Transmission Risk Comparison

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Libraries

```
library(tidyverse)
library(ggplot2)
require("knitr")
library(gridExtra)
library(grid)
library(lubridate)
library(dplyr)
library(hms)
library(truncdist)
library(crch)
library(stats)
library(LaplacesDemon)
library(ggstatsplot)
library(MASS)
library(fitdistrplus)
```

Data

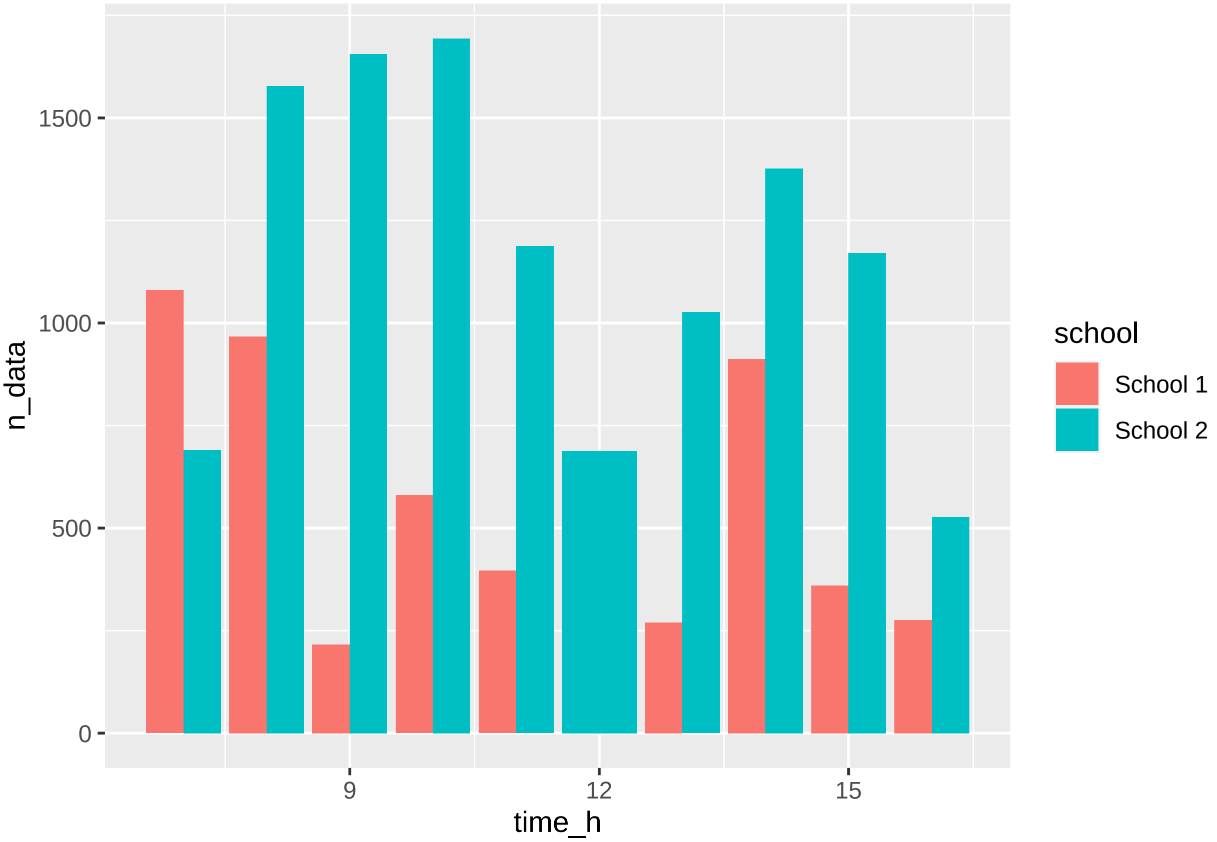
```
ch <- readRDS("data-clean/co2-ch.rds") #swiss data
satz <- readRDS("data-clean/co2-sa-tz.rds")

ch <- ch %>%
  filter(co2 > 400)

sa <- satz %>%
  filter(country == "South Africa") %>%
  filter(co2 < 3000) %>%
  filter(co2 > 400) #south africa data

tz <- satz %>%
  filter(country == "Tanzania") %>%
  filter(co2 < 3000) %>%
  filter(co2 > 400) #tanzania data
```

Methods

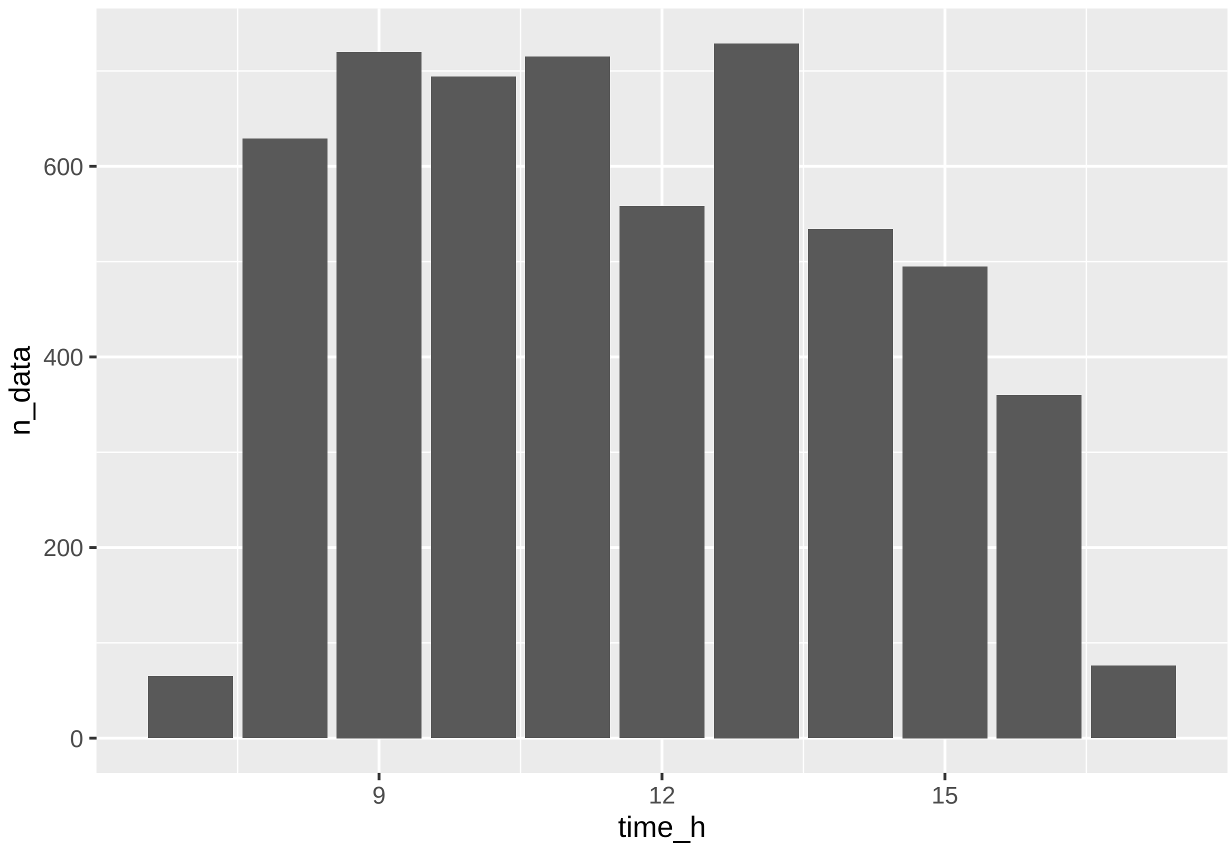
Indoor Co2 concentration
* mean or distribution from data
* C_o := Outdoor Co2 concentration * from literature https://www.fsis.usda.gov/sites/default/files/media_file/2020-08/Carbon-Dioxide.pdf
* C_a := Volume fraction of CO2 added to exhaled breath during breathing
* Persily and de Jonge [Table 3 and 4] doi: 10.1111/ina.12383
* $\bar{f} := \int_{t=0}^{t=max} f dt$
* integrating over f values from different times (2) or using a distribution based on the data
* I := Number of infectors in the class
* estimated using prevalence of the age group in the country
* q := Quantum per hour
* assuming a distribution from literature
* t := time
* changing this parameter to compare
* n := number of people in the class
* data (Switzerland) or assumption (South Africa, Tanzania)

Preprocess

```r
ch_hourly <- ch %>%
  mutate(time_h = hour(time)) %>%
  group_by(school, time_h) %>%
  summarize(mean = mean(co2),
            lower = quantile(co2, 0.25),
            upper = quantile(co2, 0.75),
            n_data = n()) %>%
  ungroup()

ch_hourly %>%
  ggplot(aes(x = time_h, y = n_data, fill = school)) +
  geom_bar(stat = "identity", position = position_dodge())
```



```
# there is a reasonable number of data points per hour but missing data at hour 12 for school 2 (no les

tz_hourly <- tz %>%
  mutate(time_h = hour(date)) %>%
  group_by(time_h) %>%
  summarize(mean = mean(co2),
            lower = quantile(co2, 0.25),
            upper = quantile(co2, 0.75),
            n_data = n()) %>%
  ungroup()

tz_hourly %>%
  ggplot(aes(x = time_h, y = n_data)) +
  geom_bar(stat = "identity", position = position_dodge())
```

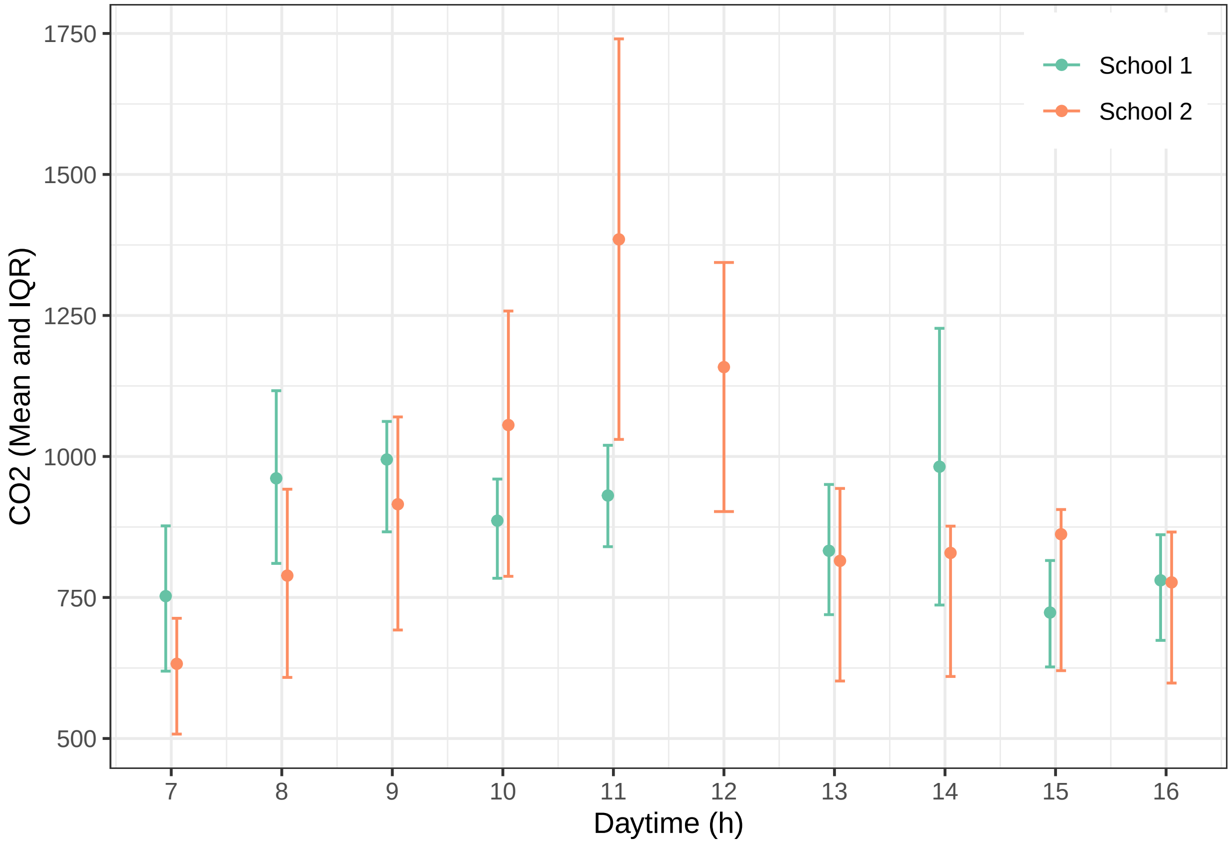


```
# data is measured throughout the day in south africa
```

