Package: BBMBC (via r-universe)

October 31, 2026

Title Beta-Binomial Models for Immune Cell Frequencies and Power Calculations

Version 1.0.1

Description Provides tools to model overdispersed immune cell frequencies using Beta-Binomial generalized linear models. Originally designed for memory B cells, the framework generalizes to evaluate rare cellular immune responses across vaccinology, immuno-oncology, and related fields. Includes method-of-moments dispersion estimation, likelihood ratio testing across experimental arms, and Monte Carlo simulation to calculate statistical power and Type I error rates. The methodologies are directly motivated by the analysis of immunology data in ``Vaccination with mRNA-encoded membrane-anchored HIV envelope trimers elicited tier 2 neutralizing antibodies in a phase 1 clinical trial" (Parks et al. 2025) <doi:10.1126/scitranslmed.ady6831>.

Encoding UTF-8

Depends R (>= 4.1.0)

Imports doParallel, foreach, glmmTMB, parallel, stats, utils

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Config/roxygen2/version 8.0.0

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NeedsCompilation no

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Repository https://cran.r-universe.dev

Date/Publication 2026-10-31 12:48:14 UTC

RemoteUrl https://github.com/cran/BBMBC

RemoteRef HEAD

RemoteSha 5bae70e736108e6d714f604b5fbf2e5be16218f0

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`calc_power_bb` *Calculate Statistical Power for Beta-Binomial Models (Parallelized)*

Description

Simulates overdispersed cell frequency data under the alternative hypothesis to estimate the statistical power of a Beta-Binomial generalized linear model.

Usage

```
calc_power_bb(
  n_0 = 20,
  n_1 = 20,
  p_base = 0.005,
  fold_change = 2,
  rho_0 = 0.006,
  rho_1 = 0.006,
  alpha = 0.05,
  min_cells = 1e+05,
  max_cells = 1e+06,
  seed = 2025,
  n_sims = 1000,
  n_cores = min(2, max(1, parallel::detectCores() - 1))
)
```

Arguments

`n_0`	Integer. Biological replicates in control arm (default: 20).
`n_1`	Integer. Biological replicates in treatment arm (default: 20).
`p_base`	Numeric. Baseline proportion in control group (default: 0.005).
`fold_change`	Numeric. Ratio of treatment mean to control mean (default: 2.0).
`rho_0`	Numeric. Overdispersion for control group (default: 0.006).
`rho_1`	Numeric. Overdispersion for treatment group (default: 0.006).
`alpha`	Numeric. Significance threshold for likelihood ratio test (default: 0.05).
`min_cells`	Integer. Minimum total cells per sample (default: 1e5).
`max_cells`	Integer. Maximum total cells per sample (default: 1e6).

seed	Integer. Random seed for reproducibility (default: 2025).
n_sims	Integer. Number of simulations to run (default: 1000).
n_cores	Integer. Number of cores for parallel processing. Defaults to 2 (CRAN safe default).

Value

A list of class power_result containing the estimated statistical power, convergence metrics, and the input parameters used.

Examples

```
# Evaluate statistical power across a range of sample sizes
sample_sizes <- c(10, 15, 20, 25)
power_results <- numeric(length(sample_sizes))
names(power_results) <- paste0("N=", sample_sizes, "/arm")

for (i in seq_along(sample_sizes)) {
  n <- sample_sizes[i]

  # Run simulation for the current sample size
  # Note: n_sims = 100 is used here for demonstration speed.
  # For formal analysis, use n_sims = 1000 or higher.
  pwr_res <- calc_power_bb(
    n_0 = n, n_1 = n,
    p_base = 0.005,
    fold_change = 2.0,
    rho_0 = 0.006, rho_1 = 0.006,
    n_sims = 100,
    n_cores = 1
  )

  power_results[i] <- pwr_res$power
}

# Print the resulting power curve estimates
print(power_results)
```

---

calc_rho_mom *Estimate Overdispersion (Rho) via Method of Moments*

Description

Calculates a rapid empirical estimate of the intra-class correlation (overdispersion parameter, rho) for proportion data. This method of moments estimator uses the ratio of the sample variance of the proportions to the theoretical maximum variance of a true binomial distribution with the same mean.

Usage

```
calc_rho_mom(props, na.rm = TRUE)
```

Arguments

props	Numeric vector of observed proportions (must be between 0 and 1).
na.rm	Logical. Should missing values (including NaN) be removed before computation? (default: TRUE).

