Logistic Regression (cont.)

Lecture 06

Dr. Colin Rundel

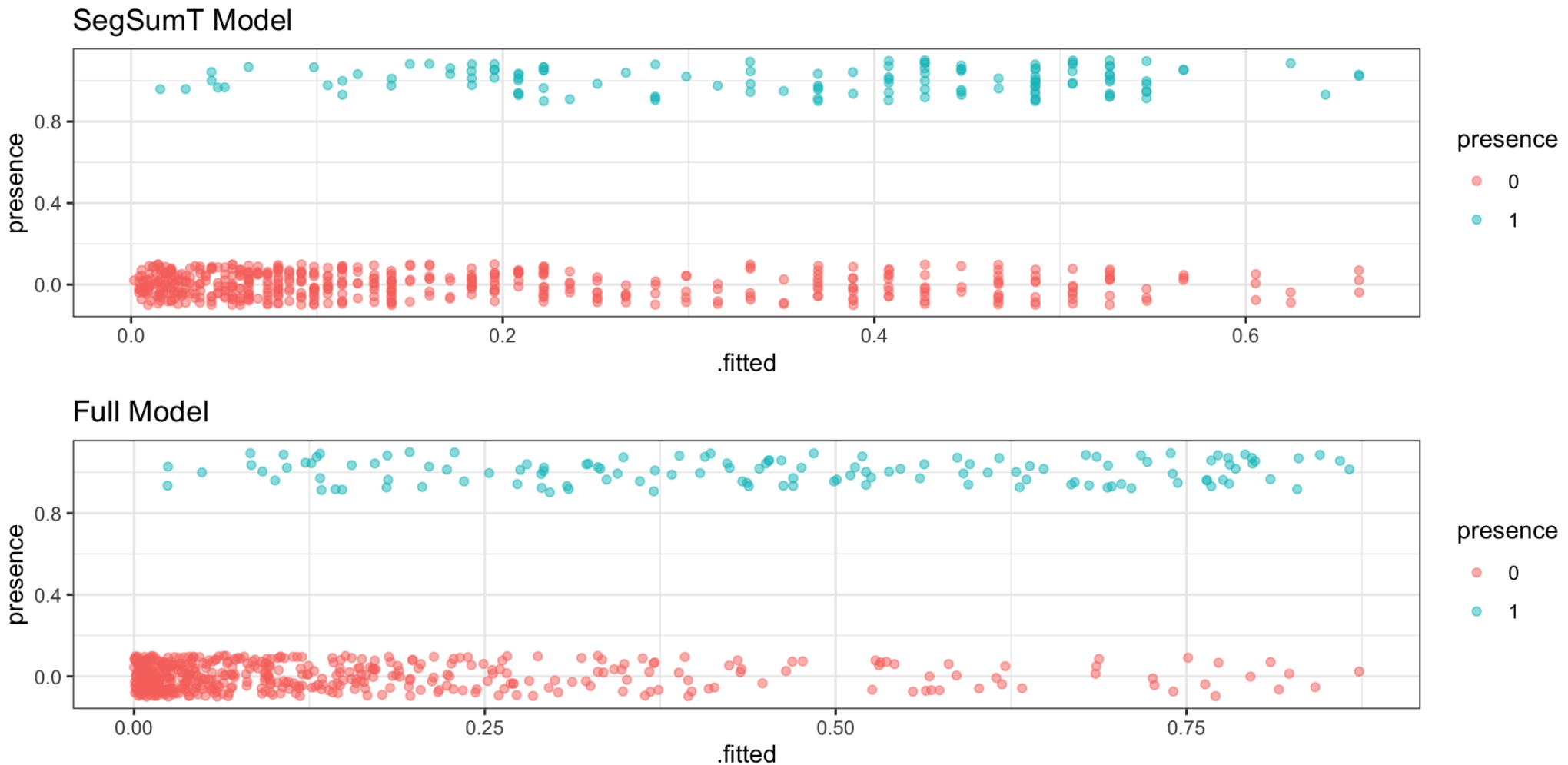
Full Model

Model

```r
f = glm(presence~., family=binomial, data=anguilla_train)
summary(f)
```

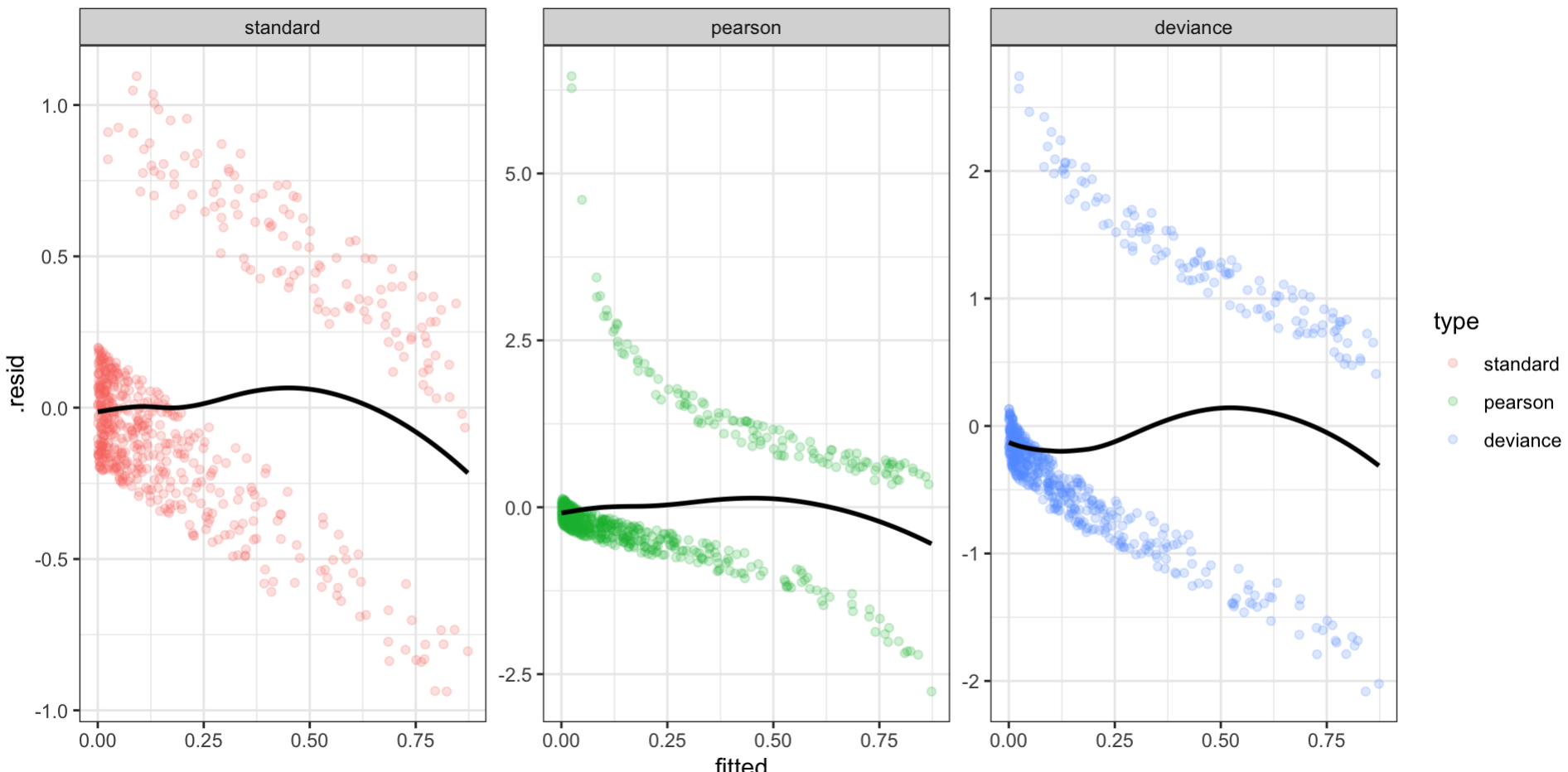
```
Call:
glm(formula = presence ~ ., family = binomial, data = anguilla_train)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -9.352885   1.761202  -5.311 1.09e-07 ***
SegSumT        0.654186   0.096921   6.750 1.48e-11 ***
DSDist        -0.004837   0.002302  -2.102  0.03559 *
DSMaxSlope    -0.030776   0.061995  -0.496  0.61959
USRainDays    -0.710920   0.225814  -3.148  0.00164 **
USSlope       -0.069814   0.025443  -2.744  0.00607 **
USNative      -0.456598   0.455261  -1.003  0.31589
DSDam         -1.095360   0.516960  -2.119  0.03410 *
Methodmixture -0.430351   0.475411  -0.905  0.36535
Methodnet     -0.066214   0.559162  -0.118  0.90574
Methodspo     -1.583905   0.701902  -2.257  0.02403 *
Methodtrap    -2.958398   0.688146  -4.299 1.72e-05 ***
LocSed        -0.140495   0.096849  -1.451  0.14688
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Separation


SegSumT Model
presence
0.0
0.4
0.8
0.0
0.2
0.4
0.6
.fitted
presence
0
1
Full Model
presence
0.0
0.4
0.8
0.00
0.25
0.50
0.75
.fitted
presence
0
1

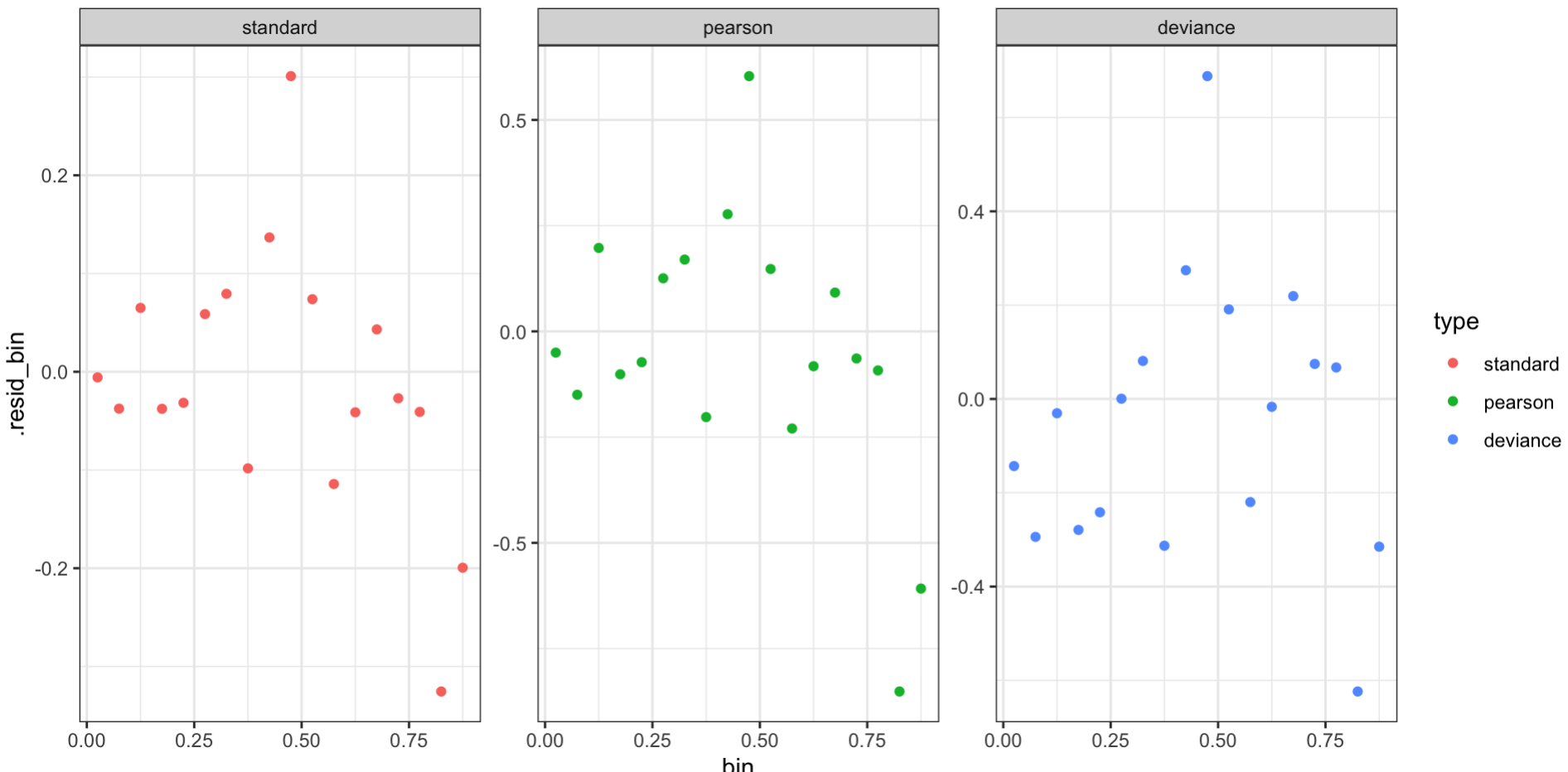
Residuals vs fitted

