

Overview:

- Participants will be introduced to a variety of **methods** for studying the complex microbial populations that surround us, including applications, limitations, and health and legal implications.
- Students will apply high-throughput sequencing techniques to mine the genetic diversity of complex populations such as the community of microbes growing happily in a **kitchen sink**.



Lectures:

1. Introduction to metagenomics and microbial communities
2. Exploiting genome sequencing for drug and biotechnology product discovery.
3. **Approaches** and limitations of metagenomic surveys.
4. Analyzing and visualizing metagenomic data (R and online tools for sequence analysis)

Labs:

1. Isolation of DNA from student-selected microbial community and preparation (Q/C) for high-throughput sequencing.
2. Assembly and gene annotation of sequence data from microbial community using cloud computing.
3. Use of bioinformatics software for analyses of metagenomic surveys.
4. Use of cloud-based pipelines for analyzing 16S sequences.
5. Use of QIIME for diversity analyses.