Package: densemlp (via r-universe)

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Title Dense Neural Networks for Tabular Regression, Classification and Survival

Version 0.7.1

Description Dense feed-forward neural networks (multilayer perceptrons) for tabular regression, classification and survival analysis, with a formula or x/y interface. Supports residual and gated hidden blocks, batch normalization, per-layer dropout, learned cross-feature interactions, exponential moving-average weights, learning-rate schedules, internal bootstrap ensembles and Adam optimization. Survival outcomes are trained with either a batch-wise Breslow-tie Cox partial likelihood or a discrete-time inverse-probability-of-censoring-weighted integrated Brier score. The numerical kernels are implemented natively in C++ via 'RcppArmadillo', with no external deep learning framework dependency (no 'torch' / 'libtorch'). Companion helpers provide k-fold cross-validation, hyperparameter search and task-aware evaluation metrics.

URL https://CRAN.R-project.org/package=densemlp

BugReports https://github.com/ielbadisy/densemlp/issues

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Encoding UTF-8

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LinkingTo Rcpp, RcppArmadillo

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`cv_densemlp` *Cross-validate a densemlp model*

Description

Fits `densemlp()` on each of `folds` training splits and evaluates it on the held-out fold via `densemlp_metrics()`.

Usage

```
cv_densemlp(
  x,
  y,
  task = c("auto", "regression", "binary", "multiclass", "survival"),
  folds = 5L,
  seed = 1L,
  ncores = 1L,
  verbose = FALSE,
  ...
)
```

Arguments

x	Predictor data.frame or matrix.
y	Outcome vector.
task	"auto" infers the task from y, as in densemlp(). Pass "survival" explicitly for a survival outcome.
folds	Number of cross-validation folds.
seed	Random seed for fold assignment; fold k fits with seed = seed + k.
ncores	Number of cores used to fit folds in parallel (see densemlp()'s ncores).
verbose	Print per-fold progress.
...	Additional arguments passed to densemlp() for every fold (e.g. hidden_units, epochs, lr).

Value

A list of class densemlp_cv with fold_metrics (one row per fold), summary (mean and SD per metric across folds), and task.

Examples

```
set.seed(1)
x <- data.frame(a = rnorm(60), b = rnorm(60))
y <- x$a - 0.5 * x$b + rnorm(60, sd = 0.1)
cv <- cv_densemlp(x, y, folds = 3, epochs = 20, hidden_units = c(8))
cv$summary
```

---

densemlp *Fit a fast dense multilayer perceptron*

Description

A compact feedforward network for regression and classification on tabular data. Forward propagation, backpropagation, and Adam optimization are all implemented natively in C++ via RcppArmadillo – no torch / libtorch dependency.

