

# Reference Conditions

## **Objective:**

- Represent all types of perennial streams in California
- Ensure biological integrity at reference sites

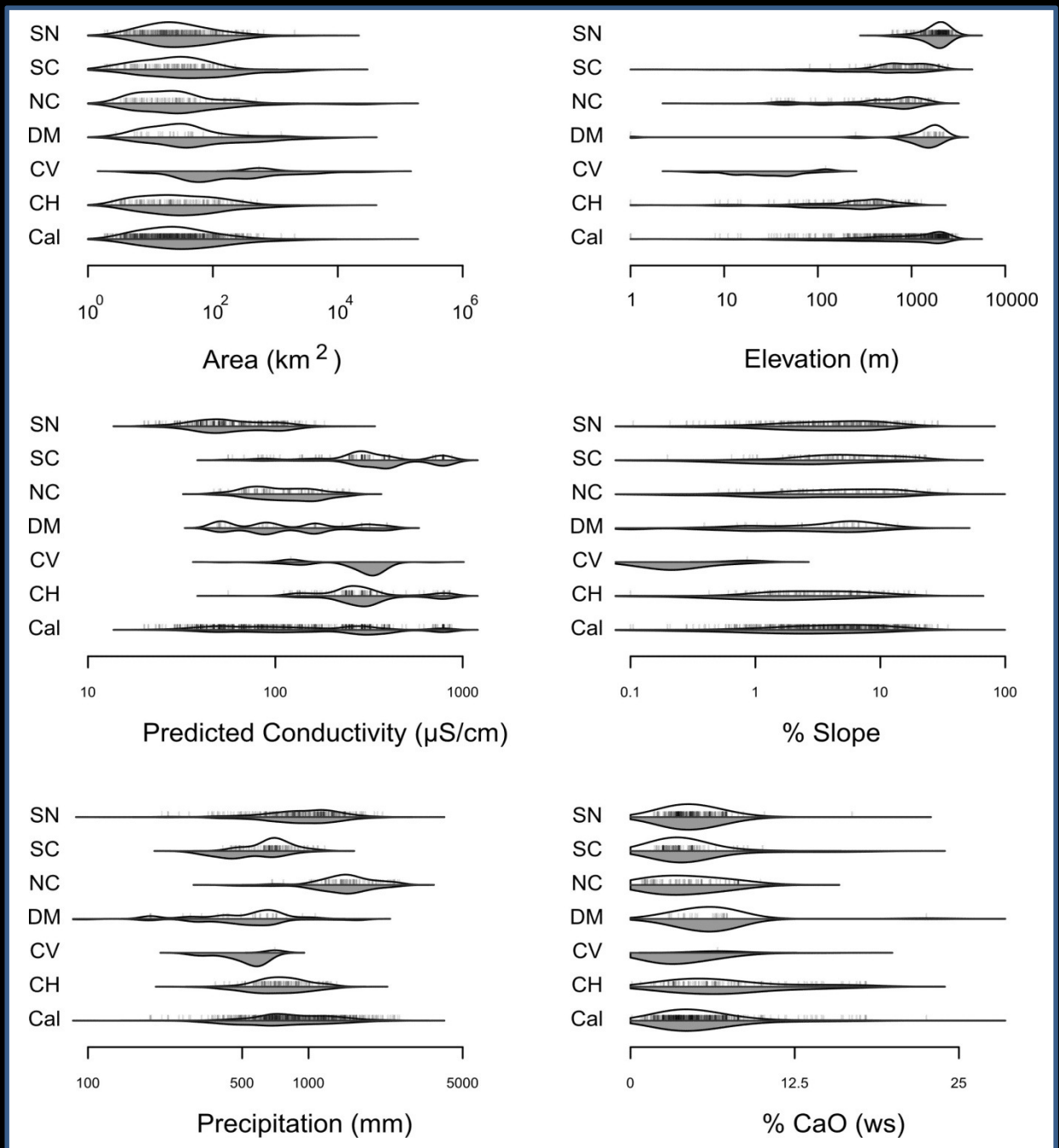
# Reference Sites

REGION	n
North Coast	79
Central Valley	1
Coastal Chaparral	87
Interior Chaparral	30
South Coast Mountains	96
South Coast Xeric	22
Western Sierra	131
Central Lahontan	142
Deserts + Modoc	27
<b>TOTAL</b>	<b>615</b>



