

# Package: SelectBoost.FDA (via r-universe)

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**Title** SelectBoost-Style Variable Selection for Functional Data Analysis

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**Description** Implements 'SelectBoost'-style variable selection workflows for functional data analysis. The package provides FDA-native design and preprocessing objects for raw curves, spline-basis expansions, Functional principal component analysis scores, and scalar covariates; grouped stability-selection routines based on repeated subject-level subsampling; multiple selector backends including lasso, group lasso, and sparse-group lasso; FDA-aware grouping functions and calibration helpers for 'SelectBoost'; method-comparison utilities; a formula interface; simulation, benchmarking, and validation helpers with mapped ground truth; targeted sensitivity-study utilities and shipped benchmark summaries for mean 'F1' comparisons between FDA-aware and plain 'SelectBoost' workflows; small example datasets; and an optional adapter to the native stability-selection interface from the 'FDboost' package.

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---

`apply_fda_preprocessor`  
*Apply an FDA Preprocessor*

---

**Description**

Applies a fitted preprocessor to new functional predictors and optional scalar covariates, returning an `fda_matrix` object compatible with the selection routines.

**Usage**

`apply_fda_preprocessor(object, predictors, scalar_covariates = NULL, ...)`

**Arguments**

`object`           A fitted `fda_preprocessor`.  
`predictors`       New functional predictors.  
`scalar_covariates`  
                    Optional scalar covariates.  
`...`             Not used.

**Value**

An object of class `fda_matrix`.

---

as\_functional\_matrix *Flatten Functional Predictors Into a Matrix*

---

### Description

Accepts a standard numeric matrix/data frame or a named list of functional blocks. List inputs are column-bound while preserving the original block membership of each coefficient, which is later reused for grouped stability selection and FDA-aware SelectBoost grouping.

### Usage

```
as_functional_matrix(x, center = FALSE, scale = FALSE)
```

### Arguments

**x** A numeric matrix/data frame, an `fda_grid`, an `fda_basis`, an `fda_design`, or a list of such objects. Each list element is treated as one functional block.

**center, scale** Passed to `base::scale()` when either argument is TRUE.

### Value

An object of class `fda_matrix` with elements `x`, `blocks`, and `positions`.

---

benchmark\_selection\_methods

*Benchmark FDA Selection Methods on Shared Ground Truth*

---

### Description

Runs `compare_selection_methods()` on a simulated dataset and evaluates the fitted objects against the mapped truth.

### Usage

```
benchmark_selection_methods(
  data,
  methods = c("stability", "interval", "selectboost", "plain_selectboost"),
  levels = c("feature", "group"),
  stability_args = list(),
  interval_args = list(),
  selectboost_args = list(),
  plain_selectboost_args = list(),
  fdboost_model = NULL,
  fdboost_args = list(),
  keep_comparison = TRUE
)
```

**Arguments**

**data** An object returned by `simulate_fda_scenario()`.  
**methods** Methods passed to `compare_selection_methods()`.  
**levels** Evaluation levels.  
**stability\_args, interval\_args, selectboost\_args,**  
**plain\_selectboost\_args** Additional arguments passed to `compare_selection_methods()`.  
**fdboost\_model, fdboost\_args** Optional FDboost inputs forwarded to `compare_selection_methods()`.  
**keep\_comparison** Should the fitted comparison object be stored?

**Value**

An object of class `fda_benchmark`.

**Examples**

```

sim <- simulate_fda_scenario(n = 24, grid_length = 16, seed = 1)
bench <- benchmark_selection_methods(
  sim,
  methods = c("selectboost", "plain_selectboost"),
  selectboost_args = list(B = 3, steps.seq = 0.5, c0lim = FALSE),
  plain_selectboost_args = list(B = 3, steps.seq = 0.5, c0lim = FALSE)
)
head(bench$metrics)

```

---

calibrate\_interval\_width

*Calibrate Interval Widths*

---

**Description**

Runs interval stability selection over candidate interval widths.

**Usage**

```

calibrate_interval_width(
  design,
  widths,
  step = NULL,
  overlap = FALSE,
  selector = "lasso",
  keep_fits = FALSE,
  seed = NULL,
  ...
)

```

**Arguments**

design	An fda_design object.
widths	Candidate interval widths.
step	Optional step size. Defaults to widths.
overlap	Should the interval groups overlap?
selector	Base selector passed to <a href="#">interval_stability_selection()</a> .
keep_fits	Should the fitted objects be stored in the result?
seed	Optional seed used to create deterministic per-grid seeds.
...	Additional arguments passed to <a href="#">interval_stability_selection()</a> .

**Value**

An object of class `fda_calibration_grid`.

---

`calibrate_selectboost` *Calibrate SelectBoost c0 Values*

---

**Description**

Runs FDA-SelectBoost on a user-provided or suggested `c0` grid.

**Usage**

```
calibrate_selectboost(
  design,
  selector = "msgps",
  c0_grid = NULL,
  grid_method = c("quantile", "linear"),
  association_method = c("correlation", "neighborhood", "hybrid", "interval"),
  keep_fit = TRUE,
  ...
)
```

**Arguments**

design	An fda_design object.
selector	Base selector passed to <a href="#">fit_selectboost()</a> .
c0_grid	Optional explicit <code>c0</code> grid.
grid_method	Rule used by <a href="#">suggest_c0_grid()</a> when <code>c0_grid</code> is omitted.
association_method	Passed to <a href="#">suggest_c0_grid()</a> and <a href="#">fit_selectboost()</a> .
keep_fit	Should the fitted object be stored in the result?
...	Additional arguments passed to <a href="#">fit_selectboost()</a> .

