Logistic Regression and Residual Analysis

Lecture 05

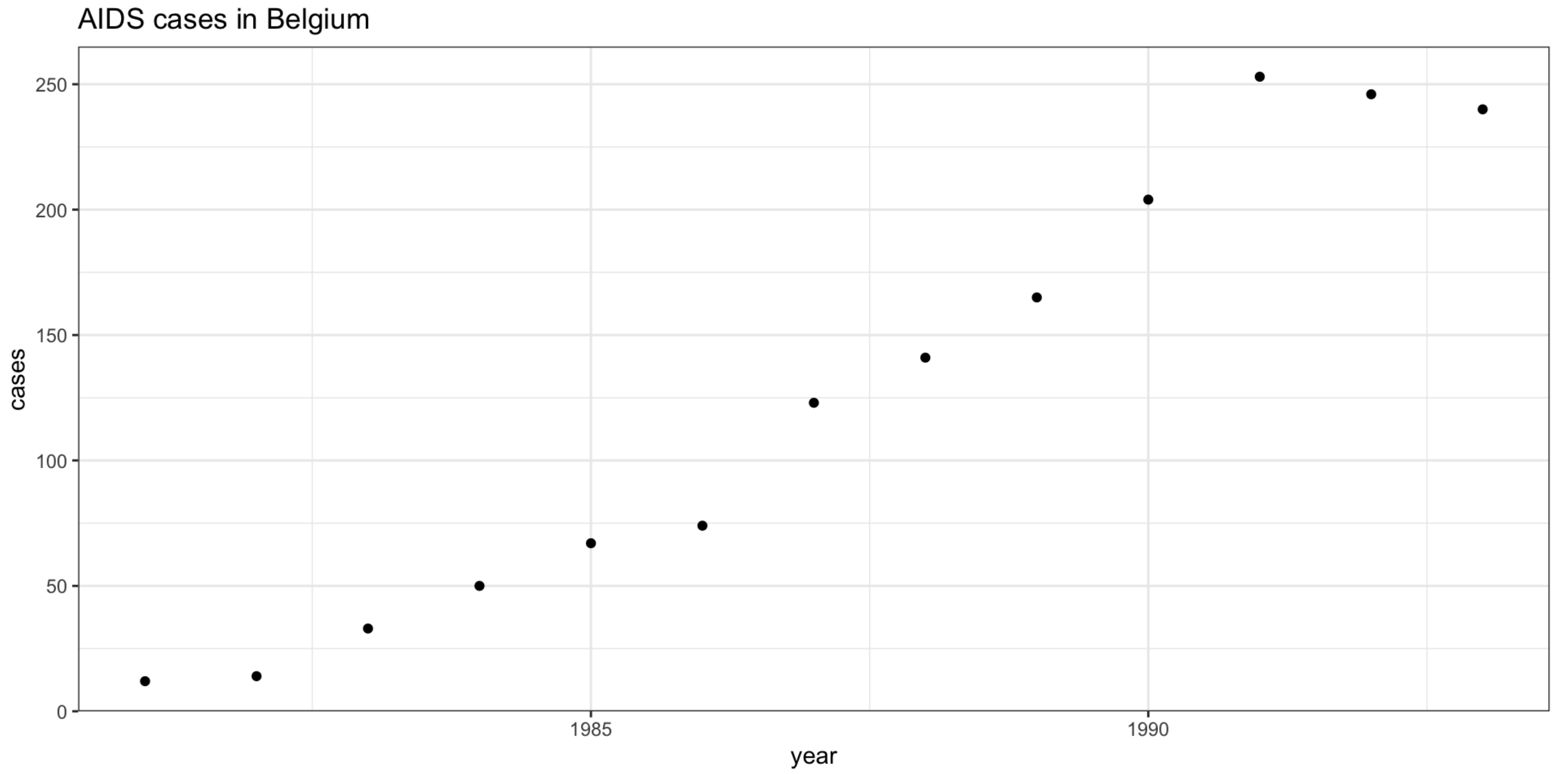
Dr. Colin Rundel

Last time

Last time

```
1  aids
```

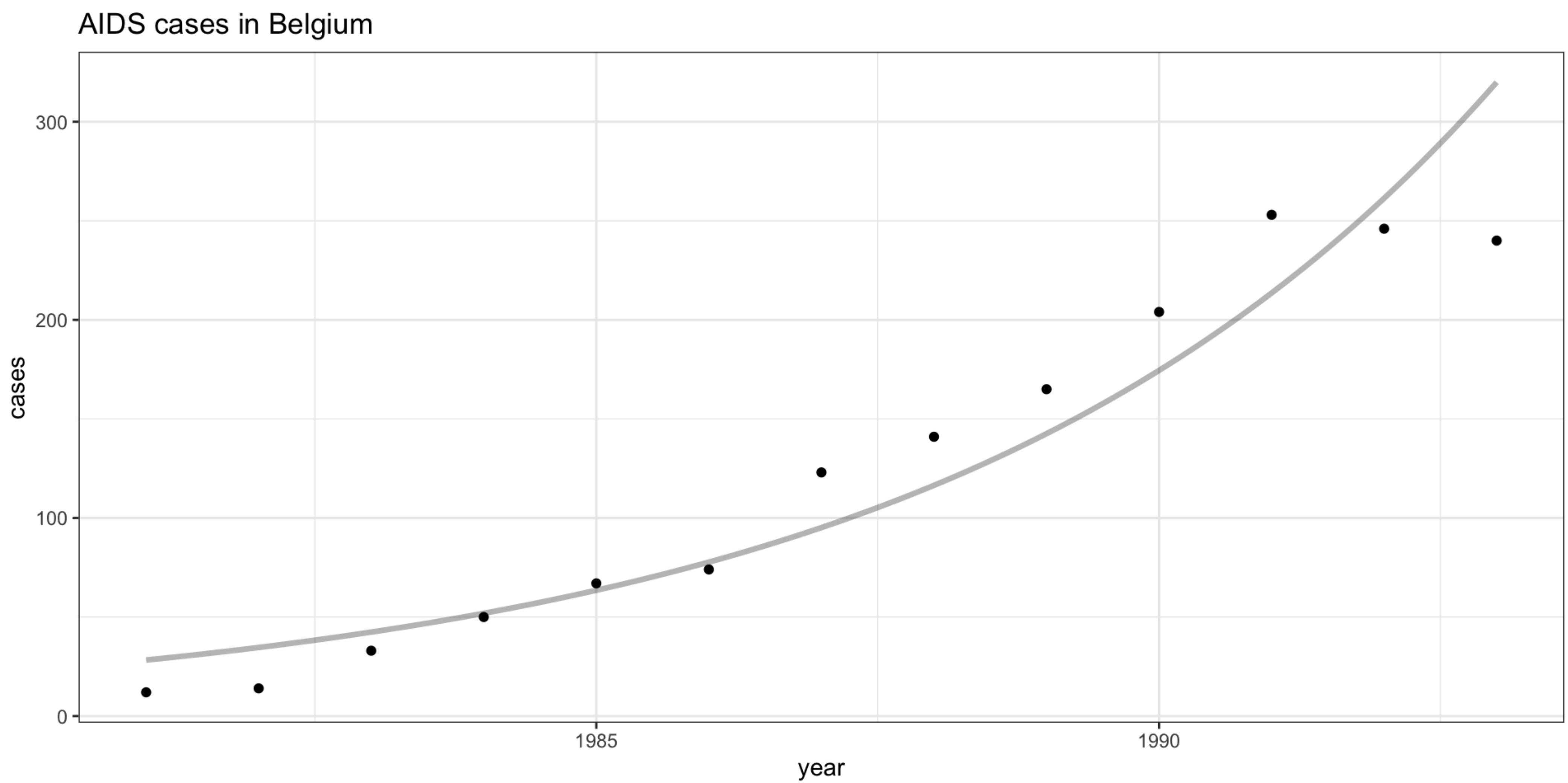
```
# A tibble: 13 × 2
    year cases
   <int> <int>
 1  1981    12
 2  1982    14
 3  1983    33
 4  1984    50
 5  1985    67
 6  1986    74
 7  1987   123
 8  1988   141
 9  1989   165
10  1990   204
11  1991   253
12  1992   246
13  1993   240
```



Model Fit

```r
g = glm(cases~year, data=aids, family=poisson)
g_pred = broom::augment(
  g, type.predict = "response",
  newdata = tibble(year=seq(1981,1993,by=0.1))
)
g
```

```
Call:  glm(formula = cases ~ year, family = poisson, data = aids)

Coefficients:
(Intercept)         year
  -397.0594       0.2021

Degrees of Freedom: 12 Total (i.e. Null);  11 Residual
Null Deviance:      872.2
Residual Deviance: 80.69    AIC: 166.4
```

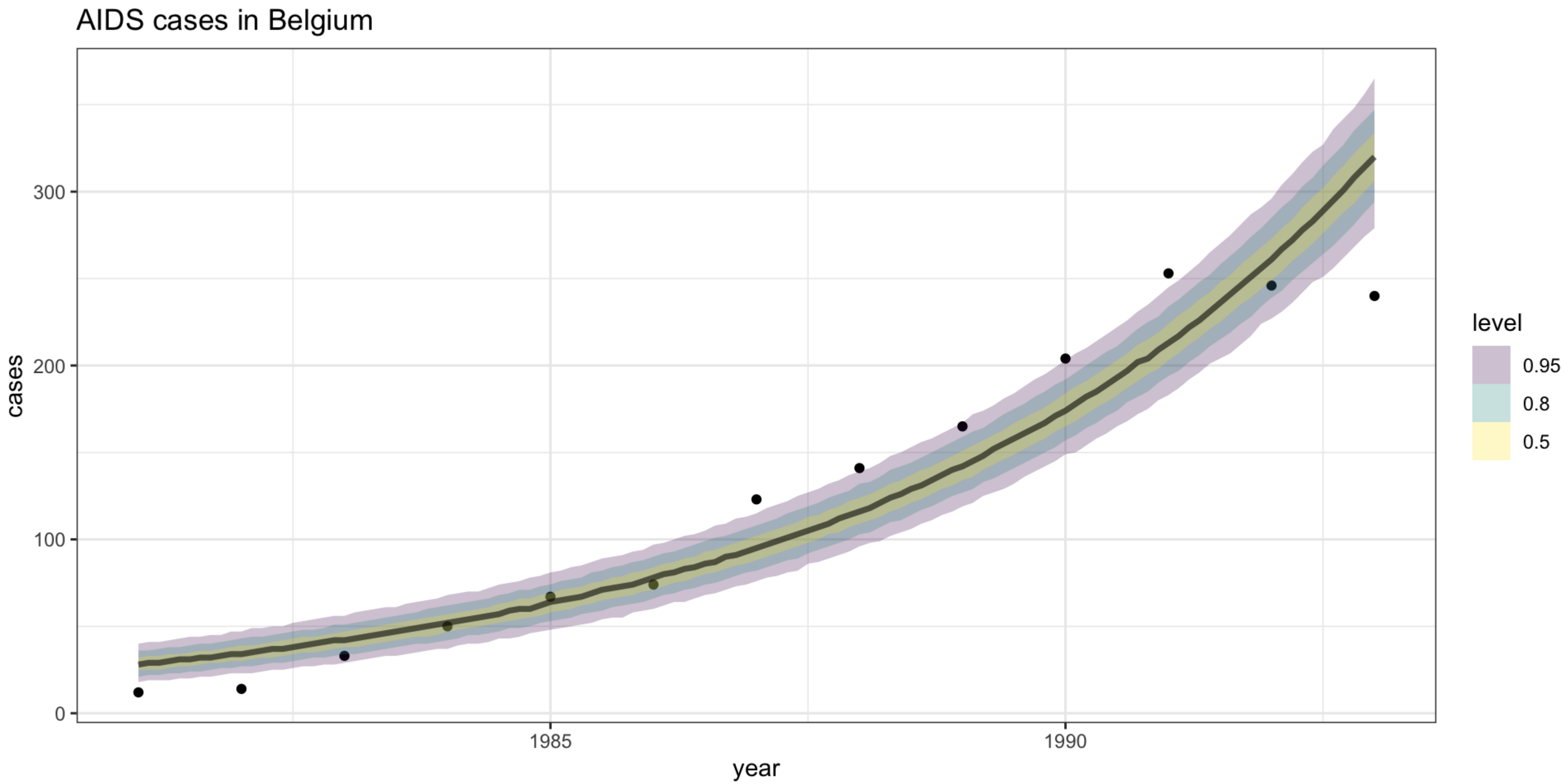

AIDS cases in Belgium
300
200
100
0
cases
1985
1990
year

Bayesian Poisson Regression Model

```r
( g_bayes = brms::brm(
    cases~year, data=aids, family=poisson,
    refresh=0, backend = "cmdstanr"
) )
```

```
 Family: poisson 
  Links: mu = log 
Formula: cases ~ year 
   Data: aids (Number of observations: 13) 
  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  -396.97     15.07  -427.48  -368.01 1.00     1638     1965
year          0.20      0.01     0.19     0.22 1.00     1639     2007

Draws were sampled using sample(hmc). 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).
```

