

Bird metabolic rate and abundance

Load the data and packages

```
library(plyr)
library(socorro)
library(MASS)

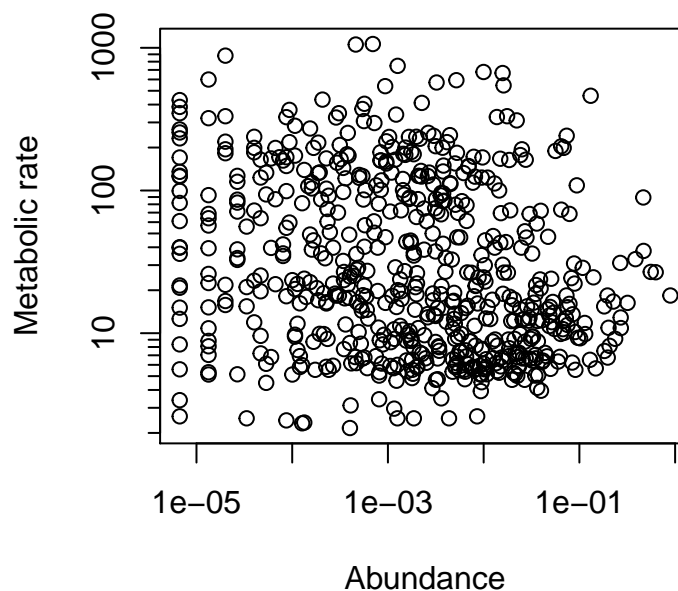
bbs <- read.csv('data/bbs/bbs2011.csv', as.is = TRUE)
bbsSpInfo <- read.csv('data/bbs/speciesTableBody.csv', as.is = TRUE)
bbsSpInfo <- bbsSpInfo[, c('sppKey', 'mass')]
names(bbsSpInfo) <- c('spp', 'mass')

x <- merge(bbs, bbsSpInfo, by = 'spp')
x$metab <- x$mass0.75
```

A naive plot of mean abundance versus metabolism

```
foo <- ddply(x, 'spp', function(X) {
  data.frame(n = sum(X$abund) / nrow(x), b = mean(X$metab))
})

plot(foo[, 2:3], xlab = 'Abundance', ylab = 'Metabolic rate', log = 'xy',
      axes = FALSE, frame.plot = TRUE)
logAxis(1:2)
```

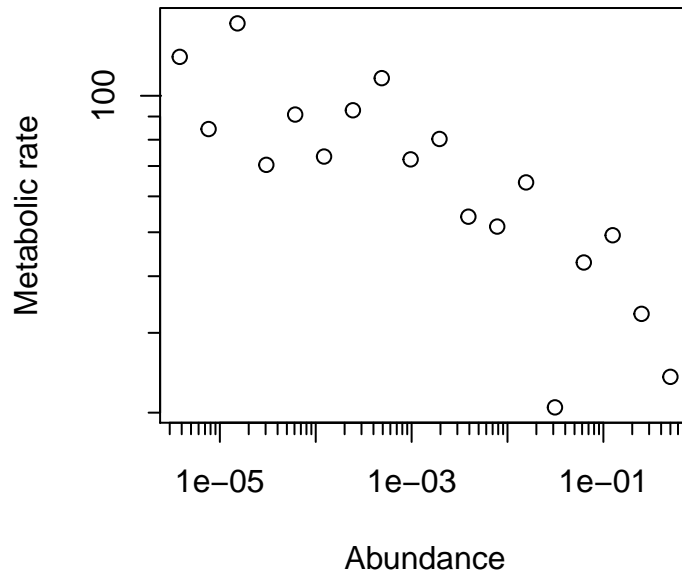


Now we take the mean metabolic rate for different log₂ abundance classes and a clearer pattern emerges

```
foo$log2bin <- floor(log(foo$n, 2))
foo2 <- ddply(foo, 'log2bin', function(X) {
  data.frame(bmean = mean(X$b))
})

plot(2foo2$log2bin, foo2$bmean, log = 'xy', axes = FALSE,
      frame.plot = TRUE,
```

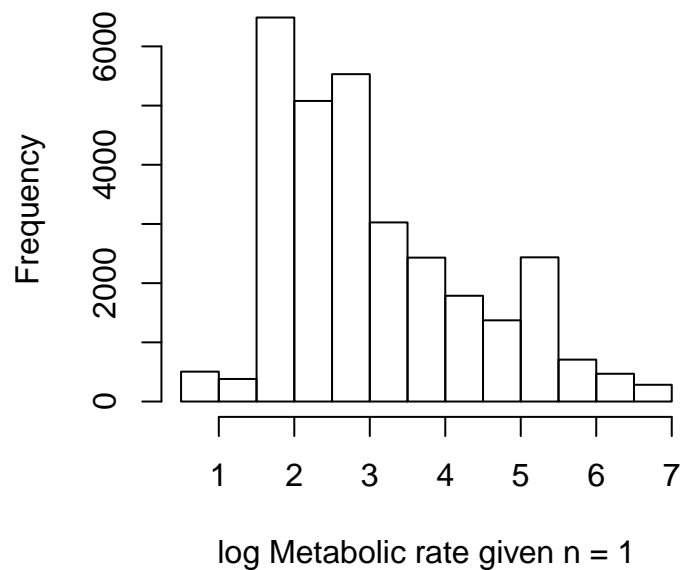
```
xlab = 'Abundance', ylab = 'Metabolic rate')
logAxis(1:2)
```



That's cleaner but still not $b \propto 1/n$.

We also investigated the distribution of $P(b \mid n)$. It's not anything pretty so far as we can tell.

```
hist(log(x$metab[x$abund == 1]), xlab = 'log Metabolic rate given n = 1', main = '')
```



Finally, we look at the mean of b given n but computed across all sites and species. This means that any given species could contribute multiple times to this mean. For example, if species `spX` has abundance n_j at 12 different sites then its metabolic rate will figure into $E(b \mid n_j)$ 12 times.

```
nn <- 1:70
meanGivenN <- sapply(nn, function(n) {
  dat <- x[x$abund == n, ]

  return(mean(dat$metab))
})
```

```
plot(nn, meanGivenN, log = 'x', xlab = 'Abundance', ylab = 'Metabolic rate',  
      xaxt = 'n')  
logAxis(1)
```

