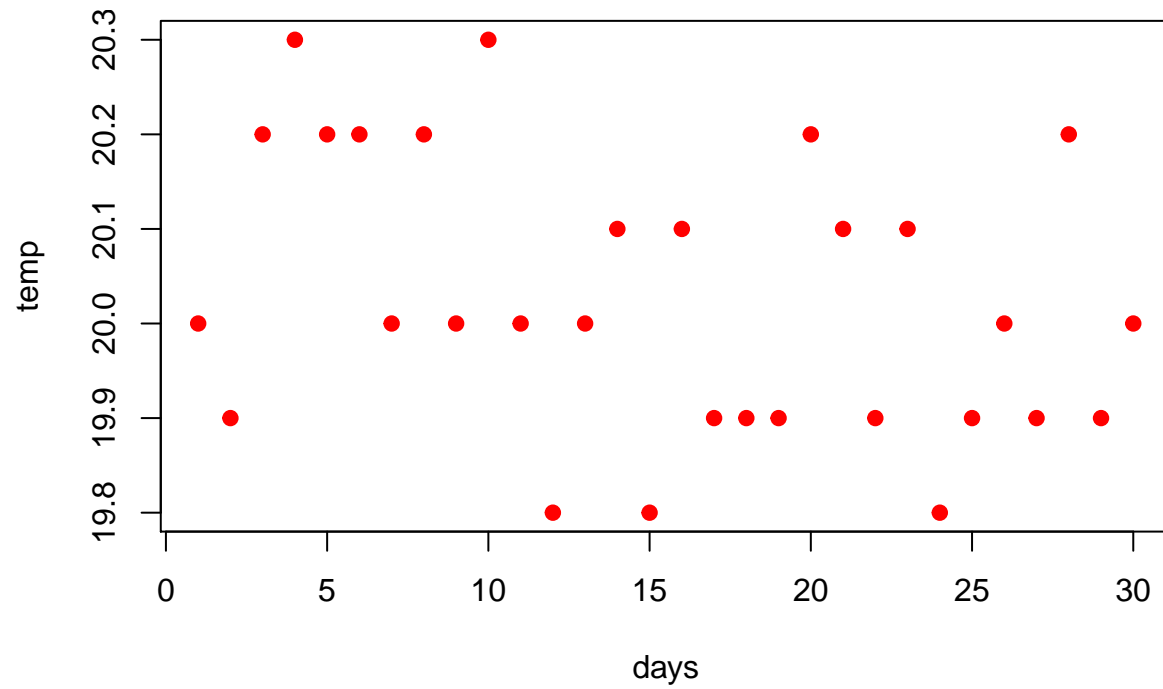


exam

Andreas Dahlberg

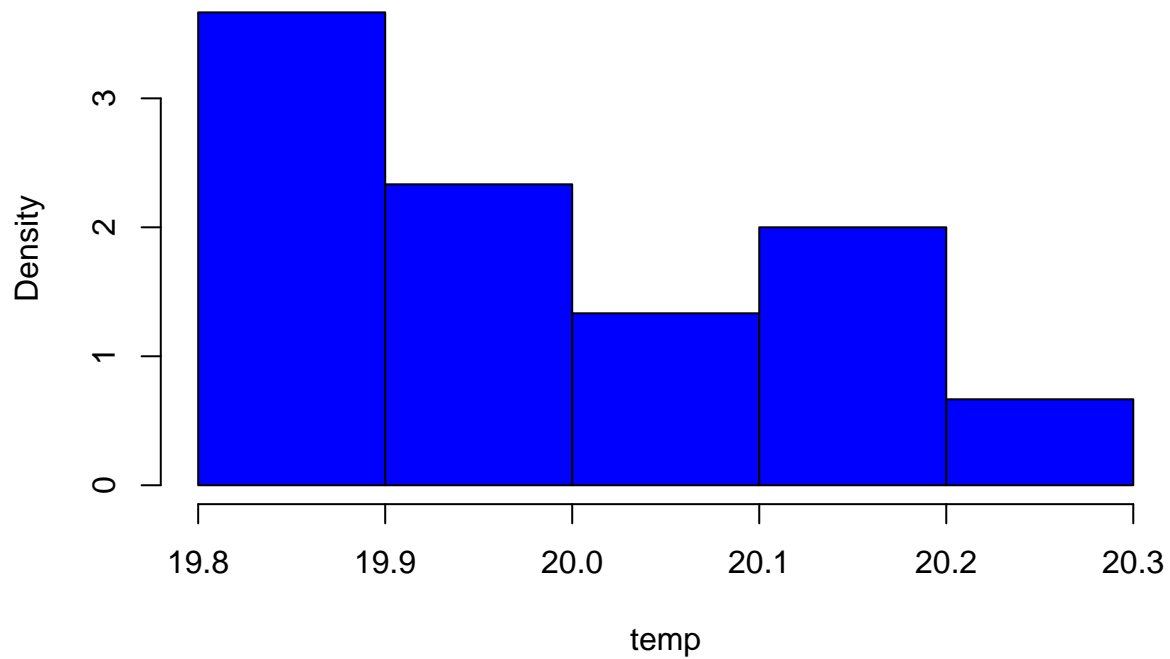
asd

```
data = read.csv("temperature23.csv")
temp = data$temp
days = data$X
plot(days,temp,type="p",col="red",pch=19)
```



```
hist(temp,prob="TRUE",col="BLUE",breaks=5)
```

