*Have microbial metagenome data?  Don't quite know what to do with it?  Don't fret!*

*Now accepting applications for SUMMER 2015*

# Explorations in Data Analyses for Metagenomic Advances in Microbial Ecology

# (EDAMAME)

Instructors:  Dr. Ashley Shade and Dr. Josh Herr
Michigan State University Department of Microbiology and Molecular Genetics

Kellogg Biological Station
22 June – 02 July 2015

EDAMAME is an intensive, hands-on course in microbial metagenome analyses, covering workflows from raw sequence analysis through to multivariate statistics and ecological interpretation.

By the end of the course, learners will be able to:

- Explain the process of high-throughput sequencing, provide an overview of data-handling specific to these technologies, and discuss their biases.
- Choose appropriate statistical analyses to explore datasets and to test hypotheses.
- Visualize patterns in microbial community using different methods and tools.
- Transfer data and run analyses in Amazon EC2 cloud and HPCC
- Develop a working proficiency with QIIME, mothur, and R, cite alternatives available, and identify resources for troubleshooting and further reading
- Choose and execute an appropriate workflow for shotgun metagenome data, including annotation and assembly
- Become familiar with publicly accessible microbial sequence databases and the tools that they offer for deposition and analyses

Please see **edamame-course.org** for more information and to apply!

Limited spaces available; Application available at: http://goo.gl/forms/m1ZlRWC6e9