



# BIOINFORMATICS SEMINAR

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### COMPUTATIONAL APPROACHES ENABLING NON-STANDARD AMINO ACID BIOSYNTHESIS AND APPLICATION

Non-standard amino acids (nsAAs) are amino acids beyond the natural twenty building blocks used for protein synthesis. These amino acids were synthesized by chemists decades ago to test fundamental biological hypotheses or to probe biological insights. The latter application became more powerful when chemical biologists developed tools that achieve template-directed incorporation of nsAAs into proteins within living cells. In this talk, I describe how biomolecular engineers have advanced this technology to applications such as control of cell proliferation by achieving selective incorporation. I highlight computational approaches, especially computational protein design, that were critical for achieving this goal. I also describe nascent efforts in my lab to engineer biosynthetic routes to nsAAs and where bioinformatics plays a major role, such as in metabolic pathway design and optimization.

#### BIOGRAPHY

Dr. Aditya Kunjapur is an Assistant Professor in Chemical & Biomolecular Engineering at the University of Delaware, where he started his lab in January 2019. Aditya earned his bachelor's degree in Chemical Engineering from the University of Texas at Austin in 2010 and his doctoral degree in Chemical Engineering from the Massachusetts Institute of Technology in 2015. At MIT, Aditya trained in metabolic engineering under Dr. Kristala Prather. Afterwards, he conducted post-doctoral research under the supervision of Dr. George Church at Harvard Medical School. Aditya was awarded an Emerging Leader in Biosecurity Initiative (ELBI) Fellowship in 2019.

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