Bertinelli_Gabriele_rlab06

June 1, 2023

1 RLab06 - Gabriele Bertinelli (1219907 - tri)

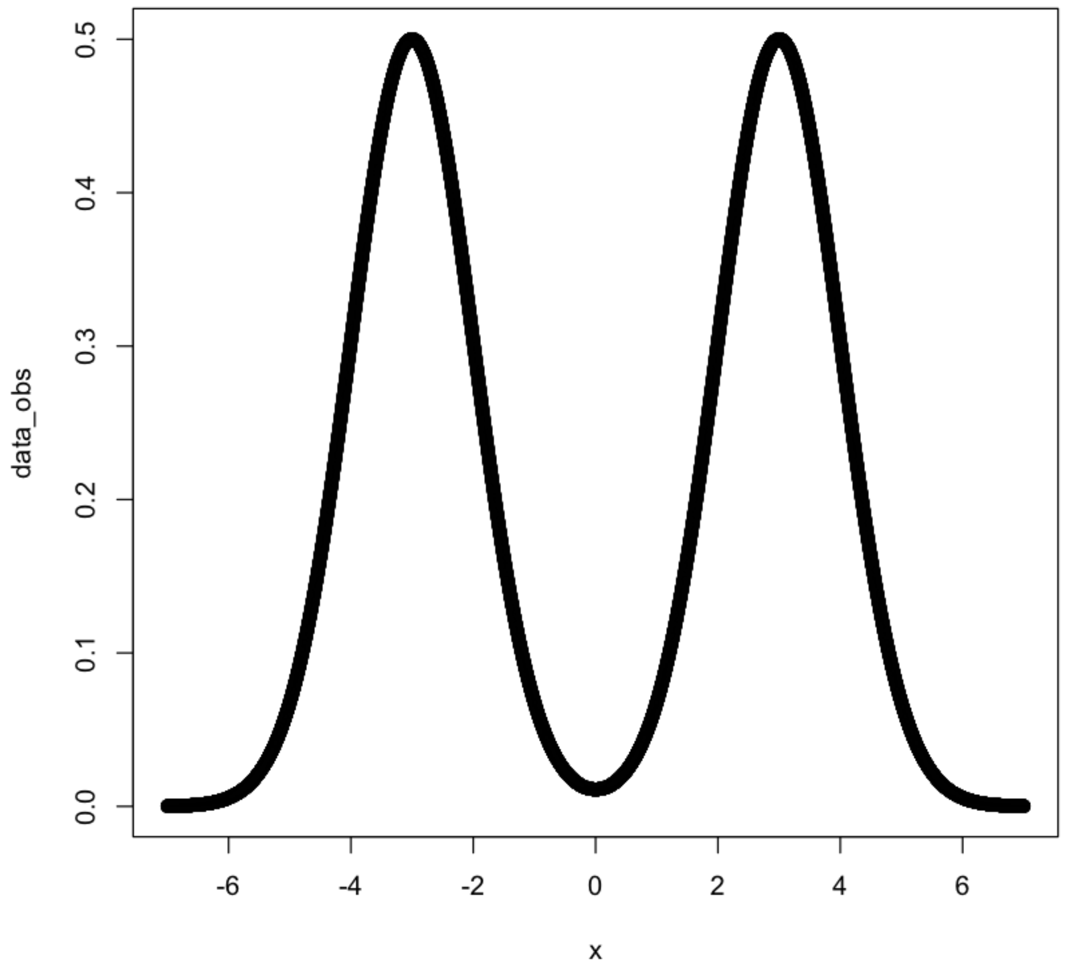
[34]:
```
library(tidyverse)
library(emdbook)
library(gridExtra)
library(rjags)
library(tidybayes)
library(emdbook)
```

2 1)

[2]:
```
g<-function(t){

    0.5*exp((-(t+3)**2/2))+0.5*exp(-0.5*(t-3)**2)
}
```

[3]:
```
data_size <- 1000

x<-seq(-7,7,1/data_size)

data_obs<- g(x)

data <- NULL
data$X <- data_obs
```

[4]:
```
plot(x,data_obs)
```

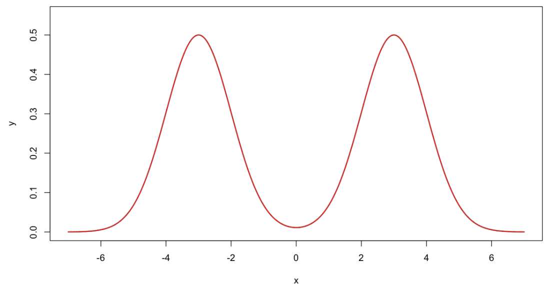


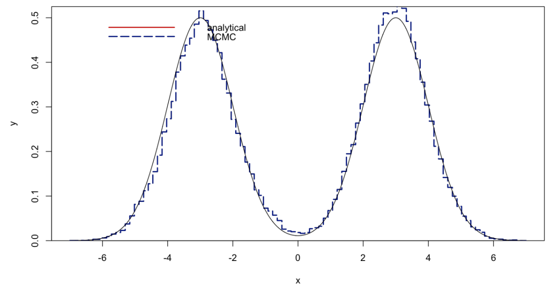
[5]:
```
# func : a function whose first argument is a real vector of parameters
# func returns a log10 of the likelihood function
# theta.init : the initial value of the Markov Chain (and of func)
# n.sample: number of required samples
# sigma : standar deviation of the gaussian MCMC sampling pdf

metropolis.1dim <- function(func, theta.init, n.sample , sigma) {

    theta.cur <- theta.init
    func.Cur <- func(theta.cur)

    func.Samp <- matrix(data=NA, nrow=n.sample , ncol=2+1)
    n.accept <- 0
    rate.accept <- 0.0

    for (n in 1:n.sample) {

        theta.prop <- rnorm(n=1, mean = theta.cur, sigma)
        func.Prop <- func(theta.prop)
        logMR <- func.Prop - func.Cur # Log10 of the Metropolis ratio

        if ( logMR >=0 || logMR>log10(runif(1)) ) {
            theta.cur <- theta.prop
            func.Cur <- func.Prop
            n.accept <- n.accept + 1
        }

        func.Samp[n, 1] <- func.Cur
        func.Samp[n, 2] <- theta.cur

    }

    return(func.Samp)

}



# - interface for the metropolis function , gets the log10 of test function
testfunc.metropolis <- function(theta) {
    return(log10(g(theta))) }
```