Value

A numeric value representing the estimated overdispersion parameter (rho). Returns NA if the sample mean is exactly 0 or 1, as the denominator becomes 0.

Examples

```
# Simulate 100 proportions with a known mean of 0.2 and overdispersion of 0.05
set.seed(123)
p_base <- 0.2
rho_true <- 0.05
shape1 <- p_base * (1 - rho_true) / rho_true
shape2 <- (1 - p_base) * (1 - rho_true) / rho_true

sim_props <- stats::rbeta(100, shape1, shape2)

# Estimate rho empirically
estimated_rho <- calc_rho_mom(sim_props)
print(estimated_rho)
```

---

calc_t1_bb *Calculate Type I Error for Beta-Binomial Models*

Description

Simulates immunology data under the null hypothesis of equal means (no biological difference in cell frequency) using parallel processing. Handles balanced/unbalanced sample sizes and dynamic overdispersion.

Usage

```
calc_t1_bb(
  n_0 = 20,
  n_1 = 20,
  p_base = 0.005,
  rho_0 = 0.006,
  rho_1 = 0.006,
  alpha = 0.05,
  min_cells = 1e+05,
```

```
  max_cells = 1e+06,
  seed = 2026,
  n_sims = 1000,
  n_cores = min(2, max(1, parallel::detectCores() - 1))
)
```

Arguments

n_0	Integer. The number of biological replicates in the control arm (default: 20).
n_1	Integer. The number of biological replicates in the treatment arm (default: 20).
p_base	Numeric. Baseline proportion of the target cell population for BOTH groups (default: 0.005).
rho_0	Numeric. Intra-class correlation (overdispersion) for the control group (default: 0.006).
rho_1	Numeric. Intra-class correlation (overdispersion) for the treatment group (default: 0.006).
alpha	Numeric. Significance threshold for the likelihood ratio test (default: 0.05).
min_cells	Integer. Minimum number of total cells analyzed per sample (default: 1e5).
max_cells	Integer. Maximum number of total cells analyzed per sample (default: 1e6).
seed	Integer. Random seed for reproducibility (default: 2026).
n_sims	Integer. The number of simulations to run (default: 1000).
n_cores	Integer. Number of cores to use for parallel processing. Defaults to 2 (CRAN safe default).

Value

A list of class `t1_error_result` containing the estimated Type I error rate, convergence metrics, and the input parameters.

Examples

```
# Run small simulation example
res <- calc_t1_bb(
  n_0 = 10, n_1 = 10,
  rho_0 = 0.006, rho_1 = 0.006,
  n_sims = 10,
  n_cores = 1
)
print(res$type_1_error_rate)
```

`test_diff_bb` *Beta-Binomial Likelihood Ratio Test for Group Differences*

Description

Performs a Likelihood Ratio Test (LRT) using Beta-Binomial models to evaluate whether the underlying proportion of events differs significantly between two groups.

Usage

```
test_diff_bb(
  data,
  success_col,
  total_col,
  group_col,
  unequal_dispersion = FALSE
)
```

Arguments

`data`	A data frame containing the experimental data.
`success_col`	Character string specifying the column name for successes.
`total_col`	Character string specifying the column name for total trials.
`group_col`	Character string specifying the column name with group labels (must have 2 levels).
`unequal_dispersion`	Logical. If TRUE, models group-specific overdispersion. Default: FALSE.

Value

A list of class `bb_test_result` containing p-value, chi-square statistic, degrees of freedom, log-odds ratio, and its standard error.

Examples

```
set.seed(2025)
trial_data <- data.frame(
  arm = rep(c("Control", "Vaccine"), each = 15),
  total_bcells = as.integer(stats::runif(30, 100000, 500000))
)
trial_data$target_cells <- ifelse(
  trial_data$arm == "Control",
  stats::rbinom(15, trial_data$total_bcells, stats::rbeta(15, 5, 995)),
  stats::rbinom(15, trial_data$total_bcells, stats::rbeta(15, 10, 990))
)

result <- test_diff_bb(
```

```
  data = trial_data,
  success_col = "target_cells",
  total_col = "total_bcells",
  group_col = "arm",
  unequal_dispersion = FALSE
)
print(result$p_value)
```

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