

# Package ‘BioM2’

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**Title** Biologically Explainable Machine Learning Framework

**Version** 1.0.7

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**Description** Biologically Explainable Machine Learning Framework for Phenotype Prediction using omics data described in Chen and Schwarz (2017) <[doi:10.48550/arXiv.1712.00336](https://doi.org/10.48550/arXiv.1712.00336)>. Identifying reproducible and interpretable biological patterns from high-dimensional omics data is a critical factor in understanding the risk mechanism of complex disease. As such, explainable machine learning can offer biological insight in addition to personalized risk scoring. In this process, a feature space of biological pathways will be generated, and the feature space can also be subsequently analyzed using WGCNA (Described in Horvath and Zhang (2005) <[doi:10.2202/1544-6115.1128](https://doi.org/10.2202/1544-6115.1128)> and Langfelder and Horvath (2008) <[doi:10.1186/1471-2105-9-559](https://doi.org/10.1186/1471-2105-9-559)> ) methods.

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---

AddUnmapped	<i>Add unmapped probe</i>
-------------	---------------------------

---

## Description

Add unmapped probe

## Usage

```
AddUnmapped(
  train = NULL,
  test = NULL,
  Unmapped_num = NULL,
  Add_FeartureSelection_Method = "wilcox.test",
  anno = NULL,
  len = NULL,
  verbose = TRUE,
  cores = 1
)
```

## Arguments

train	The input training dataset. The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.
test	The input test dataset. The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.
Unmapped_num	The number of unmapped probes.

Add_FeatureSelection_Method	Feature selection methods. Available options are c('cor', 'wilcox.test').
anno	The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'. (For details, please refer to data(data("MethylAnno")))
len	The number of unmapped probes
verbose	Whether to print running process information to the console
cores	The number of cores used for computation.

**Value**

Matrix of unmapped probes

---

baseModel	<i>Prediction by Machine Learning</i>
-----------	---------------------------------------

---

**Description**

Prediction by Machine Learning with different learners ( From 'mlr3' )

**Usage**

```
baseModel(
  trainData,
  testData,
  predMode = "probability",
  classifier,
  paramlist = NULL,
  inner_folds = 10
)
```

**Arguments**

trainData	The input training dataset. The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.
testData	The input test dataset. The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.
predMode	The prediction mode. Available options are c('probability', 'classification').
classifier	Learners in mlr3
paramlist	Learner parameters
inner_folds	k-fold cross validation ( Only supported when testData = NULL )

**Value**

The predicted output for the test data.

**Author(s)**

Shunjie Zhang

**Examples**

```
library(mlr3verse)
library(caret)
library(BioM2)
data=MethylData_Test
set.seed(1)
part=unlist(createDataPartition(data$label,p=0.8))#Split data
predict=baseModel(trainData=data[part,1:10],
                  testData=data[-part,1:10],
                  classifier = 'svm')#Use 10 features to make predictions,Learner uses svm
```

---

BioM2

*Biologically Explainable Machine Learning Framework*

---

**Description**

Biologically Explainable Machine Learning Framework

**Usage**

```
BioM2(
  TrainData = NULL,
  TestData = NULL,
  pathlistDB = NULL,
  FeatureAnno = NULL,
  resampling = NULL,
  nfolds = 5,
  classifier = "liblinear",
  predMode = "probability",
  PathwaySizeUp = 200,
  PathwaySizeDown = 20,
  MinfeatureNum_pathways = 10,
  Add_UnMapped = TRUE,
  Unmapped_num = 300,
  Add_FeatureSelection_Method = "wilcox.test",
  Inner_CV = TRUE,
  inner_folds = 10,
  Stage1_FeatureSelection_Method = "cor",
  cutoff = 0.3,
  Stage2_FeatureSelection_Method = "RemoveHighcor",
  cutoff2 = 0.95,
  classifier2 = NULL,
```

```

target = "predict",
p.adjust.method = "fdr",
save_pathways_matrix = FALSE,
cores = 1,
verbose = TRUE
)

