Package ‘MixRF’

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Title A Random-Forest-Based Approach for Imputing Clustered Incomplete Data

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Description It offers random-forest-based functions to impute clustered incomplete data. The package is tailored for but not limited to imputing multitissue expression data, in which a gene's expression is measured on the collected tissues of an individual but missing on the uncollected tissues.

License GPL

Depends doParallel, randomForest, lme4, foreach

URL https://github.com/randel/MixRF

BugReports https://github.com/randel/MixRF/issues

RoxygenNote 5.0.1

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MixRF-package

A random-forest-based algorithm for imputing clustered incomplete data

Description

This package offers random-forest-based functions to impute clustered incomplete data. The package is tailored for but not limited to imputing multitissue expression data, in which a gene’s expression is measured on the collected tissues of an individual but missing on the uncollected tissues.

Details

Package: MixRF
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License: GPL
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Author(s)

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References


See Also

MixRF.impute

MixRF

Mixed Random Forest

Description

The function to fit a random forest with random effects.
MixRF.impute

Usage

MixRF(Y, X, random, data, initialRandomEffects = 0, ErrorTolerance = 0.001, MaxIterations = 1000)

Arguments

Y  The outcome variable.
X  A data frame or matrix contains the predictors.
random  A string in lme4 format indicates the random effect model.
data  The data set as a data frame.
initialRandomEffects  The initial values for random effects.
ErrorTolerance  The tolerance for log-likelihood.
MaxIterations  The maximum iteration times.

Value

A list contains the random forest ($forest), mixed model ($MixedModel), and random effects ($RandomEffects). See the example below for the usage.

Examples

data(sleepstudy)

tmp = MixRF(Y = sleepstudy$Reaction, X = as.data.frame(sleepstudy$Days),
            random = "(Days|Subject)", data = sleepstudy, initialRandomEffects = 0,
            ErrorTolerance = 0.01, MaxIterations = 100)

# tmp$forest
# tmp$MixedModel
# tmp$RandomEffects

MixRF.impute  Impute a large number of genes using the MixRF algorithm with parallel computing

Description

This function impute the expression of a large number of genes using the MixRF algorithm with parallel computing.
MixRF.impute

Usage

MixRF.impute(Ydat, eqtl.lis, snp.dat, cov = NULL, iPC = TRUE,
               idx.selected.gene.iPC = NULL, parallel.size = 1, correlation = FALSE,
               nCV = 3)

Arguments

Ydat An array of expression data of dimension sample-by-gene-by-tissue, nxpxT,
      where n is sample size, p is the number of genes, and T is the number of tissues.
      Ydat[,1,] is a matrix of the first gene expression in T tissues for n individuals,
      nxT. Ydat[,1] is a nxp matrix of the expression data of p genes in the first tissue.

eqtl.lis A list of eQTL names of length p. Each element in the list contains the name of
         the eQTLs for the corresponding gene. The order of the list should correspond
         to the order of genes in Ydat. The code and example to calculate eQTLs can be
         found at https://github.com/randel/MixRF/blob/master/R/eqtl.r.

snp.dat A matrix of genotype. Each row is a sample and each column corresponds to
         one SNP. The column names should match eqtl.lis.

cov A matrix of covariates. Each row is a sample and each column corresponds to
      one covariate. For example, age, gender.

iPC An option. When it is TRUE, the imputed PCs (iPCs) for each tissue type will be
      constructed based on the combined observed and imputed data on the selected
      genes. The iPCs will be adjusted as covariates in the imputation.

idx.selected.gene.iPC The option is used only when iPC=TRUE. When it is, one may select a subset
                      of genes and impute those first to construct iPCs.

parallel.size A numerical value specifying the number of CPUs/cores/processors available
                for parallel computing.

correlation The option to calculate the imputation correlation using cross-validation or not.
               The default is FALSE.

nCV The option is used only when correlation=TRUE. The number of folds for cross-
     validation. The default is 3 folds.

Value

An nxpxT array of imputed and observed expression data. The observed values in Ydat are still
kept and the missing values in Ydat are imputed. When the user chooses to calculate the imputation
correlation using cross-validation (correlation=TRUE), the estimated imputation correlation (cor)
will also be returned in a list together with the imputed data (Yimp).

Examples

```r
## Not run:
data(sim)

idx.selected.gene.iPC = which(sapply(sim$eqtl.lis, length) >= 1)

Yimp = MixRF.impute(sim$Ydat, sim$eqtl.lis, sim$snp.dat, sim$cov, iPC = TRUE,
```
**Description**

This simulated data list is for demonstration.

**Value**

- **Ydat**
  An array of expression data of dimension sample-by-gene-by-tissue, nxpxT, where n is sample size, p is the number of genes, and T is the number of tissues. Ydat[,1,] is a matrix of the first gene expression in T tissues for n individuals, nxT. Ydat[,,1] is a nxp matrix of the expression data of p genes in the first tissue.

- **eqtl.lis**
  A list of eQTL names of length p. Each of the element in the list contains the name of the eQTLs for the corresponding gene. The order of the list should correspond to the order of genes in Ydat.

- **snp.dat**
  A matrix of genotype. Each row is a sample and each column corresponds to one SNP. The column names should match eqtl.lis.

- **cov**
  A matrix of covariates. Each row is a sample and each column corresponds to one covariate. For example, age, gender.

**See Also**

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