | <i>Exports getSequence results to FASTA format</i> |
|-------------|--|

---

**Description**

Exports getSequence results to FASTA format

**Usage**

```
exportFASTA(sequences, file)
```

**Arguments**

|           |  |
|-----------|--|
| sequences | A data.frame that was the output of the getSequence function |
| file      | File to which you want to write the data                     |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){  
  mart <- useMart("ensembl", dataset="hsapiens_gene_ensembl")  
  
  #seq<-getSequence(chromosome=c(2,2),start=c(100000,30000),end=c(100300,30500),mart=mart)  
  #exportFASTA(seq,file="test.fasta")  
  
  martDisconnect(mart = mart)  
}
```

---

|               |                                    |
|---------------|------------------------------------|
| filterOptions | <i>Displays the filter options</i> |
|---------------|------------------------------------|

---

**Description**

Displays a set of predetermined values for the specified filter (if available).

**Usage**

```
filterOptions(filter,mart)
```

**Arguments**

|        |  |
|--------|--|
| filter | A valid filter name.                                   |
| mart   | object of class Mar created using the useMart function |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){  
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")  
  filterOptions("chromosome_name", mart)  
}
```

---

**filterType***Displays the filter type*

---

**Description**

Displays the type of the filter given a filter name.

**Usage**

```
filterType(filter, mart)
```

**Arguments**

|        |  |
|--------|--|
| filter | A valid filter name. Valid filters are given by the listFilters function |
| mart   | object of class Mart, created using the useMart function                 |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){  
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")  
  filterType("chromosome_name", mart)  
}
```

---

getBM

*Retrieves information from the BioMart database*


---

### Description

This function is the main biomaRt query function. Given a set of filters and corresponding values, it retrieves the user specified attributes from the BioMart database one is connected to.

### Usage

```
getBM(attributes, filters = "", values = "", mart, curl = NULL, checkFilters = TRUE, verbose = FALSE, u
```

### Arguments

|              |   |
|--------------|---|
| attributes   | Attributes you want to retrieve. A possible list of attributes can be retrieved using the function listAttributes.  |
| filters      | Filters (one or more) that should be used in the query. A possible list of filters can be retrieved using the function listFilters.   |
| values       | Values of the filter, e.g. vector of affy IDs. If multiple filters are specified then the argument should be a list of vectors of which the position of each vector corresponds to the position of the filters in the filters argument.   |
| mart         | object of class Mart, created with the useMart function.  |
| curl         | An optional 'CURLHandle' object, that can be used to speed up getBM when used in a loop.  |
| checkFilters | Sometimes attributes where a value needs to be specified, for example upstream\_flank with value 20 for obtaining upstream sequence flank regions of length 20bp, are treated as filters in BioMart. To enable such a query to work, one must specify the attribute as a filter and set checkFilters = FALSE for the query to work. |
| verbose      | When using biomaRt in webservice mode and setting verbose to TRUE, the XML query to the webservice will be printed.   |
| uniqueRows   | If the result of a query contains multiple identical rows, setting this argument to TRUE (default) will result in deleting the duplicated rows in the query result at the server side.  |
| bmHeader     | Boolean to indicate if the result retrieved from the BioMart server should include the data headers or not, defaults to FALSE. This should only be switched on if the default behavior results in errors, setting to on might still be able to retrieve your data in that case  |

### Value

A data.frame. There is no implicit mapping between its rows and the function arguments (e.g. filters, values), therefore make sure to have the relevant identifier(s) returned by specifying them in attributes. See Examples.

**Author(s)**

Steffen Durinck

**Examples**

```

if (interactive()) {
  mart <- useMart("ensembl")
  datasets <- listDatasets(mart)
  mart <- useDataset("hsapiens_gene_ensembl",mart)
  getBM(attributes = c("affy_hg_u95av2", "hgnc_symbol", "chromosome_name", "band"),
        filters    = "affy_hg_u95av2",
        values     = c("1939_at", "1503_at", "1454_at"),
        mart       = mart)
  # rows are sorted by `affy_hg_u95av2`, and in different order than the `values` argument
}

```

---

getBMlist

*Retrieves information from the BioMart database*


---

**Description**

This function is the main biomaRt query function. Given a set of filters and corresponding values, it retrieves the user specified attributes from the BioMart database one is connected to

**Usage**

