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Supplementary file 2

sum(p>0.05)/nsim

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

```
# R-script for performing simulations of datasets and testing outcomes
# based on treatment means and variance within and between replicates
#
mu < -c(5, 4, 2.6, 3.8)
                            # means per treatment
varPlotEffects<-0.5*var(mu) # the multiplier (proportion of variance) can be changed
                            # 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
n<-30
                            # sample size per site, change this to decide the sample size
                            # how many times to try
nsim<-100
p<-rep(NA,nsim)</pre>
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))</pre>
                                                                  # generate 12 plot effects
       y<-rep(mu,each=nrep*n)+</pre>
          rep(ranef,each=n) +
         rnorm(4*nrep*n,mean=0,sd=max(sd))
                                                                   # generate v
       plot<-rep(1:(nrep*4),each=n)</pre>
                                                                   # generate plot id
       data<-data.frame(y=y,plot=plot,trmt=rep(trmt,each=nrep*n))</pre>
       mod<-lme(y~trmt,random=~1|plot,data=data)</pre>
       p[i] <- anova (mod) $"p-value"[2]</pre>
# Efficiency: how often null hypothesis was not rejected (p=0.05)
```

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