

A short horizontal bar with a teal segment on the left and an orange segment on the right.

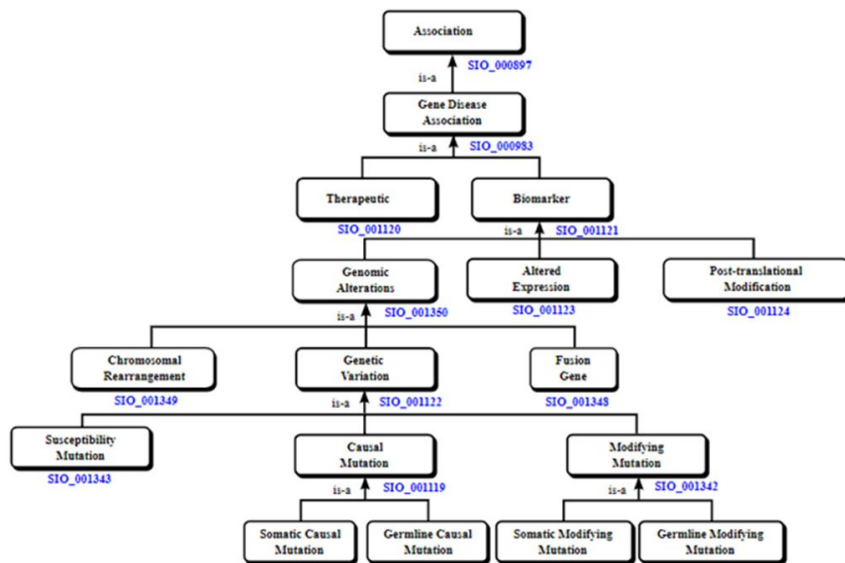
# Exploration and Analysis of Gene-Disease Associations

Arun Agarwal, Anna Yannakopoulos, Arjun Krishnan



# Introduction

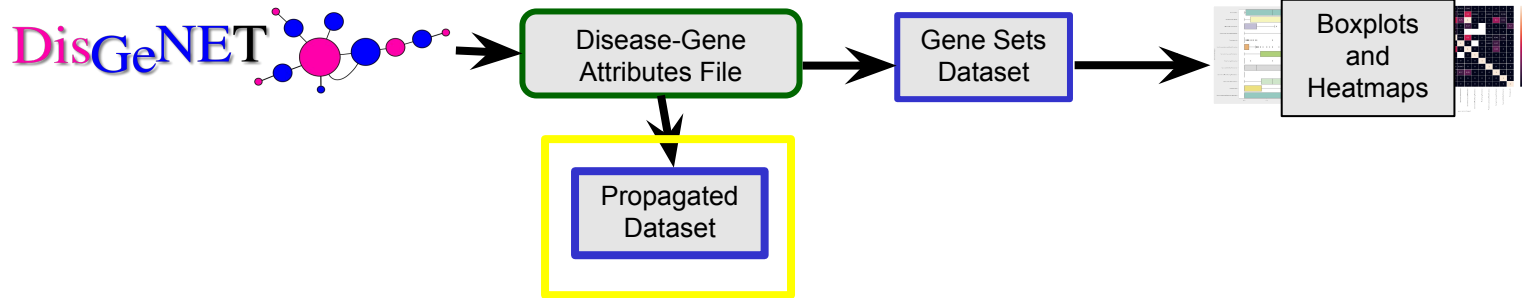
- Many diseases arise due to disruptions of multiple genes
- To work towards cures, the human genome has been studied through various experimental methods that provide different understandings of the disease's genetic cause
- **Hypothesis:** The genomic basis of complex diseases can be understood on a holistic level through the exploration and combination of genetic data from distinct sources, experimental methods, and association types
- DisGeNET: database used with human gene-disease associations



