

# Spatial vs. temporal storage: The dual role of microbial seed banks in driving geographical patterns of microbial diversity

August 4, 2015

## Overview

### 1.) Set up the environment

A. working directory

B. Load packages

C. Import functions

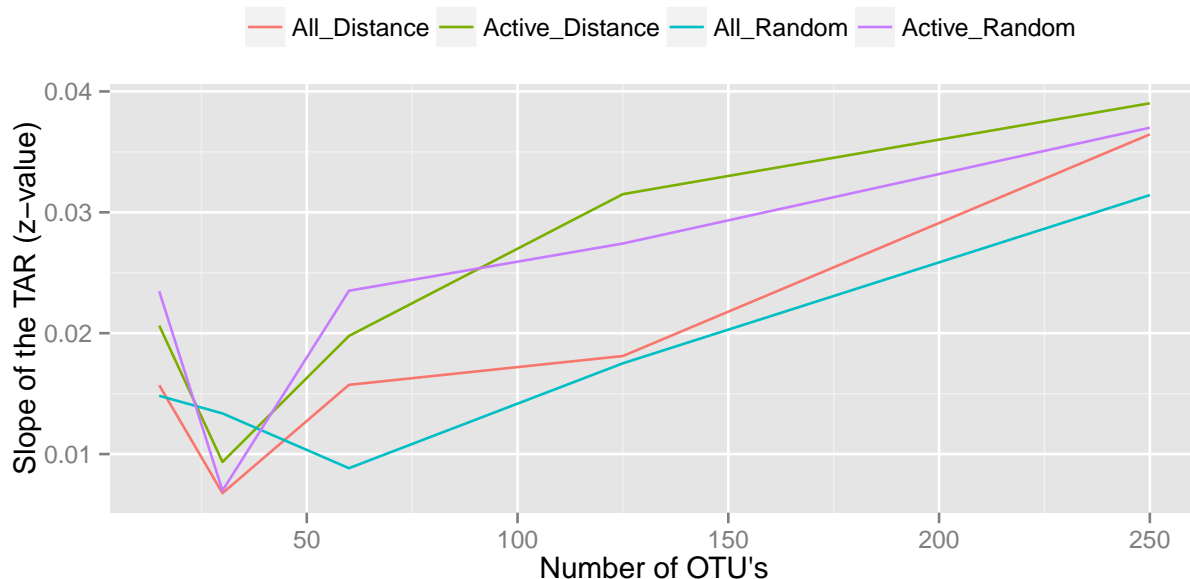
D. Import data and prepare data for analyses

### 2.) Analysis

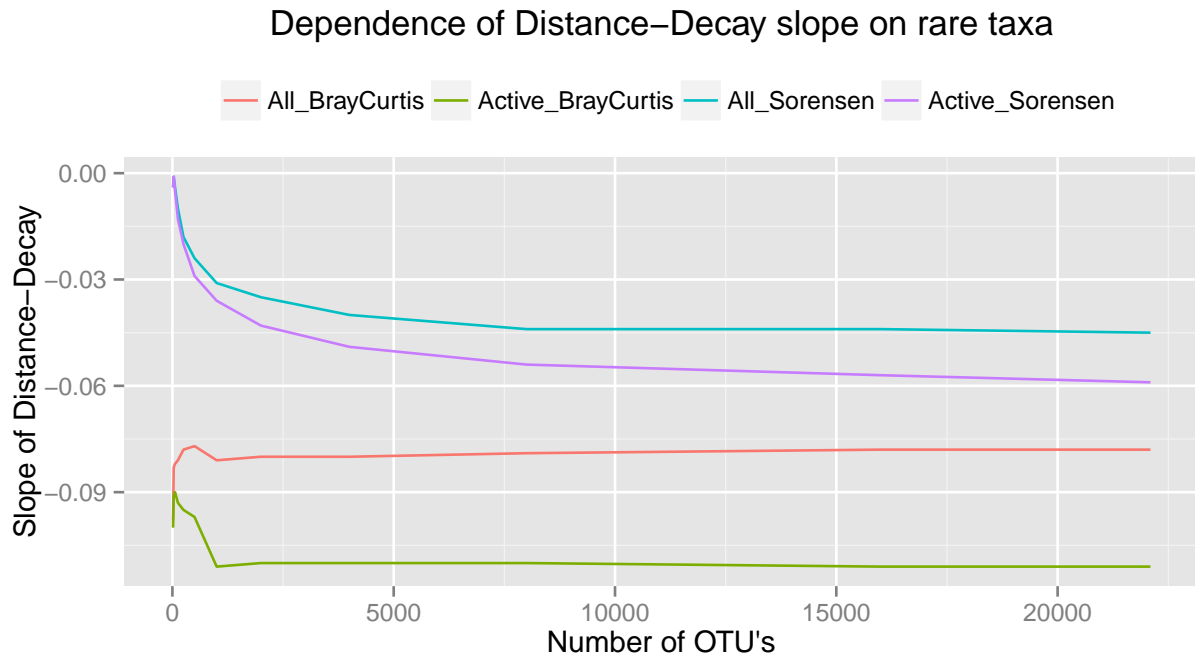
#### 1.) Dependence of the TAR on the number (detection) of rare taxa