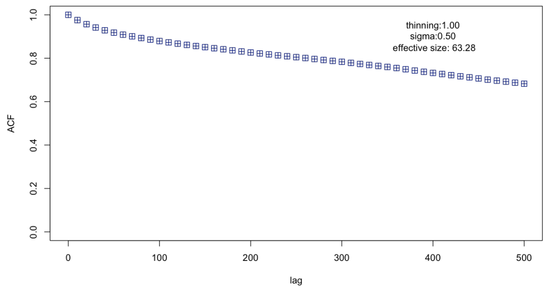
[6]:
```
options(repr.plot.width=20, repr.plot.height=6)


sigma<-c(0.5,1,5,10)

for (i in 1:length(sigma)){

### Running parameters
theta.init <- 3
sample.sig <- sigma[i]
n.sample <- 10**5


chain <- metropolis.1dim(func=testfunc.metropolis ,
                         theta.init = theta.init, n.sample = n.sample ,
                         sigma = sample.sig**2)
```

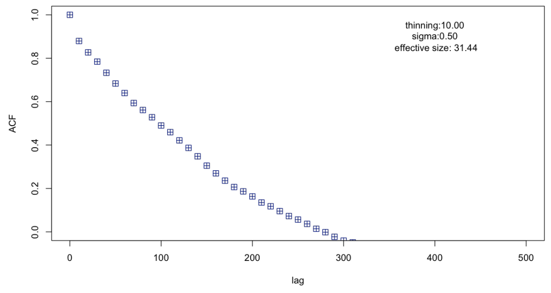
```r
par(mfrow=c(1,2))

x <- seq(-7, 7, length.out=10**4)
y <- g(x)
ymax <- 1.05 * max(y)

# Compute normalization function: used later to put on same as histogram
Zfunc <- sum(y)*diff(range(x))/(length(x))

plot(x, y, ylim=c(0,max(y)*1.10), type='l', lwd=2, col='firebrick3')

plot(x, y, type="n" , yaxs="i" , ylim=c(0,1.05*max(y)))

sa <- which(chain[,2]>=min(x) & chain[,2]<=max(x))

hist <- hist(chain[sa,2], breaks=seq(from=min(x), to=max(x),length.out=100),␣
  ↪plot=FALSE)
Zhist <- sum(hist$counts)*diff(range(hist$breaks))/(length(hist$counts))
lines(hist$breaks , c(hist$counts*Zfunc/Zhist,0), col='navy', type="s" , lwd=2,␣
  ↪lty=5)

lines(x, y, lwd=1, lty=1)

leg.labels = c('analytical', 'MCMC')
leg.ltype = c(1, 5)
leg.colors = c('firebrick3','navy')
legend("topleft" , inset=.05, bty='n', legend = leg.labels, lty=leg.ltype,␣
  ↪col=leg.colors,lwd = 2)


c.chain1 <- as.mcmc(chain[,2])

my.lags = seq(0,500,10)

y1 <- autocorr(c.chain1, lags=my.lags)

thin<-1
plot(my.lags, y1, ylim=c(0,1), pch=12, col='navy', xlab='lag', ylab='ACF',␣
  ↪cex=1.3)
text(400,0.9, sprintf('sigma:%.2f',sample.sig))
text(400,0.85,sprintf(" effective size: %.2f" , effectiveSize(c.chain1)))
text(400,0.95, sprintf('thinning:%.2f',thin))


allSamp<-chain
thin<-10
thinSel <- seq(from=1, to=nrow(allSamp), by=thin) # thin by factor 25
```

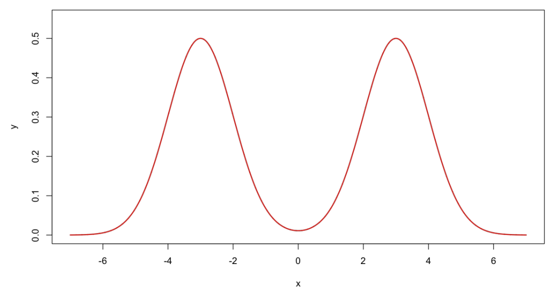
```r
postSamp <- allSamp[thinSel ,]

c.chain1 <- as.mcmc(postSamp[,2])

my.lags = seq(0,500,10)

y1 <- autocorr(c.chain1, lags=my.lags)

plot(my.lags, y1, ylim=c(0,1), pch=12, col='navy', xlab='lag', ylab='ACF', cex=1.3)
text(400,0.9, sprintf('sigma:%.2f',sample.sig))
text(400,0.85,sprintf(" effective size: %.2f" , effectiveSize(c.chain1)))
text(400,0.95, sprintf('thinning:%.2f',thin))

}
```