Model fit


AIDS cases in Belgium
cases
0
100
200
300
1985
1990
year
level
0.95
0.8
0.5

Model performance - rmse, crps

```
predicted_draws_fix(g_bayes, newdata = aids) |>
  group_by(.chain, .row) |>
  summarize(
    rmse = yardstick::rmse_vec(cases, .prediction),
    crps = dukestm::calc_crps(.prediction, cases)
  ) |>
  group_by(.chain) |>
  summarize(
    rmse = mean(rmse),
    crps = mean(crps)
  )
```

```
# A tibble: 4 × 3
  .chain  rmse  crps
   <int> <dbl> <dbl>
1      1  26.2  17.6
2      2  26.2  17.5
3      3  26.3  17.7
4      4  26.3  17.6
```

Model performance - emp coverage

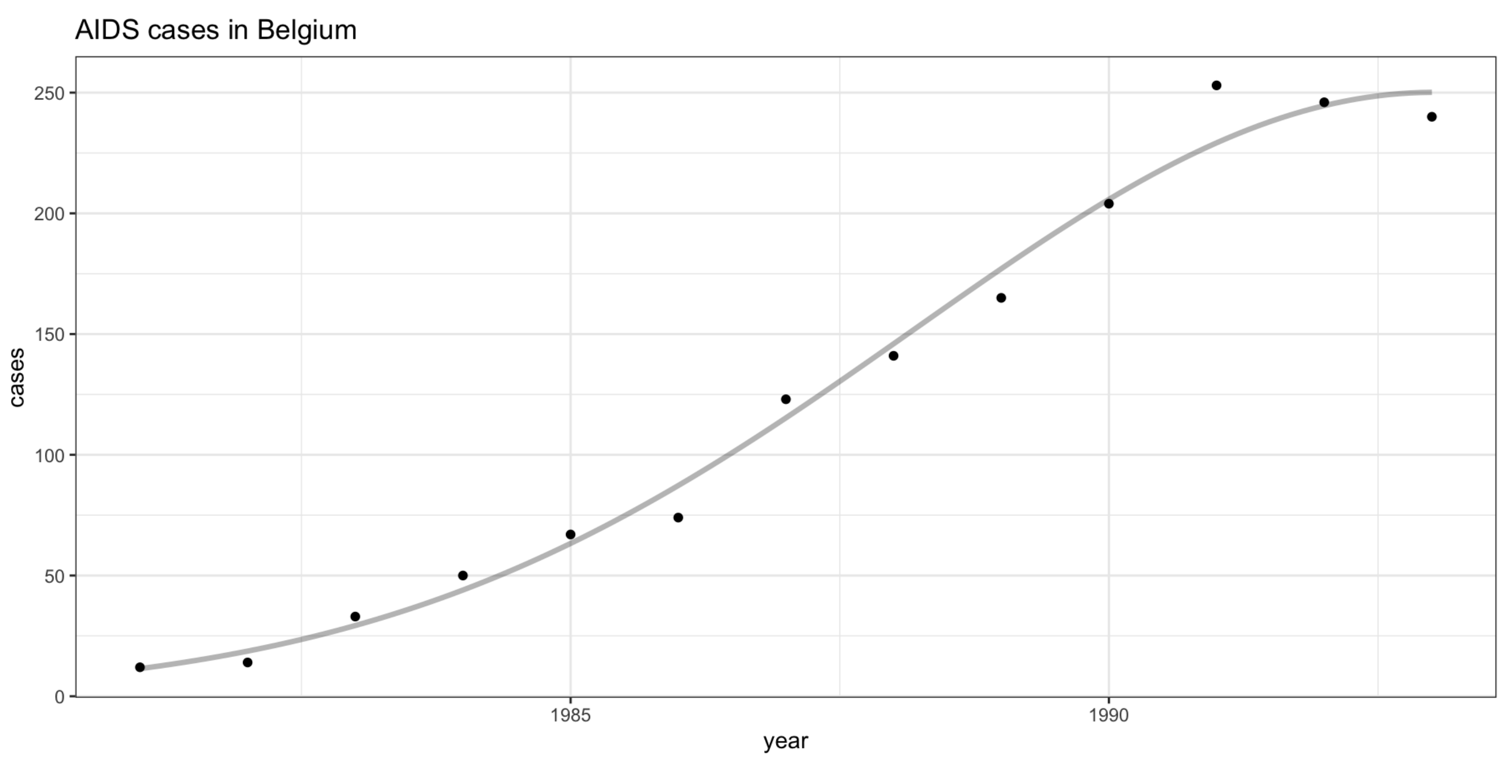
```
predicted_draws_fix(g_bayes, newdata = aids) |>
  group_by(.row, cases) |>
  ggdist::mean_hdi(
    .prediction, .width = c(0.5,0.9,0.95)
  ) |>
  mutate(contains = cases >= .lower & cases <= .upper) %>%
  group_by(.width) |>
  summarize(
    emp_cov = sum(contains)/n()
  )
```

```
# A tibble: 3 × 2
  .width emp_cov
   <dbl>   <dbl>
1   0.5    0.231
2   0.9    0.385
3   0.95   0.462
```

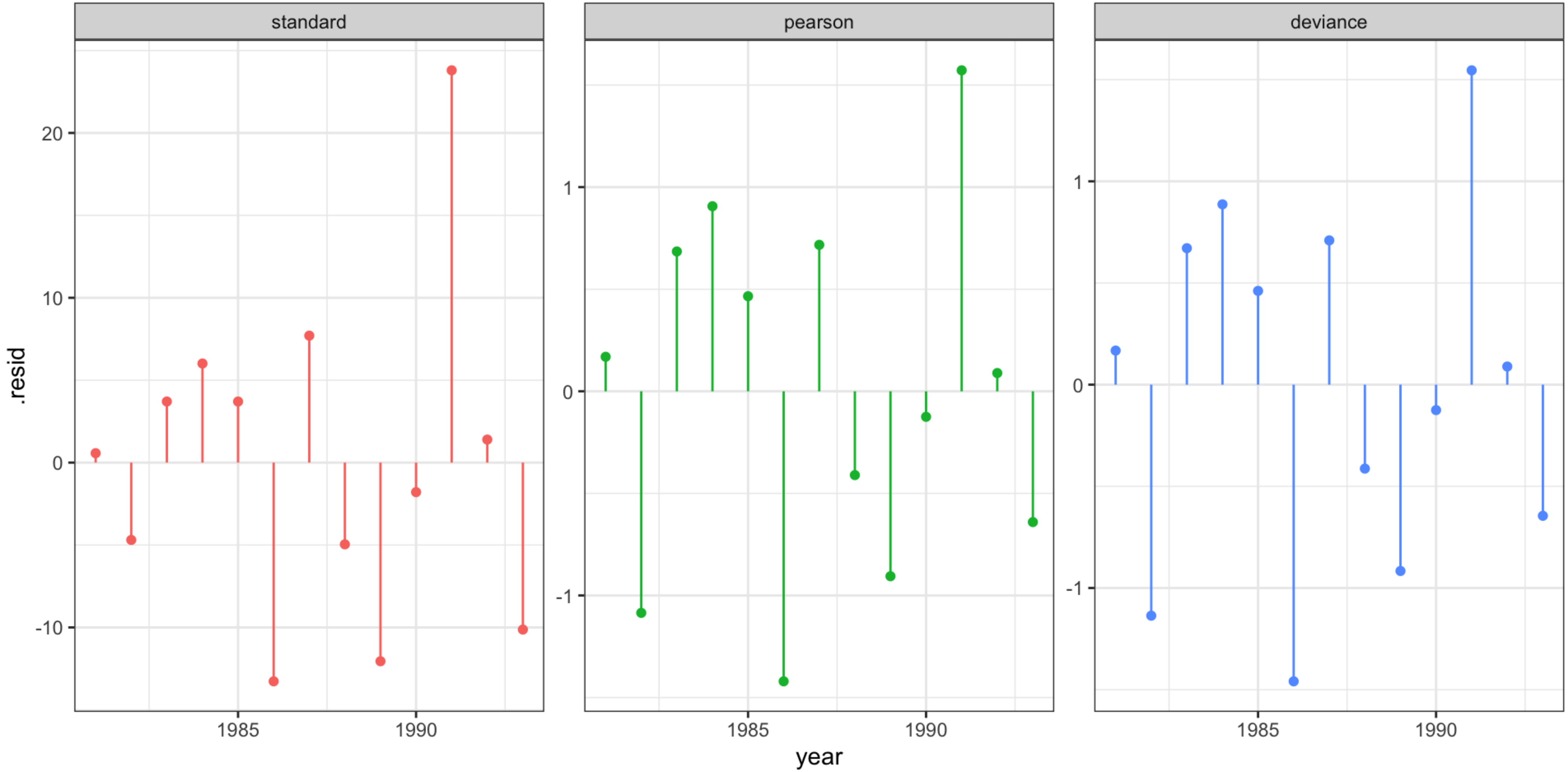
Updating the model

Quadratic fit

```
g2 = glm(cases~year+I(year^2), data=aids, family=poisson)

g2_pred = broom::augment(
  g2, type.predict = "response",
  newdata=tibble(year=seq(1981,1993,by=0.1))
)
```



Quadratic fit - residuals



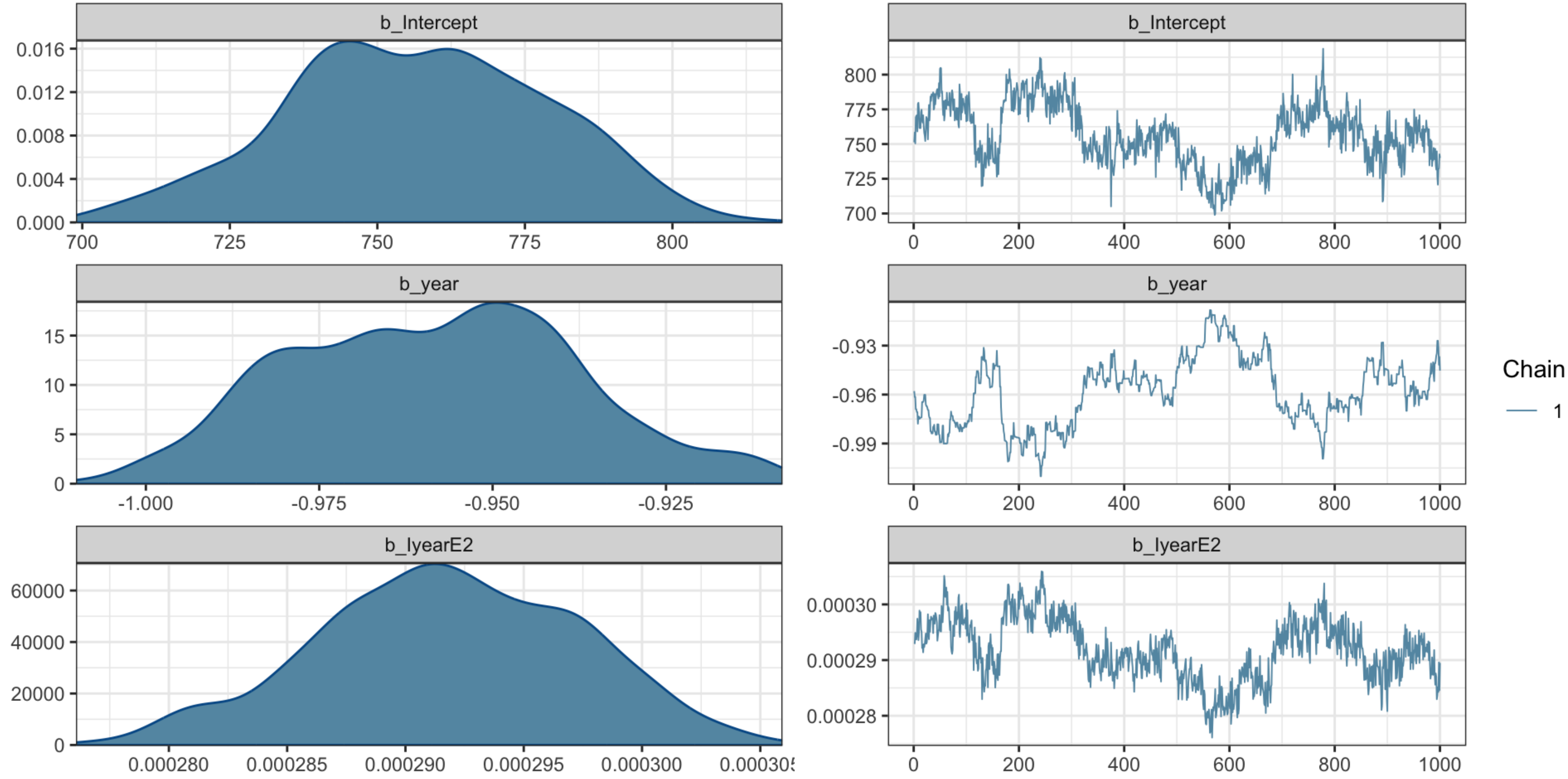
Bayesian quadratic fit

```
( g2_bayes = brms::brm(
  cases~year+I(year^2), data=aids, family=poisson,
  refresh=0, backend = "cmdstanr"
) )
```

```
 Family: poisson
  Links: mu = log
Formula: cases ~ year + I(year^2)
   Data: aids (Number of observations: 13)
  Draws: 1 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 1000

Population-Level Effects:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept   756.71     21.92   713.71   796.44 1.17        6       17
year         -0.96      0.02    -1.00    -0.92 1.22        4       21
IyearE2       0.00      0.00     0.00     0.00 1.19        5       14

Draws were sampled using sample(hmc). 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).
```