**Value**

An object of class `fda_calibration_grid`.

---

`calibrate_stability_selection`  
*Calibrate Stability-Selection Parameters*

---

**Description**

Runs grouped stability selection over a grid of subsampling fractions and cutoff values.

**Usage**

```
calibrate_stability_selection(  
  design,  
  selector = "group_lasso",  
  sample_fraction_grid = c(0.5, 0.632, 0.75),  
  cutoff_grid = c(0.6, 0.75, 0.9),  
  keep_fits = FALSE,  
  seed = NULL,  
  ...  
)
```

**Arguments**

<code>design</code>	An <code>fda_design</code> object.
<code>selector</code>	Base selector passed to <code>fit_stability()</code> .
<code>sample_fraction_grid</code>	Candidate subsampling fractions.
<code>cutoff_grid</code>	Candidate cutoff values.
<code>keep_fits</code>	Should the fitted objects be stored in the result?
<code>seed</code>	Optional seed used to create deterministic per-grid seeds.
<code>...</code>	Additional arguments passed to <code>fit_stability()</code> .

**Value**

An object of class `fda_calibration_grid`.

---

 compare\_selection\_methods

*Compare FDA Selection Methods*


---

## Description

Runs multiple selection workflows on the same `fda_design` object and returns both the fitted objects and a comparison table.

## Usage

```
compare_selection_methods(
  design,
  methods = c("stability", "interval", "selectboost"),
  stability_args = list(),
  interval_args = list(),
  selectboost_args = list(),
  plain_selectboost_args = list(),
  fdboost_model = NULL,
  fdboost_args = list()
)
```

## Arguments

<code>design</code>	An <code>fda_design</code> object.
<code>methods</code>	Methods to run. Supported values are "stability", "interval", "selectboost", "plain_selectboost", and "fdboost".
<code>stability_args</code> , <code>interval_args</code> , <code>selectboost_args</code> , <code>plain_selectboost_args</code>	Named lists of arguments passed to the corresponding fitting functions.
<code>fdboost_model</code>	Optional fitted FDboost object used when methods includes "fdboost".
<code>fdboost_args</code>	Additional arguments passed to <a href="#">fdboost_stability_selection()</a> .

## Value

An object of class `fda_method_comparison`.

## Examples

```
sim <- simulate_fda_scenario(n = 24, grid_length = 16, seed = 1)
comparison <- compare_selection_methods(
  sim$design,
  methods = c("selectboost", "plain_selectboost"),
  selectboost_args = list(B = 3, steps.seq = 0.5, c0lim = FALSE),
  plain_selectboost_args = list(B = 3, steps.seq = 0.5, c0lim = FALSE)
)
summary(comparison)
```

---

evaluate_selection	<i>Evaluate Selection Recovery Against Ground Truth</i>
--------------------	---

---

**Description**

Computes support-recovery metrics for fitted selection objects against the truth generated by `simulate_fda_scenario()`.

**Usage**

```
evaluate_selection(x, truth, level = c("feature", "group", "basis"), ...)
```

**Arguments**

<code>x</code>	A fitted selection object or an <code>fda_method_comparison</code> .
<code>truth</code>	Ground-truth object, typically the value returned by <code>simulate_fda_scenario()</code> .
<code>level</code>	Evaluation level: "feature", "group", or "basis".
<code>...</code>	Additional arguments passed to the relevant method.

**Value**

A data frame with recovery metrics.

---

fda_basis	<i>Basis-Expanded Functional Predictor</i>
-----------	--

---

**Description**

Constructor for a functional predictor represented by basis coefficients or FPCA scores.

**Usage**

```
fda_basis(
  coefficients,
  basis_type = c("generic", "spline", "wavelet", "fpga"),
  argvals = NULL,
  component_names = NULL,
  name = NULL,
  unit = NULL
)
```

**Arguments**

coefficients	Numeric matrix with one row per observation.
basis_type	Label describing the representation.
argvals	Optional labels or positions for basis functions/components.
component_names	Optional names for coefficient columns.
name	Optional predictor name.
unit	Optional unit for the basis domain.

**Value**

An object of class `fda_basis`.

---

fda_bspline	<i>Spline-Basis Preprocessing Spec</i>
-------------	--

---

**Description**

Spline-Basis Preprocessing Spec

**Usage**

```
fda_bspline(
  df = 6L,
  degree = 3L,
  intercept = TRUE,
  center = FALSE,
  scale = FALSE
)
```

**Arguments**

df	Degrees of freedom used by <code>splines::bs()</code> .
degree	Spline degree.
intercept	Should the spline basis include an intercept column?
center, scale	Logical flags controlling column-wise centering and scaling of the resulting coefficients.

**Value**

An object of class `fda_preprocess_spec`.

---

fda\_design

*Functional Design Object*


---

**Description**

Bundles the response, functional predictors, family, and a reversible feature map. This is the FDA-native entry point for the higher-level fitting functions.