The species-area relationship describes the rate at which species are discovered with increasing area. The SAR one of ecology's oldest and most intensively studied patterns. Arrhenius (1921) first described the general form of the *species-area relationship* (SAR) as a power-law:  $S = cA^z$  where S is species richness and A is area. Arrhenius's formula predicts a rate of increase in richness that is approximately linear in log-log space. That is,  $\log(S) = c + z\log(A)$ , where z is the scaling exponent.

#### Dependence of TAR slope on rare taxa



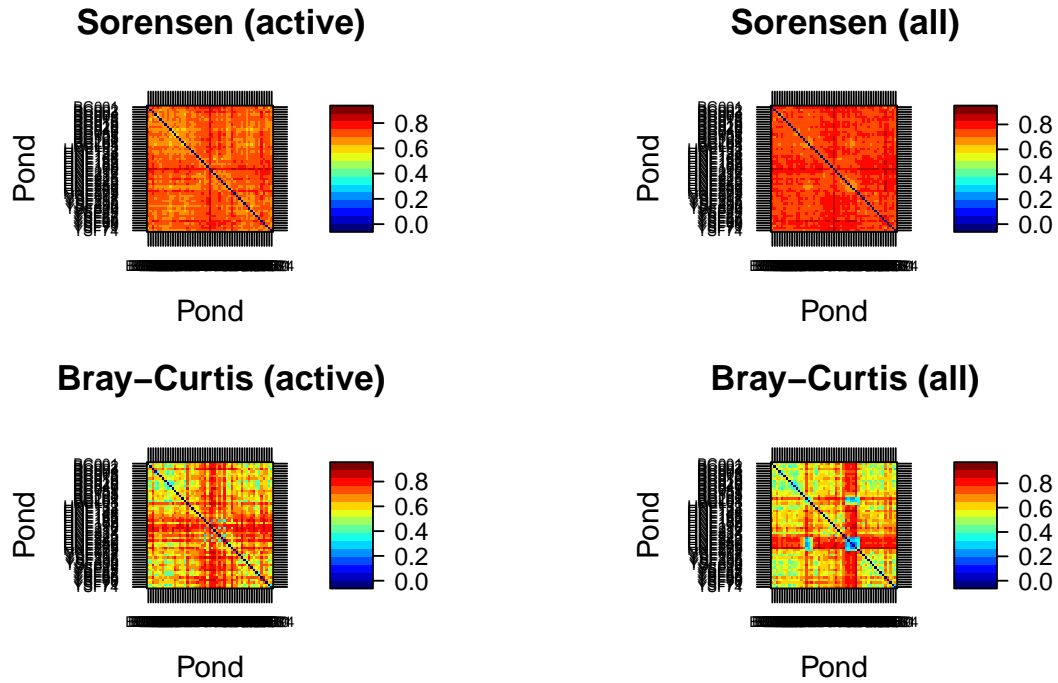
### 3.) Slight differences in distance-decay relationships



### 4.)

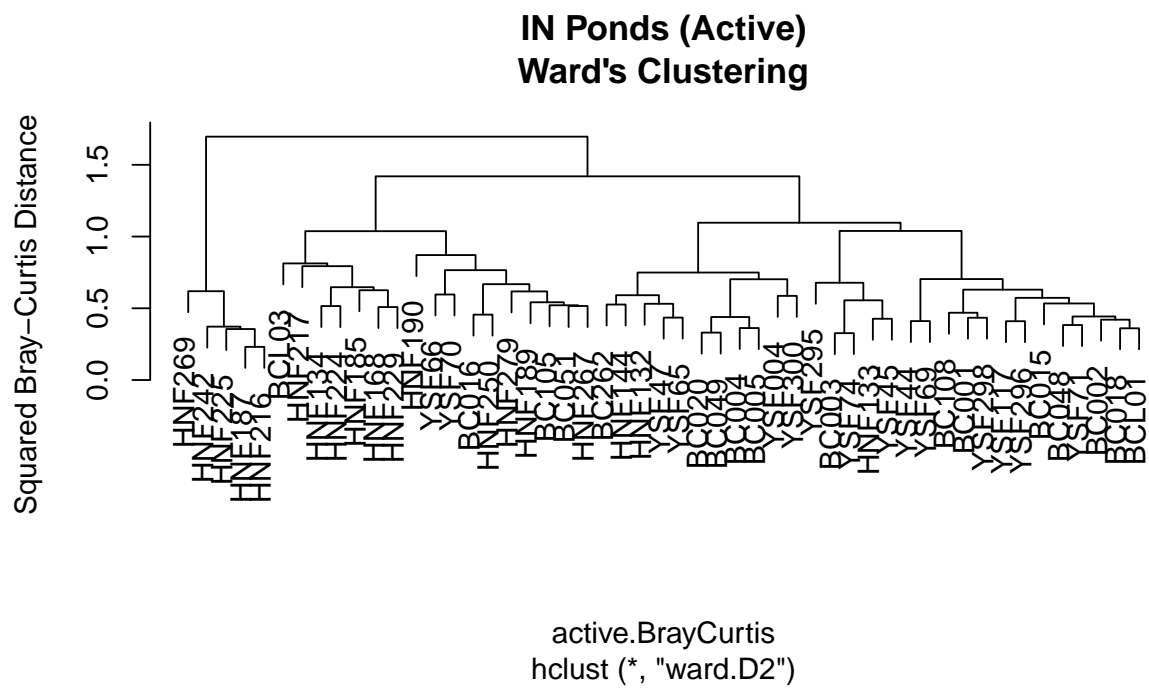
Little difference in community distance matrices between Active and All when using presence-absence, but generally high dissimilarity between all sites. Clearer differences between Active and All based on Bray-Curtis, but also decreasing dissimilarity among sites.

