Lecture 3

Residual Analysis + Generalized Linear Models

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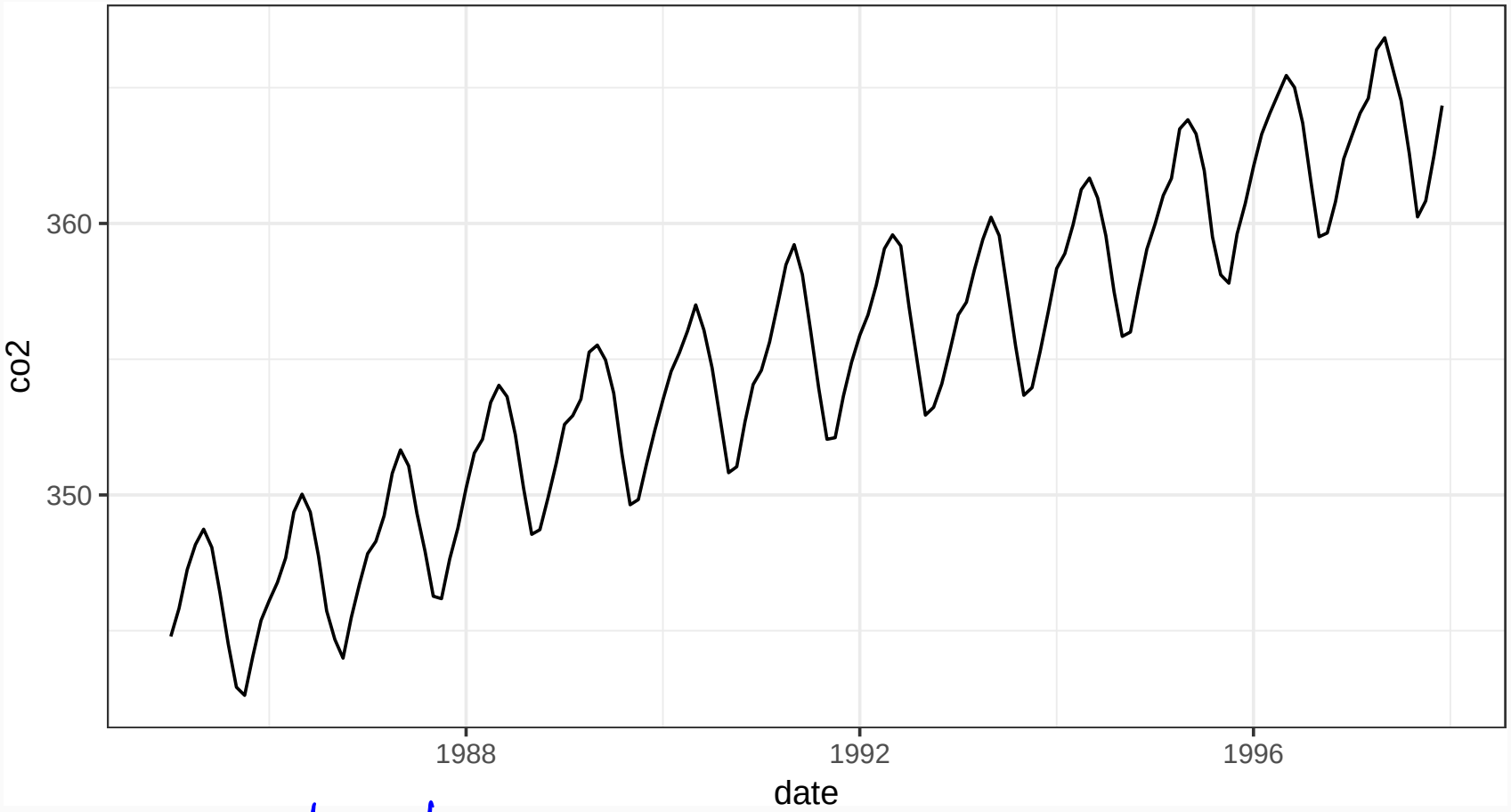
1/23/2018

Residual Analysis

Atmospheric CO_2 (ppm) from Mauna Loa



Add things along the way

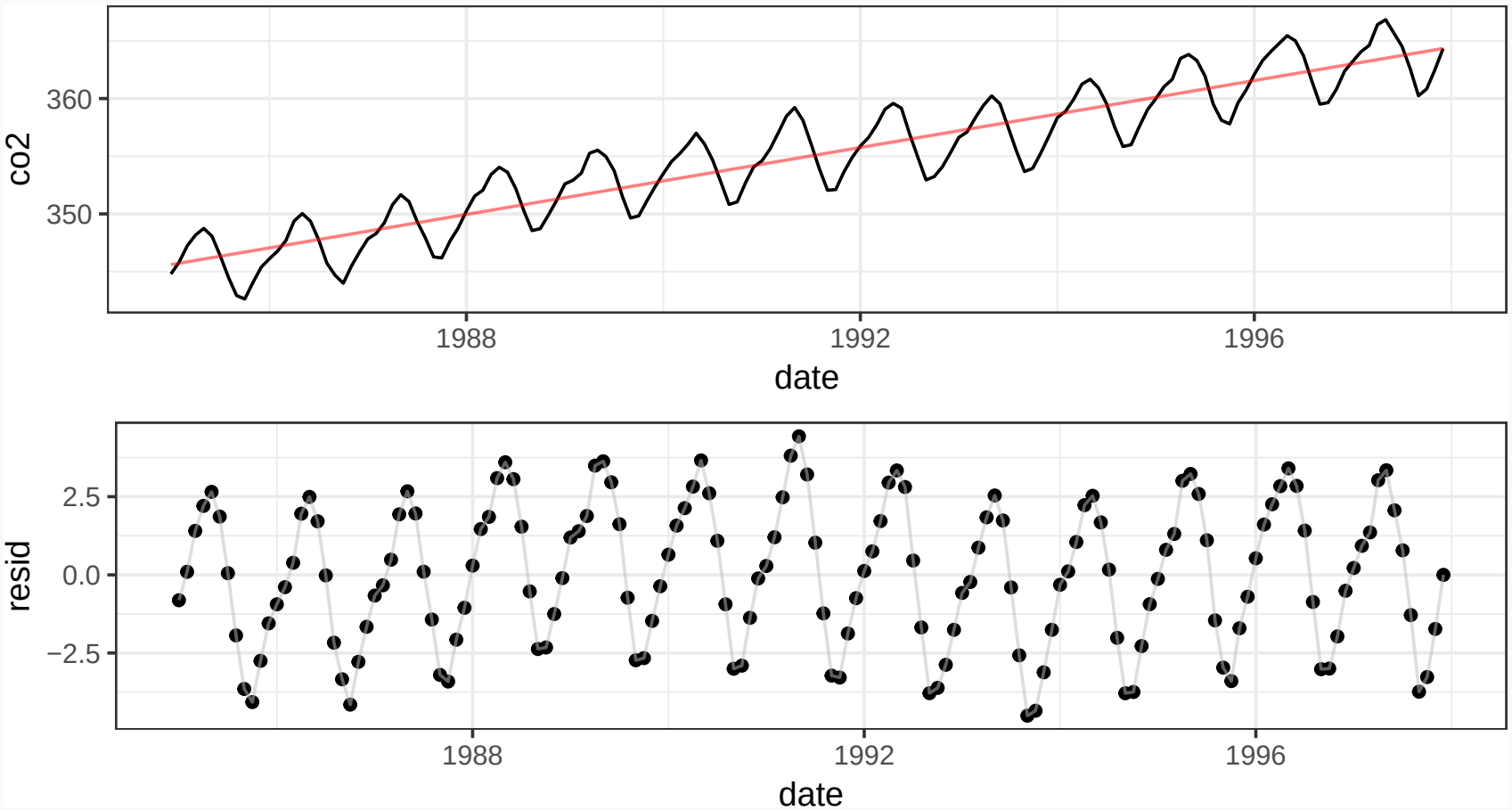
Where to start?

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

Where to start?

Start from simple model

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

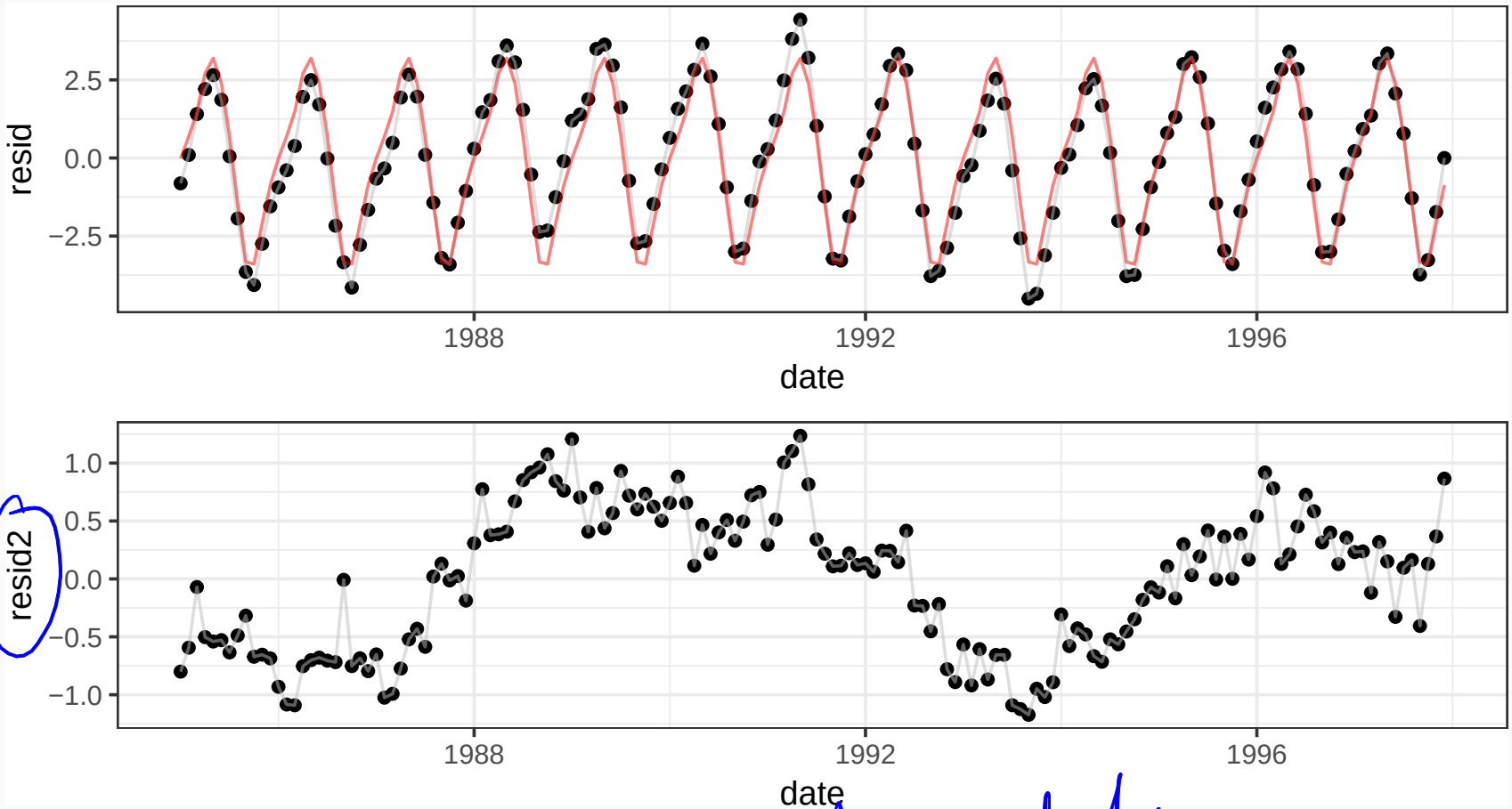


and then?