**Usage**

```
fda_design(
  response = NULL,
  predictors,
  scalar_covariates = NULL,
  family = c("gaussian", "binomial"),
  id = NULL,
  center = FALSE,
  scale = FALSE,
  transforms = NULL,
  scalar_transform = NULL,
  preprocessor = NULL
)
```

**Arguments**

response	Response vector.
predictors	A single predictor or a named list of predictors. Elements can be <code>fda_grid</code> , <code>fda_basis</code> , <code>fda_scalar</code> , matrices, data frames, or numeric vectors.
scalar_covariates	Optional scalar covariates supplied separately from the functional predictors.
family	Model family.
id	Optional observation identifiers.
center, scale	Backward-compatible shortcuts for applying an identity transform with centering and scaling to the functional predictors.
transforms	Optional preprocessing specs for the functional predictors.
scalar_transform	Optional preprocessing specs for scalar covariates.
preprocessor	Optional fitted <code>fda_preprocessor</code> . When supplied, it is reused instead of fitting preprocessing from the current data.

**Value**

An object of class `fda_design`.

**Examples**

```

data("spectra_example", package = "SelectBoost.FDA")
idx <- 1:20
design <- fda_design(
  response = spectra_example$response[idx],
  predictors = list(
    signal = fda_grid(
      spectra_example$predictors$signal[idx, ],
      argvals = spectra_example$grid,
      name = "signal"
    ),
    nuisance = fda_grid(
      spectra_example$predictors$nuisance[idx, ],
      argvals = spectra_example$grid,
      name = "nuisance"
    )
  ),
  scalar_covariates = spectra_example$scalar_covariates[idx, ],
  scalar_transform = fda_standardize(),
  family = "gaussian"
)
summary(design)

```

---

fda\_design\_formula      *Build an FDA Design from a Formula*

---

**Description**

Supports additive formulas of the form  $y \sim \text{signal} + \text{noise} + \text{age} + \text{batch}$ , where functional terms are supplied as matrices, `fda_grid`, or `fda_basis` objects in `data`, and scalar terms are expanded through `stats::model.matrix()`.

**Usage**

```

fda_design_formula(
  formula,
  data,
  family = c("gaussian", "binomial"),
  transforms = NULL,
  scalar_transform = NULL,
  preprocessor = NULL,
  center = FALSE,
  scale = FALSE
)

```

**Arguments**

`formula`      An additive formula with a single response.

data            A list or data frame containing the variables referenced in formula.  
 family, transforms, scalar\_transform, preprocessor, center, scale  
                  Passed to `fda_design()`.

**Value**

An object of class `fda_design`.

---

fda_fpca	<i>FPCA Preprocessing Spec</i>
----------	--------------------------------

---

**Description**

FPCA Preprocessing Spec

**Usage**

```
fda_fpca(  
  n_components = 3L,  
  variance_explained = NULL,  
  center = TRUE,  
  scale = FALSE  
)
```

**Arguments**

n\_components    Number of principal components to retain.  
 variance\_explained    Optional cumulative explained variance target in  $(0, 1]$ . When supplied, it overrides n\_components.  
 center, scale    Passed to `stats::prcomp()`.

**Value**

An object of class `fda_preprocess_spec`.

---

fda\_grid

*Functional Predictor on a Common Grid*


---

**Description**

Constructor for one discretized functional predictor sampled on a common grid.

**Usage**

```
fda_grid(values, argvals = NULL, name = NULL, unit = NULL)
```

**Arguments**

values	Numeric matrix with one row per observation.
argvals	Optional vector of grid values. Defaults to <code>seq_len(ncol(values))</code> .
name	Optional predictor name.
unit	Optional unit for the grid axis.

**Value**

An object of class `fda_grid`.

---

fda\_identity

*Identity Preprocessing Spec*


---

**Description**

Identity Preprocessing Spec

**Usage**

```
fda_identity(center = FALSE, scale = FALSE)
```

**Arguments**

center, scale	Logical flags controlling column-wise centering and scaling of the transformed features.
---------------	--

**Value**

An object of class `fda_preprocess_spec`.

---

fda_scalar	<i>Scalar Predictor Constructor</i>
------------	-------------------------------------

---

**Description**

Wraps scalar covariates so they can participate in the same feature-mapping and preprocessing machinery as functional predictors.

**Usage**

```
fda_scalar(values, name = NULL, unit = NULL)
```

**Arguments**

values	Numeric vector or matrix with one row per observation.
name	Optional predictor name.
unit	Optional unit label.

**Value**

An object of class `fda_scalar`.

---

fda_standardize	<i>Standardization Preprocessing Spec</i>
-----------------	---

---

**Description**

Standardization Preprocessing Spec

**Usage**

```
fda_standardize(center = TRUE, scale = TRUE)
```

**Arguments**

center, scale	Logical flags controlling column-wise centering and scaling. Both default to TRUE.
---------------	--

**Value**

An object of class `fda_preprocess_spec`.

---

`fdboost_stability_selection`*Stability Selection for FDboost Fits*

---

**Description**

Thin adapter to the `stabsel.FDboost()` method. This is the native route when the model itself is already fitted with FDboost.

**Usage**

```
fdboost_stability_selection(model, ...)
```

**Arguments**

<code>model</code>	A fitted FDboost object.
<code>...</code>	Additional arguments forwarded to <code>stabs::stabsel()</code> .

**Value**

A `stabsel` object.