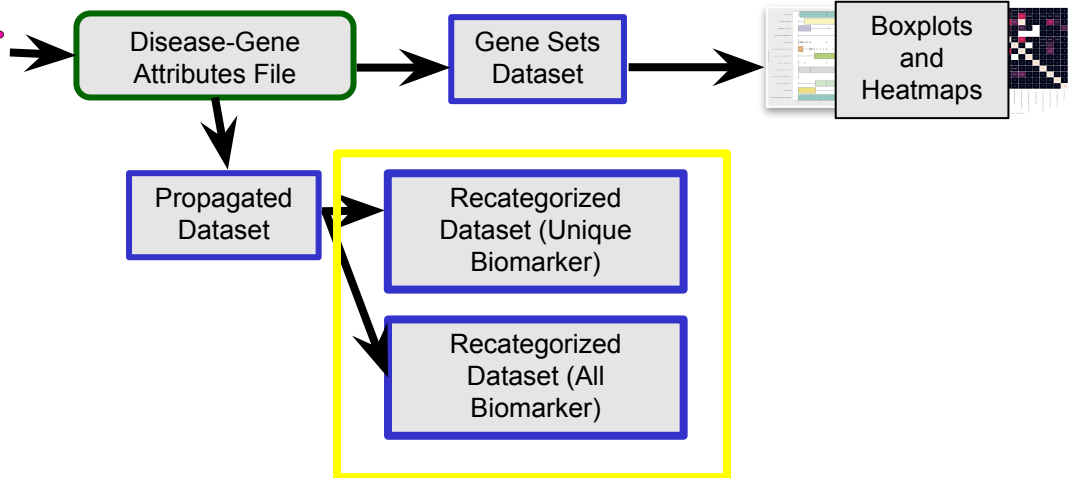
# Association Type Exploration



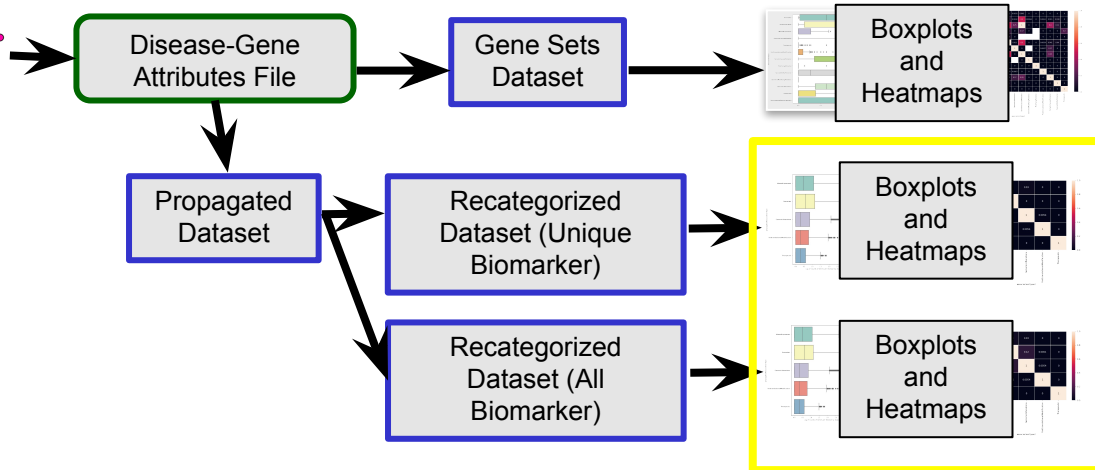
# Association Type Exploration



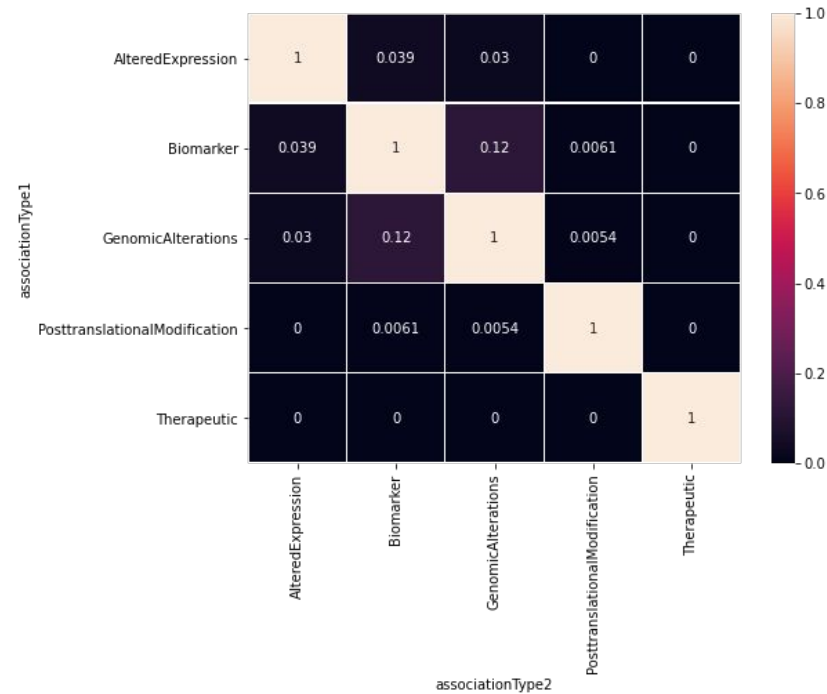
