## 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 for the state of the
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 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(1,10,Ts) \#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,TS2),ncol=7)
    m_demo=as.data.frame(m_demo)
    locus<-cbind(m_locus,m_demo)</pre>
        path <- "/home/kadurand/partage_windows/Xylella/analyses_genomiques/ABC/fastSimBac_linux/Priors_SC_</pre>
         write.table(locus,file= paste(path,i, sep="-"),col.names=FALSE,row.names =FALSE)
}
```

## Distribution des Priors

```
## 1 0.0002650113 7.398897e-05 127 1993.057 635.3898 20125.68 18.02458 ## 1 16.77433 26.7383 1993.059
```