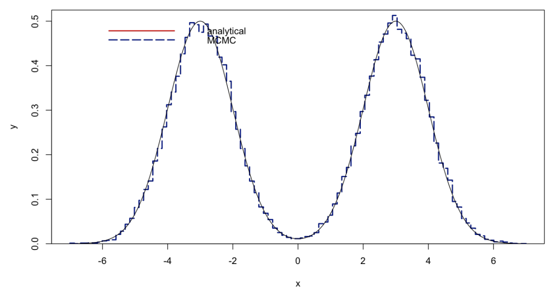


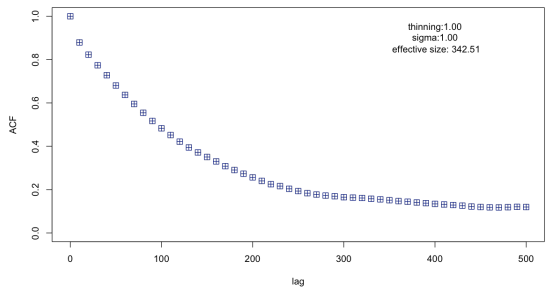


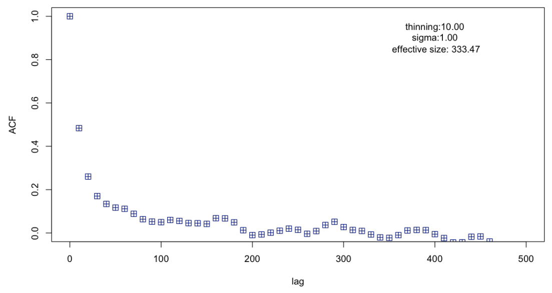


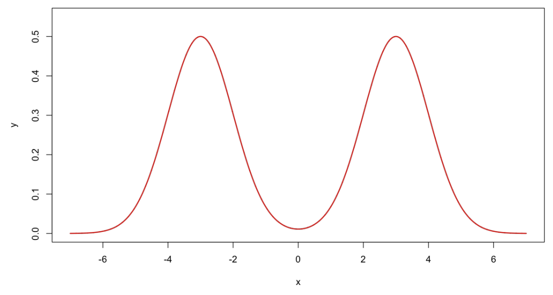


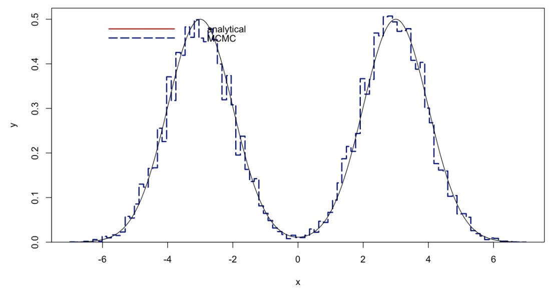

y
x

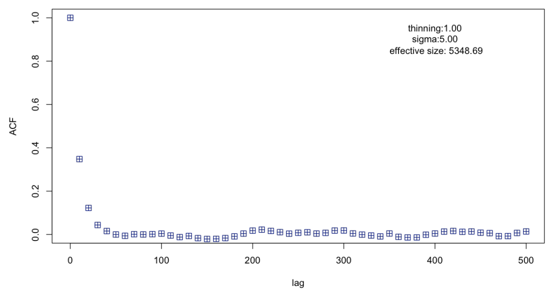

analytical
MCMC
y
x

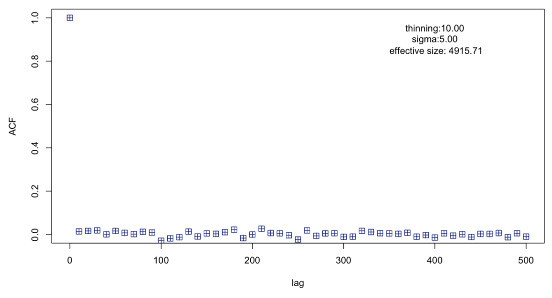

thinning:1.00
sigma:1.00
effective size: 342.51
ACF
lag

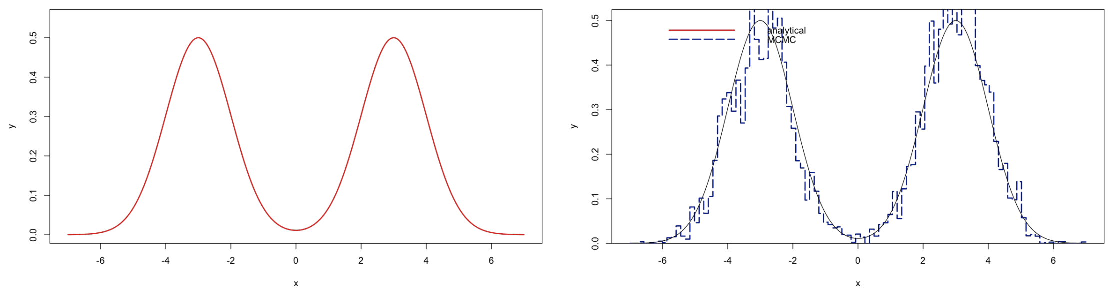

thinning:10.00
sigma:1.00
effective size: 333.47
ACF
lag

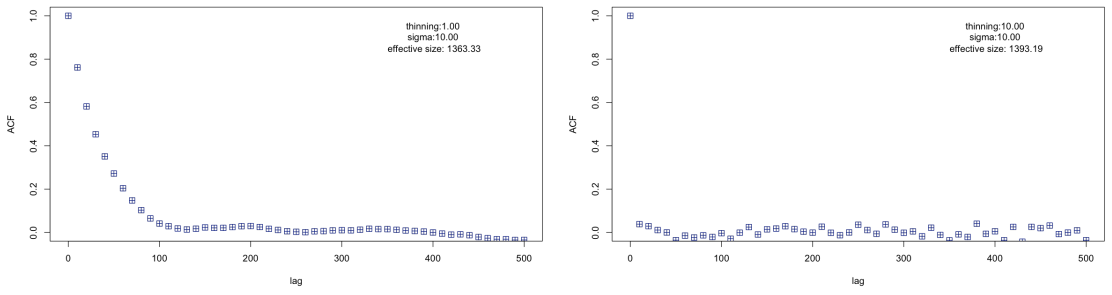

y
x


analytical
MCMC
y
x


thinning:1.00
sigma:5.00
effective size: 5348.69
ACF
lag


thinning:10.00
sigma:5.00
effective size: 4915.71
ACF
lag





3 2)

```
[107]: #janssen and Jcovden -> same vaccines

tot_vaccine <- 19630
tot_placebo <- 19691

patient <- c(rep(" Vaccine" , tot_vaccine), rep(" Placebo" , tot_placebo))

# Number of patients tested postive after RCT:

pos_vaccine <- 116
pos_placebo <- 348
tested <- c(rep(" Pos" , pos_vaccine),
            rep(" Neg" , tot_vaccine - pos_vaccine),
            rep(" Pos" , pos_placebo),
            rep(" Neg" , tot_placebo - pos_placebo))

janssen.tb <- tibble(tested = tested, patient=patient)
```

```r
table(janssen.tb[[2]], janssen.tb[[1]])
head(janssen.tb)
```

```
          Neg   Pos
Placebo 19343   348
Vaccine 19514   116
```

A tibble: 6 × 2

tested	patient
<chr>	<chr>
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine

[108]:
```r
dataList = list(tested = ifelse(janssen.tb$tested == " Neg" , 0, 1),
                patient = as.integer(factor(janssen.tb$patient)),
                Ntot = nrow(janssen.tb) ,
                Nclass = nlevels(factor(janssen.tb$patient))

)



#model
model_bugs <- "model{

for ( i in 1:Ntot ){
    tested[i] ~ dbern( theta[patient[i]] )
}

for ( k in 1:Nclass ) {
    theta[k] ~ dbeta(3 , 100) } }"







jm <- jags.model(textConnection(model_bugs), data=dataList)
```

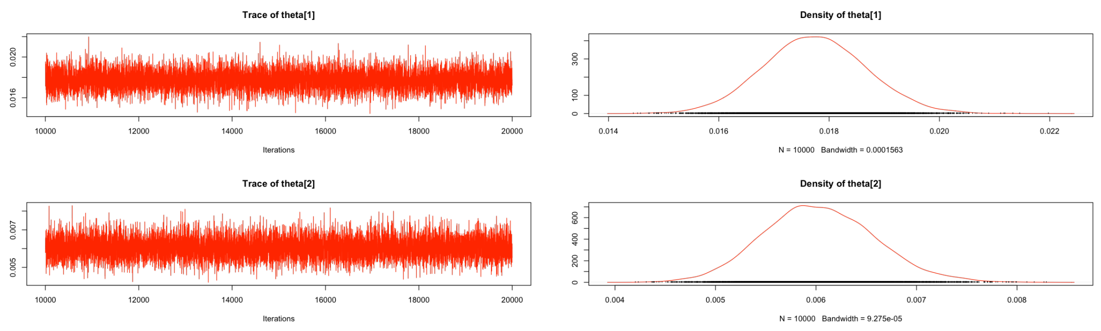
```
Compiling model graph
```

```
   Resolving undeclared variables
   Allocating nodes
Graph information:
   Observed stochastic nodes: 39321
   Unobserved stochastic nodes: 2
   Total graph size: 78648

Initializing model
```

[109]:
```r
# Update the Markov chain (Burn -in)
update (jm , 10000)
chain <- coda.samples(jm , c("theta"), n.iter=10000)
summary(chain)
```