```
getBMlist(attributes, filters = "", values = "", mart, list.names = NULL, na.value = NA, verbose = FALSE)
```

**Arguments**

|             |   |
|-------------|---|
| attributes  | Attributes you want to retrieve. A possible list of attributes can be retrieved using the function listAttributes.  |
| filters     | Filters (one or more) that should be used in the query. A possible list of filters can be retrieved using the function listFilters.   |
| values      | Values of the filter, e.g. vector of affy IDs. If multiple filters are specified then the argument should be a list of vectors of which the position of each vector corresponds to the position of the filters in the filters argument. |
| mart        | object of class Mart, created with the useMart function.  |
| list.names  | names for objects in list   |
| na.value    | value to give when result is empty  |
| verbose     | When using biomaRt in webservice mode and setting verbose to TRUE, the XML query to the webservice will be printed.   |
| giveWarning | Gives a warning about best practices of biomaRt and recommends using getBM instead of getBMlist   |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){  
  mart <- useMart("ensembl")  
  datasets <- listDatasets(mart)  
  
}
```

---

`getGene`*Retrieves gene annotation information given a vector of identifiers*

---

**Description**

This function retrieves gene annotations from Ensembl given a vector of identifiers. Annotation includes chromosome name, band, start position, end position, gene description and gene symbol. A wide variety of identifiers is available in Ensembl, these can be found with the `listFilters` function.

**Usage**

```
getGene( id, type, mart)
```

**Arguments**

|                   |   |
|-------------------|---|
| <code>id</code>   | vector of gene identifiers one wants to annotate  |
| <code>type</code> | type of identifier, possible values can be obtained by the <code>listFilters</code> function. Examples are <code>entrezgene</code> , <code>hgnc\_symbol</code> (for hugo gene symbol), <code>ensembl\_gene\_id</code> , <code>unigene</code> , <code>agilentprobe</code> , <code>affy\_hg\_u133\_plus\_2</code> , <code>refseq\_dna</code> , etc. |
| <code>mart</code> | object of class <code>Mart</code> , containing connections to the BioMart databases. You can create such an object using the function <code>useMart</code> .  |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){  
  
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")  
  
  #example using affy id  
  
  g = getGene( id = "1939_at", type = "affy_hg_u95av2", mart = mart)  
  show(g)
```

```
#example using Entrez Gene id

g = getGene( id = "100", type = "entrezgene", mart = mart)
show(g)
}
```

---

getLDS

*Retrieves information from two linked datasets*


---

## Description

This function is the main biomaRt query function that links 2 datasets and retrieves information from these linked BioMart datasets. In Ensembl this translates to homology mapping.

## Usage

```
getLDS(attributes, filters = "", values = "", mart, attributesL,
filtersL = "", valuesL = "", martL, verbose = FALSE, uniqueRows = TRUE, bmHeader=TRUE)
```

## Arguments

|             |   |
|-------------|---|
| attributes  | Attributes you want to retrieve of primary dataset. A possible list of attributes can be retrieved using the function listAttributes.   |
| filters     | Filters that should be used in the query. These filters will be applied to primary dataset. A possible list of filters can be retrieved using the function listFilters.   |
| values      | Values of the filter, e.g. list of affy IDs   |
| mart        | object of class Mart created with the useMart function.   |
| attributesL | Attributes of linked dataset that needs to be retrieved   |
| filtersL    | Filters to be applied to the linked dataset   |
| valuesL     | Values for the linked dataset filters   |
| martL       | Mart object representing linked dataset   |
| verbose     | When using biomaRt in webservice mode and setting verbose to TRUE, the XML query to the webservice will be printed. Alternatively in MySQL mode the MySQL query will be printed.  |
| uniqueRows  | Logical to indicate if the BioMart web service should return unique rows only or not. Has the value of either TRUE or FALSE   |
| bmHeader    | Boolean to indicate if the result retrieved from the BioMart server should include the data headers or not, defaults to TRUE. This should only be switched off if the default behavior results in errors, setting to off might still be able to retrieve your data in that case |

## Author(s)

Steffen Durinck

**Examples**

