Lecture 3

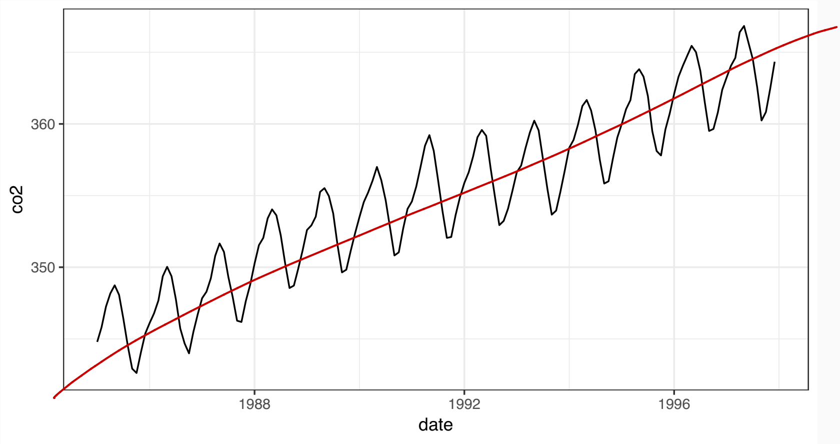
Residual Analysis + Generalized Linear Models

Colin Rundel

9/06/2018

Residual Analysis

Atmospheric CO_2 (ppm) from Mauna Loa



Where to start?

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

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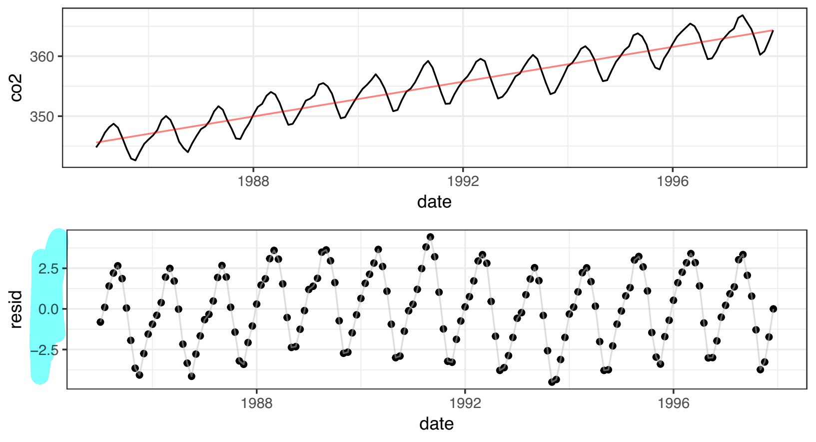

and then?

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

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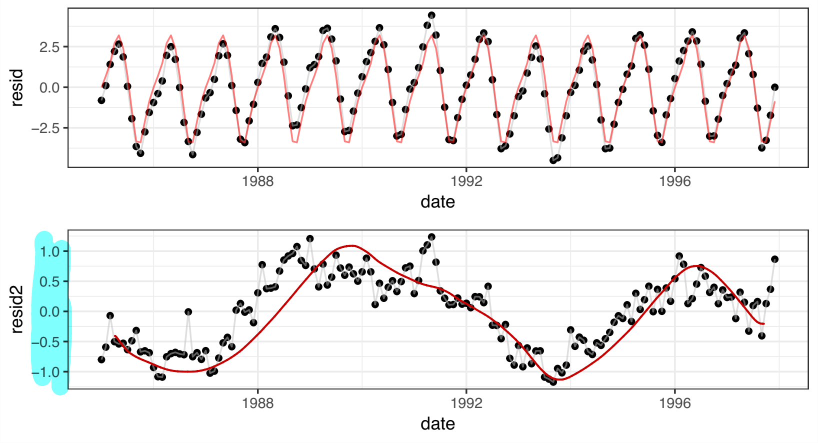

and then and then?