```
f_resid |>
  ggplot(aes(x=.fitted, y=.resid, color=type)) +
  geom_jitter(height=0.2, alpha=0.2) +
  facet_wrap(~type, ncol=3, scale="free_y") +
  geom_smooth(se = FALSE, color="black")
```



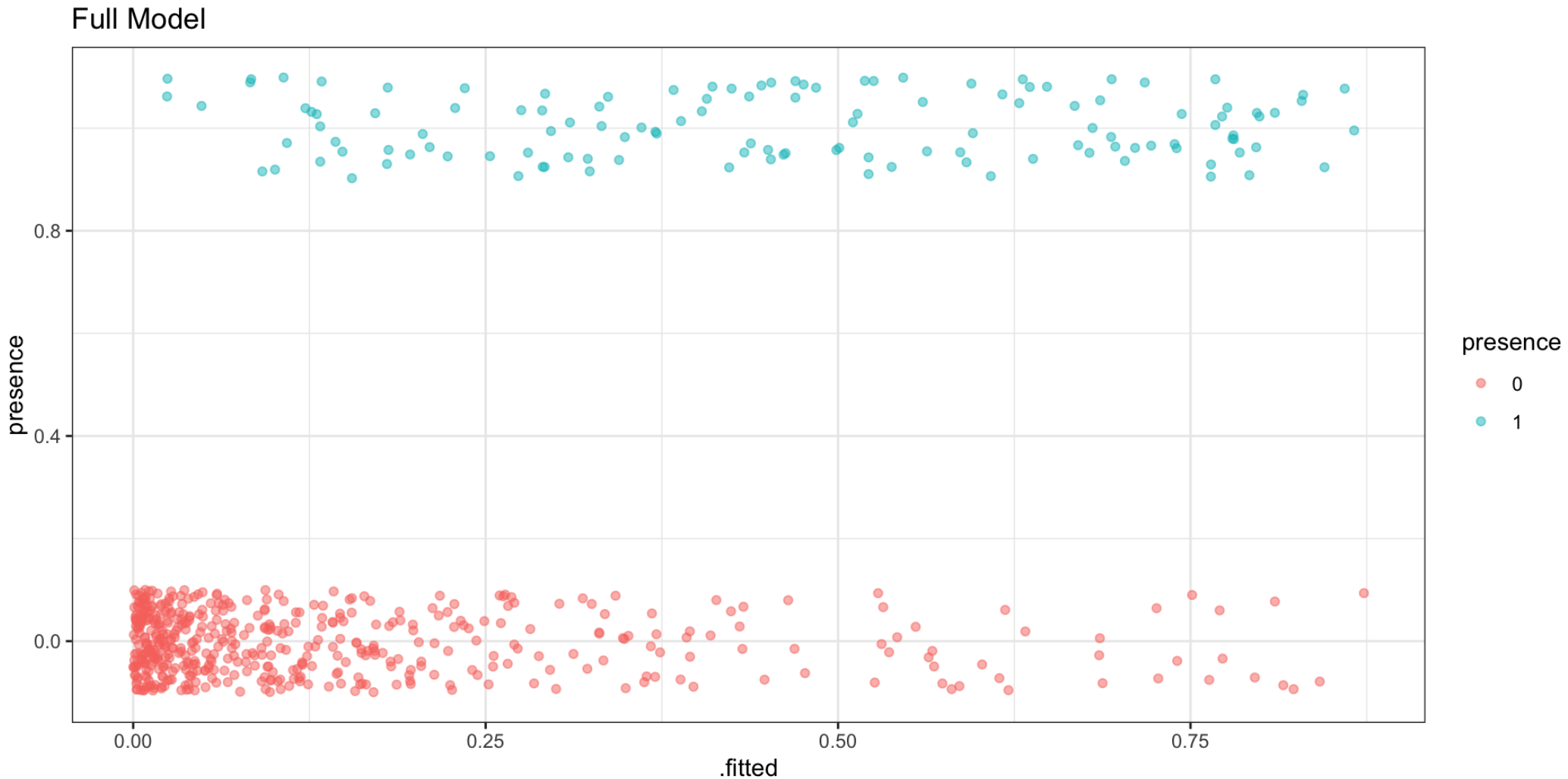
Residuals (binned) vs fitted

```
f_resid_bin |>
  mutate(type = as_factor(type)) |>
  ggplot(aes(x=bin, y=.resid_bin, color=type)) +
  geom_point() +
  facet_wrap(~type, ncol=3, scales = "free_y")
```

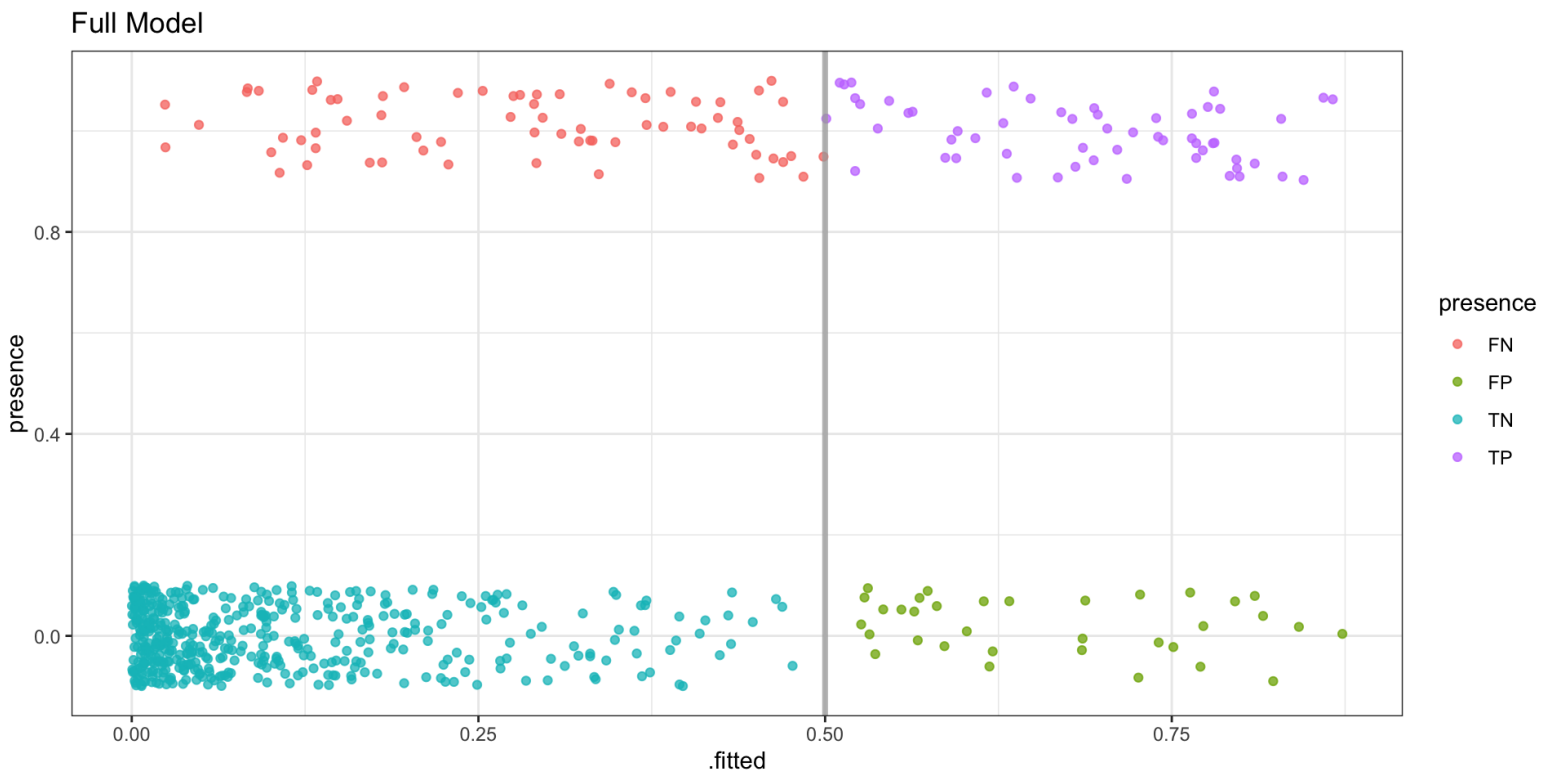


Model Performance

Confusion Matrix

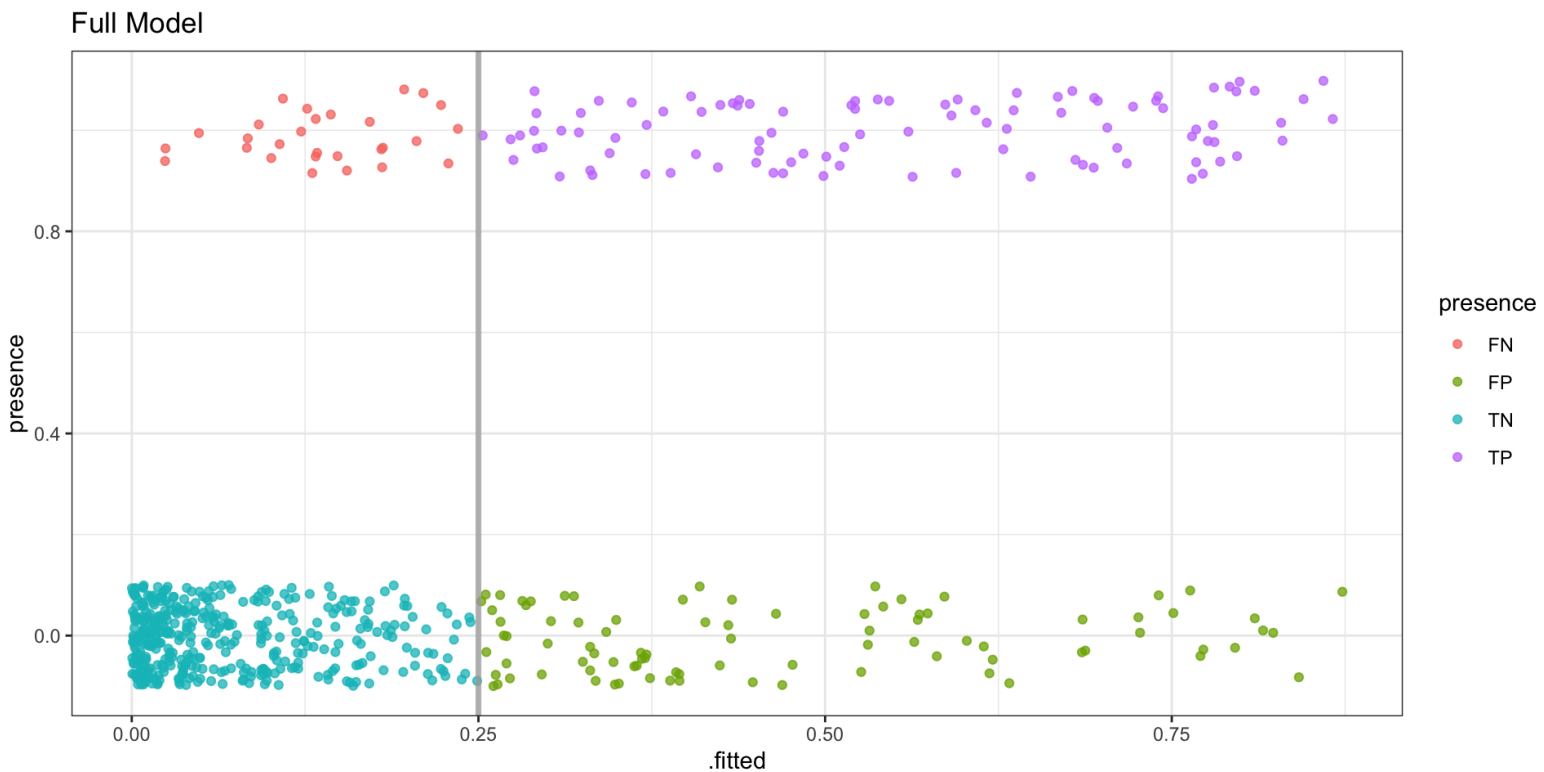


Confusion Matrix - 50% threshold



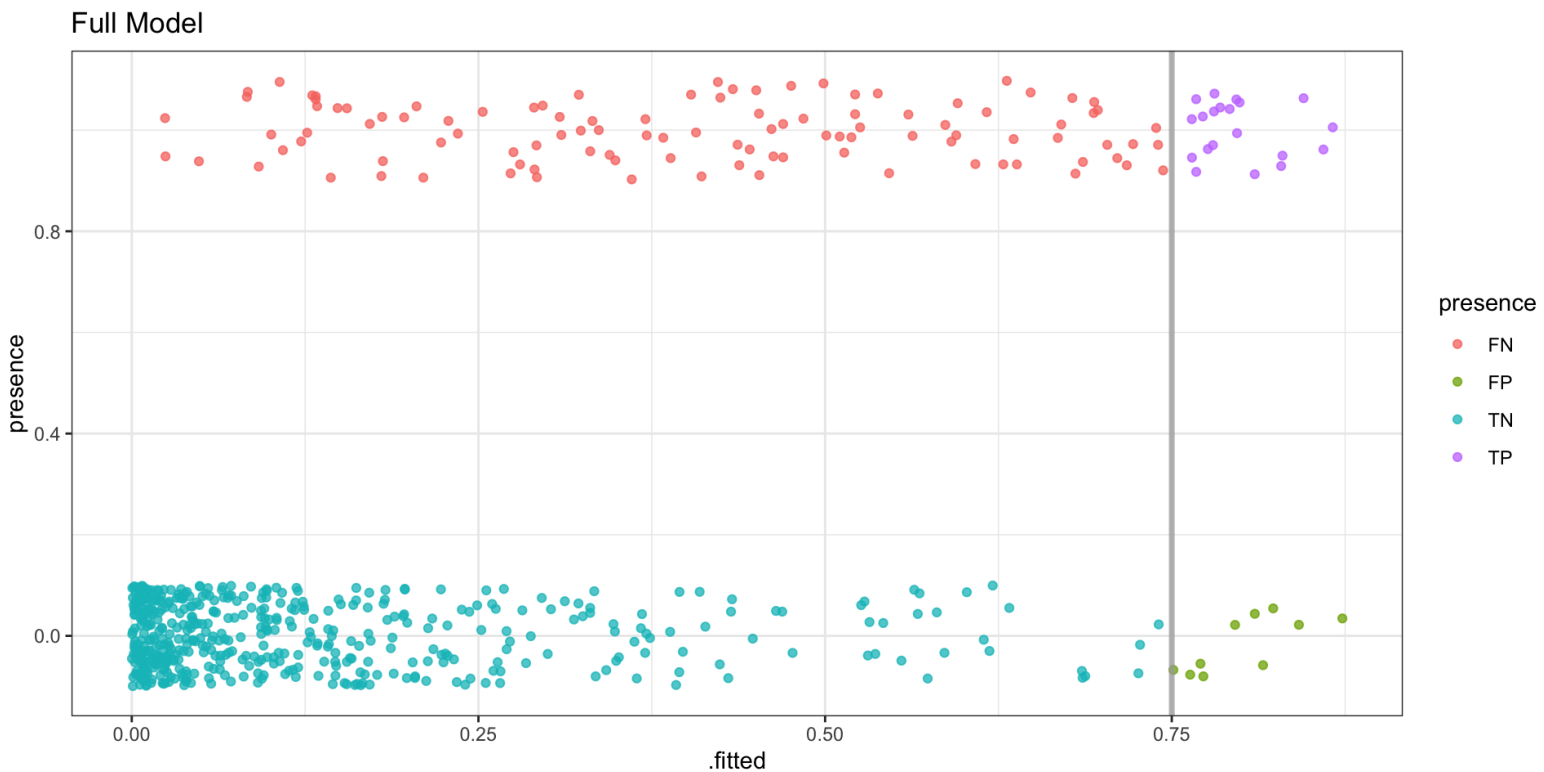
result	n
FN	70
FP	34
TN	457
TP	57

Confusion Matrix - 25% threshold



result	n
FN	28
FP	88
TN	403
TP	99

Confusion Matrix - 75% threshold



result	n
FN	107
FP	10
TN	481
TP	20

Confusion Matrix statistics

$$\text{Sensitivity= Recall} = \text{TPR} = \frac{\text{TP}}{\text{TP} + \text{FN}} = 1 - \text{FNR}$$

$$\text{Specificity} = \text{TNR} = \frac{\text{TN}}{\text{TN} + \text{FP}} = 1 - \text{FPR}$$

$$\text{Precision} = \text{PPV} = \frac{\text{TP}}{\text{TP} + \text{FP}}$$

$$\text{F}_1 = \frac{2\text{TP}}{2\text{TP} + \text{FP} + \text{FN}}$$

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}}$$

Combining model predictions