```

if(interactive()){
human = useMart("ensembl", dataset = "hsapiens_gene_ensembl")
mouse = useMart("ensembl", dataset = "mmusculus_gene_ensembl")
getLDS(attributes = c("hgnc_symbol", "chromosome_name", "start_position"), filters = "hgnc_symbol", values = "TP53")
}

```

getSequence

*Retrieves sequences***Description**

This function retrieves sequences given the chromosome, start and end position or a list of identifiers. Using getSequence in web service mode (default) generates 5' to 3' sequences of the requested type on the correct strand. The type of sequence returned can be specified by the seqType argument which takes the following values: 'cdna'; 'peptide' for protein sequences; '3utr' for 3' UTR sequences; '5utr' for 5' UTR sequences; 'gene\_exon' for exon sequences only; 'transcript\_exon\_intron' gives the full unspliced transcript, that is exons + introns; 'gene\_exon\_intron' gives the exons + introns of a gene; 'coding' gives the coding sequence only; 'coding\_transcript\_flank' gives the flanking region of the transcript including the UTRs, this must be accompanied with a given value for the upstream or downstream attribute; 'coding\_gene\_flank' gives the flanking region of the gene including the UTRs, this must be accompanied with a given value for the upstream or downstream attribute; 'transcript\_flank' gives the flanking region of the transcript excluding the UTRs, this must be accompanied with a given value for the upstream or downstream attribute; 'gene\_flank' gives the flanking region of the gene excluding the UTRs, this must be accompanied with a given value for the upstream or downstream attribute. In MySQL mode the getSequence function is more limited and the sequence that is returned is the 5' to 3'+ strand of the genomic sequence, given a chromosome, as start and an end position. So if the sequence of interest is the minus strand, one has to compute the reverse complement of the retrieved sequence, which can be done using functions provided in the matchprobes package. The biomaRt vignette contains more examples on how to use this function.

**Usage**

```
getSequence( chromosome, start, end, id, type, seqType, upstream, downstream, mart, verbose=FALSE)
```

**Arguments**

|            |  |
|------------|--|
| chromosome | Chromosome name  |
| start      | start position of sequence on chromosome   |
| end        | end position of sequence on chromosome   |
| id         | An identifier or vector of identifiers.  |
| type       | The type of identifier used. Supported types are hugo, ensembl, embl, entrez-gene, refseq, ensemblTrans and unigene. Alternatively one can also use a filter to specify the type. Possible filters are given by the listFilters function |

|            |  |
|------------|--|
| seqType    | Type of sequence that you want to retrieve. Allowed seqTypes are: cdna, peptide, 3utr, 5utr, genomic |
| upstream   | To add the upstream sequence of a specified number of basepairs to the output.                       |
| downstream | To add the downstream sequence of a specified number of basepairs to the output.                     |
| mart       | object of class Mart created using the useMart function  |
| verbose    | If verbose = TRUE then the XML query that was send to the webservice will be displayed.              |

**Author(s)**

Steffen Durinck

**Examples**

```

if(interactive()){
  mart <- useMart("ensembl",dataset="hsapiens_gene_ensembl")

  seq = getSequence(id="BRCA1", type="hgnc_symbol", seqType="peptide", mart = mart)
  show(seq)

  seq = getSequence(id="1939_at", type="affy_hg_u95av2", seqType="gene_flank",upstream = 20, mart = mart)
  show(seq)

}

```

---

getXML

*Retrieves information from the BioMart database using an XML query*


---

**Description**

This function is a low level query function bypassing lots of biomaRts internal controls. It allows for a direct XML query to a known BioMart webservice host.

**Usage**

```
getXML(host="http://www.biomart.org/biomart/martservice?", xmlquery)
```

**Arguments**

|          |   |
|----------|---|
| host     | URL to BioMart webservice, is set to <a href="http://www.biomart.org/biomart/martservice?">http://www.biomart.org/biomart/martservice?</a> by default |
| xmlquery | XML query that needs to be send to the webservice   |

**Author(s)**

Steffen Durinck

## Examples

```
if(interactive()){
  getXML(xmlquery="<?xml version='1.0' encoding='UTF-8'?><!DOCTYPE Query><Query virtualSchemaName = 'default' uni
}
```

---

|                |   |
|----------------|---|
| listAttributes | <i>lists the attributes available in the selected dataset</i> |
|----------------|---|

---

## Description

Attributes are the outputs of a biomaRt query, they are the information we want to retrieve. For example if we want to retrieve all entrez gene identifiers of genes located on chromosome X, entrezgene will be the attribute we use in the query. The listAttributes function lists the available attributes in the selected dataset

## Usage