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

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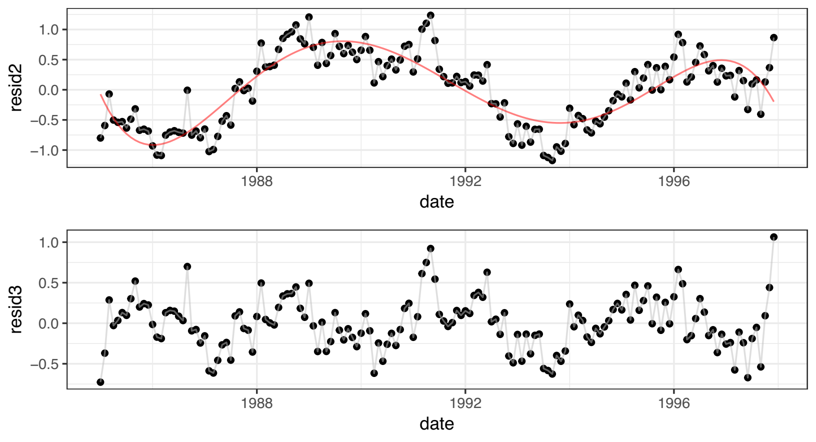
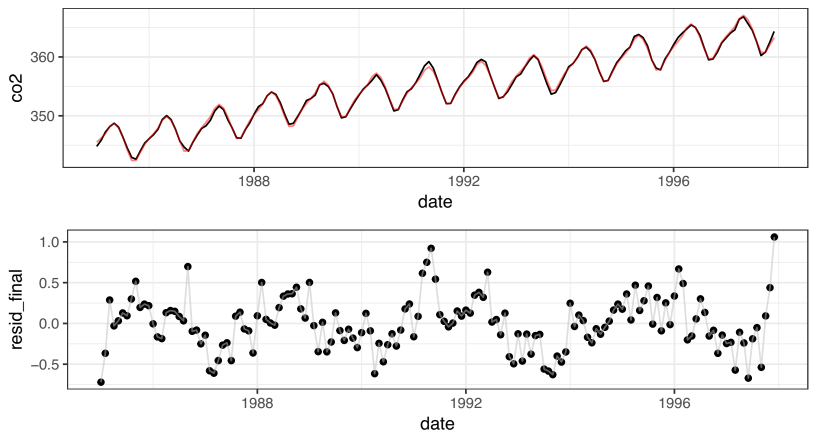


Putting it all together ...

```
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
```

Final fit + Residualss



Generalized Linear Models

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

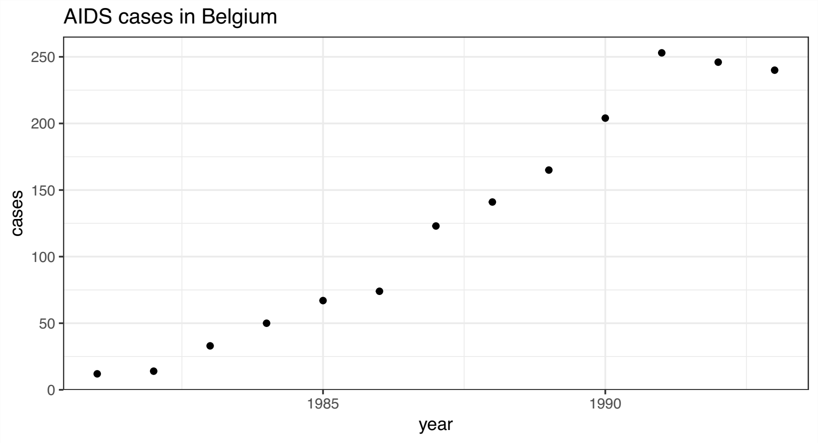
Poisson Regression

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).

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

Example - AIDS in Belgium

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



Frequentist glm fit

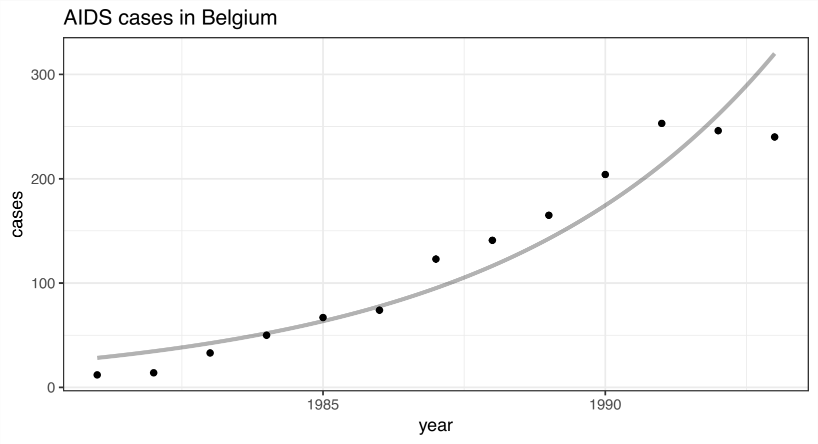
```
g = glm(cases~year, data=aids, family=poisson)

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
```

Model Fit

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

λ_i



Residuals?

