

# Package: forestsearch (via r-universe)

May 23, 2026

**Title** Exploratory Subgroup Identification in Clinical Trials with Survival Endpoints

**Version** 0.1.0

**Description** Implements statistical methods for exploratory subgroup identification in clinical trials with survival endpoints. Provides tools for identifying patient subgroups with differential treatment effects using machine learning approaches including Generalized Random Forests (GRF), LASSO regularization, and exhaustive combinatorial search algorithms. Features bootstrap bias correction using infinitesimal jackknife methods to address selection bias in post-hoc analyses. Designed for clinical researchers conducting exploratory subgroup analyses in randomized controlled trials, particularly for multi-regional clinical trials (MRCT) requiring regional consistency evaluation. Supports both accelerated failure time (AFT) and Cox proportional hazards models with comprehensive diagnostic and visualization tools. Methods are described in León et al. (2024) <doi:10.1002/sim.10163>.

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`build_classification_table`

*Build Classification Rate Table from Simulation Results*

**Description**

Constructs a publication-quality gt table summarizing subgroup identification and classification rates across one or more data generation scenarios and analysis methods. The layout mirrors Table 4 of Leon et al. (2024) with metrics grouped by model scenario (null / alt) and columns for each analysis method.

**Usage**

```
build_classification_table(
  scenario_results,
  analyses = NULL,
  digits = 2,
  title = "Subgroup Identification and Classification Rates",
  n_sims = NULL,
  bold_threshold = 0.05,
  font_size = 12
)
```

**Arguments**

scenario_results	Named list. Each element is itself a list with: <b>results</b> data.table from <a href="#">run_simulation_analysis</a> . <b>label</b> Character scenario label, e.g., "M1". <b>n_sample</b> Integer sample size. <b>dgm</b> DGM object (for true HRs and subgroup prevalence). <b>hypothesis</b> Character: "null" or "alt".
analyses	Character vector of analysis labels to include (e.g., c("FS", "FSlg", "GRF")). When NULL, all unique values of results\$analysis across scenarios are used.
digits	Integer. Decimal places for proportions. Default: 2.
title	Character. Table title. Default: "Subgroup Identification and Classification Rates".
n_sims	Integer. Number of simulations (for subtitle). Default: NULL.
bold_threshold	Numeric. Type I error threshold above which the any(H) value is shown in bold. Set NULL to disable. Default: 0.05.
font_size	Numeric. Font size in pixels for table text. Default: 12. Increase to 14 or 16 for larger display.

**Details**

For each scenario the function computes:

- any(H): Proportion of simulations identifying any subgroup.
- sens(H): Mean sensitivity (only under alternative).
- sens(Hc): Mean specificity.
- ppv(H): Mean positive predictive value (only under alternative).
- ppv(Hc): Mean negative predictive value.
- avg|H|: Mean size of identified subgroup (when found).

Under the null hypothesis the rows are reduced to any(H), sens(Hc), ppv(Hc), and avg|H|.

**Value**

A gt table object.

**See Also**

[format\\_oc\\_results](#), [summarize\\_simulation\\_results](#)

---

 build\_estimation\_table

*Build Estimation Properties Table from Simulation Results*


---

### Description

Constructs a publication-quality gt table summarizing estimation properties for hazard ratios in the identified subgroup and its complement. The layout mirrors Table 5 of Leon et al. (2024), showing average estimate, empirical SD, min, max, and relative bias for each estimator.

### Usage

```
build_estimation_table(
  results,
  dgm,
  analysis_method = "FS1g",
  n_boots = NULL,
  digits = 2,
  title = "Estimation Properties",
  subtitle = NULL,
  font_size = 12,
  cde_H = NULL,
  cde_Hc = NULL
)
```

### Arguments

results	data.table or data.frame. Simulation results from <a href="#">run_simulation_analysis</a> , optionally enriched with bootstrap bias-corrected columns (hr.H.bc, hr.Hc.bc).
dgm	DGM object. Used for true parameter values (hr_H_true, hr_Hc_true, and AHR truth via <a href="#">get_dgm_hr</a> ).
analysis_method	Character. Which analysis method to tabulate (e.g., "FS1g"). Default: "FS1g".
n_boots	Integer or NULL. Number of bootstraps. When non-NULL, appended to the subtitle as "(B = n_boots bootstraps)". Default: NULL.
digits	Integer. Decimal places. Default: 2.
title	Character. Table title.
subtitle	Character or NULL. Optional user-supplied subtitle text. Auto-populated statistics (method, estimable count, proportion) are always shown. When non-NULL, the custom text is displayed first with stats appended in parentheses, e.g. "My title (FS1g: 18/20 (90%) estimable)".
font_size	Numeric. Font size in pixels for table text. Default: 12. Increase to 14 or 16 for larger display.

cde_H	Numeric or NULL. Controlled direct effect (theta-ddagger(H)) for the true harm subgroup. When non-NULL, an additional b-ddagger bias column is shown. When NULL (default), auto-detected from dgm\$cde_H or dgm\$hazard_ratios\$CDE_harm.
cde_Hc	Numeric or NULL. Controlled direct effect for the complement. Auto-detected analogously.

### Details

Uses the paper's notation conventions:

- theta-dagger: Marginal (causal) HR truth
- theta-ddagger: Controlled direct effect (CDE) truth
- theta-hat(H-hat): Plugin Cox estimate in identified subgroup
- theta-hat\*(H-hat): Bootstrap bias-corrected estimate

Includes both Cox-based HR and AHR (Average Hazard Ratio from loghr\_po) estimators when AHR columns are present in the results.

For each subgroup (H and Hc) the function reports:

- **Avg**: Mean of the estimates across estimable simulations.
- **SD**: Empirical standard deviation.
- **Min / Max**: Range.
- **b-dagger**: Relative bias (percent) vs marginal truth,  $100 * (Avg - \text{theta\_dagger}) / \text{theta\_dagger}$ .
- **b-ddagger** (conditional): Relative bias (percent) vs CDE truth, shown when CDE values are available.

When bootstrap-corrected columns (hr.H.bc, hr.Hc.bc) are present in results, an additional bias-corrected row (theta-hat\*(H-hat)) is added per subgroup.

When AHR columns (ahr.H.hat, ahr.Hc.hat) are present, AHR estimation rows are appended using the DGM's true AHR values for relative bias calculation.

When CDE columns (cde.H.hat, cde.Hc.hat) are present and CDE truth values are available, CDE estimation rows (theta-ddagger(H-hat)) are appended. The b-dagger column for CDE rows reports bias relative to the CDE truth rather than the marginal HR.

### Value

A gt table object, or NULL if no estimable realizations exist.

### See Also

[build\\_classification\\_table](#), [format\\_oc\\_results](#), [get\\_dgm\\_hr](#)

---

calibrate\_cens\_adjust *Calibrate Censoring Adjustment to Match DGM Reference Distribution*

---

## Description

Uses root-finding to select a value of `cens_adjust` for `simulate_from_dgm` such that a chosen censoring summary statistic in the simulated data matches the corresponding statistic from the DGM reference data (`dgm$df_super`).

## Usage

```
calibrate_cens_adjust(
  dgm,
  target = c("rate", "km_median"),
  n = 1000,
  rand_ratio = 1,
  analysis_time = 48,
  max_entry = 24,
  seed = 42,
  interval = c(-3, 3),
  tol = 1e-04,
  n_eval = 2000,
  verbose = TRUE,
  ...
)
```

## Arguments

<code>dgm</code>	An "aft_dgm_flex" object from <code>generate_aft_dgm_flex</code> .
<code>target</code>	Character. Calibration target: "rate" (default) or "km_median".
<code>n</code>	Integer. Sample size passed to <code>simulate_from_dgm</code> . Default 1000.
<code>rand_ratio</code>	Numeric. Randomisation ratio passed to <code>simulate_from_dgm</code> . Default 1.
<code>analysis_time</code>	Numeric. Calendar analysis time passed to <code>simulate_from_dgm</code> . Must be on the DGM time scale. Default 48.
<code>max_entry</code>	Numeric. Maximum staggered entry time passed to <code>simulate_from_dgm</code> . Default 24.
<code>seed</code>	Integer. Base random seed. Each evaluation of the objective function uses this seed for reproducibility. Default 42.
<code>interval</code>	Numeric vector of length 2. Search interval for <code>cens_adjust</code> on the log scale. Default <code>c(-3, 3)</code> (corresponding roughly to a 20-fold decrease/increase in censoring times).
<code>tol</code>	Numeric. Root-finding tolerance. Default <code>1e-4</code> .
<code>n_eval</code>	Integer. Sample size used inside the objective function during root-finding. Smaller values are faster but noisier; increase for precision. Default 2000.

verbose Logical. Print search progress and final result. Default TRUE.  
 ... Additional arguments passed to `simulate_from_dgm` (e.g. `strata_rand`, `time_eos`).

### Details

Two calibration targets are supported:

"rate" Overall censoring rate (proportion censored). Finds `cens_adjust` such that `mean(event_sim == 0)` in simulated data equals `mean(event == 0)` in `dgm$df_super`.

"km\_median" KM-based median censoring time, estimated by reversing the event indicator so censored observations become the "event" of interest. Finds `cens_adjust` such that the simulated KM median matches the reference KM median.

#### How the objective function works:

At each candidate `cens_adjust` value, the objective function:

1. Calls `simulate_from_dgm()` with `n = n_eval` and the candidate `cens_adjust`.
2. Calls `check_censoring_dgm()` with `verbose = FALSE` to extract the target metric.
3. Returns `sim_metric - ref_metric`.

`uniroot` finds the zero crossing, i.e. the `cens_adjust` at which simulated and reference metrics are equal.

#### Monotonicity:

The objective is monotone in `cens_adjust` for both targets:

- Larger `cens_adjust` → longer censoring times → lower censoring rate and higher KM median.
- Smaller `cens_adjust` → shorter censoring times → higher censoring rate and lower KM median.

If `uniroot` fails (the target lies outside the search interval), the boundary values are printed and a wider interval should be tried.

#### Stochastic noise:

Because the objective function involves simulation, there is Monte Carlo noise. Setting a fixed seed and a sufficiently large `n_eval` ( $\geq 2000$ ) reduces noise enough for reliable root-finding. The `tol` argument controls the root-finding tolerance on the `cens_adjust` scale (not the metric scale).

### Value

A named list with elements:

`cens_adjust` Calibrated `cens_adjust` value.

`target` Calibration target used.

`ref_value` Reference metric value from `dgm$df_super`.

`sim_value` Achieved metric value in simulated data at the calibrated `cens_adjust`.

`residual` Absolute difference between `sim_value` and `ref_value`.

`iterations` Number of `uniroot` iterations.

`diagnostic` Output of `check_censoring_dgm` at the calibrated value (invisibly).

**See Also**

[simulate\\_from\\_dgm](#), [check\\_censoring\\_dgm](#), [generate\\_aft\\_dgm\\_flex](#)

**Examples**

```
library(survival)

# Build DGM on months scale
gbsg$time_months <- gbsg$rfstime / 30.4375

dgm <- generate_aft_dgm_flex(
  data = gbsg,
  continuous_vars = c("age", "size", "nodes", "pgr", "er"),
  factor_vars = c("meno", "grade"),
  outcome_var = "time_months",
  event_var = "status",
  treatment_var = "hormon",
  subgroup_vars = c("er", "meno"),
  subgroup_cuts = list(er = 20, meno = 0)
)

# Calibrate so simulated censoring rate matches reference
cal_rate <- calibrate_cens_adjust(
  dgm = dgm,
  target = "rate",
  n = 1000,
  analysis_time = 84,
  max_entry = 24
)
cat("Calibrated cens_adjust (rate):", cal_rate$cens_adjust, "\n")

# Calibrate to KM median censoring time instead
cal_km <- calibrate_cens_adjust(
  dgm = dgm,
  target = "km_median",
  n = 1000,
  analysis_time = 84,
  max_entry = 24
)
cat("Calibrated cens_adjust (km_median):", cal_km$cens_adjust, "\n")

# Use calibrated value in simulation
sim <- simulate_from_dgm(
  dgm = dgm,
  n = 1000,
  analysis_time = 84,
  max_entry = 24,
  cens_adjust = cal_rate$cens_adjust,
  seed = 123
)
mean(sim$event_sim) # event rate
mean(sim$event_sim == 0) # censoring rate - should match ref
```

---

calibrate\_k\_inter      *Calibrate k\_inter for Target Subgroup Hazard Ratio*

---

### Description

Finds the interaction effect multiplier (`k_inter`) that achieves a target hazard ratio in the harm subgroup.

### Usage

```
calibrate_k_inter(
  target_hr_harm,
  model = "alt",
  k_treat = 1,
  cens_type = "weibull",
  k_inter_range = c(-100, 100),
  tol = 1e-06,
  use_ahr = FALSE,
  verbose = FALSE,
  ...
)
```

### Arguments

<code>target_hr_harm</code>	Numeric. Target hazard ratio for the harm subgroup
<code>model</code>	Character. Model type ("alt" only). Default: "alt"
<code>k_treat</code>	Numeric. Treatment effect multiplier. Default: 1
<code>cens_type</code>	Character. Censoring type. Default: "weibull"
<code>k_inter_range</code>	Numeric vector of length 2. Search range for <code>k_inter</code> . Default: <code>c(-100, 100)</code>
<code>tol</code>	Numeric. Tolerance for root finding. Default: <code>1e-6</code>
<code>use_ahr</code>	Logical. If TRUE, calibrate to AHR instead of Cox-based HR. Default: FALSE
<code>verbose</code>	Logical. Print diagnostic information. Default: FALSE
<code>...</code>	Additional arguments passed to <a href="#">create_gbsg_dgm</a>

### Details

This function uses `uniroot` to find the `k_inter` value such that the empirical HR (or AHR) in the harm subgroup equals `target_hr_harm`.

### Value

Numeric value of `k_inter` that achieves the target HR

**Examples**

```
# Find k_inter for HR = 1.5 in harm subgroup
k <- calibrate_k_inter(target_hr_harm = 1.5, verbose = TRUE)

# Verify
dgm <- setup_gbsg_dgm(model = "alt", k_inter = k, verbose = FALSE)
print(dgm)

# Calibrate to AHR instead
k_ahr <- calibrate_k_inter(target_hr_harm = 1.5, use_ahr = TRUE, verbose = TRUE)
dgm_ahr <- setup_gbsg_dgm(model = "alt", k_inter = k_ahr, verbose = FALSE)
print(dgm_ahr)
```

---

check_censoring_dgm	<i>Diagnose Censoring Consistency Between DGM Source Data and Simulated Data</i>
---------------------	--

---

**Description**

Compares the censoring distribution observed in the data used to build the DGM against the censoring generated by [simulate\\_from\\_dgm](#). Reports censoring rates, time quantiles, KM-based median censoring times, and flags substantial discrepancies.

**Usage**

```
check_censoring_dgm(
  sim_data,
  dgm,
  treat_var = "treat_sim",
  rate_tol = 0.1,
  median_tol = 0.25,
  verbose = TRUE
)
```

**Arguments**

sim_data	A data.frame returned by <a href="#">simulate_from_dgm</a> .
dgm	An "aft_dgm_flex" object from <a href="#">generate_aft_dgm_flex</a> . The super population (dgm\$df_super) provides reference censoring times and event indicators on the DGM time scale.
treat_var	Character. Name of the treatment column in sim_data used for arm-stratified comparisons. Default "treat_sim".
rate_tol	Numeric. Absolute tolerance (proportion scale) for flagging a censoring-rate discrepancy. Default 0.10 (10 pp).

median_tol	Numeric. Relative tolerance for flagging a KM median censoring-time discrepancy. Default 0.25 (25 percent).
verbose	Logical. If TRUE, prints the full diagnostic table. Default TRUE.

### Details

The reference censoring distribution is derived from `dgm$df_super`, sampled with replacement from the data passed to `generate_aft_dgm_flex()`. Columns `y` (observed time) and `event` (event indicator) in `df_super` reflect the original observed censoring process on the DGM time scale.

The KM median censoring time is estimated by reversing the event indicator ( $1 - \text{event}$ ), treating events as censored and censored observations as the event of interest. This gives a non-parametric estimate of the censoring time distribution unconfounded by event occurrence.

Common causes of discrepancy: (1) time-scale mismatch (DGM built on days, `analysis_time` in months); check `exp(dgm$model_params$mu)` against your `analysis_time`. (2) Large `cens_adjust` shifting censoring substantially from the fitted model. (3) Short `analysis_time` or `time_eos` making administrative censoring dominate the censoring process.

### Value

Invisibly returns a named list. Elements are: `rates` (data frame of censoring rates overall and by arm); `quantiles` (data frame of censoring-time quantiles among censored subjects); `km_medians` (data frame of KM-based median censoring times); and `flags` (character vector of triggered warnings, empty if none).

### See Also

[simulate\\_from\\_dgm](#), [generate\\_aft\\_dgm\\_flex](#)

### Examples

```
dgm <- setup_gbsg_dgm(model = "null", verbose = FALSE)
sim_data <- simulate_from_dgm(dgm, n = 200)
check_censoring_dgm(sim_data, dgm = dgm)
```

---

compute\_detection\_probability

*Compute Probability of Detecting True Subgroup*

---

### Description

Calculates the probability that a true subgroup with given hazard ratio will be detected using the ForestSearch consistency-based criteria.