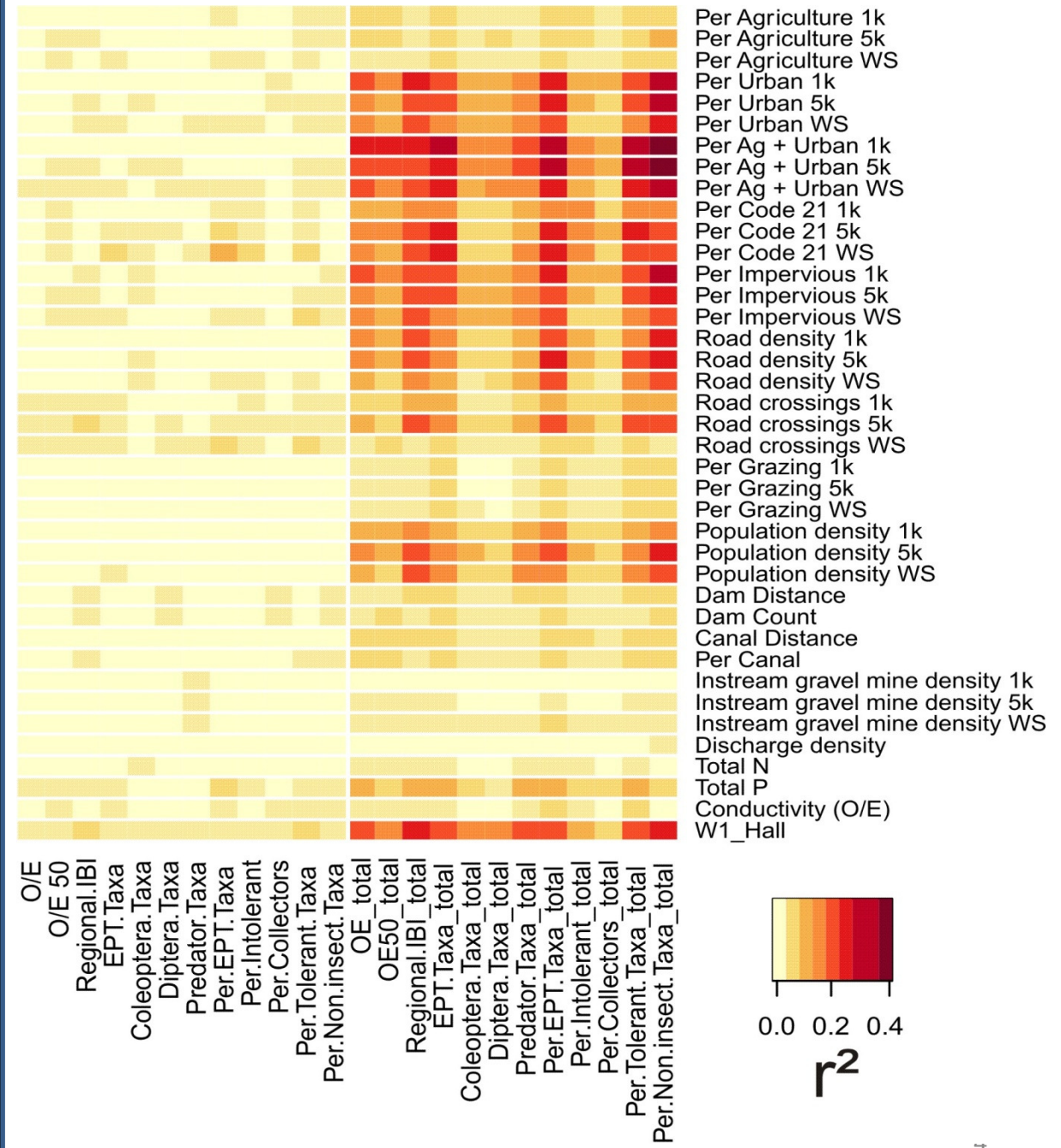
# Gradient Representation

- Overall excellent representation in most regions
- Central Valley and South Coast (xeric only) very under-represented
- Very low gradient, large watershed, low elevation settings slightly under-represented in Chaparral/ S. Coast



# Biological Integrity

- “Heatmap” of biological variation related to various stressors in both the reference population (left) and across all sites (right)
- Anthropogenic sources of variation were generally low in the reference pool



# Reference Comments

1. Add more technical detail:

*“...provide more detail on the process for identifying metrics, thresholds, or kill switches, and the differences among these”*

2. Define limits to bio-objective application

*“Define how far the traditional approach can be used in reference-poor regions like the Central Valley and South Coast Xeric”*

