

COVID-19 Deaths Analysis

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The purpose of this analysis is to analyze the relationship between COVID-19 death and time, in different countries or regions.

```
install.packages("gamm4")
```

```
library(devtools)
library(mgcv)
library(gamm4)
library(tidyverse)
```

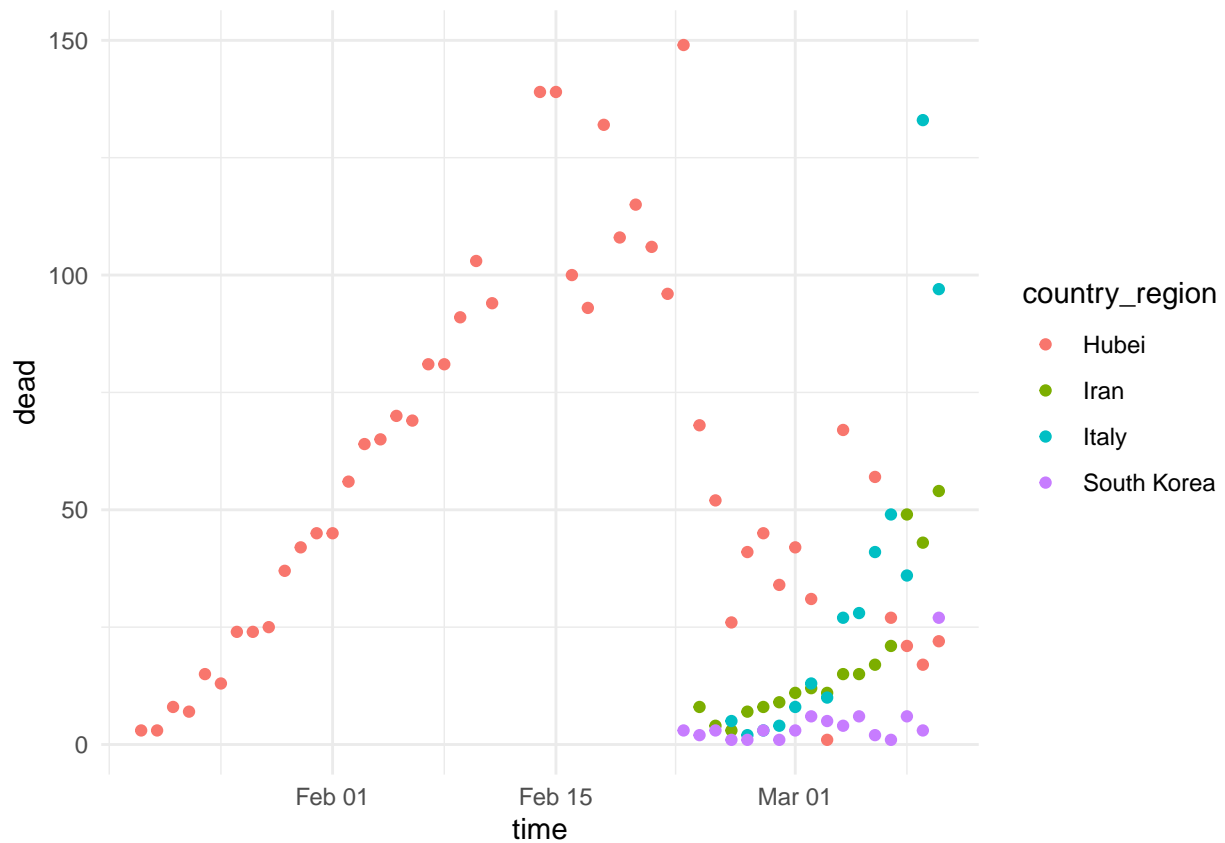
COVID-19 data

First, plot deaths from COVID-19, so we can visualize the deaths in five different regions.

