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Biological data like measured response of protein levels to presence of virus or disease, or experimentally identified protein complexes and pathways, contain many complex interactions. Hypergraphs are a natural mathematical structure to model and explore complex multi-relations and topology helps discover higher dimensional features within data. This talk will explore our recent work to understand how analogs of traditional network science concepts, like centrality and spectral clustering, can be used in the context of hypergraphs for discovery of central biological pathways, characterization of unknown transcription factors, and comparison of diseases with different pathogenesis. (Received September 10, 2019)