```

### Arguments

TrainData	The input training dataset. The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.
TestData	The input test dataset. The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.
pathlistDB	A list of pathways with pathway IDs and their corresponding genes ('entrezID' is used). For details, please refer to ( data("GO2ALLEGES_BP") )
FeatureAnno	The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'. (For details, please refer to data( data("MethylAnno") )
resampling	Resampling in mlr3verse.
nfolds	k-fold cross validation ( Only supported when TestData = NULL )
classifier	Learners in mlr3
predMode	The prediction mode. Available options are c('probability', 'classification').
PathwaySizeUp	The upper-bound of the number of genes in each biological pathways.
PathwaySizeDown	The lower-bound of the number of genes in each biological pathways.
MinfeatureNum_pathways	The minimal defined pathway size after mapping your own data to pathlistDB(KEGG database/GO database).
Add_UnMapped	Whether to add unmapped probes for prediction
Unmapped_num	The number of unmapped probes
Add_FeatureSelection_Method	Feature selection methods.
Inner_CV	Whether to perform a k-fold verification on the training set.
inner_folds	k-fold verification on the training set.
Stage1_FeatureSelection_Method	Feature selection methods.
cutoff	The cutoff used for feature selection threshold. It can be any value between 0 and 1.
Stage2_FeatureSelection_Method	Feature selection methods.
cutoff2	The cutoff used for feature selection threshold. It can be any value between 0 and 1.
classifier2	Learner for stage 2 prediction(if classifier2==NULL,then it is the same as the learner in stage 1.)

target	Is it used to predict or explore potential biological mechanisms? Available options are c('predict', 'pathways').
p.adjust.method	p-value adjustment method.(holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
save_pathways_matrix	Whether to output the path matrix file
cores	The number of cores used for computation.
verbose	Whether to print running process information to the console

### Value

A list containing prediction results and prediction result evaluation

### Examples

```

library(mlr3verse)
library(caret)
library(parallel)
library(BioM2)
data=MethylData_Test
set.seed(1)
part=unlist(createDataPartition(data$label,p=0.8))
Train=data[part,]
Test=data[-part,]
pathlistDB=G02ALLEGS_BP
FeatureAnno=MethylAnno

pred=BioM2(TrainData = Train,TestData = Test,
           pathlistDB=pathlistDB,FeatureAnno=FeatureAnno,
           classifier='svm',nfolds=5,
           PathwaySizeUp=25,PathwaySizeDown=20,MinfeatureNum_pathways=10,
           Add_UnMapped='Yes',Unmapped_num=300,
           Inner_CV='None',inner_folds=5,
           Stage1_FeatureSelection_Method='cor',cutoff=0.3,
           Stage2_FeatureSelection_Method='None',
           target='predict',cores=1
           )#(To explore biological mechanisms, set target='pathways')

```

---

FindParaModule	<i>Find suitable parameters for partitioning pathways modules</i>
----------------	---

---

## Description

Find suitable parameters for partitioning pathways modules

## Usage

```
FindParaModule(  
  pathways_matrix = NULL,  
  control_label = NULL,  
  minModuleSize = seq(10, 20, 5),  
  mergeCutHeight = seq(0, 0.3, 0.1),  
  minModuleNum = 20,  
  power = NULL,  
  exact = TRUE,  
  ancestor_anno = NULL  
)
```

## Arguments

<code>pathways_matrix</code>	A pathway matrix generated by the <code>BioM2(target='pathways')</code> function.
<code>control_label</code>	The label of the control group ( A single number, factor, or character )
<code>minModuleSize</code>	minimum module size for module detection. Detail for <code>WGCNA::blockwiseModules()</code>
<code>mergeCutHeight</code>	dendrogram cut height for module merging. Detail for <code>WGCNA::blockwiseModules()</code>
<code>minModuleNum</code>	Minimum total number of modules detected
<code>power</code>	soft-thresholding power for network construction. Detail for <code>WGCNA::blockwiseModules()</code>
<code>exact</code>	Whether to divide GO pathways more accurately (work when <code>ancestor_anno=NULL</code> )
<code>ancestor_anno</code>	Annotations for ancestral relationships (like <code>data('GO_Ancestors')</code> )

## Value

A list containing recommended parameters

---

GO2ALLEGS\_BP

*An example about pathlistDB*

---

**Description**

An example about pathlistDB

**Format**

A list :

...

