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## 2018 Seminar Series

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**Wednesday 14<sup>th</sup> of February  
12-1pm**

**Bio21 Institute Auditorium  
30 Flemington Road, Parkville**

**Dr Jonathan Monk**

*Systems Biology Research Group,  
UC San Diego*

### ***Comparative Systems Biology Analysis of Microbial Pathogens***

Genome-scale models of microbial metabolism have become a commonly used tool in the systems biology toolbox. These models can predict, based solely on an organism's genome sequence, its metabolic capabilities and unique phenotypes in different conditions and under unique perturbations. Furthermore, an array of in-silico methods have been developed that can be applied to these models to more deeply characterize an organism, re-engineer it and even to design effective ways to interrupt and kill it. This talk will focus on the creation and analysis of multiple genome-scale models of metabolism for different microbial pathogens. I will start with an overview of genome-scale modelling and techniques including flux balance analysis that can be used to predict an organism's metabolic capabilities. I will cover the process of building a comprehensive genome-scale model for Escherichia coli K-12 MG1655 as well as how these models are validated experimentally using gene-knockout studies and other techniques. Finally, I will describe applying these methods to build and analyze multiple genome-scale metabolic reconstructions of diverse Escherichia coli strains. Such analyses can be used to systematically elucidate strain-specific adaptations to nutritional environments. I will demonstrate that these models can be used to identify strain-specific pathogenic characteristics and unique metabolic capabilities that are related to infectious capabilities. Finally I will provide an overview of similar studies that are ongoing to study other microbial pathogens of interest including Shigella, Salmonella, S. aureus and Leptospira.