Well there is some periodicity lets add the month ...

and then?

Well there is some periodicity lets add the month ...



still structure in the residuals

and then and then?

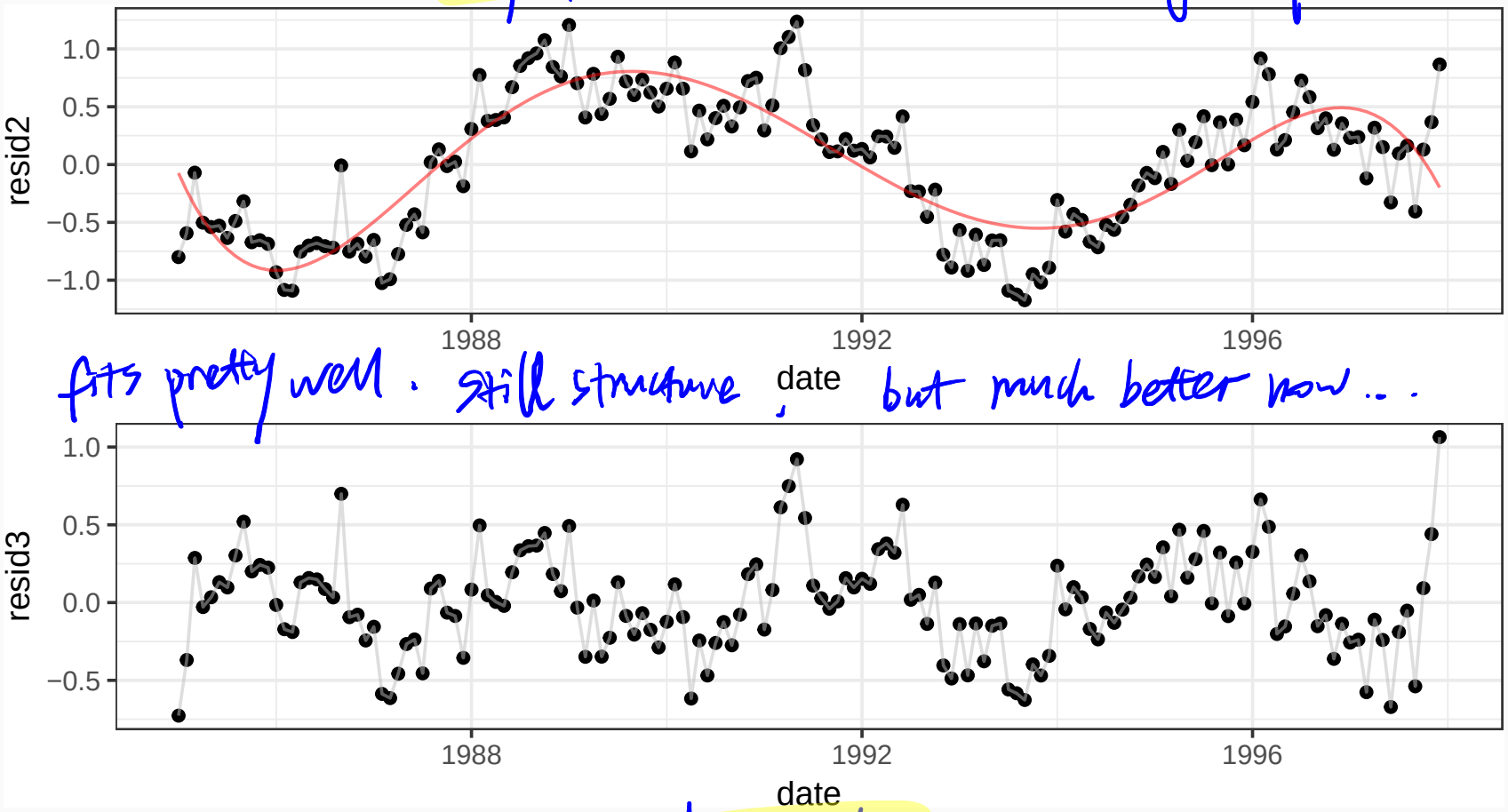
There is still some long term trend in the data, maybe a fancy polynomial can help ...

and then and then?

bad idea.

There is still some long term trend in the data, maybe a fancy polynomial can help ... lm(y ~ poly(year, 5))

large exponent.



fits pretty well. still structure, but much better now...

there's LT Annual trend

Putting it all together ...

```
l_final = lm(co2~date + month + poly(date,5), data=co2_df)
summary(l_final)
##
## Call:
## lm(formula = co2 ~ date + month + poly(date, 5), data = co2_df)
##
## 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 ***
## monthJul       -2.018e+00  1.345e-01  -15.003  < 2e-16 ***
## monthJun       -3.136e-01  1.345e-01   -2.332 0.021117 *
## monthMar       -1.233e+00  1.344e-01   -9.175 5.54e-16 ***
## monthMay        4.881e-01  1.344e-01    3.631 0.000396 ***
## monthNov       -4.799e+00  1.349e-01  -35.577  < 2e-16 ***
## monthOct       -6.102e+00  1.348e-01  -45.282  < 2e-16 ***
## monthSep       -6.036e+00  1.346e-01  -44.832  < 2e-16 ***
## poly(date, 5)1         NA         NA       NA       NA
## poly(date, 5)2 -1.920e+00  3.427e-01   -5.602 1.09e-07 ***
## poly(date, 5)3  3.920e+00  3.451e-01   11.358  < 2e-16 ***
## poly(date, 5)4  8.946e-01  3.428e-01    2.609 0.010062 *
## poly(date, 5)5 -4.340e+00  3.462e-01  -12.535  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3427 on 139 degrees of freedom
## Multiple R-squared:  0.997,  Adjusted R-squared:  0.9966
## F-statistic:  2872 on 16 and 139 DF,  p-value: < 2.2e-16
```

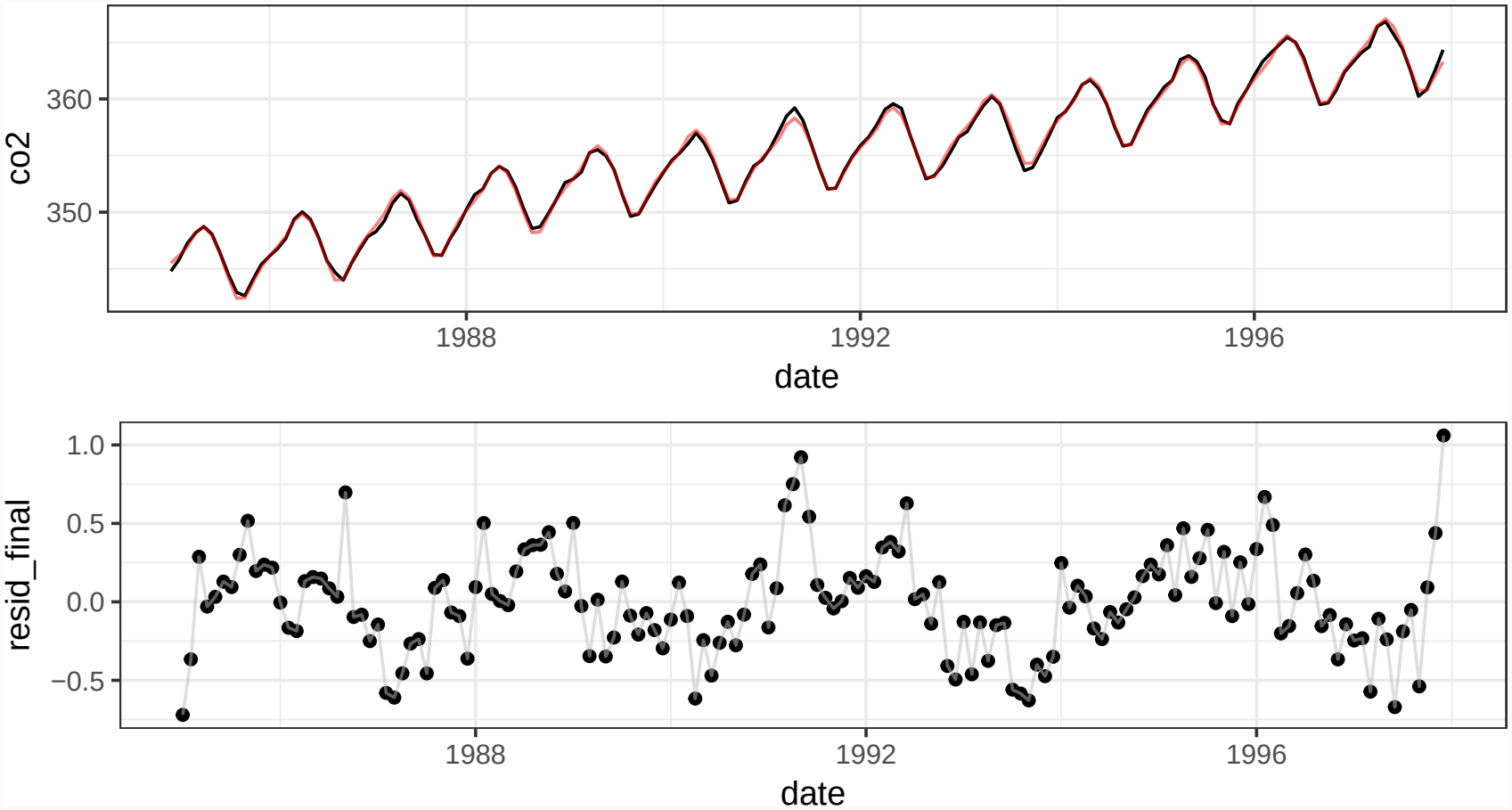
Not fit the data from scratch. fit the data to what I got last time.

final model

Additive. what we do with time series data
~ get rid of trend in residuals

good fit (sort of---)

Final fit + Residualss



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 $\boldsymbol{\eta} = \mathbf{X}\boldsymbol{\beta}$,
3. and a link function g such that $g(E(\mathbf{Y}|\mathbf{X})) = \boldsymbol{\eta}$.

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).

