

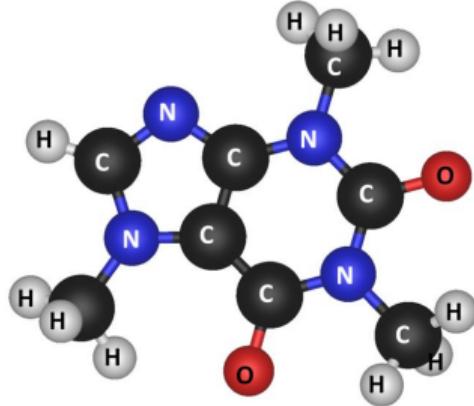
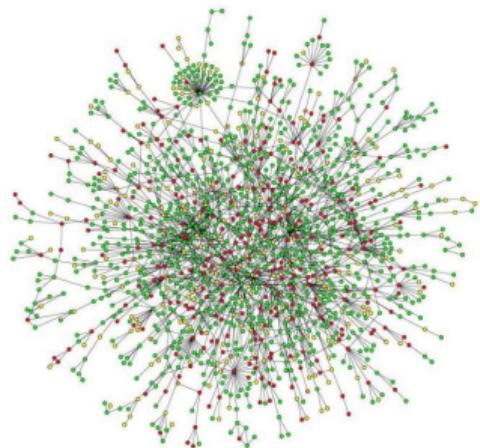
Gromov-Wasserstein Learning: A New Machine Learning Framework for Structured Data Analysis

Hongteng Xu

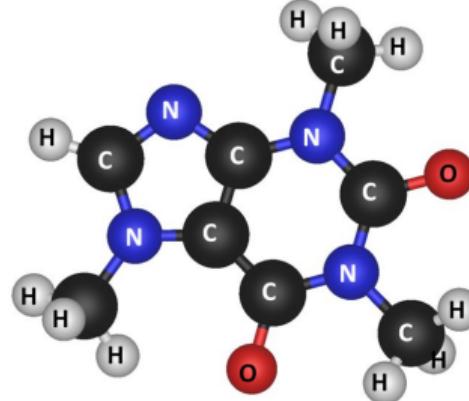
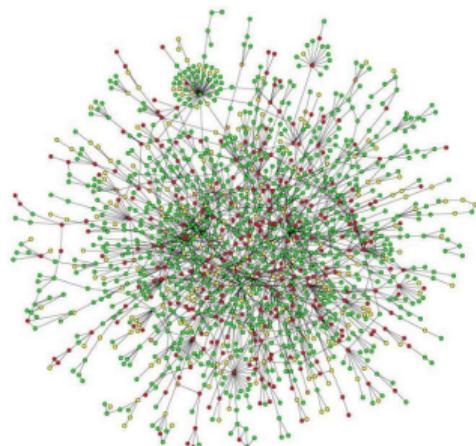
Infinia ML Inc. and Duke University



Structured data analysis



Structured data analysis



≡ Google Scholar

"structured data" OR "graph" OR "network" OR "molecule" AND "learning"

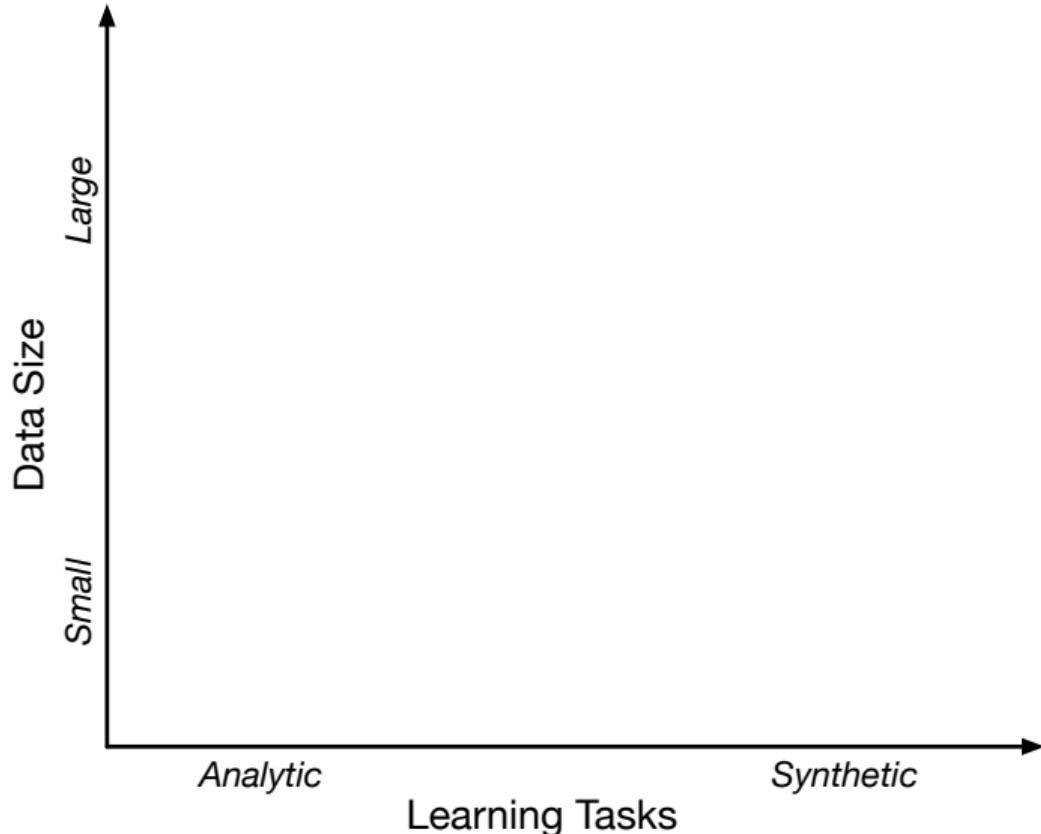


Articles

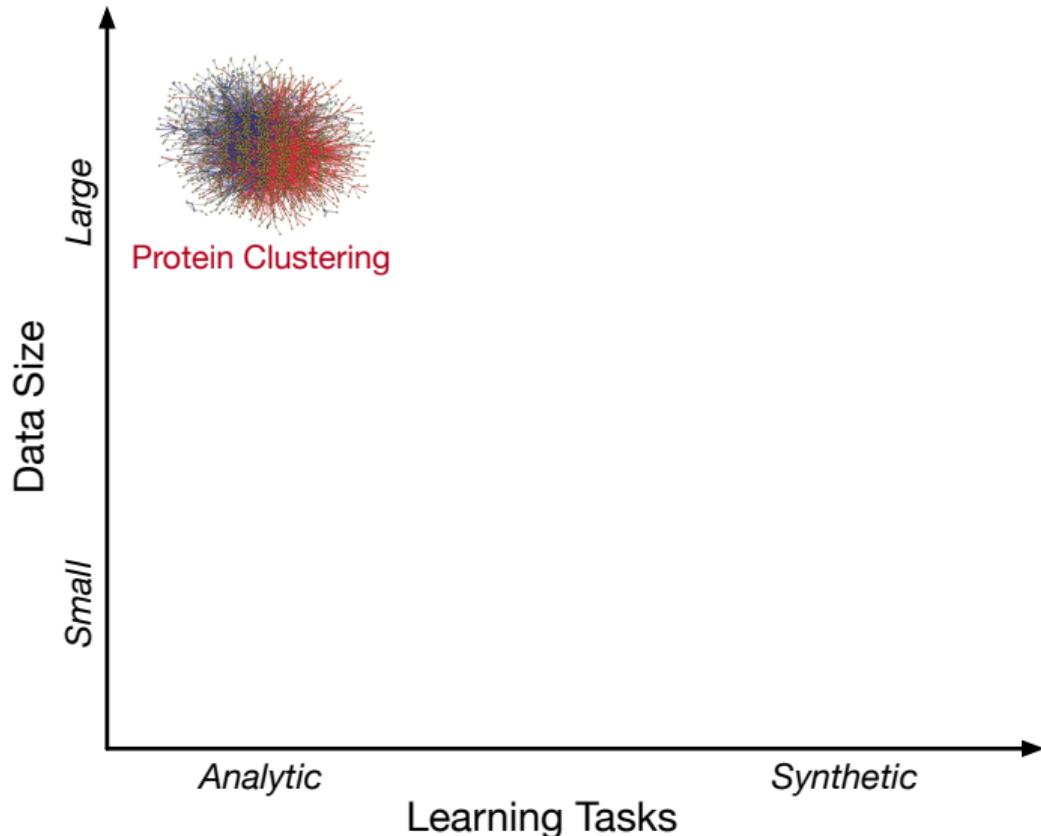
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Extract knowledge from relations effectively and efficiently.

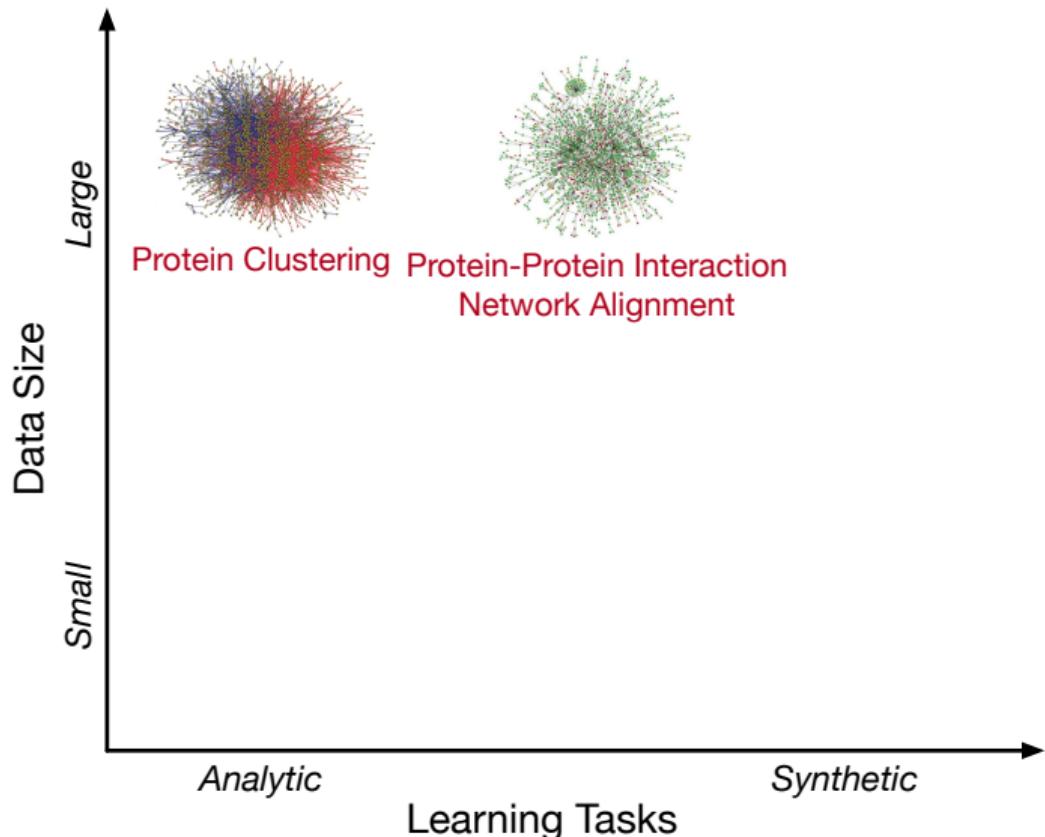
The space of problems



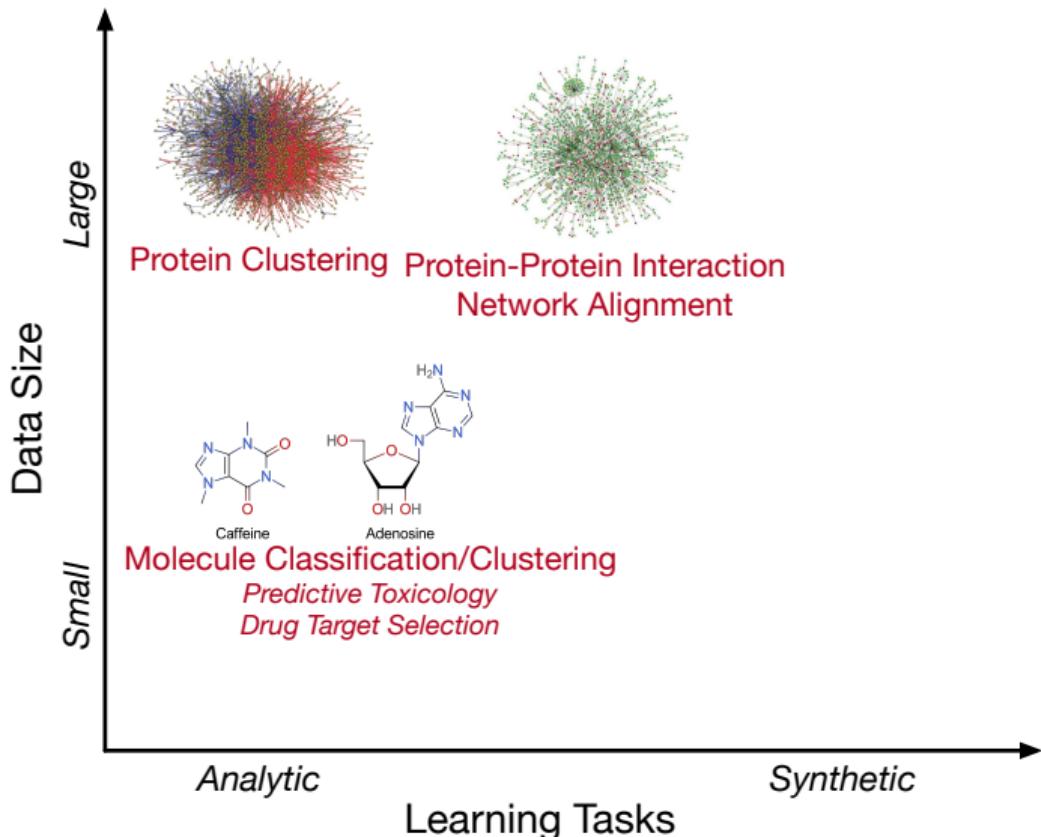
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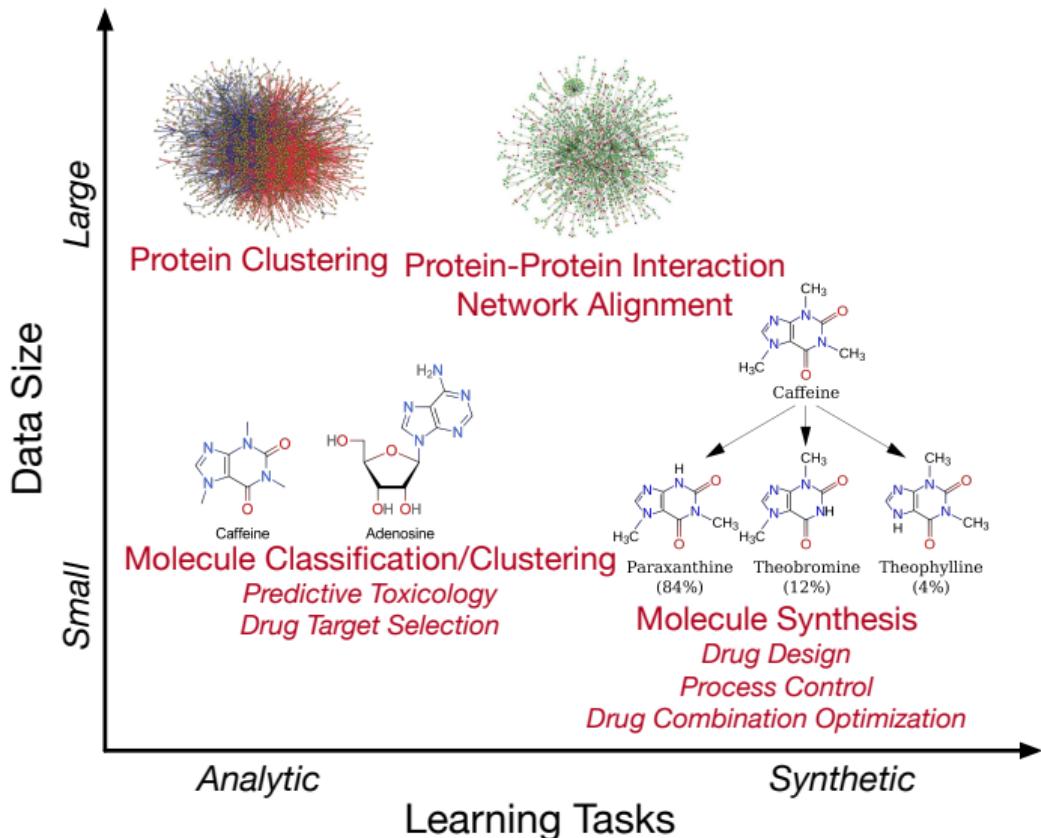
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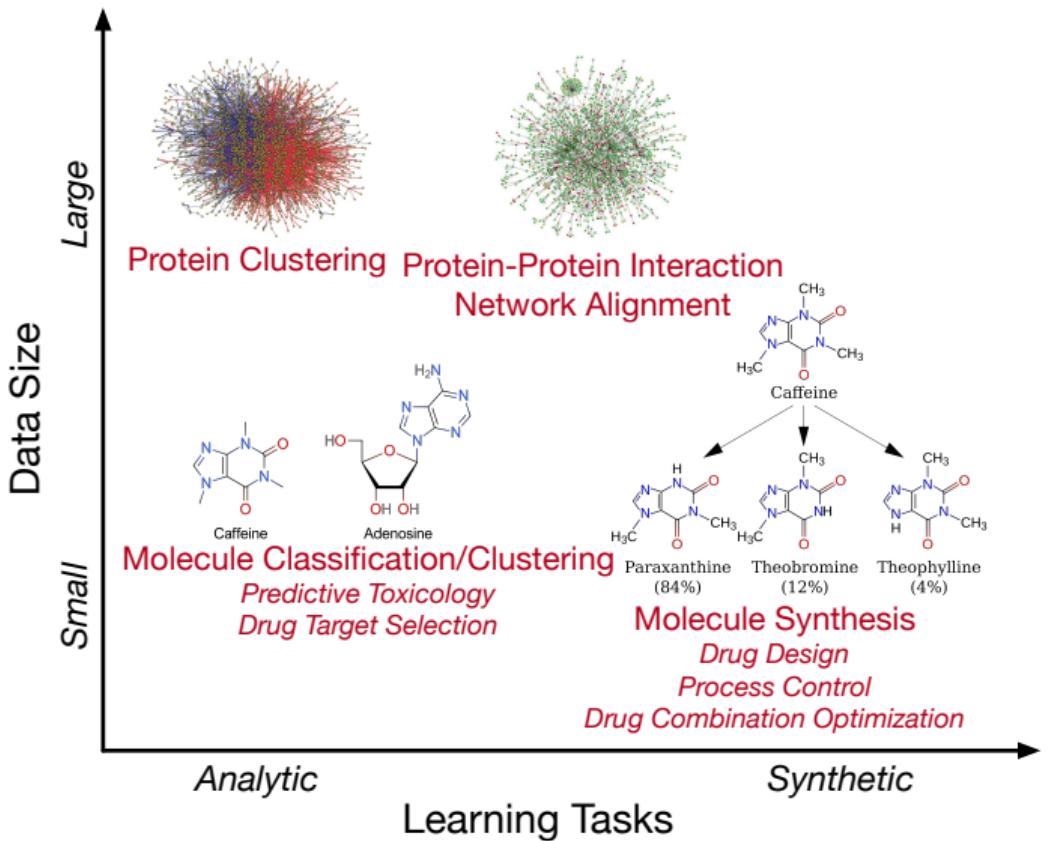
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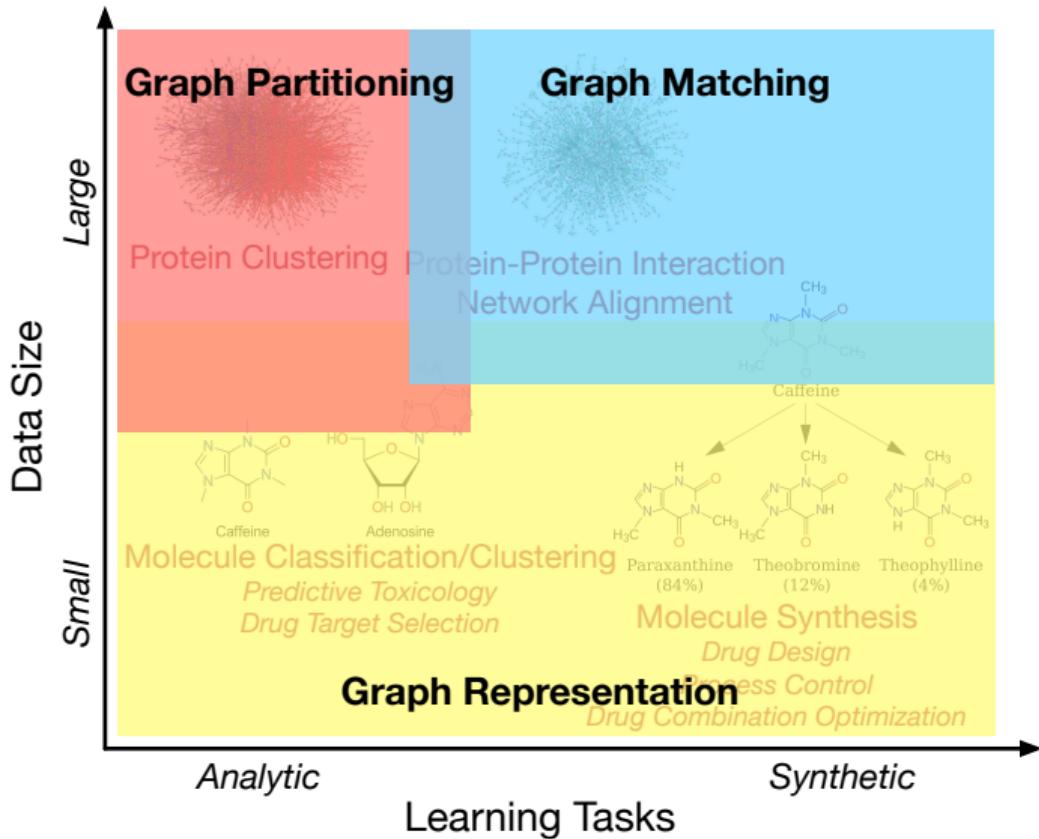
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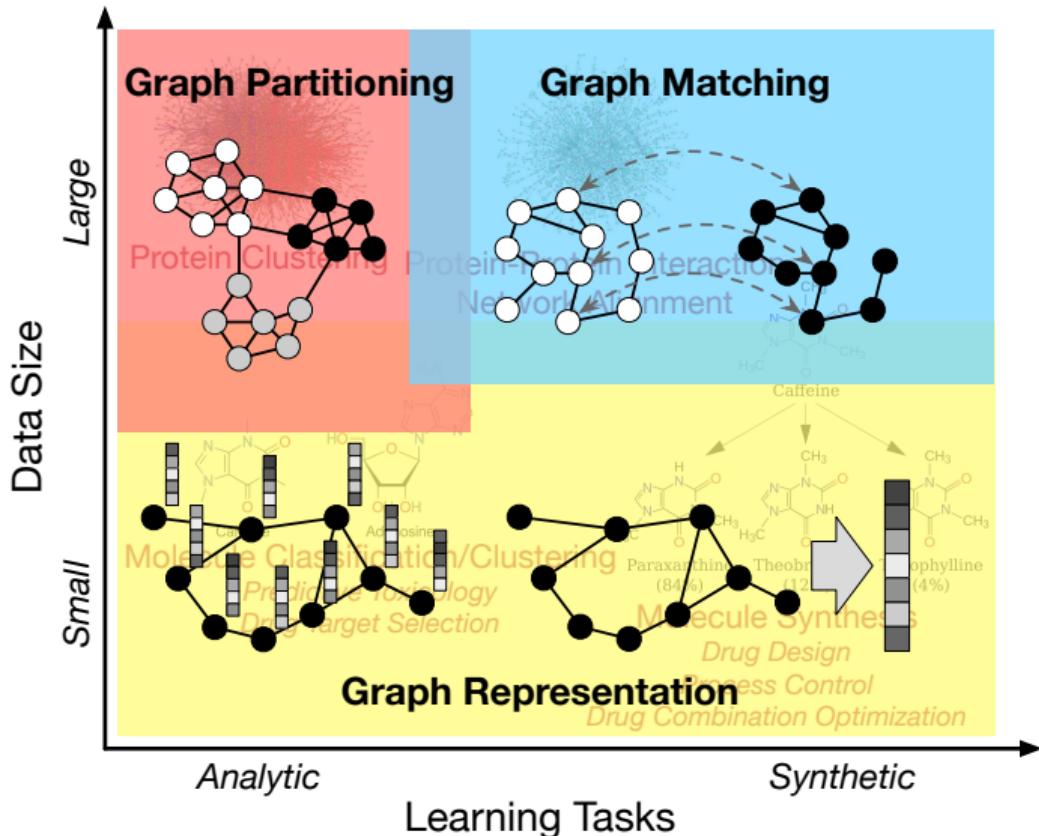
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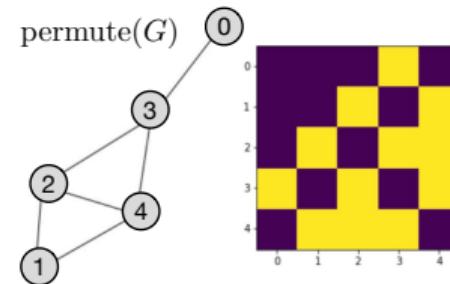
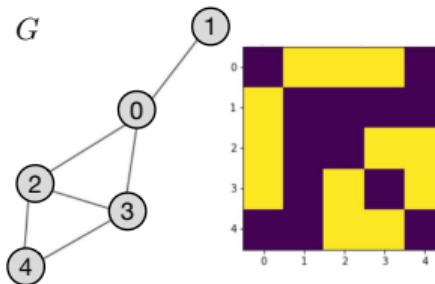
The challenges of the problems

