Priors SC

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Générer des paramètres (Priors)

Ce script permet de générer des priors pour le modèle Démographique SC selon des distributions uniforme ou log-uniforme

```
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/locality and the summary states and the summary states are summary states are summary states are summary states and the summary states are summary states are summary states are summary states and the summary states are summary states and the summary states are summary states are summary states and the summary states are summa
L<-scan("/home/kadurand/partage_windows/Xylella/analyses_genomiques/ABC/msms/lenght")#bound_taille du g
t<-runif(997,1E-11, 0.001) #bound_theta=[0-0.0003] bornes vrai pour 13pauca_multiplex augmenter la borne
r<-runif(997,0,0.0001)#bound_theta=[0-0.0003]bornes vrai pour 13pauca_multiplex augmenter la borne sup
delta<-round(runif(997,10, 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 SC
    ##Param_demo (7) = Ts, N1, N2, M12, M21, Tsc, T1,
    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 = [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]
    Tsc<-rlunif(1,100,1E+5)#bound=[0-100]borne sup <Ts
    TS2=Ts+(Ts/1E+6)
    #print( Ts, N1, N2, M12, M21, Tsc)
    m_demo=matrix(c(Ts,N2,Na,M12,M21,Tsc),ncol=6)
    m_demo=as.data.frame(m_demo)
    locus<-cbind(m_locus,m_demo)</pre>
        path <- "/home/kadurand/partage_windows/Xylella/analyses_genomiques/ABC/msms/Priors_SC_msms/SC"
        write.table(locus,file= paste(path,i, sep="-"),col.names=FALSE,row.names =FALSE)
}
```

Distribution des Priors

```
V3 V4
                                             V1
                                                      ٧2
## 1 258 0.0004760556 8.326071e-05 879 18291.48 15.52473 196448.4 19.44256
## 2 1275 0.0005266801 5.775155e-05 903 18291.48 15.52473 196448.4 19.44256
## 3 1074 0.0004399312 8.330831e-05 576 18291.48 15.52473 196448.4 19.44256
## 4 1197 0.0009617846 3.967644e-05 520 18291.48 15.52473 196448.4 19.44256
## 5 645 0.0006762178 1.541051e-05 634 18291.48 15.52473 196448.4 19.44256
## 6 1584 0.0007422637 3.914636e-05 958 18291.48 15.52473 196448.4 19.44256
           ۷5
                   ۷6
## 1 20.43025 2217.469
## 2 20.43025 2217.469
## 3 20.43025 2217.469
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## 6 20.43025 2217.469
```