```
( model_comb  = bind_rows(
    g_std |> mutate(model = "SegSumT"),
    f_std |> mutate(model = "Full")
  ) |>
    group_by(model)
)
```

```
# A tibble: 1,236 × 17
# Groups:   model [2]
   presence SegSumT .fitted  .resid    .hat .sigma   .cooksd .std.resid model
      <int>   <dbl>   <dbl>   <dbl>   <dbl>  <dbl>     <dbl>      <dbl> <chr>
 1        0    16.4  0.131  -0.131  0.00260  0.903 0.000197      -0.530 SegSumT
 2        1    17.1  0.209   0.791  0.00232  0.901 0.00443        1.77  SegSumT
 3        0    14    0.0216 -0.0216 0.00231  0.903 0.0000256     -0.209 SegSumT
 4        0    18.2  0.389  -0.389  0.00364  0.903 0.00117       -0.994 SegSumT
 5        0    15.6  0.0735 -0.0735 0.00286  0.903 0.000114      -0.391 SegSumT
 6        0    18.3  0.408  -0.408  0.00395  0.902 0.00137       -1.03  SegSumT
 7        0    18.5  0.447  -0.447  0.00466  0.902 0.00190       -1.09  SegSumT
 8        0    16.2  0.114  -0.114  0.00270  0.903 0.000174      -0.492 SegSumT
 9        0    18    0.351  -0.351  0.00313  0.903 0.000853      -0.932 SegSumT
10        1    17.3  0.236   0.764  0.00233  0.901 0.00379        1.70  SegSumT
# ℹ 1,226 more rows
# ℹ 8 more variables: DSDist <dbl>, DSMaxSlope <dbl>, USRainDays <dbl>,
#   USSlope <dbl>, USNative <dbl>, DSDam <int>, Method <fct>, LocSed <dbl>
```

Receiver operating characteristic (ROC)

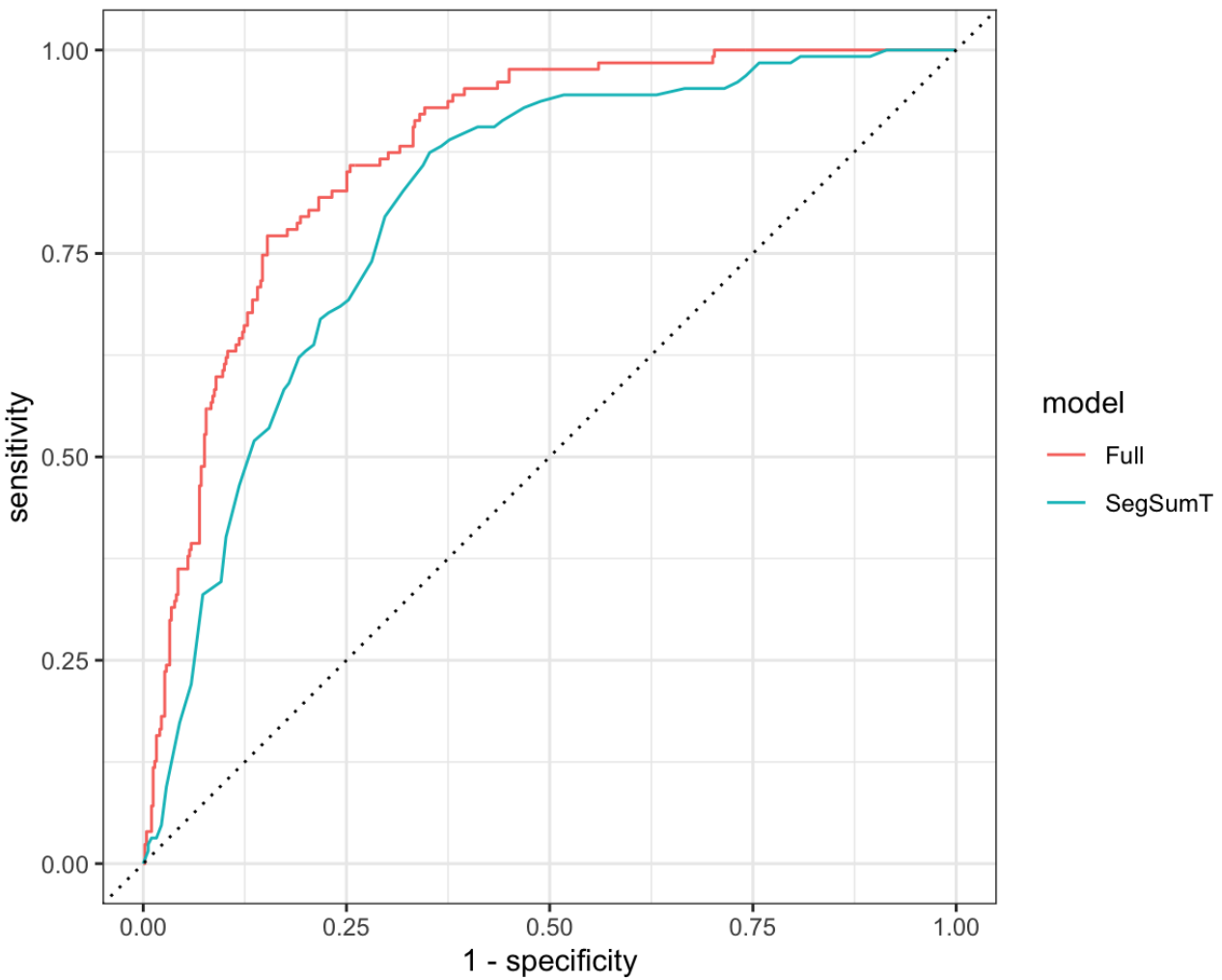
$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}} \qquad \text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}$$

```
( model_roc = model_comb |>
    mutate(presence = factor(presence, levels = c(1,0))) |>
    yardstick::roc_curve(presence, .fitted)
)
```

```
# A tibble: 696 × 4
# Groups:   model [2]
   model  .threshold specificity sensitivity
   <chr>       <dbl>       <dbl>       <dbl>
 1 Full  -Inf            0                 1
 2 Full     0.000132     0                 1
 3 Full     0.000425     0.00204           1
 4 Full     0.000453     0.00407           1
 5 Full     0.000755     0.00611           1
 6 Full     0.000761     0.00815           1
 7 Full     0.000792     0.0102            1
 8 Full     0.00108      0.0122            1
 9 Full     0.00126      0.0143            1
10 Full     0.00146      0.0163            1
# ℹ 686 more rows
```

ROC Curve

```
1 model_roc |>
2   autoplot()
```



AUC (area under the curve)

```
1 model_comb |>
2   mutate(presence = factor(presence, levels = c(1,0))) |>
3   yardstick::roc_auc(presence, .fitted)
```

