

# Package ‘GenScreenBayes’

November 21, 2025

**Title** Tweedie-Based Empirical Bayes Genomic Screening

**Version** 0.0.1

**Description** Tools for empirical Bayes genomic screening using Tweedie mixture models. Provides functions to estimate control and test Tweedie parameters, compute marginal densities and likelihood ratios, evaluate survival probabilities for test-control differences, perform posterior inference for  $\pi_0$ , and obtain gene-level screening probabilities, with plotting utilities for posterior  $\pi_0$  summaries.

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**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Depends** R ( $\geq 4.1.0$ )

**Imports** stringr,

future,

future.apply,

furrr,

mvQuad,

gtools,

purrr,

maxLik,

memoise,

tweedie,

ggplot2,

parallel,

stats,

utils

**Suggests** testthat ( $\geq 3.0.0$ ),

knitr,

rmarkdown

**Config/testthat/edition** 3

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GenScreenCalcs.fn	<i>Genomic screening calculations for Tweedie models</i>
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**Description**

Given control/test matrices and tuning parameters, perform the full Tweedie-based empirical Bayes genomic screening workflow: posterior estimation of control parameters, construction of test parameters, marginal densities, difference survival probabilities, posterior  $\pi_0$ , and screening probabilities.

**Usage**

```
GenScreenCalcs.fn(GenScrnList, xlim = NULL)
```

**Arguments**

GenScrnList	A list (typically from <a href="#">GenScreenMenu.fn</a> ) with at least components xC, xT, Tmod, TargDiffs, pi0, zeta, ngridpts, and inits.
xlim	Numeric length-2 vector giving x-axis limits for $\pi_0$ plots.

**Value**

A list with components including:

- TstMargDens – marginal densities and likelihood ratios,
- SurvDiffs – survival probabilities of differences,
- PostDenCDFpi0 – posterior density and CDF of  $\pi_0$ ,
- Pgam0 – gene-specific screening probabilities,
- ElapsedTime – elapsed time for the main computation.

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GenScreenMenu.fn	<i>Interactive menu to set up GenScreen inputs</i>
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**Description**

This function interactively collects control/test matrices and hyperparameters for the Tweedie genomic screening workflow and returns a list suitable for [GenScreenCalcs.fn](#).

**Usage**

```
GenScreenMenu.fn(
  inits_init = c(1.5, 2),
  Tmod_init = c(2, 4, 1),
  TargDiffs_init = c(2, 4, 6, 8),
  ngridpts_init = 10,
  digits_init = 3,
  zeta_init = 5,
  pi0_init = ".0001*0:10000",
  interactive = TRUE
)
```

**Arguments**

<code>inits_init</code>	Initial values for Tweedie mean & dispersion (length-2 numeric).
<code>Tmod_init</code>	Length-3 numeric giving Tweedie prior hyperparameters.
<code>TargDiffs_init</code>	Numeric vector of target difference values.
<code>ngridpts_init</code>	Number of grid points for Gauss–Hermite integration.
<code>digits_init</code>	Number of digits for printing output.
<code>zeta_init</code>	Beta(zeta, 1) prior parameter for $\pi_0$ .
<code>pi0_init</code>	Expression defining the grid for $\pi_0$ .
<code>interactive</code>	Logical; if TRUE, prompt the user and optionally run <a href="#">GenScreenCalcs.fn</a> .

**Value**

A list containing `xC`, `xT`, `inits`, `Tmod`, `TargDiffs`, `pi0`, `zeta`, `ngridpts`, and `digits`, or the result of `GenScreenCalcs.fn` if called interactively.

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