Synthetic Counterfactual Networks

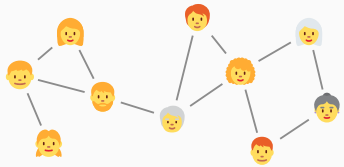
Chen-Wei Hsiang

(University College London & CeMMAP)

This version: November 7, 2026 (Click here for the latest version)

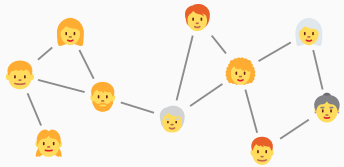
Challenges in Empirical Analysis with Network Interaction

Network structure matters for empirical analysis in multiple ways:

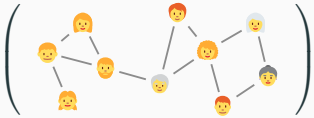


Challenges in Empirical Analysis with Network Interaction

Network structure matters for empirical analysis in multiple ways:

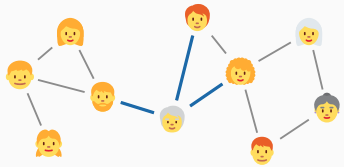


- Network itself may be the object of interest

Network statistics of 

Challenges in Empirical Analysis with Network Interaction

Network structure matters for empirical analysis in multiple ways:

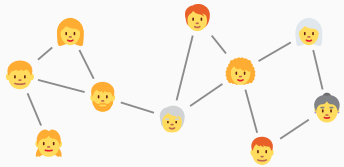


- Network itself may be the object of interest
- Individual's outcome depends on their peers' characteristics or outcomes

$$\text{'s outcome} = \beta \times \text{'s characteristics} + \gamma \times (\text{ \& \& })\text{'s characteristics}$$

Challenges in Empirical Analysis with Network Interaction

Network structure matters for empirical analysis in multiple ways:

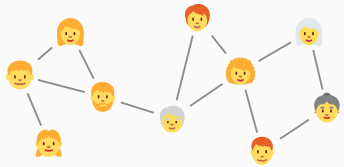


- Network itself may be the object of interest
- Individual's outcome depends on their peers' characteristics or outcomes
- Aggregate outcomes may depend on how individuals are connected



Challenges in Empirical Analysis with Network Interaction

Network structure matters for empirical analysis in multiple ways:



- Network itself may be the object of interest
- Individual's outcome depends on their peers' characteristics or outcomes
- Aggregate outcomes may depend on how individuals are connected

Studying the underlying network structure is important

Challenges in Empirical Analysis with Network Interaction

Network structure matters for empirical analysis in multiple ways:



- Network itself may be the object of interest
- Individual's outcome depends on their peers' characteristics or outcomes
- Aggregate outcomes may depend on how individuals are connected

Studying the underlying network structure is important

But treatment intervention may alter the network

Intervention Changes Network

The challenge in the empirical analysis with network interaction

Treatment intervention may alter the underlying network structure

Empirical motivation: informal risk-sharing networks (Banerjee et al., 2024)

- Microfinance (MF) lender entered 43 of 75 villages in Karnataka, India (2007-2010)
- Formal credit shrinks the informal lending network
- Relative to non-MF villages, exposure to MF dropped network density by **11%**

Intervention Changes Network

The challenge in the empirical analysis with network interaction

Treatment intervention may alter the underlying network structure

Empirical motivation: informal risk-sharing networks (Banerjee et al., 2024)

- Microfinance (MF) lender entered 43 of 75 villages in Karnataka, India (2007-2010)
- Formal credit shrinks the informal lending network
- Relative to non-MF villages, exposure to MF dropped network density by **11%**
  - The least-likely borrowers lose the most informal borrowing and risk sharing
  - Links between two *unlikely* borrowers dissolve at least as often as links involving likely ones

Intervention Changes Network

The challenge in the empirical analysis with network interaction

Treatment intervention may alter the underlying network structure

Empirical motivation: informal risk-sharing networks (Banerjee et al., 2024)

- Microfinance (MF) lender entered 43 of 75 villages in Karnataka, India (2007-2010)
- Formal credit shrinks the informal lending network
- Relative to non-MF villages, exposure to MF dropped network density by **11%**
  - The least-likely borrowers lose the most informal borrowing and risk sharing
  - Links between two *unlikely* borrowers dissolve at least as often as links involving likely ones

There is more underlying heterogeneity

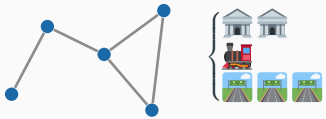
Counterfactual Network Structure is Hard to Measure

Average link probability change is not enough to tell the whole story

A policy creates some links and destroys others

In Auerbach and Cai (2025)

- Treated–control village pair selected for similarity in pre-treatment village-level covariates
  - Village no. 44 (control; non-MF) vs village no. 57 (treated; MF)





Counterfactual Network Structure is Hard to Measure

Average link probability change is not enough to tell the whole story

A policy creates some links and destroys others

In Auerbach and Cai (2025)

- Treated–control village pair selected for similarity in pre-treatment village-level covariates
  - Village no. 44 (control; non-MF) vs village no. 57 (treated; MF)
- Assuming two networks are *equal up to node relabeling* (weak isomorphism)
  - Villages no. 44 and no. 57 serve as the counterfactual networks for each other

Counterfactual Network Structure is Hard to Measure

Average link probability change is not enough to tell the whole story

A policy creates some links and destroys others

In Auerbach and Cai (2025)

- Treated–control village pair selected for similarity in pre-treatment village-level covariates
  - Village no. 44 (control; non-MF) vs village no. 57 (treated; MF)
- Assuming two networks are *equal up to node relabeling* (weak isomorphism)
  - Villages no. 44 and no. 57 serve as the counterfactual networks for each other
- Results: the structural rearrangement is beyond the net effect, but can only be *bounded*

$$\begin{cases} \text{Negative effects on connection changes:} & [8.30\%, 11.93\%] \\ \text{Positive effects on connection changes:} & [7.69\%, 11.03\%] \end{cases} \Rightarrow \text{Total disruption: } [15.99\%, 22.96\%]$$

Counterfactual Network Structure is Hard to Measure

Average link probability change is not enough to tell the whole story

A policy creates some links and destroys others

In Auerbach and Cai (2025)

- Treated–control village pair selected for similarity in pre-treatment village-level covariates
  - Village no. 44 (control; non-MF) vs village no. 57 (treated; MF)
- Assuming two networks are *equal up to node relabeling* (weak isomorphism)
  - Villages no. 44 and no. 57 serve as the counterfactual networks for each other
- Results: the structural rearrangement is beyond the net effect, but can only be *bounded*

$$\begin{cases} \text{Negative effects on connection changes:} & [8.30\%, 11.93\%] \\ \text{Positive effects on connection changes:} & [7.69\%, 11.03\%] \end{cases} \Rightarrow \text{Total disruption: } [15.99\%, 22.96\%]$$

Is there a better approach to study beyond bounds on average changes?
Moreover, can we identify/estimate the individual-level link change after intervention?

