Package ‘IBCF.MTME’

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Title Item Based Collaborative Filtering for Multi-Trait and Multi-Environment Data

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Description Implements the item based collaborative filtering (IBCF) method for continues phenotypes in the context of plant breeding where data are collected for various traits that were studied in various environments proposed by Montesinos-López et al. (2017) <doi:10.1534/g3.117.300309>.

Depends R (>= 3.0.0)

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Type Package

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BugReports https://github.com/frahik/IBCF.MTME/issues/new

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Suggests testthat, knitr, rmarkdown, covr

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Description

Barplot of the results from IBCFY object

Usage

## S3 method for class 'IBCFY'
barplot(height, select = "Pearson", ...)

Arguments

height IBCFY object, result of use the IBCF.Years() function
select character By default ("Pearson"), plot the Pearson Correlations of the IBCF Object, else ("MAAPE"), plot the MAAPE of the IBCF Object.

... Further arguments passed to or from other methods.
CV.RandomPart  

Cross-Validation with Random Partitions

Description

This method consists of randomly dividing the training data set and the test data set. For each division, the approximation function is adjusted from the training data and calculates the output values for the test data set. The result corresponds to the arithmetic mean of the values obtained for the different divisions.

Usage

CV.RandomPart(DataSet, NPartitions = 10, PTesting = 0.35, Traits.testing = NULL, Set_seed = NULL)

Arguments

Data Set data.frame The data set object is a data.frame object that contains 4 columns in the Tidy data format: $Line is the Line or genotype identifier, and the name of this column could change. $Env is the name of the evaluated environment (s). $Trait is the name of the evaluated trait (s). $Response Variable response obtained for the row corresponding to line and environment.

NPartitions integer Number of Partitions for the Cross-Validation. Is 10 by default.

PTesting Double Percentage of Testing for the Cross-Validation. Is 0.35 by default.

Traits.testing character By default is null and use all the traits to fit the model, else only part of the traits specified be used to fit the model.

Set_seed integer Number of seed for reproducible research. Is NULL by default.

Value

List A list object with length of NPartitions, every index has a matrix n × x, where n is the number of NLines and x is the number of NEnv × NTraits. The values inside is 1 for training and 2 for testing.

Examples

## Not run:
library(IBCF.MTME)

data('Wheat_IBCF')

CV.RandomPart(Wheat_IBCF)
CV.RandomPart(Wheat_IBCF, NPartitions = 10)
CV.RandomPart(Wheat_IBCF, Traits.testing = 'DH')
CV.RandomPart(Wheat_IBCF, NPartitions = 10, PTesting = .35)
CV.RandomPart(Wheat_IBCF, NPartitions = 10, Traits.testing = 'DH')
CV.RandomPart(Wheat_IBCF, NPartitions = 10, PTesting = .35, Set_seed = 5)
CV.RandomPart(Wheat_IBCF, NPartitions = 10, PTesting = .35, Traits.testing = 'DH')
CV.RandomPart(Wheat_IBCF, NPartitions = 10, PTesting = .35, Traits.testing = 'DH', Set_seed = 5)

## End(Not run)

class = getMatrixForm

DT = Tidy data format to Matrix format

Description

Tidy data format to Matrix format

Usage

getMatrixForm(Tidy_DataSet, onlyTrait = FALSE)

Arguments

Tidy_DataSet: data.frame object that contains 4 columns: $Line$: Line or genotype identifier, and the name of this column could change. $Env$: Name of the evaluated environment (s). $Trait$: Name of the evaluated trait (s). $Response$: Variable response obtained for the row corresponding to line and environment.

onlyTrait: logical by default is FALSE, if is TRUE only the column $Trait$ is transformed.

Value

A data.frame object with the $Response$ divided by $Traits$ columns.

Examples

## Not run:
  data('Wheat_IBCF')
  M <- getMatrixForm(Wheat_IBCF)

## End(Not run)

## Not run:
  data('Year_IBCF')
  M.Y <- getMatrixForm(Year_IBCF, onlyTrait = T)

## End(Not run)
**getTidyForm**

**Matrix format to Tidy data format**

**Description**

Matrix format to Tidy data format

**Usage**

getTidyForm(Matrix_DataSet, onlyTrait = FALSE)

**Arguments**

- **Matrix_DataSet** A data.frame object with the response values divided in \( n \) environments or traits columns
- **onlyTrait** logical by default is FALSE, if is TRUE only is considered the $Trait column.

**Value**

A data.frame object with the $Response divided by $Traits columns.

**Examples**

```r
## Not run:
data('Wheat_IBCF')
M <- getMatrixForm(Wheat_IBCF)
Tidy <- getTidyForm(M)
## End(Not run)

## Not run:
data('Year_IBCF')
M.Y <- getMatrixForm(Year_IBCF, onlyTrait = T)
Tidy.Y <- getTidyForm(M.Y, onlyTrait = T)
## End(Not run)
```

**IBCF**

**IBCF**

**Description**

Item Based Collaborative Filtering for multi-trait and multi-environment data.

**Usage**

IBCF(object, dec = 4)
Arguments

object  list CrossValidation object, is obtained from CV.RandomPartition function.
dec  integer Number of decimals to print in the results.

