Package: AdaptiveTrialsR (via r-universe)

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Title Bayesian and Adaptive Clinical Trial Simulation and Monitoring

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Description Provides tools for simulating and evaluating Bayesian and adaptive clinical trial designs with binary outcomes. The package includes methods for trial simulation, posterior and predictive probability monitoring, adaptive randomisation, Bayesian treatment effect estimation, dose-finding, Simon two-stage phase II designs, group sequential monitoring boundaries, operating characteristic evaluation, and interim decision support. The implementation is motivated by established Bayesian and adaptive design methodology, including Simon's two-stage design for phase II trials Simon (1989) <doi:10.1016/0197-2456(89)90015-9>, Bayesian adaptive clinical trial approaches described by Berry et al. (2010, ISBN:9781439825488), and modern adaptive trial frameworks reviewed by Pallmann et al. (2018) <doi:10.1186/s12916-018-1017-7>.

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Contents

adaptive_randomisation . . . 2
analyse_trial_data . . . 3
compare_trial_scenarios . . . 5
create_trial_template . . . 6
crm_dose_finding . . . 7
decision_summary . . . 8
estimate_treatment_effect . . . 8
export_figures_to_desktop . . . 10
export_trial_results . . . 11
group_sequential_boundary . . . 11
interim_monitoring . . . 12
plot_dose_finding . . . 13
plot_group_sequential_boundary . . . 14
plot_operating_characteristics . . . 15
plot_posterior_density . . . 16
plot_posterior_intervals . . . 17
plot_real_trial_results . . . 18
plot_sample_size_distribution . . . 19
plot_scenario_comparison . . . 20
plot_treatment_effect . . . 21
plot_trial_path . . . 22
posterior_summary . . . 22
predict_success . . . 23
predictive_probability . . . 25
sample_size_binary . . . 26
simon_two_stage . . . 27
simulate_trial . . . 28
simulate_trials . . . 29
summary_trial . . . 30
trial_report . . . 31
validate_trial_data . . . 32

Index **33**

`adaptive_randomisation`

Adaptive Randomisation Probabilities

Description

Calculates response-adaptive randomisation probabilities from posterior mean response rates. Better-performing arms receive higher allocation probabilities while preserving minimum and maximum allocation limits.

Usage

```
adaptive_randomisation(
  posterior_means,
  min_prob = 0.1,
  max_prob = 0.8,
  power = 1
)
```

Arguments

`posterior_means`
: Numeric vector of posterior mean response rates. Names may be supplied for treatment arms.

`min_prob`
: Minimum allocation probability for each arm. Default is 0.10.

`max_prob`
: Maximum allocation probability for any arm. Default is 0.80.

`power`
: Tuning parameter controlling how strongly allocation favours better-performing arms. Default is 1.

Value

A data frame with treatment arms, posterior means, and allocation probabilities.

Examples

```
adaptive_randomisation(
  posterior_means = c(Control = 0.30, Treatment = 0.50)
)

adaptive_randomisation(
  posterior_means = c(Control = 0.25, TreatmentA = 0.45, TreatmentB = 0.60),
  min_prob = 0.10,
  max_prob = 0.80
)
```

`analyse_trial_data` *Analyse Real Trial Data Using Bayesian Monitoring*

Description

Applies Bayesian posterior monitoring to real patient-level binary-outcome clinical trial data. The function compares a treatment arm with a control arm using a beta-binomial model.

Usage

```
analyse_trial_data(
  data,
  arm_col = "arm",
  outcome_col = "outcome",
  control_arm,
  treatment_arm,
  margin = 0,
  efficacy_threshold = 0.95,
  futility_threshold = 0.1,
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  seed = NULL
)
```

Arguments

`data`	A data frame containing patient-level trial data.
`arm_col`	Name of the treatment-arm column.
`outcome_col`	Name of the binary outcome column.
`control_arm`	Name of the control arm.
`treatment_arm`	Name of the treatment arm.
`margin`	Minimum clinically important treatment-control difference.
`efficacy_threshold`	Posterior probability threshold for declaring efficacy.
`futility_threshold`	Posterior probability threshold for futility.
`prior_alpha`	Beta prior alpha parameter.
`prior_beta`	Beta prior beta parameter.
`nsim`	Number of posterior simulations.
`seed`	Optional random seed.