More Information Available to Pin Down the Counterfactual Network

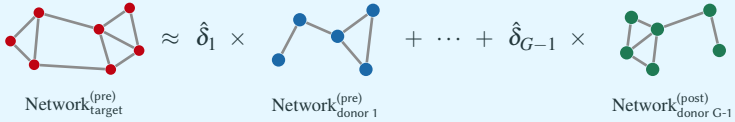
- Not only do we have village no. 44 (control; non-MF) and village no. 57 (treated; MF), but we also have a total of **75 villages**, with **43 of them being treated & 32 of them not**

More Information Available to Pin Down the Counterfactual Network

- Not only do we have village no. 44 (control; non-MF) and village no. 57 (treated; MF), but we also have a total of **75 villages**, with **43 of them being treated & 32 of them not**

Conceptual Idea (Motivated by Synthetic Control Method)

- **With pre-treatment networks, approximate the target by the convex combination of donors**

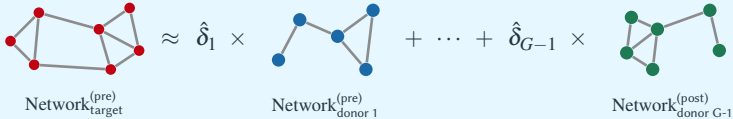


More Information Available to Pin Down the Counterfactual Network

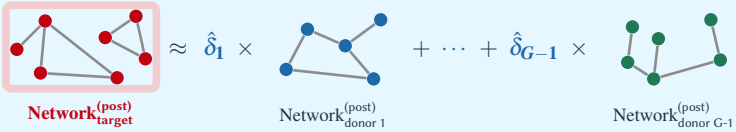
- Not only do we have village no. 44 (control; non-MF) and village no. 57 (treated; MF), but we also have a total of **75 villages**, with **43 of them being treated & 32 of them not**

Conceptual Idea (Motivated by Synthetic Control Method)

- **With pre-treatment networks, approximate the target by the convex combination of donors**



- **Carry forward the learned weights to post-treatment period and estimate $\text{Network}^{(\text{post})}_{\text{target}}$**

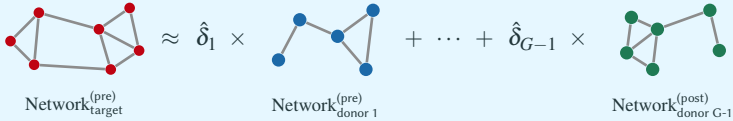


More Information Available to Pin Down the Counterfactual Network

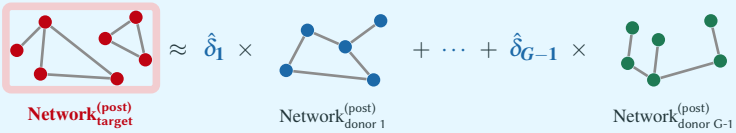
- Not only do we have village no. 44 (control; non-MF) and village no. 57 (treated; MF), but we also have a total of **75 villages**, with **43 of them being treated & 32 of them not**

Conceptual Idea (Motivated by Synthetic Control Method)

- **With pre-treatment networks, approximate the target by the convex combination of donors**



- **Carry forward the learned weights to post-treatment period and estimate $\text{Network}^{(\text{post})}_{\text{target}}$**



Unlike scalar outcomes in SCM, which can be "compared" by simple subtraction, how should we "compare" networks?

Challenges and Contribution

Challenges when trying to compare networks

- **Different network sizes**
  - $N_g \neq N_G$: two networks cannot be lined up node-by-node the way scalar outcomes are
  - Even if $N_g = N_G$, directly subtracting two networks won't work as nodes are exchangeable

Challenges and Contribution

Challenges when trying to compare networks

- **Different network sizes**
  - $N_g \neq N_G$: two networks cannot be lined up node-by-node the way scalar outcomes are
  - Even if $N_g = N_G$, directly subtracting two networks won't work as nodes are exchangeable
- **Two entangled sources of heterogeneity**
  - *Individual characteristics* are distributed differently across different networks
  - *Network formation models* themselves differ across environments

Challenges and Contribution

Challenges when trying to compare networks

- **Different network sizes**
  - $N_g \neq N_G$: two networks cannot be lined up node-by-node the way scalar outcomes are
  - Even if $N_g = N_G$, directly subtracting two networks won't work as nodes are exchangeable
- **Two entangled sources of heterogeneity**
  - *Individual characteristics* are distributed differently across different networks
  - *Network formation models* themselves differ across environments
- **Pair-level information**
  - Recovering the entire counterfactual network is already hard
  - We aim to *trace every individual pair link across two treatment statuses* for the target network

Challenges and Contribution

Challenges when trying to compare networks

- **Different network sizes**
  - $N_g \neq N_G$: two networks cannot be lined up node-by-node the way scalar outcomes are
  - Even if $N_g = N_G$, directly subtracting two networks won't work as nodes are exchangeable
- **Two entangled sources of heterogeneity**
  - *Individual characteristics* are distributed differently across different networks
  - *Network formation models* themselves differ across environments
- **Pair-level information**
  - Recovering the entire counterfactual network is already hard
  - We aim to *trace every individual pair link across two treatment statuses* for the target network

All of these challenges are addressed

- Proposed method imputes the counterfactual network
- It can be used in situations where the counterfactual network itself is the target of interest or for downstream regression with another outcome variable

Related Literature

Synthetic control method and its extension

- Synthetic control method

  Abadie et al. (2010); Abadie (2021); ...

- Functional SC: can only recover entire functional data but not able to trace individuals

  Gunsilius (2023); Lin (2025); Kurisu et al. (2025); ...

Network estimation

- Denoising through neighborhood approach

  Zhang et al. (2017); Zeleneev (2020); Deaner et al. (2025); ...

Optimal transport

- Gromov-Wasserstein distance and barycenter

  Mémoli (2011); Peyré et al. (2016); Zhang et al. (2024); Chowdhury and Needham (2020); Martín et al. (2026); ...

Overview

1. **How to "Compare" Networks?** Challenges and Conceptual Solutions
2. Proposed Method: **Synthetic Counterfactual Networks**
3. Identification in the Population Problem
4. Large Sample Theory
5. Simulation
6. Empirical Illustration

How to “Compare” Networks?