The challenges of the problems

- ▶ NP-completeness
 - ▶ Approximation algorithms with high stability and scalability

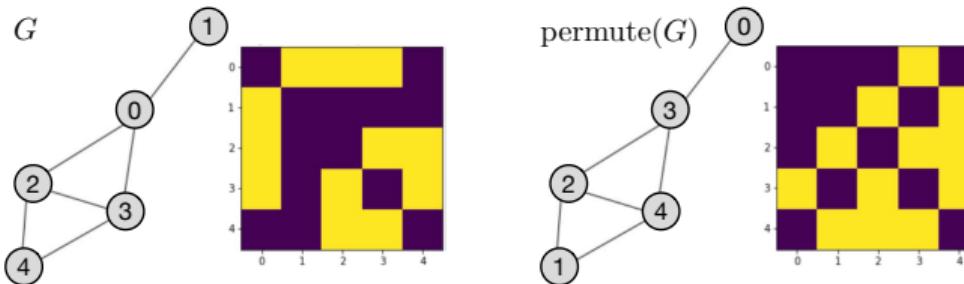
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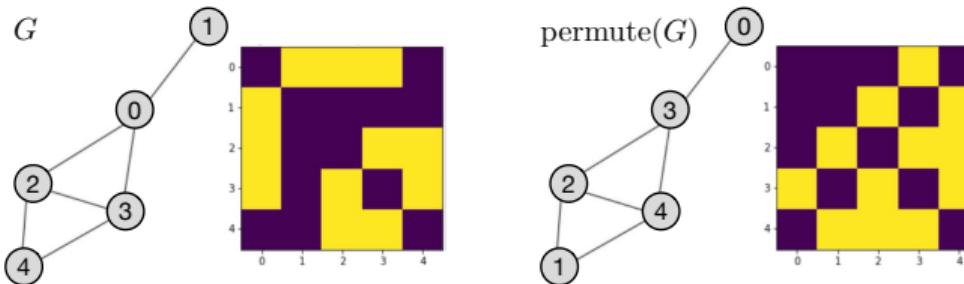
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- ▶ A permutation-invariant metric d : $d(G_X, G_Y) = d(G_X, \text{permute}(G_Y))$
- ▶ A permutation-invariant representation model f : $f(G) = f(\text{permute}(G))$

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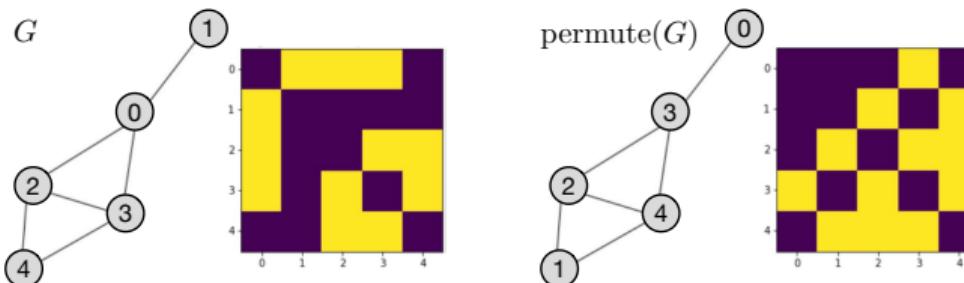
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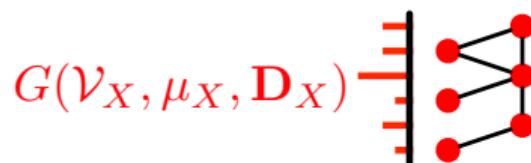
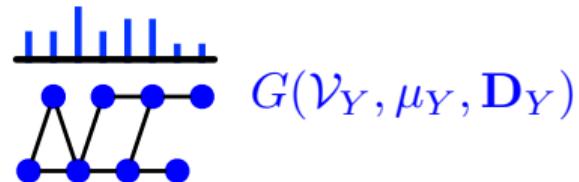


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Gromov-Wasserstein Learning (GWL) provides a potential solution.
Applications: PPI network alignment, molecule clustering and classification.

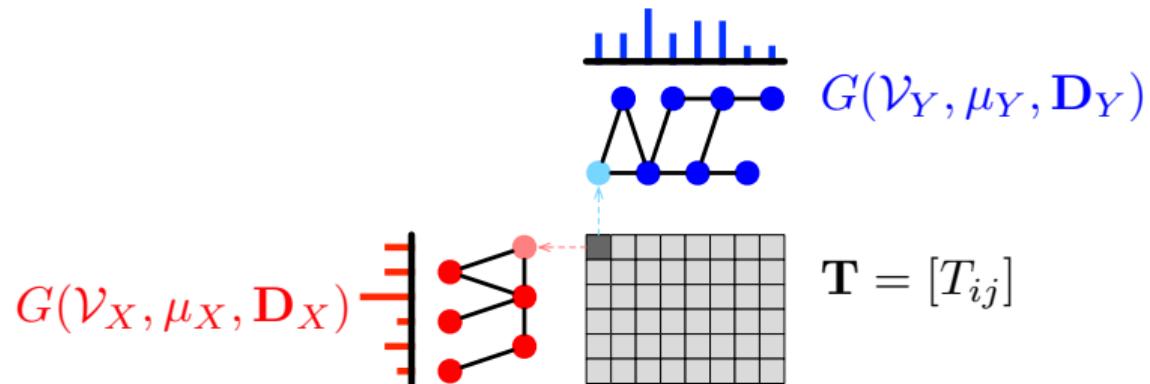
Gromov-Wasserstein distance (GWD) for structured data

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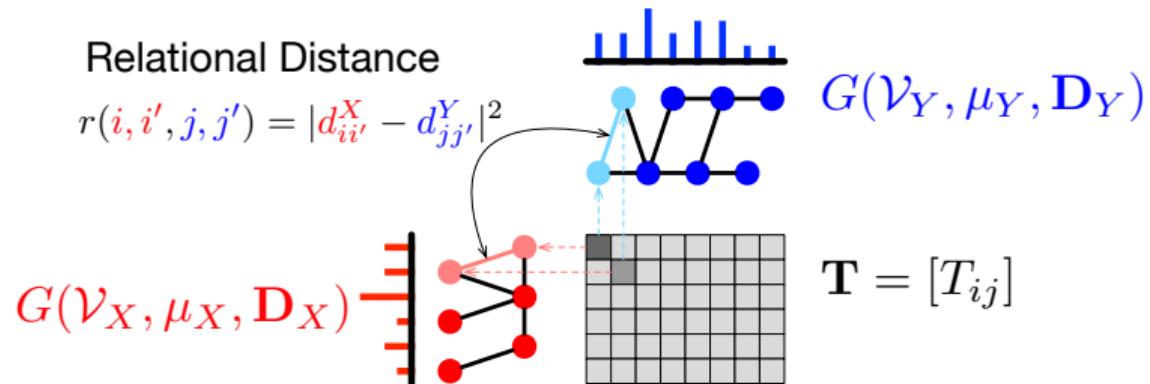
- ▶ \mathcal{V} : the node set
- ▶ μ : a predefined distribution of nodes
- ▶ $\mathbf{D} = [d_{ii'}]$: the adjacency / distance / kernel matrix

Gromov-Wasserstein distance (GWD) for structured data



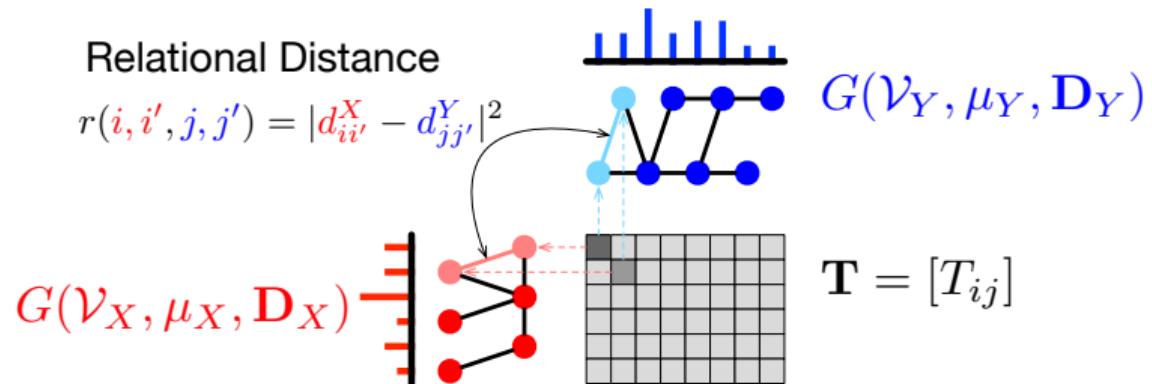
- ▶ $\mathbf{T} = [T_{ij}]$: a joint distribution of nodes
- ▶ $(i \in \mathcal{V}_X, j \in \mathcal{V}_Y) \sim \mathbf{T}$.
- ▶ $\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \boldsymbol{\mu}_Y) = \{\mathbf{T} \geq \mathbf{0} \mid \mathbf{T}\mathbf{1} = \boldsymbol{\mu}_X, \mathbf{T}^\top\mathbf{1} = \boldsymbol{\mu}_Y\}$

Gromov-Wasserstein distance (GWD) for structured data



- ▶ $\underbrace{\mathbf{T} \otimes \mathbf{T}}$: a joint distribution of edges.
Kronecker product
- ▶ The pair of edges $(d_{ii'}^X, d_{jj'}^Y) \sim \mathbf{T} \otimes \mathbf{T}$.
- ▶ Relational distance $r(i, i', j, j')$: the difference between the edges.

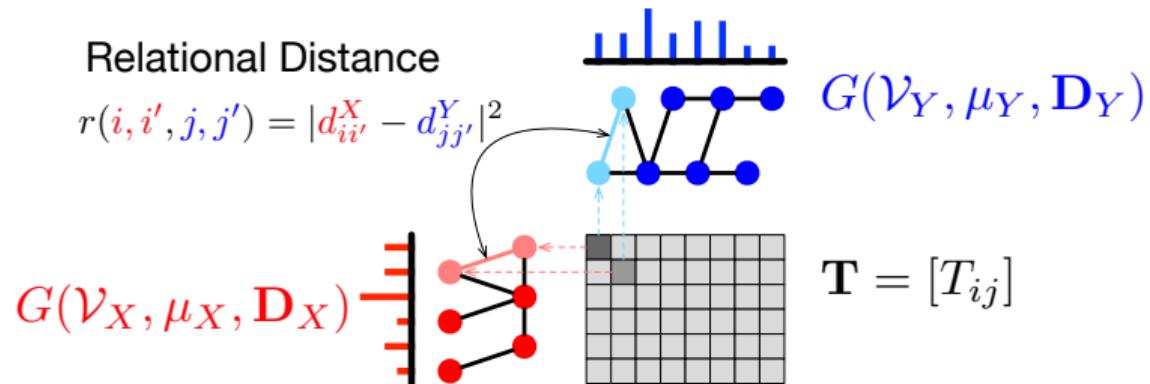
Gromov-Wasserstein distance (GWD) for structured data



The GWD is **the minimum expectation of the relational distance**:

$$\begin{aligned} d_{gw}(G_X, G_Y) &:= \min_{\mathbf{T} \in \Pi(\mu_X, \mu_Y)} \mathbb{E}_{(i, i', j, j') \sim \mathbf{T} \otimes \mathbf{T}} [r(i, i', j, j')] \\ &= \min_{\mathbf{T} \in \Pi(\mu_X, \mu_Y)} \sum_{i, i'} \sum_{j, j'} \underbrace{|d_{ii'}^X - d_{jj'}^Y|^2}_{\text{distance } r} \underbrace{T_{ij} T_{i'j'}}_{\text{prob}(r)} \quad (1) \end{aligned}$$

Gromov-Wasserstein distance (GWD) for structured data

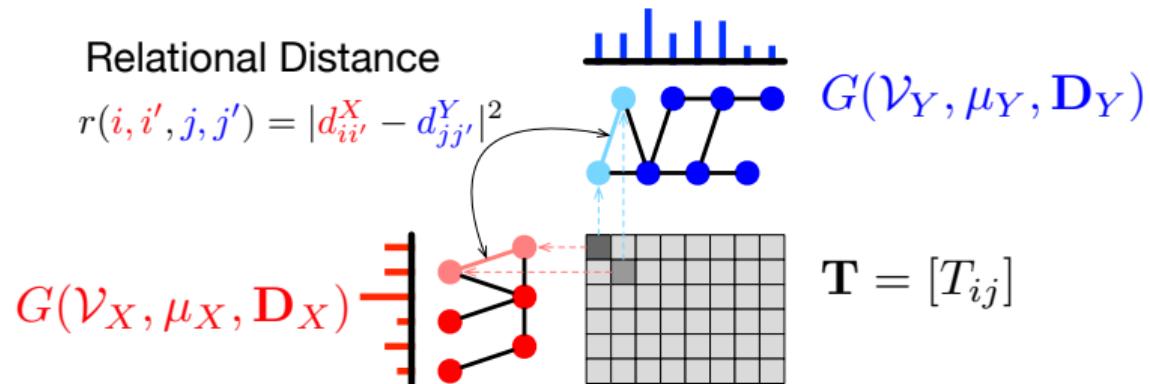


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► $\mathbf{D}_{XY} = (\mathbf{D}_X \odot \mathbf{D}_X) \mu_X \mathbf{1}_{|\mathcal{V}_Y|}^\top + \mathbf{1}_{|\mathcal{V}_X|} \mu_Y^\top (\mathbf{D}_Y \odot \mathbf{D}_Y)^\top.$

