

Abstract Submitted
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Dynamic network analysis of protein interactions¹ EIVIND ALMAAS, 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 previously 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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