**Usage**

```
compute_detection_probability(
  theta,
  n_sg,
  prop_cens = 0.3,
  hr_threshold = 1.25,
  hr_consistency = 1,
  method = c("cubature", "monte_carlo"),
  n_mc = 100000L,
  tol = 1e-04,
  verbose = FALSE
)
```

**Arguments**

theta	Numeric. True hazard ratio in the subgroup. Can be a vector for computing detection probability across multiple HR values.
n_sg	Integer. Subgroup sample size.
prop_cens	Numeric. Proportion censored (0-1). Default: 0.3
hr_threshold	Numeric. HR threshold for detection (e.g., 1.25). This is the threshold that the average HR across splits must exceed.
hr_consistency	Numeric. HR consistency threshold (e.g., 1.0). This is the threshold each individual split must exceed. Default: 1.0
method	Character. Integration method: "cubature" (recommended for accuracy) or "monte_carlo" (faster for exploration). Default: "cubature"
n_mc	Integer. Number of Monte Carlo samples if method = "monte_carlo". Default: 100000
tol	Numeric. Relative tolerance for cubature integration. Default: 1e-4
verbose	Logical. Print progress for vector inputs. Default: FALSE

**Details**

This function computes  $P(\text{detect} \mid \theta)$  using the asymptotic normal approximation for the log hazard ratio estimator. The detection criterion is based on ForestSearch's split-sample consistency evaluation:

1. The subgroup HR estimate must exceed `hr_threshold` on average
2. Each split-half must individually exceed `hr_consistency`

The approximation assumes:

- Large sample sizes (CLT applies)
- $\text{Var}(\log(\text{HR})) \sim 4/d$  per treatment arm
- Independence between split-halves (conditional on true effect)

**Value**

If theta is scalar, returns a single probability. If theta is a vector, returns a data.frame with columns: theta, probability.

**Examples**

```
# Single HR value
prob <- compute_detection_probability(
  theta = 1.5,
  n_sg = 60,
  prop_cens = 0.2,
  hr_threshold = 1.25
)

# Vector of HR values for power curve
hr_values <- seq(1.0, 2.5, by = 0.1)
results <- compute_detection_probability(
  theta = hr_values,
  n_sg = 60,
  prop_cens = 0.2,
  hr_threshold = 1.25,
  verbose = TRUE
)

# Plot detection probability curve
plot(results$theta, results$probability, type = "l",
      xlab = "True HR", ylab = "P(detect)")
```

---

compute\_dgm\_cde

*Compute and Attach CDE Values to a DGM Object*


---

**Description**

Calculates Controlled Direct Effect (CDE) hazard ratios from the super-population potential outcomes (theta\_0, theta\_1) and attaches them to the DGM's hazard\_ratios list. This enables automatic CDE detection by [build\\_estimation\\_table](#).

**Usage**

```
compute_dgm_cde(dgm, harm_col = NULL)
```

**Arguments**

dgm	A DGM object (e.g., from create_gbsg_dgm or generate_aft_dgm_flex). Must contain df_super_rand with columns theta_0 and theta_1.
harm_col	Character. Name of the subgroup indicator column in dgm\$df_super_rand. If NULL (default), auto-detected from flag.harm, flag_harm, or H.

**Details**

The CDE for subgroup S is defined as:

$$\text{CDE}(S) = \text{mean}(\exp(\text{theta}_1[S])) / \text{mean}(\exp(\text{theta}_0[S]))$$

which is the ratio of average hazard contributions on the natural scale. This differs from the AHR ( $\exp(\text{mean}(\text{loghr\_po}))$ ) due to Jensen's inequality. In the notation of Leon et al. (2024), CDE corresponds to theta-ddagger.

The function detects the subgroup indicator column automatically, checking for `flag_harm`, `flag_harm`, and `H` in the super-population data frame.

**Value**

The DGM object with CDE values added to `dgm$hazard_ratios` (CDE, CDE\_harm, CDE\_no\_harm) and to top-level fields (`dgm$CDE`, `dgm$cde_H`, `dgm$cde_Hc`).

**See Also**

[build\\_estimation\\_table](#), [get\\_dgm\\_hr](#)

**Examples**

```
dgm <- setup_gbsg_dgm(model = "alt", k_inter = 2.0, verbose = FALSE)
dgm <- compute_dgm_cde(dgm)
dgm$hazard_ratios$CDE_harm # theta-ddagger(H)
dgm$hazard_ratios$CDE     # theta-ddagger overall
```

---

cox\_ahr\_cde\_analysis *Comprehensive Wrapper for Cox Spline Analysis with AHR and CDE Plotting*

---

**Description**

This wrapper function combines Cox spline fitting with comprehensive visualization of Average Hazard Ratios (AHRs) and Controlled Direct Effects (CDEs) as described in the MRCT subgroups analysis documentation.

**Usage**

```
cox_ahr_cde_analysis(
  df,
  tte_name = "os_time",
  event_name = "os_event",
  treat_name = "treat",
  z_name = "biomarker",
  loghr_po_name = "loghr_po",
  theta1_name = "theta_1",
```

```

theta0_name = "theta_0",
spline_df = 3,
alpha = 0.2,
hr_threshold = 0.7,
plot_style = c("combined", "separate", "grid"),
plot_select = c("all", "profile_ahr", "ahr_only"),
save_plots = FALSE,
output_dir = tempdir(),
verbose = TRUE
)

```

### Arguments

<code>df</code>	Data frame containing survival data with potential outcomes.
<code>tte_name</code>	Character string specifying time-to-event variable name. Default: "os_time".
<code>event_name</code>	Character string specifying event indicator variable name. Default: "os_event".
<code>treat_name</code>	Character string specifying treatment variable name. Default: "treat".
<code>z_name</code>	Character string specifying continuous covariate/biomarker name. Default: "biomarker".
<code>loghr_po_name</code>	Character string specifying potential outcome log HR variable. Default: "loghr_po".
<code>theta1_name</code>	Optional: variable name for theta_1 (treated potential outcome). Default: "theta_1".
<code>theta0_name</code>	Optional: variable name for theta_0 (control potential outcome). Default: "theta_0".
<code>spline_df</code>	Integer degrees of freedom for spline fitting. Default: 3.
<code>alpha</code>	Numeric significance level for confidence intervals. Default: 0.20.
<code>hr_threshold</code>	Numeric hazard ratio threshold for subgroup identification, or NULL to suppress threshold-based elements. When NULL, plots omit the HR threshold line, optimal cutpoint line, and subgroup-dependent panels (Plots 5–6); subgroup statistics report only the overall population. Default: 0.7.
<code>plot_style</code>	Character: "combined", "separate", or "grid" for plot layout. Default: "combined".
<code>plot_select</code>	Character controlling which panels to display: "all" (default) shows the full grid layout; "profile_ahr" shows only the treatment effect profile (top-left) and the AHR curve for $z \geq$ threshold (top-middle) side by side, with the AHR panel's y-axis scaled to the data range; "ahr_only" shows only the AHR curve for $z \geq$ threshold as a single panel with self-contained y-axis.
<code>save_plots</code>	Logical whether to save plots to file. Default: FALSE.
<code>output_dir</code>	Character directory for saving plots. Default: tempdir().
<code>verbose</code>	Logical for diagnostic output. Default: TRUE.

### Value

List of class "cox\_ahr\_cde" containing:

**cox\_fit** Results from `cox_cs_fit` function.

**ahr\_results** AHR calculations for different subgroup definitions.

**cde\_results** CDE calculations if theta variables available.

**optimal\_cutpoint** Optimal biomarker cutpoint, or NULL when hr\_threshold is NULL.

**subgroup\_stats** Statistics for recommended and questionable subgroups, or overall-only when hr\_threshold is NULL.

**data** List with z\_values, loghr\_po, and subgroup assignments.

### Examples

```
# Build a small synthetic dataset with required columns
set.seed(42)
n <- 200
df_ex <- data.frame(
  os_time = rexp(n, rate = 0.01),
  os_event = rbinom(n, 1, 0.6),
  treat = rep(0:1, each = n / 2),
  biomarker = rnorm(n),
  loghr_po = rnorm(n, mean = -0.3, sd = 0.5)
)

# With threshold - full subgroup analysis
results <- cox_ahr_cde_analysis(
  df = df_ex, z_name = "biomarker",
  hr_threshold = 1.25, plot_style = "grid",
  verbose = FALSE
)

# Without threshold - pure AHR curves
results <- cox_ahr_cde_analysis(
  df = df_ex, z_name = "biomarker",
  hr_threshold = NULL, plot_select = "ahr_only",
  verbose = FALSE
)
```

---

 cox\_cs\_fit

*Fit Cox Model with Cubic Spline for Treatment Effect Heterogeneity*


---

### Description

Estimates treatment effects as a function of a continuous covariate using a Cox proportional hazards model with natural cubic splines. The function models treatment-by-covariate interactions to detect effect modification.

### Usage

```
cox_cs_fit(
  df,
  tte_name = "os_time",
  event_name = "os_event",
```

```

  treat_name = "treat",
  strata_name = NULL,
  z_name = "bm",
  alpha = 0.2,
  spline_df = 3,
  z_max = Inf,
  z_by = 1,
  z_window = 0,
  z_quantile = 0.9,
  show_plot = TRUE,
  plot_params = NULL,
  truebeta_name = NULL,
  verbose = TRUE
)

```

### Arguments

df	Data frame containing survival data
tte_name	Character string specifying time-to-event variable name. Default: "os_time"
event_name	Character string specifying event indicator variable name (1=event, 0=censored). Default: "os_event"
treat_name	Character string specifying treatment variable name (1=treated, 0=control). Default: "treat"
strata_name	Character string specifying stratification variable name. If NULL, no stratification is used. Default: NULL
z_name	Character string specifying continuous covariate name for effect modification. Default: "bm"
alpha	Numeric value for confidence level (two-sided). Default: 0.20 (80% confidence intervals)
spline_df	Integer specifying degrees of freedom for natural spline. Default: 3
z_max	Numeric maximum value for z in predictions. Values beyond this are truncated. Default: Inf (no truncation)
z_by	Numeric increment for z values in prediction grid. Default: 1
z_window	Numeric half-width for counting observations near each z value. Default: 0.0 (exact matches only)
z_quantile	Numeric quantile (0-1) for upper limit of z profile. Default: 0.90 (90th percentile)
show_plot	Logical indicating whether to display plot. Default: TRUE
plot_params	List of plotting parameters (see Details). Default: NULL
truebeta_name	Character string specifying variable containing true log(HR) values for validation/simulation. Default: NULL
verbose	Logical indicating whether to print diagnostic information. Default: TRUE

## Details

### Model Structure:

The function fits:

$$h(t|Z, A) = h_0(t) \exp(\beta_0 A + f(Z) + g(Z) \cdot A)$$

Where:

- A is treatment (0/1)
- Z is the continuous effect modifier
- f(Z) is modeled with natural splines (main effect)
- g(Z) is modeled with natural splines (interaction)
- The log hazard ratio is:  $\beta(Z) = \beta_0 + g(Z)$

### Plot Parameters:

The plot\_params argument accepts a list with:

- xlab: x-axis label
- main\_title: plot title
- ylimit: y-axis limits c(min, max)
- y\_pad\_zero: padding below zero line
- y\_delta: extra space for count labels
- cex\_legend: legend text size
- cex\_count: count text size
- show\_cox\_primary: show standard Cox estimate line
- show\_null: show null effect line (log(HR)=0)
- show\_target: show target effect line (e.g., log(0.80))

## Value

List containing:

**z\_profile** Vector of z values where treatment effect is estimated

**loghr\_est** Point estimates of log(HR) at each z value

**loghr\_lower** Lower confidence bound

**loghr\_upper** Upper confidence bound

**se\_loghr** Standard errors of log(HR) estimates

**counts\_profile** Number of observations near each z value

**cox\_primary** Log(HR) from standard Cox model (no interaction)

**model\_fit** The fitted coxph model object

**spline\_basis** The natural spline basis object

**Examples**

```

# Simulate data
set.seed(123)
df <- data.frame(
  os_time = rexp(500, 0.01),
  os_event = rbinom(500, 1, 0.7),
  treat = rbinom(500, 1, 0.5),
  bm = rnorm(500, 50, 10)
)

# Fit model
result <- cox_cs_fit(df, z_name = "bm", alpha = 0.20)

# Custom plotting
result <- cox_cs_fit(
  df,
  z_name = "bm",
  plot_params = list(
    xlab = "Biomarker Level",
    main_title = "Treatment Effect by Biomarker",
    cex_legend = 1.2
  )
)

```

---

 cox\_summary

*Cox model summary for subgroup (OPTIMIZED)*


---

**Description**

Called in `analyze_subgroup() <- SG_tab_estimates`

**Usage**

```

cox_summary(
  Y,
  E,
  Treat,
  Strata = NULL,
  use_strata = !is.null(Strata),
  return_format = c("formatted", "numeric")
)

```

**Arguments**

Y                    Numeric vector of outcome.  
 E                    Numeric vector of event indicators.

Treat	Numeric vector of treatment indicators.
Strata	Vector of strata (optional).
use_strata	Logical. Whether to use strata in the model (default: TRUE if Strata provided).
return_format	Character. "formatted" (default) or "numeric" for downstream use.

### Details

Calculates hazard ratio and confidence interval for a subgroup using Cox regression. Optimized version with reduced overhead and better error handling.

### Value

Character string with formatted HR and CI (or numeric vector if return\_format="numeric").

### Examples

```
library(survival)
cox_summary(
  Y = gbsg$rfstime / 30.4375,
  E = gbsg$status,
  Treat = gbsg$hormon
)
```

---

create\_dgm\_for\_mrct    *Create Data Generating Mechanism for MRCT Simulations*

---

### Description

Wrapper function to create a data generating mechanism (DGM) for MRCT simulation scenarios using [generate\\_aft\\_dgm\\_flex](#).

### Usage

```
create_dgm_for_mrct(
  df_case,
  model_type = c("alt", "null"),
  log_hrs = NULL,
  confounder_var = NULL,
  confounder_effect = NULL,
  include_regA = TRUE,
  verbose = FALSE
)
```

**Arguments**

df_case	Data frame containing case study data
model_type	Character. Either "alt" (alternative hypothesis with heterogeneous treatment effects) or "null" (uniform treatment effect)
log_hrs	Numeric vector. Log hazard ratios for spline specification. If NULL, defaults are used based on model_type
confounder_var	Character. Name of a confounder variable to include with a forced prognostic effect. Default: NULL (no forced effect)
confounder_effect	Numeric. Log hazard ratio for confounder_var effect. Only used if confounder_var is specified
include_regA	Logical. Include regA as a factor in the model. Default: TRUE
verbose	Logical. Print detailed output. Default: FALSE

**Details****Model Types:**

**alt** Alternative hypothesis: Treatment effect varies by biomarker level (heterogeneous treatment effect). Default log\_hrs create HR ranging from 2.0 (harm) to 0.5 (benefit) across biomarker range

**null** Null hypothesis: Uniform treatment effect regardless of biomarker level. Default log\_hrs = log(0.7) uniformly

**Confounder Effects:**

By default, NO prognostic confounder effect is forced. The confounder\_var and confounder\_effect parameters allow optionally specifying ANY baseline covariate to have a fixed prognostic effect in the outcome model.

The regA variable (region indicator) is included as a factor by default but without a forced effect - its coefficient is estimated from data.

**Value**

An object of class "aft\_dgm\_flex" for use with [simulate\\_from\\_dgm](#) and [mrct\\_region\\_sims](#)

**See Also**

[generate\\_aft\\_dgm\\_flex](#) for underlying DGM creation [mrct\\_region\\_sims](#) for running simulations with the DGM

---

create\_forest\_theme     *Create Forest Plot Theme with Size Controls*

---

### Description

Creates a forestploter theme with parameters that control overall plot sizing and appearance. This is the primary way to control how large the forest plot renders.

