GGdata
August 10, 2009

R topics documented:

\begin{verbatim}
fheadFits ................................................. 1
hmceuB36 ..................................................... 2
\end{verbatim}

Index

\begin{verbatim}
fheadFits  forhead box F2 gene set eQTL search result using CEU
\end{verbatim}

Description

forhead 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

data(fheadFits)
fheadFits
fheadFits["CPNE1"]
library(GGtools)
topSnps(fheadFits["CPNE1"])[[20]]
**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**


**Examples**

data(hmceuB36)  
# be patient  
exprs(hmceuB36)[1:4,1:4]  
as(smList(hmceuB36)[[1]][1:4,1:4], "character")  
library(GGtools)  
tt = gwSnpTests(genesym("CPNE1")~male, hmceuB36, snpdepth(500))  
tt  
plot(tt)
Index

*Topic datasets
  fheadFits, 1

*Topic models
  hmceuB36, 1

fheadFits, 1
hmceuB36, 1
smlSet, 2