The naive approach is to use standard residuals,

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

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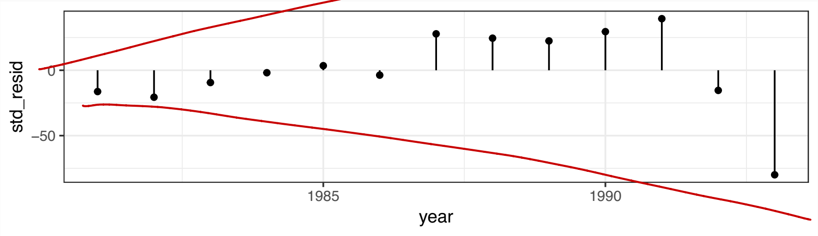
$Var(Y_i|X) = \hat{\lambda}_i$

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

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

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



Pearson residuals:

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

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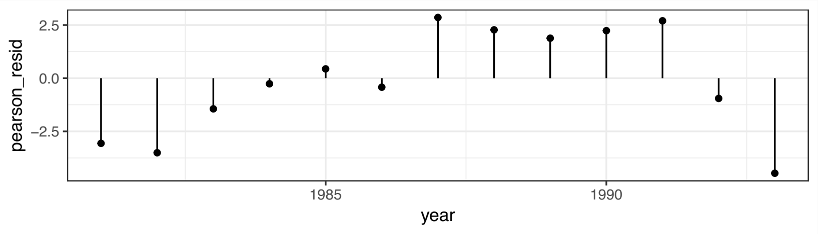
```
aids_glm = aids_glm %>%
  mutate(pearson_resid = (cases - pred)/sqrt(pred))

ggplot(aids_glm, aes(x=year, y=pearson_resid)) +
  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,

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

Derivation - Normal

$$\mathcal{L}(\mu|y) = \prod \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\frac{(y-\mu)^2}{\sigma^2}} \qquad \ell(\mu|y) = \sum_{i=1}^{n} -\frac{1}{2}\log 2\pi\sigma^2 - \frac{1}{2}\frac{(y_i-\mu)^2}{\sigma^2}$$

$$D = 2\left(\ell(\overset{y_i}{\overset{\uparrow}{\mu_{best}}}|y) - \ell(\hat{\mu}|y)\right)$$

$$= 2\left(\sum_{i=1}^{n}\left(-\frac{1}{2}\cancel{2\pi\sigma^2} - \frac{1}{2}\cancel{\frac{(y_i-y_i)^2}{\sigma^2}}\right) - \sum_{i=1}^{n}\left(\cancel{-\frac{1}{2}2\pi\sigma^2} - \frac{1}{2}\frac{(y_i-\hat{\mu})^2}{\sigma^2}\right)\right)$$

$$= \sum_{i=1}^{n}\frac{(y_i-\hat{\mu})^2}{\sigma^2} = \sum d_i^2$$

$$\mathcal{L}(\lambda|y) = \prod_{i=1}^{n} \frac{\lambda^{y_i} e^{-\lambda}}{y_i!} \qquad \ell(\lambda|y) = \sum_{i=1}^{n} y_i \log \lambda - \lambda - \log y_i!$$

$$D = 2\left(\ell(\overset{y_i}{\lambda_{best}} \mid y_i) - \ell(\hat{\lambda} \mid y)\right)$$

$$= 2\left(\sum_{i=1}^{n}\left(y_i \log y_i - y_i - \cancel{\log y_i!}\right) - \sum\left(y_i \log \hat{\lambda}_i - \hat{\lambda}_i - \cancel{\log y_i!}\right)\right)$$

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

$$= \sum_{i=1}^{n}\left(\sqrt{\;\cdots\;}\right)^2$$

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

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. In the Poisson case we have,

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

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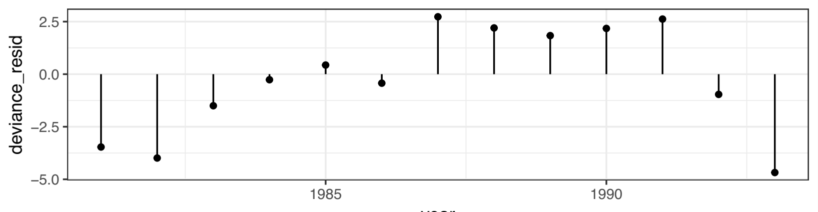
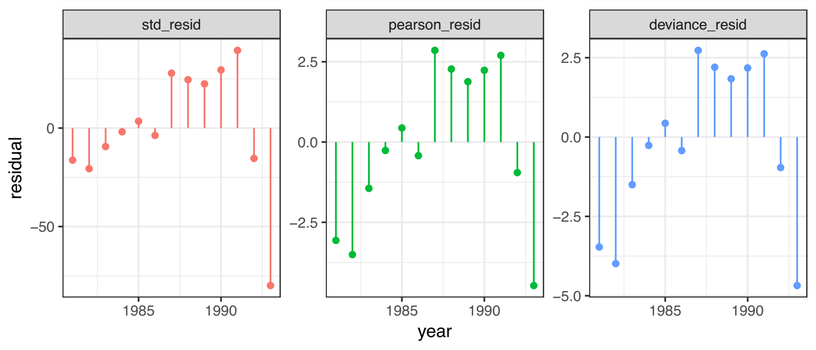
```
dev_resid = function(obs,pred)
  sign(obs-pred) * sqrt(2*(obs*log(obs/pred)-(obs-pred)))

