Code to reproduce power analysis in 'Letten and Cornwell (2014) The relative importance of recent and ancient evolution for contemporary ecology'

Load required packages into library.

```
library(picante)
library(ggplot2)
library(OUwie)
library(phytools)
```

Source functions provided in `power_funcs.r`

```
source('power_funcs.r')
```

Simulate a Yule phylogeny comprising 1000 tips/taxa.

```
tree.sim <- tree.evolve(tree.choice = "sim", pool.size = 1000)
```

Download real tree from http://datadryad.org/resource/doi:10.5061/dryad.63q27.2/3.1 (Zanne et al. 2013)

```
temp <- tempfile(fileext=".zip")
download.file(
  "http://datadryad.org//bitstream/handle/10255/dryad.55548/PhylogeneticResources.zip",
  temp)
tanktree <- read.tree(unz(temp,'PhylogeneticResources/Vascular_Plants_rooted.dated.tre'))
unlink(temp)
```

Randomly sample 1000 tips/taxa from real tree.

```
tree.real <- tree.evolve(tree.choice = "real", pool.size = 1000)
```

Simulate trait evolution (1000 reps) on simulated and real tree under Brownian motion.

```
out.mc.bm.sim <- trait.evolve(tree = tree.sim, num.reps = 1000, mode.of.evolution = "BM")
out.mc.bm.real <- trait.evolve(tree = tree.real, num.reps = 1000, mode.of.evolution = "BM")
```

Calculate pairwise phylogenetic distances on both trees.

```
phydist.sim <- cophenetic(tree.sim)
phydist.real <- cophenetic(tree.real)
```

Calculate standardised effect sizes for MNTD and MPD under 'filtering-derived' and 'neutral' models of community assembly (filtering algorithms follow Kraft et al. 2007). Analyses conducted on both real and simualted trees using raw and square root transformed phylogenetic distances.

Neutral filter (40 taxa sampled randomly with respect to trait value).

```
num.runs <- 999 # number of null model simulations (slow!)

comm.matrix.sim <- make.picante.format.bm(out.mc.bm.sim,ca="neutral")

phy.clust.mntd <- ses.mntd(comm.matrix.sim, phydist.sim, null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)
phy.clust.mntd.sq <- ses.mntd(comm.matrix.sim, sqrt(phydist.sim), null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)

out.df.neut.mntd <- data.frame(phy.clust = phy.clust.mntd$mntd.obs.z,
                            phy.clust.sq = phy.clust.mntd.sq$mntd.obs.z, metric="mntd",
                            comm.assem.algo="neutral",tree="sim")

phy.clust.mpd <- ses.mpd(comm.matrix.sim, phydist.sim, null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)
phy.clust.mpd.sq <- ses.mpd(comm.matrix.sim, sqrt(phydist.sim), null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)

out.df.neut.mpd <- cbind(phy.clust=phy.clust.mpd$mpd.obs.z,
                            phy.clust.sq = phy.clust.mpd.sq$mpd.obs.z, metric="mpd",
                            comm.assem.algo = "neutral", tree= "sim")

out.df <- rbind(out.df.neut.mntd, out.df.neut.mpd)

comm.matrix.real <- make.picante.format.bm(out.mc.bm.real, ca="neutral")

phy.clust.mntd <- ses.mntd(comm.matrix.real, phydist.real, null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)
phy.clust.mntd.sq <- ses.mntd(comm.matrix.real, sqrt(phydist.real), null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)

out.df.neut.mntd <- cbind(phy.clust = phy.clust.mntd$mntd.obs.z,
                            phy.clust.sq = phy.clust.mntd.sq$mntd.obs.z, metric = "mntd",
                            comm.assem.algo = "neutral", tree = "real")

phy.clust.mpd <- ses.mpd(comm.matrix.real, phydist.real, null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)
phy.clust.mpd.sq <- ses.mpd(comm.matrix.real, sqrt(phydist.real), null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)

out.df.neut.mpd <- cbind(phy.clust = phy.clust.mpd$mpd.obs.z,
                            phy.clust.sq = phy.clust.mpd.sq$mpd.obs.z, metric="mpd",
                            comm.assem.algo="neutral",tree="real")

out.df <- rbind(out.df, out.df.neut.mntd, out.df.neut.mpd)
```

