

Package ‘survdnn’

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Title Deep Neural Networks for Survival Analysis with R 'torch'

Version 0.7.5

Description Provides deep learning models for right-censored survival data using the 'torch' backend. Supports multiple loss functions, including Cox partial likelihood, L2-penalized Cox, time-dependent Cox, and accelerated failure time (AFT) loss. Offers a formula-based interface, built-in support for cross-validation, hyperparameter tuning, survival curve plotting, and evaluation metrics such as the C-index, Brier score, and integrated Brier score. For methodological details, see Kvamme et al. (2019) <<https://www.jmlr.org/papers/v20/18-424.html>>.

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BugReports <https://github.com/ielbadisy/survdnn/issues>

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brier	<i>Brier Score for Right-Censored Survival Data at a Fixed Time</i>
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Description

Computes the Brier score at a fixed time point using inverse probability of censoring weights (IPCW).

Usage

```
brier(object, pre_sp, t_star)
```

Arguments

- object A ‘Surv’ object with observed time and status.
- pre_sp A numeric vector of predicted survival probabilities at ‘t_star’.
- t_star The evaluation time point.

Value

A single numeric value representing the Brier score a a specific time point.

Examples

```
library(survival)
data(veteran, package = "survival")
mod <- survdnn(Surv(time, status) ~
  age + karno + celltype, data = veteran, epochs = 50, verbose = FALSE)
pred <- predict(mod, newdata = veteran, type = "survival", times = c(30, 90, 180))
y <- model.response(model.frame(mod$formula, veteran))
survdnn::brier(y, pre_sp = pred[["t=90"]], t_star = 90)
```

callback_early_stopping

Early stopping callback for survdnn

Description

Simple early stopping on a monitored scalar, typically the training loss.

Usage

```
callback_early_stopping(
  patience = 10L,
  min_delta = 0,
  mode = c("min", "max"),
  verbose = FALSE
)
```

Arguments

patience	Integer. Number of epochs with no improvement before stopping.
min_delta	Minimum change to qualify as an improvement (default: 0).
mode	Character. "min" (for losses) or "max" (for metrics to maximize).
verbose	Logical. Whether to print a message when early stopping is triggered.

Value

A function of the form ‘function(epoch, current)’ that returns TRUE if training should stop, FALSE otherwise.

cindex_survmat

Concordance Index from a Survival Probability Matrix

Description

Computes the time-dependent concordance index (C-index) from a predicted survival matrix at a fixed time point. The risk is computed as $1 - S(t_{\text{star}})$.

Usage

```
cindex_survmat(object, predicted, t_star = NULL)
```

Arguments

object	A 'Surv' object representing the observed survival data.
predicted	A data frame or matrix of predicted survival probabilities. Each column corresponds to a time point (e.g., 't=90', 't=180').
t_star	A numeric time point corresponding to one of the columns in 'predicted'. If 'NULL', the last column is used.

Value

A single numeric value representing the C-index.

Examples

```
library(survival)
data(veteran, package = "survival")
mod <- survdnn(Surv(time, status) ~
  age + karno + celltype, data = veteran, epochs = 50, verbose = FALSE)
pred <- predict(mod, newdata = veteran, type = "survival", times = c(30, 90, 180))
y <- model.response(model.frame(mod$formula, veteran))
cindex_survmat(y, pred, t_star = 180)
```

cv_survdnn

K-Fold Cross-Validation for survdnn Models

Description

Performs cross-validation for a 'survdnn' model using the specified evaluation metrics.

Usage

```
cv_survdnn(
  formula,
  data,
  times,
  metrics = c("cindex", "ibs"),
  folds = 5,
  .seed = NULL,
  .device = c("auto", "cpu", "cuda"),
  na_action = c("omit", "fail"),
  ...
)
```

Arguments

formula	A survival formula, e.g., 'Surv(time, status) ~ x1 + x2'.
data	A data frame.
times	A numeric vector of evaluation time points.
metrics	A character vector: any of "cindex", "brier", "ibs".
folds	Integer. Number of folds to use.
.seed	Optional. Set random seed for reproducibility.
.device	Character string indicating the computation device used when fitting the models in each fold. One of "auto", "cpu", or "cuda". "auto" uses CUDA if available, otherwise falls back to CPU.
na_action	Character. How to handle missing values within each fold: "omit" drops incomplete rows; "fail" errors if any NA is present.
...	Additional arguments passed to [survdnn()].