```
listAttributes(mart, page, what = c("name", "description"))
```

## Arguments

|      |  |
|------|--|
| mart | object of class Mart created using the useMart function  |
| page | Show only the attributes that belong to the specified attribute page.  |
| what | vector of types of information about the attributes that need to be displayed. Can have values like name, description, fullDescription, page |

## Author(s)

Steffen Durinck

## Examples

```
if(interactive()){
  ensembl = useMart("ensembl", dataset="hsapiens_gene_ensembl")
  listAttributes(ensembl)
}
```

---

|              |  |
|--------------|--|
| listDatasets | <i>lists the datasets available in the selected BioMart database</i> |
|--------------|--|

---

**Description**

Lists the datasets available in the selected BioMart database

**Usage**

```
listDatasets(mart, verbose = FALSE)
```

**Arguments**

|         |  |
|---------|--|
| mart    | object of class Mart created with the useMart function                   |
| verbose | Give detailed output of what the method is doing, for debugging purposes |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){  
  
#marts <- listMarts()  
#index<-grep("ensembl",marts)  
  
#mart <- useMart(marts[index])  
  
#listDatasets(mart = mart)  
  
#martDisconnect(mart = mart)  
}
```

---

|             |  |
|-------------|--|
| listEnsembl | <i>lists the available BioMart databases hosted by Ensembl</i> |
|-------------|--|

---

**Description**

This function returns a list of BioMart databases hosted by Ensembl. To establish a connection use the useMart function.

**Usage**

```
listEnsembl(mart = NULL, host = "www.ensembl.org", version = NULL, GRCh = NULL, mirror = NULL, verbose = FALSE)
```

**Arguments**

|         |  |
|---------|--|
| mart    | mart object created with the useEnsembl function. This is optional, as you usually use listMarts to see which marts there are to connect to. |
| host    | Host to connect to if different then www.ensembl.org   |
| version | Ensembl version to connect to when wanting to connect to an archived Ensembl version   |
| GRCh    | GRCh version to connect to if not the current GRCh38, currently this can only be 37  |
| mirror  | Mirror to connect to [uswest,useast,asia], If no mirror is specified the default will be used which is www.ensembl.org hosted in the UK      |
| verbose | Give detailed output of what the method is doing, for debugging purposes   |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){
  listEnsembl()
}
```

---

|             |  |
|-------------|--|
| listFilters | <i>lists the filters available in the selected dataset</i> |
|-------------|--|

---

**Description**

Filters are what we use as inputs for a biomaRt query. For example, if we want to retrieve all entrezgene identifiers on chromosome X, chromosome will be the filter, with corresponding value X.

**Usage**

```
listFilters(mart, what = c("name", "description"))
```

**Arguments**

|      |  |
|------|--|
| mart | object of class Mart created using the <a href="#">useMart</a> function  |
| what | character vector indicating what information to display about the available filters. Valid values are name, description, options, fullDescription, filters, type, operation, filters8, filters9. |

**Author(s)**

Steffen Durinck

**Examples**

```

if(interactive()){
  mart = useMart("ensembl", dataset="hsapiens_gene_ensembl")
  listFilters(mart)
}

```

---

|           |  |
|-----------|--|
| listMarts | <i>lists the available BioMart databases</i> |
|-----------|--|

---

**Description**

This function returns a list of BioMart databases to which biomaRt can connect to. By default all public BioMart databases are displayed. To establish a connection use the useMart function.

**Usage**

```
listMarts(mart = NULL, host="www.ensembl.org", path="/biomart/martservice", port=80, includeHosts = F
```

**Arguments**

|                |   |
|----------------|---|
| mart           | mart object created with the useMart function. This is optional, as you usually use listMarts to see which marts there are to connect to. |
| host           | host to connect to if different then www.biomart.org  |
| path           | path to martservice that should be pasted behind the host to get to web service URL   |
| port           | port to use in HTTP communication   |
| includeHosts   | boolean to indicate if function should return host of the BioMart databases   |
| archive        | Boolean to indicate if you want to access archived versions of BioMart database   |
| ssl.verifypeer | Set SSL peer verification on or off. By default ssl.verifypeer is set to TRUE   |
| verbose        | Give detailed output of what the method is doing, for debugging purposes  |

**Author(s)**

Steffen Durinck

**Examples**