### Usage

```
create_forest_theme(  
  base_size = 10,  
  scale = 1,  
  row_padding = NULL,  
  ci_pch = 15,  
  ci_lwd = NULL,  
  ci_lty = NULL,  
  ci_col = "black",  
  header_fontsize = NULL,  
  body_fontsize = NULL,  
  footnote_fontsize = NULL,  
  footnote_col = "darkcyan",  
  title_fontsize = NULL,  
  cv_fontsize = NULL,  
  cv_col = "gray30",  
  refline_lwd = NULL,  
  refline_lty = "dashed",  
  refline_col = "gray30",  
  vertline_lwd = NULL,  
  vertline_lty = "dashed",  
  vertline_col = "gray20",  
  arrow_type = "closed",  
  arrow_col = "black",  
  summary_fill = "black",  
  summary_col = "black"  
)
```

### Arguments

base_size	Numeric. Base font size in points. This is the primary scaling parameter - increasing it will proportionally scale all fonts, row padding, and line widths. Default: 10.
scale	Numeric. Additional scaling multiplier applied on top of base_size. Use for quick overall scaling. Default: 1.0.
row_padding	Numeric vector of length 2. Padding around row content in mm as c(vertical, horizontal). If NULL, auto-calculated from base_size. Default: NULL.

ci_pch	Integer. Point character for CI. 15=square, 16=circle, 18=diamond. Default: 15.
ci_lwd	Numeric. Line width for CI lines. If NULL, auto-calculated from base_size. Default: NULL.
ci_Theight	Numeric. Height of T-bar ends on CI. If NULL, auto-calculated from base_size. Default: NULL.
ci_col	Character. Color for CI lines and points. Default: "black".
header_fontsize	Numeric. Font size for column headers. If NULL, auto-calculated as base_size * scale + 1. Default: NULL.
body_fontsize	Numeric. Font size for body text. If NULL, auto-calculated as base_size * scale. Default: NULL.
footnote_fontsize	Numeric. Font size for footnotes. If NULL, auto-calculated as base_size * scale - 1. Default: NULL.
footnote_col	Character. Color for footnote text. Default: "darkcyan".
title_fontsize	Numeric. Font size for title. If NULL, auto-calculated as base_size * scale + 4. Default: NULL.
cv_fontsize	Numeric. Font size for CV annotation text. If NULL, auto-calculated as base_size * scale. Default: NULL.
cv_col	Character. Color for CV annotation text. Default: "gray30".
refline_lwd	Numeric. Reference line width. If NULL, auto-calculated. Default: NULL.
refline_lty	Character. Reference line type. Default: "dashed".
refline_col	Character. Reference line color. Default: "gray30".
vertline_lwd	Numeric. Vertical line width. If NULL, auto-calculated. Default: NULL.
vertline_lty	Character. Vertical line type. Default: "dashed".
vertline_col	Character. Vertical line color. Default: "gray20".
arrow_type	Character. Arrow type: "open" or "closed". Default: "closed".
arrow_col	Character. Arrow color. Default: "black".
summary_fill	Character. Fill color for summary diamonds. Default: "black".
summary_col	Character. Border color for summary diamonds. Default: "black".

## Details

The `base_size` parameter is the primary way to control plot size. When you change `base_size`, the following are automatically scaled:

- All font sizes (body, header, footnote, CV, title)
- Row padding (vertical and horizontal)
- CI line width and T-bar height
- Reference and vertical line widths

The scaling formula uses `base_size = 10` as the reference point:

- base\_size = 10: Default sizing
- base\_size = 12: 20% larger
- base\_size = 14: 40% larger
- base\_size = 16: 60% larger

You can override any individual parameter by specifying it explicitly.

The theme does NOT set row background colors - those are determined automatically by `plot_subgroup_results_forestplot` based on row types (ITT, reference, posthoc, etc.).

### Value

A list of class "fs\_forest\_theme" containing all theme parameters.

### See Also

[plot\\_subgroup\\_results\\_forestplot](#), [render\\_forestplot](#)

### Examples

```
# Simple: just increase base_size for larger plot
large_theme <- create_forest_theme(base_size = 14)
print(large_theme)

# Or use scale for quick adjustment
large_theme <- create_forest_theme(base_size = 10, scale = 1.4)

# Fine-tune specific elements
custom_theme <- create_forest_theme(
  base_size = 14,
  cv_fontsize = 12,
  ci_lwd = 2.5
)
```

---

create\_summary\_table *Create Enhanced Summary Table for Baseline Characteristics*

---

### Description

Generates a formatted summary table comparing baseline characteristics between treatment arms. Supports continuous, categorical, and binary variables with p-values, standardized mean differences (SMD), and missing data summaries.

**Usage**

```

create_summary_table(
  data,
  treat_var = "treat",
  vars_continuous = NULL,
  vars_categorical = NULL,
  vars_binary = NULL,
  var_labels = NULL,
  digits = 1,
  show_pvalue = TRUE,
  show_smd = TRUE,
  show_missing = TRUE,
  table_title = "Baseline Characteristics by Treatment Arm",
  table_subtitle = NULL,
  source_note = NULL,
  font_size = 12,
  header_font_size = 14,
  footnote_font_size = 10,
  use_alternating_rows = TRUE,
  stripe_color = "#f9f9f9",
  indent_size = 20,
  highlight_pval = 0.05,
  highlight_smd = 0.2,
  highlight_color = "#ff3cd",
  compact_mode = FALSE,
  column_width_var = 200,
  column_width_stats = 120,
  show_column_borders = FALSE,
  custom_css = NULL
)

```

**Arguments**

<code>data</code>	Data frame containing the analysis data
<code>treat_var</code>	Character. Name of treatment variable (must have 2 levels)
<code>vars_continuous</code>	Character vector. Names of continuous variables
<code>vars_categorical</code>	Character vector. Names of categorical variables
<code>vars_binary</code>	Character vector. Names of binary (0/1) variables
<code>var_labels</code>	Named list. Custom labels for variables (optional)
<code>digits</code>	Integer. Number of decimal places for continuous variables
<code>show_pvalue</code>	Logical. Include p-values column
<code>show_smd</code>	Logical. Include SMD (effect size) column
<code>show_missing</code>	Logical. Include missing data rows
<code>table_title</code>	Character. Main title for the table

table_subtitle	Character. Subtitle for the table (optional)
source_note	Character. Source note at bottom (optional)
font_size	Numeric. Base font size in pixels (default: 12)
header_font_size	Numeric. Header font size in pixels (default: 14)
footnote_font_size	Numeric. Footnote font size in pixels (default: 10)
use_alternating_rows	Logical. Apply zebra striping (default: TRUE)
stripe_color	Character. Color for alternating rows (default: "#f9f9f9")
indent_size	Numeric. Indentation for sub-levels in pixels (default: 20)
highlight_pval	Numeric. Highlight p-values below this threshold (default: 0.05)
highlight_smd	Numeric. Highlight SMD values above this threshold (default: 0.2)
highlight_color	Character. Color for highlighting (default: "#fff3cd")
compact_mode	Logical. Reduce spacing for compact display (default: FALSE)
column_width_var	Numeric. Width for Variable column in pixels (default: 200)
column_width_stats	Numeric. Width for stat columns in pixels (default: 120)
show_column_borders	Logical. Show vertical column borders (default: FALSE)
custom_css	Character. Additional custom CSS styling (optional)

### Details

Binary variables specified via `vars_binary` display a single row showing the count and proportion for the "1" level. Categorical variables specified via `vars_categorical` that happen to be binary-coded (i.e., have exactly two levels: 0 and 1) are automatically detected and displayed in the same compact single-row format, showing only the "1" proportion.

### Value

A gt table object (or data frame if gt not available)

---

cv_metrics_tables	<i>Create Metrics Tables for Cross-Validation Results</i>
-------------------	---

---

### Description

Formats the `find_summary` and `sens_summary` outputs from `forestsearch_tenfold` or `forestsearch_kfold` into publication-ready gt tables.

**Usage**

```
cv_metrics_tables(
  cv_result,
  sg_definition = NULL,
  title = "Cross-Validation Metrics",
  show_percentages = TRUE,
  digits = 1,
  include_raw = FALSE,
  table_style = c("combined", "separate", "minimal"),
  use_gt = TRUE
)
```

**Arguments**

cv_result	List. Result from forestsearch_tenfold() or forestsearch_Kfold(). Must contain find_summary and sens_summary elements.
sg_definition	Character vector. Subgroup factor definitions for labeling (optional). If NULL, extracted from cv_result\$sg_analysis.
title	Character. Main title for combined table. Default: "Cross-Validation Metrics".
show_percentages	Logical. Display metrics as percentages (0-100) instead of proportions (0-1). Default: TRUE.
digits	Integer. Decimal places for formatting. Default: 1.
include_raw	Logical. Include raw matrices (sens_out, find_out) in the output for detailed analysis. Default: FALSE.
table_style	Character. One of "combined", "separate", or "minimal". <ul style="list-style-type: none"> <li>• "combined": Single table with both agreement and finding metrics</li> <li>• "separate": Two separate gt tables</li> <li>• "minimal": Compact single-row summary</li> </ul> Default: "combined".
use_gt	Logical. Return gt table(s) if TRUE, data.frame(s) if FALSE. Default: TRUE.

**Value**

Depending on table\_style:

- "combined": A single gt table (or data.frame)
- "separate": A list with agreement\_table and finding\_table
- "minimal": A single-row gt table (or data.frame)

If include\_raw = TRUE, also includes sens\_out and find\_out matrices in the returned list.

**See Also**

[cv\\_summary\\_tables](#) for formatting forestsearch\_KfoldOut(outall=TRUE) results

---

cv\_summary\_tables      *Create Summary Tables from forestsearch\_KfoldOut Results*

---

### Description

Formats the detailed output from `forestsearch_KfoldOut` (`outall=TRUE`) into publication-ready gt tables. This includes ITT estimates, original subgroup estimates, and K-fold subgroup estimates.

### Usage

```
cv_summary_tables(
  kfold_out,
  title = "Cross-Validation Summary",
  subtitle = NULL,
  show_metrics = TRUE,
  digits = 3,
  font_size = 12,
  use_gt = TRUE
)
```

### Arguments

<code>kfold_out</code>	List. Result from <code>forestsearch_KfoldOut(res, outall = TRUE)</code> . Must contain <code>itt_tab</code> , <code>SG_tab_original</code> , <code>SG_tab_Kfold</code> , and optionally <code>tab_all</code> .
<code>title</code>	Character. Main title for combined table. Default: "Cross-Validation Summary".
<code>subtitle</code>	Character. Subtitle for table. Default: NULL (auto-generated).
<code>show_metrics</code>	Logical. Include agreement and finding metrics in output. Default: TRUE.
<code>digits</code>	Integer. Decimal places for numeric formatting. Default: 3.
<code>font_size</code>	Integer. Font size in pixels. Default: 12.
<code>use_gt</code>	Logical. Return gt table if TRUE, data.frame if FALSE. Default: TRUE.

### Value

If `use_gt = TRUE`, returns a list with gt table objects:

- `combined_table`: Combined ITT and subgroup estimates
- `itt_table`: ITT estimates only
- `original_table`: Original full-data subgroup estimates
- `kfold_table`: K-fold subgroup estimates
- `metrics_table`: Agreement and finding metrics (if `show_metrics = TRUE`)

If `use_gt = FALSE`, returns equivalent data.frames.

### See Also

[cv\\_metrics\\_tables](#) for formatting `forestsearch_tenfold()` results

---

figure_note	<i>Generate Figure Note for Quarto/RMarkdown</i>
-------------	--

---

### Description

Formats the figure note from `plot_sg_weighted_km()` output for use in Quarto or RMarkdown documents.

### Usage

```
figure_note(
  x,
  prefix = "*Note*: ",
  include_definition = TRUE,
  include_hr_explanation = TRUE,
  custom_text = NULL
)
```

### Arguments

<code>x</code>	Output from <code>plot_sg_weighted_km()</code>
<code>prefix</code>	Character. Prefix for the note. Default uses italic Note.
<code>include_definition</code>	Logical. Include subgroup definition. Default: TRUE
<code>include_hr_explanation</code>	Logical. Include HR(bc) explanation. Default: TRUE
<code>custom_text</code>	Character. Additional custom text to append. Default: NULL

### Value

Character string formatted as a figure note, or NULL if no content

---

forestsearch	<i>ForestSearch: Exploratory Subgroup Identification</i>
--------------	--

---

### Description

Identifies subgroups with differential treatment effects in clinical trials using a combination of Generalized Random Forests (GRF), LASSO variable selection, and exhaustive combinatorial search with split-sample validation.

**Usage**

```
forestsearch(  
  df.analysis,  
  outcome.name = "tte",  
  event.name = "event",  
  treat.name = "treat",  
  id.name = "id",  
  potentialOutcome.name = NULL,  
  flag_harm.name = NULL,  
  confounders.name = NULL,  
  parallel_args = list(plan = "callr", workers = 6, show_message = TRUE),  
  df.predict = NULL,  
  df.test = NULL,  
  is.RCT = TRUE,  
  seedit = 8316951,  
  est.scale = "hr",  
  use_lasso = TRUE,  
  use_grf = TRUE,  
  grf_res = NULL,  
  grf_cuts = NULL,  
  max_n_confounders = 1000,  
  grf_depth = 2,  
  dmin.grf = 12,  
  frac.tau = 0.6,  
  return_selected_cuts_only = TRUE,  
  conf_force = NULL,  
  defaultcut_names = NULL,  
  cut_type = "default",  
  exclude_cuts = NULL,  
  replace_med_grf = FALSE,  
  cont.cutoff = 4,  
  conf.cont_medians = NULL,  
  conf.cont_medians_force = NULL,  
  n.min = 60,  
  hr.threshold = 1.25,  
  hr.consistency = 1,  
  sg_focus = "hr",  
  fs.splits = 1000,  
  m1.threshold = Inf,  
  pconsistency.threshold = 0.9,  
  stop_threshold = 0.95,  
  showten_subgroups = FALSE,  
  d0.min = 12,  
  d1.min = 12,  
  max.minutes = 3,  
  minp = 0.025,  
  details = FALSE,  
  maxk = 2,
```

```

by.risk = 12,
plot.sg = FALSE,
plot.grf = FALSE,
max_subgroups_search = 10,
vi.grf.min = -0.2,
use_twostage = TRUE,
twostage_args = list()
)

```

## Arguments

<code>df.analysis</code>	Data frame. Analysis dataset with required columns.
<code>outcome.name</code>	Character. Name of time-to-event outcome variable. Default "tte".
<code>event.name</code>	Character. Name of event indicator (1=event, 0=censored). Default "event".
<code>treat.name</code>	Character. Name of treatment variable (1=treatment, 0=control). Default "treat".
<code>id.name</code>	Character. Name of subject ID variable. Default "id".
<code>potentialOutcome.name</code>	Character. Name of potential outcome variable (optional).
<code>flag_harm.name</code>	Character. Name of true harm flag for simulations (optional).
<code>confounders.name</code>	Character vector. Names of candidate subgroup-defining variables.
<code>parallel_args</code>	List. Parallel processing configuration: <b>plan</b> Character. One of "multisession", "multicore", "callr", "sequential" <b>workers</b> Integer. Number of parallel workers <b>show_message</b> Logical. Show parallel setup messages
<code>df.predict</code>	Data frame. Prediction dataset (optional).
<code>df.test</code>	Data frame. Test dataset (optional).
<code>is.RCT</code>	Logical. Is this a randomized controlled trial? Default TRUE.
<code>seedit</code>	Integer. Random seed. Default 8316951.
<code>est.scale</code>	Character. Estimation scale ("hr" or "rmst"). Default "hr".
<code>use_lasso</code>	Logical. Use LASSO for variable selection. Default TRUE.
<code>use_grf</code>	Logical. Use GRF for variable importance. Default TRUE.
<code>grf_res</code>	GRF results object (optional, for reuse).
<code>grf_cuts</code>	List. Custom GRF cut points (optional).
<code>max_n_confounders</code>	Integer. Maximum confounders to consider. Default 1000.
<code>grf_depth</code>	Integer. GRF tree depth. Default 2.
<code>dmin.grf</code>	Integer. Minimum events for GRF. Default 12.
<code>frac.tau</code>	Numeric. Fraction of tau for RMST. Default 0.6.
<code>return_selected_cuts_only</code>	Logical. If TRUE (default), GRF returns only cuts from the tree depth that identified the selected subgroup meeting <code>dmin.grf</code> . If FALSE returns all cuts from all fitted trees (depths 1 through <code>grf_depth</code> ). See <a href="#">grf.subg.harm survival</a> for details.

conf_force	Character vector. Variables to force include (optional).
defaultcut_names	Character vector. Default cut variable names (optional).
cut_type	Character. Cut type ("default" or "custom"). Default "default".
exclude_cuts	Character vector. Variables to exclude from cutting (optional).
replace_med_grf	Logical. Replace median with GRF cuts. Default FALSE.
cont.cutoff	Integer. Cutoff for continuous vs categorical. Default 4.
conf.cont_medians	Named numeric vector. Median values for continuous variables (optional).
conf.cont_medians_force	Named numeric vector. Forced median values (optional).
n.min	Integer. Minimum subgroup size. Default 60.
hr.threshold	Numeric. Minimum HR for candidate subgroups. Default 1.25.
hr.consistency	Numeric. Minimum HR for consistency validation. Default 1.0.
sg_focus	Character. Subgroup selection focus. One of "hr", "hrMaxSG", "maxSG", "hrMinSG", "minSG". Default "hr".
fs.splits	Integer. Number of splits for consistency evaluation (or maximum splits when use_twostage = TRUE). Default 1000.
m1.threshold	Numeric. Maximum median survival threshold. Default Inf.
pconsistency.threshold	Numeric. Minimum consistency proportion. Default 0.90.
stop_threshold	Numeric in $[\emptyset, 1]$ or NULL. Early stopping threshold for consistency evaluation. When a candidate subgroup's consistency probability (Pcons) meets or exceeds this threshold, evaluation stops early — remaining candidates are skipped. Set to NULL to disable early stopping and force evaluation of all candidates up to max_subgroups_search. Default 0.95. <b>Note:</b> Values > 1.0 are not permitted. To disable early stopping, use stop_threshold = NULL, not a value above 1. Automatically reset to NULL (with a warning) when sg_focus is "hrMaxSG" or "hrMinSG", as these compound criteria require comparing HR <i>and</i> size across all candidates.
showten_subgroups	Logical. Show top 10 subgroups. Default FALSE.
d0.min	Integer. Minimum control arm events. Default 12.
d1.min	Integer. Minimum treatment arm events. Default 12.
max.minutes	Numeric. Maximum search time in minutes. Default 3.
minp	Numeric. Minimum prevalence threshold. Default 0.025.
details	Logical. Print progress details. Default FALSE.
maxk	Integer. Maximum number of factors per subgroup. Default 2.
by.risk	Integer. Risk table interval. Default 12.
plot.sg	Logical. Plot subgroup survival curves. Default FALSE.