**Details**

A list of pathways with pathway IDs and their corresponding genes ('entrezID' is used).

---

GO\_Ancessor

*Pathways in the GO database and their Ancestor*

---

**Description**

Inclusion relationships between pathways

**Format**

A data frame :

...

**Details**

In the GO database, each pathway will have its own ancestor pathway. Map pathways in GO database to about 20 common ancestor pathways.

**Source**

From GO.db



---

GO\_Ancessor\_exact      *Pathways in the GO database and their Ancestor*

---

**Description**

Inclusion relationships between pathways

**Format**

A data frame :

...

**Details**

In the GO database, each pathway will have its own ancestor pathway. Map pathways in GO database to about 400 common ancestor pathways.

**Source**

From GO.db

---

HybaseModel      *Selection of the optimal base model*

---

**Description**

Selection of the optimal base model

**Usage**

```
HybaseModel(
  data = NULL,
  pathlistDB = NULL,
  FeatureAnno = NULL,
  resampling = NULL,
  nfolds = 5,
  classifiers = "liblinear",
  predMode = "probability",
  PathwaySizeUp = 200,
  PathwaySizeDown = 20,
  MinfeatureNum_pathways = 10,
  Add_UnMapped = TRUE,
  Unmapped_num = 300,
  Add_FeatureSelection_Method = "wilcox.test",
  Inner_CV = TRUE,
```

```

inner_folds = 10,
Stage1_FeatureSelection_Method = "cor",
cutoff = 0.3,
Stage2_FeatureSelection_Method = "RemoveHighcor",
cutoff2 = 0.95,
cores = 1,
verbose = TRUE
)

```

### Arguments

data	The input training dataset. The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.
pathlistDB	A list of pathways with pathway IDs and their corresponding genes ('entrezID' is used). For details, please refer to ( data("GO2ALLEGES_BP") )
FeatureAnno	The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'. (For details, please refer to data("MethylAnno") )
resampling	Resampling in mlr3verse.
nfolds	k-fold cross validation
classifiers	A string of character vectors(Learners in mlr3)
predMode	The prediction mode. Available options are c('probability', 'classification').
PathwaySizeUp	The upper-bound of the number of genes in each biological pathways.
PathwaySizeDown	The lower-bound of the number of genes in each biological pathways.
MinfeatureNum_pathways	The minimal defined pathway size after mapping your own data to pathlistDB(KEGG database/GO database).
Add_UnMapped	Whether to add unmapped probes for prediction
Unmapped_num	The number of unmapped probes
Add_FeatureSelection_Method	Feature selection methods.
Inner_CV	Whether to perform a k-fold verification on the training set.
inner_folds	k-fold verification on the training set.
Stage1_FeatureSelection_Method	Feature selection methods.
cutoff	The cutoff used for feature selection threshold. It can be any value between 0 and 1.
Stage2_FeatureSelection_Method	Feature selection methods.
cutoff2	The cutoff used for feature selection threshold. It can be any value between 0 and 1.
cores	The number of cores used for computation.
verbose	Whether to print running process information to the console

**Value**

A data frame containing the predictive performance of each basemodel

---

MethylAnno	<i>An example about FeatureAnno for methylation data</i>
------------	--

---

**Description**

An example about FeatureAnno for methylation data

**Format**

A data frame :

...

**Details**

The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'.

---

MethylData_Test	<i>An example about TrainData/TestData for methylation data</i>
-----------------	---

---

**Description**

An example about TrainData/TestData for methylation data MethylData\_Test.

**Format**

A data frame :

...

**Details**

The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.