Adjacency Matrix and Link Probability

- Consider following two (pre-treatment) networks g and G



Network g



Network G

Adjacency Matrix and Link Probability

- Consider following two (pre-treatment) networks g and G



Network g



Network G

- Rewrite them as adjacency matrices $\left\{A^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]}$ and $\left\{A^{(0)}_{G,k,\ell}\right\}_{k,\ell\in[N_G]}$



Adjacency matrix of g



Adjacency matrix of G

with the model: $\textbf{Link } A^{(w)}_{g,i,j} = \underbrace{\textbf{Link Probability } P^{(w)}_{g,i,j}}_{\text{link probability between individual } i,j\in[N_g]} + \textbf{Noise } e^{(w)}_{g,i,j}$

Adjacency Matrix and Link Probability

- Consider following two (pre-treatment) networks g and G



Network g

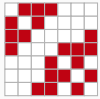


Network G

- Rewrite them as adjacency matrices $\left\{A^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]}$ and $\left\{A^{(0)}_{G,k,\ell}\right\}_{k,\ell\in[N_G]}$



Adjacency matrix of g



Adjacency matrix of G

with the model: **Link** $A^{(w)}_{g,i,j}$ $=$ **Link Probability** $P^{(w)}_{g,i,j}$ $+$ **Noise** $e^{(w)}_{g,i,j}$

$$= f^{(w)}\Big(\underbrace{\xi_{g,i}\ ,\ \xi_{g,j}}\ ,\ \underbrace{\gamma_g}\ \Big) + e^{(w)}_{g,i,j}$$

individual latent characteristics $\xi_{g,i} \overset{i.i.d.}{\sim} \mu_g$, where μ_g can be different in different networks

unobserved network-specific effect, where γ_g and γ_G can be different

Adjacency Matrix and Link Probability

- Consider following two (pre-treatment) networks g and G



Network g



Network G

- Rewrite them as adjacency matrices $\left\{A^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]}$ and $\left\{A^{(0)}_{G,k,\ell}\right\}_{k,\ell\in[N_G]}$



Adjacency matrix of g



Adjacency matrix of G

with the model: **Link** $A^{(w)}_{g,i,j}$ = **Link Probability** $P^{(w)}_{g,i,j}$ + **Noise** $e^{(w)}_{g,i,j}$

$= f^{(w)}(\ \xi_{g,i}\ ,\ \xi_{g,j}\ ,\ \gamma_g\ ) + e^{(w)}_{g,i,j}$

But "comparing" observed adjacency matrices is complicated by realization noise E

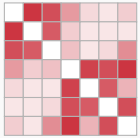
- Differences reflect both underlying link probabilities and random link realizations
- Link probabilities can better capture economically relevant interaction propensities (Cai, 2026)

Denoise and Attempt to Compare Estimated Link Probability

- Denoise adjacency matrices and work on link probabilities $\left\{\hat{P}^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]}$ and $\left\{\hat{P}^{(0)}_{G,k,\ell}\right\}_{k,\ell\in[N_G]}$



Link probabilities of g



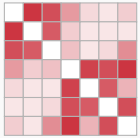
Link probabilities of G

Denoise and Attempt to Compare Estimated Link Probability

- Denoise adjacency matrices and work on link probabilities $\left\{\hat{P}^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]}$ and $\left\{\hat{P}^{(0)}_{G,k,\ell}\right\}_{k,\ell\in[N_G]}$



Link probabilities of g



Link probabilities of G

- Within the same network, we can "compare graphon slices"

$\hat{P}^{(0)}_{g,i,\cdot} = i$  vs $\hat{P}^{(0)}_{g,j,\cdot} = j$ 

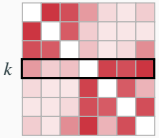
- Individual i and j in network g are similar if they happen to have similar connection profile

Denoise and Attempt to Compare Estimated Link Probability

- Denoise adjacency matrices and work on link probabilities $\left\{\hat{P}^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]}$ and $\left\{\hat{P}^{(0)}_{G,k,\ell}\right\}_{k,\ell\in[N_G]}$



Link probabilities of g



Link probabilities of G

- Can we extend this concept and "compare graphon slices across different networks g & G"?

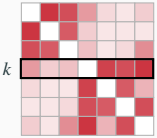
$\hat{P}^{(0)}_{g,i,\cdot} = i$  vs $\hat{P}^{(0)}_{G,k,\cdot} = k$ 

Denoise and Attempt to Compare Estimated Link Probability

- Denoise adjacency matrices and work on link probabilities $\left\{\hat{P}^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]}$ and $\left\{\hat{P}^{(0)}_{G,k,\ell}\right\}_{k,\ell\in[N_G]}$



Link probabilities of g



Link probabilities of G

- Can we extend this concept and "compare graphon slices across different networks g & G"?

$\hat{P}^{(0)}_{g,i,\cdot} = i$  vs $\hat{P}^{(0)}_{G,k,\cdot} = k$ 

- Cross network graphon slices comparison does not work:
  - **Network sizes are different $N_g \neq N_G$, and so are their graphon slices**
  - **Even if $N_g = N_G$, exchangeability means there is no entry-by-entry correspondence**
  - **Even if $\hat{P}^{(0)}_{g,i,\cdot} = \hat{P}^{(0)}_{G,k,\cdot}$, the individual characteristics behind them can be very different**

Entangled Heterogeneity: Individual Characteristics & Network Formation

- After sorting connection profile for i in network g and connection profile for k in network G

$$\text{sort}\left(\hat{P}^{(0)}_{g,i,\cdot}\right) = i \qquad \text{sort}\left(\hat{P}^{(0)}_{G,k,\cdot}\right) = k$$

their graphon slices happen to have similar link probabilities empirical distributions



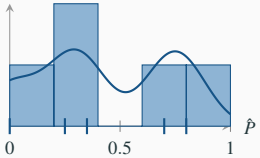
Entangled Heterogeneity: Individual Characteristics & Network Formation

- After sorting connection profile for i in network g and connection profile for k in network G

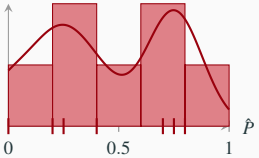
$\text{sort}\left(\hat{P}^{(0)}_{g,i,\cdot}\right) = i$ 

$\text{sort}\left(\hat{P}^{(0)}_{g,i,\cdot}\right) = k$ 

their graphon slices happen to have similar link probabilities empirical distributions



vs



- In network g
  - 👴 Age: $\{20, \overset{\boldsymbol{i}}{22}, 24, 25, 27\}$
  - 🏘️ Sparse living environment

  $\hat{P}$ are mostly driven by physical distances

In network G

- 👴 Age: $\{21, 27, 40, 54, \overset{\boldsymbol{k}}{57}, 62, 70\}$
- 🏘️ Dense living environment

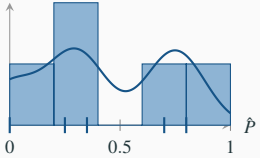
$\hat{P}$ are mostly driven by age differences

Entangled Heterogeneity: Individual Characteristics & Network Formation

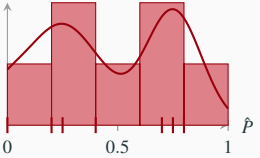
- After sorting connection profile for i in network g and connection profile for k in network G

$$\text{sort}\left(\hat{P}^{(0)}_{g,i,\cdot}\right) = i \qquad \text{sort}\left(\hat{P}^{(0)}_{g,i,\cdot}\right) = k$$

their graphon slices happen to have similar link probabilities empirical distributions



vs



- In network g
  - 👴 Age: $\{20, \overset{i}{22}, 24, 25, 27\}$
  - 🏘 Sparse living environment