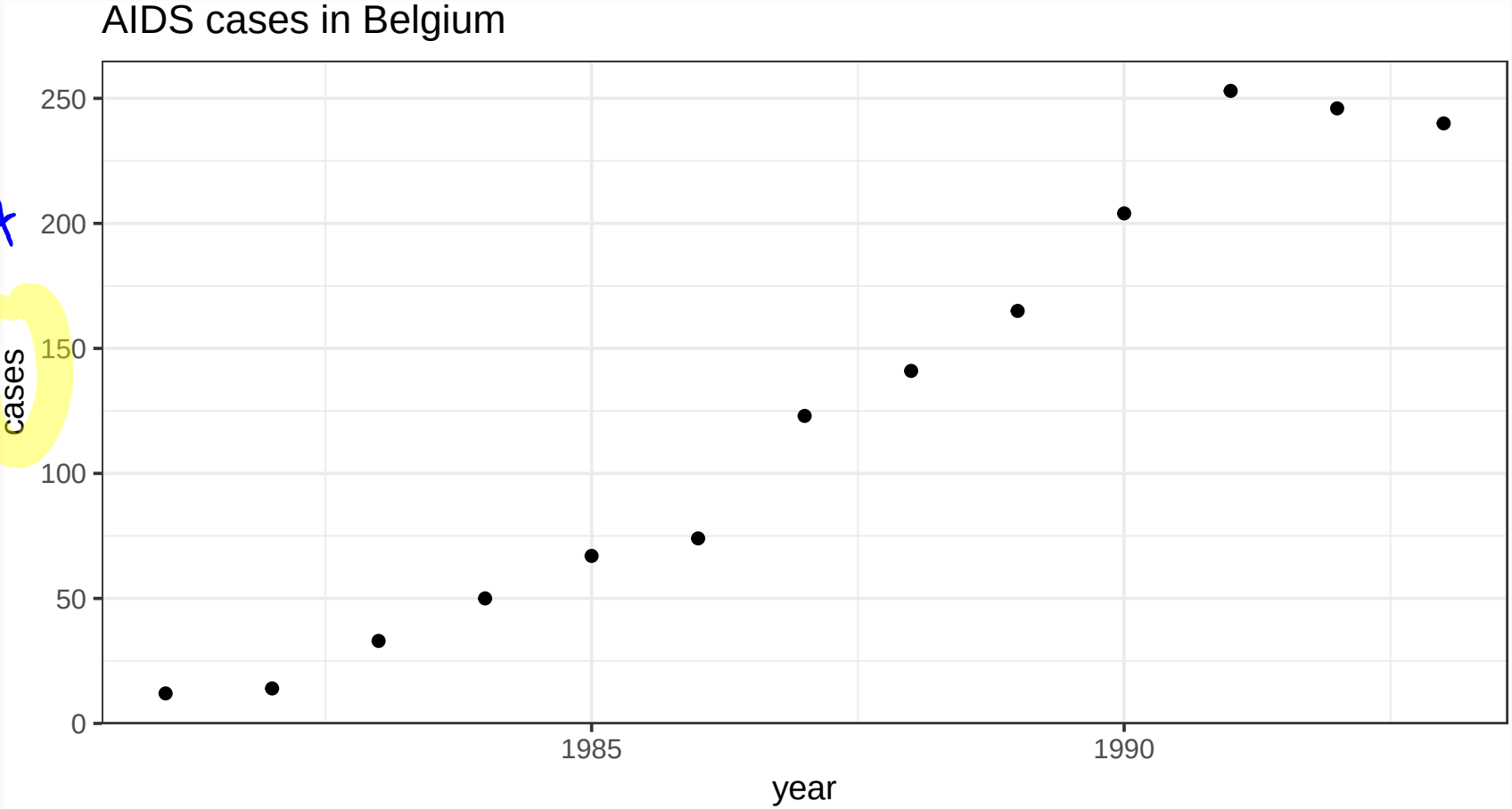
$$Y_i \sim \text{Poisson}(\lambda_i)$$
$$\log E(Y_i|\mathbf{X}_{i\cdot}) = \log \lambda_i = \mathbf{X}_{i\cdot}\boldsymbol{\beta}$$

$\lambda_i = \exp\{X_i\beta\}$.

$\in [0, \infty]$

Example - AIDS in Belgium

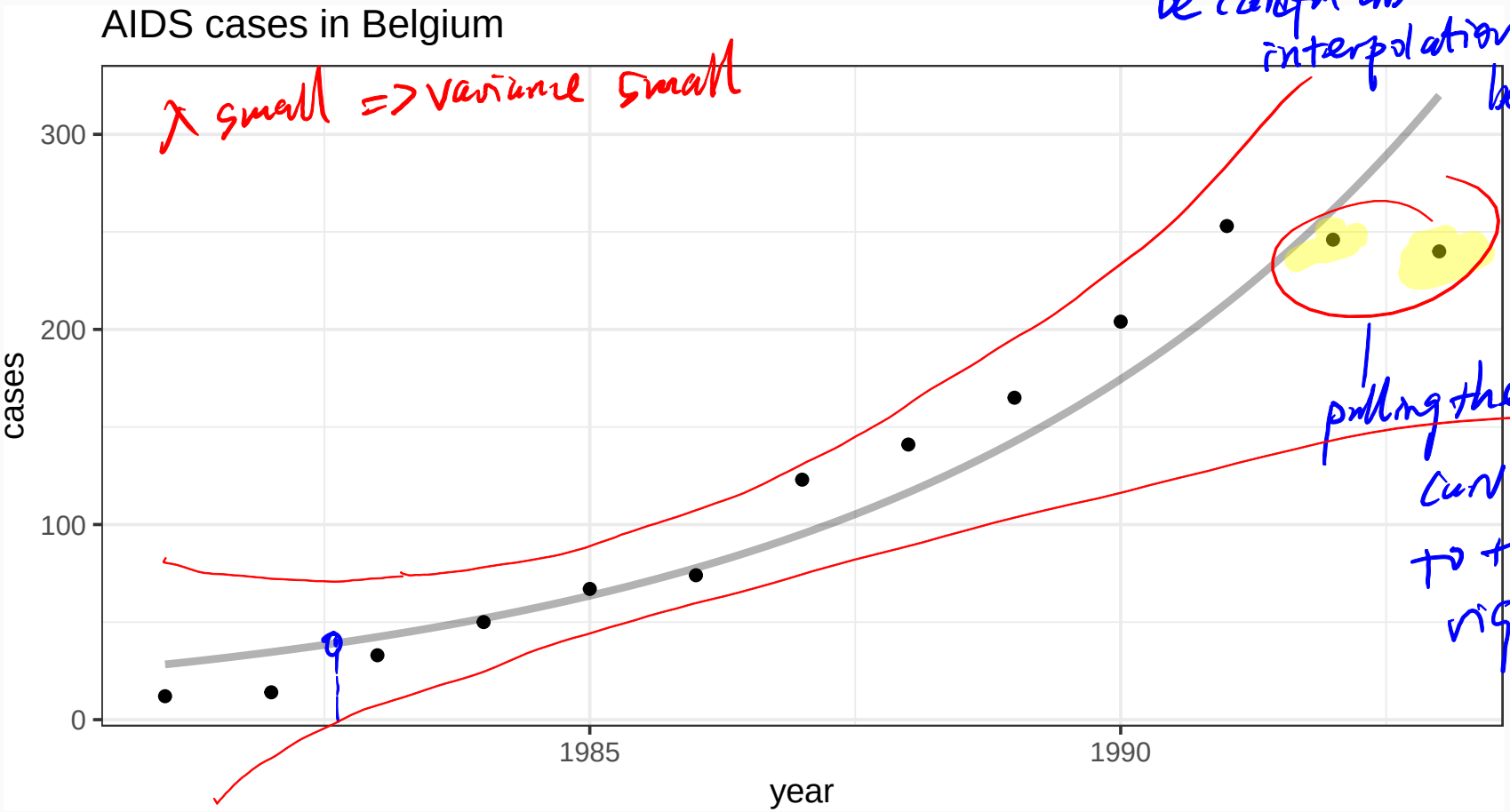
These data represent the total number of new AIDS cases reported in Belgium during the early stages of the epidemic.



Count

Frequentist glm fit

```
g = glm(cases~year, data=aids, family=poisson)
pred = data_frame(year=seq(1981,1993,by=0.1)) %>%
  mutate(cases = predict(g, newdata=., type = "response"))
```



Residuals?

The naive approach is to use standard residuals,

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

Residuals?

The naive approach is to use standard residuals,

What's the problem

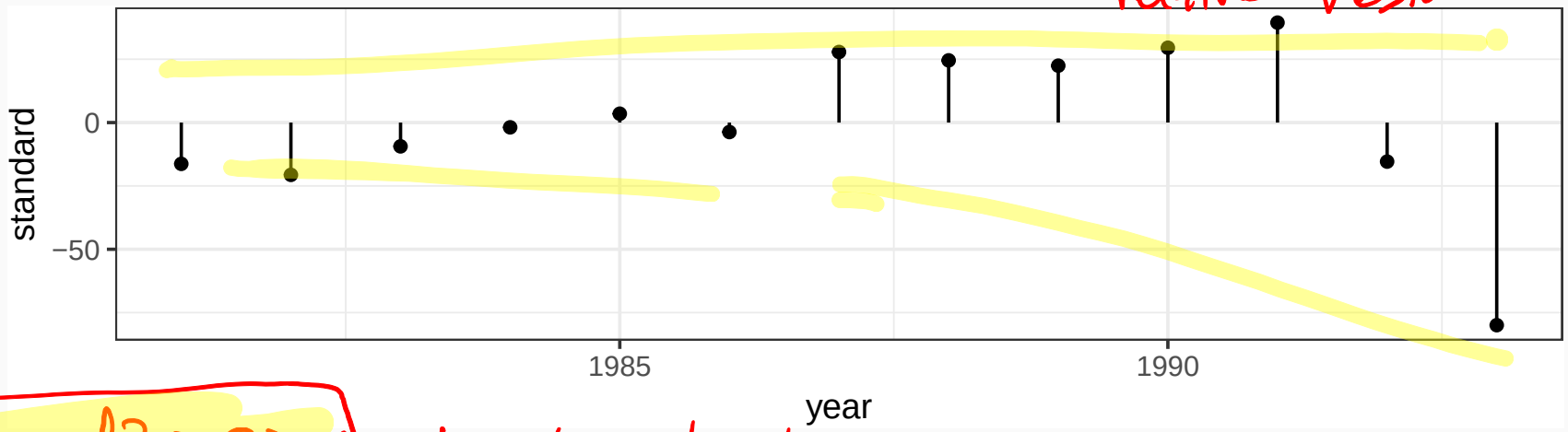
$$r_i = Y_i - E(Y_i|X) = Y_i - \hat{\lambda}_i$$

Key

Variance depends on λ : Var = E(·).

```
aids = aids %>%
  mutate(pred = predict(g, newdata=., type = "response")) %>%
  mutate(standard = cases - pred)

ggplot(aids, aes(x=year, y=standard)) +
  geom_point() + geom_segment(aes(xend=year, yend=0))
```

Miss leading plot of relative residual.



over-dispersion

Variation too large.

