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Developing and leveraging improved RNA-Seq methodologies to explore the cellular functions and interactions that drive infectious disease

To survive and proliferate in their human hosts, microbes must rapidly alter their physiology in response to myriad environmental changes and diverse interactions with other microbes and with host cells. Often these physiological responses are mediated by changes in expression of genes that make up complex and inter-connecting transcriptional networks. RNA-Seq has emerged as a uniquely effective tool for mapping transcriptomes and profiling changes in gene expression in both microbes and eukaryotes. In this talk I will highlight some of the key methodological advances made by our group to expand the power of RNA-Seq in infectious disease research and describe several recent and ongoing studies we have undertaken that leverage this technology to study diverse aspects of microbial physiology, evolution, and pathogenesis.