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)

License LGPL-3

Encoding UTF-8

LazyData true

Type Package

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

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Imports lsa, tidyr, dplyr

Suggests testthat, knitr, rmarkdown, covr

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Description

Barplot of the results from IBCFY object

Usage

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

Arguments

- **height**: IBCFY object 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.
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.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.
- **integer** Number of Partitions for the Cross-Validation. Is 10 by default.
- **Double** Percentage of Testing for the Cross-Validation. Is 0.35 by default.
- **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.
- **integer** Number of seed for reproducible research. Is NULL by default.

Value

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

Examples

```r
## 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')
```
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**

```r
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)
```

**ICBF**

**ICBF**

**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)

IBCF.MTME

IBCF.MTME: Item Based Collaborative Filtering for Multi-Trait and Multi-Environment Data.

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 continuous 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**

```r
IBCF.Years(DataSet, colYears = 1, colID = 2, Years.testing = "", Traits.testing = "", dec = 4)
```

**Arguments**

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

**Value**

A list with the next components

- `Year.testing` : vector a vector with the Years used for the testing data
- `Traits.testing` : vector a vector with the Traits used for the testing data
- `Data_Obs_Pred` : data.frame Contains the values observed and predicted (the predicted values has `.1` after the name)
- `predictions_Summary` : 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

**Plot IBCF graph**

**Description**
Plot from IBCF object

**Usage**

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

**Arguments**

- **x**
  - IBCF object IBCF object, result of use the IBCF() 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.

### print.IBCF

**Print IBCF information object**

**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
**Description**

Print IBCFY information object

**Usage**

```
```

**Arguments**

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

**Value**

printable object

---

**Description**

Summary of IBCF object

**Usage**

```
```

**Arguments**

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

Description

Summary of IBCFY object

Usage

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

Arguments

- `object`  IBCFY 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.

Description


Usage

```r
data(Wheat_IBCF)
```

Format

- A tidyData format, 3000 row per 4 columns.

Author(s)

Montesinos-Lopez, O. A.
Description

Dataset based on simulated data with the next code:

```
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, 0.7^0.5, 0.9^0.5, 0.8^0.5, 0.7^0.5, 0.7^0.5, 0.7^0.5, 0.7^0.5, 0.7^0.5))
Sigma <- Sdv
No.Lines <- 60
Z <- rmvnorm(No.Lines, mean=c(5, 5, 5, 6, 5, 7, 6, 5, 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

```
data(Year_IBCF)
```

Format

a TidyData format, 750 row per 4 columns.

Author(s)

Montesinos-Lopez, O. A.
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