3. Explain how reference data will be used

*“It is not clear how reference data will be used in a regulatory context”*



# Predictive Models: (Observed/ Expected Models)

*Developed in UK (Wright and others 1970s-1980s, RlvPACS),  
adapted in Australia (AusRivAS) and US (Chuck Hawkins, Utah  
State... source of most of these slides)*

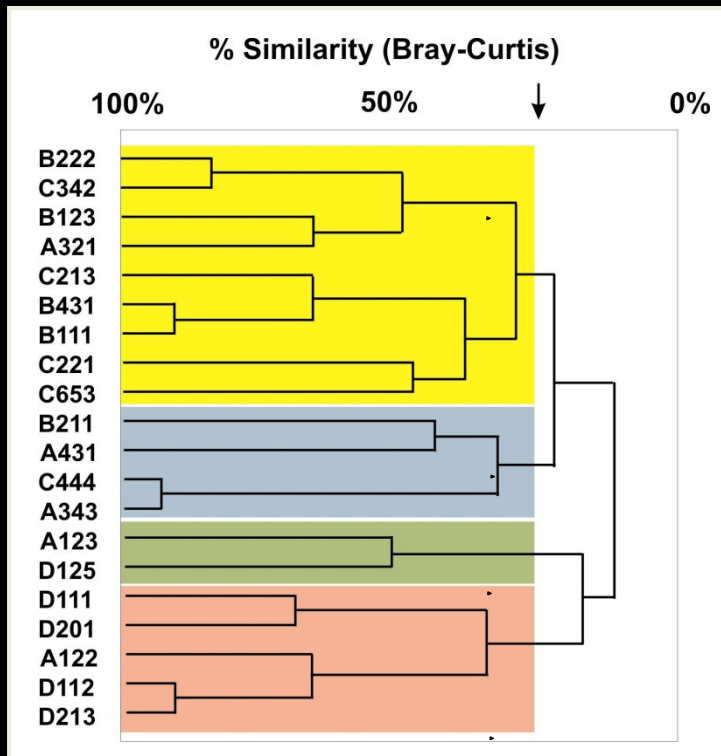
**Species-based approach:** Compare number of **observed** (“O”) taxa to number of **expected** (“E”) taxa

“Expected” taxa derived from predictive modeling techniques

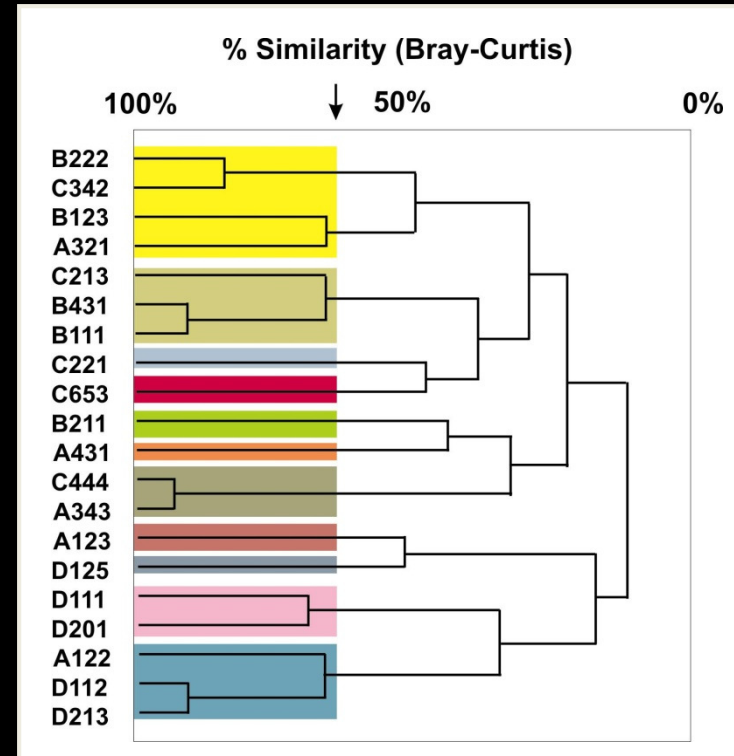
# Estimating “E”

Step 1. Classify reference sites based on biological similarity

Clustering techniques used to identify groups of reference sites with similar species composition



