

Metagenomic Data Visualization: R Shiny and Other Resources

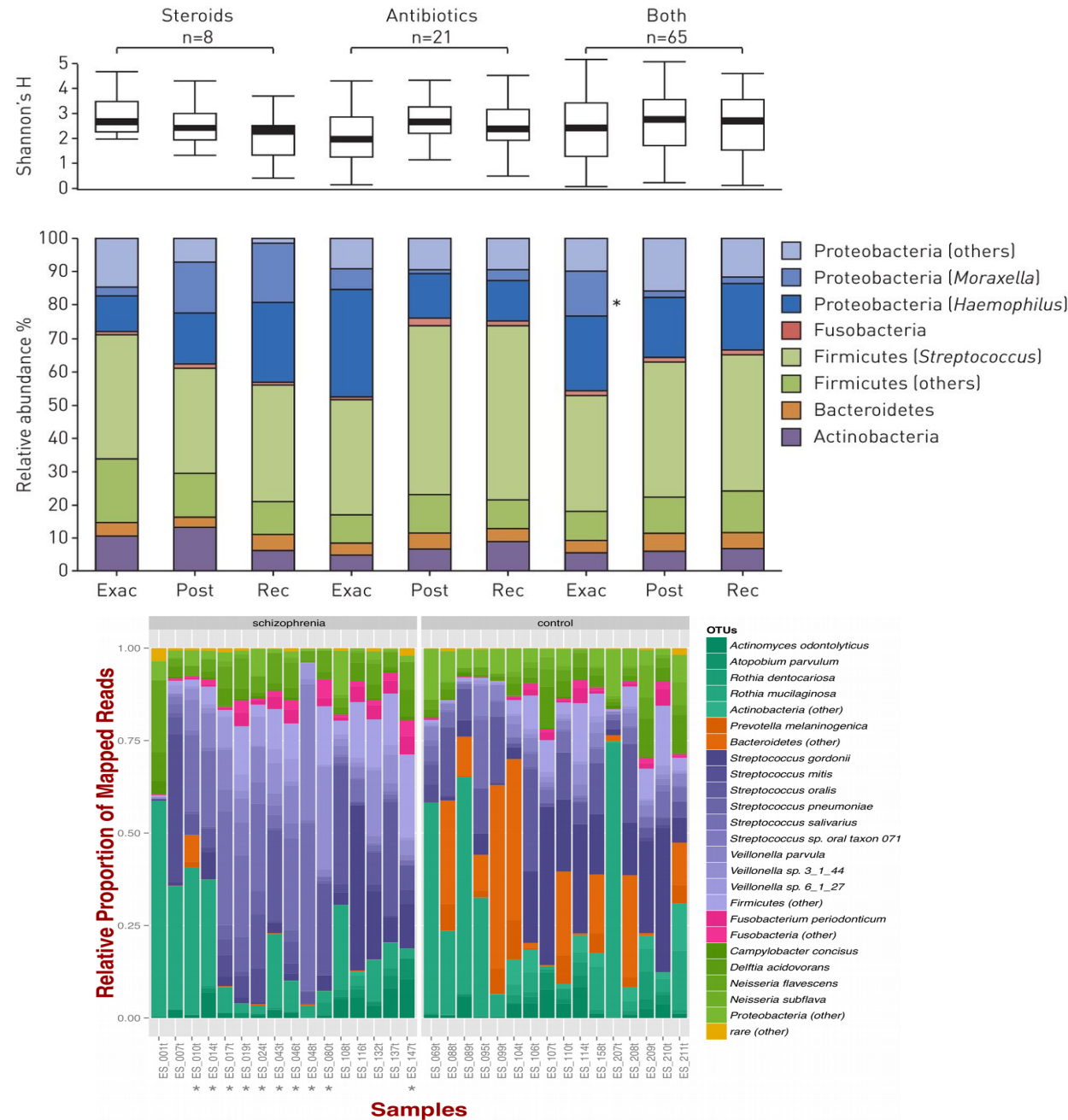
Steven Lakin

Goals of Microbiome Visualization

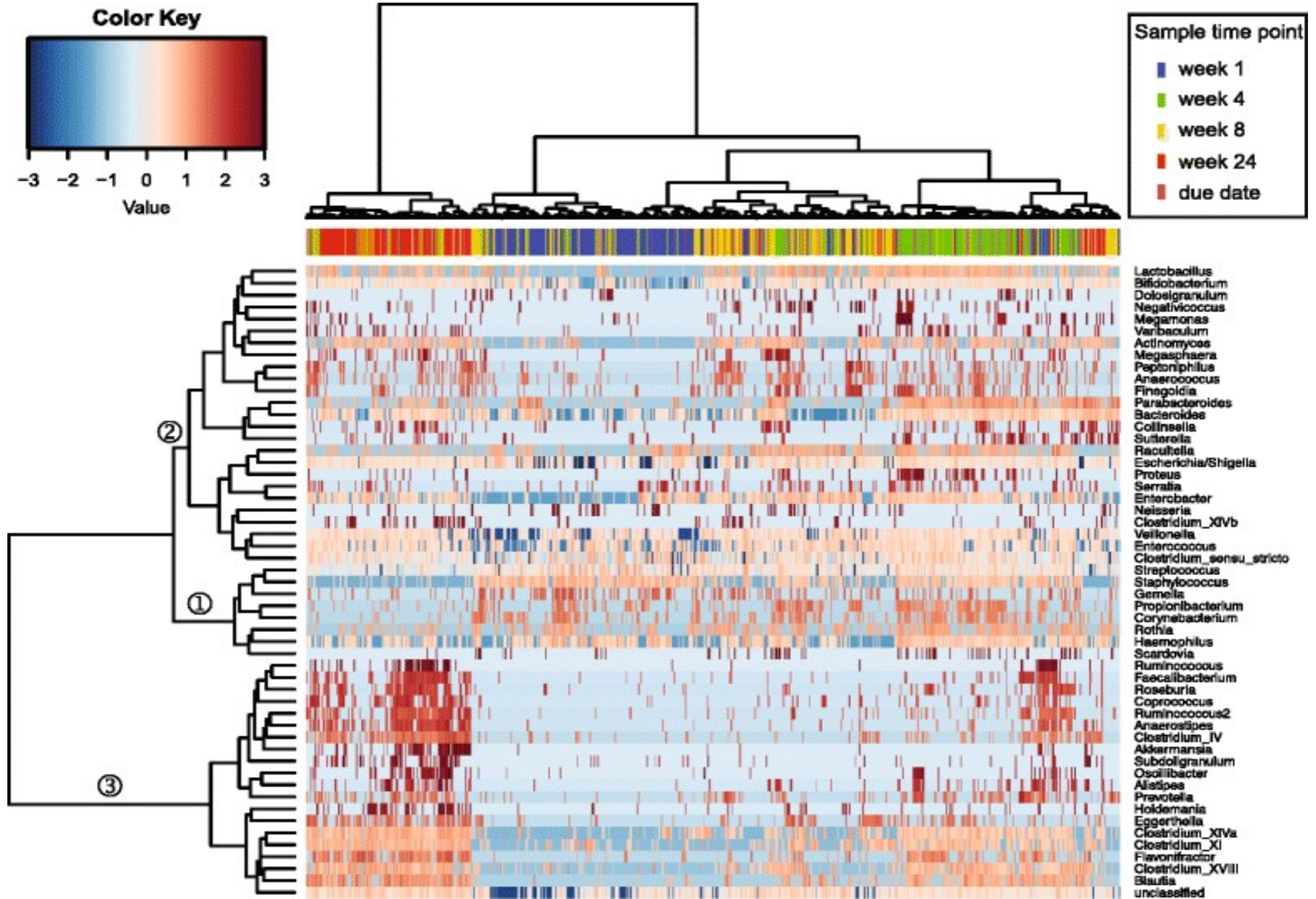
- Dimension reduction: high to low
- Similarity or differences:
 - Composition
 - Sample/Experimental group
 - Changes over space/time/measure
 - Differential abundance (statistical)
- Simply communicate high dimensionality
- Static vs. Dynamic

Composition

- Stacked bar
- Heatmap
- D3.js: interactive
 - Circular
 - Phylogeny (unrooted)
 - Line charts
- Animated figures
- Other tools:
 - BURRITO (functional)
 - MetaViz
 - Tableau

