

BM formula

```
brown<-function(param, tree, trait){

require(MASS)
sigma<-abs(param[1]) # paramètre à estimer
n<-length(trait)
tree.vcv<-vcv(tree) # estimation de la matrice vcv sous l'hypothèse BM
s_vcv3<- sigma^2 * tree.vcv # sigma intégrés dans vcv
d_vcv3 <- ginv(s_vcv3) # inverse de s_vcv3
anc_estim <- ace(trait, tree)$ace[[1]] # estimation de l'ancêtre
one<-matrix(1,n,1)

(-t(trait-one*anc_estim)%*%d_vcv3)%*%(trait-one*anc_estim))/2- n*log(2*pi)/2-
log( det(s_vcv3))/2 # MLE
}

optim(c(0.1), brown, control=list(fnscale=-1), NULL, tree=utree, trait=bio10, method = "L-BFGS-
B", hessian = TRUE) # estimation des paramètres
```

Vérification BM formula

On teste pour le même arbre notre formule avec celle préexistante de geiger, pour 100 répétition.

```
require(geiger)

#function Berto-Anna
brown<-function(param, tree, trait, anc){
  require(MASS)
  sigma<-param[1]

  n<-length(trait)
  tree.vcv<-vcv.phylo(tree)
  s_vcv3<- sigma^2 * tree.vcv
  d_vcv3 <- ginv(s_vcv3)

  if(anc==1) {
    if(length(param)<=1) {
      error("needs 2 paramters for this option");
    }
    anc_estim <- param[2]
  }
  else if(anc==2) {
    anc_estim <- ace(trait, tree)$ace[[1]]
  }
  else if(anc==3) {
    anc_estim <- colSums(d_vcv3)%*%trait/sum(d_vcv3)
  }

  (-t(trait-anc_estim)%*%d_vcv3)%*%(trait-anc_estim))/2 - n*log(2*pi)/2 - log(det(s_vcv3))/2
```

```
}
```

```
tree10<-rcoal(10)
```

```
#estimate with brown function (Berto-Anna) - I only store positive sigmas(!)
```

```
res_brown<-matrix(0,nrow=100, ncol=2)
```

```
for (i in 1:100){
```

```
  traits_sigma01<-rTraitCont(tree10, model="BM", sigma = 0.1)
```

```
  #val<-abs(optim(c(0.2), brown, control=list(fnscale=-1), NULL, tree=tree10, trait=traits_sigma01,  
method = "L-BFGS-B", hessian = TRUE)$par )
```

```
  res_brown[i,1]<-optim(c(0.2,0.0), fn<-function(p) brown(p, tree10, traits_sigma01, anc=1),  
control=list(fnscale=-1), lower=c(0.000000001,-100), upper=c(100,100), method = "L-BFGS-B",  
hessian = TRUE)$par[1]
```

```
  res_brown[i,2]<-sqrt(fitContinuous(tree10,traits_sigma01, model="BM")$Trait1$beta)
```

```
}
```

```
par(mfrow=c(1,2))
```

```
#
```

```
hist(res_brown[,1])
```

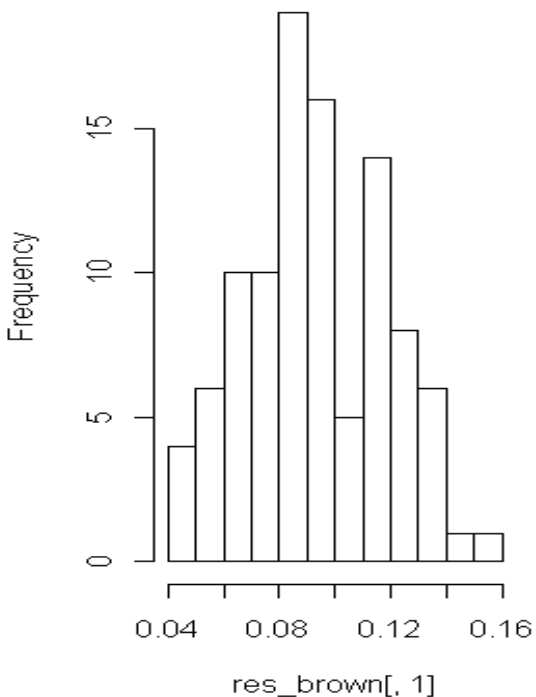
```
#
```

```
hist(res_brown[,2])
```

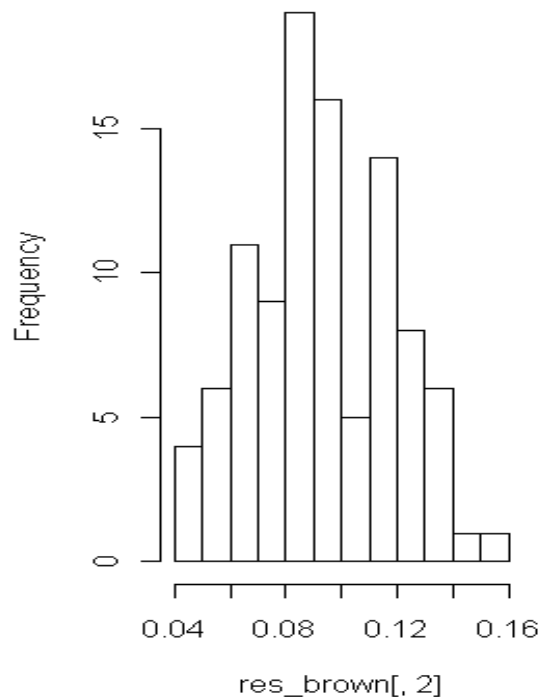
```
#
```

```
apply(res_brown, 2, mean) # pour voire graphiquement l'équivalence
```

Histogram of res_brown[, 1]



Histogram of res_brown[, 2]



Résultat:

	bio1	bio2	bio10
Sigma	84.5	21.9	52.3
MLE	-51.2	-38.9	-46.8

C'est un modèle affecté uniquement par la **dérive**.