Network Reconciliation Approach to Extracting Similarly and Differentially Regulated Pathways of Gene Expression

Ravi Sood

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TODOS:
- Normalize sums
- Threshold, s.t. max(size) ≥ 100
- separate + and - subgraphs
- Summary of consensus functions in subgraphs
1 Introduction

2 Prior Work

3 Methods

4 Results

Figure 1: First Figure: shows that weighted average homogeneity of the returned subnetworks increases somewhat as the difference threshold (the amount of difference in expression levels between nodes in the reconciled network and nodes in the ex vivo network above which nodes are returned in subnetworks) increases. The homogeneity is also generally greater when the ex vivo network is weighted higher in the reconciliation, perhaps because this simulates the effect of having a higher difference threshold (fewer nodes are further away from the ex vivo values)

5 Conclusion

“I always thought something was fundamentally wrong with the universe” [1]

References