

# Bird metabolic rate and abundance

Load the data and packages

```
library(pika)
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$metab <- x$mass^0.75

# summarize by species
summ <- ddply(x, 'spp', function(dat) {
  c(abund = sum(dat$abund), metab = mean(dat$metab))
})
```

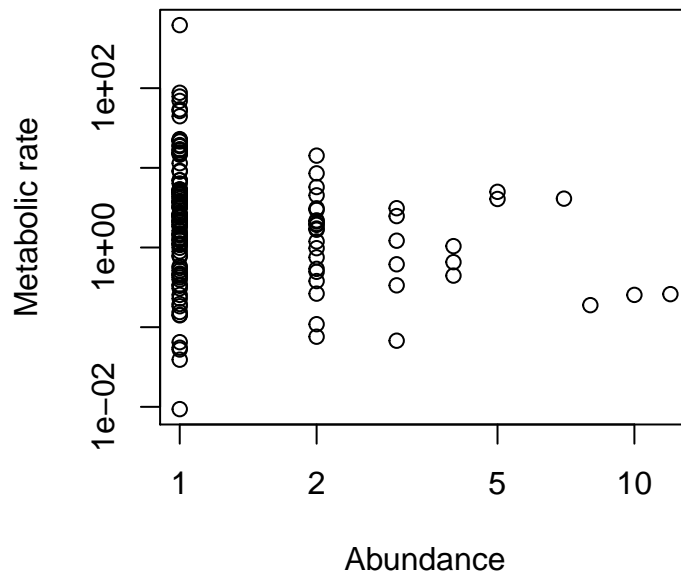
Now parameterize a model where metabolic rate  $r_i$  for a species  $i$  with abundance  $n_i$  is distributed  $P(r_i) \propto e^{-\beta n_i r_i}$  and where abundances are log-series distributed.

```
b <- 1 / mean(summ$metab[summ$abund == 1])
S <- 1000
aprop <- 0.01

nn <- rfish(S, 0.01)
rr <- rexp(S, b * nn)
```

Now we can simulate subsampling from this global pattern. We know that in ecology, spatial subsamples are often negative binomial in distribution, so we can start with that.

```
nhathat <- rnbino(S, size = 1, mu = nn * apropr)
plot(nhathat[nhathat > 0], rr[nhathat > 0], log = 'xy', xlab = 'Abundance', ylab = 'Metabolic rate')
```



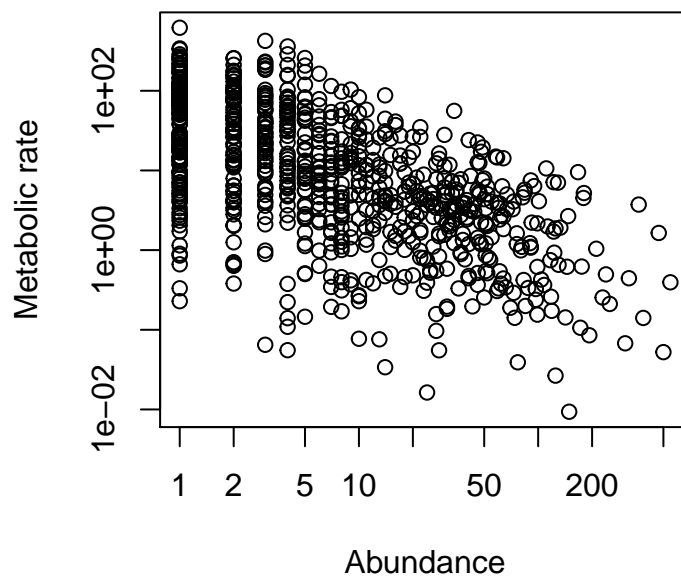
```
modSamp <- lm(log(rr[nhat > 0]) ~ log(nhat[nhat > 0]))
modSamp$coefficients
```

```
##      (Intercept) log(nhat[nhat > 0])
##      0.8509991      -0.7128041
```

The “Damuth rule” pattern disappears for a small spatial subsample. Note: the size of the spatial subsample is determined by `aprop` (the proportion of the local sample relative to the “metacommunity” size) and in this case is equal to 0.01.

Interestingly, when we make `aprop` 1 and keep negative binomial sampling we do not re-arrive at Damuth:

```
aprop <- 1
nhat <- rnbino(m, size = 1, mu = nn * apropr)
plot(nhat[nhat > 0], rr[nhat > 0], log = 'xy', xlab = 'Abundance', ylab = 'Metabolic rate')
```

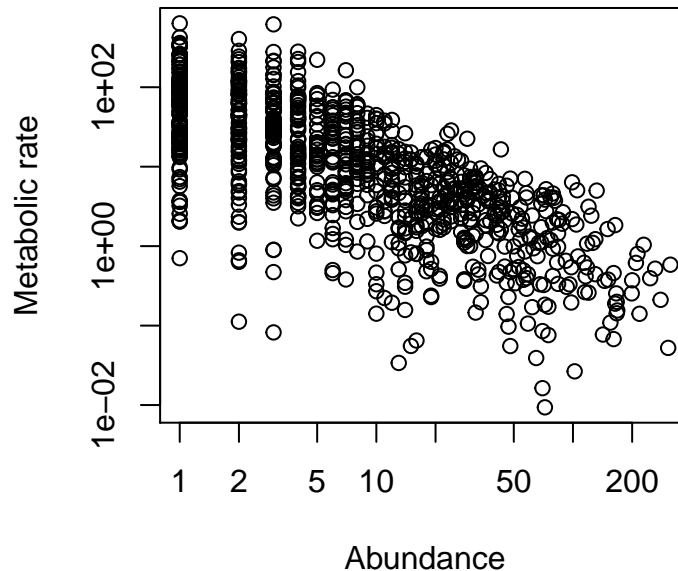


```
modSamp <- lm(log(rr[nhat > 0]) ~ log(nhat[nhat > 0]))
modSamp$coefficients
```

```
##          (Intercept) log(nhat[nhat > 0])
##          3.615212      -0.776380
```

To get back Damuth we need to have a Poisson sample of the metacommunity. Equivalently to Poisson, we can make the `size` parameter of the negative binomial very large:

```
aprop <- 1
nhat <- rnbinom(S, size = 1000, mu = nn * apropr)
plot(nhat[nhat > 0], rr[nhat > 0], log = 'xy', xlab = 'Abundance', ylab = 'Metabolic rate')
```



```
modSamp <- lm(log(rr[nhat > 0]) ~ log(nhat[nhat > 0]))
modSamp$coefficients
```

```
##          (Intercept) log(nhat[nhat > 0])
##          4.1337613      -0.9570805
```

Now we get Damuth's rule again.

Taken all together these results imply that (1) the lack of energy equivalence or Damuth's rule at small scales does not negate the possibility that it operates at larger scales (i.e. sampling matters) and that the `size` parameter of the negative binomial must increase with the size of the spatial sample for Damuth to hold at large scale, but not at small scale.