Histogram of temp



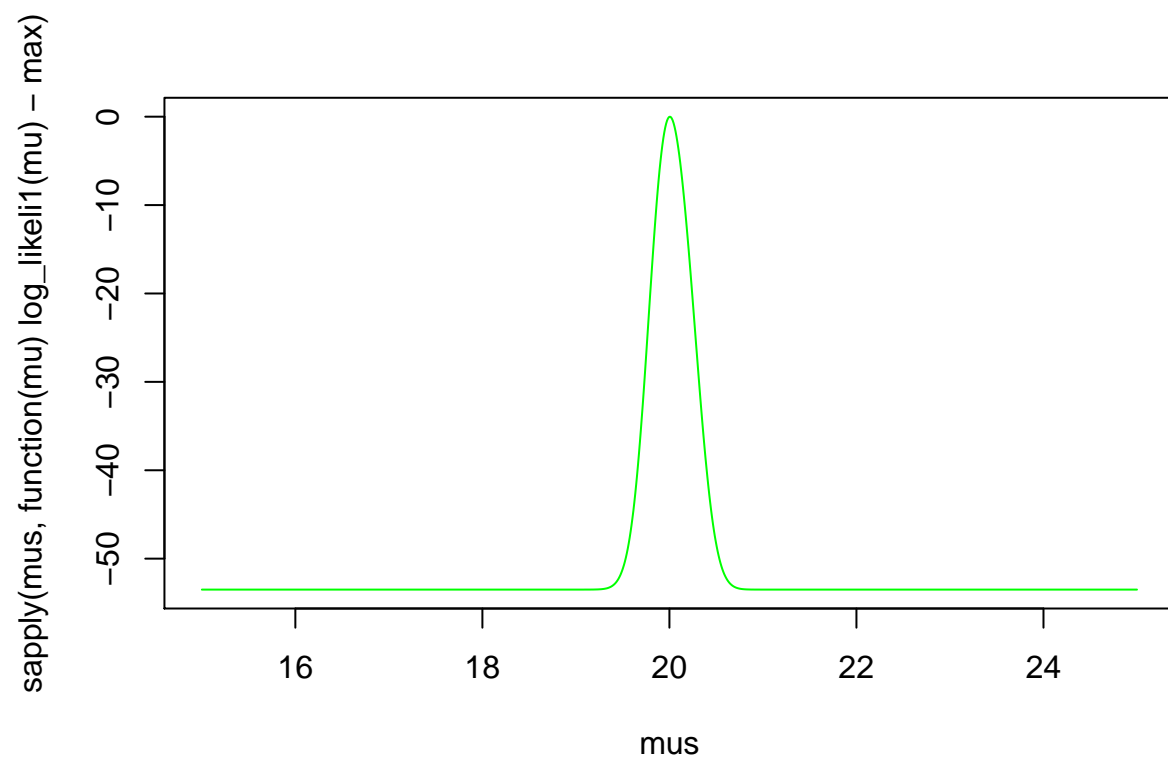
```
mean(temp)
```

```
## [1] 20.02667
```

