a network analysis of three yeast cell populations in starvation and exponential growth conditions. A high-level analysis of the modular structure of these networks suggests that quiescent cells are significantly under-annotated, highlighting the need to study these cells. Our analysis suggests that the non-quiescent cells share more characteristics with exponential cells as compared to quiescent. Analysis of individual subgraphs indicates that quiescent and non-quiescent cells exhibit similarities in their mechanisms to adapt to glucose starvation. However, there are processes specific to quiescent cells such as sporulation, which suggest alternative response mechanisms that might be active in these cells. Finally, we find that non-quiescent hubs are enriched in homologs of human disease genes. In summary, our network-based analysis has identified both previously known and novel biological processes that are important in these cells, giving a finer understanding of the mechanisms conserved and specific to these cells.

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