aids_glm = aids_glm %>%
  mutate(deviance_resid = dev_resid(cases, pred))

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



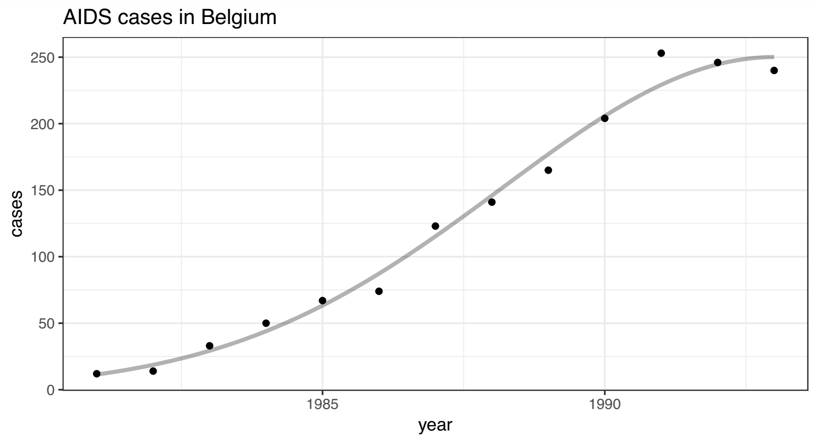
Comparing Residuals



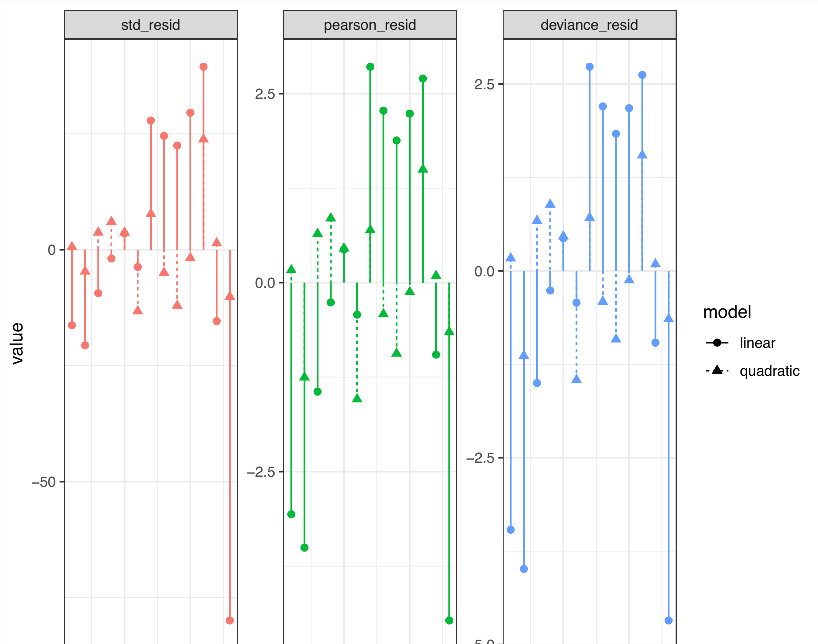
Updating the model

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

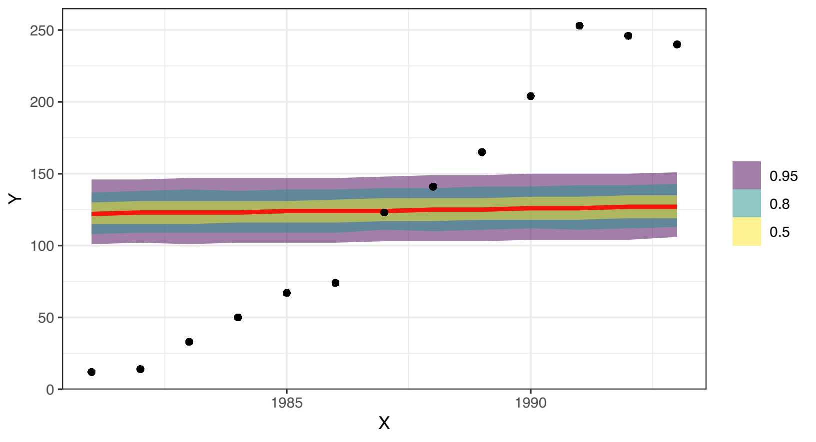
```
poisson_model =
"model{
  # Likelihood
  for (i in 1:length(Y)) {
