ABC inference for Normal mean and variance

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Regular ABC algorithm

The main steps for conducting parameter inference using ABC are to simulate data from prior distributions for the parameters of interest, followed by comparing this simulated data to the observed data to determine how similar they are. Parameters values from the prior that produce data that are similar to the observed data can then be saved and form an approximated posterior distribution for those parameters.

In the example below, we have 30 observations from a Normal distribution with unknown mean and variance. To infer these unknown parameters, we will use ABC to simulate data that can be compared to our observed data and will save the parameter values that produce the closest matching data sets. To compare simulated data sets and our observed data, we sort the data and use the Euclidean distance.

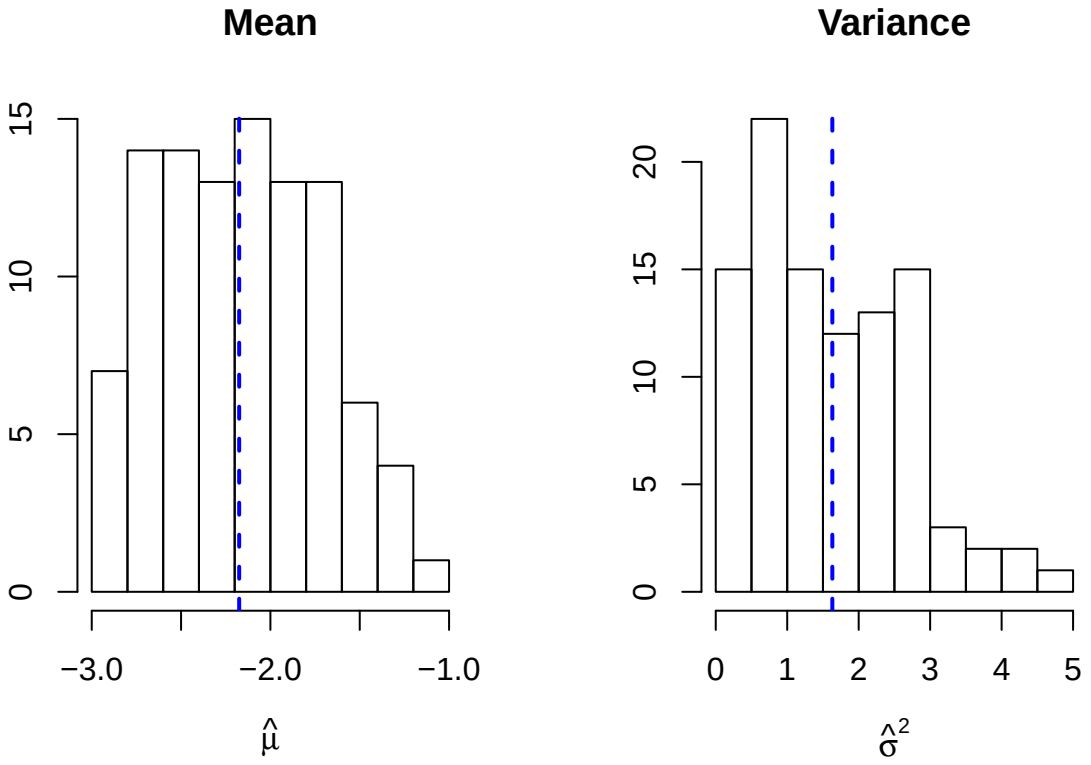
We use uninformative, uniform distributions as priors for both of the mean and variance and simulate 50,000 data sets to compare with our observed data. After comparing with the observed data, we keep the parameters for the 100 simulated data sets that produce data that is most similar to our observed data. These 100 samples of the mean and variance can be considered draws from their approximate posterior distributions.

```
normal_start_time <- proc.time()
# Step 1: Read in the data and sort it
dat <- as.vector(read.table("data.txt",header=F))
dat <- sort(dat[,1])

# Step 2: Set up number of simulations and number of parameters to save
reps <- 50000
save <- 100
dist_vals <- rep(NA,reps)

# Step 3: Draw values from the prior distributions
tmp_mean <- runif(reps, -20, 20)
tmp_variance <- runif(reps, 0, 50)

# Step 3: Loop through the prior values, simulate data and compare to observed data
# using the Euclidean distance
for(i in 1:reps){
  tmp_dat <- rnorm(length(dat), tmp_mean[i], sqrt(tmp_variance[i]))
  tmp_dat <- sort(tmp_dat)
  dist_vals[i] <- dist(rbind(dat,tmp_dat))
}

# Step 4: Sort distance values (summary stat) and keep the indexes
dist_indexes <- sort(dist_vals, index.return=T)

# Step 5: Get the indexes of the top values based on the number of parameter values you want to save
save_indexes <- dist_indexes$ix[1:save]

# Step 6: Get the corresponding parameter values with the lowest distances from the observed data
```

```r
saved_means <- tmp_mean[save_indexes]
saved_variances <- tmp_variance[save_indexes]
normal_total_time <- proc.time() - normal_start_time

# Store in a data frame and print as a knitr table
res <- data.frame(Parameter=c("Normal Mean","Normal Variance"),
                  Mean=c(mean(saved_means), mean(saved_variances)),
                  SD=c(sd(saved_means),sd(saved_variances)))

knitr::kable(res, digits=3)
```