The mean temperature is about 20.027 and the histogram indicates that it doesn't seem to be normal distributed, though we will use normality anyways. We see that the pdf is normally distributed with mean μ and $sd = 1/\sqrt{2k}$

sdasd

```
log_likeli1 <- function(mu){  
  sum(dnorm(temp,mu,sqrt(1/(2*mu))),log=TRUE)  
}  
  
mus = seq(15,25,length=1000)  
opt = optim(15,function(mu) -log_likeli1(mu),method="Brent",lower=0,upper=50)  
ML = opt$par  
max = -opt$val  
  
plot(mus,sapply(mus,function(mu)log_likeli1(mu)-max),type="l",col="green")
```

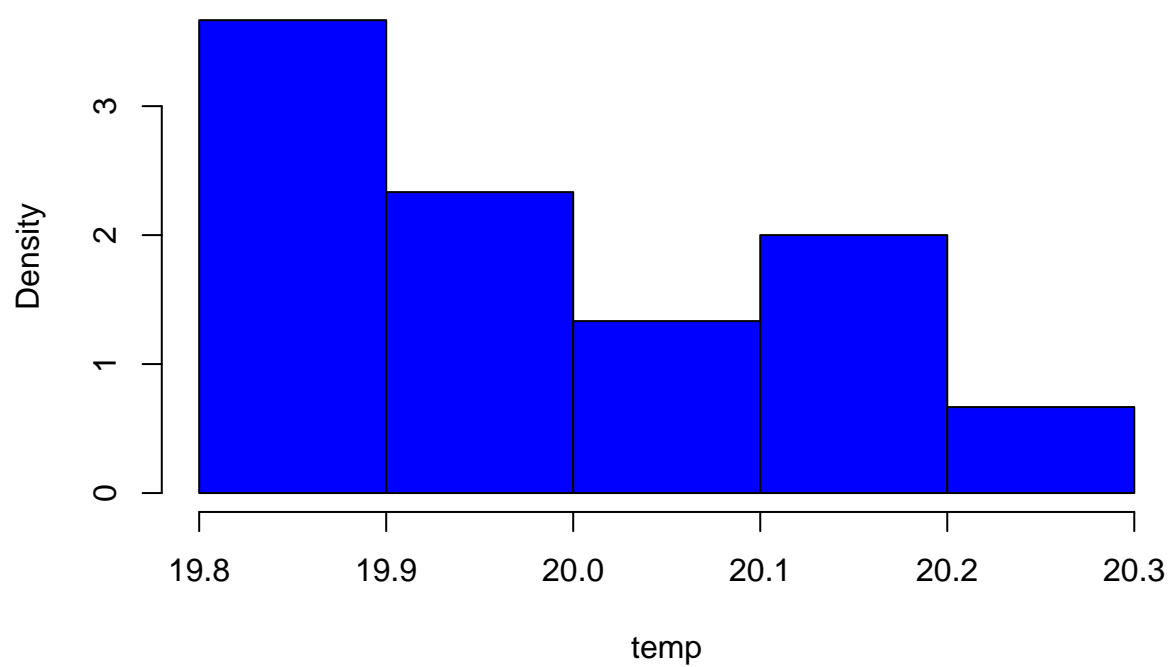


ML

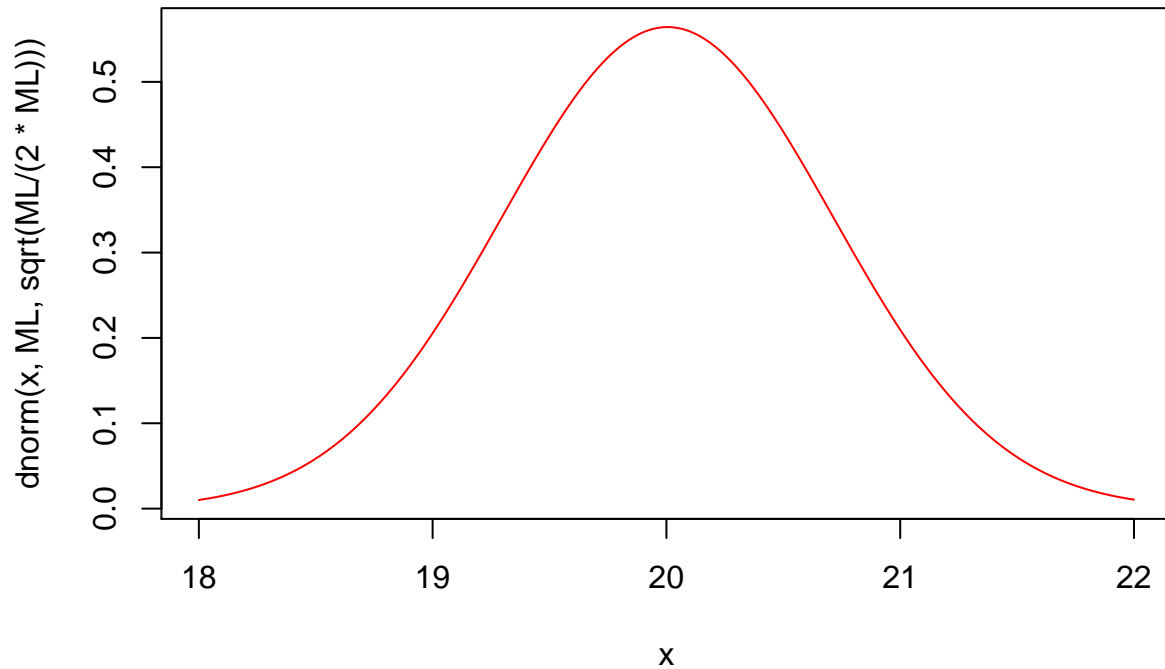
```
## [1] 20.00493
```

```
hist(temp,prob="TRUE",col="BLUE",breaks=5)
