Data-Driven Approaches for Drug Repurposing

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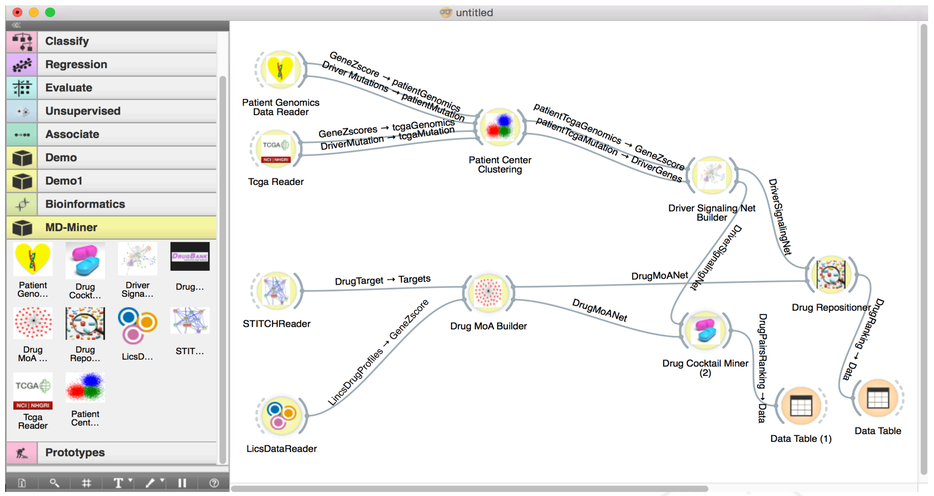
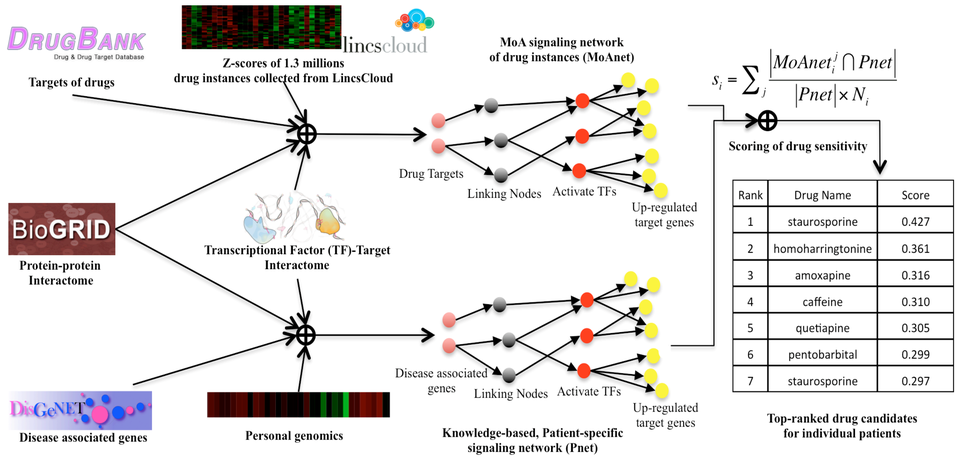
Due to advances in next generation sequencing (NGS) technologies and corresponding reductions in cost, it is now attainable to investigate genome-wide gene expression and variants at a patient-level, so as to better understand and anticipate heterogeneous responses to therapy. Consequently, it is feasible to design personalized drug treatment based on personal genomics data. However, there is a lack of reliable computational approaches for predicting effective drugs for individual patients. In our lab, we are developing data-driven computational approaches, and an open-source, visual programming computational platform to facilitate the fast development of drug repositioning approaches integrating personal genomics data with public available big data of pharmacogenomics.



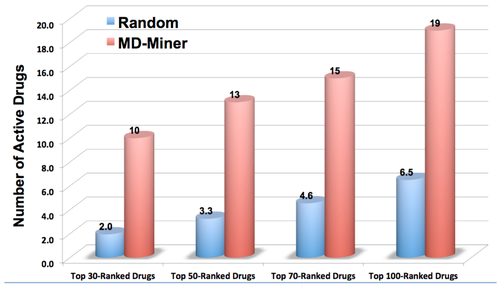
MD-Miner: an open source, visual programming computational platform (no such platform exists specifically designed for personalized drug discovery) to enable the following: 1) help collect, clean, format and integrate diverse data sets (time-consuming and nontrivial); 2) provide completed computational pipelines for predicting personalized drugs (germane to teaching and training new team members); 3) make methods development easy, fun and fast (even for those who are not computer-savvy) by visual programming to build a pipeline, similar to assembling LEGO toys. It is designed to help both clinical and bioinformatics researchers to develop and discover personalized precision medicine in a fast manner.

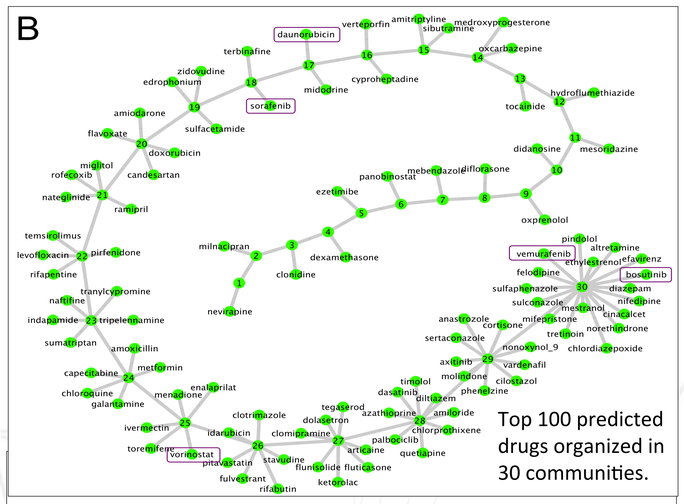
Acknowledgement:
We would like to thank the support of Biomedical Informatics (BMI) Department, summer intern program of BMI, Translational Data Analytics (TDA).