<code>plot.grf</code>	Logical. Plot GRF results. Default FALSE.
<code>max_subgroups_search</code>	Integer. Maximum subgroups to evaluate. Default 10.
<code>vi.grf.min</code>	Numeric. Minimum GRF variable importance. Default -0.2.
<code>use_twostage</code>	Logical. Use two-stage sequential consistency algorithm for improved performance. Default FALSE for backward compatibility. When TRUE, <code>fs.splits</code> becomes the maximum number of splits, and early stopping is enabled. See Details.
<code>twostage_args</code>	List. Parameters for two-stage algorithm (only used when <code>use_twostage = TRUE</code> ): <ul style="list-style-type: none"> <li><b>n.splits.screen</b> Integer. Splits for Stage 1 screening. Default 30.</li> <li><b>screen.threshold</b> Numeric. Consistency threshold for Stage 1. Default is automatically calculated to provide ~2.5 SE margin.</li> <li><b>batch.size</b> Integer. Splits per batch in Stage 2. Default 20.</li> <li><b>conf.level</b> Numeric. Confidence level for early stopping. Default 0.95.</li> <li><b>min.valid.screen</b> Integer. Minimum valid Stage 1 splits. Default 10.</li> </ul>

## Details

### Algorithm Overview:

1. **Variable Selection:** GRF identifies variables with treatment effect heterogeneity; LASSO selects most predictive
2. **Subgroup Discovery:** Exhaustive search over factor combinations up to `maxk`
3. **Consistency Validation:** Split-sample validation ensures reproducibility
4. **Selection:** Choose subgroup based on `sg_focus` criterion

**Two-Stage Consistency Algorithm:** When `use_twostage = TRUE`, the consistency evaluation uses an optimized algorithm that can provide 3-10x speedup:

- **Stage 1:** Quick screening with `n.splits.screen` splits eliminates clearly non-viable candidates
- **Stage 2:** Sequential batched evaluation with early stopping for candidates passing Stage 1

The two-stage algorithm is recommended for:

- Exploratory analyses with many candidate subgroups
- Large `fs.splits` values (>200)
- Iterative model development

For final regulatory submissions, `use_twostage = FALSE` may be preferred for exact reproducibility.

**Value**

A list of class "forestsearch" containing:

**grp.consistency** Consistency evaluation results including:

- **out\_sg**: Selected subgroup based on **sg\_focus**
- **sg\_focus**: Focus criterion used
- **df\_flag**: Treatment recommendations
- **algorithm**: "twostage" or "fixed"
- **n\_candidates\_evaluated**: Number evaluated
- **n\_passed**: Number passing threshold

**find.grps** Subgroup search results

**confounders.candidate** Candidate confounders considered

**confounders.evaluated** Confounders after variable selection

**df.est** Analysis data with treatment recommendations

**df.predict** Prediction data with recommendations (if provided)

**df.test** Test data with recommendations (if provided)

**minutes\_all** Total computation time

**grf\_res** GRF results object

**sg\_focus** Subgroup focus criterion used

**sg.harm** Selected subgroup definition

**grf\_cuts** GRF cut points used

**prop\_maxk** Proportion of max combinations searched

**max\_sg\_est** Maximum subgroup HR estimate

**grf\_plot** GRF plot object (if `plot.grf = TRUE`)

**args\_call\_all** All arguments for reproducibility

**References**

- FDA Guidance for Industry: Enrichment Strategies for Clinical Trials
- Athey & Imbens (2016). Recursive partitioning for heterogeneous causal effects. PNAS.
- Wager & Athey (2018). Estimation and inference of heterogeneous treatment effects using random forests. JASA.

**See Also**

[subgroup.consistency](#) for consistency evaluation details [forestsearch\\_bootstrap\\_dofuture](#) for bootstrap inference [forestsearch\\_Kfold](#) for cross-validation

Package website: <https://larry-leon.github.io/forestsearch/>

Source code: <https://github.com/larry-leon/forestsearch>

---

 forestsearch\_bootstrap\_dofuture

*ForestSearch Bootstrap with doFuture Parallelization*


---

## Description

Orchestrates bootstrap analysis for ForestSearch using doFuture parallelization. Implements bias correction methods to adjust for optimism in subgroup selection.

## Usage

```
forestsearch_bootstrap_dofuture(
  fs.est,
  nb_boots,
  seed = 8316951L,
  details = FALSE,
  show_three = FALSE,
  parallel_args = list()
)
```

## Arguments

fs.est	List. ForestSearch results object from <a href="#">forestsearch</a> . Must contain df.est (data frame) and args_call_all (list of arguments).
nb_boots	Integer. Number of bootstrap samples (recommend 500-1000).
seed	Integer. Random seed for reproducibility of bootstrap sample generation. Default 8316951L. The value is passed to both <a href="#">bootstrap_ystar</a> (which constructs the $n \times B$ bootstrap index matrix) and <a href="#">bootstrap_results</a> (which reruns the ForestSearch algorithm on each replicate); both calls must use the same seed to ensure bootstrap index alignment. Set to NULL for a non-reproducible run.
details	Logical. If TRUE, prints detailed progress information. Default: FALSE.
show_three	Logical. If TRUE, shows verbose output for first 3 bootstrap iterations for debugging. Default: FALSE.
parallel_args	List. Parallelization configuration with elements: <ul style="list-style-type: none"> <li>• plan: Character. One of "multisession", "multicore", "callr", or "sequential"</li> <li>• workers: Integer. Number of parallel workers</li> <li>• show_message: Logical. Show parallel setup messages</li> </ul> If empty list, inherits settings from original forestsearch call.

**Value**

List with the following components:

**results** Data.table with bias-corrected estimates for each bootstrap iteration

**SG\_CIs** List of confidence intervals for H and Hc (raw and bias-corrected)

**FSsg\_tab** Formatted table of subgroup estimates

**Ystar\_mat** Matrix (nb\_boots x n) of bootstrap sample indicators

**H\_estimates** Detailed estimates for subgroup H

**Hc\_estimates** Detailed estimates for subgroup Hc

**summary** (If create\_summary=TRUE) Enhanced summary with tables and diagnostics

**Bias Correction Methods**

Two bias correction approaches are implemented:

1. **Method 1 (Simple Optimism):**

$$H_{adj1} = H_{obs} - (H_*^* - H_{obs}^*)$$

where  $H_*^*$  is the new subgroup HR on bootstrap data and  $H_{obs}^*$  is the new subgroup HR on original data.

2. **Method 2 (Double Bootstrap):**

$$H_{adj2} = 2 \times H_{obs} - (H_* + H_*^* - H_{obs}^*)$$

where  $H_*$  is the original subgroup HR on bootstrap data.

**Variable Naming Convention**

- H: Original subgroup (harm/questionable, treat.recommend == 0)
- Hc: Complement subgroup (recommend, treat.recommend == 1)
- \_obs: Estimate from original data
- \_star: Estimate from bootstrap data
- \_biasadj\_1: Bias correction method 1
- \_biasadj\_2: Bias correction method 2

**Performance**

Typical runtime: 1-5 seconds per bootstrap iteration. For 1000 bootstraps with 6 workers, expect 3-10 minutes total. Memory usage scales with dataset size and number of workers.

**Requirements**

- Original fs.est must have identified a valid subgroup
- Requires packages: data.table, foreach, doFuture, survival
- For plots: requires ggplot2

**See Also**

[forestsearch](#) for initial subgroup identification [bootstrap\\_results](#) for the core bootstrap worker function [build\\_cox\\_formula](#) for Cox formula construction [fit\\_cox\\_models](#) for Cox model fitting

---

forestsearch\_Kfold      *ForestSearch K-Fold Cross-Validation*

---

**Description**

This function assesses the stability and reproducibility of ForestSearch subgroup identification through cross-validation. For each fold:

1. Train ForestSearch on (K-1) folds
2. Apply the identified subgroup to the held-out fold
3. Compare predictions to the original full-data analysis

**Usage**

```
forestsearch_Kfold(
  fs.est,
  Kfolds = nrow(fs.est$df.est),
  seedit = 8316951L,
  parallel_args = list(plan = "multisession", workers = 6, show_message = TRUE),
  sg0.name = "Not recommend",
  sg1.name = "Recommend",
  details = FALSE
)
```

**Arguments**

<code>fs.est</code>	List. ForestSearch results object from <a href="#">forestsearch</a> . Must contain <code>df.est</code> (data frame) and <code>args_call_all</code> (list of arguments).
<code>Kfolds</code>	Integer. Number of folds (default: <code>nrow(fs.est\$df.est)</code> for LOO).
<code>seedit</code>	Integer. Random seed for fold assignment (default: 8316951).
<code>parallel_args</code>	List. Parallelization configuration with elements: <ul style="list-style-type: none"> <li>• <code>plan</code>: Character. One of "multisession", "multicore", "sequential"</li> <li>• <code>workers</code>: Integer. Number of parallel workers</li> <li>• <code>show_message</code>: Logical. Show parallel setup messages</li> </ul>
<code>sg0.name</code>	Character. Label for subgroup 0 (default: "Not recommend").
<code>sg1.name</code>	Character. Label for subgroup 1 (default: "Recommend").
<code>details</code>	Logical. Print progress details (default: FALSE).

## Details

Performs K-fold cross-validation for ForestSearch, evaluating subgroup identification and agreement between training and test sets.

## Value

List with components:

**resCV** Data frame with CV predictions for each observation

**cv\_args** Arguments used for CV ForestSearch calls

**timing\_minutes** Execution time in minutes

**prop\_SG\_found** Percentage of folds where a subgroup was found

**sg\_analysis** Original subgroup definition from full-data analysis

**sg0.name, sg1.name** Subgroup labels

**Kfolds** Number of folds used

**sens\_summary** Named vector of sensitivity metrics (sens\_H, sens\_Hc, ppv\_H, ppv\_Hc)

**find\_summary** Named vector of subgroup-finding metrics (Any, Exact, etc.)

## Cross-Validation Types

- **Leave-One-Out (LOO)**: When `Kfolds = nrow(df)`, each observation is held out once. Most thorough but computationally intensive.
- **K-Fold**: When `Kfolds < nrow(df)`, data is split into K roughly equal folds. Good balance of bias-variance tradeoff.

## Output Metrics

The returned `resCV` data frame contains:

- `treat.recommend`: Prediction from CV model
- `treat.recommend.original`: Prediction from full-data model
- `cvindex`: Fold assignment
- `sg1, sg2`: Subgroup definitions found in each fold

## See Also

[forestsearch](#) for initial subgroup identification [forestsearch\\_KfoldOut](#) for summarizing CV results [forestsearch\\_tenfold](#) for repeated K-fold simulations

---

 forestsearch\_KfoldOut *ForestSearch K-Fold Cross-Validation Output Summary*


---

**Description**

Summarizes cross-validation results for ForestSearch, including subgroup agreement and performance metrics.

**Usage**

```
forestsearch_KfoldOut(res, details = FALSE, outall = FALSE)
```

**Arguments**

res	List. Result object from ForestSearch cross-validation, must contain elements: cv_args, sg_analysis, sg0.name, sg1.name, Kfolds, resCV.
details	Logical. Print details during execution (default: FALSE).
outall	Logical. If TRUE, returns all summary tables; if FALSE, returns only metrics (default: FALSE).

**Value**

If outall=FALSE, a list with sens\_metrics\_original and find\_metrics. If outall=TRUE, a list with summary tables and metrics.

---

 forestsearch\_tenfold *ForestSearch Repeated K-Fold Cross-Validation*


---

**Description**

This function performs multiple independent K-fold cross-validations to assess the variability in subgroup identification. Each simulation:

1. Randomly shuffles the data
2. Performs K-fold CV
3. Records sensitivity and agreement metrics

Results are summarized across all simulations.

**Usage**

```
forestsearch_tenfold(
  fs.est,
  sims,
  Kfolds = 10,
  details = TRUE,
  seed = 8316951L,
  parallel_args = list(plan = "multisession", workers = 6, show_message = TRUE)
)
```

**Arguments**

<code>fs.est</code>	List. ForestSearch results object from <a href="#">forestsearch</a> .
<code>sims</code>	Integer. Number of simulation repetitions.
<code>Kfolds</code>	Integer. Number of folds per simulation (default: 10).
<code>details</code>	Logical. Print progress details (default: TRUE).
<code>seed</code>	Integer. Base random seed for fold shuffling. Default 8316951L. Each simulation uses <code>seed + 1000 * ksim</code> for reproducibility.
<code>parallel_args</code>	List. Parallelization configuration.

**Details**

Runs repeated K-fold cross-validation simulations for ForestSearch and summarizes subgroup identification stability across repetitions.

**Value**

List with components:

**sens\_summary** Named vector of median sensitivity metrics across simulations

**find\_summary** Named vector of median subgroup-finding metrics

**sens\_out** Matrix of sensitivity metrics (sims x metrics)

**find\_out** Matrix of finding metrics (sims x metrics)

**timing\_minutes** Total execution time

**sims** Number of simulations run

**Kfolds** Number of folds per simulation

**Parallelization Strategy**

Unlike the single K-fold function which parallelizes across folds, this function parallelizes across simulations for better efficiency when running many repetitions. Each simulation runs its K-fold CV sequentially.

**See Also**

[forestsearch\\_Kfold](#) for single K-fold CV [forestsearch\\_KfoldOut](#) for summarizing CV results

---

format\_oc\_results      *Format Operating Characteristics Results as GT Table*

---

### Description

Creates a formatted gt table from simulation operating characteristics results.

### Usage

```
format_oc_results(
  results,
  analyses = NULL,
  metrics = "all",
  digits = 3,
  digits_hr = 3,
  title = "Operating Characteristics Summary",
  subtitle = NULL,
  use_gt = TRUE
)
```

### Arguments

results	data.table or data.frame. Simulation results from <a href="#">run_simulation_analysis</a> or combined results from multiple simulations.
analyses	Character vector. Analysis methods to include. Default: NULL (all analyses in results)
metrics	Character vector. Metrics to display. Options include: "detection", "classification", "hr_estimates", "ahr_estimates", "cde_estimates", "subgroup_size", "all". Default: "all"
digits	Integer. Decimal places for proportions. Default: 3
digits_hr	Integer. Decimal places for hazard ratios. Default: 3
title	Character. Table title. Default: "Operating Characteristics Summary"
subtitle	Character. Table subtitle. Default: NULL
use_gt	Logical. Return gt table if TRUE, data.frame if FALSE. Default: TRUE

### Details

The function summarizes simulation results across multiple metrics:

- **Found:** Proportion of simulations finding a subgroup (any.H)
- **Classification:** Sen, spec, PPV, NPV
- **HR Estimates:** Mean Cox hazard ratios in true (H) and identified (H-hat) subgroups and their complements
- **AHR Estimates:** Mean average hazard ratios (from loghr\_po) in true and identified subgroups

- **CDE Estimates:** Controlled direct effects (from  $\theta_0/\theta_1$ ) in true and identified subgroups
- **Subgroup Size:** Average, min, max sizes

Column notation aligns with [build\\_estimation\\_table](#) and Leon et al. (2024): H = true (oracle) subgroup, H-hat = identified subgroup. The asterisk (\*) is reserved for bootstrap bias-corrected estimates and is not used in this summary table.

## Value

A gt table object (if use\_gt = TRUE and gt package available) or data.frame

---

generate\_aft\_dgm\_flex *Generate Synthetic Survival Data using AFT Model with Flexible Subgroups*

---

## Description

Creates a data generating mechanism (DGM) for survival data using an Accelerated Failure Time (AFT) model with Weibull distribution. Supports flexible subgroup definitions and treatment-subgroup interactions.

