

Do It Yourself microBIOMES



<https://qubeshub.org/community/groups/remnet>

Participants:

Alice Tarun – St. Lawrence University
Melanie Lenahan - Raritan Valley CC
Christine Girtain – Toms River High School
Caitlin Fisher-Reid - Bridgewater State University
Maira Goytia - Spelman College

Facilitators:

David Smyth – The New School
Theodore Muth – Brooklyn College
With support from Geena Sompanya

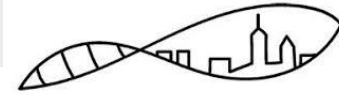
Guest Facilitators:

Bruce Nash - CSHL
Carlos Goller – North Carolina State University



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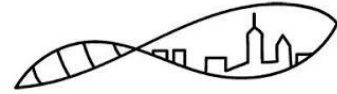




MicroBIOMEs for ALL!!

- What was our plan
- What did we do
- What are our plans for going forward

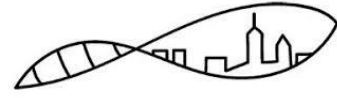




What was our plan

- We are a diverse group of instructors wishing to implement microbiome-based classroom research experiences
- We had a range of experiences with data analysis
 - Wanted to focus on being able to “Do It Yourself”
- We were looking for faculty and student friendly approaches
- Plan was to test out two and implement in Spring





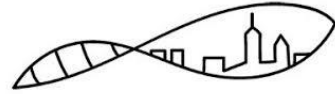
Our goal is to increase access and equity in microbiome associated classroom research

- By making datasets available
- By making analysis accessible
- By generating microbiome case studies (REMNet + HITs)



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What did we do

- We reached out to Bruce Nash about DNA Subway and the purple line
- Held two workshops to walkthrough the platform
- Used Christine Girtain's data as a pilot and then tried it at home with our own
- Learned the background and nitty gritty of the platform



Zoom Meeting Participants:

- Davida Smyth
- Bruce Nash
- NJ Christine Girtain
- Alice's iPad

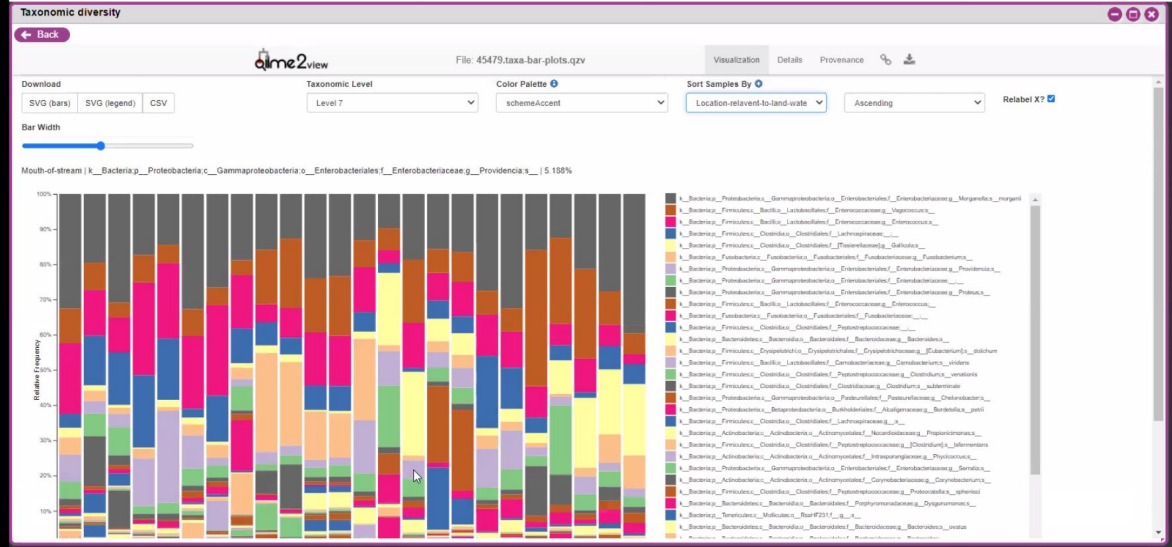
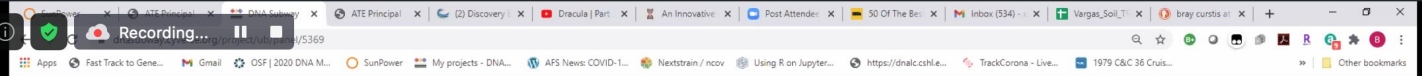
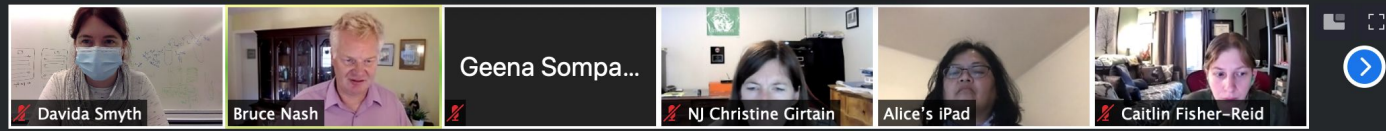
Browser Tab: dnasubway.cyverse.org/project/ub/panel/5369

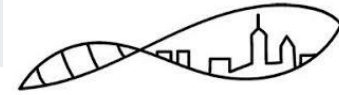
QIIME2 File: 45122.alpha-rarefaction-trim45118.qzv

Metric: observed_otus

Sample Metadata Column: Description

Graph: observed_otus vs. Sample Size





What did we do continued

- We reached out to Carlos Goller from NCSU about Nephele
- Held two workshops to walkthrough the platform
- Learned about Carlos's applications of Nephele and his use of published datasets and associated manuscripts with his postdoc Meghan.
- Started to work on a manual and will continue in the Spring





New to Nephele? [Get started here.](#)

Select your analysis type below to start.