Value

A data frame containing arm-level summaries, posterior probability, and Bayesian decision.

Examples

```
trial_data <- data.frame(
  arm = c("Control", "Control", "Control", "Treatment", "Treatment", "Treatment"),
  outcome = c(0, 1, 0, 1, 1, 0)
)

analyse_trial_data(
  data = trial_data,
```

```
  control_arm = "Control",
  treatment_arm = "Treatment",
  seed = 123
)
```

`compare_trial_scenarios` *Compare Operating Characteristics Across Trial Scenarios*

Description

Runs repeated Bayesian adaptive trial simulations across multiple true-response scenarios and summarises the resulting operating characteristics.

Usage

```
compare_trial_scenarios(
  scenarios,
  n_sim = 100,
  n_total = 100,
  interim_every = 20,
  margin = 0,
  efficacy_threshold = 0.95,
  futility_threshold = 0.1,
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  seed = NULL
)
```

Arguments

`scenarios`	A data frame with columns control_response and treatment_response.
`n_sim`	Number of simulated trials per scenario.
`n_total`	Maximum total sample size per trial.
`interim_every`	Frequency of interim analyses.
`margin`	Minimum clinically important treatment-control difference.
`efficacy_threshold`	Posterior probability threshold for stopping early for efficacy.
`futility_threshold`	Posterior probability threshold for stopping early for futility.
`prior_alpha`	Beta prior alpha parameter.
`prior_beta`	Beta prior beta parameter.
`nsim`	Number of posterior simulations used inside each trial.
`seed`	Optional random seed.

Value

A data frame of operating characteristics by scenario.

Examples

```
scenarios <- data.frame(
  control_response = c(0.25, 0.25, 0.25),
  treatment_response = c(0.25, 0.35, 0.45)
)

compare_trial_scenarios(
  scenarios = scenarios,
  n_sim = 10,
  n_total = 100,
  interim_every = 20,
  nsim = 1000,
  seed = 123
)
```

---

create_trial_template *Create a Trial Data Template*

Description

Creates a simple patient-level clinical trial data template for use with AdaptiveTrialsR. The template includes patient ID, treatment arm, and binary outcome columns.

Usage

```
create_trial_template(n = 20, arms = c("Control", "Treatment"), path = NULL)
```

Arguments

n	Number of rows to create. Default is 20.
arms	Character vector of treatment arms. Default is c("Control", "Treatment").
path	Optional file path for saving the template as a CSV file.

Value

A data frame containing a trial data template.

Examples

```
create_trial_template(n = 10)

temp_file <- tempfile(fileext = ".csv")
create_trial_template(n = 10, path = temp_file)
```

crm_dose_finding *Simple Bayesian CRM Dose-Finding Summary*

Description

Provides a simplified Bayesian continual reassessment method-style dose-finding summary for Phase I trials. The function estimates posterior toxicity probabilities for each dose and recommends the dose closest to the target toxicity rate.

Usage

```
crm_dose_finding(
  dose_data,
  dose_col = "dose",
  n_col = "n",
  tox_col = "tox",
  target_toxicity = 0.25,
  prior_alpha = 1,
  prior_beta = 1
)
```

Arguments

`dose_data`	A data frame containing dose-level data.
`dose_col`	Name of the dose column.
`n_col`	Name of the column containing number treated.
`tox_col`	Name of the column containing number with toxicity.
`target_toxicity`	Target toxicity probability.
`prior_alpha`	Beta prior alpha parameter.
`prior_beta`	Beta prior beta parameter.

Value

A data frame with posterior toxicity summaries and recommended dose.

Examples

```
dose_data <- data.frame(
  dose = c(1, 2, 3, 4),
  n = c(3, 3, 3, 3),
  tox = c(0, 0, 1, 2)
)

crm_dose_finding(dose_data)
```

decision_summary *Summarise Final Decisions from Adaptive Trial Simulations*

Description

Creates a clean summary table of final trial decisions from repeated Bayesian adaptive clinical trial simulations.

Usage

```
decision_summary(simulations)
```

Arguments

simulations	An object returned by simulate_trials().

Value

A data frame containing decision counts and percentages.