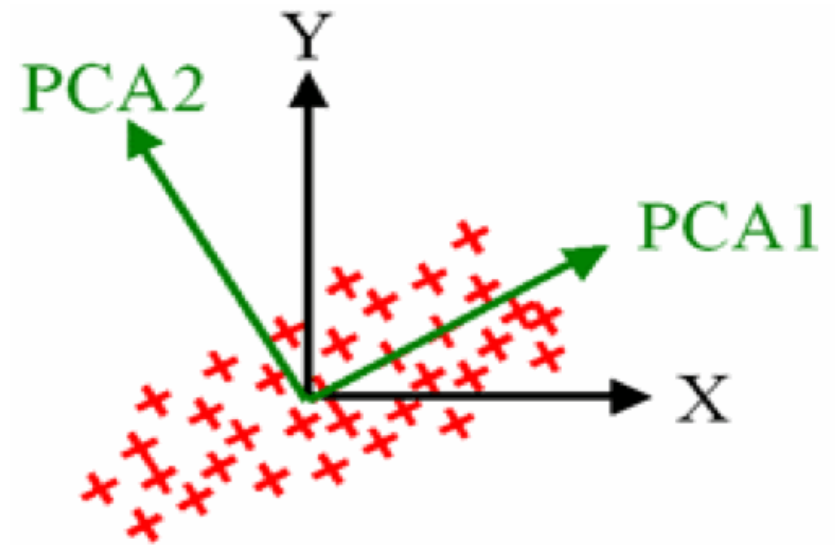


Composition

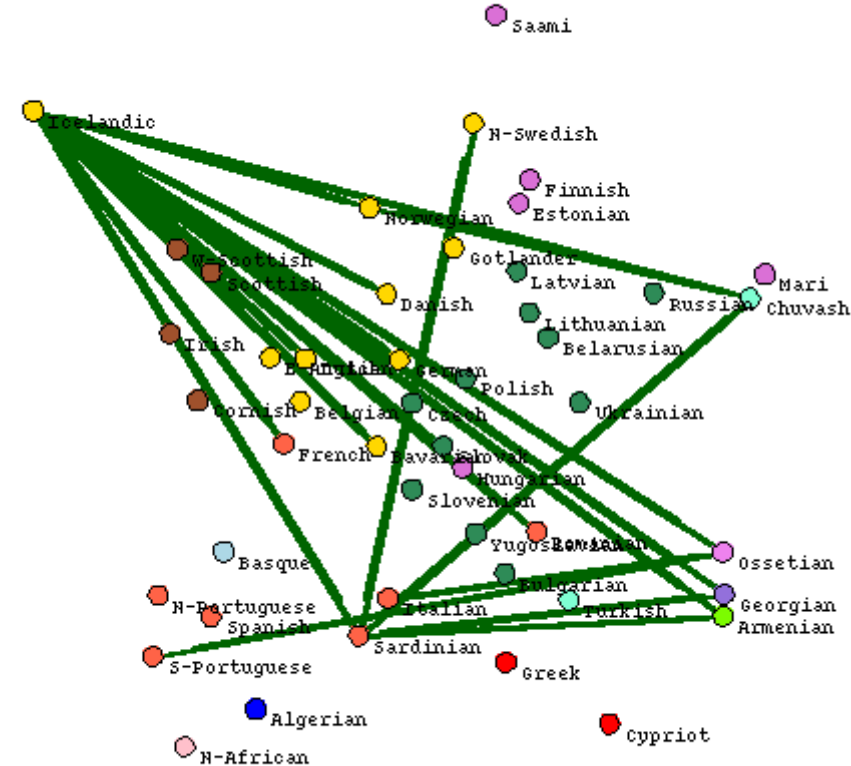


Ordination

- Principal Components Analysis (PCA)
- Multi-dimensional Scaling (MDS)
- Non-metric Multi-dimensional Scaling (NMDS)