Value

A tibble containing metric values per fold and (optionally) per time point.

Examples

```
library(survival)
data(veteran)
cv_survdnn(
  Surv(time, status) ~ age + karno + celltype,
  data = veteran,
  times = c(30, 90, 180),
  metrics = "ibs",
  folds = 3,
  .seed = 42,
  hidden = c(16, 8),
  epochs = 5
)
```

`evaluate_survdnn`*Evaluate a survdnn Model Using Survival Metrics*

Description

Computes evaluation metrics for a fitted ‘survdnn’ model at one or more time points. Supported metrics include the concordance index (“cindex”), Brier score (“brier”), and integrated Brier score (“ibs”).

Usage

```
evaluate_survdnn(  
  model,  
  metrics = c("cindex", "brier", "ibs"),  
  times,  
  newdata = NULL,  
  na_action = c("omit", "fail"),  
  verbose = FALSE  
)
```

Arguments

<code>model</code>	A fitted ‘survdnn’ model object.
<code>metrics</code>	A character vector of metric names: “cindex”, “brier”, “ibs”.
<code>times</code>	A numeric vector of evaluation time points.
<code>newdata</code>	Optional. A data frame on which to evaluate the model. Defaults to training data.
<code>na_action</code>	Character. How to handle missing values in evaluation data: “omit” drops incomplete rows, “fail” errors if any NA is present.
<code>verbose</code>	Logical. If TRUE and ‘na_action=“omit”’, prints a message when rows are removed.

Value

A tibble with evaluation results, containing at least ‘metric’, ‘value’, and possibly ‘time’.

gridsearch_survdnn	<i>Grid Search for survdnn Hyperparameters</i>
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Description

Performs grid search over user-specified hyperparameters and evaluates performance on a validation set.

Usage

```
gridsearch_survdnn(  
  formula,  
  train,  
  valid,  
  times,  
  metrics = c("cindex", "ibs"),  
  param_grid,  
  .seed = 42,  
  .device = c("auto", "cpu", "cuda")  
)
```

Arguments

formula	A survival formula (e.g., 'Surv(time, status) ~ .')
train	Training dataset
valid	Validation dataset
times	Evaluation time points (numeric vector)
metrics	Evaluation metrics (character vector): any of "cindex" and "ibs".
param_grid	A named list of hyperparameters to search over. Currently supported entries are hidden, lr, activation, epochs, and loss.
.seed	Optional random seed for reproducibility
.device	Character string indicating the computation device used when fitting all models in the grid search. One of "auto", "cpu", or "cuda". This is a runtime setting and is not part of the hyperparameter grid.

Value

A tibble with configurations and their validation metrics

Examples

```
library(survdnn)  
library(survival)  
set.seed(123)  
  
# Simulate small dataset
```

```

n <- 300
x1 <- rnorm(n); x2 <- rbinom(n, 1, 0.5)
time <- rexp(n, rate = 0.1)
status <- rbinom(n, 1, 0.7)
df <- data.frame(time, status, x1, x2)

# Split into training and validation
idx <- sample(seq_len(n), 0.7 * n)
train <- df[idx, ]
valid <- df[-idx, ]

# Define formula and param grid
formula <- Surv(time, status) ~ x1 + x2
param_grid <- list(
  hidden    = list(c(16, 8), c(32, 16)),
  lr         = c(1e-3),
  activation = c("relu"),
  epochs     = c(100),
  loss       = c("cox", "coxtime")
)

# Run grid search
results <- gridsearch_survnn(
  formula = formula,
  train    = train,
  valid    = valid,
  times    = c(10, 20, 30),
  metrics  = c("cindex", "ibs"),
  param_grid = param_grid
)

# View summary
dplyr::group_by(results, hidden, lr, activation, epochs, loss, metric) |>
  dplyr::summarise(mean = mean(value, na.rm = TRUE), .groups = "drop")

```

 ibs_survmat

Integrated Brier Score (IBS) from a Survival Probability Matrix

Description

Computes the Integrated Brier Score (IBS) over a set of evaluation time points, using trapezoidal integration and IPCW adjustment for right-censoring.

