COVID-19 patients, deaths, and death rate

01/04/2020

Source of the data

The data is compiled from https://github.com/CSSEGISandData/COVID-19.

The python script *script.py* is a modification of https://github.com/JacopoPan/JHU-2019nCoV-to-pandas-DF

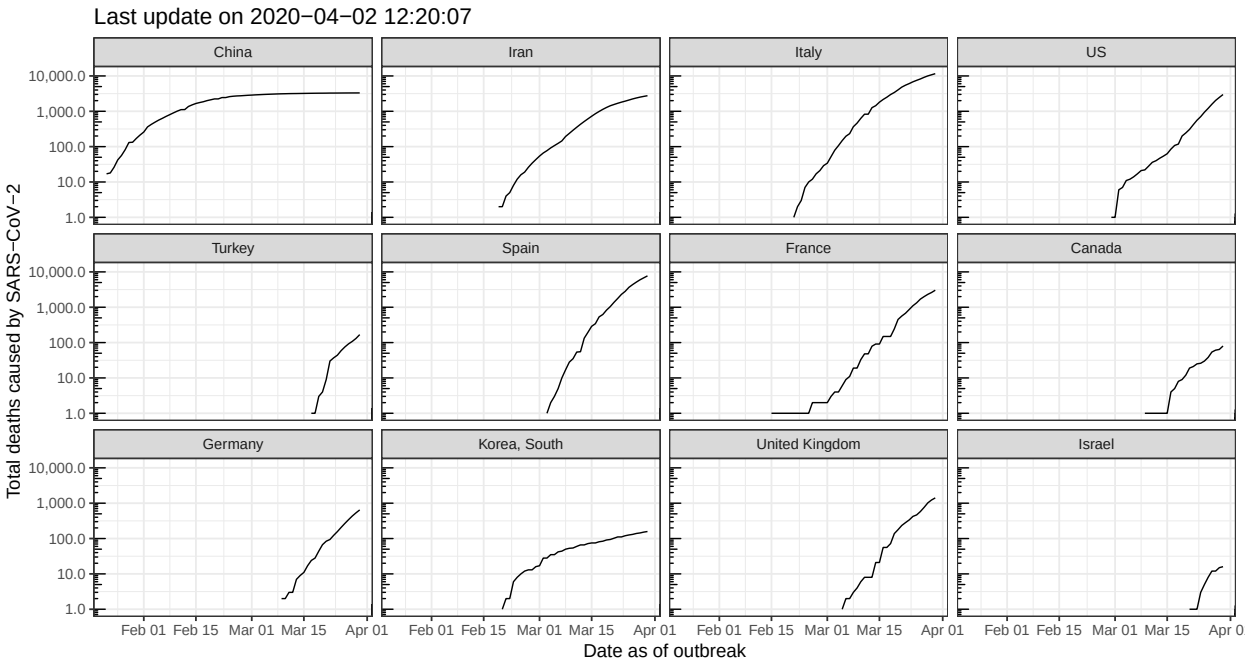
Here I avoided any data modeling and am just showing the raw number of diagnosed patients, deaths, death rate, new cases by day, and new deaths by day.

Total morbidity

```
deathmat = read.csv("deaths.tsv", header=T,
                    sep="\t", check.names=F, row.names=1)
countries = c("China", "Iran", "Italy",
              "US", "Turkey", "Spain",
              "France", "Canada", "Germany",
              "Korea, South", "United Kingdom", "Israel")
deathmat = deathmat[,c(countries, "date")]

moltendf = melt(deathmat)
```

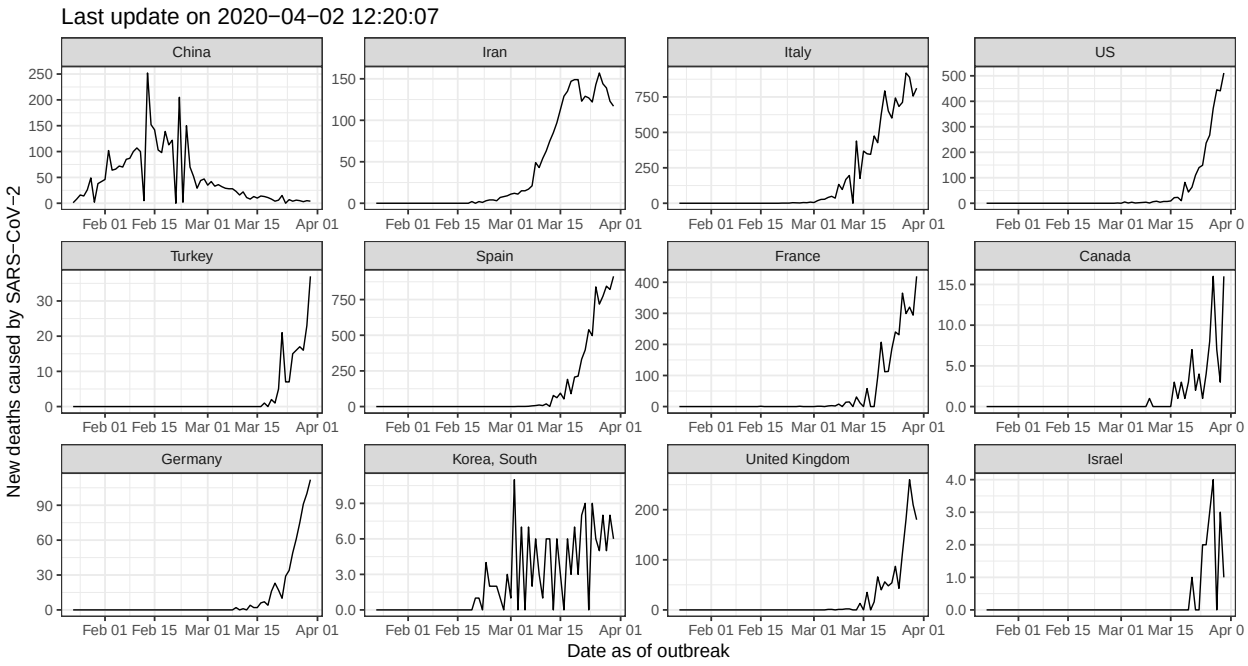
```
## Using date as id variables
```

```
moltendf$date = as.Date(moltendf$date)

P2 = ggplot(moltendf[moltendf$value > 0,],
            aes(x=date, y=(value),
                group=variable)) +
  geom_line() +
  theme_bw(base_size=14) +
  facet_wrap(~variable) +
  scale_y_log10(
    name="Total deaths caused by SARS-CoV-2", labels=comma) +
  xlab("Date as of outbreak") +
  ggtitle(paste("Last update on", Sys.time())) +
  annotation_logticks()

plot(P2)
```