```
# A tibble: 2 × 4
  model   .metric .estimator .estimate
  <chr>   <chr>   <chr>          <dbl>
1 Full    roc_auc binary         0.875
2 SegSumT roc_auc binary         0.806
```

A model that randomly assigns classes to the data is expected to achieve an AUC of 0.5 (dotted line on the previous plot) while a perfect model would achieve an AUC of 1.

Precision / Recall

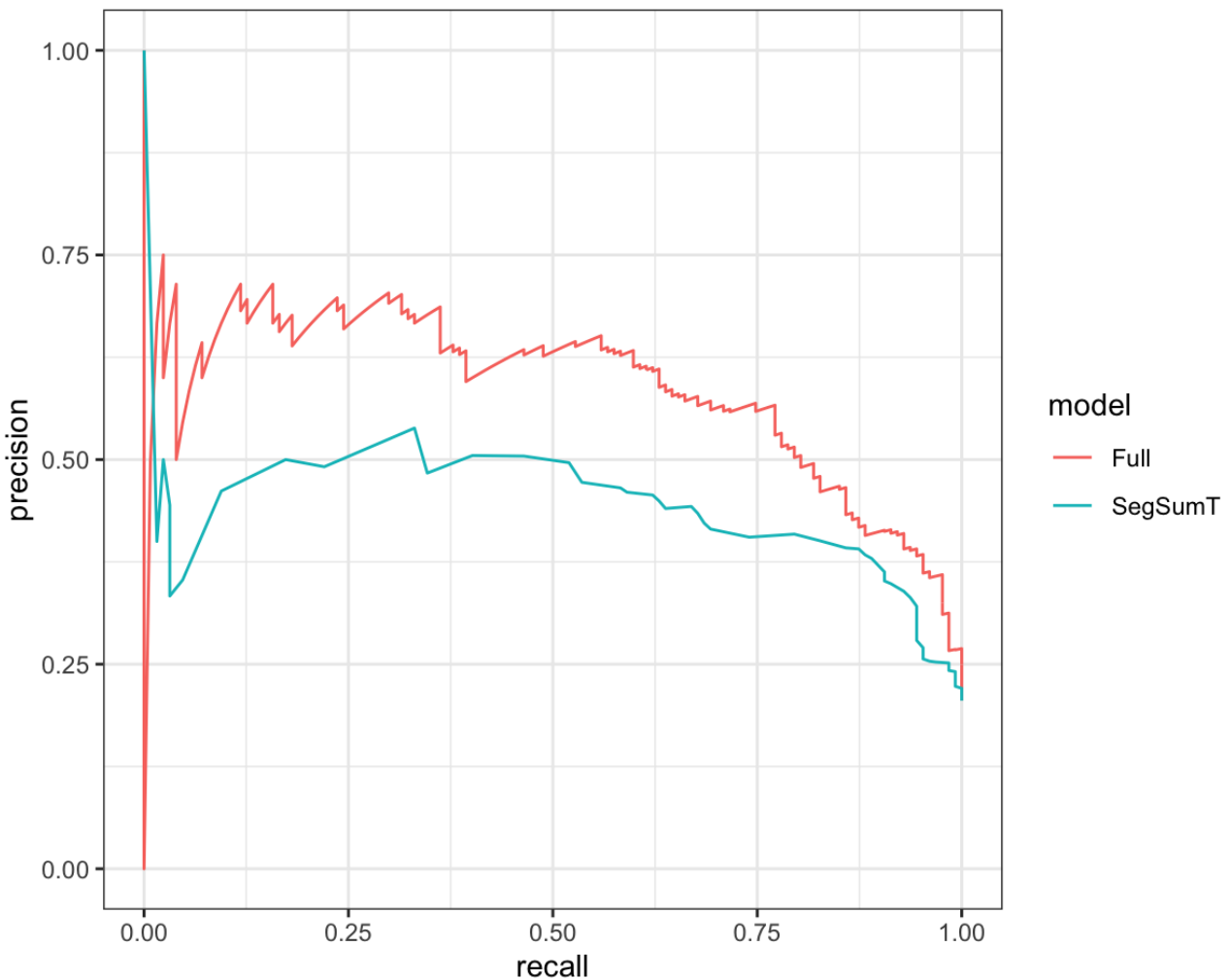
$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \qquad \text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

```
( model_pr = model_comb |>
    mutate(presence = factor(presence, levels = c(1,0))) |>
    yardstick::pr_curve(presence, .fitted)
)
```

```
# A tibble: 694 × 4
# Groups:   model [2]
   model .threshold  recall precision
   <chr>       <dbl>   <dbl>     <dbl>
 1 Full      Inf     0           1
 2 Full        0.873 0           0
 3 Full        0.866 0.00787     0.5
 4 Full        0.859 0.0157      0.667
 5 Full        0.845 0.0236      0.75
 6 Full        0.842 0.0236      0.6
 7 Full        0.830 0.0315      0.667
 8 Full        0.829 0.0394      0.714
 9 Full        0.823 0.0394      0.625
10 Full        0.816 0.0394      0.556
# ℹ 684 more rows
```

Precision Recall curve

```
1 model_pr |>
2   autoplot()
```



Precision Recall AUC

```
1 model_comb |>
2   mutate(presence = factor(presence, levels = c(1,0))) |>
3   yardstick::pr_auc(presence, .fitted)
```

```
# A tibble: 2 × 4
  model    .metric .estimator .estimate
  <chr>    <chr>   <chr>          <dbl>
1 Full     pr_auc  binary         0.583
2 SegSumT pr_auc  binary         0.447
```

A model that randomly assigns classes to the data is expected to achieve an PR-AUC of # successes / n while a perfect model would achieve an PR-AUC of 1 (a point at a coordinate of (1,1)).

What about the test data?

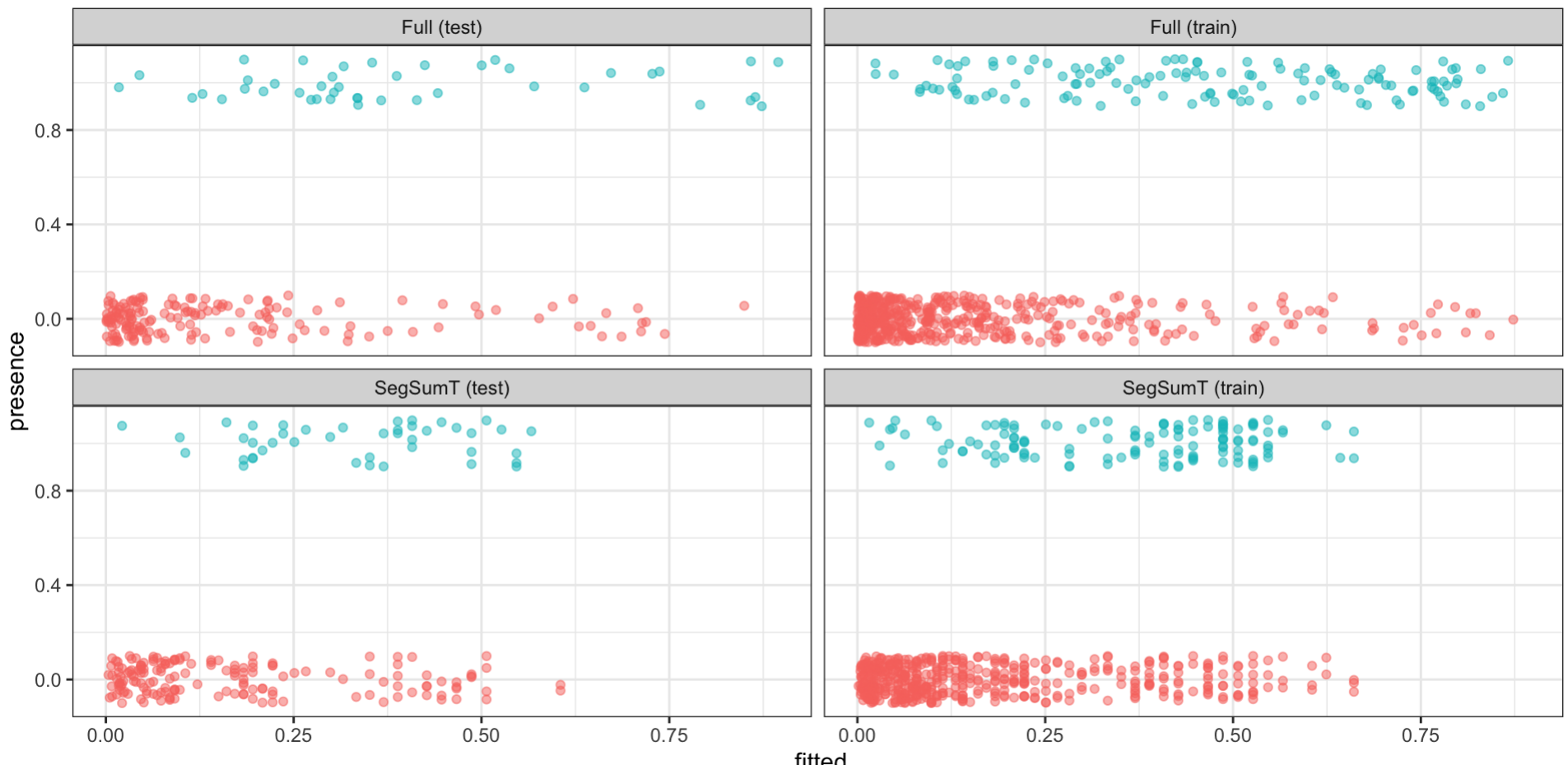
Combining predicitons

```
(model_comb = bind_rows(
    broom::augment(g, newdata=anguilla_train, type.predict="response") |> mutate(model = "SegSum
    broom::augment(g, newdata=anguilla_test,  type.predict="response") |> mutate(model = "SegSum
    broom::augment(f, newdata=anguilla_train, type.predict="response") |> mutate(model = "Full (
    broom::augment(f, newdata=anguilla_test,  type.predict="response") |> mutate(model = "Full (
  ) |>
    group_by(model)
)
```

```
# A tibble: 1,648 × 12
# Groups:   model [4]
   presence SegSumT DSDist DSMaxSlope USRainDays USSlope USNative DSDam Method
      <int>   <dbl>  <dbl>      <dbl>      <dbl>   <dbl>    <dbl> <int> <fct>
 1        0    16.4  97.8        6.28      1.51     24.6     0.81     0 electric
 2        1    17.1  13.9        0.57      1.98      3.3     0.13     0 net
 3        0    14     1.84       0.57      0.29     10.1     0.37     0 electric
 4        0    18.2 121.         0.57      0.894     1.1     0.02     0 trap
 5        0    15.6  55.1        5.14      3.3      27.6     0.98     0 electric
 6        0    18.3 107.         0.57      0.85      1.1     0        0 trap
 7        0    18.5  81.5        2.29      1.26     22.8     0.94     0 electric
 8        0    16.2 272.         3.43      0.56     27.2     0.95     1 electric
 9        0    18    24.4        0.17      0.601    19.5     0.16     0 electric
10        1    17.3  11.9        0.57      2.14      3.9     0.04     0 electric
# ℹ 1,638 more rows
# ℹ 3 more variables: LocSed <dbl>, .fitted <dbl>, model <chr>
```

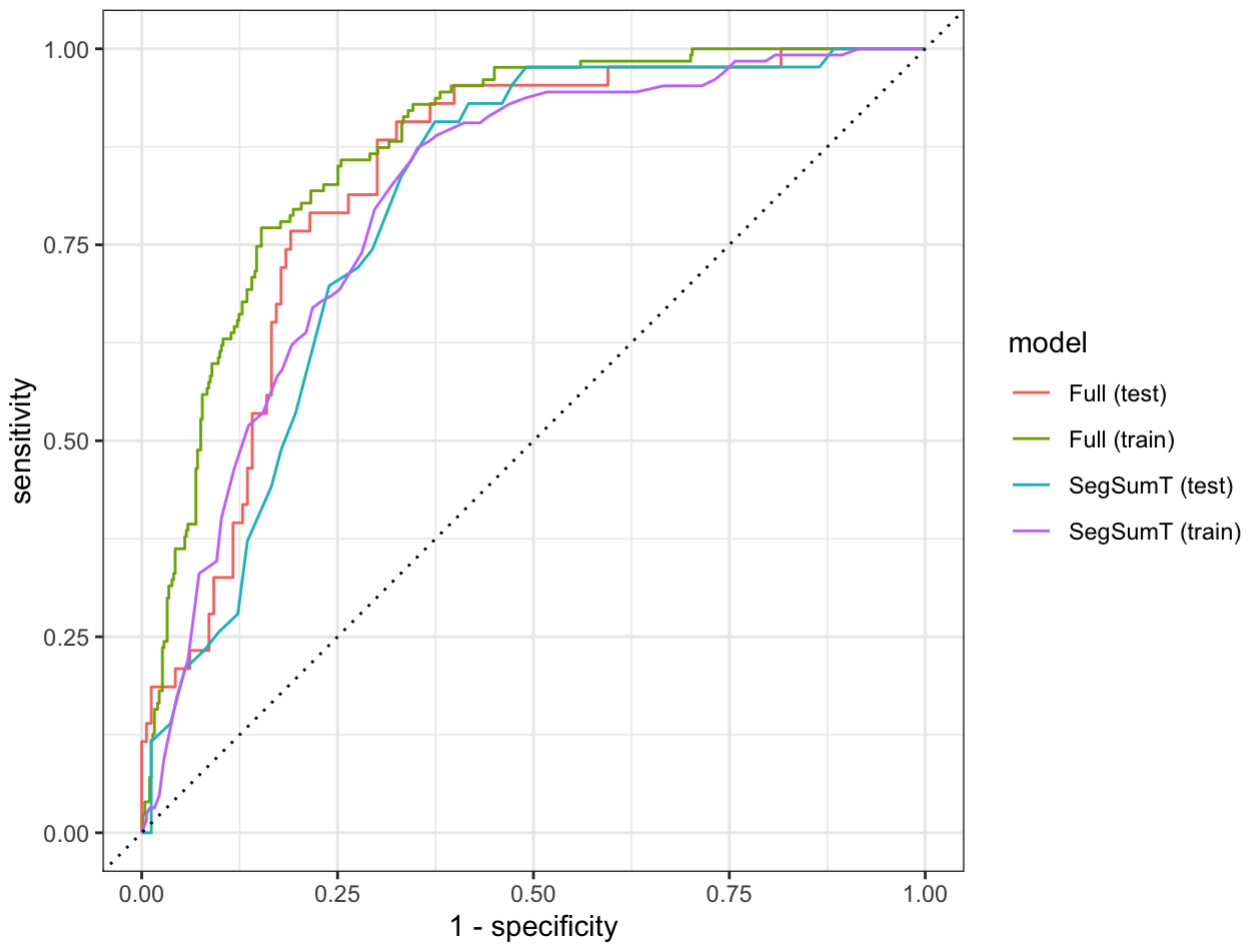
Separation

