Package: qtl2bioc (via r-universe)

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Title Connect to Bioconductor for QTL Experiments

Description Functions to connect to genome databases via Bioconductor, such as to obtain gene annotation information. Part of R/qtl2, a reimplementation of the R/qtl package to better handle high-dimensional data and complex cross designs.

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Depends R (>= 3.1.0)

Imports GenomicRanges, AnnotationHub

Suggests testthat, devtools, roxygen2

License GPL-3

URL `https://kbroman.org/qtl2`, `https://github.com/rqtl/qtl2bioc`

BugReports `https://github.com/rqtl/qtl2bioc/issues`

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RemoteUrl https://github.com/rqtl/qtl2bioc

RemoteRef HEAD

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Contents

`create_ensembl_query_func` *Create a function to query genes*

Description

Create a function that will query genes from a GenomicRanges object with ensembl gene annotations and return a data frame with gene information for a selected region.

Usage

```
create_ensembl_query_func(ensembl, full_genes_only = TRUE)
```

Arguments

`ensembl`	Ensembl gene annotations as a GenomicRanges object.
`full_genes_only`	If TRUE, filter by `type=="gene"`

Details

Note that this function assumes that the database has `start` and `end` fields that are in basepairs, but the selection uses positions in Mbp, and the output data frame should have `start` and `stop` columns in Mbp.

Value

Function with three arguments, `chr`, `start`, and `end`, which returns a data frame with the genes overlapping that region, with `start` and `end` being in Mbp. The output should contain at least the columns `Name`, `chr`, `start`, and `stop`, the latter two being positions in Mbp.

Examples

```
# small version of ensembl data
ensembl <- readRDS(system.file("extdata", "ensembl_small.rds", package="qtl2bioc"))

# create query function, pulling only full genes
query_ensembl <- create_ensembl_query_func(ensembl)

# genes on chr 2 overlapping (96.5 - 97.0)
genes <- query_ensembl("2", 96.5, 97.0)
```

`grab_ensembl` *Grab ensembl gene annotations*

Description

Grab ensembl gene annotations from the Bioconductor AnnotationHub.

Usage

```
grab_ensembl(organism = "mus musculus", set = "AH51040")
```

Arguments

`organism`	Character string with name of organism
`set`	Character string with name of dataset

Value

A GenomicRanges object with the gene annotation information.

Examples

```
## Not run:
ensembl <- grab_ensembl()

## End(Not run)
```

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