Gromov-Wasserstein distance (GWD) for structured data

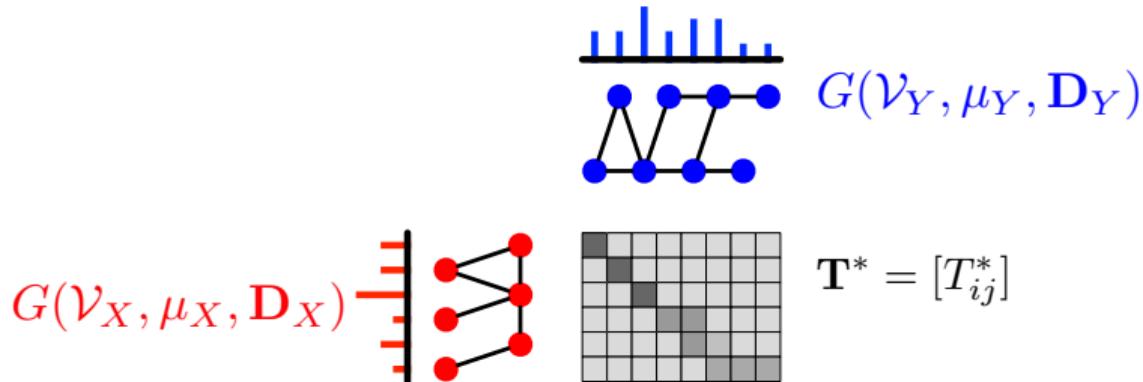


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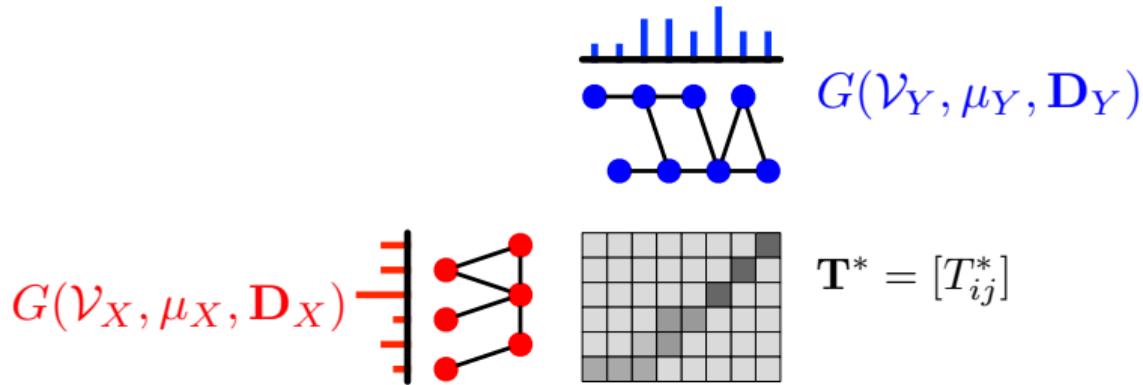
- ▶ $\mathbf{D}_{XY} = (\mathbf{D}_X \odot \mathbf{D}_Y) \mu_X \mathbf{1}_{|\mathcal{V}_Y|}^\top + \mathbf{1}_{|\mathcal{V}_X|} \mu_Y^\top (\mathbf{D}_Y \odot \mathbf{D}_Y)^\top.$
- ▶ Given comparable node attributes, $\mathbf{D}_{XY} \leftarrow \mathbf{D}_{XY} + \mathbf{D}(\mathbf{F}_X, \mathbf{F}_Y)$

Advantages of GWD



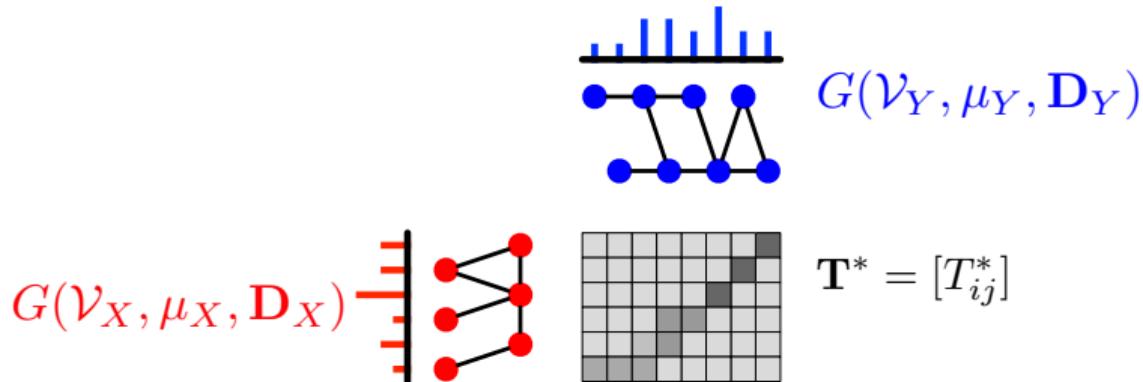
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- ▶ The optimal joint distribution \mathbf{T}^* (or called “**optimal transport**” matrix) indicates the correspondence between the two graphs.
- ▶ A **permutation-invariant** (pseudo) metric
 - ▶ $d_{gw}(G_X, G_Y) = d_{gw}(G_X, \text{permute}(G_Y))$
- ▶ Applicable to the graphs with different sizes, *i.e.*, $|\mathcal{V}_X| \neq |\mathcal{V}_Y|$.
- ▶ Applicable to the graphs with/without node attributes.

Straightforward applications

Graph matching and partitioning

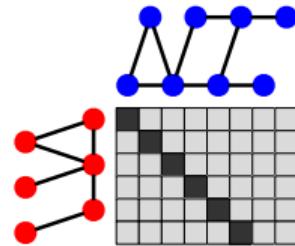
Apply the Gromov-Wasserstein distance as objective functions

Matching via learning optimal transport

Quadratic assignment problem (QAP):

$$\max_{\mathbf{P} \in \mathcal{P}} \langle \mathbf{D}_X \mathbf{P} \mathbf{D}_Y^\top, \mathbf{P} \rangle,$$

$$\mathcal{P} = \{\mathbf{P} \in \{0, 1\}^{|\mathcal{V}_X| \times |\mathcal{V}_Y|} \mid \mathbf{P}\mathbf{1} = \mathbf{1}, \mathbf{P}^\top \mathbf{1} \leq \mathbf{1}\}.$$

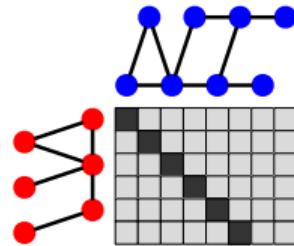


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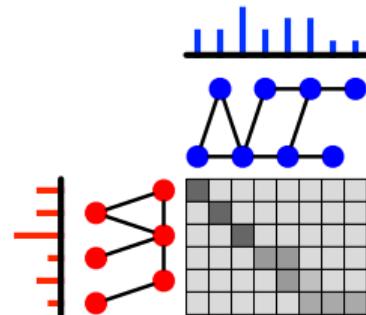
$$\mathcal{P} = \{P \in \{0, 1\}^{|\mathcal{V}_X| \times |\mathcal{V}_Y|} \mid P\mathbf{1} = \mathbf{1}, P^\top \mathbf{1} \leq \mathbf{1}\}.$$



Gromov-Wasserstein distance (GWD):

$$\min_{T \in \Pi(\mu_X, \mu_Y)} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X T \mathbf{D}_Y^\top, T \rangle,$$

$$\Pi(\mu_X, \mu_Y) = \{T \geq 0 \mid T\mathbf{1} = \mu_X, T^\top \mathbf{1} = \mu_Y\}$$

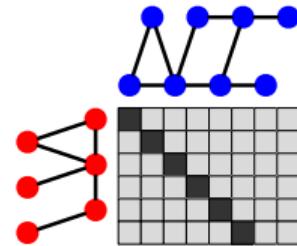


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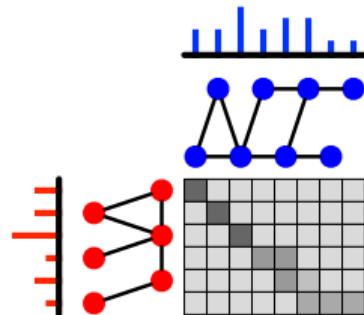
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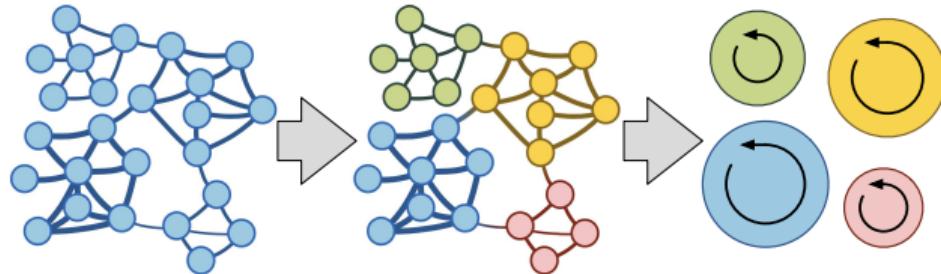
- ▶ Conditional prob. $\mathbf{P}^* = \frac{\mathbf{T}^*}{\boldsymbol{\mu}_X \mathbf{1}^\top} = [P^*(j|i)].$
- ▶ For each node $i \in \mathcal{V}_X$, $j^* = \arg \max_j P^*(j|i).$

Partitioning is also matching

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Modularity maximization principle

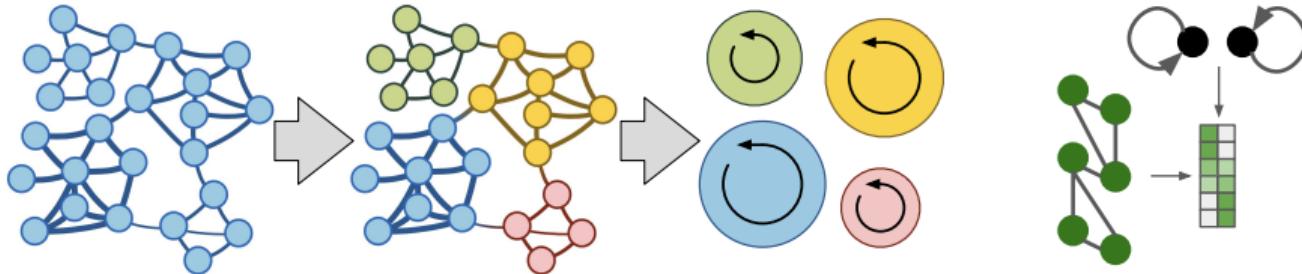
- ▶ Dense internal edges + sparse external edges.



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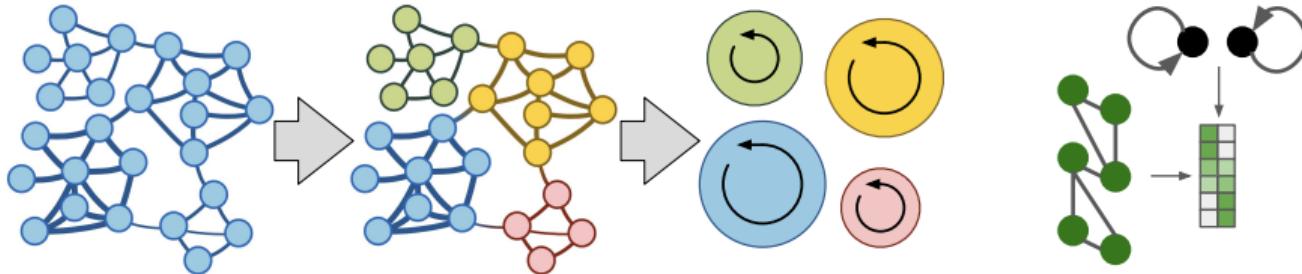
A GWD-based solution [*Xu, et al., NeurIPS 2019*]:

- ▶ $\mathbf{T}^* \in \mathbb{R}^{|\mathcal{V}| \times N} \leftarrow d_{gw}(G, G_{iso})$
- ▶ $G_{iso}(\mathcal{V}_{iso}, \frac{1}{N} \mathbf{1}_N, \mathbf{I}_{N \times N})$

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Proposed algorithms

$$\min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \boldsymbol{\mu}_Y)} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{T} \mathbf{D}_Y^\top, \mathbf{T} \rangle$$

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Proximal Gradient Algorithm [Xu, et al., ICML 2019]

$$\min_{T \in \Pi(\mu_X, \mu_Y)} \underbrace{\langle D_{XY} - 2D_X \mathbf{T}^{(m)} D_Y^\top, T \rangle}_{\text{GW term}} + \gamma \underbrace{\text{KL}(T \| \mathbf{T}^{(m)})}_{\text{Proximal term}}$$

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Sinkhorn distance

Bregman ADMM [Xu, AAAI 2020]

$$\underbrace{\min_{\substack{T \in \Pi(\mu_X, \cdot), S \in \Pi(\cdot, \mu_Y), \mathbf{T} = \mathbf{S}}} \langle D_{XY} - 2D_X S D_Y^\top, T \rangle}_{\text{Decoupling constraints by Aux.}}$$

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$$\rightarrow \min_{\substack{\mathbf{T} \in \Pi(\mu_X, \cdot), \\ \mathbf{S} \in \Pi(\cdot, \mu_Y), \\ \mathbf{Z}}} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S} \mathbf{D}_Y^\top, \mathbf{T} \rangle + \underbrace{\langle \mathbf{Z}, \mathbf{T} - \mathbf{S} \rangle}_{\text{Augmented Lagrangian}} + \underbrace{\gamma B(\mathbf{T}, \mathbf{S})}_{\text{Bregman Div.}}$$

Further analysis

Convergence

- ▶ $\lim_{m \rightarrow \infty} T^{(m)}$ is a stationary point.
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- ▶ $\mathbf{D}_X, \mathbf{D}_Y$ are dense distance/kernel matrices: $\mathcal{O}(V^3)$.

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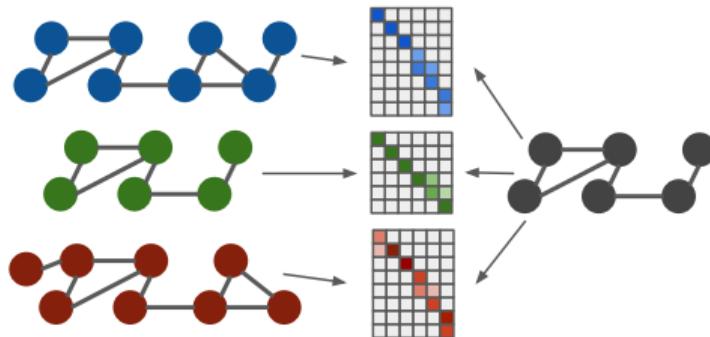
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- ▶ $\mathbf{D}_X, \mathbf{D}_Y$ are adjacency matrices: $\mathcal{O}(VE)$.
- ▶ When $V = |\mathcal{V}_X| \gg |\mathcal{V}_Y| = N$ (graph partitioning): $\mathcal{O}(N(E + V))$.

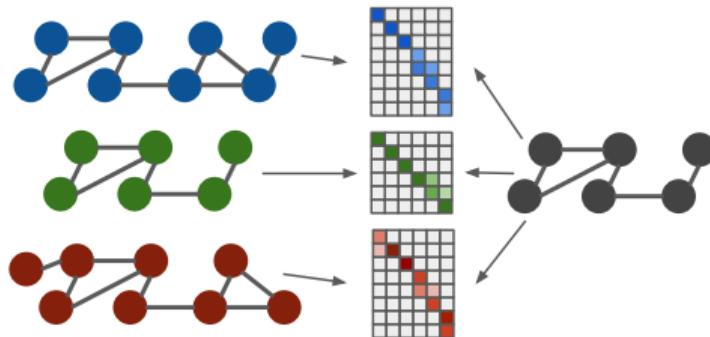
Large-scale matching based on GW barycenters



Given $\{G_k\}_{k=1}^K$, $K \geq 2$, their GW barycenter is defined as

$$\underbrace{B_{gw}(\bar{\mathcal{V}}, \bar{\boldsymbol{\mu}}, \bar{\mathbf{B}}^*)}_{\text{Barycenter graph}}, \quad \underbrace{\{\mathbf{T}_k^*\}_{k=1}^K}_{\text{OT matrices}} := \arg \min_B \sum_{k=1}^K \lambda_k d_{gw}(B, G_k), \quad (4)$$

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Learn $\{\mathbf{T}_k^*\}_{k=1}^K$ and \mathbf{B}^* via **alternating optimization**.

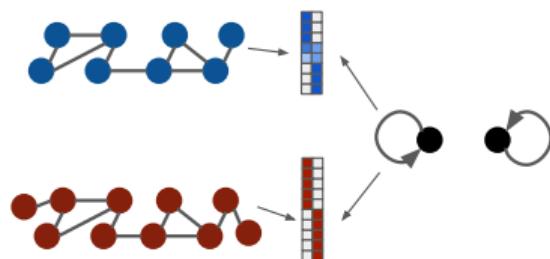
$$\mathbf{B}^* = \frac{1}{\bar{\boldsymbol{\mu}} \bar{\boldsymbol{\mu}}^\top} \sum_{k=1}^K \lambda_k (\mathbf{T}_k^*)^\top \mathbf{D}_k \mathbf{T}_k^* \quad (5)$$

Large-scale matching based on GW barycenters

Co-partition two graphs:

$$B^*, T_X^*, T_Y^* = \arg \min \frac{|\mathcal{V}_X|}{|\mathcal{V}_X| + |\mathcal{V}_Y|} d_{gw}(B, G_X) + \frac{|\mathcal{V}_Y|}{|\mathcal{V}_X| + |\mathcal{V}_Y|} d_{gw}(B, G_Y)$$

Initialize the barycenter graph by a disconnected graph.

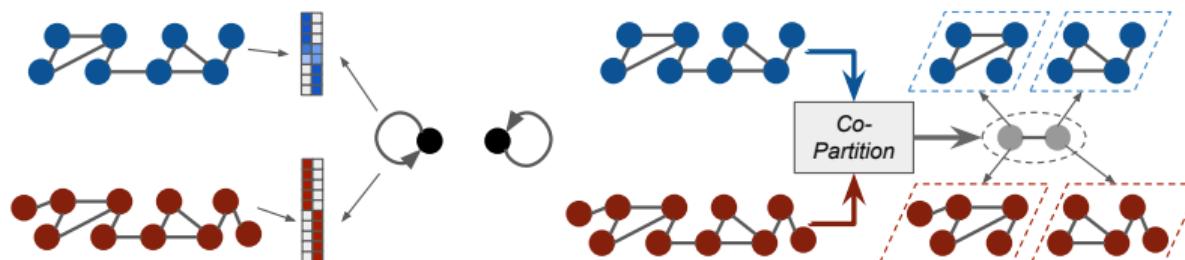


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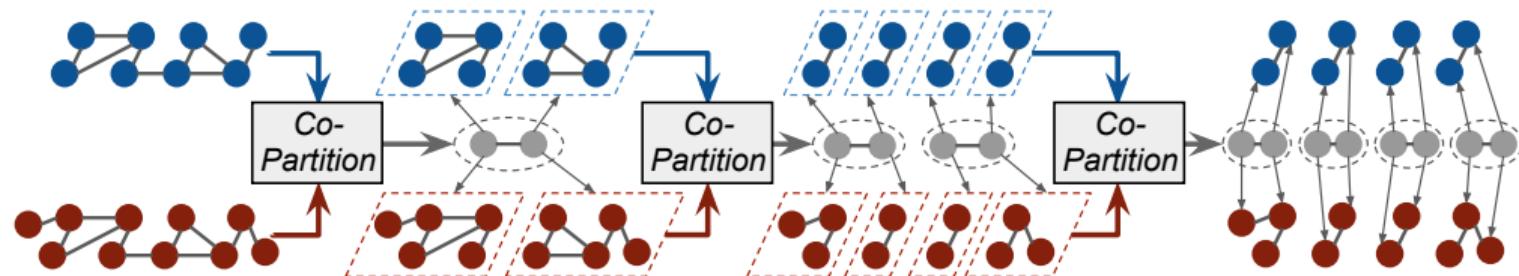
Initialize the barycenter graph by a disconnected graph.