Accounting for variability

Pearson residuals:

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

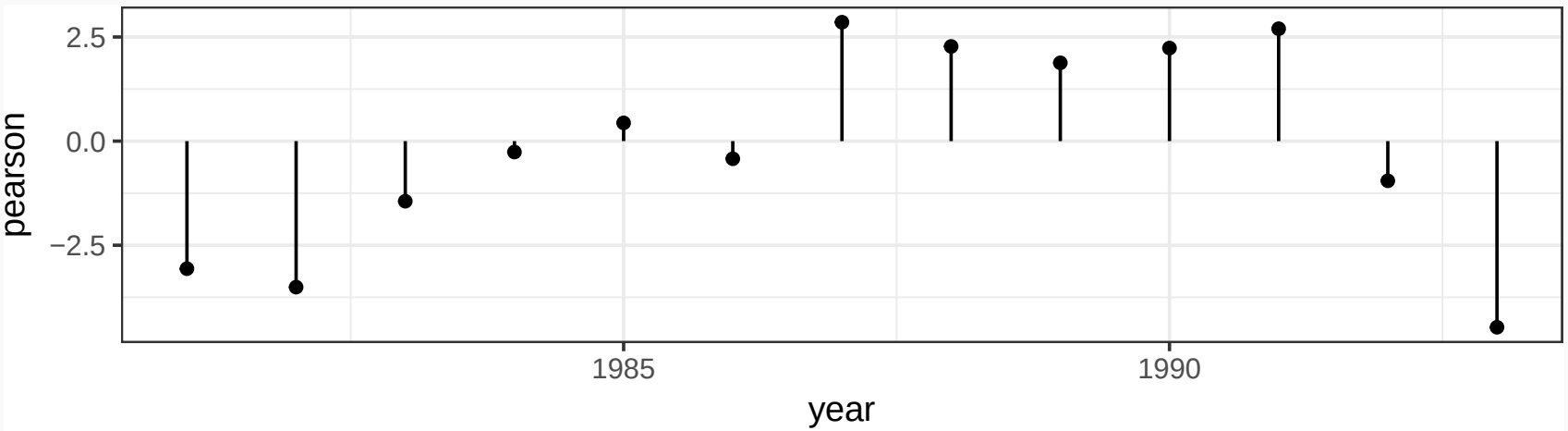
Question: Is there a generic approach of diagnose?

Accounting for variability

Pearson residuals:

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

```
aids = aids %>%
  mutate(pearson = (cases - pred)/sqrt(pred))

ggplot(aids, aes(x=year, y=pearson)) +
  geom_point() + geom_segment(aes(xend=year, yend=0))
```



Deviance

Deviance is a way of measuring the difference between your glm's fit and the fit of a perfect model (where $E(\hat{Y}_i|X) = Y_i$).

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

$$\begin{aligned} D &= 2\log(\mathcal{L}(\theta_{best}|Y)/\mathcal{L}(\hat{\theta}|Y)) \\ &= 2(l(\theta_{best}|Y) - l(\hat{\theta}|Y)) \end{aligned}$$

$= -2(l(\hat{\theta}|Y) - l(\theta_{best}|Y))$

from the saturated model.

Derivation - Normal

$$\ell = -\frac{1}{2}\log 2\pi\sigma^2 - \frac{1}{2}\frac{(y_i-\mu)^2}{\sigma^2}$$

Best: $E(y_i|x) = y_i = \mu$

model: $E(y_i|x_i) = \hat{\mu} = X\hat{\beta}$

$$\ell(\theta_{best}|y_i) - \ell(\hat{\theta}|y_i)$$

$$= -\frac{1}{2}\log 2\pi\sigma^2 - \frac{1}{2}\frac{(y_i-y_i)^2}{\sigma^2}^{0} - \left(-\frac{1}{2}\log 2\pi\sigma^2 - \frac{1}{2}\frac{(y_i-\hat{\mu})^2}{\sigma^2}\right)$$

$$= \frac{1}{2}\frac{(y_i-\hat{\mu})^2}{\sigma^2}$$

$$D = \sum_{i=1}^{n}\frac{(y_i-\hat{\mu})^2}{\sigma^2} = r_{DS}^2$$ standard residual

Derivation - Poisson

log-likelihood

$$l = y_i \log\lambda - \lambda - \log y_i!$$

Best $E(y_i|x) = y_i = \lambda$.

model : $E(y_i|x) = \hat{\lambda} = e^{x\hat{\beta}}$

$$l(\theta_{best}|y_i) - l(\hat{\theta}|y_i)$$

$$= y_i \log y_i - y_i - \log y_i! - (y_i \log\hat{\lambda} - \hat{\lambda} - \log y_i!)$$

$$= y_i \log\frac{y_i}{\hat{\lambda}} - (y_i - \hat{\lambda})$$

something weird... not same as stat. we know

$$D = 2\sum_{i=1}^{n}\left[y_i \log\frac{y_i}{\hat{\lambda}} - (y_i - \hat{\lambda})\right] = 2\sum_{i=1}^{n} d_i^2$$

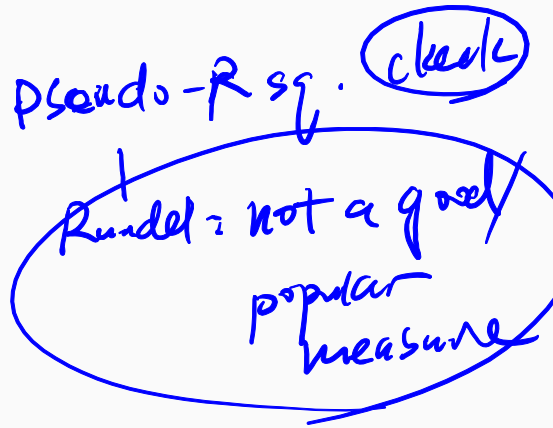
$$d_i = \text{sign}(y_i - \hat{\lambda})\sqrt{2\left(y_i \log\frac{y_i}{\hat{\lambda}} - (y_i - \hat{\lambda})\right)}$$

generally Applicable

HW: derive deviance for Bernoulli

glm output

```
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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 872.206  on 12  degrees of freedom
## Residual deviance:  80.686  on 11  degrees of freedom
## AIC: 166.37
##
## Number of Fisher Scoring iterations: 4
```



Deviance residuals

We can therefore think of deviance as $D = \sum_{i=1}^{n} d_i^2$ where d_i is a generalized residual. So in the Poisson case we can define,

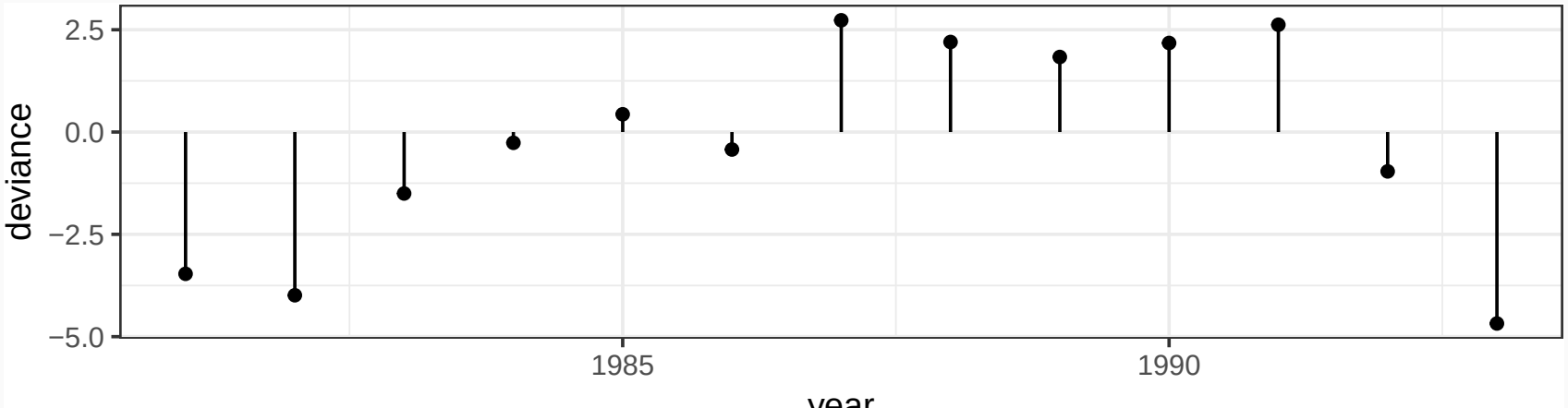
$$d_i = \text{sign}(y_i - \lambda_i)\sqrt{2(y_i \log(y_i/\hat{\lambda}_i) - (y_i - \hat{\lambda}_i))}$$

Deviance residuals

We can therefore think of deviance as $D = \sum_{i=1}^{n} d_i^2$ where d_i is a generalized residual. So in the Poisson case we can define,

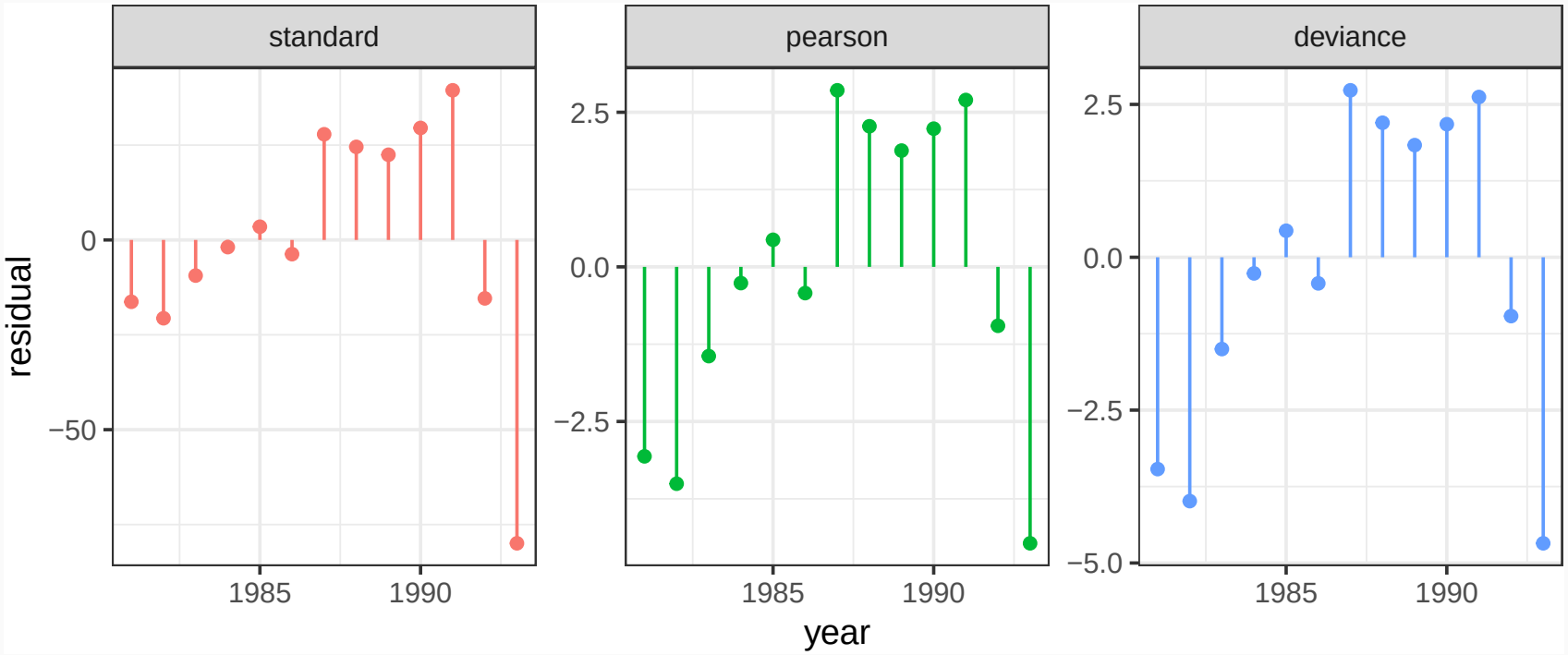
$$d_i = \text{sign}(y_i - \lambda_i)\sqrt{2(y_i \log(y_i/\hat{\lambda}_i) - (y_i - \hat{\lambda}_i))}$$

```
dev_resid = function(obs,pred)
  sign(obs-pred) * sqrt(2*(obs*log(obs/pred)-(obs-pred)))

aids = aids %>%
  mutate(deviance = dev_resid(cases, pred))

ggplot(aids, aes(x=year, y=deviance)) +
  geom_point() + geom_segment(aes(xend=year, yend=0))
```