---

`fit_fda_preprocessor` *Fit an FDA Preprocessor*

---

**Description**

Learns train/test-safe preprocessing transforms for functional predictors and optional scalar covariates. The fitted object can be reused to create compatible `fda_design` objects on new data.

**Usage**

```
fit_fda_preprocessor(  
  predictors,  
  scalar_covariates = NULL,  
  transforms = NULL,  
  scalar_transform = NULL  
)
```

**Arguments**

predictors      One predictor or a named list of predictors.  
 scalar\_covariates      Optional scalar covariates supplied as a vector, matrix/data frame, fda\_scalar, or a named list.  
 transforms      Optional preprocessing specs for functional predictors.  
 scalar\_transform      Optional preprocessing specs for scalar covariates.

**Value**

An object of class fda\_preprocessor.

---

fit_selectboost	<i>Fit SelectBoost from an FDA Design</i>
-----------------	---

---

**Description**

Fit SelectBoost from an FDA Design

**Usage**

```
fit_selectboost(design, ...)
```

**Arguments**

design      An fda\_design object.  
 ...      Additional arguments forwarded to selectboost\_fda().

**Value**

An object inheriting from selectboost\_fda\_result.

**Examples**

```

sim <- simulate_fda_scenario(n = 24, grid_length = 16, seed = 1)
fit <- fit_selectboost(
  sim$design,
  mode = "fast",
  steps.seq = 0.5,
  c0lim = FALSE,
  B = 3
)
head(selection_map(fit, c0 = colnames(fit$feature_selection)[1]))

```

---

`fit_selectboost_formula`*Fit FDA-SelectBoost from a Formula*

---

**Description**

Fit FDA-SelectBoost from a Formula

**Usage**

```
fit_selectboost_formula(  
  formula,  
  data,  
  family = c("gaussian", "binomial"),  
  transforms = NULL,  
  scalar_transform = NULL,  
  preprocessor = NULL,  
  center = FALSE,  
  scale = FALSE,  
  ...  
)
```

**Arguments**

formula, data, family, transforms, scalar\_transform, preprocessor,  
center, scale

Passed to `fda_design_formula()`.

... Additional arguments passed to `fit_selectboost()`.

**Value**

An object inheriting from `selectboost_fda_result`.

---

`fit_stability`*Fit Grouped Stability Selection from an FDA Design*

---

**Description**

Fit Grouped Stability Selection from an FDA Design

**Usage**

```
fit_stability(design, ...)
```



**Value**

An object inheriting from `fda_stability_selection`.

---

`functional_association`

*Functional Association Matrix*

---

**Description**

Computes or post-processes an absolute association matrix for discretized or basis-expanded functional predictors.

**Usage**

```
functional_association(
  x,
  association = NULL,
  method = c("correlation", "neighborhood", "hybrid", "interval"),
  within_blocks = TRUE,
  bandwidth = NULL,
  interval_groups = NULL,
  width = NULL,
  step = width,
  decay = 1
)
```

**Arguments**

<code>x</code>	Any input accepted by <code>as_functional_matrix()</code> .
<code>association</code>	Optional square association matrix supplied by the user. When omitted, <code>abs(stats::cor(X))</code> is used.
<code>method</code>	Association structure. "correlation" uses the absolute correlation matrix, "neighborhood" uses local positional similarity, "hybrid" multiplies correlation by a neighborhood kernel, and "interval" induces associations within interval groups.
<code>within_blocks</code>	Should cross-block associations be zeroed out?
<code>bandwidth</code>	Optional maximum within-block lag retained in the association matrix.
<code>interval_groups</code>	Optional interval grouping used when <code>method = "interval"</code> .
<code>width, step</code>	Interval parameters used when <code>method = "interval"</code> and <code>interval_groups</code> is omitted.
<code>decay</code>	Positive exponent controlling the neighborhood kernel.

**Value**

A square absolute association matrix with unit diagonal.

---

 functional\_block\_groups

*Block-Level Groups for Functional Predictors*


---

**Description**

Returns one group label per column, with each functional block defining a group.

**Usage**

```
functional_block_groups(x)
```

**Arguments**

x Any input accepted by `as_functional_matrix()`.

**Value**

An integer vector of group memberships.

---

functional\_interval\_groups

*Interval Groups for Discretized Functional Predictors*


---

**Description**

Creates non-overlapping interval groups within each functional block. This is useful when one wants region-level stability summaries instead of pointwise selection frequencies.

**Usage**

```
functional_interval_groups(x, width, step = width, overlap = FALSE)
```

**Arguments**

x Any input accepted by `as_functional_matrix()`.

width Positive integer interval width within each block.

step Step size between interval starts. Only non-overlapping intervals are supported by default.

overlap Logical; should intervals be allowed to overlap? When TRUE, the result is returned as an overlapping group structure.

**Value**

Either an integer group vector with an `interval_table` attribute or an overlapping group structure of class `fda_group_list`.

---

```
interval_stability_selection
      Interval Stability Selection
```

---

**Description**

Convenience wrapper around `stability_selection_fda()` that first creates non-overlapping interval groups within each functional block.