Examples

```
sims <- simulate_trials(
  n_sim = 20,
  n_total = 100,
  true_response = c(0.25, 0.45),
  interim_every = 20,
  nsim = 1000,
  seed = 123
)

decision_summary(sims)
```

estimate_treatment_effect *Estimate Bayesian Treatment Effect for Binary Trial Outcomes*

Description

Estimates the posterior distribution of the treatment-control difference in response probabilities using a beta-binomial model.

Usage

```
estimate_treatment_effect(
  data,
  arm_col = "arm",
  outcome_col = "outcome",
  control_arm,
  treatment_arm,
  margin = 0,
  efficacy_threshold = 0.95,
  futility_threshold = 0.1,
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  cred_level = 0.95,
  seed = NULL
)
```

Arguments

`data`	A data frame containing patient-level trial data.
`arm_col`	Name of the treatment-arm column.
`outcome_col`	Name of the binary outcome column.
`control_arm`	Name of the control arm.
`treatment_arm`	Name of the treatment arm.
`margin`	Minimum clinically important treatment-control difference.
`efficacy_threshold`	Posterior probability threshold for declaring efficacy.
`futility_threshold`	Posterior probability threshold for futility.
`prior_alpha`	Beta prior alpha parameter.
`prior_beta`	Beta prior beta parameter.
`nsim`	Number of posterior simulations.
`cred_level`	Credible interval level.
`seed`	Optional random seed.

Value

A data frame containing posterior treatment-effect summaries.

Examples

```
trial_data <- data.frame(
  arm = c("Control", "Control", "Treatment", "Treatment"),
  outcome = c(0, 1, 1, 1)
)
```

```
estimate_treatment_effect(
  data = trial_data,
  control_arm = "Control",
  treatment_arm = "Treatment",
  seed = 123
)
```

`export_figures_to_desktop`

Export Package Figures Folder to Desktop

Description

Copies the package figures folder to the user's Desktop. This is useful for backing up figures for GitHub, manuscripts, presentations, or supplementary materials.

Usage

```
export_figures_to_desktop(
  figures_dir = "figures",
  folder_name = "AdaptiveTrialsR_figures",
  overwrite = TRUE
)
```

Arguments

`figures_dir`	Source figures directory. Default is "figures".
`folder_name`	Name of the destination folder on Desktop.
`overwrite`	Logical. Should an existing destination folder be overwritten? Default is TRUE.

Value

Invisibly returns the destination folder path.

Examples

```
## Not run:
export_figures_to_desktop()

## End(Not run)
```

export_trial_results *Export Adaptive Trial Simulation Results*

Description

Exports simulation-level results, operating characteristics, and decision summaries from repeated Bayesian adaptive trial simulations to CSV files.

Usage

```
export_trial_results(simulations, path = ".", prefix = "adaptive_trial")
```

Arguments

simulations	An object returned by simulate_trials().
path	Directory where CSV files should be saved.
prefix	Prefix used in exported file names.

Value

Invisibly returns a character vector of written file paths.

Examples

```
sims <- simulate_trials(
  n_sim = 10,
  n_total = 100,
  true_response = c(0.25, 0.45),
  interim_every = 20,
  nsim = 1000,
  seed = 123
)

temp_dir <- tempdir()
export_trial_results(sims, path = temp_dir)
```

group_sequential_boundary *Group Sequential Monitoring Boundaries*

Description

Creates simple group sequential monitoring boundaries for interim analyses in a clinical trial. The function provides approximate efficacy and futility boundaries across planned information fractions.

Usage

```
group_sequential_boundary(
  looks = 5,
  alpha = 0.05,
  beta = 0.2,
  boundary = "obrien_fleming"
)
```

Arguments

`looks`	Number of interim looks including the final analysis.
`alpha`	Overall type I error rate. Default is 0.05.
`beta`	Type II error rate. Default is 0.20.
`boundary`	Type of efficacy boundary. Options are "obrien_fleming" and "pocock".

Value

A data frame containing information fractions and monitoring boundaries.

Examples

```
group_sequential_boundary(
  looks = 5,
  alpha = 0.05,
  beta = 0.20,
  boundary = "obrien_fleming"
)
```

`interim_monitoring` *Bayesian Interim Monitoring for Adaptive Clinical Trials*

Description

Performs Bayesian interim monitoring using a beta-binomial model and calculates the posterior probability that the treatment response rate exceeds the control response rate by a specified margin.

