

(Robust) Seeded graph matching

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 Given two graphs, the Graph matching problem (GMP) seeks to find an alignment of the vertex sets of the two graphs that best preserves the connectivity structure of the graphs

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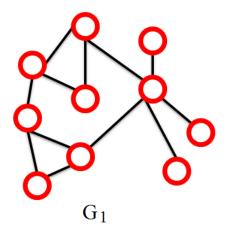


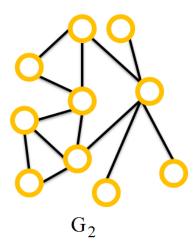
THIRTY YEARS OF GRAPH MATCHING IN PATTERN RECOGNITION

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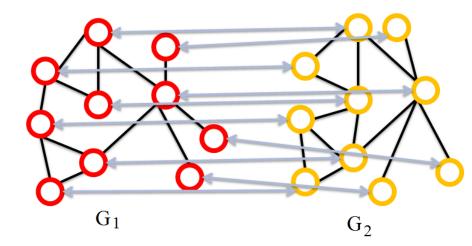
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- Given two graphs, the Graph matching problem (GMP) seeks to find an alignment of the vertex sets of the two graphs that best preserves the connectivity structure of the graphs
- In the seeded graph matching problem, we are further provided subsets of the vertices (Seeds)

$$S_1 \subset V_1, S_2 \subset V_2$$

and a seeding function

 $\phi \subset S_1 \times S_2$, i.e. $(u, v) \in \phi \Rightarrow$ u and v are "matched"

Goal: Leverage ϕ to match the remaining vertices

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- Our proceudre: The Joint Optimization of Fidelity and Commensurability (JOFC) graph matching algorithm of Lyzinski et al. (2014)
- Adapted from the manifold matching methodologies of Priebe et al. (2013)
- Is robust
- Briefly, the JOFC algorithm proceeds as follows:
 - 1. Jointly embed the seeded vertices into a common Euclidean space
 - 2. Separately out-of-sample embed the nonseeded vertices
 - 3. Match the embedded nonseeded vertices—this is equivalent to solving the generalized assignment problem

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Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

We begin with ∆₁ and ∆₂, dissimilarity representations of the graphs G₁ and G₂ resp.

Let

 $X_1^{(1)}, X_2^{(1)}, \ldots, X_{s_1}^{(1)}$ be the embedded seeded vertices of G_1 ,

and

 $X_1^{(2)}, X_2^{(2)}, \dots, X_{s_2}^{(2)}$ the embedded seeded vertices of \mathcal{G}_2

- We want the embedding to simultaneously preserve:
 - 1. The within graph dissimilarities amongst the seeded vertices (fidelity)
 - 1b. The across graph relationship provided by the seeding between non-matched seeded vertices (separability)
 - The across graph relationship given by the seeding (commensurability)



Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

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- We want the embedding to simultaneously preserve:
 - 1. The within graph dissimilarities amongst the seeded vertices i.e. we wish to minimize the within graph squared fidelity error of the embedding given by

$$arepsilon_{F_1}^2 := \sum_{i,j} \left(d(X_i^{(1)}, X_j^{(1)}) - \Delta_1(i,j) \right)^2$$

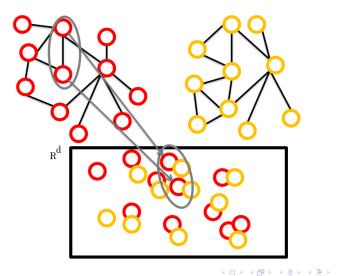
and

$$arepsilon_{F_2}^2 := \sum_{i,j} \left(d(X_i^{(2)}, X_j^{(2)}) - \Delta_2(i,j) \right)^2$$

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Minimize the squared fidelity error of the embedding

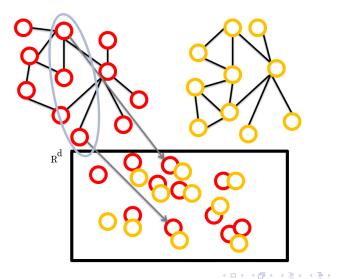


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Minimize the squared fidelity error of the embedding



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Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

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- We want the embedding to simultaneously preserve:
 - 1b. The dissimilarities amongst the non-matched seeded vertices across graphs

i.e. we wish to minimize the across graph squared separability error of the embedding given by

$$\varepsilon_{S}^{2} := \sum_{\substack{i, j \text{ s.t. } i \text{ and } j \text{ are non-matched} \\ \text{seeded vertices}}} \left(d(X_{i}^{(1)}, X_{j}^{(2)}) - \delta(i, j) \right)^{2}$$

 δ here is an unknown across graph dissimilarity, and must be imputed or treated as missing data



Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

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- We want the embedding to simultaneously preserve:
 - 2. The across graph relationship given by the seeding i.e. we wish to minimize the within graph squared commensurability error of the embedding given by

