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A Network Approach to Rare Disease Modeling SUSAN GHIASSIAN, SABRINA RABELLO, AMITABH SHARMA, CCNR Northeastern University, OLAF WIEST, University of Notre Dame, ALBERT-LASZLO BARABASI, CCNR Northeastern University — Network approaches have been widely used to better understand different areas of natural and social sciences. Network Science had a particularly great impact on the study of biological systems. In this project, using biological networks, candidate drugs as a potential treatment of rare diseases were identified. Developing new drugs for more than 2000 rare diseases (as defined by ORPHANET) is too expensive and beyond expectation. Disease proteins do not function in isolation but in cooperation with other interacting proteins. Research on FDA approved drugs have shown that most of the drugs do not target the disease protein but a protein which is 2 or 3 steps away from the disease protein in the Protein-Protein Interaction (PPI) network. We identified the already known drug targets in the disease gene's PPI subnetwork (up to the 3rd neighborhood) and among them those in the same sub cellular compartment and higher coexpression coefficient with the disease gene are expected to be stronger candidates. Out of 2177 rare diseases, 1092 were found not to have any drug target. Using the above method, we have found the strongest candidates among the rest in order to further experimental validations.

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