Learning Outcomes

- To define metagenomics.

- To describe ways the iPlant Discovery Environment (DE) can be used to teach metagenomics data analyses to undergraduates and graduate students.

- To evaluate different approaches for metagenomics education using the iPlant DE and research-based educational approaches.

Metagenomics is a culture-independent analysis method that involves:
- obtaining DNA from communities of (micro)organisms
- sequencing it in a “shotgun” fashion and characterizing genes
- and comparing genes and genomes with known sequences

Q – How can we study complex communities of microorganisms?

What microorganisms are in your kitchen sink?
Metagenomics Workflow

(1) Sample Communities
(2) Extract Total DNA
(3) Sequence DNA
(4) Analyze Sequences

1) iPlant activities...

- Work with your lab partner.
- Navigate to: https://de.iplantcollaborative.org/de/
- Follow the worksheet.
- We will stop to discuss key procedures and functions.

2) iPlant activities: The DE

3) iPlant activities: Worksheets
Teaching Students How to Analyze Metagenomic Data with the iPlant DE

- iPlant DE provides an environment that is user-friendly yet has powerful tools (e.g., for taxonomic inference from short reads).
- The iPlant DE allows both students and instructors to share data and results fostering collaborations.
- iPlant DE provides flexibility, allowing students to choose different tools and then reflect on the outcomes.
ABSTRACT

Sifting Through Metagenomes Using the iPlant Discovery Environment

Teaching undergraduate and graduate students about metagenomics and analyzing sequence data can be challenging when participants are not familiar with the software. The iPlant Discovery Environment provides a user-friendly yet powerful platform to begin to perform metagenomic analyses in a classroom setting. Since the fall of 2013, the Biotechnology Program at North Carolina State University has used the iPlant Discovery Environment to introduce students to cloud-based computing. A series of computer activities based on worksheets familiarize students with procedures to download sequences from databases, assess the quality of next-generation sequencing reads, launch applications to analyze sequences to infer taxonomy, and assemble metagenomes. Sharing of large sequence files and results with groups of students allows instructors to easily manage laboratory sessions. Pairs of students are then tasked with diagramming the procedures they followed to reinforce the steps for each workflow and propose alternatives. Combined with reflective questioning, diagramming helps students break down complex processes into simple steps. The iPlant Discovery Environment offers an increasing number of tools for analyses of next-generation sequencing data, genomics, and metagenomics on a platform that is user-friendly, powerful, and promotes interaction among student groups.