Usage

```
interim_monitoring(
  y_treatment,
  n_treatment,
  y_control,
  n_control,
  margin = 0,
  efficacy_threshold = 0.95,
  futility_threshold = 0.1,
  prior_alpha = 1,
```

```
  prior_beta = 1,
  nsim = 10000,
  seed = NULL
)
```

Arguments

`y_treatment`	Number of responders in the treatment arm.
`n_treatment`	Number of patients in the treatment arm.
`y_control`	Number of responders in the control arm.
`n_control`	Number of patients in the control arm.
`margin`	Minimum clinically important difference. Default is 0.
`efficacy_threshold`	Posterior probability threshold for stopping early for efficacy. Default is 0.95.
`futility_threshold`	Posterior probability threshold for stopping early for futility. Default is 0.10.
`prior_alpha`	Beta prior alpha parameter. Default is 1.
`prior_beta`	Beta prior beta parameter. Default is 1.
`nsim`	Number of posterior simulations. Default is 10000.
`seed`	Optional random seed.

Value

A data frame containing interim monitoring results.

Examples

```
interim_monitoring(
  y_treatment = 18,
  n_treatment = 40,
  y_control = 10,
  n_control = 40
)
```

`plot_dose_finding` *Plot Bayesian Dose-Finding Results*

Description

Creates a publication-quality plot of posterior toxicity probabilities across dose levels from a Bayesian CRM-style dose-finding summary.

Usage

```
plot_dose_finding(
  dose_result,
  title = "Bayesian Phase I Dose-Finding Summary",
  subtitle = "Posterior toxicity estimates by dose level"
)
```

Arguments

dose_result	A data frame returned by crm_dose_finding().
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object.

Examples

```
dose_data <- data.frame(
  dose = c(1, 2, 3, 4),
  n = c(3, 3, 3, 3),
  tox = c(0, 0, 1, 2)
)

dose_result <- crm_dose_finding(dose_data)
plot_dose_finding(dose_result)
```

---

plot_group_sequential_boundary

Plot Group Sequential Monitoring Boundaries

Description

Creates a publication-quality plot of efficacy and futility monitoring boundaries across planned interim analyses.

Usage

```
plot_group_sequential_boundary(
  boundary_data,
  title = "Group Sequential Monitoring Boundaries",
  subtitle = "Approximate efficacy and futility boundaries across interim looks"
)
```

Arguments

boundary_data	A data frame returned by group_sequential_boundary().
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object.

Examples

```
boundaries <- group_sequential_boundary(
  looks = 5,
  alpha = 0.05,
  beta = 0.20
)

plot_group_sequential_boundary(boundaries)
```

---

plot_operating_characteristics *Plot Operating Characteristics from Simulated Adaptive Trials*

Description

Creates a publication-quality bar plot of key operating characteristics from repeated Bayesian adaptive clinical trial simulations.

Usage

```
plot_operating_characteristics(
  simulations,
  title = "Operating Characteristics of Bayesian Adaptive Trial Design",
  subtitle = "Estimated from repeated trial simulations"
)
```

Arguments

simulations	An object returned by simulate_trials().
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object showing key operating characteristics.

Examples

```
sims <- simulate_trials(
  n_sim = 10,
  n_total = 100,
  true_response = c(0.25, 0.45),
  interim_every = 20,
  nsim = 1000,
  seed = 123
)

plot_operating_characteristics(sims)
```

---

plot_posterior_density

Plot Posterior Density for Trial Arms

Description

Creates a publication-quality density plot of posterior response probabilities for each trial arm using a beta-binomial model.

Usage

```
plot_posterior_density(
  data,
  arm_col = "arm",
  outcome_col = "outcome",
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  seed = NULL,
  title = "Posterior Response Distributions by Trial Arm",
 subtitle = "Beta-binomial posterior densities for binary clinical trial outcomes"
)
```

Arguments

data	A data frame containing patient-level trial data.
arm_col	Name of the treatment-arm column.
outcome_col	Name of the binary outcome column.
prior_alpha	Beta prior alpha parameter.
prior_beta	Beta prior beta parameter.
nsim	Number of posterior simulations.
seed	Optional random seed.
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object.

