

BIOLOGY SEMINAR

BIOLOGY GRADUATE STUDENT ASSOCIATION AND
DEPARTMENT OF BIOLOGICAL SCIENCES



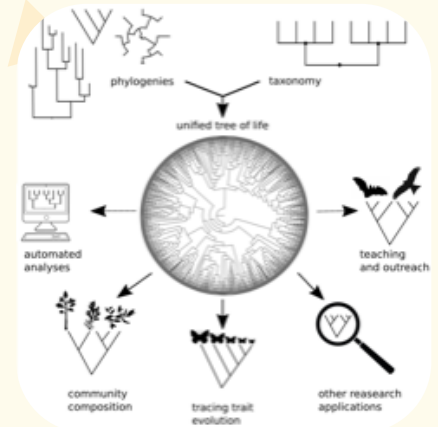
**Emily Jane
McTavish, PhD**
University of
California, Merced

FRIDAY, MAY 3 @ 4 PM
SCI B 133

Large scale phylogenetics, from within STD outbreaks to across the tree of life

In order to answer biological questions about organisms it is necessary to understand their evolutionary history. Recent technological developments have made it possible to generate sequence data rapidly and inexpensively. These data are providing new opportunities for phylogenetic inference, but are also creating new computational challenges. We need to combine not only large amounts and kinds of data, but data being generated using a wide variety of methods. I will present on-going work addressing these problems at two very different biological scales - within gonorrhea outbreaks, and across the tree of life through the Open Tree of life project.

We have developed a phylogenetic updating procedure that leverages existing phylogenetic inferences and core genome alignments, and applied it to tracing *Neisseria gonorrhoeae* relationships. This approach, which is being developed in collaboration with the CDC, improves our ability to efficiently and accurately infer evolutionary relationships of new gonorrhea isolates. At a much broader taxonomic scale, I will discuss new developments in the Open Tree of Life project. The Open Tree of Life is a collaborative effort to synthesize, share and update a comprehensive tree of life, by combining published phylogenetic estimates. The synthesis tree is revised as new data become available, and captures conflict and consensus across studies. The current draft contains 2.3 million named species.



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