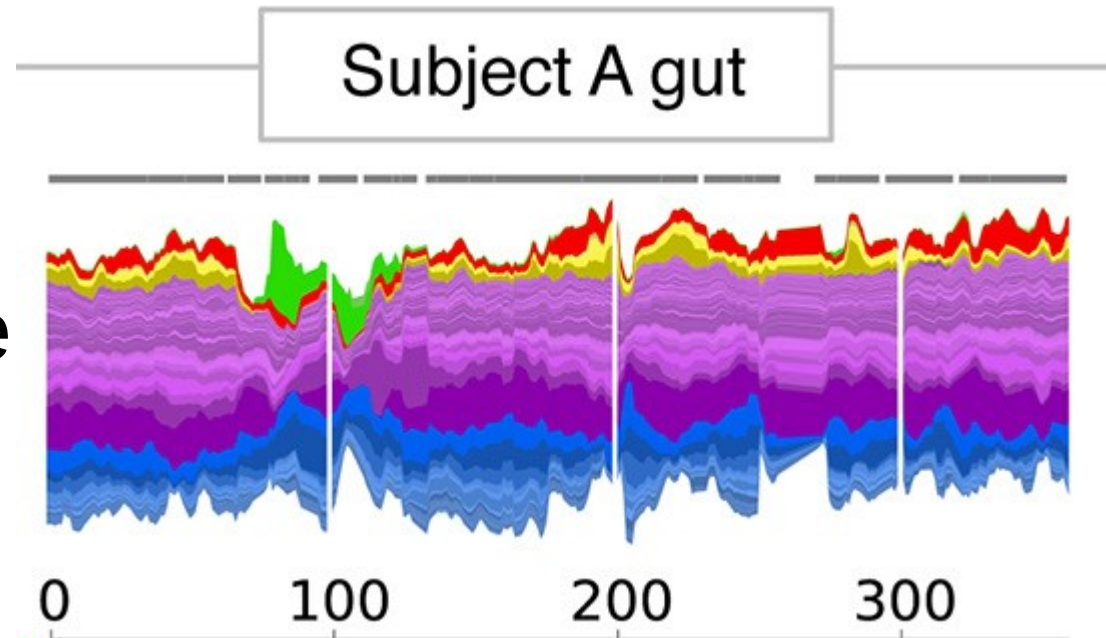


0.57799



Changes Over Space/Time

- Animation (D3.js/Emperor)
- Time/measure/space plots
- Other tools: TIME



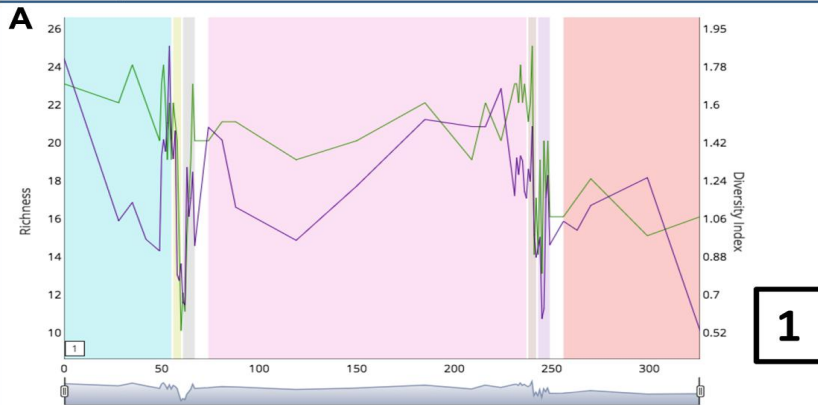
Changes Over Space/Time

PreCp | FirstCp | FirstWPC | Interim | SecondCp | SecondWPC | PostCp