Computational complexity: $\mathcal{O}(2(V + E))$

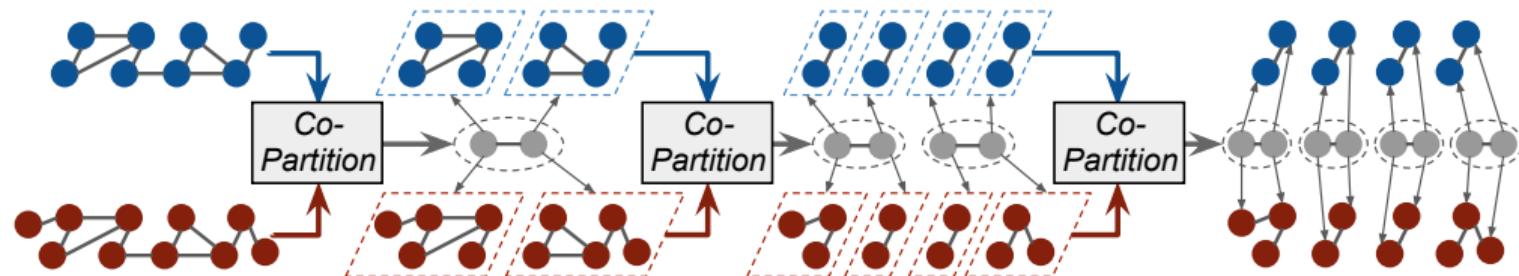
Large-scale matching based on GW barycenters

A “Divide and Conquer” strategy based on recursive co-partitioning [Xu, et al., NeurIPS 2019]



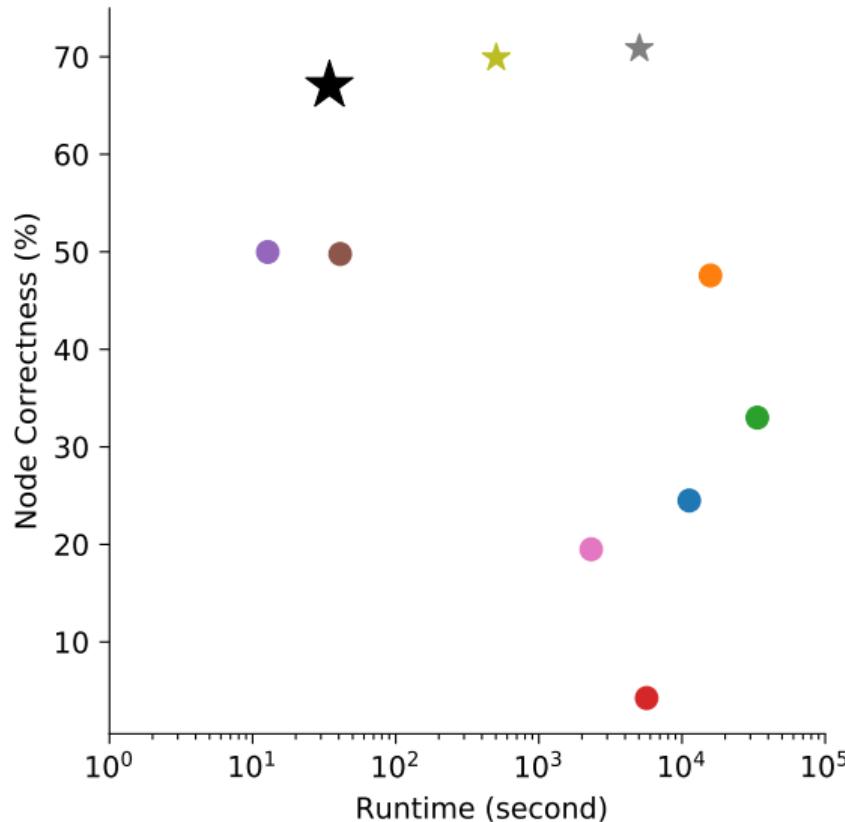
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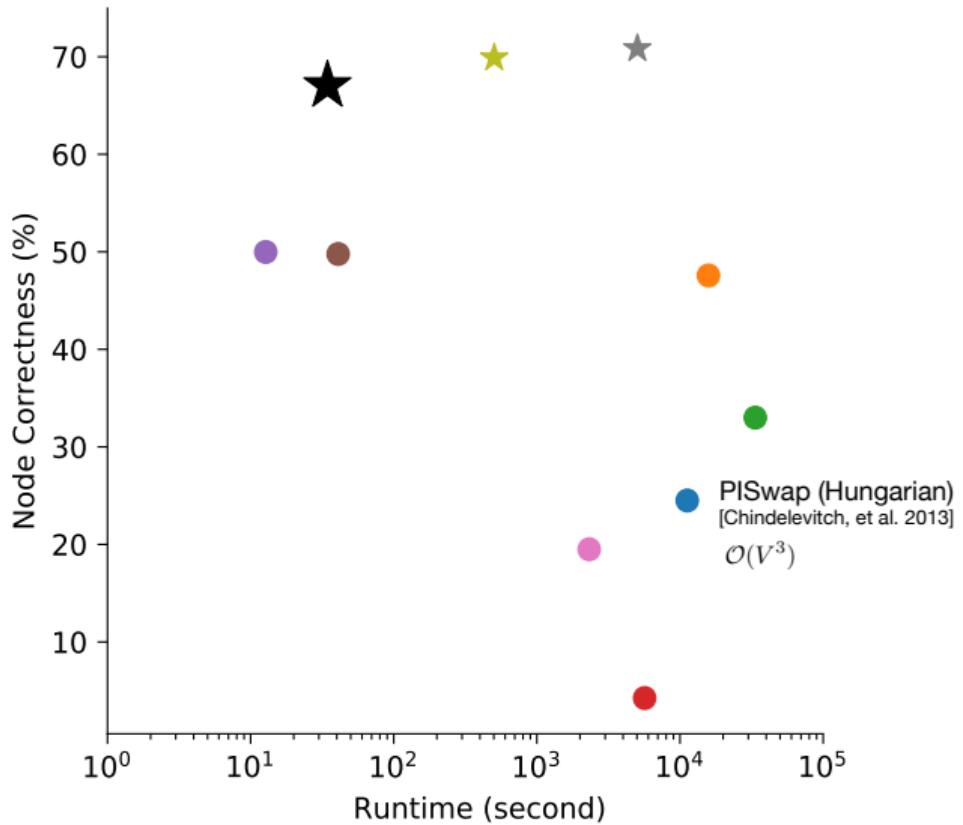


Computational complexity: $\mathcal{O}((E + V) \log V)$

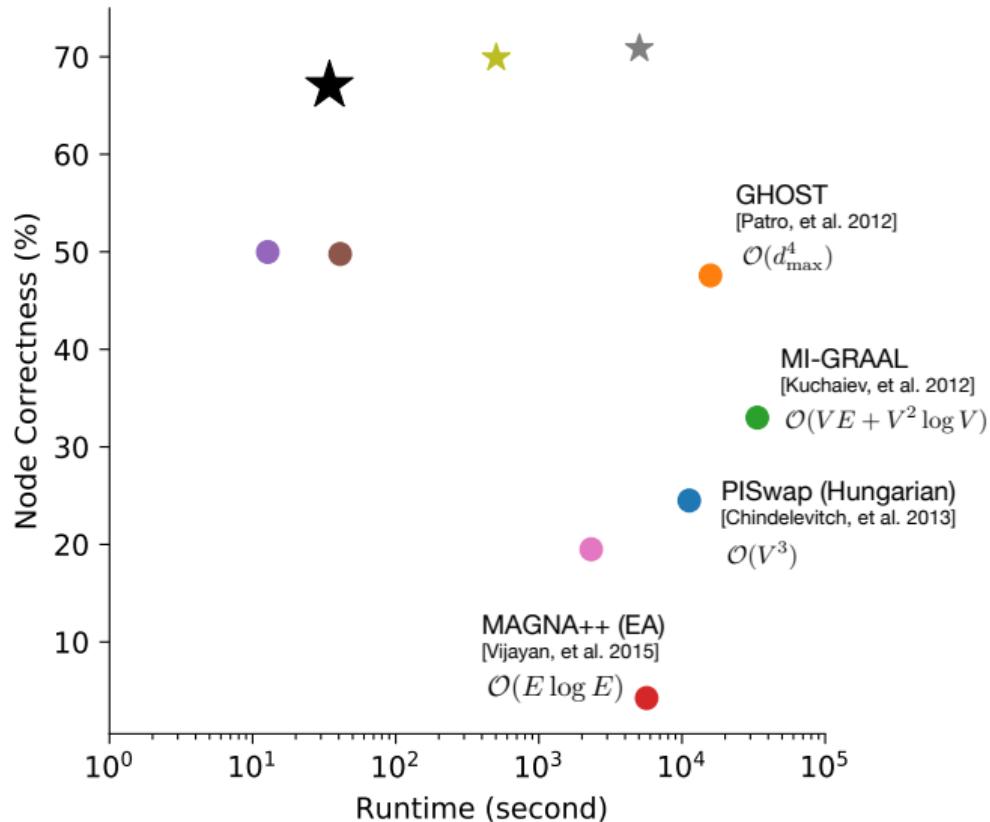
Matching synthetic graphs



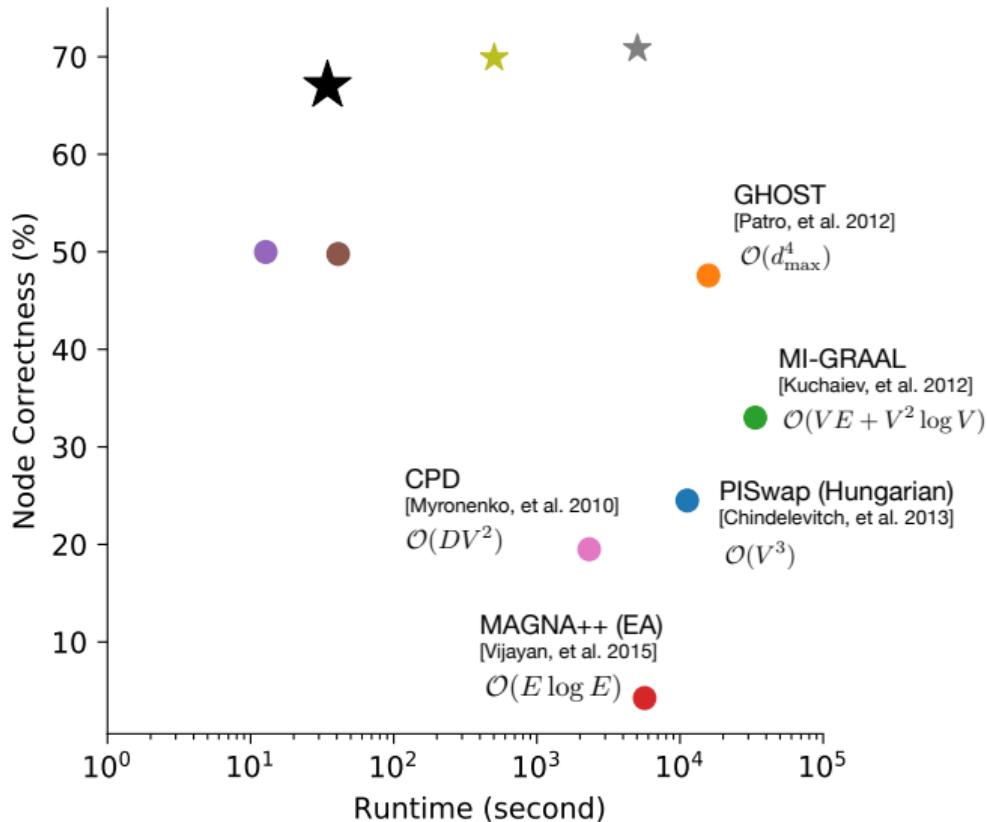
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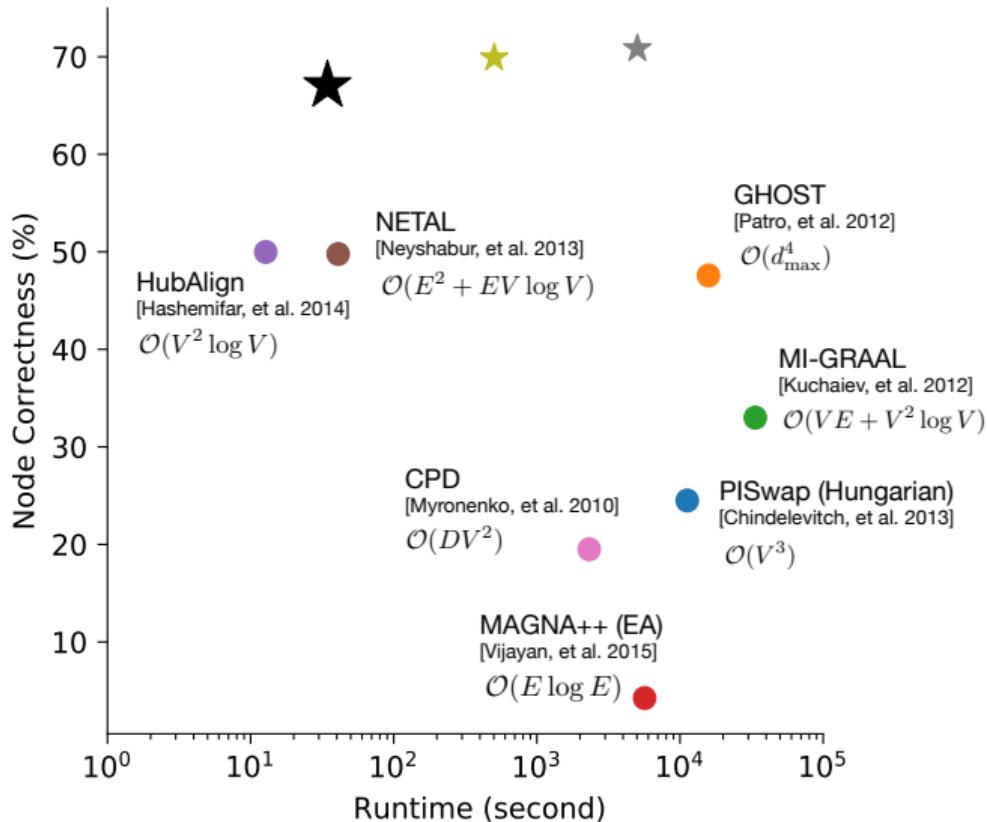
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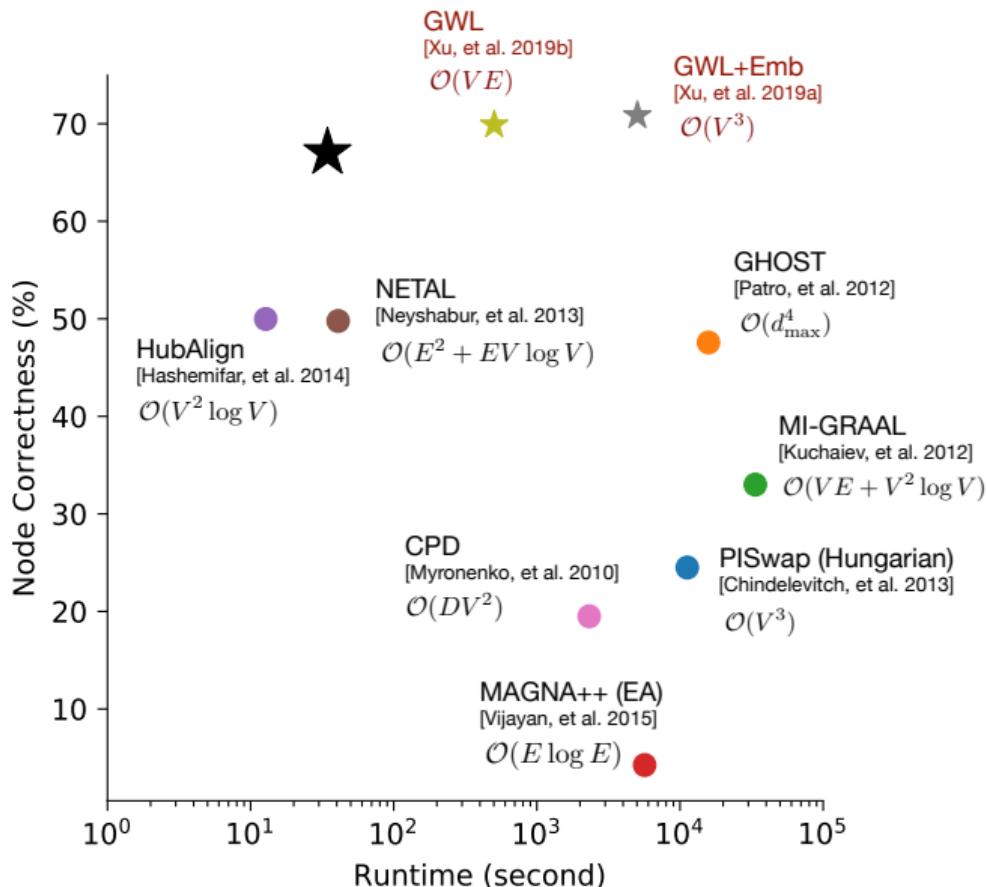
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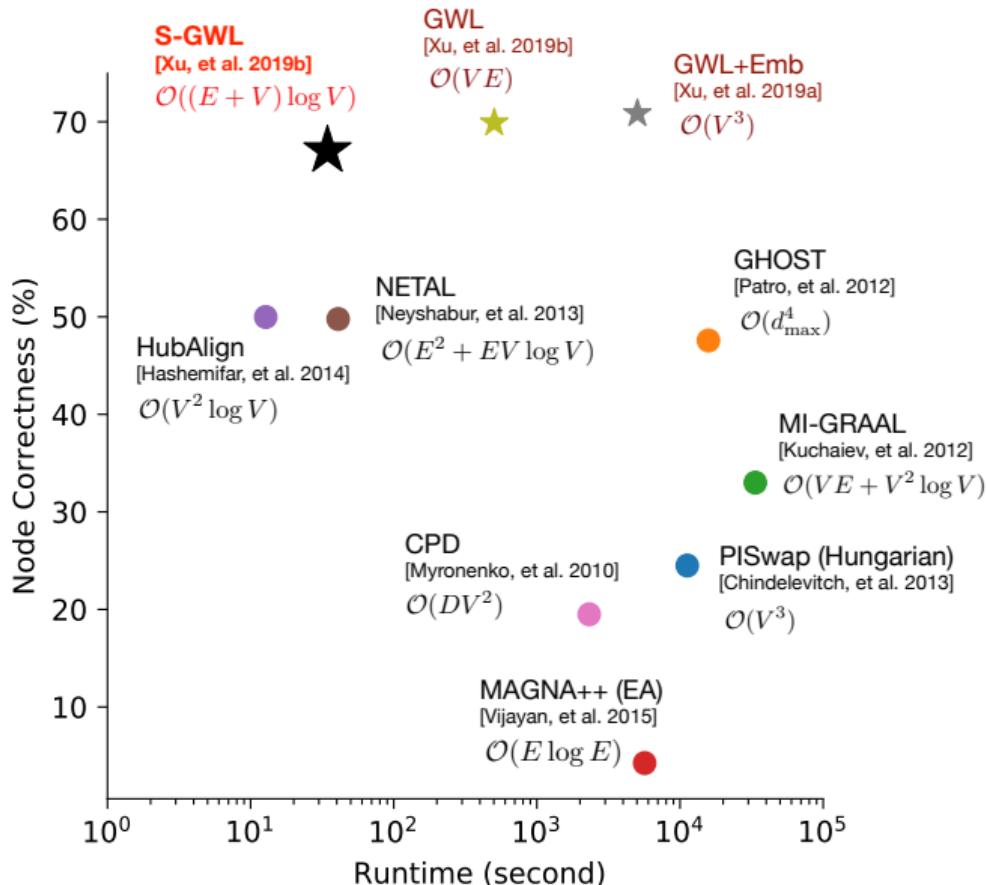
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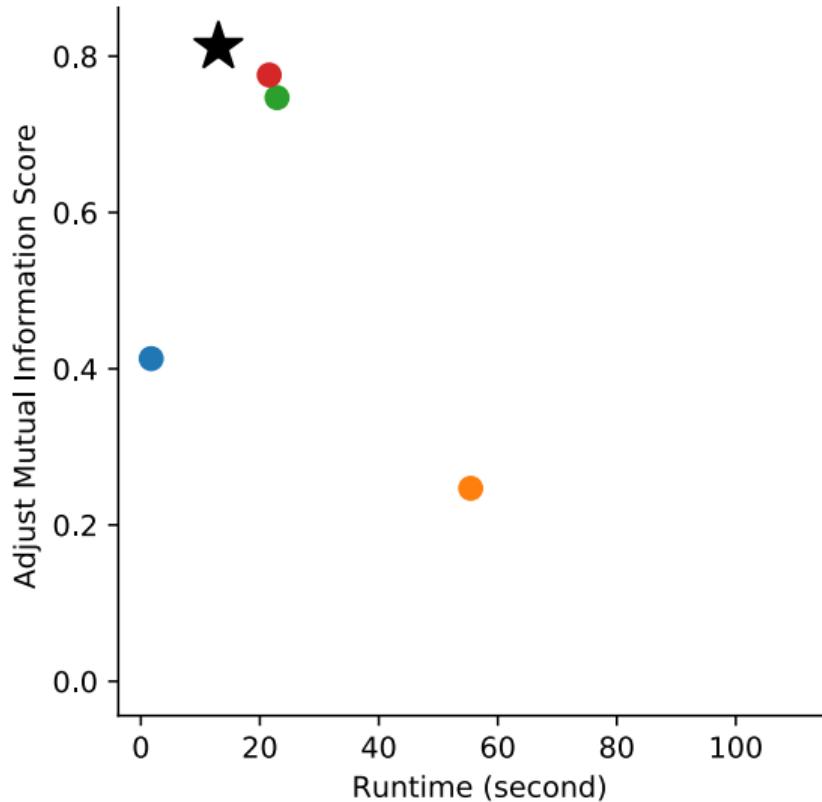
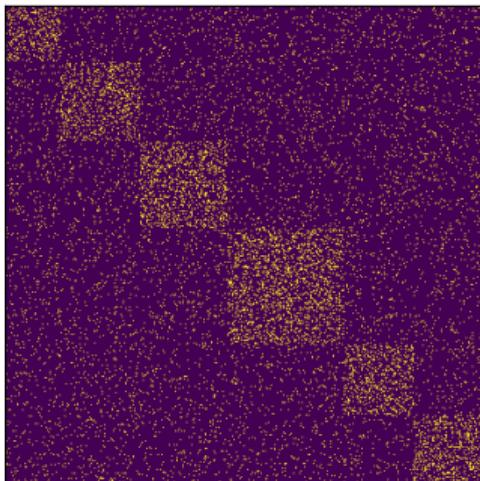