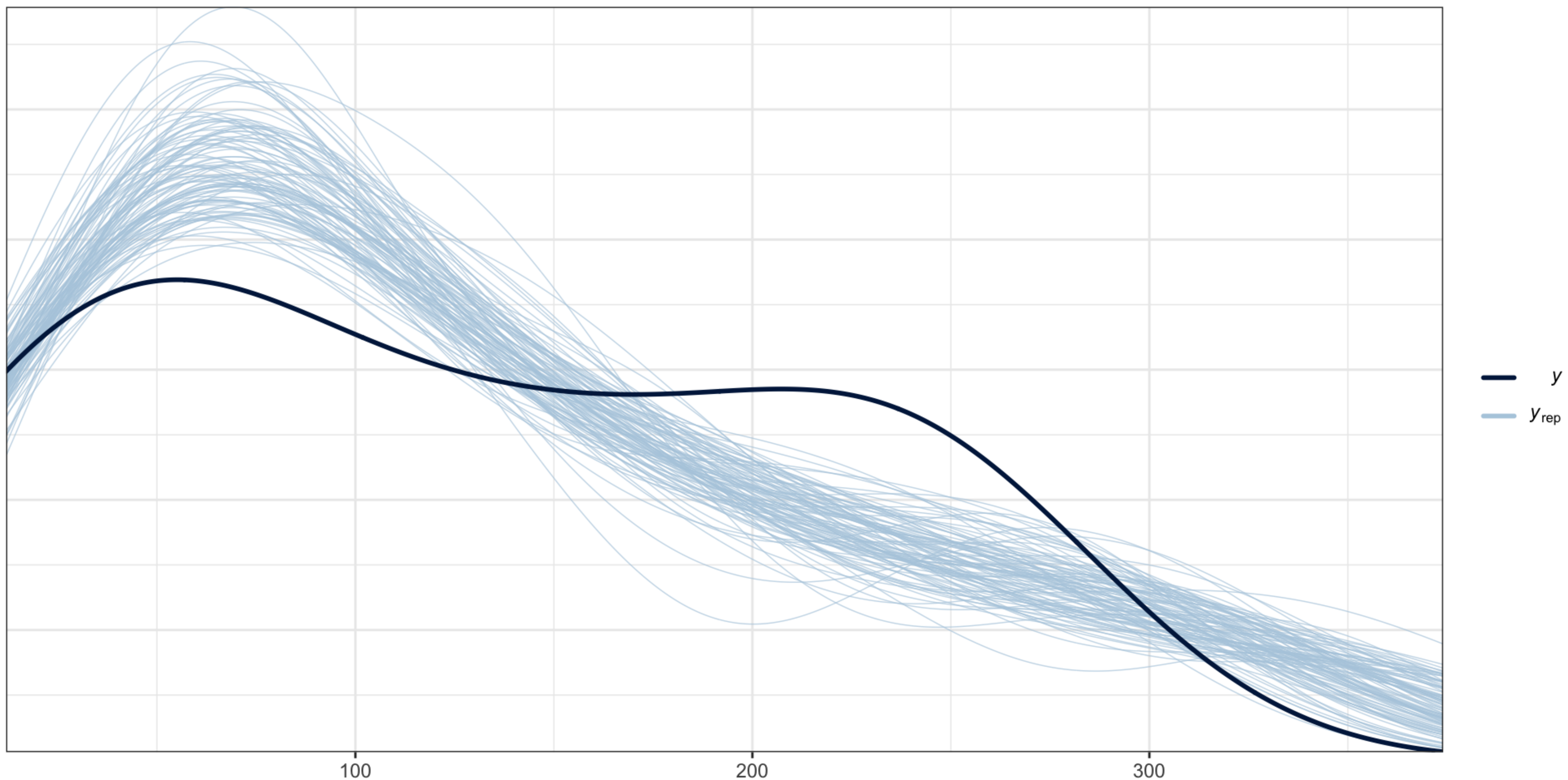
Diagnostics

```
plot(g2_bayes)
```



PP Checks

```r
brms::pp_check(g2_bayes, ndraws=100)
```



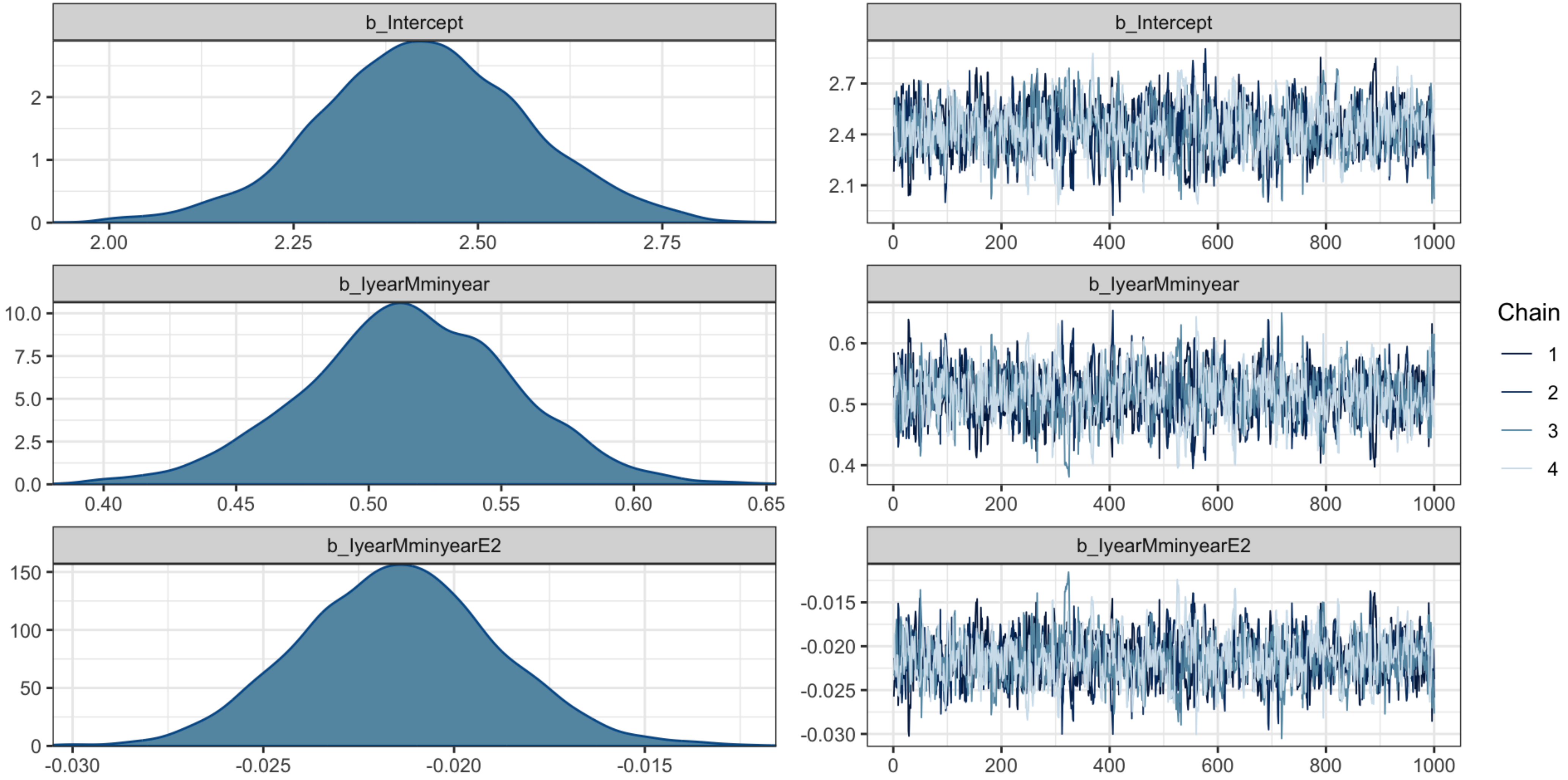
Bayesian quadratic fit (fixed)

```r
( g2_bayes = brms::brm(
  cases~I(year-min(year))+I((year-min(year))^2), data=aids, family=poisson,
  refresh=0, backend = "cmdstanr"
) )
```

```
 Family: poisson
  Links: mu = log
Formula: cases ~ I(year - min(year)) + I((year - min(year))^2)
   Data: aids (Number of observations: 13)
  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           2.43      0.14     2.14     2.71 1.00     1025     1238
IyearMminyear       0.52      0.04     0.44     0.59 1.00     1025     1389
IyearMminyearE2    -0.02      0.00    -0.03    -0.02 1.00     1066     1402

Draws were sampled using sample(hmc). 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).
```

