**Temporal phosphorylation and network analysis of yeast signaling**

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**Abstract**

Current methods for identifying protein interaction networks due to a cellular stress response do not completely utilize all of the data that has now become available. The computational method, Temporal Pathway Synthesizer (TPS), uses temporal phosphoproteomic data to identify signaling pathways. Using this newfound temporal phosphorylation data, TPS can determine pathways by checking all possible pathways from the receptor node, and eliminate any potential paths that do not match the temporal data. TPS is used here to analyze the osmotic stress signal transduction pathways, and to determine whether or not the method is successful in identifying the potential proteins involved in the stress response compared to the literature already known. The results indicate that TPS is effective in its determination of the signaling pathway, but the methods also have room for improvement.