# Residual Analysis + Generalized Linear Models

## Lecture 04

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# Lecture 3 wrap up

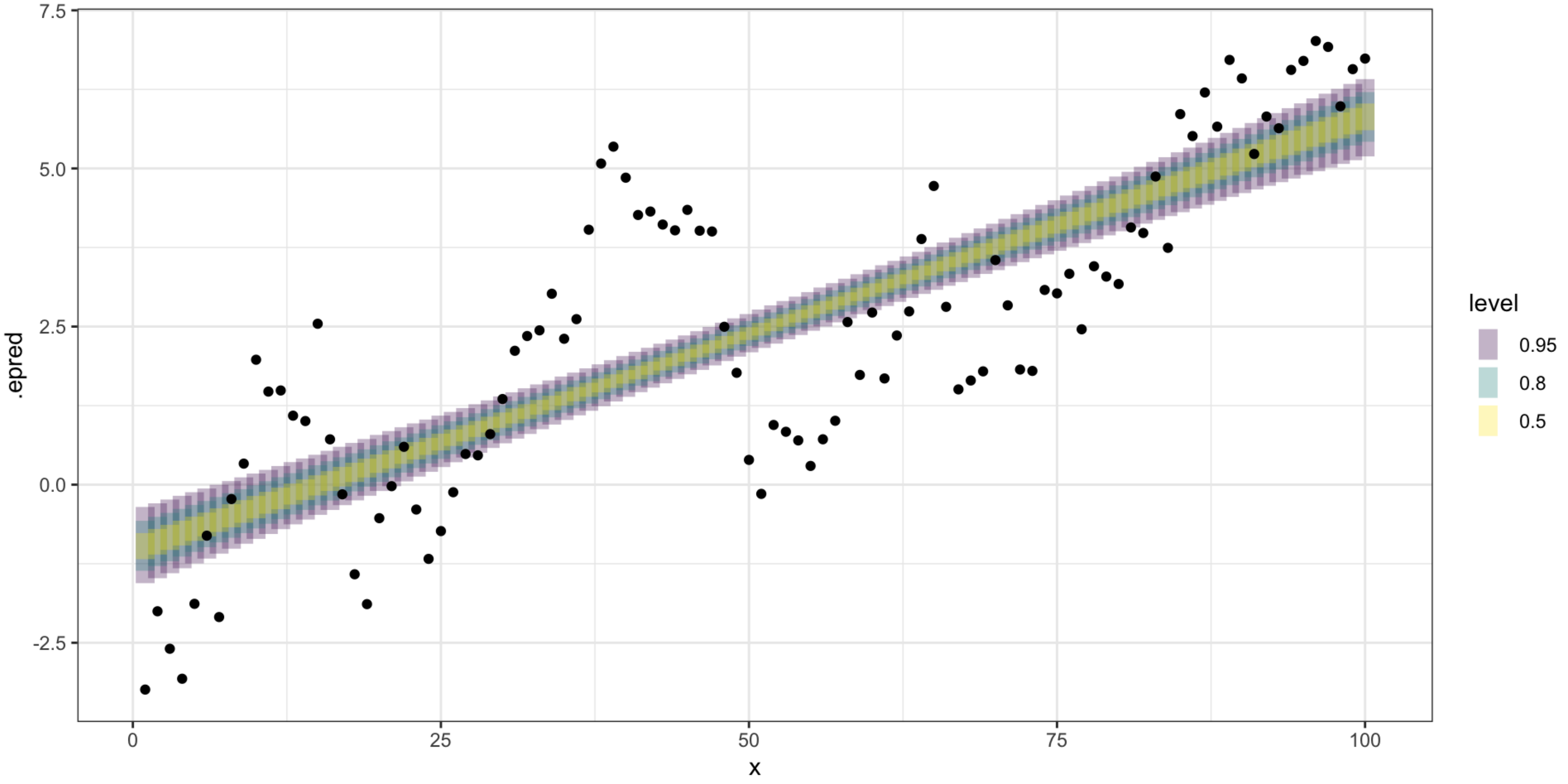
# Where we left it - Empirical Coverage ($\hat{y}$)

```r
( epred_draws_fix(b, newdata=d) %>%
    group_by(x, y) %>%
    tidybayes::mean_hdi(
      .epred, .width = c(0.5,0.9,0.95)
    ) %>%
    mutate(contains = y >= .lower & y <= .upper) %>%
    group_by(prob = .width) %>%
    summarize(
      emp_cov = sum(contains)/n()
    )
)
```

```
# A tibble: 3 × 2
   prob emp_cov
  <dbl>   <dbl>
1  0.5     0.02
2  0.9     0.11
3  0.95    0.14
```

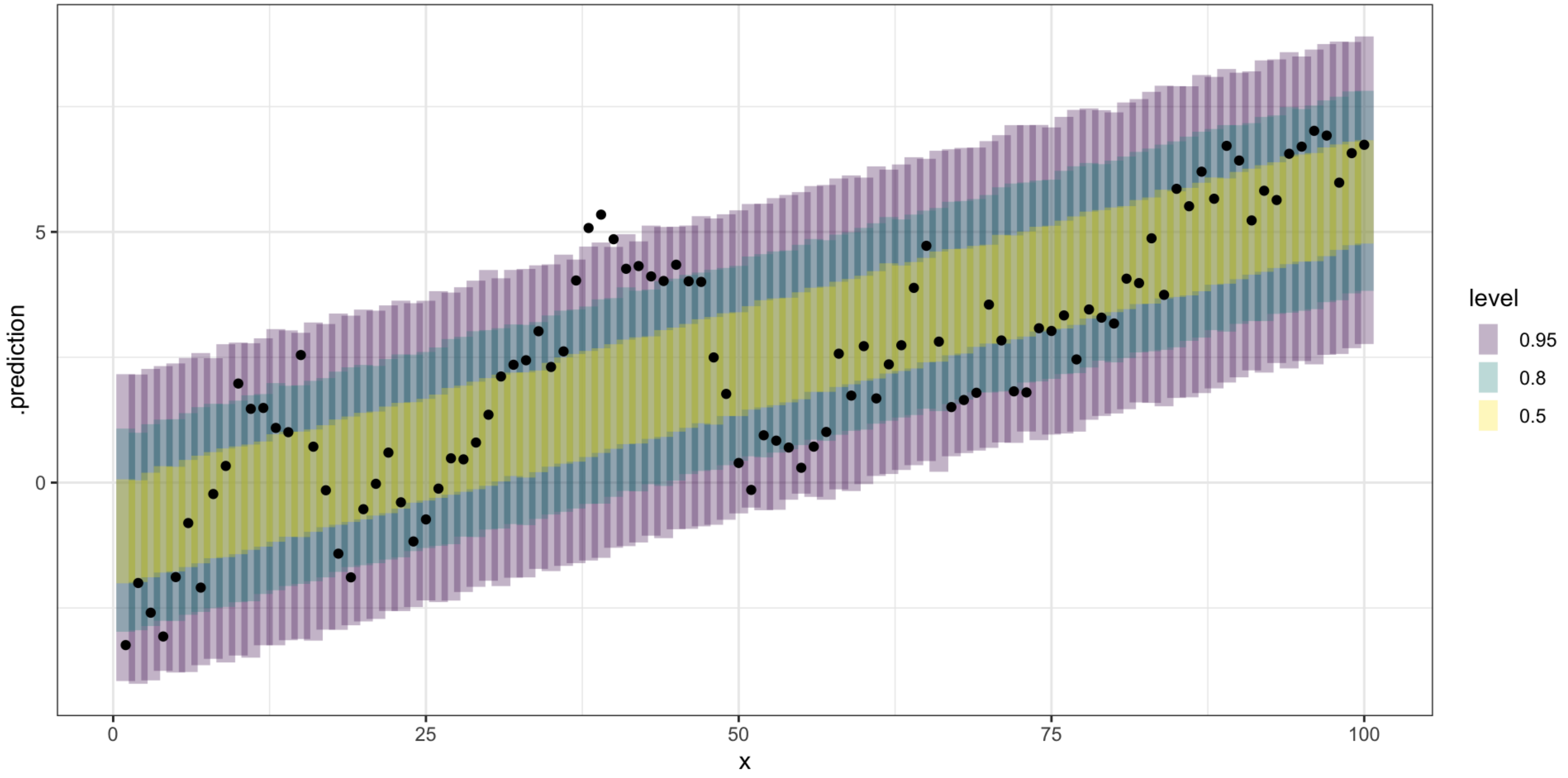
# What went wrong?

```r
epred_draws_fix(b, newdata=d) %>%
  ggplot(aes(x=x)) +
    tidybayes::stat_interval(alpha=0.3, aes(y=.epred, group=x)) +
    geom_point(data=d, aes(y=y))
```



# The right predictions

```r
predicted_draws_fix(b, newdata=d) %>%
  ggplot(aes(x=x)) +
    tidybayes::stat_interval(alpha=0.3, aes(y=.prediction, group=x)) +
    geom_point(data=d, aes(y=y))
```