'Derived filter' (takes the maximum simulated trait value and selects 40 taxa with nearest trait values).

```
comm.matrix.sim <- make.picante.format.bm(out.mc.bm.sim,ca="filter")

phy.clust.mntd <- ses.mntd(comm.matrix.sim, phydist.sim, null.model = "phylogeny.pool",
                            abundance.weighted = F, runs = num.runs)
phy.clust.mntd.sq <- ses.mntd(comm.matrix.sim, sqrt(phydist.sim), null.model = "phylogeny.pool",
```

```
                              abundance.weighted = F, runs = num.runs)

out.df.filt.mntd <- data.frame(phy.clust = phy.clust.mntd$mntd.obs.z,
                                phy.clust.sq = phy.clust.mntd.sq$mntd.obs.z,
                                metric = "mntd", comm.assem.algo = "filter", tree="sim")

phy.clust.mpd <- ses.mpd(comm.matrix.sim, phydist.sim, null.model = "phylogeny.pool",
                     abundance.weighted = F, runs = num.runs)
phy.clust.mpd.sq <- ses.mpd(comm.matrix.sim, sqrt(phydist.sim), null.model = "phylogeny.pool",
                     abundance.weighted = F, runs = num.runs)

out.df.filt.mpd <- data.frame(phy.clust = phy.clust.mpd$mpd.obs.z,
                               phy.clust.sq = phy.clust.mpd.sq$mpd.obs.z,
                               metric = "mpd",comm.assem.algo = "filter", tree = "sim")

out.df <- rbind(out.df,out.df.filt.mntd,out.df.filt.mpd)

comm.matrix.real <- make.picante.format.bm(out.mc.bm.real,ca="filter")

phy.clust.mntd <- ses.mntd(comm.matrix.real, phydist.real, null.model = "phylogeny.pool",
                     abundance.weighted = F, runs = num.runs)
phy.clust.mntd.sq <- ses.mntd(comm.matrix.real, sqrt(phydist.real), null.model = "phylogeny.pool",
                     abundance.weighted = F, runs = num.runs)

out.df.filt.mntd <- data.frame(phy.clust = phy.clust.mntd$mntd.obs.z,
                                phy.clust.sq = phy.clust.mntd.sq$mntd.obs.z,metric="mntd",
                                comm.assem.algo="filter",tree="real")

phy.clust.mpd <- ses.mpd(comm.matrix.real, phydist.real, null.model = "phylogeny.pool",
                     abundance.weighted = F, runs = num.runs)
phy.clust.mpd.sq <- ses.mpd(comm.matrix.real, sqrt(phydist.real), null.model = "phylogeny.pool",
                     abundance.weighted = F, runs = num.runs)

out.df.filt.mpd <- data.frame(phy.clust = phy.clust.mpd$mpd.obs.z,
                               phy.clust.sq = phy.clust.mpd.sq$mpd.obs.z,
                               metric="mpd",comm.assem.algo = "filter", tree = "real")

out.df<-rbind(out.df,out.df.filt.mntd,out.df.filt.mpd)
```

```
out.df$phy.clust<-as.numeric(out.df$phy.clust)
out.df$phy.clust.sq<-as.numeric(out.df$phy.clust.sq)
```

Quantify difference in standadized effect sizes (MNTD/MPD) when using raw vs square-root transformed phylogenetic distance.

```
out.df$diff <- out.df$phy.clust.sq-out.df$phy.clust
```

Generate Figure 4 from manuscript.

```
out.df.fig <- out.df
levels(out.df.fig$tree) <- c("Simulated birth-death tree", "Vascular plant tree")
levels(out.df.fig$metric) <- c("MNTD", "MPD")
```

```
p <- ggplot(out.df.fig,aes(x = metric, y = diff, fill = comm.assem.algo))
p + geom_boxplot(outlier.size = 1) + theme_bw() + facet_grid(.~tree) +
  theme(legend.key = element_blank(), legend.position= "none",
        axis.line = element_line(colour = "black"),
        legend.key = element_blank(),
        axis.line = element_line(colour = "black"),
        legend.key = element_blank(),
        panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        strip.background = element_rect(colour = 'NA', fill = 'NA')) +
  scale_fill_manual(values = c("grey", "firebrick")) +
  xlab("") + ylab(expression(paste(Delta, "SES", sep = "")))
```