

Brownian Motion

LOAD PACKAGES

```
library(phytools)
```

```
## Loading required package: ape
```

```
## Loading required package: maps
```

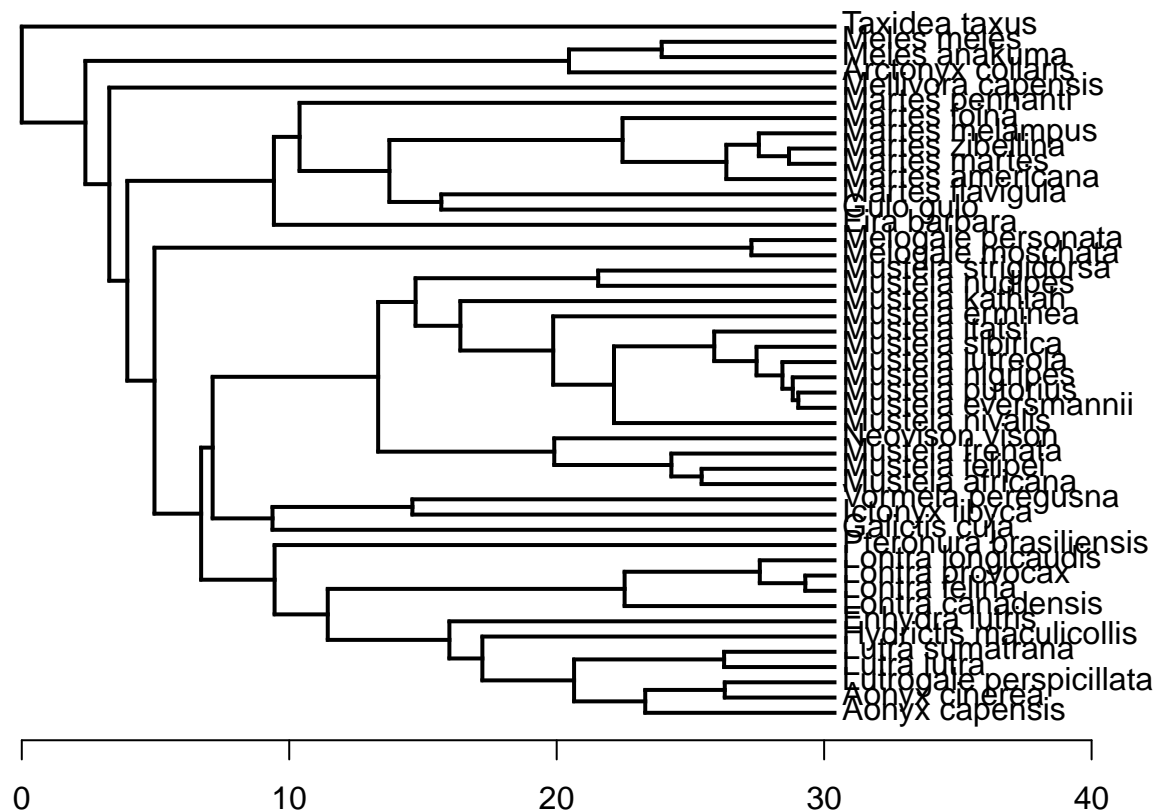
HOMEWORK EXERCISE

Load tree and calculate rates

```
prac.tree<-read.nexus("../Lab1/consensusTree_10kTrees_Carnivora_Version1.nex") #load tree
t<-15 # total time
n<-50 # total taxa
b<-(log(n)-log(2))/t #birth rate
```

Visualize tree:

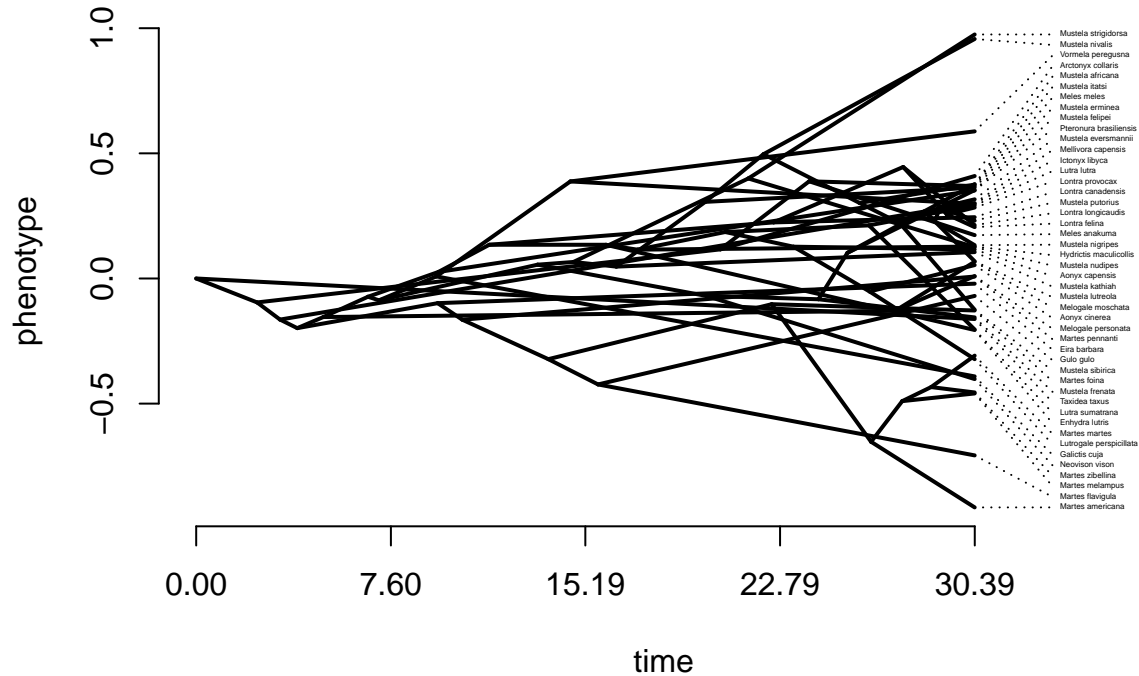
```
plotTree(prac.tree,mar=c(3.1,0.1,0.1,0.1))
axis(1)
```



Simulate branches with Brownian Motion:

```
sig2<-0.01
x<-fastBM(prac.tree,sig2=sig2,internal=TRUE)
phenogram(prac.tree,x,spread.labels=TRUE,spread.cost=c(1,0),spread.labels=TRUE,fsz = 0.25)
```

Optimizing the positions of the tip labels...

