NOBEL SYMPOSIA SERIES

Universe

Neil Turok

Higgs Chair of Theoretical Physics, University of Edinburgh
Emeritus Director, Perimeter Institute for Theoretical Physics, Canada
Founder and Board Chair, African Institute for Mathematical Sciences

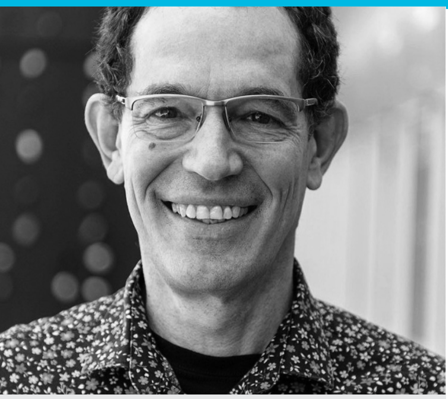
Learning the shape of the protein universe

Armita Nourmohammad

Assistant Professor of Physics at the University of Washington
Affiliate investigator, Fred Hutchinson Cancer Research Center, Seattle

NOBEL IN AFRICA
A STIAS INITIATIVE

Monday, 31 October 2022 | 13:00-14:30
3rd Floor Seminar Room, Physics Building, Westville Campus, UKZN



BIOGRAPHY

Neil Turok was born in South Africa. He founded the African Institute for Mathematical Sciences (AIMS) in 2003.

Neil's research focuses on testing and developing theories of the universe. Formerly a Professor of Physics at Princeton and of Mathematical Physics at Cambridge, he currently serves as the inaugural Higgs Chair for Theoretical Physics at the University of Edinburgh. He is also Emeritus Director of the Perimeter Institute for Theoretical Physics in Canada and Chair of AIMS International Governing Board.

ABSTRACTS

Neil Turok's lecture

Recent observations of the universe on very large and very small scales, have revealed an astonishing simplicity in its structure and basic laws. Meanwhile, fundamental theory has trended in the opposite direction, predicting a profusion of extra particles, dimensions of space and even a "multiverse," none observed. In this talk, I will outline a radically minimal and far more predictive theory which provides new explanations for the cosmos's extraordinary symmetry on large scales, for the nature of the dark matter and the role of dark energy, as well as predicting the fluctuations which seeded the formation of galaxies. It also gives us a picture of the big bang itself. I will also outline the theory's predictions, several of which will be tested in the decade ahead.

Armita Nourmohammad's lecture

Proteins are the machinery of life facilitating the key processes that drive living organisms. The physical arrangement of amino acids dictates how proteins fold and interact with their environment. Recent advances have increased the number of experimentally resolved or computationally predicted tertiary structures, however we still lack a practical understanding of how 3D structure determines the function of a protein. While machine learning has been at the forefront of protein science, the inferred models are often hard to interpret physically. In this talk I will introduce physically motivated machine learning approaches to learn interpretable models of protein micro-environments, reflecting the underlying biophysics. With these models we infer amino acid preferences given a surrounding atomic neighborhood, and predict the impact of evolutionary substitutions in proteins. Our computational approach establishes an interpretable model for how biological function emerges from protein micro-environments. The flexibility and efficiency of this approach also show promise for building generative models to design novel protein structures with desired function.

BIOGRAPHY

Armita Nourmohammad is a theoretical physicist by training. She is interested in the interplay between physics and biology, especially with regards to the complex dynamics of evolving populations. Her research comprises a broad range of topics, including non-equilibrium statistical physics, evolutionary biology, and immunology. Her research group aims to contribute to the understanding of biological systems through theoretical models and statistical inference from molecular data. Her team aims to understand the principles underlying the organization and encoding of information in the adaptive immune system, in light of host-pathogen coevolution.

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