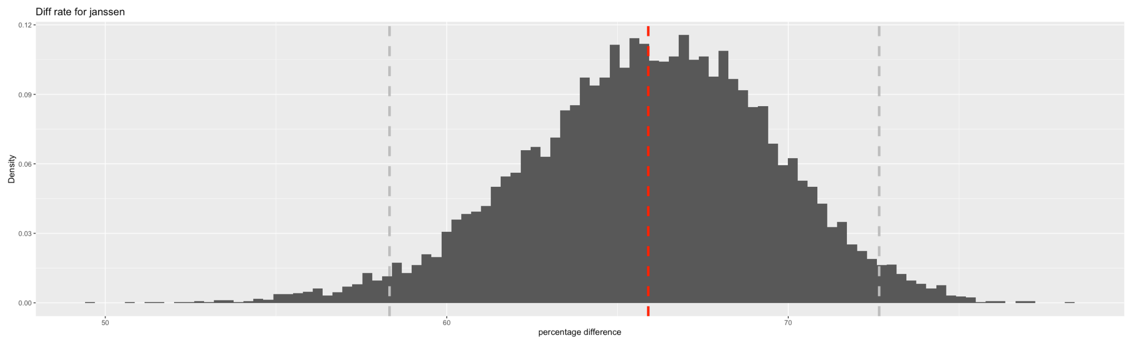
```
Iterations = 10001:20000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

             Mean        SD  Naive SE Time-series SE
theta[1] 0.017744 0.0009314 9.314e-06      9.314e-06
theta[2] 0.006034 0.0005521 5.521e-06      5.521e-06

2. Quantiles for each variable:

            2.5%      25%      50%      75%    97.5%
theta[1] 0.01594 0.017119 0.017735 0.018366 0.019589
theta[2] 0.00500 0.005656 0.006016 0.006401 0.007173
```

[110]:
```r
plot(chain, col="red")
```



```
[111]: janssen_res<- tidybayes::tidy_draws(chain) %>%
                       select('theta[1]':'theta[2]') %>%
                       rename(Placebo = 'theta[1]', Vaccine = 'theta[2]') %>%
                       mutate(diff_rate = (Placebo - Vaccine) / Placebo * 100,
                           Placebo_perc = Placebo * 100, Vaccine_perc = Vaccine * 100)

       allmcmc2 <- as.mcmc(janssen_res, vars="diff_rate" )

       df<-as.data.frame(allmcmc2)

       rates<-as_tibble(janssen_res$diff_rate)

       ci<-summarise_draws(rates, mean,~quantile(.x,probs = c(0.025, 0.975)))

       print(ci)

       a <- ggplot() +
         geom_histogram(aes(df$diff_rate, y=after_stat(density)), bins=100)  +
                     geom_vline(xintercept =ci[[3]],linetype='dashed',␣
        ↪color='grey',linewidth=1.5)+
                      geom_vline(xintercept␣
        ↪=ci[[4]],linetype='dashed',color='grey',linewidth=1.5)+
                       geom_vline(xintercept␣
        ↪=ci[[2]],linetype='dashed',color='red',linewidth=1.5)+

               labs(title='Diff rate for janssen', x='percentage difference',
                                       y='Density')
       a
```

```
# A tibble: 1 × 4
  variable  mean `2.5%` `97.5%`
  <chr>    <num>  <num>
<num>
1 value     65.9   58.3    72.7
```



[103]:
```
#Spikevax

tot_vaccine <- 14134
tot_placebo <- 14073

patient <- c(rep(" Vaccine" , tot_vaccine), rep(" Placebo" , tot_placebo))

# Number of patients tested postive after RCT:

pos_vaccine <- 11
pos_placebo <- 185
tested <- c(rep(" Pos" , pos_vaccine),
            rep(" Neg" , tot_vaccine - pos_vaccine),
            rep(" Pos" , pos_placebo),
            rep(" Neg" , tot_placebo - pos_placebo))

spikevax.tb <- tibble(tested = tested, patient=patient)



table(spikevax.tb[[2]], spikevax.tb[[1]])
head(spikevax.tb)
```

```
             Neg   Pos
  Placebo 13888   185
  Vaccine 14123    11
```

A tibble: 6 × 2

tested <chr>	patient <chr>
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine

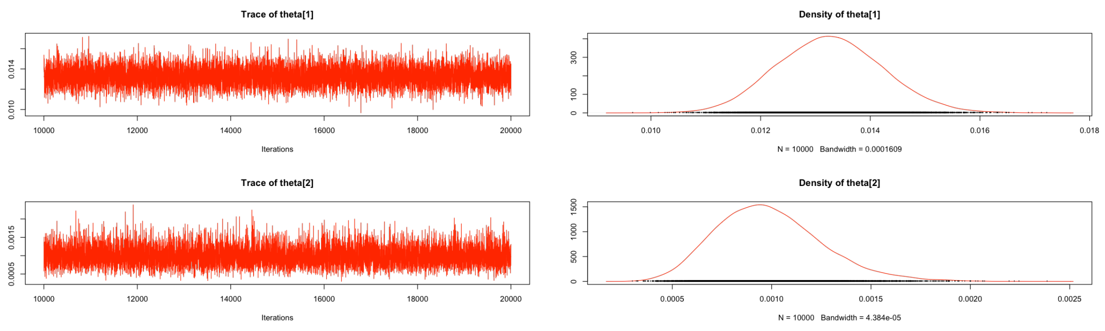
[104]:
```
dataList = list(tested = ifelse(spikevax.tb$tested == " Neg" , 0, 1),
                patient = as.integer(factor(spikevax.tb$patient)),
                Ntot = nrow(spikevax.tb) ,
                Nclass = nlevels(factor(spikevax.tb$patient))

)

#model
model_bugs <- "model{
```

```
for ( i in 1:Ntot ){
    tested[i] ~ dbern( theta[patient[i]] )
}

for ( k in 1:Nclass ) {
    theta[k] ~ dbeta(3 , 100) } }"

jm <- jags.model(textConnection(model_bugs), data=dataList)
```

```
Compiling model graph
   Resolving undeclared variables
   Allocating nodes
Graph information:
   Observed stochastic nodes: 28207
   Unobserved stochastic nodes: 2
   Total graph size: 56420

Initializing model
```

