



MARQUETTE  
UNIVERSITY

HELEN WAY KLINGLER  
COLLEGE OF ARTS AND SCIENCES

Department of Mathematics, Statistics and Computer Science

## COLLOQUIUM ANNOUNCEMENT

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### *Modeling Protein Aggregation Concentration in Saccharomyces cerevisiae*

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**3:30 PM, Thursday, December 7, 2017**

Cudahy Hall, Room 401

#### **Abstract**

Proteins are the foundation for almost all biological processes. Some, when misfolded, turn into disease-associated proteins. A prime example is the prion, which is an infectious agent that is composed only of proteins. Under normal circumstances, proteins are flexible and can take on different shapes. However, when misfolded, prions have an added infectious characteristic and can force normal protein to change into the misfolded state. One by one, a few misfolded prions can corrupt a whole population. As more prions accumulate, they tend to aggregate into clumps or long fibrils. These aggregates then wreak havoc on the organism's system, such as the brain in CJD, mad cow, and scrapie. Understanding the aggregation processes will provide insight into how prion diseases progress and spread. In the case for prions, some of these dynamics are not easily observed. Mathematical modeling, specifically compartmental modeling, can be used to describe the unobservable system.

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For further information: see <http://www.marquette.edu/mscs/resources-colloquium.shtml>

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*POST COLLOQUIUM REFRESHMENTS SERVED IN  
CUDAHY HALL, ROOM 342 AT 4:30 P.M.*