**Usage**

```
interval_stability_selection(
  x,
  y = NULL,
  width,
  step = width,
  overlap = FALSE,
  ...
)
```

**Arguments**

<code>x</code>	Any input accepted by <code>as_functional_matrix()</code> , or an <code>fda_design</code> object.
<code>y</code>	Response vector. Leave as <code>NULL</code> when <code>x</code> is an <code>fda_design</code> .
<code>width</code>	Positive interval width.
<code>step</code>	Step size between interval starts.
<code>overlap</code>	Logical; should the interval groups overlap?
<code>...</code>	Additional arguments forwarded to <code>stability_selection_fda()</code> .

**Value**

An object of class `fda_interval_stability_selection`.

---

```
make_functional_grouping_function
      FDA-Aware Grouping Function for SelectBoost
```

---

**Description**

Builds a closure that can be passed directly to `group=` in `SelectBoost::fastboost()` or `SelectBoost::autoboost()`. The returned grouping function respects functional block boundaries and can optionally restrict groups to local neighborhoods along the observation grid.

**Usage**

```

make_functional_grouping_function(
  x,
  association = NULL,
  method = c("threshold", "community"),
  association_method = c("correlation", "neighborhood", "hybrid", "interval"),
  within_blocks = TRUE,
  bandwidth = NULL,
  interval_groups = NULL,
  width = NULL,
  step = width,
  decay = 1
)

```

**Arguments**

x	Any input accepted by <code>as_functional_matrix()</code> .
association	Optional square association matrix. When omitted, the correlation matrix supplied by <code>SelectBoost</code> is reused after applying the FDA-specific masks.
method	Grouping strategy. "threshold" wraps <code>SelectBoost::group_func_1()</code> and "community" wraps <code>SelectBoost::group_func_2()</code> .
association_method	Association structure passed to <code>functional_association()</code> .
within_blocks	Should groups be restricted to features coming from the same functional block?
bandwidth	Optional maximum within-block lag retained in groups.
interval_groups, width, step, decay	Additional arguments passed to <code>functional_association()</code> when using region-aware associations.

**Value**

A function with signature `(absXcor, c0)` compatible with `SelectBoost`.

---

 motion\_example

*Smooth Trajectory Functional Example*


---

**Description**

Simulated smooth trajectories used to demonstrate spline-basis and FPCA preprocessing from raw curves.

**Usage**

```

motion_example

```

**Format**

A list with four components:

**grid** Numeric vector of observation times.

**response** Numeric response vector.

**predictors** Named list of functional predictor matrices.

**scalar\_covariates** Data frame with scalar covariates.

**Source**

Simulated for package examples.

---

plain\_selectboost      *Plain SelectBoost Baseline for Functional Predictors*

---

**Description**

Runs `SelectBoost` directly on the flattened predictor matrix without the FDA-specific grouping heuristics used by `selectboost_fda()`. This is useful as a benchmark against the FDA-aware variant.

**Usage**

```
plain_selectboost(
  x,
  y = NULL,
  mode = c("fast", "auto"),
  selector = "msgps",
  selector_fun = NULL,
  selector_args = list(),
  groups = NULL,
  family = c("gaussian", "binomial"),
  association = NULL,
  group_method = c("threshold", "community"),
  ...
)
```

**Arguments**

<code>x</code>	Any input accepted by <code>as_functional_matrix()</code> , or an <code>fda_design</code> object.
<code>y</code>	Response vector. Leave as <code>NULL</code> when <code>x</code> is an <code>fda_design</code> .
<code>mode</code>	"fast" for a fixed <code>c0</code> grid or "auto" for the adaptive version.
<code>selector</code>	Base selector used inside <code>SelectBoost</code> . Choose from "msgps", "lasso", "group_lasso", "sparse_group_lasso", the backend-specific aliases "glmnet", "grpreg", "sgl", or provide a custom function.

selector_fun	Optional custom base selector. It must return a coefficient vector of length $p$ .
selector_args	Optional named list of arguments forwarded to the base selector.
groups	Optional feature groups used by grouped base selectors such as "grpreg". Defaults to block-level groups for list inputs.
family	Model family passed to built-in selectors.
association	Optional absolute association matrix used directly by the raw SelectBoost grouping function.
group_method	Functional grouping backend: threshold-based or community-based.
...	Additional arguments passed to <code>SelectBoost::fastboost()</code> or <code>SelectBoost::autoboost()</code> .

**Value**

An object of class `plain_selectboost_result`.

---

`plot.fda_selection`      *Plot FDA Selection Results*

---

**Description**

Plots feature-, group-, interval-, and basis-level summaries derived from `selection_map()`. The available views depend on the fitted object:

**Usage**

```
## S3 method for class 'fda_stability_selection'
plot(
  x,
  type = c("feature", "group", "interval", "basis"),
  value = c("group", "mean", "max"),
  facet = c("none", "predictor"),
  palette = selection_palette(),
  show_legend = TRUE,
  legend_title = NULL,
  legend_n_ticks = 3L,
  legend_digits = 2L,
  legend_cex = 0.75,
  cutoff = x$cutoff,
  ...
)

## S3 method for class 'selectboost_fda_result'
plot(
  x,
  type = c("feature", "group", "basis"),
  value = c("max", "mean"),
```

```

palette = selection_palette(),
show_legend = TRUE,
legend_title = NULL,
legend_n_ticks = 3L,
legend_digits = 2L,
legend_cex = 0.75,
c0 = NULL,
...
)