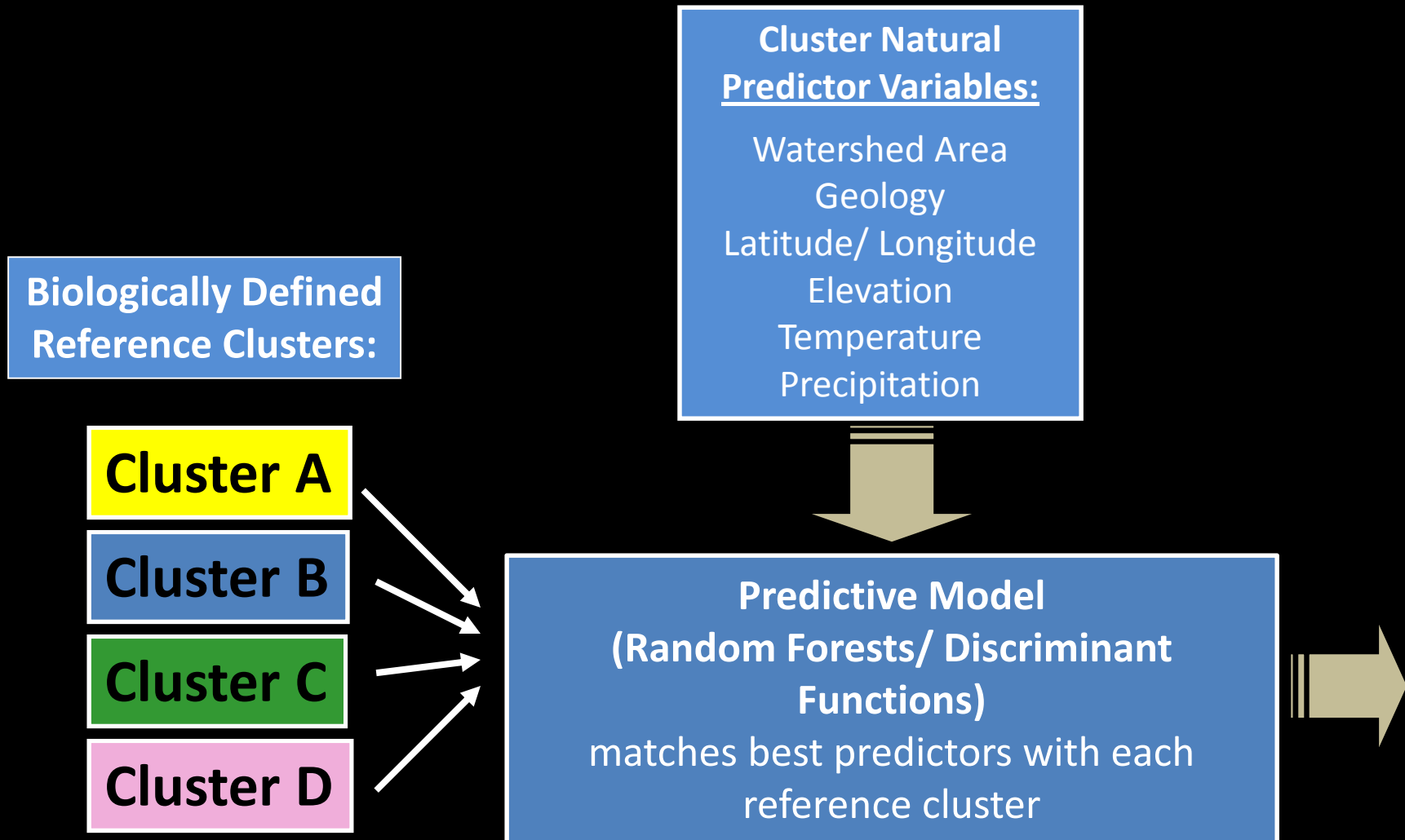
4 classes



11 classes

# Estimating “E”

Step 2. Develop model that will predict class membership for new sites





# Estimating “E”

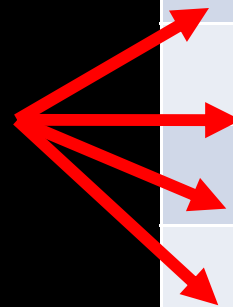
## Step 3. Estimate capture probabilities

Use discriminant model output + frequencies of occurrence within each class to estimate **probabilities of capture (PC)** for each taxon at a given site

Predictor Variables



**Predictive Model**  
(matches predictors with each reference class)



Cluster	Site's probability of cluster membership	Frequency of species X ( <i>Farula sp.</i> ) in cluster	Expected contribution to PC
A	0.5	0.6	0.30
B	0.4	0.2	0.08
C	0.1	0.0	0.00
D	0.0	0.0	0.00
Probability of <i>Farula sp.</i> being in sample if site is in reference condition			<b>0.38</b>

# Estimating “E”

Step 4. Sum of taxon occurrence probabilities is an estimate of the number of native taxa (E) that should be observed (O)