```

Histogram of temp



```
x = seq(18,22,length=1000)
plot(x,dnorm(x,ML,sqrt(ML/(2*ML))),col="red",type="l")
```

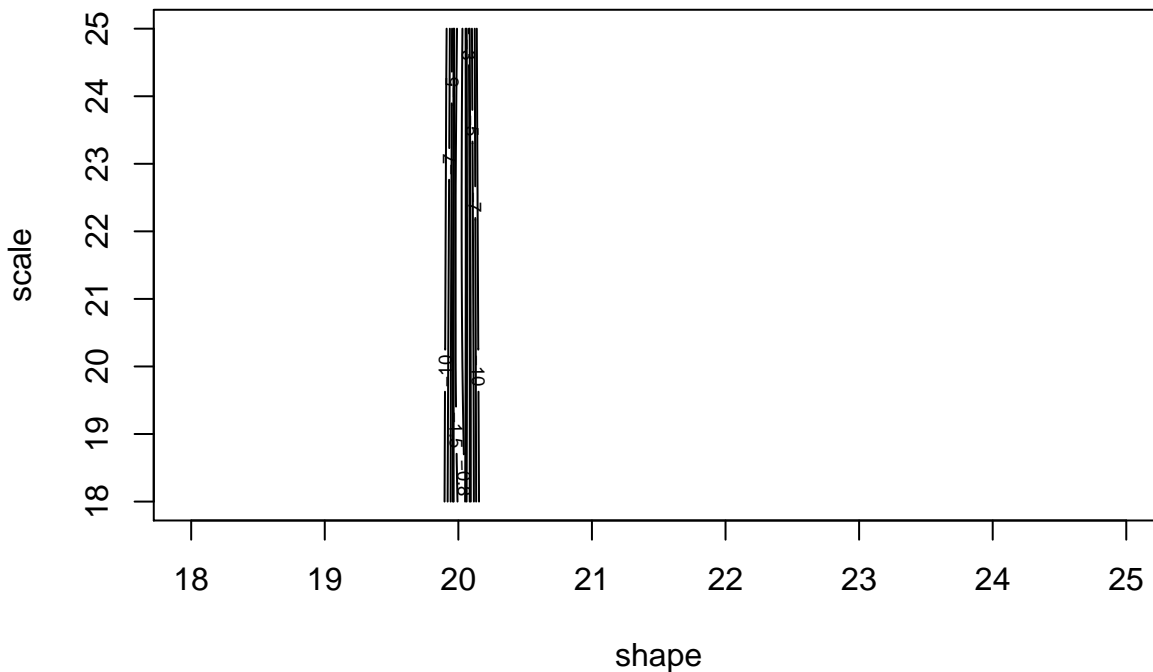


```
log_likeli2 <- function(params){
  mu = params[1]
  k = params[2]
  sum(dnorm(temp,mu,sqrt(1/(2*k)),log=TRUE))
}
```

```
optt = optim(c(18,45),function(params)-log_likeli2(params),hessian=TRUE)
ML2 = optt$par
max = -optt$val
ML2
```

```
## [1] 20.02672 23.51564
```

```
mus = seq(18,25,length=100)
k = seq(18,25,length=100)
grid = expand.grid(mus,k)
z = apply(grid,1,function(params)log_likeli2(params)-max)
z = array(z,c(100,100))
contour(mus,k,z,levels=c(0,-0.3,-0.8,-1.5,-3.0,-3.5,-5,-7,-10),xlab="shape",ylab="scale")
```