  $\hat{P}$ are mostly driven by physical distances

In network G

- 👴 Age: $\{21, 27, 40, 54, \overset{k}{57}, 62, 70\}$
- 🏘 Dense living environment

$\hat{P}$ are mostly driven by age differences

- **Proposed solution:**

  Change the object of comparison and fix one source of heterogeneity

Internal Relational Structures

Instead of comparing $\hat{P}$ across networks, we compare the internal relational structures

- For a pair i and j in network g, take the difference between their graphon slices

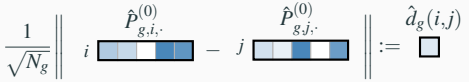
$$\frac{1}{\sqrt{N_g}} \left\| \hat{P}^{(0)}_{g,i,\cdot} - \hat{P}^{(0)}_{g,j,\cdot} \right\| := \hat{d}_g(i,j)$$



Internal Relational Structures

Instead of comparing $\hat{P}$ across networks, we compare the internal relational structures

- For a pair i and j in network g, take the difference between their graphon slices



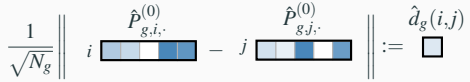
- $\hat{d}_g(i,j)$ measures similarity between i & j by comparing their connection profiles in g

Internal Relational Structures

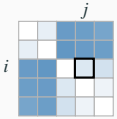
Instead of comparing $\hat{P}$ across networks, we compare the internal relational structures

- For a pair i and j in network g, take the difference between their graphon slices

$$\frac{1}{\sqrt{N_g}} \left\| \hat{P}^{(0)}_{g,i,\cdot} - \hat{P}^{(0)}_{g,j,\cdot} \right\| := \hat{d}_g(i,j)$$



- $\hat{d}_g(i,j)$ measures similarity between i & j by comparing their connection profiles in g



Internal structure of g
measured by $\hat{d}_g(i,j)\ \forall i,j \in [N_g]$

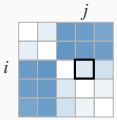
Internal Relational Structures

Instead of comparing $\hat{P}$ across networks, we compare the internal relational structures

- For a pair i and j in network g, take the difference between their graphon slices

$$\frac{1}{\sqrt{N_g}} \left\| \hat{P}^{(0)}_{g,i,\cdot} - \hat{P}^{(0)}_{g,j,\cdot} \right\| := \hat{d}_g(i,j)$$

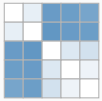
- $\hat{d}_g(i,j)$ measures similarity between i & j by comparing their connection profiles in g



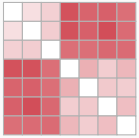
Internal structure of g
measured by $\hat{d}_g(i,j)\ \forall i,j \in [N_g]$

- Since $\hat{P}^{(0)}_{g,i,\cdot}$ and $\hat{P}^{(0)}_{g,j,\cdot}$ are both in network g, network-specific formation is held the same
- $\hat{d}_g(i,j)$ only reflects **how different i and j's characteristics are**

Alignment via Internal Relational Structures $\hat{d}_g$ and $\hat{d}_G$

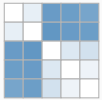


Internal structure of g
measured by $\hat{d}_g(i,j)\ \forall i,j \in [N_g]$

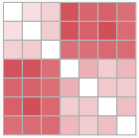


Internal structure of G
measured by $\hat{d}_G(k,\ell)\ \forall k,\ell \in [N_G]$

Alignment via Internal Relational Structures $\hat{d}_g$ and $\hat{d}_G$



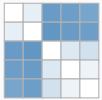
Internal structure of g
measured by $\hat{d}_g(i,j)\ \forall i,j \in [N_g]$



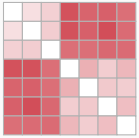
Internal structure of G
measured by $\hat{d}_G(k,\ell)\ \forall k,\ell \in [N_G]$

- Despite that *network-specific effects are removed by using internal relational structures*
  - There is still no cross-network entry-by-entry correspondence
  - Matrix sizes are still different, so an one-to-one alignment cannot work

Alignment via Internal Relational Structures $\hat{d}_g$ and $\hat{d}_G$



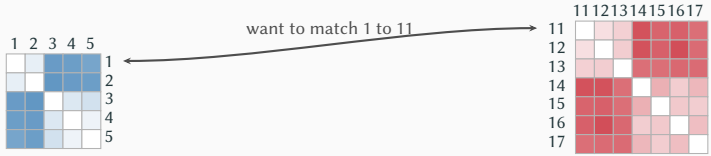
Internal structure of g
measured by $\hat{d}_g(i,j)\ \forall i,j \in [N_g]$



Internal structure of G
measured by $\hat{d}_G(k,\ell)\ \forall k,\ell \in [N_G]$

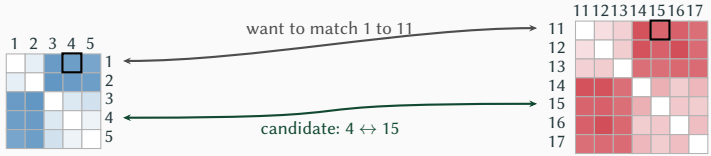
- Despite that *network-specific effects are removed by using internal relational structures*
  - There is still no cross-network entry-by-entry correspondence
  - Matrix sizes are still different, so an one-to-one alignment cannot work
- We tackle this issue by *softly aligning the networks*

Alignment via Internal Relational Structures $\hat{d}_g$ and $\hat{d}_G$



For example, if we want to match 1 in network g to 11 in network G

Alignment via Internal Relational Structures $\hat{d}_g$ and $\hat{d}_G$

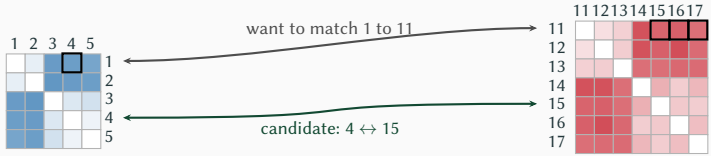


For example, if we want to match 1 in network g to 11 in network G

- Notice that $\begin{cases} \text{in network } g\text{, nodes 1 and 4 are far apart as } \hat{d}_g(1,4) = \square \\ \text{in network } G\text{, nodes 11 and 15 are also far apart as } \hat{d}_G(11,15) = \square \end{cases}$

  If 1 is matched to 11, then 4 should go to someone equally far from 11 inside G, e.g., 15

Alignment via Internal Relational Structures $\hat{d}_g$ and $\hat{d}_G$



For example, if we want to match 1 in network g to 11 in network G

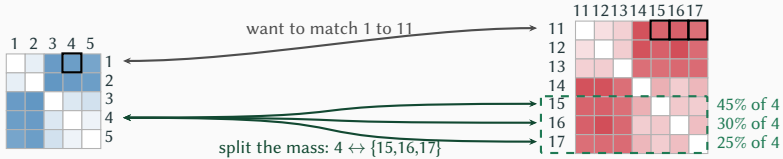
- Notice that $\begin{cases} \text{in network } g, \text{ nodes 1 and 4 are far apart as } \hat{d}_g(1,4) = \square \\ \text{in network } G, \text{ nodes 11 and 15 are also far apart as } \hat{d}_G(11,15) = \square \end{cases}$

