

# Package: regport (via r-universe)

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**Title** Regression Model Processing Port

**Version** 0.3.0

**Description** Provides R6 classes, methods and utilities to construct, analyze, summarize, and visualize regression models.

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**URL** <https://github.com/ShixiangWang/regport>,  
<https://shixiangwang.github.io/regport/>

**BugReports** <https://github.com/ShixiangWang/regport/issues>

**Imports** broom.helpers, data.table, dplyr, forestploter, glue, parameters, R6, rlang (>= 0.4.11), stats, survival

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**Repository** <https://shixiangwang.r-universe.dev>

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`REGModel`*R6 class representing a regression model*

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### Description

Contains fields storing data and methods to build, process and visualize a regression model. Currently, this class is designed for CoxPH and GLM regression models.

### Public fields

`data` a `data.table` storing modeling data.

`recipe` an R formula storing model formula.

`terms` all terms (covariables, i.e. columns) used for building model.

`args` other arguments used for building model.

`model` a constructed model.

`type` model type (class).

`result` model result, a object of `parameters_model`. Can be converted into `data.frame` with `as.data.frame()` or `data.table::as.data.table()`.

`forest_data` more detailed data used for plotting forest.

### Methods

#### Public methods:

- `REGModel$new()`
- `REGModel$get_forest_data()`
- `REGModel$plot_forest()`
- `REGModel$plot()`
- `REGModel$print()`
- `REGModel$clone()`

**Method** `new()`: Build a `REGModel` object.

*Usage:*

```
REGModel$new(  
  data,  
  recipe,  
  ...,  
  f = c("coxph", "binomial", "gaussian", "Gamma", "inverse.gaussian", "poisson",  
        "quasi", "quasibinomial", "quasipoisson"),  
  exp = NULL,  
  ci = 0.95  
)
```

*Arguments:*

`data` a `data.table` storing modeling data.

recipe an R formula or a list with two elements 'x' and 'y', where 'x' is for covariables and 'y' is for label. See example for detail operation.

... other parameters passing to corresponding regression model function.

f a length-1 string specifying modeling function or family of `glm()`, default is 'coxph'. Other options are members of GLM family, see `stats::family()`. 'binomial' is logistic, and 'gaussian' is linear.

exp logical, indicating whether or not to exponentiate the the coefficients.

ci confidence Interval (CI) level. Default to 0.95 (95%). e.g. `survival::coxph()`.

*Returns:* a REGModel R6 object.

**Method** `get_forest_data()`: get tidy data for plotting forest.

*Usage:*

```
REGModel$get_forest_data(separate_factor = FALSE, global_p = FALSE)
```

*Arguments:*

`separate_factor` separate factor/class as a blank row.

`global_p` if TRUE, return global p value.

**Method** `plot_forest()`: plot forest.

*Usage:*

```
REGModel$plot_forest(ref_line = NULL, xlim = NULL, ...)
```

*Arguments:*

`ref_line` reference line, default is 1 for HR.

`xlim` limits of x axis.

... other plot options passing to `forestploter::forest()`. Also check <https://github.com/adayim/forestploter> to see more complex adjustment of the result plot.

**Method** `plot()`: print the `REGModel$result` with default plot methods from `see` package.

*Usage:*

```
REGModel$plot(...)
```

*Arguments:*

... other parameters passing to `plot()` in `see::plot.see_parameters_model` function.

**Method** `print()`: print the REGModel object

*Usage:*

```
REGModel$print(...)
```

*Arguments:*

... unused.

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
REGModel$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

**Examples**

```

library(survival)
test1 <- data.frame(
  time = c(4, 3, 1, 1, 2, 2, 3),
  status = c(1, 1, 1, 0, 1, 1, 0),
  x = c(0, 2, 1, 1, 1, 0, 0),
  sex = c(0, 0, 0, 0, 1, 1, 1)
)
test1$sex <- factor(test1$sex)

# -----
# Build a model
# -----

# way 1:
mm <- REGModel$new(
  test1,
  Surv(time, status) ~ x + strata(sex)
)
mm
as.data.frame(mm$result)
if (require("see")) mm$plot()
mm$print() # Same as print(mm)

# way 2:
mm2 <- REGModel$new(
  test1,
  recipe = list(
    x = c("x", "strata(sex)"),
    y = c("time", "status")
  )
)
mm2

# Add other parameters, e.g., weights
# For more, see ?coxph
mm3 <- REGModel$new(
  test1,
  recipe = list(
    x = c("x", "strata(sex)"),
    y = c("time", "status")
  ),
  weights = c(1, 1, 1, 2, 2, 2, 3)
)
mm3$args

# -----
# Another type of model
# -----
library(stats)
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- gl(3, 1, 9)