Examples

```
trial_data <- data.frame(
  arm = c("Control", "Control", "Treatment", "Treatment"),
  outcome = c(0, 1, 1, 1)
)

plot_posterior_density(trial_data, seed = 123)
```

---

plot_posterior_intervals

Plot Posterior Credible Intervals for Trial Arms

Description

Creates a publication-quality forest-style plot of posterior mean response rates and credible intervals for each trial arm.

Usage

```
plot_posterior_intervals(
  posterior_data,
  title = "Posterior Response Estimates by Trial Arm",
  subtitle = "Posterior means with 95% credible intervals"
)
```

Arguments

posterior_data	A data frame returned by posterior_summary().
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object.

Examples

```
trial_data <- data.frame(
  arm = c("Control", "Control", "Treatment", "Treatment"),
  outcome = c(0, 1, 1, 1)
)

post <- posterior_summary(trial_data)
plot_posterior_intervals(post)
```

plot_real_trial_results

Plot Real Trial Analysis Results

Description

Creates a publication-quality bar plot comparing observed response rates between control and treatment arms from real patient-level trial data.

Usage

```
plot_real_trial_results(
  analysis_result,
  title = "Bayesian Analysis of Real Trial Data",
  subtitle = "Observed response rates by treatment arm"
)
```

Arguments

analysis_result	A data frame returned by analyse_trial_data().
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object.

Examples

```
trial_data <- data.frame(
  arm = c("Control", "Control", "Control", "Treatment", "Treatment", "Treatment"),
  outcome = c(0, 1, 0, 1, 1, 0)
)

result <- analyse_trial_data(
  data = trial_data,
  control_arm = "Control",
  treatment_arm = "Treatment",
  seed = 123
)

plot_real_trial_results(result)
```

plot_sample_size_distribution

Plot Sample Size Distribution from Adaptive Trial Simulations

Description

Creates a publication-quality histogram showing the distribution of enrolled sample sizes across repeated Bayesian adaptive clinical trial simulations.

Usage

```
plot_sample_size_distribution(
  simulations,
  title = "Sample Size Distribution Across Adaptive Trial Simulations",
  subtitle =
   "Distribution of enrolled patients before stopping or reaching maximum sample size"
)
```

Arguments

`simulations`	An object returned by `simulate_trials()`.
`title`	Plot title.
`subtitle`	Plot subtitle.

Value

A ggplot object.

Examples

```
sims <- simulate_trials(
  n_sim = 20,
  n_total = 100,
  true_response = c(0.25, 0.45),
  interim_every = 20,
  nsim = 1000,
  seed = 123
)

plot_sample_size_distribution(sims)
```

plot_scenario_comparison

Plot Scenario Comparison for Adaptive Trial Simulations

Description

Creates a publication-quality plot comparing operating characteristics across multiple true treatment-effect scenarios.

Usage

```
plot_scenario_comparison(
  scenario_results,
  metric = "probability_stop_efficacy",
  title = "Operating Characteristics Across Trial Scenarios",
 subtitle = "Bayesian adaptive trial performance under different treatment effects"
)
```

Arguments

`scenario_results`	A data frame returned by `compare_trial_scenarios()`.
`metric`	Operating characteristic to plot. Default is "probability_stop_efficacy".
`title`	Plot title.
`subtitle`	Plot subtitle.

Value

A ggplot object.

Examples

```
scenarios <- data.frame(
  control_response = c(0.25, 0.25, 0.25),
  treatment_response = c(0.25, 0.35, 0.45)
)

scenario_results <- compare_trial_scenarios(
  scenarios = scenarios,
  n_sim = 10,
  n_total = 100,
  interim_every = 20,
  nsim = 1000,
  seed = 123
)

plot_scenario_comparison(scenario_results)
```

plot_treatment_effect *Plot Bayesian Treatment Effect*

Description

Creates a publication-quality plot of the posterior treatment-control difference with a Bayesian credible interval.

Usage

```
plot_treatment_effect(
  effect_result,
  title = "Bayesian Treatment Effect Estimate",
  subtitle = "Posterior treatment-control difference with credible interval"
)
```

Arguments

effect_result	A data frame returned by estimate_treatment_effect().
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object.