the estimate of μ is about 20.0 which is approx the sample mean of temperature. This is good. We see that the pdf and the histogram of temperatures don't align good but not bad either. Probably a sample of size 30 is too little.

```
data = c(17.5,22.1,10.2,16.9,20.0,8.1,14.6,21.3,16.4)
n = length(data)

log_likeli <- function(x){
  mu = x[1]
  a = x[2]
  n*log(a)-a*n*log(mu)+(a-1)*sum(log(data))-1/(mu^a)*sum(data^a)
}

opt = optim(c(5,5),function(x)-log_likeli(x),hessian=TRUE)

## Warning in log(a): NaNs produced

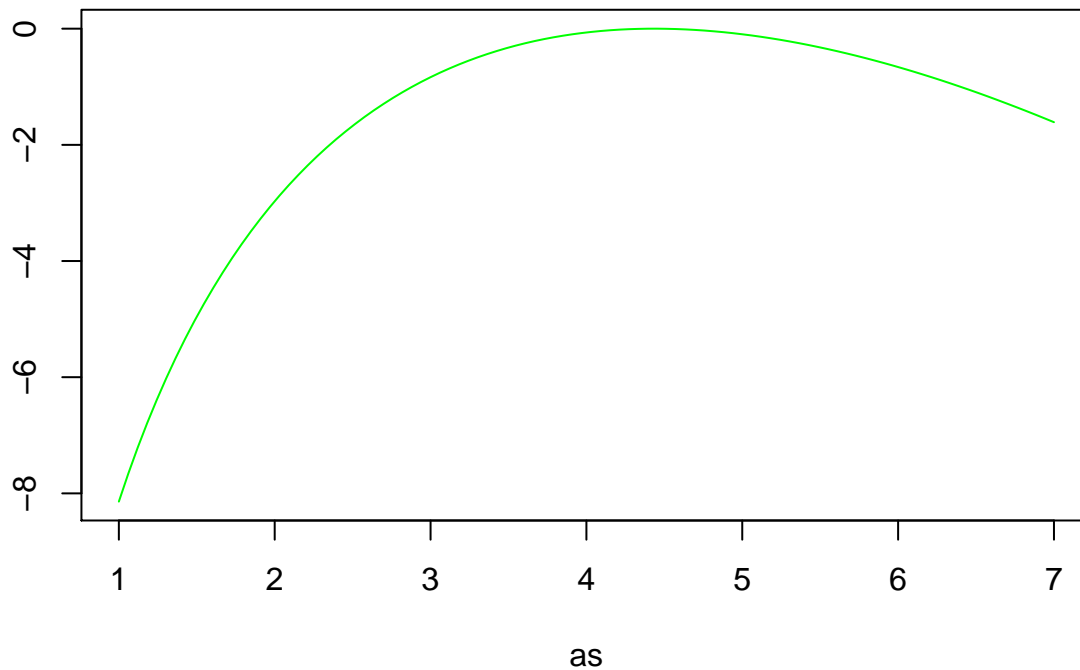
## Warning in log(a): NaNs produced

## Warning in log(a): NaNs produced

ML = opt$par
max = -opt$val
observed_fisher=opt$hessian
se = sqrt(diag(solve(observed_fisher)))

profile_likeli <- function(a){
  optim(15,function(mu)-log_likeli(c(mu,a)),method="Brent",lower=0,upper=50)$par
}

as = seq(1,7,length=100)
plot(as,sapply(as,function(a) log_likeli(c(profile_likeli(a),a)))-max,col="green",type="l",ylab="")
```