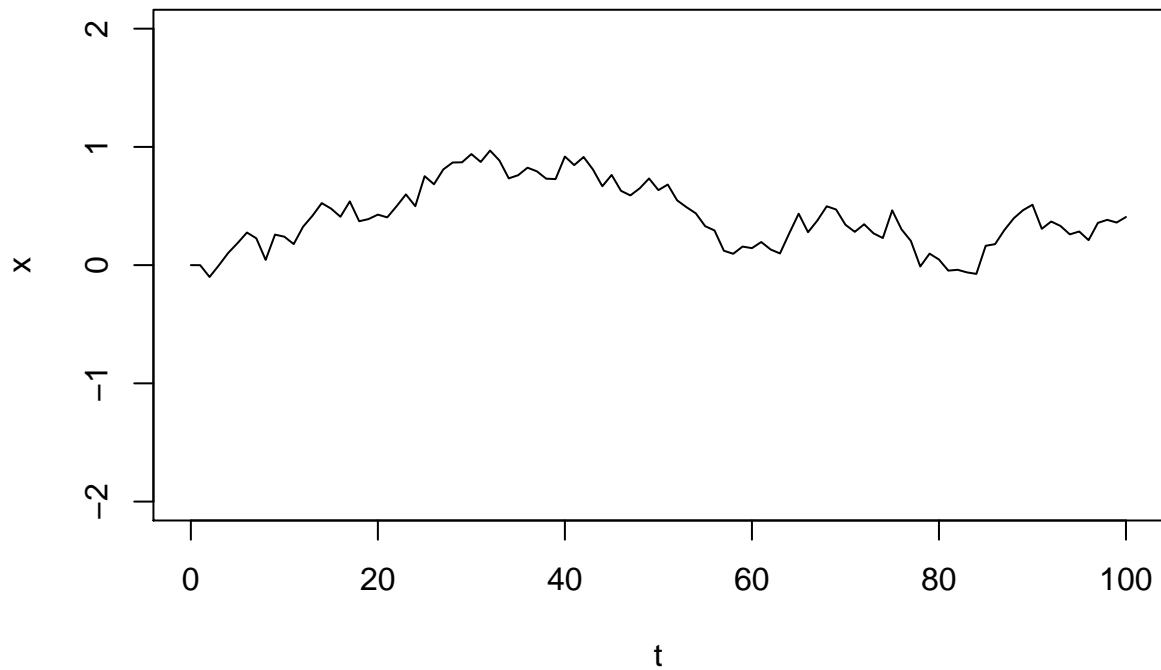


TUTORIAL

Discrete Time: Single Simulation

$\sigma^2=0.01$ for 100 generations

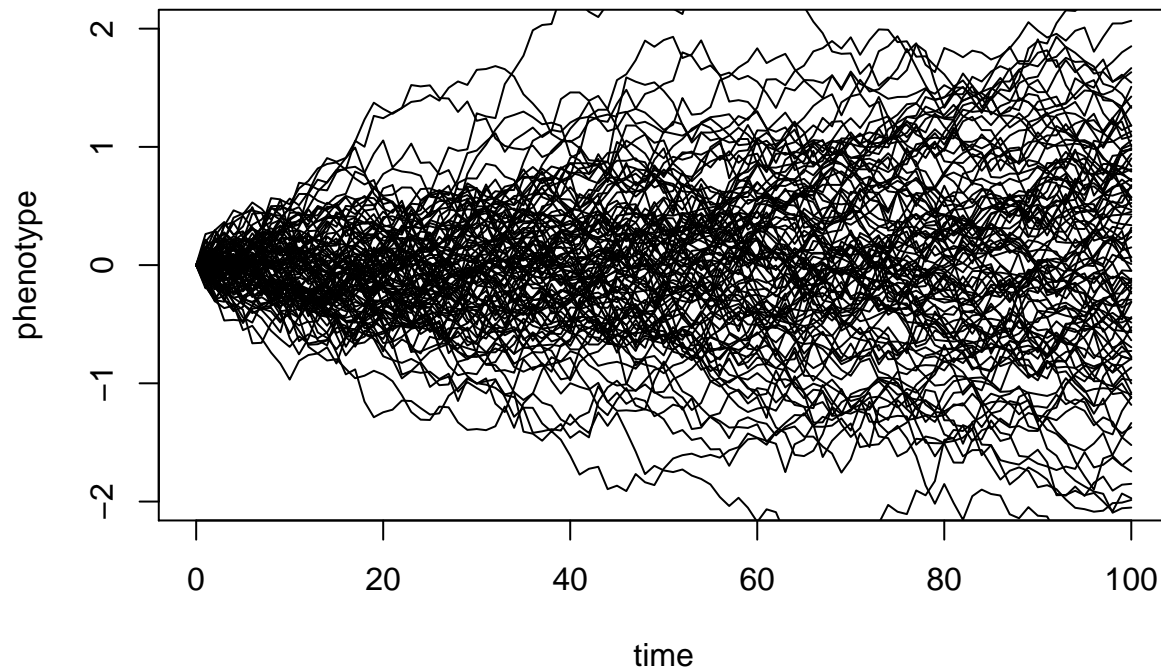
```
t<-0:100 #time sequence
sig2<-0.01
x<-rnorm(n=length(t)-1,sd=sqrt(sig2)) #create a sequence of normally distributed numbers with a standard deviation of 0.01
x<-c(0,cumsum(x)) #start vector x with 0 and then add each successive step to get the new position
plot(t,x,type="l",ylim=c(-2,2)) #plot time versus step
```



Discrete Time: Multiple Simulations

Number of simulations: 100

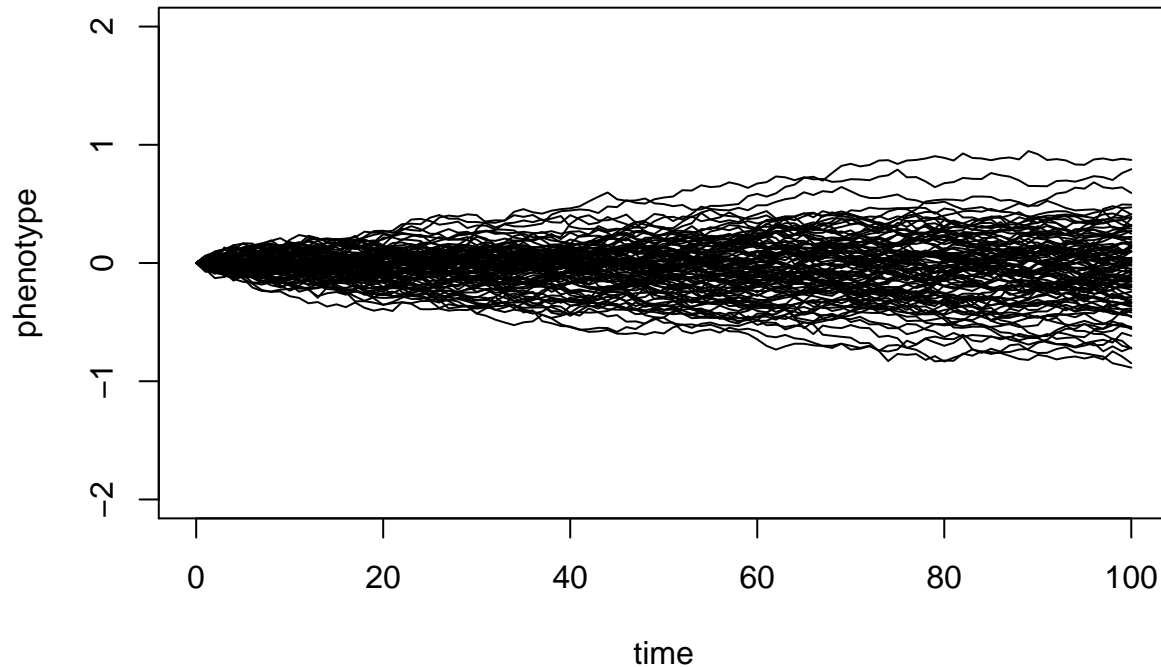
```
nsim<-100
X<-matrix(rnorm(n=nsim*(length(t)-1),sd=sqrt(sig2)),nsim,length(t)-1) #create a matrix of simulation steps
X<-cbind(rep(0,nsim),t(apply(X,1,cumsum))) #make the time steps a row in the matrix
plot(t,X[1,],xlab="time",ylab="phenotype",ylim=c(-2,2),type="l") #blank plot
apply(X[2:nsim,],1,function(x,t) lines(t,x),t=t) #plot the steps for each simulation over time
```



