

# Package ‘biobtreeR’

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**Type** Package

**Title** Using biobtree tool from R

**Version** 1.16.0

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**Description** The biobtreeR package provides an interface to [biobtree](https://github.com/tamerh/biobtree) tool which covers large set of bioinformatics datasets and allows search and chain mappings functionalities.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyLoad** yes

**NeedsCompilation** no

**URL** <https://github.com/tamerh/biobtreeR>

**BugReports** <https://github.com/tamerh/biobtreeR/issues>

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, testthat, rmarkdown, markdown

**Imports** httr, httpuv, stringi, jsonlite, methods, utils

**biocViews** Annotation

**RoxygenNote** 6.1.1

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bbBuildCustomDB	<i>Build custom DB</i>
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### Description

biobtree covers all the genomes in ensembl and ensembl genomes. If the the studied organism genome is not included in the default pre built in databases then this function is used and build the biobtree database locally for given genomes.

### Usage

```
bbBuildCustomDB(taxonomyIDs = NULL, rawArgs = NULL)
```

### Arguments

taxonomyIDs	Comma seperated list of taxonomy identifiers for building the genomes
rawArgs	For using all available biobtree command line arguments directly

### Value

returns empty

### Author(s)

Tamer Gur

**Examples**

```
## Not run:

bbUseOutDir("your directory path")
bbBuildCustomDB(taxonomyIDs="1408103,206403")

## End(Not run)
```

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bbBuiltInDB	<i>Get pre build biobtree database</i>
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**Description**

Pre build biobtree database for commonly studied datasets and model organism genomes. Once this function called it retrieves the pre build database saves to users output directory.

**Usage**

```
bbBuiltInDB(type = "1")
```

**Arguments**

type	<p>built in database type accepted values are 1,2,3 and 4. Currently there are 4 different builtin database; Type 1 Requires ~ 5 GB free storage Included datasets hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro Included uniprot proteins and ensembl genomes belongs to following organisms</p> <p>homo_sapiens 9606 -&gt; ensembl danio_rerio 7955 zebrafish -&gt; ensembl galus_gallus 9031 chicken -&gt; ensembl mus_musculus 10090 -&gt; ensembl Rattus norvegicus 10116 -&gt; ensembl saccharomyces_cerevisiae 4932-&gt; ensembl,ensembl_fungi arabidopsis_thaliana 3702-&gt; ensembl_plants drosophila_melanogaster 7227 -&gt; ensembl,ensembl_metazoa caenorhabditis_elegans 6239 -&gt; ensembl,ensembl_metazoa Escherichia coli 562 -&gt; ensembl_bacteria Escherichia coli str. K-12 substr. MG1655 511145 -&gt; ensembl_bacteria Escherichia coli K-12 83333 -&gt; ensembl_bacteria</p> <p>Type 2 Requires ~ 5 GB free storage Instead of genomes in in the type 1 it contains human and all the mouse strains genomes with their uniprot proteins. In addition hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro datasets are included</p> <p>Type 3 Requires ~ 4 GB storage Contains no genome but it contains all the uniprot data with hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro</p> <p>Type 4 Requires ~ 13 GB storage Contains no genome but full uniprot and chembl data with hgnc,hmdb,taxonomy,go,efo,eco,chebi,interpro</p>
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**Value**

returns empty

**Author(s)**

Tamer Gur

**Examples**

```
bbUseOutDir(tempdir()) # temp dir for demo purpose
bbBuiltInDB("demo") # small demo database for real database use 1, 2, 3 or 4
```

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bbConfig-class	<i>Class for biobtreeR config</i>
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**Description**

This class holds the datasets meta data and web service endpoints and used while executing the search/mapping queries. Instance of this class with name bbConfig is globally set by bbStart function. About dataset meta data, this class instance holds all the datasets unique identifiers, entry url templates etc. In biobtree each dataset has unique character and numeric identifier. For instance Uniprot's character identifier is "uniprot" and numeric identifier is 1. When performing queries the dataset character identifier is used for convenience but in actual database it is saved numerically.

