

# Parameterization of the LN of the speciation rate.

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```
m=-13.58; s=1.85
```

```
q01=qlnorm(0.1, meanlog=m, sdlog=s) # proper limits for our distribution, we are keeping the 90%  
of the possible values
```

```
q09=qlnorm(0.9, meanlog=m, sdlog=s) # proper limits for our distribution, we are keeping the 90%  
of the possible values
```

## this is the plot of the distribution

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```
probs=seq(0,1,length.out=1000)  
q=qlnorm(probs,meanlog=m,sdlog=s)  
plot(probs,log10(q), main=paste0("LN:",m,",",s), xlab="Prob", ylab="log10(q)",axes=F) # | q0.1:  
",q01, " q0.9: ",q09 )  
axis(2); axis(1, at=seq(0,1,by=0.1), labels=seq(0,1,by=0.1), las=2)
```

```
meanLeaves=mean(c(4,20)) # these are the old values (remember, haploid individual for simphy)  
E_Height_200Ky_Lima=log(meanLeaves)/200000 # same values as before, i was generating  
wrong years, but now I'm doing the correct ones  
E_Height_20My_Lima=log(meanLeaves)/20000000 # same values as before, i was generating  
wrong years, but now I'm doing the correct ones  
pEH20a=plnorm(E_Height_20My_Lima, mean=m, sdlog=s)  
pEH200a=plnorm(E_Height_200Ky_Lima, mean=m, sdlog=s)  
points(c(pEH20a,pEH200a),log10(c(E_Height_20My_Lima,E_Height_200Ky_Lima)), col="blue",  
pch=19)
```

```
meanLeaves=mean(c(4,12)) # these are our new number of leaves (remember, haploid individual  
for simphy)  
E_Height_200Ky_Limb=log(meanLeaves)/200000  
E_Height_20My_Limb=log(meanLeaves)/20000000  
pEH20b=plnorm(E_Height_20My_Limb, mean=m, sdlog=s)  
pEH200b=plnorm(E_Height_200Ky_Limb, mean=m, sdlog=s)  
points(c(pEH20b,pEH200b),log10(c(E_Height_20My_Limb,E_Height_200Ky_Limb)), col="red",  
pch=19)
```

```
qs=c(q01,q09)
```

```
opta=c(E_Height_20My_Lima,E_Height_200Ky_Lima)
optb=c(E_Height_20My_Limb,E_Height_200Ky_Limb)
c(opta[1] >qs[1], opta[2] <qs[1],optb[2] <qs[2])
```

```
#####
####
```

## Parameterization of the LN of the speciation rate.

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```
png(filename="ln.parameterization.simphy.png", width=400, height=400)
m=-13.58; s=1.85
```

## this is the plot of the distribution

---

```
probs=seq(0,1,length.out=1000)
q=qlnorm(probs,meanlog=m,sdlog=s)
plot(probs,log10(q), main=paste0("LN:",m,",",s), xlab="Probs.", ylab="log10(q)",axes=F) # | q0.1:
",q01, " q0.9: ",q09 ))
axis(2); axis(1, at=seq(0,1,by=0.1), labels=seq(0,1,by=0.1), las=2)
meanLeaves=mean(c(4,12)) # these are our new number of leaves (remember, haploid individual
for simphy)
E_Height_200Ky_Limb=log(meanLeaves)/200000
E_Height_20My_Limb=log(meanLeaves)/20000000
pEH20b=plnorm(E_Height_20My_Limb, mean=m, sdlog=s)
pEH200b=plnorm(E_Height_200Ky_Limb, mean=m, sdlog=s)
lines(c(pEH20b,pEH20b), c(log10(E_Height_20My_Limb), -10), col="red")>
lines(c(pEH200b,pEH200b), c(log10(E_Height_200Ky_Limb), -10), col="red")
dev.off()
```