    Y[i] ~ dpois(lambda[i])
    log(lambda[i]) <- beta[1] + beta[2]*X[i]

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

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

Fit Model

```r
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"
)
```

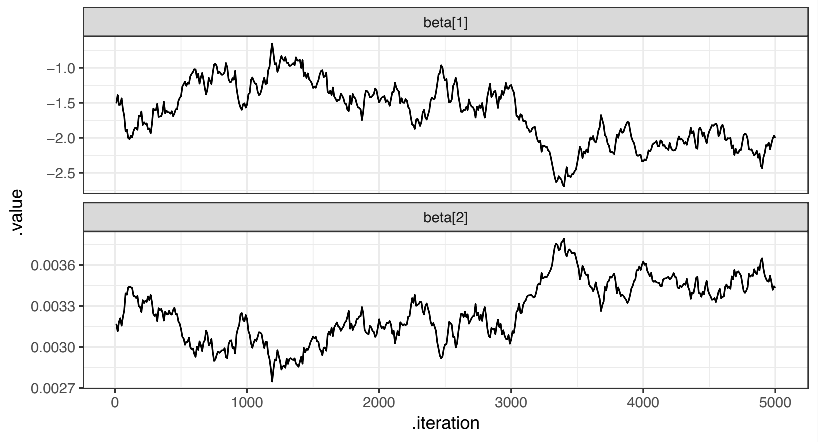
Model Fit?

```
tidybayes::spread_draws(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()
```



MCMC Diagnostics