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bbEntry	<i>Retrieve entry</i>
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**Description**

Returns entry for an identifier and dataset. Entry contains all the data raw data for and entry such as mappings, attributes and paging info if exists.

**Usage**

```
bbEntry(identifier, source)
```

**Arguments**

identifier	Identifier for the entry. Note that keywords are not accepted. For instance instead of "vav_human" keyword "p15498" identifier must be passed
source	Dataset identifier

**Value**

returns biobtree json object

**Author(s)**

Tamer Gur

**Examples**

```
bbStart() # if not already started  
bbEntry("HGNC:12009", "hgnc")
```

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bbEntryFilter	<i>Retrieve entry with filtered dataset</i>
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**Description**

Similar with entry retrieval but filtered mapping entries with given datasets.

**Usage**

```
bbEntryFilter(identifer, source, filters, page = NULL)
```

**Arguments**

identifer	Identifer for the entry.
source	Dataset identifier
filters	Comma seperated dataset identifier to retrieve
page	Page index if results is more than default biobtree paging size.

**Value**

returns biobtree json object

**Author(s)**

Tamer Gur

**Examples**

```
bbStart() # if not already started  
bbEntryFilter("HGNC:12009", "hgnc", "uniprot,ensembl")
```

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bbEntryPage	<i>Retrieve entry result page</i>
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**Description**

If an entry contains large set of mapping entries it is paginated by biobtree with configured paging size. This function retrieve these paging for an entry. Biobtree paging size for each entry is 200.

**Usage**

```
bbEntryPage(identifer, source, page, totalPage)
```

**Arguments**

identifer	Identifer for the entry.
source	Dataset identifier
page	Page index it starts from 0
totalPage	Total number of page for the entry. This value needs to calculate by user via using total number of entries which is available at the root result for the entry and divide it to the paging size of 200

**Value**

returns biobtree json object

**Author(s)**

Tamer Gur

**Examples**

```
bbStart() # if not already started  
bbEntryPage("ENSG00000141956", "ensembl", 0, 0)
```

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bbListAttrs	<i>Retrieve attributes of dataset</i>
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**Description**

Provides list of available attributes for a dataset to use in search and mapping queries.

**Usage**

```
bbListAttrs(dataset)
```

**Arguments**

dataset          Dataset identifier

**Value**

attributes names

**Examples**

```
bbListAttrs("hgnc")  
bbListAttrs("ensembl")
```

---

bbListDatasets	<i>List available datasets</i>
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**Description**

Lists the available source and target datasets with their numeric identifiers.

**Usage**

```
bbListDatasets()
```

**Value**

returns datasets

**Examples**

```
bbListDatasets()
```

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 bbMapping
 

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*Chain mapping and filtering*


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**Description**

Chain mapping identifiers or keywords with filtering and retrieving attributes if available.

**Usage**

```
bbMapping(terms, mapfilter, page = NULL, source = NULL, lite = TRUE,
          limit = 1000, inattrs = NULL, attrs = NULL,
          showInputColumn = FALSE)
```

**Arguments**

terms	Input terms for the mapping. Same with search functionality they can be comma separated identifiers or keywords
mapfilter	Mapping query which consist of map and optional filter functions in the form of map(dataset).filter(Boolean query expression) The boolean expressions are based on datasets attributes and dataset attributes can be list with bbAttr function. Dataset attributes which used in the filters starts with their dataset name. In biobtree boolean expressions feature has been implemented via Google common expression language so its full capability can be checked in its documentation.
page	Optional parameter works similar with bbSearch page paramter.
source	Optional dataset identifiers for searching input terms within the given dataset.
lite	By default it is TRUE and allow function return quickly with data.frame with mapping identifiers and attributes. If set to TRUE function return raw results converted from json.
limit	Limits the number of mapping results. By default without any limit all the results returned.
inattrs	Optional comma seperated attribute names for input identifiers and if available their values includes in result data.frame
attrs	Optional comma seperated attribute names for mapping identifiers and if available their values includes in result data.frame
showInputColumn	Optional logical parameter to show the input identifiers in the result data.frame

