ses.mpd weighting explored

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```r
set.seed(123) # for repro
g<-matrix(rpois(144,2),nrow=12) # col=hosts(12),row=para(12)
```

A hypothetical matrix with parasites as rows, hosts as columns, and cells referring to number of HxP records

```r
g
```

```
##       [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
##  [1,]    1    3    2    3    1    2    3    0    3     2     2     2
##  [2,]    3    2    3    1    4    0    0    2    0     1     1     3
##  [3,]    2    0    2    1    0    1    2    6    2     4     1     2
##  [4,]    4    4    2    1    2    1    1    4    2     1     1     2
##  [5,]    4    1    1    1    3    3    1    4    2     0     1     3
##  [6,]    0    0    1    2    0    2    2    1    1     5     6     3
##  [7,]    2    1    5    2    2    3    1    0    2     3     1     5
##  [8,]    4    5    4    1    1    3    0    2    5     1     0     2
##  [9,]    2    4    3    1    0    3    1    1    2     2     1     1
## [10,]    2    3    3    1    3    2    2    2    4     5     3     2
## [11,]    5    2    0    1    4    3    2    1    4     2     2     0
## [12,]    2    6    2    2    1    2    3    1    2     1     4     1
```

According to help file, this is the weighting applied to host PD metrics

```r
w<-t(g) %*% g # a weighting - to be explained
w
```

```
##       [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
##  [1,]  103   87   69   37   69   67   39   71   83    53    43    61
##  [2,]   87  121   79   44   52   67   47   52   86    53    55    54
##  [3,]   69   79   86   40   46   59   35   50   69    64    43    71
##  [4,]   37   44   40   29   26   36   30   26   40    40    38    39
##  [5,]   69   52   46   26   61   42   27   41   52    39    34    46
##  [6,]   67   67   59   36   42   63   38   42   69    55    47    53
##  [7,]   39   47   35   30   27   38   38   32   45    47    46    34
##  [8,]   71   52   50   26   41   42   32   84   55    52    35    51
##  [9,]   83   86   69   40   52   69   45   55   91    66    50    55
## [10,]   53   53   64   40   39   55   47   52   66    91    68    62
## [11,]   43   55   43   38   34   47   46   35   50    68    75    48
## [12,]   61   54   71   39   46   53   34   51   55    62    48    74
```

This is the abundance of each host
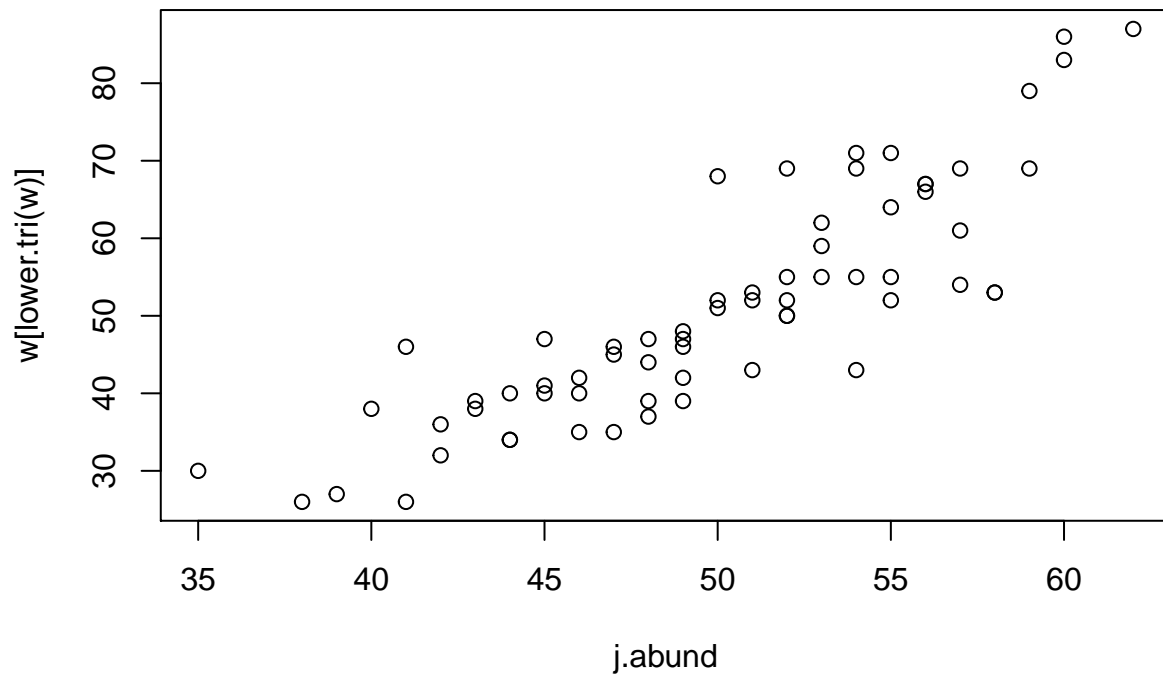
```r
colSums(g) # host abundances
```

```
##  [1] 31 31 28 17 21 25 18 24 29 27 23 26
```

This is the correlation of (x) the pairwise abundances of hosts and (y) the weighting applied

```r
j.abund<-NULL # joint abundances of pairs of hosts
for (i in 1:11){
  for (j in (i+1):12){
    j.abund<-c(j.abund,sum(g[,i],g[,j]))
  }
```

```
}
```

```
plot(j.abund,w[lower.tri(w)])
```


So I guess this weighting is an approximation to the pairwise abundances of hosts.