```

### Arguments

x	An object returned by <code>stability_selection_fda()</code> , <code>interval_stability_selection()</code> , <code>fit_stability()</code> , <code>selectboost_fda()</code> , or <code>fit_selectboost()</code> .
type	Summary view to plot. Stability-selection fits support "feature", "group", "interval", and "basis". SelectBoost fits support "feature", "group", and "basis".
value	Quantity summarized in group, interval, and basis views. Stability-selection fits accept "group", "mean", and "max". SelectBoost fits accept "mean" and "max".
facet	Faceting mode for interval heatmaps. Currently only type = "interval" uses this argument.
palette	Vector of colors used for heatmaps.
show_legend	Logical; should heatmap views draw a legend?
legend_title	Optional legend title for heatmap views. By default an informative title is chosen from type and value.
legend_n_ticks	Approximate number of tick marks used in the heatmap legend.
legend_digits	Number of significant digits used for heatmap legend labels.
legend_cex	Character expansion used for heatmap legend text.
cutoff	Stability threshold. Only used for <code>fda_stability_selection</code> objects.
...	Additional graphical parameters passed to bar-plot-based views.
c0	Optional SelectBoost correlation threshold. When omitted, SelectBoost heatmaps are drawn across all available <code>c0</code> values.

### Details

- `fda_stability_selection` supports type = "feature", "group", "interval", and "basis".
- `selectboost_fda_result` supports type = "feature", "group", and "basis".

Heatmap-based views are used for interval summaries and for SelectBoost summaries over multiple `c0` values. Bar-plot views are used otherwise.

### Value

Invisibly returns the helper output used to build the plot.

### See Also

[selection\\_map\(\)](#)

---

run\_selectboost\_sensitivity\_study

*Run a Targeted Sensitivity Study for FDA-SelectBoost*


---

## Description

Repeats the FDA benchmark over a grid of simulation settings and a grid of FDA-aware SelectBoost settings. This is intended to answer the specific benchmark question of when selectboost\_fda() improves on plain SelectBoost.

## Usage

```
run_selectboost_sensitivity_study(
  n_rep = 10L,
  simulate_grid = expand.grid(scenario = c("localized_dense", "confounded_blocks"),
    confounding_strength = c(0.4, 0.9), active_region_scale = c(1, 0.7),
    local_correlation = c(0, 2), stringsAsFactors = FALSE),
  selectboost_grid = expand.grid(association_method = c("correlation", "neighborhood",
    "hybrid", "interval"), bandwidth = c(NA, 4, 8), stringsAsFactors = FALSE),
  simulate_args = list(),
  benchmark_args = list(),
  seed = NULL,
  keep_results = FALSE
)
```

## Arguments

n_rep	Number of replications per setting combination.
simulate_grid	Data frame of simulation-setting combinations. Columns are merged into simulate_args and can include scenario, confounding_strength, active_region_scale, and local_correlation.
selectboost_grid	Data frame of selectboost_fda() setting combinations. Columns are merged into benchmark_args\$selectboost_args and can include association_method, bandwidth, width, or step.
simulate_args	Named list forwarded to simulate_fda_scenario().
benchmark_args	Named list forwarded to benchmark_selection_methods(). When omitted, the study compares FDA-aware SelectBoost, plain SelectBoost, and grouped stability selection.
seed	Optional seed used to derive deterministic per-replication and per-setting seeds.
keep_results	Should the individual benchmark objects be returned?

## Value

An object inheriting from fda\_selectboost\_sensitivity\_study and fda\_simulation\_study.

**Examples**

```

grid <- data.frame(
  scenario = "confounded_blocks",
  confounding_strength = 0.9,
  active_region_scale = 0.7,
  local_correlation = 2,
  stringsAsFactors = FALSE
)
methods <- data.frame(
  association_method = c("correlation", "hybrid"),
  bandwidth = c(NA, 4),
  stringsAsFactors = FALSE
)
study <- run_selectboost_sensitivity_study(
  n_rep = 1,
  simulate_grid = grid,
  selectboost_grid = methods,
  simulate_args = list(n = 24, grid_length = 16),
  benchmark_args = list(
    methods = c("selectboost", "plain_selectboost"),
    levels = "feature",
    selectboost_args = list(B = 3, steps.seq = 0.5, c0lim = FALSE),
    plain_selectboost_args = list(B = 3, steps.seq = 0.5, c0lim = FALSE)
  ),
  seed = 1
)
summarise_benchmark_advantage(
  study,
  target = "selectboost",
  reference = "plain_selectboost",
  level = "feature"
)

```

---

run\_simulation\_study *Run a Repeated FDA Simulation Study*

---

**Description**

Repeats `simulate_fda_scenario()` and `benchmark_selection_methods()` over multiple replications and aggregates the resulting recovery metrics.

**Usage**

```

run_simulation_study(
  n_rep = 10L,
  simulate_args = list(),
  benchmark_args = list(),
  seed = NULL,
  keep_results = FALSE
)

```

**Arguments**

n_rep	Number of simulation replications.
simulate_args	Named list forwarded to <code>simulate_fda_scenario()</code> .
benchmark_args	Named list forwarded to <code>benchmark_selection_methods()</code> .
seed	Optional seed used to derive deterministic per-replication seeds.
keep_results	Should the individual benchmark objects be returned?

**Value**

An object of class `fda_simulation_study`.

