

Project #02: **Mark Borodovsky** and **Huaiqiu Zhu**: *New gene finding methods for shotgun DNA sequences of microbial communities coexisting with a human host*

The recent advent of shotgun metagenomic sequencing of DNA molecules isolated from microbe communities made a revolution in the methods of exploration of microbial world. Particularly, phylogenetic and functional diversity of tens of thousands of microbial species localized and coexisting in tiny environments within a human host can now be directly surveyed and the genes critically important for host-microbe interactions can be identified. Still, the research on specialized methods of metagenomic sequence analysis is in a stage of infancy. Development of methods of DNA sequence analysis has been a major focus of research conducted by Dr. Borodovsky (Georgia Tech) and Dr. Zhu (PKU). Therefore, we propose a collaborative project to develop new computational methods and tools for gene finding in metagenomes. The quality of these new tools is expected to be sufficiently high for being selected by leading genome sequencing centers for sequence analysis of metagenomes, including the human health related metagenomes.