

Exploring the Role of Visual Analytics in the Design and Management of Multidisciplinary Translational Teams

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Abstract

Numerous institutions conducting translational research have assembled teams to enable the two-way translation of scientific discoveries between bench, clinical, and community-based research. However, the design and management of such teams can be a challenge given the wide range of goals and disciplines involved, often resulting in an explosion of textual information. Here we explore the role of bipartite visual analytics to enable the comprehension of multiple team variables in a single representation. A bipartite network analysis of 11 multidisciplinary translational teams consisting of 119 members from 26 different affiliations revealed patterns related to team overlap, homogeneity, and size. Besides helping to comprehend the topology of the teams, the results led to hypotheses about inter- and intra-team dynamics, which could lead to more effective approaches for designing and managing translational teams.

Introduction

A wide range of institutions that conduct translational research¹ have explored different models to assemble and support translational teams of researchers. However, the comprehension and tracking of team information is a challenge often because of the many variables and relationships involved. Here we explore whether a bipartite network of teams and members could lead to new insights into the design and management of translational teams.

Method and Results

We used a bipartite network² where nodes represented 11 teams and 119 members, and edges between the nodes represented team membership. The colors of the nodes represented members' departmental affiliations, and the size of each node was proportional to the number of connecting edges, so teams with many members were larger compared to those that had fewer members. The nodes were laid out using the *Kamada Kawai*² algorithm suitable for networks up to 500 nodes. The algorithm pushes together nodes that share many connections and pushes apart nodes that do not, resulting in a layout that approximates the relationship between nodes. The network was presented to principal investigators (PIs) of a Clinical and Translational Award (CTSA) site, who collaboratively analyzed the network for insights related to team design and management.

The analysis led to three insights about team structure. (1) **Team Overlap:** Four teams in the center of the network shared four or more members, three teams shared at least two members, and two teams shared no members. The shared members were mostly researchers who specialized in methods (e.g., biostatistics, proteomics analysis), or were PIs of the CTSA. (2) **Team Homogeneity:** Three teams were more homogenous in terms of member affiliation compared to the rest. For example, 7 out of 10 members from the Pediatric Otitis Media team were from the Department of Pediatrics. (3) **Team Size:** The teams ranged from 22 members (Obesity) to 5 members (MFM). The overall observations led to the hypothesis that shared members could enhance inter-team exchange of ideas warranting a closer inspection of the role such researchers played in motivating generalizable methodologies.

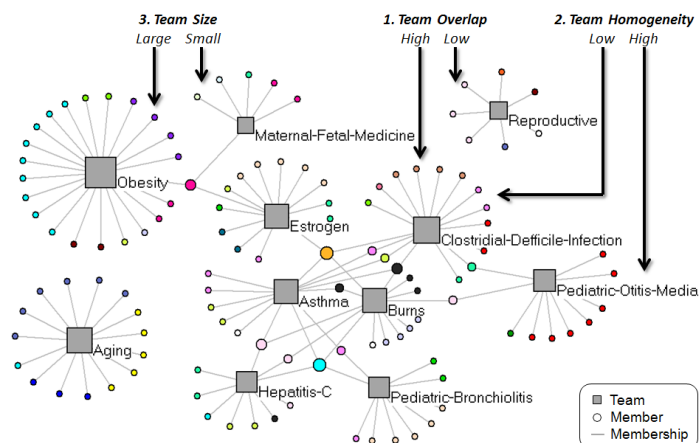


Figure 1. A bipartite network of 11 translational teams and 119 members revealed patterns related to team overlap, size, and homogeneity.

Furthermore, there appeared to be a correlation between team heterogeneity and the number of shared members, which could be a precursor for higher productivity in translation research. The results suggest that while networks of a much larger size might be less easy to comprehend, a bipartite network of ~130 nodes shows promise in enabling PIs to derive new insights about the design and management of translational teams.

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References

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