```

```
treatment <- gl(3, 3)
data <- data.frame(treatment, outcome, counts)

mm4 <- REGModel$new(
  data,
  counts ~ outcome + treatment,
  f = "poisson"
)
mm4
mm4$plot_forest()
mm4$get_forest_data()
mm4$plot_forest()
```

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REGModelList

*R6 class representing a list of regression model*

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## Description

Contains fields storing data and methods to build, process and visualize a list of regression model. Currently, this class is designed for CoxPH and GLM regression models.

## Public fields

`data` a `data.table` storing modeling data.

`x` focal variables (terms).

`y` predicted variables or expression.

`covars` covariables.

`mlist` a list of `REGModel`.

`args` other arguments used for building model.

`type` model type (class).

`result` model result, a object of `parameters_model`. Can be converted into `data.frame` with `as.data.frame()` or `data.table::as.data.table()`.

`forest_data` more detailed data used for plotting forest.

## Methods

### Public methods:

- `REGModelList$new()`
- `REGModelList$build()`
- `REGModelList$plot_forest()`
- `REGModelList$print()`
- `REGModelList$clone()`

**Method** `new()`: Create a `REGModelList` object.

*Usage:*

```
REGModelList$new(data, y, x, covars = NULL)
```

*Arguments:*

`data` a `data.table` storing modeling data.

`y` predicted variables or expression.

`x` focal variables (terms).

`covars` covariables.

*Returns:* a `REGModelList` R6 object.

**Method** `build()`: Build `REGModelList` object.

*Usage:*

```
REGModelList$build(
  f = c("coxph", "binomial", "gaussian", "Gamma", "inverse.gaussian", "poisson",
        "quasi", "quasibinomial", "quasipoisson"),
  exp = NULL,
  ci = 0.95,
  parallel = FALSE,
  ...
)
```

*Arguments:*

`f` a length-1 string specifying modeling function or family of `glm()`, default is 'coxph'. Other options are members of GLM family, see `stats::family()`. 'binomial' is logistic, and 'gaussian' is linear.

`exp` logical, indicating whether or not to exponentiate the the coefficients.

`ci` confidence Interval (CI) level. Default to 0.95 (95%). e.g. `survival::coxph()`.

`parallel` if TRUE, use N-1 cores to run the task.

... other parameters passing to corresponding regression model function.

*Returns:* a `REGModel` R6 object.

**Method** `plot_forest()`: plot forest.

*Usage:*

```
REGModelList$plot_forest(
  ref_line = NULL,
  xlim = NULL,
  vars = NULL,
  p = NULL,
  ...
)
```

*Arguments:*

`ref_line` reference line, default is 1 for HR.

`xlim` limits of x axis.

`vars` selected variables to show.

`p` selected variables with level' pvalue lower than p.

... other plot options passing to `forestploter::forest()`. Also check <https://github.com/adayim/forestploter> to see more complex adjustment of the result plot.

**Method** print(): print the REGModelList object

*Usage:*

```
REGModelList$print(...)
```

*Arguments:*

... unused.

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

```
REGModelList$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

### Examples

```
m1 <- REGModelList$new(  
  data = mtcars,  
  y = "mpg",  
  x = c("factor(cyl)", colnames(mtcars)[3:5]),  
  covars = c(colnames(mtcars)[8:9], "factor(gear)")  
)  
m1  
m1$print()  
m1$plot_forest()  
  
m1$build(f = "gaussian")  
## Not run:  
m1$build(f = "gaussian", parallel = TRUE)  
  
## End(Not run)  
m1$print()  
m1$result  
m1$forest_data  
m1$plot_forest()
```

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