

# Package: ensModelVis (via r-universe)

May 21, 2026

**Title** Visualisations for Model Ensembles

**Version** 0.2.0

**Description** Displays for model fits of multiple models and their ensembles. For classification models, the plots are heatmaps, for regression, scatterplots.

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**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Depends** R (>= 4.1.0)

**Imports** dplyr, forcats, ggplot2, rlang, tidyr

**URL** <https://github.com/domijan/ensModelVis>

**BugReports** <https://github.com/domijan/ensModelVis/issues>

**Suggests** discrim, glmnet, kernlab, knitr, MASS, nnet, ranger, rmarkdown, stacks, stringr, tidymodels

**VignetteBuilder** knitr

**Config/pak/sysreqs** libicu-dev

**Repository** <https://domijan.r-universe.dev>

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plot_ensemble	<i>Draws a plot for model predictions of ensembles of models. For classification the plot is a heatmap, for regression, scatterplot.</i>
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### Description

Draws a plot for model predictions of ensembles of models. For classification the plot is a heatmap, for regression, scatterplot.

### Usage

```
plot_ensemble(
  truth,
  tibble_pred,
  incorrect = FALSE,
  tibble_prob = NULL,
  order = NULL,
  facet = FALSE
)
```

### Arguments

truth	The y variable. In regression this is numeric vector, in classification this is a factor vector.
tibble_pred	A data.frame of predictions. Each column corresponds to a candidate model.
incorrect	If TRUE, for observations that were correctly classified by all models, remove all but a single observation per class. Classification only.
tibble_prob	If not NULL, a data.frame with same column names as tibble_pred. Applies transparency based on the predicted probability of the predicted class. Classification only.
order	default ordering of columns in a heatmap (classification) or facets (regression) is by accuracy (classification) or RMSE (regression). Can submit any other ordering for heatmaps e.g. AUC, which should be a data.frame with same column names as tibble_pred.
facet	whether to facet the plots by model (regression only).

### Value

a ggplot

### Examples

```
data(iris)
if (require("MASS")){
  lda.model <- lda(Species~., data = iris)
  lda.pred <- predict(lda.model)
```

```
}
if (require("ranger")){
  ranger.model <- ranger(Species~., data = iris)
  ranger.pred <- predict(ranger.model, iris)
}

library(ensModelVis)

plot_ensemble(iris$Species,
  data.frame(LDA = lda.pred$class,
  RF = ranger.pred$predictions))

plot_ensemble(iris$Species,
  data.frame(LDA = lda.pred$class,
  RF = ranger.pred$predictions),
  incorrect= TRUE)

if (require("ranger")){
  ranger.model <- ranger(Species~., data = iris, probability = TRUE)
  ranger.prob <- predict(ranger.model, iris)
}

plot_ensemble(iris$Species,
  data.frame(LDA = lda.pred$class,
  RF = ranger.pred$predictions),
  tibble_prob = data.frame(LDA = apply(lda.pred$posterior, 1, max),
  RF = apply(ranger.prob$predictions, 1, max)))
```

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