```
tidybayes::gather_draws(samp, beta[i]) %>%
  mutate(param = paste0(.variable,"[",i,"]")) %>%
  filter(.iteration %% 10 == 0) %>%
  ggplot(aes(x=.iteration, y=.value)) +
    geom_line() +
    facet_wrap(~param, ncol=1, scale="free_y")
```



Now what?

Maybe more iterations will fix everything …

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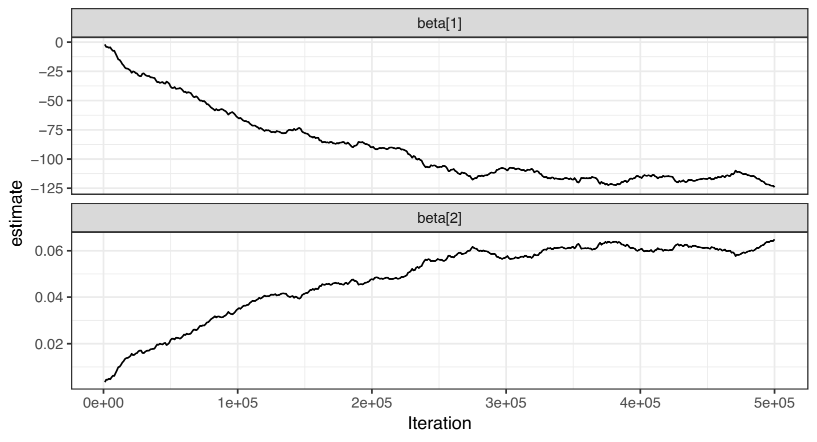

What went wrong?

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```r
summary(g)
##
## Call:
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##
## 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

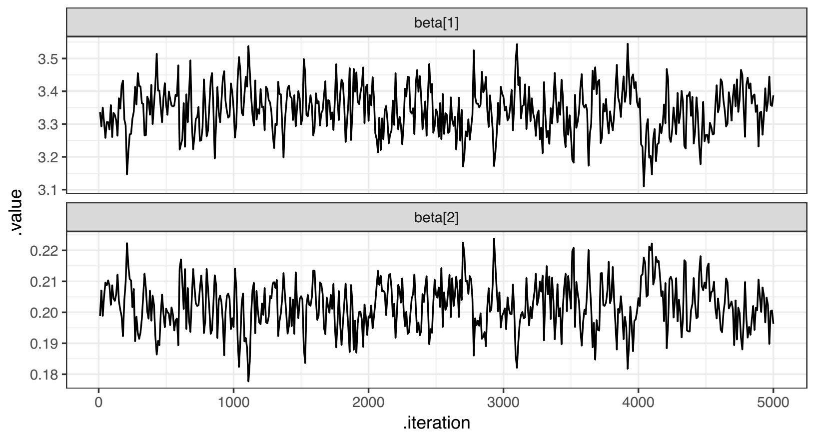
```
poisson_model2 =
"model{
  # Likelihood
  for (i in 1:length(Y)) {
    Y[i] ~ dpois(lambda[i])
    log(lambda[i]) <- beta[1] + beta[2]*(X[i] - 1981)

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

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

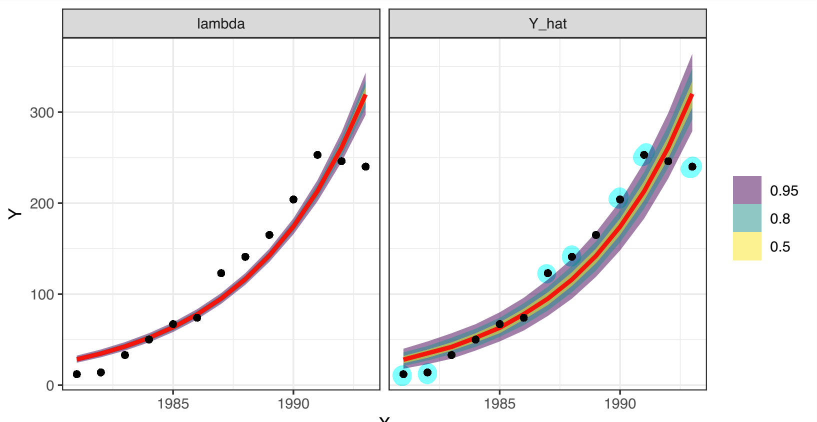
MCMC Diagnostics

```
tidybayes::gather_draws(samp2, beta[i]) %>%
  mutate(param = paste0(.variable,"[",i,"]")) %>%
  filter(.iteration %% 10 == 0) %>%
  ggplot(aes(x=.iteration, y=.value)) +
    geom_line() +
    facet_wrap(~param, ncol=1, scale="free_y")
```

