Diagnostic plots are always a nice, visually explicit way to assess our data and predictions, and I’ve just added a new one to the `modEvA` R package. The **‘*predPlot*‘** function plots **predicted values separated into observed presences and absences, and coloured according to whether they’re above or below a given prediction threshold** (the default threshold is species prevalence, i.e. proportion of presences, in the observed data). It shows whether there’s a visible split in the predicted values for presences and absences (see also functions `predDensity` and `plotGLM` in the same package, for alternative/complementary ways of visualizing this). The plot imitates (with permission from the author) one of the graphical outputs of the ‘`summary`‘ of models built with the ‘`embarcadero`‘ package (Carlson, 2020), but it can be applied to any ‘`glm`‘ object or any set of observed and predicted values, and it allows specifying a user-defined prediction threshold. The ‘`predPlot`‘ function is now included in package `modEvA` (version >= 2.1, currently available on R-Forge).

```
predPlot <- function(model = NULL, obs = NULL, pred = NULL, thresh = "preval",
main = "Classified predicted values", legend.pos = "bottomright") {
  # version 1.0 (20 Jan 2021)

  if (!is.null(model)) {
    if (!("glm" %in% class(model)) || family(model)$family != "binomial")
stop("'model' must be of class 'glm' and family 'binomial'.")
    if (!is.null(obs)) message("Argument 'obs' ignored in favour of 'model'.")
    if (!is.null(pred)) message("Argument 'pred' ignored in favour of
'model'.")
    obs <- model$y
    pred <- model$fitted.values
  } else {
    if (is.null(obs) || is.null(pred)) stop ("You must provide either 'model'
or a combination of 'obs' and 'pred'.")
    if (!is.numeric(obs) || !is.numeric(pred)) stop ("'obs' and 'pred' must be
numeric.")
    if (length(obs) != length(pred)) stop("'obs' and 'pred' must have the same
length.")
  }

  if (!(thresh == "preval" || (is.numeric(thresh) && thresh >= 0 && thresh <=
1))) stop ("'thresh' must be either 'preval' or a numeric value between 0 and
1.")
  if (thresh == "preval")  thresh <- prevalence(obs)

  pred0 <- pred[obs == 0]
  pred1 <- pred[obs == 1]

  opar <- par(no.readonly = TRUE)
  on.exit(par(opar))
  par(mar = c(5, 5.2, 3, 1))

  plot(x = c(0, 1), y = c(-0.5, 1.5), xlab = "Predicted value", type = "n",
ylab = "", yaxt = "n", main = main)
  axis(side = 2, at = c(0, 1), tick = FALSE, labels = c("Observed\nabsences",
"Observed\npresences"), las = 1)
  abline(v = thresh, lty = 2)
  points(x = pred0, y = sapply(rep(0, length(pred0)), jitter, 10), col =
ifelse(pred0 < thresh, "grey", "black"))
  points(x = pred1, y = sapply(rep(1, length(pred1)), jitter, 10), col =
ifelse(pred1 < thresh, "grey", "black"))
```

```
  if (!is.na(legend.pos) && legend.pos != "n")  legend(legend.pos, legend =
c("Predicted presence", "Predicted absence"), pch = 1, col = c("black",
"grey"))
}
```

Usage examples:

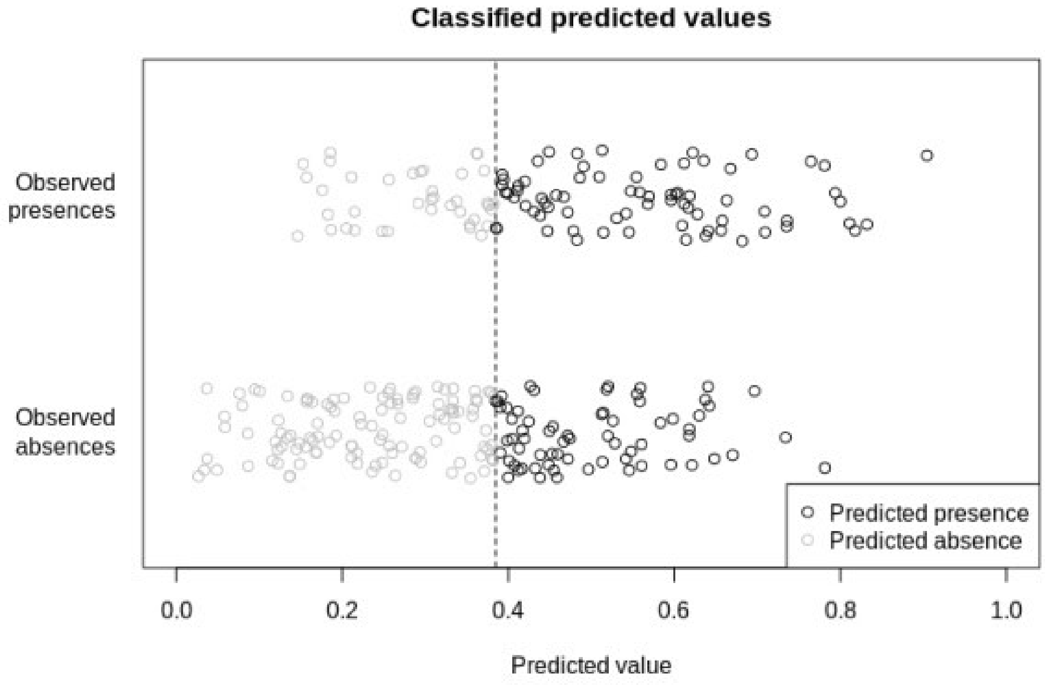
```
library(modEvA)

# load sample models:
data(rotif.mods)

# choose a particular model to play with:
mod <- rotif.mods$models[[1]]

# make some predPlots:
predPlot(model = mod)
predPlot(model = mod, thresh = 0.5)

# you can also use 'predPlot' with vectors of observed and predicted values
instead of a model object:
myobs <- mod$y
mypred <- mod$fitted.values
predPlot(obs = myobs, pred = mypred)
```



References

Carlson C.J. (2020) `embarcadero`: Species distribution modelling with Bayesian additive regression trees in R. *Methods in Ecology and Evolution*, 11: 850-858.