```

if(interactive()){
  listMarts()
}

```

---

Mart-class

*Class Mart*

---

**Description**

Represents a Mart class, containing connections to different BioMarts

**Methods**

show Print summary of the object

**Author(s)**

Steffen Durinck

---

NP2009code

*Display the analysis code from the 2009 Nature protocols paper*

---

**Description**

This function opens an editor displaying the analysis code of the Nature Protocols 2009 paper

**Usage**

```
NP2009code()
```

**Details**

The `edit` function uses `getOption("editor")` to select the editor. Use, for instance, `options(editor="emacs")` to set another editor.

**Author(s)**

Steffen Durinck, Wolfgang Huber

**See Also**

[edit](#)

**Examples**

```
if(interactive()){  
  NP2009code()  
}
```

select-methods

*Retrieve information from the BioMart databases***Description**

`select`, `columns` and `keys` are used together to extract data from a Mart object. These functions work much the same as the classic biomaRt functions such as `getBM` etc. and are provide here to make this easier for people who are comfortable using these methods from other Annotation packages. Examples of other objects in other packages where you can use these methods include (but are not limited to): `ChipDb`, `OrgDb`, `GODb`, `InparanoidDb` and `ReactomeDb`.

`columns` shows which kinds of data can be returned from the Mart object.

`keytypes` allows the user to discover which keytypes can be passed in to `select` or `keys` as the `keytype` argument.

`keys` returns keys from the Mart of the type specified by it's `keytype` argument.

`select` is meant to be used with these other methods and has arguments that take the kinds of values that these other methods return. `select` will retrieve the results as a `data.frame` based on parameters for selected keys and columns and `keytype` arguments.

**Usage**

```
columns(x)
keytypes(x)
keys(x, keytype, ...)
select(x, keys, columns, keytype, ...)
```

**Arguments**

|                      |   |
|----------------------|---|
| <code>x</code>       | the Mart object. The dataset of the Mart object must already be specified for all of these methods.   |
| <code>keys</code>    | the keys to select records for from the database. Keys for some keytypes can be extracted by using the <code>keys</code> method.  |
| <code>columns</code> | the columns or kinds of things that can be retrieved from the database. As with <code>keys</code> , all possible columns are returned by using the <code>columns</code> method.   |
| <code>keytype</code> | the keytype that matches the keys used. For the <code>select</code> methods, this is used to indicate the kind of ID being used with the <code>keys</code> argument. For the <code>keys</code> method this is used to indicate which kind of keys are desired from <code>keys</code>  |
| <code>...</code>     | other arguments. These include: <ul style="list-style-type: none"> <li><b>pattern:</b> the pattern to match (used by <code>keys</code>)</li> <li><b>column:</b> the column to search on. This is used by <code>keys</code> and is for when the thing you want to pattern match is different from the <code>keytype</code>, or when you want to simply want to get keys that have a value for the thing specified by the <code>column</code> argument.</li> <li><b>fuzzy:</b> TRUE or FALSE value. Use fuzzy matching? (this is used with <code>pattern</code> by the <code>keys</code> method)</li> </ul> |

**Value**

keys, columns and keytypes each return a character vector or possible values. select returns a data.frame.

**Author(s)**

Marc Carlson

**Examples**

```
## 1st create a Mart object and specify the dataset
mart<-useMart(dataset="hsapiens_gene_ensembl",biomart='ensembl')
## you can list the keytypes
keytypes(mart)
## you can list the columns
columns(mart)
## And you can extract keys when this is supported for your keytype of interest
k = keys(mart, keytype="chromosome_name")
head(k)
## You can even do some pattern matching on the keys
k = keys(mart, keytype="chromosome_name", pattern="LRG")
head(k)
## Finally you can use select to extract records for things that you are
## interested in.
affy=c("202763_at", "209310_s_at", "207500_at")
select(mart, keys=affy, columns=c('affy_hg_u133_plus_2', 'entrezgene'),
       keytype='affy_hg_u133_plus_2')
```

---

useDataset

*Select a dataset to use and updates Mart object*

---

**Description**

This function selects a dataset and updates the Mart object

**Usage**