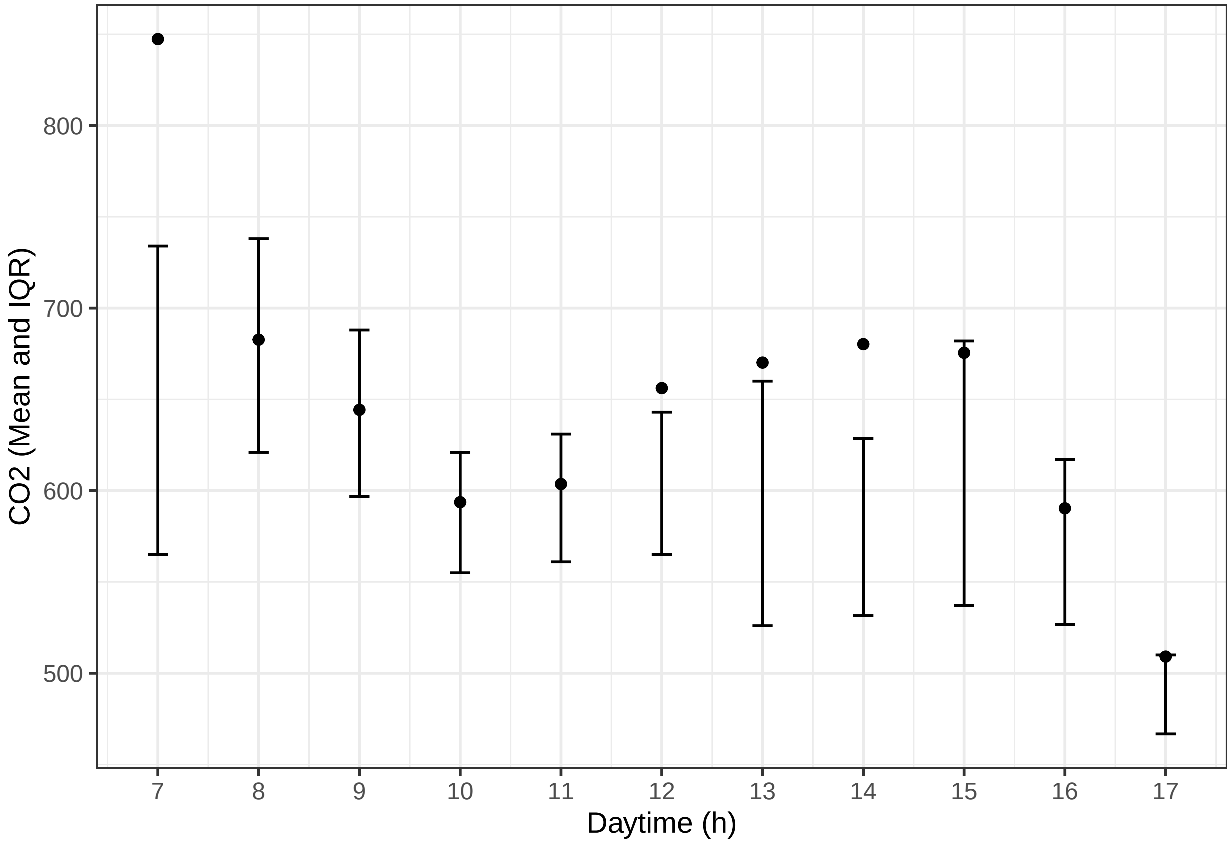
Analysis

Co2 over time

```
ch_hourly %>% #plot co2 during the day (ch)
  ggplot(aes(x = time_h, group = school, color = school)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = .2, position =     position_dodge2(width = .2))
  geom_point(aes(y = mean), position = position_dodge2(width = .2)) +
  scale_color_brewer(palette = "Set2") +
  scale_x_continuous(breaks = seq(7, 16, 1)) +
  labs(x = "Daytime (h)", y = "CO2 (Mean and IQR)") +
  theme_bw() +
  theme(legend.position = c(0.9,0.9), legend.title = element_blank())
```



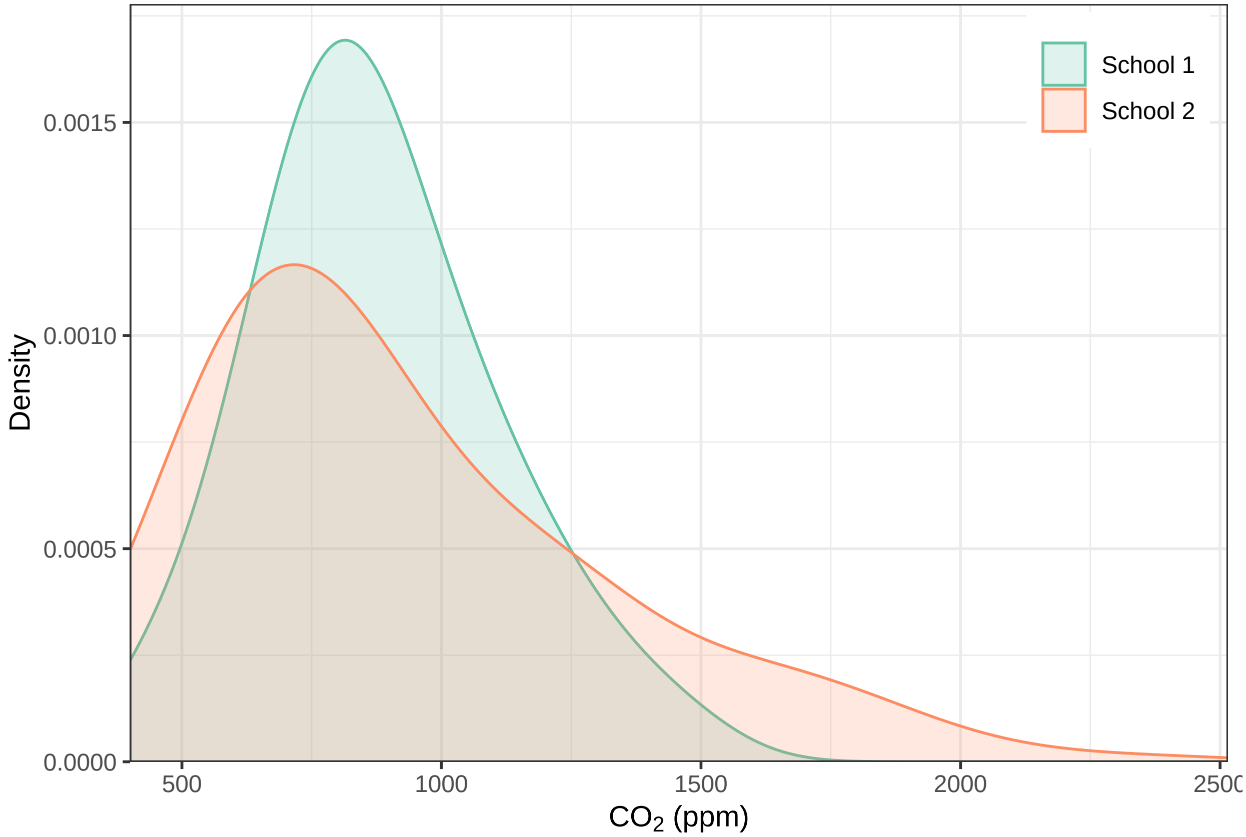
```
tz_hourly %>% #plot co2 during the day (tz)
  ggplot(aes(x = time_h)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = .2, position =    position_dodge2(width = .2))
  geom_point(aes(y = mean), position = position_dodge2(width = .2)) +
  scale_color_brewer(palette = "Set2") +
  scale_x_continuous(breaks = seq(7, 17, 1)) +
  labs(x = "Daytime (h)", y = "CO2 (Mean and IQR)") +
  theme_bw() +
  theme(legend.position = c(0.9,0.9), legend.title = element_blank())
```



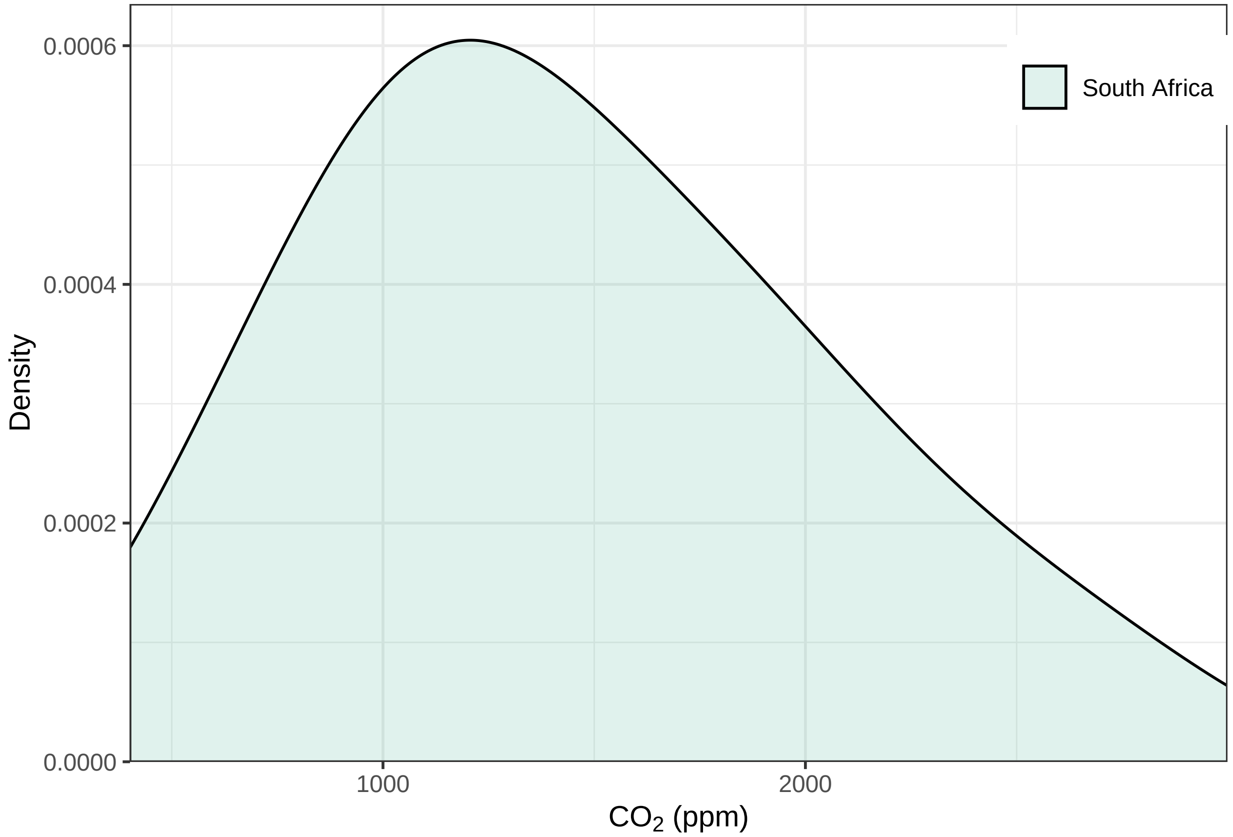
```
#no time data available for south africa
```

