

RSNPper

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SNPperMeta-class	<i>Class "SNPperMeta" representing data on SNPs curated at snpper.chip.org</i>
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Description

gives immediate access to location and allele, methods extract material on allele frequencies in different populations, and relationships to particular mRNAs/genes.

Objects from the Class

Objects can be created by calls of the form `new("SNPperMeta", . . .)`. The extend matrix (so that colnames are propagated).

Slots

- .Data:** Object of class "matrix" see example
- popDetails:** Object of class "data.frame" information on populations that have been genotyped for reference
- geneDetails:** Object of class "data.frame" information on mRNAs (typically) near the SNP; putative SNP roles (in Promoter, 3' UTR, or Exon) are often denoted
- submitters:** Object of class "ANY" unprocessed XML on submitter identity.

Extends

Class "matrix", from data part. Class "structure", by class "matrix". Class "array", by class "matrix". Class "vector", by class "matrix", with explicit coerce. Class "vector", by class "matrix", with explicit coerce.

Methods

popDetails, geneDetails, submitters functions are available.

Author(s)

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References

snpper.chip.org

Examples

```
if (interactive()) {
  lkc = SNPinfo("6060535")
  lkc
  popDetails(lkc)
  geneDetails(lkc)
  lkg = geneInfo("CPNE1")
  lkg
  dim(allGeneMeta(lkg))
}
```

geneInfo

use CHIP SNPPER XML-RPC service to extract gene or SNP information

Description

SNPPER is a web service at chip.org (see Riva and Kohane, Bioinformatics 2002). This function sets up the XML RPC call for the GENEINFO service.

Usage

```
geneInfo(name=NA, acc=NA, id=NA, useOldOutput=FALSE)
SNPinfo(dbsnpid=NA, useOldOutput=FALSE)
geneLayout(id=NA)
geneSNPs(id=NA, acc=NA)
itemsInRange(item="genes", chr, start, end)
useSNPPER(cmd, parmstring)
useSNPPER2(cmd, parmstring)
```

Arguments

name	name: standard gene name
acc	acc: mrna accession number
id	id: SNPPER gene id. This is a 'private' nomenclature, to find the value for a given gene, use geneInfo.
dbsnpid	dbsnpid: numeric value after 'rs' in dbSNP id
item	item: string, either "genes", "snps", or "countsnps"
useOldOutput	logical: should the 1.5 output format be used? newer format uses an S4 object
cmd	cmd: character string identifying an XML-RPC call honored by SNPPER; see list .rpcCalls in package
parmstring	parmstring: character string supplying parm=value information

chr	chr: string beginning with 'chr' identifying chromosome of interest
start	start: start in base pair count of region of interest; use a string to avoid problems with scientific notation
end	end: end in base pair count of region of interest; use a string to avoid problems with scientific notation

Details

runs an xmlEventParse on the XML-RPC response and packages the results.

Value

an attributed, named character vector. The attribute gives version info for the SNPper database build.

Note

The itemsInRange function with item argument 'countsnp' is a hack that does not use XML parsing because the countsnp XML-RPC returns illegitimate XML tags. Thus there is no toolInfo attribute for this specific call. All other functions return textual information coupled with a 'toolInfo' attribute which details the SNPper database version, the golden path build version, and the dbSNP database version from which the SNPper resources were constructed.

NB: A revised version of the XML package now allows direct parsing of R connection streams. This will be employed ASAP, once the necessary general XML infrastructure becomes prevalent.

Author(s)

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References

Riva A and Kohane IS, SNPper: retrieval and analysis of human SNPs, Bioinformatics 18(12) 2002, pp1681-1685.

Examples

```
if (interactive())
{
  print(geneInfo("CRP"))
  print(geneLayout("546"))
  tmp <- geneSNPs("546")
  print(length(tmp))
  glist <- itemsInRange("genes","chr1", "155000000", "157000000")
  print(SNPinfo("25"))
  print(length(glist))
  print(itemsInRange("countsnp","chr1", "156000000", "157000000"))
  print(useSNPper("geneinfo",&name=CRP))
}
```

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