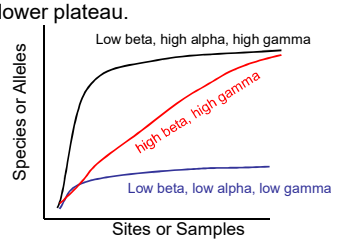
Review

- Dropping rows and columns based on criteria.
  - Apply function – create a vector summarizing rows or columns (mean, min, max, sd etc.)
  - Test that criteria using logical operators (>, <, == etc.) to create a vector of TRUE/FALSE
  - Use that vector to drop rows or columns
    - matrix[,vector] to drop columns
    - Matrix[vector,] to drop rows

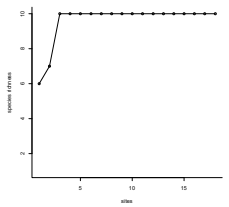
Species Accumulation and Rarefaction

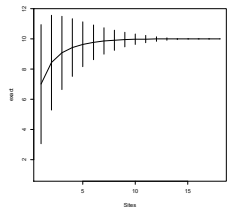
- As you accumulate more samples, the number of observed rare events increases.
- Curves display the rate of new species addition with additional sampling.
- Alpha, beta and gamma diversity
- Diverse ecosystems (high gamma and high beta diversity) will display rapid increase to higher plateau. Less diverse: slow increase to lower plateau.

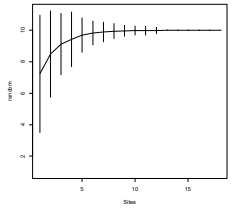


Species Accumulation and Rarefaction

- Function: specaccum
  - specaccum(matrix,method)
- Methods:
  - Accumulate species by:
    - Adding samples in the order collected (“collector”)
    - Adding samples in random order (“random”)
    - Calculating expected (mean) number for each sample size (“exact”)
    - Follow methods of Coleman 1982 (“coleman”)
    - Permuting individuals instead of samples (“rarefaction”)
- “collector” does not provide error estimates.
- “exact” provides a mean and standard deviation for observed data
- “random” provides mean and standard deviation for permuted data







```
species_accumulation<-
specaccum(community,method="collector")

species_accumulation<-
specaccum(community,method="exact")

species_accumulation<-
specaccum(community,method="random")
```

Randomizations, bootstraps, jacknifes, Monte Carlo, MCMC

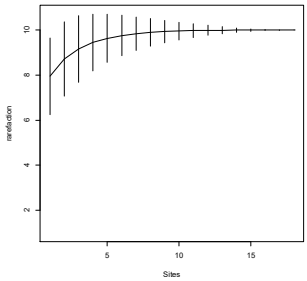
- Function sample can be used to randomly sample any data
  - sample(thing to sample, number of samples, replace)
  - **Bootstrapping** – estimating some parameter by randomly sampling with replacement
  - See also functions in permute package
- In our sample community dataset:
  - `mean(community)` = 14.283
  - `sample(community,100,replace=TRUE)` # pick 100 values
  - `sample(community,100000,replace=TRUE)` # pick 100000, take mean
  - `sample(community,180,replace=FALSE)` # sample all without replacement

Species Accumulation and Rarefaction

- **Rarefaction** – most commonly used technique for estimating diversity
- Pool **individuals** within a dataset and resample individuals and not individual cells within the matrix.
- Use the same specaccum function (method="rarefaction").
- Rarefaction requires integer (count) data, untransformed. Other methods will work with log or proportional transformed data.
- **Number of individuals sampled is set as the mean number of individuals per sample in the dataset.**

Species Accumulation and Rarefaction

- Rarefaction curve for sample community data using specaccum, method="rarefaction" which set the number of individuals per sample to 143.



Species Accumulation and Rarefaction

- The specaccum function uses the function rrarefy to do the resampling. You can use rrarefy directly if you want more control.
- Function rrarefy(communty,sample)
  - Provide the community matrix and how many individuals to sample and it will return a permuted sample.
- To duplicate what specaccum did:
  - Pool all individuals into 1 sample
    - `pooled<-apply(community,2,sum)`
  - Select 143 individual at random
    - `rrarefy(pooled,sample=143)`
  - Repeat…

Species Accumulation and Rarefaction

- One common use for rarefaction is to control for sampling effort (or efficiency) in estimating diversity.
- In the sample community, the number of individuals per sample ranges from 39 to 630.
  - `apply(community,1,sum)`

```
A_08 B_08 C_08 D_08 E_08 F_08 A_09 B_09 C_09 D_09 E_09 F_09 A_07 B_07 C_07 D_07 E_07 F_07
 340  125  132  138   39   99  630   62  123   87   86  157  110   40  111   89   98  105
```

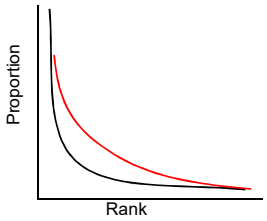
- Diversity and the number of individuals is correlated, What is sample diversity if we control for this?

Species Accumulation and Rarefaction

- Function rarefy will select a constant number of individuals from each sample
  - rarefy(community,sample,se)
    - Provide community data, number to subsample and whether or not you want standard error calculated
- How many individuals should you sample?
  - The number should be less than the number in your least abundant sample
    - `min_individuals<-min(apply(community,1,sum))`
    - `rarefy(community,sample=min_individuals,se=TRUE)`
  - Note that sampling this number results in no error for the sample with the fewest individuals (all individuals are sampled in each permutation)

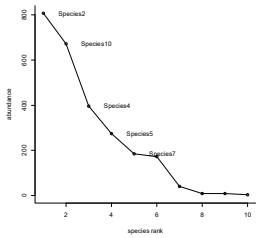
Species Abundance Curves

- Plot of rank abundance (x-axis) vs abundance or P_i (y-axis).
- More diverse communities lack numerically dominant species, flatter line.



Species Abundance Curves

- Functions: rankabundance, rankabuncomp in the BiodiversityR package
- rankabundance(community)
  - Can use either raw abundance or proportion data
  - rankabuncomp allows for comparison among factors
  - rankabunplot will plot the results




```
rank_data<-rankabundance(community)
rankabunplot(rank_data)
```