The Medical College of Wisconsin

Division of Biostatistics

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A Statistical Research Seminar
Talk By:

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Title: Structural Bioinformatics and the Next Frontiers of Genetic Data Interpretation

ABSTRACT: Clinical genomics sequencing has revolutionized healthcare by providing more precise tools for defining, diagnosing, and treating genetic diseases, as well as unraveling the genetic component of complex diseases. Because these methods are relatively new, key information regarding genetic variation remains uninterpreted and therefore unable to be used in healthcare or even further research. For example, existing clinical workflows estimate the impact of DNA changes on protein function by their effect on linear protein sequence. This approach fails to accommodate changes to protein structural (3D) and time-dynamic (4D) properties, including stability, chemistry, and local mobility, that could impair or dysregulate the protein. We believe it is imperative to develop an approach that systematically evaluates many protein properties and how they are each altered by genomic variants, to reach the right interpretation.

Computational tools for simulating the detailed effects of mutations are used in basic science fields but have not yet been parameterized and standardized for more wide application to clinically observed and cancer-associated genetic variants. Thus, improved tools are needed for genomic data interpretation. The Zimmermann lab focuses on the development, translation, and application of molecular modeling