Protein interaction network (PIN) studies in different organisms have provided a wealth of data. However, the reliability of the datasets and the predicted interactions have become clear concerns in evaluating these studies. Therefore, most studies of protein networks neglect the structural and chemical aspects of each interaction. [1]

A new study [2] by Mark Gerstein’s group at Yale University provides an additional dimension to protein interaction networks in the form of structural modeling that characterizes interactions by using atomic-resolution information from three-dimensional protein structures. This more rigorous approach (see figure) is intended to increase the reliability of the reported protein interactions.

Beginning with the yeast protein interaction network, the approach involves first removing low confidence interactions, and then incorporating structural and chemical information on protein interactions. 3D structural modeling also is applied to exclude possible configurations of complexes that appear mutually exclusive, and thus narrow the range of possible interactions.

The result is termed the structural interaction network (SIN), which consists of 873 proteins and 1269 interactions, 438 which were found to be mutually exclusive. In initial analyses of the SIN, notable properties include a maximum of 14 interaction partners per “hub” protein, in contrast to earlier interactome studies reporting much higher ranges. The approach also distinguishes between “multi-interface” hubs that involve simultaneously possible interactions and “singlish-interface” hubs with mutually exclusive interactions, and shows that the former are more likely to be essential, co-expressed, and show lower evolutionary rate (dN/dS). The SIN dataset and updates can be found at http://sin.gersteinlab.org.

References