New deaths by day

```
list.data = lapply(colnames(deathmat)[1:(ncol(deathmat)-1)], function(country){
  new_cases = diff(deathmat[,country])
  addf = data.frame(date=deathmat$date[2:nrow(deathmat)],
                    variable=country,
                    value=new_cases)
})
moltendf = do.call("rbind", list.data)

moltendf$date = as.Date(moltendf$date)

P = ggplot(moltendf, aes(x=date, y=value, group=variable)) +
  geom_line() +
  theme_bw(base_size=14) +
  facet_wrap(~variable, scales="free") +
  scale_y_continuous(
    name="New deaths caused by SARS-CoV-2", labels=comma) +
  ggtitle(paste("Last update on", Sys.time())) +
  xlab("Date as of outbreak")
plot(P)
```



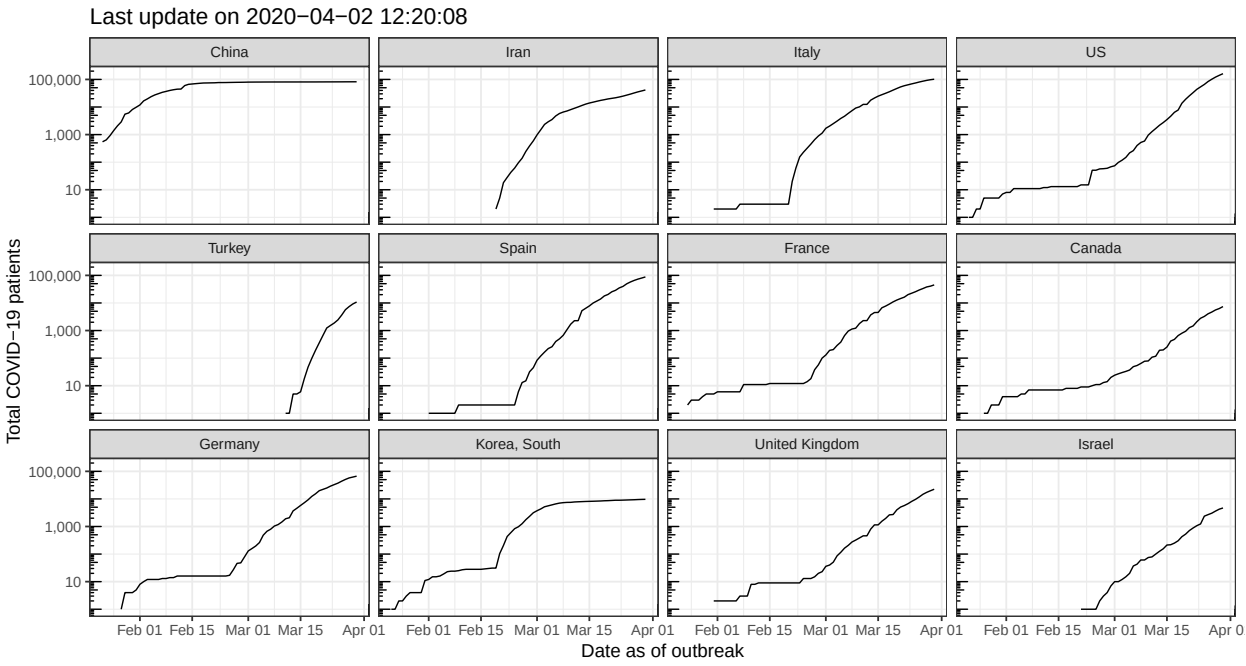
Total COVID-19 patients

```
casemat = read.csv("confirmed.tsv",
                   header=T, sep="\t", check.names=F, row.names=1)

casemat = casemat[,c(countries, "date")]

moltendf = melt(casemat)
```

```
## Using date as id variables
```

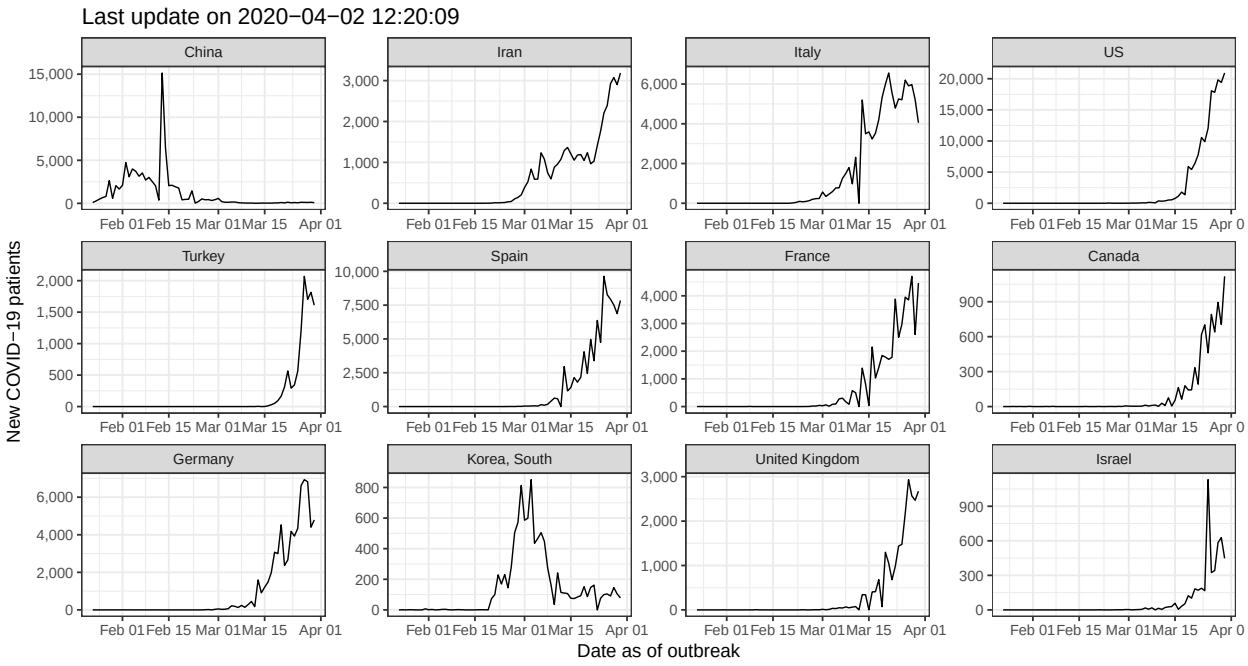
```
moltendf$date = as.Date(moltendf$date)
```

```
P2 = ggplot(moltendf[moltendf$value > 0, ], aes(x=date, y=(value), group=variable)) +
  geom_line() +
  theme_bw(base_size=14) +
  facet_wrap(~variable) +
  scale_y_log10(
    name="Total COVID-19 patients", labels=comma) +
  xlab("Date as of outbreak") +
  ggtitle(paste("Last update on", Sys.time())) +
  annotation_logticks()

plot(P2)
```