# Association Type Exploration



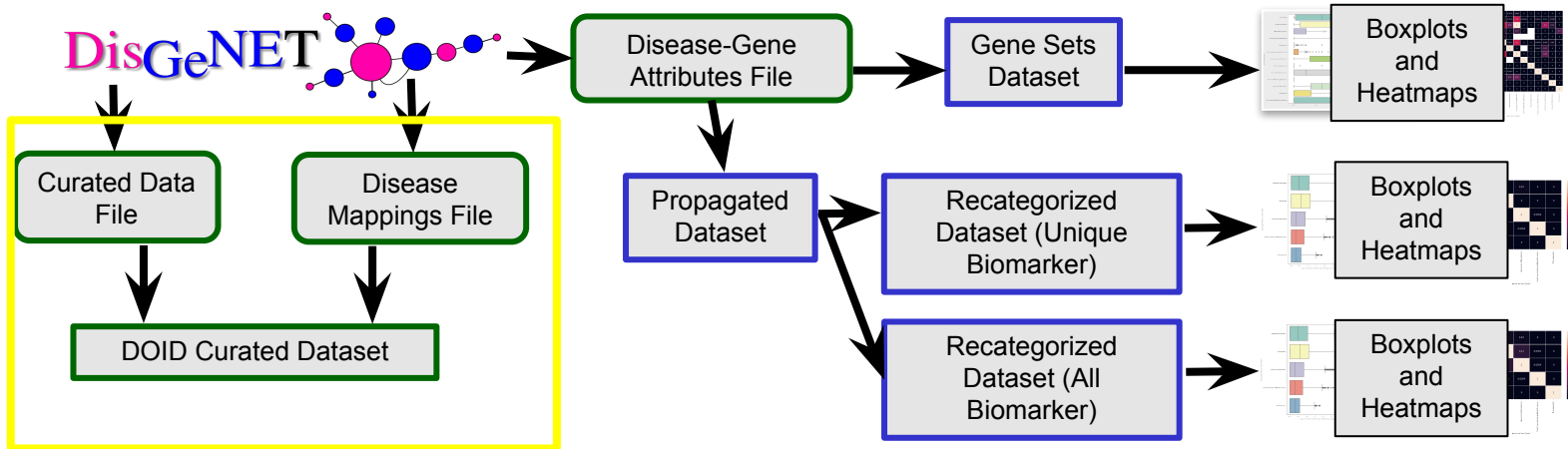
# Association Type Exploration



## Heatmap of Median Correlation