# Empirical Coverage (y)

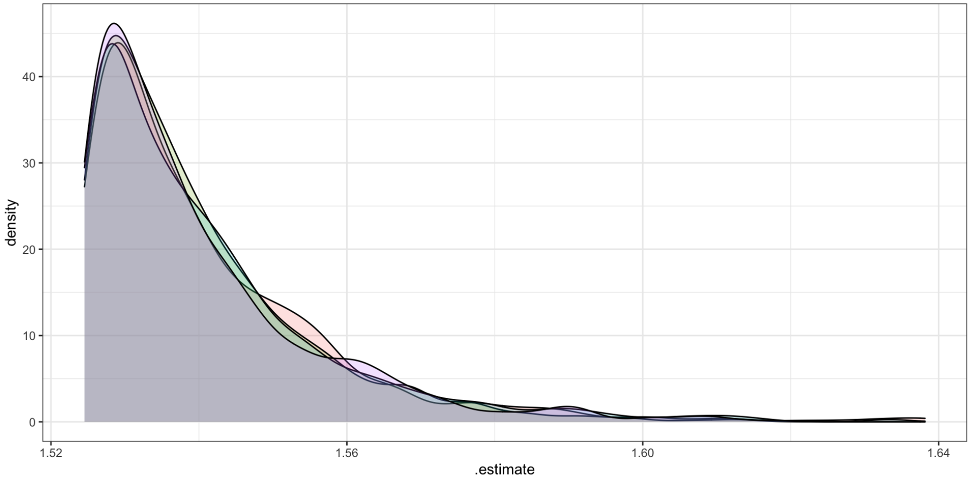
```r
predicted_draws_fix(b, newdata=d) %>%
  group_by(x, y) %>%
  tidybayes::mean_hdi(
    .prediction, .width = c(0.5,0.8,0.9,0.95)
  ) %>%
  mutate(contains = y >= .lower & y <= .upper) %>%
  group_by(prob = .width) %>%
  summarize(
    emp_cov = sum(contains)/n()
  )
```

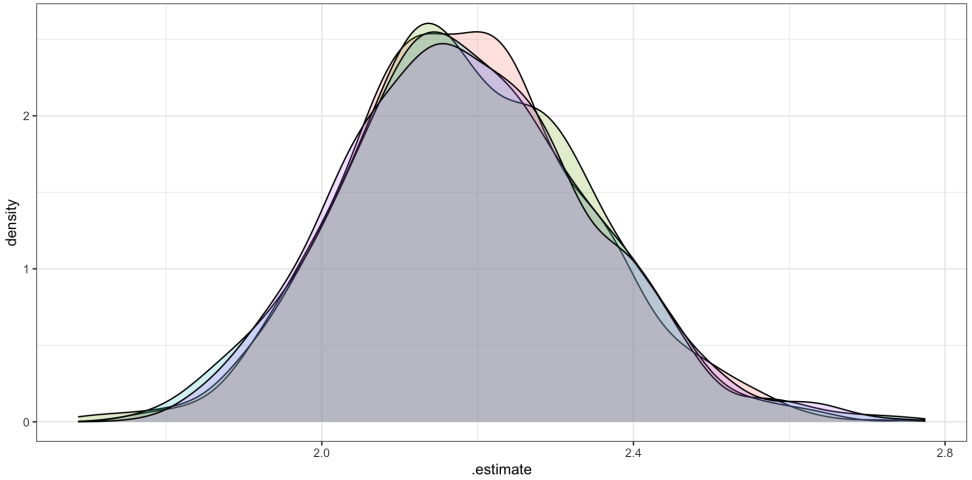
```
# A tibble: 4 × 2
   prob emp_cov
  <dbl>   <dbl>
1  0.5     0.44
2  0.8     0.81
3  0.9     0.97
4  0.95    0.97
```

# RMSE - $y$ vs $\hat{y}$

```r
epred_draws_fix(b, newdata=d) %>%
  group_by(.iteration, .chain) %>%
  yardstick::rmse(truth = y, estimate = .epre
  ggplot(aes(x=.estimate, fill=as.factor(.cha
    geom_density(alpha=0.2) +
    guides(fill="none")
```

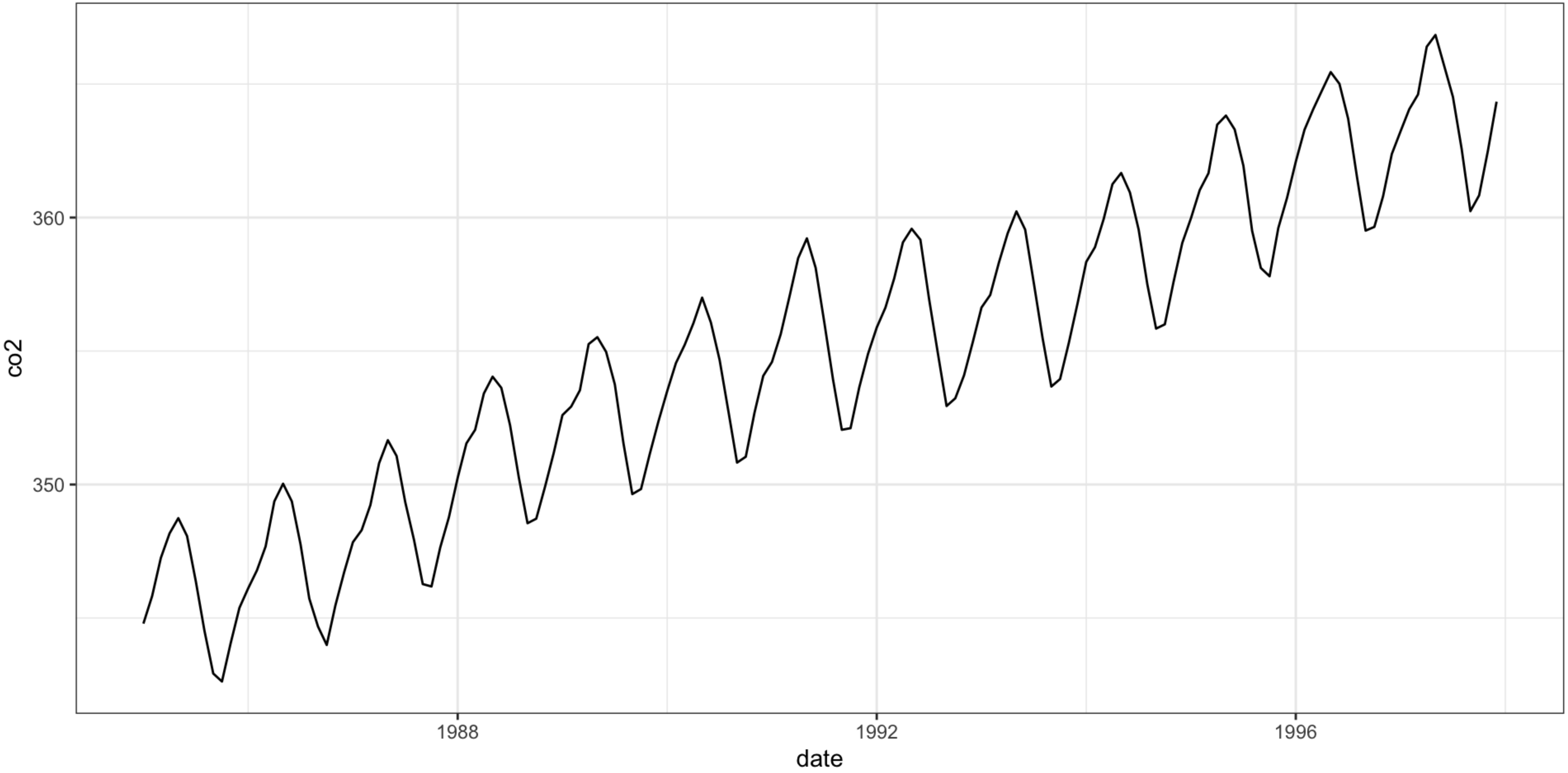
```r
predicted_draws_fix(b, newdata=d) %>%
  group_by(.iteration, .chain) %>%
  yardstick::rmse(truth = y, estimate = .pred
  ggplot(aes(x=.estimate, fill=as.factor(.cha
    geom_density(alpha=0.2)+
    guides(fill="none")
```





