

GENOME: THE GIS SPEAKER SERIES

Bioinformatics Challenges In Complete Genomics And Metagenomics

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In-person @ GIS Seminar Room (L2)



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Even though the first draft human genome was generated two decades ago, many biomedically important regions (such as centromeres) represented the terra incognita of the genome sequencing until recently. The long-read DNA sequencing technologies are now transforming genome sequencing toward generating complete genomes and metagenomes. They also raised novel bioinformatics challenges that represent the key bottlenecks for the ongoing large-scale genomics and metagenomics projects. I will describe some bioinformatics challenges in complete genomics/metagenomics, discuss the recently developed approaches for their solution, show how these approaches bring us closer to the goal of complete genome/metagenome sequencing, and illustrate some applications of these approaches in metagenomics-based search for novel antibiotics.

Pavel Pevzner is Ronald R. Taylor Chair and Distinguished Professor of Computer Science and Engineering at University of California, San Diego. He holds Ph.D. from Moscow Institute of Physics and Technology, Russia. He was named Howard Hughes Medical Institute Professor in 2006. He was elected the Association for Computing Machinery (ACM) Fellow, the International Society for Computational Biology (ISCB) Fellow, the American Association for Advancement in Science (AAAI) Fellow, and the European Academy of Sciences member (Academia Europaea) member. He was awarded honorary degrees from Simon Fraser and Tel Aviv Universities, the ISCB Senior Scientist Award, and the ACM Kanellakis Theory and Practice Award. Dr. Pevzner authored textbooks "Computational Molecular Biology: An Algorithmic Approach", "Introduction to Bioinformatics Algorithms" (with Neal Jones), "Bioinformatics Algorithms: an Active Learning Approach" (with Phillip Compeau), and "Learning Algorithms through Programming and Puzzle Solving" (with Alexander Kulikov). He co-developed the "Bioinformatics" and "Data Structure and Algorithms" online specializations on Coursera with over a million enrollments since 2014.