Partitioning synthetic graphs

$V = 4,000$

$p_{\text{within}} = 0.2$

$p_{\text{across}} = 0.05$

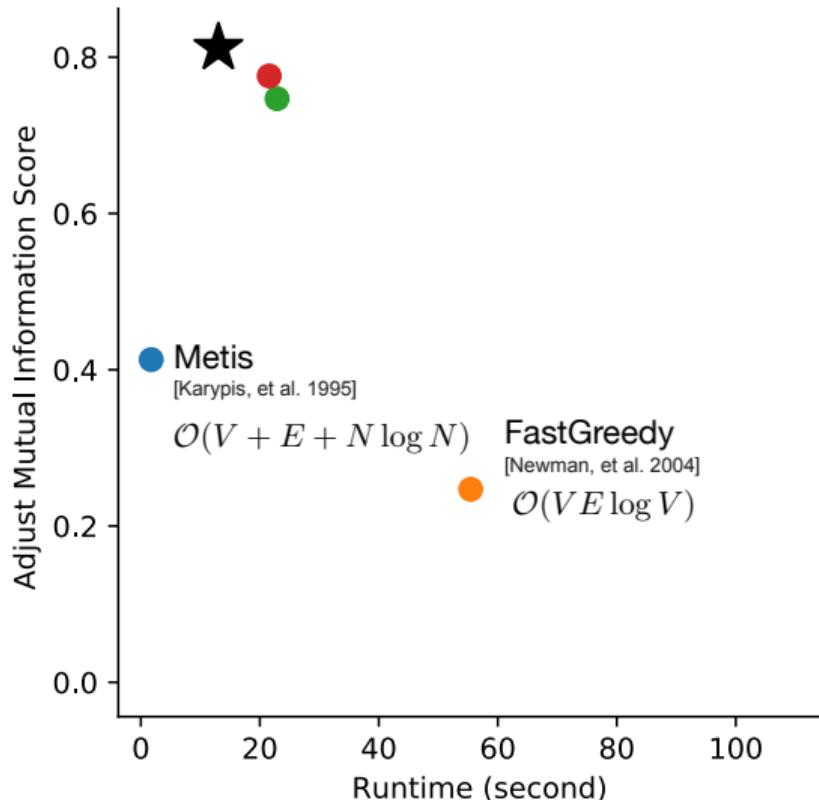
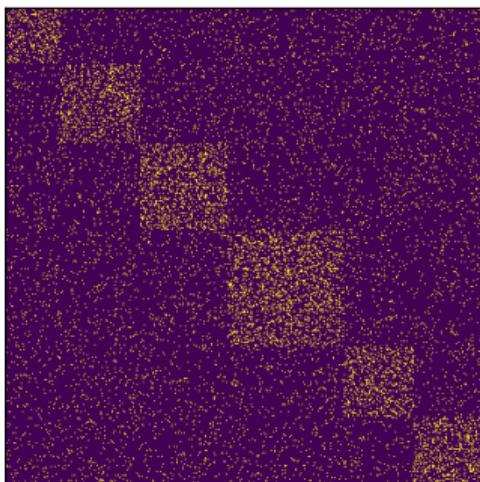


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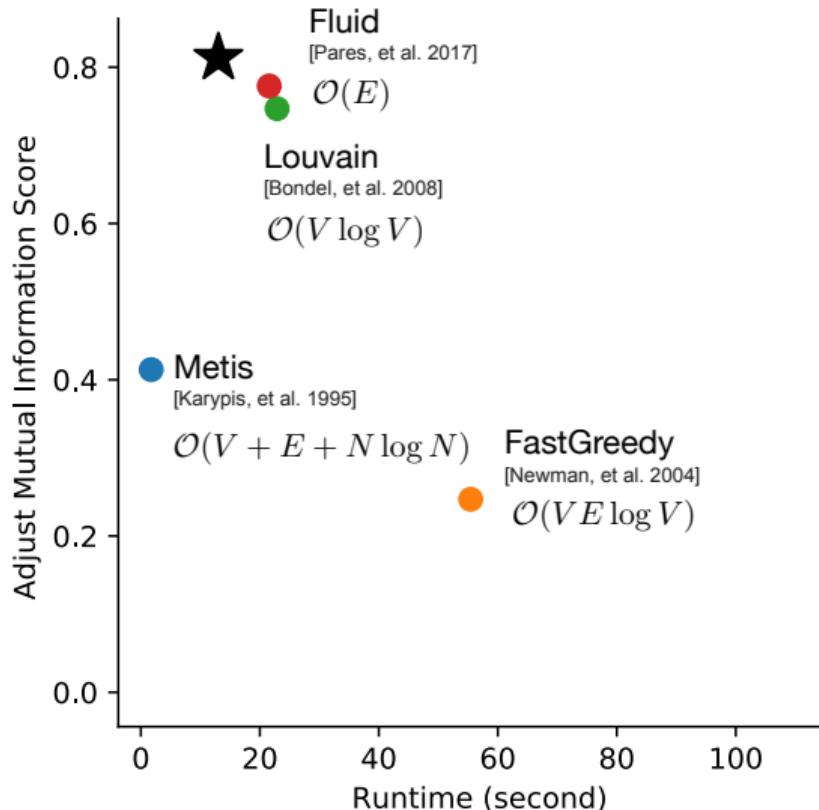
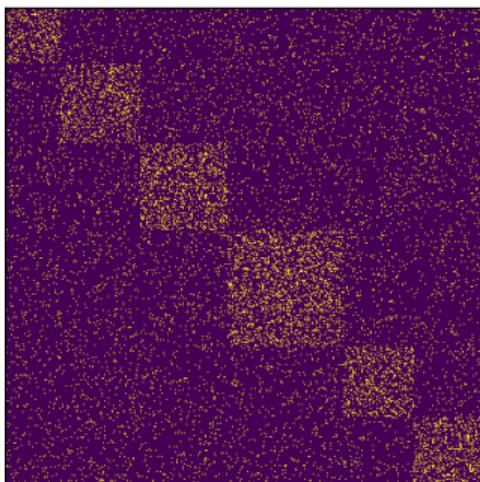


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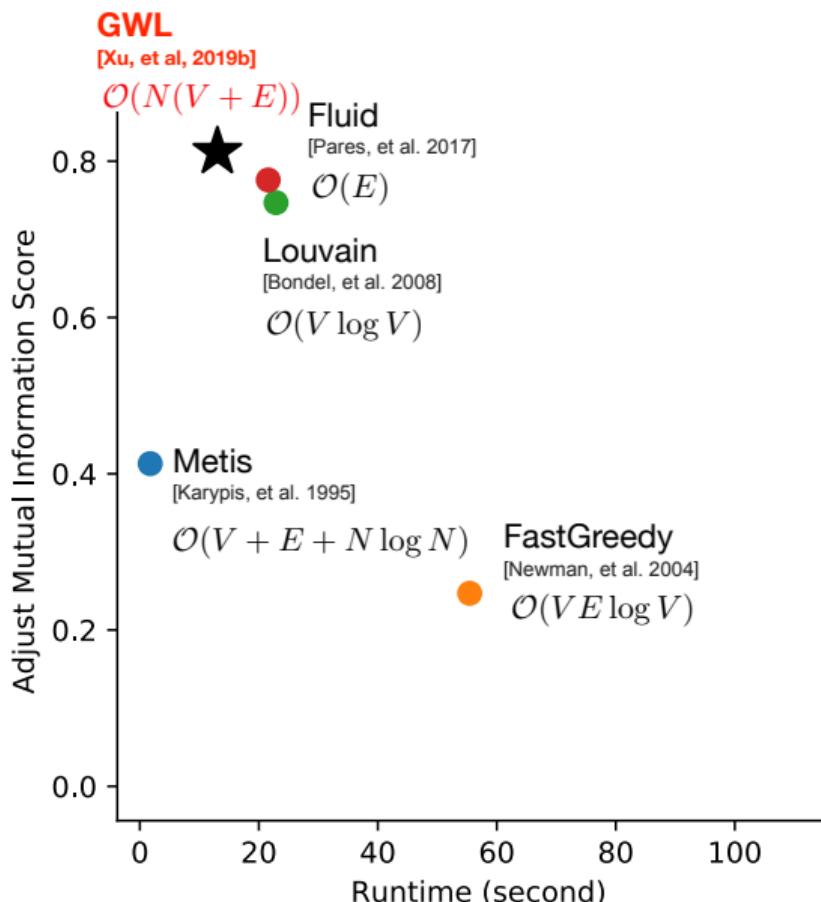
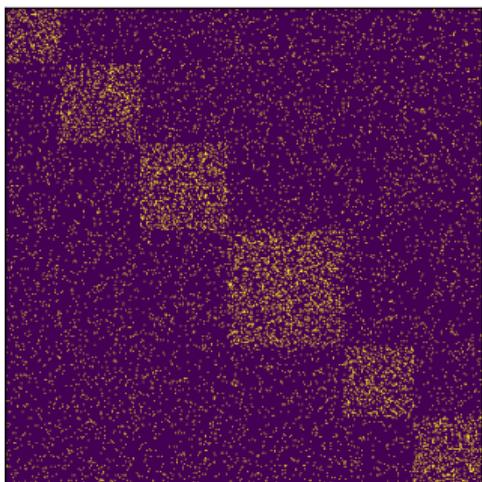


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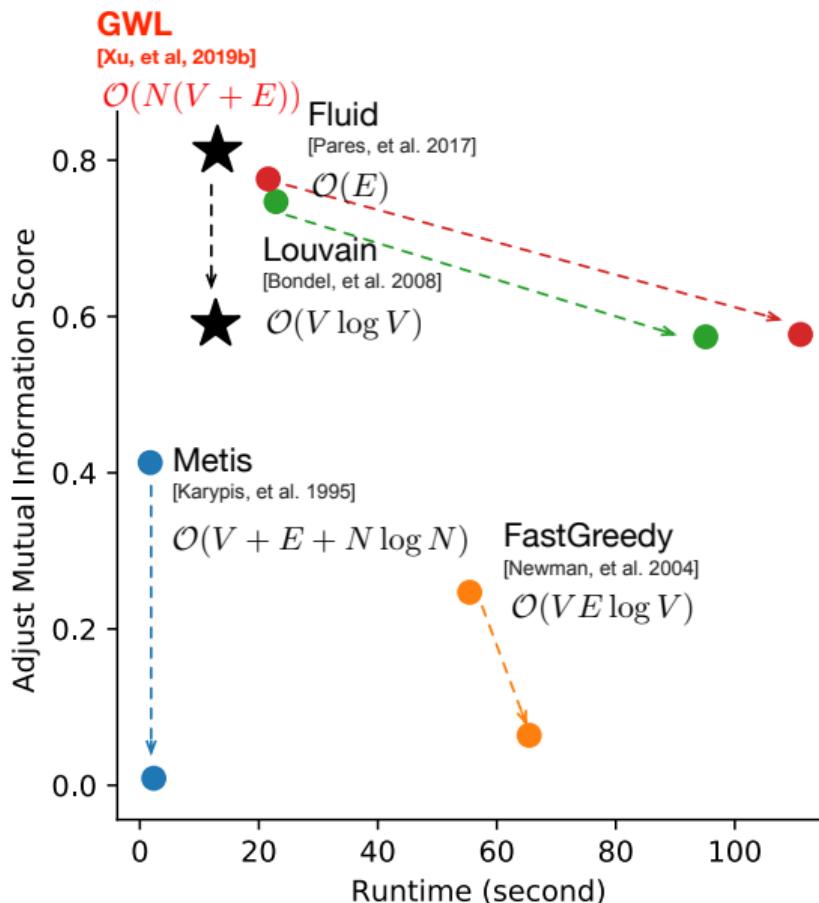
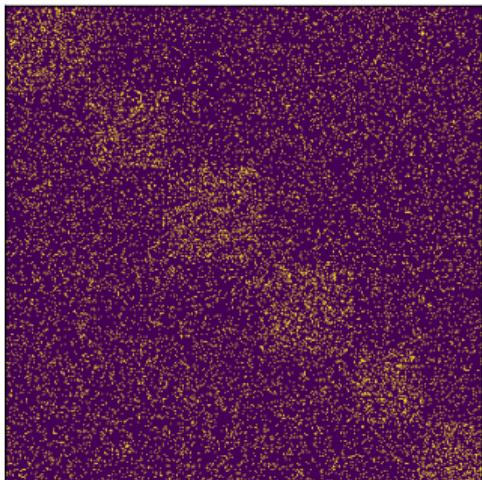


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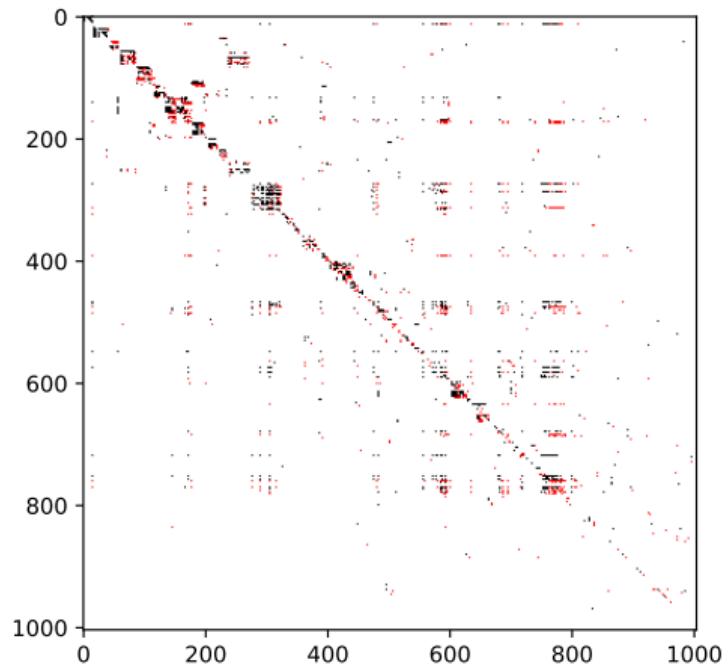
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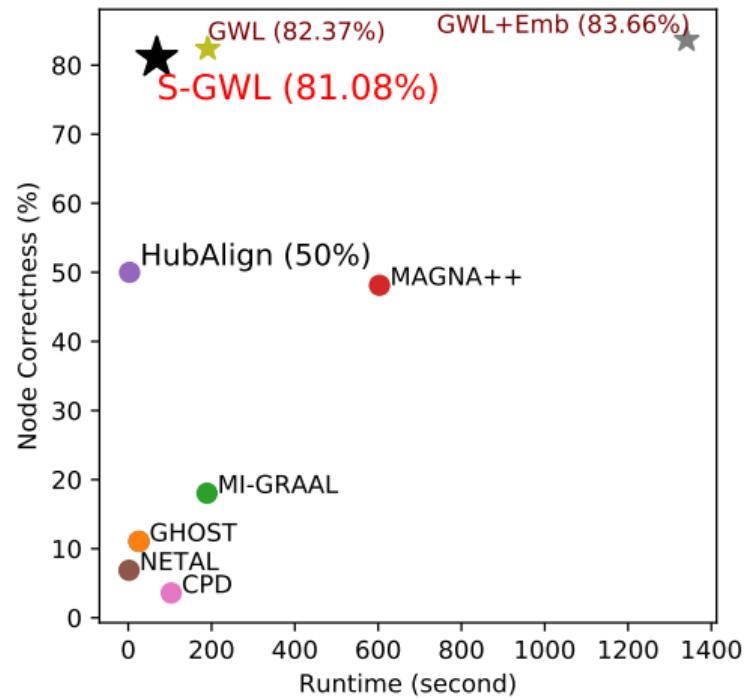
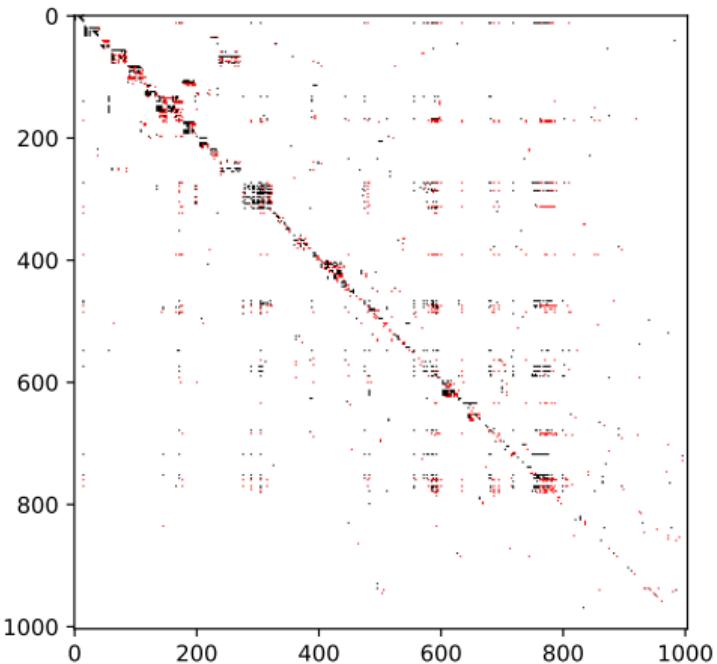
Real-world PPI network alignment