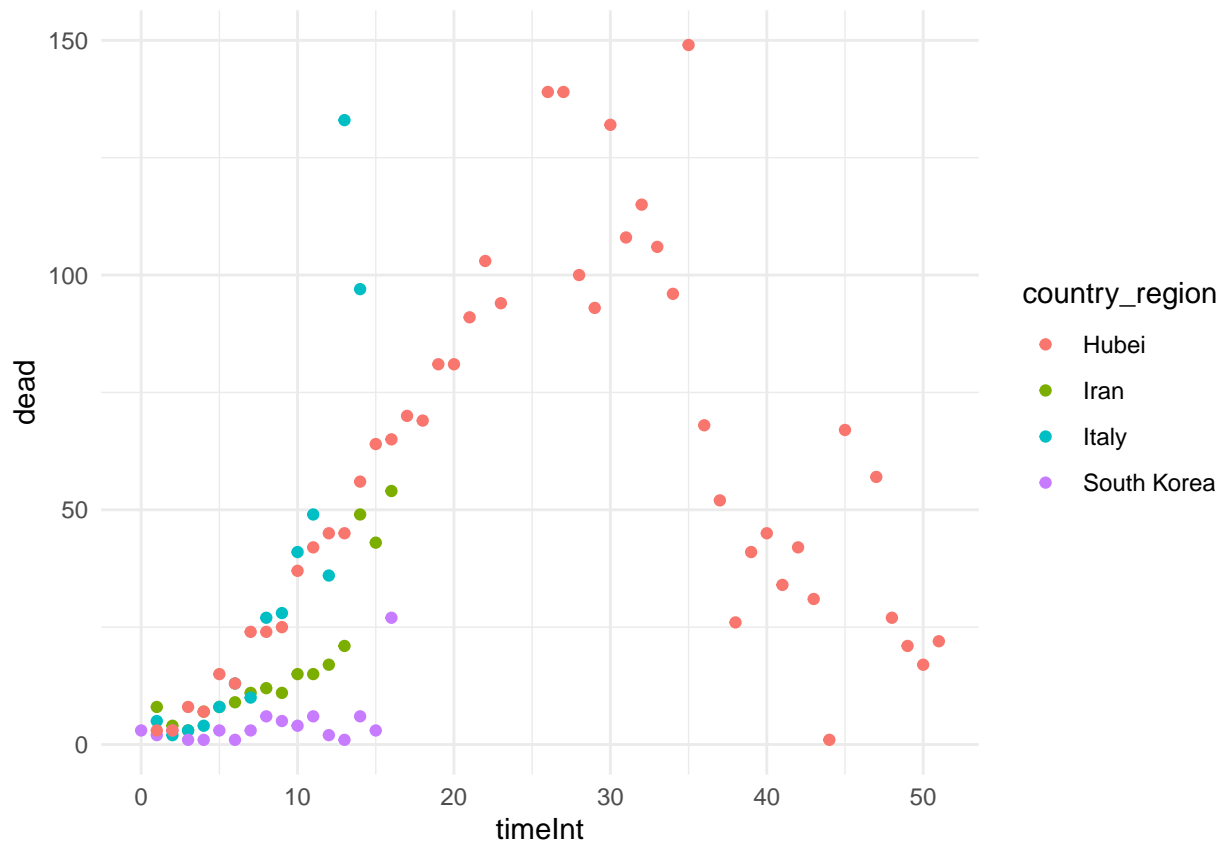
```
# Load nCOVID-19 data
covid_data <- read_csv("covid_data.csv")
```

```
## Parsed with column specification:
## cols(
##   time = col_date(format = ""),
##   timeInt = col_double(),
##   cum_confirm = col_double(),
##   cum_dead = col_double(),
##   incidence = col_double(),
##   dead = col_double(),
##   country_region = col_character()
## )
```

```
# Plot over time
covid_data %>%
  filter(country_region %in% c('Hubei', 'Italy', 'Iran', 'South Korea', 'USA')) %>%
  na.omit() %>%
  ggplot(aes(time, dead, color=country_region)) +
  geom_point() +
  theme_minimal()
```



```
# Plot from initial death in region
covid_data %>%
  filter(country_region %in% c('Hubei', 'Italy', 'Iran', 'South Korea', 'USA')) %>%
  na.omit() %>%
  ggplot(aes(timeInt, dead, color=country_region)) +
  geom_point() +
  theme_minimal()
```



Now fit it a GAM resGam with `dead` as the response a smooth on `timeInt` and `country_region` as covariates.

```
resGam= mgcv::gam(
  dead ~ s(timeInt, pc=0) + country_region,
  data=covid_data,
  family=poisson(link='log'))
```

Now we summarize and get the conclusion of the model, then plot it.

```
summary(resGam)
```

```
##
## Family: poisson
## Link function: log
##
## Formula:
## dead ~ s(timeInt, pc = 0) + country_region
##
## Parametric coefficients:
##
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.160352	0.583136	-0.275	0.783329
country_regionAustralia	0.078106	1.155196	0.068	0.946094
country_regionBeijing	-1.940556	0.739512	-2.624	0.008688 **
country_regionChongqing	-0.535153	0.819679	-0.653	0.513833
country_regionFrance	1.127419	0.610845	1.846	0.064940 .
country_regionGuangdong	-1.608135	0.771882	-2.083	0.037215 *

```
##
```

```

## country_regionHainan      -2.168937    0.824279   -2.631 0.008506 **
## country_regionHebei       -0.763389    0.823787   -0.927 0.354092
## country_regionHeilongjiang -1.118993    0.666038   -1.680 0.092943 .
## country_regionHenan       -1.208796    0.631050   -1.916 0.055425 .
## country_regionHubei        1.815819    0.589066    3.083 0.002052 **
## country_regionHunan        0.078106    1.155196    0.068 0.946094
## country_regionIran         1.321243    0.590201    2.239 0.025180 *
## country_regionIraq         0.171690    0.764797    0.224 0.822375
## country_regionItaly        2.117238    0.588802    3.596 0.000323 ***
## country_regionJapan       -1.361864    0.654921   -2.079 0.037578 *
## country_regionShandong     0.215099    0.817422    0.263 0.792440
## country_regionSouth Korea  -0.005497    0.597876   -0.009 0.992664
## country_regionSpain        2.033865    0.605583    3.359 0.000784 ***
## country_regionUnited Kingdom 1.258965    0.820598    1.534 0.124979
## country_regionUnited States 0.827315    0.621365    1.331 0.183042
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##              edf Ref.df Chi.sq p-value
## s(timeInt) 8.758  8.982   1309  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.894   Deviance explained = 93.5%
## UBRE = 2.0019   Scale est. = 1           n = 170

```