  If 1 is matched to 11, then 4 should go to someone equally far from 11 inside G, e.g., 15

- But $\begin{cases} \hat{d}_G(11,16) = \square \\ \hat{d}_G(11,17) = \square \end{cases}$ also have similar color gradient,

  which means that in network G, 16 and 17 sit just as far from 11 as 15 does

Alignment via Internal Relational Structures $\hat{d}_g$ and $\hat{d}_G$



For example, if we want to match 1 in network g to 11 in network G

- Notice that $\begin{cases} \text{in network } g\text{, nodes 1 and 4 are far apart as } \hat{d}_g(1,4) = \blacksquare \\ \text{in network } G\text{, nodes 11 and 15 are also far apart as } \hat{d}_G(11,15) = \blacksquare \end{cases}$

  If 1 is matched to 11, then 4 should go to someone equally far from 11 inside G, e.g., 15

- But $\begin{cases} \hat{d}_G(11,16) = \blacksquare \\ \hat{d}_G(11,17) = \blacksquare \end{cases}$ also have similar color gradient,

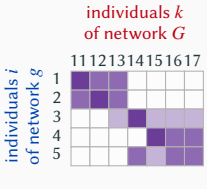
  which means that in network G, 16 and 17 sit just as far from 11 as 15 does

- **So the alignment should be soft**: 4 is shared out over 15, 16, and 17, in proportions

  Every individual of g is spread over the individuals of G with the same **relative position**

What Would Individuals from G Look Like if They Lived in Network g?

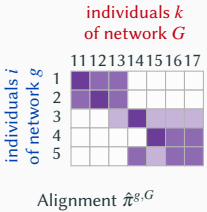
Optimize for soft alignment, we have



Alignment $\hat{\pi}^{g,G}$

What Would Individuals from G Look Like if They Lived in Network g?

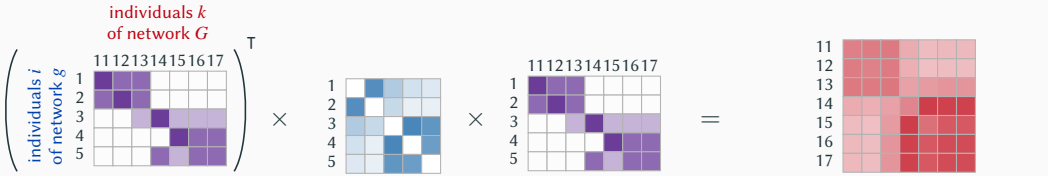
Optimize for soft alignment, we have



- This concept is known as **Gromov-Wasserstein optimal transport** (Mémoli, 2011)
  - Compare two spaces via their within-space distances, rather than through points themselves
  - The alignment  is the **optimal coupling** for the optimal transport problem
  - Matching needs no $N_g = N_G$ & cross-network comparable individuals

What Would Individuals from G Look Like if They Lived in Network g?

Optimize for soft alignment, we have



- This concept is known as **Gromov-Wasserstein optimal transport** (Mémoli, 2011)
  - Compare two spaces via their within-space distances, rather than through points themselves
  - The alignment  is the **optimal coupling** for the optimal transport problem
  - Matching needs no $N_g = N_G$ & cross-network comparable individuals
- With such *soft* matching, captured by **Gromov-Wasserstein optimal coupling**, we answer "*What would the individuals $k \in \{1, \ldots, N_G\}$ look like if they lived in network environment g?*"

Synthetic Counterfactual Networks

Framework, Observed Data, and Estimand

For each network $g \in \{1, \ldots, G\}$ and treatment status $w \in \{0, 1\}$,

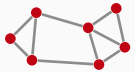
$$
\begin{aligned}
A_{g,i,j}^{(w)} &= P_{g,i,j}^{(w)} + e_{g,i,j}^{(w)} \\
&= f^{(w)}\left(\xi_{g,i}, \xi_{g,j}, \gamma_g\right) + e_{g,i,j}^{(w)}
\end{aligned}
$$

Framework, Observed Data, and Estimand

For each network $g \in \{1, \ldots, G\}$ and treatment status $w \in \{0, 1\}$,

$$\begin{aligned} \boldsymbol{A}_{g,i,j}^{(w)} &= \boldsymbol{P}_{g,i,j}^{(w)} + \boldsymbol{e}_{g,i,j}^{(w)} \\ &= \boldsymbol{f}^{(w)}\left(\boldsymbol{\xi}_{g,i}, \boldsymbol{\xi}_{g,j}, \boldsymbol{\gamma}_g\right) + \boldsymbol{e}_{g,i,j}^{(w)} \end{aligned}$$