```
model_comb |>
  ggplot(aes(x=.fitted, y=presence, color=as.factor(presence))) +
    geom_jitter(height=0.1, alpha=0.5) +
    facet_wrap(~model, ncol=2) +
    guides(color="none")
```



ROC

```
model_comb |>
  mutate(presence = factor(presence, levels = c(1,0))) |>
  yardstick::roc_curve(presence, .fitted) |>
  autoplot()
```



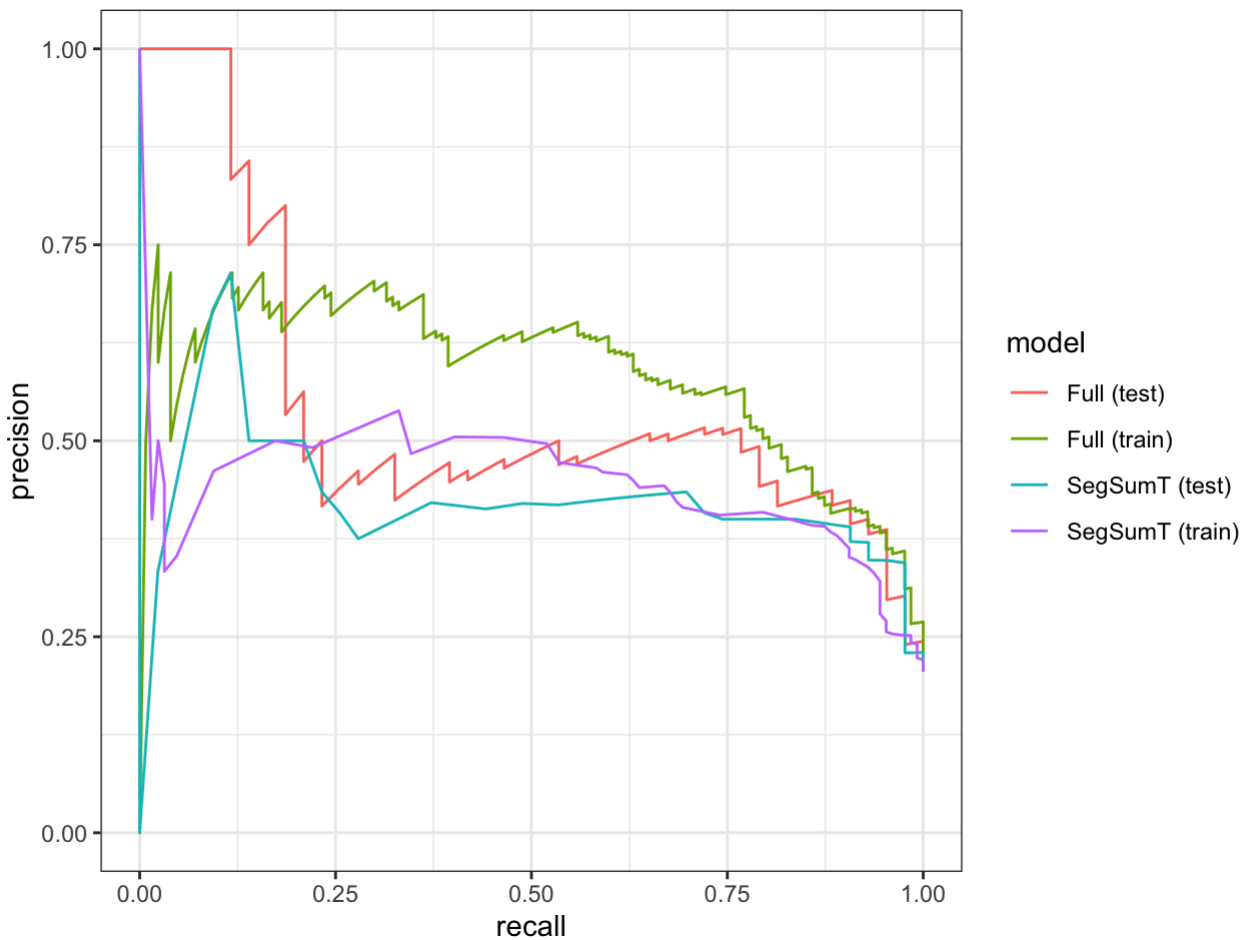
AUC

```
model_comb |>
  mutate(presence = factor(presence, levels = c(1,0))) |>
  yardstick::roc_auc(presence, .fitted)
```

```
# A tibble: 4 × 4
  model            .metric .estimator .estimate
  <chr>            <chr>   <chr>          <dbl>
1 Full (test)      roc_auc binary         0.831
2 Full (train)     roc_auc binary         0.875
3 SegSumT (test)   roc_auc binary         0.796
4 SegSumT (train)  roc_auc binary         0.806
```

Precision / Recall

```
model_comb |>
  mutate(presence = factor(presence, levels = c(1,0))) |>
  yardstick::pr_curve(presence, .fitted) |>
  autoplot()
```



PR-AUC

```
1 model_comb |>
2   mutate(presence = factor(presence, levels = c(1,0))) |>
3   yardstick::pr_auc(presence, .fitted)
```

```
# A tibble: 4 × 4
  model            .metric .estimator .estimate
  <chr>            <chr>   <chr>          <dbl>
1 Full (test)      pr_auc  binary         0.543
2 Full (train)     pr_auc  binary         0.583
3 SegSumT (test)   pr_auc  binary         0.422
4 SegSumT (train)  pr_auc  binary         0.447
```

Aside: Species Distribution Modeling

Model Choice

We have been fitting a model that looks like the following,

$$y_i \sim \text{Bern}(p_i)$$

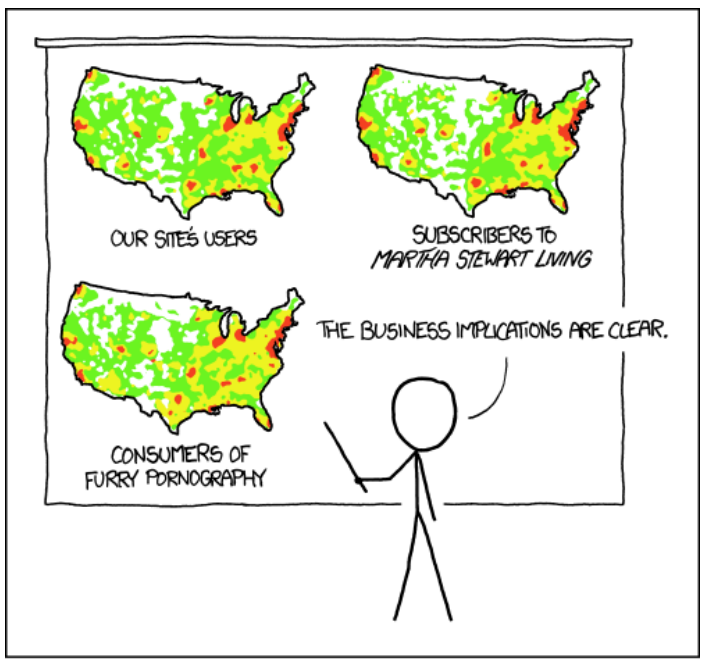
$$\text{logit}(p_i) = \boldsymbol{X}_i \cdot \boldsymbol{\beta}$$

Interpretation of y_i and p_i?

Absence of evidence ...

If we observe a species at a particular location what does that tell us?

If we *don't* observe a species at a particular location what does that tell us?



PET PEEVE #208:
GEOGRAPHIC PROFILE MAPS WHICH ARE BASICALLY JUST POPULATION MAPS

Revised Model

If we allow for crypsis, then

$$y_i \sim \text{Bern}(q_i\, z_i)$$
$$z_i \sim \text{Bern}(p_i)$$

$$\text{logit}(q_i) = \boldsymbol{X}^{\star}_{i\cdot}\boldsymbol{\gamma}$$
$$\text{logit}(p_i) = \boldsymbol{X}_{i\cdot}\boldsymbol{\beta}$$

How should we interpret the parameters / variables: y_i, z_i, p_i, and q_i?

- y_i indicates if the species was detected or not
- z_i indicates if the species is present or not
- q_i is the probability of detecting the species
- p_i is the probability of the species being present

Bayesian Model

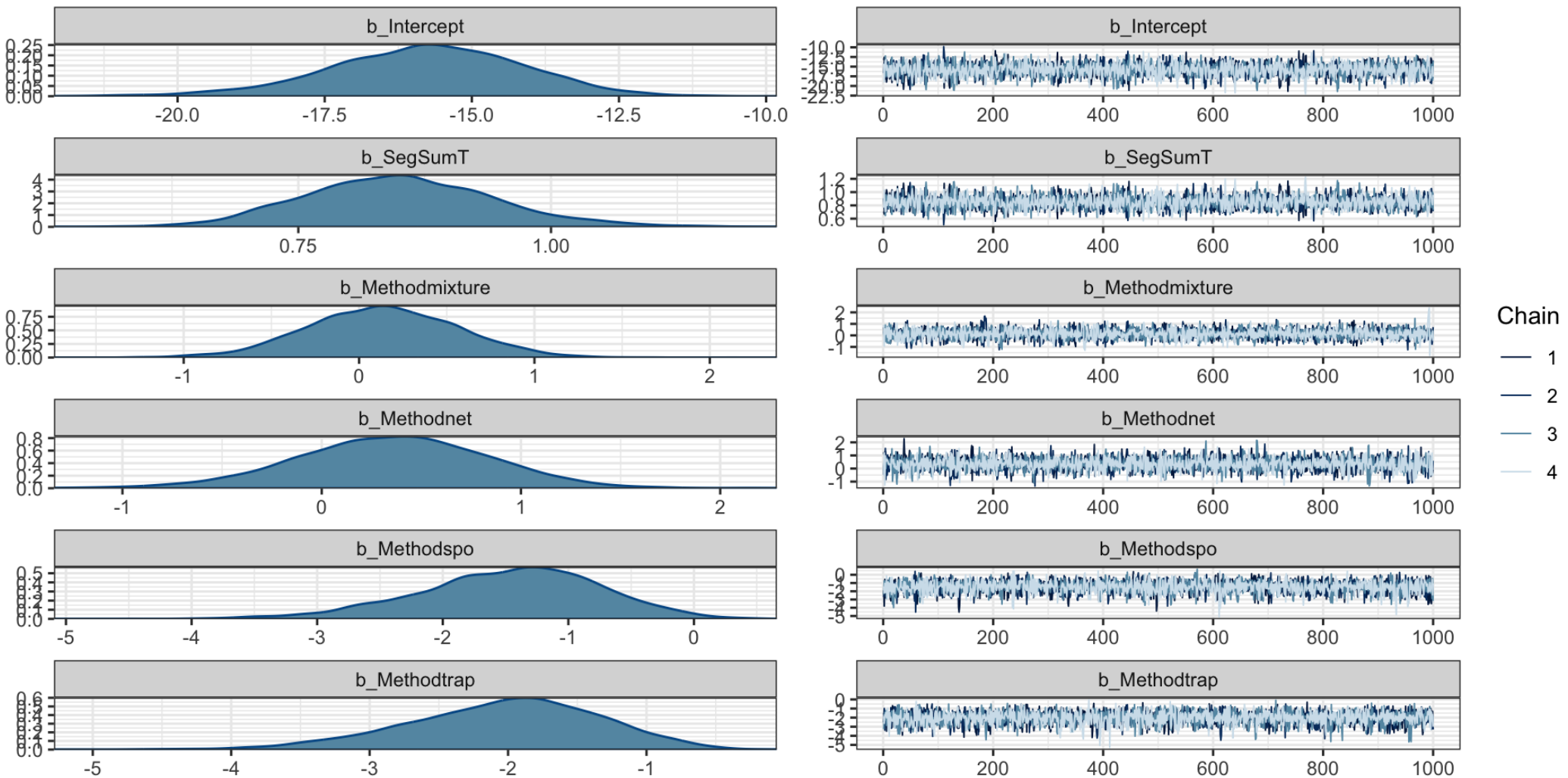
brms + logistic regression