```
coef(resGam)
```

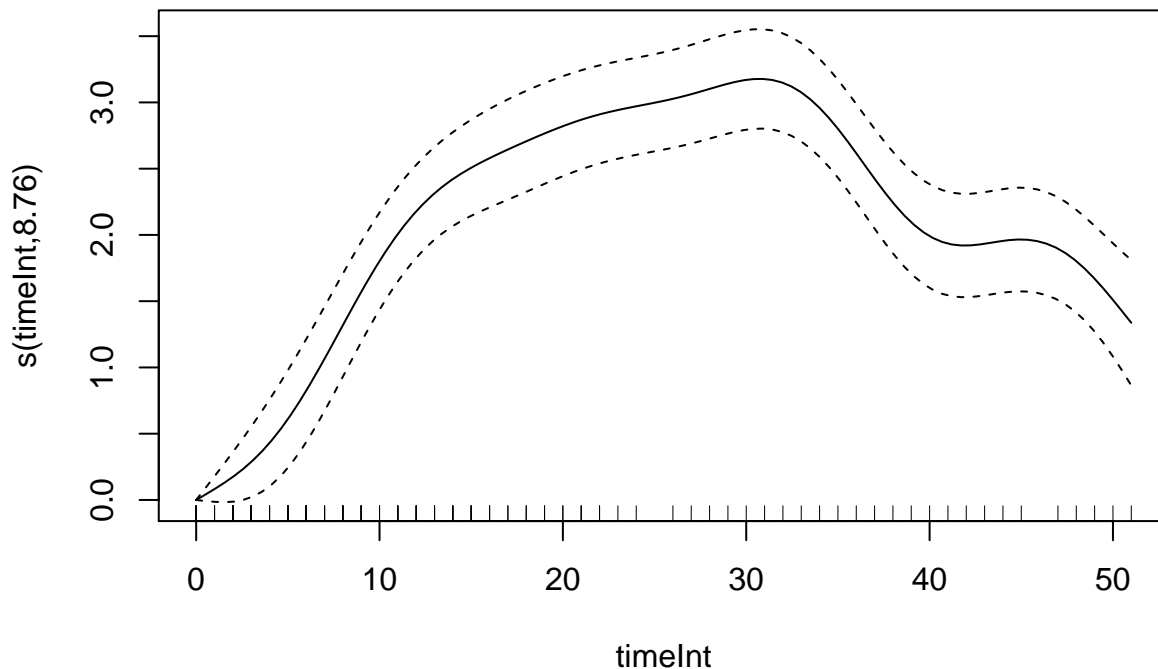
```

##              (Intercept)      country_regionAustralia
##              -0.160352456          0.078105515
## country_regionBeijing      country_regionChongqing
##              -1.940556292          -0.535153159
## country_regionFrance      country_regionGuangdong
##              1.127419488          -1.608135374
## country_regionHainan      country_regionHebei
##              -2.168937066          -0.763389041
## country_regionHeilongjiang      country_regionHenan
##              -1.118993096          -1.208796089
## country_regionHubei      country_regionHunan
##              1.815818734          0.078105515
## country_regionIran      country_regionIraq
##              1.321243223          0.171690309
## country_regionItaly      country_regionJapan
##              2.117237701          -1.361864231
## country_regionShandong      country_regionSouth Korea
##              0.215099168          -0.005496802
## country_regionSpain      country_regionUnited Kingdom
##              2.033864959          1.258964745
## country_regionUnited States      s(timeInt).1
##              0.827314895          0.436070190
##              s(timeInt).2          s(timeInt).3
##              0.162668721          0.695995274
##              s(timeInt).4          s(timeInt).5

```

