

# Package: iPRISM (via r-universe)

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**Type** Package

**Title** Intelligent Predicting Response to Cancer Immunotherapy Through Systematic Modeling

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**Description** Immunotherapy has revolutionized cancer treatment, but predicting patient response remains challenging. Here, we presented Intelligent Predicting Response to cancer Immunotherapy through Systematic Modeling (iPRISM), a novel network-based model that integrates multiple data types to predict immunotherapy outcomes. It incorporates gene expression, biological functional network, tumor microenvironment characteristics, immune-related pathways, and clinical data to provide a comprehensive view of factors influencing immunotherapy efficacy. By identifying key genetic and immunological factors, it provides an insight for more personalized treatment strategies and combination therapies to overcome resistance mechanisms.

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iPRISM-package	<i>Intelligent Predicting Response to Cancer Immunotherapy Through Systematic Modeling</i>
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## Description

Immunotherapy has revolutionized cancer treatment, but predicting patient response remains challenging. Here, we presented Intelligent Predicting Response to cancer Immunotherapy through Systematic Modeling (iPRISM), a novel network-based model that integrates multiple data types to predict immunotherapy outcomes. It incorporates gene expression, biological functional network, tumor microenvironment characteristics, immune-related pathways, and clinical data to provide a comprehensive view of factors influencing immunotherapy efficacy. By identifying key genetic and immunological factors, it provides an insight for more personalized treatment strategies and combination therapies to overcome resistance mechanisms.

## Details

iPRISM

## Examples

```
# if (!"devtools" %in% as.data.frame(installed.packages())$Package)
#   install.packages("devtools")
# devtools::install_github("hanjunwei-lab/iPRISM")
```

---

cor\_plot

*Correlation Plot with Significance Points*

---

## Description

This function generates a correlation plot between two datasets, displaying correlation coefficients as a heatmap and significant correlations as scatter points.

## Usage

```
cor_plot(
  data1,
  data2,
  sig.name1 = "value1",
  sig.name2 = "value2",
  cutoff.pvalue = 0.05,
  color = c("#62CCC9", "#FF9999")
)
```

## Arguments

data1	A data frame or matrix representing the first dataset.
data2	A data frame or matrix representing the second dataset.
sig.name1	A character string specifying the name of the first dataset (default: "value1").
sig.name2	A character string specifying the name of the second dataset (default: "value2").
cutoff.pvalue	The significance threshold for correlation (default: 0.05).
color	A vector of two colors for the heatmap gradient (default: c("#62CCC9", "#FF9999")).

## Details

The function computes correlation coefficients between corresponding columns in the two datasets and identifies significant correlations based on p-values.

## Value

A ggplot object displaying the correlation heatmap and scatter points.

**Examples**

```
# Read all data into memory
data(data.path, package = "iPRISM")
data(data.cell, package = "iPRISM")
# Draw the plot
cor_plot(data1 = data.path, data2 = data.cell, sig.name1 = "path", sig.name2 = "cell")
```

---

data.cell

*data.cell*


---

**Description**

The ‘data.cell’ represents the second type of feature matrix used for calculating correlations (in this case, cell abundances), where rows correspond to samples, and columns correspond to features.

**Usage**

```
data.cell
```

**Format**

An object of class `matrix` (inherits from `array`) with 121 rows and 21 columns.

**Examples**

```
library(iPRISM)
data(data.cell, package = "iPRISM")
dim(data.cell)
```

---

data.path

*data.path*


---

**Description**

The ‘data.path’ represents the first type of feature matrix used for calculating correlations (in this case, pathway expression levels), where rows correspond to samples, and columns correspond to features.

**Usage**

```
data.path
```

**Format**

An object of class `matrix` (inherits from `array`) with 121 rows and 17 columns.

**Examples**

```
library(iPRISM)
data(data.path, package = "iPRISM")
plot(data.path)
```

---

 data\_sig

*data\_sig*


---

**Description**

The 'data\_sig' represents the sample feature matrix, where rows correspond to samples, and columns correspond to features.

**Usage**

```
data_sig
```

**Format**

An object of class `matrix` (inherits from `array`) with 121 rows and 31 columns.

**Examples**

```
library(iPRISM)
data(data_sig, package = "iPRISM")
plot(data_sig)
```

---

 ESScore

*Enrichment Score Calculation*


---

**Description**

Calculates the enrichment score (ES) for a given set of labels and correlation vector.

**Usage**

```
ESScore(labels.list, correl.vector = NULL)
```

**Arguments**

`labels.list` A binary vector indicating membership in a gene set (1 for inclusion, 0 for exclusion).

`correl.vector` A vector of correlation values (e.g., gene expression correlations).

**Value**

The enrichment score (ES) for the given labels and correlation vector.

---

ESscore_weighted	<i>Weighted Enrichment Score Calculation</i>
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---

**Description**

Calculates the weighted enrichment score (ES) for a given set of labels and correlation vector.

**Usage**

```
ESscore_weighted(labels.list, correl.vector = NULL)
```

**Arguments**

`labels.list` A binary vector indicating membership in a gene set (1 for inclusion, 0 for exclusion).

`correl.vector` A vector of correlation values (e.g., gene expression correlations).

**Value**

The weighted enrichment score (ES) for the given labels and correlation vector.

---

genelist_cp	<i>TME gene list after random walks</i>
-------------	---

---

**Description**

This gene list includes genes from tumor microenvironment (TME). Random Walk with Restart (RWR) is applied to prioritize genes that are relevant to immunotherapy responses.

**Usage**

```
genelist_cp
```

**Format**

An object of class `numeric` of length 15867.

