



06 Interpreting Ecological Niche Modeling

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06 Continued

dismo

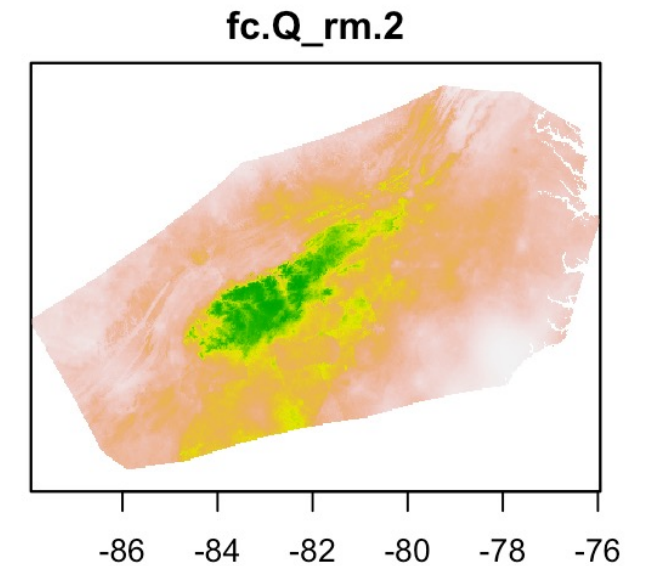
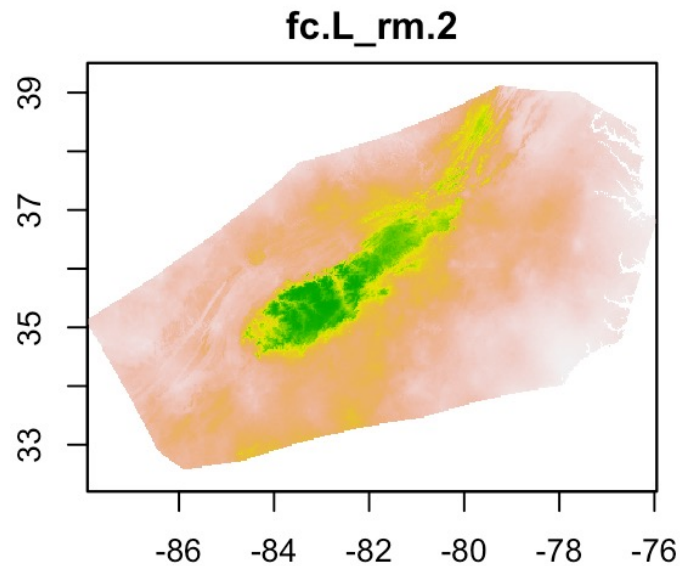
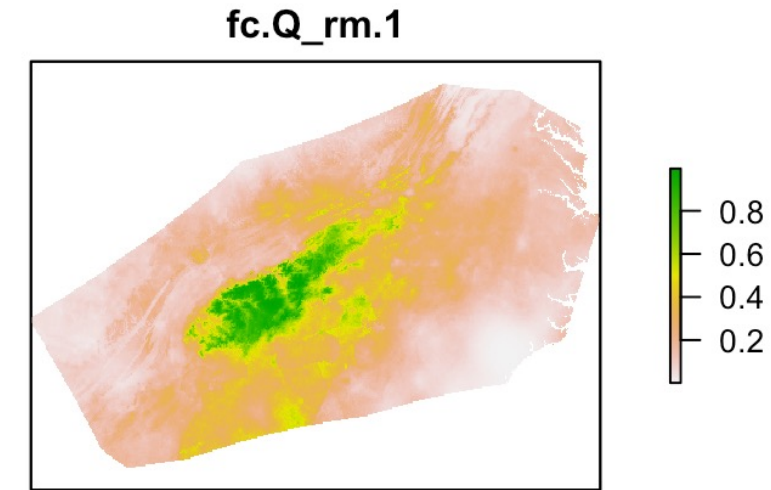
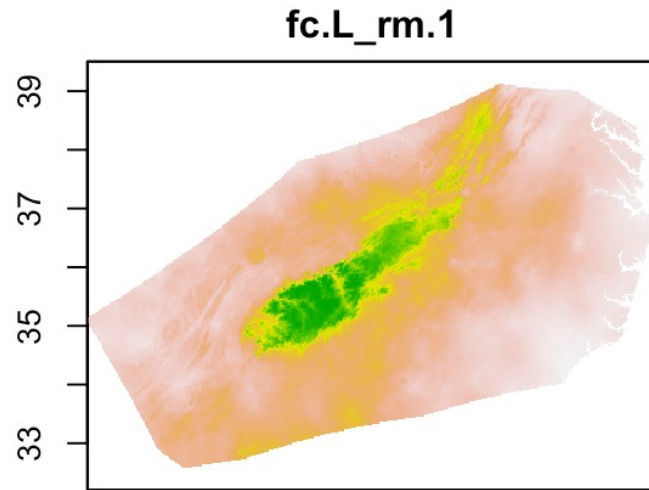
Inspect the dismo model based on the html

```
browseURL(evaldis@html)
```