Usage

```
ibs_survmat(object, sp_matrix, times)
```

Arguments

object	A 'Surv' object with observed time and status.
sp_matrix	A data frame or matrix of predicted survival probabilities. Each column corresponds to a time point in 'times'.
times	A numeric vector of time points. Must match the columns of 'sp_matrix'.

Value

A single numeric value representing the integrated Brier score.

Examples

```
set.seed(123)
library(survival)
data(veteran, package = "survival")
idx <- sample(nrow(veteran), 0.7 * nrow(veteran))
train <- veteran[idx, ]; test <- veteran[-idx, ]
mod <- survdn(Surv(time, status) ~
  age + karno + celltype, data = train, epochs = 50, verbose = FALSE)
pred <- predict(mod, newdata = test, times = c(30, 90, 180), type = "survival")
y_test <- model.response(model.frame(mod$formula, test))
ibs_survmat(y_test, sp_matrix = pred, times = c(30, 90, 180))
```

plot.survdn

Plot survdn Survival Curves using ggplot2

Description

Visualizes survival curves predicted by a fitted 'survdnn' model. Curves can be grouped by a categorical variable in 'newdata' and optionally display only the group-wise means or overlay them.

Usage

```
## S3 method for class 'survdnn'
plot(
  x,
  newdata = NULL,
  times = 1:365,
  group_by = NULL,
  plot_mean_only = FALSE,
  add_mean = TRUE,
  alpha = 0.3,
  mean_lwd = 1.3,
  mean_lty = 1,
  ...
)
```

Arguments

x	A fitted 'survdnn' model object.
newdata	Optional data frame for prediction (defaults to training data).
times	A numeric vector of time points at which to compute survival probabilities.
group_by	Optional name of a column in 'newdata' used to color and group curves.
plot_mean_only	Logical; if 'TRUE', plots only the mean survival curve per group.
add_mean	Logical; if 'TRUE', adds mean curves to the individual lines.
alpha	Alpha transparency for individual curves (ignored if 'plot_mean_only = TRUE').
mean_lwd	Line width for mean survival curves.
mean_lty	Line type for mean survival curves.
...	Reserved for future use.

Value

A 'ggplot' object.

Examples

```
library(survival)
data(veteran)
set.seed(42)

mod <- survdnn(Surv(time, status) ~ age + karno + celltype, data = veteran,
               hidden = c(16, 8), epochs = 100, verbose = FALSE)
plot(mod, group_by = "celltype", times = 1:300)
```

plot_loss

Plot Training Loss for a survdnn Model

Description

Visualize the evolution of the training loss across epochs for a fitted 'survdnn' model. Helps inspect convergence, instability, or callback effects (e.g., early stopping).

Usage

```
plot_loss(object, smooth = FALSE, log_y = FALSE, ...)
```

Arguments

object	A fitted 'survdnn' model.
smooth	Logical; if 'TRUE', overlays a smoothed loess curve.
log_y	Logical; if 'TRUE', uses a log10 y-scale.
...	Reserved for future use.

Value

A ‘ggplot’ object.

predict.survdmn	<i>Predict from a survdmn Model</i>
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Description

Generate predictions from a fitted ‘survdmn’ model for new data. Supports linear predictors, survival probabilities at specified time points, or cumulative risk estimates.

Usage

```
## S3 method for class 'survdmn'
predict(object, newdata, times = NULL, type = c("survival", "lp", "risk"), ...)
```

Arguments

object	An object of class “survdmn” returned by [survdmn()].
newdata	A data frame of new observations to predict on.
times	Numeric vector of time points at which to compute survival or risk probabilities. Required if ‘type = “survival”’ or ‘type = “risk”’ for Cox/AFT models. For CoxTime, ‘times = NULL’ is allowed when ‘type=“survival”’ and defaults to event times.
type	Character string specifying the type of prediction to return: "lp" Linear predictor. For “cox”/“cox_l2” this is a log-risk score (higher implies worse prognosis, consistent with training sign convention). For “aft”, this is the predicted location parameter $\mu(x)$ on the log-time scale. For “coxtime”, this is $g(t_0, x)$ evaluated at a reference time t_0 (the first event time). "survival" Predicted survival probabilities at each value of ‘times’. "risk" Cumulative risk (1 - survival) at **a single** time point.
...	Currently ignored (for future extensions).