## Usage

```
generate_aft_dgm_flex(
  data,
  continuous_vars,
  factor_vars,
  continuous_vars_cens = NULL,
  factor_vars_cens = NULL,
  set_beta_spec = list(set_var = NULL, beta_var = NULL),
  outcome_var,
  event_var,
  treatment_var = NULL,
  subgroup_vars = NULL,
  subgroup_cuts = NULL,
  draw_treatment = FALSE,
  model = "alt",
  k_treat = 1,
  k_inter = 1,
  n_super = 5000,
  select_censoring = TRUE,
  cens_type = "weibull",
  cens_params = list(),
  seed = 8316951,
  verbose = TRUE,
  standardize = FALSE,
  spline_spec = NULL
)
```

**Arguments**

<code>data</code>	A <code>data.frame</code> containing the input dataset to base the simulation on
<code>continuous_vars</code>	Character vector of continuous variable names to be standardized and included as covariates
<code>factor_vars</code>	Character vector of factor/categorical variable names to be converted to dummy variables (largest value as reference)
<code>continuous_vars_cens</code>	Character vector of continuous variable names to be used for censoring model. If NULL, uses same as <code>continuous_vars</code> . Default NULL
<code>factor_vars_cens</code>	Character vector of factor variable names to be used for censoring model. If NULL, uses same as <code>factor_vars</code> . Default NULL
<code>set_beta_spec</code>	List with elements 'set_var' and 'beta_var' for manually setting specific beta coefficients. Default list(set_var = NULL, beta_var = NULL)
<code>outcome_var</code>	Character string specifying the name of the outcome/time variable
<code>event_var</code>	Character string specifying the name of the event/status variable (1 = event, 0 = censored)
<code>treatment_var</code>	Character string specifying the name of the treatment variable. If NULL, treatment will be randomly simulated with 50/50 allocation
<code>subgroup_vars</code>	Character vector of variable names defining the subgroup. Default is NULL (no subgroups)
<code>subgroup_cuts</code>	Named list of cutpoint specifications for subgroup variables. See Details section for flexible specification options
<code>draw_treatment</code>	Logical indicating whether to redraw treatment assignment in simulation. Default is FALSE (use original assignments)
<code>model</code>	Character string: "alt" for alternative model with subgroup effects, "null" for null model without subgroup effects. Default is "alt"
<code>k_treat</code>	Numeric treatment effect modifier. Values >1 increase treatment effect, <1 decrease it. Default is 1 (no modification)
<code>k_inter</code>	Numeric interaction effect modifier for treatment-subgroup interaction. Default is 1 (no modification)
<code>n_super</code>	Integer specifying size of super population to generate. Default is 5000
<code>select_censoring</code>	Logical. If TRUE (default), fits the censoring distribution to the observed censoring times in data using <code>survreg</code> with AIC-based selection among Weibull and log-normal models (with and without covariates). If FALSE, no model is fitted; the censoring distribution is specified entirely by <code>cens_params</code> . Default TRUE.
<code>cens_type</code>	Character string specifying censoring distribution type: "weibull" or "uniform". Controls which parametric family is considered when <code>select_censoring</code> = TRUE, and determines the required structure of <code>cens_params</code> when <code>select_censoring</code> = FALSE. Default "weibull".

cens_params	<p>Named list of censoring distribution parameters. Interpretation depends on <code>select_censoring</code> and <code>cens_type</code>:</p> <p><code>select_censoring = TRUE</code> Ignored; all parameters are estimated from data.</p> <p><code>select_censoring = FALSE, cens_type = "uniform"</code> Must supply <code>min</code> and <code>max</code>. If either is absent, defaults to <math>0.5 * \min(y)</math> and <math>1.5 * \max(y)</math> with a message.</p> <p><code>select_censoring = FALSE, cens_type = "weibull"</code> Must supply <code>mu</code> (log-scale location) and <code>tau</code> (scale). Optionally supply <code>type</code> ("weibull" or "lognormal"); defaults to "weibull". Censoring is treated as intercept-only (no covariate or treatment dependence): <code>lin_pred_cens_0 = lin_pred_cens_1 = mu</code>.</p> <p>Default <code>list()</code>.</p>
seed	Integer random seed for reproducibility. Default is 8316951
verbose	Logical indicating whether to print diagnostic information during execution. Default is TRUE
standardize	Logical indicating whether to standardize continuous variables. Default is FALSE
spline_spec	List specifying spline configuration for treatment effect. Must include 'var' (variable name), 'knot', 'zeta', and 'log_hrs' (vector of length 3). Default NULL (no spline)

## Details

### Subgroup Cutpoint Specifications:

The `subgroup_cuts` parameter accepts multiple flexible specifications:

*Fixed Value:*

```
subgroup_cuts = list(er = 20) # er <= 20
```

*Quantile-based:*

```
subgroup_cuts = list(
  er = list(type = "quantile", value = 0.25) # er <= 25th percentile
)
```

*Function-based:*

```
subgroup_cuts = list(
  er = list(type = "function", fun = median) # er <= median
)
```

*Range:*

```
subgroup_cuts = list(
  age = list(type = "range", min = 40, max = 60) # 40 <= age <= 60
)
```

*Greater than:*

```
subgroup_cuts = list(
  nodes = list(type = "greater", quantile = 0.75) # nodes > 75th percentile
)
```

*Multiple values (for categorical):*

```

subgroup_cuts = list(
  grade = list(type = "multiple", values = c(2, 3)) # grade in (2, 3)
)
Custom function:
subgroup_cuts = list(
  er = list(
    type = "custom",
    fun = function(x) x <= quantile(x, 0.3) | x >= quantile(x, 0.9)
  )
)

```

**Model Structure:**

The AFT model with Weibull distribution is specified as:

$$\log(T) = \mu + \gamma'X + \sigma\epsilon$$

Where:

- $T$  is the survival time
- $\mu$  is the intercept
- $\gamma$  contains the covariate effects
- $X$  includes treatment, covariates, and treatment x subgroup interaction
- $\sigma$  is the scale parameter
- $\epsilon$  follows an extreme value distribution

**Interaction Term:**

The model creates a SINGLE interaction term representing the treatment effect modification when ALL subgroup conditions are simultaneously satisfied. This is not multiple separate interactions but one combined indicator.

**Value**

A named list of class `aft_dgm` containing:

<code>data</code>	Simulated trial data frame with outcome, event, and treatment columns.
<code>model_params</code>	Model parameters used for data generation (coefficients, dispersion, spline info if applicable).
<code>subgroup_info</code>	Subgroup definition and membership indicators, if a heterogeneous treatment effect was specified.
<code>censoring_info</code>	Censoring model parameters and observed censoring rate.
<code>call_args</code>	Arguments used in the call, for reproducibility.

**Author(s)**

Your Name

## References

Leon, L.F., et al. (2024). Statistics in Medicine.

Kalbfleisch, J.D. and Prentice, R.L. (2002). The Statistical Analysis of Failure Time Data (2nd ed.). Wiley.

## Examples

```
df <- survival::gbsg
dgm <- generate_aft_dgm_flex(
  data      = df,
  outcome_var = "rfstime",
  event_var  = "status",
  treatment_var = "hormon",
  continuous_vars = c("age", "size", "nodes", "pgr", "er"),
  factor_vars  = "meno",
  model        = "null",
  verbose      = FALSE
)
str(dgm)
```

---

generate\_detection\_curve

*Generate Detection Probability Curve*

---

## Description

Computes detection probability across a range of hazard ratios to create a power-like curve for subgroup detection.

## Usage

```
generate_detection_curve(
  theta_range = c(0.5, 3),
  n_points = 50L,
  n_sg,
  prop_cens = 0.3,
  hr_threshold = 1.25,
  hr_consistency = 1,
  include_reference = TRUE,
  method = "cubature",
  verbose = TRUE
)
```

**Arguments**

theta_range	Numeric vector of length 2. Range of HR values to evaluate. Default: c(0.5, 3.0)
n_points	Integer. Number of points to evaluate. Default: 50
n_sg	Integer. Subgroup sample size.
prop_cens	Numeric. Proportion censored (0-1). Default: 0.3
hr_threshold	Numeric. HR threshold for detection. Default: 1.25
hr_consistency	Numeric. HR consistency threshold. Default: 1.0
include_reference	Logical. Include reference HR values (0.5, 0.75, 1.0). Default: TRUE
method	Character. Integration method. Default: "cubature"
verbose	Logical. Print progress. Default: TRUE

**Value**

A data.frame with columns:

theta	Hazard ratio values
probability	Detection probability
n_sg	Subgroup size (repeated)
prop_cens	Censoring proportion (repeated)
hr_threshold	Detection threshold (repeated)

---

gg_forest	<i>ggplot2 / patchwork forest plot</i>
-----------	--

---

**Description**

Creates a publication-quality forest plot using ggplot2 for the CI panel and patchwork to assemble label and annotation columns alongside it. Unlike forestploter, fig.height maps directly to row density —  $\text{row\_height} = \text{fig.height} / \text{n\_rows}$  with no hidden scaling.

**Usage**

```
gg_forest(
  subgroups,
  est,
  lo,
  hi,
  cat_vec = NULL,
  cat_colours = NULL,
  annot = NULL,
  ref_line = 1,
```

```

vert_lines = NULL,
ref_col = "firebrick",
ref_lty = "dashed",
vert_col = "grey50",
vert_lty = "dotted",
xlim = NULL,
ticks_at = NULL,
tick_labels = NULL,
xlog = TRUE,
xlab = "Hazard Ratio",
title = NULL,
subtitle = NULL,
footnote = NULL,
point_size = 2.5,
line_size = 0.8,
point_shape = 21,
base_size = 11,
widths = NULL,
row_expand = 0.6
)

```

### Arguments

subgroups	Character vector of subgroup names (displayed top to bottom).
est	Numeric vector of point estimates (median HR or similar).
lo	Numeric vector of lower bounds (e.g. 1st percentile ECI).
hi	Numeric vector of upper bounds (e.g. 99th percentile ECI).
cat_vec	Optional character vector of category labels (one per row). Used to colour CI lines and label text.
cat_colours	Optional named character vector mapping category labels to colours. Defaults to grey for all rows.
annot	Optional named list of character vectors, one per annotation column. Names become column headers. Each vector must match length(subgroups).
ref_line	Numeric. X position of the primary reference line (default 1). Drawn as a dashed red line.
vert_lines	Numeric vector. X positions of secondary vertical lines (default NULL). Drawn as dotted grey lines.
ref_col	Colour of the primary reference line (default "firebrick").
ref_lty	Line type of the primary reference line (default "dashed").
vert_col	Colour of secondary vertical lines (default "grey50").
vert_lty	Line type of secondary vertical lines (default "dotted").
xlim	Numeric vector length 2. X-axis limits for the CI panel.
ticks_at	Numeric vector. X-axis tick positions.
tick_labels	Character vector. Custom tick labels (default: as.character(ticks_at)).

xlog	Logical. If TRUE (default), x-axis on log scale.
xlab	Character. X-axis label (default "Hazard Ratio").
title	Character. Overall plot title (default NULL).
subtitle	Character. Plot subtitle (default NULL).
footnote	Character. Footnote appended below the CI panel (default NULL).
point_size	Numeric. Size of point estimate symbol (default 2.5).
line_size	Numeric. Line width of CI segments (default 0.8).
point_shape	Integer. pch for point estimates (default 21, filled circle).
base_size	Numeric. ggplot2 base font size in pt (default 11). Controls all text — increase to make the plot larger; no other knob needed.
widths	Numeric vector. Relative patchwork column widths: c(label, ci, annot_1, annot_2, ...). Default: c(3.5, 5, rep(1, n_annot)).
row_expand	Numeric. Extra space above and below row range on y-axis, in row units (default 0.6).

**Value**

A patchwork object. Render with `print()` or `plot()`. Control dimensions entirely via knitr chunk options `fig.width / fig.height`: `row height = fig.height / n_rows`.

---

grf.subg.harm.survival

*GRF Subgroup Identification for Survival Data*

---

**Description**

Identifies subgroups with differential treatment effect using generalized random forests (GRF) and policy trees. This function uses causal survival forests to identify heterogeneous treatment effects and policy trees to create interpretable subgroup definitions.

**Usage**

```
grf.subg.harm.survival(
  data,
  confounders.name,
  outcome.name,
  event.name,
  id.name,
  treat.name,
  frac.tau = 1,
  n.min = 60,
  dmin.grf = 0,
  RCT = TRUE,
  details = FALSE,
```

```

sg.criterion = "mDiff",
maxdepth = 2,
seedit = 8316951,
return_selected_cuts_only = FALSE
)

```

## Arguments

<code>data</code>	Data frame containing the analysis data.
<code>confounders.name</code>	Character vector of confounder variable names.
<code>outcome.name</code>	Character. Name of outcome variable (e.g., time-to-event).
<code>event.name</code>	Character. Name of event indicator variable (0/1).
<code>id.name</code>	Character. Name of ID variable.
<code>treat.name</code>	Character. Name of treatment group variable (0/1).
<code>frac.tau</code>	Numeric. Fraction of tau for GRF horizon (default: 1.0).
<code>n.min</code>	Integer. Minimum subgroup size (default: 60).
<code>dmin.grf</code>	Numeric. Minimum difference in subgroup mean (default: 0.0).
<code>RCT</code>	Logical. Is the data from a randomized controlled trial? (default: TRUE)
<code>details</code>	Logical. Print details during execution (default: FALSE).
<code>sg.criterion</code>	Character. Subgroup selection criterion ("mDiff" or "Nsg").
<code>maxdepth</code>	Integer. Maximum tree depth (1, 2, or 3; default: 2).
<code>seedit</code>	Integer. Random seed (default: 8316951).
<code>return_selected_cuts_only</code>	Logical. If TRUE, returns only cuts from the tree depth that identified the selected subgroup meeting <code>dmin.grf</code> . If FALSE (default), returns all cuts from all fitted trees (depths 1 through <code>maxdepth</code> ).

## Details

The `return_selected_cuts_only` parameter controls which cuts are returned:

**FALSE (default)** Returns all cuts from all fitted trees (depths 1 to `maxdepth`). This provides the full set of candidate splits for downstream exploration and is the original behavior for backward compatibility.

**TRUE** Returns only cuts from the tree at the depth that identified the "winning" subgroup meeting the `dmin.grf` criterion. This is useful when you want a focused set of cuts associated with the selected subgroup, reducing noise from non-selected trees.

When `return_selected_cuts_only = TRUE` and no subgroup meets the criteria, `tree.cuts` will be empty (`character(0)`).

**Value**

A list with GRF results, including:

data	Original data with added treatment recommendation flags
grf.gsub	Selected subgroup information
sg.harm.id	Expression defining the identified subgroup
tree.cuts	Cut expressions - either all cuts from all trees (if return_selected_cuts_only = FALSE) or only cuts from the selected tree depth (if return_selected_cuts_only = TRUE)
tree.names	Unique variable names used in cuts
tree	Selected policy tree object
tau.rmst	Time horizon used for RMST
harm.any	All subgroups with positive treatment effect difference
selected_depth	Depth of the tree that identified the subgroup (when found)
return_selected_cuts_only	Logical indicating which cut extraction mode was used

Additional tree-specific cuts and objects (tree1, tree2, tree3) based on maxdepth

---

interpret\_estimation\_table

*Generate Narrative Interpretation of Estimation Properties*

---

**Description**

Produces a templated text summary of the estimation properties table, automatically populating numerical results from the simulation output. Useful for reproducible vignettes where interpretation paragraphs should update when simulations are re-run.

**Usage**

```
interpret_estimation_table(
  results,
  dgm,
  analysis_method = "FSlg",
  n_sims = NULL,
  n_boots = 300,
  digits = 2,
  scenario = NULL,
  cat = TRUE
)
```

**Arguments**

results	Data frame of simulation results (same as for <a href="#">build_estimation_table</a> ).
dgm	DGM object with true parameter values.
analysis_method	Character. Which analysis method to summarise. Default: "FS1g".
n_sims	Integer. Total number of simulations (for detection rate). If NULL (default), derived from <code>nrow(results)</code> after filtering to the analysis method.
n_boots	Integer. Number of bootstraps (for narrative). Default: 300.
digits	Integer. Decimal places for reported values. Default: 2.
scenario	Character. One of "null" or "alt" (default). Controls the interpretive framing: <ul style="list-style-type: none"> <li>• "null": emphasises false-positive rate and selection bias</li> <li>• "alt": emphasises power, bias relative to true effect</li> </ul> If NULL, inferred from the DGM ( <code>hr_H_true == hr_Hc_true</code> implies null).
cat	Logical. If TRUE (default), prints the paragraph via <code>cat()</code> . If FALSE, returns it invisibly as a character string (useful for programmatic insertion into Rmd via <code>results = "asis"</code> ).

**Value**

Invisibly returns the interpretation as a character string.

**See Also**

[build\\_estimation\\_table](#), [format\\_oc\\_results](#), [get\\_dgm\\_hr](#)

---

mrct_region_sims	<i>MRCT Regional Subgroup Simulation</i>
------------------	--

---

**Description**

Simulates multi-regional clinical trials and evaluates ForestSearch subgroup identification. Splits data by region into training and testing populations, identifies subgroups using ForestSearch on training data, and evaluates performance on the testing region.

