

Abstract Submitted  
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**Dynamic network analysis of protein interactions**<sup>1</sup> EIVIND AL-  
MAAS, Lawrence Livermore Natl Lab, JOYA DERI, Lawrence Livermore Natl Lab  
and Stanford University — Network approaches have recently become a popular tool  
to study complex systems such as cellular metabolism and protein interactions. A  
substantial number of analyses of the protein interaction network (PIN) of the yeast  
*Saccharomyces cerevisiae* have considered this network as a static entity, not taking  
the network's dynamic nature into account. Here, we examine the time-variation  
of gene regulation superimposed on the PIN by defining mRNA expression profiles  
throughout the cell cycle as node weights. To characterize these network dynamics,  
we have both developed a set of novel network measures as well as studied previ-  
ously published measures for weighted networks. We expect that our approach will  
provide a deeper understanding of protein regulation during the cell cycle.

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