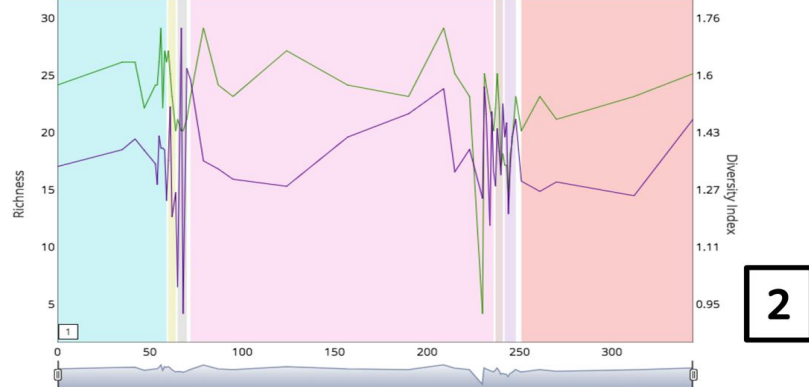
Diversity and Richness

Core taxa

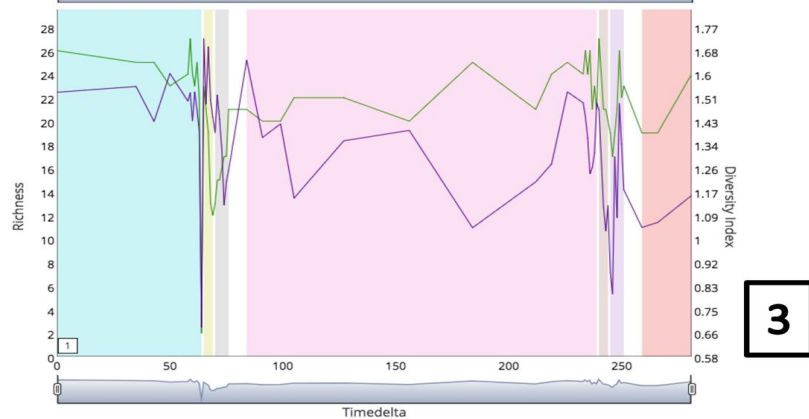
D (Female, 54 years)



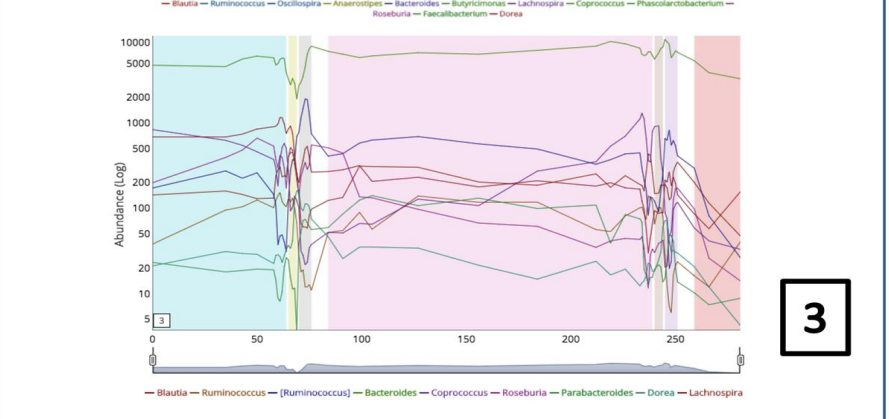
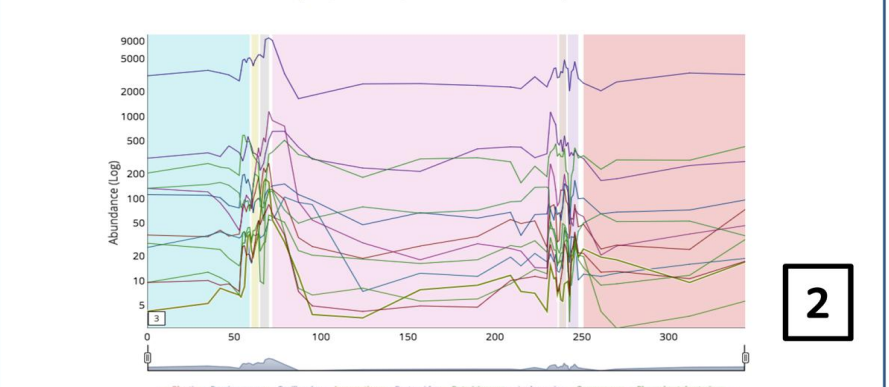
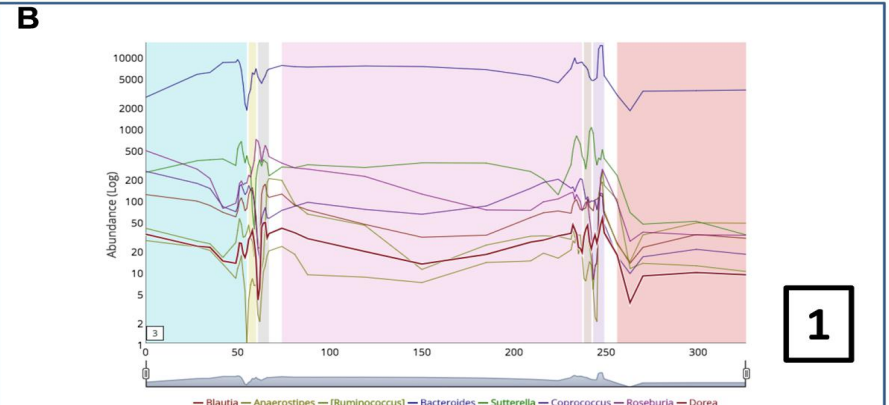
E (Female, 34 years)



