

Q&A SESSION WITH TAMIR TULLER

At our Synthetic Biology Congress this coming November you will deliver a presentation entitled 'Computational Based Approaches for Accelerating Viral Engineering.' Why is there currently a need for new computational approaches in this field?

Engineering viruses for various biotechnological objectives is a very challenging and tedious mission: viruses tend to be populated with many confounding regulatory signals and overlapping coding regions, which makes the effect of their modification unexpected. Moreover, they have a relatively high mutation rate and undergo fast evolution, which may render their modification unstable. Furthermore, much of the viral genetic material is RNA and not DNA making its manipulation challenging. Finally, viruses undergo complex interactions with the host cell and specifically its immune system. Consequently the development of a viral product can take dozens of years and cost hundreds of millions of dollars. Integrating computational models into the process can accelerate it, via, inter alia, cheaper screening of the desired viral properties in-silico.

How can viruses be designed for useful purposes?

We design viruses via modulating various gene expression codes which are part of the viral genetic material, and often interleaved with the genetic code at the viral coding regions. We have various models that enable us to detect these codes and modify them to effect viruses according to the required biotechnological objectives. For example, we can attenuate viruses to generate live attenuated vaccines, increase to viral titer in certain cell lines to improve the production of inactivated vaccines, or improve the efficiency of viral products such as oncolytic viruses. Similarly, our algorithms can be used for optimizing the expression of transgenes that are often introduced into viruses to generate novel viral products.

Tamir Tuller,
Associate Professor,
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Tamir Tuller is an Associate Professor, the head of the Laboratory of Computational Systems and Synthetic Biology at Tel-Aviv University. He has a multidisciplinary academic background in engineering, life science, computer science, and medical science (four BSc, two MSc studies, and two PhD titles). Prof. Tuller is the author of over 130 peer reviewed scientific articles, and received numerous awards and fellowships. He performs multidisciplinary research focusing on various aspects of gene expression and specifically mRNA translation. Among others, he aims at developing novel approaches for modeling and engineering gene expression, and employs synthetic biology tools for understanding the way gene expression is encoded in the genetic material.

How do you draw upon expertise from other scientific fields?

We developed a computational-experimental pipeline for viral engineering which is based on my expertise and academic background from various scientific fields: First, we developed computational efficient algorithms for scanning large numbers of viral genomes optimization solutions. Second, we developed various in-silico biophysical simulations of diverse aspects related to gene expression that enable us to predict the effect of mutations on viral fitness. Third, the entire pipeline was designed and inspired by engineering concepts such as modularity and simplicity. Fourth, we extensively employ tools from disciplines such as molecular evolution to analyze viral genomes and detect functional genomics codes that can be designed and implemented. Finally, we employ and develop sophisticated statistical tools tailored for analyzing the different types of relevant genomic and experimental data ■

Tamir Tuller will be speaking on Day 1 of our Synthetic Biology Congress, with his talk 'Computational Based Approaches for Accelerating Viral Engineering.'