Between Gene Sets for Chosen Association Types

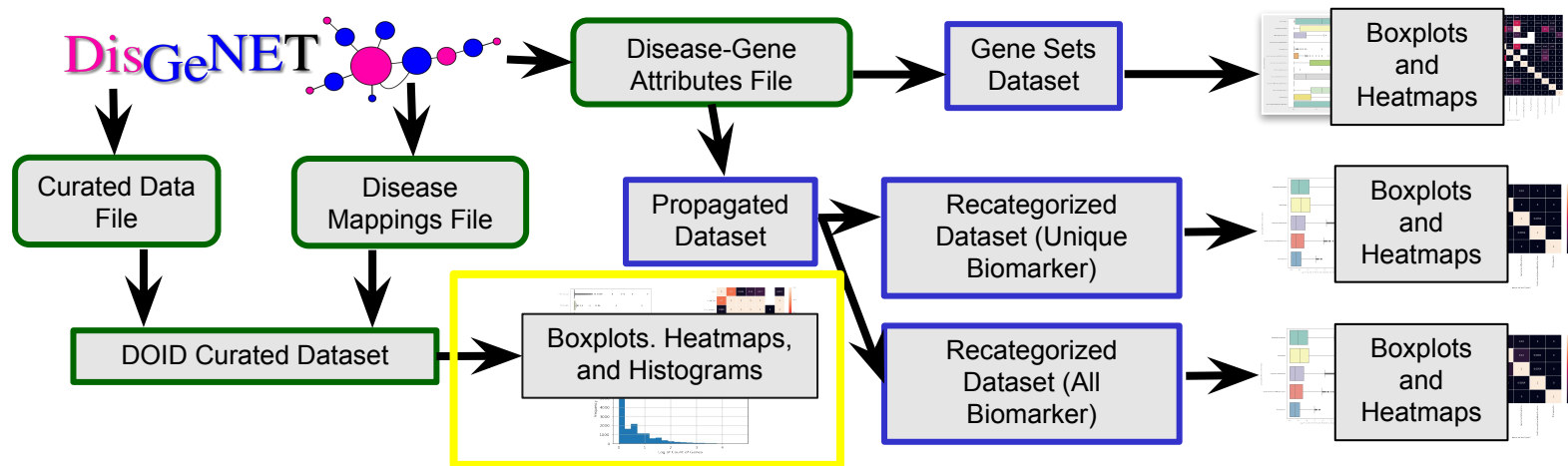


# Sources Exploration

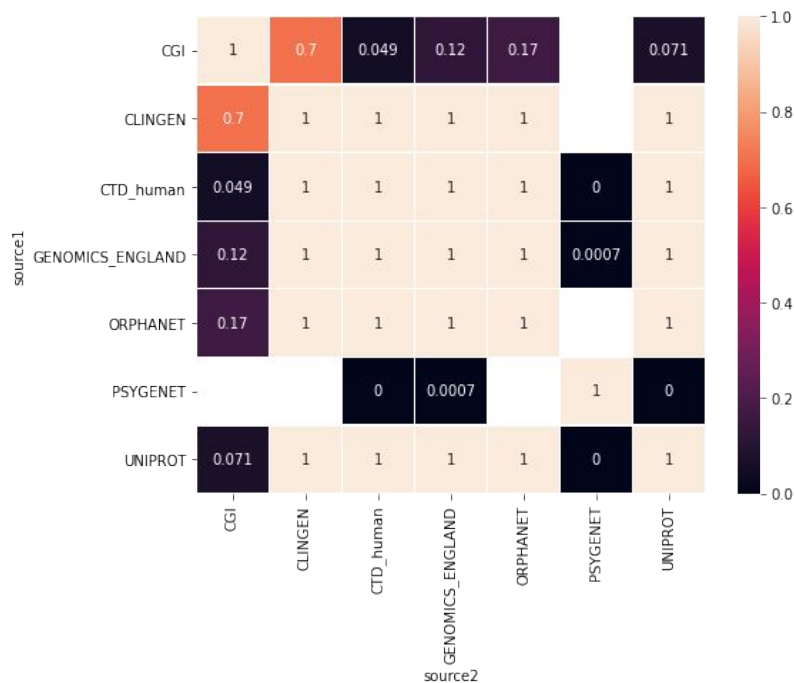