Co2 distribution

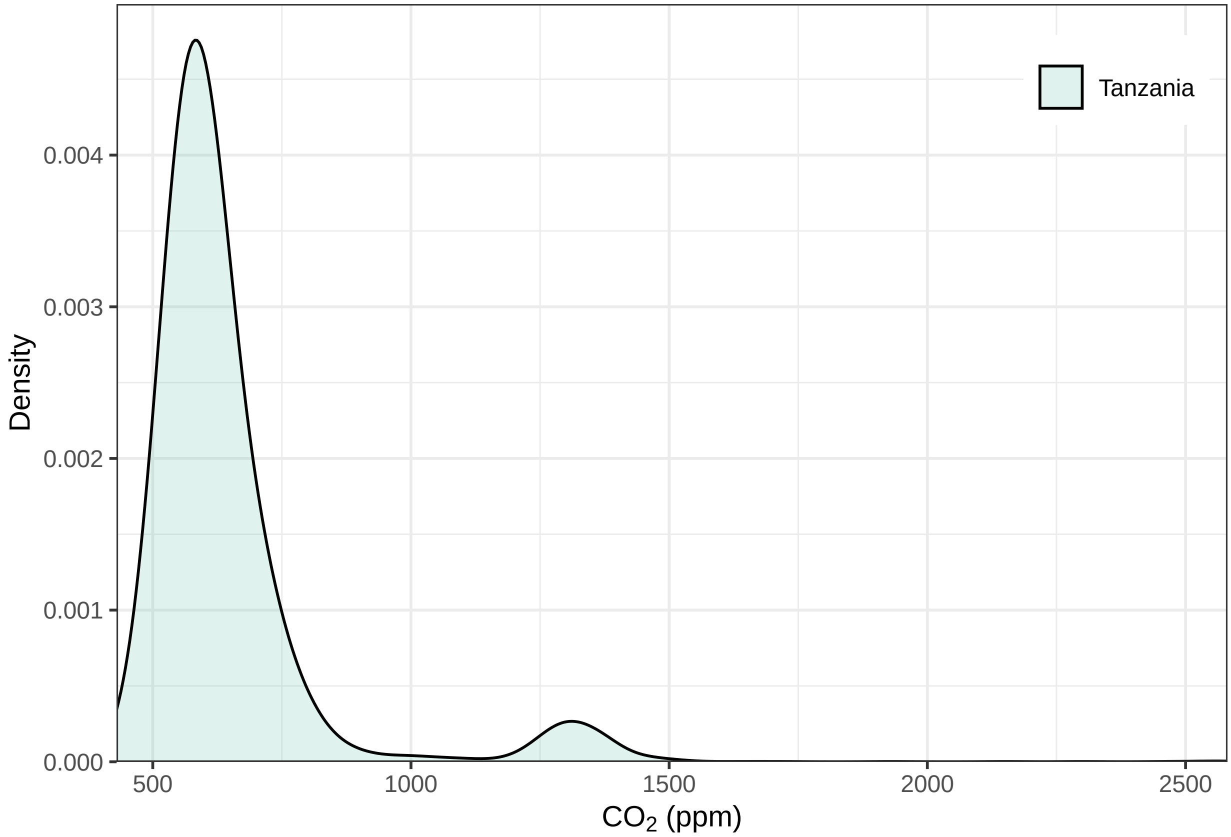
```
ch %>% #density plot ch
  ggplot(aes(x = co2, color = school, fill = school)) +
  geom_density(alpha = .2, kernel = "gaussian", adjust = 3) +
  scale_x_continuous(expand = c(0,0)) +
  scale_color_brewer(palette = "Set2") +
  scale_fill_brewer(palette = "Set2") +
  scale_y_continuous(expand = expansion(mult = c(0, 0.05))) +
  labs(x = expression(CO[2]*" (ppm)"), y = "Density") +
  theme_bw() +
  theme(legend.position = c(0.9,0.9), legend.title = element_blank())
```



```
sa %>% #density plot sa
  ggplot(aes(x = co2, fill = country)) +
  geom_density(alpha = .2, kernel = "gaussian", adjust = 4) +
  scale_x_continuous(expand = c(0,0)) +
  scale_color_brewer(palette = "Set2") +
  scale_fill_brewer(palette = "Set2") +
  scale_y_continuous(expand = expansion(mult = c(0, 0.05))) +
  labs(x = expression(CO[2]*" (ppm)"), y = "Density") +
  theme_bw() +
  theme(legend.position = c(0.9,0.9), legend.title = element_blank())
```

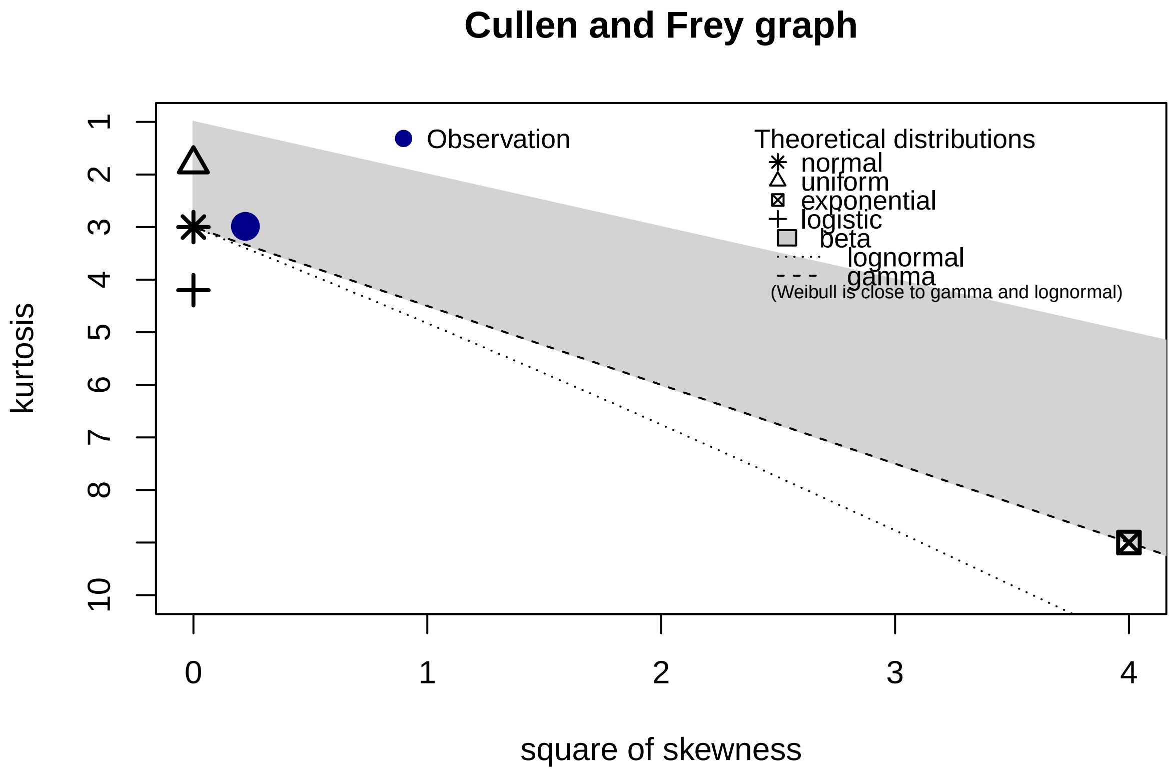


```
tz %>% #density plot tz
  ggplot(aes(x = co2, fill = country)) +
  geom_density(alpha = .2, kernel = "gaussian", adjust = 3) +
  scale_x_continuous(expand = c(0,0)) +
  scale_color_brewer(palette = "Set2") +
  scale_fill_brewer(palette = "Set2") +
  scale_y_continuous(expand = expansion(mult = c(0, 0.05))) +
  labs(x = expression(CO[2]*" (ppm)"), y = "Density") +
  theme_bw() +
  theme(legend.position = c(0.9,0.9), legend.title = element_blank())
```



### Distribution co2

```
#C_a
C_a <- (((0.0048+0.0041+0.0053 +0.0042)/4)*60)/8 #https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5666301/

#C_o
C_o <- 400 #p.p.m (taking a higher estimate because higher values ar possible when a lot of traffic ect
## all schools are directly on the side of a road (no info for tanzania), so i won't make a distinction

#school1
x_ch1 <- ch %>%
  filter(school == "School 1") %>%
  pull(co2)

descdist(x_ch1, discrete = FALSE) #normal distribution fits well
```

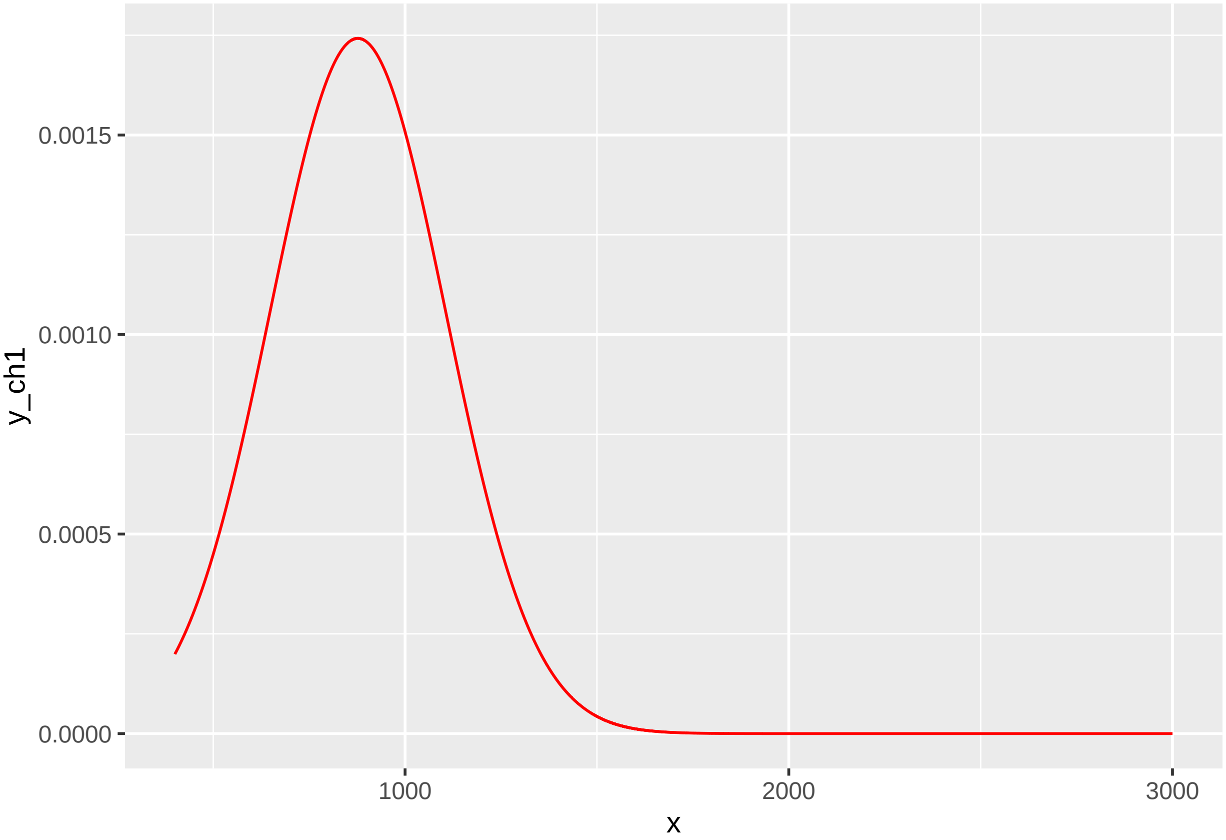


```
## summary statistics
## ------
## min:  431.17   max:  1561.93
## median:  848.87
## mean:  877.1516
## estimated sd:  228.6292
## estimated skewness:  0.4714223
## estimated kurtosis:  2.986206
```

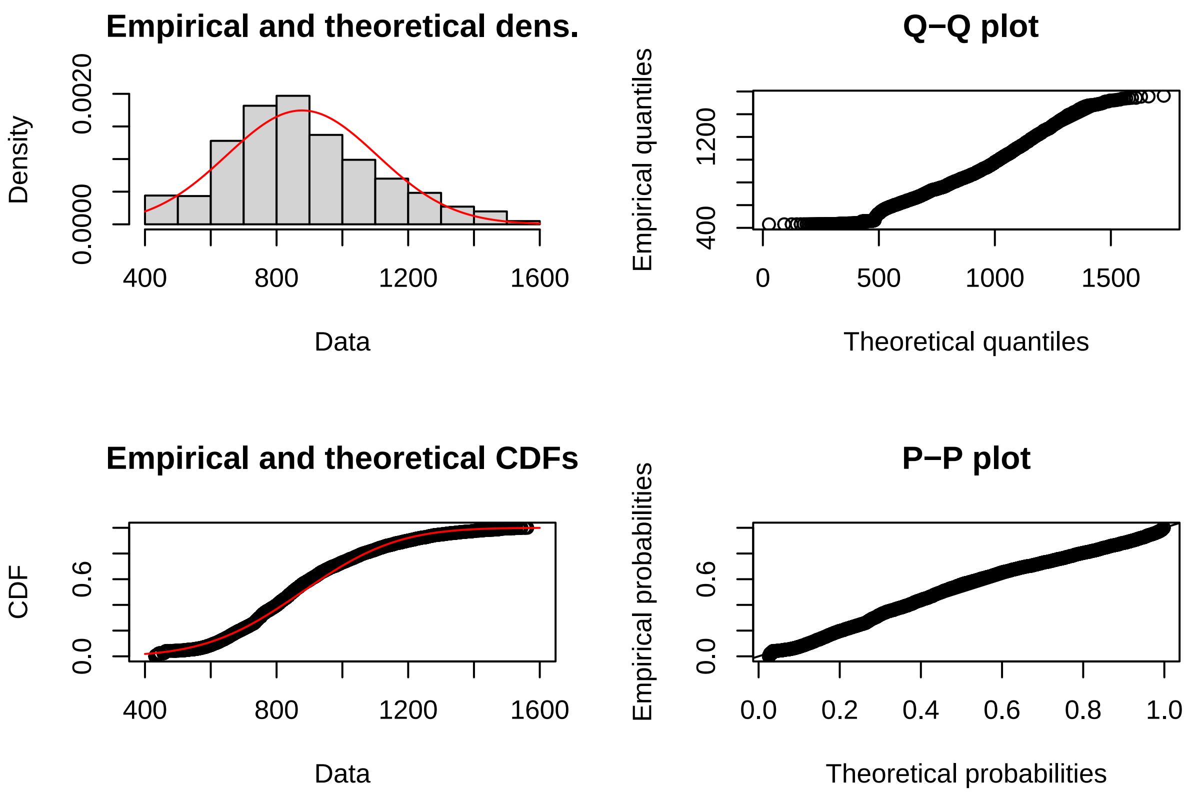
```
fitdistr(x_ch1, "normal") #get parameters
```

```
##       mean          sd
##   877.151602   228.606581
##  (  3.214713) (  2.273146)
```

```
x <- seq(400, 3000, by = .1)
y_ch1 <- dnorm(x, mean = 877, sd = 229)
x_ch1_norm <- data.frame(cbind(x,y_ch1))

x_ch1_norm %>%
  ggplot(aes(x=x,y=y_ch1)) +
  geom_line(color= "red") #plot density
```