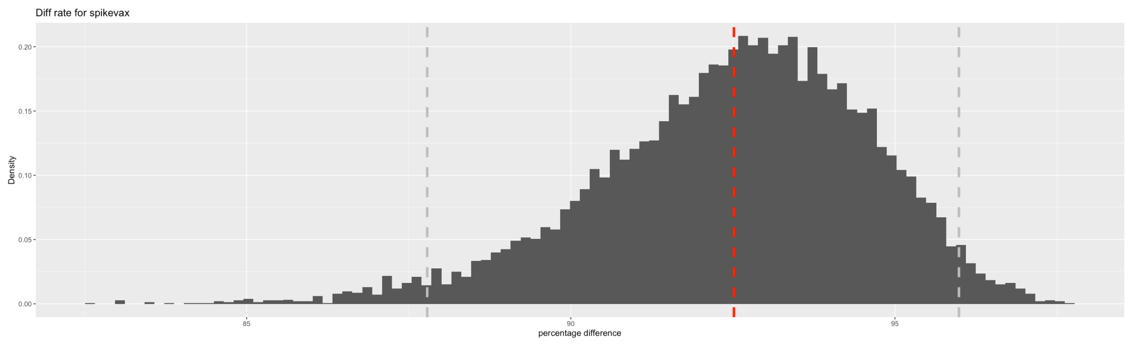
[105]:
```
# Update the Markov chain (Burn -in)
update (jm , 10000)
chain <- coda.samples(jm , c("theta"), n.iter=10000)
summary(chain)
plot(chain, col="red")
```

```
Iterations = 10001:20000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

              Mean        SD  Naive SE Time-series SE
theta[1] 0.0132698 0.0009578 9.578e-06      9.435e-06
theta[2] 0.0009881 0.0002653 2.653e-06      2.653e-06

2. Quantiles for each variable:

              2.5%     25%       50%     75%    97.5%
theta[1] 0.0114572 0.01261 0.0132538 0.01391 0.015202
theta[2] 0.0005394 0.00080 0.0009665 0.00115 0.001576
```



```
[106]: spikevax_res<- tidybayes::tidy_draws(chain) %>%
                       select('theta[1]':'theta[2]') %>%
                       rename(Placebo = 'theta[1]', Vaccine = 'theta[2]') %>%
                       mutate(diff_rate = (Placebo - Vaccine) / Placebo * 100,
                           Placebo_perc = Placebo * 100, Vaccine_perc = Vaccine * 100)

       allmcmc2 <- as.mcmc(spikevax_res, vars="diff_rate" )

       df<-as.data.frame(allmcmc2)

       rates<-as_tibble(spikevax_res$diff_rate)

       ci<-summarise_draws(rates, mean,~quantile(.x,probs = c(0.025, 0.975)))

       print(ci)

       a <- ggplot() +
         geom_histogram(aes(df$diff_rate, y=after_stat(density)), bins=100)  +
                     geom_vline(xintercept =ci[[3]],linetype='dashed',␣
         ↪color='grey',linewidth=1.5)+
                      geom_vline(xintercept␣
         ↪=ci[[4]],linetype='dashed',color='grey',linewidth=1.5)+
                       geom_vline(xintercept␣
         ↪=ci[[2]],linetype='dashed',color='red',linewidth=1.5)+

               labs(title='Diff rate for spikevax', x='percentage difference',
                                       y='Density')
       a
```

```
# A tibble: 1 × 4
  variable  mean `2.5%` `97.5%`
  <chr>    <num>  <num>
<num>
1 value     92.5   87.8    96.0
```



[95]:
```r
#astrazeneca
tot_vaccine <- 5258
tot_placebo <- 5210

patient <- c(rep(" Vaccine" , tot_vaccine), rep(" Placebo" , tot_placebo))

# Number of patients tested postive after RCT:

pos_vaccine <- 64
pos_placebo <- 154
tested <- c(rep(" Pos" , pos_vaccine),
            rep(" Neg" , tot_vaccine - pos_vaccine),
            rep(" Pos" , pos_placebo),
            rep(" Neg" , tot_placebo - pos_placebo))

astrazeneca.tb <- tibble(tested = tested, patient=patient)



table(astrazeneca.tb[[2]], astrazeneca.tb[[1]])
head(astrazeneca.tb)
```

```
          Neg  Pos
 Placebo 5056  154
 Vaccine 5194   64
```

A tibble: 6 × 2

tested <chr>	patient <chr>
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine
Pos	Vaccine

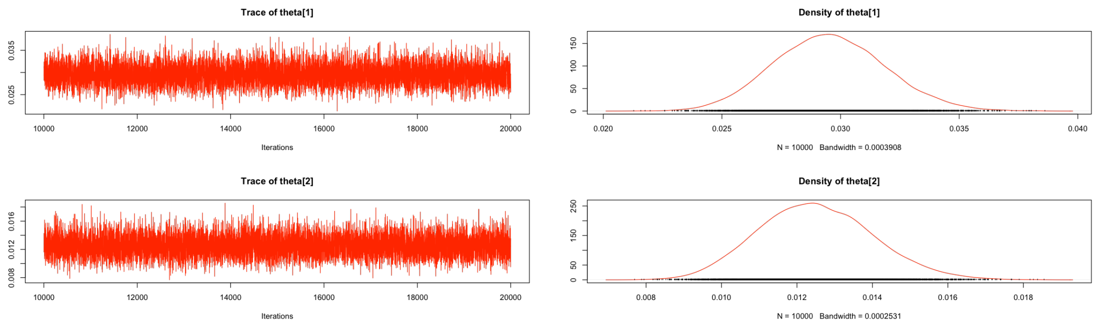
[96]:
```
dataList = list(tested = ifelse(astrazeneca.tb$tested == " Neg" , 0, 1),
                patient = as.integer(factor(astrazeneca.tb$patient)),
                Ntot = nrow(astrazeneca.tb) ,
                Nclass = nlevels(factor(astrazeneca.tb$patient))

)

#model
model_bugs <- "model{

for ( i in 1:Ntot ){
    tested[i] ~ dbern( theta[patient[i]] )
}

for ( k in 1:Nclass ) {
    theta[k] ~ dbeta(3 , 100) } }"

jm <- jags.model(textConnection(model_bugs), data=dataList)
```

```
Compiling model graph
   Resolving undeclared variables
   Allocating nodes
Graph information:
   Observed stochastic nodes: 10468
   Unobserved stochastic nodes: 2
   Total graph size: 20942

Initializing model
```

[97]:
```
# Update the Markov chain (Burn -in)
update (jm , 10000)
chain <- coda.samples(jm , c("theta"), n.iter=10000)
summary(chain)
plot(chain, col="red")
```

```
Iterations = 10001:20000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

            Mean       SD  Naive SE Time-series SE
theta[1] 0.02955 0.002326 2.326e-05      2.326e-05
theta[2] 0.01250 0.001507 1.507e-05      1.464e-05
```

