Yale SCHOOL OF PUBLIC HEALTH
Biostatistics

Graph Matching and Network Inference in Biological Applications

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ABSTRACT

While many multiple graph inference methodologies operate under the implicit assumption that an explicit vertex correspondence is known across the vertex sets of the graphs, in practice these correspondences may only be partially or errorfully known. In these instances, graph matching---find an alignment between the vertex sets of the graphs that best preserves common structure across graphs---can be used to recover the lost vertex alignment before performing subsequent inference. We study the theoretical and practical impact that noisily observed vertex correspondences can have on applications in hypothesis testing, joint graph clustering, and noisy induced subgraph detection.

12:00 Noon, Tuesday, September 25, 2018
47 College Street, Room 106B
11:45 AM - Lunch served outside Room 106B