# Priors_production_AM.Rmd

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## production des priors AM

**mon_script**

```
library(stats)
library("KScorrect", lib.loc="~/R/x86_64-pc-linux-gnu-library/3.3")
######partie locus
#variables locus
#-L=taille du gene
#-t=theta
#-r=rho
#-delta=taille du track recombinant
#boucle de 1000000 iterations(1000000 tirage demographique)
demo<-NULL
locus<-NULL
tbs<-NULL
#####TIRER un prior locus dans une distribution uniforme de bornes
L<-scan("/home/kadurand/partage_windows/Xylella/analyses_genomiques/ABC/1368oRTHOLOGUES_summarystats/le
t<--runif(1368,0, 0.001)#bound_theta=[0-0.0003]bornes vrai pour 13pauca_multiplex augmenter la borne su
r<-runif(1368,0,0.001)#bound_theta=[0-0.0003]bornes vrai pour 13pauca_multiplex augmenter la borne sup
delta<-round(runif(1368,10, 1000))#bound=[10-1000]
#print(L,t,r,delta)
m_locus=matrix(c(L,t,r,delta),ncol=4)
m_locus=as.data.frame(m_locus)

for (i in 1:10000){#tirage des priors demographiques
  #variables demographique modéle SI
  ##Param_demo (5) = Ts  N1, N2,  M12, M21
  Ts<-rlunif(1,100,1E+8)#bound=[1,100,1E+8]
  N1<-rlunif(1,100,1E+6)#bound=[100,1E+6]
  N2<-rlunif(1,100,1E+6)#bound=[100,1E+6]
  Na<-rlunif(1,100,1E+6)#Bound=[100,1E+6]
  M12<-runif(1,0.01,30)#bound=[0.01-30]
  M21<-runif(1,0.01,30)#bound=[0.01-30]
  Tam<-rlunif(1,100,Ts)#)#bound=[0-100]
  #print( Ts , N1, N2,  M12, M21,Tam)
m_demo=matrix(c(Ts,N1,N2,M12,M21,Tam),ncol=6)
m_demo=as.data.frame(m_demo)
locus<-cbind(m_locus,m_demo)

path <- "/home//kadurand/partage_windows/Xylella/analyses_genomiques/ABC/fastSimBac_linux/Priors_AM_100
write.table(locus,file= paste(path,i, sep="-"),col.names=FALSE,row.names =FALSE)
}
```