New COVID-19 patients by day

```
list.data = lapply(colnames(casemat)[1:(ncol(casemat)-1)], function(country){
  new_cases = diff(casemat[,country])
  addf = data.frame(date=casemat$date[2:nrow(casemat)],
                    variable=country,
                    value=new_cases)
})
moltendf = do.call("rbind", list.data)

moltendf$date = as.Date(moltendf$date)

P = ggplot(moltendf, aes(x=date, y=value, group=variable)) +
  geom_line() +
  theme_bw(base_size=14) +
  facet_wrap(~variable, scales="free") +
  scale_y_continuous(
    name="New COVID-19 patients", labels=comma) +
  ggtitle(paste("Last update on", Sys.time())) +
  xlab("Date as of outbreak")
plot(P)
```

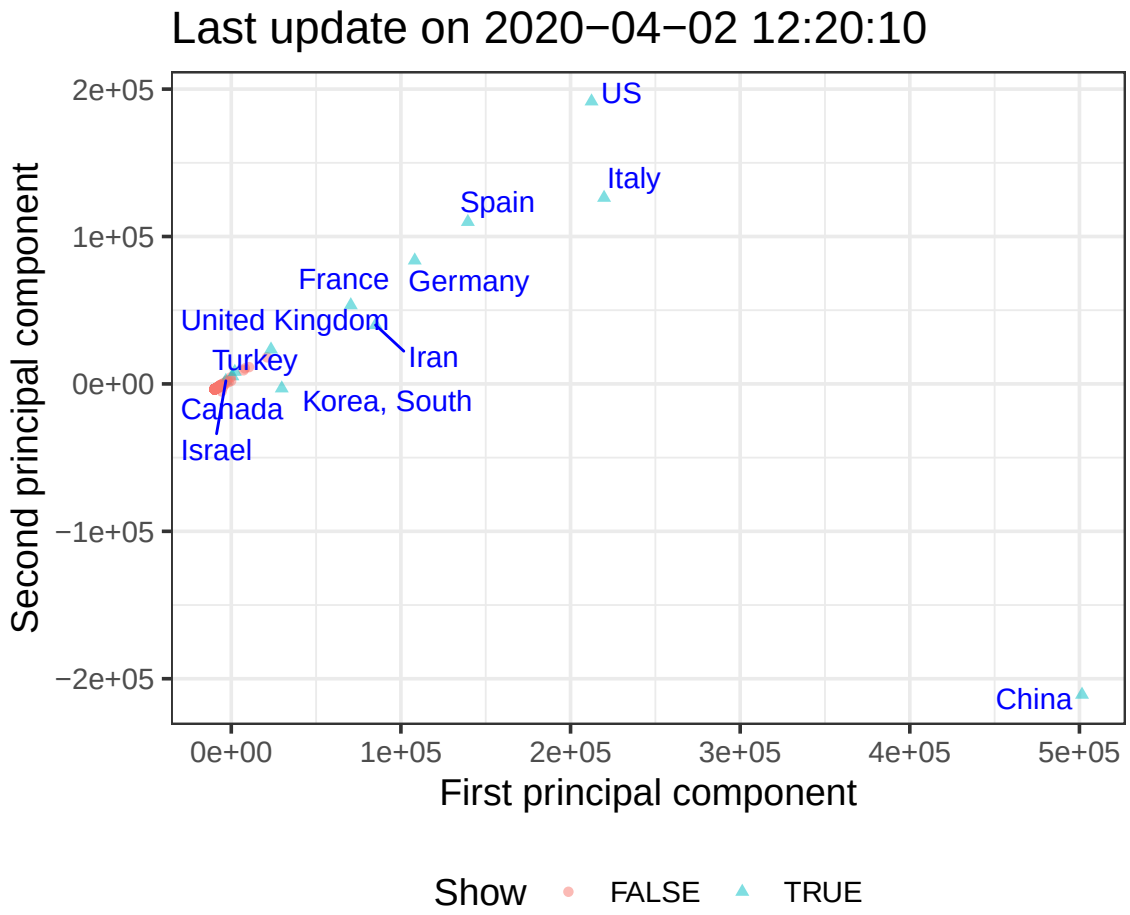


PCA of countries by total patients

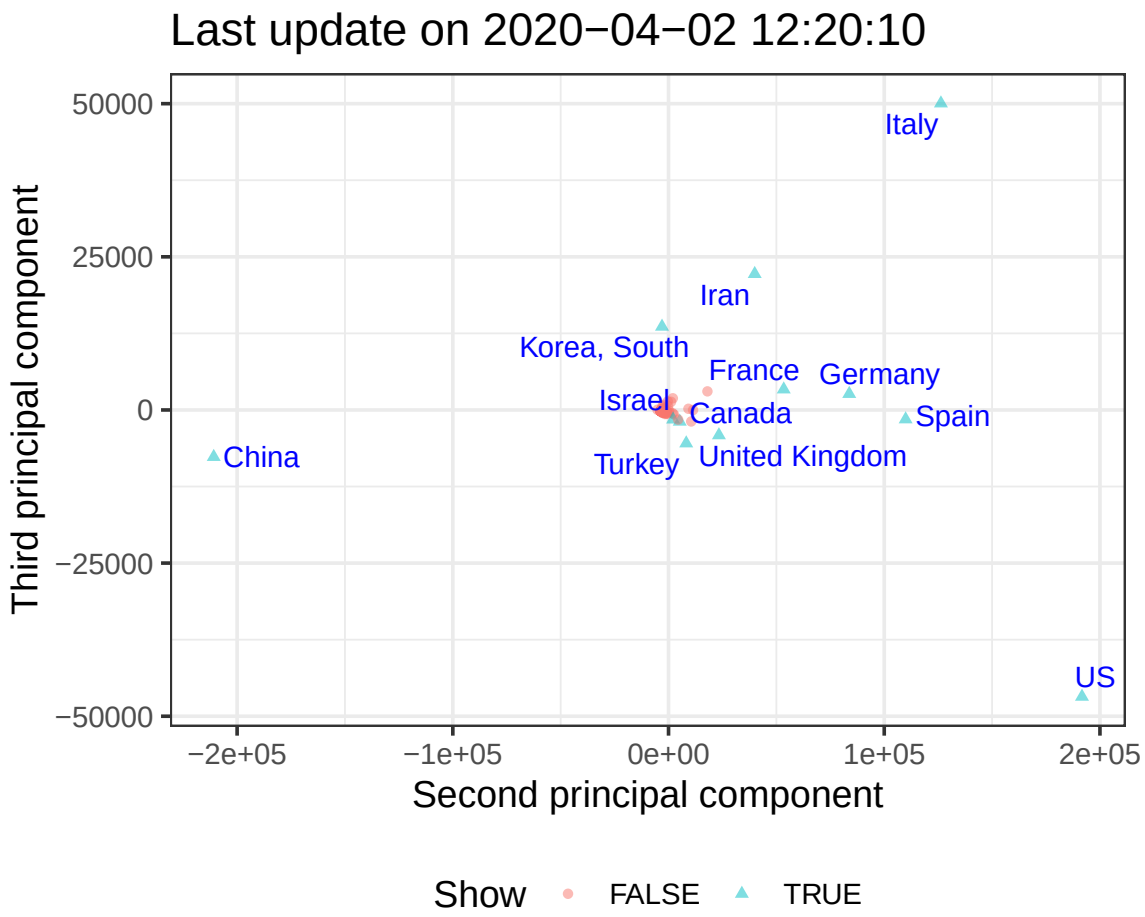
Principal component analysis identifies non-correlating variables (components) from the data and here can identify outlier countries according to a single variable.