```r
( b = brms::brm(
    presence~SegSumT+Method, family="bernoulli",
    data=anguilla_train
) )
```

```
 Family: bernoulli
  Links: mu = logit
Formula: presence ~ SegSumT + Method
   Data: anguilla_train (Number of observations: 618)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Population-Level Effects:
             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept       -15.78      1.64   -19.26   -12.74 1.00     3174     2355
SegSumT           0.85      0.09     0.68     1.05 1.00     3238     2493
Methodmixture     0.13      0.43    -0.69     0.96 1.00     4248     2850
Methodnet         0.35      0.48    -0.63     1.27 1.00     5319     2455
Methodspo        -1.48      0.73    -3.05    -0.18 1.00     5061     2614
Methodtrap       -2.04      0.70    -3.52    -0.81 1.00     4693     2667

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

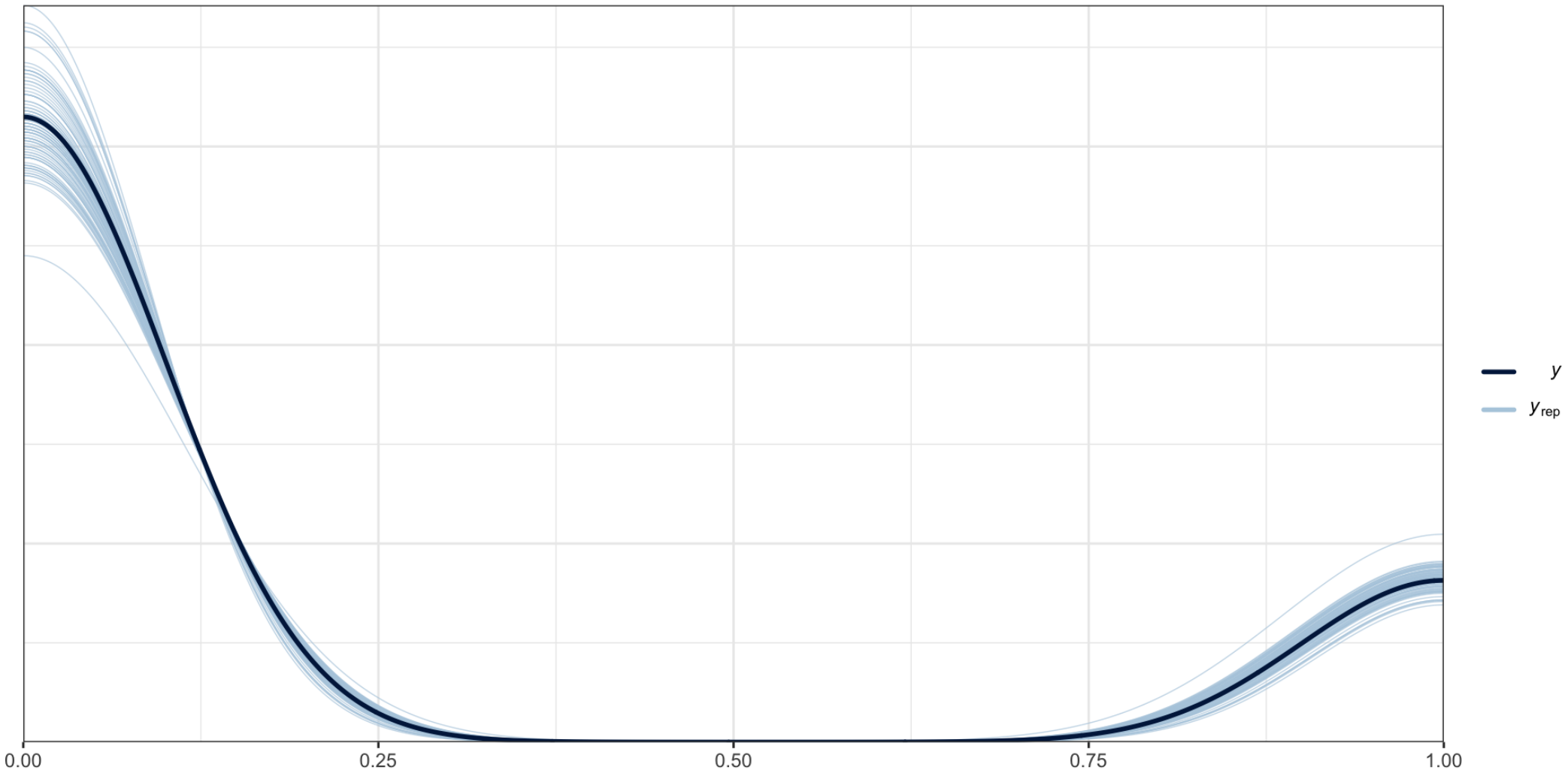
Diagnostics

```
1  plot(b, N=6)
```



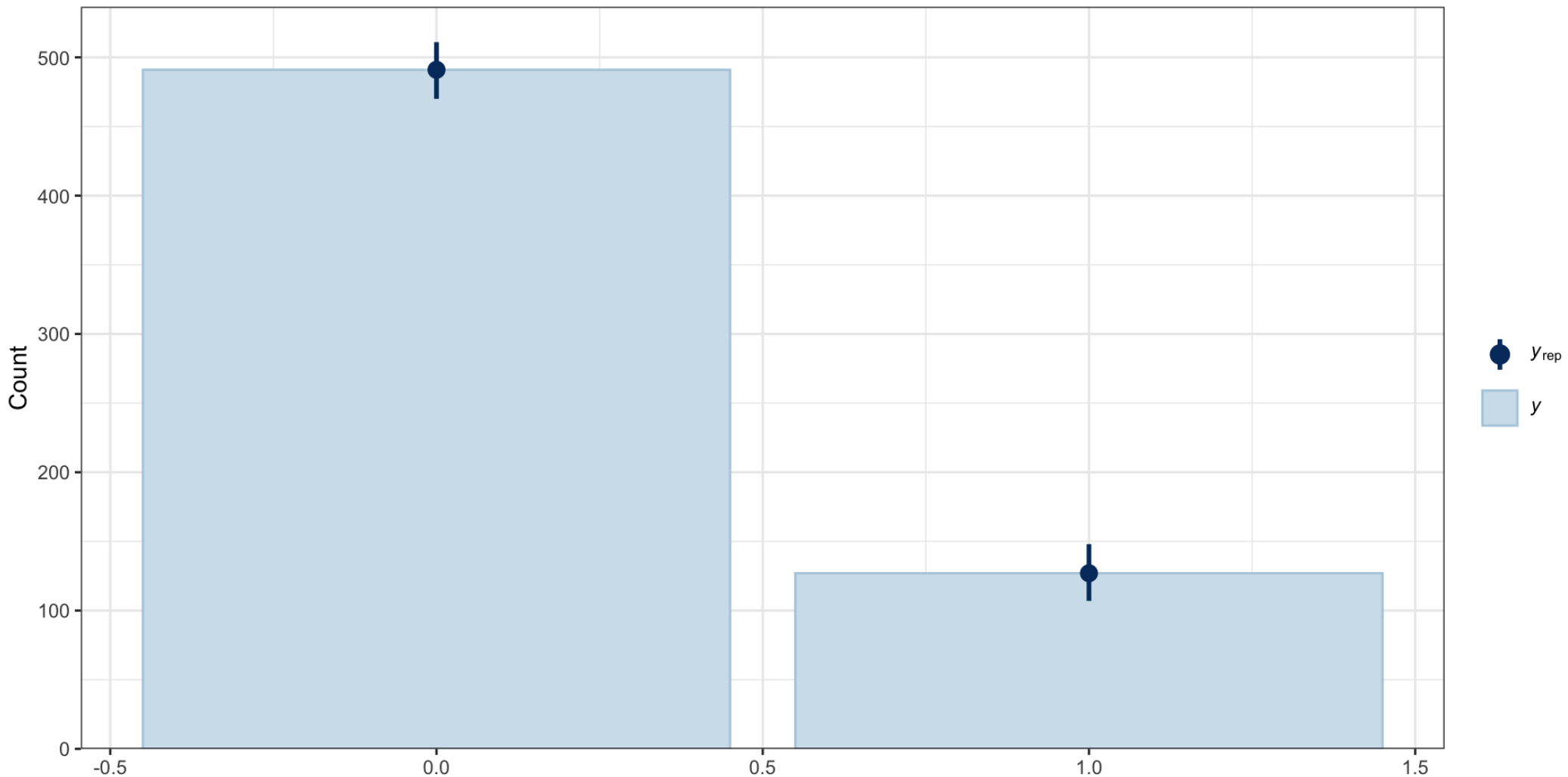
PP checks

```
1  brms::pp_check(b, ndraws=100)
```



PP check - bars

```
brms::pp_check(b, type="bars", ndraws=1000)
```



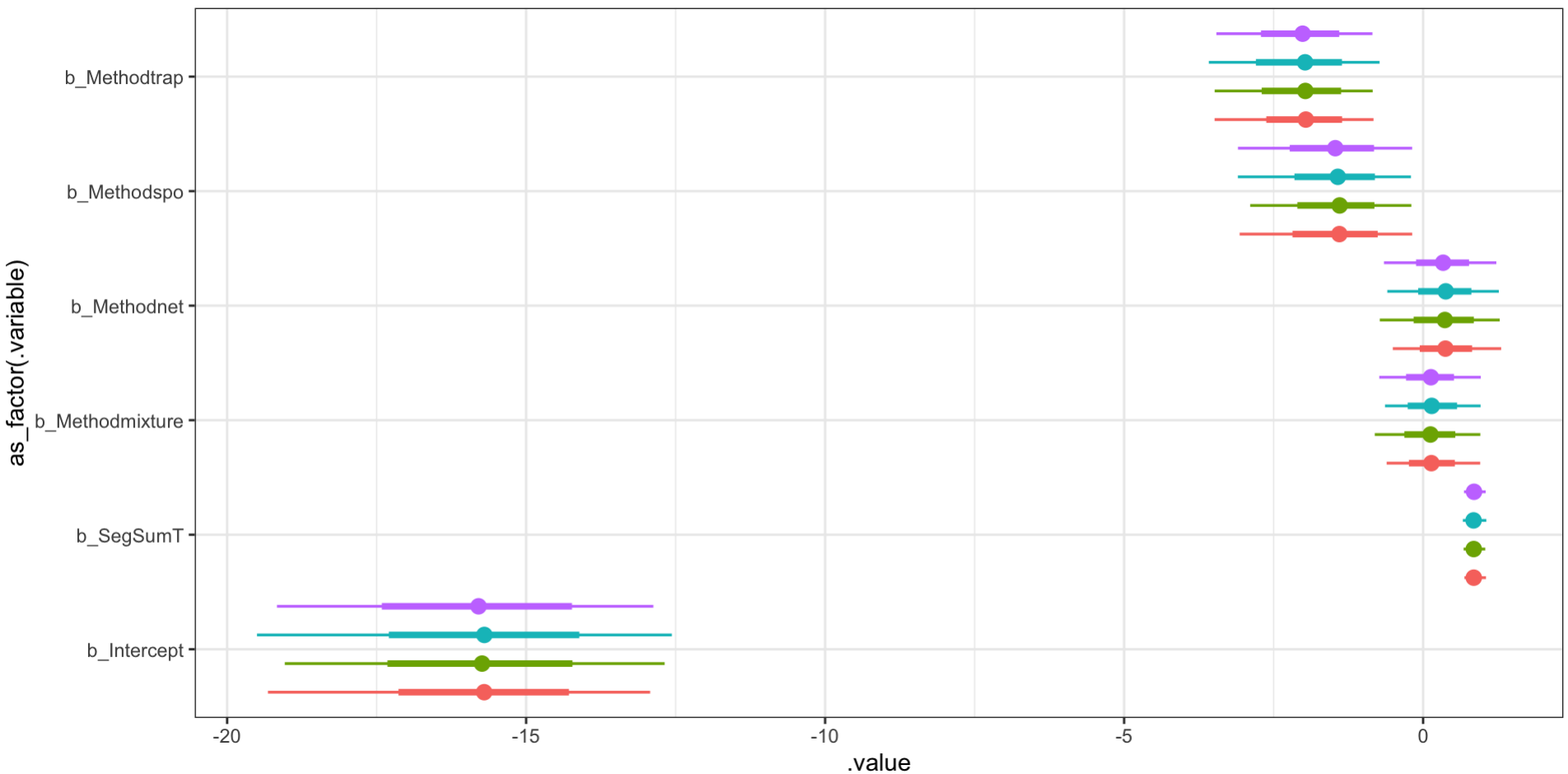
Gathering parameters

```
( b_param = b |>
    tidybayes::gather_draws( `b_.*`, regex = TRUE)
)
```

```
# A tibble: 24,000 × 5
# Groups:   .variable [6]
   .chain .iteration .draw .variable   .value
    <int>      <int> <int> <chr>        <dbl>
 1      1          1     1 b_Intercept  -13.3
 2      1          2     2 b_Intercept  -12.6
 3      1          3     3 b_Intercept  -18.2
 4      1          4     4 b_Intercept  -15.1
 5      1          5     5 b_Intercept  -16.9
 6      1          6     6 b_Intercept  -19.0
 7      1          7     7 b_Intercept  -18.1
 8      1          8     8 b_Intercept  -17.8
 9      1          9     9 b_Intercept  -16.6
10      1         10    10 b_Intercept  -16.7
# ℹ 23,990 more rows
```