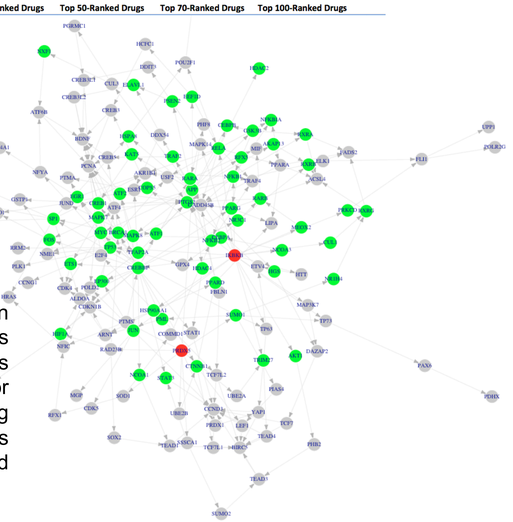


Rank	Drug Name	Score
1	staurosporine	0.427
2	homoharringtonine	0.361
3	amoxapine	0.316
4	caffeine	0.310
5	quetiapine	0.305
6	pentobarbital	0.299
7	staurosporine	0.297

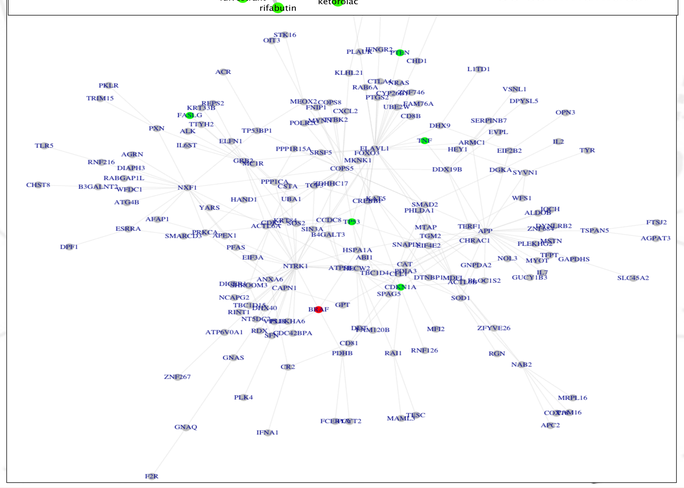
Method Overview of MD-Miner for drug repurposing.



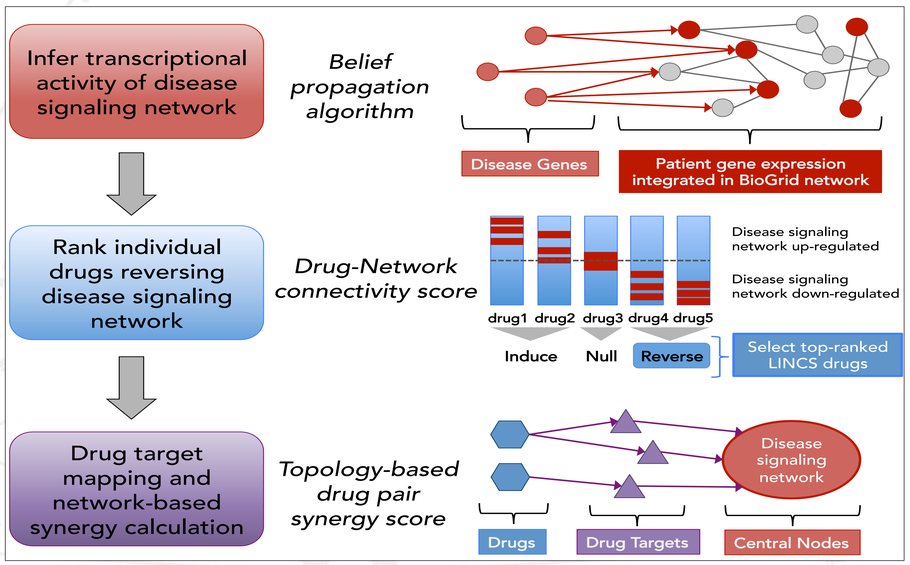




MoAnet of Auranofil instance on A549 cell line. There are 121 genes (nodes) and 214 interactions (edges). Red, gray and green color represents drug targets, linking genes and common genes appeared in both Pnet of PC-3 and MoAnet of Auranofil instance.



Drug target and melanoma disease signaling network for vemurafenib + vorinostat drug combination predicted by SynGeNet. Nodes highlighted in red and green represent gene targets of the first and second drug of the combination, respectively. Cyan nodes represent drug target genes shared by both drugs paired in the combination.



Method Overview of SynGeNet drug combination prediction approach integrating disease signaling network and transcriptomics data.