**Usage**

```
mrct_region_sims(
  dgm,
  n_sims,
  n_sample = NULL,
  region_var = "z_regA",
  sg_focus = "minSG",
  maxk = 1,
  hr.threshold = 0.9,
```

```

hr.consistency = 0.8,
pconsistency.threshold = 0.9,
confounders.name = NULL,
conf_force = NULL,
fs_args = list(),
sim_args = list(rand_ratio = 1, draw_treatment = TRUE),
analysis_time = 60,
cens_adjust = 0,
parallel_args = list(plan = "multisession", workers = NULL, show_message = TRUE),
details = FALSE,
verbose_n_sims = 2L,
seed = NULL
)

```

### Arguments

dgm	Data generating mechanism object from <a href="#">generate_aft_dgm_flex</a>
n_sims	Integer. Number of simulations to run
n_sample	Integer. Sample size per simulation. If NULL (default), uses the entire super-population from dgm
region_var	Character. Name of the region indicator variable used to split data into training (region_var == 0) and testing (region_var == 1) populations. Default: "z_regA"
sg_focus	Character. Subgroup selection criterion passed to <a href="#">forestsearch</a> : "minSG", "hr", or "maxSG". Default: "minSG"
maxk	Integer. Maximum number of factors in subgroup combinations (1 or 2). Default: 1
hr.threshold	Numeric. Hazard ratio threshold for subgroup identification. Default: 0.90
hr.consistency	Numeric. Consistency threshold for hazard ratio. Default: 0.80
pconsistency.threshold	Numeric. Probability threshold for consistency. Default: 0.90
confounders.name	Character vector. Confounder variable names for ForestSearch. If NULL, automatically extracted from dgm
conf_force	Character vector. Forced cuts to consider in ForestSearch. Default: c("z_age <= 65", "z_bm <= 0", "z_bm <= 1", "z_bm <= 2", "z_bm <= 5")
fs_args	Named list. Additional arguments passed directly to <a href="#">forestsearch</a> inside each simulation replicate. Use this to control parameters not exposed by mrct_region_sims (e.g., use_grf, use_lasso, cut_type, d0.min, d1.min, n.min, max_subgroups_search, use_twostage, twostage_args). Parameters already in the mrct_region_sims signature (hr.threshold, hr.consistency, pconsistency.threshold, sg_focus, maxk, confounders.name, conf_force) take precedence over values in fs_args. Default: list() (uses forestsearch defaults)
sim_args	Named list. Additional arguments passed to <a href="#">simulate_from_dgm</a> inside each replicate (e.g., rand_ratio, draw_treatment). Parameters already in the mrct_region_sims signature (analysis_time, cens_adjust) take precedence. Default: list(rand_ratio = 1, draw_treatment = TRUE)

analysis_time	Numeric. Time of analysis for administrative censoring. Default: 60
cens_adjust	Numeric. Adjustment factor for censoring rate on log scale. Default: 0
parallel_args	List. Parallel processing configuration with components: <ul style="list-style-type: none"> <li>• plan: "multisession", "multicore", "callr", or "sequential"</li> <li>• workers: Number of workers (NULL for auto-detect)</li> <li>• show_message: Logical for progress messages</li> </ul>
details	Logical. Print detailed progress information. Default: FALSE
verbose_n_sims	Integer. When details = TRUE, print full ForestSearch diagnostics (including internal output) for only the first verbose_n_sims simulation replicates. Set to 0 to suppress per-sim output, or Inf to print all. Default: 2
seed	Integer. Base random seed for reproducibility. Default: NULL

## Details

### Simulation Process:

For each simulation:

1. Sample from super-population using [simulate\\_from\\_dgm](#)
2. Split by region\_var into training and testing populations
3. Estimate HRs in ITT, training, and testing populations
4. Run [forestsearch](#) on training population
5. Apply identified subgroup to testing population
6. Calculate subgroup-specific estimates

### Region Variable:

The region\_var parameter is used ONLY for splitting data into training/testing populations. It does not imply any prognostic effect. To include prognostic confounder effects, specify them when creating the DGM using [create\\_dgm\\_for\\_mrct](#) or [generate\\_aft\\_dgm\\_flex](#).

## Value

A data.table with simulation results containing:

<b>sim</b>	Simulation index
<b>n_itt</b>	ITT sample size
<b>hr_itt</b>	ITT hazard ratio (stratified if strat variable present)
<b>hr_ittX</b>	ITT hazard ratio stratified by region
<b>n_train</b>	Training (non-region A) sample size
<b>hr_train</b>	Training population hazard ratio
<b>n_test</b>	Testing (region A) sample size
<b>hr_test</b>	Testing population hazard ratio
<b>any_found</b>	Indicator: 1 if subgroup identified, 0 otherwise
<b>sg_found</b>	Character description of identified subgroup
<b>n_sg</b>	Subgroup sample size

**hr\_sg** Subgroup hazard ratio in testing population  
**POhr\_sg** Potential outcome hazard ratio in subgroup (testing)  
**prev\_sg** Subgroup prevalence (proportion of testing population)  
**n\_sg\_train** Subgroup sample size in training population  
**hr\_sg\_train** Subgroup hazard ratio in training population  
**POhr\_sg\_train** Potential outcome hazard ratio in subgroup (training)  
**hr\_sg\_null** Subgroup HR when found, NA otherwise

### See Also

[forestsearch](#) for subgroup identification algorithm [generate\\_aft\\_dgm\\_flex](#) for DGM creation [simulate\\_from\\_dgm](#) for data simulation [create\\_dgm\\_for\\_mrct](#) for MRCT-specific DGM wrapper [summaryout\\_mrct](#) for summarizing simulation results

---

plot.forestsearch      *Plot ForestSearch Results*

---

### Description

Dispatches to [plot\\_sg\\_results](#) for Kaplan-Meier curves, hazard-ratio forest plots, or combined panels.

### Usage

```
## S3 method for class 'forestsearch'
plot(
  x,
  type = c("combined", "km", "forest", "summary"),
  outcome.name = "Y",
  event.name = "Event",
  treat.name = "Treat",
  ...
)
```

### Arguments

x	A forestsearch object returned by <a href="#">forestsearch</a> .
type	Character. Type of plot: "combined" KM curves + forest plot (default) "km" Kaplan-Meier survival curves only "forest" Hazard-ratio forest plot only "summary" Summary statistics panel
outcome.name	Character. Name of time-to-event column. Default: "Y".
event.name	Character. Name of event indicator column. Default: "Event".

treat.name	Character. Name of treatment column. Default: "Treat".
...	Additional arguments passed to <a href="#">plot_sg_results</a> , such as <code>by.risk</code> , <code>conf.level</code> , <code>est.scale</code> , <code>sg0_name</code> , <code>sg1_name</code> , <code>treat_labels</code> , <code>colors</code> , <code>title</code> , <code>show_events</code> , <code>show_ci</code> , <code>show_logrank</code> , <code>show_hr</code> .

**Value**

Invisibly returns the plot result from [plot\\_sg\\_results](#).

**See Also**

[plot\\_sg\\_results](#) for full control over appearance, [plot\\_sg\\_weighted\\_km](#) for weighted KM curves, [plot\\_subgroup\\_results\\_forestplot](#) for publication-ready forest plots.

---

plot\_detection\_curve *Plot Detection Probability Curve*

---

**Description**

Creates a visualization of the detection probability curve.

**Usage**

```
plot_detection_curve(
  curve_data,
  add_reference_lines = TRUE,
  add_threshold_line = TRUE,
  title = NULL,
  ...
)
```

**Arguments**

curve_data	A data.frame from <a href="#">generate_detection_curve</a> or with columns: <code>theta</code> , <code>probability</code> .
add_reference_lines	Logical. Add horizontal reference lines at 0.05, 0.10, 0.80. Default: TRUE
add_threshold_line	Logical. Add vertical line at <code>hr_threshold</code> . Default: TRUE
title	Character. Plot title. Default: auto-generated
...	Additional arguments passed to <code>plot()</code>

**Value**

Invisibly returns the input data.

---

`plot_km_band_forestsearch`*Plot Kaplan-Meier Survival Difference Bands for ForestSearch Subgroups*

---

**Description**

Creates Kaplan-Meier survival difference band plots comparing the identified ForestSearch subgroup (sg.harm) and its complement against the ITT population. This function wraps `plotKM.band_subgroups()` from the `weightsurv` package, automatically extracting subgroup definitions from ForestSearch results.

**Usage**

```
plot_km_band_forestsearch(  
  df,  
  fs.est = NULL,  
  sg_cols = NULL,  
  sg_labels = NULL,  
  sg_colors = NULL,  
  itt_color = "azure3",  
  outcome.name = "tte",  
  event.name = "event",  
  treat.name = "treat",  
  xlabel = "Time",  
  ylabel = "Survival differences",  
  yseq_length = 5,  
  draws_band = 1000,  
  tau_add = NULL,  
  by_risk = 6,  
  risk_cex = 0.75,  
  risk_delta = 0.035,  
  risk_pad = 0.015,  
  ymax_pad = 0.11,  
  show_legend = TRUE,  
  legend_pos = "topleft",  
  legend_cex = 0.75,  
  ref_subgroups = NULL,  
  verbose = FALSE  
)
```

**Arguments**

<code>df</code>	Data frame. The analysis dataset containing all required variables including subgroup indicator columns.
<code>fs.est</code>	A forestsearch object containing the identified subgroup, or NULL if using pre-defined subgroup indicators.

sg_cols	Character vector. Names of columns in df containing subgroup indicators (0/1). These columns must already exist in df. If NULL and fs.est is provided, columns will be created automatically. Default: NULL
sg_labels	Character vector. Subsetting expressions for each subgroup, corresponding to sg_cols. These are passed to plotKM.band_subgroups() which evaluates them as R expressions (e.g., "age < 65", "er <= 0", "Qrecommend == 1"). Must be same length as sg_cols. Default: NULL (auto-generated as "colname == 1").
sg_colors	Character vector. Colors for each subgroup curve, corresponding to sg_cols. Must be same length as sg_cols. Default: NULL (uses default color palette).
itt_color	Character. Color for ITT population band. Default: "azure3".
outcome.name	Character. Name of time-to-event column. Default: "tte".
event.name	Character. Name of event indicator column. Default: "event".
treat.name	Character. Name of treatment column. Default: "treat".
xlabel	Character. X-axis label. Default: "Time".
ylabel	Character. Y-axis label. Default: "Survival differences".
yseq_length	Integer. Number of y-axis tick marks. Default: 5.
draws_band	Integer. Number of bootstrap draws for confidence band. Default: 1000.
tau_add	Numeric. Time horizon for the plot. If NULL, auto-calculated from data. Default: NULL.
by_risk	Numeric. Interval for risk table. Default: 6.
risk_cex	Numeric. Character expansion for risk table text. Default: 0.75.
risk_delta	Numeric. Vertical spacing for risk table. Default: 0.035.
risk_pad	Numeric. Padding for risk table. Default: 0.015.
ymax_pad	Numeric. Y-axis maximum padding. Default: 0.11.
show_legend	Logical. Whether to display the legend. Default: TRUE.
legend_pos	Character. Legend position (e.g., "topleft", "bottomright"). Default: "topleft".
legend_cex	Numeric. Character expansion for legend text. Default: 0.75.
ref_subgroups	Named list. Optional additional reference subgroups to include. Each element should be a list with: <b>subset_expr</b> Character. R expression to define subgroup (e.g., "age < 65") <b>label</b> Character. Display label (optional, defaults to subset_expr) <b>color</b> Character. Color for the curve The function automatically creates indicator columns from the expressions. Default: NULL.
verbose	Logical. Print diagnostic messages. Default: FALSE.

## Details

This function simplifies the workflow of creating KM survival difference band plots for ForestSearch-identified subgroups. It can work in two modes:

### Mode 1: With ForestSearch result (fs.est provided)

1. Extracts the subgroup definition from the ForestSearch result
2. Creates binary indicator columns (Qrecommend, Brecommend) in df
3. Generates appropriate labels from the subgroup definition
4. Calls plotKM.band\_subgroups() with configured parameters

### Mode 2: With pre-defined columns (sg\_cols provided)

1. Uses existing indicator columns in df
2. Requires sg\_labels and sg\_colors to match sg\_cols

The sg.harm subgroup (Qrecommend) represents patients with questionable treatment benefit (where `treat.recommend == 0` in ForestSearch output). The complement (Brecommend) represents patients recommended for treatment.

### Value

Invisibly returns a list containing:

**df** The modified data frame with subgroup indicators

**sg\_cols** Character vector of subgroup column names used

**sg\_labels** Character vector of subgroup labels used

**sg\_colors** Character vector of colors used

**sg\_harm\_definition** The subgroup definition extracted from fs.est

**ref\_subgroups** The reference subgroups list (if provided)

### Subgroup Extraction

When `fs.est` is provided, the subgroup definition is extracted from:

- `fs.est$grp.consistency$out_sg$sg.harm_label` - Human-readable labels
- `fs.est$sg.harm` - Technical factor names (fallback)
- `fs.est$df.est$treat.recommend` - Subgroup membership indicator

### Note

This function requires the **weightedsurv** package, which can be installed from GitHub: `devtools::install_github("larr")`

### See Also

[forestsearch](#) for running the subgroup analysis [plot\\_sg\\_weighted\\_km](#) for weighted KM plots  
[plot\\_sg\\_results](#) for comprehensive subgroup visualization

---

plot\_sg\_weighted\_km *Plot Weighted Kaplan-Meier Curves for ForestSearch Subgroups*

---

### Description

Creates weighted Kaplan-Meier survival curves for the identified subgroups (H and Hc) using the `weightedSurv` package, matching the pattern used in `sg_consistency_out()`.

### Usage

```
plot_sg_weighted_km(
  fs.est,
  fs_bc = NULL,
  outcome.name = "Y",
  event.name = "Event",
  treat.name = "Treat",
  by.risk = NULL,
  sg0_name = NULL,
  sg1_name = NULL,
  conf.int = TRUE,
  show.logrank = TRUE,
  show.cox = TRUE,
  show.cox.bc = TRUE,
  put.legend.lr = "topleft",
  ymax = 1.05,
  xmed.fraction = 0.65,
  hr_bc_position = "bottomright",
  hr_bc_cex = 0.725,
  title = NULL,
  verbose = FALSE
)
```

### Arguments

<code>fs.est</code>	A forestsearch object containing <code>df.est</code> with <code>treat.recommend</code> column, or a data frame directly.
<code>fs_bc</code>	Optional. Bootstrap results from <code>forestsearch_bootstrap_dofuture()</code> containing bias-corrected HR estimates. If provided, bias-corrected HRs will be annotated on the plots.
<code>outcome.name</code>	Character. Name of time-to-event column. Default: "Y"
<code>event.name</code>	Character. Name of event indicator column. Default: "Event"
<code>treat.name</code>	Character. Name of treatment column. Default: "Treat"
<code>by.risk</code>	Numeric. Risk interval for plotting. Default: NULL (auto-calculated as $\max(\text{outcome})/12$ )
<code>sg0_name</code>	Character. Label for H subgroup ( <code>treat.recommend == 0</code> ). Default: NULL (auto-extracted from forestsearch object as "H: {definition}" or "Questionable (H)" if not available)

<code>sg1_name</code>	Character. Label for Hc subgroup ( <code>treat.recommend == 1</code> ). Default: NULL (auto-generated as "Hc: NOT {definition}" or "Recommend (Hc)" if not available)
<code>conf.int</code>	Logical. Show confidence intervals. Default: TRUE
<code>show.logrank</code>	Logical. Show log-rank test. Default: TRUE
<code>show.cox</code>	Logical. Show unadjusted Cox HR from <code>weightedsurv</code> . Default: TRUE
<code>show.cox.bc</code>	Logical. Show bootstrap bias-corrected HR annotation (requires <code>fs_bc</code> ). Default: TRUE
<code>put.legend.lr</code>	Character. Legend position. Default: "topleft"
<code>ymax</code>	Numeric. Max y-axis value. Default: 1.05
<code>xmed.fraction</code>	Numeric. Fraction for median lines. Default: 0.65
<code>hr_bc_position</code>	Character. Position for bias-corrected HR annotation. One of "bottomright", "bottomleft", "topright", "topleft". Default: "bottomright"
<code>hr_bc_cex</code>	Numeric. Character expansion factor for bias-corrected HR annotation text. Default: 0.725 (matches <code>weightedsurv</code> <code>cox.cex</code> default)
<code>title</code>	Character. Overall plot title. Default: NULL
<code>verbose</code>	Logical. Print diagnostic messages. Default: FALSE

### Details

This function uses the exact same calling pattern as `plot_subgroup()` in the `ForestSearch` package. Column names are mapped internally to the standard names (Y, Event, Treat) expected by `weightedsurv`.

Subgroup definitions are automatically extracted from the `forestsearch` object if available:

- `fs$grp.consistency$out_sg$sg.harm_label` - Human-readable labels
- `fs$sg.harm` - Technical factor names (fallback)

HR display options controlled by `show.cox` and `show.cox.bc`:

- Both TRUE (default): Shows unadjusted HR from `weightedsurv` AND bias-corrected HR annotation
- `show.cox = TRUE`, `show.cox.bc = FALSE`: Shows only unadjusted HR
- `show.cox = FALSE`, `show.cox.bc = TRUE`: Shows only bias-corrected HR
- Both FALSE: Shows neither HR estimate

### Value

Invisibly returns a list with subgroup data frames and counting data

---

plot\_spline\_treatment\_effect  
*Plot Spline Treatment Effect Function*

---

**Description**

Plot Spline Treatment Effect Function

**Usage**

```
plot_spline_treatment_effect(dgm_result, add_points = TRUE)
```

**Arguments**

dgm_result	Result object from generate_aft_dgm_flex with spline
add_points	Logical; add observed data points. Default TRUE

**Value**

No return value, called for side effects (produces a plot).