---

PathwaysModule	<i>Delineate differential pathway modules with high biological interpretability</i>
----------------	---

---

### Description

Delineate differential pathway modules with high biological interpretability

### Usage

```
PathwaysModule(
  pathways_matrix = NULL,
  control_label = NULL,
  power = NULL,
  minModuleSize = NULL,
  mergeCutHeight = NULL,
  cutoff = 70,
  MinNumPathways = 5,
  p.adjust.method = "fdr",
  exact = TRUE,
  ancestor_anno = NULL
)
```

### Arguments

pathways_matrix	A pathway matrix generated by the BioM2( target='pathways') function.
control_label	The label of the control group ( A single number, factor, or character )
power	soft-thresholding power for network construction. Detail for WGCNA::blockwiseModules()
minModuleSize	minimum module size for module detection. Detail for WGCNA::blockwiseModules()
mergeCutHeight	dendrogram cut height for module merging. Detail for WGCNA::blockwiseModules()
cutoff	Thresholds for Biological Interpretability Difference Modules
MinNumPathways	Minimum number of pathways included in the biologically interpretable difference module
p.adjust.method	p-value adjustment method.(holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
exact	Whether to divide GO pathways more accurately (work when ancestor_anno=NULL)
ancestor_anno	Annotations for ancestral relationships (like data('GO_Ancestors'))

### Value

A list containing differential module results that are highly biologically interpretable

---

 PlotCorModule

*Correlalogram for Biological Differences Modules*


---

**Description**

Correlalogram for Biological Differences Modules

**Usage**

```
PlotCorModule(
  PathwaysModule_obj = NULL,
  alpha = 0.7,
  begin = 0.2,
  end = 0.9,
  option = "C",
  family = "serif"
)
```

**Arguments**

PathwaysModule_obj	Results produced by PathwaysModule()
alpha	The alpha transparency, a number in (0,1). Detail for scale_fill_viridis()
begin	The (corrected) hue in (0,1) at which the color map begins. Detail for scale_fill_viridis().
end	The (corrected) hue in (0,1) at which the color map ends. Detail for scale_fill_viridis()
option	A character string indicating the color map option to use. Detail for scale_fill_viridis()
family	calligraphic style

**Value**

a ggplot object

---

 PlotPathFeatue

*Visualisation of significant pathway-level features*


---

**Description**

Visualisation of significant pathway-level features

**Usage**

```
PlotPathFeature(
  BioM2_pathways_obj = NULL,
  pathlistDB = NULL,
  top = 10,
  p.adjust.method = "none",
  begin = 0.1,
  end = 0.9,
  alpha = 0.9,
  option = "C",
  seq = 1
)
```

**Arguments**

BioM2_pathways_obj	Results produced by BioM2( <i>target='pathways'</i> )
pathlistDB	A list of pathways with pathway IDs and their corresponding genes ( <i>'entrezID'</i> is used). For details, please refer to ( <code>data("GO2ALLEGS_BP")</code> )
top	Number of significant pathway-level features visualised
p.adjust.method	p-value adjustment method.( <i>holm</i> , <i>hochberg</i> , <i>hommel</i> , <i>bonferroni</i> , <i>BH</i> , <i>BY</i> , <i>fdr</i> , <i>none</i> )
begin	The (corrected) hue in (0,1) at which the color map begins. Detail for <code>scale_fill_viridis()</code> .
end	The (corrected) hue in (0,1) at which the color map ends. Detail for <code>scale_fill_viridis()</code>
alpha	The alpha transparency, a number in (0,1). Detail for <code>scale_fill_viridis()</code>
option	A character string indicating the color map option to use. Detail for <code>scale_fill_viridis()</code>
seq	Interval of x-coordinate

**Value**

a ggplot2 object

---

 PlotPathInner

---

*Visualisation Original features that make up the pathway*


---

**Description**

Visualisation Original features that make up the pathway

**Usage**

```
PlotPathInner(
  data = NULL,
  pathlistDB = NULL,
  FeatureAnno = NULL,
  PathNames = NULL,
  p.adjust.method = "none",
  save_pdf = FALSE,
  alpha = 1,
  cols = NULL
)
```

