Package ‘ROCModels’

May 7, 2026

Title ROC Models and AUC Estimation

Version 1.0.0

Description

The receiver operating characteristic (ROC) curve is one of the most widely used tools for evaluating diagnostic and prognostic biomarkers across diverse scientific fields, particularly in medicine. Despite its ubiquity, ROC estimation and testing methods differ substantially in their assumptions and resulting curve properties. This package provides a unified framework for constructing, visualizing, and comparing parametric, nonparametric, semiparametric, and Bayesian ROC curves. 'ROCModels' helps researchers identify and implement ROC inference methods most suitable for their data. See the accompanying vignette 'ROCModels_Package_Doc' for a detailed introduction. Alonzo, T. A., and Pepe, M. S. (2002) <doi:10.1093/biostatistics/3.3.421>, Andrews, D. F., and Herzberg, A. M. (1985) <doi:10.1007/978-1-4612-5098-2>, Bamber, D. (1975) <doi:10.1016/0022-2496(75)90001-2>, Cox, D. R. (1972) <doi:10.1111/j.2517-6161.1972.tb00899.x>, Cox, D. R. (1975) <doi:10.1093/biomet/62.2.269>, DeLong, E. R., DeLong, D. M., and Clarke-Pearson, D. L. (1988) <doi:10.2307/2531595>, Dorfman, D. D., and Alf, E. (1969) <doi:10.1016/0022-2496(69)90019-4>, Dorfman, D. D., Berbaum, K. S., and Metz, C. E. (1997) <doi:10.1016/s1076-6332(97)80013-x>, Erkanli, A., Sung, L., and Stamey, J. D. (2006) <doi:10.1002/sim.2496>, Faraggi, D., and Reiser, B. (2002) <doi:10.1002
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0258(19971015)16:19%3C2143::AID-SIM655%3E3.0.CO;2-3>.

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Imports ggplot2, kedd, dplyr, survival, nleqslv, HDInterval, ROCit, doParallel, foreach, pbivnorm, nor1mix, parallel, readr, MASS, doRNG

Depends R (>= 3.5)

LazyData true

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.2

NeedsCompilation no

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Contents

`AUC` *Calculates AUC, confidence intervals, and generates a ROC plot.*

Description

Calculates AUC, confidence intervals, and generates a ROC plot.

Usage

```
AUC(
  data,
  method,
  ci = TRUE,
  ci_method = "delong",
```

```
  siglevel = 0.05,
  boot_iter = 1000,
  seed = NULL
)
```

Arguments

`data`	A data frame containing at least two columns: **biomarker** Numeric values representing the diagnostic marker. **status** Character or factor with levels ‘"0"‘ (controls) and ‘"1"‘ (cases).
`method`	A character string specifying the ROC/AUC modeling approach. Supported options include: • ‘"empirical"‘ – empirical ROC • ‘"order"‘ – ROC curve under stochastic order constraints • ‘"norm_silver"‘ – kernel ROC with normal kernel and Silverman bandwidth • ‘"norm_ucv"‘ – kernel ROC with normal kernel and UCV bandwidth • ‘"bi_silver"‘ – kernel ROC with biweight kernel and Silverman bandwidth • ‘"bi_ucv"‘ – kernel ROC with biweight kernel and UCV bandwidth • ‘"binormal"‘ – classical binormal ROC model • ‘"biweibull"‘ – parametric bi-Weibull ROC • ‘"bigamma"‘ – parametric ROC assuming gamma distributions • ‘"lehmann"‘ – ROC under the Lehmann alternative • ‘"bayesbiweibull"‘ – Bayesian bi-Weibull ROC (MCMC-based) • ‘"BB"‘ – Bayesian bootstrap ROC • ‘"dpm"‘ – Dirichlet process mixture ROC
`ci`	Logical; if ‘TRUE‘ (default), computes confidence intervals for the AUC (or credible intervals for Bayesian methods).
`ci_method`	Character string specifying the type of interval estimation. Not all CI methods are compatible with every model: • ‘"delong"‘ – DeLong’s variance-based normal approximation • ‘"bootstrap"‘ – nonparametric bootstrap interval • ‘"hm"‘ – Hanley–McNeil variance-based interval • ‘"mle"‘ – likelihood-based interval • ‘"all"‘ – computes all applicable interval types for the selected method
`siglevel`	Numeric; significance level α for the confidence interval. The corresponding confidence level is $1 - \alpha$.
`boot_iter`	Integer; number of bootstrap resamples (used when ‘ci_method = "bootstrap"‘ or ‘"all"‘). Larger values give more stable intervals but increase computation time.
`seed`	Integer; random seed for reproducibility.

Value

A list with the following elements:

summary Printed output of the AUC and confidence intervals.

plot A ‘ggplot‘ object visualizing the ROC curve.

The exact structure may vary depending on the chosen model.

Examples

```
# Import well formated dataset
data(DMDmodified)
# Calculate AUC summary and ROC plot
auc <- AUC(
  data=DMDmodified,
  method = "empirical",
  ci        = TRUE
)
# Get the AUC summary
cat(auc$summary)
# Get the ROC plot
auc$plot
```

`DMDmodified` *DMDmodified dataset*

Description

A dataset used for ROC modeling examples.

Usage

```
DMDmodified
```

Format

A data frame with X rows and Y variables:

X ID for the row

biomarker Biomarker value

status Status

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