- View an html output for models made with **dismo**

ENMeval – Visualize

```
maps <- eval1@predictions  
plot(maps)
```



ENMeval – Model Overlap

```
mod_overlap <- calc.niche.overlap(eval1@predictions, overlapStat = "D")
```

```
kable(mod_overlap) %>%  
  kable_styling(bootstrap_options = c("striped", "hover", "condensed", font_size = 10)) %>%  
  scroll_box(width = "100%", height = "200px")
```

| | fc.L_rm.1 | fc.Q_rm.1 | fc.L_rm.2 | fc.Q_rm.2 |
|-----------|-----------|-----------|-----------|-----------|
| fc.L_rm.1 | NA | NA | NA | NA |
| fc.Q_rm.1 | 0.8951659 | NA | NA | NA |
| fc.L_rm.2 | 0.9864079 | 0.8870755 | NA | NA |
| fc.Q_rm.2 | 0.9062003 | 0.9801491 | 0.8992666 | NA |

ENMeval – Select Best Model

Inspect the results

Identify the best model selecting models with the lowest average test omission rate and the highest average validation AUC

```
results <- eval.results(eval1)
opt.seq <- results %>%
  dplyr::filter(or.10p.avg == min(or.10p.avg)) %>%
  dplyr::filter(auc.val.avg == max(auc.val.avg))
kable(opt.seq) %>%
kable_styling(bootstrap_options = c("striped", "hover", "condensed", font_size = 10)) %>%
  scroll_box(width = "100%", height = "200px")
```

| | fc | rm | tune.args | auc.train | cbi.train | auc.diff.avg | auc.diff.sd | auc.val.avg | auc.val.sd | cbi.val.avg | cbi.val.sd | or.10p.avg | or. |
|---|----|-----------|-----------|-----------|-----------|--------------|-------------|-------------|------------|-------------|------------|------------|-----|
| L | 2 | fc.L_rm.2 | 0.8777198 | 0.995 | 0.0647308 | 0.0290278 | 0.8587255 | 0.0598812 | 0.9325 | 0.0859477 | 0.1319444 | 0.0 | |

