

Package: fastmart (via r-universe)

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Title What the Package Does (One Line, Title Case)
Version 0.0.0.9000
Description What the package does (one paragraph).
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Remotes selkamand/assertions
URL <https://github.com/selkamand/fastmart>
BugReports <https://github.com/selkamand/fastmart/issues>
Repository <https://selkamand.r-universe.dev>
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fastmart_annotate_biotype

Annotate ENSEMBL GENES with BIOTYPE

Description

Annotate ENSEMBL GENES with BIOTYPE

Usage

```
fastmart_annotate_biotype(  
  ensemble_gene_id,  
  GRCh = c("38", "37"),  
  cache_dir = fastmart_default_cache()  
)
```

Arguments

ensemble_gene_id	ensembl gene id (can be versioned / not versioned)
GRCh	assembly to use. Can only be set to
cache_dir	directory to store cache in

Value

matched biotype for each sample (character)

Examples

```
## Not run:  
fastmart_annotate_biotype('ENSG00000282455.1')  
#> IG_D_gene  
  
## End(Not run)
```

fastmart_cache_tables *Cache Tables*

Description

Cache Tables

Usage

```
fastmart_cache_tables(
  ensembl_version = 109,
  overwrite = FALSE,
  GRCh = c("38", "37"),
  cache_dir = fastmart_default_cache()
)
```

Arguments

ensembl_version	ensembl version. Older versions may not be supported. Will be ignored if GRCh != 38
overwrite	overwrite existing cache (flag)
GRCh	assembly to use. Can only be set to
cache_dir	directory to store cache in

Value

invisible(TRUE). This function is run for its side effects

Examples

```
## Not run:
fastmart_cache_tables()

## End(Not run)
```

```
fastmart_convert_hgnc_to_ensembl
      Convert HGNC -> ENSEMBL IDs
```

Description

Because ENSEMBL IDs are more granular than HGNC / HUGO symbols we require the start & stop coordinates

Usage

```
fastmart_convert_hgnc_to_ensembl(
  hgnc_symbols,
  chrom,
  start,
  end,
  GRCh = c("38", "37"),
  exact_match = TRUE,
  no_pos_required = FALSE,
  cache_dir = fastmart_default_cache()
)
```

Arguments

hgnc_symbols	HGNC symbols
chrom	Chromosome of Gene. Required to resolve ambiguous mappings (character)
start	Start position of Gene. Required to resolve ambiguous mappings (numeric)
end	End position of Gene. Required to resolve ambiguous mappings (numeric)
GRCh	assembly to use. Can only be set to
exact_match	Is an exact match between chrom-start-end required (TRUE), or should the omst similar interval be returned (FALSE) (flag)
cache_dir	directory to store cache in

Value

matched ENSEMBL IDs (character)

Examples

```
## Not run:
fastmart_convert_hgnc_to_ensembl('TBCE', chrom='1', start='235530675', end='235612283', GRCh = "37")
# > ENSG00000116957.8

## End(Not run)
```

fastmart_default_cache

Default Cache

Description

Default Cache

Usage

```
fastmart_default_cache()
```

Value

default path to cache

Examples

```
fastmart_default_cache()
```

<code>fastmart_init</code>	<i>Initialise fastmart</i>
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Description

Creates a folder (by default at `~/fastmart`) where any database caches will be stored

Usage

```
fastmart_init(cache_dir = fastmart_default_cache())
```

Arguments

`cache_dir` directory to store cache in

Value

path to the newly created fastmart cache

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