In the following plots, I show the first three principal components for total diagnosed patients by day, total deaths by day, and also death rate by day.

```
casemat = read.csv("confirmed.tsv", header=T, sep="\t", check.names=F, row.names=1)

pcamat = casemat[,1:(ncol(casemat) - 1)]
PCA = prcomp(t(pcamat))
pcadf = as.data.frame(PCA$x)
pcadf$Country = colnames(casemat)[1:nrow(pcadf)]
pcadf$Show = ifelse(pcadf$Country %in% countries, TRUE, FALSE)

P = ggplot(pcadf, aes(x=PC1, y=PC2)) +
  geom_point(aes(colour=Show, shape=Show), alpha=0.5) +
  geom_text_repel(data=pcadf[pcadf$Show,], aes(label=Country), colour="blue", size=4) +
  theme_bw(base_size=14) +
  xlab("First principal component") +
  ylab("Second principal component") +
  ggtitle(paste("Last update on", Sys.time())) +
  theme(legend.position="bottom")
plot(P)
```

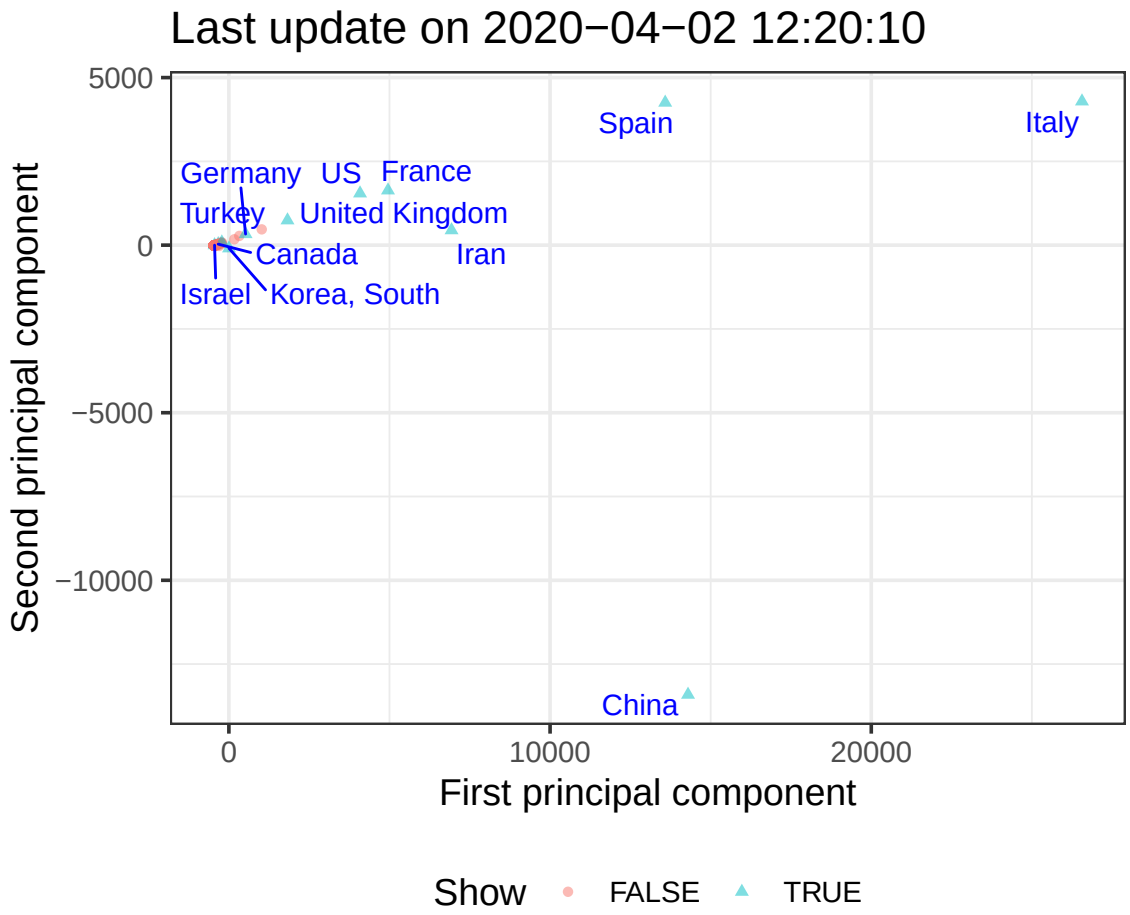



```
P = ggplot(pcadf, aes(x=PC2, y=PC3)) +
  geom_point(aes(colour=Show, shape=Show), alpha=0.5) +
  geom_text_repel(data=pcadf[pcadf$Show,], aes(label=Country), colour="blue", size=4) +
  theme_bw(base_size=14) +
  ylab("Third principal component") +
  xlab("Second principal component") +
  ggtitle(paste("Last update on", Sys.time())) +
  theme(legend.position="bottom")
plot(P)
```