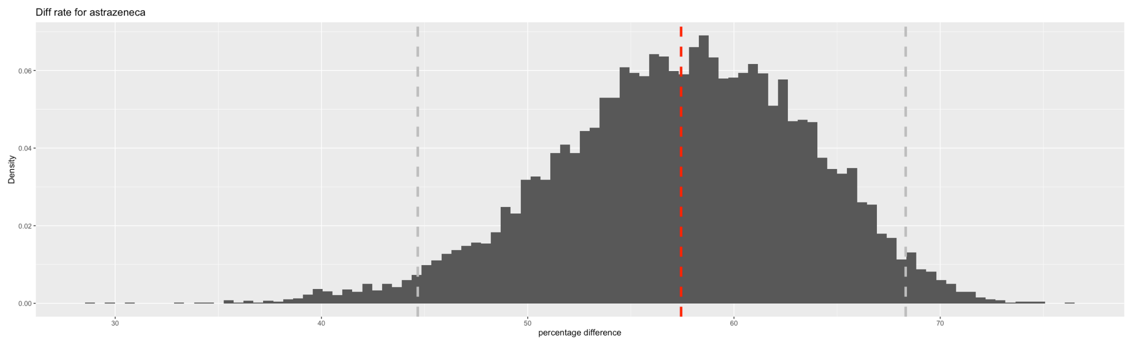
```
2. Quantiles for each variable:

             2.5%     25%     50%     75%   97.5%
theta[1] 0.025156 0.02794 0.02950 0.03109 0.03423
theta[2] 0.009735 0.01144 0.01245 0.01350 0.01559
```



[102]:
```
astrazeneca_res<- tidybayes::tidy_draws(chain) %>%
                select('theta[1]':'theta[2]') %>%
                rename(Placebo = 'theta[1]', Vaccine = 'theta[2]') %>%
                mutate(diff_rate = (Placebo - Vaccine) / Placebo * 100,
                    Placebo_perc = Placebo * 100, Vaccine_perc = Vaccine * 100)

allmcmc2 <- as.mcmc(astrazeneca_res, vars="diff_rate" )

df<-as.data.frame(allmcmc2)

rates<-as_tibble(astrazeneca_res$diff_rate)

ci<-summarise_draws(rates, mean,~quantile(.x,probs = c(0.025, 0.975)))

print(ci)

a <- ggplot() +
  geom_histogram(aes(df$diff_rate, y=after_stat(density)), bins=100)  +
              geom_vline(xintercept =ci[[3]],linetype='dashed',␣
 ↪color='grey',linewidth=1.5)+
               geom_vline(xintercept␣
 ↪=ci[[4]],linetype='dashed',color='grey',linewidth=1.5)+
                geom_vline(xintercept␣
 ↪=ci[[2]],linetype='dashed',color='red',linewidth=1.5)+

        labs(title='Diff rate for astrazeneca', x='percentage difference',
                            y='Density')
```

```
a
```

```
# A tibble: 1 × 4
  variable  mean `2.5%` `97.5%`
  <chr>     <num>  <num>
<num>
1 value      57.4   44.7    68.3
```



4 3

[167]:
```
covid <- read.delim("owid-covid-data.csv", header = TRUE, sep = ",",)
```

[168]:
```
colnames(covid)
```

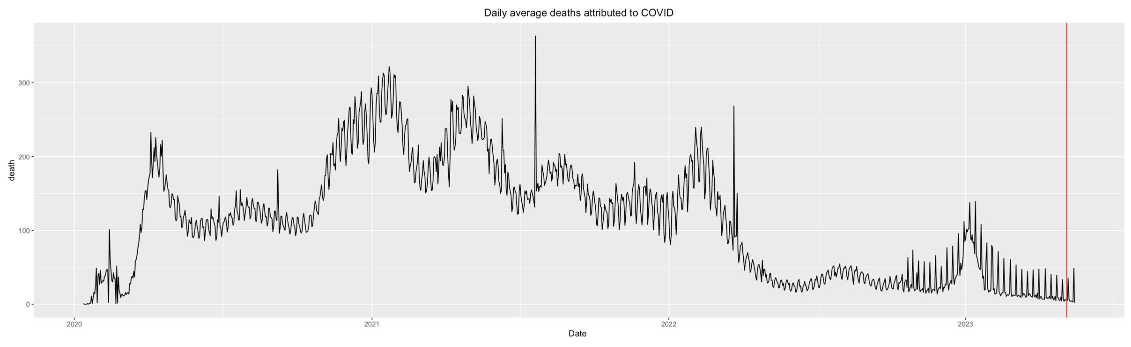
1. 'iso_code' 2. 'continent' 3. 'location' 4. 'date' 5. 'total_cases' 6. 'new_cases' 7. 'new_cases_smoothed' 8. 'total_deaths' 9. 'new_deaths' 10. 'new_deaths_smoothed' 11. 'total_cases_per_million' 12. 'new_cases_per_million' 13. 'new_cases_smoothed_per_million' 14. 'total_deaths_per_million' 15. 'new_deaths_per_million' 16. 'new_deaths_smoothed_per_million' 17. 'reproduction_rate' 18. 'icu_patients' 19. 'icu_patients_per_million' 20. 'hosp_patients' 21. 'hosp_patients_per_million' 22. 'weekly_icu_admissions' 23. 'weekly_icu_admissions_per_million' 24. 'weekly_hosp_admissions' 25. 'weekly_hosp_admissions_per_million' 26. 'total_tests' 27. 'new_tests' 28. 'total_tests_per_thousand' 29. 'new_tests_per_thousand' 30. 'new_tests_smoothed' 31. 'new_tests_smoothed_per_thousand' 32. 'positive_rate' 33. 'tests_per_case' 34. 'tests_units' 35. 'total_vaccinations' 36. 'people_vaccinated' 37. 'people_fully_vaccinated' 38. 'total_boosters' 39. 'new_vaccinations' 40. 'new_vaccinations_smoothed' 41. 'total_vaccinations_per_hundred' 42. 'people_vaccinated_per_hundred' 43. 'people_fully_vaccinated_per_hundred' 44. 'total_boosters_per_hundred' 45. 'new_vaccinations_smoothed_per_million' 46. 'new_people_vaccinated_smoothed' 47. 'new_people_vaccinated_smoothed_per_hundred' 48. 'stringency_index' 49. 'population_density' 50. 'median_age' 51. 'aged_65_older' 52. 'aged_70_older' 53. 'gdp_per_capita' 54. 'extreme_poverty' 55. 'cardiovasc_death_rate' 56. 'diabetes_prevalence' 57. 'female_smokers' 58. 'male_smokers' 59. 'handwashing_facilities' 60. 'hospital_beds_per_thousand' 61. 'life_expectancy' 62. 'human_development_index'

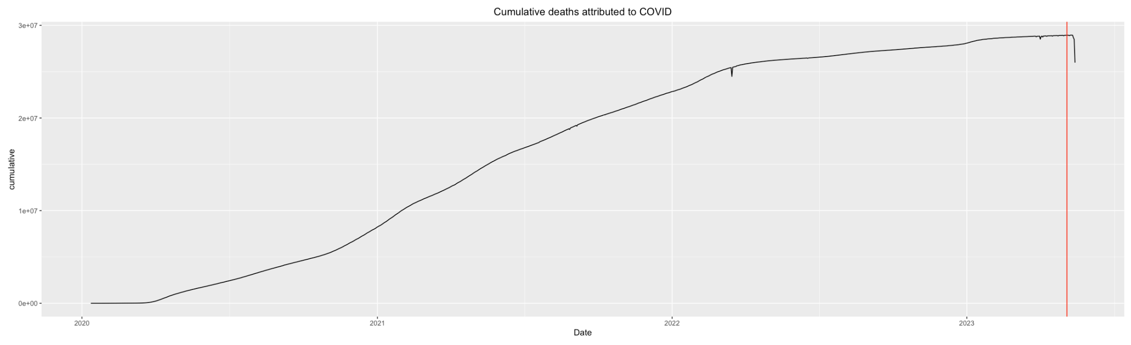
63. ’population’ 64. ’excess_mortality_cumulative_absolute’ 65. ’excess_mortality_cumulative’ 66. ’excess_mortality’ 67. ’excess_mortality_cumulative_per_million’