<p>Pre-processing quality check</p> <p>QC</p>	<p>Amplicon Data</p> <p>16S ITS</p>	<p>WGS Data</p> <p>WGS</p>	<p>Downstream analysis</p> <p>DA</p>
Details	Details	Details	Details

Need to re-run previous job?



Select your pipeline and upload your data



Select the parameters for your microbiome analysis



Your pipeline starts and runs in the cloud



Download and visualize your results

CONNECT



LINKS

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[National Institute of Allergy & Infectious Diseases](#)
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Pipeline Features	mothur [*]	QIIME1	DADA2
Join forward and reverse short reads as contigs	✓	✓	✓
Screen contigs to reduce sequencing errors			✓
Dereplicate contig sequences	✓	✓	✓
Taxonomic assignment based on selected database	✓	✓	✓
Remove sequences likely due to sequencing errors	✓		✓
Identify and remove chimeric sequences	✓	✓	✓
Classify sequences based on k-nearest neighbor	✓		
Remove sequences belonging to undesirable lineages	✓		
Remove rare OTUs in the samples	✓	✓	
Detect differentially abundant features in samples		✓	
Construct phylogenetic tree	✓	✓	
Calculate various measures of diversity	✓	✓	✓
Ion Torrent Processing - Beta			✓

Select See details^{*}
Select See details
Select See details

Upload your Single End FASTQ sequence files (max file size 1GB)

Drag and Drop Files Here (The maximum size allowed per file is 1GB)
or
[Add Files...](#)

20.38 MB/s | C000-40 | 4.10 % | 4.36 MB / 106.39 MB

SRR10425893_1.fastq	48.01 MB	Start Cancel
SRR10425902_1.fastq	16.49 MB	Start Cancel
SRR10425903_1.fastq	41.89 MB	Start Cancel

Help

On File Uploads:

- You can **drag & drop** files from your desktop on this webpage (see [Browser support](#)).
- The maximum size allowed per file is 1GB.

On the Blueimp library:

- Please refer to the [documentation](#) for more information on how the multi-file uploader works.

What are our plans for the Spring?

- We are going to complete our walkthroughs for the Purple Line and Nephele – we'll be using them in our Spring classes
- We're working on case-studies that relate to the microbiome
 - Using our own narratives and our own data – share it!
 - Salamanders, microbiomes and climate change
 - Superfund sites and beneficial microbes
- Investigate KBase



Final words from the Team!

Slide from Caitlin

- What did you want to know
- What did you learn
- What are you going to do

Slide from Christine

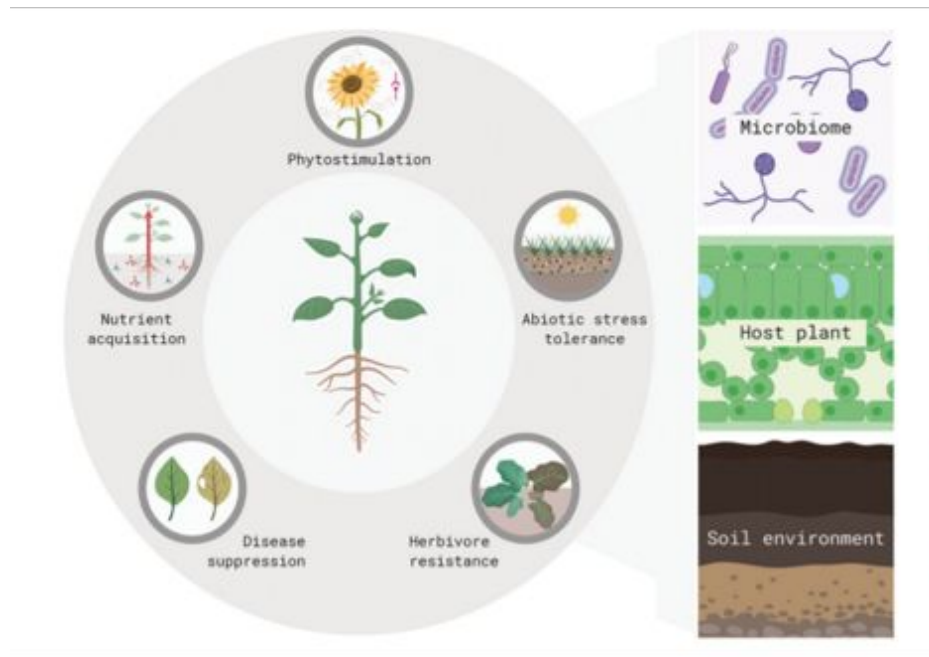
- What did you want to know
- What did you learn
- What are you going to do

Slide from Maira

- What did you want to know
- What did you learn
- What are you going to do

Slide from Alice

- What did you want to know
- What did you learn
- What are you going to do



Alice Tarun, Ph.D.

Research:

- Microbiome Analysis of soil and plant rhizosphere in sustainable agriculture practices;
- Microbiome analysis in wetland bioremediation

What did you learn:

- Microbiome protocols and analysis

What are you going to do:

- Incorporate microbiome analysis in CURE and URE for Summer 2021