NULL

Discrete Time: Multiple Simulations, $\sigma^2/2$

```
X<-matrix(rnorm(n=nsim*(length(t)-1),sd=sqrt(sig2/10)),nsim,length(t)-1)
X<-cbind(rep(0,nsim),t(apply(X,1,cumsum)))
plot(t,X[1,],xlab="time",ylab="phenotype",ylim=c(-2,2),type="l")
apply(X[2:nsim,],1,function(x,t) lines(t,x),t=t)
```



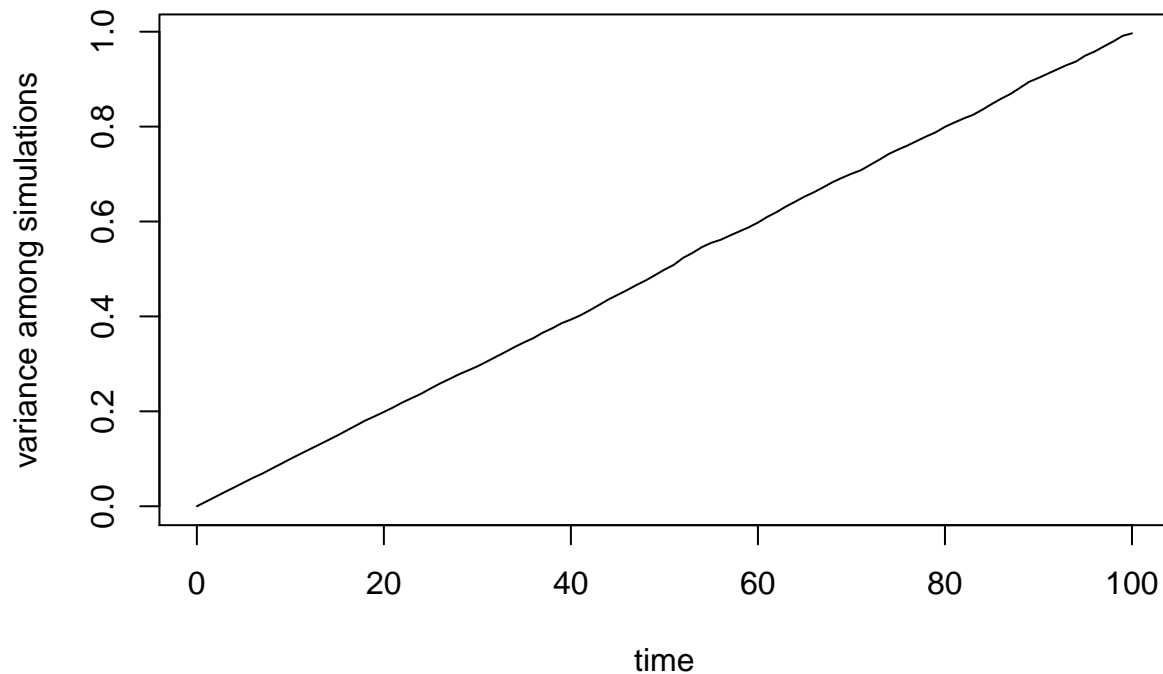
NULL

Brownian Motion Expected Variance

The expected variance is $\sigma^2 * \text{time step}$.