---

plot\_subgroup\_results\_forestplot  
*Plot Subgroup Results Forest Plot*

---

**Description**

Generates a comprehensive forest plot showing:

- ITT (Intent-to-Treat) population estimate
- Reference subgroups (e.g., by biomarker levels)
- Post-hoc identified subgroups with bias-corrected estimates
- Cross-validation agreement metrics as annotations

**Usage**

```
plot_subgroup_results_forestplot(  
  fs_results,  
  df_analysis,  
  subgroup_list = NULL,  
  outcome.name,  
  event.name,  
  treat.name,  
  E.name = "Experimental",
```

```

C.name = "Control",
est.scale = "hr",
xlog = TRUE,
title_text = NULL,
arrow_text = c("Favors Experimental", "Favors Control"),
footnote_text = c("Eg 80% of training found SG: 70% of B (+) also B in CV testing"),
xlim = c(0.25, 1.5),
ticks_at = c(0.25, 0.7, 1, 1.5),
show_cv_metrics = TRUE,
cv_source = c("auto", "kfold", "oob", "both"),
posthoc_colors = c("powderblue", "beige"),
reference_colors = c("yellow", "powderblue"),
ci_column_spaces = 20,
conf.level = 0.95,
theme = NULL
)

```

## Arguments

<code>fs_results</code>	List. A list containing ForestSearch analysis results with elements: <ul style="list-style-type: none"> <li>• <code>fs.est</code>: ForestSearch estimation object from <a href="#">forestsearch</a></li> <li>• <code>fs.bc</code>: Bootstrap bias-corrected results from <a href="#">forestsearch_bootstrap_dofuture</a></li> <li>• <code>fs.kfold</code>: K-fold cross-validation results from <a href="#">forestsearch_Kfold</a> or <a href="#">forestsearch_tenfold</a> (optional)</li> <li>• <code>fs.OOB</code>: Out-of-bag cross-validation results (optional, alternative to <code>fs.kfold</code>)</li> </ul>
<code>df_analysis</code>	Data frame. The analysis dataset with outcome, event, and treatment variables.
<code>subgroup_list</code>	List. Named list of subgroup definitions to include in the plot. Each element should be a list with: <ul style="list-style-type: none"> <li>• <code>subset_expr</code>: Character string for subsetting (e.g., "BM&gt; 1")</li> <li>• <code>name</code>: Display name for the subgroup</li> <li>• <code>type</code>: Either "reference" for pre-specified or "posthoc" for identified</li> </ul>
<code>outcome.name</code>	Character. Name of the survival time variable.
<code>event.name</code>	Character. Name of the event indicator variable.
<code>treat.name</code>	Character. Name of the treatment variable.
<code>E.name</code>	Character. Label for experimental arm (default: "Experimental").
<code>C.name</code>	Character. Label for control arm (default: "Control").
<code>est.scale</code>	Character. Estimate scale: "hr" or "1/hr" (default: "hr").
<code>xlog</code>	Logical. If TRUE (default), the x-axis is plotted on a logarithmic scale. This is standard for hazard ratio forest plots where equal distances represent equal relative effects.
<code>title_text</code>	Character. Plot title (default: NULL).
<code>arrow_text</code>	Character vector of length 2. Arrow labels for forest plot (default: c("Favors Experimental", "Favors Control")).

footnote_text	Character vector. Footnote text for the plot explaining CV metrics (default provides CV interpretation guidance; set to NULL to omit).
xlim	Numeric vector of length 2. X-axis limits (default: c(0.25, 1.5)).
ticks_at	Numeric vector. X-axis tick positions (default: c(0.25, 0.70, 1.0, 1.5)).
show_cv_metrics	Logical. Whether to show cross-validation metrics (default: TRUE if fs_kfold or fs_OOB available).
cv_source	Character. Source for CV metrics: "auto" (default, uses both if available, otherwise whichever is present), "kfold" (use fs_kfold only), "oob" (use fs_OOB only), or "both" (explicitly use both fs_kfold and fs_OOB, with K-fold first then OOB).
posthoc_colors	Character vector. Colors for post-hoc subgroup rows (default: c("powderblue", "beige")).
reference_colors	Character vector. Colors for reference subgroup rows (default: c("yellow", "powderblue")).
ci_column_spaces	Integer. Number of spaces for the CI plot column width. More spaces = wider CI column (default: 20).
conf.level	Numeric. Confidence level for intervals (default: 0.95 for 95% CI). Used to calculate the z-multiplier as $qnorm(1 - (1 - conf.level)/2)$ .
theme	An fs_forest_theme object from create_forest_theme(). Use this to control plot sizing (fonts, row height, CI appearance, CV annotation font size). Default: NULL (uses default theme).

## Details

Creates a publication-ready forest plot displaying identified subgroups with hazard ratios, bias-corrected estimates, and cross-validation metrics. This wrapper integrates ForestSearch results with the forestploter package.

### ForestSearch Labeling Convention:

ForestSearch identifies subgroups based on hazard ratio thresholds:

- `sg.harm`: Contains the definition of the "harm" or "questionable" subgroup (H)
- `treat.recommend == 0`: Patient is IN the harm subgroup (H)
- `treat.recommend == 1`: Patient is in the COMPLEMENT subgroup (Hc, typically benefit)

For `est.scale = "hr"` (searching for harm):

- H (`treat.recommend=0`): Subgroup defined by `sg.harm` with elevated HR (harm/questionable)
- Hc (`treat.recommend=1`): Complement of `sg.harm` (potential benefit)

For `est.scale = "1/hr"` (searching for benefit):

- Roles are reversed: H becomes the benefit group

**Value**

A list containing:

**plot** The forestploter grob object (can be rendered with plot())

**data** The data frame used for the forest plot

**row\_types** Character vector of row types for styling reference

**cv\_metrics** Cross-validation metrics text (if available)

**See Also**

[forestsearch](#) for running the subgroup analysis [forestsearch\\_bootstrap\\_dofuture](#) for bootstrap bias correction [forestsearch\\_Kfold](#) for cross-validation [create\\_forest\\_theme](#) for customizing plot appearance [render\\_forestplot](#) for rendering the plot

---

print.cox\_ahr\_cde      *Print method for cox\_ahr\_cde objects*

---

**Description**

Print method for cox\_ahr\_cde objects

**Usage**

```
## S3 method for class 'cox_ahr_cde'
print(x, ...)
```

**Arguments**

x                    A cox\_ahr\_cde object from [cox\\_ahr\\_cde\\_analysis](#).

...                  Additional arguments (not used).

**Value**

Invisibly returns the input object.

---

print.forestsearch      *Print Method for forestsearch Objects*

---

**Description**

Displays a concise summary of ForestSearch results including the identified subgroup definition, consistency metrics, algorithm details, and computation time.

**Usage**

```
## S3 method for class 'forestsearch'  
print(x, ...)
```

**Arguments**

x                      A forestsearch object returned by [forestsearch](#).  
...                    Additional arguments (currently unused).

**Value**

Invisibly returns x.

**See Also**

[summary.forestsearch](#) for detailed output, [plot.forestsearch](#) for visualization.

---

print.fs\_kfold              *Print Method for K-Fold CV Results*

---

**Description**

Print Method for K-Fold CV Results

**Usage**

```
## S3 method for class 'fs_kfold'  
print(x, ...)
```

**Arguments**

x                      An fs\_kfold object  
...                    Additional arguments (ignored)

**Value**

Invisibly returns x.

---

print.fs\_tenfold      *Print Method for Repeated K-Fold CV Results*

---

**Description**

Print Method for Repeated K-Fold CV Results

**Usage**

```
## S3 method for class 'fs_tenfold'  
print(x, ...)
```

**Arguments**

x                    An fs\_tenfold object  
...                  Additional arguments (ignored)

**Value**

Invisibly returns x.

---

print.gbsg\_dgm      *Print Method for gbsg\_dgm Objects*

---

**Description**

Print Method for gbsg\_dgm Objects

**Usage**

```
## S3 method for class 'gbsg_dgm'  
print(x, ...)
```

**Arguments**

x                    A gbsg\_dgm object  
...                  Additional arguments (unused)

**Value**

Invisibly returns x.

**Examples**

```
dgm <- setup_gbsg_dgm(model = "alt", verbose = FALSE)  
print(dgm)
```

---

render\_forestplot      *Render ForestSearch Forest Plot*

---

**Description**

Renders a forest plot from `plot_subgroup_results_forestplot()`.

**Usage**

```
render_forestplot(x, newpage = TRUE)
```

**Arguments**

`x`                      An `fs_forestplot` object from `plot_subgroup_results_forestplot()`.  
`newpage`                Logical. Call `grid.newpage()` before drawing. Default: `TRUE`.

**Details**

To control plot sizing, create a custom theme using `create_forest_theme()` and pass it to `plot_subgroup_results_forestplot()`.

```
my_theme <- create_forest_theme(base_size = 14, row_padding = c(6, 4))
result <- plot_subgroup_results_forestplot(..., theme = my_theme)
render_forestplot(result)
```

**Value**

Invisibly returns the grob object.

---

render\_reference\_table      *Render Reference Simulation Table as gt*

---

**Description**

Converts a data frame of pre-computed reference simulation results (e.g., digitized from a published LaTeX table) into a styled `gt` table. This is useful for displaying published benchmark results alongside new simulation output within vignettes or reports.

**Usage**

```
render_reference_table(
  ref_df,
  title = "Reference Simulation Results",
  subtitle = NULL,
  bold_threshold = 0.05
)
```

**Arguments**

ref_df	data.frame. Must contain a Metric column and one column per analysis method, with a Scenario column for row grouping.
title	Character. Table title.
subtitle	Character. Table subtitle. Default: NULL.
bold_threshold	Numeric. Values in any(H) rows exceeding this threshold are shown in bold. Set NULL to disable. Default: 0.05.

**Value**

A gt table object.

**Examples**

```
ref <- data.frame(
  Scenario = "M1 Null: N=700",
  Metric   = "any(H)",
  FS       = 0.02,
  FS1g     = 0.03,
  GRF      = 0.25
)
render_reference_table(ref, title = "Reference Results")
```

---

```
run_simulation_analysis
```

*Run One Simulation Replicate*

---

**Description**

General replacement for the legacy `run_simulation_analysis()` that was coupled to `simulate_from_gbsg_dgm()` and GBSG-specific column names. This version calls `simulate_from_dgm` and accepts explicit column-name parameters, making it applicable to any DGM built with `generate_aft_dgm_flex`.

**Usage**

```
run_simulation_analysis(
  sim_id,
  dgm,
  n_sample,
  analysis_time = Inf,
  cens_adjust = 0,
  max_follow = NULL,
  muC_adj = NULL,
  confounders_base = c("v1", "v2", "v3", "v4", "v5", "v6", "v7"),
  n_add_noise = 0L,
```

```

outcome_name = "y_sim",
event_name = "event_sim",
treat_name = "treat_sim",
harm_col = "flag_harm",
run_fs = TRUE,
run_fs_grf = TRUE,
run_grf = TRUE,
fs_params = list(),
grf_params = list(),
cox_formula = NULL,
cox_formula_adj = NULL,
n_sims_total = NULL,
seed_base = 8316951L,
verbose = FALSE,
verbose_n = NULL,
debug = FALSE
)

```

### Arguments

sim_id	Integer. Simulation replicate index (used as seed offset).
dgm	An "aft_dgm_flex" object from <a href="#">generate_aft_dgm_flex</a> or <a href="#">setup_gbsg_dgm</a> .
n_sample	Integer. Per-replicate sample size.
analysis_time	Numeric. Calendar time of analysis on the DGM time scale. Use Inf (default) for no administrative censoring — equivalent to the legacy max_follow = Inf.
cens_adjust	Numeric. Log-scale shift to censoring times passed to <code>simulate_from_dgm(cens_adjust = ...)</code> . Replaces legacy muC_adj. Default 0.
max_follow	<b>Deprecated.</b> Use analysis_time instead. If supplied, its value is forwarded to analysis_time with a warning. Retained for backward compatibility with legacy scripts.
muC_adj	<b>Deprecated.</b> Use cens_adjust instead. If supplied, its value is forwarded to cens_adjust with a warning. Retained for backward compatibility with legacy scripts.
confounders_base	Character vector of base confounder names.
n_add_noise	Integer. Number of independent N(0,1) noise variables to append. Default 0L.
outcome_name	Name of the observed time column in simulated data. Default "y_sim".
event_name	Name of the event indicator column. Default "event_sim".
treat_name	Name of the treatment column. Default "treat_sim".
harm_col	Name of the true-subgroup indicator column. Default "flag_harm".
run_fs	Logical. Run ForestSearch (LASSO). Default TRUE.
run_fs_grf	Logical. Run ForestSearch (LASSO + GRF). Default TRUE.
run_grf	Logical. Run standalone GRF. Default TRUE.
fs_params	Named list of ForestSearch parameter overrides.

grf_params	Named list of GRF parameter overrides.
cox_formula	Optional Cox formula for unadjusted ITT.
cox_formula_adj	Optional adjusted Cox formula.
n_sims_total	Integer. Total simulations (for progress messages).
seed_base	Integer. Base seed; replicate seed = seed_base + sim_id. Default 8316951L.
verbose	Logical. Print progress messages. Default FALSE.
verbose_n	Integer. If set, only print for sim_id <= verbose_n. Default NULL.
debug	Logical. Print detailed debug output. Default FALSE.

**Value**

A data.table with one row per analysis method, containing subgroup size, HR, AHR, CDE, and classification metrics.

**See Also**

[simulate\\_from\\_dgm](#), [generate\\_aft\\_dgm\\_flex](#), [setup\\_gbsg\\_dgm](#)

---

select\_best\_subgroup *Select best subgroup based on criterion*

---

**Description**

Identifies the optimal subgroup according to the specified criterion

**Usage**

```
select_best_subgroup(values, sg.criterion, dmin.grf, n.max)
```

**Arguments**

values	Data frame. Node metrics from policy trees
sg.criterion	Character. "mDiff" for maximum difference, "Nsg" for largest size
dmin.grf	Numeric. Minimum difference threshold
n.max	Integer. Maximum allowed subgroup size (total sample size)

**Value**

Data frame row with best subgroup or NULL if none found

**Examples**

```
vals <- data.frame(diff = c(8.5, 6.2, 3.1), Nsg = c(120, 95, 80))
select_best_subgroup(values = vals, sg.criterion = "mDiff",
                     dmin.grf = 6, n.max = 500)
```

---

 setup\_gbsg\_dgm

 Set Up a GBSG-Based AFT Data Generating Mechanism
 

---

### Description

Creates a GBSG-based data generating mechanism that is fully compatible with `simulate_from_dgm`. This is the replacement for `create_gbsg_dgm()`: it accepts exactly the same arguments and produces the same numeric output, but returns an object of class "aft\_dgm\_flex" instead of "gbsg\_dgm".

### Usage

```
setup_gbsg_dgm(
  model = c("alt", "null"),
  k_treat = 1,
  k_inter = 1,
  k_z3 = 1,
  z1_quantile = 0.25,
  n_super = 5000L,
  cens_type = c("weibull", "uniform"),
  use_rand_params = FALSE,
  seed = 8316951L,
  verbose = FALSE
)
```

### Arguments

model	Character. Either "alt" for alternative hypothesis with heterogeneous treatment effects, or "null" for uniform treatment effect. Default: "alt"
k_treat	Numeric. Treatment effect multiplier applied to the treatment coefficient from the fitted AFT model. Values > 1 strengthen the treatment effect. Default: 1
k_inter	Numeric. Interaction effect multiplier for the treatment-subgroup interaction ( $z1 * z3$ ). Only used when model = "alt". Higher values create more heterogeneity between HR(H) and HR(Hc). Default: 1
k_z3	Numeric. Effect multiplier for the z3 (menopausal status) coefficient. Default: 1
z1_quantile	Numeric. Quantile threshold for z1 (estrogen receptor). Observations with ER <= quantile are coded as z1 = 1. Default: 0.25
n_super	Integer. Size of super-population for empirical HR estimation. Default: 5000
cens_type	Character. Censoring distribution type: "weibull" or "uniform". Default: "weibull"
use_rand_params	Logical. If TRUE, modifies confounder coefficients using estimates from randomized subset (meno == 0). Default: FALSE
seed	Integer. Random seed for super-population generation. Default: 8316951
verbose	Logical. Print diagnostic information. Default: FALSE

**Details**

Internally the function calls `create_gbsg_dgm()` and then:

1. Adds a `df_super` field with column names aligned to `simulate_from_dgm()` conventions (`lin_pred_1`, `lin_pred_0`, `lin_pred_cens_1`, `lin_pred_cens_0`, `flag_harm`).
2. Adds a `model_params$tau` field (= `model_params$sigma`) and a `model_params$censoring` sub-list.
3. Sets class to `c("aft_dgm_flex", "gbsg_dgm", "list")`.

The original `df_super_rand` field is kept so that `compute_dgm_cde()` and `print.gbsg_dgm` continue to work.

**Value**

An object of class `c("aft_dgm_flex", "gbsg_dgm", "list")` with all fields from `create_gbsg_dgm()` plus:

`df_super` Super-population data frame with `simulate_from_dgm()`-compatible column names.

`model_params$tau` Copy of `model_params$sigma`.

`model_params$censoring` Sub-list with `type`, `mu`, `tau` for the censoring model.

**See Also**

[create\\_gbsg\\_dgm](#), [simulate\\_from\\_dgm](#), [compute\\_dgm\\_cde](#)

**Examples**

```
dgm <- setup_gbsg_dgm(model = "alt", k_inter = 2, verbose = FALSE)
dgm <- compute_dgm_cde(dgm)
print(dgm)
sim <- simulate_from_dgm(dgm, n = 400, seed = 1)
```

**Description**

Returns formatted summary tables for subgroups using the `gt` package, with search metadata and customizable decimal precision. Produces two tables: a treatment effect estimates table and an identified subgroups table, each with fully customizable titles and subtitles.