Columns used: - new_vaccinations: New COVID-19 vaccination doses administered (only calculated for consecutive days) - total_vaccinations: Total number of COVID-19 vaccination doses administered - new_deaths: New deaths attributed to COVID-19. Counts can include probable deaths, where reported. - total_deaths: Total deaths attributed to COVID-19. Counts can include probable deaths, where reported.

https://github.com/owid/covid-19-data/tree/master/public/data

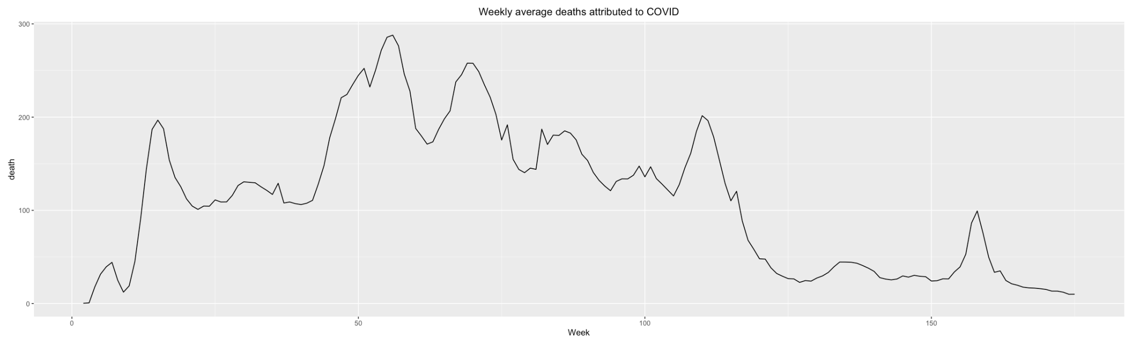
[333]:
```
deaths<-data.frame(covid$date,covid$new_deaths,covid$total_deaths)

deaths$covid.date <- as.Date(deaths$covid.date, "%Y-%m-%d")

deaths<-as_tibble(deaths)



tda<-deaths$covid.date
deaths$week <- (interval(min(tda), tda) %/% weeks(1)) + 1



a<-deaths %>% drop_na() %>% group_by(covid.date)%>%
                    summarise(death = mean(covid.new_deaths),
                             cumulative=sum(covid.total_deaths))
a<-slice(a, 1:(n() - 2))



ggplot(data=a,aes(x=covid.date,y=death))+geom_line(aes(y=death))+␣
 ↪geom_vline(xintercept =as.Date('2023-05-05',"%Y-%m-%d"),color='red')+
    ggtitle("Daily average deaths attributed to COVID") +
   theme(plot.title = element_text(hjust = 0.5)) +
   xlab("Date ")
ggplot(data=a,aes(x=covid.date,y=cumulative))+geom_line(aes(y=cumulative))+␣
 ↪geom_vline(xintercept =as.Date('2023-05-05',"%Y-%m-%d"),color='red')+
ggtitle("Cumulative deaths attributed to COVID") +
   theme(plot.title = element_text(hjust = 0.5)) +
   xlab("Date")
```

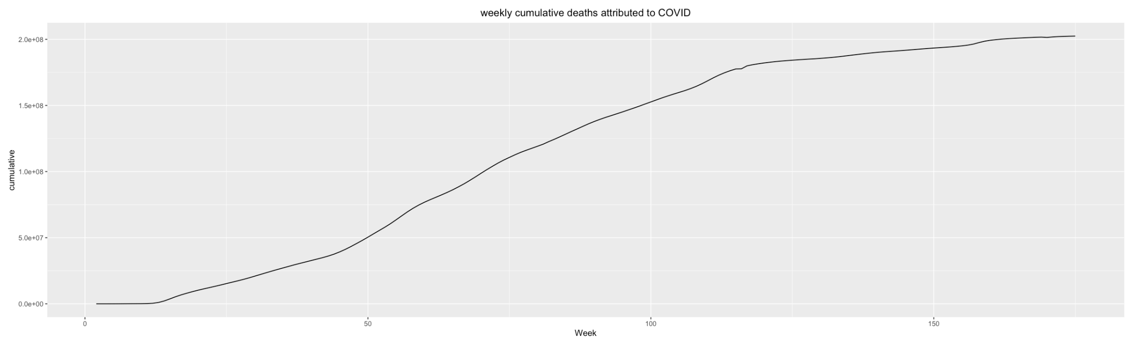




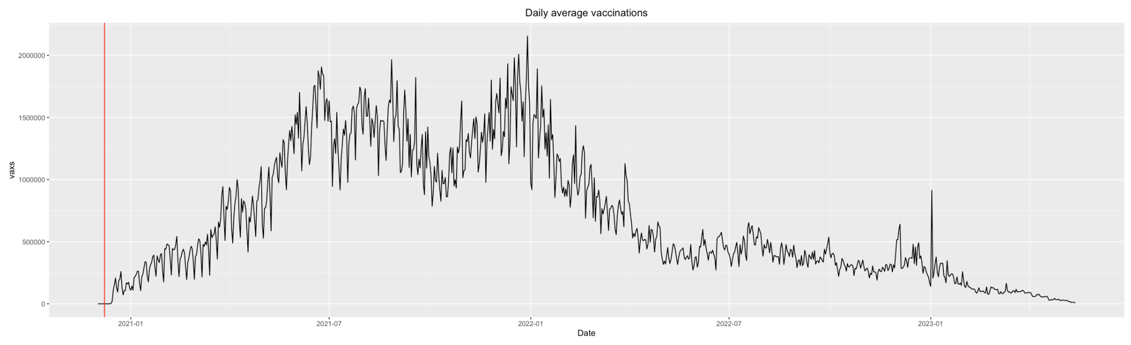
On 2023-05-05 WHO declared the end of the covid pandemic (red line).

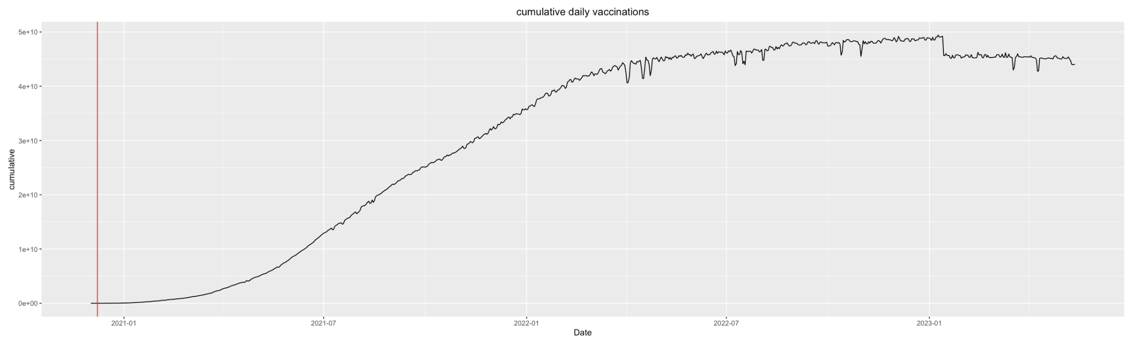
[334]:
```
a<-deaths %>% drop_na() %>% group_by(week)%>%
                        summarise(death = mean(covid.new_deaths),
                                  cumulative=sum(covid.total_deaths))
a<-slice(a, 1:(n() - 2))

ggplot(data=a,aes(x=week,y=death))+geom_line(aes(y=death))+ ggtitle("Weekly␣
 ↪average deaths attributed to COVID") +
   theme(plot.title = element_text(hjust = 0.5)) +
   xlab("Week")
ggplot(data=a,aes(x=week,y=cumulative))+geom_line(aes(y=cumulative))+ggtitle("weekly␣
 ↪cumulative deaths attributed to COVID") +
   theme(plot.title = element_text(hjust = 0.5)) +
   xlab("Week")
```





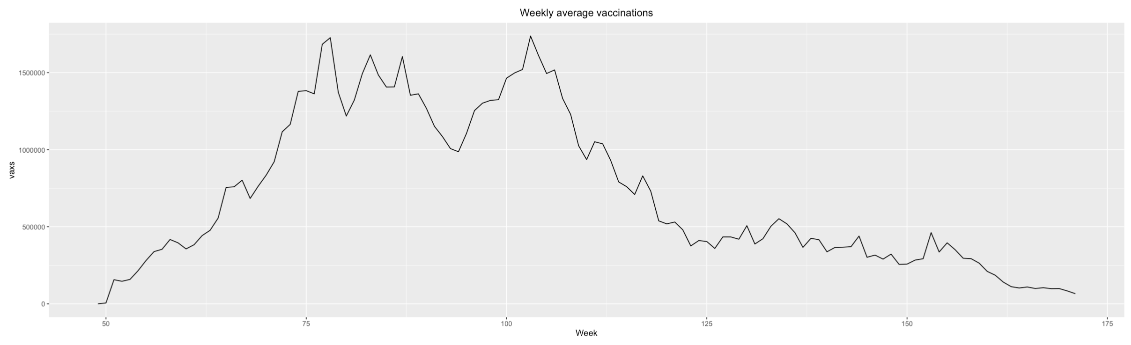
```
[335]: vax<-data.frame(covid$date,covid$new_vaccinations,covid$total_vaccinations)

       vax$covid.date <- as.Date(vax$covid.date, "%Y-%m-%d")

       vax<-as_tibble(vax)


       tda<-vax$covid.date
       vax$week <- (interval(min(tda), tda) %/% weeks(1)) + 1





       a<-vax %>% drop_na() %>% group_by(covid.date)%>%
                           summarise(vaxs = mean(covid.new_vaccinations),
                                     cumulative=sum(covid.total_vaccinations))

       a<-slice(a, 1:(n() - 6)) #discarded last six rows



       ggplot(data=a,aes(x=covid.date,y=vaxs))+geom_line(aes(y=vaxs))+␣
        ↪geom_vline(xintercept =as.Date('2020-12-8',"%Y-%m-%d"),color='red')+
        ggtitle("Daily average vaccinations") +
          theme(plot.title = element_text(hjust = 0.5)) +
          xlab("Date")

       ggplot(data=a,aes(x=covid.
        ↪date,y=cumulative))+geom_line(aes(y=cumulative))+geom_vline(xintercept =as.
        ↪Date('2020-12-8',"%Y-%m-%d"),color='red')+
        ggtitle("cumulative daily vaccinations") +
          theme(plot.title = element_text(hjust = 0.5)) +
          xlab("Date")
```

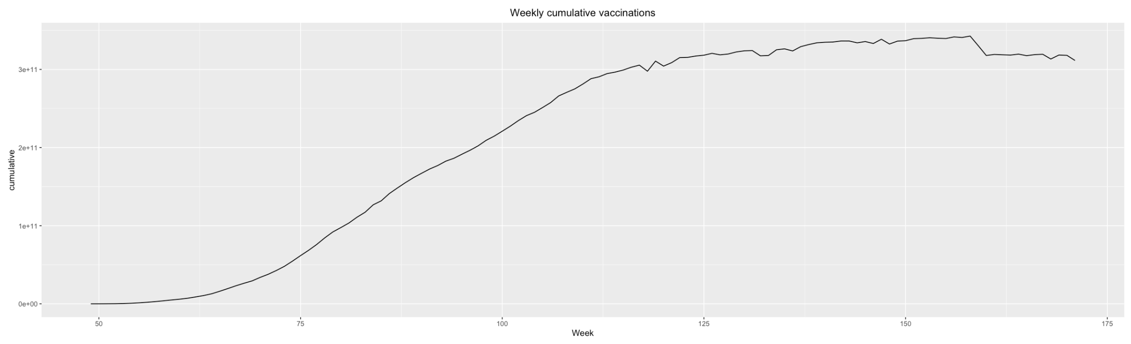




On 2020-12-8 (red line) the first person had received the vaccine.

[336]:
```
a<-vax %>% drop_na() %>% group_by(week)%>%
                    summarise(vaxs = mean(covid.new_vaccinations),
                             cumulative=sum(covid.total_vaccinations))
a<-slice(a, 1:(n() - 6)) #removing last six weeks for plotting purposes, data␣
 ↪is not updated correctly and cumulative drops to zero


ggplot(data=a,aes(x=week,y=vaxs))+geom_line(aes(y=vaxs))+ ggtitle("Weekly␣
 ↪average vaccinations") +
   theme(plot.title = element_text(hjust = 0.5)) +
   xlab("Week")

ggplot(data=a,aes(x=week,y=cumulative))+geom_line(aes(y=cumulative))+␣
 ↪ggtitle("Weekly cumulative vaccinations") +
   theme(plot.title = element_text(hjust = 0.5)) +
   xlab("Week")
```


Weekly average vaccinations
vaxs
1500000
1000000
500000
0
50
75
100
125
150
175
Week


Weekly cumulative vaccinations
cumulative
3e+11
2e+11
1e+11
0e+00
50
75
100
125
150
175
Week