# Residual Analysis

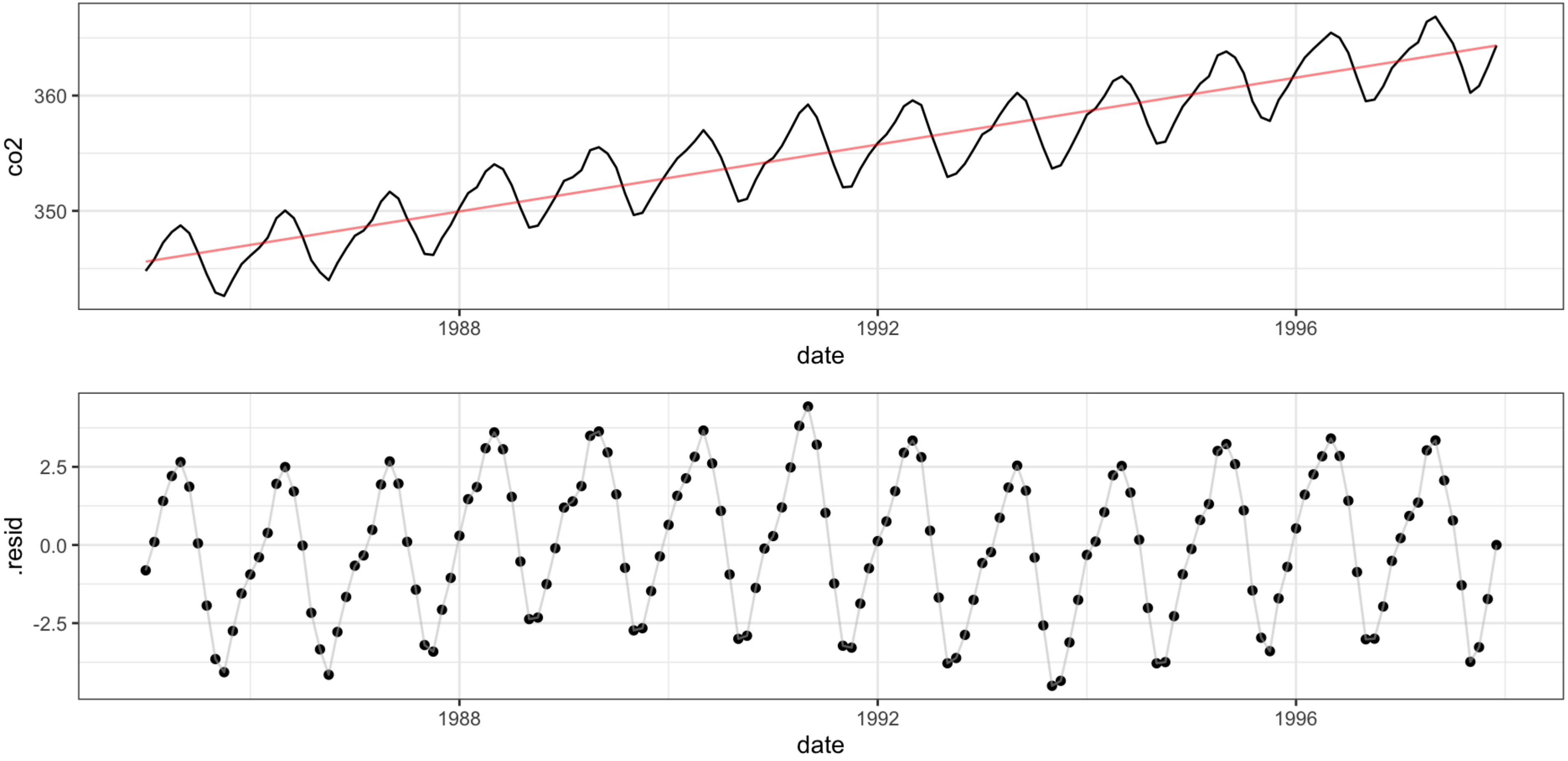
# Atmospheric $\mathrm{CO_2}$ (ppm) from Mauna Loa



# Where to start?

Well, it looks like stuff is going up on average …

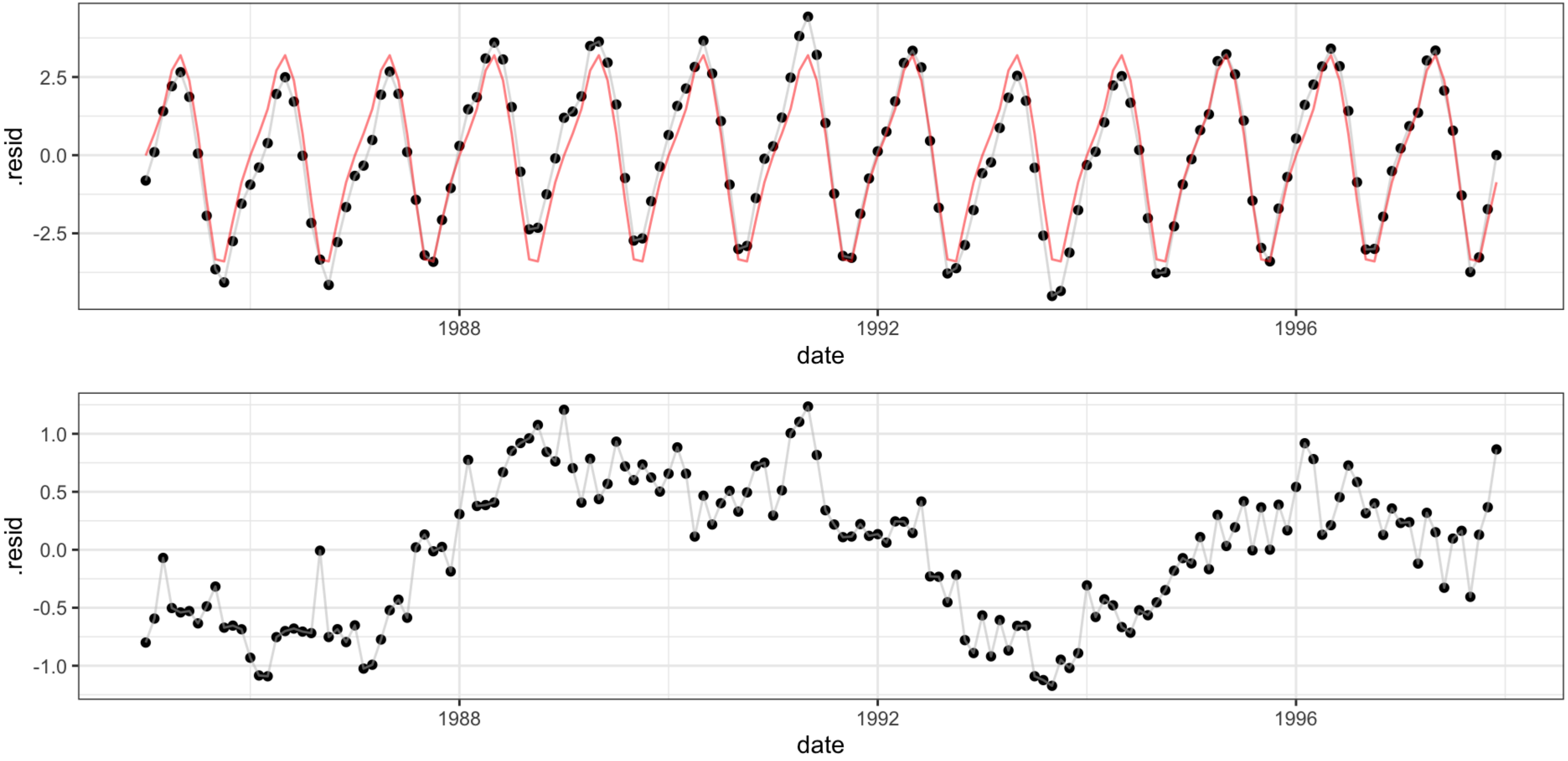
```r
l = lm(co2~date, data=mauna_loa)
```



# and then?

Well there is some periodicity lets add the month …

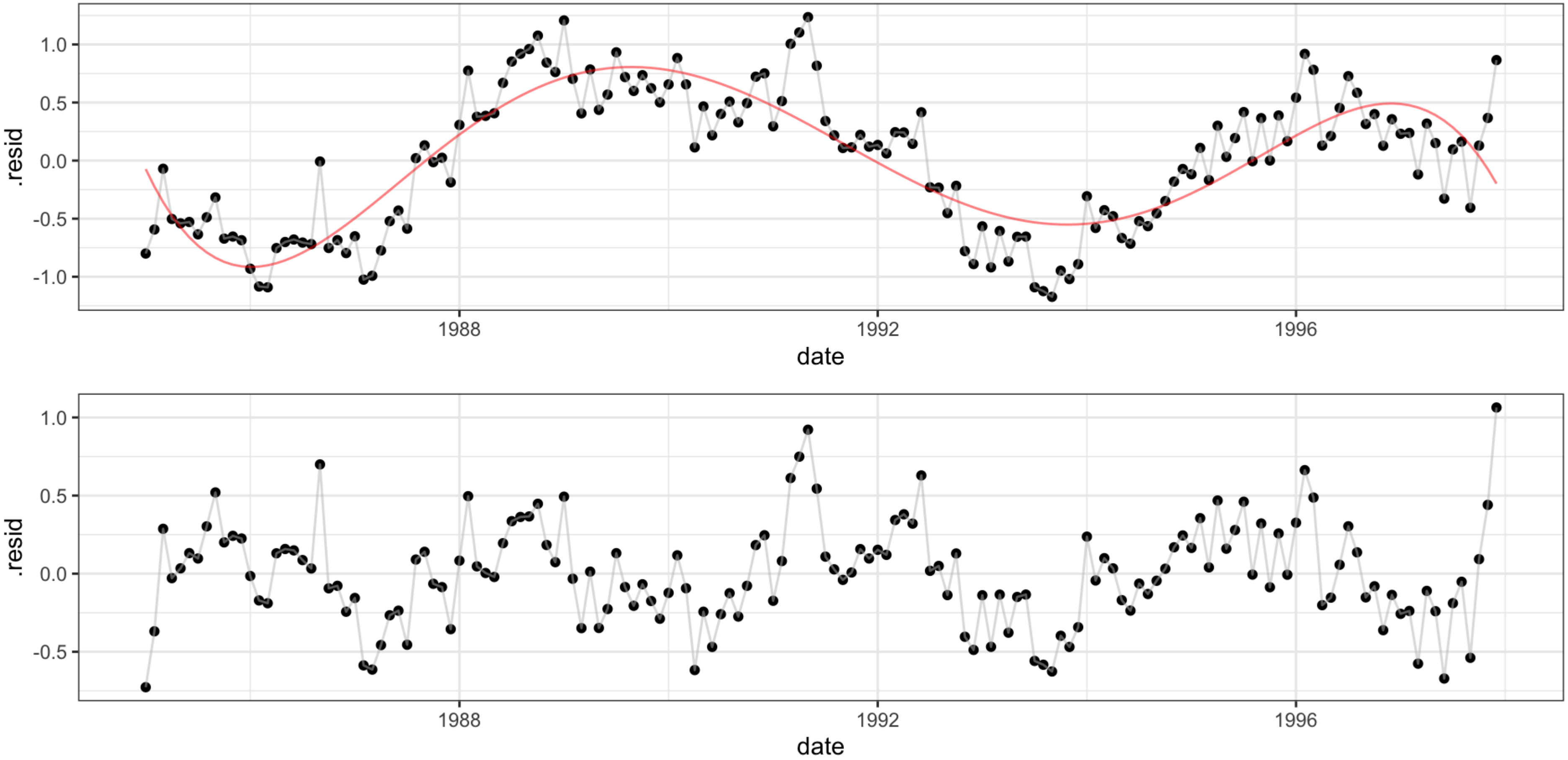
```r
ls = lm(.resid~month, data=mauna_loa_l)
```