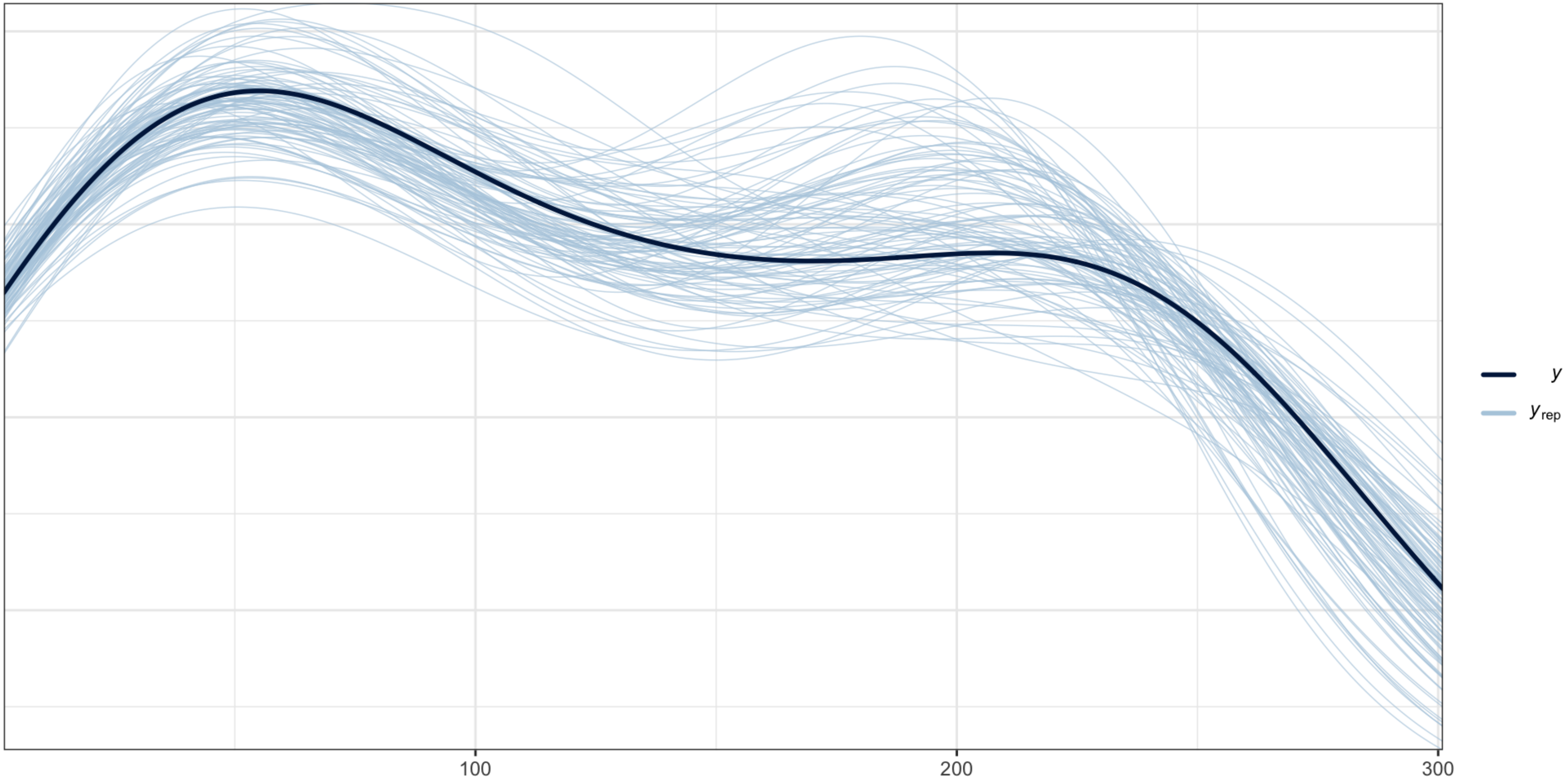
Diagnostics

```r
plot(g2_bayes)
```



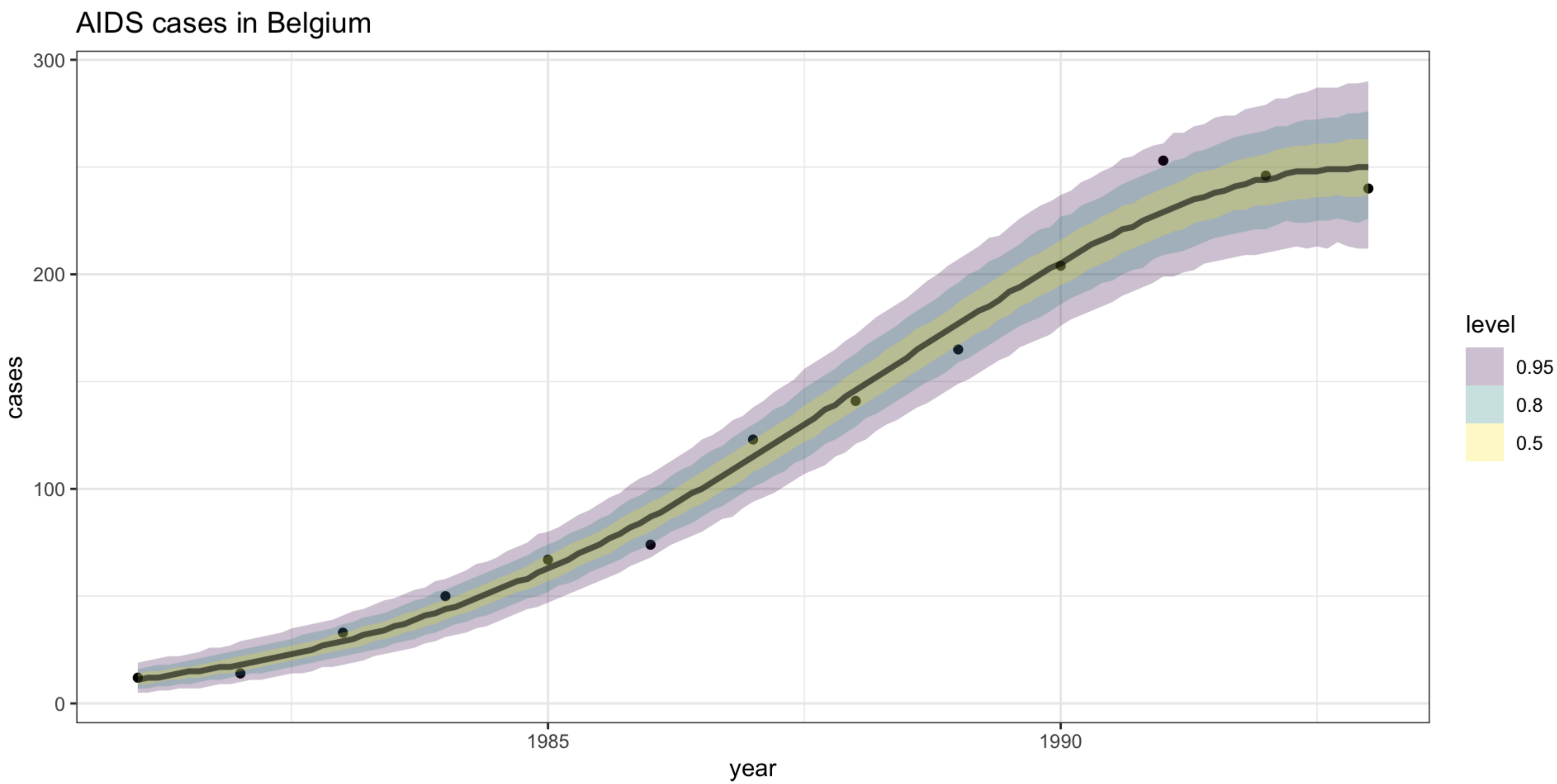
PP Checks

```r
brms::pp_check(g2_bayes, ndraws=100)
```



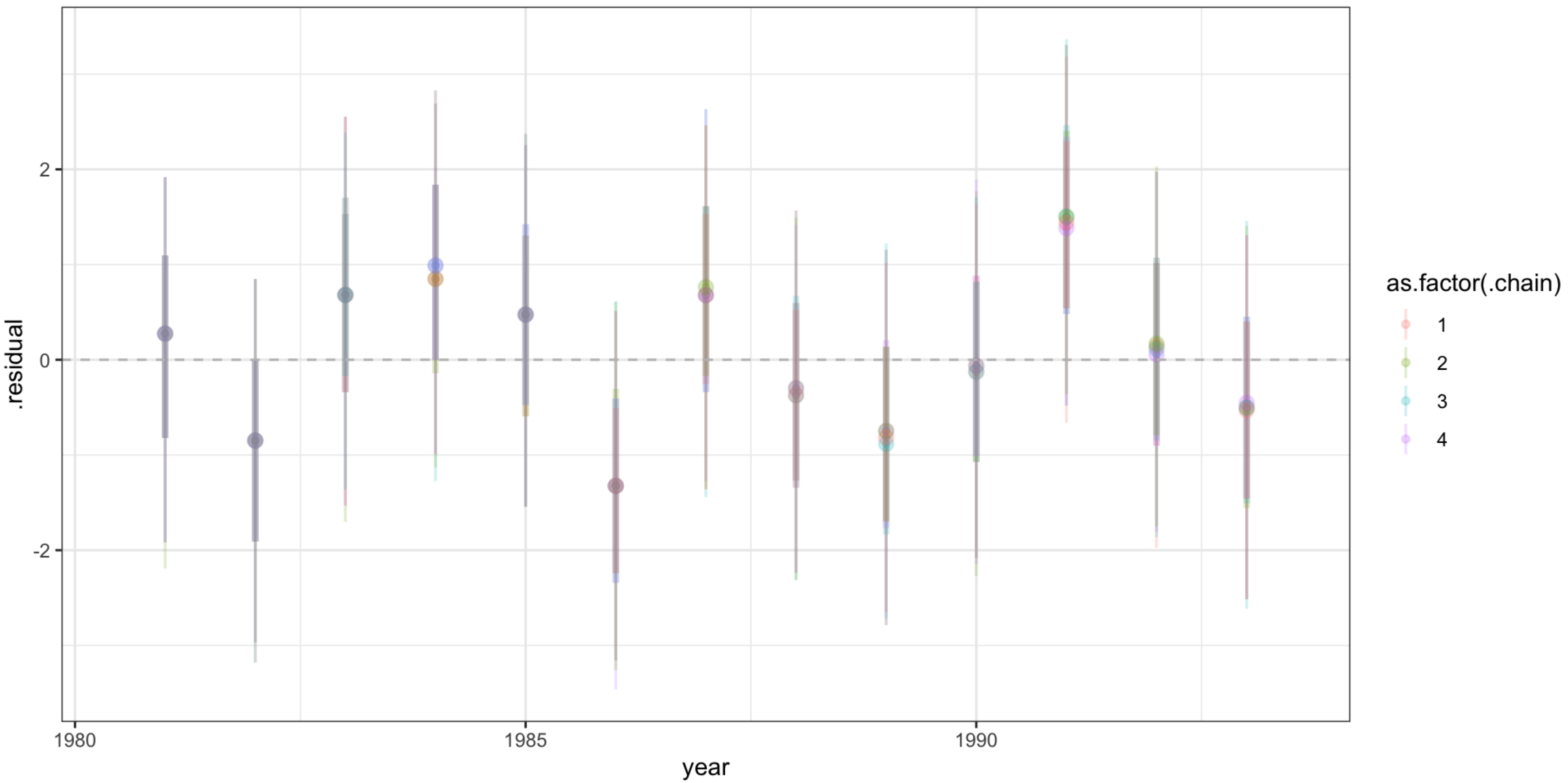
Model fit - Y CI

```
aids_base +
  tidybayes::stat_lineribbon(
    data = g2_bayes_pred, aes(y=.prediction), alpha=0.25
  )
```



Residuals (pearson)

```
residual_draws_fix(g2_bayes, newdata = aids, type = "pearson") |>
  ggplot(aes(y = .residual, x = year, color=as.factor(.chain), group=.chain)) +
    tidybayes::stat_pointinterval(alpha=0.2) +
    geom_hline(yintercept = 0, color='grey', linetype=2)
```



Model performance - rmse, crps

```
predicted_draws_fix(g2_bayes, newdata = aids) |>
  group_by(.chain, .row) |>
  summarize(
    rmse = yardstick::rmse_vec(cases, .prediction),
    crps = calc_crps(.prediction, cases)
  ) |>
  group_by(.chain) |>
  summarize(
    rmse = mean(rmse),
    crps = mean(crps)
  )
```

```
# A tibble: 4 × 3
  .chain  rmse  crps
   <int> <dbl> <dbl>
1      1  14.2  5.15
2      2  14.2  5.16
3      3  14.3  5.18
4      4  14.1  5.14
```

Model performance - emp coverage

```r
predicted_draws_fix(g2_bayes, newdata = aids) |>
  group_by(.row, cases) |>
  tidybayes::mean_hdi(
    .prediction, .width = c(0.5,0.9,0.95)
  ) |>
  mutate(contains = cases >= .lower & cases <= .upper) %>%
  group_by(.width) |>
  summarize(
    emp_cov = sum(contains)/n()
  )
```

```
# A tibble: 3 × 2
  .width emp_cov
   <dbl>   <dbl>
1   0.5    0.538
2   0.9    1
3   0.95   1
```

Logistic regression

Logistic regression as a GLM

This is another case of a generalized linear model, specifically where the outcome is 0-1 data (i.e. Bernoulli draws),

$$\begin{aligned} Y_i &\sim \text{Bern}(p_i) \\ \text{logit}\, E(Y_i | \boldsymbol{X}_{i\cdot}) &= \text{logit}(p_i) = \boldsymbol{X}_{i\cdot}\boldsymbol{\beta} \end{aligned}$$

$$\begin{aligned} E(Y_i) &= p_i \\ Var(Y_i) &= p_i(1 - p_i) \end{aligned}$$

$$\begin{aligned} \text{logit}(p_i) &= \log \frac{p_i}{1 - p_i} \\ \text{logit}^{-1}(x) &= \frac{\exp(x)}{1 + \exp(x)} = \frac{1}{1 + \exp(-x)} \end{aligned}$$

Background

Next we'll be looking at data on the presence and absence of the short-finned eel (Anguilla australis) at a number of sites in New Zealand.

These data come from

- Leathwick, J. R., Elith, J., Chadderton, W. L., Rowe, D. and Hastie, T. (2008), Dispersal, disturbance and the contrasting biogeographies of New Zealand's diadromous and non-diadromous fish species. Journal of Biogeography, 35: 1481–1497.

Species Distribution

Codebook:

- `presence` - presence (`1`) or absence (`0`) of Anguilla australis at the sampling location
- `SegSumT` - Summer air temperature (degrees C)
- `DSDist` - Distance to coast (km)
- `DSMaxSlope` - Maximum downstream slope (degrees)
- `USRainDays` - days per month with rain greater than 25 mm
- `USSlope` - average slope in the upstream catchment (degrees)
- `USNative` - area with indigenous forest (proportion)
- `DSDam` - Presence of known downstream obstructions, mostly dams
- `Method` - fishing method (`electric`, `net`, `spot`, `trap`, or `mixture`)
- `LocSed` - weighted average of proportional cover of bed sediment

1. mud
2. sand
3. fine gravel
4. coarse gravel
5. cobble
6. boulder
7. bedrock

Data

```r
( anguilla = readRDS("data/anguilla.rds") )
```

```
   presence SegSumT   DSDist DSMaxSlope USRainDays USSlope USNative DSDam
1         0    16.0  50.2000       0.57      2.470     9.8     0.81     0
2         1    18.7 132.5300       1.15      1.153     8.3     0.34     0
3         0    18.3 107.4400       0.57      0.847     0.4     0.00     0
4         0    16.7 166.8200       1.72      0.210     0.4     0.22     1
5         1    17.2   3.9500       1.15      1.980    21.9     0.96     0
6         0    15.1  11.1700       1.72      3.300    25.7     1.00     0
7         0    12.7  42.3700       2.86      0.430     9.6     0.09     0
10        1    18.2  94.3960       3.43      0.847    20.5     0.92     0
11        0    14.9  45.7370       2.29      2.249     3.9     0.38     0
12        1    18.3  91.8920       1.72      0.861     6.7     0.58     1
13        1    17.1   6.8000       0.52      0.620     0.7     0.00     0
14        0    13.4 190.3900       3.43      0.770    20.1     0.99     0
15        0    13.1 224.4400       6.84      0.290     9.8     0.98     0
17        0    17.0   1.3800       9.09      1.980    10.5     1.00     0
18        1    18.5   1.8685       1.72      0.847    11.8     0.30     0
19        0    15.7  13.8800       0.57      3.300     2.7     0.29     0
20        0    16.6  28.0200       1.15      0.860    19.0     0.57     0
```

See https://github.com/sta344-644-fa23/sta344-644-fa23.github.io/tree/main/static/slides/data for all

Test / train split

```r
set.seed(20220908)
part = rsample::initial_split(anguilla, prop = 3/4)

anguilla_train = rsample::training(part)
anguilla_test  = rsample::testing(part)
```