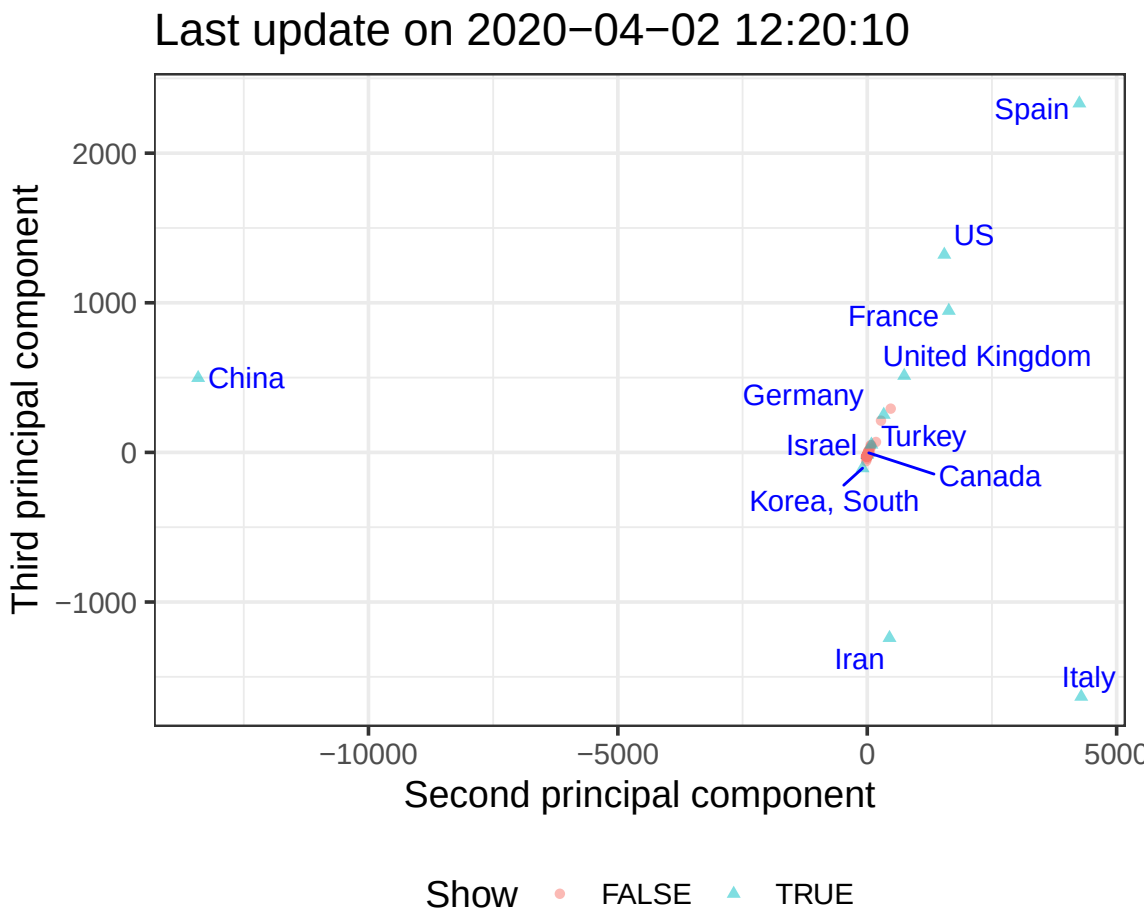


PCA of countries by morbidity

```
deathmat = read.csv("deaths.tsv", header=T,
                    sep="\t", check.names=F, row.names=1)

pcamat = deathmat[,1:(ncol(deathmat) - 1)]
PCA = prcomp(t(pcamat))
pcadf = as.data.frame(PCA$x)
pcadf$Country = colnames(deathmat)[1:nrow(pcadf)]
pcadf$Show = ifelse(pcadf$Country %in% countries, TRUE, FALSE)

P = ggplot(pcadf, aes(x=PC1, y=PC2)) +
  geom_point(aes(colour=Show, shape=Show), alpha=0.5) +
  geom_text_repel(data=pcadf[pcadf$Show,], aes(label=Country), colour="blue", size=4) +
  theme_bw(base_size=14) +
  xlab("First principal component") +
  ylab("Second principal component") +
  ggtitle(paste("Last update on", Sys.time())) +
  theme(legend.position="bottom")
plot(P)
```




```
P = ggplot(pcadf, aes(x=PC2, y=PC3)) +
  geom_point(aes(colour=Show, shape=Show), alpha=0.5) +
  geom_text_repel(data=pcadf[pcadf$Show,], aes(label=Country), colour="blue", size=4) +
  theme_bw(base_size=14) +
  ylab("Third principal component") +
  xlab("Second principal component") +
  ggtitle(paste("Last update on", Sys.time())) +
  theme(legend.position="bottom")
plot(P)
```



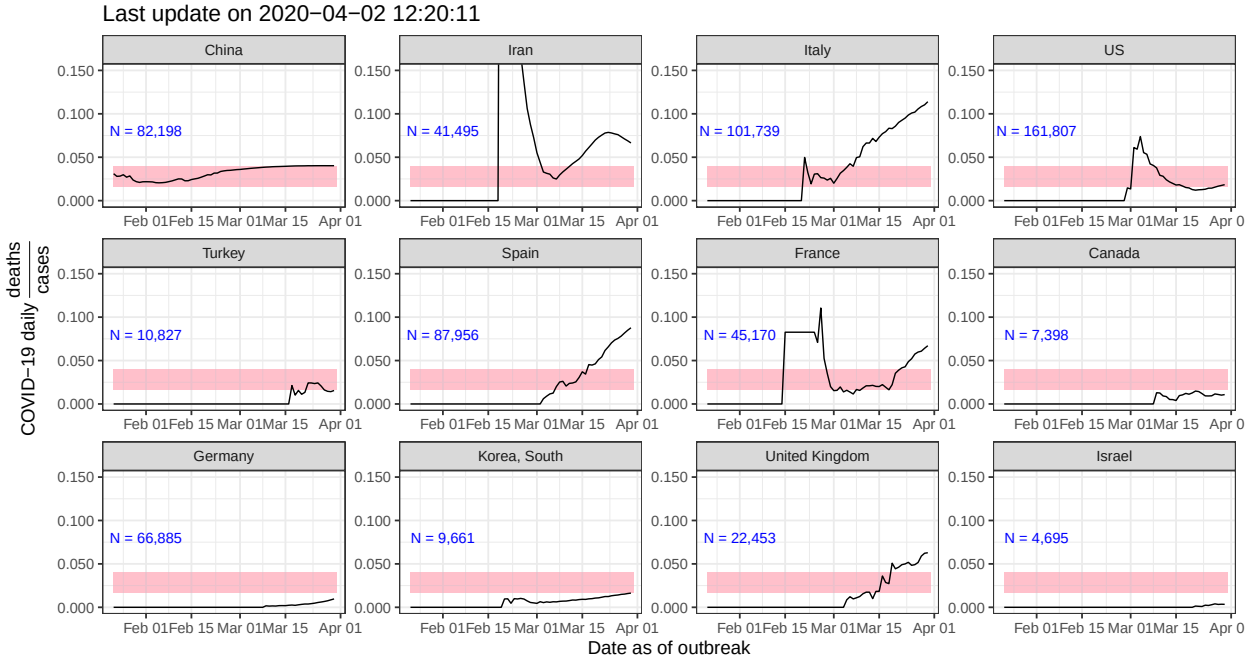
Death rate

The two countries which succeeded in stopping the spread, China and South Korea, provide the most accurate measurement of true death rate. In the death rate plot below, the range of the death rate of these two countries is shown by pink.

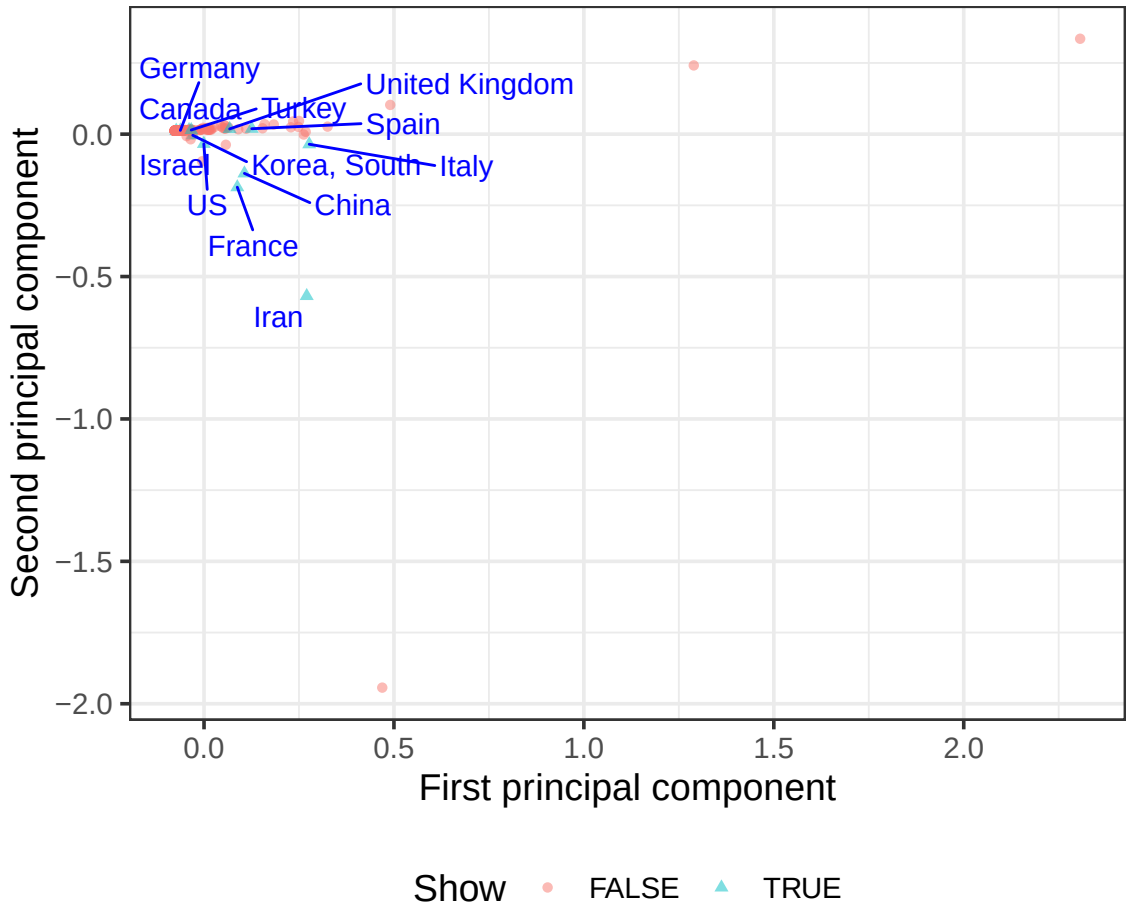
```
deathmat = read.csv("deaths.tsv", header=T,
                    sep="\t", check.names=F, row.names=1)
casemat = read.csv("confirmed.tsv", header=T, sep="\t", check.names=F, row.names=1)
deathrate = deathmat[,1:(ncol(deathmat) - 1)] / (0.1  + casemat[,setdiff(colnames(deathmat), "date")])

deathratedf = deathrate
deathratedf$date = casemat$date
moltendf = melt(deathratedf[,c(countries, "date")])


## Using date as id variables

moltendf$date = as.Date(moltendf$date)

moltendf$Label = NA
deathratedf$date = as.Date(deathratedf$date)
```

```
textmat = casemat[which.max(casemat[,"China"]), ]
textdf = melt(as.data.frame(textmat[,c(countries, "date")]))


## Using date as id variables
```

```
textdf$date = min(as.Date(deathratedf$date)) + 10
textdf$Label = paste("N =", comma(textdf$value))
textdf$value = 0.08

P = ggplot(moltendf, aes(x=date, y=value, group=variable)) +
  geom_rect(xmin=min(deathratedf$date),
            xmax=max(deathratedf$date+1),
            ymin=max(deathratedf$China),
            ymax=max(deathratedf[,"Korea, South"]),
            alpha=0.05,
            fill="pink") +
  geom_line() +
  geom_text(data=textdf, aes(x=date, y=value, label=Label), colour='blue') +
  theme_bw(base_size=14) +
  facet_wrap(~variable, scales="free") +
  scale_y_continuous(
    name=expression("COVID-19 daily "*frac("deaths", "cases")),
    labels=comma) +
  xlab("Date as of outbreak") +
  ggtitle(paste("Last update on", Sys.time())) +
  coord_cartesian(ylim=c(0, 0.15))
plot(P)
```

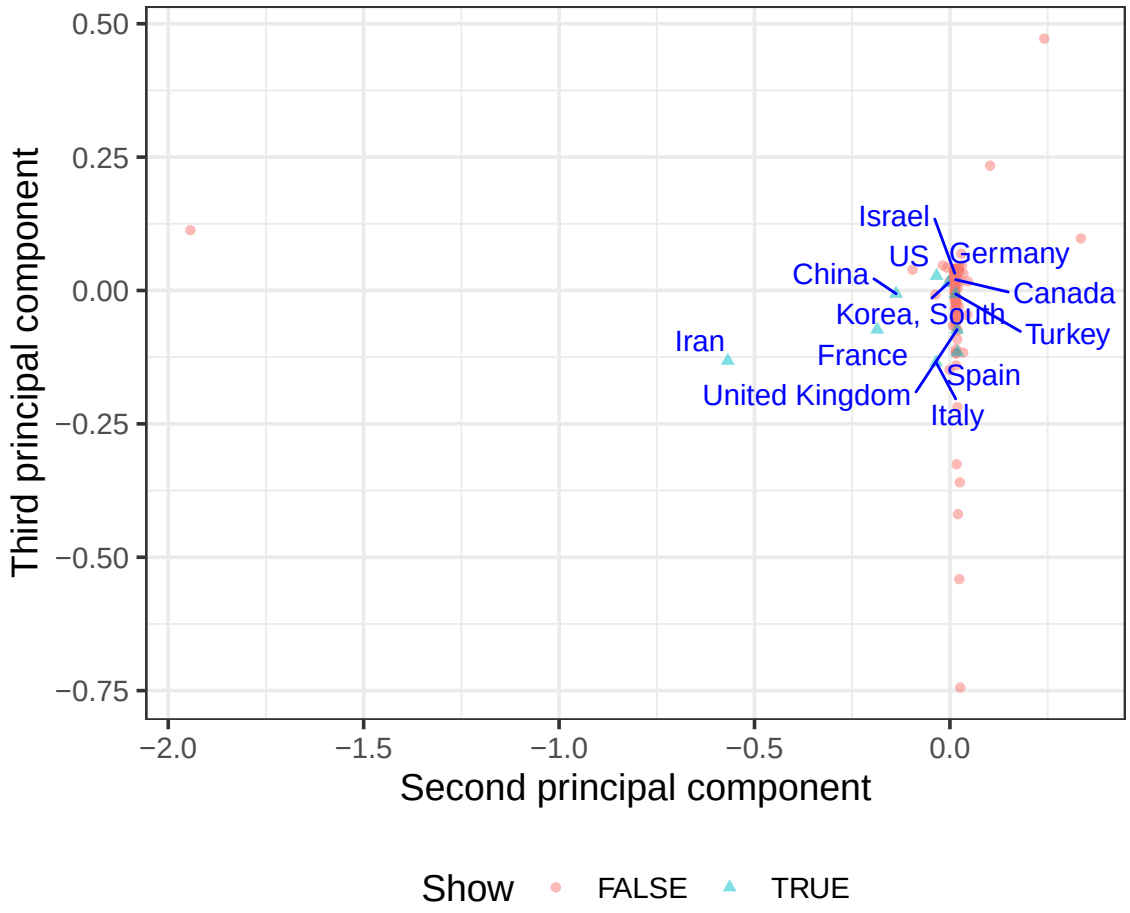


```
pcamat = deathrate
PCA = prcomp(t(pcamat))
pcadf = as.data.frame(PCA$x)
pcadf$Country = colnames(deathmat)[1:nrow(pcadf)]
pcadf$Show = ifelse(pcadf$Country %in% countries, TRUE, FALSE)

P = ggplot(pcadf, aes(x=PC1, y=PC2)) +
  geom_point(aes(colour=Show, shape=Show), alpha=0.5) +
  geom_text_repel(data=pcadf[pcadf$Show,], aes(label=Country), colour="blue", size=4) +
  theme_bw(base_size=14) +
  xlab("First principal component") +
  ylab("Second principal component") +
  theme(legend.position="bottom")
plot(P)
```




```
P = ggplot(pcadf, aes(x=PC2, y=PC3)) +
  geom_point(aes(colour=Show, shape=Show), alpha=0.5) +
  geom_text_repel(data=pcadf[pcadf$Show,], aes(label=Country), colour="blue", size=4) +
  theme_bw(base_size=14) +
  ylab("Third principal component") +
  xlab("Second principal component") +
  theme(legend.position="bottom")
```

```
plot(P)
```



Canada

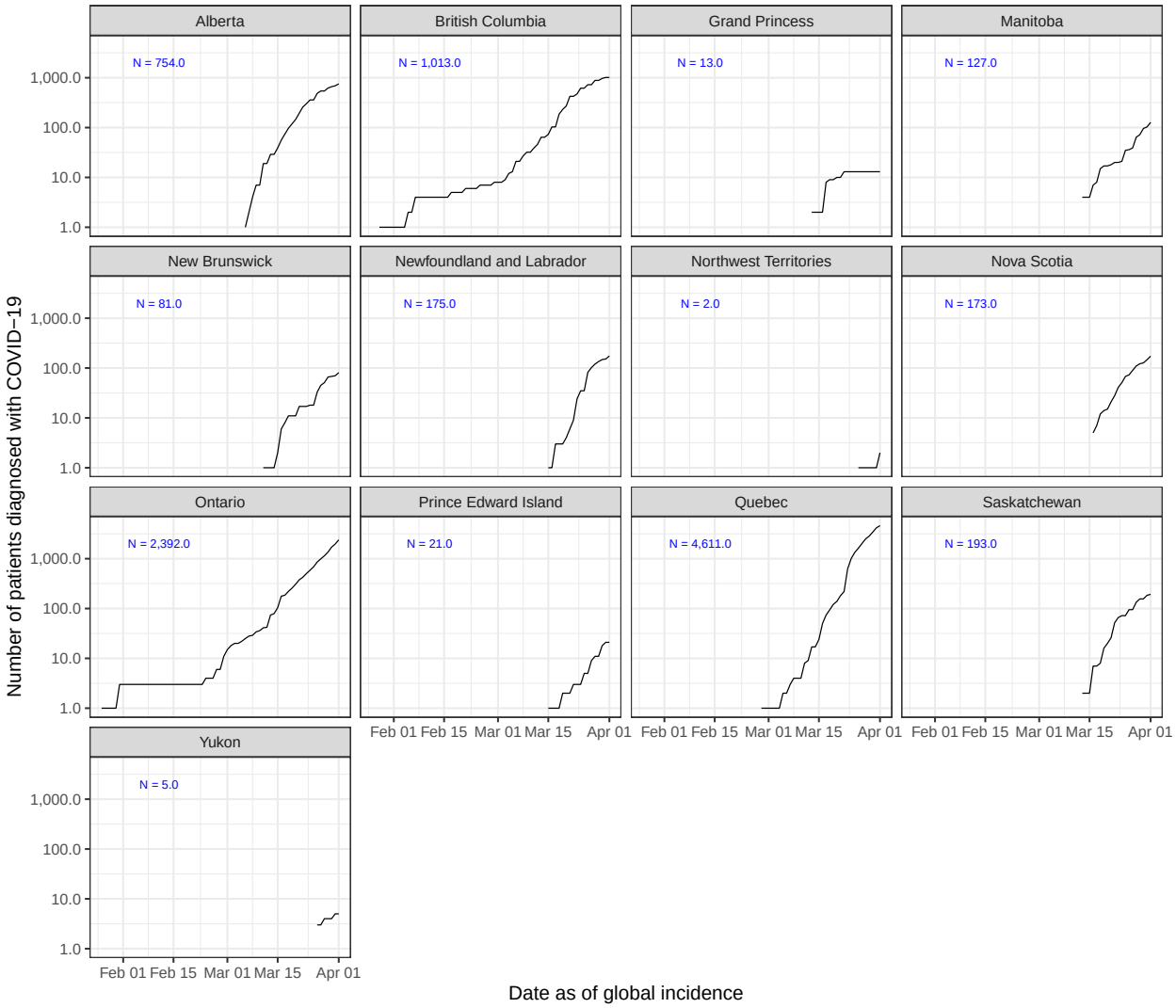
```
setwd("COVID-19/csse_covid_19_data/csse_covid_19_time_series")
casedf = read.csv("time_series_covid19_confirmed_global.csv", header=T, check.names=F)
casedf = casedf[casedf[,2]=="Canada", c(1, 5:ncol(casedf))]
provinces = casedf[apply(casedf[,2:ncol(casedf)], 1, sum) > 0, 1]
casedf = casedf[casedf[,1] %in% provinces,]


moltendf = melt(casedf)
```

```
## Using Province/State as id variables
```

```
moltendf$date = as.Date(as.character(moltendf$variable), tryFormats="%m/%d/%y")

textdf = melt(casedf[,c(1, ncol(casedf))])
```

```
## Using Province/State as id variables
```

```
textdf$date = as.Date(as.character(textdf$variable), tryFormats="%m/%d/%y")
textdf$date = min(as.Date(textdf$date)) - 50
textdf$Label = paste("N =", comma(round(textdf$value)))
textdf$value = 2000

P = ggplot(moltendf[moltendf$value > 0,], aes(x=date, y=value, group=`Province/State`)) +
  geom_line() +
  geom_text(data=textdf, aes(label=Label), colour="blue") +
  theme_bw(base_size=18) +
  facet_wrap(~`Province/State`) +
  scale_y_log10("Number of patients diagnosed with COVID-19", labels=comma) +
  xlab("Date as of global incidence")
plot(P)
```