Comparing Residuals

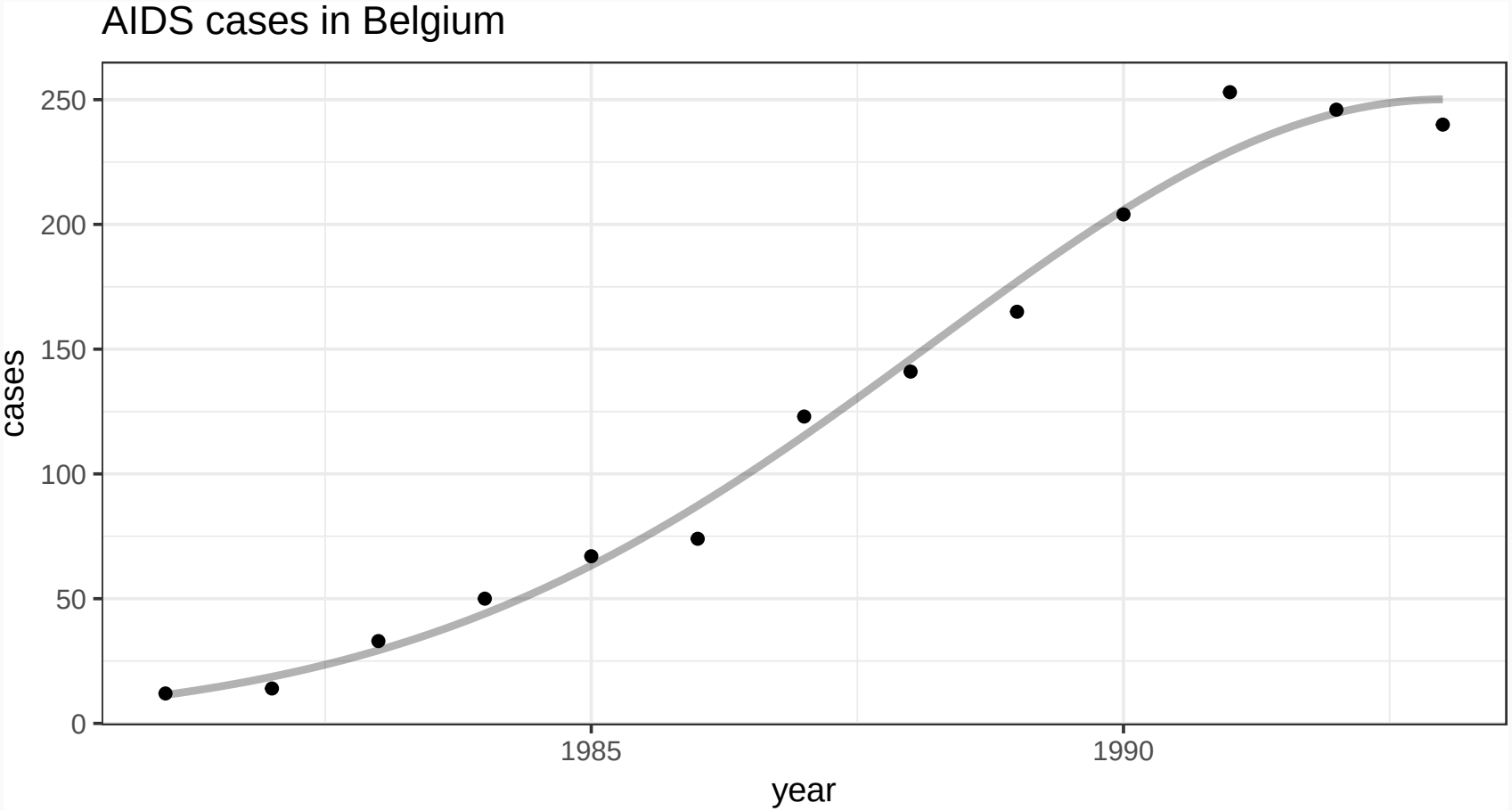
show same pattern



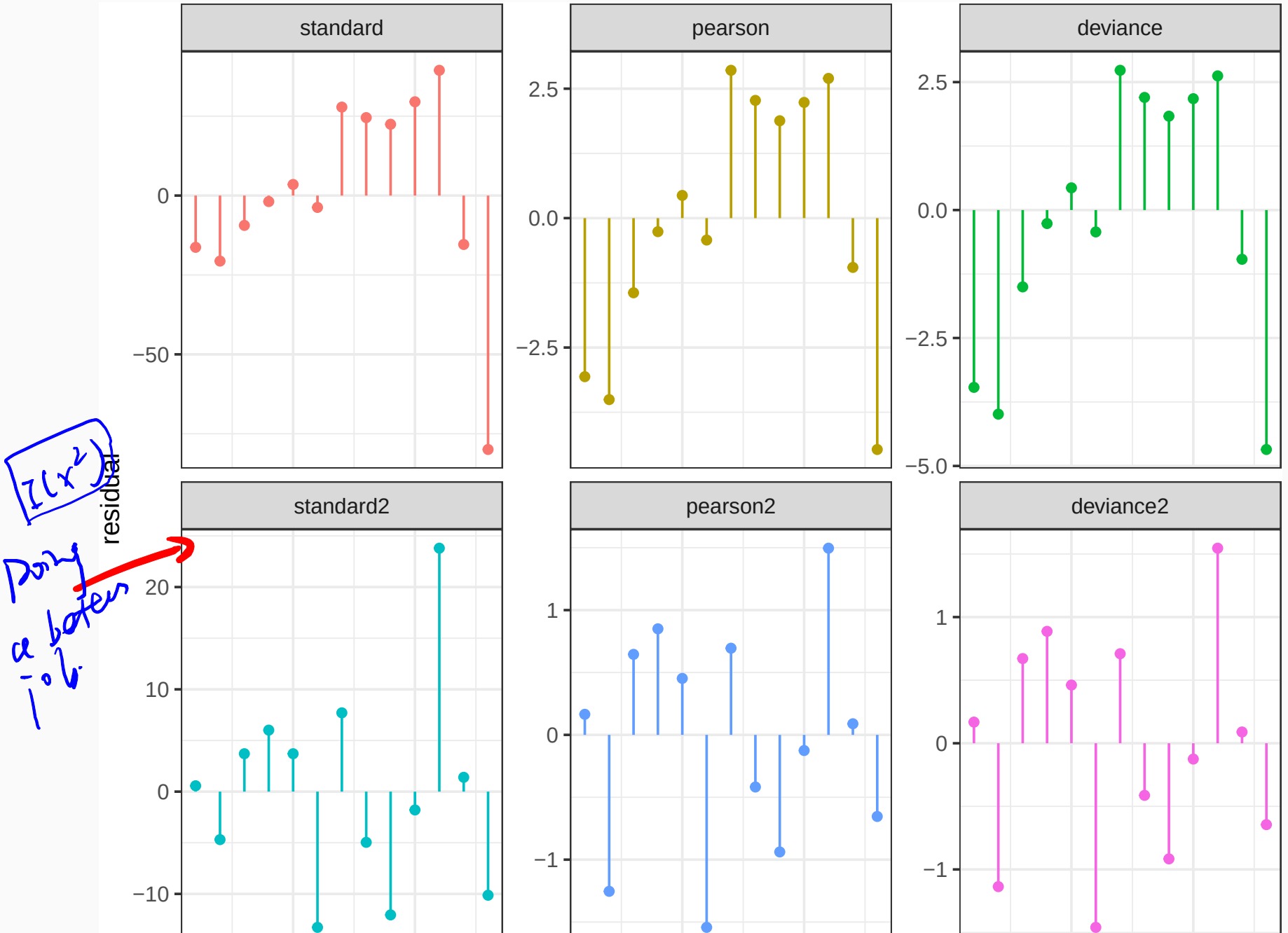
Updating the model

Quadratic fit

```
g2 = glm(cases~year+I(year^2), data=aids, family=poisson)
pred2 = data_frame(year=seq(1981,1993,by=0.1)) %>%
  mutate(cases = predict(g2, newdata=., type = "response"))
```



Quadratic fit - residuals



Bayesian Model

Bayesian Poisson Regression Model

```
poisson_model =
"model{
  # Likelihood
  for (i in 1:length(Y)) {
    Y[i] ~ dpois(lambda[i])
    log(lambda[i]) <- beta[1] + beta[2]*X[i]

    # In-sample prediction
    Y_hat[i] ~ dpois(lambda[i])
  }

  # Prior for beta
  for(j in 1:2){
    beta[j] ~ dnorm(0,1/100)
  }
}"
```

Poisson

no conjugacy.

⇒ slower ⇒ M-H algorithm

will get a saxon access!

