psi\_code

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library(meteR)  
devtools::install\_github('ajrominger/socorro')  
library(socorro)  
  
setwd('~/Dropbox/Research/psi\_mete')  
  
# load data  
  
rmbl <- read.csv('RMBL\_PSI\_test.csv', as.is = TRUE)  
  
bci <- read.csv('BCIS.csv', as.is = TRUE)  
bci <- bci[bci$year == 1995, ]  
bcitest <- read.csv('BCI\_PSI\_test.csv', as.is = TRUE)  
  
arth <- read.csv('gruner\_kohala.csv', as.is = TRUE)  
  
# make METE objects  
  
rmblIPD <- ipd(meteESF(S0 = 31, N0 = 877, E0 = sum(rmbl$observed)))  
# need to custom add data to IPD for rmbl  
rmblIPD$data <- sort(rmbl$observed, decreasing = TRUE)  
  
bciIPD <- ipd(meteESF(spp = bci$spp, abund = bci$count,   
 power = bci$dbh^2))  
  
arthIPD <- ipd(meteESF(spp = arth$SpeciesCode, abund = arth$Abundance,   
 power = arth$IND\_BIOM^0.75))  
  
  
# plotting theory for BCI  
e <- exp(seq(log(1), log(500000), length = 1000))  
  
jpeg('ms/fig\_PsiThr.jpg', width = 6, height = 3, units = 'in',   
 res = 380)  
  
par(mfrow = 1:2, mar = c(3, 3, 0.7, 0) + 0.5, mgp = c(2, 0.75, 0))  
plot(e, bciIPD$d(e), log = 'xy', type = 'l', col = 'red',  
 xaxt = 'n', yaxt = 'n', ylim = 10^c(-12, 0),  
 xlab = 'Metabolic rate', ylab = 'Probability density',  
 panel.first = {  
 rect(xleft = 10, xright = 10000, ybottom = 10^par('usr')[3],   
 ytop = 10^par('usr')[4],  
 col = 'gray60', border = NA)  
 rect(xleft = 10000, xright = 10^par('usr')[2],   
 ybottom = 10^par('usr')[3], ytop = 10^par('usr')[4],  
 col = 'gray80', border = NA)  
 })  
logAxis(1, expLab = TRUE)  
axis(2, at = 10^seq(-12, 0, by = 3),   
 labels = sapply(seq(-12, 0, by = 3),   
 function(p)   
 eval(substitute(expression(10^p),   
 list(p = p)))))  
mtext('A', side = 3, at = 10^(par('usr')[1] + 0.05 \*   
 diff(par('usr')[1:2])),   
 line = 0.2)  
  
# plot rank plot  
n <- bciIPD$state.var['N0']  
plot(approx(bciIPD$p(exp(seq(log(1), log(10^7), length = 5000))),   
 exp(seq(log(1), log(10^7), length = 5000)),   
 xout = seq(1, 1/n, length.out = n) - 1/(2 \* n))$y,   
 log = 'xy', xlab = 'Rank', ylab = 'Metabolic rate',   
 axes = FALSE, frame.plot = TRUE, type = 'l', col = 'red',  
 panel.first = {  
 rect(ybottom = 10, ytop = 10000, xleft = 10^par('usr')[1],   
 xright = 10^par('usr')[2],  
 col = 'gray60', border = NA)  
 rect(ybottom = 10000, ytop = 10^par('usr')[4],   
 xleft = 10^par('usr')[1], xright = 10^par('usr')[2],  
 col = 'gray80', border = NA)  
 })  
logAxis(1, expLab = TRUE)  
logAxis(2, expLab = TRUE)  
  
mtext('B', side = 3, at = 10^(par('usr')[1] + 0.05 \*  
 diff(par('usr')[1:2])),   
 line = 0.2)  
  
  
# plotting data and theory  
  
jpeg('ms/fig\_PsiData.jpg', width = 8, height = 3, units = 'in',   
 res = 380)  
  
par(mfrow = c(1, 3), oma = c(3, 2, 0, 0) + 0.5,   
 mar = c(0, 2, 1, 0) + 0.2, cex = 1, mgp = c(2, 0.75, 0))  
  
plot(exp(bcitest$ln.rank.), exp(bcitest$ln.dbh2.), log = 'xy',  
 ylim = c(1, 300000), xaxt = 'n', yaxt = 'n',  
 xlab = '', ylab = '')  
points(exp(bcitest$ln.rank.), exp(bcitest$ln.PRED\_METE.), type = 'l',   
 col = 'red')  
logAxis(1, expLab = TRUE)  
logAxis(2, expLab = TRUE)  
legend('topright', legend = c('Data', 'METE'), pch = c(1, NA),   
 lwd = c(NA, 1), col = c('black', 'red'), bty = 'n', cex = 0.9)  
mtext('A', side = 3, at = 10^(par('usr')[1] + 0.05 \*   
 diff(par('usr')[1:2])),   
 line = 0.2)  
  
plot(rmblIPD, ptype = 'rad', log = 'xy', add.legend = FALSE,   
 ylim = c(1, 100000), xaxt = 'n', yaxt = 'n',  
 xlab = '', ylab = '')  
logAxis(1, expLab = TRUE)  
logAxis(2, expLab = TRUE)  
mtext('B', side = 3, at = 10^(par('usr')[1] + 0.05 \*   
 diff(par('usr')[1:2])),   
 line = 0.2)  
  
plot(arthIPD, ptype = 'rad', log = 'xy', add.legend = FALSE,  
 xaxt = 'n', yaxt = 'n', xlab = '', ylab = '')  
logAxis(1, expLab = TRUE)  
logAxis(2, expLab = TRUE)  
mtext('C', side = 3, at = 10^(par('usr')[1] + 0.05 \*   
 diff(par('usr')[1:2])),   
 line = 0.2)  
  
mtext('Metabolic rate', side = 2, line = 0.5, outer = TRUE)  
mtext('Rank', side = 1, line = 2, outer = TRUE)  
  
dev.off()