Value

A numeric vector (if ‘type = “lp”’ or “risk”), or a data frame (if ‘type = “survival”’) with one row per observation and one column per ‘times’.

<code>print.survnn</code>	<i>Print a survnn Model</i>
---------------------------	-----------------------------

Description

Pretty prints a fitted ‘survnn’ model. Displays the formula, network architecture, training configuration, and final training loss.

Usage

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

Arguments

<code>x</code>	An object of class “survnn”, returned by [survnn()].
<code>...</code>	Ignored (for future compatibility).

Value

The model object, invisibly.

Examples

```
library(survival)
data(veteran, package = "survival")
mod <- survnn(Surv(time, status) ~
  age + karno + celltype, data = veteran, epochs = 20, verbose = FALSE)
print(mod)
```

<code>summarize_cv_survnn</code>	<i>Summarize Cross-Validation Results from survnn</i>
----------------------------------	---

Description

Computes mean, standard deviation, and confidence intervals for metrics from cross-validation.

Usage

```
summarize_cv_survnn(cv_results, by_time = TRUE, conf_level = 0.95)
```

Arguments

<code>cv_results</code>	A tibble returned by [cv_survnn()].
<code>by_time</code>	Logical. Whether to stratify results by ‘time’ (if present).
<code>conf_level</code>	Confidence level for the intervals (default: 0.95).

Value

A tibble summarizing mean, sd, and confidence bounds per metric (and per time if applicable).

Examples

```
library(survival)
data(veteran)
res <- cv_survdnn(
  Surv(time, status) ~ age + karno + celltype,
  data = veteran,
  times = c(30, 90, 180, 270),
  metrics = c("cindex", "ibs"),
  folds = 3,
  .seed = 42,
  hidden = c(16, 8),
  epochs = 5
)
summarize_cv_survdnn(res)
```

summarize_tune_survdnn

Summarize survdnn Tuning Results

Description

Aggregates cross-validation results from ‘tune_survdnn(return = "all")’ by configuration, metric, and optionally by time point.

Usage

```
summarize_tune_survdnn(tuning_results, by_time = TRUE)
```

Arguments

tuning_results The full tibble returned by ‘tune_survdnn(..., return = "all”)’.

by_time Logical; whether to group and summarize separately by time points.

Value

A summarized tibble with mean and standard deviation of performance metrics.

summary.survdnn

Summarize a Deep Survival Neural Network Model

Description

Provides a structured summary of a fitted ‘survdnn’ model, including the network architecture, training configuration, and data characteristics. The summary is printed automatically with a styled header and sectioned output using {cli} and base formatting. The object is returned invisibly.

Usage

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

Arguments

object An object of class “survdnn” returned by the [survdnn()] function.
 ... Currently ignored (for future compatibility).

Value

Invisibly returns an object of class “summary.survdnn”.

Examples

```
set.seed(42)
sim_data <- data.frame(
  age = rnorm(100, 60, 10),
  sex = factor(sample(c("male", "female"), 100, TRUE)),
  trt = factor(sample(c("A", "B"), 100, TRUE)),
  time = rexp(100, 0.05),
  status = rbinom(100, 1, 0.7)
)
mod <- survdnn(Surv(time, status) ~ age + sex + trt, data = sim_data, epochs = 50, verbose = FALSE)
summary(mod)
```

survdnn

Fit a Deep Neural Network for Survival Analysis

Description

Trains a deep neural network (DNN) to model right-censored survival data using one of the predefined loss functions: Cox, AFT, or Coxtime.

Usage

```

survdnn(
  formula,
  data,
  hidden = c(32L, 16L),
  activation = "relu",
  lr = 1e-04,
  epochs = 300L,
  loss = c("cox", "cox_l2", "aft", "coxtime"),
  optimizer = c("adam", "adamw", "sgd", "rmsprop", "adagrad"),
  optim_args = list(),
  verbose = TRUE,
  dropout = 0.3,
  batch_norm = TRUE,
  callbacks = NULL,
  .seed = NULL,
  .device = c("auto", "cpu", "cuda"),
  na_action = c("omit", "fail")
)