Examples

```
trial_data <- data.frame(
  arm = c("Control", "Control", "Treatment", "Treatment"),
  outcome = c(0, 1, 1, 1)
)

effect <- estimate_treatment_effect(
  data = trial_data,
  control_arm = "Control",
  treatment_arm = "Treatment",
  seed = 123
)

plot_treatment_effect(effect)
```

plot_trial_path *Plot Interim Monitoring Path for an Adaptive Trial*

Description

Creates a publication-quality plot of posterior probability across interim analyses for a simulated Bayesian adaptive clinical trial.

Usage

```
plot_trial_path(
  trial,
  title = "Bayesian Interim Monitoring Path",
  subtitle = "Posterior probability of treatment benefit across interim analyses"
)
```

Arguments

trial	An object returned by simulate_trial().
title	Plot title.
subtitle	Plot subtitle.

Value

A ggplot object showing the Bayesian interim monitoring path.

Examples

```
trial <- simulate_trial(
  n_total = 100,
  true_response = c(0.25, 0.45),
  interim_every = 20,
  seed = 123
)

plot_trial_path(trial)
```

posterior_summary *Posterior Summary for Binary Trial Outcomes*

Description

Computes Bayesian posterior summaries for binary response rates in each treatment arm using a beta-binomial model.

Usage

```
posterior_summary(
  data,
  arm_col = "arm",
  outcome_col = "outcome",
  prior_alpha = 1,
  prior_beta = 1,
  cred_level = 0.95
)
```

Arguments

`data`	A data frame containing patient-level trial data.
`arm_col`	Name of the treatment-arm column.
`outcome_col`	Name of the binary outcome column.
`prior_alpha`	Beta prior alpha parameter.
`prior_beta`	Beta prior beta parameter.
`cred_level`	Credible interval level. Default is 0.95.

Value

A data frame containing posterior summaries by treatment arm.

Examples

```
trial_data <- data.frame(
  arm = c("Control", "Control", "Treatment", "Treatment"),
  outcome = c(0, 1, 1, 1)
)

posterior_summary(trial_data)
```

`predict_success` *Predict Bayesian Probability of Trial Success*

Description

Calculates the posterior probability that the treatment response rate exceeds the control response rate by at least a specified margin using a beta-binomial model.

Usage

```
predict_success(
  y_treatment,
  n_treatment,
  y_control,
  n_control,
  margin = 0,
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  seed = NULL
)
```

Arguments

`y_treatment`	Number of responders in the treatment arm.
`n_treatment`	Number of patients in the treatment arm.
`y_control`	Number of responders in the control arm.
`n_control`	Number of patients in the control arm.
`margin`	Minimum clinically important difference. Default is 0.
`prior_alpha`	Beta prior alpha parameter. Default is 1.
`prior_beta`	Beta prior beta parameter. Default is 1.
`nsim`	Number of posterior simulations. Default is 10000.
`seed`	Optional random seed.

Value

A data frame containing posterior probability and decision.

Examples

```
predict_success(
  y_treatment = 18,
  n_treatment = 40,
  y_control = 10,
  n_control = 40
)
```

predictive_probability

Predictive Probability of Trial Success

Description

Estimates the predictive probability that a trial will meet its final success criterion if recruitment continues to the planned maximum sample size. This is useful for Bayesian futility monitoring in adaptive trials.

Usage

```
predictive_probability(
  y_treatment,
  n_treatment,
  y_control,
  n_control,
  n_total,
  margin = 0,
  success_threshold = 0.95,
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  seed = NULL
)
```

Arguments

`y_treatment`	Current number of responders in the treatment arm.
`n_treatment`	Current number of patients in the treatment arm.
`y_control`	Current number of responders in the control arm.
`n_control`	Current number of patients in the control arm.
`n_total`	Planned total sample size across both arms.
`margin`	Minimum clinically important treatment-control difference.
`success_threshold`	Posterior probability threshold for final success.
`prior_alpha`	Beta prior alpha parameter.
`prior_beta`	Beta prior beta parameter.
`nsim`	Number of simulation draws.
`seed`	Optional random seed.

Value

A data frame containing predictive probability and decision.