Observed data



Pre-treatment target G

$\left\{A_{G,k,\ell}^{(0)}\right\}_{k,\ell \in [N_G]}$

&



Pre-treatment source $g = 1$

$\left\{A_{1,i,j}^{(0)}\right\}_{i,j \in [N_1]}$

$\cdots$



Pre-treatment source $g = G - 1$

$\left\{A_{G-1,m,n}^{(0)}\right\}_{m,n \in [N_{G-1}]}$

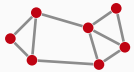
Framework, Observed Data, and Estimand

For each network $g \in \{1, \ldots, G\}$ and treatment status $w \in \{0, 1\}$,

$$A_{g,i,j}^{(w)} = P_{g,i,j}^{(w)} + e_{g,i,j}^{(w)}$$

$$= f^{(w)}(\xi_{g,i}, \xi_{g,j}, \gamma_g) + e_{g,i,j}^{(w)}$$

Observed data



Pre-treatment target G

$\left\{A_{G,k,\ell}^{(0)}\right\}_{k,\ell \in [N_G]}$

&



Pre-treatment source $g = 1$

$\left\{A_{1,i,j}^{(0)}\right\}_{i,j \in [N_1]}$

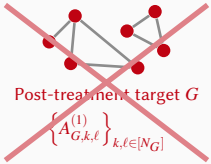
$\cdots$



Pre-treatment source $g = G - 1$

$\left\{A_{G-1,m,n}^{(0)}\right\}_{m,n \in [N_{G-1}]}$

Cannot observe post-treatment target network G



Post-treatment target G

$\left\{A_{G,k,\ell}^{(1)}\right\}_{k,\ell \in [N_G]}$

&



Post-treatment source $g = 1$

$\left\{A_{1,i,j}^{(1)}\right\}_{i,j \in [N_1]}$

$\cdots$



Post-treatment source $g = G - 1$

$\left\{A_{G-1,m,n}^{(1)}\right\}_{m,n \in [N_{G-1}]}$

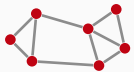
Framework, Observed Data, and Estimand

For each network $g \in \{1, \ldots, G\}$ and treatment status $w \in \{0, 1\}$,

$$A_{g,i,j}^{(w)} = P_{g,i,j}^{(w)} + e_{g,i,j}^{(w)}$$

$$= f^{(w)}(\xi_{g,i}, \xi_{g,j}, \gamma_g) + e_{g,i,j}^{(w)}$$

Observed data



Pre-treatment target G

$\left\{A_{G,k,\ell}^{(0)}\right\}_{k,\ell \in [N_G]}$

&



Pre-treatment source $g = 1$

$\left\{A_{1,i,j}^{(0)}\right\}_{i,j \in [N_1]}$

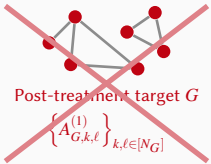
$\cdots$



Pre-treatment source $g = G - 1$

$\left\{A_{G-1,m,n}^{(0)}\right\}_{m,n \in [N_{G-1}]}$

Cannot observe post-treatment target network G



Post-treatment target G

$\left\{A_{G,k,\ell}^{(1)}\right\}_{k,\ell \in [N_G]}$

&



Post-treatment source $g = 1$

$\left\{A_{1,i,j}^{(1)}\right\}_{i,j \in [N_1]}$

$\cdots$



Post-treatment source $g = G - 1$

$\left\{A_{G-1,m,n}^{(1)}\right\}_{m,n \in [N_{G-1}]}$

Goal: Impute the link probability matrix of target network $\left\{P_{G,k,\ell}^{(1)}\right\}_{k,\ell \in [N_G]}$



Proposed Method Overview

- **Step 0. Denoising the adjacency matrices**

Denoise $\{A\} =$  $\cdots$  $=$  $\cdots$  and get $\{\hat{P}\} =$  $\cdots$ 

Proposed Method Overview

- **Step 0. Denoising the adjacency matrices**

  Denoise $\{A\} =$  $\cdots$  $=$  $\cdots$  and get $\{\hat{P}\} =$  $\cdots$ 

- **Step 1. Gromov-Wasserstein alignment and projection**

  For all $\hat{P}$, calculate internal relational structure $\left\{\hat{d}_g\right\}_{g\in[G]}$  $\cdots$ 

  For each sources $\left\{\hat{d}_g\right\}_{g\in[G-1]}$ and the target $\left\{\hat{d}_G\right\}$, find the soft alignment $\hat{\pi}^{g,G}$ 

  With $\hat{\pi}^{g,G}$, project all G's individuals to each source g's environment, get $\hat{Q}_g :=$ 

Proposed Method Overview

- **Step 0. Denoising the adjacency matrices**

  Denoise $\{A\} =$  $\cdots$  $=$  $\cdots$  and get $\{\hat{P}\} =$  $\cdots$ 

- **Step 1. Gromov-Wasserstein alignment and projection**

  For all $\hat{P}$, calculate internal relational structure $\left\{\hat{d}_g\right\}_{g\in[G]}$  $\cdots$ 

  For each sources $\left\{\hat{d}_g\right\}_{g\in[G-1]}$ and the target $\left\{\hat{d}_G\right\}$, find the soft alignment $\hat{\pi}^{g,G}$ 

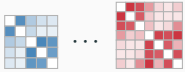
  With $\hat{\pi}^{g,G}$, project all G's individuals to each source g's environment, get $\hat{Q}_g :=$ 

- **Step 2. Gromov-Wasserstein barycentric weights**

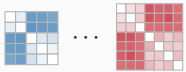
  With projected link probability $\hat{Q}_g$, fit the convex weights $\left\{\hat{\delta}_g\right\}_{g=1}^{G-1} = \underset{\delta\in\Delta^{G-2}}{\arg\min} \left\| \hat{P}_G^{(0)} - \sum_{g=1}^{G-1} \delta_g \hat{Q}_g^{(0)} \right\|_F^2$

Proposed Method Overview

- **Step 0. Denoising the adjacency matrices**

  Denoise $\{A\} =$  $=$  and get $\{\hat{P}\} =$ 

- **Step 1. Gromov-Wasserstein alignment and projection**

  For all $\hat{P}$, calculate internal relational structure $\{\hat{d}_g\}_{g\in[G]}$ 

  For each sources $\{\hat{d}_g\}_{g\in[G-1]}$ and the target $\{\hat{d}_G\}$, find the soft alignment $\hat{\pi}^{g,G}$ 

  With $\hat{\pi}^{g,G}$, project all G's individuals to each source g's environment, get $\hat{Q}_g :=$ 

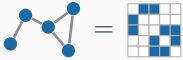
- **Step 2. Gromov-Wasserstein barycentric weights**

  With projected link probability $\hat{Q}_g$, fit the convex weights $\left\{\hat{\delta}_g\right\}_{g=1}^{G-1} = \underset{\delta\in\Delta^{G-2}}{\arg\min} \left\| \hat{P}_G^{(0)} - \sum_{g=1}^{G-1} \delta_g \hat{Q}_g^{(0)} \right\|_F^2$

- **Step 3. Extension to the post-treatment period**

  Impute the target network post-treatment link probability $\hat{P}_G^{(1)} = \sum_{g=1}^{G-1} \hat{\delta}_g \hat{Q}_g^{(1)}$

Step 0. Denoising

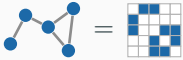
- We only have access to the adjacency matrices  $=$

$$\left\{A^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G] \quad \text{and} \quad \left\{A^{(1)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G-1]$$

but for the matching across networks, we would want to work on link probabilites 

$$\left\{\hat{P}^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G] \quad \text{and} \quad \left\{\hat{P}^{(1)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G-1]$$

Step 0. Denoising

- We only have access to the adjacency matrices  $=$

$$\left\{A^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G] \quad \text{and} \quad \left\{A^{(1)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G-1]$$

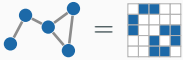
but for the matching across networks, we would want to work on link probabilites 

$$\left\{\hat{P}^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G] \quad \text{and} \quad \left\{\hat{P}^{(1)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G-1]$$

- If ξ's were observed, we could use the Nadaraya-Watson type estimator for link probability

$$\hat{P}^{(w)}_{g,i,j} = \frac{\sum_{k\in[N_g]} K\left(\left\|\xi_{g,i}-\xi_{g,k}\right\|/h\right) A^{(w)}_{g,k,j}}{\sum_{k\in[N_g]} K\left(\left\|\xi_{g,i}-\xi_{g,k}\right\|/h\right)}, \qquad \text{for } i,j\in[N_g]$$

Step 0. Denoising

- We only have access to the adjacency matrices  =

$$\left\{A^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G] \quad \text{and} \quad \left\{A^{(1)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G-1]$$

but for the matching across networks, we would want to work on link probabilites 

$$\left\{\hat{P}^{(0)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G] \quad \text{and} \quad \left\{\hat{P}^{(1)}_{g,i,j}\right\}_{i,j\in[N_g]} \text{ for } g\in[G-1]$$