```
##          -0.257405570          0.133254518
##          s(timeInt).6          s(timeInt).7
##          1.140898783          -0.022139449
##          s(timeInt).8          s(timeInt).9
##          4.992873514          -1.020359041
```

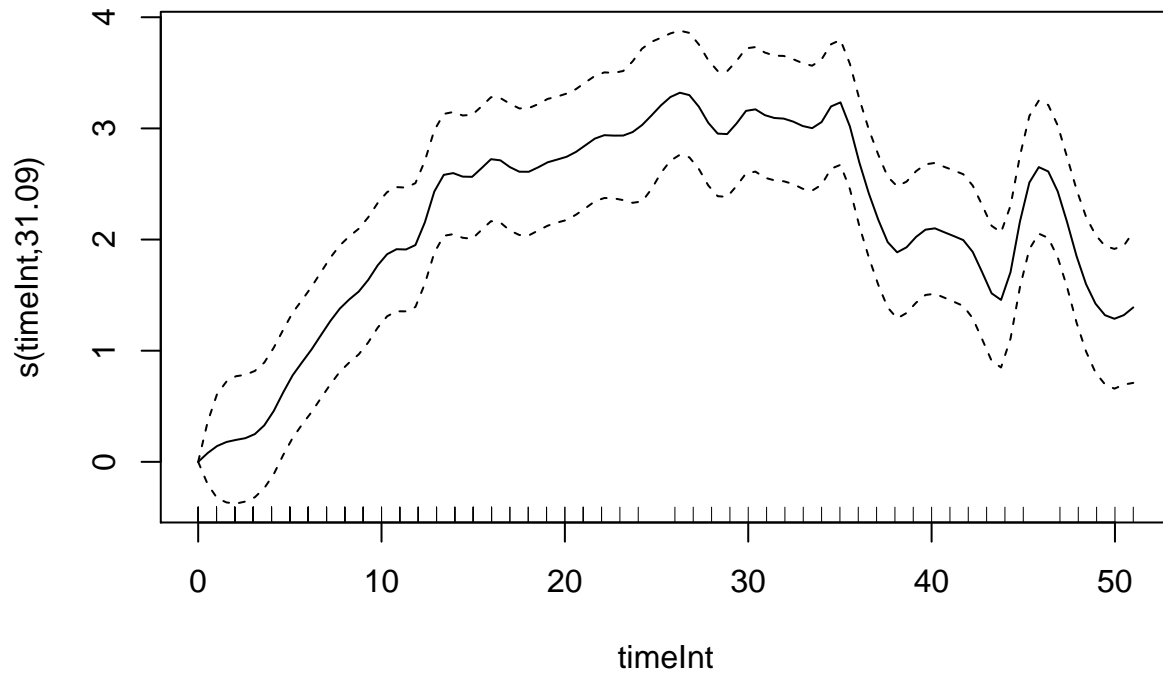
```
plot(resGam)
```



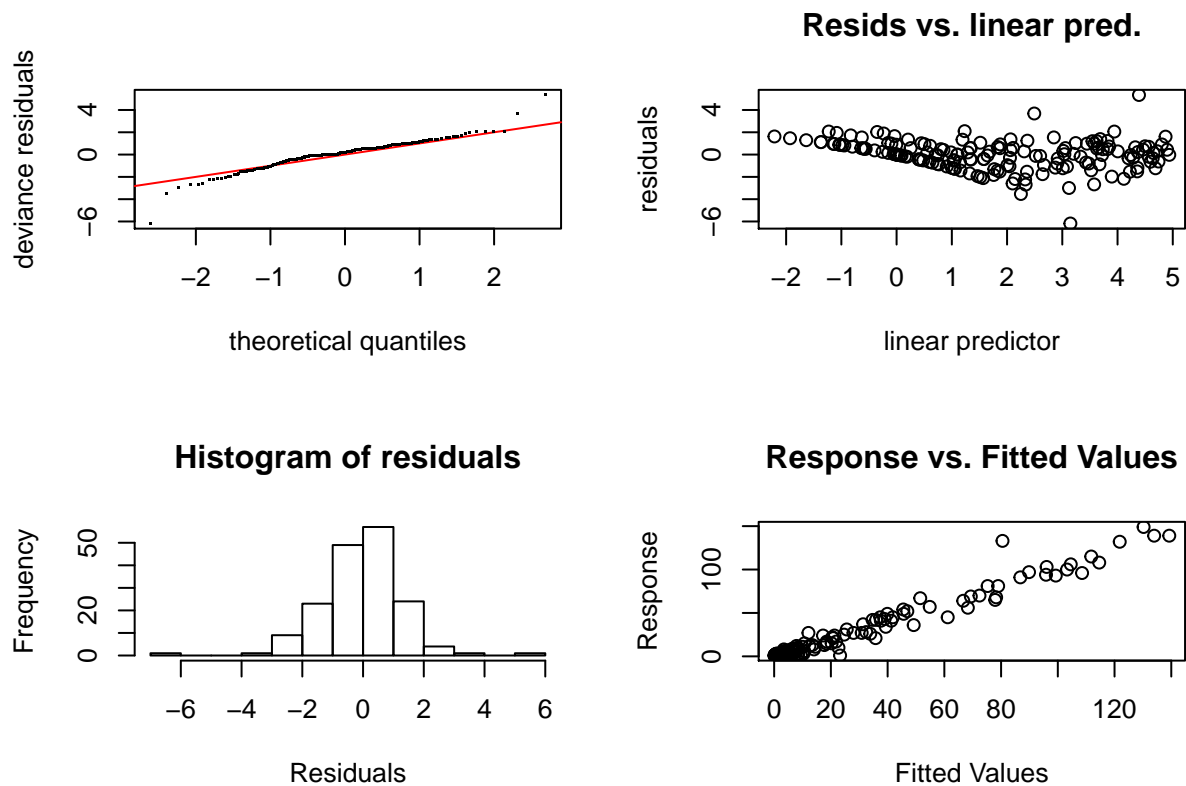
Conclusion from above The estimated degrees of freedom for the smooth of `timeInt` is 8.758, we see an edf is much higher than 1(which is 8.758), which means the relationship between deaths and time is not close to linear. We can interpret the coefficients for `country_region`. For example, `country_regionAustralia` has a coefficient of 0.078, means time has a positive relationship with deaths due to COVID-19 in Australia, one unit of time will cause 0.078 more deaths in Australia.

Next, we fit and plot two more GAMs with the same model but with `k = 50` and `k = 20`.