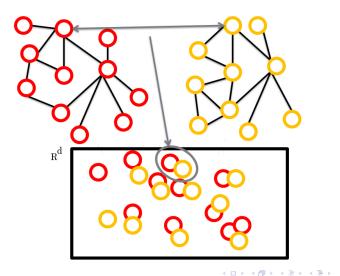
$$\varepsilon_{C}^{2} := \sum_{\substack{i, j \text{ s.t. } i \text{ and } j \text{ are matched} \\ by the seeding}} \left(d(X_{i}^{(1)}, X_{j}^{(2)}) - \delta(i, j) \right)^{2}$$

Again δ here is an unknown across graph dissimilarity, though if *i* and *j* are matched by the seeding, it is reasonable to impute $\delta(i, j) = 0$

Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

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2. Minimize the squared commensurability error of the embedding



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- ► We embed the seeded vertices using the SMACOF algorithm of de Leeuw (1977)—a version of weighted MDS
- With a judicious choice of weightings here, SMACOF seeks to minimize

$$w(\epsilon_{F_1}^2 + \epsilon_{F_2}^2 + \epsilon_S^2) + (1 - w)\epsilon_{C^2}$$

In our applications, we found best performance with w = 0.8; see Adali et al. (2013) for motivation Graph Matching JOFC Summary Summary JOFC

- We next out-of-sample embed the unseeded vertices of G_1 $(\{Y_i^{(1)}\})$ and of G_2 $(\{Y_i^{(2)}\})$ using the weighted MDS procedure of Tang et al. (2013)
- Through a judicious choice of weightings, we seek to minimize the stress function

$$\sigma(\mathbf{Y}) = \sum_{i} \sum_{j} \left(d(X_i^{(1)}, Y_j^{(1)}) - \Delta^{(1)}(i, j) \right)^2 \\ + \sum_{i} \sum_{j} \left(d(X_i^{(2)}, Y_j^{(2)}) - \Delta^{(2)}(i, j) \right)^2$$

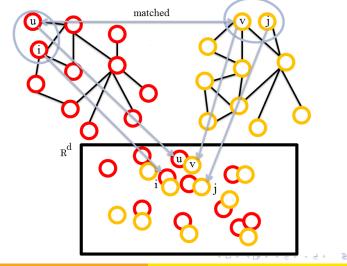
i.e. we wish to preserve the within graph dissimilarities between the seeded and unseeded vertices

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Then match embedded vertices based on Euclidean distance: closer together=more likely to be matched

Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

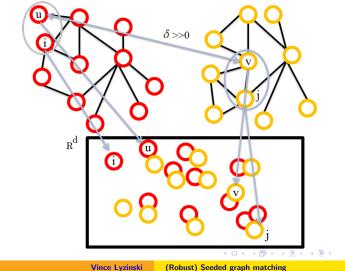
Suppose i ∈ V(G₁) and j ∈ V(G₂) are unseeded vertices that should be matched to each other



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Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

Suppose i ∈ V(G₁) and j ∈ V(G₂) are unseeded vertices that should NOT be matched to each other



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We then match the unseeded embedded vertices by minimizing

$$\sum_{i,j \text{ unseeded vertices}} d(Y_i^{(1)}, Y_j^{(2)}).$$

matched by M

over all matchings $M \subset V(G_1) \times V(G_2)$ of the unseeded vertices

 This is equivalent to a generalized assignment problem— NP-hard in general, but are good approximation algorithms



- Ex Matching C. elegans connectomes
 - The C. elegans nervous system is believed to be composed of 302 labelled vertices (279 with synapses to other neurons)
 - There are two types of connections between neurons: electrical and chemical
 - We match the chemical connectome to the electrical connectome to understand the extent to which connectivity structure alone is enough to identify neurons across the connectomes

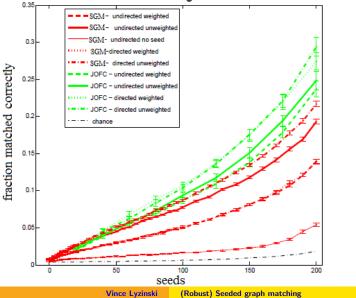
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Embedding the seeded vertices Out-of-sample embedding the unseeded vertices Why this works? Results

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- This procedure is flexible enough to handle:
 - 1. $|V(G_1)| \neq |V(G_2)|$ —allow for many-to-many, many-to-one or many-to-none matchings in the embedded graphs
 - 2. Weighted directed graphs—use a dissimilarity that allows for weightedness and directedness in the graphs for the embedding
 - The case of "soft" seeds—suitably weight the MDS embeddings
- Is easily modified for vertex classification
- Working on scaling the SMACOF subroutine—would lead to our algorithm scaling

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