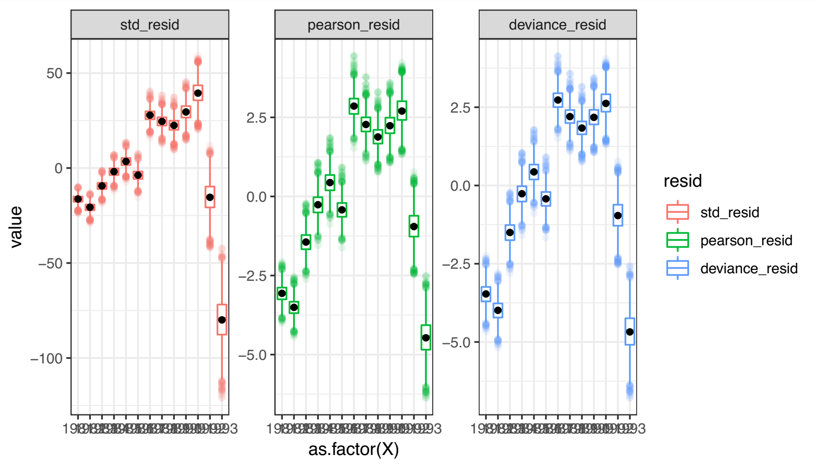


Model Fit

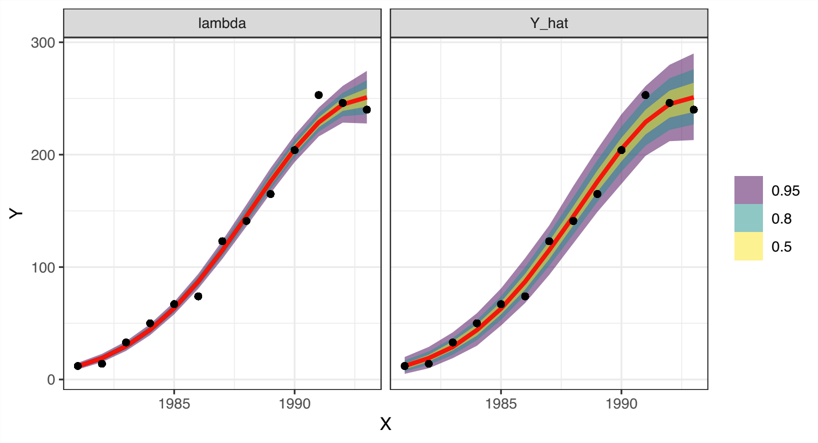
```
tidybayes::spread_draws(samp2, Y_hat[i], lambda[i], X[i], Y[i]) %>%
  ungroup() %>%
  tidyr::gather(param, value, Y_hat, lambda) %>%
  ggplot(aes(x=X,y=Y)) +
    tidybayes::stat_lineribbon(aes(y=value), alpha=0.5) +
    geom_point() +
    facet_wrap(~param)
```



Residual Plots

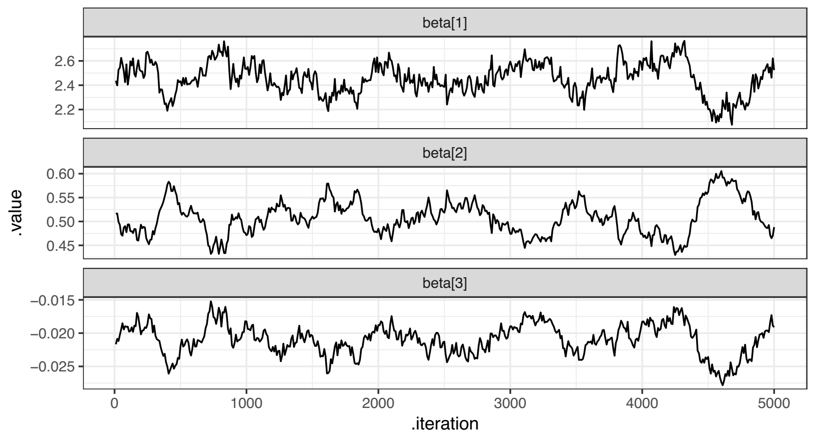


Quadratic Fit



MCMC Diagnostics

```r
tidybayes::gather_draws(samp3, beta[i]) %>%
  mutate(param = paste0(.variable,"[",i,"]")) %>%
  filter(.iteration %% 10 == 0) %>%
  ggplot(aes(x=.iteration, y=.value)) +
    geom_line() +
    facet_wrap(~param, ncol=1, scale="free_y")
```



Residual Plots