```
resGam3= mgcv::gam(
  dead ~ s(timeInt, k=50, pc=0) + country_region, data=covid_data,
  family=poisson(link='log'), method='ML')
plot(resGam3)
```



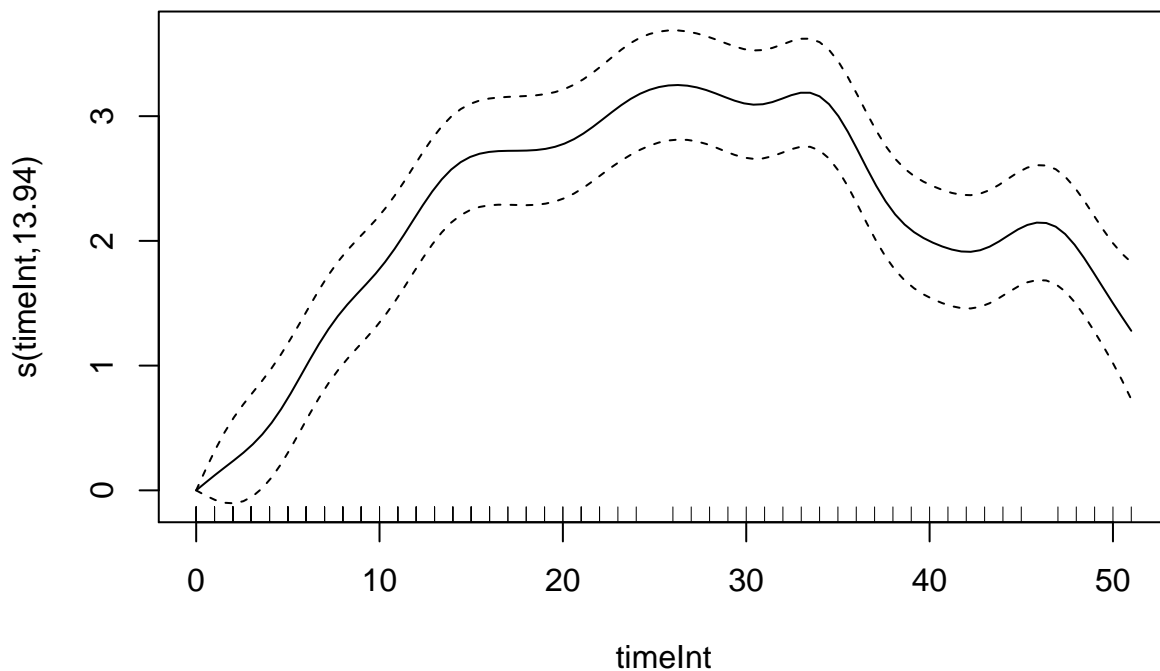
```
gam.check(resGam3)
```



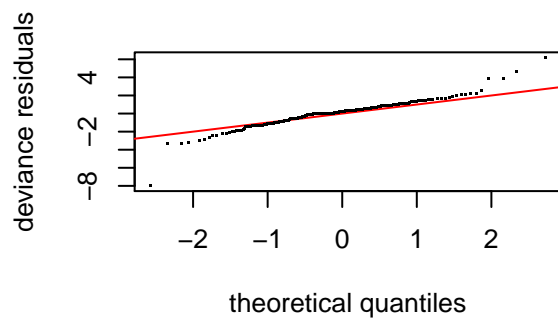
```
##
## Method: ML    Optimizer: outer newton
## full convergence after 6 iterations.
## Gradient range [-1.704072e-05,-1.704072e-05]
```