This section plots the variance among simulations to confirm this assumption.

```
nsim<-10000
X<-matrix(rnorm(n=nsim*(length(t)-1),sd=sqrt(sig2)),nsim,length(t)-1)
X<-cbind(rep(0,nsim),t(apply(X,1,cumsum)))
v<-apply(X,2,var) #calculates the variance among simulations
plot(t,v,type="l",xlab="time",ylab="variance among simulations")
```



Confirm the slope of the line is roughly equal to 1:

```
var(X[,length(t)])
```

```
## [1] 0.9964872
```

Brownian Motion along Tree Branches

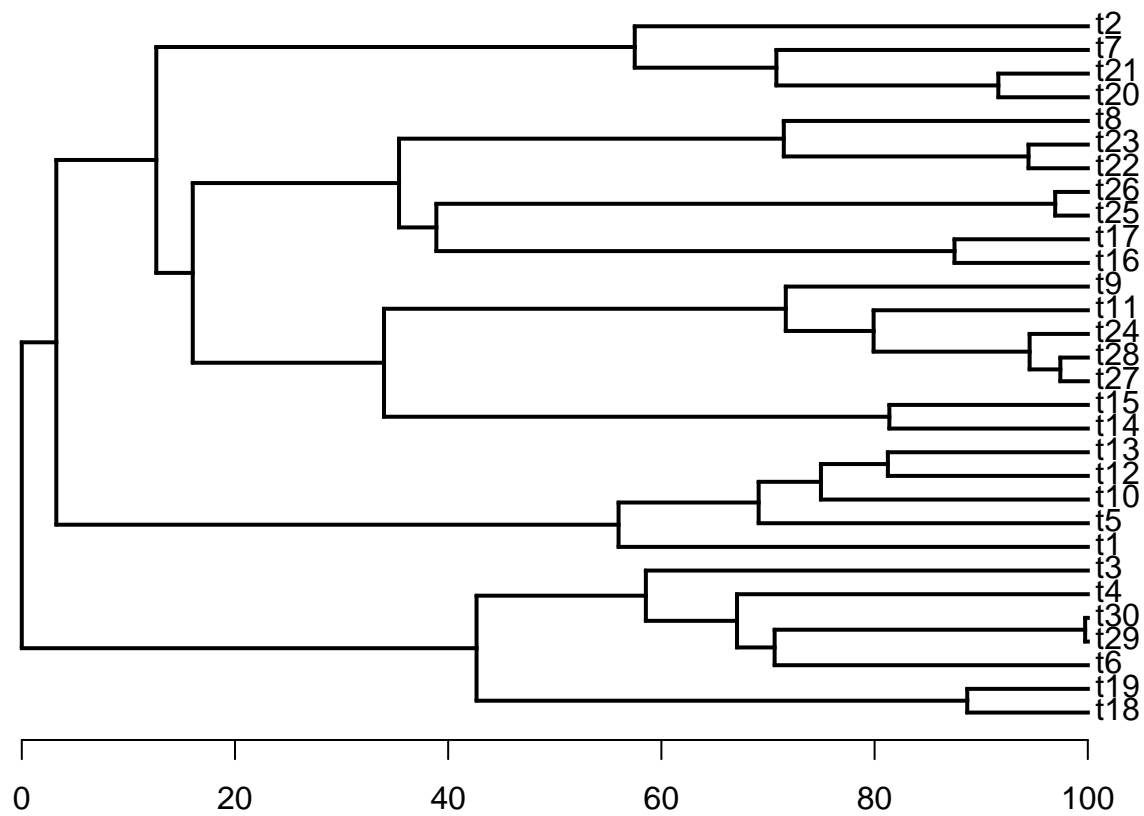
Simulate using a 30 taxa tree with 100 time steps:

```
t<-100 # total time
n<-30 # total taxa
b<-(log(n)-log(2))/t #birth rate
tree<-pbtree(b=b,n=n,t=t)
```

```
## simulating with both taxa-stop (n) and time-stop (t) is
## performed via rejection sampling & may be slow
##
## 65 trees rejected before finding a tree
```

Visualize tree:

```
plotTree(tree,mar=c(3.1,0.1,0.1,0.1))
axis(1)
```



Simulate branches with new branches offset to end point of source branch:

```
## simulate Brownian evolution on a tree with fastBM
x<-fastBM(tree,sig2=sig2,internal=TRUE)
## visualize Brownian evolution on a tree
phenogram(tree,x,spread.labels=TRUE,spread.cost=c(1,0))
```