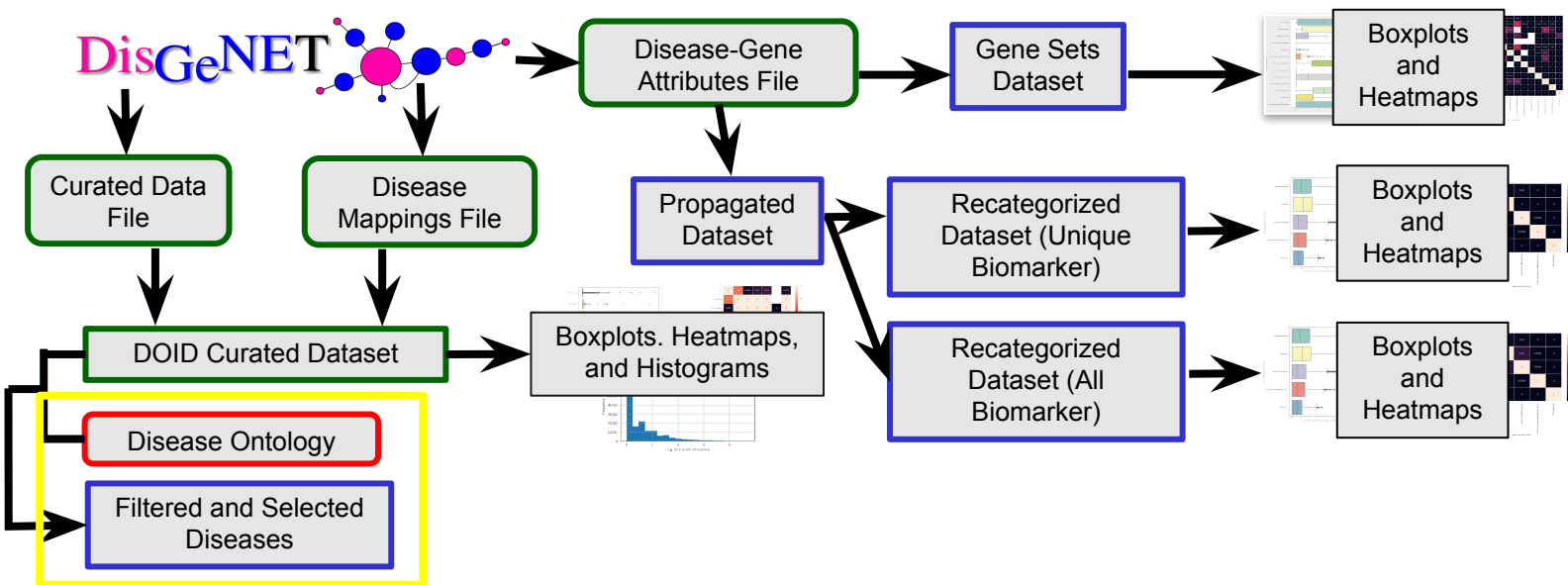
# Sources Exploration



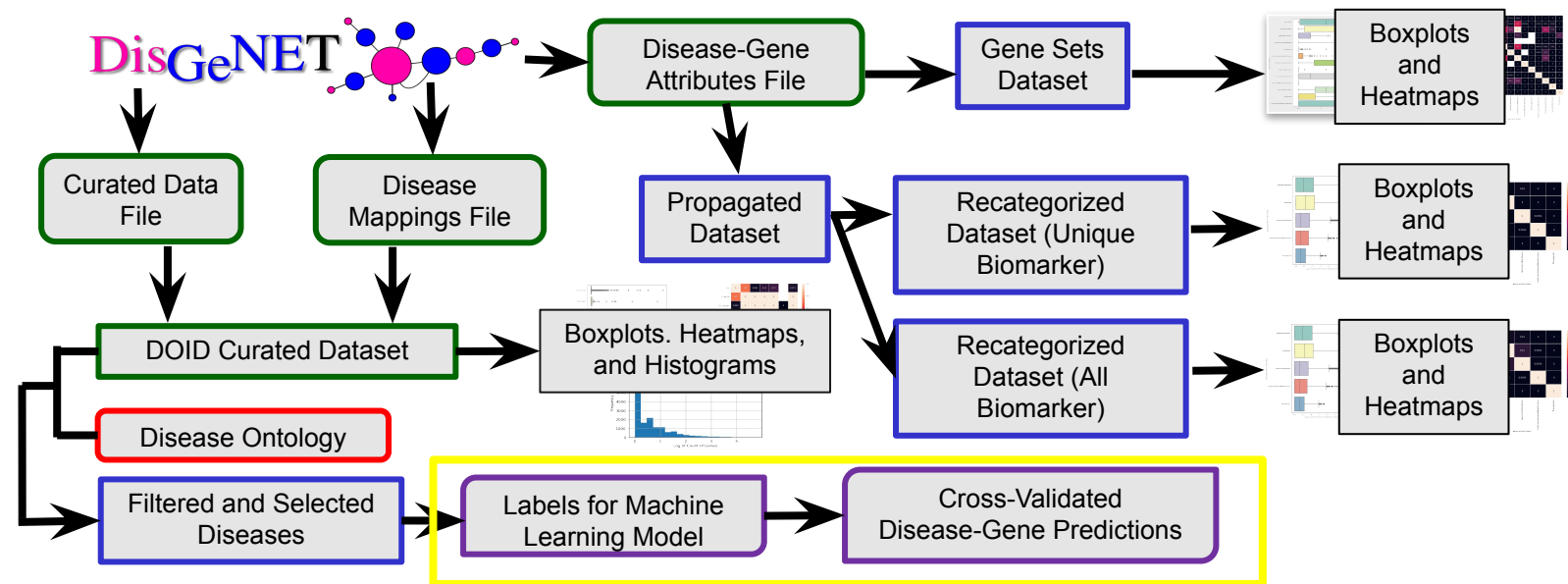
## Heatmap of Median Correlation Between Gene Sets for All Sources