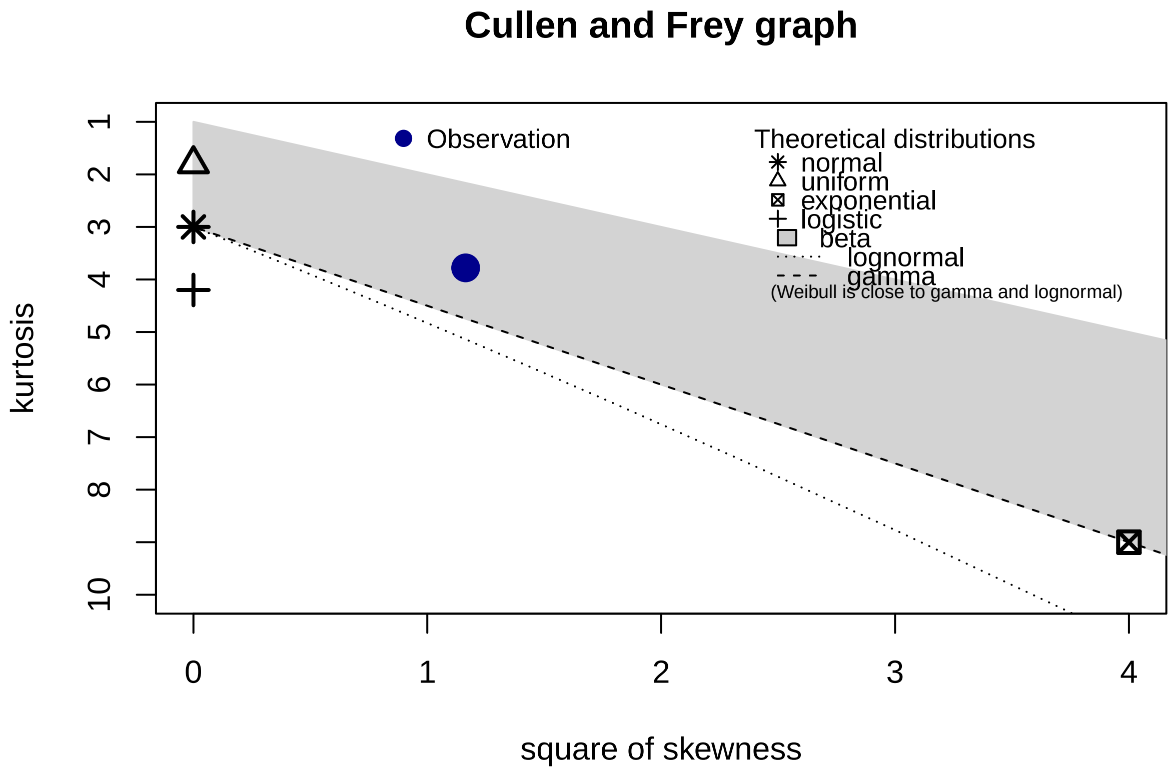


```
ch1_fit_norm <- fitdist(x_ch1, "norm", lower=c(0,0)) #different fitting function
plot(ch1_fit_norm) #plots comparison
```



```
co2_distr_ch1 <- data.frame(co2 = seq(400, 3000, .1)) %>%
  mutate(prob = dnorm(co2,877,299))

sample_co2_ch1 <- sample(co2_distr_ch1$co2, 1000, replace = TRUE, prob = co2_distr_ch1$prob) #sample co
sample_f_ch1 <- tibble(co2 = sample_co2_ch1, f = ((co2-C_o)/C_a)/1000000) %>% #sample f
  dplyr::select(-co2)
```

```
#school 2
x_ch2 <- ch %>%
  filter(school == "School 2") %>%
  pull(co2)

descdist(x_ch2, discrete = FALSE) #gamma or beta distribution fits well
```

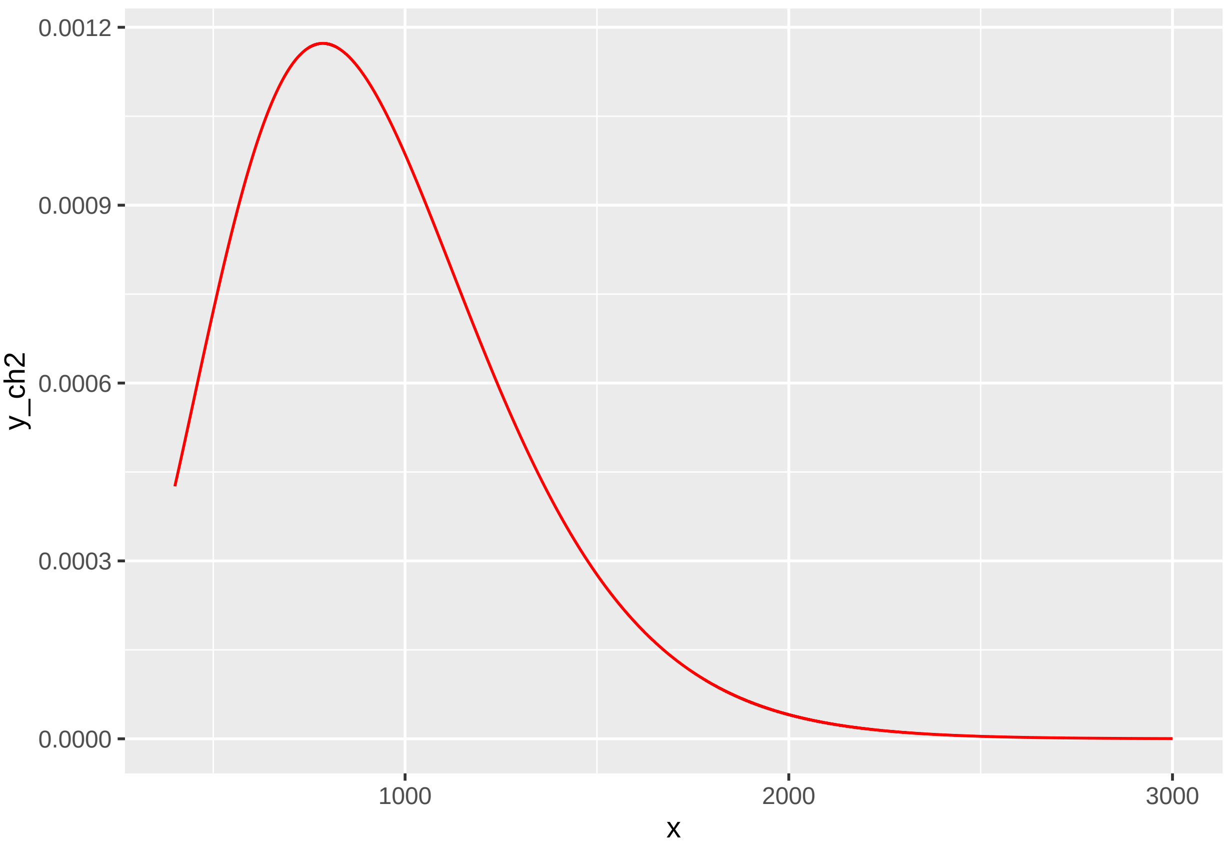


```
## summary statistics
## ------
## min:  400.03   max:  2515.03
## median:  828.6
## mean:  933.4951
## estimated sd:  389.1754
## estimated skewness:  1.078812
## estimated kurtosis:  3.778963
```

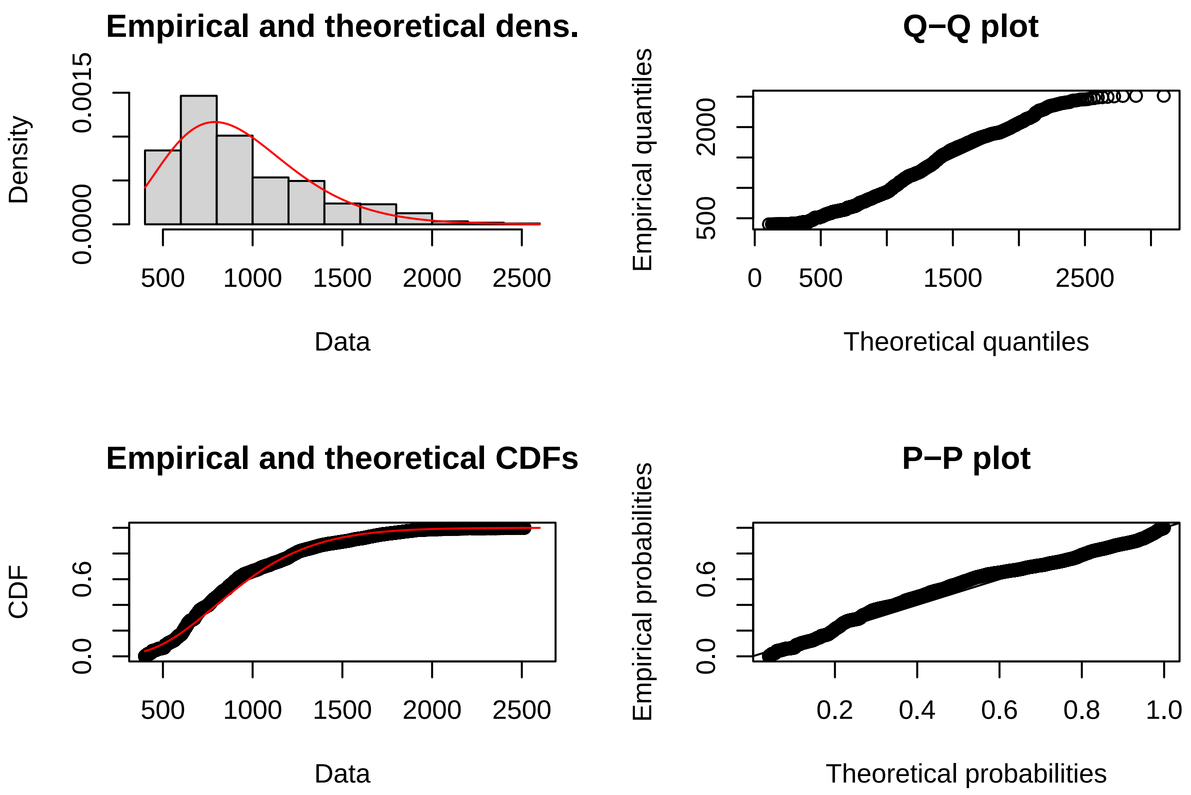
```
fitdistr(x_ch2, "gamma") #get parameters
```

```
##        shape            rate
##    6.49189374456   0.00695440525
##   (0.07685943654) (0.00008471348)
```

```
y_ch2 <- dgamma(x, 6.5, 0.007)
x_ch2_gamma <- data.frame(cbind(x,y_ch2))

x_ch2_gamma %>%
  ggplot(aes(x=x,y=y_ch2)) +
  geom_line(color= "red") #plot density
```