---

selectboost_fda	<i>FDA-Oriented SelectBoost Wrapper</i>
-----------------	---

---

**Description**

Wraps `SelectBoost::fastboost()` or `SelectBoost::autoboost()` while adding FDA-specific structure through block-aware and region-aware grouping.

**Usage**

```
selectboost_fda(
  x,
  y = NULL,
  mode = c("fast", "auto"),
  selector = "msgps",
  selector_fun = NULL,
  selector_args = list(),
  groups = NULL,
  family = c("gaussian", "binomial"),
  association = NULL,
  group_method = c("threshold", "community"),
  association_method = c("correlation", "neighborhood", "hybrid", "interval"),
  within_blocks = TRUE,
  bandwidth = NULL,
  interval_groups = NULL,
  width = NULL,
  step = width,
  decay = 1,
  ...
)
```

**Arguments**

x	Any input accepted by <code>as_functional_matrix()</code> , or an <code>fda_design</code> object.
y	Response vector. Leave as NULL when x is an <code>fda_design</code> .
mode	"fast" for a fixed $c_0$ grid or "auto" for the adaptive version.
selector	Base selector used inside SelectBoost. Choose from "msgps", "lasso", "group_lasso", "sparse_group_lasso", the backend-specific aliases "glmnet", "grpreg", "sgl", or provide a custom function.
selector_fun	Optional custom base selector. It must return a coefficient vector of length p.
selector_args	Optional named list of arguments forwarded to the base selector.
groups	Optional feature groups used by grouped base selectors such as "grpreg". Defaults to block-level groups for list inputs.
family	Model family passed to built-in selectors.
association	Optional custom association matrix used to define FDA-aware groups.
group_method	Functional grouping backend: threshold-based or community-based.
association_method	Association structure used to build FDA-aware groups.
within_blocks	Should SelectBoost groups stay within functional blocks?
bandwidth	Optional maximum within-block lag retained in groups.
interval_groups, width, step, decay	Additional arguments passed to <code>make_functional_grouping_function()</code> .
...	Additional arguments passed to <code>SelectBoost::fastboost()</code> or <code>SelectBoost::autoboost()</code> .

**Value**

An object of class `selectboost_fda_result`.

---

selected	<i>Extract Selected Features or Groups</i>
----------	--

---

**Description**

Returns the selected rows from `selection_map()` for stability-selection or SelectBoost fits.

**Usage**

```
selected(x, ...)
```

**Arguments**

x	A fitted selection object.
...	Additional arguments passed to the relevant method.

**Value**

A data frame.

---

selection_map	<i>Feature-Level Selection Map</i>
---------------	------------------------------------

---

**Description**

Returns a feature map augmented with selection summaries from a fit object.

**Usage**

```
selection_map(x, level = c("feature", "group", "basis"), ...)
```

**Arguments**

x	An <code>fda_design</code> , <code>fda_stability_selection</code> , or <code>selectboost_fda_result</code> object.
level	Summary level. "feature" returns one row per coefficient, "group" returns one row per stability/interval group, and "basis" returns one row per basis-expanded predictor.
...	Additional arguments passed to the relevant method.

**Value**

A data frame.

---

simulate_fda_scenario	<i>Simulate an FDA Benchmark Scenario</i>
-----------------------	---

---

**Description**

Generates raw functional predictors, scalar covariates, a response, and the mapped ground truth for the transformed design matrix.

**Usage**

```
simulate_fda_scenario(
  n = 80L,
  grid_length = 60L,
  family = c("gaussian", "binomial"),
  representation = c("grid", "basis", "fpca"),
  transforms = NULL,
  basis_df = 7L,
  n_components = 5L,
  scenario = c("localized_dense", "distributed_smooth", "confounded_blocks"),
  confounding_strength = NULL,
  active_region_scale = 1,
```

```

    local_correlation = 0,
    include_scalar = TRUE,
    noise_sd = 0.4,
    seed = NULL
  )

```

### Arguments

<code>n</code>	Number of observations.
<code>grid_length</code>	Number of grid points per functional predictor.
<code>family</code>	Model family used to generate the response.
<code>representation</code>	Representation used when building the returned <code>fda_design()</code> : "grid" keeps the raw curves, "basis" applies a spline-basis transform, and "fpca" applies FPCA scores.
<code>transforms</code>	Optional transform list passed to <code>fda_design()</code> . When omitted, a sensible default is chosen from representation.
<code>basis_df</code>	Degrees of freedom used when representation = "basis".
<code>n_components</code>	Number of FPCA components used when representation = "fpca".
<code>scenario</code>	Benchmark scenario. "localized_dense" emphasizes narrow active regions under strong local correlation, "distributed_smooth" spreads the effect over broader smooth regions, and "confounded_blocks" adds stronger nuisance structure near the active block.
<code>confounding_strength</code>	Strength of cross-block confounding injected into the nuisance curve. Higher values make plain SelectBoost less able to separate true local signals from correlated nuisance structure.
<code>active_region_scale</code>	Positive multiplier applied to the width of the active regions. Values below 1 create narrower active regions.
<code>local_correlation</code>	Non-negative smoothing parameter applied to the simulated curves. Larger values increase local correlation along the grid.
<code>include_scalar</code>	Should scalar covariates be included in the design and truth object?
<code>noise_sd</code>	Observation noise level.
<code>seed</code>	Optional random seed.