**Value**

returns mapping results in data.frame by default if lite set it true returns json object

**Author(s)**

Tamer Gur



**Examples**

```

bbStart()

bbMapping("tpi1", 'map(uniprot)')

bbMapping("shh", 'map(ensembl)')

## Not run:
# run these examples with building the default dataset with bbBuildData()
#Map protein to its go terms and retrieve go term types
bbMapping("AT5G3_HUMAN", 'map(go)', attrs = "type")

#Map protein to its go terms with filter by its type and retrieve their types
bbMapping("AT5G3_HUMAN", 'map(go).filter(go.type=="biological_process")', attrs = "type")

#Map gene names to exon identifiers and retrieve the region
bbMapping("ATP5MC3,TP53", 'map(transcript).map(exon)', attrs = "seq_region_name")

#Map Affymetrix identifiers to Ensembl identifiers and gene names
bbMapping("202763_at,213596_at,209310_s_at", source = "affy_hg_u133_plus_2"
, 'map(transcript).map(ensembl)', attrs = "name")

## End(Not run)

```

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bbSearch

*Search identifiers or special keywords*


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**Description**

Search identifiers or special keywords terms uniformly and resolve their actual unique identifiers and datasets. Keywords can be several things for instance for uniprot an accession like "vav\_human" can be a keyword which points to its original identifier "P15498". Or gene name can be also a keyword like "tpi1" which could points multiple dataset like ensembl and hgnc.

**Usage**

```

bbSearch(terms, source = NULL, filter = NULL, page = NULL,
         limit = 1000, showURL = FALSE, lite = TRUE)

```

**Arguments**

terms	Comma seperated identifiers or keywords
source	Optional dataset identifiers to search only within this dataset.
filter	Filter expression useful to filter out results when a keyword point several results. For instance if the biobtree index with multiple organism a same gene search could hit several results for different species to filter only a specific species a filter can apply to search function.

page	By default no need to pass this parameter since it returns all the results. It can be used with limit parameter for very large results to process them in paginated manner. About paging every long search or mapping result paginated in biobtree and for paginated results every response contains a key to get the next page results. So if this parameter is set with this key specified next page results returned for the given search term.
limit	Limits the number of search results. By default without any limit all the results returned.
showURL	allows returning the dataset source url
lite	By default it is TRUE and allow function return quickly with data.frame containing most important fields. If set to TRUE function return raw results converted from json.

**Value**

returns search results in data.frame by default if lite set it true returns json object

**Author(s)**

Tamer Gur

**Examples**

```
bbSearch("hunk,vav_human")
```

```
bbSearch("hunk","ensembl",filter='ensembl.genome=="homo_sapiens"')
```

---

bbStart

*Start biobtreeR*


---

**Description**

Once target datasets is built with bbBuildData this function used to start biobtree server in the background for performing search/mapping queries.

**Usage**

```
bbStart()
```

**Value**

character

**Examples**

```
bbStart()
```

```
bbStop()
```

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bbStop	<i>Stop biobtree</i>
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**Description**

Stops running background biobtree process which started with bbStart

**Usage**

```
bbStop()
```

**Value**

returns empty

**Examples**

```
bbStop()
```

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bbUseOutDir	<i>Output directory for biobtreeR</i>
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**Description**

Allows to set the directory for the package for its files. It is required to set a valid directory.

**Usage**

```
bbUseOutDir(outDir)
```

**Arguments**

outDir            path for the output directory.

**Value**

returns empty

**Examples**

```
bbUseOutDir(tempdir())
```

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