Parameter	Mean	SD
Normal Mean	-2.175	0.448
Normal Variance	1.631	1.067

```r
# Plot the posterior distributions for the mean and variance
par(mfrow=c(1,2))
hist(saved_means, main="Mean", xlab=expression(hat(mu)), ylab="")
abline(v=mean(saved_means),col="blue",lty="dashed",lwd=2)
hist(saved_variances, main="Variance", xlab=expression(hat(sigma)^2), ylab="")
abline(v=mean(saved_variances),col="blue",lty="dashed",lwd=2)
```



ABC–Sequential Monte Carlo algorithm

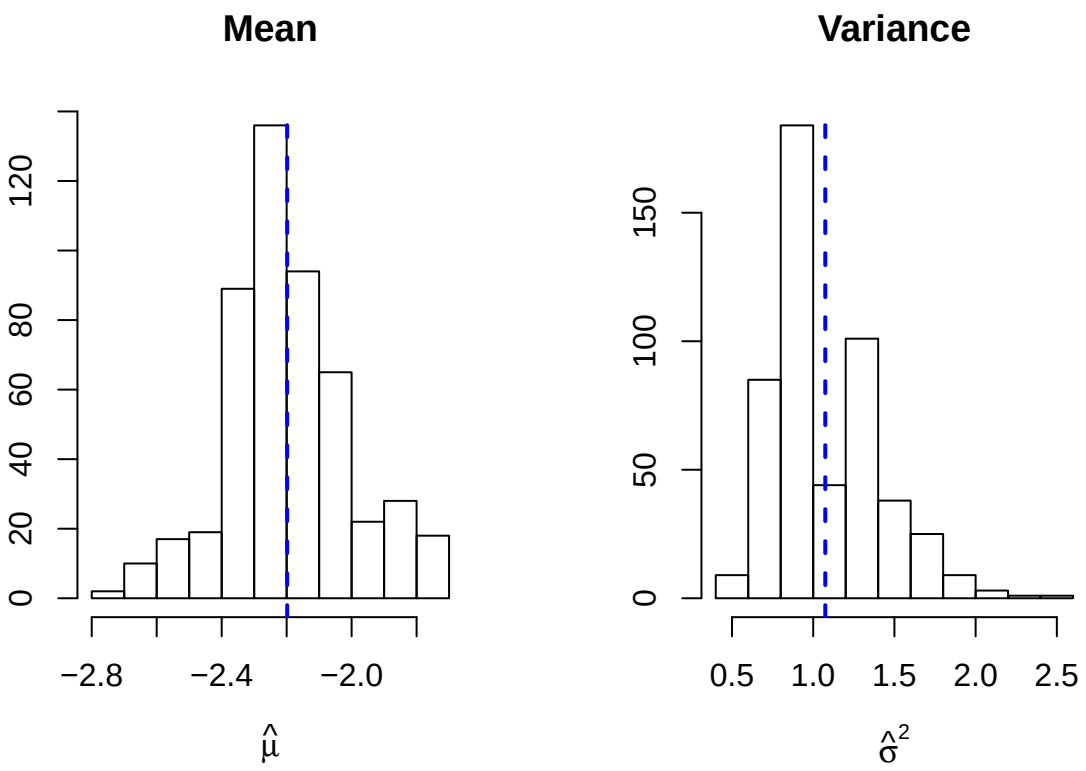
The setup for this example is the same as above, except that we use a sequential Monte Carlo algorithm with 5 rounds of sampling.

```r
sequential_start_time <- proc.time()
# Read in data
dat <- as.vector(read.table("data.txt",header=F))
dat <- sort(dat[,1])

# Number of SMC rounds
rounds <- 5

# Number of iterations per round
N <- 10000

# Fraction of samples to save per round
tau <- c(0.2,rep(0.25,rounds-1))

# Number of samples to save from first round
Q <- N*tau[1]

# Threshold value for simulated vectors to be saved
epsilon <- rep(NA,rounds)

# Storage vector for dist measure from simulated data
dist_vals <- rep(NA,N)

# Draw initial mean and variance samples for first round from prior
tmp_mean <- runif(N, -20, 20)
tmp_variance <- runif(N, 0, 50)

## -------- 1st round -------- ##

# Draw N data sets and compare
for(i in 1:N){
  tmp_dat <- rnorm(length(dat), tmp_mean[i], sqrt(tmp_variance[i]))
  tmp_dat <- sort(tmp_dat)
  dist_vals[i] <- dist(rbind(dat,tmp_dat))
}

# Sort dist values and save the top Q means and variances
dist_indexes <- sort(dist_vals, index.return=T)
save_indexes <- dist_indexes$ix[1:Q]
epsilon[1] <- dist_indexes$x[Q] # first epsilon is the max dist value
saved_means <- tmp_mean[save_indexes]
saved_variances <- tmp_variance[save_indexes]


## -------- 2nd through rth rounds -------- ##

for(r in 2:rounds){

  curr_num_saved <- 0
  dist_vals <- rep(NA,Q)
  tmp_saved_means <- rep(NA,Q)
  tmp_saved_variances <- rep(NA,Q)
```

```
  while(curr_num_saved < Q){
    curr_mean <- sample(saved_means,1)
