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Protein function and structure prediction

Because proteins are the workhorses of the cell, defining much of who we are, our disease susceptibility, and more, scientists in both academia and industry are devoting enormous resources and time to understanding protein function and structure. Partly due to the cost and difficulty of experimental ("wet-bench") methods, computational methods of predicting protein function and structure are being increasingly relied upon.

In this talk, I will present some new methods for the prediction of protein function and structure, using a combination of information-theoretic and probabilistic tools. These statistical approaches have been shown to be very powerful for the recognition of related family members, prediction of key functional positions in proteins, construction of evolutionary trees, and identification of functional subfamilies.