

Package ‘ceu1kg’

October 7, 2015

Title CEU (N=60) genotypes from 1000 genomes pilot phase I

Version 0.6.0

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Description CEU genotypes from 1000 genomes ``low coverage" pilot phase I (approx 8 million SNP calls released July 2010); includes Wellcome trust GENEVAR expression for 43 indiv

Depends R (>= 2.12.0), GGBase (>= 3.9.0), GGtools, Biobase

Suggests SNPlocs.Hsapiens.dbSNP.20101109

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License Artistic-2.0

biocViews SNPData, HapMap, Project1000genomes

NeedsCompilation no

R topics documented:

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Description

CEU genotypes from 1000 genomes pilot phase I (approx 8 million SNP); includes wellcome trust GENEVAR expression for 41 individuals

Details

Package: ceulkg
Version: 0.0.10
Depends: R (>= 2.11.1), GGBase (>= 3.9.0)
License: Artistic-2.0
LazyLoad: yes
Built: R 2.12.0; ; 2010-07-01 01:14:27 UTC; unix

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ceulkg-package 60 hapmap CEU samples, 47K expression, 8mm 1000
 genomes SNP

There are three two data resources provided here.

First, the 1000 genomes SNP calls for 60 CEU individuals were extracted from the pilot data VCF file ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/pilot_data/release/2010_07/low_coverage/snps/CEU.low_coverage.2010_07.genotypes.vcf.gz.

Second, a `smlSet-class` is provided for 43 individuals in the 1000 genomes CEU SNP call set for whom expression data are available via the Sanger GENEVAR distribution (ftp://ftp.sanger.ac.uk/pub/genevar/CEU_parents_norm_march2007.zip).

Author(s)

The R package was created by VJ Carey <stvjc@channing.harvard.edu>

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Examples

```
library(ceulkg)
```

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