- If ξ's were observed, we could use the Nadaraya-Watson type estimator for link probability

$$\hat{P}^{(w)}_{g,i,j} = \frac{\sum_{k\in[N_g]} K\left(\left\|\xi_{g,i}-\xi_{g,k}\right\|/h\right) A^{(w)}_{g,k,j}}{\sum_{k\in[N_g]} K\left(\left\|\xi_{g,i}-\xi_{g,k}\right\|/h\right)}, \qquad \text{for } i,j\in[N_g]$$

- Because of non-identifiable ξ, following Zhang et al. (2017) and Deaner et al. (2025), replace unknown $\|\xi_{g,i}-\xi_{g,k}\|$ by pseudo distance $\hat{d}^{\text{pseudo}}_g(i,k) := \max_{\ell\neq i,k} \frac{1}{N_g}\left|\left\langle A^{(0)}_{g,i,\cdot} - A^{(0)}_{g,k,\cdot}, A^{(0)}_{g,\ell,\cdot}\right\rangle\right|$

$$\hat{P}^{(w)}_{g,i,j} = \frac{\sum_{k\in[N_g]} K\left(\hat{d}^{\text{pseudo}}_g(i,k)/h\right) A^{(w)}_{g,k,j}}{\sum_{k\in[N_g]} K\left(\hat{d}^{\text{pseudo}}_g(i,k)/h\right)}$$

Step 1. Gromov-Wasserstein Alignment and Projection

With **pre-treatment** period, solve the Gromov-Wasserstein problem between networks g and G:



$$\hat{\pi}^{g,G} = \underset{\pi \in \Pi^{g,G}}{\arg\min} \sum_{i,j \in [N_g]} \sum_{k,\ell \in [N_G]} \left[\hat{d}_g^2(i,j) - \hat{d}_G^2(k,\ell)\right]^2 \pi_{i,k}\, \pi_{j,\ell}$$

with internal distances  $\hat{d}_g(i,j) = \frac{1}{N_g} \left\| \hat{P}^{(0)}_{g,i,\cdot} - \hat{P}^{(0)}_{g,j,\cdot} \right\|_2$ and  $\hat{d}_G(k,\ell) = \frac{1}{N_G} \left\| \hat{P}^{(0)}_{G,k,\cdot} - \hat{P}^{(0)}_{G,\ell,\cdot} \right\|_2$

- Coupling π is a **joint distribution of individual characteristics ξ between g and G**
- Optimal coupling aligns units by *how they connect to everyone else within their own network*

Step 1. Gromov-Wasserstein Alignment and Projection

With **pre-treatment** period, solve the Gromov-Wasserstein problem between networks g and G:



$$\hat{\pi}^{g,G} = \underset{\pi \in \Pi^{g,G}}{\arg\min} \sum_{i,j \in [N_g]} \sum_{k,\ell \in [N_G]} \left[\hat{d}_g^2(i,j) - \hat{d}_G^2(k,\ell)\right]^2 \pi_{i,k}\, \pi_{j,\ell}$$

with internal distances  $\hat{d}_g(i,j) = \frac{1}{N_g} \left\| \hat{P}^{(0)}_{g,i,\cdot} - \hat{P}^{(0)}_{g,j,\cdot} \right\|_2$ and  $\hat{d}_G(k,\ell) = \frac{1}{N_G} \left\| \hat{P}^{(0)}_{G,k,\cdot} - \hat{P}^{(0)}_{G,\ell,\cdot} \right\|_2$

Then, project all $k, \ell \in [N_G]$ to network environment g



$\hat{Q}^{(0)}_{g,k,\ell}$:= Link probabilities for $k, \ell \in [N_G]$ as if they lived in network environment g

$$= \sum_{i \in [N_g]} \sum_{j \in [N_g]} \frac{\hat{\pi}^{g,G}_{i,k}}{1/N_G} \frac{\hat{\pi}^{g,G}_{j,\ell}}{1/N_G} \hat{P}^{(0)}_{g,i,j} \qquad \text{for all } k, \ell \in [N_G]$$

Step 2. Gromov-Wasserstein barycenteric weights

Gromov-Wasserstein barycenter analysis for convex weights:

$$\left\{\hat{\delta}_g\right\}_{g=1}^{G-1} = \underset{\delta \in \Delta^{G-2}}{\arg\min} \left\| \hat{P}_G^{(0)} - \sum_{g=1}^{G-1} \delta_g \, \hat{Q}_g^{(0)} \right\|_{\mathrm{F}}^2$$

Step 2. GW Barycenter & Step 3. Extend to Post-treatment

Step 2. Gromov-Wasserstein barycenteric weights

Gromov-Wasserstein barycenter analysis for convex weights:

$$\left\{\hat{\delta}_g\right\}_{g=1}^{G-1} = \underset{\delta \in \Delta^{G-2}}{\arg\min} \left\| \hat{P}_G^{(0)} - \sum_{g=1}^{G-1} \delta_g \hat{Q}_g^{(0)} \right\|_{\mathrm{F}}^2$$

Step 3. Extend to the post-treatment period

$$\hat{Q}_{g,k,\ell}^{(1)} = \sum_{i \in [N_g]} \sum_{j \in [N_g]} \frac{\hat{\pi}_{i,k}^{g,G}}{1/N_G} \frac{\hat{\pi}_{j,\ell}^{g,G}}{1/N_G} \hat{P}_{g,i,j}^{(1)}$$

Impute the target post-treatment network G

$$\hat{P}_G^{(1)} = \sum_{g \in [G-1]} \hat{\delta}_g \hat{Q}_g^{(1)}$$

Step 2. GW Barycenter & Step 3. Extend to Post-treatment

Step 2. Gromov-Wasserstein barycenteric weights

Gromov-Wasserstein barycenter analysis for convex weights:

$$\left\{\hat{\delta}_g\right\}_{g=1}^{G-1} = \underset{\delta \in \Delta^{G-2}}{\arg\min} \left\| \hat{P}_G^{(0)} - \sum_{g=1}^{G-1} \delta_g \hat{Q}_g^{(0)} \right\|_{\mathrm{F}}^2$$

Step 3. Extend to the post-treatment period

$$\hat{Q}_{g,k,\ell}^{(1)} = \sum_{i \in [N_g]} \sum_{j \in [N_g]} \frac{\hat{\pi}_{i,k}^{g,G}}{1/N_G} \frac{\hat{\pi}_{j,\ell}^{g,G}}{1/N_G} \hat{P}_{g,i,j}^{(1)}$$

Impute the target post-treatment network G

$$\hat{P}_G^{(1)} = \sum_{g \in [G-1]} \hat{\delta}_g \hat{Q}_g^{(1)}$$

Remark: Similar to synthetic control method, ...

- Estimate network weights in the pre-treatment period, then carry to the post-treatment
- Additionally, relative relations between individuals across networks remain the same

Identification in the Population Problem

Population Problem

Different networks have very different population ...

- Both $\begin{cases} \textbf{network formation environment } f_g^{(w)} \\ \textbf{individual latent characteristics distribution } \mu_g \end{cases}$ **are different**
- Want to study what **"commonness"** they need to have for the proposed method to work

Population Problem

Different networks have very different population ...

