R-script for performing the Monte Carlo analysis of power (simulations of the sampling outcomes)

```r
# R-script for performing simulations of datasets and testing outcomes
# based on treatment means and variance within and between replicates

#means per treatment
mu<-c(5,4,2.6,3.8)
#the multiplier (proportion of variance) can be changed
varPlotEffects<-0.5*var(mu)
#assume that half of the variance
#between treatments was actually due to the
#normal variation between sites
sd<-sqrt(c(3,2.7,2.1,2.7))
#variances per treatment
#note: in the code below it is assumed that all treatments
#have the same variance (the maximum of these)

#We assume that there are nrep replicates of sites per treatment
nrep<-3
#sample size per site, change this to decide the sample size
n<-30
#how many times to try
nsim<-100
p<-rep(NA,nsim)
trmt<-c("UBNC","BNC","B50","UBCC")
for (i in 1:nsim) {
  if (!(i%%10)) print(i)
  ranef<-rnorm(4*nrep,mean=0,sd=sqrt(varPlotEffects))
  y<-rep(mu,each=nrep*n)+rep(ranef,each=n)+rnorm(4*nrep*n,mean=0,sd=max(sd))
  plot<-rep(1:(nrep*4),each=n)
  data<-data.frame(y=y,plot=plot,trmt=rep(trmt,each=nrep*n))
  mod<-lme(y~trmt,random=~1|plot,data=data)
  p[i]<-anova(mod)$"p-value"[2]
}
#Efficiency: how often null hypothesis was not rejected (p=0.05)
sum(p>0.05)/nsim
```