GGdata

March 19, 2011

`fheadFits` *forkhead box F2 gene set eQTL search result using CEU*

Description

forkhead box F2 gene set eQTL search result using CEU

Usage

```
data(fheadFits)
```

Format

The format is: Formal class 'filteredMultiGwSnpScreenResult' [package "GGBase"] with 4 slots, the list of filtered results (.Data), geneset (the set of genes tested), call, and sessionInfo.

Examples

```
## Not run:   # requires bioc 2.7
data(fheadFits)
fheadFits
fheadFits[["CPNE1"]]
library(GGtools)
topSnps(fheadFits[["CPNE1"]])[[20]]

## End(Not run)
```

`hmceuB36` *representations of HapMap snp data + expression data*

Description

representations of HapMap snp data + expression data

Usage

```
data(hmceuB36)
```

Details

These instances of class `smlSet` are created from two basic sources.

First, the expression data for 90 CEU families in CEPH were obtained from SANGER GENEVAR project.

Second, data on forward non-redundant SNPs in these individuals the HapMap build 36 ftp site in march 2008. Full provenance information still to be supplied.

Value

instances of class `smlSet`

Author(s)

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References

Cheung VG., Spielman RS., Ewens KG., Weber TM., Morley M & Burdick JT.: *Mapping determinants of human gene expression by regional and whole genome association.* Nature, 437: 1365-1369, 2005

Examples

```
## Not run:   # requires bioc 2.7
data(hmceuB36)
# be patient
exprs(hmceuB36)[1:4,1:4]
as(smList(hmceuB36)[[1]][1:4,1:4], "character")
library(ff)
library(GGtools)
tt = gwSnpTests(genesym("CPNE1")~male, hmceuB36, snpdepth(500))
tt
plot(tt)

## End(Not run)
```

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