Package 'UKB.COVID19'

January 20, 2025

Type Package

Title UK Biobank COVID-19 Data Processing and Risk Factor Association Tests

Version 0.1.6

Date 2024-08-17

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Description Process UK Biobank COVID-19 test result data for susceptibility, severity and mortality analyses, perform potential non-genetic COVID-19 risk factor and co-morbidity association tests. Wang et al. (2021) <doi:10.5281/zenodo.5174381>.

Imports questionr, data.table, tidyverse, magrittr, here, dplyr

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URL https://github.com/bahlolab/UKB.COVID19

Encoding UTF-8

RoxygenNote 7.3.1

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

Repository CRAN

Date/Publication 2024-08-17 10:20:59 UTC

VignetteBuilder knitr

Contents

`comorbidity_asso` *Generate comorbidity association result file*

Description

Association tests between each co-morbidity and given phenotype (susceptibility, mortality or severity) with the adjustment of covariates.

Usage

```
comorbidity_asso(
  pheno,
  covariates,
  cormorbidity,
  population = "all",
  cov.name = c("sex", "age", "bmi"),
  phe.name,
  ICD10.file
)
```

Arguments

`pheno`	phenotype dataframe - output from makePheno function
`covariates`	covariate dataframe - output from risk.factor function. Optional.
`cormorbidity`	Comorbidity summary generated from comorbidity.summary.
`population`	Choose self-report population/ethnic background group from "all", white", "black", "asian", "mixed", or "other". By default, population="all", include all ethnic groups.
`cov.name`	Selected covariates names. By default, cov.name=c("sex","age","bmi"), covariates are sex age and BMI.
`phe.name`	Phenotype name.
`ICD10.file`	The ICD10 code file, which is included in the package.

Value

Outputs a comorbidity association test result with OR, 95% CI and p-value.

Examples

```
## Not run:
comorb.asso <- comorbidity_asso(pheno=phe,
covariates=covar,
cormorbidity=comorb,
population="white",
cov.name=c("sex","age","bmi","SES","smoke","inAgedCare"),
phe.name="hospitalisation",
ICD10.file=covid_example("ICD10.coding19.txt.gz"))

## End(Not run)
```

`comorbidity_summary` *Create comorbidity summary file*

Description

summarise disease history records of each individual from the hospital inpatient diagnosis data.

Usage

```
comorbidity_summary(
  ukb.data,
  hesin.file,
  hesin_diag.file,
  primary = FALSE,
  ICD10.file,
  Date.start = NULL,
  Date.end = NULL
)
```

Arguments

`ukb.data`	tab delimited UK Biobank phenotype file, containing sample qc fields (with default UKBiobank codes as column names)
`hesin.file`	Latest hospital inpatient master file.
`hesin_diag.file`	Latest hospital inpatient diagnosis file.
`primary`	TRUE: include primary diagnosis only; FALSE: include all diagnoses.
`ICD10.file`	The ICD10 code file, which is included in the package.
`Date.start`	Date, dd/mm/yyyy, select the start date of hospital inpatient record period.
`Date.end`	Date, dd/mm/yyyy, select the end date of hospital inpatient record period.

Value

Outputs comorbidity summary table, named comorbidity_<Date.start>_<Date.end>.RData, including phenotype, non-genetic risk factors and all comorbidities, which will be used in the comorbidity association tests.

Examples

```
## Not run:
comorb <- comorbidity_summary(ukb.data=covid_example("sim_ukb.tab.gz"),
hesin.file=covid_example("sim_hesin.txt.gz"),
hesin_diag.file=covid_example("sim_hesin_diag.txt.gz"),
ICD10.file=covid_example("ICD10.coding19.txt.gz"),
primary = FALSE,
Date.start = "16/03/2020")

## End(Not run)
```

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covid_example *Provide working directory for UKB.COVID19 example files*

Description

Provide working directory for UKB.COVID19 example files

Usage

```
covid_example(path)
```

Arguments

path	path to file

Value

Outputs the working directory for UKB.COVID19 example files.

Examples

```
covid_example('results/covariate.txt')
```

data_reform *Reform variables*

Description

Reform variables

Usage

```
data_reform(res, type)
```

Arguments

res	Merged data of phenotype from makePhenotypes or comorbidity_summary and covariates from risk_factor.
type	Data type: susceptibility, severity, mortality or comorbidity.