**Usage**

```
sg_tables(
  fs,
  which_df = "est",
  est_title = "Treatment Effect Estimates",
  est_caption = "Training data estimates",
  sg_title = "Identified Subgroups",
  sg_subtitle = NULL,
  potentialOutcome.name = NULL,
  hr_1a = NA,
  hr_0a = NA,
  ndecimals = 3,
  include_search_info = TRUE,
  font_size = 12
)
```

**Arguments**

fs	ForestSearch results object.
which_df	Character. Which data frame to use ("est" or "testing").
est_title	Character or NULL. Main title for the estimates table (default: "Treatment Effect Estimates"). Rendered as bold markdown. Set to NULL to suppress the title and display only est_caption.
est_caption	Character. Subtitle for the estimates table (default: "Training data estimates").
sg_title	Character or NULL. Main title for the identified subgroups table (default: "Identified Subgroups"). Rendered as bold markdown. Set to NULL to suppress the title and display only sg_subtitle.
sg_subtitle	Character or NULL. Subtitle for the identified subgroups table. When NULL (default), an informative subtitle is auto-generated from maxk (e.g., "Two-factor subgroups (maxk=2)").
potentialOutcome.name	Character. Name of potential outcome variable (optional).
hr_1a	Character. Adjusted HR for subgroup 1 (optional).
hr_0a	Character. Adjusted HR for subgroup 0 (optional).
ndecimals	Integer. Number of decimals for formatted numbers (default: 3).
include_search_info	Logical. Include search metadata table (default: TRUE).
font_size	Numeric. Font size in pixels for table text (default: 12).

**Value**

List with gt tables for estimates, subgroups, and optionally search info.

---

simulate\_from\_dgm      *Simulate Survival Data from AFT Data Generating Mechanism*

---

### Description

Generates simulated survival data from a previously created AFT data generating mechanism (DGM). Samples from the super population and generates survival times with specified censoring.

### Usage

```
simulate_from_dgm(
  dgm,
  n = NULL,
  rand_ratio = 1,
  entry_var = NULL,
  max_entry = 24,
  analysis_time = 48,
  cens_adjust = 0,
  draw_treatment = TRUE,
  seed = NULL,
  strata_rand = NULL,
  hrz_crit = NULL,
  keep_rand = FALSE,
  time_eos = NULL
)
```

### Arguments

dgm	An object of class "aft_dgm_flex" created by <a href="#">generate_aft_dgm_flex</a> .
n	Integer specifying the sample size. If NULL (default), uses the entire super population without sampling.
rand_ratio	Numeric randomisation ratio (treatment:control). Default 1 (1:1 allocation).
entry_var	Character string naming an entry-time variable in the super population. If NULL, entry times are drawn as $\text{Uniform}(0, \text{max\_entry})$ . Default NULL.
max_entry	Numeric maximum entry time for staggered entry simulation. Only used when <code>entry_var = NULL</code> . Default 24.
analysis_time	Numeric calendar time of analysis. Follow-up is <code>analysis_time - entry_time</code> . Must be on the same time scale as the DGM (i.e. the same units as <code>outcome_var</code> passed to <code>generate_aft_dgm_flex</code> ). Default 48.
cens_adjust	Numeric log-scale adjustment to censoring distribution. Positive values increase censoring times; negative values decrease them. Default 0 (no adjustment).
draw_treatment	Logical. If TRUE (default), reassigns treatment according to <code>rand_ratio</code> . If FALSE, retains original treatment assignments from the super population.
seed	Integer random seed. Default NULL.

strata_rand	Character string naming a column in the sampled data for within-stratum balanced treatment allocation. If NULL, marginal allocation is used. Default NULL.
hrz_crit	Numeric log-HR threshold. If supplied, a column hrz_flag is added marking subjects with $\text{lin\_pred}_1 - \text{lin\_pred}_0 \geq \text{hrz\_crit}$ . Default NULL.
keep_rand	Logical. If TRUE, appends a rand_order column preserving the randomisation sequence. Default FALSE.
time_eos	Numeric secondary administrative censoring cutoff (end-of-study time on the DGM scale). Applied after follow_up censoring. Default NULL.

## Details

### Time-scale consistency:

All time parameters (analysis\_time, max\_entry, time\_eos) must be expressed in the same units as outcome\_var supplied to generate\_aft\_dgm\_flex(). A common error is building the DGM on days (e.g. rfstime) and then passing analysis\_time in months, which causes follow-up windows far shorter than the DGM event-time scale and produces universal administrative censoring (event\_sim = 0 for all subjects).

Verify with:  $\exp(\text{dgm}\$model\_params\$\mu)$  — the implied median event time should be plausible given your analysis\_time.

### n = NULL path:

When n = NULL the entire super population is used as-is, with no staggered entry and no administrative censoring (follow\_up = Inf). Treatment assignments and linear predictors already stored in dgm\$df\_super are retained unchanged.

### Censoring adjustment:

cens\_adjust shifts the log-scale location parameter of the censoring distribution:

- cens\_adjust = log(2) doubles expected censoring times.
- cens\_adjust = log(0.5) halves expected censoring times.

## Value

A data.frame with columns:

id Subject identifier.

treat Original treatment from super population.

treat\_sim Simulated treatment assignment.

flag\_harm Subgroup indicator (1 = all subgroup conditions met).

z\_\* Covariate values.

lin\_pred\_1, lin\_pred\_0 Counterfactual log-time linear predictors.

y\_sim Observed survival time ( $\min(T, C)$ ).

event\_sim Event indicator (1 = event, 0 = censored).

t\_true Latent true survival time (pre-censoring).

c\_time Effective censoring time (post admin-censoring).

hrz\_flag (Optional) Individual harm-zone indicator.

rand\_order (Optional) Randomisation sequence index.

**See Also**

[generate\\_aft\\_dgm\\_flex](#), [check\\_censoring\\_dgm](#)

**Examples**

```
dgm <- setup_gbsg_dgm(model = "null", verbose = FALSE)
sim_data <- simulate_from_dgm(dgm, n = 200, seed = 42)
dim(sim_data)
head(sim_data[, c("y_sim", "event_sim", "treat_sim")])
```

---

subgroup.consistency *Evaluate Subgroup Consistency*

---

**Description**

Evaluates candidate subgroups using split-sample consistency validation. For each candidate, repeatedly splits the data and checks whether the treatment effect direction is consistent across splits.

**Usage**

```
subgroup.consistency(
  df,
  hr.subgroups,
  hr.threshold = 1,
  hr.consistency = 1,
  pconsistency.threshold = 0.9,
  m1.threshold = Inf,
  n.splits = 100,
  details = FALSE,
  by.risk = 12,
  plot.sg = FALSE,
  maxk = 7,
  Lsg,
  confs_labels,
  sg_focus = "hr",
  stop_Kgroups = 10,
  stop_threshold = NULL,
  shorten_subgroups = FALSE,
  pconsistency.digits = 2,
  seed = 8316951,
  checking = FALSE,
  use_twostage = FALSE,
  twostage_args = list(),
  parallel_args = list()
)
```

**Arguments**

<code>df</code>	Data frame containing the analysis dataset. Must include columns for outcome (Y), event indicator (Event), and treatment (Treat).
<code>hr.subgroups</code>	Data.table of candidate subgroups from subgroup search, containing columns: HR, n, E, K, d0, d1, m0, m1, grp, and factor indicators.
<code>hr.threshold</code>	Numeric. Minimum hazard ratio threshold for candidates. Default: 1.0
<code>hr.consistency</code>	Numeric. Minimum HR required in each split for consistency. Default: 1.0
<code>pconsistency.threshold</code>	Numeric. Minimum proportion of splits that must be consistent. Default: 0.9
<code>m1.threshold</code>	Numeric. Maximum m1 threshold for filtering. Default: Inf
<code>n.splits</code>	Integer. Number of splits for consistency evaluation. Default: 100
<code>details</code>	Logical. Print progress details. Default: FALSE
<code>by.risk</code>	Numeric. Risk interval for KM plots. Default: 12
<code>plot.sg</code>	Logical. Generate subgroup plots. Default: FALSE
<code>maxk</code>	Integer. Maximum number of factors in subgroup. Default: 7
<code>Lsg</code>	List of subgroup parameters.
<code>confs_labels</code>	Character vector mapping factor names to labels.
<code>sg_focus</code>	Character. Subgroup selection criterion: "hr", "maxSG", or "minSG". Default: "hr"
<code>stop_Kgroups</code>	Integer. Maximum number of candidates to evaluate. Default: 10
<code>stop_threshold</code>	Numeric in $[\emptyset, 1]$ or NULL. When a candidate subgroup's consistency probability (Pcons) meets or exceeds this threshold, evaluation stops early — remaining candidates are skipped. Set to NULL to disable early stopping and evaluate all candidates up to <code>stop_Kgroups</code> . Default: NULL. <b>Note:</b> Values > 1.0 are not permitted. To disable early stopping, use <code>stop_threshold = NULL</code> , not a value above 1.
	<b>Interaction with <code>sg_focus</code>:</b>
	"hr", "maxSG", "minSG" Early stopping is valid because candidates are sorted by a single criterion. The first candidate passing the threshold is optimal under that criterion.
	"hrMaxSG", "hrMinSG" Should generally be NULL, because these compound criteria require comparing HR <i>and</i> size across all candidates. <code>forestsearch()</code> automatically resets to NULL with a warning for these.
	For parallel execution, early stopping is checked after each batch completes, so some additional candidates beyond the first meeting the threshold may be evaluated. Use a smaller <code>batch_size</code> in <code>parallel_args</code> for finer-grained early stopping.
<code>shorten_subgroups</code>	Logical. If TRUE, prints up to 10 candidate subgroups after sorting by <code>sg_focus</code> , showing their rank, HR, sample size, events, and factor definitions. Useful for reviewing which candidates will be evaluated for consistency. Default: FALSE

pconsistency.digits	Integer. Decimal places for consistency proportion. Default: 2
seed	Integer. Random seed for reproducible consistency splits. Default: 8316951. Set to NULL for non-reproducible random splits. The seed is used both for sequential execution (via set.seed()) and parallel execution (via future.seed).
checking	Logical. Enable additional validation checks. Default: FALSE
use_twostage	Logical. Use two-stage adaptive algorithm. Default: FALSE
twostage_args	List. Parameters for two-stage algorithm: <b>n.splits.screen</b> Splits for Stage 1 screening. Default: 30 <b>screen.threshold</b> Consistency threshold for Stage 1. Default: auto <b>batch.size</b> Splits per batch in Stage 2. Default: 20 <b>conf.level</b> Confidence level for early stopping. Default: 0.95 <b>min.valid.screen</b> Minimum valid Stage 1 splits. Default: 10
parallel_args	List. Parallel processing configuration: <b>plan</b> Future plan: "multisession", "multicore", or "sequential" <b>workers</b> Number of parallel workers <b>batch_size</b> Number of candidates to evaluate per batch. Smaller values provide finer-grained early stopping but may increase overhead. Default: When stop_threshold is set and sg_focus is "hr" or "minSG", defaults to 1 (stop immediately when first candidate passes). For other sg_focus values with stop_threshold, defaults to min(workers, n_candidates/4). When stop_threshold is NULL, defaults to workers*2 for efficiency. <b>show_message</b> Print parallel config messages

## Value

A list containing:

<b>out_sg</b>	Selected subgroup results
<b>sg_focus</b>	Selection criterion used
<b>df_flag</b>	Data frame with treatment recommendations
<b>sg.harm</b>	Subgroup definition labels
<b>sg.harm.id</b>	Subgroup membership indicator
<b>algorithm</b>	"twostage" or "fixed"
<b>n_candidates_evaluated</b>	Number of candidates actually evaluated
<b>n_candidates_total</b>	Total candidates available
<b>n_passed</b>	Number meeting consistency threshold
<b>early_stop_triggered</b>	Logical indicating if early stop occurred
<b>early_stop_candidate</b>	Index of candidate triggering early stop
<b>stop_threshold</b>	Threshold used for early stopping
<b>seed</b>	Random seed used for reproducibility (NULL if not set)

---

 summarize\_bootstrap\_events

*Summarize Bootstrap Event Counts*


---

### Description

Provides summary statistics for event counts across bootstrap iterations, helping assess the reliability of HR estimates when events are sparse.

### Usage

```
summarize_bootstrap_events(boot_results, threshold = 5)
```

### Arguments

**boot\_results** List. Output from forestsearch\_bootstrap\_dofuture()  
**threshold** Integer. Minimum event threshold for flagging low counts (default: 5)

### Details

This function summarizes event counts in four scenarios:

1. ORIGINAL subgroup H evaluated on BOOTSTRAP samples
2. ORIGINAL subgroup Hc evaluated on BOOTSTRAP samples
3. NEW subgroup H\* (found in bootstrap) evaluated on ORIGINAL data
4. NEW subgroup Hc\* (found in bootstrap) evaluated on ORIGINAL data

Low event counts (below threshold) can lead to unstable HR estimates. This summary helps identify potential issues with sparse events.

### Value

Invisibly returns a list with summary statistics:

**threshold** The event threshold used

**nb\_boots** Total number of bootstrap iterations

**n\_successful** Number of iterations that found a new subgroup

**original\_H** List with low event counts for original H on bootstrap samples

**original\_Hc** List with low event counts for original Hc on bootstrap samples

**new\_Hstar** List with low event counts for new H\* on original data

**new\_Hcstar** List with low event counts for new Hc\* on original data

---

 summarize\_bootstrap\_results

*Enhanced Bootstrap Results Summary*


---

## Description

Creates comprehensive output including formatted table with subgroup footnote, diagnostic plots, bootstrap quality metrics, and detailed timing analysis.

## Usage

```
summarize_bootstrap_results(
  sgharm,
  boot_results,
  create_plots = FALSE,
  est.scale = "hr"
)
```

## Arguments

sgharm	The selected subgroup object from forestsearch results. Can be: <ul style="list-style-type: none"> <li>• Character vector of factor definitions (e.g., c("{age}&gt;=50}", "{nodes}&gt;=3}"))</li> <li>• List with sgharm element containing factor definitions</li> <li>• List with sg.harm_label element (human-readable labels)</li> </ul>
boot_results	List. Output from forestsearch_bootstrap_dofuture()
create_plots	Logical. Generate diagnostic plots (default: FALSE)
est.scale	Character. "hr" or "1/hr" for effect scale

## Details

The table output includes a footnote displaying the identified subgroup definition, analogous to the tab\_estimates table from [sg\\_tables](#). This is achieved by extracting the subgroup definition from sgharm and passing it to [format\\_bootstrap\\_table](#).

## Value

List with components:

**table** gt table with treatment effects and subgroup footnote

**diagnostics** List of bootstrap quality metrics

**diagnostics\_table\_gt** gt table of diagnostics

**plots** List of ggplot2 diagnostic plots (if create\_plots=TRUE)

**timing** List of timing analysis (if timing data available)

**subgroup\_summary** List from summarize\_bootstrap\_subgroups()

**See Also**

[format\\_bootstrap\\_table](#) for table creation [sg\\_tables](#) for analogous main analysis tables [summarize\\_bootstrap\\_subgro](#) for subgroup stability analysis

---

summarize\_simulation\_results

*Summarize Simulation Results*

---

**Description**

Creates a summary table of operating characteristics across all simulations. Includes both HR and AHR metrics.

**Usage**

```
summarize_simulation_results(
  results,
  analyses = NULL,
  digits = 2,
  digits_hr = 3
)
```

**Arguments**

results	data.table with simulation results from run_simulation_analysis
analyses	Character vector. Analysis methods to include. Default: all
digits	Integer. Decimal places for proportions. Default: 2
digits_hr	Integer. Decimal places for hazard ratios. Default: 3

**Value**

Data frame with summary statistics

---

summary.cox\_ahr\_cde *Summary method for cox\_ahr\_cde objects*

---

**Description**

Summary method for cox\_ahr\_cde objects

**Usage**

```
## S3 method for class 'cox_ahr_cde'
summary(object, ...)
```

**Arguments**

object            A cox\_ahr\_cde object from `cox_ahr_cde_analysis`.  
 ...              Additional arguments (not used).

**Value**

Invisibly returns the input object.

---

`summary.forestsearch`    *Summary Method for forestsearch Objects*

---

**Description**

Provides a detailed summary of a ForestSearch analysis including input parameters, variable selection results, consistency evaluation, and the selected subgroup with key metrics.

**Usage**

```
## S3 method for class 'forestsearch'
summary(object, ...)
```

**Arguments**

object            A forestsearch object returned by `forestsearch`.  
 ...              Additional arguments (currently unused).

**Value**

Invisibly returns object.

---

`validate_k_inter_effect`  
                           *Validate k\_inter Effect on HR Heterogeneity*

---

**Description**

Test function to verify that `k_inter` properly modulates the difference between HR(H) and HR(Hc), and that AHR metrics align with Cox-based HRs.

**Usage**

```
validate_k_inter_effect(  
  k_inter_values = c(-2, -1, 0, 1, 2, 3),  
  verbose = TRUE,  
  ...  
)
```

**Arguments**

`k_inter_values` Numeric vector of `k_inter` values to test. Default: `c(-2, -1, 0, 1, 2, 3)`  
`verbose` Logical. Print results. Default: `TRUE`  
`...` Additional arguments passed to `create_gbsg_dgm`

**Value**

Data frame with `k_inter`, `hr_H`, `hr_Hc`, `AHR_H`, `AHR_Hc`, and `ratio` columns

**Examples**

```
# Test k_inter effect
results <- validate_k_inter_effect()

# k_inter = 0 should give hr_H approximately equals hr_Hc (ratio approximately 1)
```

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