

# Package: MantaID (via r-universe)

January 8, 2025

**Title** A Machine-Learning Based Tool to Automate the Identification of Biological Database IDs

**Version** 1.0.4

**Description** The number of biological databases is growing rapidly, but different databases use different IDs to refer to the same biological entity. The inconsistency in IDs impedes the integration of various types of biological data. To resolve the problem, we developed 'MantaID', a data-driven, machine-learning based approach that automates identifying IDs on a large scale. The 'MantaID' model's prediction accuracy was proven to be 99%, and it correctly and effectively predicted 100,000 ID entries within two minutes. 'MantaID' supports the discovery and exploitation of ID patterns from large quantities of databases. (e.g., up to 542 biological databases). An easy-to-use freely available open-source software R package, a user-friendly web application, and API were also developed for 'MantaID' to improve applicability. To our knowledge, 'MantaID' is the first tool that enables an automatic, quick, accurate, and comprehensive identification of large quantities of IDs, and can therefore be used as a starting point to facilitate the complex assimilation and aggregation of biological data across diverse databases.

**License** GPL (>= 3)

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Depends** R (>= 4.4.0),biomaRt,caret,keras,mlr3tuning,mlr3

**LazyData** true

**URL** <https://molaison.github.io/MantaID/>

**Imports**

ggplot2,data.table,magrittr,stringr,tibble,tidyr,tidysselect,ggcorrplot,reshape2,scutr,paradox,RColorBrewer,purrr,dplyr

**Suggests** mlr3hyperband,mlr3learners,ranger,rpart,xgboost

**NeedsCompilation** no

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Example	<i>ID example dataset.</i>
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**Description**

ID example dataset.

**Usage**

Example

**Format**

A tibble with 5000 rows and 2 variables.

**ID** A identifier character.

**class** The database the ID belongs to.

---

mi	<i>A wrapper function that executes MantaID workflow.</i>
----	---

---

**Description**

A wrapper function that executes MantaID workflow.

**Usage**

```
mi(  
  cores = NULL,  
  levels = c("*", 0:9, letters, LETTERS, "_", ".", "-", " ", "/", "\\", ":"),  
  ratio = 0.3,  
  para_blc = FALSE,  
  model_path = NULL,  
  batch_size = 128,  
  epochs = 64,  
  validation_split = 0.3,  
  graph_path = NULL  
)
```

**Arguments**

cores	The number of cores used when balancing data.
levels	The vector that includes all the single characters occurred in IDs.
ratio	The ratio of the test set.
para_blc	A logical value whether using parallel computing when balancing data.
model_path	The path to save models.
batch_size	The batch size of deep learning model fitting.
epochs	The epochs of deep learning model fitting.
validation_split	The validation ratio of deep learning model fitting.
graph_path	The path to save graphs.

**Value**

The list of models and graphs.

---

mi_balance_data	<i>Data balance. Most classes adopt random undersampling, while a few classes adopt smote method to oversample to obtain relatively balanced data.</i>
-----------------	--

---

**Description**

Data balance. Most classes adopt random undersampling, while a few classes adopt smote method to oversample to obtain relatively balanced data.

**Usage**

```
mi_balance_data(data, ratio = 0.3, parallel = FALSE)
```

**Arguments**

data	A data frame. Except for class column, all are numeric types.
ratio	Numeric between 0 and 1. The percent of the test set split from data.
parallel	Logical.

**Value**

A list contains a train set and a test set.

---

mi_clean_data	<i>Reshape data and delete meaningless rows.</i>
---------------	--

---

**Description**

Reshape data and delete meaningless rows.

**Usage**

```
mi_clean_data(data, cols = everything(), placeholder = c("-"))
```

**Arguments**

data	A dataframe or tibble or data.table or matrix. Names of the column will be regard as the class of ID included in column.
cols	Character vectors. Columns of data that contain the IDs
placeholder	Character vectors. IDs included in placeholder will be omitted.

**Value**

A tibble with two columns("ID" and "class")

**Examples**

```
data <- tibble::tibble(  
  "class1" = c("A", "B", "C", "D"),  
  "class2" = c("E", "F", "G", "H"),  
  "class3" = c("L", "M", "-", "O")  
)  
mi_clean_data(data)
```

---

mi_data_attributes	<i>ID-related datasets in biomed.</i>
--------------------	---------------------------------------

---

**Description**

ID-related datasets in biomed.