Usage

```
densemlp(
  x = NULL,
  y = NULL,
  task = c("auto", "regression", "binary", "multiclass", "survival"),
  loss = c("cox", "brier"),
  n_bins = 10L,
  hidden_units = c(32, 16),
  epochs = 100L,
  batch_size = 32L,
```

```
  lr = 0.001,
  validation = 0.2,
  early_stopping = TRUE,
  patience = 10L,
  min_delta = 0,
  min_epochs = max(10L, floor(epochs * 0.2)),
  residual = FALSE,
  gated = FALSE,
  dropout = 0,
  batch_norm = TRUE,
  input_projection = NULL,
  interaction = FALSE,
  ema_decay = 0,
  ensemble = 1L,
  ensemble_bootstrap = TRUE,
  lr_schedule = c("none", "cosine", "step"),
  seed = 1L,
  verbose = FALSE,
  ncores = 1L,
  formula = NULL,
  data = NULL
)

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

Arguments

x	A densemlp object.
y	Outcome (x/y interface): numeric for regression, a factor/character (2 levels for binary, 3+ for multiclass) for classification, or, for task = "survival", a survival::Surv() object or a two-column matrix/data.frame giving (time, event) (event coded 1 = event, 0 = censored).
task	"auto" infers the task from y (a survival::Surv() response, from either interface, is always detected as "survival"); otherwise one of "regression", "binary", "multiclass", "survival".
loss	For task = "survival" only: "cox" (batch-wise Breslow-tie Cox partial likelihood, a single linear risk score) or "brier" (IPCW integrated Brier score over a discrete-time grid of n_bins hazard outputs; see the "Survival" section below). Ignored otherwise.
n_bins	For task = "survival", loss = "brier" only: number of discrete-time bins (quantile cutpoints of the observed follow-up times).
hidden_units	Integer vector of hidden layer sizes.
epochs	Maximum number of training epochs (an upper bound when early_stopping is used).
batch_size	Mini-batch size.

lr	Adam learning rate.
validation	Validation fraction held out for early stopping. Set to 0 to disable (trains for the full epochs, no BN running-stat evaluation set).
early_stopping	Logical; stop once validation loss stops improving. Ignored if validation = 0.
patience	Number of non-improving epochs to wait before stopping.
min_delta	Minimum validation loss improvement to reset patience.
min_epochs	Minimum number of epochs before early stopping can trigger. Defaults to max(10, floor(epochs * 0.2)).
residual	Logical; add a residual skip to every hidden block. A learned linear projection is used when the block dimensions differ.
gated	Logical; use a learned sigmoid gate in every hidden block.
dropout	Dropout probability, either one value or one per hidden layer. Values must be in [0, 1).
batch_norm	Logical; apply batch normalization inside every hidden block (Linear -> BatchNorm -> ReLU). When FALSE, hidden blocks are Linear -> ReLU with no normalization and no learned BN affine parameters.
input_projection	Optional positive integer. When set, a plain linear layer (no activation, no batch normalization) maps the encoded predictors to input_projection dimensions before the first hidden block. NULL (default) disables it. Cannot be combined with interaction.
interaction	Logical; prepend an efficient learned cross-feature layer that models explicit second-order interactions in O(p) parameters.
ema_decay	Exponential moving-average decay for model parameters. Set to 0 to disable; values such as 0.99 enable EMA evaluation and best-epoch restoration.
ensemble	Number of internally fitted members whose predictions are averaged. 1 fits a single model and preserves the standard behavior.
ensemble_bootstrap	Logical; bootstrap rows independently for each member when ensemble > 1.
lr_schedule	Learning-rate schedule: "none", cosine annealing over epochs, or "step" decay by 0.5 every max(5, floor(epochs / 3)) epochs.
seed	Integer seed.
verbose	Logical; print training/validation loss every 10 epochs.
ncores	Number of cores used to fit ensemble members in parallel when ensemble > 1 (via parallel::mclapply on Unix-alikes, serially on Windows). Ignored when ensemble = 1.
formula	A formula, e.g. y ~ . or, for survival, survival::Surv(time, status) ~ ., as an alternative to x/y. Use either formula/data or x/y, not both. A formula may be given as the first positional argument – densemlp(y ~ ., df), densemlp(formula = y ~ ., data = df) and densemlp(x, y) all work.
data	A data.frame used with formula.
...	Unused.

Details

Hidden layers are `Linear -> BatchNorm -> ReLU -> optional gate -> optional dropout -> optional residual` (batch statistics during training, running mean/var at prediction time, exponential decay 0.9), with He initialization for the linear weights. Set `batch_norm = FALSE` to drop the normalization step, leaving `Linear -> ReLU` hidden blocks. Residual blocks use a learned linear projection when dimensions differ. With `input_projection = k`, a bare linear layer maps the encoded inputs to `k` dimensions before the first hidden block (mutually exclusive with `interaction`). The optional interaction layer is a one-layer cross network initialized as the identity. With `ema_decay > 0`, validation and final predictions use moving-average parameters. With `ensemble > 1`, fully fitted internal members are trained with successive seeds and optionally bootstrapped rows, and their response probabilities/predictions are averaged transparently. The output layer is plain `Linear -> task activation` (no BN): linear (regression, MSE loss), sigmoid (binary, binary cross-entropy), softmax (multiclass, categorical cross-entropy), or a linear risk score (survival, Cox partial likelihood); the first three share the output-gradient simplification `dZ = (yhat - y) / n`, while survival uses its own closed-form Cox gradient (see the "Survival" section below). With `validation > 0` and `early_stopping = TRUE` (both on by default), the parameters (weights, biases, and BN affine/running-stat parameters) from the best validation epoch are restored at the end.

Value

A `densemlp` object.

Survival

`task = "survival"` supports two losses, both trained batch-wise against a `(time, event)` outcome:

- `loss = "cox"` (the default) trains a single linear risk score using a batch-wise Breslow-tie Cox partial log-likelihood – the same "risk set = current mini-batch" approximation used by DeepSurv/pycox, which turns Cox regression into an ordinary per-batch loss compatible with masked-free Adam training, BN, and early stopping unchanged. For a batch sorted by descending time, with each observation's risk set approximated by the sorted prefix of observations with a time at least as large, the loss is the negative mean, over events, of the risk score minus the log of the cumulative sum of exponentiated risk scores over its risk set – computed via a single cumulative sum with a closed-form O(n) gradient (no autodiff).
- `loss = "brier"` trains a discrete-time hazard head with `n_bins` outputs (a quantile grid of the observed follow-up times) directly against the IPCW (Graf et al.) integrated Brier score. Bin `k`'s sigmoid output is a conditional hazard, and the survival probability at that bin is the running product of one minus every hazard up to and including it, which is monotonically non-increasing by construction. Each bin's Brier term is inverse-probability-of-censoring weighted using a Kaplan-Meier estimate of the *censoring* distribution fit once on the training data; subjects censored before a bin are excluded from that bin's term, per Graf's correction. The gradient is closed-form (no autodiff): a bin's survival probability depends on every hazard logit at or before it, so each bin's Brier-score gradient is distributed back across all of them.

`predict(fit, newdata, type = "response")` returns a linear risk score for either loss (for `"brier"`, the negative log of the predicted survival probability at the final time bin, so higher is still riskier);

with `loss = "brier"`, `type = "survival"` additionally returns the full `n_bins`-column survival-probability matrix. `densemlp_metrics()` reports Harrell's concordance index for `task = "survival"` regardless of loss.

Examples

