Priors_production

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production des priors SI

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mon_script

```r
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/l
t<-runif(1,1E-11, 0.001 )#bound_theta=[0-0.0003]bornes vrai pour 13pauca_multiplex augmenter la borne s
r<-runif(1,0,0.0001)##bound_rho=[0,0.0006]bornes vrai pour 13pauca_multiplex augmenter la borne sup à 0
delta<-round(runif(1,10, 1000))#bound=[10-1000]
#print(L,t,r,delta)
m_locus=matrix(c(t,r,delta),ncol=3)
m_locus=as.data.frame(m_locus)

for (i in 1:10000){#tirage des priors demographiques
#variables demographique modéle SI
#Param_demo (3) =   Ts, N1, N2,
  Ts<-rlunif(1,100,1E+8)#bound=[1,100,1E+8]
  #N1<-rlunif(1,100,1E+6)#bound=[100,1E+6]
  N2<-rlunif(1,1E-3,1E+3)#bound=[1E-3,1E+3]
  Na<-rlunif(1,100,1E+6)#Bound=[100,1E+6]
  TS2=Ts+(Ts/1E+6)


#print( N1, N2, Ts)
m_demo=matrix(c(Ts,N2,Na,TS2),ncol=4)
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_SI_100
write.table(locus,file= paste(path,i, sep="-"),col.names=FALSE,row.names =FALSE)
}
```