Taxon	pc	O
<i>Atherix</i>	0.70	*
<i>Baetis</i>	0.92	*
<i>Caenis</i>	0.86	
<i>Drunella</i>	0.63	
<i>Epeorus</i>	0.51	*
<b><i>Farula</i></b>	<b>0.38</b>	
<i>Gyrinus</i>	0.07	
<i>Hyaella</i>	0.00	*
E	4.07	3

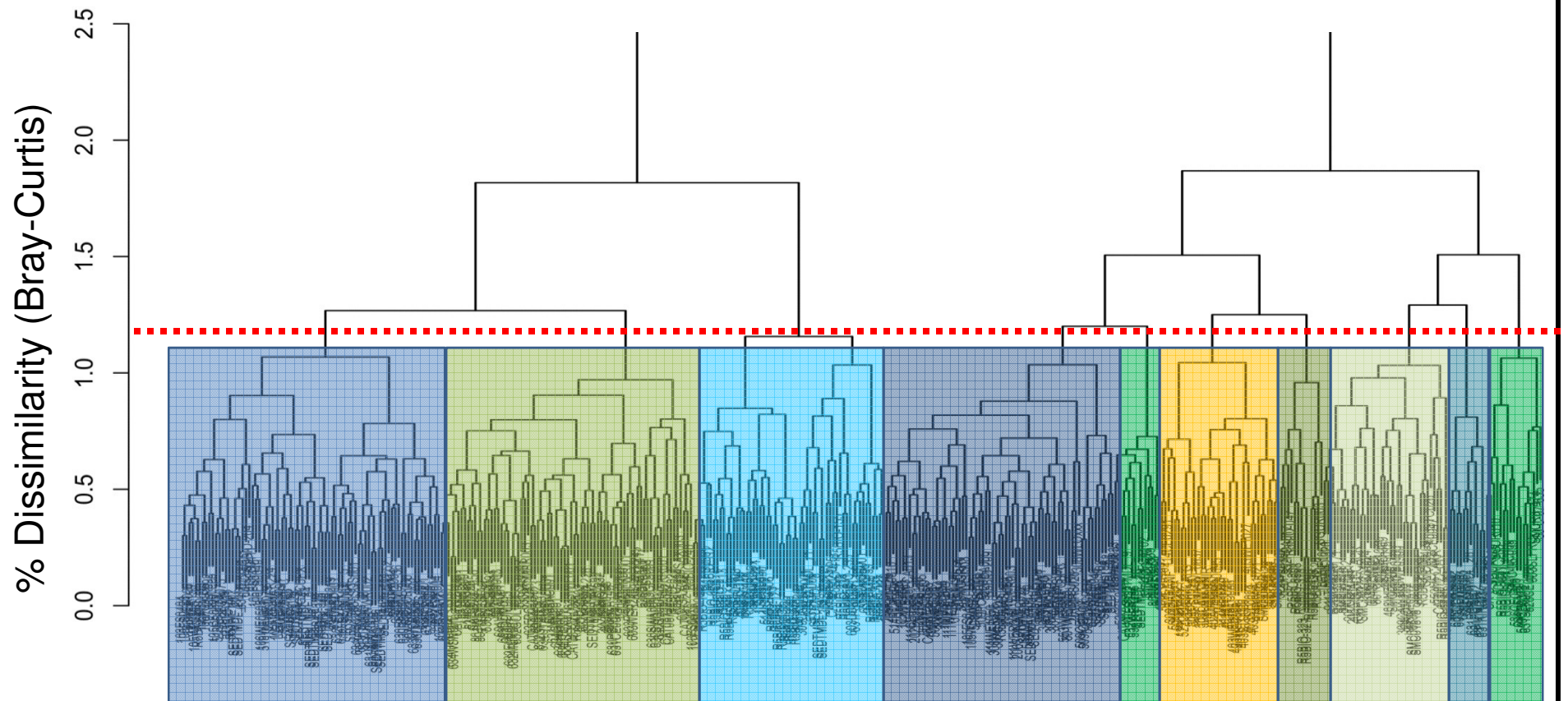
$$O/E = 3 / 4.07$$

$$O/E = 0.74$$

O/E (scaled 0.0 to 1.0):  
represents proportion of  
native assemblage present  
at test site

# Step 2: Cluster biological similarity

*(Bray-Curtis dissimilarity, flexible- $\beta = -0.25$ , rare taxa removed if  $< 2.5\%$  of sites)*



# Scoring Tool Performance Measures

1. Precision
2. Accuracy
3. Responsiveness
4. Repeatability
5. Applicability