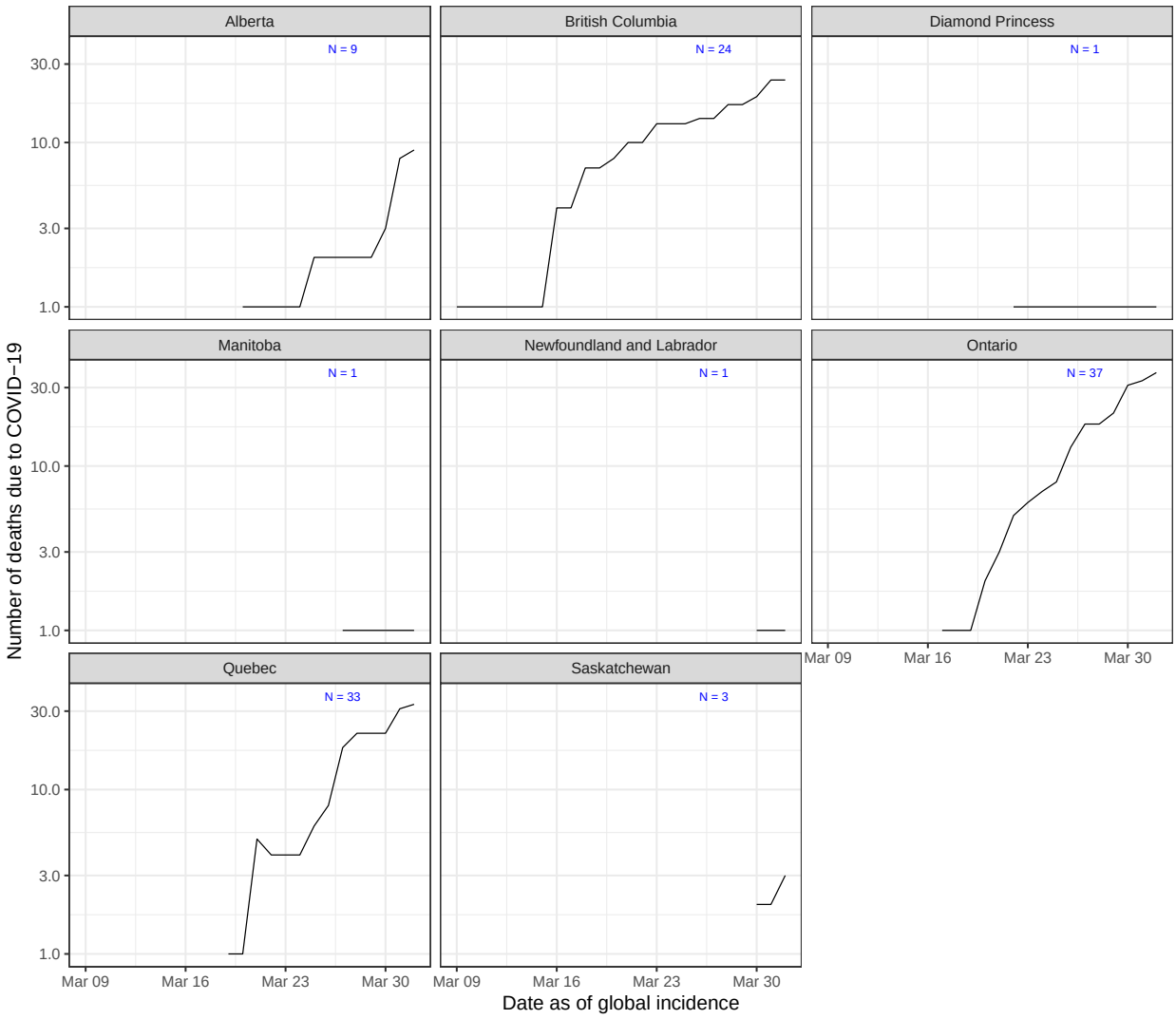


Canada's deaths

```
setwd("COVID-19/csse_covid_19_data/csse_covid_19_time_series")
casedf = read.csv("time_series_covid19_deaths_global.csv", header=T, check.names=F)
casedf = casedf[casedf[,2]=="Canada", c(1, 5:ncol(casedf))]
provinces = casedf[apply(casedf[,2:ncol(casedf)], 1, sum) > 0, 1]
casedf = casedf[casedf[,1] %in% provinces,]


moltendf = melt(casedf)


## Using Province/State as id variables
```

```
moltendf$date = as.Date(as.character(moltendf$variable), tryFormats="%m/%d/%y")

textdf = melt(casedf[,c(1, ncol(casedf))])


## Using Province/State as id variables
```

```
textdf$date = as.Date(as.character(textdf$variable), tryFormats="%m/%d/%y")
textdf$date = min(as.Date(textdf$date)) - 5
textdf$Label = paste("N =", comma(round(textdf$value)))
textdf$value = max(moltendf$value)

P = ggplot(moltendf[moltendf$value > 0,], aes(x=date, y=value, group=`Province/State`)) +
  geom_line() +
  geom_text(data=textdf, aes(label=Label), colour="blue") +
  theme_bw(base_size=18) +
  facet_wrap(~`Province/State`) +
  scale_y_log10("Number of deaths due to COVID-19", labels=comma) +
  xlab("Date as of global incidence")
plot(P)
```


Alberta
N = 9
British Columbia
N = 24
Diamond Princess
N = 1
Manitoba
N = 1
Newfoundland and Labrador
N = 1
Ontario
N = 37
Quebec
N = 33
Saskatchewan
N = 3
30.0
10.0
3.0
1.0
Number of deaths due to COVID−19
Mar 09
Mar 16
Mar 23
Mar 30
Date as of global incidence