EKU Department of Mathematics & Statistics

Colloquium

presenting...

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A Mathematical Graph–Theoretic Model of Single Point Mutations Associated with Sickle Cell Anemia Disease

Mutations in the amino acid sequence of a protein might prevent a protein from assuming the appropriate conformation needed for proper protein functions. Many diseases such as cystic fibrosis and sickle cell anemia disease, COVID-19, and others arise from point mutations in the respective proteins. How mutations, especially point mutation might lead to a global devastating consequence on a protein remains an intellectual mystery hence an improved understanding might offer insight into protein engineering, with potential therapeutic intervention in view.

We present mathematical graph-theoretic modeling interfaced with unsupervised machine learning as a tool to gain meaningful insight into how single point mutations in a protein might lead to different phenotypes of diseases. Our results suggest this tool should be added to the toolbox for drug discovery for diseases arising from single point mutations.

Wednesday, February 16th, 2022
2:30 – 3:20 p.m.   Wallace Bldg. Room 348