

# ceulkg

March 19, 2011

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ceulkg-package	<i>CEU (N=60) genotypes from 1000 genomes pilot phase I</i>
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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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There are three basic 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](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, metadata `GRanges-class` instances are provided in chromosome-specific containers.

Third, 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](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](mailto:stvjc@channing.harvard.edu)>

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**Examples**

```
# all genotypes
if ("package:snpMatrix2" %in% search()) {
  # note this will not run in Bioconductor 2.7
  library(ceulkg)
  data(ceulkg.sml)
  names(ceulkg.sml)
  ceulkg.sml[[1]]
  data(ceulkgMeta_20)
  ceulkgMeta_20
  data(ceulkg)
  ceulkg
}
```

ceulkg.sml

*SnpMatrix instances of 1000 genomes low coverage data for CEU***Description**

SnpMatrix instances of 1000 genomes low coverage data for CEU

**Usage**

```
data(ceulkg.sml)
```

**Format**

The format is:

List of 22

\$ chr1 :Formal class 'SnpMatrix' [package "snpMatrix2"] with 1 slots

.. ..@ .Data: raw [1:60, 1:605756] 01 01 01 01 ...

.. .. - attr(\*, "dimnames")=List of 2

.. .. .. \$ : chr [1:60] "NA06985" "NA06986" "NA06994" "NA07000" ...

.. .. .. \$ : chr [1:605756] "chr1:533" "chr1:41342" "chr1:41791" "chr1:44449" ...

\$ chr2 :Formal class 'SnpMatrix' [package "snpMatrix2"] with 1 slots

.. ..@ .Data: raw [1:60, 1:664326] 01 01 02 02 ...

.. .. - attr(\*, "dimnames")=List of 2

.. .. .. \$ : chr [1:60] "NA06985" "NA06986" "NA06994" "NA07000" ...

.. .. .. \$ : chr [1:664326] "chr2:361" "chr2:536" "chr2:572" "chr2:1320" ...

....

\$ chr22:Formal class 'SnpMatrix' [package "snpMatrix2"] with 1 slots

.. ..@ .Data: raw [1:60, 1:101568] 01 01 01 01 ...

.. .. - attr(\*, "dimnames")=List of 2

.. .. .. \$ : chr [1:60] "NA06985" "NA06986" "NA06994" "NA07000" ...

.. .. .. \$ : chr [1:101568] "rs62224609" "rs6518413" "rs4965019" "chr22:14433730" ...

**Details**

see provenance folder in installed folder for notes on construction

**Source**

[ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/pilot\\_data/release/2010\\_07/low\\_coverage/snps/CEU.low\\_coverage.2010\\_07.genotypes.vcf.gz](ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/pilot_data/release/2010_07/low_coverage/snps/CEU.low_coverage.2010_07.genotypes.vcf.gz)

**References**

1000genomes.org

**Examples**

```
# data(ceulkg.sml)
```

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ceulkgMeta\_20

*GRanges instances of SNP location and allele coding data*

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**Description**

GRanges instances of SNP location and allele coding data

**Usage**

```
data(ceulkgMeta_20)
```

**Format**

The format is: Formal class 'GRanges' [package "GenomicRanges"] with 7 slots ..@ seqnames : Formal class 'Rle' [package "IRanges"] with 5 slots ..@ values : Factor w/ 1 level "chr20": 1 ..@ lengths : int 174484 ..@ elementMetadata: NULL ..@ elementType : chr "ANY" ..@ metadata : list() ..@ ranges : Formal class 'IRanges' [package "IRanges"] with 6 slots ..@ start : int [1:174484] 9098 9795 10731 11244 11541 11799 13288 13532 13900 14370 ... ..@ width : int [1:174484] 1 1 1 1 1 1 1 1 1 ... ..@ NAMES : chr [1:174484] "rs6078030" "rs4814683" "rs34147676" "rs6139074" ... ..@ elementMetadata: NULL ..@ elementType : chr "integer" ..@ metadata : list() ..@ strand : Formal class 'Rle' [package "IRanges"] with 5 slots ..@ values : Factor w/ 3 levels "+","-","\*": 3 ..@ lengths : int 174484 ..@ elementMetadata: NULL ..@ elementType : chr "ANY" ..@ metadata : list() ..@ seqlengths : Named int NA ..- attr(\*, "names")= chr "chr20" ..@ elementMetadata: Formal class 'DataFrame' [package "IRanges"] with 6 slots ..@ rownames : NULL ..@ nrows : int 174484 ..@ elementMetadata: NULL ..@ elementType : chr "ANY" ..@ metadata : list() ..@ listData : List of 3 ..- \$ ref : chr [1:174484] "C" "G" "C" "A" ... ..- \$ alt : chr [1:174484] "T" "T" "A" "C" ... ..- \$ depth : num [1:174484] 192 NA 228 NA 331 NA NA 219 325 NA ... ..@ elementType : chr "ANY" ..@ metadata : list()

**Details**

see notes.txt in provenance folder for info on detailed derivation

**Source**

[ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/pilot\\_data/release/2010\\_07/low\\_coverage/snps/CEU.low\\_coverage.2010\\_07.genotypes.vcf.gz](ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/pilot_data/release/2010_07/low_coverage/snps/CEU.low_coverage.2010_07.genotypes.vcf.gz)

**References**

1000genomes.org

**Examples**

```
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ceukgMeta_20
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