Description

representations of HapMap snp data + expression data

Usage

# getSS("GGdata", "20")  # for example, to get full expression, + genotypes
# on chr20

Format

ExpressionSet and SnpMatrix instances to be combined using getSS
Details

Instances of class \texttt{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 \texttt{smlSet}

Note

As of March 2011 the smlSet is no longer serialized. Instead, use \texttt{getSS(“GGdata”, \[chrs\])} to create an smlSet with all probes and selected chromosomes. There is an instance of \texttt{ExpressionSet-class} named \texttt{ex} in the data folder of this package that will be united with genotype data using \texttt{getSS}.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

References


Examples

library(GGtools)
hmceuB36 = getSS(“GGdata”, c(“20”)) # just 1 chromosome
exprs(hmceuB36)[1:4,1:4] as(smList(hmceuB36)[][1][1:4,1:4], “character”)
library(GGtools)
library(illuminaHumanv1.db)
cptag = get(“CPNE1”, revmap(illuminaHumanv1SYMBOL))
tt = eqtlTests(hmceuB36[[probeId(cptag)],], ~male)
topFeats(probeId(cptag), mgr=tt, ffind=1)
Index

«Topic packages
  hmceuB36, 1
ex (hmceuB36), 1
getSS, 2
hmceuB36, 1
hmceuB36-package (hmceuB36), 1
sm1Set, 2