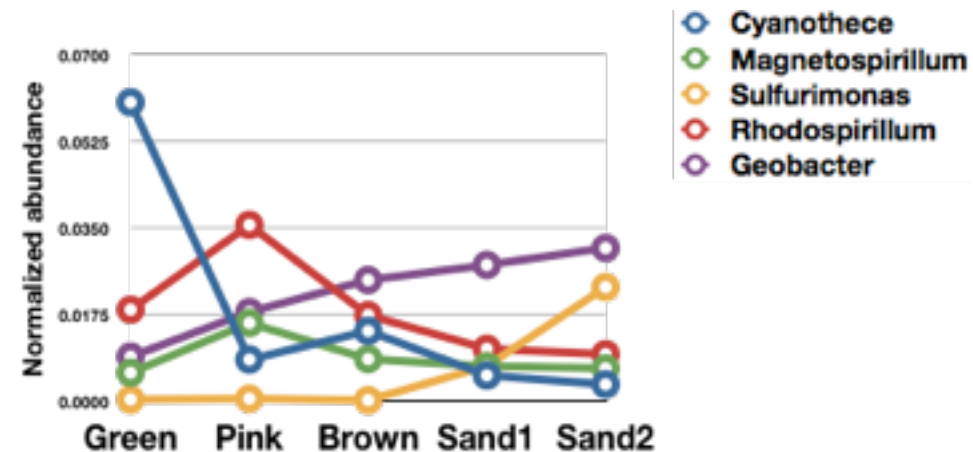


UCA Biodiversity Workshop

May16-18 2016

Martin Polz
Libusha Kelly
Fatima Hussain
Dave VanInsberghe



Useful tools and best practices for studying biodiversity

- Conducting a barcoding and/or high-throughput sequence-based study
- Knowing what kinds of questions you can ask *before* sample collection
- Better consumers and reviewers of bioinformatics tools and analyses
- Communicating with potential (super awesome) collaborators

microbial mat + diatom



Start with the questions

- **What factors shape community structure and membership?**
- **What factors contribute to ecosystem diversity, stability, and organization?**
- **How do interactions between organisms contribute to stability or instability in ecosystems?**
- **How does the abundance and activity of a target phylotype/species change over time, space, and environmental conditions?**

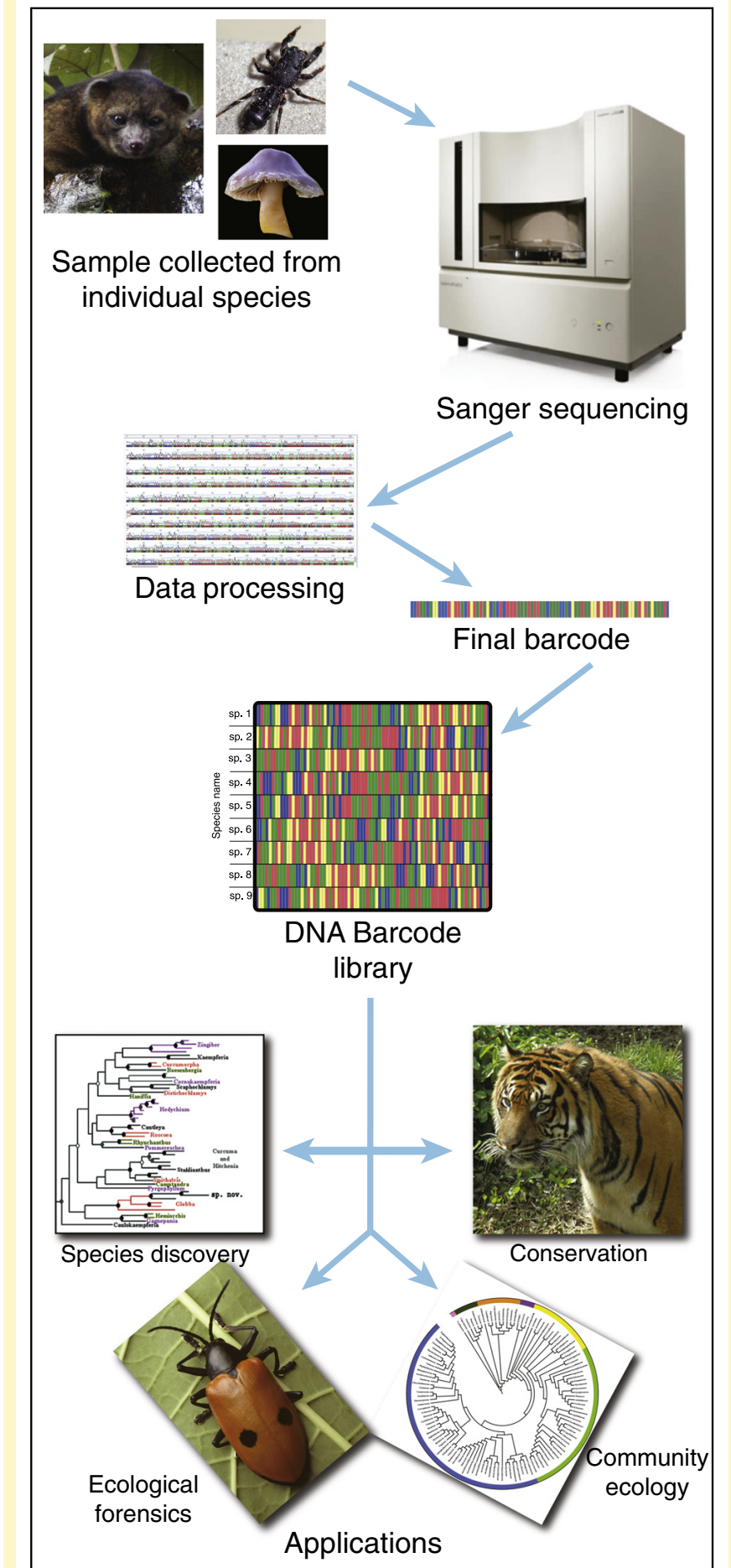
Tools to address questions in biodiversity