Notably, for 'all', a group of Hoosier National Forest (HNF) sites and a group of Brown County State Park (BC) sites share relatively high similarity. Also, the same subgroup of HNF sites is highly dissimilar to all other sites in the dataset. Perhaps these results are explained by environmental similarity.



5.)

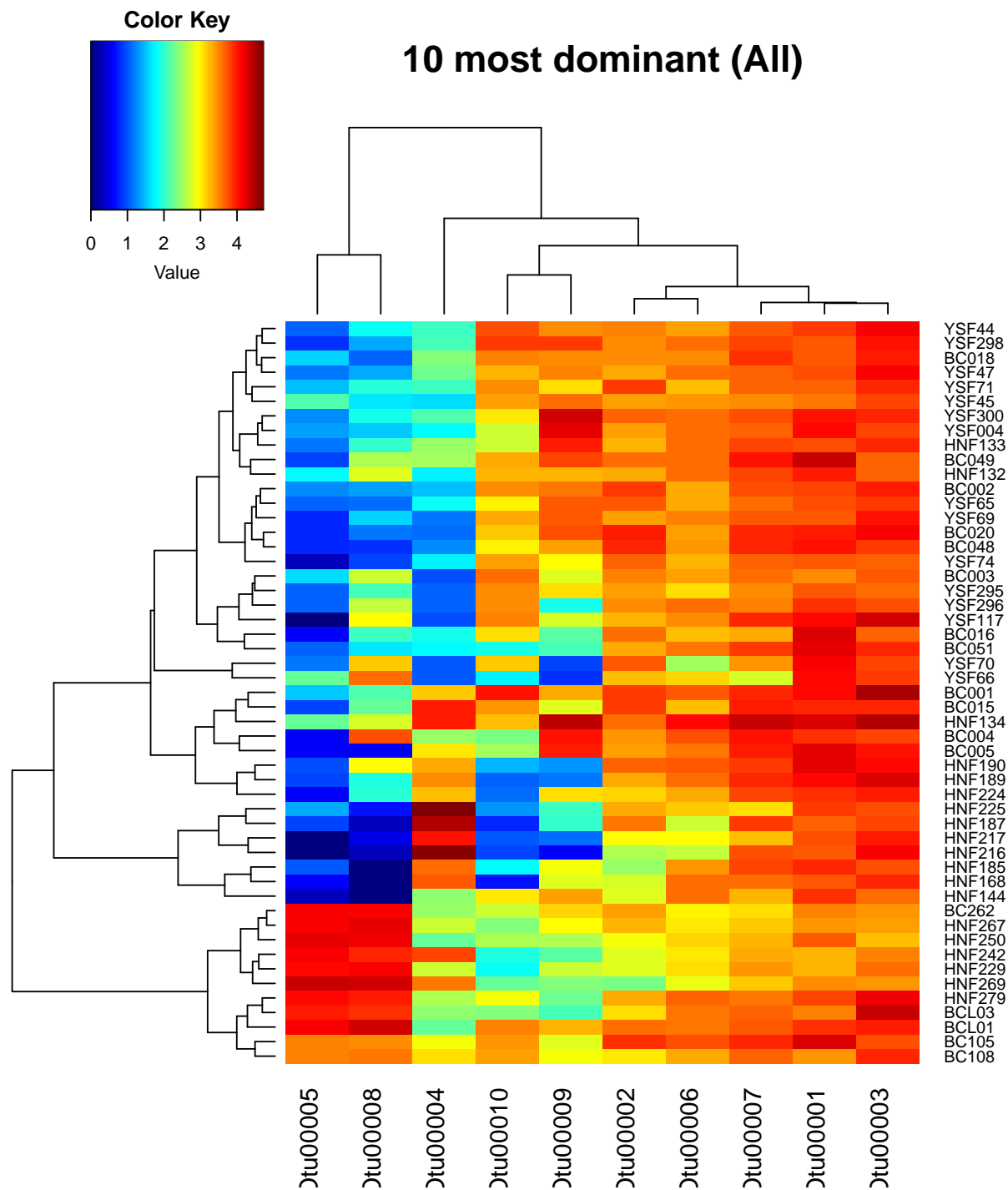
Cluster analysis reveals greater clustering based on relative activity than based on relative abundance.