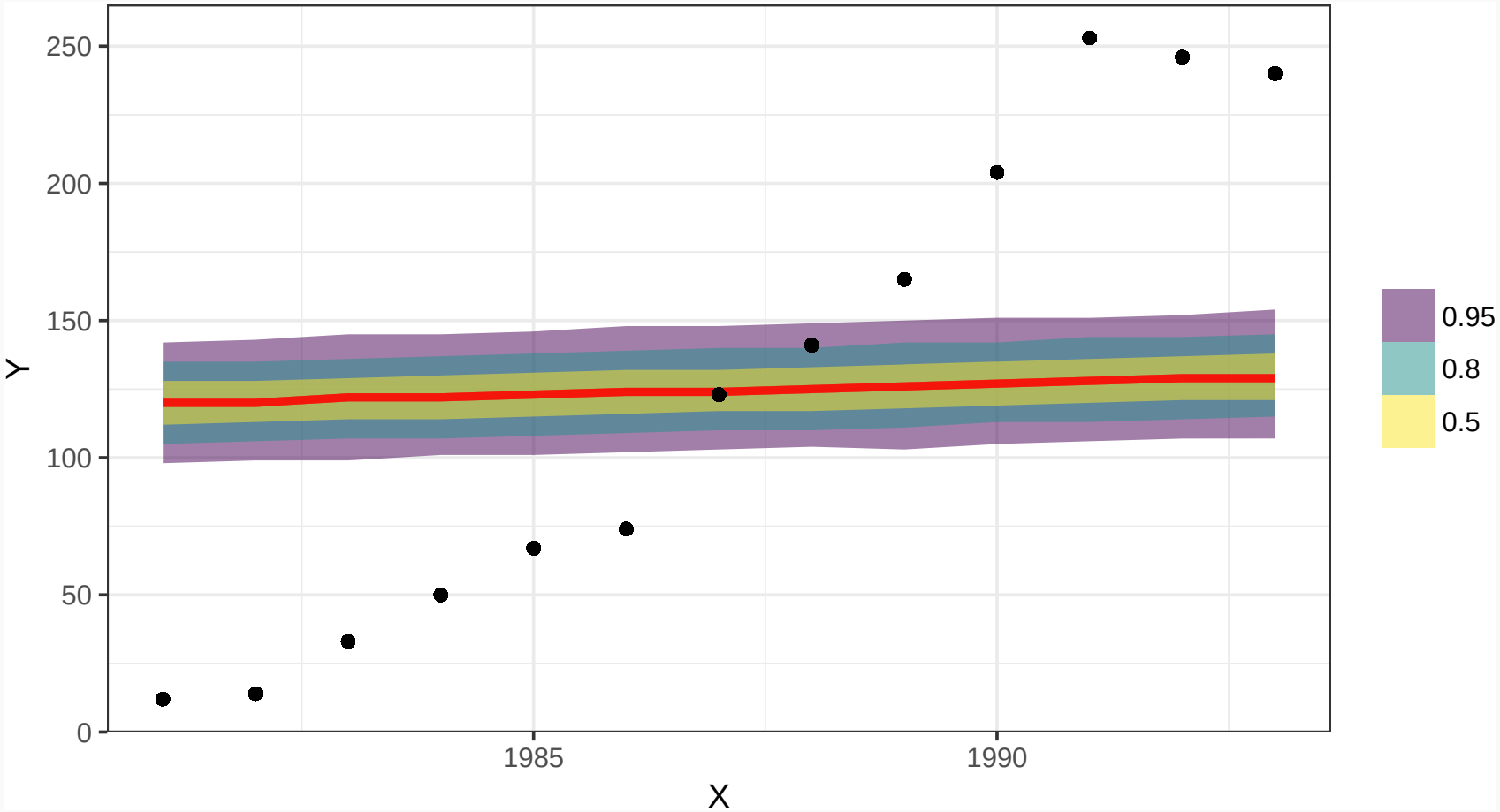
Fit Model

```
n_burn=1000; n_iter=5000

m = rjags::jags.model(
  textConnection(poisson_model), quiet = TRUE,
  data = list(Y=aids$cases, X=aids$year)
)

update(m, n.iter=1000, progress.bar="none")

samp = rjags::coda.samples(
  m, variable.names=c("beta","lambda","Y_hat","Y","X"),
  n.iter=5000, progress.bar="none"
)
```

Model Fit?

```
tidybayes::spread_samples(samp, Y_hat[i], X[i],Y[i]) %>%
  ungroup() %>%
  ggplot(aes(x=X,y=Y)) +
    tidybayes::stat_lineribbon(aes(y=Y_hat), alpha=0.5) +
    geom_point()
```

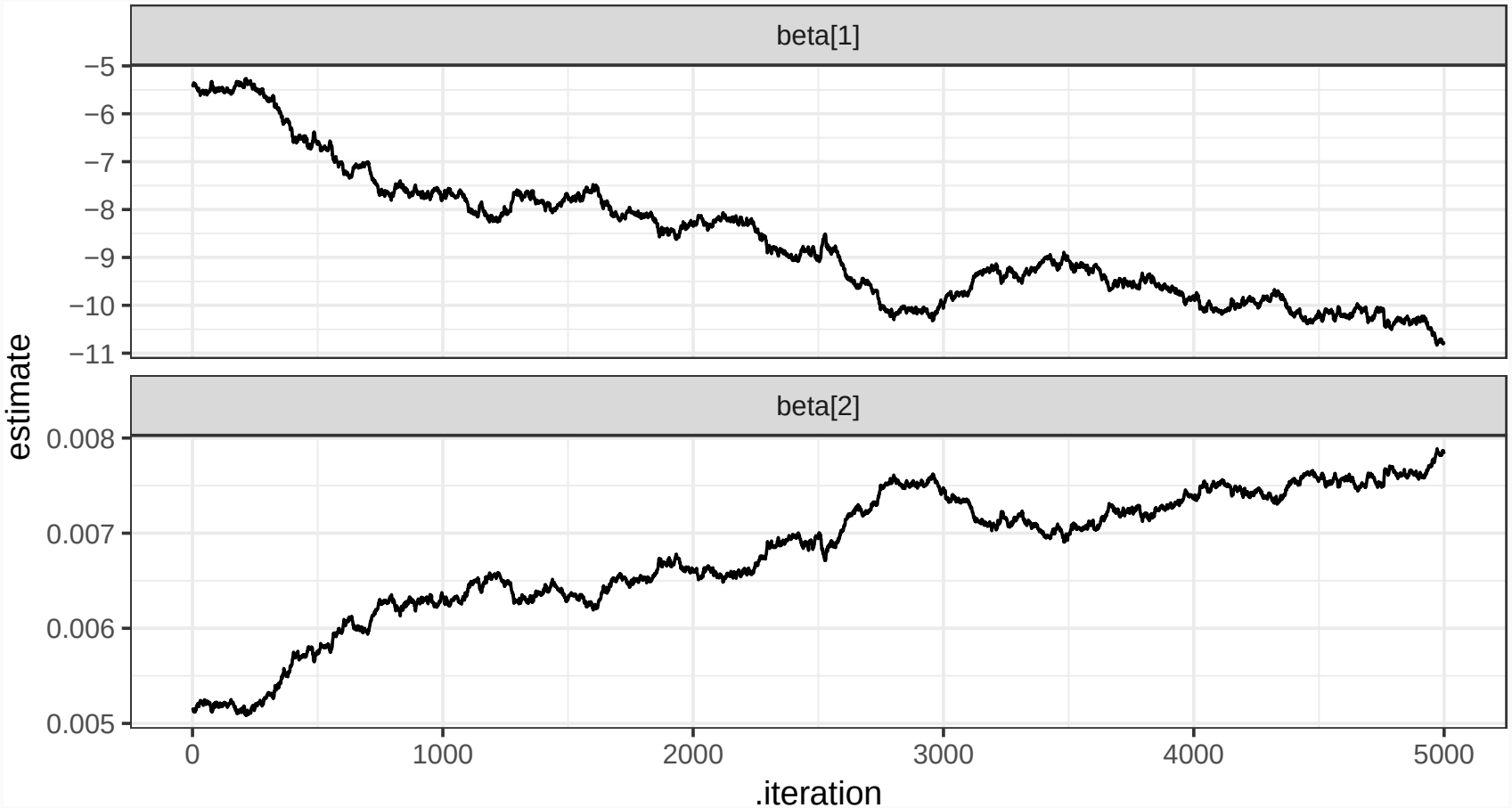
Something wrong!



MCMC Diagnostics

```
tidybayes::gather_samples(samp, beta[i]) %>%
  mutate(param = paste0(term,"[",i,"]")) %>%
  ggplot(aes(x=.iteration, y=estimate)) +
    geom_line() +
    facet_wrap(~param, ncol=1, scale="free_y")
```

No convergence !



Now what?

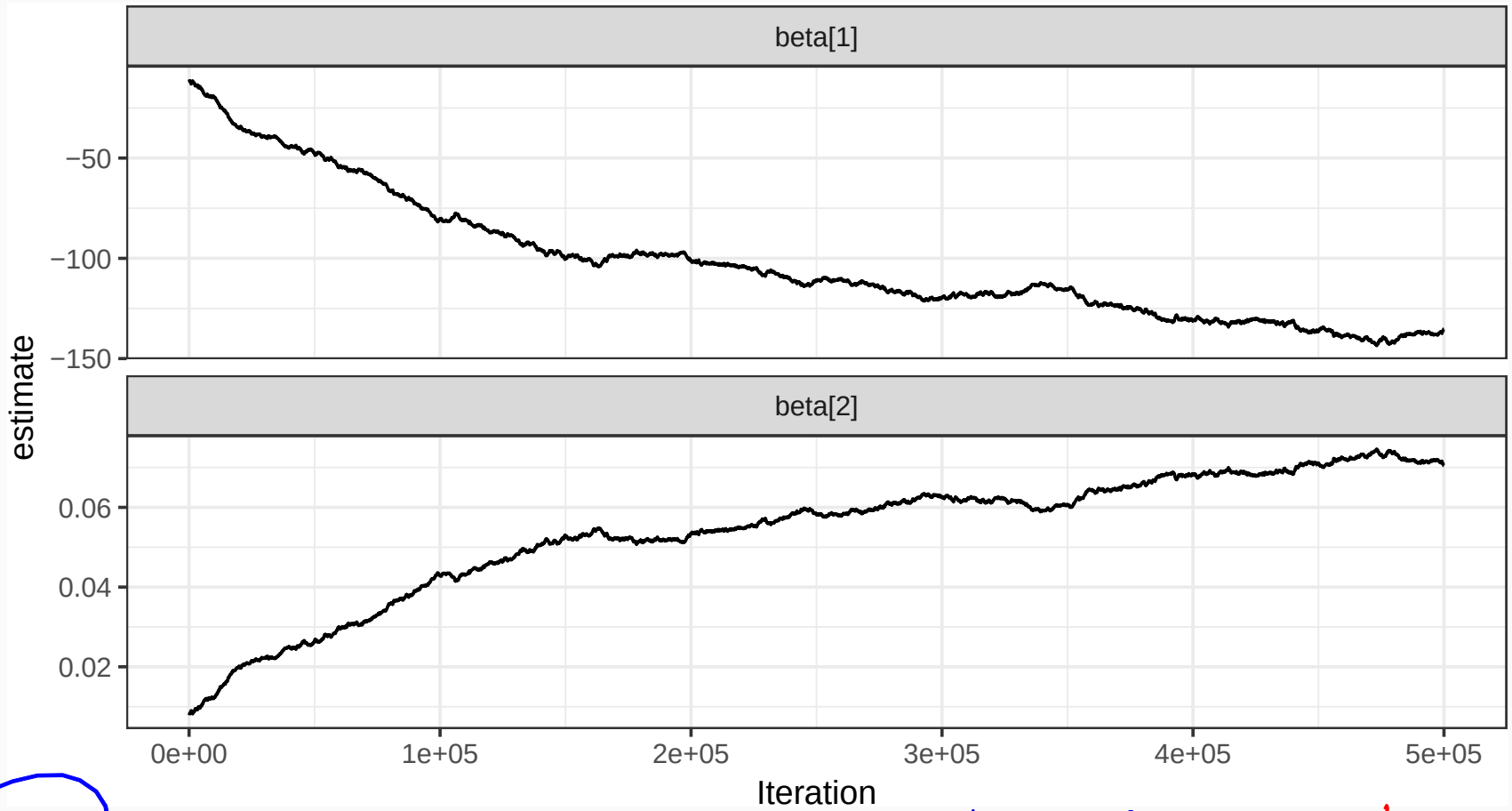
Maybe more iterations will fix everything ...

LoL

Now what?

Maybe more iterations will fix everything ...

not good.



problem

prior of β.

set to $\tau = \frac{1}{100}$

check the frequentist output.

solution: use a diffuse prior.

make prior more diffuse?

? standardize input

What went wrong?

rescale scale & center

if scaled, won't be weird behavior with not-so-diffused prior.

What went wrong?

```
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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 872.206  on 12  degrees of freedom
## Residual deviance:  80.686  on 11  degrees of freedom
## AIC: 166.37
##
## Number of Fisher Scoring iterations: 4
```

A simple fix

```
summary(glm(cases~I(year-1981), data=aids, family=poisson))
##
## Call:
## glm(formula = cases ~ I(year - 1981), 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)    3.342711   0.070920   47.13   <2e-16 ***
## I(year - 1981) 0.202121   0.007771   26.01   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 872.206  on 12  degrees of freedom
## Residual deviance:  80.686  on 11  degrees of freedom
## AIC: 166.37
##
## Number of Fisher Scoring iterations: 4
```

Revising the jags model

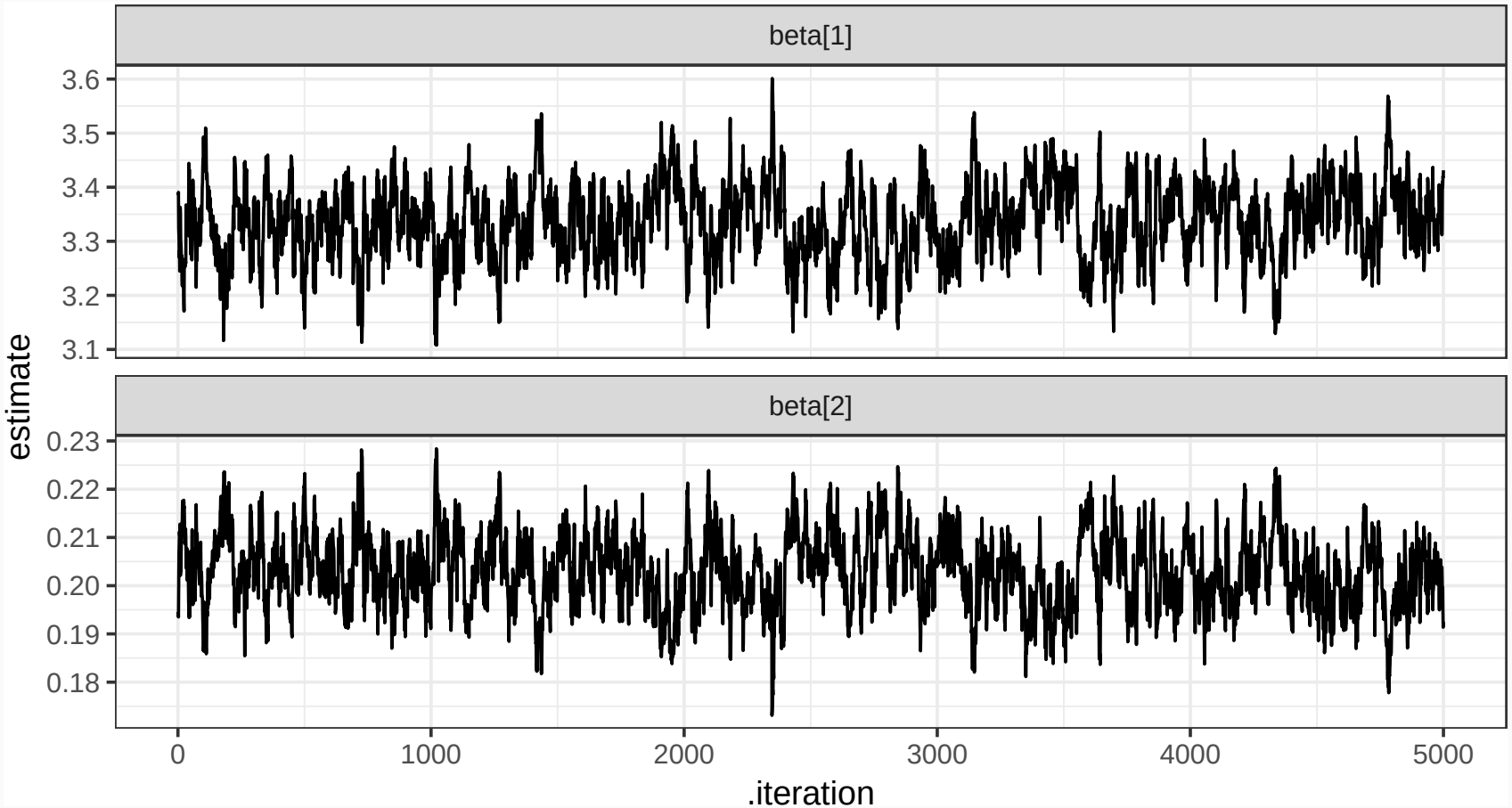
```
poisson_model2 =
"model{
  # Likelihood
  for (i in 1:length(Y)) {
    Y[i] ~ dpois(lambda[i])
    log(lambda[i]) <- beta[1] + beta[2]*(X[i] - 1981)

    Y_hat[i] ~ dpois(lambda[i])
  }

  # Prior for beta
  for (j in 1:2) {
    beta[j] ~ dnorm(0,1/100)
  }
}"
```

not enough variance

MCMC Diagnostics

```
tidybayes::gather_samples(samp2, beta[i]) %>%
  mutate(param = paste0(term,"[",i,"]")) %>%
  ggplot(aes(x=.iteration, y=estimate)) +
    geom_line() +
    facet_wrap(~param, ncol=1, scale="free_y")
```

