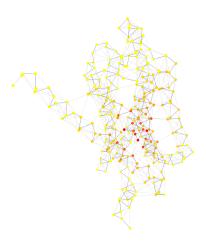
Network-based analysis of membrane protein structures

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Aim: Proteins are made of chains of aminoacids folded into 3-dimensional structures. They rely on this assembly to be able to perform their function, whether is is catalysis, transport, recognition, shaping or any other function necessary for the cell. Progress in structural biology has led to the resolution of many protein structures. Here we describe proteins as networks and use network analysis tools to find similarities and particularities of proteins, and to understand how the details of the 3-d assembly participate in shaping their function

Context and impact: This research project aims at exploiting data analysis tools (in this case, tools from network theory) for biological applications. Understanding protein function has implications for drug design and other aspects of biotechnology.

What you will do in practice: You will be given a set of membrane protein structures (G-protein coupled receptors, kinases, enzymes and ion channels) and will analyze them using python scripts. Basic scripts will be provided and one of your roles will be to modify them to fit the needs of the projects. You will interpret the results using molecular visualization tools.