Examples

```
predictive_probability(
  y_treatment = 12,
  n_treatment = 30,
  y_control = 8,
  n_control = 30,
  n_total = 100,
  seed = 123
)
```

`sample_size_binary` *Sample Size for Two-Arm Binary Endpoint Trial*

Description

Calculates an approximate sample size for a two-arm clinical trial with binary outcomes using a normal approximation for comparing two proportions.

Usage

```
sample_size_binary(
  p_control,
  p_treatment,
  alpha = 0.05,
  power = 0.8,
  allocation_ratio = 1
)
```

Arguments

`p_control`	Expected response probability in the control arm.
`p_treatment`	Expected response probability in the treatment arm.
`alpha`	Type I error rate. Default is 0.05.
`power`	Desired statistical power. Default is 0.80.
`allocation_ratio`	Allocation ratio treatment/control. Default is 1.

Value

A data frame containing sample size calculations.

Examples

```
sample_size_binary(
  p_control = 0.25,
  p_treatment = 0.45
)
```

simon_two_stage *Simon Two-Stage Phase II Trial Design*

Description

Searches for a Simon two-stage design for a single-arm Phase II trial with a binary outcome. The design tests an unacceptable response rate against a desirable response rate while controlling the type I error rate and ensuring the required power.

Usage

```
simon_two_stage(p0, p1, alpha = 0.05, power = 0.8, n_max = 100)
```

Arguments

p0	Unacceptable response probability under the null hypothesis.
p1	Desirable response probability under the alternative hypothesis.
alpha	Maximum type I error rate. Default is 0.05.
power	Minimum desired power. Default is 0.80.
n_max	Maximum total sample size to search. Default is 100.

Value

A data frame containing the selected Simon two-stage design.

Examples

```
simon_two_stage(
  p0 = 0.20,
  p1 = 0.40,
  alpha = 0.10,
  power = 0.70,
  n_max = 35
)

## Not run:
simon_two_stage(
  p0 = 0.20,
  p1 = 0.40,
  alpha = 0.05,
  power = 0.80,
  n_max = 80
)

## End(Not run)
```

simulate_trial — *Simulate a Bayesian Adaptive Clinical Trial*

Description

Simulates a two-arm Bayesian adaptive clinical trial with binary outcomes. The trial can include interim monitoring for early stopping based on posterior probability thresholds.

Usage

```
simulate_trial(
  n_total = 100,
  true_response = c(0.25, 0.4),
  arm_names = c("Control", "Treatment"),
  interim_every = 20,
  margin = 0,
  efficacy_threshold = 0.95,
  futility_threshold = 0.1,
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  seed = NULL
)
```

Arguments

`n_total`	Maximum total sample size.
`true_response`	Numeric vector of true response probabilities for control and treatment arms.
`arm_names`	Character vector of treatment arm names.
`interim_every`	Frequency of interim analyses.
`margin`	Minimum clinically important treatment-control difference.
`efficacy_threshold`	Posterior probability threshold for stopping early for efficacy.
`futility_threshold`	Posterior probability threshold for stopping early for futility.
`prior_alpha`	Beta prior alpha parameter.
`prior_beta`	Beta prior beta parameter.
`nsim`	Number of posterior simulations.
`seed`	Optional random seed.

Value

A list containing patient-level data, interim results, and final trial decision.

Examples

```
simulate_trial(
  n_total = 100,
  true_response = c(0.25, 0.40),
  interim_every = 20,
  seed = 123
)
```

---

simulate_trials *Simulate Multiple Bayesian Adaptive Clinical Trials*

Description

Runs repeated simulations of a Bayesian adaptive clinical trial and estimates key operating characteristics, including stopping probability, efficacy stopping rate, futility stopping rate, mean sample size, and probability of trial success.

Usage

```
simulate_trials(
  n_sim = 100,
  n_total = 100,
  true_response = c(0.25, 0.4),
  arm_names = c("Control", "Treatment"),
  interim_every = 20,
  margin = 0,
  efficacy_threshold = 0.95,
  futility_threshold = 0.1,
  prior_alpha = 1,
  prior_beta = 1,
  nsim = 10000,
  seed = NULL
)
```

Arguments

`n_sim`	Number of simulated trials.
`n_total`	Maximum total sample size per trial.
`true_response`	Numeric vector of true response probabilities for control and treatment arms.
`arm_names`	Character vector of treatment arm names.
`interim_every`	Frequency of interim analyses.
`margin`	Minimum clinically important treatment-control difference.
`efficacy_threshold`	Posterior probability threshold for stopping early for efficacy.