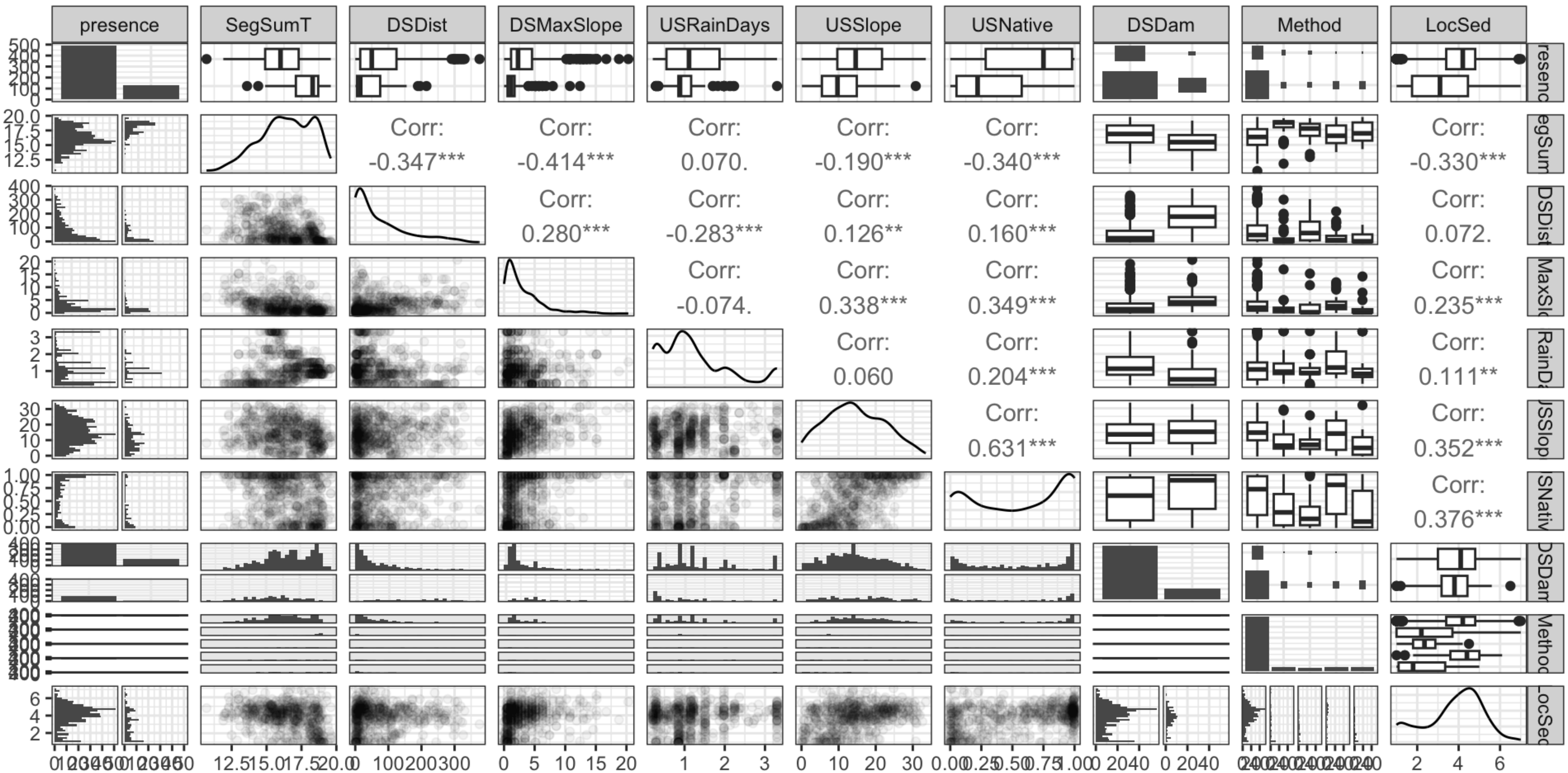
```r
dim(anguilla_train)
```

```
[1] 618  10
```

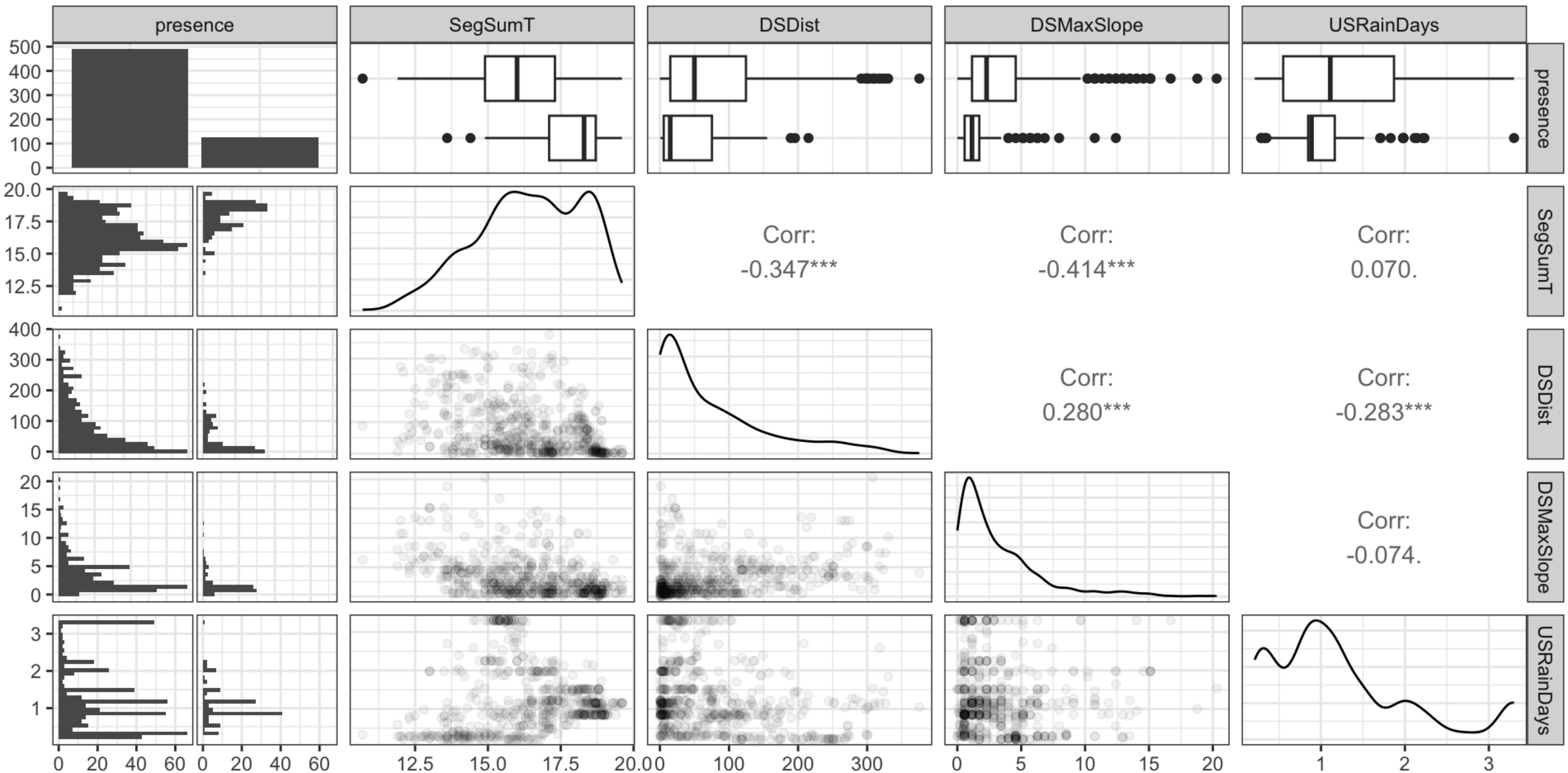
```r
dim(anguilla_test)
```

```
[1] 206  10
```

EDA

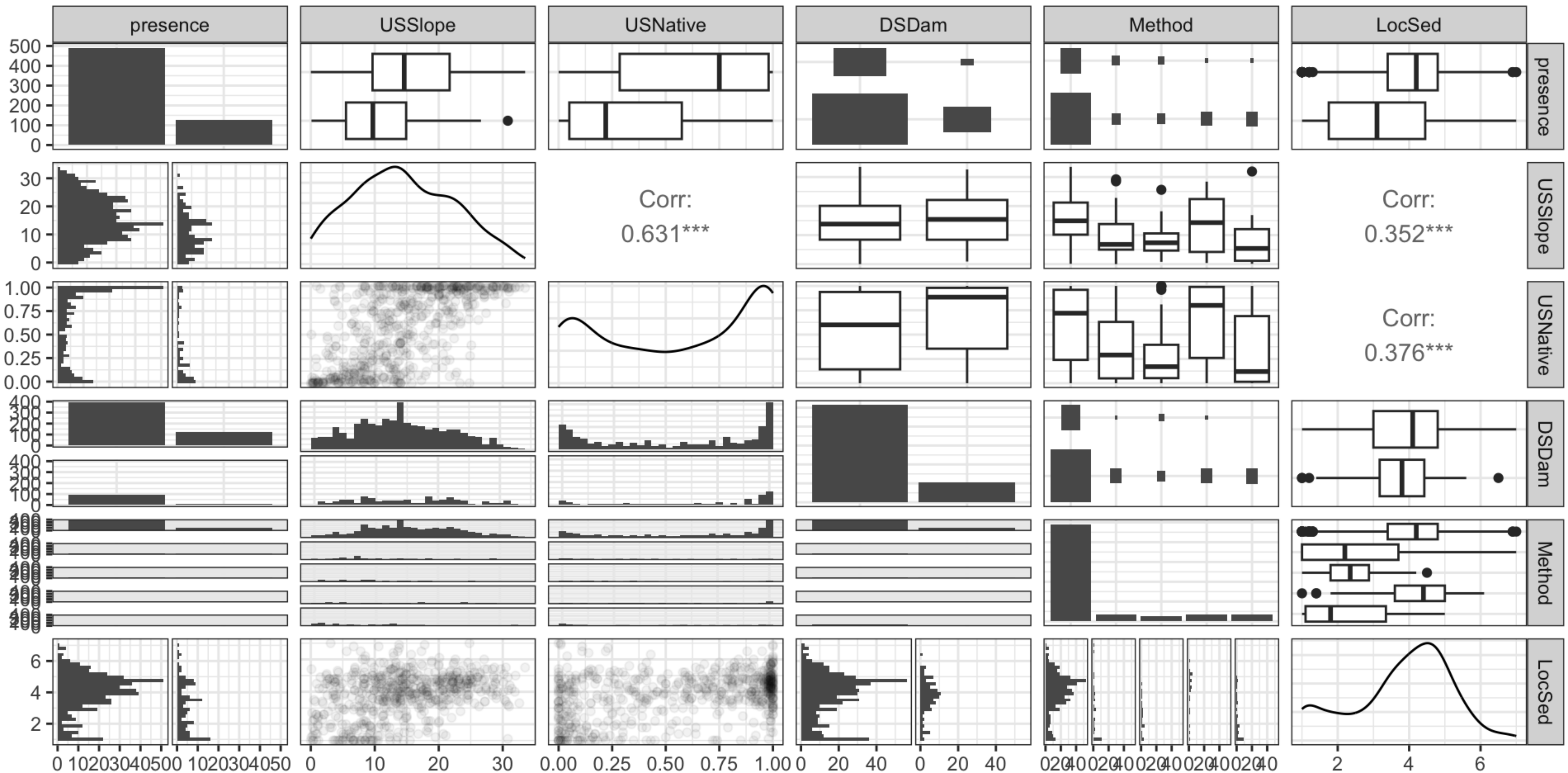

presence
SegSumT
DSDist
DSMaxSlope
USRainDays
USSlope
USNative
DSDam
Method
LocSed
Corr: -0.347***
Corr: -0.414***
Corr: 0.070.
Corr: -0.190***
Corr: -0.340***
Corr: -0.330***
Corr: 0.280***
Corr: -0.283***
Corr: 0.126**
Corr: 0.160***
Corr: 0.072.
Corr: -0.074.
Corr: 0.338***
Corr: 0.349***
Corr: 0.235***
Corr: 0.060
Corr: 0.204***
Corr: 0.111**
Corr: 0.631***
Corr: 0.352***
Corr: 0.376***

EDA (part 1)

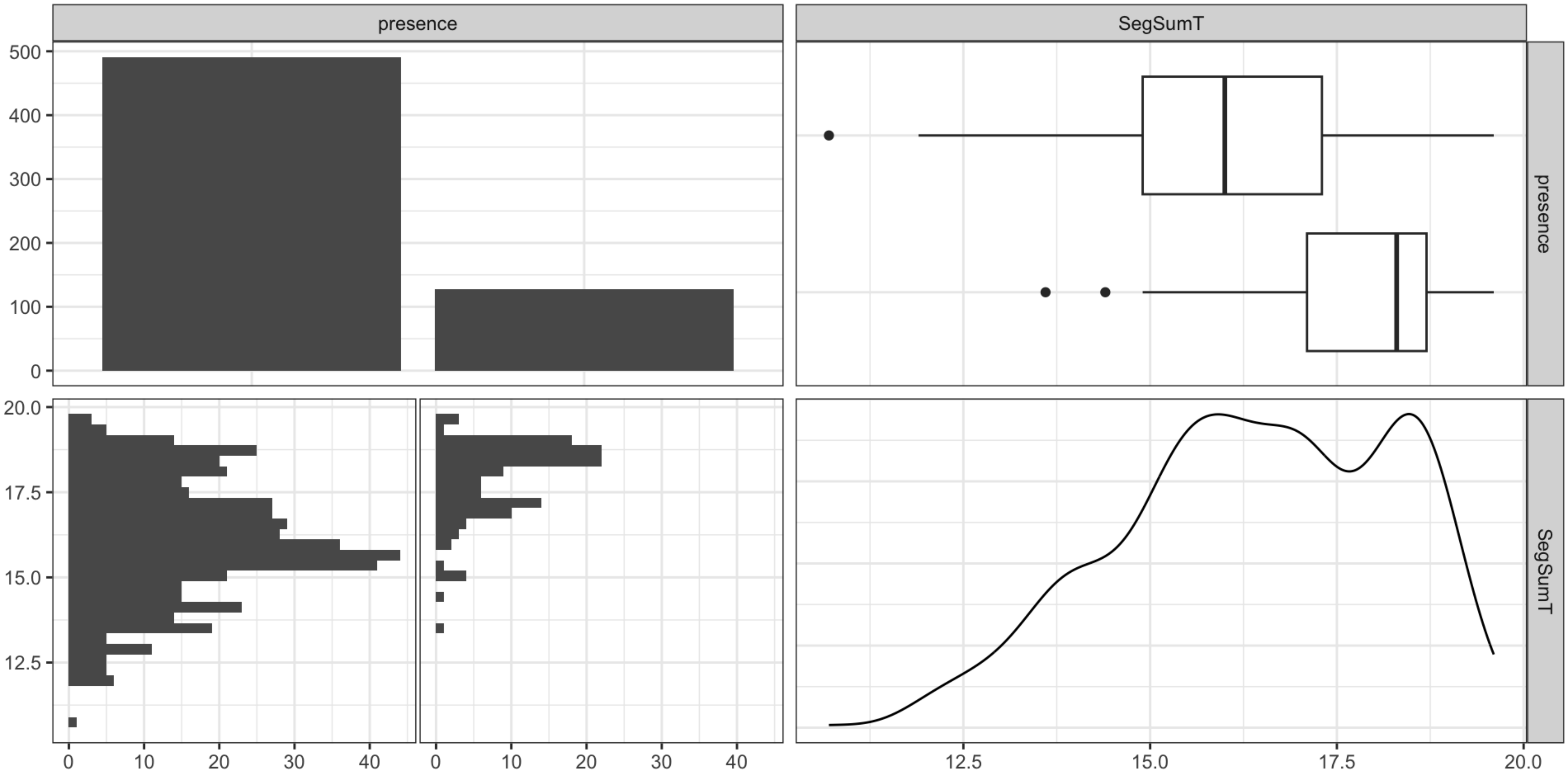


presence
SegSumT
DSDist
DSMaxSlope
USRainDays
Corr:
-0.347***
Corr:
-0.414***
Corr:
0.070.
Corr:
0.280***
Corr:
-0.283***
Corr:
-0.074.

