

```

library(EasyABC)
library(SimInf)

# specifying initial compartmental values
u0 = data.frame(S=c(90000), I=c(10000), R=c(0)) # where N=100000

# specifying model
model <- SIR(u0, 1:75, beta = 0.5, gamma = 0.025 )
result <- run(model, threads = 1)
plot(result)
result@U
result@U[2,50]
result@U[2,75]

# creating a loop around the function
set.seed(123)
save_prevs= matrix(c(0,0),10000,2) # a 10000x2 matrix that receives the prevalences at 50 and 75 per model run
for(i in 1:10000){

modelABC= function(parameters){
  library(SimInf)
  u0 = data.frame(S=c(90000), I=c(10000), R=c(0)) #specifying initial compartmental values
  model <- SIR(u0, 1:75, beta=parameters[1], gamma=parameters[2]) # specifying the model
  result <- run(model, threads = 1) # running the model
  pop= numeric()
  pop[1]=result@U[2,50] # number of infected individuals at time 50
  pop[2]=result@U[2,75] # number of infected individuals at time 75
  prevs=pop/sum(u0) # prevalence at times 50 and 75
  return(prevs)
}
save_prevs[i,]= modelABC(c(0.5,0.025))
}

### random selection of rows implies random selection of model runs

targets=save_prevs[sample(nrow(save_prevs), 1000), ] ### obtaining a sample of size, 1000 as the targets

hist(targets[,1]) # histogram of sample prev at 50
hist(targets[,2]) # histogram of sample prev at 75

c(max(targets[,1]), max(targets[,2])) #Peak prevalence level

### some illustrative code

modelABC= function(parameters,N,inf){
  library(SimInf)
  u0 = data.frame(S=(1-inf)*N, I=inf*N, R=c(0)) #specifying initial compartmental values
  model <- SIR(u0, 1:75, beta=parameters[1], gamma=parameters[2]) # specifying the model
  result <- run(model, threads = 1) # running the model
  pop= numeric()
  pop[1]=result@U[2,50] # number of infected individuals at time 50
  pop[2]=result@U[2,75] # number of infected individuals at time 75
  prevs=pop/sum(u0) # prevalence at times 50 and 75
  return(prevs)
  return(plot(results))
}

res1= modelABC(c(0.5,0.025),100000,inf=0.1)
plot(res1)

u0 = data.frame(S=c(90000), I=c(10000), R=c(0)) #specifying initial compartmental values
model <- SIR(u0, 1:75, beta=0.5, gamma=0.025) # specifying the model
result <- run(model, threads = 1)
plot(result)

resultst50= c(result@U[1,50], result@U[2,50], result@U[3,50])
sum(resultst50)

?sample

summat= matrix(c(0,0),100000,2) # a 10000x2 matrix that receives the prevalences at 50 and 75 per model run

for(i in 1:100000){
xsamp= sample(x=c("S","I","R"),prob= resultst50/100000, size= 1000, replace=T)

```

```
summat[i,]= summary(as.factor(xsamp))
}  
mean(summat[,1])
```

```
# peak prevalence  
max(result@U[2,])  
# time at peak prevalence  
which.max(result@U[2,])
```

```
?rnorm()  
x1= rnorm(100000, mean=10,sd=1)  
mean(x1)
```

```
mean(sample(x1,10))
```