Package 'GWASdata'

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Title Data used in the examples and vignettes of the GWASTools package

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Description Selected Affymetrix and Illlumina SNP data for HapMap subjects. Data provided by the Center for Inherited Disease Research at Johns Hopkins University and the Broad Institute of MIT and Harvard University.

Depends GWASTools

Suggests ncdf4

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GWASdata-package *Data used in the examples and vignettes of the GWASTools package.*

Description

Selected Affymetrix and Illlumina SNP data for HapMap subjects. Data provided by the Center for Inherited Disease Research (CIDR) at Johns Hopkins University and the Broad Institute of MIT and Harvard University.

Details

77 HapMap subjects were genotyped by CIDR on the Illumina Human1Mv_C array. Selected data includes 1000 SNPs on each of chromosomes 21, 22, and X, and 100 SNPs on each of Y, the pseudoautosomal region, and mitochondrial DNA. SNP and scan annotation are provided as R data frames. Genotype data, X and Y intensity data with quality scores, and B allele frequency / log R ratio data are stored in NetCDF files. Text files with raw data are provided for 3 subjects.

47 of the HapMap subjects were genotyped by the Broad on the Affymetrix GenomeWideSNP_6 array. Identical SNPs to the Illumina data were selected for chromosomes 21, 22, and X. SNP and scan annotation are provided as R data frames. Genotype data and X and Y intensity data with quality scores are stored in NetCDF files. Text files with raw data are provided for 3 subjects.

List of datasets:

- affy_scan_annot: data.frame with Affymetrix scan annotation
- affy_snp_annot: data.frame with Affymetrix SNP annotation
- affyScanADF: `ScanAnnotationDataFrame` with Affymetrix scan annotation
- affySNPADF: `SnpAnnotationDataFrame` with Affymetrix SNP annotation
- illumina_scan_annot: data.frame with Illumina scan annotation
- illumina_snp_annot: data.frame with Illumina SNP annotation
- illuminaScanADF: `ScanAnnotationDataFrame` with Illumina scan annotation
- illuminaSnpADF: `SnpAnnotationDataFrame` with Illumina SNP annotation

List of files in "extdata":

- affy_geno.nc: NetCDF file with Affymetrix genotypes
- affy_qxy.nc: NetCDF file with Affymetrix XY intensity data and quality scores
- affy_raw_data: Directory with Affymetrix raw data in text files
- illumina_geno.nc: NetCDF file with Illumina genotypes
- illumina_qxy.nc: NetCDF file with Illumina XY intensity data and quality scores
- illumina_bl.nc: NetCDF file with Illumina BAlleleFreq and LogRRatio data
- illumina_geno.gds: GDS file with Illumina genotypes
- illumina_qxy.gds: GDS file with Illumina XY intensity data and quality scores
- illumina_bl.gds: GDS file with Illumina BAlleleFreq and LogRRatio data

- illumina_raw_data: Directory with Illumina raw data in text files
- illumina_subj.ped: PLINK PED file with Illumina genotypes
- illumina_subj.map: PLINK MAP file with Illumina SNP info
- illumina_subj.bim: PLINK extended MAP file with Illumina SNP info and alleles

See Also

ScanAnnotationDataFrame, SnpAnnotationDataFrame, NcdfGenotypeReader, NcdfIntensityReader, GdsGenotypeReader, GdsIntensityReader, GenotypeData, IntensityData

Examples

```
library(GWASdata)
data(illumina_scan_annot)
data(illumina_snp_annot)

data(illuminaScanADF) # ScanAnnotationDataFrame
data(illuminaSnpADF) # SnpAnnotationDataFrame
varMetadata(illuminaSnpADF)

# NetCDF
file <- system.file("extdata", "illumina_geno.nc", package="GWASdata")
nc <- NcdfGenotypeReader(file)
geno <- getGenotype(nc, snp=c(1,10), scan=c(1,5))
genoData <- GenotypeData(nc, snpAnnot=illuminaSnpADF, scanAnnot=illuminaScanADF)

# GDS
file <- system.file("extdata", "illumina_geno.gds", package="GWASdata")
gds <- GdsGenotypeReader(file)
geno <- getGenotype(gds, snp=c(1,10), scan=c(1,5))
genoData <- GenotypeData(gds, snpAnnot=illuminaSnpADF, scanAnnot=illuminaScanADF)

# raw data
list.files(system.file("extdata", "illumina_raw_data", package="GWASdata"))
```

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