

# Package ‘PosiR’

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**Type** Package

**Title** Post-Selection Inference via Simultaneous Confidence Intervals

**Version** 0.1.2

**Description** Post-selection inference in linear regression models,  
constructing simultaneous confidence intervals across a user-specified universe of models.  
Implements the methodology described in Kuchibhotla, Kolassa, and Kuffner (2022) ``Post-  
Selection Inference"  
<[doi:10.1146/annurev-statistics-100421-044639](https://doi.org/10.1146/annurev-statistics-100421-044639)> to ensure valid inference after model  
selection, with applications in high-dimensional settings like Lasso selection.

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**Encoding** UTF-8

**Suggests** knitr, pbapply, rmarkdown, testthat (>= 3.0.0), dplyr, glmnet

**Config/testthat/edition** 3

**RoxygenNote** 7.3.2

**URL** <https://github.com/Chukyhenry/PosiR>

**BugReports** <https://github.com/Chukyhenry/PosiR/issues>

**Imports** graphics, parallel, stats

**VignetteBuilder** knitr

**Depends** R (>= 4.0.0)

**NeedsCompilation** no

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**Repository** CRAN

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plot.simultaneous\_ci\_result

*Plot Simultaneous Confidence Intervals*


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## Description

Visualizes confidence intervals returned by `simultaneous_ci()` using base R graphics. Estimates are shown as points with corresponding CI segments, grouped and labeled by model and coefficient name. Supports customization for log scale, character sizes, label trimming, and reference lines.

## Usage

```
## S3 method for class 'simultaneous_ci_result'
plot(
  x,
  y = NULL,
  subset_pars = NULL,
  log.scale = FALSE,
  cex = 0.8,
  cex.labels = 0.8,
  las.labels = 1,
  pch = 16,
  col.estimate = "blue",
  col.ci = "darkgray",
  col.ref = "red",
  ref.line.pos = 0,
  lty.ref = 2,
  main = "Simultaneous Confidence Intervals",
  xlab = NULL,
  label.trim = NULL,
  ...
)
```

## Arguments

<code>x</code>	An object of class <code>simultaneous_ci_result</code> , typically returned by <code>simultaneous_ci()</code> .
<code>y</code>	Ignored.
<code>subset_pars</code>	Optional character vector. Coefficient names to subset the plot. Default: all.
<code>log.scale</code>	Logical. Plot on logarithmic scale. Intervals crossing 0 or with nonpositive bounds are excluded.
<code>cex</code>	Point size for estimates. Default = 0.8.
<code>cex.labels</code>	Label size for y-axis. Default = 0.8.
<code>las.labels</code>	Orientation of y-axis labels (0, 1, 2, or 3). Default = 1.
<code>pch</code>	Plot character for point estimates. Default = 16.

<code>col.estimate</code>	Color of point estimates. Default = "blue".
<code>col.ci</code>	Color of confidence interval lines. Default = "darkgray".
<code>col.ref</code>	Color of reference line(s). Default = "red".
<code>ref.line.pos</code>	Position(s) for vertical reference line(s). Default = 0. Set to NULL to omit.
<code>lty.ref</code>	Line type for reference lines. Default = 2 (dashed).
<code>main</code>	Plot title. Default = "Simultaneous Confidence Intervals".
<code>xlab</code>	X-axis label. If NULL and <code>log.scale = TRUE</code> , label defaults to "Log Estimate".
<code>label.trim</code>	Integer. Trims long coefficient labels to this width (adds "..."). Optional.
<code>...</code>	Additional arguments passed for future use (currently ignored).

## Value

Invisibly returns a list:

- `ycoords`: Named vector of y-axis positions for each label
- `xlim`: Range of x-axis limits used
- `ylim`: Range of y-axis limits used

If no valid intervals are available for plotting, returns `invisible(NULL)`.

## Examples

```
set.seed(1)
X <- matrix(rnorm(100*2), 100, 2, dimnames = list(NULL, c("X1", "X2")))
y <- 1 + X[,1] - X[,2] + rnorm(100)
res <- simultaneous_ci(X, y, list(mod = 1:3), B = 100, add_intercept = TRUE)
plot(res)
```

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<code>simultaneous_ci</code>	<i>Compute Simultaneous Confidence Intervals via Bootstrap (Post-Selection Inference)</i>
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## Description

Implements Algorithm 1 from the reference paper using bootstrap-based max-t statistics to construct valid simultaneous confidence intervals for selected regression coefficients across a user-specified universe of linear models.

**Usage**

```
simultaneous_ci(
  X,
  y,
  Q_universe,
  alpha = 0.05,
  B = 1000,
  add_intercept = TRUE,
  bootstrap_method = "pairs",
  cores = 1,
  use_pbapply = TRUE,
  seed = NULL,
  verbose = TRUE,
  ...
)
```

**Arguments**

<code>X</code>	Numeric matrix (n x p): Design matrix. Must have unique column names. Do not include an intercept if <code>add_intercept = TRUE</code> .
<code>y</code>	Numeric vector (length n): Response vector.
<code>Q_universe</code>	Named list of numeric vectors. Each element specifies a model as a vector of column indices (accounting for intercept if <code>add_intercept = TRUE</code> ). Names are used to identify each model in results.
<code>alpha</code>	Significance level for the confidence intervals. Default is 0.05.
<code>B</code>	Integer. Number of bootstrap samples. Default is 1000.
<code>add_intercept</code>	Logical. If <code>TRUE</code> , adds an intercept as the first column of the design matrix. Default is <code>TRUE</code> .
<code>bootstrap_method</code>	Character. Bootstrap type. Only "pairs" is currently supported.
<code>cores</code>	Integer. Number of CPU cores to use for bootstrap parallelization. Default is 1.
<code>use_pbapply</code>	Logical. Use <code>pbapply</code> for progress bars if available. Default is <code>TRUE</code> .
<code>seed</code>	Optional numeric. Random seed for reproducibility. Used for parallel-safe RNG.
<code>verbose</code>	Logical. Whether to display status messages. Default is <code>TRUE</code> .
<code>...</code>	Reserved for future use.

**Details**

Supports parallel execution, internal warnings capture, and returns structured results with estimates, intervals, bootstrap diagnostics, and inference statistics.

**Value**

A list of class `simultaneous_ci_result` with elements:

- `intervals`: Data frame with estimates, confidence intervals, variances, and SEs
- `K_alpha`: Bootstrap  $(1 - \alpha)$  quantile of max-t statistics
- `T_star_b`: Vector of bootstrap max-t statistics
- `n_valid_T_star_b`: Number of finite bootstrap max-t statistics
- `alpha, B, bootstrap_method`: Metadata
- `warnings_list`: Internal warnings collected during bootstrap/model fitting
- `valid_bootstrap_counts`: Valid bootstrap replicates per parameter
- `n_bootstrap_errors`: Total bootstrap fitting errors

**References**

Kuchibhotla, A., Kolassa, J., & Kuffner, T. (2022). Post-selection inference. *Annual Review of Statistics and Its Application*, 9(1), 505–527.

**Examples**

```
set.seed(123)
X <- matrix(rnorm(100 * 2), 100, 2, dimnames = list(NULL, c("X1", "X2")))
y <- X[,1] * 0.5 + rnorm(100)
Q <- list(model = 1:2)
res <- simultaneous_ci(X, y, Q, B = 100, cores = 1)
print(res$intervals)
plot(res)
```

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