**Usage**

```
mi_data_attributes
```

**Format**

A dataframe with 65 variables and 3 variables.

**name** The name of dataset.

**description** Description of dataset.

**page** collection of attributes.

---

mi_data_procID	<i>Processed ID data.</i>
----------------	---------------------------

---

**Description**

Processed ID data.

**Usage**

mi\_data\_procID

**Format**

A tibble dataframe with 5000 rows and 21 variables.

**pos1 to pos20** Splited ID.

**class** The databases that ID belongs to.

---

mi_data_rawID	<i>ID dataset for testing.</i>
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---

**Description**

ID dataset for testing.

**Usage**

mi\_data\_rawID

**Format**

A tibble with 5000 rows and 2 variables.

**ID** A identifier character.

**class** The database the ID belongs to.

---

mi_filter_feat	<i>Performing feature selection in a automatic way based on correlation and feature importance.</i>
----------------	---

---

**Description**

Performing feature selection in a automatic way based on correlation and feature importance.

**Usage**

```
mi_filter_feat(data, cor_thresh = 0.7, imp_thresh = 0.99, union = FALSE)
```

**Arguments**

data	The data frame returned by mi_to_numer().
cor_thresh	The threshold set for Pearson correlation. If correlation value is over this threshold, the two features will be viewed as redundant and one of them will be removed.
imp_thresh	The threshold set for feature importance. The last several features with the lowest importance will be removed if remained importance lower than imp_thresh.
union	The method for combining the decisions of correlation method and importance method. If TRUE, any of the features calculated by the two methods will be returned. Otherwise, only features in the results of both methods will be returned.

**Value**

The names of the features that should be removed.

---

mi_get_confusion	<i>Compute the confusion matrix for the predicted result.</i>
------------------	---

---

**Description**

Compute the confusion matrix for the predicted result.

**Usage**

```
mi_get_confusion(result_list, ifnet = FALSE)
```

**Arguments**

result_list	A list returned from model training functions.
ifnet	Logical. Whether the data is obtained by a deep learning model.

**Value**

A confusionMatrix object.

---

mi\_get\_ID

*Get ID data from the Biomart database using attributes.*


---

### Description

Get ID data from the Biomart database using attributes.

### Usage

```
mi_get_ID(
  attributes,
  biomart = "genes",
  dataset = "hsapiens_gene_ensembl",
  mirror = "asia"
)
```

### Arguments

attributes	A dataframe. The information we want to retrieve. Use mi_get_ID_attr to have a try.
biomart	BioMart database name you want to connect to. Use biomaRt::listEnsembl to retrieve the possible database names.
dataset	Datasets of the selected BioMart database.
mirror	Specify an Ensembl mirror to connect to.

### Value

A tibble dataframe.

---

mi\_get\_ID\_attr

*Get ID attributes from the Biomart database.*


---

### Description

Get ID attributes from the Biomart database.

### Usage

```
mi_get_ID_attr(
  biomart = "genes",
  dataset = "hsapiens_gene_ensembl",
  mirror = "asia"
)
```



**Arguments**

biomart	BioMart database name you want to connect to. Use <code>biomaRt::listEnsembl</code> to retrieve the possible database names.
dataset	Datasets of the selected BioMart database.
mirror	Specify an Ensembl mirror to connect to.

**Value**

A dataframe.

---

mi_get_importance	<i>Plot the bar plot for feature importance.</i>
-------------------	--

---

**Description**

Plot the bar plot for feature importance.

**Usage**

```
mi_get_importance(data)
```

**Arguments**

data	A table.
------	----------

**Value**

A bar plot.

---

mi_get_miss	<i>Observe the distribution of the false response of the test set.</i>
-------------	--

---

**Description**

Observe the distribution of the false response of the test set.

**Usage**

```
mi_get_miss(predict)
```

**Arguments**

predict	An R6 class <code>PredictionClassif</code> .
---------	--

**Value**

A tibble data frame that records the number of wrong predictions for each category ID

---

mi_get_padlen	<i>Get max length of ID data.</i>
---------------	-----------------------------------

---

**Description**

Get max length of ID data.

**Usage**

```
mi_get_padlen(data)
```

**Arguments**

data	A dataframe.
------	--------------

**Value**

An int object.

