



Public Lecture Offerings

Artificial Intelligence in Clinical Medicine: What makes a good machine learning model for clinical applications?*

Although applications of Machine Learning (ML) are now pervasive in the clinical literature, ML has yet to be embraced by the clinical community. So, what constitutes a good machine learning model for clinical applications? Certainly, a necessary condition for the success of any machine learning model is that it achieves an accuracy that is superior to pre-existing methods. In the healthcare sphere, however, accuracy alone does not, nor should it, ensure that a model will gain clinical acceptance. In view of the fact that no model, in practice, has 100% accuracy, attempts to understand when a given model is likely to fail should form an important part of the evaluation of any machine learning model that will be used clinically. Moreover, the most useful clinical models are explainable in the sense that it is possible to clearly articulate why the model arrives at a particular result for a given set of inputs. In this talk I will expand upon these challenges that make the creation of clinically useful ML models particularly difficult, and discuss ways in which they can be overcome.

Modeling Unfolded States of Proteins*

A typical introductory course in biochemistry describes most proteins as adopting a well-defined structure, which is defined as the "native state". It is now apparent, however, that proteins are not static molecules in that their structures fluctuate at physiologic temperature. Indeed, normal fluctuations in protein structure can be significant, and in the extreme cases, proteins need to adopt unfolded "flexible" conformations to carry out their normal functions. Characterizing these unfolded states, therefore, is needed if one wishes to have a comprehensive understanding of protein

function. Yet, since the direct observation of unfolded states is difficult to achieve experimentally, additional methods are needed to fully characterize these proteins. In this talk I will discuss a combination of computational and experimental methods for studying unfolded states of proteins and demonstrate how these approaches can be leveraged to gain insight into the pathogenesis of common diseases such as Alzheimer's disease and atherosclerosis.

***Request:** I will need to project a PowerPoint presentation from a PC.

Classroom Discussion Topics

The topics listed above can be explored in more detail and I can also talk about:

- **Building Interpretable Machine Learning Models for Clinical Applications**
- **Atherosclerosis: A disease of protein unfolding?**