```
useDataset(dataset,mart, verbose = FALSE)
```

**Arguments**

|         |   |
|---------|---|
| dataset | Dataset you want to use. List of possible datasets can be retrieved using the function listDatasets |
| mart    | Mart object created with the useMart function   |
| verbose | Give detailed output of what the method is doing, for debugging                                     |

**Author(s)**

Steffen Durinck

**Examples**

```

if(interactive()){
  mart=useMart("ensembl")
  mart=useDataset("hsapiens_gene_ensembl", mart = mart)
}

```

---

|            |  |
|------------|--|
| useEnsembl | <i>Connects to the selected BioMart database and dataset hosted by Ensembl</i> |
|------------|--|

---

**Description**

A first step in using the biomaRt package is to select a BioMart database and dataset to use. The useEnsembl function enables one to connect to a specified BioMart database and dataset hosted by Ensembl without having to specify the Ensembl URL. To know which BioMart databases are available see the listEnsembl function. To know which datasets are available within a BioMart database, first select the BioMart database using useMart and then use the listDatasets function on the selected BioMart, see listDatasets function.

**Usage**

```
useEnsembl(biomart, dataset, host="www.ensembl.org", version = NULL, GRCh = NULL, mirror = NULL, verbose)
```

**Arguments**

|         |   |
|---------|---|
| biomart | BioMart database name you want to connect to. Possible database names can be retrieved with the function listEnsembl  |
| dataset | Dataset you want to use. To see the different datasets available within a biomaRt you can e.g. do: mart = useEnsembl('ENSEMBL_MART_ENSEMBL'), followed by listDatasets(mart). |
| host    | Host to connect to if different then www.ensembl.org  |
| version | Ensembl version to connect to when wanting to connect to an archived Ensembl version  |
| GRCh    | GRCh version to connect to if not the current GRCh38, currently this can only be 37   |
| mirror  | Mirror to connect to [uswest,useast,asia], If no mirror is specified the default will be used which is www.ensembl.org hosted in the UK                                       |
| verbose | Give detailed output of what the method is doing while in use, for debugging  |

**Author(s)**

Steffen Durinck

**Examples**

```

if(interactive()){

  mart = useEnsembl("ENSEMBL_MART_ENSEMBL")
  mart=useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl")
}

```

---

useMart

*Connects to the selected BioMart database and dataset*


---

**Description**

A first step in using the biomaRt package is to select a BioMart database and dataset to use. The useMart function enables one to connect to a specified BioMart database and dataset within this database. To know which BioMart databases are available see the listMarts function. To know which datasets are available within a BioMart database, first select the BioMart database using useMart and then use the listDatasets function on the selected BioMart, see listDatasets function.

**Usage**

```

useMart(biomart, dataset, host="www.ensembl.org",
  path="/biomart/martservice", port=80, archive=FALSE, ssl.verifypeer =
  TRUE, version, verbose = FALSE)

```

**Arguments**

|                |   |
|----------------|---|
| biomart        | BioMart database name you want to connect to. Possible database names can be retrieved with the function listMarts  |
| dataset        | Dataset you want to use. To see the different datasets available within a biomaRt you can e.g. do: mart = useMart('ensembl'), followed by listDatasets(mart).   |
| host           | Host to connect to if different then www.biomart.org  |
| path           | Path that should be pasted after to host to get access to the web service URL   |
| port           | port to connect to, will be pasted between host and path  |
| archive        | Boolean to indicate if you want to access archived versions of BioMart databases. Note that this gives access to only a limited number of archived BioMarts and the most recent archives are often not available. A better alternative is to leave archive = FALSE and to specify the url of the archived BioMart you want to access see vignette for an example. |
| ssl.verifypeer | Set SSL peer verification on or off. By default ssl.verifypeer is set to TRUE   |
| version        | Use version name instead of biomart name to specify which BioMart you want to use   |
| verbose        | Give detailed output of what the method is doing while in use, for debugging  |

**Author(s)**

Steffen Durinck

**Examples**

```
if(interactive()){  
  
  mart = useMart("ensembl")  
  mart=useMart(biomart="ensembl", dataset="hsapiens_gene_ensembl")  
}
```

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