**Examples**

```
data(mi_data_rawID)
mi_get_padlen(mi_data_rawID)
```

---

mi_plot_cor	<i>Plot correlation heatmap.</i>
-------------	----------------------------------

---

**Description**

Plot correlation heatmap.

**Usage**

```
mi_plot_cor(data, cls = "class")
```

**Arguments**

data	Data frame including IDs' position features.
cls	The name of the class column.

**Value**

A heatmap.

**Examples**

```
data(mi_data_procID)
data_num <- mi_to_numer(mi_data_procID)
mi_plot_cor(data_num)
```

---

mi_plot_heatmap	<i>Plot heatmap for result confusion matrix.</i>
-----------------	--

---

**Description**

Plot heatmap for result confusion matrix.

**Usage**

```
mi_plot_heatmap(table, name = NULL, filepath = NULL)
```

**Arguments**

table	A table.
name	Model names.
filepath	File path the plot to save. Default NULL.

**Value**

A ggplot object.

---

mi_predict_new	<i>Predict new data with a trained learner.</i>
----------------	---

---

**Description**

Predict new data with a trained learner.

**Usage**

```
mi_predict_new(data, result, ifnet = F)
```

**Arguments**

data	A dataframe.
result	The result object from a previous training.
ifnet	A boolean indicating if a neural network is used for prediction.

**Value**

A data frame that contains features and 'predict' class.

---

mi_run_bmr	<i>Compare classification models with small samples.</i>
------------	--

---

**Description**

Compare classification models with small samples.

**Usage**

```
mi_run_bmr(data, row_num = 1000, resamplings = rsmps("cv", folds = 10))
```

**Arguments**

data	A tibble. All are numeric except the first column is a factor.
row_num	The number of samples used.
resamplings	R6/Resampling.Resampling method.

**Value**

A list of R6 class of benchmark results and scores of test set. examples `data(mi_data_procID)`  
`mi_run_bmr(mi_data_procID)`

---

mi_split_col	<i>Cut the string of ID column character by character and divide it into multiple columns.</i>
--------------	--

---

**Description**

Cut the string of ID column character by character and divide it into multiple columns.

**Usage**

```
mi_split_col(data, cores = NULL, pad_len = 10)
```

**Arguments**

data	Dataframe(tibble) to be split.
cores	Int. The num of cores to allocate for computing.
pad_len	The length of longest id, i.e. the maxlength.

**Value**

A tibble with `pad_len+1` column.

---

mi_split_str	<i>Split the string into individual characters and complete the character vector to the maximum length.</i>
--------------	---

---

**Description**

Split the string into individual characters and complete the character vector to the maximum length.

**Usage**

```
mi_split_str(str, pad_len)
```

**Arguments**

str	The string to be splited.
pad_len	The length of longest ID, i.e. the maxlength.

**Value**

Splited character vector.

**Examples**

```
string_test <- "Good Job"
length <- 15
mi_split_str(string_test, length)
```

---

mi_to_numer	<i>Convert data to numeric, and for the ID column convert with fixed levels.</i>
-------------	--

---

**Description**

Convert data to numeric, and for the ID column convert with fixed levels.

**Usage**

```
mi_to_numer(
  data,
  levels = c("*", 0:9, letters, LETTERS, "_", ".", "-", " ", "/", "\\ ", ":")
)
```

**Arguments**

data	A tibble with n position column(pos1,pos2,...) and class column.
levels	Characters accommodated in IDs.

**Value**

A numeric data frame with numerical or factor type columns.

**Examples**

```
data(mi_data_procID)
mi_to_numer(mi_data_procID)
```

---

<code>mi_train_BP</code>	<i>Train a three layers neural network model.</i>
--------------------------	---

---

**Description**

Train a three layers neural network model.

**Usage**

```
mi_train_BP(
  train,
  test,
  cls = "class",
  path2save = NULL,
  batch_size = 128,
  epochs = 64,
  validation_split = 0.3,
  verbose = 0
)
```

**Arguments**

<code>train</code>	A dataframe with the class column as label.
<code>test</code>	A dataframe with the class column as label.
<code>cls</code>	A character. The name of the label column.
<code>path2save</code>	The folder path to store the model and train history.
<code>batch_size</code>	Integer or NULL. The number of samples per gradient update.
<code>epochs</code>	The number of epochs to train the model.
<code>validation_split</code>	Float between 0 and 1. Fraction of the training data to be used as validation data.
<code>verbose</code>	The verbosity mode.