EDA (part 2)


presence
USSlope
USNative
DSDam
Method
LocSed
Corr:
0.631***
Corr:
0.352***
Corr:
0.376***

EDA (part 3)



presence
SegSumT
500
400
300
200
100
0
20.0
17.5
15.0
12.5
0
10
20
30
40
0
10
20
30
40
12.5
15.0
17.5
20.0
presence
SegSumT

Basic Model

Model

```r
g = glm(presence~SegSumT, family=binomial, data=anguilla_train)
summary(g)
```

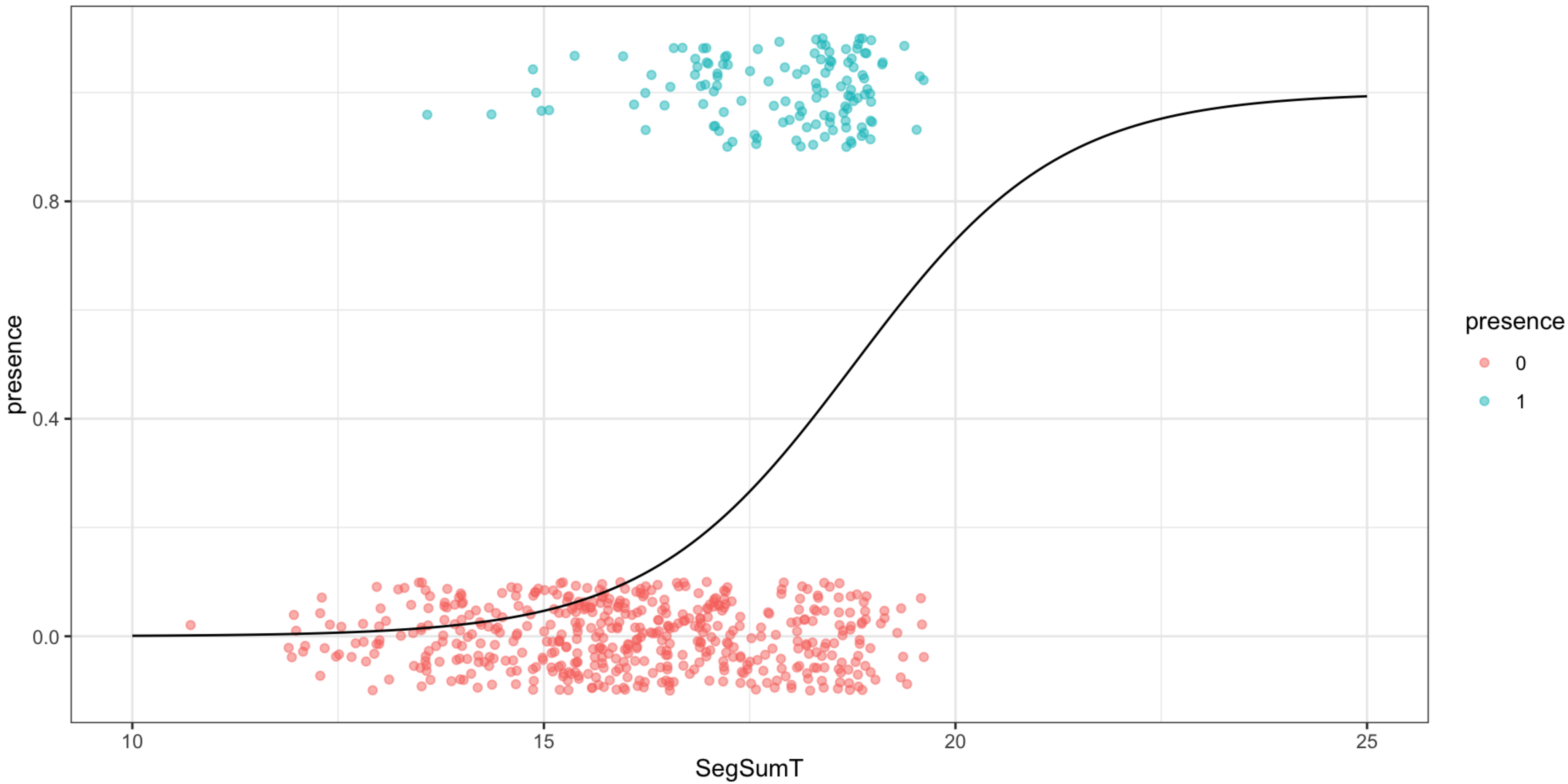
```

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

Coefficients:
             Estimate Std. Error z value Pr(>|z|)    
(Intercept) -15.02201    1.53770  -9.769   <2e-16 ***
SegSumT       0.80047    0.08726   9.173   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 627.81  on 617  degrees of freedom
Residual deviance: 501.93  on 616  degrees of freedom
AIC: 505.93

Number of Fisher Scoring iterations: 5
```

Fit

```r
( g_pred = broom::augment(g, type.predict = "response") )
```

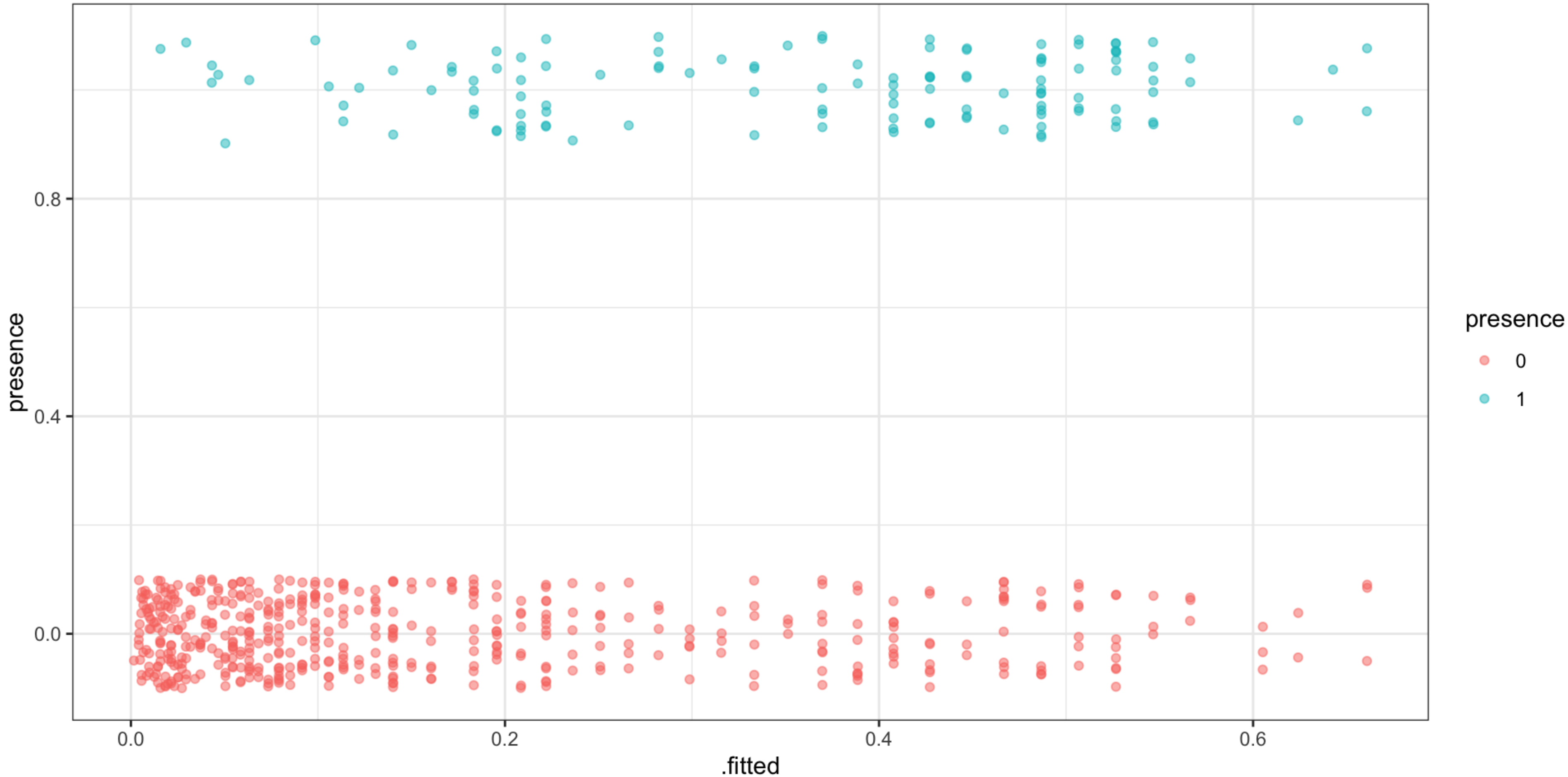
```
# A tibble: 618 × 8
   presence SegSumT .fitted .resid     .hat .sigma   .cooksd .std.resid
      <int>   <dbl>   <dbl>  <dbl>    <dbl>  <dbl>     <dbl>      <dbl>
 1        0    16.4  0.131  -0.529 0.00260   0.903 0.000197      -0.530
 2        1    17.1  0.209   1.77  0.00232   0.901 0.00443        1.77
 3        0    14    0.0216 -0.209 0.00231   0.903 0.0000256     -0.209
 4        0    18.2  0.389  -0.992 0.00364   0.903 0.00117       -0.994
 5        0    15.6  0.0735 -0.391 0.00286   0.903 0.000114      -0.391
 6        0    18.3  0.408  -1.02  0.00395   0.902 0.00137       -1.03
 7        0    18.5  0.447  -1.09  0.00466   0.902 0.00190       -1.09
 8        0    16.2  0.114  -0.491 0.00270   0.903 0.000174      -0.492
 9        0    18    0.351  -0.930 0.00313   0.903 0.000853      -0.932
10        1    17.3  0.236   1.70  0.00233   0.901 0.00379        1.70
# ℹ 608 more rows
```