Yeast PPI \leftrightarrow Yeast PPI + 5% LC edges



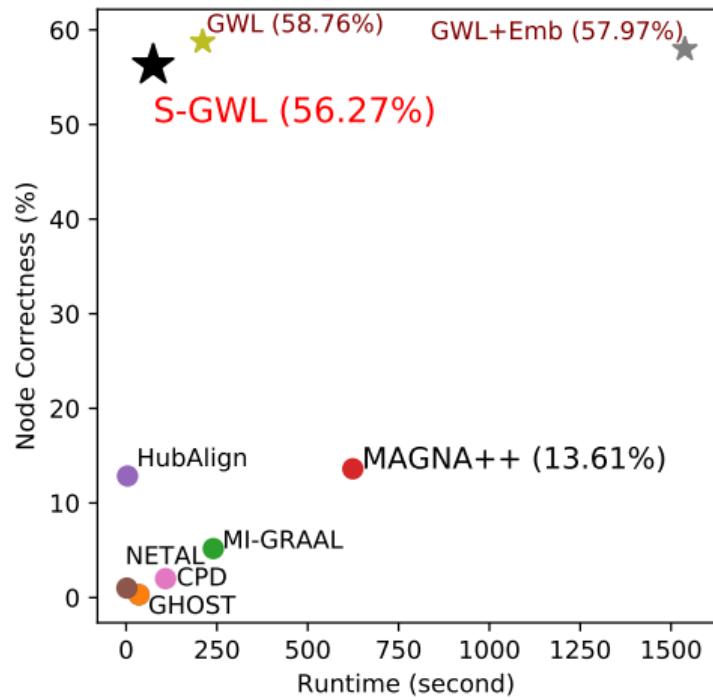
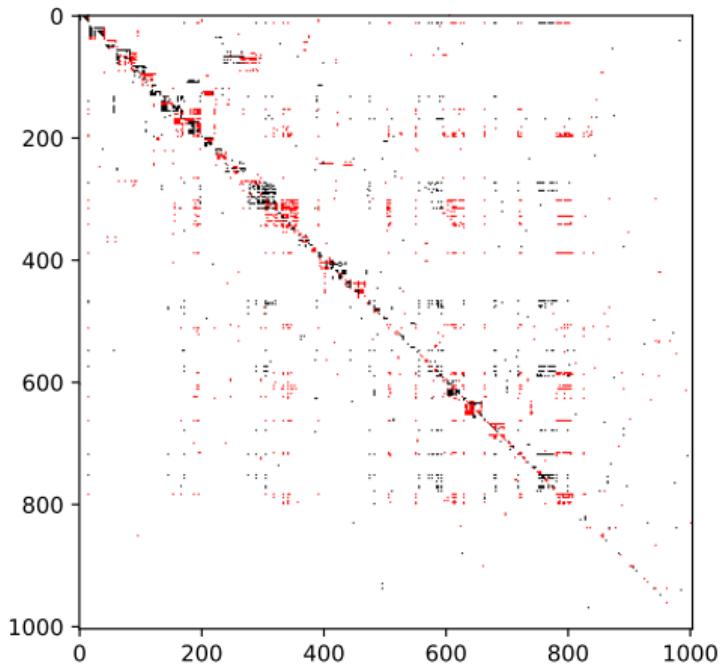
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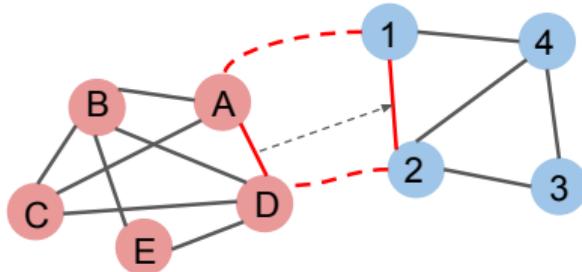
Yeast PPI \leftrightarrow Yeast PPI + 25% LC edges



Matching real-world PPI networks

Matching the PPI network of yeast (2,340 proteins) to that of human (9,141 proteins)

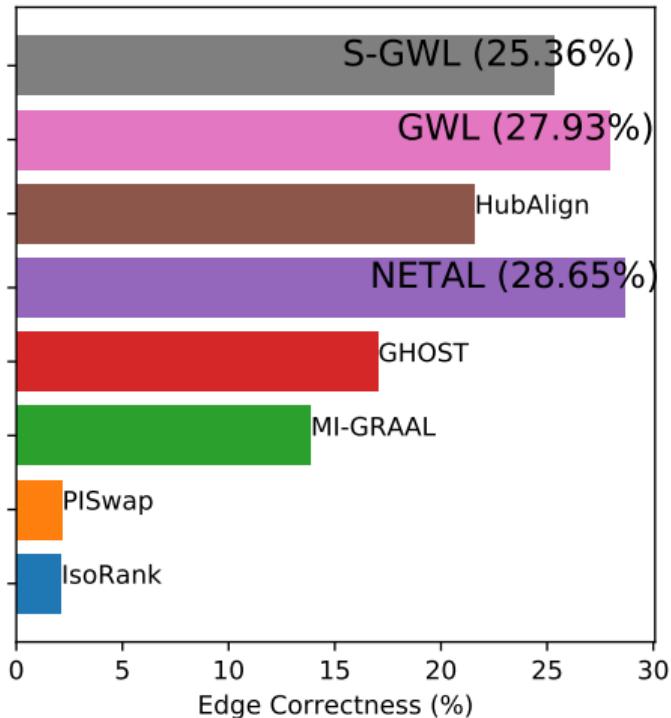
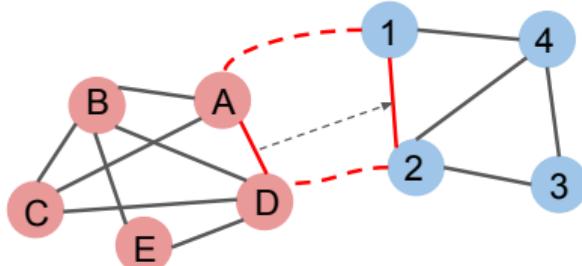
Edge correctness:



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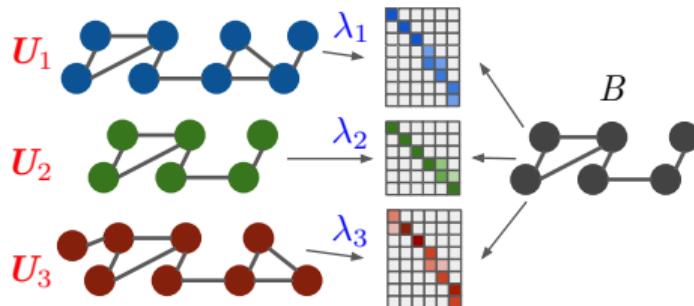
Edge correctness:



Graph representation

Extend existing representation models based on Gromov-Wasserstein distance

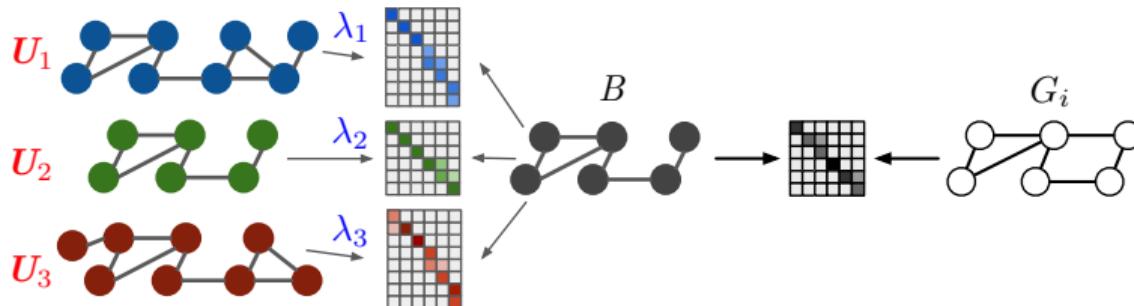
Gromov-Wasserstein factorization model



$$B_{gw}(\mathbf{U}_{1:K}, \boldsymbol{\lambda}) := \arg \min_B \sum_{k=1}^K \lambda_k d_{gw}(B, G_k(\mathbf{U}_k)). \quad (6)$$

- ▶ $\{G_k(\mathbf{U}_k)\}_{k=1}^K$: a set of graph bases.
- ▶ $\boldsymbol{\lambda} = [\lambda_k] \in \Delta^{K-1}$: the coefficients of the graph basis.

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- ▶ Estimate each graph by a GW barycenter graph [Xu, AAAI 2020]:

$$\min_{\mathbf{1} \geq \mathbf{U}_{1:K} \geq \mathbf{0}, \ \boldsymbol{\lambda}_{1:I} \in \Delta^{K-1}} \sum_{i=1}^I d_{gw}(B_{gw}(\mathbf{U}_{1:K}, \underbrace{\boldsymbol{\lambda}_i}_{\text{Rep. of } G_i}), G_i). \quad (7)$$

Gromov-Wasserstein factorization model

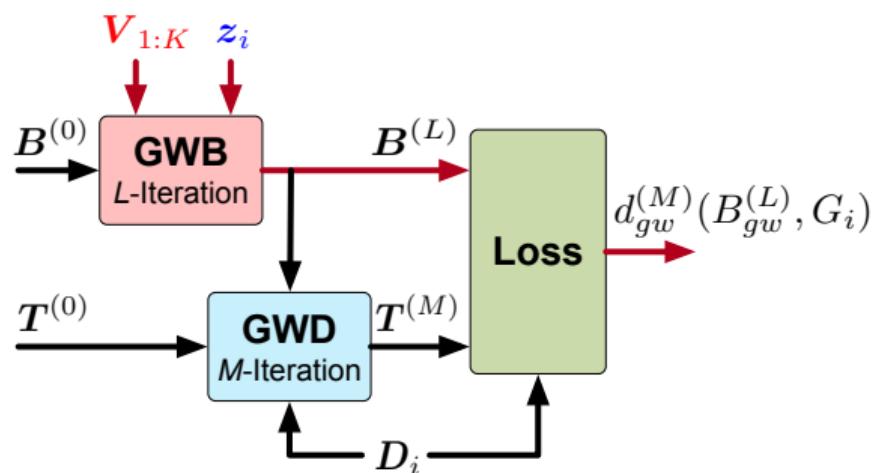
Reparameterize the problem to an unconstrained optimization problem:

$$\min_{\mathbf{V}_{1:K}, \mathbf{z}_{1:I}} \sum_{i=1}^I d_{gw}(B_{gw}(\underbrace{\sigma(\mathbf{V}_{1:K})}_{\mathbf{U}_{1:K}}, \underbrace{\text{softmax}(\mathbf{z}_i)}_{\lambda_i}), G_i). \quad (8)$$

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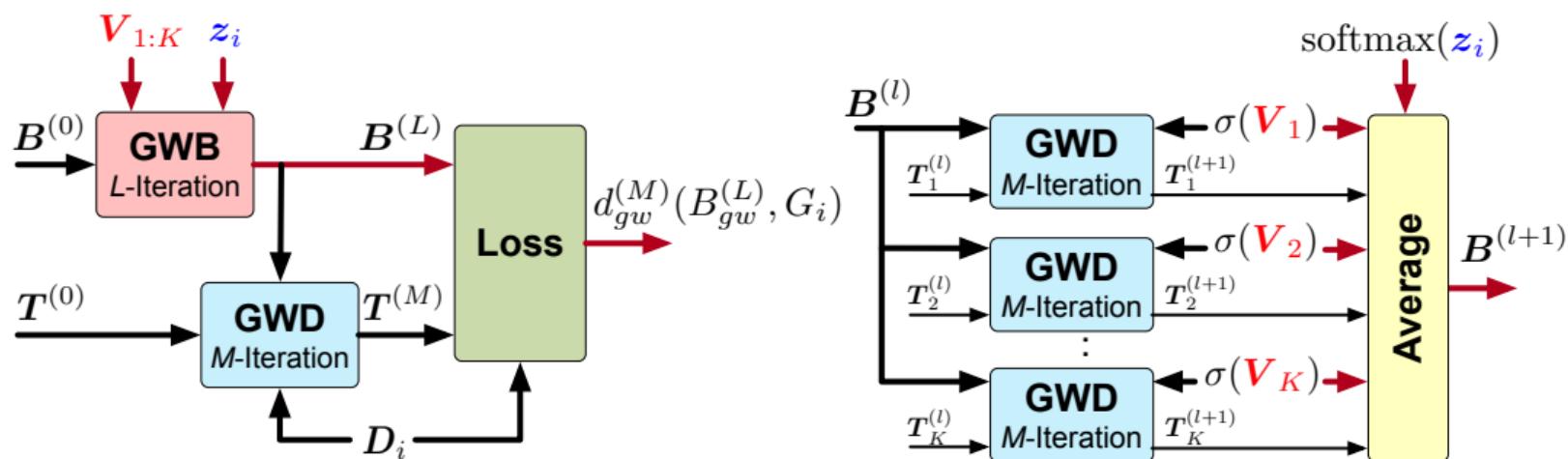
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From transductive to inductive

The GWF is a transductive model:

$$z_{\text{new}} = \arg \min_z d_{gw}(B_{gw}(\sigma(V_{1:K}), \text{softmax}(z)), G_{\text{new}}). \quad (9)$$

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Make an **inductive GWF** model [Xu, et al. ICML 2020 submission]:

$$\min_{\mathbf{V}_{1:K}, \theta} \sum_{i=1}^I d_{gw}(B_{gw}(\sigma(\mathbf{V}_{1:K}), \text{softmax}(\underbrace{\text{GCN}_{\theta}(G_i)}_{\mathbf{z}_i})), G_i). \quad (10)$$

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Experiments on molecule clustering

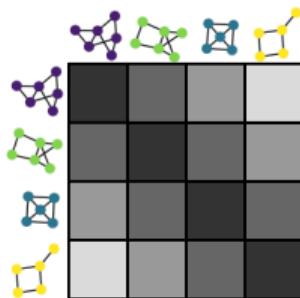
Experiments on molecule clustering

- ▶ AIDS: 2,000 compounds active/inactive to anti-HIV
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GWD Kernel



GWD+Kmeans

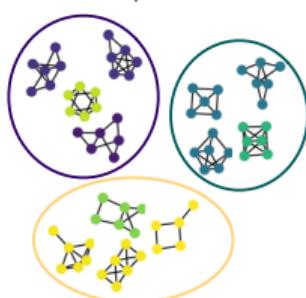


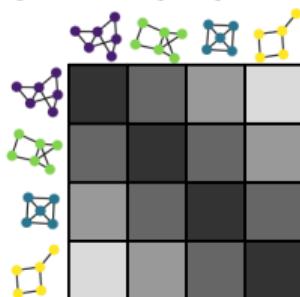
Table: Comparisons on clustering accuracy (%)

Method	AIDS	PROTEIN
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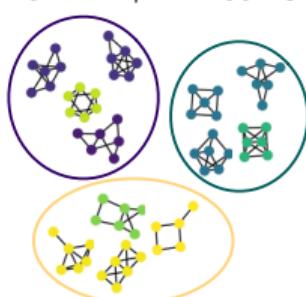
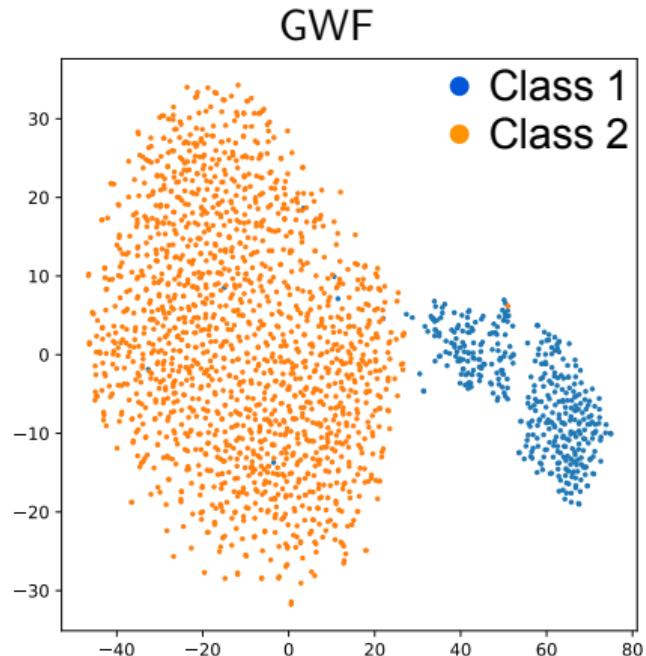


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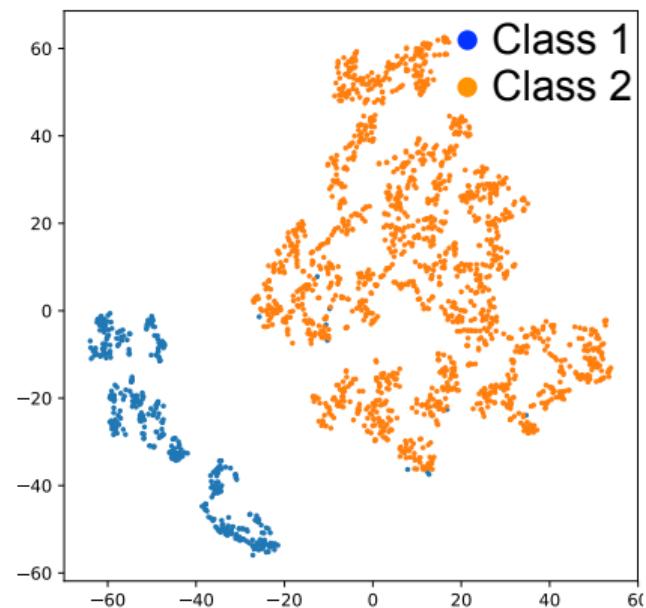
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GWF + Kmeans	99.5 ± 0.4	70.7 ± 0.7
I-GWF + Kmeans	99.2 ± 0.5	73.3 ± 0.6