```
## (score 540.3471 & scale 1).
## Hessian positive definite, eigenvalue range [4.080029,4.080029].
## Model rank = 70 / 70
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##           k'   edf k-index p-value
## s(timeInt) 49.0 31.1   1.25      1
```

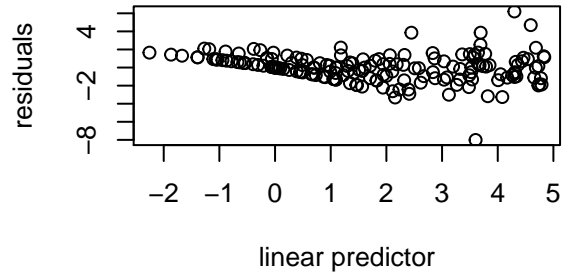
```
resGam4 = mgcv::gam(
  dead ~ s(timeInt, k=20, pc=0) + country_region, data=covid_data,
  family=poisson(link='log'), method='ML')
plot(resGam4)
```



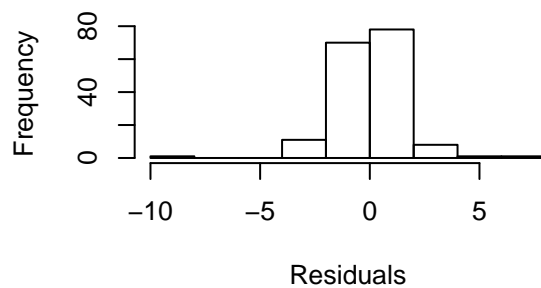
```
gam.check(resGam4)
```



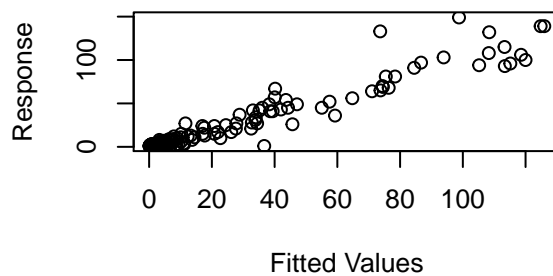
Resids vs. linear pred.



Histogram of residuals



Response vs. Fitted Values

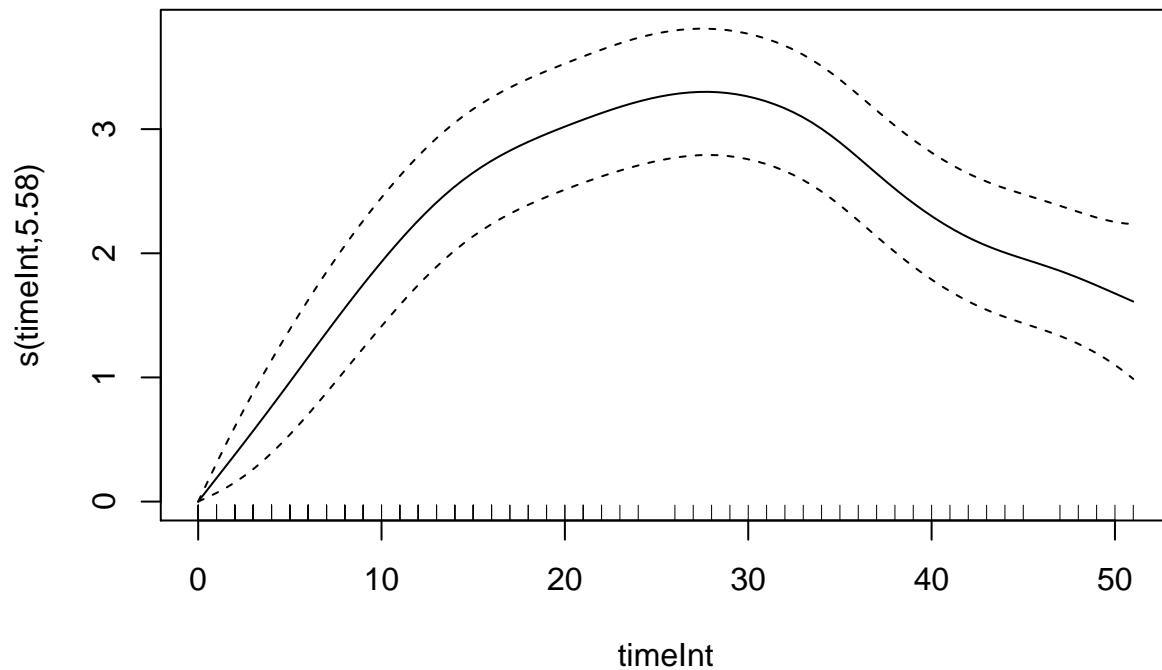


```
##
## Method: ML   Optimizer: outer newton
## full convergence after 6 iterations.
## Gradient range [3.691928e-06,3.691928e-06]
## (score 554.3095 & scale 1).
## Hessian positive definite, eigenvalue range [3.724135,3.724135].
## Model rank = 40 / 40
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##           k'   edf k-index p-value
## s(timeInt) 19.0 13.9   1.15   0.97
```

```
covid_data$timeIntInd = covid_data$timeInt

resGammInd = gamm4::gamm4(
  dead ~ country_region +
    s(timeInt, k=20, pc=0),
  random = ~ (1|timeIntInd),
  data=covid_data, family=poisson(link='log'))

plot(resGammInd$gam)
```

```
summary(resGammInd$mer)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
##
##      AIC      BIC   logLik deviance df.resid
##  1082.2   1157.4   -517.1   1034.2     146
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2542 -0.5002  0.0522  0.8694  5.2817
##
## Random effects:
##  Groups      Name      Variance Std.Dev.
## timeIntInd (Intercept) 0.08203  0.2864
## Xr              s(timeInt) 5.18868  2.2779
## Number of obs: 170, groups:  timeIntInd, 50; Xr, 18
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## X(Intercept)    -0.306160   0.605059  -0.506  0.612857
## Xcountry_regionAustralia    0.005782   1.163560   0.005  0.996035
## Xcountry_regionBeijing    -2.011839   0.741288  -2.714  0.006648 **
## Xcountry_regionChongqing   -0.657144   0.823363  -0.798  0.424800
## Xcountry_regionFrance     1.045114   0.612790   1.706  0.088101 .
## Xcountry_regionGuangdong   -1.642045   0.775352  -2.118  0.034192 *
## Xcountry_regionHainan     -2.299688   0.843723  -2.726  0.006418 **
## Xcountry_regionHebei      -0.882840   0.825789  -1.069  0.285031
## Xcountry_regionHeilongjiang -1.055389   0.668758  -1.578  0.114535
## Xcountry_regionHenan      -1.242027   0.632998  -1.962  0.049747 *
## Xcountry_regionHubei       1.771843   0.590886   2.999  0.002712 **
```