Visually



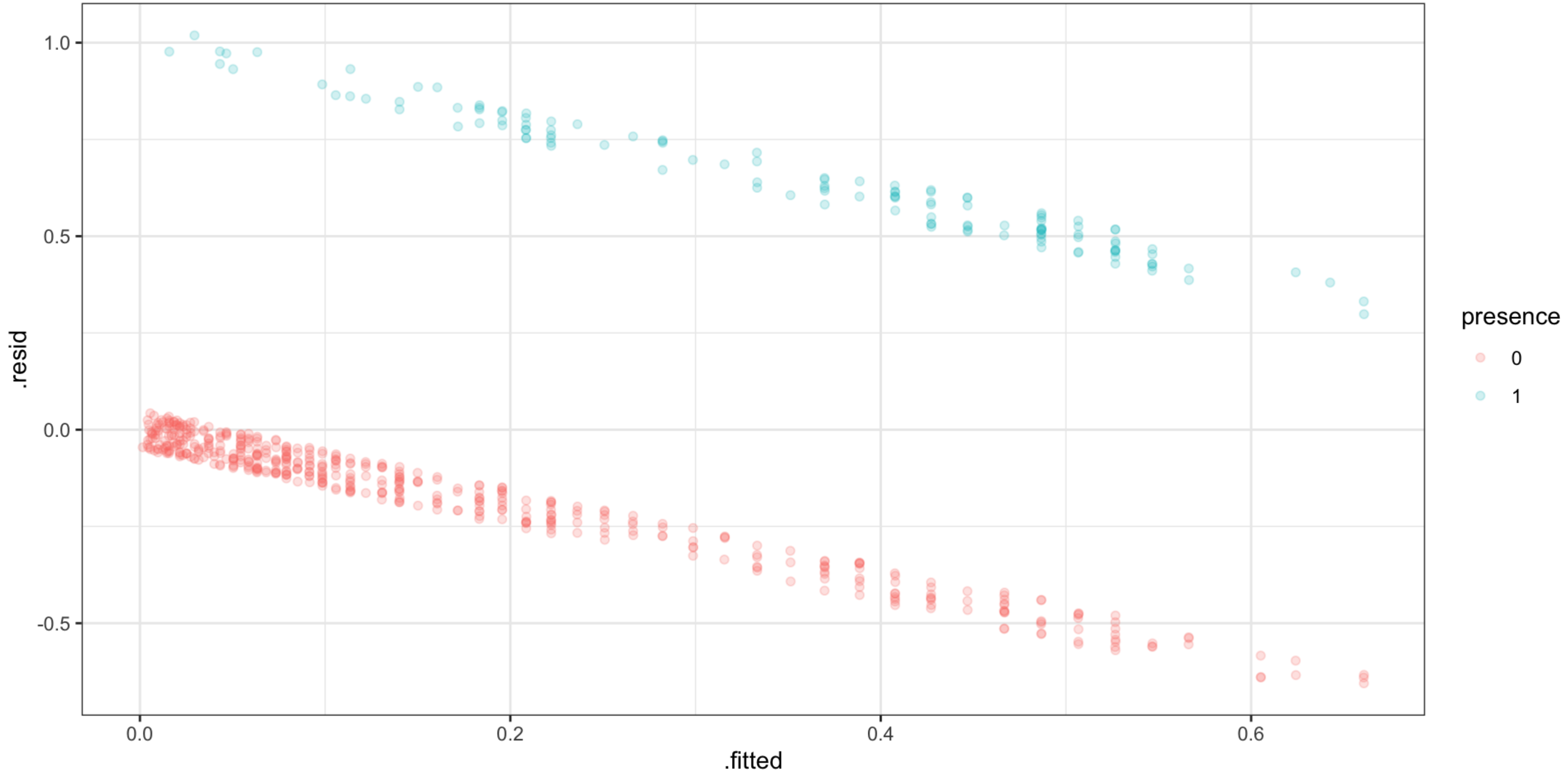
Separation

```
ggplot(g_pred, aes(x=.fitted, y=presence, color=as.factor(presence))) +
  geom_jitter(height=0.1, alpha=0.5) +
  labs(color="presence")
```



Standard Residuals

```
g_std =  broom::augment(g, type.predict = "response") |>
  mutate(.resid = presence - .fitted)
```



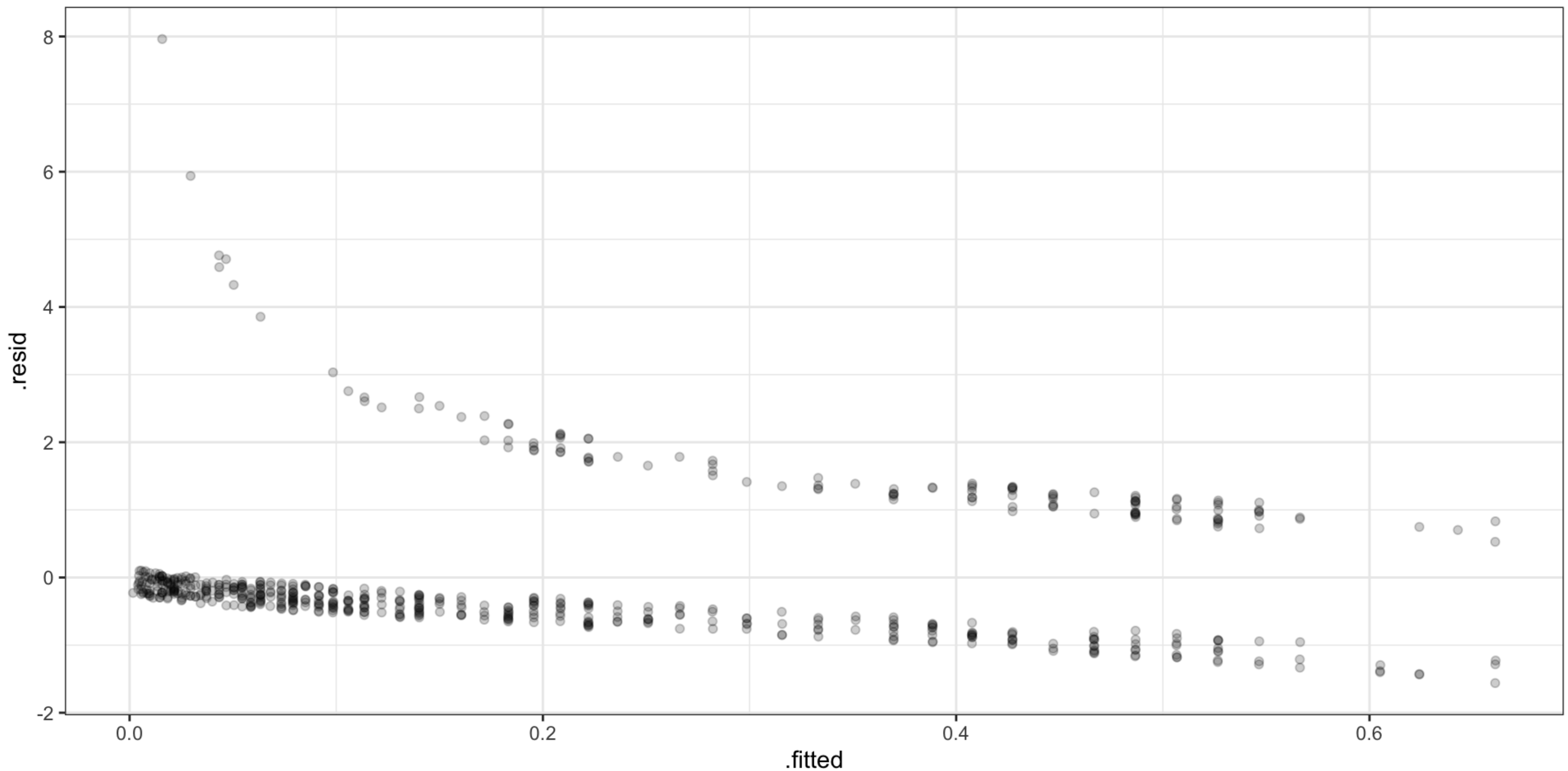
Binned Residuals

```
bin_width = 0.05
g_std_bin = g_std |>
  mutate(bin = .fitted - (.fitted %% bin_width) + bin_width/2) |>
  group_by(bin) |>
  summarize(.resid_bin = mean(presence - .fitted))
```

Pearson Residuals

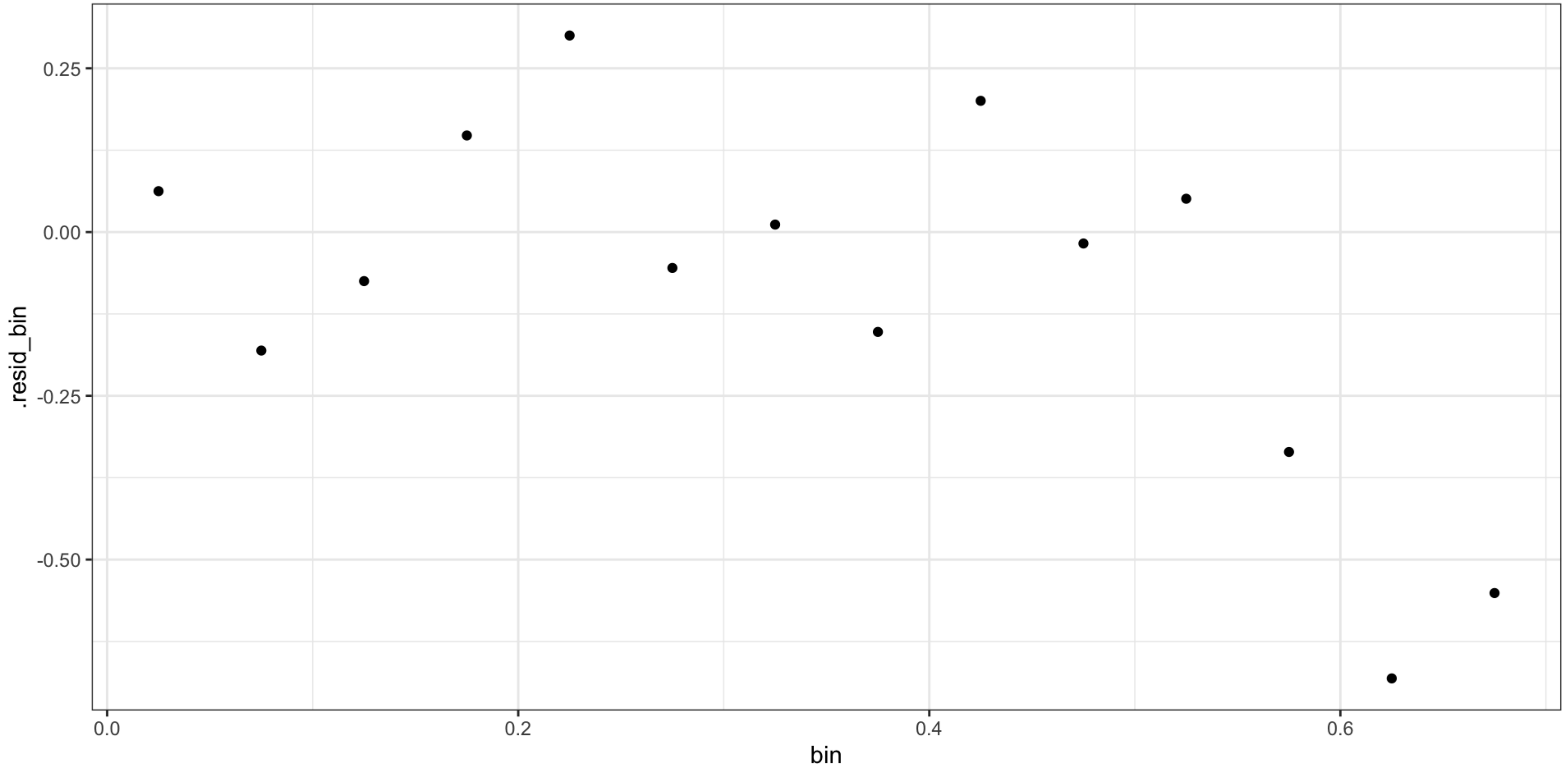
$$r_i = \frac{Y_i - E(Y_i)}{\sqrt{Var(Y_i)}} = \frac{Y_i - \hat{p}_i}{\sqrt{\hat{p}_i(1-\hat{p}_i)}}$$

```
g_pearson = broom::augment(
  g, type.predict="response",
  type.residuals="pearson"
)
```



Binned Pearson Residuals

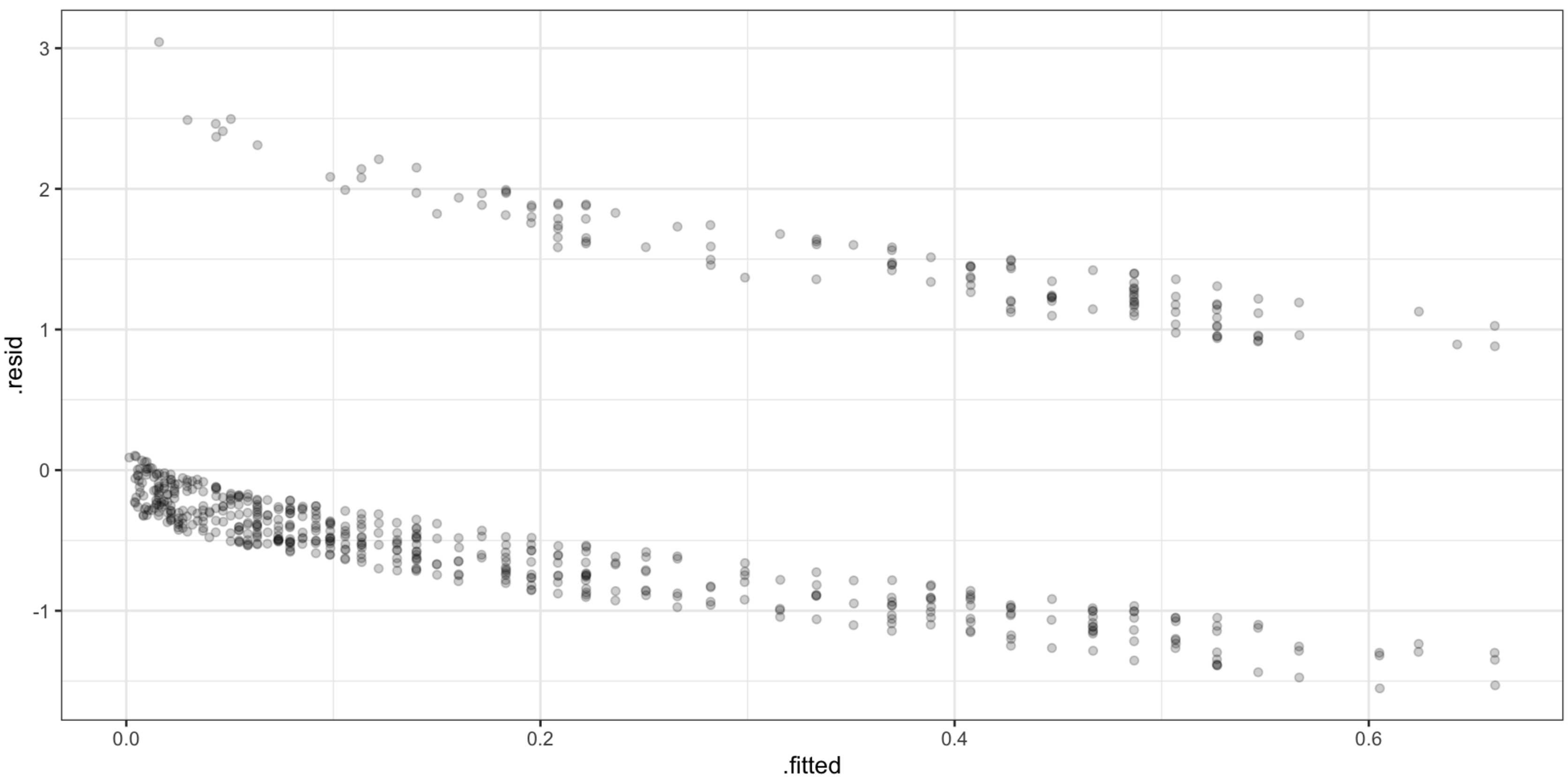
```r
g_pearson_bin = g_pearson |>
  mutate(bin = .fitted - (.fitted %% bin_width) + bin_width/2) |>
  group_by(bin) |>
  summarize(.resid_bin = mean(.resid))
```