`futility_threshold`
: Posterior probability threshold for stopping early for futility.

`prior_alpha` Beta prior alpha parameter.

`prior_beta` Beta prior beta parameter.

`nsim` Number of posterior simulations used inside each trial.

`seed` Optional random seed.

Value

A list containing simulation-level results and operating characteristics.

Examples

```
sims <- simulate_trials(
  n_sim = 10,
  n_total = 100,
  true_response = c(0.25, 0.45),
  interim_every = 20,
  nsim = 1000,
  seed = 123
)

sims$operating_characteristics
```

---

summary_trial *Summarise a Simulated Adaptive Trial*

Description

Provides a concise summary of a simulated adaptive clinical trial object produced by `simulate_trial()`.

Usage

```
summary_trial(trial)
```

Arguments

`trial` An object returned by `simulate_trial()`.

Value

A data frame summarising trial sample size, responses, stopping status, and final decision.

Examples

```
trial <- simulate_trial(
  n_total = 100,
  true_response = c(0.25, 0.40),
  interim_every = 20,
  seed = 123
)

summary_trial(trial)
```

`trial_report` *Generate a Plain-Language Adaptive Trial Report*

Description

Creates a concise plain-language report from repeated Bayesian adaptive clinical trial simulations. The report is intended for clinicians, trial teams, and non-statistical audiences.

Usage

```
trial_report(simulations)
```

Arguments

`simulations`	An object returned by `simulate_trials()`.

Value

A character vector containing a formatted trial report.

Examples

```
sims <- simulate_trials(
  n_sim = 20,
  n_total = 100,
  true_response = c(0.25, 0.45),
  interim_every = 20,
  nsim = 1000,
  seed = 123
)

trial_report(sims)
```

validate_trial_data *Validate Real Trial Data for Adaptive Trial Analysis*

Description

Checks whether a real clinical trial dataset has the minimum required structure for use with AdaptiveTrialsR functions. The dataset must contain one row per patient, a treatment-arm variable, and a binary outcome variable.

Usage

```
validate_trial_data(
  data,
  arm_col = "arm",
  outcome_col = "outcome",
  allowed_outcomes = c(0, 1)
)
```

Arguments

`data`	A data frame containing patient-level trial data.
`arm_col`	Name of the treatment-arm column.
`outcome_col`	Name of the binary outcome column.
`allowed_outcomes`	Allowed values for the binary outcome. Default is c(0, 1).

Value

A cleaned data frame with standardised columns `arm` and `outcome`.

Examples

```
trial_data <- data.frame(
  patient_id = 1:6,
  arm = c("Control", "Control", "Treatment", "Treatment", "Control", "Treatment"),
  outcome = c(0, 1, 1, 1, 0, 1)
)

validate_trial_data(trial_data)
```

Index

adaptive_randomisation, 2
analyse_trial_data, 3
analyse_trial_data(), *18*

compare_trial_scenarios, 5
compare_trial_scenarios(), *20*
create_trial_template, 6
crm_dose_finding, 7
crm_dose_finding(), *14*

decision_summary, 8

estimate_treatment_effect, 8
estimate_treatment_effect(), *21*
export_figures_to_desktop, 10
export_trial_results, 11

group_sequential_boundary, 11
group_sequential_boundary(), *15*

interim_monitoring, 12

plot_dose_finding, 13
plot_group_sequential_boundary, 14
plot_operating_characteristics, 15
plot_posterior_density, 16
plot_posterior_intervals, 17
plot_real_trial_results, 18
plot_sample_size_distribution, 19
plot_scenario_comparison, 20
plot_treatment_effect, 21
plot_trial_path, 22
posterior_summary, 22
posterior_summary(), *17*
predict_success, 23
predictive_probability, 25

sample_size_binary, 26
simon_two_stage, 27
simulate_trial, 28
simulate_trial(), *22*, *30*
simulate_trials, 29
simulate_trials(), *8*, *11*, *15*, *19*, *31*
summary_trial, 30

trial_report, 31

validate_trial_data, 32