**Examples**

```
library(iPRISM)
data(genelist_cp, package = "iPRISM")
```

---

genelist_hla	<i>HLA gene list after random walks</i>
--------------	---

---

**Description**

This gene list includes genes from human leukocyte antigen (HLA). Random Walk with Restart (RWR) is applied to prioritize genes that are relevant to immunotherapy responses.

**Usage**

```
genelist_hla
```

**Format**

An object of class numeric of length 15867.

**Examples**

```
library(iPRISM)
data(genelist_hla, package = "iPRISM")
```

---

genelist_imm	<i>ICI gene list after random walks</i>
--------------	---

---

**Description**

This gene list includes genes from immune checkpoint inhibitors (ICI). Random Walk with Restart (RWR) is applied to prioritize genes that are relevant to immunotherapy responses.

**Usage**

```
genelist_imm
```

**Format**

An object of class numeric of length 15867.

**Examples**

```
library(iPRISM)
data(genelist_imm, package = "iPRISM")
```

---

`get_gsea_path`*Gene Set Enrichment Analysis (GSEA) using Multiplex Networks*

---

### Description

This function performs gene set enrichment analysis (GSEA) based on multiplex network data.

### Usage

```
get_gsea_path(  
  seed = seed,  
  network = network,  
  gamma = 0.7,  
  pathlist = pathlist,  
  gsea.weight = 1,  
  gsea.nperm = 1000  
)
```

### Arguments

<code>seed</code>	A seed value (optional).
<code>network</code>	A network object (e.g., protein-protein interaction network).
<code>gamma</code>	A parameter for random walk restart (default: 0.7).
<code>pathlist</code>	A predefined list of gene sets (pathways).
<code>gsea.weight</code>	Weight for GSEA (default: 1).
<code>gsea.nperm</code>	Number of permutations for significance testing (default: 1000).

### Details

The function constructs a multiplex network, performs random walk restart, and calculates gene scores. It then transforms the scores and applies GSEA using the provided gene sets.

### Value

A GSEA result object.

### Examples

```
data(Seeds, package = "iPRISM")  
data(ppi, package = "iPRISM")  
data(path_list, package = "iPRISM")  
  
result <- get_gsea_path(seed = Seeds,  
  network = ppi,  
  pathlist = path_list[1:2],  
  gsea.nperm = 100)
```



```
print(result)
```

---

`get_logiModel`*Fit Logistic Regression Model*

---

**Description**

This function fits a logistic regression model to the given data.

**Usage**

```
get_logiModel(data.sig, pred.value, levels = c("R", "N"), step = TRUE)
```

**Arguments**

<code>data.sig</code>	A data frame where each row is a sample and each column is a pathway.
<code>pred.value</code>	A numeric vector representing the response variable.
<code>levels</code>	A character vector specifying the levels of the response variable (default: <code>c("R", "N")</code> ).
<code>step</code>	Logical. If TRUE, perform stepwise model selection (default: TRUE).

**Details**

The function converts the response variable to a factor with specified levels and fits a logistic regression model using the `glm` function.

**Value**

A fitted logistic regression model.

**Examples**

```
data(data_sig, package = "iPRISM")

b <- get_logiModel(data.sig = data_sig, pred.value = pred_value, step = TRUE)
summary(b)
```

---

gseafun	<i>Gene Set Enrichment Analysis (GSEA) Function</i>
---------	---

---

### Description

This function performs gene set enrichment analysis using a gene list and a set of pathways.

### Usage

```
gseafun(genelist, pathlist, nperm = 1000, weighted = 1)
```

### Arguments

genelist	A named vector of gene expression values.
pathlist	A list of gene sets (pathways) to test for enrichment.
nperm	Number of permutations for calculating p-values (default is 1000).
weighted	Logical indicating whether to use weighted enrichment scores (default is TRUE).

### Value

A data frame with enrichment scores (ES), p-values, and adjusted p-values.

### Examples

```
data(path_list, package = "iPRISM")
data(genelist_imm, package = "iPRISM")

res_gsea_imm <- gseafun(genelist = genelist_imm,
                       pathlist = path_list[1:2],
                       weighted = 1,
                       nperm = 1000)

print(res_gsea_imm)
```

---

path_list	<i>path_list</i>
-----------	------------------

---

### Description

The ‘path\_list’ contains the gene list associated with pathways.

### Usage

```
path_list
```

**Format**

An object of class `list` of length 2656.

**Examples**

```
library(iPRISM)
data(path_list, package = "iPRISM")
length(path_list)
```

---

ppi

*A protein-protein physical interaction network (PPI network)*

---

**Description**

An `igraph` object containing a protein-protein physical interaction network.

**Usage**

```
ppi
```

**Format**

An object of class `igraph` of length 15867.

**Examples**

```
library(iPRISM)
data(ppi, package = "iPRISM")

library(igraph)
graph <- simplify(ppi)
graph_comp <- components(graph)$membership == which.max(components(graph)$csize)
graph <- induced_subgraph(graph, V(graph)[graph_comp])
plot(graph)
```

---

pred_value	<i>Original Class Labels for Samples</i>
------------	--

---

**Description**

A named vector where each element corresponds to a sample name and represents the original class label.

A named vector where each element corresponds to a sample name and represents the original class label.

**Usage**

```
pred_value
```

```
pred_value
```

**Format**

An object of class character of length 121.

An object of class character of length 121.

**Examples**

```
library(iPRISM)
data(pred_value, package = "iPRISM")
table(pred_value)
```

```
library(iPRISM)
data(pred_value, package = "iPRISM")
table(pred_value)
```

---

Seeds	<i>Seed Node Names</i>
-------	------------------------

---

**Description**

A character vector with seed node names.

**Usage**

```
Seeds
```

**Format**

An object of class character of length 3.

**Examples**

```
library(iPRISM)  
data(Seeds, package = "iPRISM")
```

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