Bioinformatics: a Servant or the Queen of Molecular Biology?

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While some experimental biologists view bioinformatics as a servant, I argue that it is rapidly turning into the queen of molecular biology. I will illustrate this view by showing how recent computational developments brought down biological dogmas that remained unchallenged for at least three decades. Specifically, I will discuss the N-end theory connecting the protein half-life with N-terminal Methionine Excision, the Master Alu Theory explaining repeat proliferation in the human genome, and Random Breakage Model of genome rearrangements.

In the second part of the talk, I will discuss a century-old dogma about the traditional classroom and describe the recent efforts to repudiate it using Intelligent Tutoring Systems. I will describe a new educational technology called a **Massive Adaptive Interactive Text (MAIT)** that can prevent *individual* learning breakdowns and outperform a professor in a classroom. I will argue that computer science is a unique discipline where the transition to MAITs is about to happen and will describe a bioinformatics MAIT that has already outperformed me. In difference from existing Massive Online Open Courses (MOOCs), MAITs will capture digitized individual learning paths of all students and will transform educational psychology into a digital science. I will argue that the future MAIT revolution will profoundly affect the way we all teach and will generate large population-wide datasets containing individual learning paths through various MAITs.

Biosketch: Pavel Pevzner is Ronald R. Taylor Professor of Computer Science and Engineering and Director of the NIH Center for Computational Mass Spectrometry 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 Fellow in 2010, the International Society for Computational Biology Fellow in 2012, and European Academy of Sciences member (Academia Europaea) in 2016. He was awarded a *Honoris Causa* (2011) from Simon Fraser University in Vancouver and the Senior Scientist Award (2017) by the International Society for Computational Biology. Dr. Pevzner authored textbooks "Computational Molecular Biology: An Algorithmic Approach", "Introduction to Bioinformatics Algorithms" (with Neal Jones) and "Bioinformatics Algorithms: an Active Learning Approach" (with Phillip Compeau). He co-developed the *Bioinformatics* and *Data Structure and Algorithms* online specializations on Coursera as well as the Algorithms Micro Master Program at edX.

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