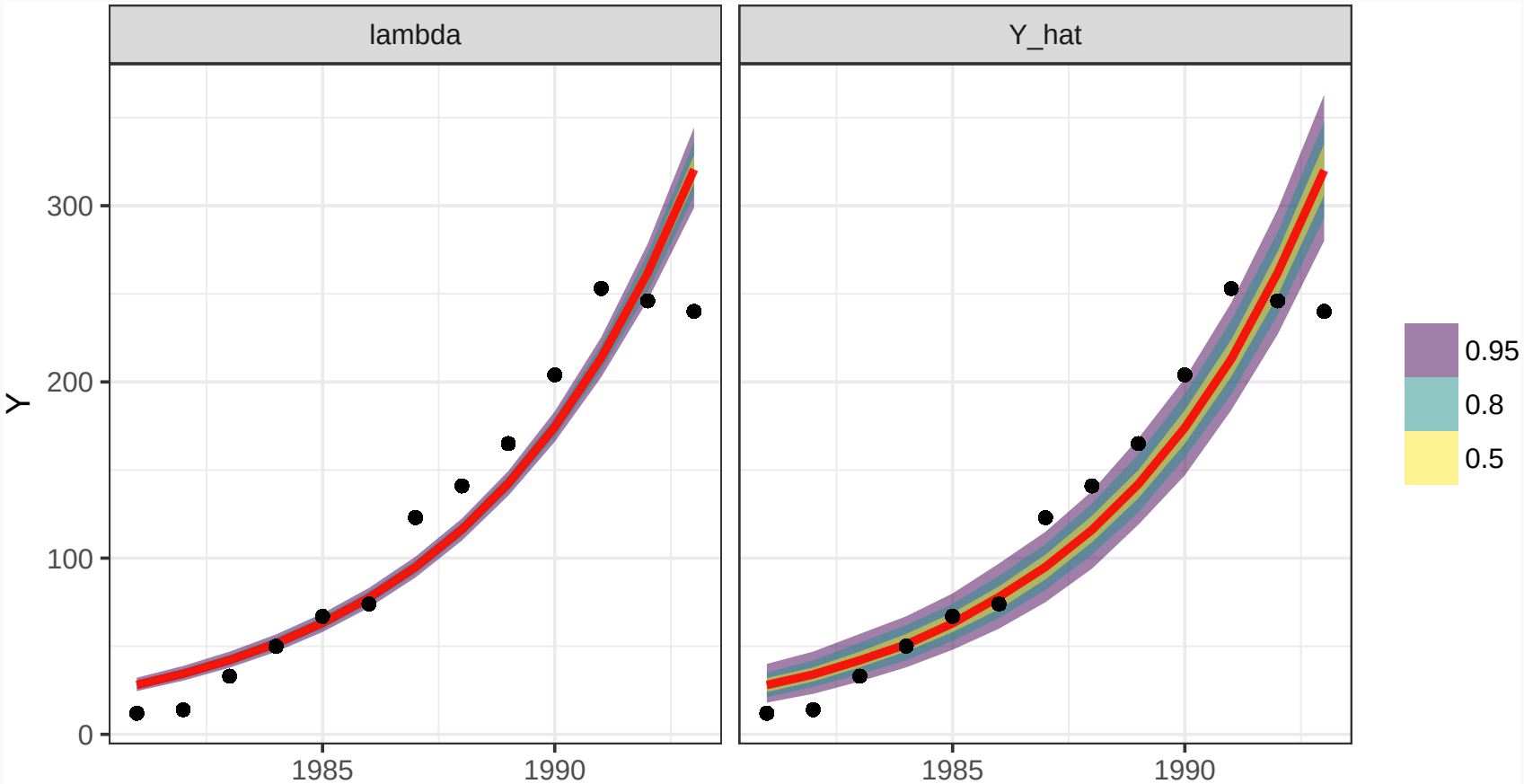
good now



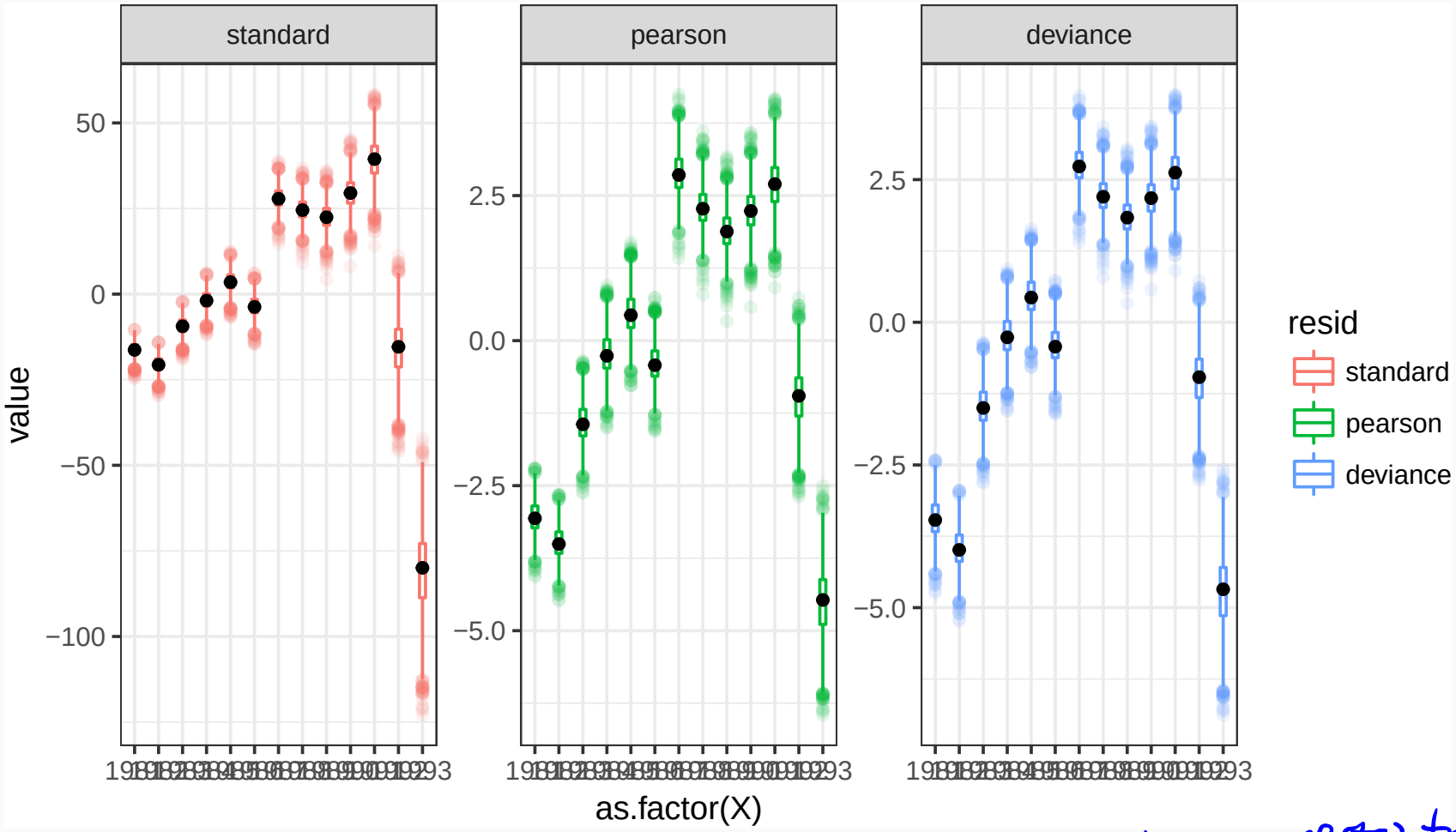
Model Fit

```
tidybayes::spread_samples(samp2, Y_hat[i], lambda[i], X[i], Y[i]) %>%
  ungroup() %>%
  tidyr::gather(param, value, Y_hat, lambda) %>%
  ggplot(aes(x=X,y=Y)) +
    tidybayes::stat_lineribbon(aes(y=value), alpha=0.5) +
    geom_point() +
    facet_wrap(~param)
```

not good:
Quasi-poiss
negative-binom

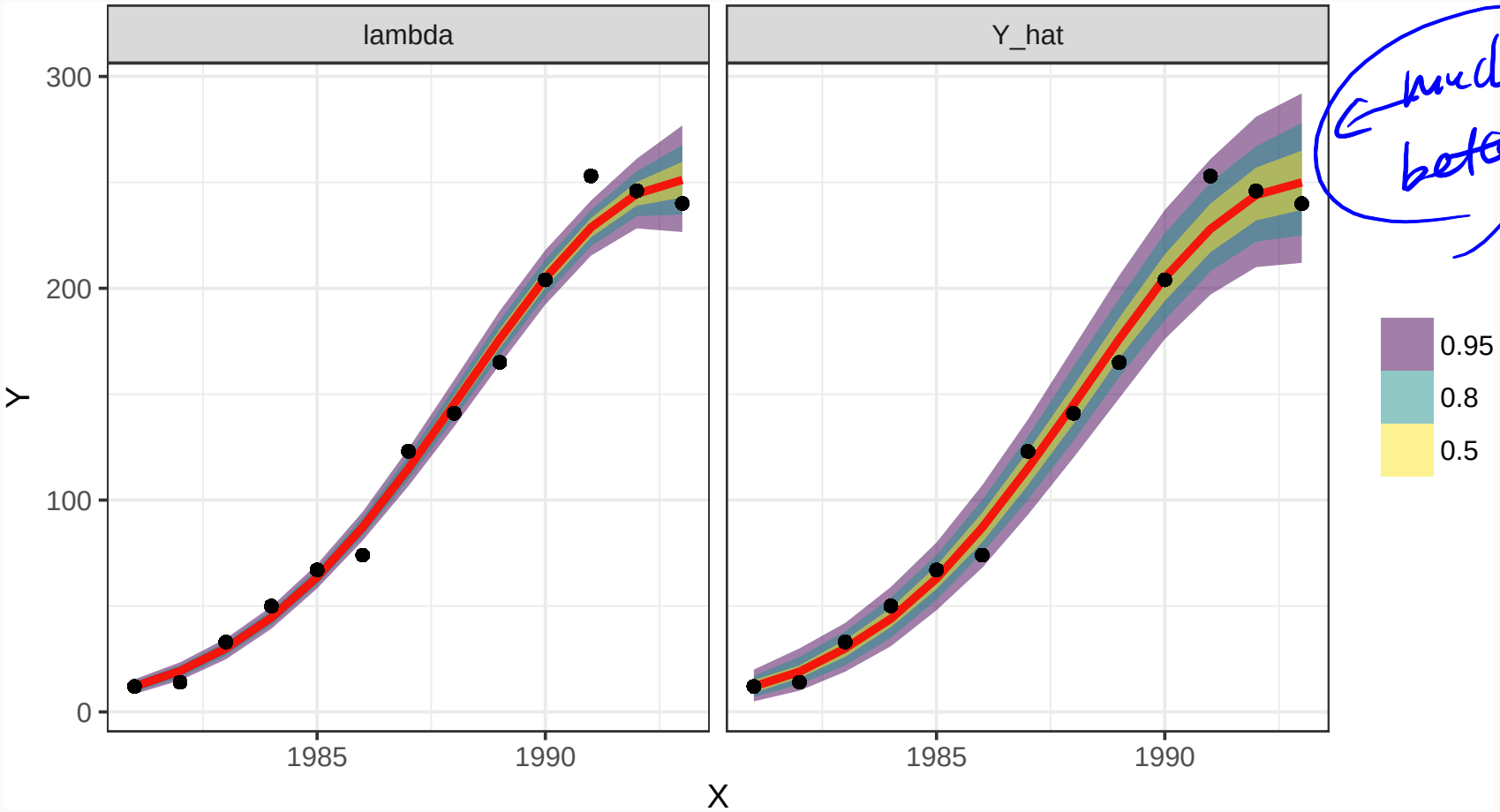


Residual Plots



Bayesian, Freq. Same answer. But Bayesian better capture uncertainty

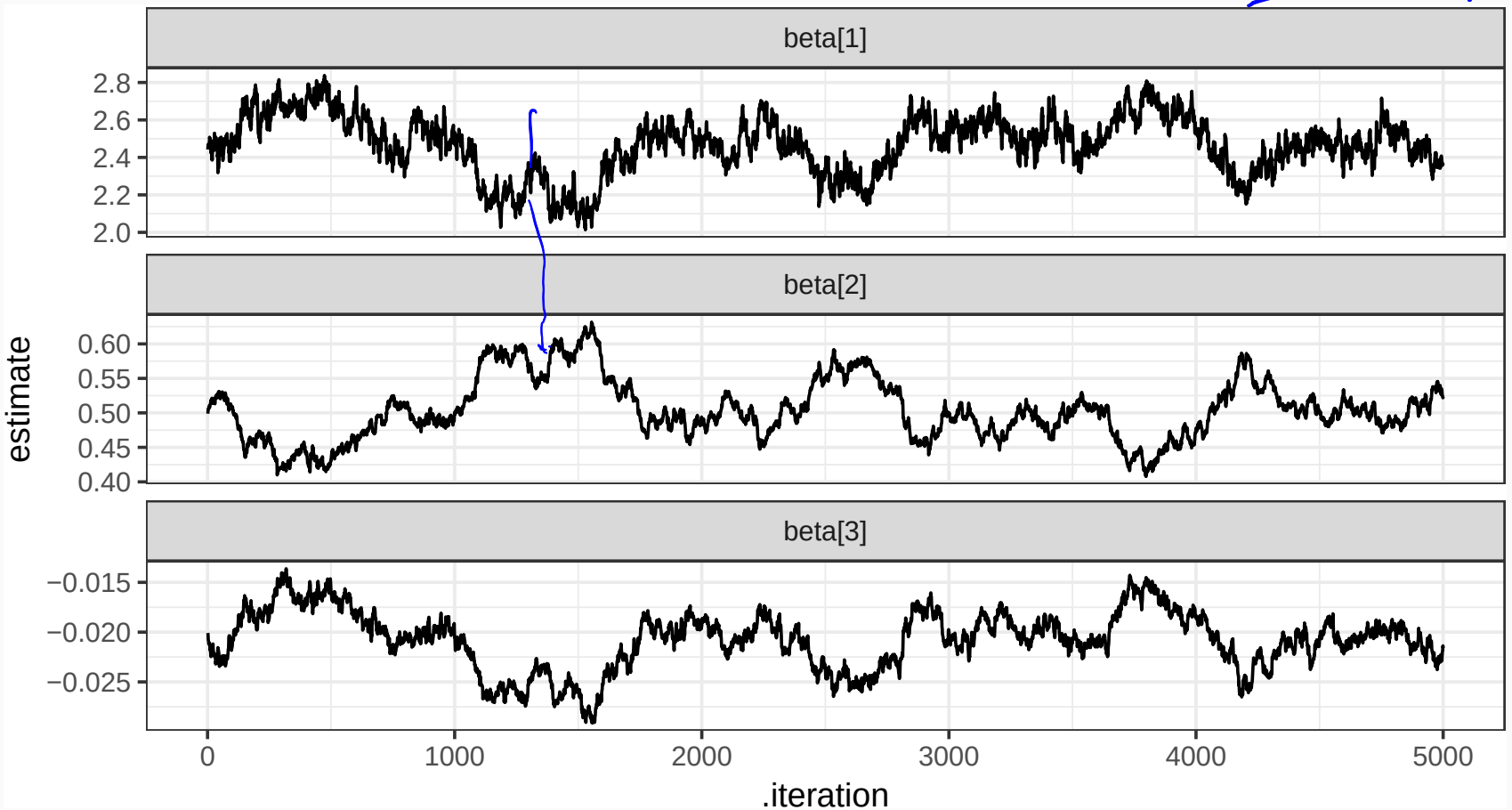
Quadratic Fit



MCMC Diagnostics

```
tidybayes::gather_samples(samp3, beta[i]) %>%
  mutate(param = paste0(term,"[",i,"]")) %>%
  ggplot(aes(x=.iteration, y=estimate)) +
    geom_line() +
    facet_wrap(~param, ncol=1, scale="free_y")
```

chains are correlated! ⇒ run longer



Residual Plots