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Poster Submissions**Poster Title**

Metabolic network percolation provides insight into microbial fastidiousness

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Please describe the extent of your work in this research

I helped design the research project, conduct the research, and write up the results.

Abstract Submission

- [Abstract_GSI1_Oct20_2015.doc](#)

Would you like your abstract to be considered for an oral presentation (students and post docs only)?

Yes

Metabolic network percolation provides insight into microbial fastidiousness

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We present a new metabolic network analysis method designed to provide quantitative insight into the dependence of microbial growth on the availability of specific environmental nutrients, also known as fastidiousness. Our method, which is inspired by the statistical mechanics concept of percolation theory, uses a Monte Carlo approach to quantify the average number of environmental nutrients necessary for a microbe to synthesize a specified metabolite (e.g. an amino acid) or set of metabolites (e.g. biomass). Alongside our algorithm, we devised a combinatorics-based theory which serves to clarify the mathematical underpinnings of our algorithm and its results. We have demonstrated the capacity of our method to capture the different biosynthetic capabilities of organisms ranging from *E. coli* to *M. genitalium*, two organisms with drastically different reliance on exogenously supplied nutrients. Additionally, we have more closely examined amino acid biosynthesis in *E. coli* and observed a strong correlation between the ease of biosynthesis, as calculated with our method, and the cellular composition. Furthermore, our method has been adapted towards analyzing incomplete metabolic networks automatically reconstructed from microbial genomes. Thus, it can provide biological insights into organisms based solely on their genomic information, and is a promising tool for the study of poorly characterized organisms such as currently uncultivable organisms or those from metagenomes of complex communities. Moving forward, our method can be further extended to study interactions between species, which will provide valuable insights into the nature of complex microbial communities. For example, we are currently working on using our method to understand the metabolic relationships that shape the structure and dynamics of the oral microbiome.