- **DNA barcoding**
 - *identifying species, community ecology, trophic interactions*
- **High throughput sequencing of 16S gene**
 - *microbial community profiling and comparison*
- **Unix**
 - *manipulating and visualizing data*
 - *QIIME package for 16S analysis*
- **Statistics**
 - *interpreting data*
 - *R statistical software package*

Conducting a barcode-based microbial diversity study

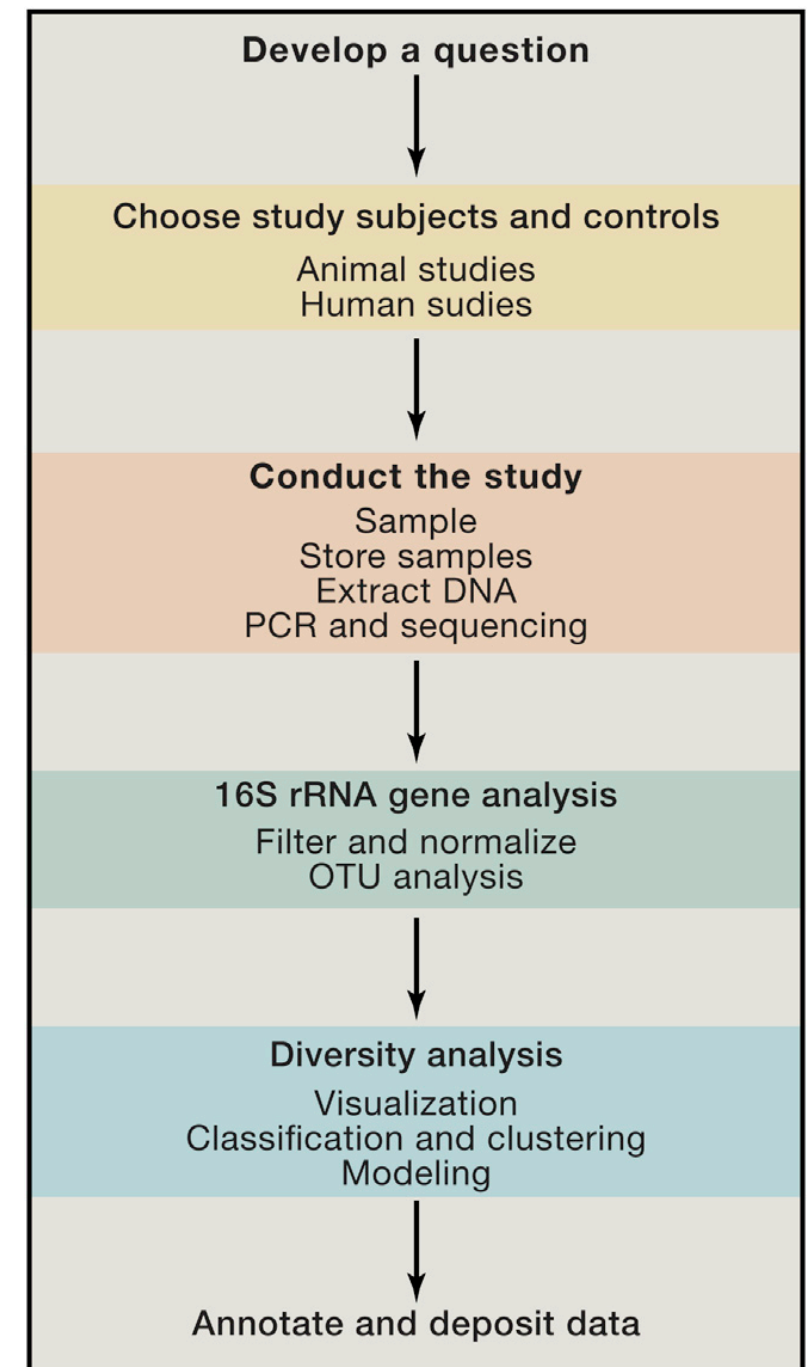
- **Discussion of your samples**
- **Context provided by available libraries**
- **Potential questions/ applications**