# and then and then?

There is still some long term trend in the data, maybe a fancy polynomial can help ...

```r
lsy = lm(.resid~poly(date,5), data=mauna_loa_ls)
```

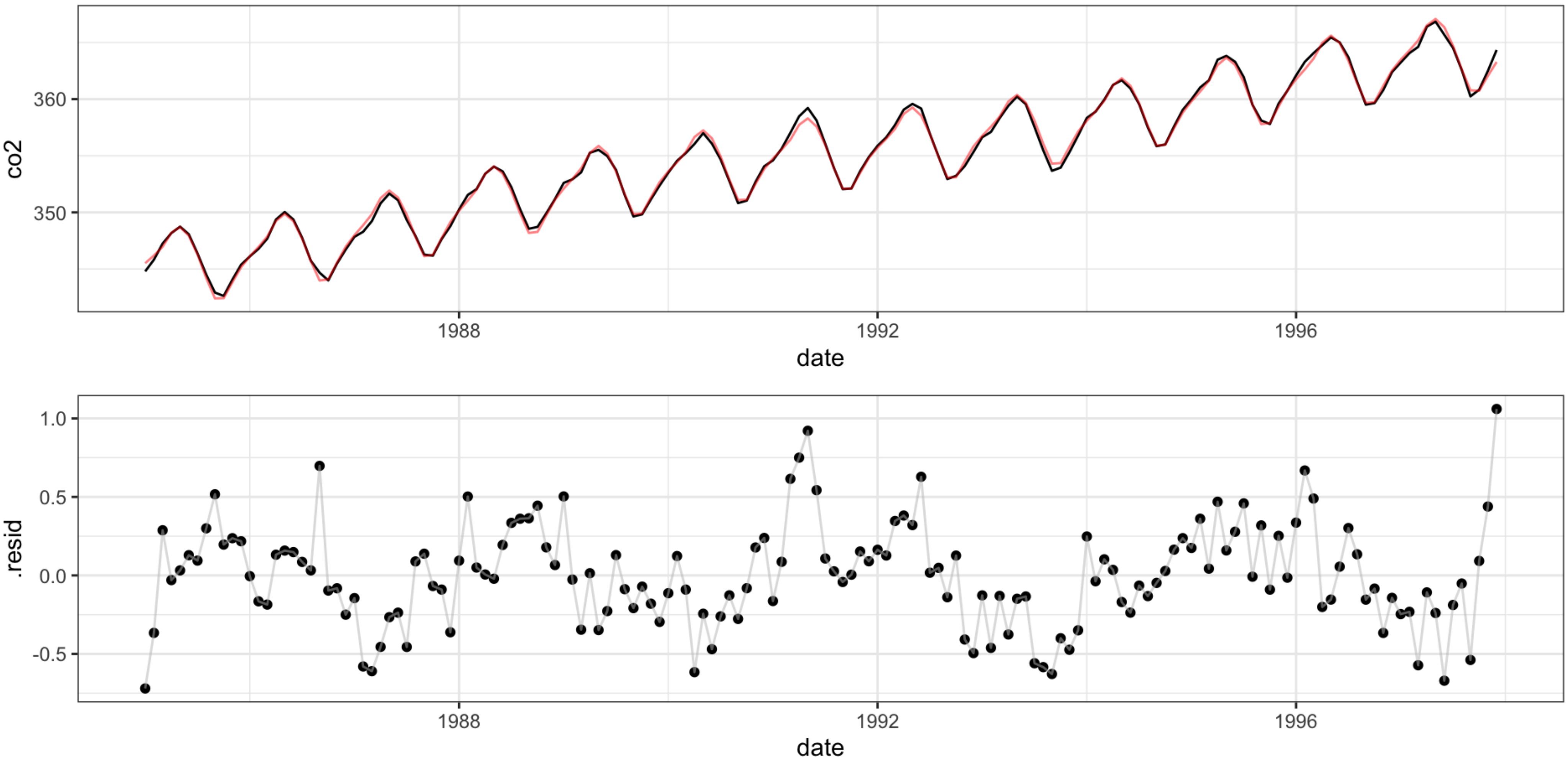

.resid
1.0
0.5
0.0
-0.5
-1.0
1988
1992
1996
date
.resid
1.0
0.5
0.0
-0.5
1988
1992
1996
date

# Putting it all together …

```r
l_comb = lm(co2~date + month + poly(date,5), data=mauna_loa)
summary(l_comb)
```

```
Call:
lm(formula = co2 ~ date + month + poly(date, 5), data = mauna_loa)

Residuals:
     Min       1Q   Median       3Q      Max 
-0.72022 -0.19169 -0.00638  0.17565  1.06026 

Coefficients: (1 not defined because of singularities)
                 Estimate Std. Error  t value Pr(>|t|)    
(Intercept)    -2.587e+03  1.460e+01 -177.174  < 2e-16 ***
date            1.479e+00  7.334e-03  201.649  < 2e-16 ***
monthAug       -4.155e+00  1.346e-01  -30.880  < 2e-16 ***
monthDec       -3.566e+00  1.350e-01  -26.404  < 2e-16 ***
monthFeb       -2.022e+00  1.345e-01  -15.041  < 2e-16 ***
monthJan       -2.729e+00  1.345e-01  -20.286  < 2e-16 ***
```

# Combined fit + Residuals



# Model performance

| Model | rmse |
|---|---|
| `co2 ~ date` | 2.248 |
| `co2 ~ month` | 5.566 |
| `co2 ~ date+month` | 0.594 |
| `co2 ~ poly(date,5)` | 2.171 |
| `co2 ~ month+poly(date,5)` | 0.323 |
| `co2 ~ date+month+poly(date,5)` | 0.323 |

# Generalized Linear Models

# Background

A generalized linear model has three key components:

1. a probability distribution (from the exponential family) that describes your response variable
2. a linear predictor $\boldsymbol{\eta} = \boldsymbol{X}\boldsymbol{\beta}$,
3. and a link function $\mathrm{g}$ such that $\mathrm{g}(\mathrm{E}(\boldsymbol{Y}|\boldsymbol{X})) = \boldsymbol{\eta}$ (or $\mathrm{E}(\boldsymbol{Y}|\boldsymbol{X}) = \mathrm{g}^{-1}(\boldsymbol{\eta})$).

# Poisson Regression

This is a special case of a generalized linear model for count data where we assume the outcome variable follows a poisson distribution (mean = variance).

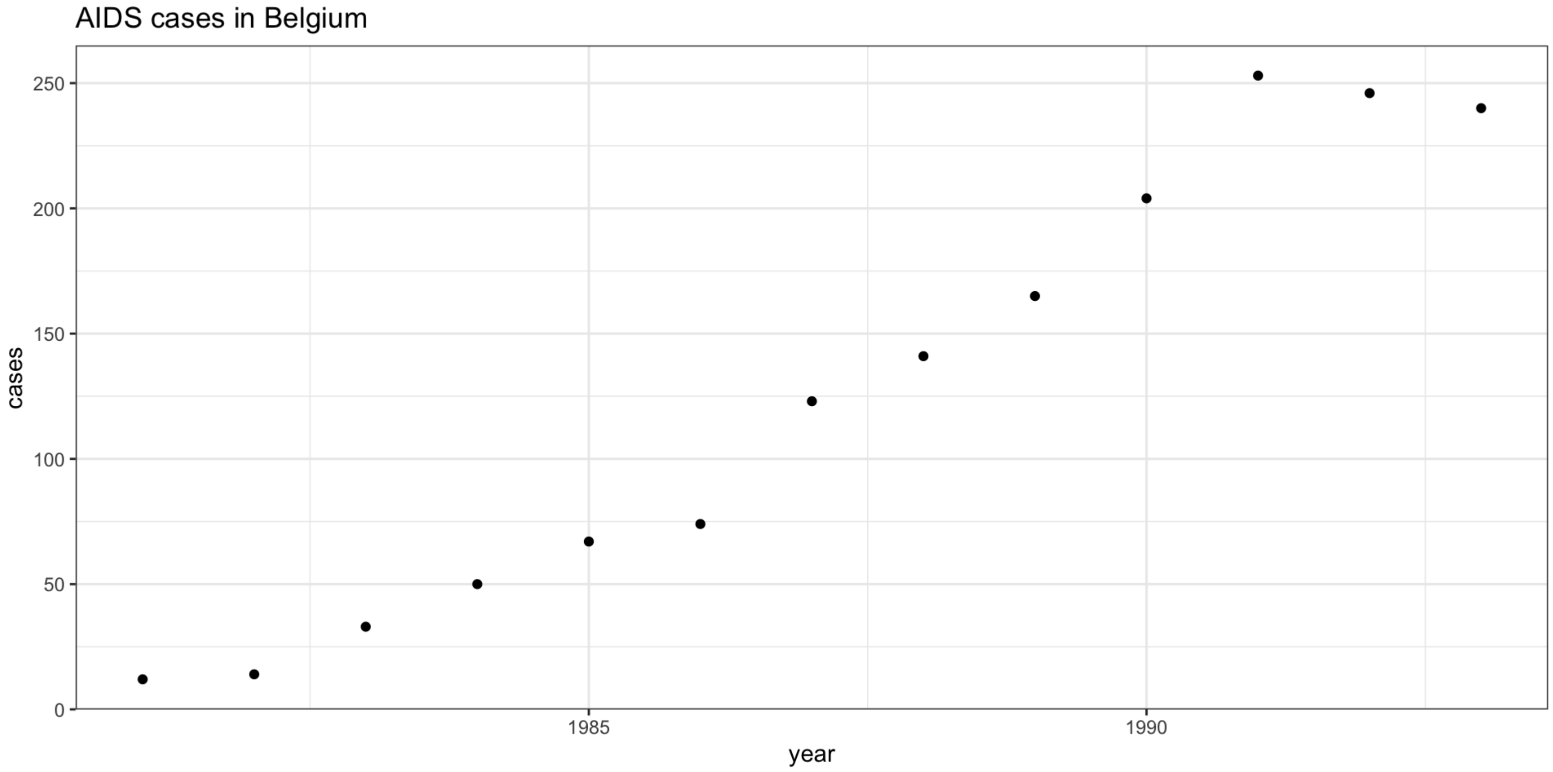
$$
\begin{aligned}
Y_i &\sim \text{Poisson}(\lambda_i) \\
\log E(Y_i | \boldsymbol{X}_{i\cdot}) = \log \lambda_i &= \underset{1\times p}{\boldsymbol{X}_{i\cdot}} \underset{p\times 1}{\boldsymbol{\beta}}
\end{aligned}
$$