Visualization of coefficient vectors

AIDS



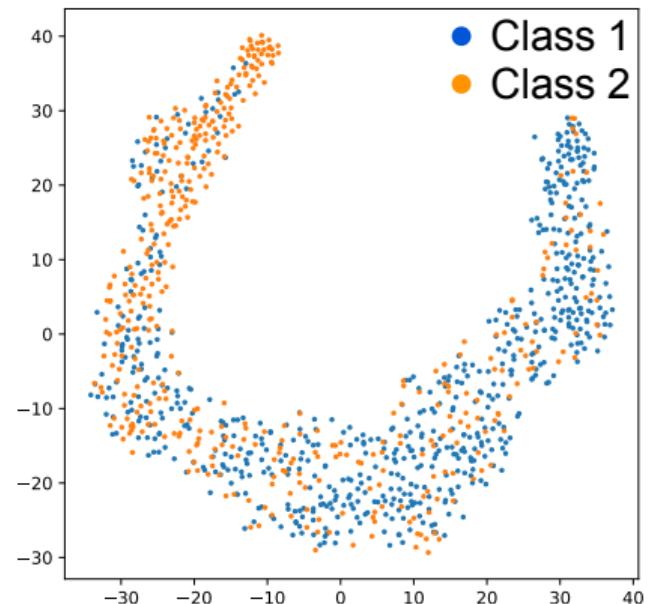
I-GWF



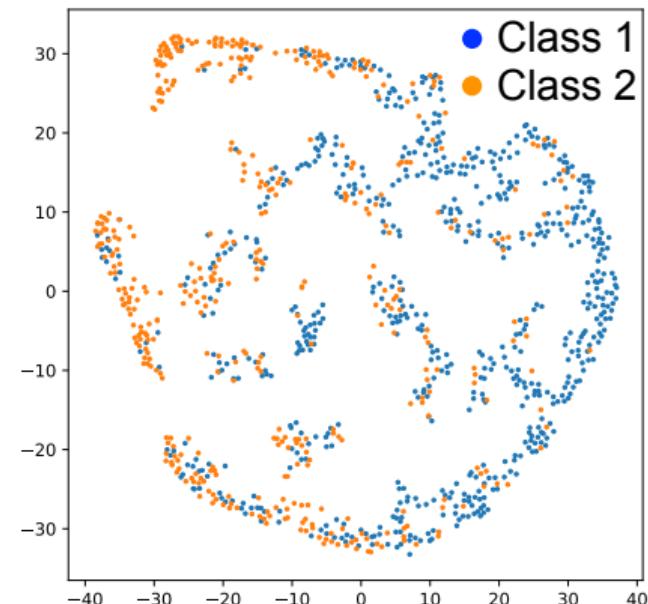
Visualization of coefficient vectors

PROTEIN

GWF



I-GWF



Semi-supervised learning of the I-GWF model

$$\min_{\mathbf{V}_{1:K}, \theta, \phi} \underbrace{\sum_{i=1}^I d_{gw}(B_{gw}(\sigma(\mathbf{V}_{1:K}), \text{softmax}(\text{GCN}_\theta(G_i))), G_i) +}_{\text{Reconstruction loss for both unlabeled and labeled graphs}} \\ \underbrace{\sum_{i \in \mathcal{G}_{\text{labeled}}} \text{loss}(\overbrace{\phi(\text{GCN}_\theta(G_i))}^{\text{classifier}}, l_i)}_{\text{MLE for labeled graphs}}. \quad (12)$$

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	Deep Graph	87.44	60.08
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Summary of the GWL framework

Theoretical
Fundamentals

Gromov-Wasserstein Distance for
Structured Data

Summary of the GWL framework

Optimization
Theoretical
Fundamentals

Proximal Gradient	ADMM	Alternating Opt.	...
Constrained Non-convex Optimization			
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Summary of the GWL framework

Models	Graph convolution networks		Factorization Model
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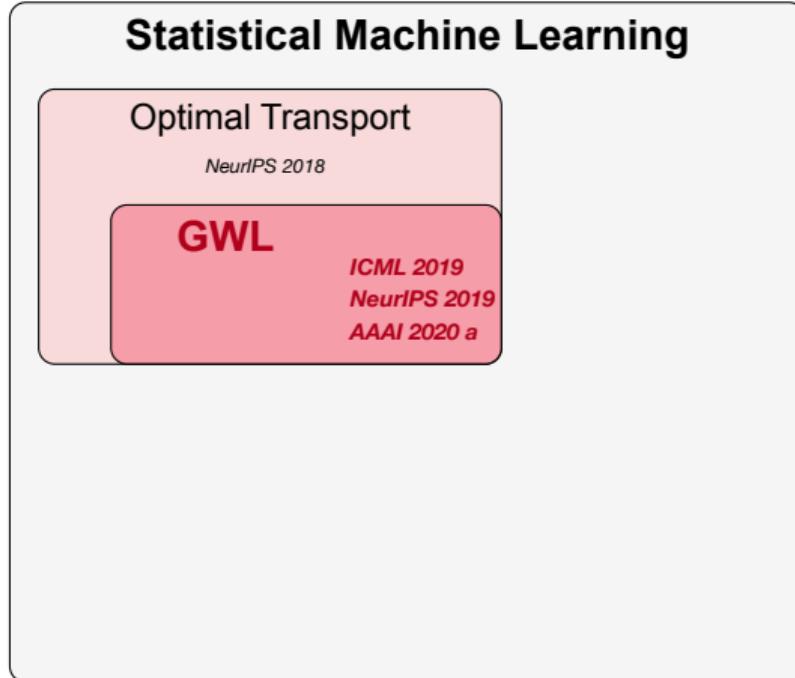
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Applications	Graph Matching	Graph Partitioning	Graph Representation
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Summary of the GWL framework

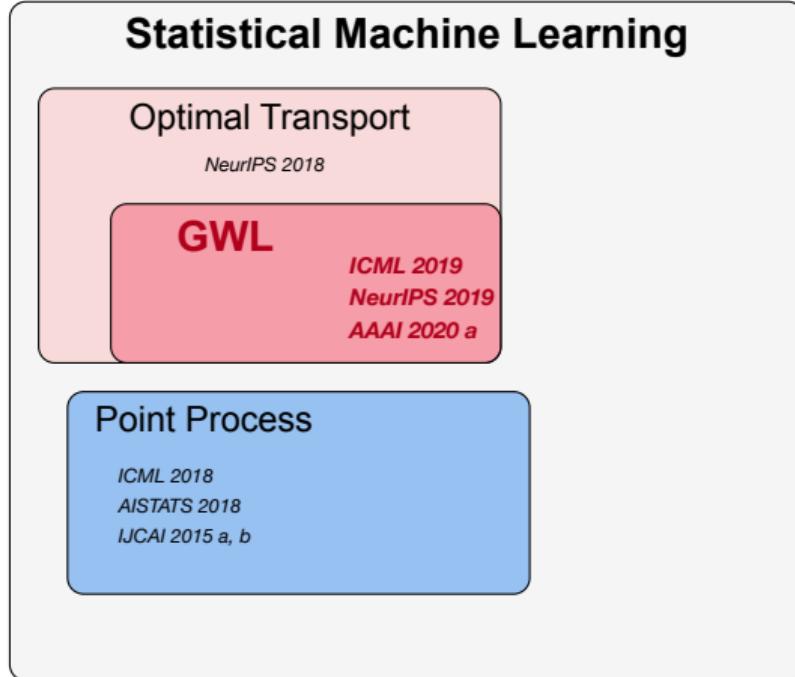
Tasks	PPI Network Alignment	Molecule Clustering and Classification	...
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Existing and ongoing work



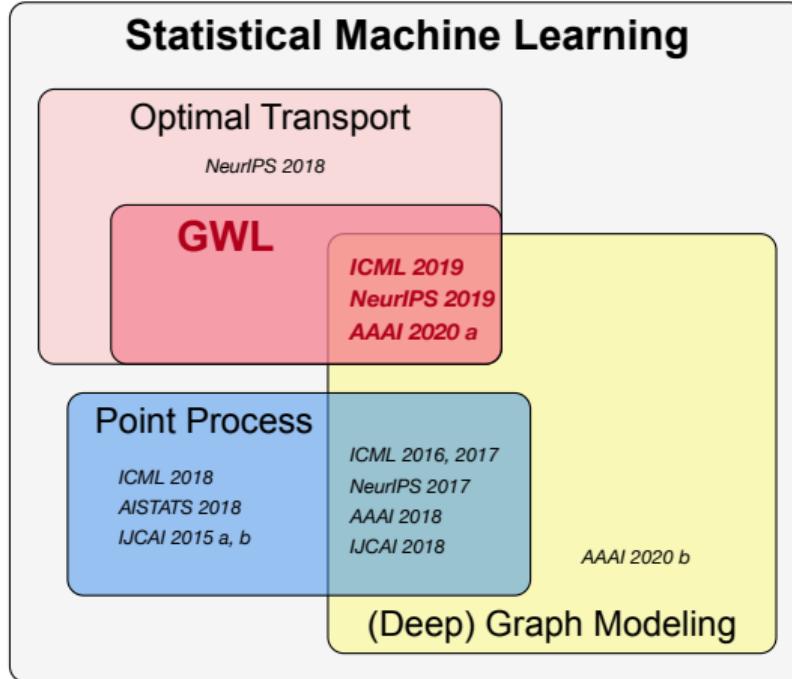
1. [ICML 2019] Hongteng Xu, D. Luo, H. Zha, and L. Carin, *Gromov-Wasserstein Learning for Graph Matching and Node Embedding*.
2. [NeurIPS 2019] Hongteng Xu, D. Luo, L. Carin, *Scalable Gromov-Wasserstein Learning for Graph Partitioning and Matching*.
3. [AAAI 2020 a] Hongteng Xu, *Gromov-Wasserstein Factorization Models for Graph Clustering*.
4. [NeurIPS 2018] Hongteng Xu, W. Wang, W. Liu, and L. Carin, *Distilled wasserstein learning for word embedding and topic modeling*.

Existing and ongoing work



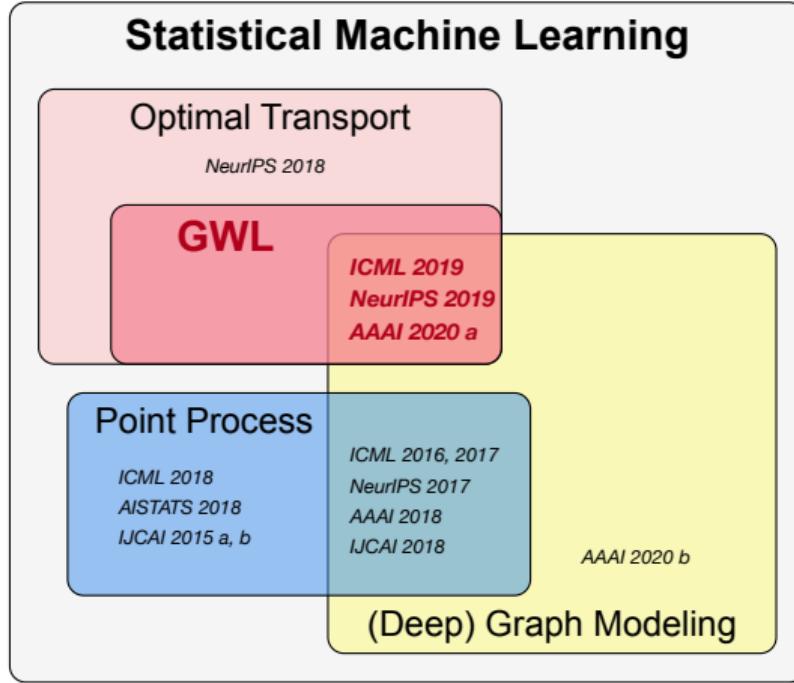
5. [ICML 2018] Hongteng Xu, H. Zha, and L. Carin, *Learning registered point processes from idiosyncratic observations*.
6. [AISTATS 2018] Hongteng Xu, D. Luo, X. Chen, and L. Carin, *Benefits from superposed hawkes processes*.
7. [IJCAI 2015 a] Hongteng Xu, D. Luo, et al., *Multi-Task Multi-Dimensional Hawkes Processes for Modeling Event Sequences*.
8. [IJCAI 2015 b] Hongteng Xu, Y. Zhen, and H. Zha, *Trailer Generation via a Point Process-Based Visual Attractiveness Model*.

Existing and ongoing work



9. [ICML 2016] Hongteng Xu, M. Farajtabar, and H. Zha, *Learning Granger Causality for Hawkes Processes*.
10. [ICML 2017] Hongteng Xu, D. Luo, and H. Zha, *Learning Hawkes processes from short doubly-censored event sequences*.
11. [NeurIPS 2017] Hongteng Xu and H. Zha, *A Dirichlet mixture model of Hawkes processes for event sequence clustering*.
12. [AAAI 2020 b] W. Wang, Hongteng Xu, et al., *Graph-Driven Generative Models for Heterogeneous Multi-Task Learning*.

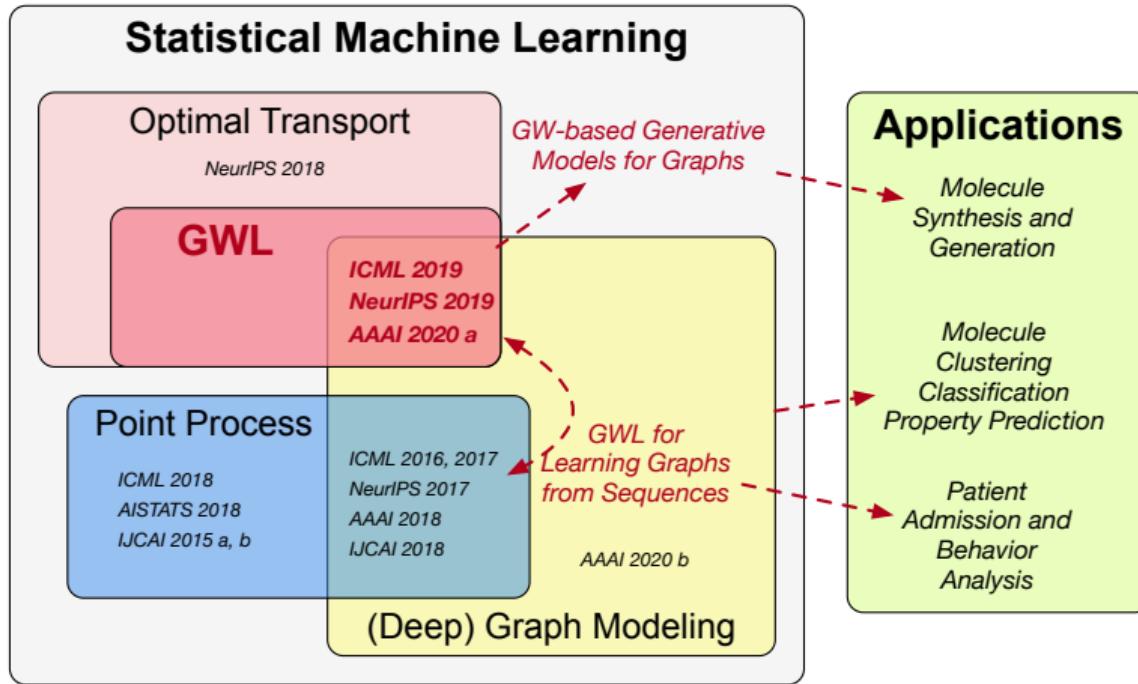
Existing and ongoing work



Miscellaneous (Manifold learning, vision, recommendation, ...)

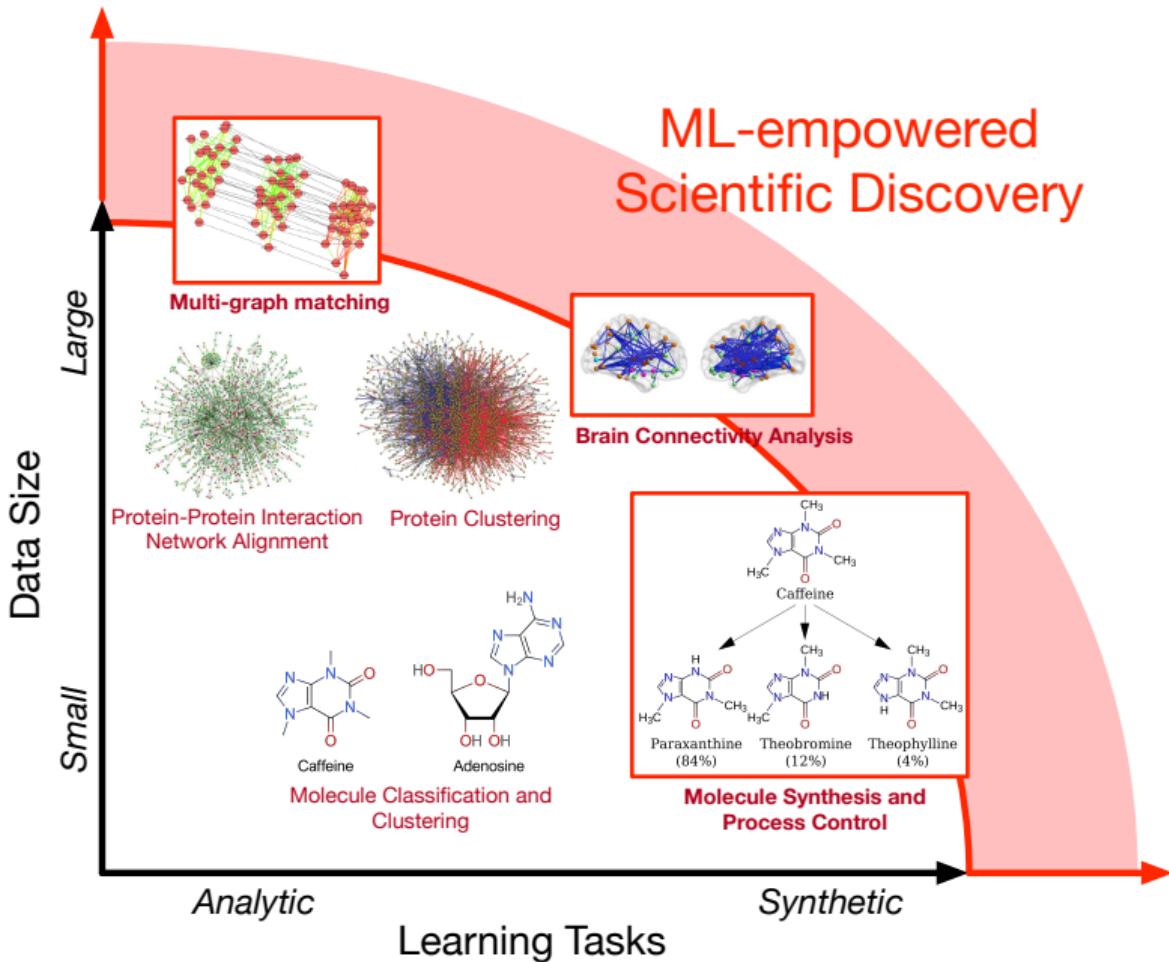
13. [AAAI 2015] Hongteng Xu, M. Davenport, et al., *Active Manifold Learning via Gershgorin Circle Guided Sample Selection*.
14. [ICCV 2015] Hongteng Xu, Y. Zhou, et al., *Unsupervised trajectory clustering via adaptive multi-kernel-based shrinkage*.
15. [CVPR 2017] Hongteng Xu, J. Yan, et al., *Fractal dimension invariant filtering and its CNN-based implementation*.
16. [WSDM 2018] X. Chen, Hongteng Xu, et al., *Sequential recommendation with user memory networks*.