    curr_mean <- curr_mean + runif(1,-0.05,0.05)
    curr_variance <- sample(saved_variances,1)
    curr_variance <- curr_variance + runif(1,0,0.05)
    curr_dat <- rnorm(30,curr_mean,sqrt(curr_variance))
    curr_dat <- sort(curr_dat)
    curr_dist <- dist(rbind(dat,curr_dat))

    # Only save value if it is better than the previously saved max
    if(curr_dist < epsilon[r-1]){

      curr_num_saved <- curr_num_saved + 1
      dist_vals[curr_num_saved] <- curr_dist
      tmp_saved_means[curr_num_saved] <- curr_mean
      tmp_saved_variances[curr_num_saved] <- curr_variance

    }

  }

  # Save mean and variance samples
  dist_indexes <- sort(dist_vals, index.return=T)
  save_indexes <- dist_indexes$ix[1:(tau[r]*Q)]
  epsilon[r] <- dist_indexes$x[(tau[r]*Q)]
  saved_means <- tmp_saved_means[save_indexes]
  saved_variances <- tmp_saved_variances[save_indexes]
}

sequential_total_time <- proc.time() - sequential_start_time

# Make a data frame and print as a knitr table
res <- data.frame(Parameter=c("Normal Mean","Normal Variance"),
                  Mean=c(mean(saved_means), mean(saved_variances)),
                  SD=c(sd(saved_means),sd(saved_variances)))

knitr::kable(res, digits=3)
```

Parameter	Mean	SD
Normal Mean	-2.198	0.187
Normal Variance	1.074	0.332

```
# Plot the posterior distribution of the parameters
par(mfrow=c(1,2))
hist(saved_means, main="Mean", xlab=expression(hat(mu)), ylab="")
abline(v=mean(saved_means),col="blue",lty="dashed",lwd=2)
hist(saved_variances, main="Variance", xlab=expression(hat(sigma)^2), ylab="")
abline(v=mean(saved_variances),col="blue",lty="dashed",lwd=2)
```




```
timing <- data.frame(Algorithm=c("ABC","ABC-SMC"),
                     Time=c(normal_total_time[3],sequential_total_time[3]),
                     Improvement=c(normal_total_time[3]/normal_total_time[3],
                                   normal_total_time[3]/sequential_total_time[3]))

knitr::kable(timing, digits=3)
```

Algorithm	Time	Improvement
ABC	2.579	1.000
ABC-SMC	1.210	2.131