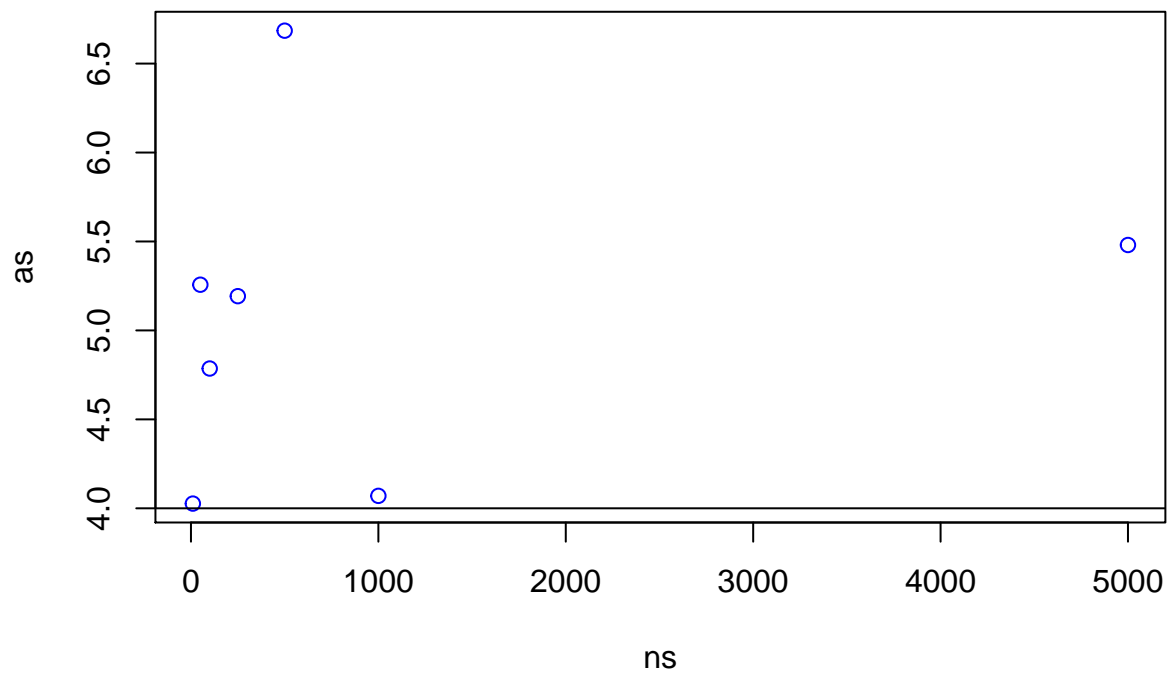


```
wald_a = ML[2]+c(-1,1)*1.96*se[2]
wald_a

## [1] 1.997932 6.857555

a = 4
as = c()
ns = c(10,50,100,250,500,1000,5000)
for (i in 1:length(ns)){
  n = ns[i]
  data = rnorm(n,17,4)

  log_likeli <- function(x){
    mu = x[1]
    a = x[2]
    n*log(a)-a*n*log(mu)+(a-1)*sum(log(data))-1/(mu^a)*sum(data^a)
  }
  ML = optim(c(15,4),function(x)-log_likeli(x),hessian=TRUE)$par
  as = append(as,ML[2])
}
plot(ns,as,type="p",col="blue")
abline(h=4)
```



The 95 percent confint for a is about 2 and 6.85