

1163-92-1655

Suzanne Sindi*, 5200 North Lake Road, Merced, CA 95343, **Mikahl Banwarth-Kuhn**, 5200 North Lake Road, Merced, CA 95343, and **Jordan Collignon**, 5200 North Lake Road, Merced, CA 95434. *Multiscale Modeling of Prion Aggregate Dynamics in Yeast*.

Prion proteins are responsible for a variety of neurodegenerative diseases in mammals such as Creutzfeldt-Jakob disease in humans and “mad-cow” disease in cattle. While these diseases are fatal to mammals, a host of harmless phenotypes have been associated with prion proteins in *S. cerevisiae*, making yeast an ideal model organism for prion diseases. Most mathematical approaches to modeling prion dynamics have focused on either the protein dynamics in isolation, absent from a changing cellular environment, or modeling prion dynamics in a population of cells by considering the “average” behavior. However, such models have been unable to recapitulate *in vivo* properties of yeast prion strains.

In this talk, I will show some results from recent individual based simulations where we study how the organization of a yeast population depends on the division and growth properties of the colonies. Each individual cell has their own configuration of prion aggregates and we study how the population level phenotypes are a natural consequence of the interplay between the cell cycle, budding cell division and aggregate dynamics. We quantify how common experimentally observed outcomes depend on population heterogeneity. (Received September 16, 2020)