GGdata

March 23, 2012

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

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 `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`

Note

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

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

```
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)
```

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