DNA barcodes for ecology, evolution and conservation. W. John Kress, Carlos Garcí'a-Robledo, Maria Uriarte, and David L. Erickson. Trends in Ecology & Evolution, January 2015, Vol. 30, No. 1 <http://dx.doi.org/10.1016/j.tree.2014.10.008>



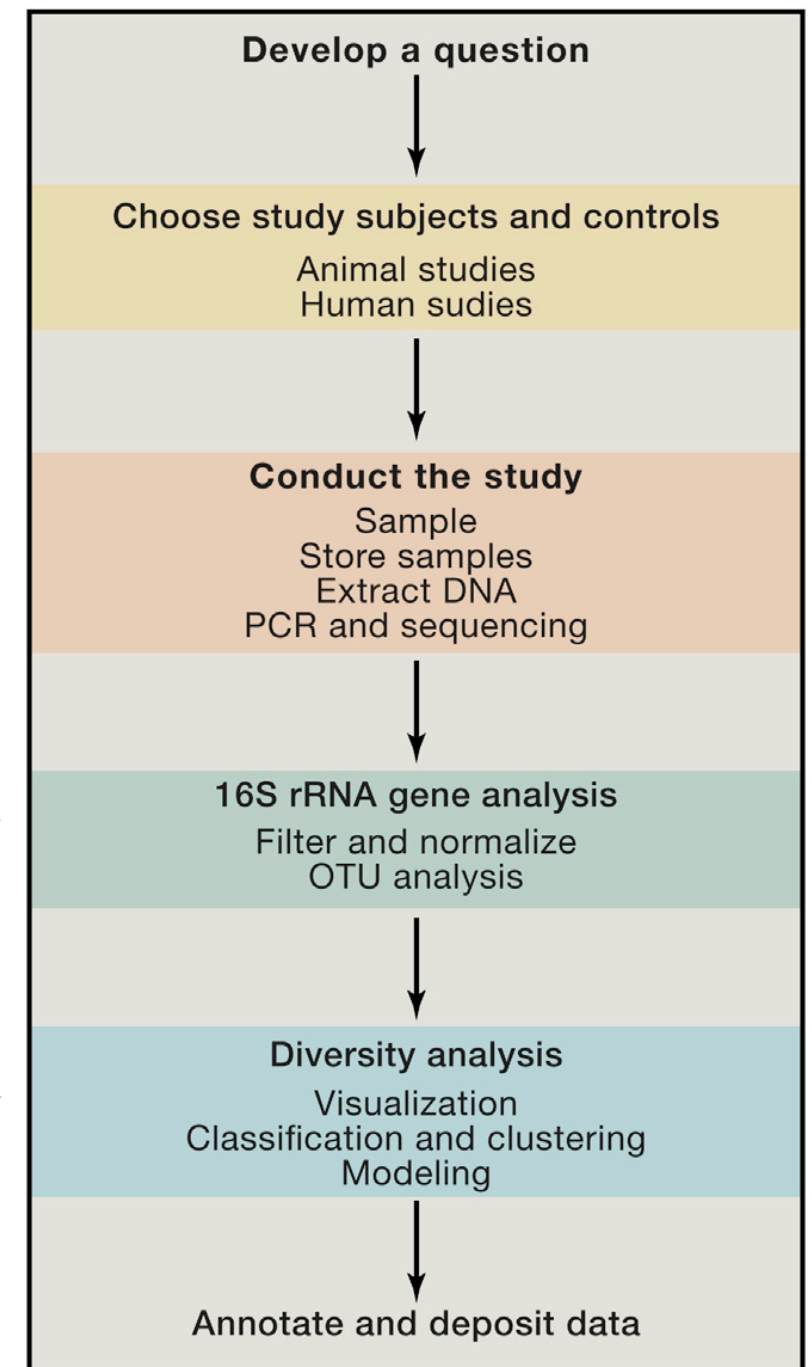
Conducting a 16S based microbial diversity study