Caterpillar plot

```
b_param |>
  ggplot(aes(x=.value, y=as_factor(.variable), color=as.factor(.chain))) +
    tidybayes::stat_pointinterval(position = "dodge") +
    guides(color="none")
```



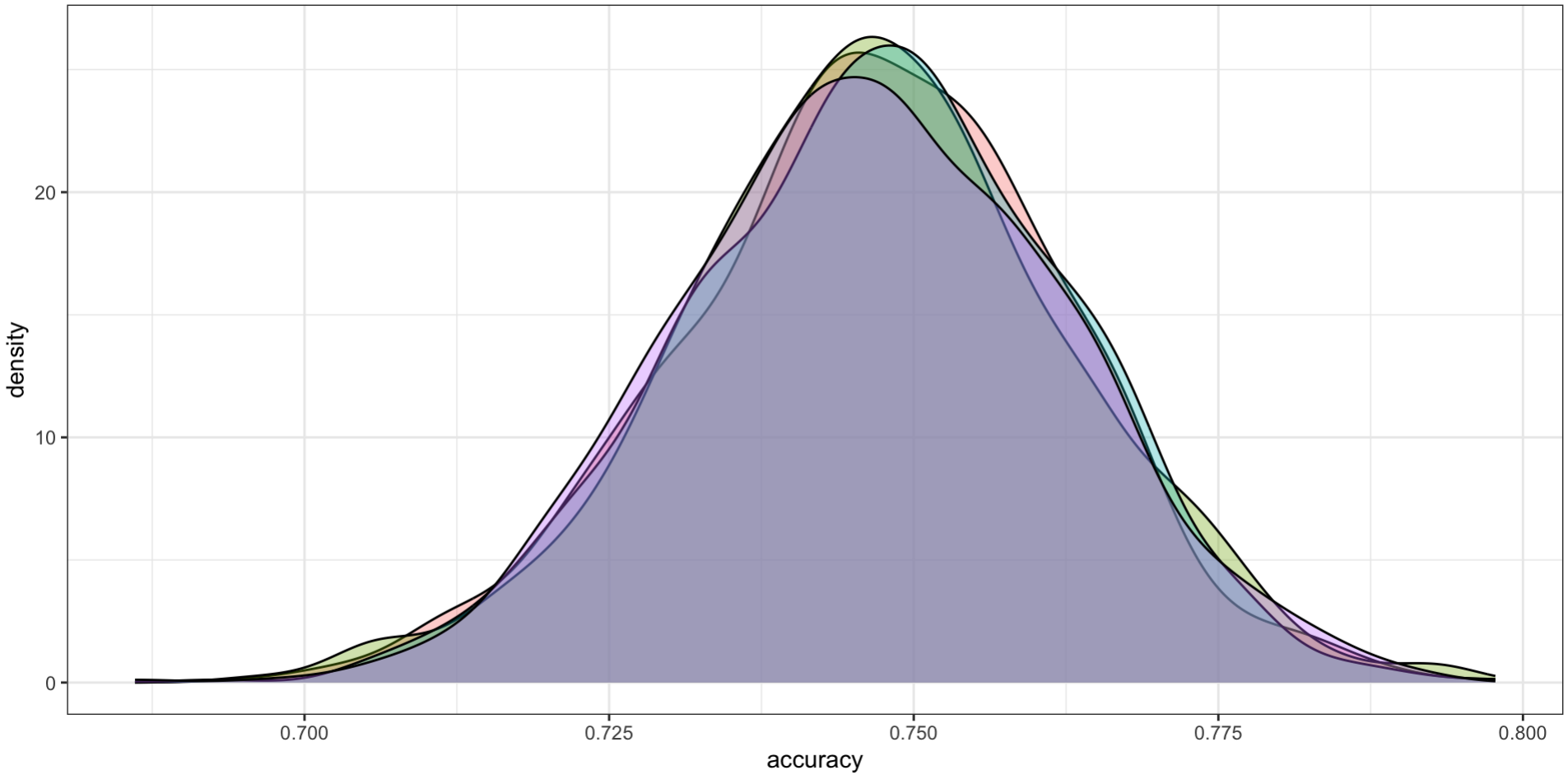
Posterior predictive

```r
( b_pred = b |>
    predicted_draws_fix(newdata = anguilla_train) |>
    select(presence, .row:.prediction) |>
    mutate( # Fix for yardstick
      presence = factor(presence, levels=c(1,0)),
      .prediction = factor(.prediction, levels=c(1,0))
    )
)
```

```
# A tibble: 2,472,000 × 6
   presence  .row .chain .iteration .draw .prediction
   <fct>    <int>  <int>      <int> <int> <fct>
 1 0            1      1          1     1 0
 2 0            1      1          2     2 0
 3 0            1      1          3     3 0
 4 0            1      1          4     4 0
 5 0            1      1          5     5 0
 6 0            1      1          6     6 0
 7 0            1      1          7     7 1
 8 0            1      1          8     8 0
 9 0            1      1          9     9 0
10 0            1      1         10    10 0
# ℹ 2,471,990 more rows
```

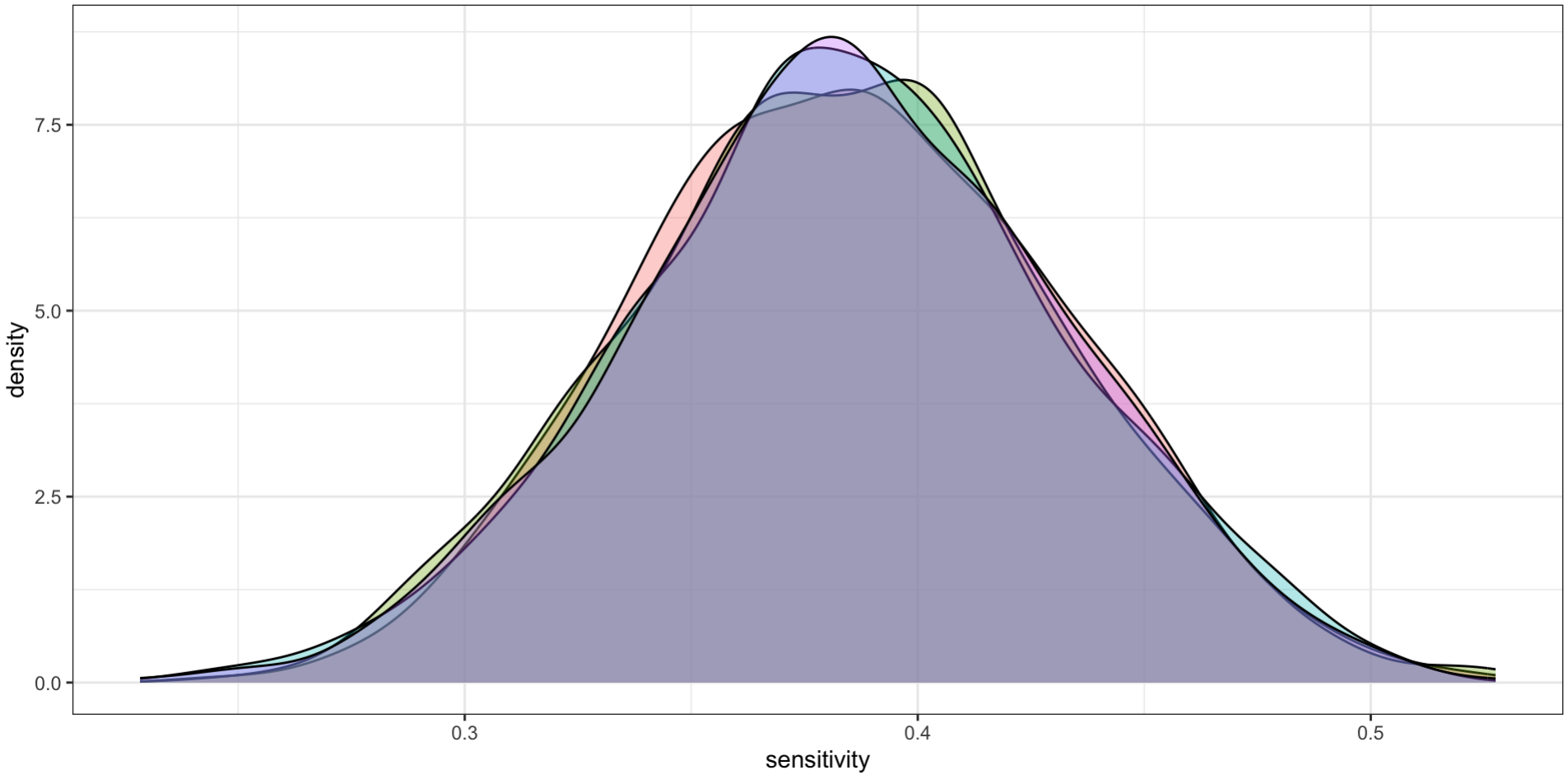
Posterior Accuracy

```
b_pred  |>
  group_by(.chain, .iteration) |>
  summarize(accuracy = yardstick::accuracy_vec(presence, .prediction)) |>
  ggplot(aes(x = accuracy, fill = as.factor(.chain))) +
    geom_density(alpha=0.33) +
    guides(fill = "none")
```


density
20
10
0
0.700
0.725
0.750
0.775
0.800
accuracy

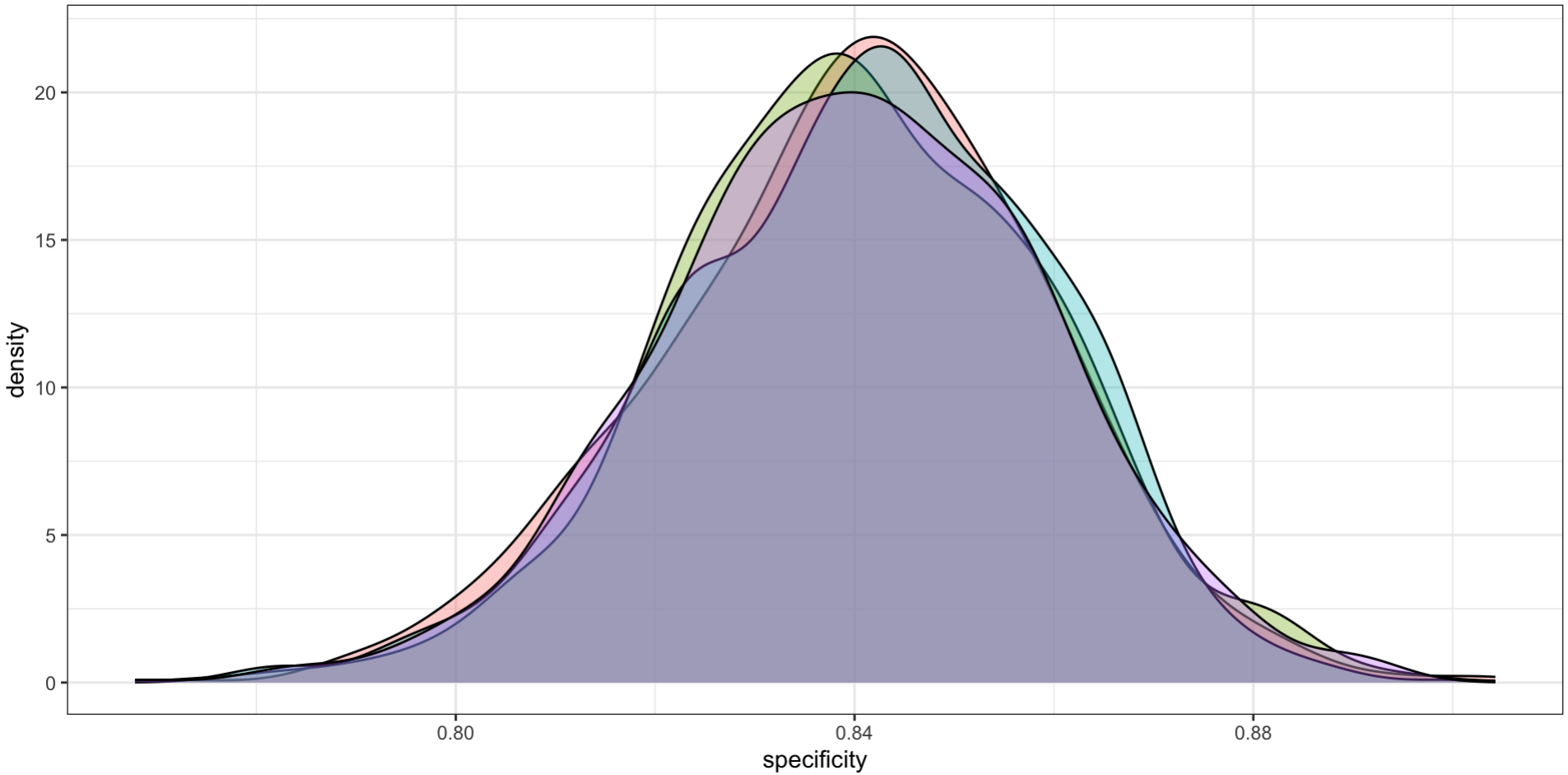
Posterior Sensitivity

```
b_pred  |>
  group_by(.chain, .iteration) |>
  summarize(sensitivity = yardstick::sensitivity_vec(presence, .prediction)) |>
  ggplot(aes(x = sensitivity, fill = as.factor(.chain))) +
    geom_density(alpha=0.33) +
    guides(fill = "none")
```


7.5
5.0
2.5
0.0
density
0.3
0.4
0.5
sensitivity

Posterior Specificity

```
b_pred  |>
  group_by(.chain, .iteration) |>
  summarize(specificity = yardstick::specificity_vec(presence, .prediction)) |>
  ggplot(aes(x = specificity, fill = as.factor(.chain))) +
    geom_density(alpha=0.33) +
    guides(fill = "none")
```


density
20
15
10
5
0
0.80
0.84
0.88
specificity

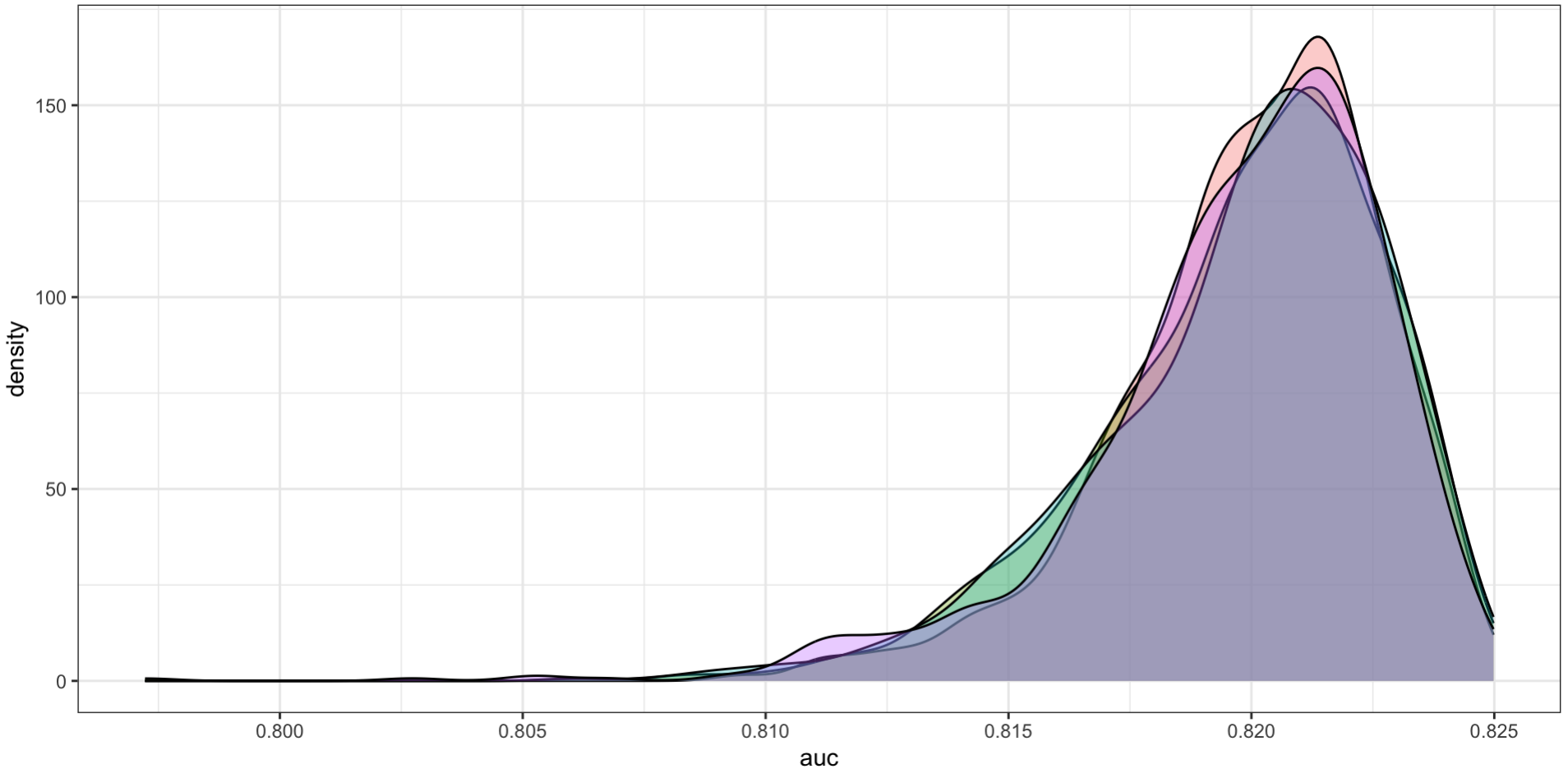
Expected posterior predictive

```r
( b_epred = b |>
    epred_draws_fix(newdata = anguilla_train) |>
    select(presence, .row:.epred) |>
    mutate( # Fix for yardstick
      presence = factor(presence, levels=c(1,0))
    )
)
```

```
# A tibble: 2,472,000 × 6
   presence  .row .chain .iteration .draw .epred
   <fct>    <int>  <int>      <int> <int>  <dbl>
 1 0            1      1          1     1  0.161
 2 0            1      1          2     2  0.165
 3 0            1      1          3     3  0.108
 4 0            1      1          4     4  0.134
 5 0            1      1          5     5  0.137
 6 0            1      1          6     6  0.116
 7 0            1      1          7     7  0.129
 8 0            1      1          8     8  0.128
 9 0            1      1          9     9  0.137
10 0            1      1         10    10  0.134
# ℹ 2,471,990 more rows
```

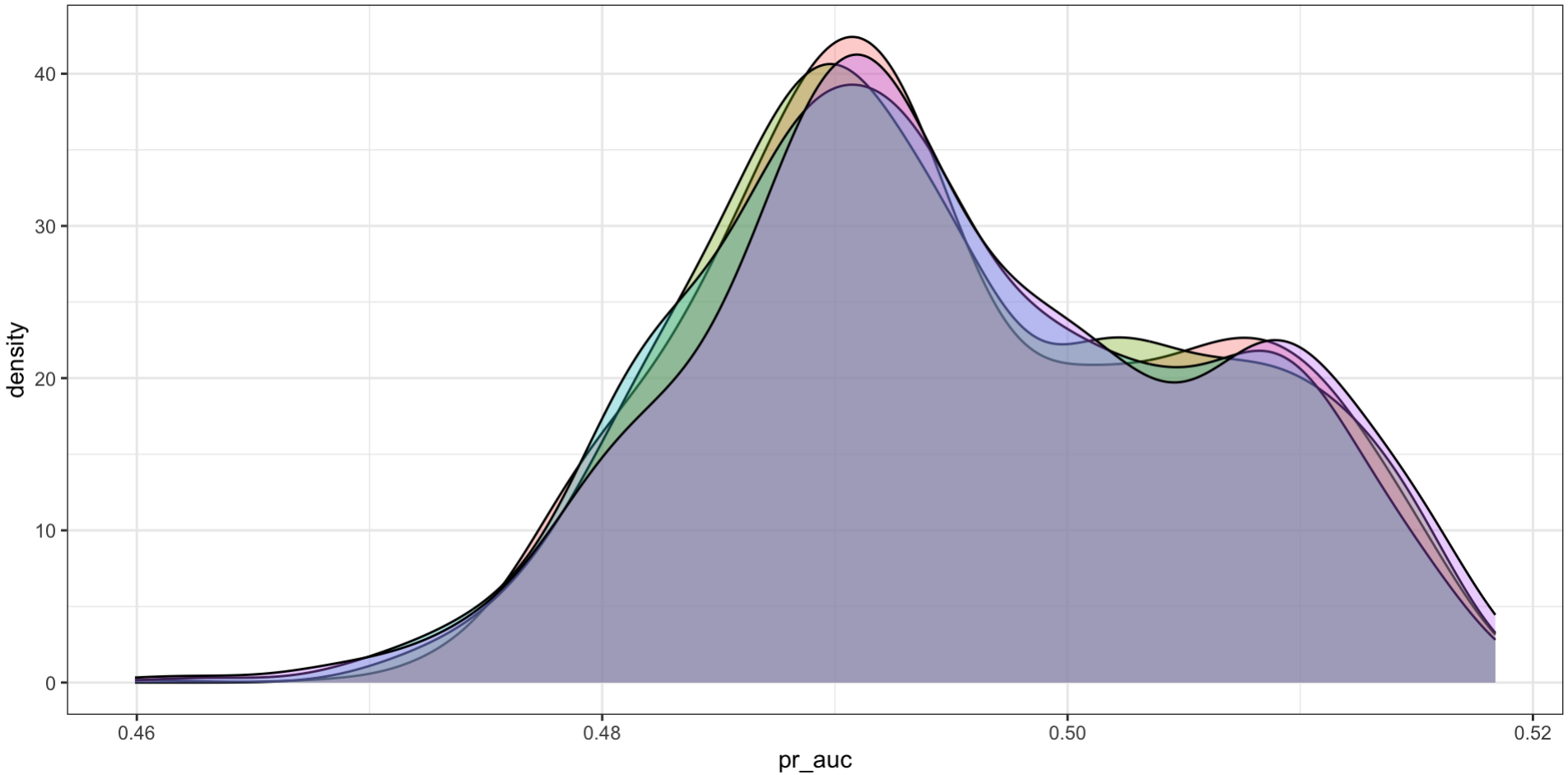
Posterior AUC

```
b_epred  |>
  group_by(.chain, .iteration) |>
  summarize(auc = yardstick::roc_auc_vec(presence, .epred)) |>
  ggplot(aes(x = auc, fill = as.factor(.chain))) +
    geom_density(alpha=0.33) +
    guides(fill = "none")
```


density
150
100
50
0
0.800
0.805
0.810
0.815
0.820
0.825
auc

Posterior PR-AUC

```
b_epred  |>
  group_by(.chain, .iteration) |>
  summarize(pr_auc = yardstick::pr_auc_vec(presence, .epred)) |>
  ggplot(aes(x = pr_auc, fill = as.factor(.chain))) +
    geom_density(alpha=0.33) +
    guides(fill = "none")
```


40
30
20
10
0
density
0.46
0.48
0.50
0.52
pr_auc

Expected posterior predictive - test

```
b_epred_test = b |>
  epred_draws_fix(newdata = anguilla_test) |>
  select(presence, .row:.epred) |>
  mutate( # Fix for yardstick
    presence = factor(presence, levels=c(1,0))
  )
```

```
b_comb = bind_rows(
  b_epred |> mutate(data = "train"),
  b_epred_test |> mutate(data = "test")
)
```

Comparing AUC / PR-AUC

```
b_comb  |>
  group_by(.chain, .iteration, data) |>
  summarize(
    auc = yardstick::roc_auc_vec(presence, .epred),
    pr_auc = yardstick::pr_auc_vec(presence, .epred)
  ) |>
  pivot_longer(cols = auc:pr_auc, names_to = "stat", values_to = "value"
  ggplot(aes(x = value, y=data)) +
    tidybayes::stat_halfeye() +
    facet_wrap(~stat, ncol=1, scales = "free_x")
```

Comparing AUC / PR-AUC