

Abstract Submitted
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Network topological analysis reveals the functional cohesiveness for the newly discovered links by Yeast 2 Hybrid approach SUSAN GHIASSIAN, CCNR, Northeastern University, SAM PEVZNER, THOMAS ROLLAND, Dana Farber Cancer Institute, MURAT TASSAN, University of Toronto, ALBERT LASZLO BARABASI, CCNR, Northeastern University, MARK VIDAL, Dana Farber Cancer Institute, CCNR, NORTHEASTERN UNIVERSITY COLLABORATION, DANA FARBER CANCER INSTITUTE COLLABORATION — Protein-protein interaction maps and interactomes are the blueprint of Network Medicine and systems biology and are being experimentally studied by different groups. Despite the wide usage of Literature Curated Interactome (LCI), these sources are biased towards different parameters such as highly studied proteins. Yeast two hybrid method is a high throughput experimental setup which screens proteins in an unbiased fashion. Current knowledge of protein interactions is far from complete. In fact the previous offered data from Y2H method (2005), is estimated to offer only 5% of all potential protein interactions. Currently this coverage has increased to 20% of what is known as reference HI In this work we study the topological properties of Y2H protein-protein interactions network with LCI and show although they both agree on some properties, LCI shows a clear unbiased nature of interaction selections. Most importantly, we assess the properties of PPI as it evolves with increasing the coverage. We show that, the newly discovered interactions tend to connect proteins that have been closer than average in the previous PPI release. reinforcing the modular structure of PPI. Furthermore, we show, some unseen effects on PPI (as opposed to LCI) can be explained by its incompleteness.

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