```
## Xcountry_regionHunan      0.005607  1.163584  0.005 0.996155
## Xcountry_regionIran       1.236077  0.592175  2.087 0.036857 *
## Xcountry_regionIraq       0.150635  0.768603  0.196 0.844621
## Xcountry_regionItaly      2.044601  0.590686  3.461 0.000537 ***
## Xcountry_regionJapan      -1.418249  0.656942 -2.159 0.030861 *
## Xcountry_regionShandong    0.083484  0.822716  0.101 0.919175
## Xcountry_regionSouth Korea -0.088985  0.599738 -0.148 0.882049
## Xcountry_regionSpain       2.017840  0.604858  3.336 0.000850 ***
## Xcountry_regionUnited Kingdom 1.337925  0.832874  1.606 0.108187
## Xcountry_regionUnited States 0.744861  0.623195  1.195 0.231998
## Xs(timeInt)Fx1            2.801306  0.765064  3.662 0.000251 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 22 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it
```

```
summary(resGammInd$gam)
```

```
##
## Family: poisson
## Link function: log
##
## Formula:
## dead ~ country_region + s(timeInt, k = 20, pc = 0)
##
## Parametric coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.306160   0.608512  -0.503 0.614874
## country_regionAustralia    0.005782   1.169958   0.005 0.996057
## country_regionBeijing     -2.011839   0.744806  -2.701 0.006910 **
## country_regionChongqing    -0.657144   0.827554  -0.794 0.427149
## country_regionFrance       1.045114   0.616594   1.695 0.090080 .
## country_regionGuangdong    -1.642045   0.779111  -2.108 0.035067 *
## country_regionHainan       -2.299688   0.850166  -2.705 0.006831 **
## country_regionHebei        -0.882840   0.829945  -1.064 0.287450
## country_regionHeilongjiang -1.055389   0.672452  -1.569 0.116540
## country_regionHenan        -1.242027   0.636659  -1.951 0.051075 .
## country_regionHubei        1.771843   0.594531   2.980 0.002880 **
## country_regionHunan        0.005607   1.170033   0.005 0.996176
## country_regionIran         1.236077   0.595806   2.075 0.038021 *
## country_regionIraq         0.150635   0.773106   0.195 0.845515
## country_regionItaly        2.044601   0.594323   3.440 0.000581 ***
## country_regionJapan       -1.418249   0.660555  -2.147 0.031789 *
## country_regionShandong     0.083484   0.827629   0.101 0.919653
## country_regionSouth Korea  -0.088985   0.603363  -0.147 0.882753
## country_regionSpain        2.017840   0.608684   3.315 0.000916 ***
## country_regionUnited Kingdom 1.337925   0.839165   1.594 0.110857
## country_regionUnited States 0.744861   0.627042   1.188 0.234874
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Approximate significance of smooth terms:
##           edf Ref.df Chi.sq p-value
## s(timeInt) 5.579  5.579  289.7  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.884
## glmer.ML = 250.06  Scale est. = 1          n = 170
```

The plot suggests a trend where we estimate a sharper increase in deaths per day over the first 25 days to a month and then the number decreases from about day 30 onwards.

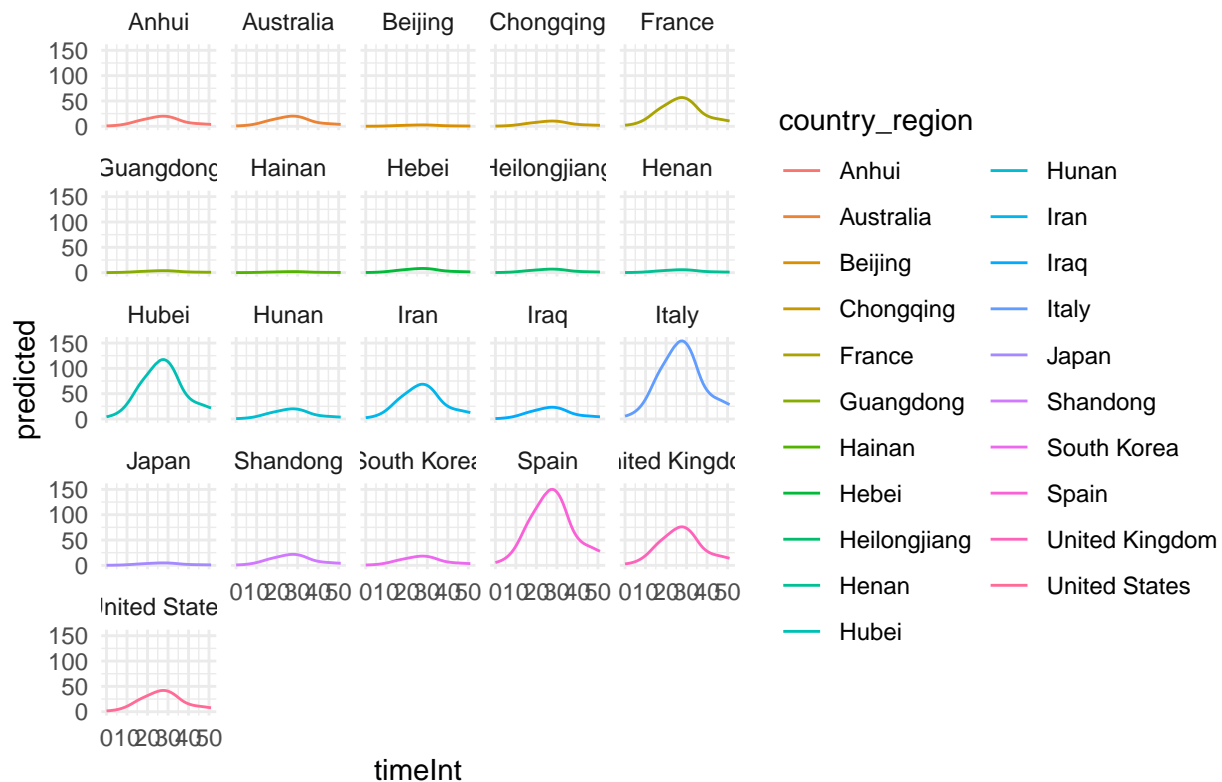
```
covid_data_2 <- expand_grid(covid_data$timeInt, covid_data$country_region) %>%
  as_tibble() %>%
  rename(timeInt = 1, country_region = 2) %>%
  distinct()