F (Female, 28 years)

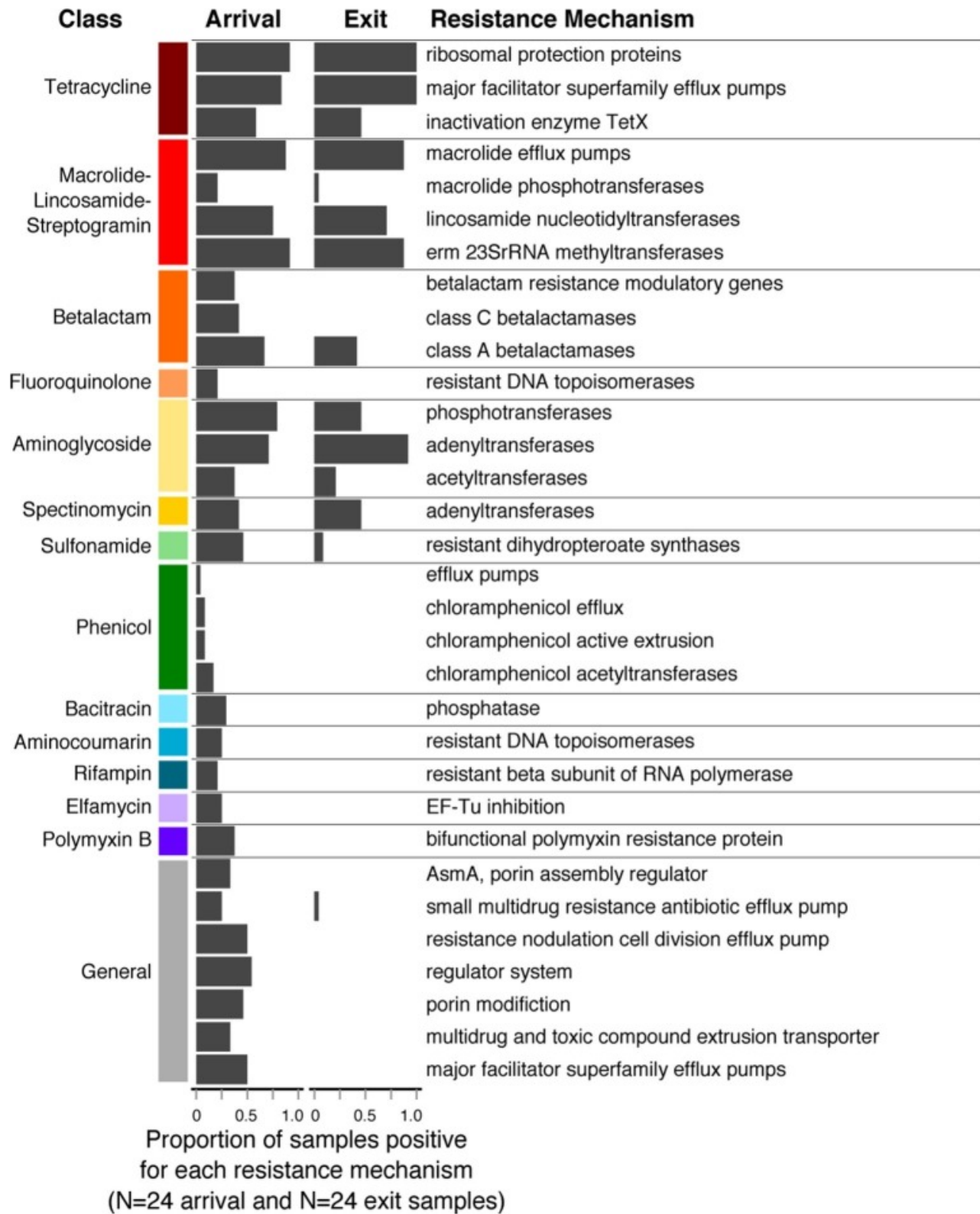


— Richness — Shannon



Differential Abundance

- Volcano plots
- Multi-column bar graphs
- Multi-faceted ggplot graphs



R Shiny

- Code in R
- Interactive in web browser
- Manipulate data in real time
- Good for real-time data vis
- HTML/CSS-based