# Example - AIDS in Belgium

These data represent the total number of new AIDS cases reported in Belgium during the early stages of the epidemic.

```r
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
```



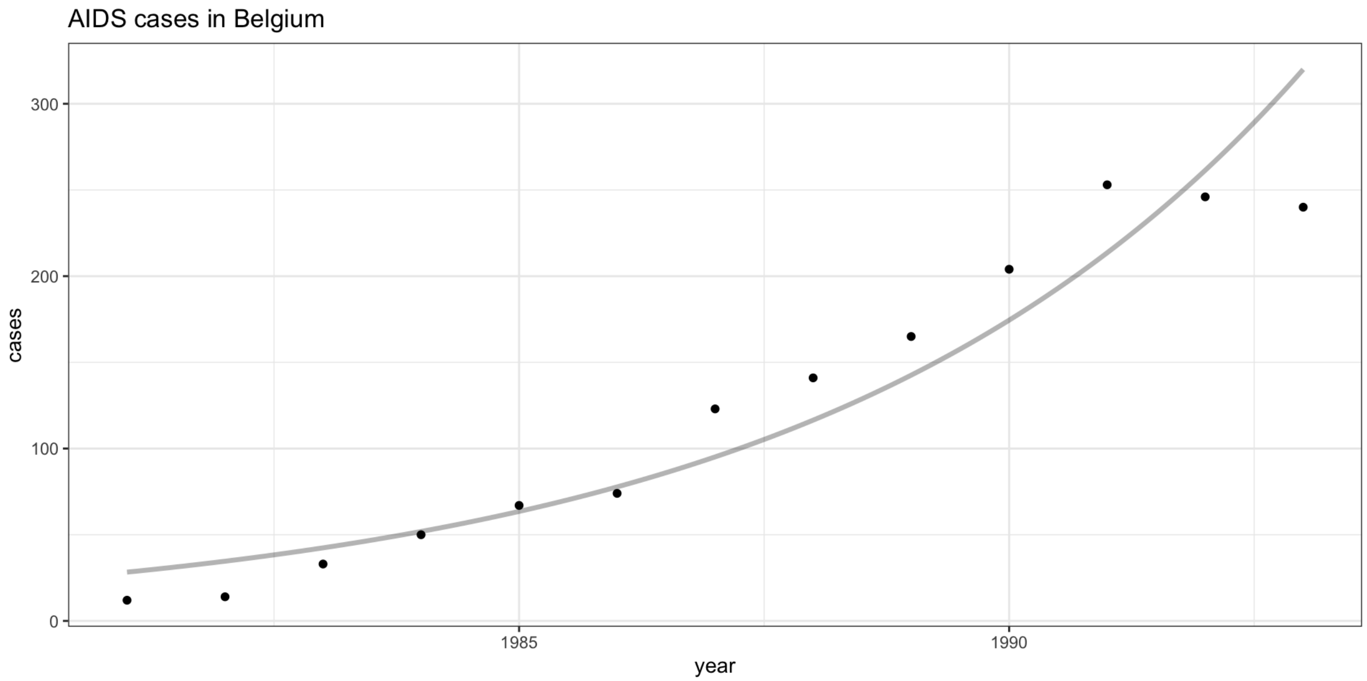
# Frequentist glm fit

```r
( g = glm(cases~year, data=aids, family=poisson) )
```

```
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
```

# Model Fit

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

aids_base +
  geom_line(data=g_pred, aes(y=.fitted), size=1.2, alpha=0.3)
```



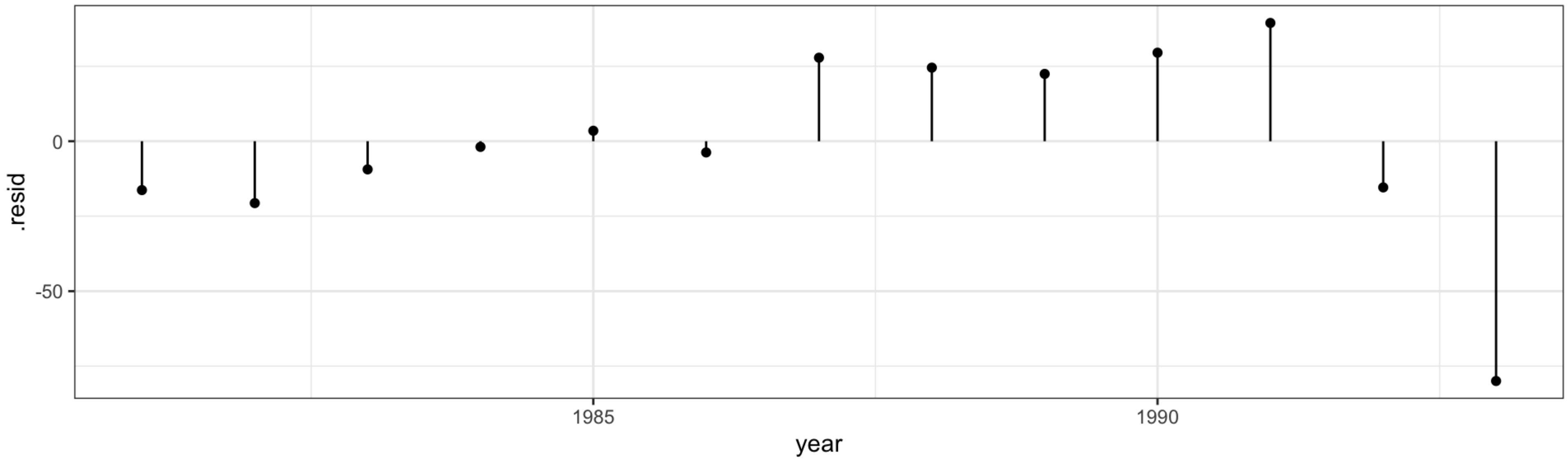
AIDS cases in Belgium

# Residuals?

The naive approach is to use standard residuals,

$$r_i = Y_i - E(Y_i|X) = Y_i - \hat{\lambda_i}$$

```r
g_pred_std = broom::augment(
  g, type.predict = "response"
) %>%
  mutate(.resid = cases - .fitted)
```

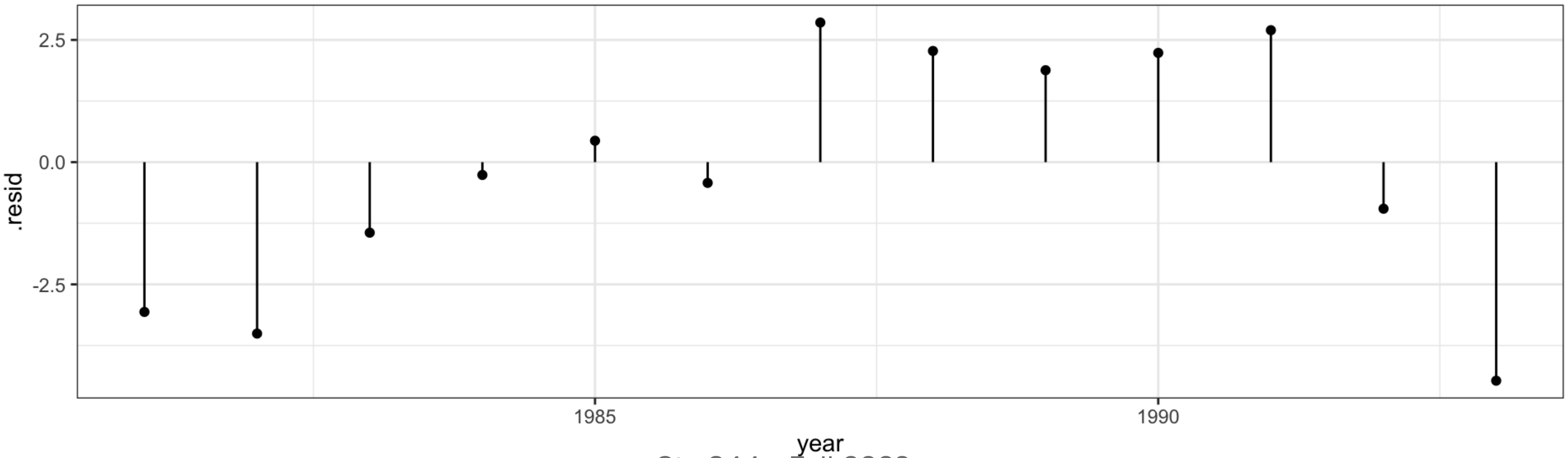


# Accounting for variability

Pearson residuals:

$$r_i = \frac{Y_i - E(Y_i|X)}{\sqrt{Var(Y_i|X)}} = \frac{Y_i - \hat{\lambda}_i}{\sqrt{\hat{\lambda}_i}}$$

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



# Deviance

Deviance is a way of measuring the difference between a GLM's fit and the fit of the perfect model (i.e. where $\theta_b est = E(Y_i|X) = Y_i$).

It is defined as twice the log of the ratio between the likelihood of the perfect model and the likelihood of the given model,

$$
\begin{aligned}
D &= 2 \log\left( \frac{(\theta_{best}|Y)}{(\hat{\theta}|Y)} \right) \\
&= 2\left( l(\theta_{best}|Y) - l(\hat{\theta}|Y) \right)
\end{aligned}
$$

# Derivation - Normal

# Derivation - Poisson

# glm output

```r
summary(g)
```

```

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

Deviance Residuals:
    Min       1Q   Median       3Q      Max  
-4.6784  -1.5013  -0.2636   2.1760   2.7306  

Coefficients:
              Estimate Std. Error z value Pr(>|z|)    
(Intercept) -3.971e+02  1.546e+01  -25.68   <2e-16 ***
year         2.021e-01  7.771e-03   26.01   <2e-16 ***
```

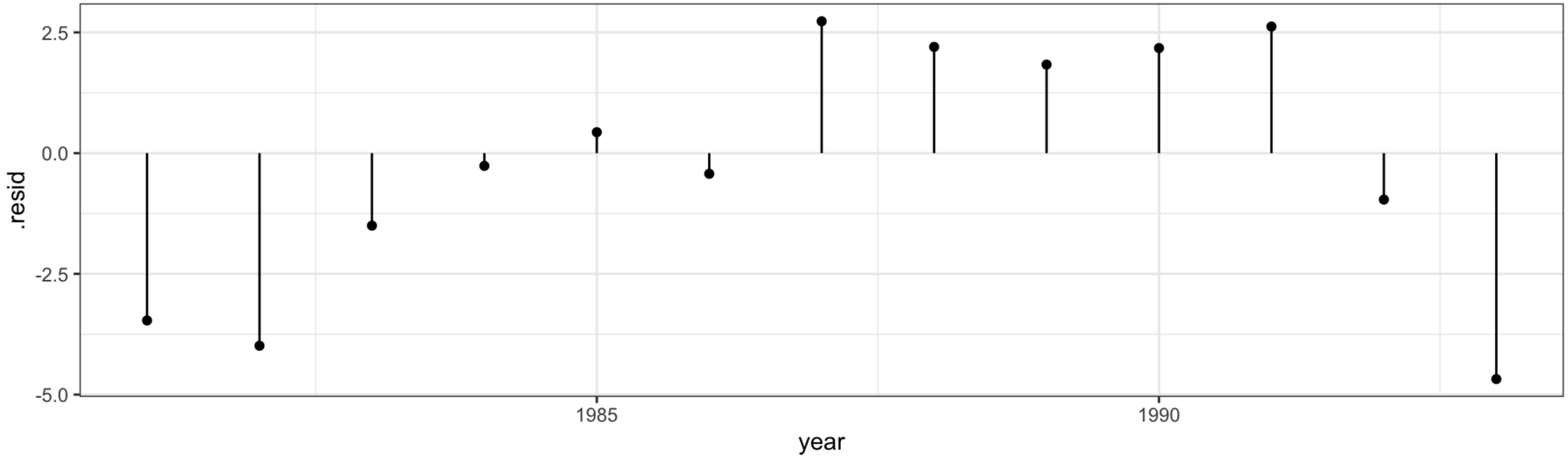
# Deviance residuals

We can therefore think of deviance as $D = \sum_{i=1}^{n} d_i^2$ where $d_i$ is a generalized residual.

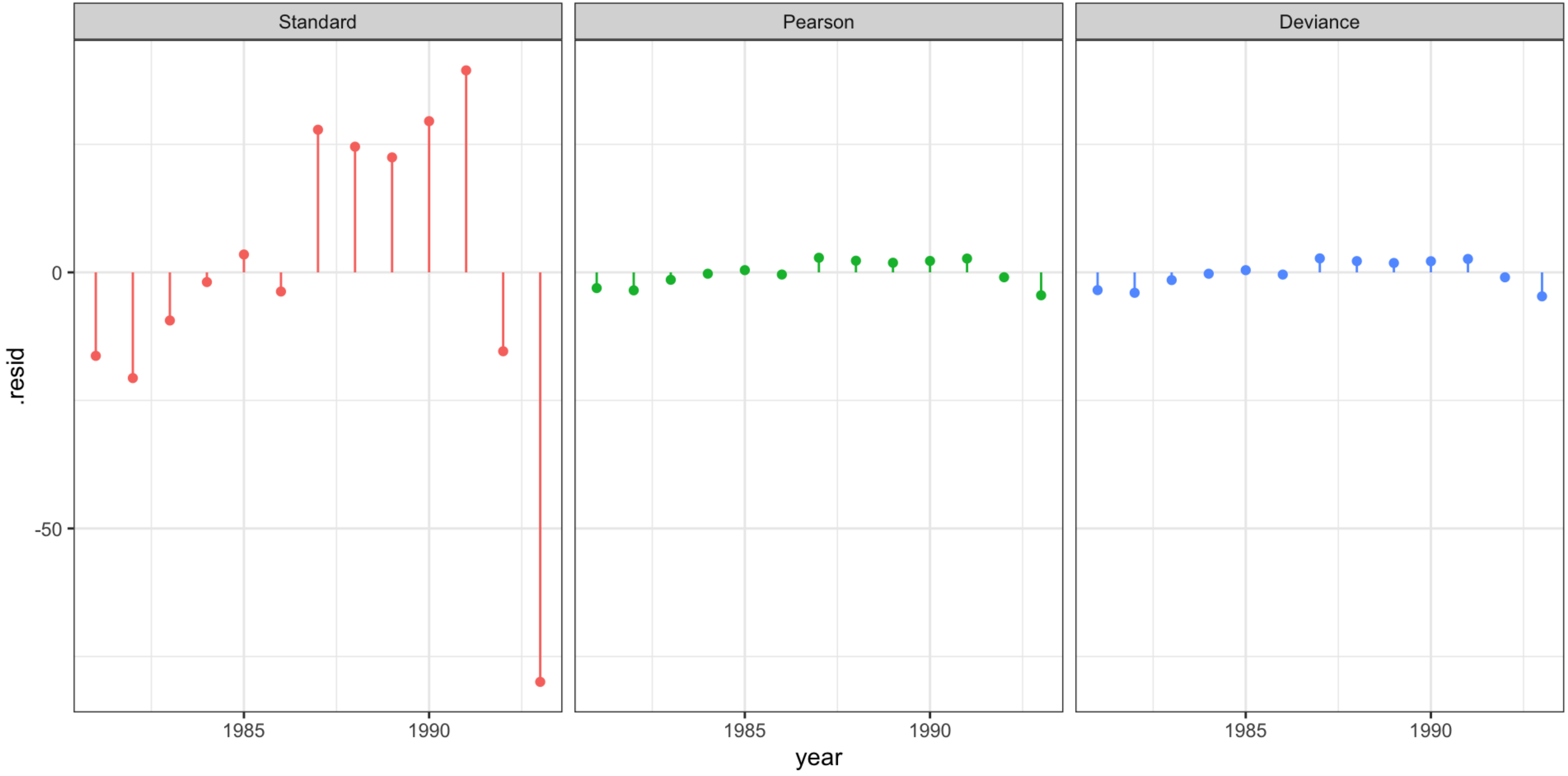
In the Poisson case we have,

$$d_i = \text{sign}(y_i - \lambda_i) \sqrt{2(y_i \log(y_i/\hat{\lambda}_i) - (y_i - \hat{\lambda}_i))}$$

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



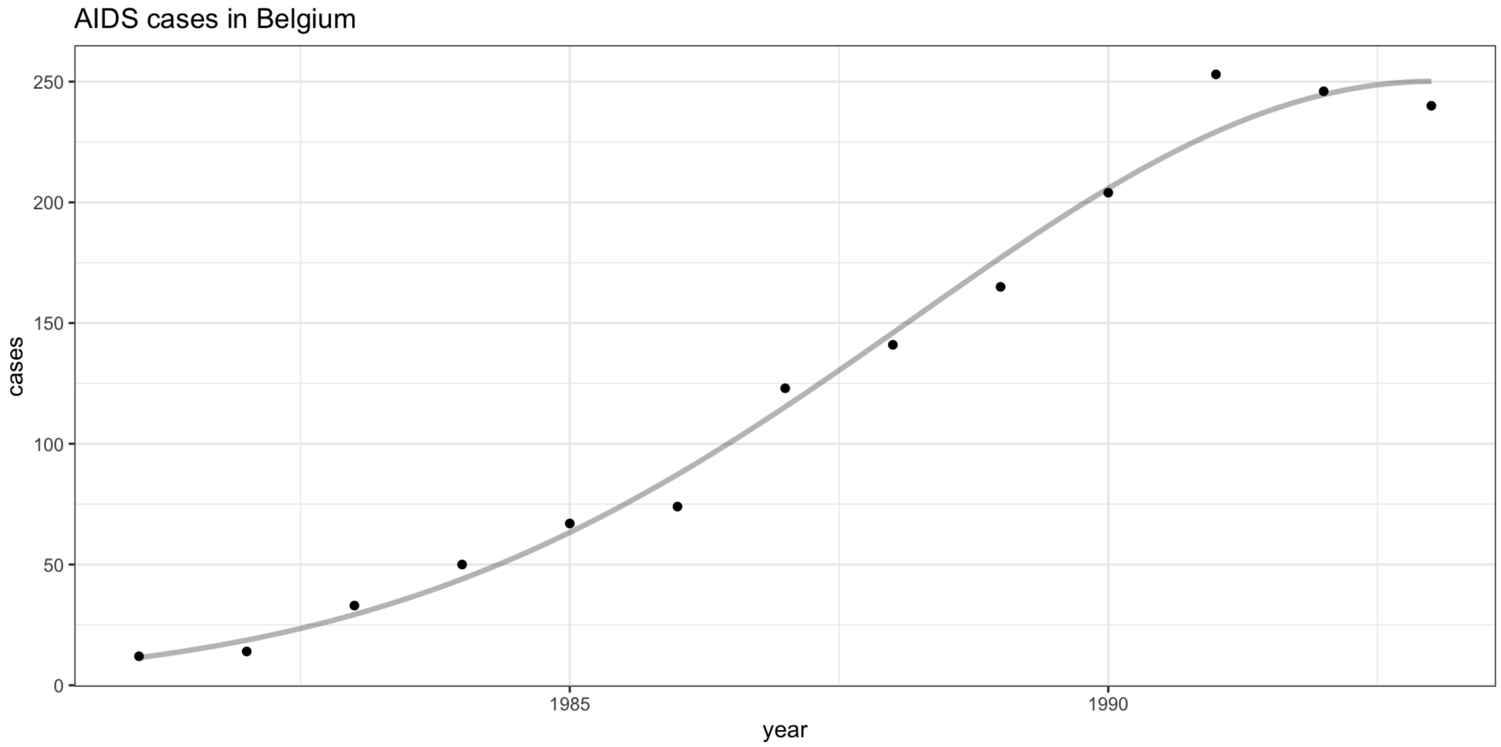
# Comparing Residuals



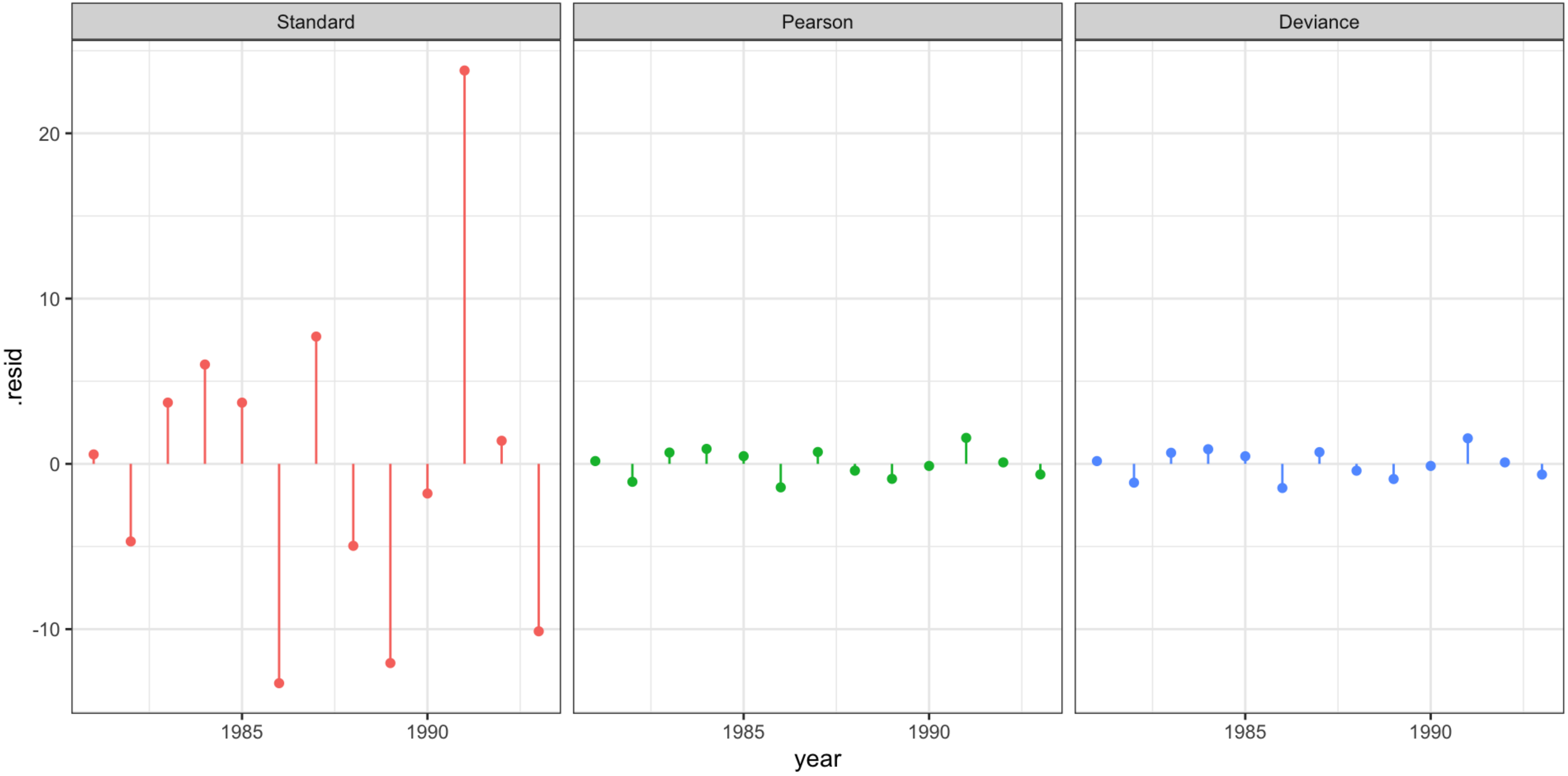
# Updating the model

# Quadratic fit

```r
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 Model

# Bayesian Poisson Regression Model

```r
( g_bayes = brms::brm(
    cases~year, data=aids, family=poisson,
    silent=2, refresh=0
) )
```

```
 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  -397.04     15.92  -428.85  -365.05 1.00     1381     1618
year          0.20      0.01     0.19     0.22 1.00     1382     1605

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).
```

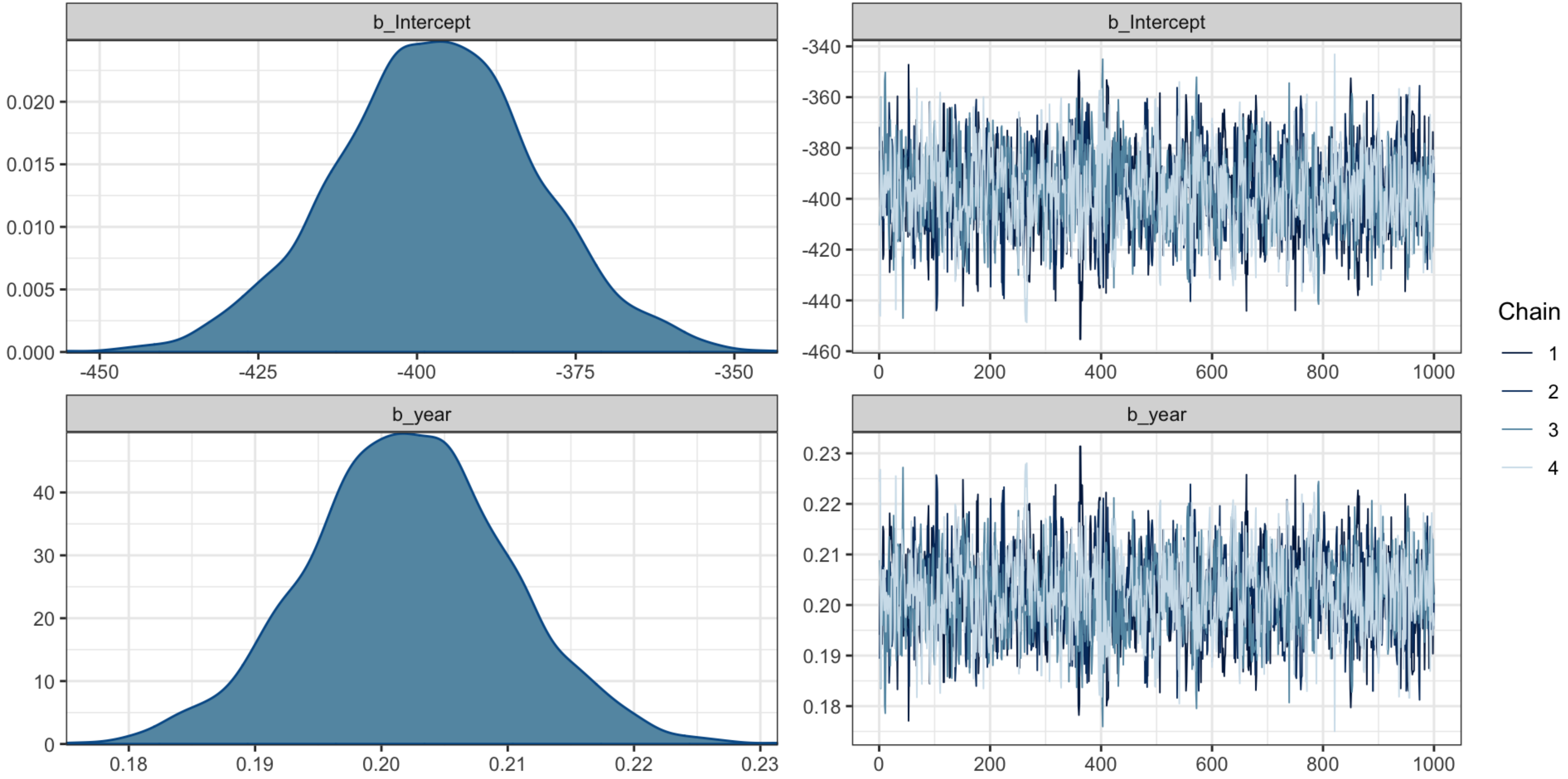
# Model priors

```r
brms::prior_summary(g_bayes)
```

```
                  prior     class coef group resp dpar nlpar lb ub
source
                 (flat)         b
default
                 (flat)         b year
(vectorized)
 student_t(3, 4.8, 2.5) Intercept
default
```

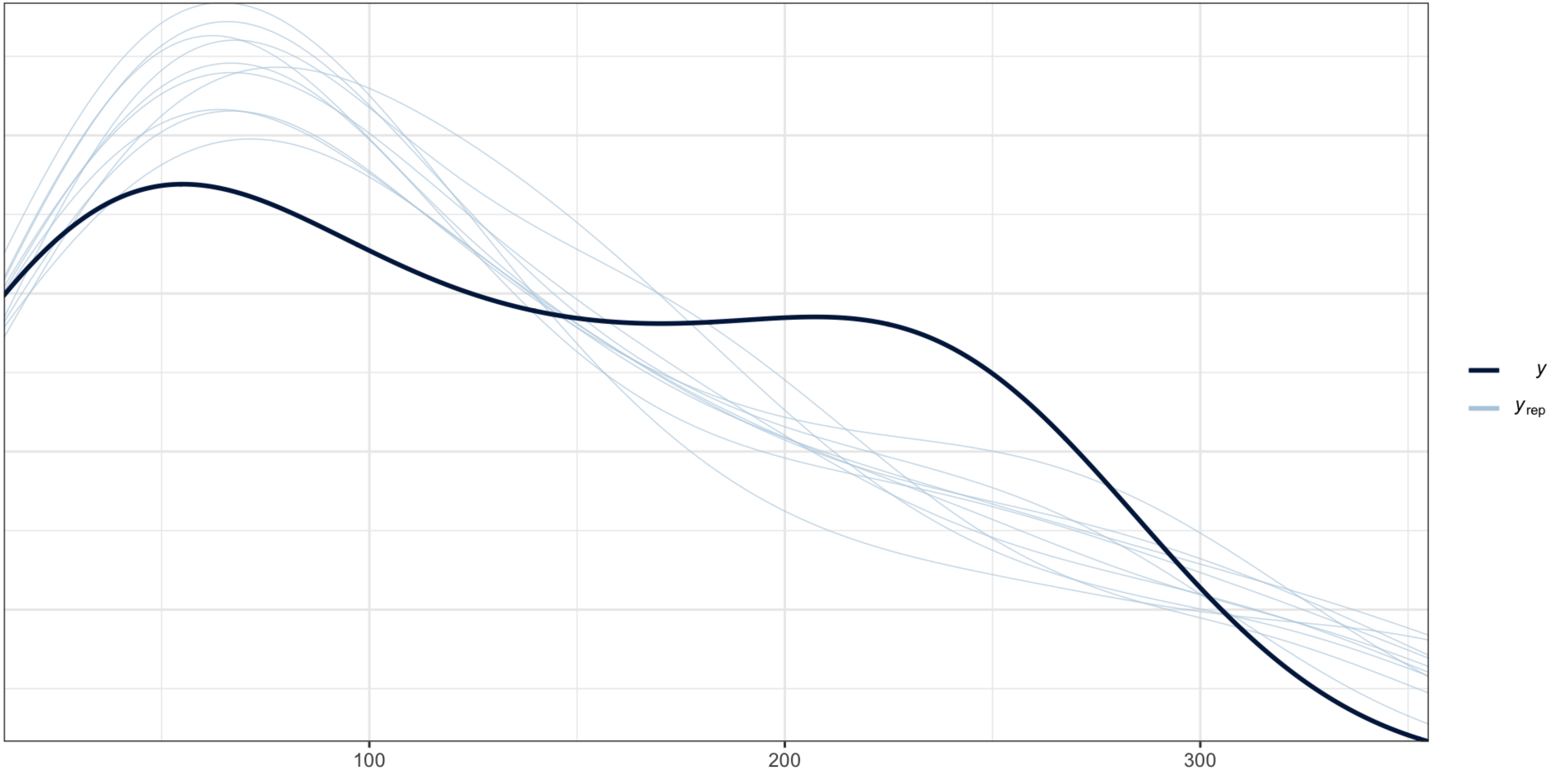
# MCMC Diagnostics

```r
plot(g_bayes)
```



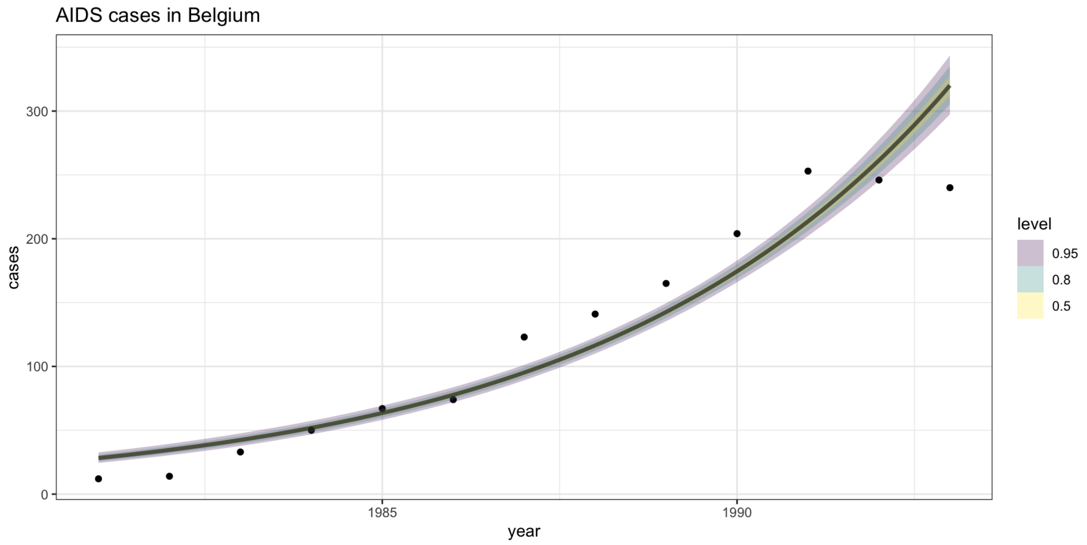
# Posterior Predictive Check

```r
brms::pp_check(g_bayes)
```



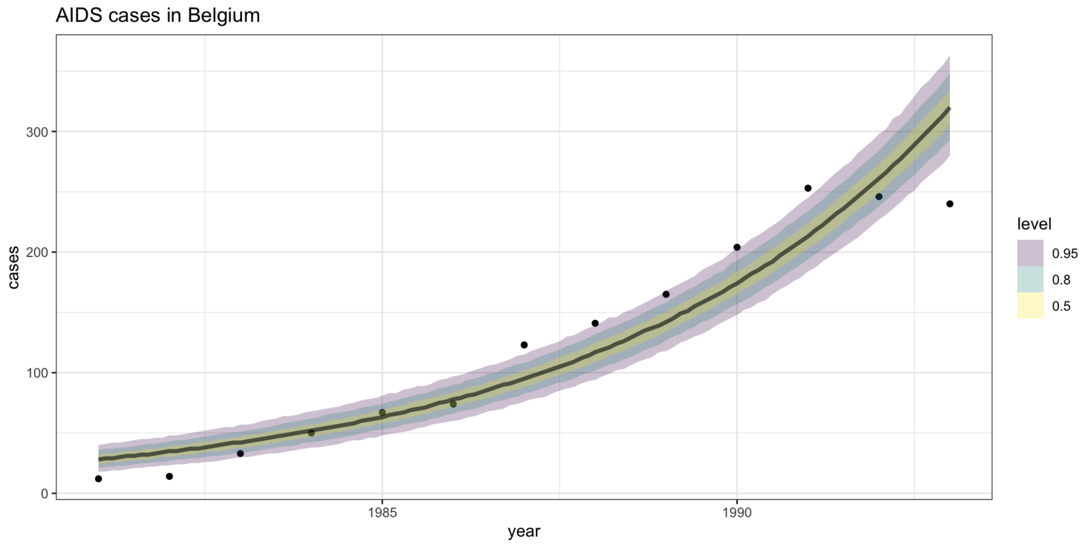
# Model fit - λ CI

```r
aids_base +
  tidybayes::stat_lineribbon(
    data = tidybayes::epred_draws(
      g_bayes,
      newdata = tibble(year=seq(1981,1993,by=0.1))
    ),
    aes(y=.epred),
    alpha=0.25
  )
```



# Model fit - $Y$ CI

```r
aids_base +
  tidybayes::stat_lineribbon(
    data = tidybayes::predicted_draws(
      g_bayes,
      newdata = tibble(year=seq(1981,1993,by=0.1))
    ),
    aes(y=.prediction),
    alpha=0.25
  )
```


AIDS cases in Belgium
cases
year
level