covid_data_2$predicted <- predict(resGammInd$gam, newdata=covid_data_2, type="response")

#covid_data_3 <- bind_cols(covid_data_2, predicted) %>%
#  mutate(lower = fit - 2*se.fit, upper = fit + 2*se.fit)

covid_data_2 %>%
  ggplot(aes(timeInt, predicted, colour=country_region)) +
  geom_line() +
  theme_minimal() +
  facet_wrap(~country_region) +
  ggtitle("Predicted deaths over time (time = 0 is first death)")
```

Predicted deaths over time (time = 0 is first death)



The plot shows the Predicted deaths over time (time = 0 is first death).

Fit a different model.

Now we fit a different model with time being a random slope.

```
covid_data$timeSlope = covid_data$timeInt/100

resGammSlope = gamm4::gamm4(
  dead ~ country_region + s(timeInt, k=30, pc=0),
  random = ~(0+timeSlope|country_region) +
    (1|timeIntInd:country_region),
  data=covid_data, family=poisson(link='log'))
#save(resGammSlope, file='resGamSlope.RData')
plot(resGammSlope$gam)
summary(resGammSlope$mer)
names(lme4::ranef(resGammSlope$mer))
theRanef = lme4::ranef(resGammSlope$mer, condVar = TRUE)$country_region
(theRanefVec = sort(drop(t(theRanef))))

Dcountry = 'France'
toPredict = expand.grid(
  timeInt = 0:100,
  country_region = Dcountry)
toPredict$timeSlope = toPredict$timeIntInd =
  toPredict$timeInt
thePred = predict(resGammSlope$gam,
```

```

newdata=toPredict, se.fit=TRUE)

matplot(toPredict$timeInt,
        exp(do.call(cbind, thePred) %*% Pmisc::ciMat(0.75)),
        type='l',
        col=c('black','grey','grey'),
        ylim = c(0, 25))
points(covid_data[covid_data$country_region == Dcountry,c('timeInt','dead')],
       col='red')

```

Appendix

1. The COVID-19 data was retrieved from GitHub and the procedure is shown below.

```

install.packages("devtools")
devtools::install_github("GuangchuangYu/nCov2019")

x1 <- nCov2019::load_nCov2019(lang = 'en')

cutoff=3

x2 = by(x1$global, x1$global[, 'country', drop=FALSE],
        function(xx) {
          xx$incidence = diff(c(0, xx$cum_confirm))
          xx$dead = diff(c(0, xx$cum_dead))
          if(any(xx$cum_dead >= cutoff)) {
            cutoffHere = min(xx[xx$cum_dead >= cutoff, 'time'], na.rm=TRUE) +1
            xx$timeInt = as.numeric(difftime(xx$time, cutoffHere, units='days'))
            xx = xx[xx$timeInt >= 0, ]
            xx=
              xx[,c('time','timeInt','cum_confirm','cum_dead','incidence','dead','cou
          } else {
            xx = NULL
          }
          xx
        }, simplify=FALSE)

x3 = by(x1$province, x1$province[, 'province', drop=FALSE],
        function(xx) {
          xx$incidence = diff(c(0, xx$cum_confirm))
          xx$dead = diff(c(0, xx$cum_dead))
          colnames(xx) = gsub("province","country", colnames(xx))
          if(any(xx$cum_dead >= cutoff)) {
            cutoffHere = min(xx[xx$cum_dead >= cutoff, 'time'], na.rm=TRUE) +1
            xx$timeInt = as.numeric(difftime(xx$time, cutoffHere, units='days'))
            xx = xx[xx$timeInt >= 0, ]
            xx=
              xx[,c('time','timeInt','cum_confirm','cum_dead','incidence','dead','cou
          } else {
            xx = NULL
          }
          xx
        }, simplify=FALSE)
class(x2) = class(x3) = 'list'

```

```

x2 = x2[grepl('China', names(x2), invert=TRUE)]
x = c(x2, x3)
x$Hubei[x$Hubei$incidence > 4000, c('dead', 'incidence')] = NA

tidy_data <- compact(x) %>% bind_rows() %>%
  rename(country_region = country) %>%
  filter(dead>0)
write_csv(tidy_data, "covid_data.csv")

```

2. Some codes were modified from the assignment of the class ran by Prof. Brown and Prof. Bolton from the University of Toronto.