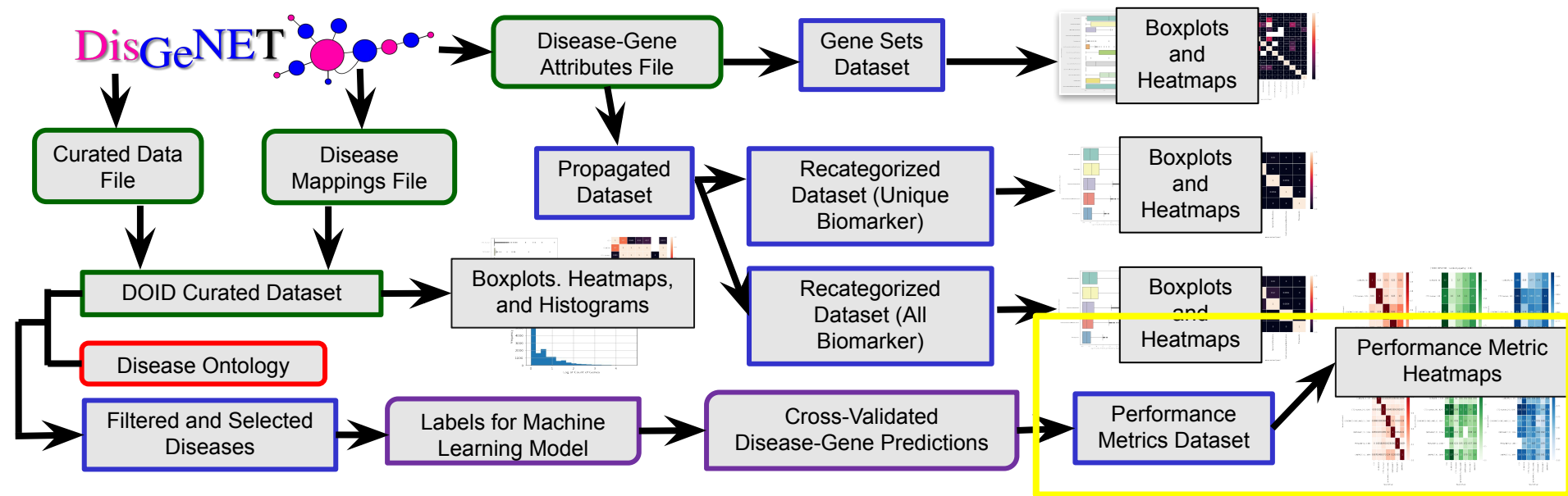
# Sources Exploration



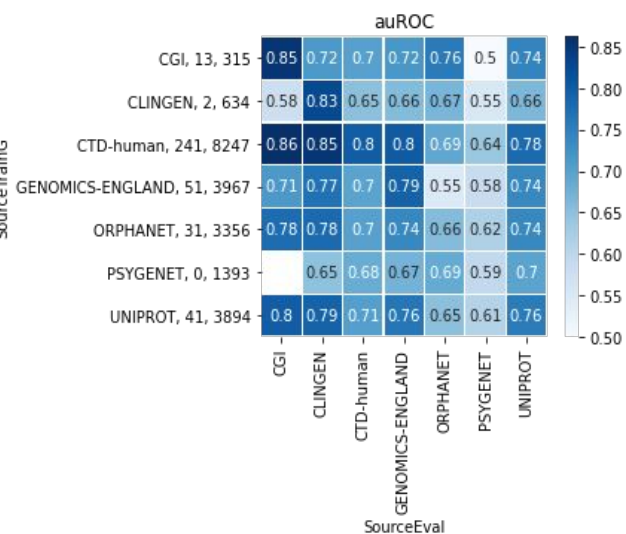
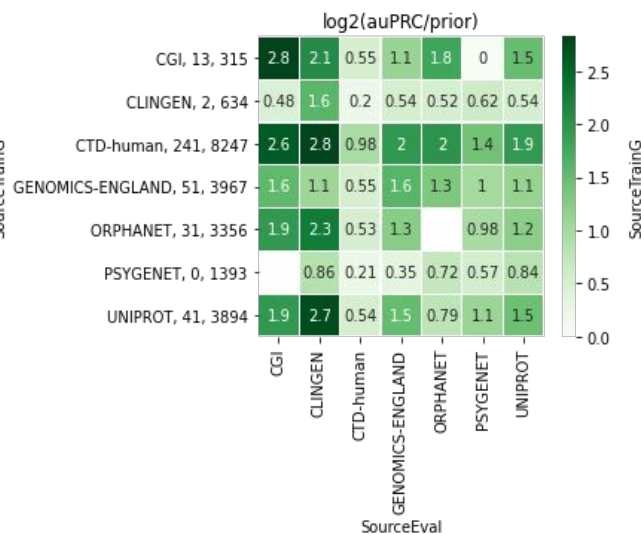
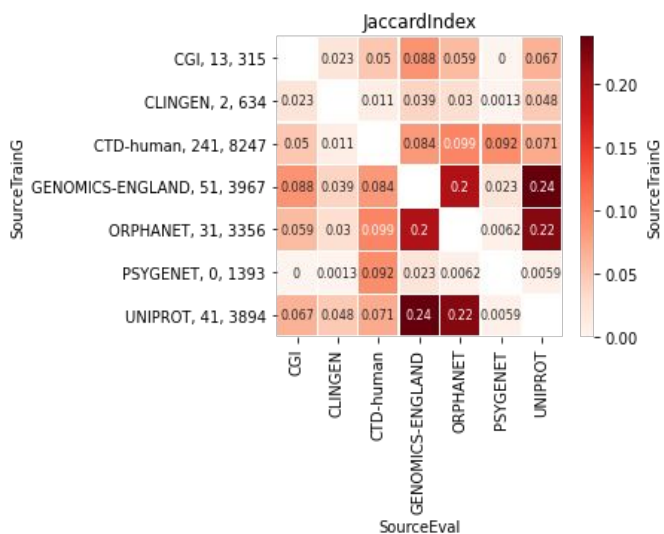
# Sources Exploration



# Sources Exploration



# Heatmaps of Median Correlation Score Between Gene Sets, $\log_2(\text{auPRC}/\text{prior})$ Score, and auROC Score for All Sources





## Conclusion

We tried to answer:

1. Do different experimental methods provide the same view of the underlying biology, or do they present different aspects of it?
2. Can models trained on one experimental method predict the genes associated to another?



## Next Steps

1. Create an ensemble model
2. Make my work available for further disease study