```
set.seed(1)
x <- data.frame(a = rnorm(100), b = rnorm(100))
y <- x$a - 0.5 * x$b + rnorm(100, sd = 0.1)
fit <- densemlp(x, y, epochs = 50, hidden_units = c(16))
predict(fit, x[1:5, ])
```

---

densemlp_integrated_brier_score

Integrated Brier score for a fitted Brier-loss survival densemlp model

---

Description

The IPCW (Graf et al.) integrated Brier score, evaluated at the model's own time grid (`object$survival_breaks`), using a Kaplan-Meier estimate of the censoring distribution fit on `y` (i.e. on whatever data is passed in – pass the held-out set's own outcome for an honest out-of-sample estimate). Lower is better; this is exactly the objective `densemlp()` minimizes when fit with `task = "survival", loss = "brier"`.

Usage

```
densemlp_integrated_brier_score(object, newdata, y)
```

Arguments

`object`	A `densemlp` object fit with `task = "survival", loss = "brier"`.
`newdata`	Predictor data to evaluate on.
`y`	The corresponding survival outcome (`survival::Surv()` or a two-column `(time, event)` matrix/data.frame).

Value

A single numeric integrated Brier score.

densemlp_metrics *Prediction metrics for a fitted densemlp model*

Description

Prediction metrics for a fitted densemlp model

Usage

```
densemlp_metrics(truth, estimate, task, prob = NULL)
```

Arguments

truth	Observed outcome values, or, for task = "survival", a survival::Surv() object or a two-column (time, event) matrix/data.frame.
estimate	Predicted values (type = "response" for regression and survival, type = "class" for classification).
task	"regression", "binary", "multiclass", or "survival".
prob	Optional matrix of class probabilities (classification only), used to compute macro_auc and log_loss.

Value

A named list of metrics: rmse, nrmse, rsq for regression, accuracy, balanced_accuracy, macro_auc, log_loss for classification, or concordance (Harrell's C-index) for survival.

perm_importance *Permutation variable importance for a fitted densemlp model*

Description

Model-agnostic permutation importance: for each predictor, the column is randomly shuffled and the drop in predictive performance (relative to the unpermuted baseline) is recorded. Larger values mean the model relied more on that predictor.

Usage

```
perm_importance(object, new_data, truth, metric = NULL, seed = object$seed)

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

Arguments

object	A fitted densemlp object (single model; ensembles are not supported).
new_data	Evaluation predictor data.
truth	Ground-truth outcome for new_data: a numeric vector (regression), a factor/character (classification), or a survival::Surv() / two-column (time, event) object (survival).
metric	Metric name understood by densemlp_metrics(). Defaults to "rmse" (regression), "accuracy" (classification) or "concordance" (survival).
seed	Random seed used for the column shuffles.
x	A densemlp_importance object.
...	Unused.

Value

A densemlp_importance object: a list with data (a data frame of feature / importance, ordered by decreasing importance), metric, baseline and task.

