Biomedical Informatics Grand Rounds

Wednesday, April 12, 2023 3:00 pm – 4:00 pm

Can Evolution, AI and Physics Shed Light on Complex Disease?

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Remote Access
Join Zoom Meeting https://stonybrook.zoom.us/j/95617197636?pwd=KytzZ2pVRG9SZGpKZUtpNXJISjNjZz09
Meeting ID: 956 1719 7636 Passcode: 924293
In-Person talk: Medical and Research Translation (MART) Building, Room location 7M-0602

Bio: Dr. Lichtarge is a Professor of Molecular and Human Genetics at Baylor College of Medicine, where he holds the Cullen Foundation Chair. His laboratory combines computational methods with experiments to investigate how genetic variations disrupt biological mechanisms or facilitate useful engineering designs. His contributions include developing equations that express basic evolutionary principles and algorithms that map functional sites in protein structures and assess the impact of coding variants. These findings have led to insights into the molecular basis of G protein signaling and the genetic basis of bacterial drug resistance and complex diseases, such as cancer and neurodegenerative disorders. His recent work integrates genomics, machine learning, and physics to characterize Alzheimer's Disease. Dr. Lichtarge trained in Mathematics and Physics at McGill University, Biophysics and Medicine at Stanford, and Internal Medicine, Endocrinology, and Molecular Pharmacology at UCSF.

Abstract: Life is complex and appears difficult to capture through simple equations. However, our research suggests that a basic model of evolution can obey such equations and predict several genomic features, including genes involved in complex human diseases such as cancer, autism, and Alzheimer's among other examples. One approach feeds this evolutionary model into machine learning, while another approach expands on the model by coupling it to statistical physics. Our findings suggest that organisms explore evolutionary fitness landscapes by maximizing entropy while remaining within a narrow energy band. In practice, this provides a quantitative framework for identifying impactful genes and variants from selected populations , potentially informing mechanistic and therapeutic studies towards personalized medicine.

Educational Objects:
- Impact analyses of variant of unknown significance
- Analyses of genetic drivers of complex diseases
- Genetic contributions to Alzheimer's disease
- Use of evolutionary information in clinical contexts

Disclosure Statement: The faculty and planners have no relevant financial relationship with ineligible companies whose primary business is producing, marketing, selling, re-selling, or distributing health care products used by or on patients.

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