Value

Reformed data for association tests using logistic regression models.

log_cov *Perform association tests between phenotype and covariates*

Description

Perform association tests between phenotype and covariates

Usage

```
log_cov(pheno, covariates, phe.name, cov.name = c("sex", "age", "bmi"))
```

Arguments

pheno	phenotype dataframe - output from makePhenotypes function
covariates	covariate dataframe - output from risk_factor function.
phe.name	Phenotype name in the data.
cov.name	Selected covariate names in the data. By default, cov.name=c("sex","age","bmi"), covariates include sex, age and BMI.

Value

Outputs association test results with OR, 95% CI, and p-value.

Examples

```
## Not run:
log_cov(pheno=phe, covariates=covar, phe.name="hospitalisation", cov.name=c("sex","age","bmi"))

## End(Not run)
```

`makeGWASFiles` *Generate files for GWAS Software. SAIGE and Plink currently supported.*

Description

Generate files for GWAS Software. SAIGE and Plink currently supported.

Usage

```
makeGWASFiles(
  ukb.data,
  pheno,
  covariates,
  phe.name,
  cov.name = NULL,
  includeSampsFile = NULL,
  software = "SAIGE",
  outDir = "",
  prefix
)
```

Arguments

`ukb.data`	tab delimited UK Biobank phenotype file, containing sample qc fields (with default UKBiobank codes as column names)
`pheno`	phenotype dataframe - output from makePhenotype function
`covariates`	covariate dataframe - output from risk.factor function. Optional.
`phe.name`	phenotypes to be included in outputted data. multiple phenotypes can be specified as a vector. if null, all phenotypes will be outputted.
`cov.name`	covariates to be included in outputted data. Optional. multiple covariates can be specified as a vector. if null, all covariates in file will be outputted
`includeSampsFile`	list of samples to be included GWAS. File with the first column containing sample IDs to be kept. Can contain other columns. output from sampleQC function may be used. Optional - if null, all samples will be outputted.
`software`	specify "SAIGE" or "plink" - defaults to "SAIGE"
`outDir`	specify directory to output file
`prefix`	prefix for file - optional

Value

outputs file, suitable for reading by chosen GWAS software

Examples

```
## Not run:
makeGWASFiles(ukb.data=covid_example("sim_ukb.tab.gz"),
pheno=phe,
covariates=covar,
phe.name="hospitalisation",
cov.name=NULL,
includeSampsFile=NULL,
software="SAIGE",
outDir=covid_example("results"),
prefix="hospitalisation")

## End(Not run)
```

---

makePhenotypes *Generate COVID-19 phenotypes*

Description

Generate COVID-19 phenotypes

Usage

```
makePhenotypes(
  ukb.data,
  res.eng,
  res.wal = NULL,
  res.sco = NULL,
  death.file,
  death.cause.file,
  hesin.file,
  hesin_diag.file,
  hesin_oper.file,
  hesin_critical.file,
  code.file,
  pheno.type = "severity",
  Date = NULL
)
```

Arguments

ukb.data	tab delimited UK Biobank phenotype file.
res.eng	Latest covid result file/files for England.
res.wal	Latest covid result file/files for Wales. Only available for downloads after April 2021.
res.sco	Latest covid result file/files for Scotland. Only available for downloads after April 2021.
death.file	Latest death register file.
death.cause.file	Latest death cause file.
hesin.file	Latest hospital inpatient master file.
hesin_diag.file	Latest hospital inpatient diagnosis file.
hesin_oper.file	Latest hospital inpatient operation file.
hesin_critical.file	Latest hospital inpatient critical care file.
code.file	The operation code file, which is included in the package.
pheno.type	The phenotype options, which include "susceptibility", "severity", and "mortality".
Date	Date, ddmmyyyy, select the results until a certain date. By default, Date = NULL, the latest hospitalization date.

Value

Returns a data.frame with phenotypes for COVID-19 susceptibility, severity and mortality.