Future work



17. [NeurIPS workshop 2019] D. Luo, **Hongteng Xu**, and L. Carin, *Fused Gromov-Wasserstein Alignment for Hawkes Processes*.
18. [TKDE 2017] **Hongteng Xu**, W. Wu, S. Nemati, et al., *Patient flow prediction via discriminative learning of mutually-correcting processes*.
19. [MLHC 2018] M. Engelhard, **Hongteng Xu**, et al., *Predicting smoking events with a time-varying semi-parametric hawkes process model*.
20. [TechReport 2019] D. Luo, **Hongteng Xu**, and L. Carin, *Interpretable ICD Code Embeddings with Self-and Mutual-Attention Mechanisms*.

Future work



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- ▶ Matthew Engelhard (Duke)



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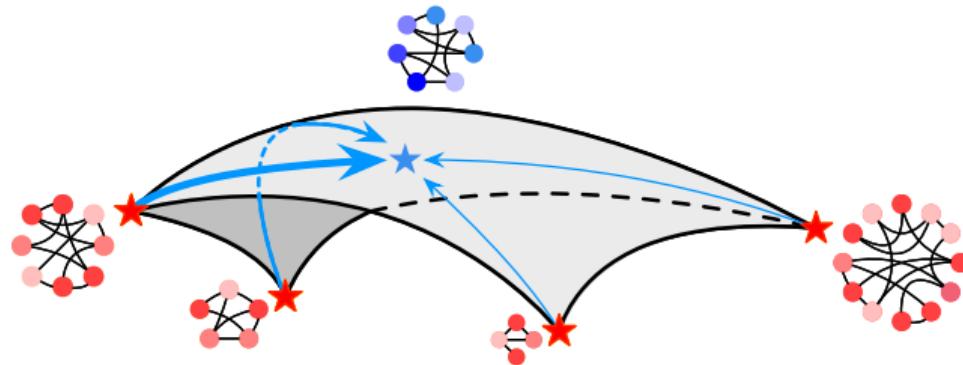
More Information

<https://sites.google.com/view/hongtengxu>

<https://github.com/HongtengXu>

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Synthesize new graphs based on the GWF model



$$\lambda_{\text{new}} \sim P_\lambda,$$

$$G_{\text{new}} = \arg \min_B \sum_{k=1}^K \lambda_k^{\text{new}} d_{gw}(B, G_k).$$

Proposed algorithm: Proximal gradient algorithm (PGA)

Obj. $\min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \boldsymbol{\mu}_Y)} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{T} \mathbf{D}_Y^\top, \mathbf{T} \rangle.$

Init. $m = 0, \mathbf{T}^{(m)} = \boldsymbol{\mu}_X \boldsymbol{\mu}_Y^\top.$

For $m = 0 : M$

$$\begin{aligned} & \min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \boldsymbol{\mu}_Y)} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{T}^{(m)} \mathbf{D}_Y^\top, \mathbf{T} \rangle + \gamma \underbrace{\text{KL}(\mathbf{T} \| \mathbf{T}^{(m)})}_{\text{Proximal}} \\ &= \min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \boldsymbol{\mu}_Y)} \underbrace{\langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{T}^{(m)} \mathbf{D}_Y^\top - \gamma \log \mathbf{T}^{(m)}, \mathbf{T} \rangle}_{\text{constant}} - \gamma \mathsf{H}(\mathbf{T}). \end{aligned} \tag{13}$$

1. Compute $\Phi = \exp\left(\frac{\mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{T}^{(m)} \mathbf{D}_Y^\top}{\gamma}\right) \odot \mathbf{T}^{(m)}, \mathbf{a} = \boldsymbol{\mu}_X.$
2. Sinkhorn-Knopp Iterations:
 - ▶ Repeat $\mathbf{b} = \frac{\boldsymbol{\mu}_Y}{\Phi^\top \mathbf{a}}$ and $\mathbf{a} = \frac{\boldsymbol{\mu}_X}{\Phi \mathbf{b}}$ until convergence
3. $\mathbf{T}^{(m+1)} = \text{diag}(\mathbf{a}) \Phi \text{diag}(\mathbf{b}).$

Proposed algorithm: Bregman ADMM (B-ADMM)

$$\min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \cdot), \mathbf{S} \in \Pi(\cdot, \boldsymbol{\mu}_Y), \mathbf{T} = \mathbf{S}} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S} \mathbf{D}_Y^\top, \mathbf{T} \rangle, \quad (14)$$

Introduce a **dual variable** \mathbf{Z} and initialize $\mathbf{Z}^{(0)} = \mathbf{0}$, $\mathbf{T}^{(0)} = \mathbf{S}^{(0)} = \boldsymbol{\mu}_X \boldsymbol{\mu}_Y^\top$:

Proposed algorithm: Bregman ADMM (B-ADMM)

$$\min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \cdot), \mathbf{S} \in \Pi(\cdot, \boldsymbol{\mu}_Y), \mathbf{T} = \mathbf{S}} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S} \mathbf{D}_Y^\top, \mathbf{T} \rangle, \quad (14)$$

Introduce a **dual variable** \mathbf{Z} and initialize $\mathbf{Z}^{(0)} = \mathbf{0}$, $\mathbf{T}^{(0)} = \mathbf{S}^{(0)} = \boldsymbol{\mu}_X \boldsymbol{\mu}_Y^\top$:

$$\begin{aligned} \mathbf{T}^{(m+1)} &= \arg \min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \cdot)} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S}^{(m)} \mathbf{D}_Y^\top, \mathbf{T} \rangle + \\ &\quad \langle \mathbf{Z}^{(m)}, \mathbf{T} - \mathbf{S}^{(m)} \rangle + \gamma \mathsf{KL}(\mathbf{T} \| \mathbf{S}^{(m)}) = \left(\frac{\boldsymbol{\mu}_X}{\Phi_T \mathbf{1}_Y} \mathbf{1}_Y^\top \right) \odot \Phi_T, \end{aligned}$$

$$\text{where } \Phi_T = \exp\left(-\frac{1}{\gamma}(\mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S}^{(m)} \mathbf{D}_Y^\top + \mathbf{Z}^{(m)})\right) \odot \mathbf{S}^{(m)}$$

Proposed algorithm: Bregman ADMM (B-ADMM)

$$\min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \cdot), \mathbf{S} \in \Pi(\cdot, \boldsymbol{\mu}_Y), \mathbf{T} = \mathbf{S}} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S} \mathbf{D}_Y^\top, \mathbf{T} \rangle, \quad (14)$$

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$$\begin{aligned} \mathbf{T}^{(m+1)} &= \arg \min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \cdot)} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S}^{(m)} \mathbf{D}_Y^\top, \mathbf{T} \rangle + \\ &\quad \langle \mathbf{Z}^{(m)}, \mathbf{T} - \mathbf{S}^{(m)} \rangle + \gamma \text{KL}(\mathbf{T} \| \mathbf{S}^{(m)}) = \left(\frac{\boldsymbol{\mu}_X}{\Phi_T \mathbf{1}_Y} \mathbf{1}_Y^\top \right) \odot \Phi_T, \end{aligned}$$

$$\text{where } \Phi_T = \exp\left(-\frac{1}{\gamma}(\mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S}^{(m)} \mathbf{D}_Y^\top + \mathbf{Z}^{(m)})\right) \odot \mathbf{S}^{(m)}$$

$$\begin{aligned} \mathbf{S}^{(m+1)} &= \arg \min_{\mathbf{S} \in \Pi(\cdot, \boldsymbol{\mu}_t)} \langle -2\mathbf{D}_X^\top \mathbf{T}^{(m+1)} \mathbf{D}_Y, \mathbf{S} \rangle + \langle \mathbf{Z}^{(m)}, \mathbf{T}^{(m+1)} - \mathbf{S} \rangle + \\ &\quad \gamma \text{KL}(\mathbf{S} \| \mathbf{T}^{(m+1)}) = (\mathbf{1}_X \left(\frac{\boldsymbol{\mu}_Y}{\Phi_S^\top \mathbf{1}_X} \right)^\top) \odot \Phi_S, \end{aligned}$$

$$\text{where } \Phi_S = \exp\left(\frac{1}{\gamma}(2\mathbf{D}_X^\top \mathbf{T}^{(m+1)} \mathbf{D}_Y + \mathbf{Z}^{(m)})\right) \odot \mathbf{T}^{(m)}$$

Proposed algorithm: Bregman ADMM (B-ADMM)

$$\min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \cdot), \mathbf{S} \in \Pi(\cdot, \boldsymbol{\mu}_Y), \mathbf{T} = \mathbf{S}} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S} \mathbf{D}_Y^\top, \mathbf{T} \rangle, \quad (14)$$

Introduce a **dual variable \mathbf{Z}** and initialize $\mathbf{Z}^{(0)} = \mathbf{0}$, $\mathbf{T}^{(0)} = \mathbf{S}^{(0)} = \boldsymbol{\mu}_X \boldsymbol{\mu}_Y^\top$:

$$\begin{aligned} \mathbf{T}^{(m+1)} &= \arg \min_{\mathbf{T} \in \Pi(\boldsymbol{\mu}_X, \cdot)} \langle \mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S}^{(m)} \mathbf{D}_Y^\top, \mathbf{T} \rangle + \\ &\quad \langle \mathbf{Z}^{(m)}, \mathbf{T} - \mathbf{S}^{(m)} \rangle + \gamma \text{KL}(\mathbf{T} \| \mathbf{S}^{(m)}) = \left(\frac{\boldsymbol{\mu}_X}{\Phi_T \mathbf{1}_Y} \mathbf{1}_Y^\top \right) \odot \Phi_T, \end{aligned}$$

$$\text{where } \Phi_T = \exp\left(-\frac{1}{\gamma}(\mathbf{D}_{XY} - 2\mathbf{D}_X \mathbf{S}^{(m)} \mathbf{D}_Y^\top + \mathbf{Z}^{(m)})\right) \odot \mathbf{S}^{(m)}$$

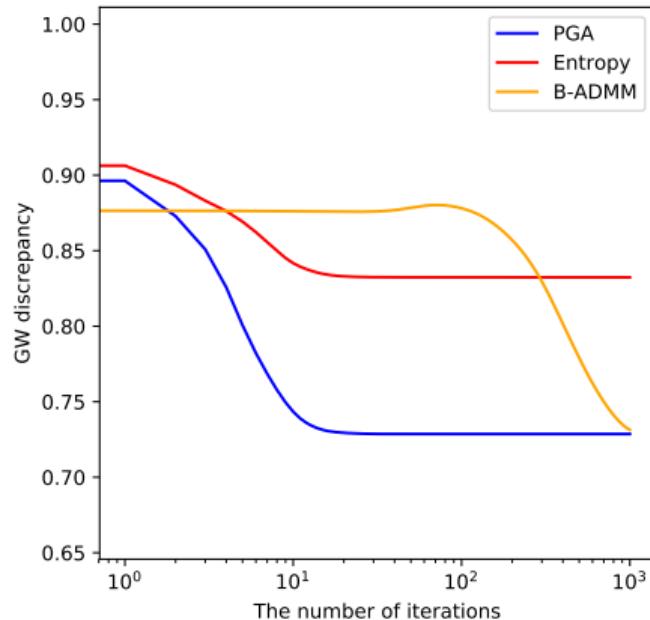
$$\begin{aligned} \mathbf{S}^{(m+1)} &= \arg \min_{\mathbf{S} \in \Pi(\cdot, \boldsymbol{\mu}_t)} \langle -2\mathbf{D}_X^\top \mathbf{T}^{(m+1)} \mathbf{D}_Y, \mathbf{S} \rangle + \langle \mathbf{Z}^{(m)}, \mathbf{T}^{(m+1)} - \mathbf{S} \rangle + \\ &\quad \gamma \text{KL}(\mathbf{S} \| \mathbf{T}^{(m+1)}) = (\mathbf{1}_X \left(\frac{\boldsymbol{\mu}_Y}{\Phi_S^\top \mathbf{1}_X} \right)^\top) \odot \Phi_S, \end{aligned}$$

$$\text{where } \Phi_S = \exp\left(\frac{1}{\gamma}(2\mathbf{D}_X^\top \mathbf{T}^{(m+1)} \mathbf{D}_Y + \mathbf{Z}^{(m)})\right) \odot \mathbf{T}^{(m)}$$

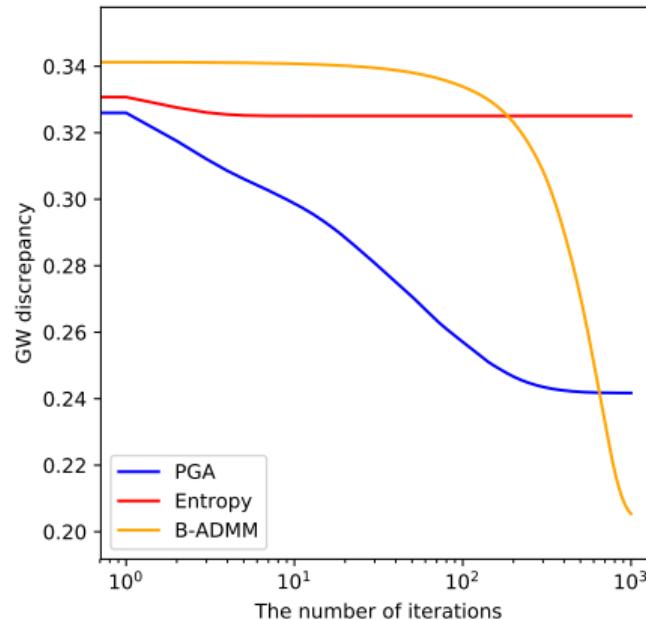
$$\mathbf{Z}^{(m+1)} = \mathbf{Z}^{(m)} + \gamma(\mathbf{T}^{(m+1)} - \mathbf{S}^{(m+1)}).$$

Empirical convergence

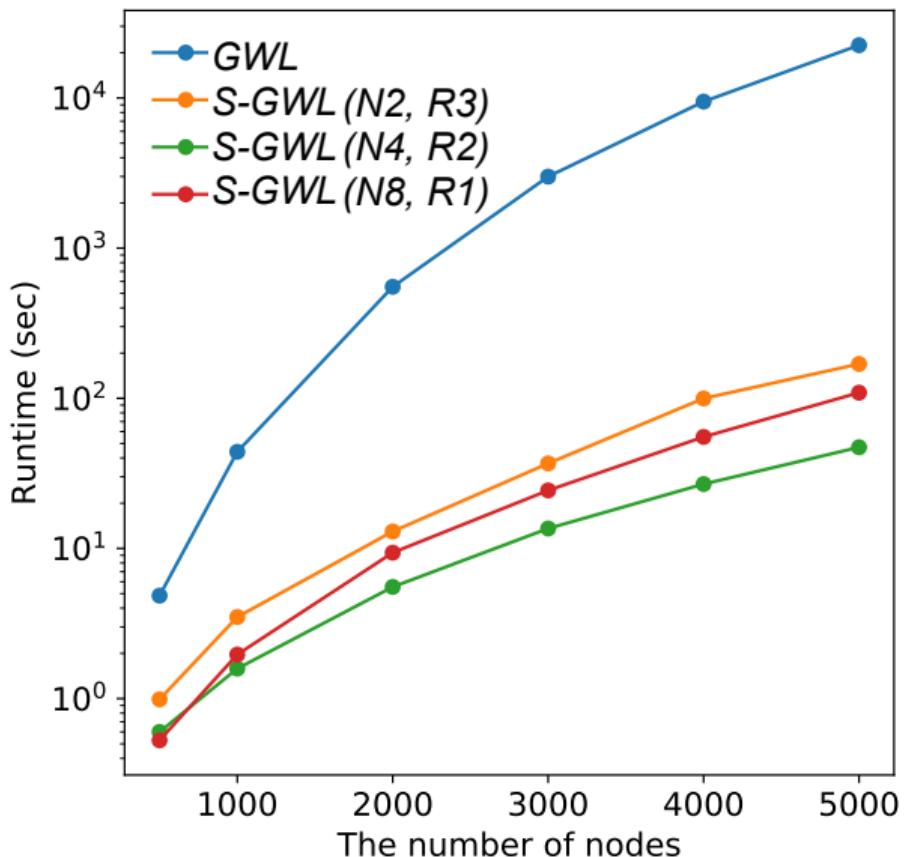
Undirected graph



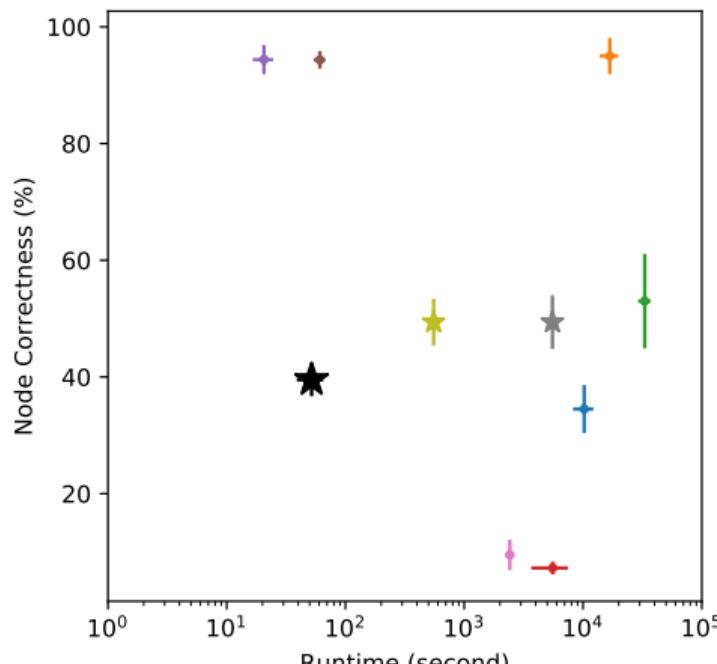
Directed graph



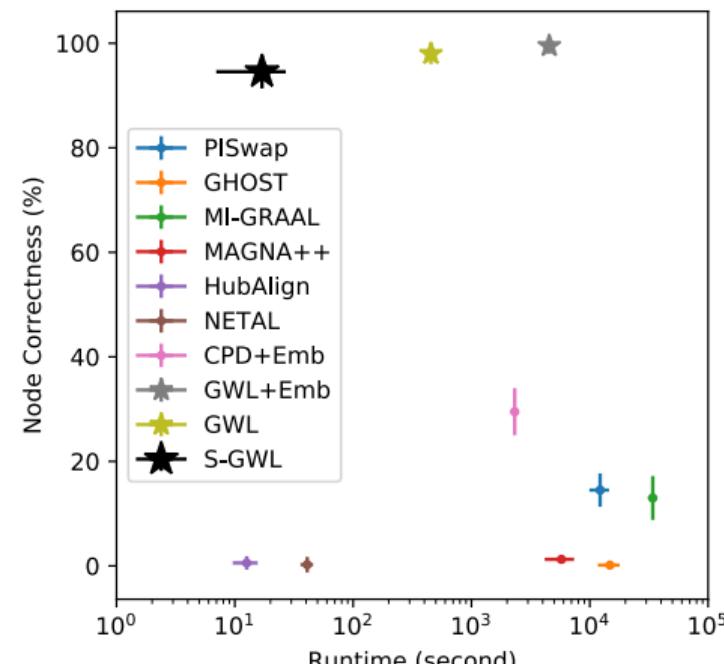
Improvements on scalability



More experimental results on graph matching



(a) BA graphs



(b) GRP graphs