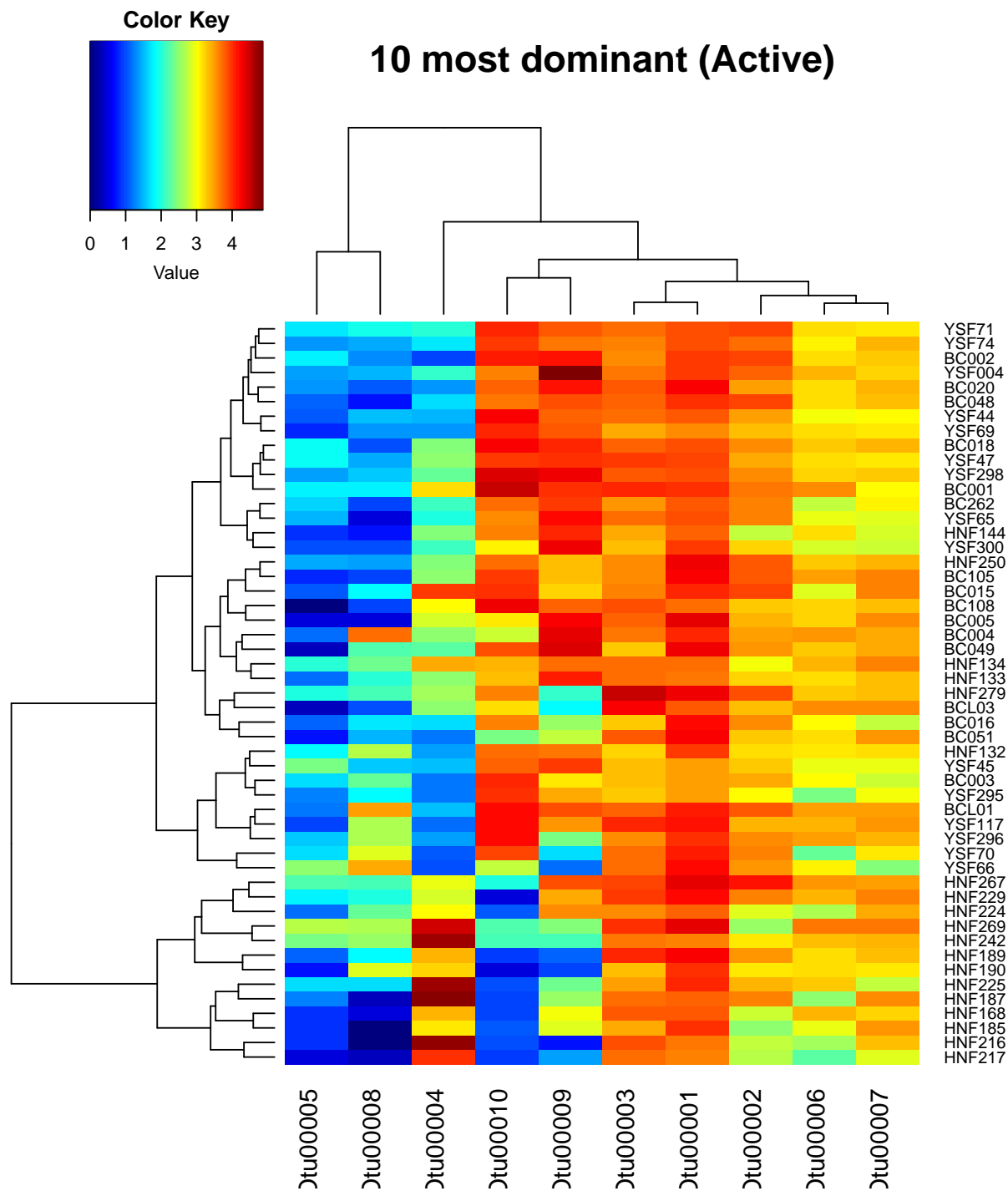


Squared Bray–Curtis Distance

**6.)**

4





## 7.) Variance partitioning:

