QUANTITATIVE & SYSTEMS BIOLOGY COLLOQUIUM:
Making hard genome editing easy (with CRISPR/Cas-induced homology-directed repair)

Thaddeus D. Seher
PhD Candidate in Quantitative & Systems Biology
University of Califoria, Merced

Date:
3/12/2021

Time:
10:30 AM-11:45 AM

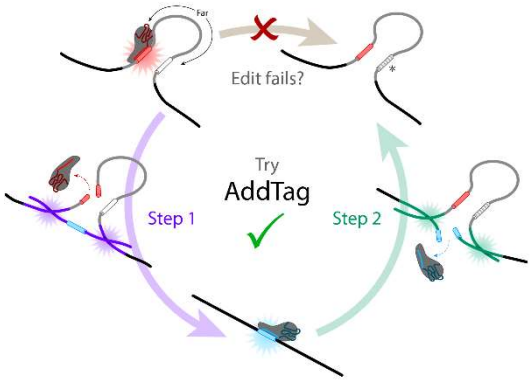
Link:
Please contact snsgradstaff@ucmerced.edu for the Zoom link and passcode.

About The Speaker:

Thaddeus D. Seher's scientific journey began as an undergraduate in the lab of Charles H. Langley (UC Davis), sequencing fruit flies to measure their worldwide genome diversity. After graduating, he analyzed sex-specific fruit fly traits using transcriptomics in the Artyom Kopp lab (UC Davis). Then he moved to William B. Ludington lab (UC Berkeley) to do metagenome assemblies of water microbes, and the Gregory M. Barton lab (UC Berkeley) to investigate how mice use antibodies to control their gut microbiomes. Finally, he came to the Clarissa J. Nobile and Suzanne S. Sindi labs (UC Merced) to study microbial symbioses and molecular biology from a bioinformatics lens in the Candida albicans model system. He spends his free time computer programming, playing Disc Golf, cooking, and making up preposterous stories to tell his young daughter.

Abstract:

CRISPR/Cas-induced genome editing is a powerful tool for genetic engineering, however targeting constraints limit which loci are editable with this method. Since the length of a DNA sequence impacts the likelihood it overlaps a unique target site, precision editing of small genomic features with CRISPR/Cas remains an obstacle. We introduce a novel genome editing strategy that virtually eliminates CRISPR/Cas targeting constraints and facilitates precision genome editing of elements as short as a single base-pair at virtually any locus in any organism that supports CRISPR/Cas-induced genome editing. Our two-step approach first replaces the locus of interest with an "AddTag" sequence, which is subsequently replaced with any engineered sequence, and thus circumvents the need for direct overlap with a unique CRISPR/Cas target site. In this study, we demonstrate the feasibility of our approach by editing transcription factor binding sites within Candida albicans that could not be targeted directly using the traditional gene editing approach. We also demonstrate the utility of the AddTag approach for combinatorial genome editing and gene complementation analysis, and we present a software package that automates the design of AddTag editing.



For more information, contact : Emily Jane McTavish
ejmctavish@ucmerced.edu