**Arguments**

data	The input omics data
pathlistDB	A list of pathways with pathway IDs and their corresponding genes ('entrezID' is used). For details, please refer to ( data("GO2ALLEGS_BP") )
FeatureAnno	The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'. (For details, please refer to data( data("MethylAnno") )
PathNames	A vector.A vector containing the names of pathways
p.adjust.method	p-value adjustment method.(holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none")
save_pdf	Whether to save images in PDF format
alpha	The alpha transparency, a number in (0,1).
cols	palette (vector of colour names)

**Value**

a plot object

---

 PlotPathNet

*Network diagram of pathways-level features*


---

**Description**

Network diagram of pathways-level features

**Usage**

```
PlotPathNet(
  data = NULL,
  BioM2_pathways_obj = NULL,
  FeatureAnno = NULL,
  pathlistDB = NULL,
  PathNames = NULL,
  cutoff = 0.2,
  num = 10
)
```

**Arguments**

data	The input omics data
BioM2_pathways_obj	Results produced by BioM2()
FeatureAnno	The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'. (For details, please refer to data("MethylAnno"))
pathlistDB	A list of pathways with pathway IDs and their corresponding genes ('entrezID' is used). For details, please refer to ( data("GO2ALLEGS_BP") )
PathNames	A vector.A vector containing the names of pathways
cutoff	Threshold for correlation between features within a pathway
num	The first few internal features of each pathway that are most relevant to the phenotype

**Value**

a ggplot object

---

ShowModule

*Display biological information within each pathway module*

---

**Description**

Display biological information within each pathway module

**Usage**

```
ShowModule(obj = NULL, ID_Module = NULL, exact = TRUE, ancestor_anno = NULL)
```

**Arguments**

obj	Results produced by PathwaysModule()
ID_Module	ID of the diff module
exact	Whether to divide GO pathways more accurately (work when ancestor_anno=NULL)
ancestor_anno	Annotations for ancestral relationships (like data('GO_Ancestors'))



**Value**

List containing biologically specific information within the module

---

Stage1\_FeatureSelection  
*Stage 1 Feature Selection*

---

**Description**

Stage 1 Feature Selection

**Usage**

```
Stage1_FeatureSelection(
  Stage1_FeatureSelection_Method = "cor",
  data = NULL,
  cutoff = NULL,
  featureAnno = NULL,
  pathlistDB_sub = NULL,
  cores = 1,
  verbose = TRUE
)
```

**Arguments**

Stage1_FeatureSelection_Method	Feature selection methods. Available options are c(NULL, 'cor', 'wilcox.test', 'cor_rank', 'wilcox.test_rank').
data	The input training dataset. The first column is the label.
cutoff	The cutoff used for feature selection threshold. It can be any value between 0 and 1. Commonly used cutoffs are c(0.5, 0.1, 0.05, 0.01, etc.).
featureAnno	The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'. (For details, please refer to data("MethylAnno"))
pathlistDB_sub	A list of pathways with pathway IDs and their corresponding genes ('entrezID' is used). For details, please refer to ( data("GO2ALLEGS_BP") )
cores	The number of cores used for computation.
verbose	Whether to print running process information to the console

**Value**

A list of matrices with pathway IDs as the associated list member names.

**Author(s)**

Shunjie Zhang

**Examples**

```
library(parallel)
data=MethylData_Test
feature_pathways=Stage1_FeatureSelection(Stage1_FeatureSelection_Method='cor',
                                         data=data,cutoff=0,
                                         featureAnno=MethylAnno,pathlistDB_sub=G02ALLEGS_BP,cores=1)
```

---

Stage2\_FeatureSelection

*Stage 2 Feature Selection*

---

**Description**

Stage 2 Feature Selection

**Usage**

```
Stage2_FeatureSelection(
  Stage2_FeatureSelection_Method = "RemoveHighcor",
  data = NULL,
  label = NULL,
  cutoff = NULL,
  preMode = NULL,
  classifier = NULL,
  verbose = TRUE,
  cores = 1
)
```

**Arguments**

Stage2_FeatureSelection_Method	Feature selection methods. Available options are c(NULL, 'cor', 'wilcox.test', 'RemoveHighcor', 'RemoveLinear').
data	The input training dataset. The first column is the label.
label	The label of dataset
cutoff	The cutoff used for feature selection threshold. It can be any value between 0 and 1.
preMode	The prediction mode. Available options are c('probability', 'classification').
classifier	Learners in mlr3
verbose	Whether to print running process information to the console
cores	The number of cores used for computation.