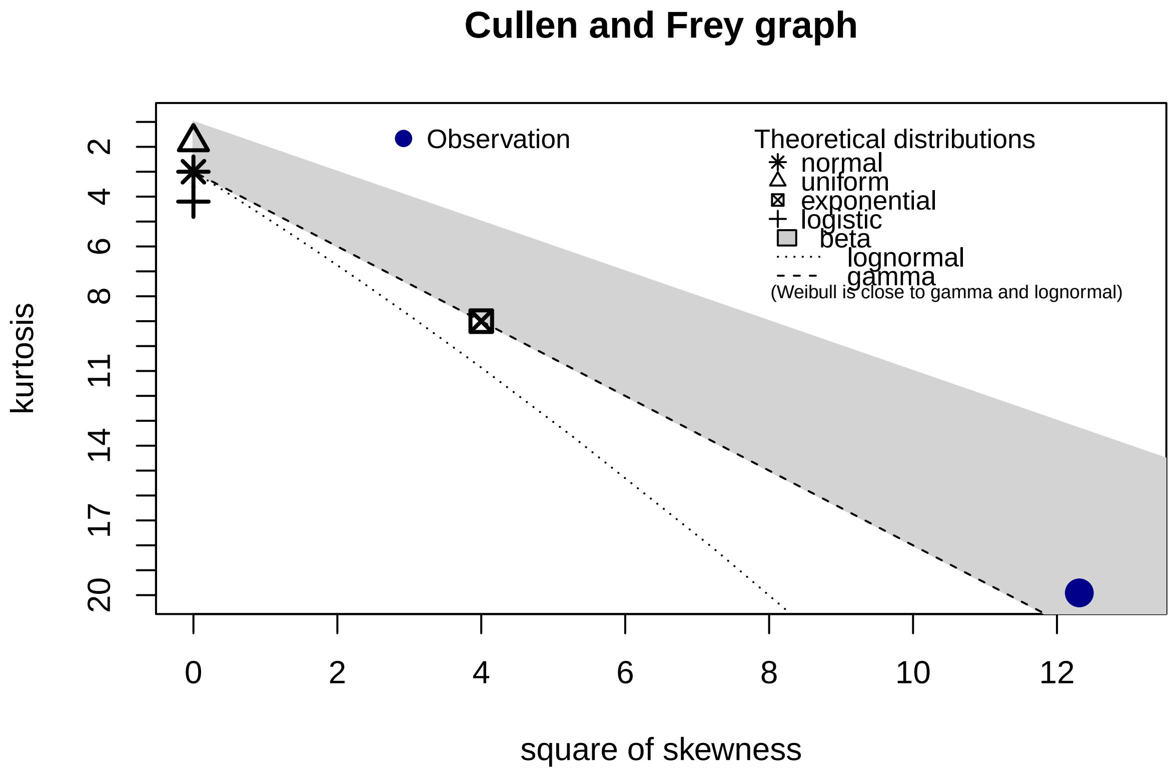


```
ch2_fit_gamma <- fitdist(x_ch2, "gamma") #different fitting function
plot(ch2_fit_gamma) #plots comparison
```



```
co2_distr_ch2 <- data.frame(co2 = seq(400, 3000, .1)) %>%
  mutate(prob = dgamma(co2,6.5,0.007))

sample_co2_ch2 <- sample(co2_distr_ch2$co2, 1000, replace = TRUE, prob = co2_distr_ch2$prob) #sample
sample_f_ch2 <- tibble(co2 = sample_co2_ch2, f = ((co2-C_o)/C_a)/1000000) %>%
  dplyr::select(-co2)
```

```
#tanzania

x_tz <- tz %>%
  pull(co2)

x_tz <- as.numeric(x_tz)

descdist(x_tz, discrete = FALSE) #gamma fits ok
```

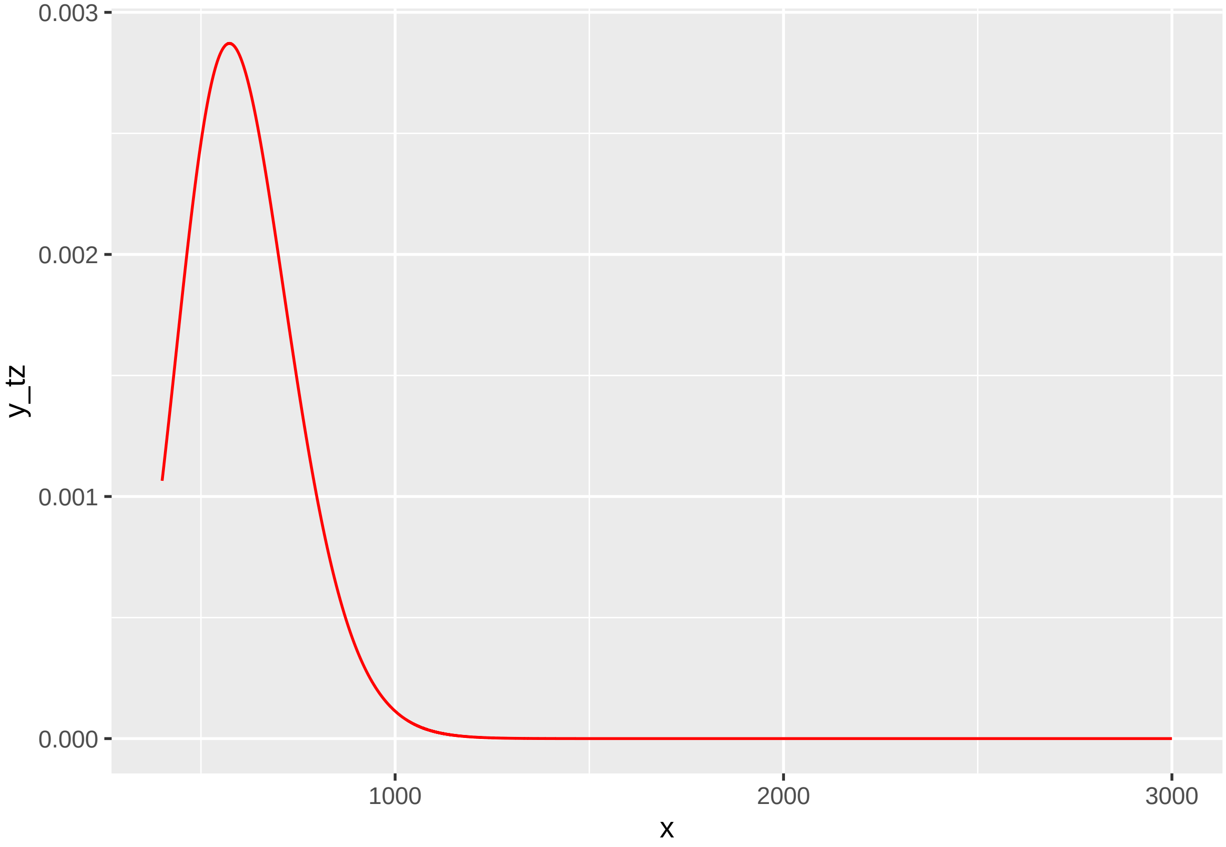


```
## summary statistics
## ------
## min:  430   max:  2581
## median:  601
## mean:  644.9383
## estimated sd:  184.4097
## estimated skewness:  3.508629
## estimated kurtosis:  19.91035
```

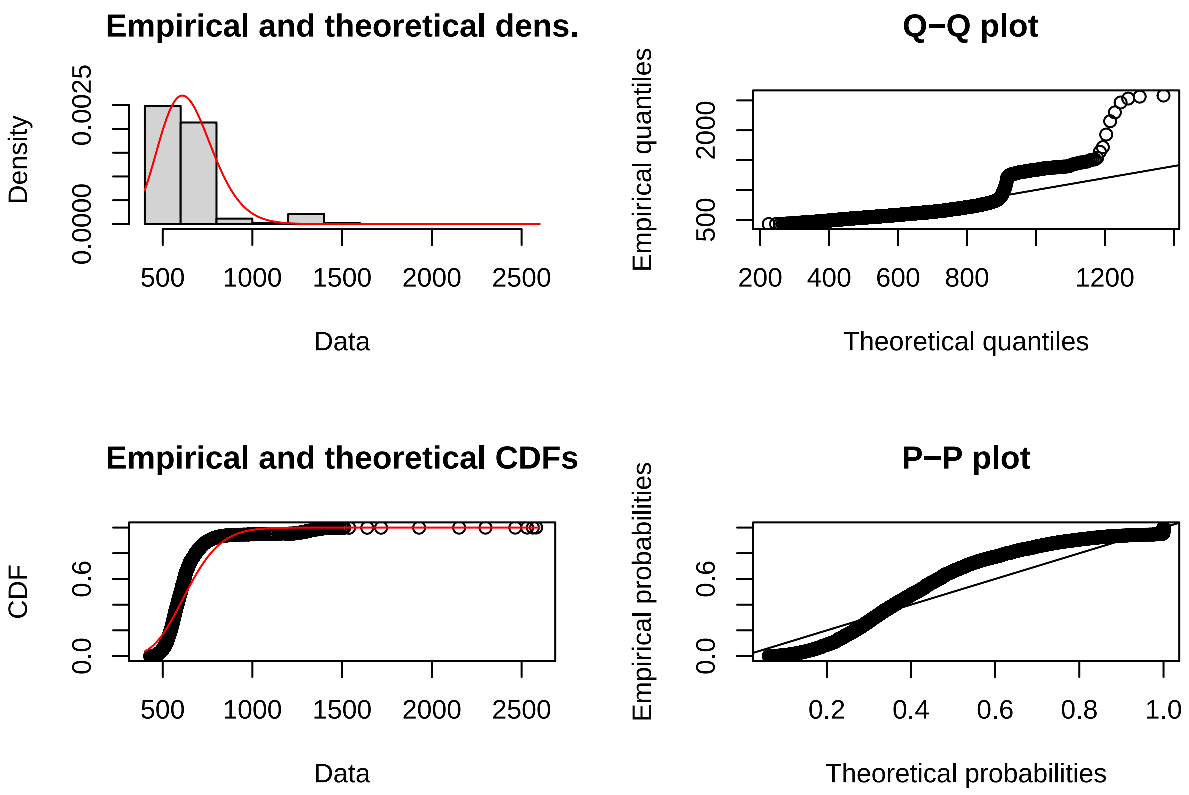
```
fitdistr(x_tz, "gamma") #get parameters
```

```
##        shape           rate
##   18.1844020924    0.0281955963
##  ( 0.3363085749) ( 0.0005283763)
```

```
#fitdistr(x_tz, "beta", start = list (shape1 = 8, shape2 = 8)) # funktioniert nicht

y_tz <- dgamma(x, 18.2, 0.03)
x_tz_gamma <- data.frame(cbind(x,y_tz))

x_tz_gamma %>%
  ggplot(aes(x=x,y=y_tz)) +
  geom_line(color= "red")
```

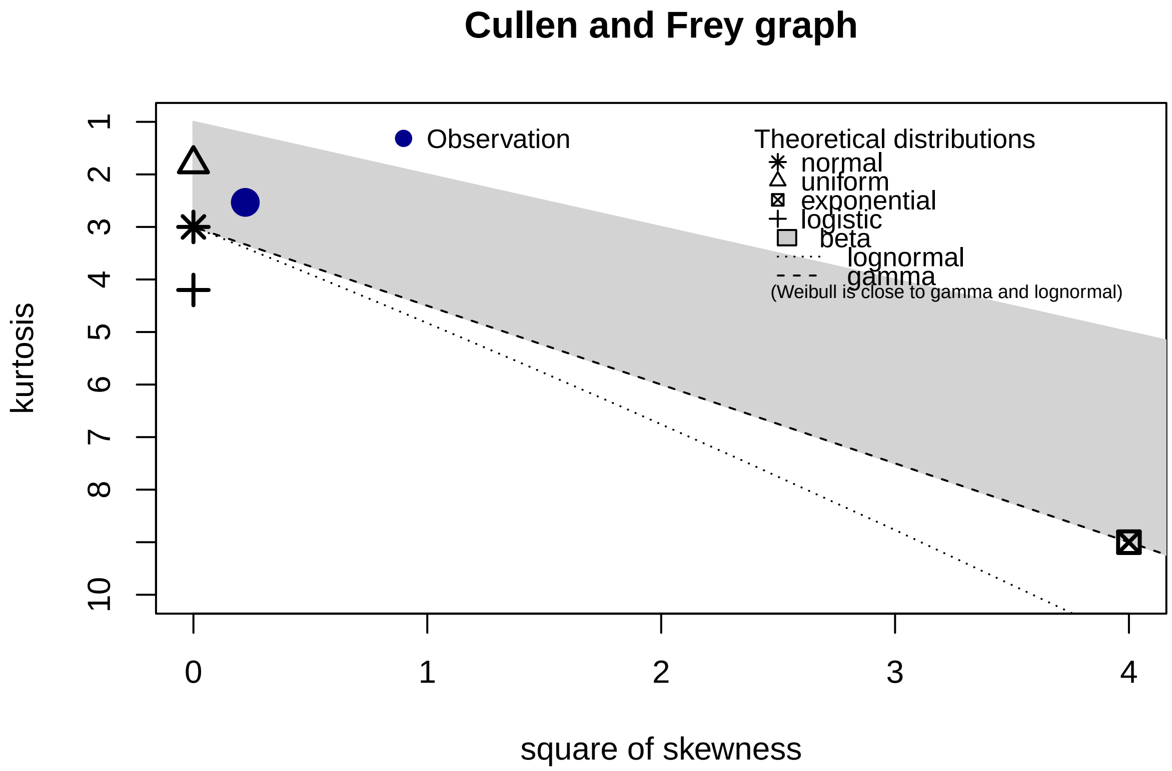


```
tz_fit_gamma <- fitdist(x_tz, "gamma") #different fitting function
plot(tz_fit_gamma) #plots comparison
```



```
co2_distr_tz <- data.frame(co2 = seq(400, 3000, .1)) %>%
  mutate(prob = dnorm(co2,648,209))

sample_co2_tz <- sample(co2_distr_tz$co2, 1000, replace = TRUE, prob = co2_distr_tz$prob) #sample
sample_f_tz <- tibble(co2 = sample_co2_tz, f = ((co2-C_o)/C_a)/1000000) %>%
  dplyr::select(-co2)
```

```
#south africa

x_sa <- sa %>%
  pull(co2)

x_sa <- as.numeric(x_sa)

descdist(x_sa, discrete = FALSE) #normal/gamma fits ok -> after comparison --> gamma is better
```

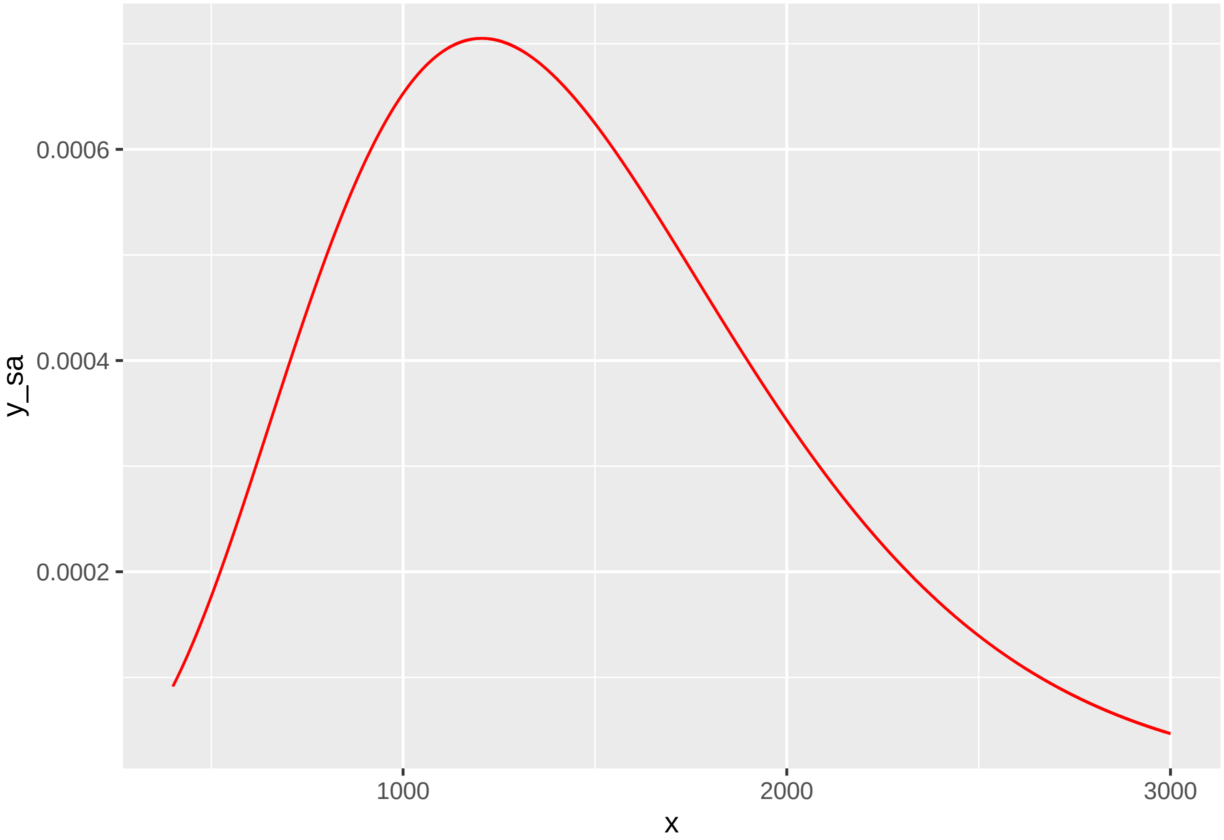


```
## summary statistics
## ------
## min:  401   max:  2999
## median:  1377
## mean:  1456.939
## estimated sd:  596.1244
## estimated skewness:  0.4709815
## estimated kurtosis:  2.532455
```

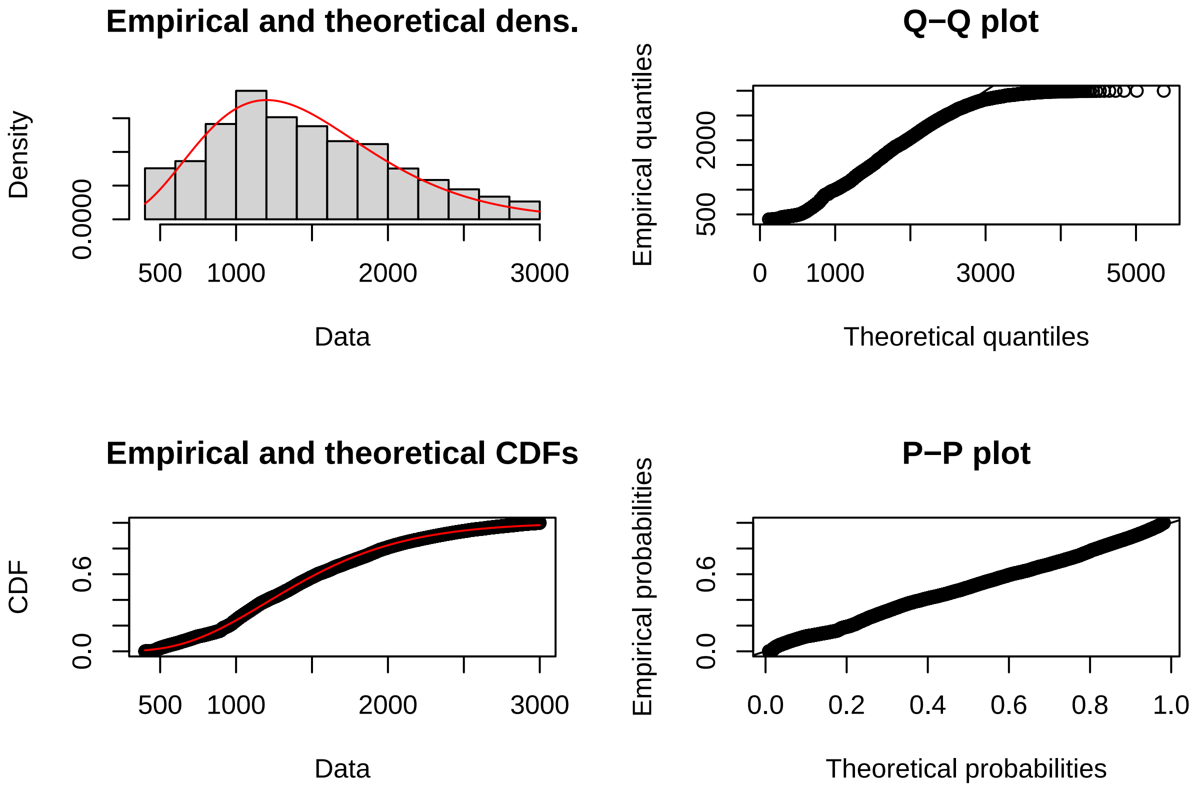
```
fitdistr(x_sa, "gamma") #get parameters
```

```
##        shape           rate
##   5.70826320474   0.00391798932
##  (0.04222129369) (0.00002928928)
```

```
y_sa <- dgamma(x, 5.7, 0.0039)
x_sa_gamma <- data.frame(cbind(x,y_sa))

x_sa_gamma %>%
  ggplot(aes(x=x,y=y_sa)) +
  geom_line(color= "red")
```



```
sa_fit_gamma<- fitdist(x_sa, "gamma") #different fitting function
plot(sa_fit_gamma) #plots comparison
```



```
co2_distr_sa <- data.frame(co2 = seq(400, 3000, .1)) %>%
  mutate(prob = dgamma(co2,5.7,0.0039))

sample_co2_sa <- sample(co2_distr_sa$co2, 1000, replace = TRUE, prob = co2_distr_sa$prob) #sample
sample_f_sa <- tibble(co2 = sample_co2_sa, f = ((co2-C_o)/C_a)/1000000) %>%
  dplyr::select(-co2)
```

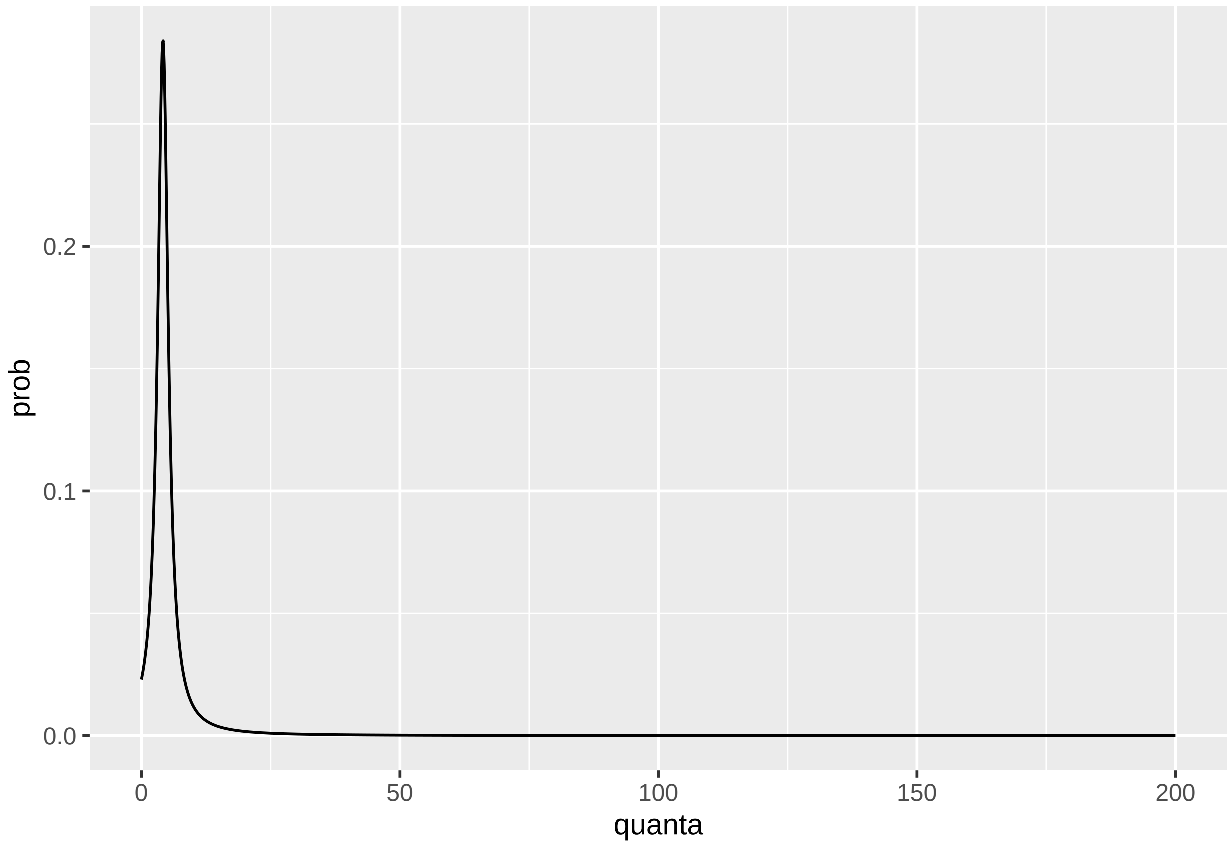
Quanta

I'll use the following studies for calculating the meanparameter:

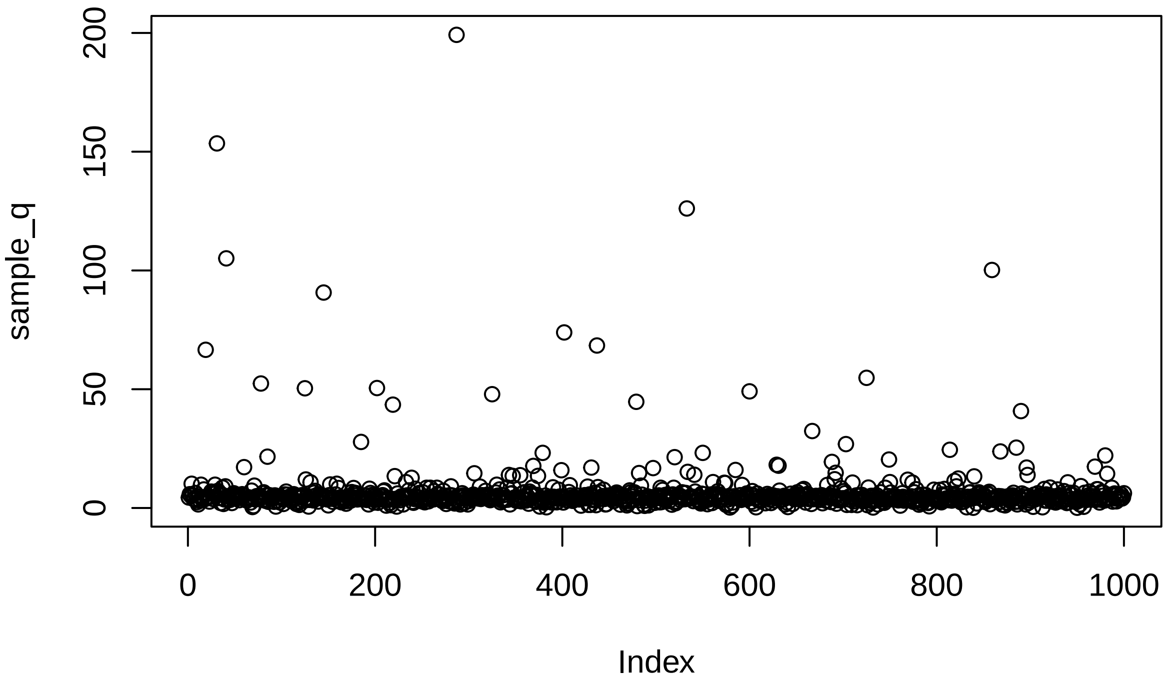
Riley (1962): 130 patients, q: 1.25 Escombe (2008): 117 patients, q: 8.2 Nardell (1991) : 1 patients, q: 12.5 Andrews (2014) : 571 patients, q: 0.89 Dhamadhakari (2012) : 17 patients, q: 138/34 (no mask/mask)

```
q <- (1.25*130+8.2*117+12.5+0.89*571+138*17)/(130+117+1+571+138) #weighted mean from different studies

#Escombe Table 2
mean_one_inf <- mean(c(12,3,5.5,1.8,18,12)) #mean quanta of pers. which infected one pig
mean_two_inf <- mean(c(2.9,40)) #mean quanta of pers. which infected two pigs
q_inf_persons <- c(12,3,2.9,5.5,1.8,18,40,12,226,52,mean_two_inf,rep(mean_one_inf,11))
#reported quanta plus the two missing
q_sample_total_unif <- c(q_inf_persons, runif(117-length(q_inf_persons), min = 0, max =1))
#rest unif in [0,1], as quanta below 1 isnt enough to infect an indidual

#density function for q
```

```
dq <- function(x) {
  dtrunc(x, spec = "st", a = 0, b = 300, mu = q, sigma = 1.235, nu = 1) #sigma aus Escombe (mean über 1
}

rq_distr <- data.frame(quanta = seq(0, 200, .1)) %>%
  mutate(prob = dq(quanta))

rq_distr %>%
  ggplot(aes(x = quanta, y = prob)) +
  geom_line()
```



```
sample_q <- sample(rq_distr$quanta, 1000, replace = TRUE, prob = rq_distr$prob) #sample q for calculati
plot(sample_q)
```



Rest of the parameters

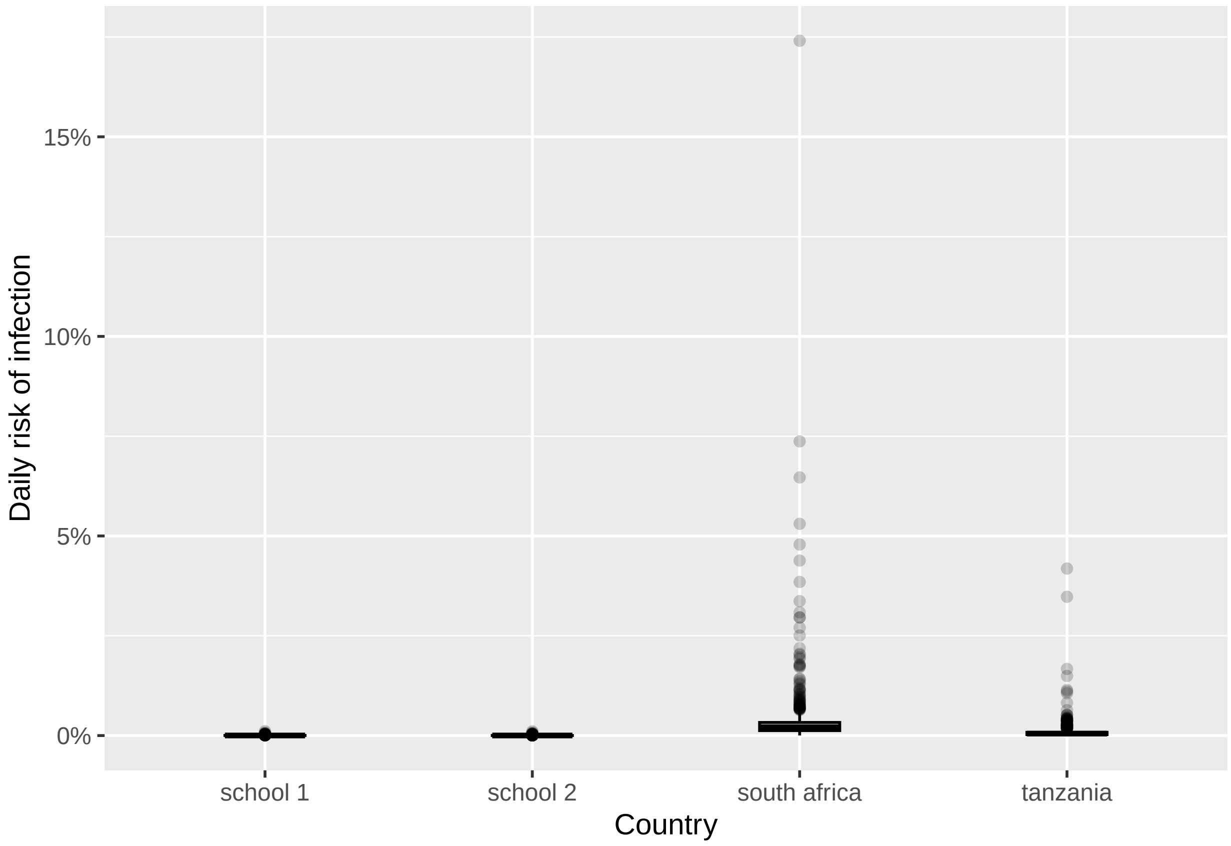
```
#n
n_ch <- 20
n_sa <- 30 #Powerpoint
n_tz <- 50 #Powerpoint

#I
prev_ch <- (0.46 + 8.23)/200000 #decimal; values for age group 10-14 and 15-19 https://www.bag.admin.ch

age_group <- sum(c(2837833, 2766037,2890269, 2824108, 2566719, 2534956, 2351752, 2327273))
#https://www.statista.com/statistics/1330839/population-of-south-africa-by-age-group-and-gender/
prev_sa <- (6500+6500+20000+12000)/age_group
 #https://worldhealthorg.shinyapps.io/tb_profiles/?_inputs_&entity_type=%22country%22&lan=%22EN%22&iso2
# Ansteckungen in Altersgruppe 5-24 durch Population in dieser Altersgruppe (nicht 5-24 genommen, da so

prev_tz <- 0.003
#https://ntlp.go.tz/tuberculosis/paediatric-tb/

I_ch <- prev_ch*n_ch #prevalence per class (per year)
I_sa <- prev_sa*n_sa
I_tz <- prev_tz*n_sa

day <- 8
```

```
week <- 8*5
month <- 8*5*4
year <- 8*5*4*10
```

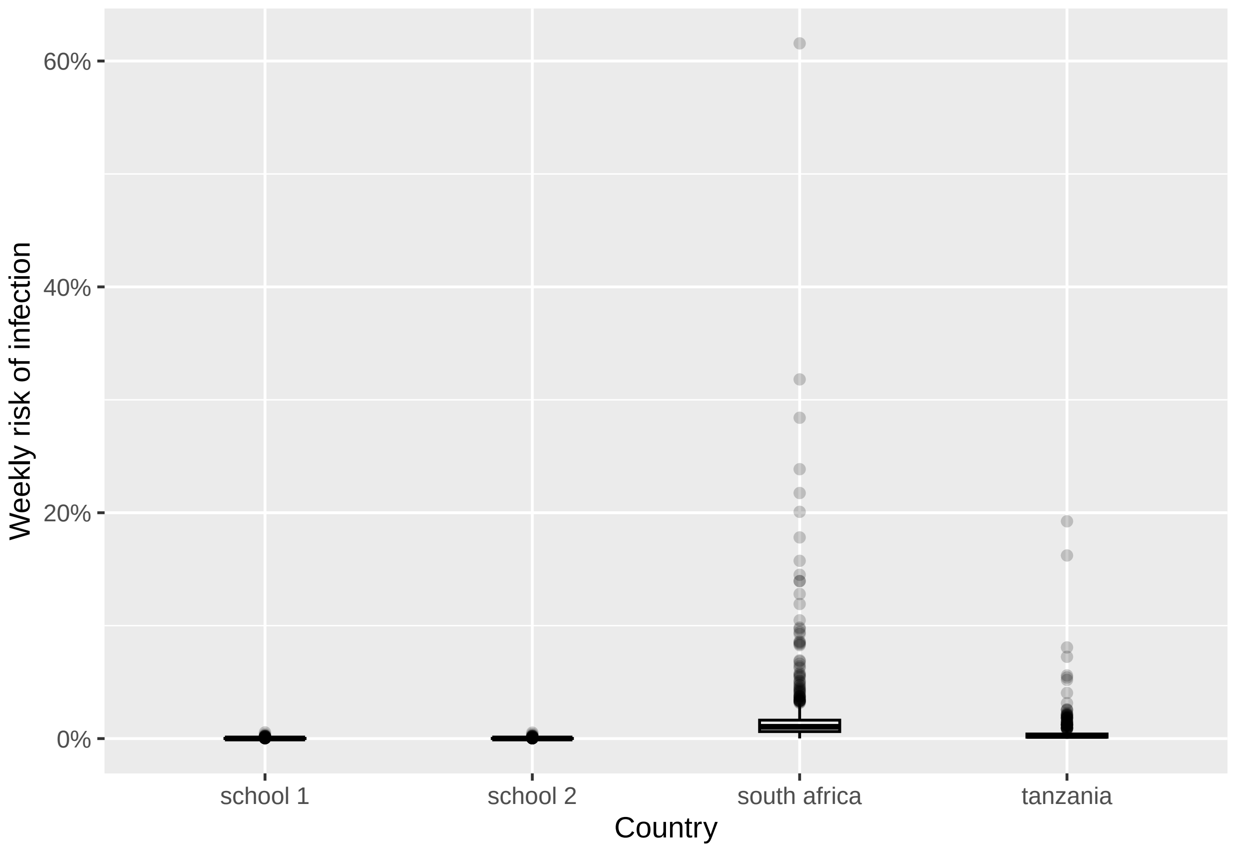
```
#preparing datasets for plotting
df_ch1 <- tibble(school = c(rep("school 1", 1000)), f = sample_f_ch1, q = sample_q) %>%
  mutate(P_year = 1 - exp(-(f*I_ch*q*year)/n_ch)) %>%
  mutate(P_month = 1 - exp(-(f*I_ch*q*month)/n_ch)) %>%
  mutate(P_week = 1 - exp(-(f*I_ch*q*week)/n_ch)) %>%
  mutate(P_day = 1 - exp(-(f*I_ch*q*day)/n_ch)) %>%
  mutate(P_year_one = 1 - exp(-(f*0.01*q*year)/n_ch)) %>%
  mutate(P_month_one = 1 - exp(-(f*0.01*q*month)/n_ch)) %>%
  mutate(P_week_one = 1 - exp(-(f*0.01*q*week)/n_ch)) %>%
  mutate(P_day_one = 1 - exp(-(f*0.01*q*day)/n_ch))

df_ch2 <- tibble(school = c(rep("school 2", 1000)), f = sample_f_ch2, q = sample_q) %>%
  mutate(P_year = 1 - exp(-(f*I_ch*q*year)/n_ch)) %>%
  mutate(P_month = 1 - exp(-(f*I_ch*q*month)/n_ch)) %>%
  mutate(P_week = 1 - exp(-(f*I_ch*q*week)/n_ch)) %>%
  mutate(P_day = 1 - exp(-(f*I_ch*q*day)/n_ch)) %>%
  mutate(P_year_one = 1 - exp(-(f*0.01*q*year)/n_ch)) %>%
  mutate(P_month_one = 1 - exp(-(f*0.01*q*month)/n_ch)) %>%
  mutate(P_week_one = 1 - exp(-(f*0.01*q*week)/n_ch)) %>%
  mutate(P_day_one = 1 - exp(-(f*0.01*q*day)/n_ch))

df_tz <- tibble(school = c(rep("tanzania", 1000)), f = sample_f_tz, q = sample_q) %>%
  mutate(P_year = 1 - exp(-(f*I_tz*q*year)/n_tz)) %>%
  mutate(P_month = 1 - exp(-(f*I_tz*q*month)/n_tz)) %>%
  mutate(P_week = 1 - exp(-(f*I_tz*q*week)/n_tz)) %>%
  mutate(P_day = 1 - exp(-(f*I_tz*q*day)/n_tz)) %>%
  mutate(P_year_one = 1 - exp(-(f*0.01*q*year)/n_ch)) %>%
  mutate(P_month_one = 1 - exp(-(f*0.01*q*month)/n_ch)) %>%
  mutate(P_week_one = 1 - exp(-(f*0.01*q*week)/n_ch)) %>%
  mutate(P_day_one = 1 - exp(-(f*0.01*q*day)/n_ch))

df_sa <- tibble(school = c(rep("south africa", 1000)), f = sample_f_sa, q = sample_q) %>%
  mutate(P_year = 1 - exp(-(f*I_sa*q*year)/n_sa)) %>%
  mutate(P_month = 1 - exp(-(f*I_sa*q*month)/n_sa)) %>%
  mutate(P_week = 1 - exp(-(f*I_sa*q*week)/n_sa)) %>%
  mutate(P_day = 1 - exp(-(f*I_sa*q*day)/n_sa)) %>%
  mutate(P_year_one = 1 - exp(-(f*0.01*q*year)/n_ch)) %>%
  mutate(P_month_one = 1 - exp(-(f*0.01*q*month)/n_ch)) %>%
  mutate(P_week_one = 1 - exp(-(f*0.01*q*week)/n_ch)) %>%
  mutate(P_day_one = 1 - exp(-(f*0.01*q*day)/n_ch))

df_complet <- bind_rows(df_ch1, df_ch2, df_sa, df_tz)
```

Plots of the transmission risk

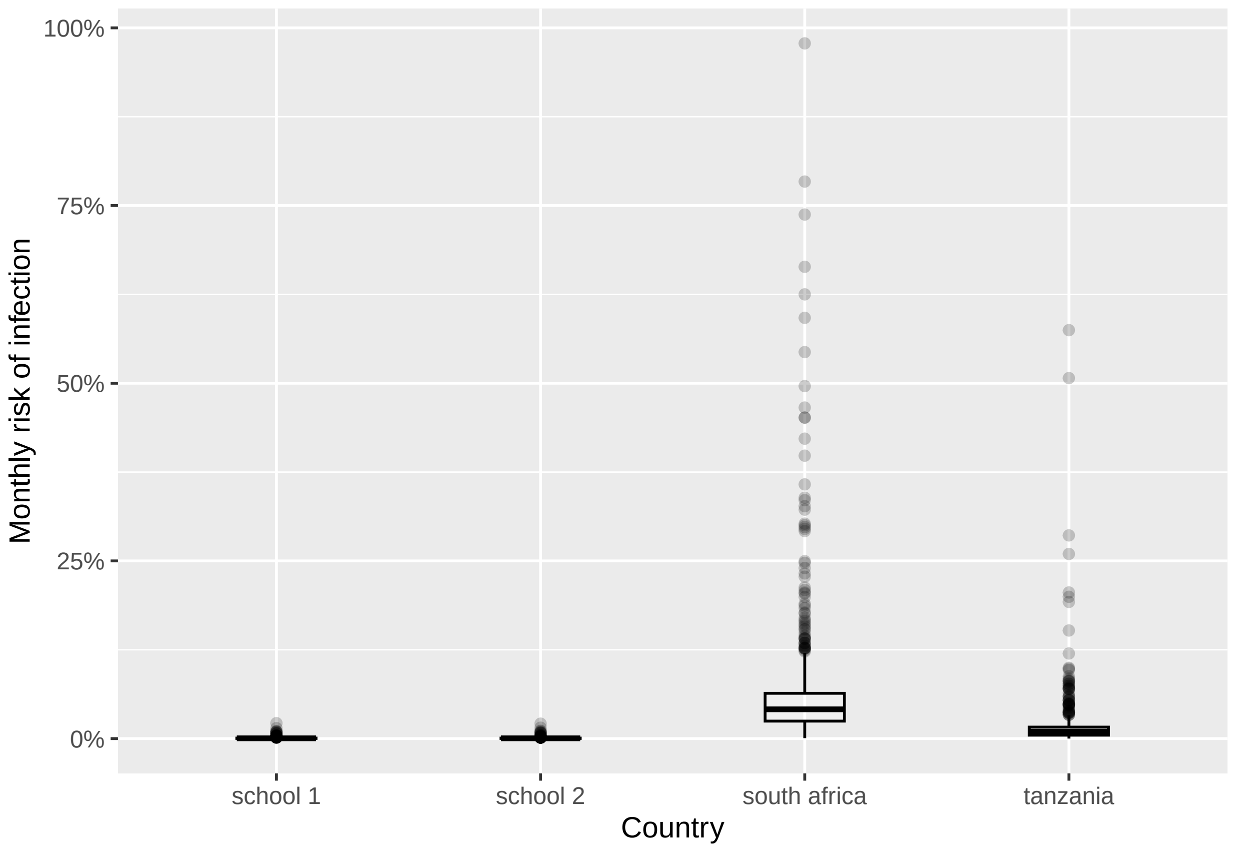
```
df_complet %>%
  ggplot(aes(x = school, y=P_day$f, colour = school))+
  geom_boxplot(width=0.3, color="black", alpha=0.2) +
  scale_y_continuous(labels = scales::percent_format(scale = 100)) +
  xlab("Country") +
  ylab("Daily risk of infection")
```



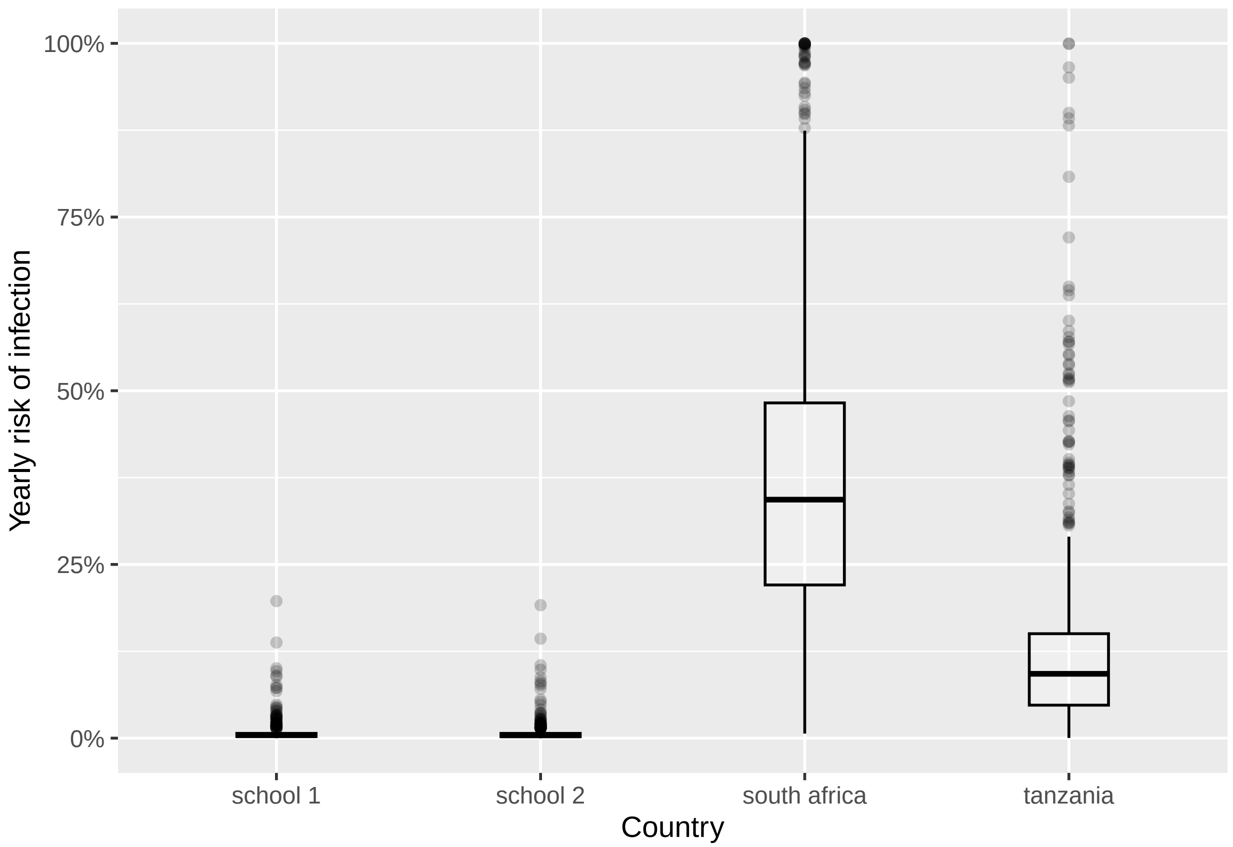
```
df_complet %>%
  ggplot(aes(x = school, y=P_week$f, colour = school))+
  geom_boxplot(width=0.3, color="black", alpha=0.2) +
  scale_y_continuous(labels = scales::percent_format(scale = 100)) +
  xlab("Country") +
  ylab("Weekly risk of infection")
```



```
df_complet %>%
  ggplot(aes(x = school, y=P_month$f, colour = school))+
  geom_boxplot(width=0.3, color="black", alpha=0.2) +
  scale_y_continuous(labels = scales::percent_format(scale = 100)) +
  xlab("Country") +
  ylab("Monthly risk of infection")
```

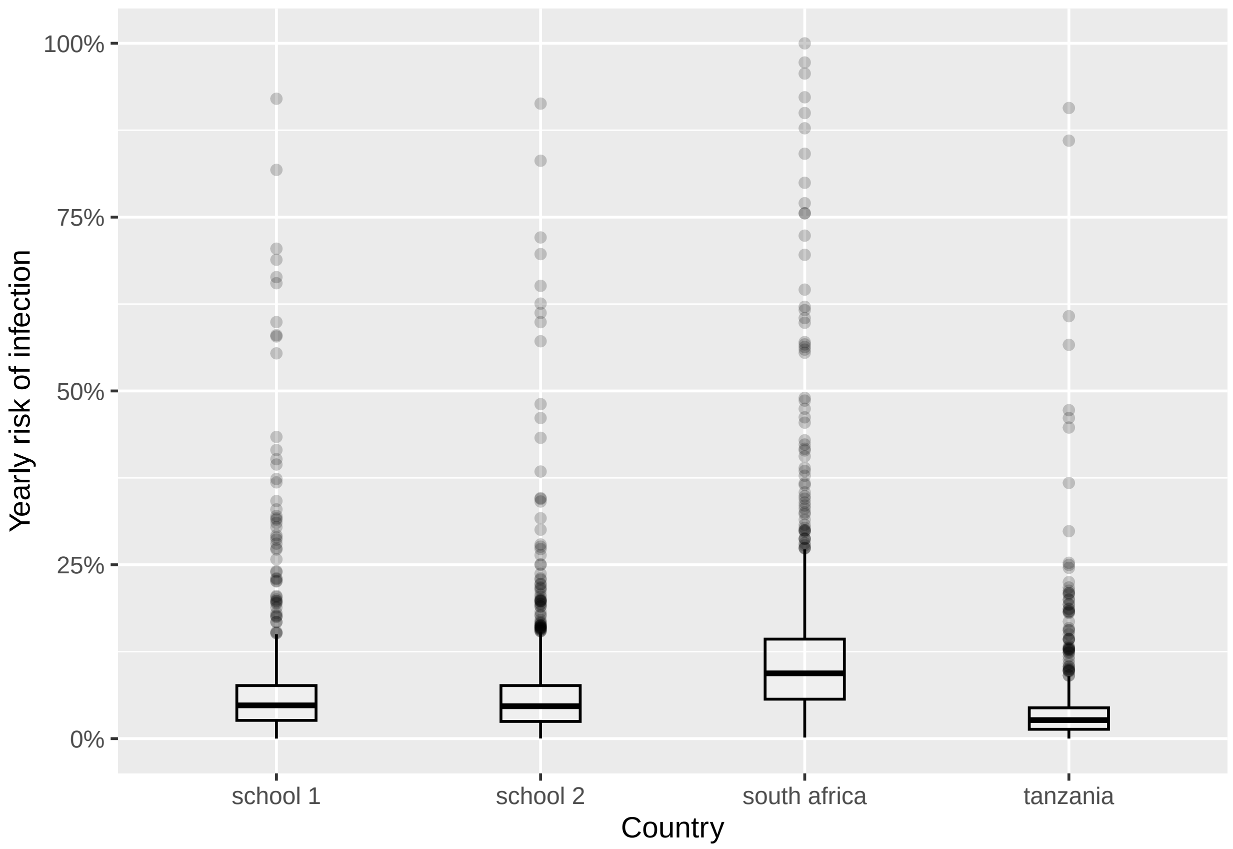


```
df_complet %>%
  ggplot(aes(x = school, y=P_year$f, colour = school))+
  geom_boxplot(width=0.3, color="black", alpha=0.2) +
  scale_y_continuous(labels = scales::percent_format(scale = 100)) +
  xlab("Country") +
  ylab("Yearly risk of infection")
```



Now I will compare the risks of infection, assuming that the prevalence is the same for every country and also assuming that the class size is the same. The prevalence per country is not used. This is to highlight the influence of air quality.

```
df_complet %>%
  ggplot(aes(x = school, y=P_year_one$f, colour = school)) +
  geom_boxplot(width=0.3, color="black", alpha=0.2) +
  scale_y_continuous(labels = scales::percent_format(scale = 100)) +
  xlab("Country") +
  ylab("Yearly risk of infection")
```


Yearly risk of infection
100%
75%
50%
25%
0%
school 1
school 2
south africa
tanzania
Country