Genome-scale metabolic models are invaluable tools that serve as organism knowledge bases and can help guide metabolic engineering efforts. We have constructed a model of *Methanococcus maripaludis S2*, a model methanogenic archaeon, that accounts for 477 of the 1722 protein coding genes (28%) in its genome

*Methanococcus maripaludis S2* is a model methanogenic archaeon with a fast doubling time and well-developed set of genetic tools. To better our understanding of this organism and the unique properties of its methanogenic enzymes, we have constructed a genome-scale metabolic model of *M. maripaludis* that accounts for 477 of the 1722 protein coding genes (28%) in its genome. Our model is the first for this organism to accurately depict the Wolfe cycle, the central catabolic pathway for methane and energy production in hydrogenotrophic methanogens, and the first model of any organism constructed using the maximum likelihood gap filling approach. This model will provide a platform to generate quantitative and qualitative hypotheses for how to turn the methanogenic enzymes in reverse to oxidize methane to methanol and how to add exergonic sulfate reduction pathways that can make the process energetically viable.

RELEVANT ACTIVITIES

In the box below, please indicate your particular activities which justify favorable consideration of you as a participant and contributor to this meeting.   
This information is important, as it allows the Scientific Organizers to make a thorough assessment when reviewing and selecting participants (max. 1700 characters).

I am a graduate student at the University of Illinois at Urbana-Champaign and conduct my research under Dr. Nathan Price at the Institute for Systems Biology (ISB) in Seattle, WA. Outside of my time in the research lab, I am highly active in education outreach efforts with the Logan Center at ISB and have worked with educators at both K-12 and community college levels. At the K-12 level, I serve as a scientific content expert to groups of 5-10 teachers and help the group design class lessons that conform to new Washington education standards. As part of my role, I supply examples of how concepts from each lesson can be applied in the real world and propose ways the teachers could bring these real world examples into their classrooms to get students excited about science. At the community college level, I have acted as a “big data mentor” to groups of teachers working to integrate big data concepts from systems biology into their curricula. In this role, I have helped assess vital ideas to big data science and suggested ways to make these ideas accessible to all students in their programs. I am also a member of the Editorial Board at ISB, a group of scientific researchers whose goal is to increase public awareness of the scientific advances at the institute. As a board member, I write short pieces aimed at a general audience that highlight recent publications by members of the institute and make the information accessible to individuals outside of the scientific community. These pieces generally describe research conducted by the Price lab and several were published in ISB’s monthly newsletter, Molecular Me.

In addition to the work presented here, I have begun a project to create a tool that uses the maximum likelihood gap filling tool to make a new fully-functional genome scale model by incrementally modifying an existing model. The expected outcome of this project will be a homology-based method that reduces the time and effort necessary to produce a high-quality model.

Synthesizing methanol, a liquid fuel, from methane, a greenhouse gas, is an expensive procedure that could alter both our environmental outlook and our fuel economy if it were achieved efficiently. To solve this problem, we will metabolically engineer *Methanococcus maripaludis S2*, a fast-growing methanogenic archaeon with well-developed genetic tools, to generate methanol from methane by inserting reaction pathways native to methanotrophic organisms. We have constructed a genome-scale metabolic model of *M. maripaludis* that allows us to predict the experimental outcomes of our engineering efforts and accounts for 477 of the 1722 protein coding genes (28%) in the *M. maripaludis* genome. Our model is the first for this organism to accurately depict the Wolfe cycle, the central catabolic pathway for methane and energy production in hydrogenotrophic methanogens that must function in reverse to achieve our proposed strain design. This model will provide a platform to generate hypotheses for how to turn the methanogenic enzymes backwards to oxidize methane to methanol and how to add exergonic sulfate reduction pathways that can make the process energetically viable. It is also the first model of any organism constructed using the likelihood-based gap filling approach, a method that we are currently expanding as a tool to make new fully-functional genome scale models by incrementally modifying existing models. Thus, this model represents both a vital piece of our work to modify *M. maripaludis* to efficiently convert methane to methanol and a first step toward the creation of a homology-based model morphing tool that will reduce the time and effort necessary to produce a high-quality genome scale model.