Value

A list with the next components

NPartitions  integer Number of partitions used for testing data
predictions_Summary  data.frame A data.frame with the results of the test
Predictions  list A list with the predicted results for each partition

Examples

## Not run:
library(IBCF.MTME)
data('Wheat_IBCF')
CV <- CV.RandomPart(Wheat_IBCF)
IBCF(CV)
## End(Not run)

Description

The Item Based Collaborative Filtering for Multi-Trait and Multi-Environment Data (IBCF.MTME) package was developed to implement the item based collaborative filtering (IBCF) method for continues phenotypes in the context of plant breeding where data are collected for various traits that were studied in various environments. It is important to point out that the main difference of this package with the available packages that can implement IBCF is that this package was developed for continuous phenotypes which cannot be implemented in the current packages that can implement IBCF that only work for binary and ordinary phenotypes.
Description

Item Based Collaborative Filtering for Years data

Usage

\[
\text{IBCF.Years(DataSet, colYears = 1, colID = 2, Years.testing = "", }
\text{Traits.testing = "", dec = 4)}
\]

Arguments

- **DataSet** \(\text{data.frame}\) A data set in Matrix Form.
- **colYears** \(\text{string or integer}\) A name or the position of the 'Years' column just in case that is not the first column.
- **colID** \(\text{string or integer}\) A name or the position of the 'ID' column, just in case that is not the second column.
- **Years.testing** \(\text{vector}\) A vector with the names of the years to use in test.
- **Traits.testing** \(\text{vector}\) A vector with the names of the traits to use in test.
- **dec** \(\text{integer}\) Number of decimals to print in the results.

Value

A list with the next components

- **Year.testing** \(\text{vector}\) a vector with the Years used for the testing data
- **Traits.testing** \(\text{vector}\) a vector with the Traits used for the testing data
- **Data.Obs.Pred** \(\text{data.frame}\) Contains the values observed and predicted (the predicted values has ',1' after the name)
- **predictions_Summary** \(\text{data.frame}\) Contains the summary of the correlation of the predictions and the MAAPE

Examples

```r
## Not run:
library(IBCF.MTME)
data(Year_IBCF)
DataSet <- getMatrixForm(Year_IBCF, onlyTrait = TRUE)
IBCF.Years(DataSet, Years.testing = c('2015', '2016'), Traits.testing = c('T5', 'T6'))
## End(Not run)
```
## plot.IBCF

### Description

Plot from IBCF object

### Usage

```r
## S3 method for class 'IBCF'
plot(x, select = "Pearson", ...)
```

### Arguments

- `x` IBCF object
- `select` character By default ("Pearson"), plot the Pearson Correlations of the IBCF Object, else ("MAAPE"), plot the MAAPE of the IBCF Object.
- `...` Further arguments passed to or from other methods.

## print.IBCF

### Description

Print IBCF information object

### Usage

```r
## S3 method for class 'IBCF'
print(x, ...)
```

### Arguments

- `x` IBCF object
- `...` Further arguments passed to or from other methods.

### Value

printable object
Print IBCFY information object

**Description**
- Print IBCFY information object

**Usage**
```r
## S3 method for class 'IBCFY'
print(x, ...)
```

**Arguments**
- `x` IBCFY object
- `...` Further arguments passed to or from other methods.

**Value**
- printeable object

Summary of IBCF object

**Usage**
```r
## S3 method for class 'IBCF'
summary(object, information = "compact", digits = 4, 
         ...)
```

**Arguments**
- `object` IBCF object, result of use the IBCF() function
- `information` string...
- `digits` numeric...
- `...` Further arguments passed to or from other methods.
**summary.IBCFY**

### Summary

Summary of IBCFY object

### Usage

```r
# S3 method for class 'IBCFY'
summary(object, digits = 4, ...)
```

### Arguments

- **object**: IBCFY object, result of use the IBCF.Years() function
- **digits**: numeric, Number of digits of the output.
- **...**: Further arguments passed to or from other methods.

---

**Wheat_IBCF**

### Wheat Data

**Description**


**Usage**

```r
data(Wheat_IBCF)
```

**Format**

A TidyData format, 3000 row per 4 columns.

**Author(s)**

Montesinos-Lopez, O. A.
Year_IBCF Data

Description

Dataset based on simulated data with the next code:

```r
set.seed(2)
A <- matrix(0.65, ncol=12, nrow=12)
diag(A) <- 1
Sdv <- diag(c(0.9^0.5, 0.8^0.5, 0.9^0.5, 0.8^0.5, 0.86^0.5, 0.7^0.5, 0.9^0.5, 0.8^0.5, 0.9^0.5, 0.7^0.5, 0.7^0.5, 0.85^0.5))
Sigma <- Sdv
No.Lines <- 60
Z <- rmvnorm(No.Lines, mean=c(5, 5.5, 6, 5.5, 7, 6.5, 6, 6.6, 6.8, 6.3, 8), sigma=Sigma)
Gids <- c(1:No.Lines)

Data.Final <- data.frame(cbind(Years, Gids, Z))

head(Data.Final)
Year_IBCF <- getTidyForm(Data.Final, onlyTrait = T)
```

Usage

```r
data(Year_IBCF)
```

Format

A TidyData format, 750 row per 4 columns.

Author(s)

Montesinos-Lopez, O. A.
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