Examples

```
## Not run:
pheno <- makePhenotypes(ukb.data=covid_example("sim_ukb.tab.gz"),
res.eng=covid_example("sim_result_england.txt.gz"),
death.file=covid_example("sim_death.txt.gz"),
death.cause.file=covid_example("sim_death_cause.txt.gz"),
hesin.file=covid_example("sim_hesin.txt.gz"),
hesin_diag.file=covid_example("sim_hesin_diag.txt.gz"),
hesin_oper.file=covid_example("sim_hesin_oper.txt.gz"),
hesin_critical.file=covid_example("sim_hesin_critical.txt.gz"),
code.file=covid_example("coding240.txt.gz"),
pheno.type = "severity")

## End(Not run)
```

`risk_factor` *Generate covariate file*

Description

This function formats and outputs a covariate table, used for input for other functions.

Usage

```
risk_factor(
  ukb.data,
  ABO.data = NULL,
  hesin.file,
  res.eng,
  res.wal = NULL,
  res.sco = NULL,
  fields = NULL,
  field.names = NULL
)
```

Arguments

`ukb.data`	tab delimited UK Biobank phenotype file. The file should include fields of gender, year of birth, BMI, ethnic background, SES, and smoking.
`ABO.data`	Latest yyyymmdd_covid19_misc.txt file.
`hesin.file`	Latest yyyymmdd_hesin.txt file.
`res.eng`	Latest covid result file/files for England.
`res.wal`	Latest covid result file/files for Wales. Only available for downloads after April 2021.
`res.sco`	Latest covid result file/files for Scotland. Only available for downloads after April 2021.
`fields`	User specified field codes from ukb.data file.
`field.names`	User specified field names.

Value

Outputs a covariate table, used for input for other functions. Automatically returns sex, age at birthday in 2020, SES, self-reported ethnicity, most recently reported BMI, most recently reported pack-years, whether they reside in aged care (based on hospital admissions data, and covid test data) and blood type. Function also allows user to specify fields of interest (field codes, provided by UK Biobank), and allows the users to specify more intuitive names, for selected fields.

Examples

```
## Not run:
covars <- risk_factor(ukb.data=covid_example("sim_ukb.tab.gz"),
ABO.data=covid_example("sim_covid19_misc.txt.gz"),
hesin.file=covid_example("sim_hesin.txt.gz"),
res.eng=covid_example("sim_result_england.txt.gz"))

## End(Not run)
```

`sampleQC` *Sample QC for genetic analyses*

Description

Sample QC for genetic analyses

Usage

```
sampleQC(ukb.data, withdrawnFile, ancestry = "all", software = "SAIGE", outDir)
```

Arguments

`ukb.data`	tab delimited UK Biobank phenotype file, containing sample qc fields (with default UKBiobank codes as column names)
`withdrawnFile`	csv file with withdrawn IDs from UK Biobank
`ancestry`	specify "WhiteBritish" or "all" - defaults to "all"
`software`	specify "SAIGE" or "plink" - defaults to "SAIGE"
`outDir`	specify directory for sample QC file and inclusion/exclusion lists

Value

outputs sample QC file, and sample inclusion / exclusion lists for specified software

Examples

```
## Not run:
sampleQC(ukb.data=covid_example("sim_ukb.tab.gz"),
withdrawnFile=covid_example("sim_withdrawn.csv.gz"),
ancestry="all",
software="SAIGE",
outDir=covid_example("results"))

## End(Not run)
```

variantQC *Variant QC for Genetic Analyses*

Description

Variant QC for Genetic Analyses

Usage

```
variantQC(snpQcFile, mfiDir, mafFilt = 0.001, infoFilt = 0.5, outDir)
```

Arguments

snpQcFile	file containing SNP QC info (ukb_snp_qc.txt)
mfiDir	directory where the per chromosome UKBiobank MAF/INFO files (ukb_mfi_chr*_v3.txt) are located
mafFilt	minor allele frequency filter - default 0.001
infoFilt	imputation quality (INFO) score filter - default 0.5
outDir	output directory

Value

outputs SNP inclusion lists (SNPID and rsID formats) for given MAF/INFO filters. Also outputs list of SNPs to be used for genetic Relatedness Matrix (GRM) calculations.

Examples

```
## Not run:
variantQC(snpQcFile=covid_example("sim_ukb_snp_qc.txt.gz"),
mfiDir=covid_example("alleleFreqs"),
mafFilt=0.001,
infoFilt=0.5,
outDir=covid_example("results"))

## End(Not run)
```

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