



**CALIFORNIA SCIENCE & ENGINEERING FAIR  
2018 PROJECT SUMMARY**

<b>Name(s)</b> <b>Rishi M. Desai</b>	<b>Project Number</b> <b>S0810</b>
<b>Project Title</b> <b>New Cartographic Network Visualization Technique for Analyzing Alignments of Protein-Protein Interaction Networks</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives/Goals</b> In cartographic visualization, nodes are represented as horizontal lines and edges as vertical lines. This method provides advantages over node-link diagrams because nodes and edges cannot overlap. However, there is no software currently available that utilizes cartographic visualization of network alignments. I developed a network visualization tool based on cartographic visualization to analyze the alignments of protein-protein interaction (PPI) networks. This tool was added as a new feature to BioFabric, network visualization software developed by the Institute for Systems Biology, Seattle.</p> <p><b>Methods/Materials</b> I calculated topological measures such as Edge Coverage (EC) and Symmetric Substructure Score (S3) with the alignment of PPI networks rat to yeast. I generated several alignments between the PPI networks yeast2K to yeast5K to analyze objective functions in alignment algorithms. I devised novel measures Node Group Distance (NGD) and Link Group Distance (LGD) to automate topological analysis.</p> <p><b>Results</b> Using the width of link groups, I calculated the <math>EC = .54</math> and <math>S3 = .41</math> for the alignment between rat and yeast. The topological similarity between the two PPI networks can be visualized with the relative sizes of link groups. Researchers can alter the alignment so certain nodes do or do not align to each other. Cartographic visualization helps compare topology between the yeast2K to yeast5K alignments generated by different objective functions. I found that objective functions that utilize a combination of measures produce alignments closer to the perfect alignment than those that utilize only one measure. Alignments generated with a combination of measures consistently produced lower NGD and LGD values than those that utilized only one measure such as S3 and Importance.</p> <p><b>Conclusions/Discussion</b> I developed a novel method using cartographic visualization to analyze PPI network alignments. I am the first to use cartographic visualization in the context of network alignments, and any other software currently available uses node-link diagrams. My layout shows topological measures, network connectivity, and allows researchers to improve alignment algorithms. I created novel numerical measures for the automation of topological analysis.</p>	
<b>Summary Statement</b> I developed a novel software tool based on cartographic visualization that allows researchers to analyze topology in the alignments of protein-protein interaction networks.	
<b>Help Received</b> Mr. Longabaugh at Institute for Systems Biology, Seattle, and Prof. Hayes at UC Irvine provided guidance and valuable comments.	