- **Focus on human studies but simple framework is applicable to any microbial diversity study**

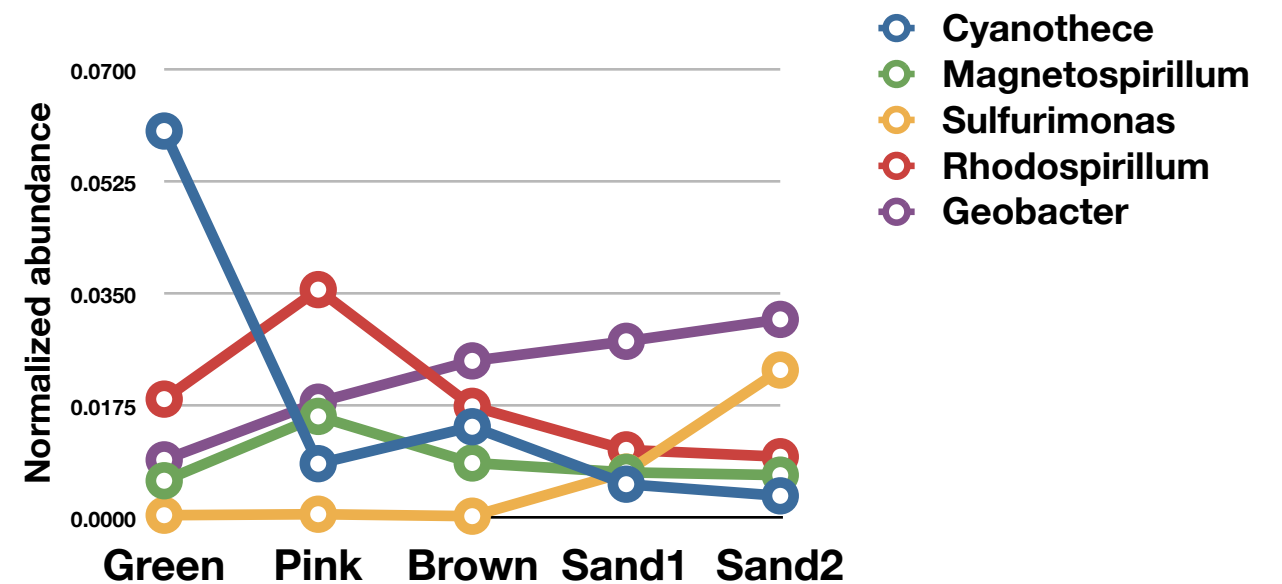


Conducting a 16S based microbial diversity study

- **Focus on human studies but simple framework is applicable to any microbial diversity study**



QIIME for 16S amplicon analysis



- High throughput 16S amplicon sequencing for five layers of a microbial mat

Armitage DW, Gallagher KL, Youngblut ND, Buckley DH, Zinder SH.
Millimeter-scale patterns of phylogenetic and trait diversity in a salt marsh
microbial mat. *Front Microbiol.* 2012 Aug 10;3:293.

Unix for biodiversity analysis

- **How files are organized**
- **How to navigate around your files**
- **Some useful commands**
- **Walk through a specific, complex example of a Qiime command to split libraries from the microbial mat dataset based on barcodes**
QIIME package for 16S analysis

Statistical analysis and R

- **All this descriptive stuff is great (we found these organisms here and these organisms there...) but you need statistics to demonstrate significant differences between microbial populations**
- **Basic stats, pitfalls, and software for diversity analysis**
 - **Data visualization**
 - **Basic statistics**
 - **Multiple comparisons**
 - **Probability**
 - **Sampling bias**
 - **Diversity tutorial in R, a powerful and flexible statistical software package**