Examples

```
set.seed(1)
x <- data.frame(a = rnorm(120), b = rnorm(120), c = rnorm(120))
y <- x$a - 0.5 * x$b + rnorm(120, sd = 0.1)
fit <- densemlp(x, y, epochs = 40, hidden_units = c(16))
perm_importance(fit, x, y)
```

---

plot.densemlp *Plot training history*

Description

Plot training history

Usage

```
## S3 method for class 'densemlp'
plot(x, ...)
```

Arguments

x	A fitted densemlp object (single model; ensembles are not supported since members don't share an epoch axis).
...	Additional arguments passed to graphics::matplot().

Value

x, invisibly.

plot.densemlp_importance *Plot permutation importance*

Description

Plot permutation importance

Usage

```
## S3 method for class 'densemlp_importance'
plot(x, top = 20L, ...)
```

Arguments

x	A densemlp_importance object.
top	Number of top features to show.
...	Passed to graphics::barplot().

Value

x, invisibly.

plot_history *Plot the training history of a fitted densemlp model*

Description

A named wrapper around the plot.densemlp() method: draws the per-epoch training and validation loss curves.

Usage

```
plot_history(object, ...)
```

Arguments

object	A fitted densemlp object (single model).
...	Passed to graphics::matplot().

Value

object, invisibly.

Examples

```
set.seed(1)
x <- data.frame(a = rnorm(80), b = rnorm(80))
y <- x$a - 0.5 * x$b + rnorm(80, sd = 0.1)
fit <- densemlp(x, y, epochs = 40, hidden_units = c(16))
plot_history(fit)
```

`predict.densemlp` *Predict from a fitted densemlp model*

Description

Predict from a fitted densemlp model

Usage

```
## S3 method for class 'densemlp'
predict(
  object,
  newdata,
  type = c("response", "class", "prob", "survival"),
  ...
)
```

Arguments

`object`	A fitted `densemlp` object.
`newdata`	New predictor data, in the same representation used to fit.
`type`	`"response"` (regression: unscaled prediction; binary: predicted probability of the second factor level; survival: a linear risk score, higher = riskier, for either `loss`), `"class"` (classification only: predicted factor label), `"prob"` (classification only: a matrix of class probabilities), or `"survival"` (survival with `loss = "brier"` only: the full `n_bins`-column survival-probability matrix).
`...`	Unused.

Value

A numeric vector (`"response"`), a factor (`"class"`), or a matrix (`"prob"` or `"survival"`).

tune_densemlp *Tune a densemlp model over a hyperparameter grid*

Description

Fits densemlp() for every combination in grid (each repeated repeats times with successive seeds), ranks candidates by their best internal validation loss, and optionally refits the best configuration on the full data.

Usage

```
tune_densemlp(
  x,
  y,
  task = c("auto", "regression", "binary", "multiclass", "survival"),
  grid = NULL,
  validation = 0.2,
  seed = 1L,
  repeats = 3L,
  ncores = 1L,
  verbose = FALSE,
  refit = TRUE
)
```

Arguments

x	Predictor data.frame or matrix.
y	Outcome vector.
task	"auto" infers the task from y, as in densemlp().
grid	A named list of candidate values. Supported names: hidden_units (a list of integer vectors), dropout (a list of numeric vectors, recycled to hidden_units length), residual, gated, ema_decay, lr_schedule, epochs, batch_size, lr. Any name omitted falls back to a single-value default. interaction is intentionally not tunable here: it is numerically unstable on small/wide data (see package NEWS) and is left at FALSE.
validation	Validation fraction used for every candidate fit.
seed	Base random seed.
repeats	Number of repeated seeds per candidate.
ncores	Number of cores used to fit candidates in parallel (see densemlp()'s ncores).
verbose	Print per-candidate progress.
refit	Refit the best configuration on the supplied data.

Value

A list of class densemlp_tuned with results (one row per candidate, ranked best first by mean validation loss), best_config, and, when refit = TRUE, best_fit.

Examples

```
set.seed(1)
x <- data.frame(a = rnorm(80), b = rnorm(80))
y <- x$a - 0.5 * x$b + rnorm(80, sd = 0.1)
tuned <- tune_densemlp(
  x, y, repeats = 1,
  grid = list(hidden_units = list(c(8), c(16, 8)), epochs = c(20))
)
tuned$best_config
```

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