Priors_production

karine Durand

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production des priors SI

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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/l
L<-scan("/home/kadurand/partage_windows/Xylella/analyses_genomiques/ABC/msms/lenght")#bound_taille du g
t<-runif(997,0, 0.004 )#bound_theta=[0-0.0003]bornes vrai pour 13pauca_multiplex augmenter la borne sup
r<-runif(997,0,0.004)#bound_rho=[0-0.0003]bornes vrai pour 13pauca_multiplex augmenter la borne sup à 0
#delta<-round(runif(997,10, 1000))#bound=[10-1000]
#print(L,t,r,delta)
m_locus=matrix(c(L,t*L,r*L),ncol=3)
m_locus=as.data.frame(m_locus)

for (i in 1:1000){#tirage des priors demographiques
#variables demographique modéle SI
#Param_demo (3) =   Ts, N1, N2,
  ##Param_demo (5) = Ts  N1, N2,  M12, M21
  Ts<-runif(1,0,20)#bound=[1,100,1E+7] Ts/4N0
  N1<-runif(1,0,30)#bound=[100,1E+6] X=N1/N0
  N2<-runif(1,0,30)#bound=[100,1E+6]
  Na<-runif(1,0,60)#Bound=[100,1E+6]

#print( N1, N2, Ts)
m_demo=matrix(c(Ts,N1,N2,Na),ncol=4)
m_demo=as.data.frame(m_demo)
locus<-cbind(m_locus,m_demo)

path <- "/home//kadurand/partage_windows/Xylella/analyses_genomiques/ABC/msms/Priors_SI_ms_13/SI"
write.table(locus,file= paste(path,i, sep="-"),col.names=FALSE,row.names =FALSE)
}
```