**Introduction:**

With increasingly more data becoming available, there is much more opportunity for the analyses of cellular processes in ways that were unimaginable before this wealth of information. One particular dataset which is of great importance is protein activity tracked over time. Analyzing phosphoproteomic data can help identify the protein signaling networks that occur within the cell. When a stimulus response affects a cell, there is a cascade of protein interactions that occur from the stimulus as the cell adapts to its new environment. This cascade can lead to a variety of effects from conformational changes to providing a regulatory role in downstream events.

**Why analyze protein interaction networks?**

In evaluating protein interaction networks, one could learn what proteins are involved for particular cellular responses. Knowing the subnetwork of proteins involved, one could potentially know which proteins to inhibit, for example, in order to prevent a particular cellular response from occurring.

**Hypothesis/Research Question:**

Is the Temporal Pathway Synthesizer effective in using temporal phosphoproteomic data to determine the osmotic stress response protein signaling pathway in yeast?

**Experimental/Project Design:**

* Prepare yeast phosphorylation and network data from mass spectrometry to run the Omics Integrator software for the identification of an initial coarse network. This software uses the Prize-Collecting Steiner Forest algorithm to identify the potential networks based on node prizes and edge costs.
* Use the time series phosphorylation data to better understand the possible interactions in the prospective networks obtained from the Omics Integrator software. Using the time series data, elimination of possible paths from the initial coarse network would be possible, and a more directed network becomes much more likely.
* Assess the quality of the predicted yeast signaling pathway using pathway databases and related literature.

**Expected Results:**

The Temporal Pathway Synthesizer will predict which protein interactions are used to transmit information from the osmotic stress response receptor proteins to the downstream proteins that undergo phosphorylation changes. The number of significantly phosphorylated proteins is far greater than those traditionally considered to be osmotic stress pathway members. Therefore, it is expected that the predicted network will partly overlap with components of the known pathway and also reveal many new connections.