Deviance Residuals

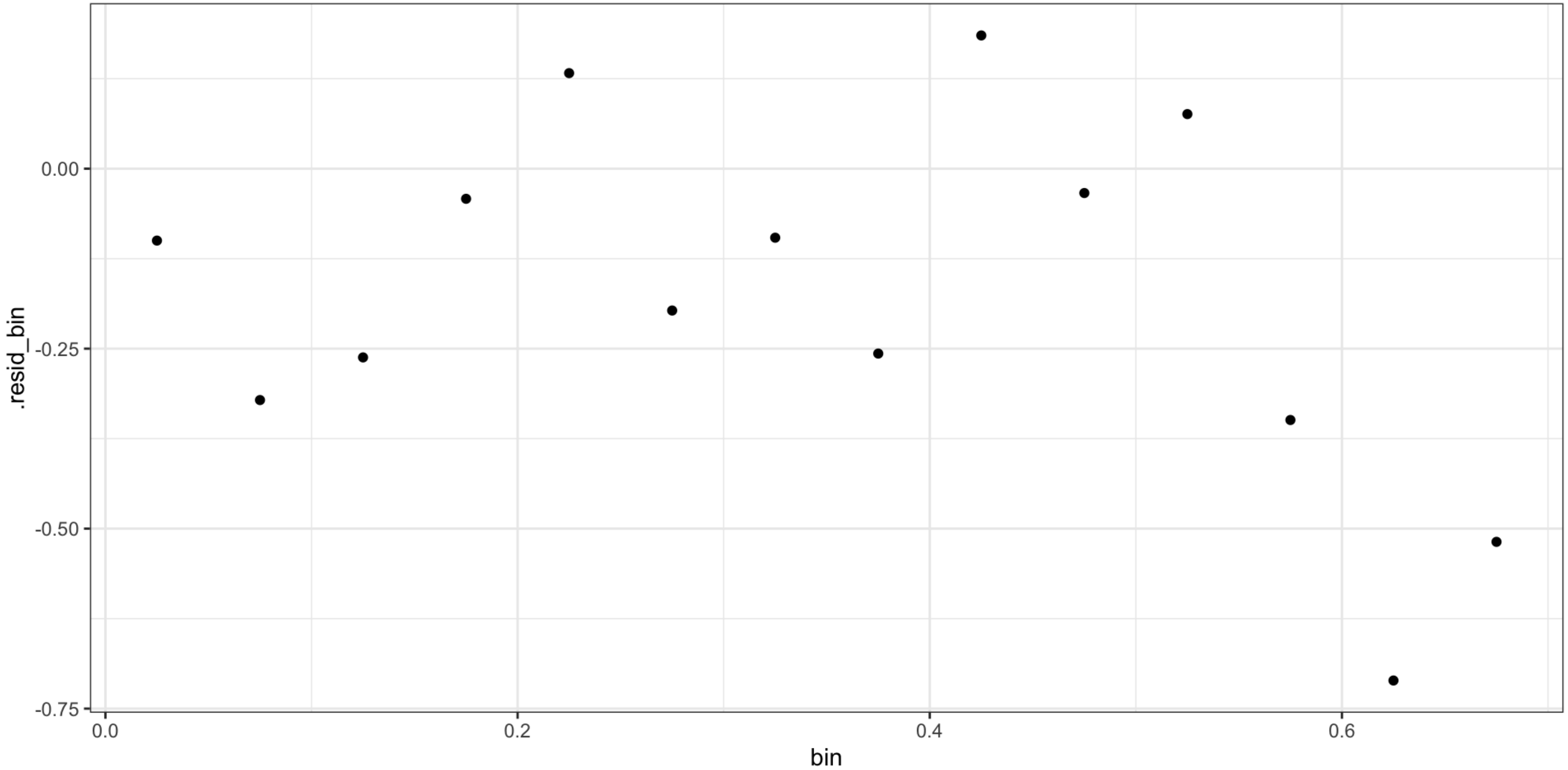
$$d_i = \text{sign}(Y_i - \hat{p}_i) \times \sqrt{-2\left(Y_i \log \hat{p}_i + (1 - Y_i)\log(1 - \hat{p}_i)\right)}$$

```r
g_deviance = broom::augment(
  g, type.predict = "response",
  type.residuals = "deviance"
)
```



Binned Deviance Residuals

```r
g_deviance_bin = g_deviance |>
  mutate(bin = .fitted - (.fitted %% bin_width) + bin_width/2) |>
  group_by(bin) |>
  summarize(.resid_bin = mean(.resid))
```



Checking Deviance

```r
g
```

```

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

Coefficients:
(Intercept)      SegSumT  
   -15.0220       0.8005  

Degrees of Freedom: 617 Total (i.e. Null);  616 Residual
Null Deviance:	    627.8 
Residual Deviance: 501.9 	AIC: 505.9
```

```r
summarize(g_deviance, sum(.resid^2))
```

```
# A tibble: 1 × 1
  `sum(.resid^2)`
            <dbl>
1            502.
```

Full Model

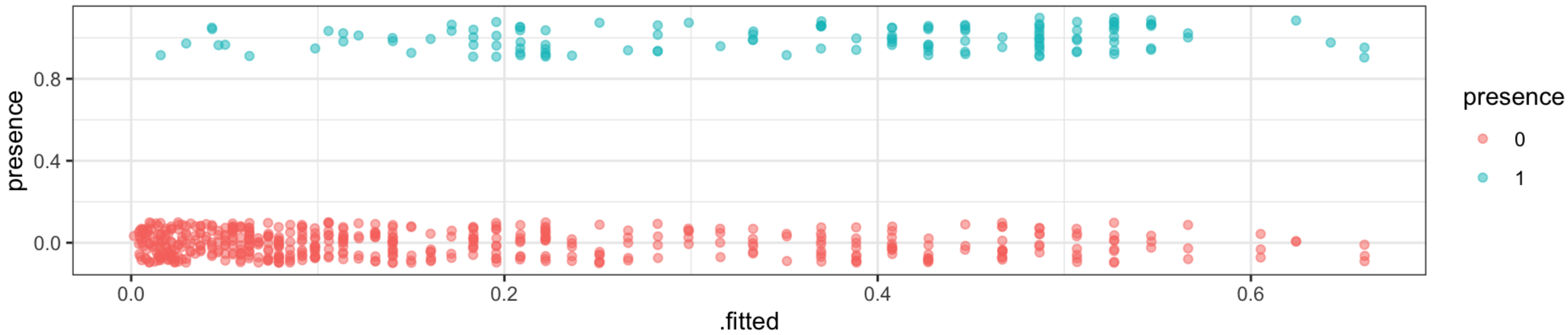
Model

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

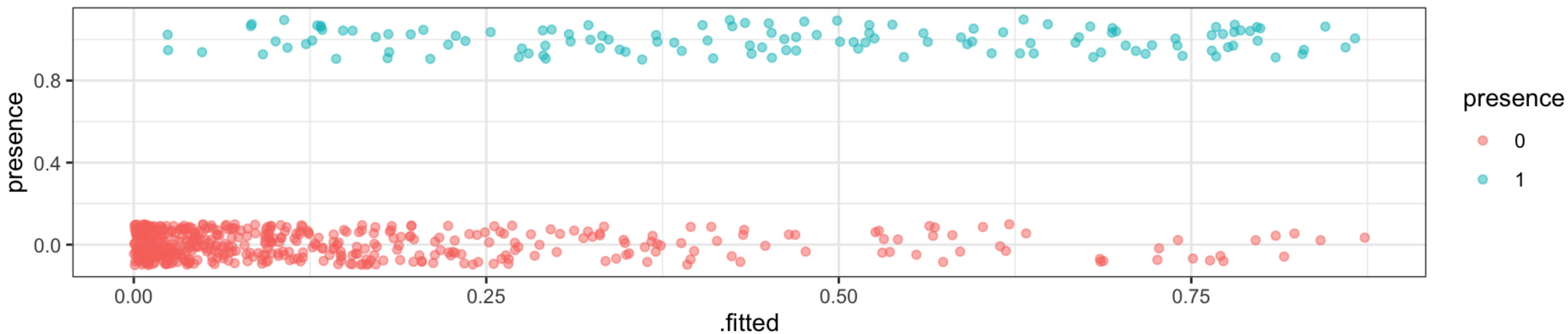
```
Call:
glm(formula = presence ~ ., family = binomial, data = anguilla_train)

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

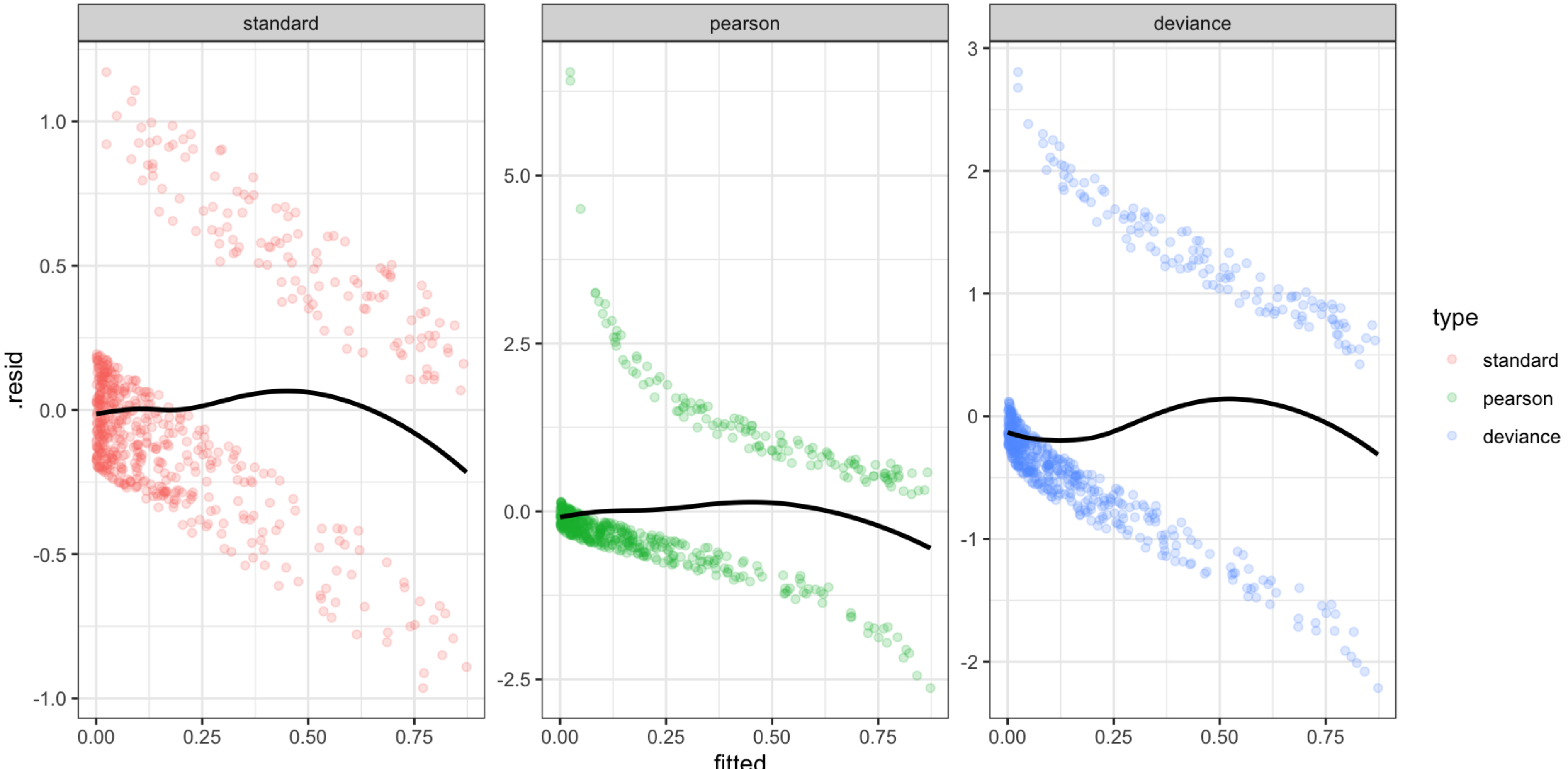


Full Model



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

```r
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")
```