```

Arguments

formula	A survival formula of the form ‘Surv(time, status) ~ predictors’.
data	A data frame containing the variables in the model.
hidden	Integer vector. Sizes of the hidden layers (default: c(32, 16)).
activation	Character string specifying the activation function to use in each layer. Supported options: "relu", "leaky_relu", "tanh", "sigmoid", "gelu", "elu", "softplus".
lr	Learning rate for the optimizer (default: ‘1e-4’).
epochs	Number of training epochs (default: 300).
loss	Character name of the loss function to use. One of "cox", "cox_l2", "aft", or "coxtime".
optimizer	Character string specifying the optimizer to use. One of "adam", "adamw", "sgd", "rmsprop", or "adagrad". Defaults to "adam".
optim_args	Optional named list of additional arguments passed to the underlying torch optimizer (e.g., ‘list(weight_decay = 1e-4, momentum = 0.9)’).
verbose	Logical; whether to print loss progress every 50 epochs (default: TRUE).
dropout	Numeric between 0 and 1. Dropout rate applied after each hidden layer (default = 0.3). Set to 0 to disable dropout.
batch_norm	Logical; whether to add batch normalization after each hidden linear layer (default = TRUE).
callbacks	Optional list of callback functions. Each callback should have signature ‘function(epoch, current)’ and return TRUE if training should stop, FALSE otherwise. Used, for example, with [callback_early_stopping()].

<code>.seed</code>	Optional integer. If provided, sets both R and torch random seeds for reproducible weight initialization, shuffling, and dropout.
<code>.device</code>	Character string indicating the computation device. One of "auto", "cpu", or "cuda". "auto" uses CUDA if available, otherwise falls back to CPU.
<code>na_action</code>	Character. How to handle missing values in the model variables: "omit" drops incomplete rows (and reports how many were removed when 'verbose=TRUE'); "fail" stops with an error if any missing values are present.

Value

An object of class "survdnn" containing:

model Trained 'nn_module' object.

formula Original survival formula.

data Training data used for fitting.

xnames Predictor variable names.

x_center Column means of predictors.

x_scale Column standard deviations of predictors.

loss_history Vector of loss values per epoch.

final_loss Final training loss.

loss Loss function name used ("cox", "aft", etc.).

activation Activation function used.

hidden Hidden layer sizes.

lr Learning rate.

epochs Number of training epochs.

optimizer Optimizer name used.

optim_args List of optimizer arguments used.

device Torch device used for training ('torch_device').

aft_log_sigma Learned global log(sigma) for 'loss="aft"'; 'NA_real_' otherwise.

aft_loc AFT log-time location offset used for centering when 'loss="aft"'; 'NA_real_' otherwise.

covertime_time_center Mean used to scale time for CoxTime; 'NA_real_' otherwise.

covertime_time_scale SD used to scale time for CoxTime; 'NA_real_' otherwise.

Description

Performs k-fold cross-validation over a user-defined hyperparameter grid and selects the best configuration according to the specified evaluation metric.

Usage

```
tune_survdnn(
  formula,
  data,
  times,
  metrics = "cindex",
  param_grid,
  folds = 3,
  .seed = 42,
  .device = c("auto", "cpu", "cuda"),
  na_action = c("omit", "fail"),
  refit = FALSE,
  return = c("all", "summary", "best_model")
)
```

Arguments

formula	A survival formula, e.g., ‘Surv(time, status) ~ x1 + x2’.
data	A data frame.
times	A numeric vector of evaluation time points.
metrics	A character vector of evaluation metrics: "cindex", "brier", or "ibs". Only the first metric is used for model selection.
param_grid	A named list defining hyperparameter combinations to evaluate. Required names: ‘hidden’, ‘lr’, ‘activation’, ‘epochs’, ‘loss’.
folds	Number of cross-validation folds (default: 3).
.seed	Optional seed for reproducibility.
.device	Character string indicating the computation device used when fitting models during cross-validation and refitting. One of "auto", "cpu", or "cuda". "auto" uses CUDA if available, otherwise falls back to CPU.
na_action	Character. How to handle missing values: "omit" drops incomplete rows; "fail" errors if any NA is present.
refit	Logical. If TRUE, refits the best model on the full dataset.
return	One of "all", "summary", or "best_model": "all" Returns the full cross-validation result across all combinations. "summary" Returns averaged results per configuration. "best_model" Returns the refitted model or best hyperparameters.

Value

A tibble or model object depending on the 'return' value.

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