



James Stapleton

NIH NRSA Postdoctoral Fellow
Dept. of Chemical Engineering and Materials Science
Michigan State University

Research Seminar

Thursday, December 4, 2014
9:30 - 10:30 a.m. - ABE 301

"Synthetic Long Sequencing Reads for Data-Driven Biomolecular Engineering"

Abstract:

Next-generation sequencing has transformed biology into a data science. However, the challenge of assembling the short sequencing reads delivered by the dominant platforms hinders the analysis of complex genomes and homologous mixed populations. I will present a high-throughput method to reconstruct the sequences of individual 10-kb nucleic acids from a homologous population. The method has assembled 99.95%-accurate synthetic long reads from bacterial, plant, and animal genomic samples, and individual homologous HIV *env* gene variants from a mixture. This approach relieves a fundamental limitation of short-read sequencing, extending the utility of the vast investment made by institutions around the world in next-generation DNA sequencing infrastructure.

Biological engineering is also beginning to transition to data-intensive approaches. A major impediment is the lack of high-throughput phenotypic assays to match the throughput of DNA sequencing. I will discuss methods that overcome this limitation and generate huge sets of linked genotype-phenotype data.

Teaching Seminar

Friday, December 5, 2014
9:00 - 10:00 a.m. - ABE 301