Subset model

```
mod.seq <- eval.models(eval1)[[opt.seq$tune.args]]
```

ENMeval – Inspect

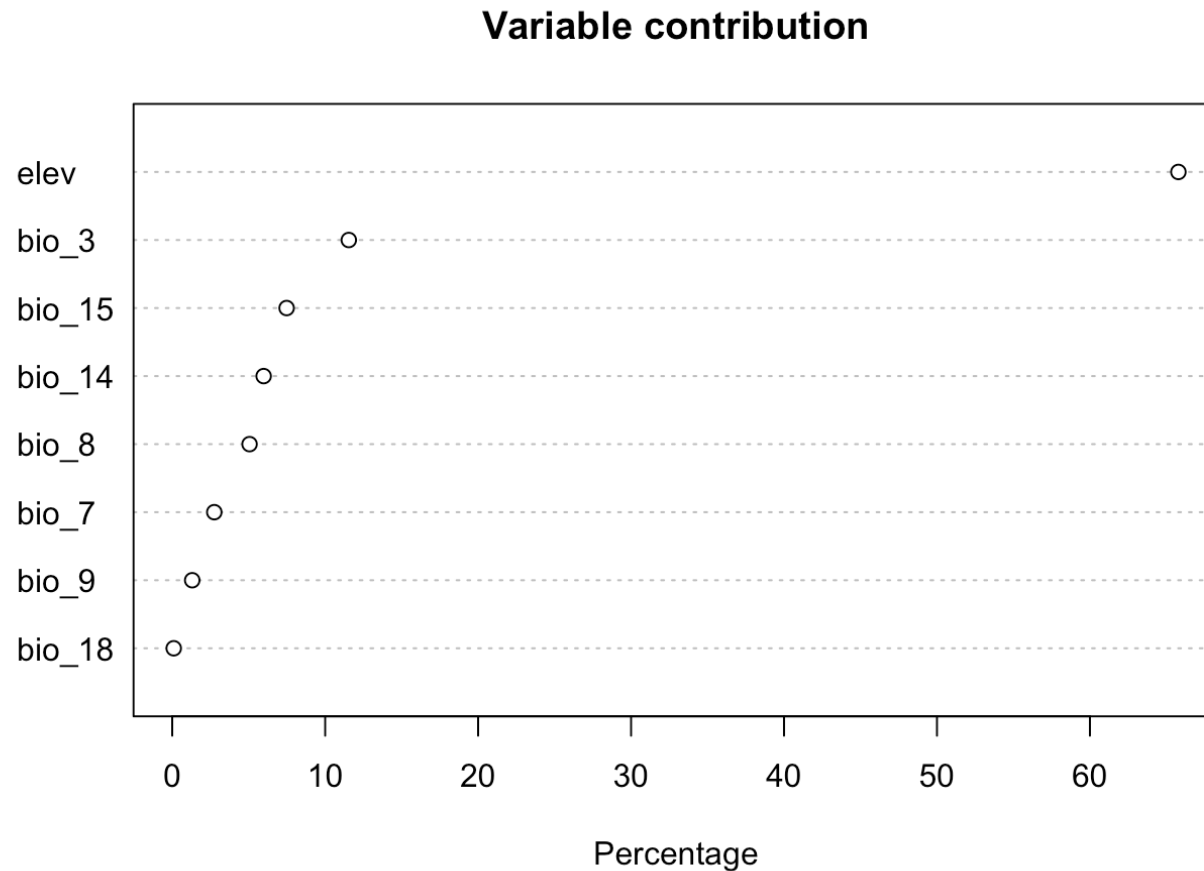
```
kable(mod.seq@results) %>%  
  kable_styling(bootstrap_options = c("striped", "hover", "condensed", font_size = 10)) %>%  
  scroll_box(width = "100%", height = "200px")
```

| | |
|-----------------------------|------------|
| X.Training.samples | 1728.0000 |
| Regularized.training.gain | 0.6747 |
| Unregularized.training.gain | 0.7039 |
| Iterations | 140.0000 |
| Training.AUC | 0.8227 |
| X.Background.points | 11704.0000 |
| ... | ... |

ENMeval – Variable Contribution

Look at variable contribution

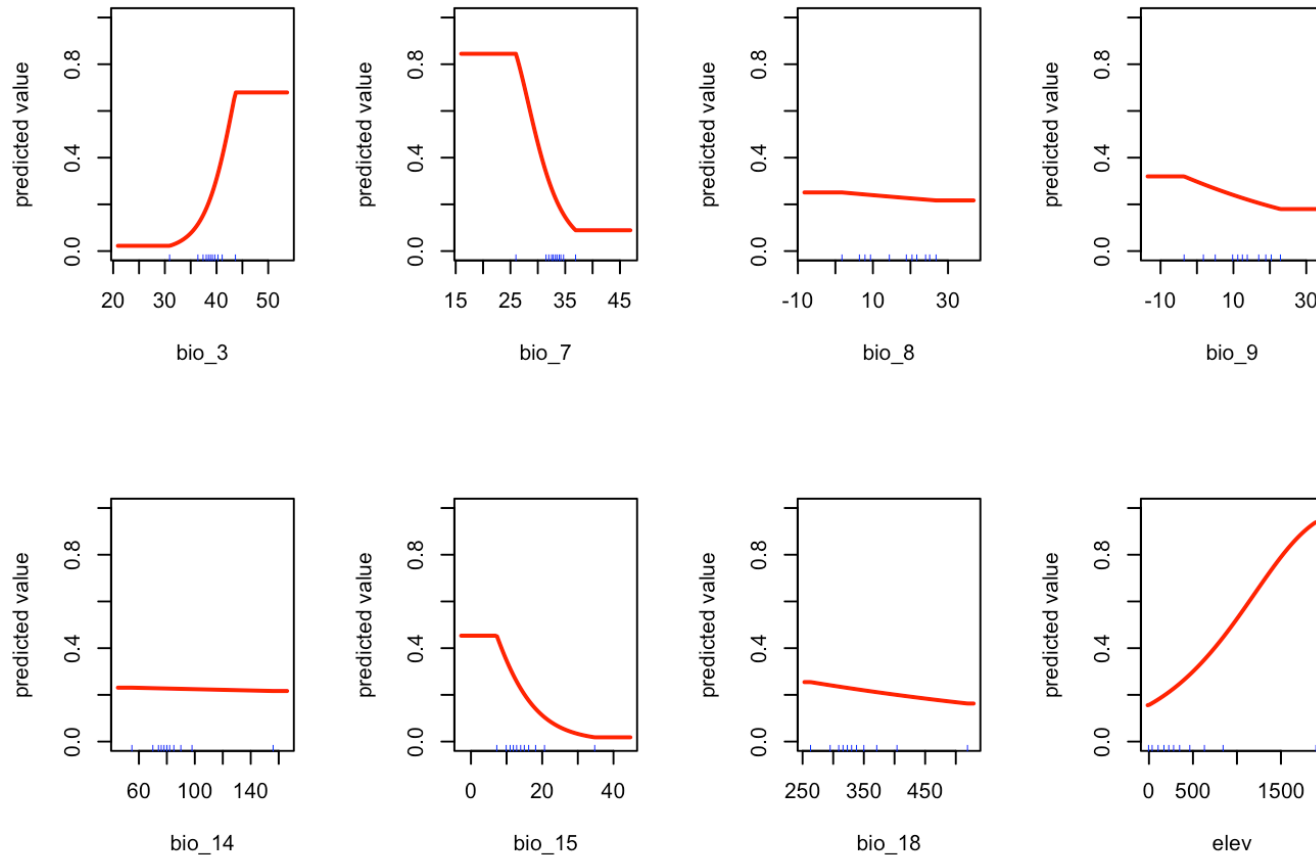
```
plot(mod.seq)
```



ENMeval – Response curves

Look at the response curves

```
dismo::response(mod.seq)
```



ENMeval – Project and Plot

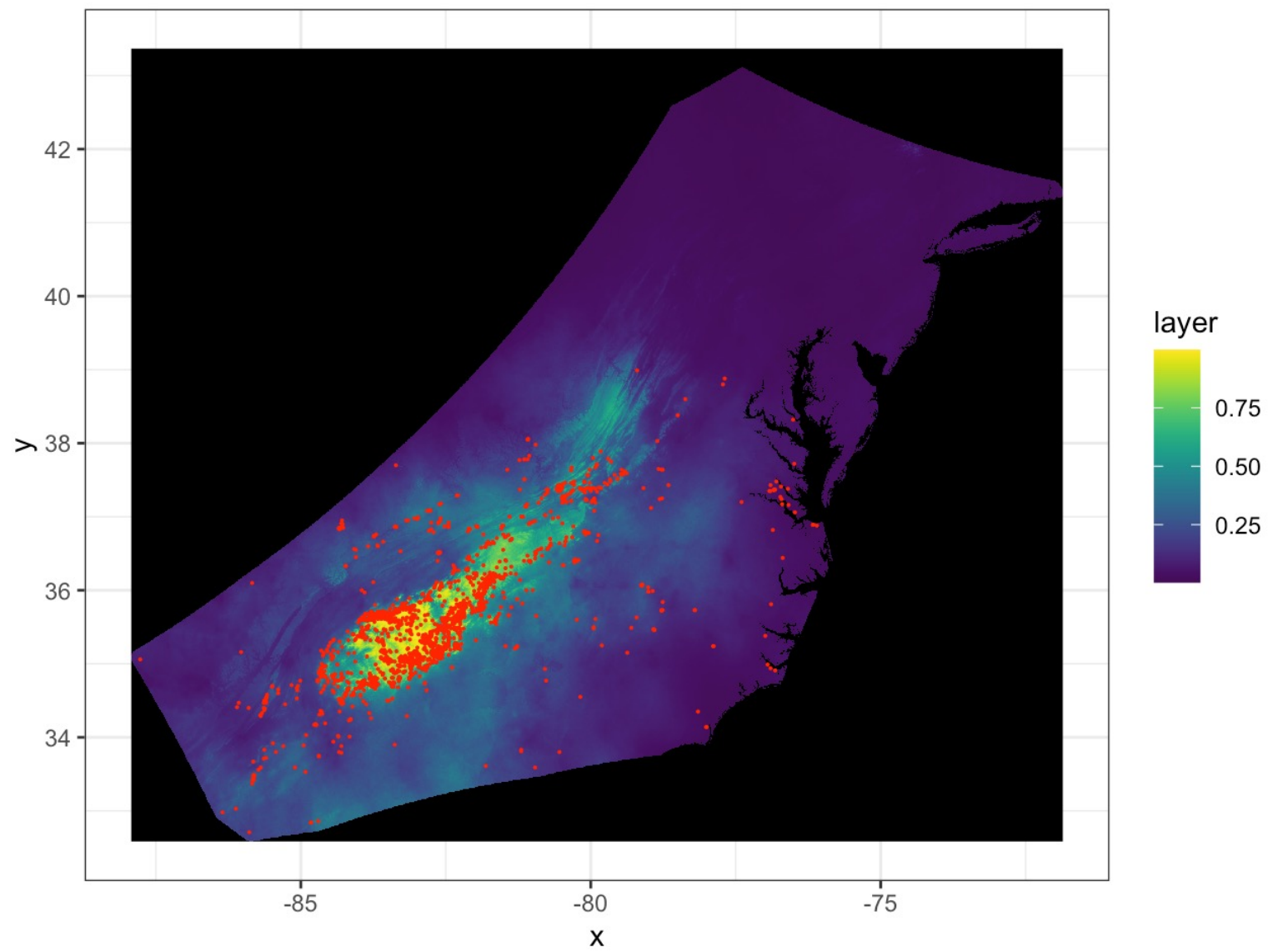
Project model to allstack

```
p <- predict(mod.seq, allstack)
```

Visualize

```
# Make into a data frame
p_df <- as.data.frame(p, xy = TRUE)

# Plot
ggplot() +
  geom_raster(data = p_df, aes(x = x, y = y, fill = layer)) +
  geom_point(data= Galax_urceolata,
            mapping = aes(x = longitude, y = latitude),
            col='red', cex=0.05) +
  coord_quickmap() +
  theme_bw() +
  scale_fill_gradientn(colours = viridis::viridis(99),
                      na.value = "black")
```



ENMeval – Save Model

Save outputs

R saved dataset

```
save(mod.seq, file = "data/Ecological_Niche_Modeling/enm_output/ENMeval/GalaxENM.rda")
```

Save Raster

```
writeRaster(x = p, filename = "data/Ecological_Niche_Modeling/enm_output/ENMeval/GalaxEN  
M.asc",  
            format = "ascii", NAFlag = "-9999", overwrite = T)
```

Interpreting ENMs

Step 1: Look at the output

Step 2: Evaluate the models

Step 3: Additional Analysis