**Value**

A list object containing the prediction confusion matrix, the model object, and the mapping of predicted numbers to classes.

---

mi_train_rg	<i>Random Forest Model Training.</i>
-------------	--------------------------------------

---

**Description**

Random Forest Model Training.

**Usage**

```
mi_train_rg(train, test, measure = msr("classif.acc"), instance = NULL)
```

**Arguments**

train	A dataframe.
test	A dataframe.
measure	Model evaluation method.
instance	A tuner.

**Value**

A list of learner for predicting and predicted result of test set.

---

mi_train_rp	<i>Classification tree model training.</i>
-------------	--

---

**Description**

Classification tree model training.

**Usage**

```
mi_train_rp(train, test, measure = msr("classif.acc"), instance = NULL)
```

**Arguments**

train	A dataframe.
test	A dataframe.
measure	Model evaluation method. Use mlr_measures and msr() to view and choose metrics.
instance	A tuner.

**Value**

A list of learner for predicting and predicted result of test set.

---

mi_train_xgb	<i>Xgboost model training</i>
--------------	-------------------------------

---

**Description**

Xgboost model training

**Usage**

```
mi_train_xgb(train, test, measure = msr("classif.acc"), instance = NULL)
```

**Arguments**

train	A dataframe.
test	A dataframe.
measure	Model evaluation method.
instance	A tuner.

**Value**

A list of learner for predicting and predicted result of test set.

---

mi_tune_rg	<i>Tune the Random Forest model by hyperband.</i>
------------	---

---

**Description**

Tune the Random Forest model by hyperband.

**Usage**

```
mi_tune_rg(
  data,
  resampling = rsmpl("cv", folds = 5),
  measure = msr("classif.acc"),
  eta = 3
)
```

**Arguments**

data	A tibble. All are numeric except the first column is a factor.
resampling	R6/Resampling.
measure	Model evaluation method. Use mlr_measures and msr() to view and choose metrics.
eta	The percent parameter configurations discarded.



**Value**

A list of tuning instance and stage plot.

---

mi_tune_rp	<i>Tune the Decision Tree model by hyperband.</i>
------------	---

---

**Description**

Tune the Decision Tree model by hyperband.

**Usage**

```
mi_tune_rp(
  data,
  resampling = rsmp("bootstrap", ratio = 0.8, repeats = 5),
  measure = msr("classif.acc"),
  eta = 3
)
```

**Arguments**

data	A tibble. All are numeric except the first column is a factor.
resampling	R6/Resampling.
measure	Model evaluation method. Use mlr_measures and msr() to view and choose metrics.
eta	The percent parameter configurations discarded.

**Value**

A list of tuning instance and stage plot.

---

mi_tune_xgb	<i>Tune the Xgboost model by hyperband.</i>
-------------	---

---

**Description**

Tune the Xgboost model by hyperband.

**Usage**

```
mi_tune_xgb(
  data,
  resampling = rsmp("cv", folds = 5),
  measure = msr("classif.acc"),
  eta = 3
)
```

**Arguments**

data	A tibble. All are numeric except the first column is a factor.
resampling	R6/Resampling.
measure	Model evaluation method. Use <code>mlr_measures</code> and <code>msr()</code> to view and choose metrics.
eta	The percent parameter configurations discarded.

**Value**

A list of tuning instance and stage plot.

---

mi_unify_mod	<i>Predict with four models and unify results by the sub-model's specificity score to the four possible classes.</i>
--------------	--

---

**Description**

Predict with four models and unify results by the sub-model's specificity score to the four possible classes.

**Usage**

```
mi_unify_mod(
  data,
  col_id,
  result_rg,
  result_rp,
  result_xgb,
  result_BP,
  c_value = 0.75,
  pad_len = 30
)
```

**Arguments**

data	A dataframe contains the ID column.
col_id	The name of ID column.
result_rg	The result from the Random Forest model.
result_rp	The result from the Decision Tree model.
result_xgb	The result from the XGBoost model.
result_BP	The result from the Backpropagation Neural Network model.
c_value	A numeric value used in the final prediction calculation.
pad_len	The length to pad the ID characters to.

*mi\_unify\_mod*

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**Value**

A dataframe.

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