

## Vignette for:

Blarquez O., Finsinger W. and C. Carcaillet. 2013. Assessing  
Paleo-Biodiversity Using Low Proxy Influx. PLoS ONE 8(4):  
e65852

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June 12, 2013

This example is intended to present the methods developed for the paper Blarquez *et al.* (2013). We will use the macroremain record of the Lac du Loup a small subalpine lake with continuous macroremain counts for the last 11 750 years. More details on this site can be found in Blarquez *et al.* (2010). First load the macroremain data:

```
> dataMacro=read.csv("http://blarquez.com/public/code/dataMacro.csv")
> # Macroremain counts
> paramMacro=read.csv("http://blarquez.com/public/code/paramMacro.csv")
> # Associated depths, ages and sample volumes
> dataMacro[is.na(dataMacro)]=0
> # Set missing values to zero
```

We now calculate the median resolution of the record and the interpolated ages at which the influx will be calculated:

```
> resMed=median(diff(paramMacro[,3]))
> Ages=seq(-50, 11750, resMed)
```

We reconstruct the influx matrix using the pretreatment function which is the R implementation of the CharAnalysis CharPretreatment.m function originally developed by P. Higuera and available at <https://sites.google.com/site/charanalysis>

Requires a matrix as input with the following columns:

CmTop CmBot AgeTop AgeBot Volume (params)

A serie from which to calculate accumulation rates (serie)

```
> source("http://blarquez.com/public/code/pretreatment.R")
> infMacro=matrix(ncol=length(dataMacro[1,]),nrow=length(Ages))
> for (i in 1:length(dataMacro[1,])){
+   infMacro[,i]=c(pretreatment(params=paramMacro,serie=dataMacro[,i],
+                               yrInterp=resMed,first=-50,last=11750,
+                               plotit=F,Int=F)$accI)
+ }
```

Calculate samples macroremain sums and the minimum influx sum:

```
> S=rowSums(infMacro)
> nMin=min(na.omit(S[1:length(S)-1]))
```

We exclude the last sample (not calculated because of unknown accumulation rate) and samples with NA (because of vol==0):

```
> del=which(S==0 | is.na(S))
> infMacro=infMacro[-del,]
> Ages=Ages[-del]
> S=S[-del]
```

We calculate a proportion matrix which is used to replicate the rarefaction procedure:

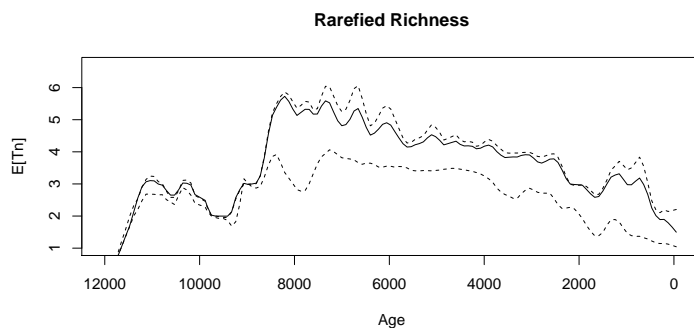
```
> S_=matrix(ncol=ncol(infMacro),nrow=nrow(infMacro))
> for (i in 1:length(infMacro[1,])){
+   S_[,i]=c(S)
+ }
> propMat=infMacro/S_
```

Replicate rarefaction with min influx  $n=1,2,\dots,500$ . We will use the rarefy function from the package vegan:

```
> library(vegan)
> rare_=matrix(nrow=nrow(infMacro),ncol=500)
> for (n in 1:500){
+   infN=ceiling(S_*n/nMin*propMat)
+   rare_[,n]=c(rarefy(infN,sample=n))
+ }
```

And finally calculates the 90 percent confidence intervals and plot the rarefied richness using a 500 years locally weighted scatter plot smoother:

```
> CI_=t(apply(rare_, 1, quantile, probs = c(0.05, 0.5, .95), na.rm = TRUE))
> span=500/resMed/length(Ages)
> plot(Ages,lowess(CI_[,2], f =span)$y,type="l",ylab="E[Tn]",ylim=c(min(CI_),
+   max(CI_)),xlab="Age",main="Rarefied Richness",xlim=c(12000,-100))
> lines(Ages,lowess(CI_[,1], f =span)$y,type="l",lty=2)
> lines(Ages,lowess(CI_[,3], f =span)$y,type="l",lty=2)
```



## References:

Blarquez O., Finsinger W. and C. Carcaillet. 2013. Assessing paleo-biodiversity using low proxy influx. PLoS ONE 8(4): e65852

Blarquez O., Carcaillet C., Mourier B., Bremond L. and O. Radakovitch. 2010. Trees in the subalpine belt since 11 700 cal. BP : origin, expansion and alteration of the modern forest. The Holocene 20 : 139-146. DOI : 10.1177/0959683609348857