**Value**

Column index of feature

**Author(s)**

Shunjie Zhang

---

TransAnno

*An example about FeatureAnno for gene expression*

---

**Description**

An example about FeatureAnno for gene expression

**Format**

A data frame :

...

**Details**

The annotation data stored in a data.frame for probe mapping. It must have at least two columns named 'ID' and 'entrezID'.

---

TransData\_Test

*An example about TrainData/TestData for gene expression*

---

**Description**

An example about TrainData/TestData for gene expression MethylData\_Test.

**Format**

A data frame :

...

**Details**

The first column is the label or the output. For binary classes, 0 and 1 are used to indicate the class member.

---

 VisMultiModule

*Visualisation of the results of the analysis of the pathway modules*


---

## Description

Visualisation of the results of the analysis of the pathway modules

## Usage

```

VisMultiModule(
  BioM2_pathways_obj = NULL,
  FindParaModule_obj = NULL,
  ShowModule_obj = NULL,
  PathwaysModule_obj = NULL,
  exact = TRUE,
  ancestor_anno = NULL,
  type_text_table = FALSE,
  text_table_theme = ttheme("mOrange"),
  volin = FALSE,
  control_label = 0,
  module = NULL,
  cols = NULL,
  n_neighbors = 8,
  spread = 1,
  min_dist = 2,
  target_weight = 0.5,
  size = 1.5,
  alpha = 1,
  ellipse = TRUE,
  ellipse.alpha = 0.2,
  theme = ggthemes::theme_base(base_family = "serif"),
  save_pdf = FALSE,
  width = 7,
  height = 7
)

```

## Arguments

BioM2_pathways_obj	Results produced by BioM2(,target='pathways')
FindParaModule_obj	Results produced by FindParaModule()
ShowModule_obj	Results produced by ShowModule()
PathwaysModule_obj	Results produced by PathwaysModule()
exact	Whether to divide GO pathways more accurately (work when ancestor_anno=NULL)

ancestor_anno	Annotations for ancestral relationships (like data('GO_Ancestors'))
type_text_table	Whether to display it in a table
text_table_theme	The topic of this table. Detail for ggtexttable()
volin	Can only be used when PathwaysModule_obj exists. ( Violin diagram )
control_label	Can only be used when PathwaysModule_obj exists. ( Control group label )
module	Can only be used when PathwaysModule_obj exists. ( PathwaysModule ID )
cols	palette (vector of colour names)
n_neighbors	The size of local neighborhood (in terms of number of neighboring sample points) used for manifold approximation. Larger values result in more global views of the manifold, while smaller values result in more local data being preserved. In general values should be in the range 2 to 100.
spread	The effective scale of embedded points. In combination with min_dist, this determines how clustered/clumped the embedded points are.
min_dist	The effective minimum distance between embedded points. Smaller values will result in a more clustered/clumped embedding where nearby points on the manifold are drawn closer together, while larger values will result on a more even dispersal of points. The value should be set relative to the spread value, which determines the scale at which embedded points will be spread out.
target_weight	Weighting factor between data topology and target topology. A value of 0.0 weights entirely on data, a value of 1.0 weights entirely on target. The default of 0.5 balances the weighting equally between data and target. Only applies if y is non-NULL.
size	Scatter plot point size
alpha	Alpha for ellipse specifying the transparency level of fill color. Use alpha = 0 for no fill color.
ellipse	logical value. If TRUE, draws ellipses around points.
ellipse.alpha	Alpha for ellipse specifying the transparency level of fill color. Use alpha = 0 for no fill color.
theme	Default: theme_base(base_family = "serif")
save_pdf	Whether to save images in PDF format
width	image width
height	image height

**Value**

a ggplot2 object

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