### Value

An object of class `fda_simulation_data`.

### Examples

```

sim <- simulate_fda_scenario(n = 24, grid_length = 16, seed = 1)
sim
head(sim$truth$active_features)

```

---

spectra_example	<i>Spectroscopy-Style Functional Example</i>
-----------------	--

---

**Description**

Simulated dense spectra with one signal block, one nuisance block, and two scalar covariates. The response is continuous and depends on localized regions of the signal spectrum plus the scalar covariates.

**Usage**

```
spectra_example
```

**Format**

A list with four components:

**grid** Numeric vector of wavelength locations.

**response** Numeric response vector.

**predictors** Named list of functional predictor matrices.

**scalar\_covariates** Data frame with scalar covariates.

**Source**

Simulated for package examples.

---

stability_selection_fda	<i>Grouped Stability Selection for Functional Predictors</i>
-------------------------	--

---

**Description**

Repeatedly subsamples observations, refits a sparse base selector, and computes exact feature- and group-level selection frequencies. This is the generic FDA recipe for basis expansions, discretized curves, or FPCA scores.

**Usage**

```
stability_selection_fda(  
  x,  
  y = NULL,  
  selector = "group_lasso",  
  selector_fun = NULL,  
  groups = NULL,  
  family = c("gaussian", "binomial"),
```

```

    B = 100L,
    sample_fraction = 0.5,
    cutoff = 0.75,
    seed = NULL,
    keep_subsamples = FALSE,
    ...
)

```

### Arguments

x	Any input accepted by <code>as_functional_matrix()</code> , or an <code>fda_design</code> object.
y	Response vector. Leave as <code>NULL</code> when x is an <code>fda_design</code> .
selector	Either "lasso", "group_lasso", "sparse_group_lasso", one of the backend-specific aliases ("glmnet", "grpreg", "sgl"), or a custom function.
selector_fun	Optional custom selector. It must accept X, y, groups, and family, and return either a coefficient vector or a logical selection vector of length p.
groups	Optional grouping structure. Defaults to block-level groups when x is supplied as a list, and otherwise to one group per feature.
family	Model family passed to the built-in selectors.
B	Number of subsampling replicates.
sample_fraction	Fraction of observations drawn without replacement in each subsample.
cutoff	Stability threshold used to define <code>selected_features</code> and <code>selected_groups</code> .
seed	Optional random seed.
keep_subsamples	Should the sampled row indices be returned?
...	Additional arguments forwarded to the built-in or custom selector.

### Value

An object of class `fda_stability_selection`.

---

suggest_c0_grid	<i>Suggest a c0 Grid for FDA-SelectBoost</i>
-----------------	--

---

### Description

Builds a data-driven `c0` grid from an FDA-aware association matrix.

**Usage**

```
suggest_c0_grid(
  x,
  n = 5L,
  method = c("quantile", "linear"),
  association_method = c("correlation", "neighborhood", "hybrid", "interval"),
  within_blocks = TRUE,
  bandwidth = NULL,
  interval_groups = NULL,
  width = NULL,
  step = width,
  decay = 1
)
```

**Arguments**

`x` Any input accepted by `as_functional_matrix()`.

`n` Number of grid values to return.

`method` Grid construction rule: "quantile" or "linear".

`association_method` Association structure passed to `functional_association()`.

`within_blocks`, `bandwidth`, `interval_groups`, `width`, `step`, `decay` Passed to `functional_association()`.

**Value**

A decreasing numeric vector of  $c_0$  values.

---

summarise\_benchmark\_advantage

*Summarize the Advantage of FDA-SelectBoost Over Baselines*

---

**Description**

Computes the per-scenario and per-level gain of a target method over one or more reference methods. This is intended to make the benchmark story explicit when comparing FDA-aware SelectBoost to existing baselines.

**Usage**

```
summarise_benchmark_advantage(
  x,
  target = "selectboost",
  reference = c("plain_selectboost", "stability"),
  level = c("feature", "group", "basis"),
  metric = "f1",
```

```

  optimize = c("max", "min"),
  select_c0 = c("best", "all")
)

```

### Arguments

x	An <code>fda_benchmark</code> or <code>fda_simulation_study</code> object.
target	Method whose gain should be assessed.
reference	One or more baseline methods.
level	Evaluation level.
metric	Metric used both for best- <code>c0</code> selection and for the reported gains.
optimize	Should larger or smaller values of <code>metric</code> be preferred?
select_c0	Keep all <code>c0</code> rows or only the best one per method and replicate.

### Value

A data frame.

---

```
summarise_benchmark_performance
```

*Summarize Benchmark Performance by Method*

---

### Description

Collapses raw benchmark rows into method-level performance summaries, with an option to retain only the best `c0` per method and replication.

### Usage

```

summarise_benchmark_performance(
  x,
  level = c("feature", "group", "basis"),
  metric = "f1",
  optimize = c("max", "min"),
  select_c0 = c("best", "all")
)

```

### Arguments

x	An <code>fda_benchmark</code> or <code>fda_simulation_study</code> object.
level	Evaluation level.
metric	Metric used to pick the best <code>c0</code> when <code>select_c0 = "best"</code> .
optimize	Should larger or smaller values of <code>metric</code> be preferred?
select_c0	Keep all <code>c0</code> rows or only the best one per method and replicate.

**Value**

A data frame.

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