- Both $\begin{cases} \textbf{network formation environment } f_g^{(w)} \\ \textbf{individual latent characteristics distribution } \mu_g \end{cases}$ **are different**
- Want to study what **"commonness"** they need to have for the proposed method to work

We called this problem the **population problem**, and in such idealized problem ...

- **Noises can be removed perfectly**: We work with link probability (denoising is not needed)
- **Population algorithm**: We acquire the oracle estimator $\tilde{\mathbf{P}}_G^{(1)}$

Population Problem

Different networks have very different population ...

- Both $\begin{cases} \textbf{network formation environment } f_g^{(w)} \\ \textbf{individual latent characteristics distribution } \mu_g \end{cases}$ **are different**
- Want to study what **"commonness"** they need to have for the proposed method to work

We called this problem the **population problem**, and in such idealized problem ...

- **Noises can be removed perfectly**: We work with link probability (denoising is not needed)
- **Population algorithm**: We acquire the oracle estimator $\tilde{\mathbf{P}}_G^{(1)}$

Want to study under what cross-network conditions on $f_g^{(w)}$ and μ_g can we get $\tilde{\mathbf{P}}_G^{(1)} = \mathbf{P}_G^{(1)}$

Assumption 1: Convex Hull

For simplicity, let us work with the case where $\mu := \mu_g = \mu_{g'} \quad \forall\, g, g' \in [G]$

(Results for more general $\mu_g \neq \mu_{g'}$ can be found in the paper ▶)

Assumption 1: Convex Hull

For simplicity, let us work with the case where $\mu := \mu_g = \mu_{g'} \quad \forall\, g, g' \in [G]$

(Results for more general $\mu_g \neq \mu_{g'}$ can be found in the paper)

Assumption 1 (Convex hull)

There exists $\delta^* \in \Delta_{G-2}$ such that, for both $w \in \{0,1\}$,

$$f_G^{(w)} = \sum_{g=1}^{G-1} \delta_g^* f_g^{(w)} \qquad \text{in } L^2(\mu \otimes \mu),$$

with the same weights δ^* for both treatment statuses $w \in \{0,1\}$.

Assumption 2: Comonotone Geometries

To have a valid projection between g and G, *their network formation "logic" needs to be "similar"*

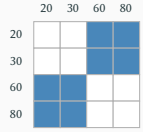
Assumption 2: Comonotone Geometries

To have a valid projection between g and G, *their network formation "logic" needs to be "similar"*

- **Toy example:** suppose there are four individuals with ages $\{20, 30, 60, 80\}$
- Formations of network g / network G are driven by age group (young vs old) / age gap

$P_g(\xi, \xi') = 0.8$ same group, 0.2 o.w.

$P_G(\xi, \xi') = 0.8 - |\xi - \xi'|/100$



Internal structure of g



Internal structure of G

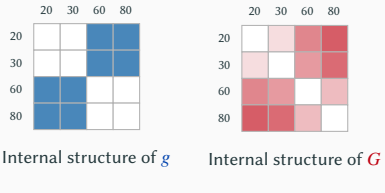
Assumption 2: Comonotone Geometries

To have a valid projection between g and G, *their network formation "logic" needs to be "similar"*

- **Toy example:** suppose there are four individuals with ages $\{20, 30, 60, 80\}$
- Formations of network g / network G are driven by age group (young vs old) / age gap

$P_g(\xi, \xi') = 0.8$ same group, 0.2 o.w.

$P_G(\xi, \xi') = 0.8 - |\xi - \xi'|/100$



- **Both networks agree:** every cross-group pair is more dissimilar than within-group pair

Assumption 2: Comonotone Geometries

To have a valid projection between g and G, *their network formation "logic" needs to be "similar"*

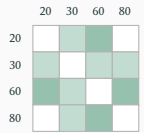
- **Toy example:** suppose there are four individuals with ages $\{20, 30, 60, 80\}$
- Formations of network g / network X are driven by age group (young vs old) / leisure time

$$P_g(\xi, \xi') = 0.8 \text{ same group, } 0.2 \text{ o.w.}$$

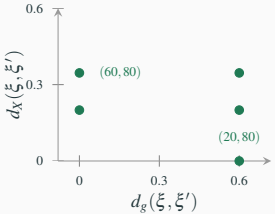
$$P_X(\xi, \xi') = 0.8 - \big||\xi - 50| - |\xi' - 50|\big|/50$$



Internal structure of g



Internal structure of X



- **Two networks disagree on which individuals are alike:** rescaling d_g cannot recover d_X

Assumption 2: Comonotone Geometries

To have a valid projection between g and G, *their network formation "logic" needs to be "similar"*

Assumption 2 (Alignment of comonotone geometries across different networks)

For every $g \in [G-1]$ and for every pair of pairs of coordinates $\big((\xi,\xi'),(\zeta,\zeta')\big)$,

$$\left[d_g^2(\xi,\xi') - d_g^2(\zeta,\zeta')\right]\left[d_G^2(\xi,\xi') - d_G^2(\zeta,\zeta')\right] \geq 0$$

All networks *rank* (ξ,ξ') *consistently by how dissimilarly two* ξ*'s connect to rest of its population*

- **If network g regards one pair of characteristics as more dissimilar than another pair, so does the target network G**
- Passing from G to g may stretch/compress dissimilarities, but must not scramble order

Assumption 3: Rigidity

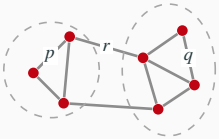
But comonotone geometries are not enough to pin down target counterfactual network

- Gromov-Wasserstein can only see internal distances; it's invariant to rigid transformation

Assumption 3: Rigidity

But comonotone geometries are not enough to pin down target counterfactual network

- Gromov-Wasserstein can only see internal distances; it's invariant to rigid transformation
- **Toy example:** suppose we have two communities in the network
  - Within-community link probabilities are p and q
  - Cross-community link probabilities are r
  - $d_G(\text{points in left community}) = d_G(\text{points in right community}) = 0$
  - GW cannot tell the two communities apart:
    aligning to either is optimal, so imputation fails whenever $p \neq q$



Assumption 3: Rigidity

But comonotone geometries are not enough to pin down target counterfactual network

- Gromov-Wasserstein can only see internal distances; it's invariant to rigid transformation

Following assumption closes the gap between what GW aligns and what imputation consumes

Assumption 3 (Rigidity of the target structure) ▸ Detailed Assumption 3

(i) Strengthen comonotonicity into deterministic link ($\exists$ Borel b_g such that $d_G^2 = b_g \circ d_g^2$)

(ii) Whatever d_G^2 cannot distinguish, the link probabilities do not either

Doesn't force unique optimal π; only requires all optimal π's to be equivalent for imputation

Identification in the Population Problem

Note that Assumptions 2 & 3 are conditions on internal geometries across networks

- They are not restrictions on which network formation model is allowed
- Most of the common network formation models without strategic interaction are included

Theorem 1 (Identification in the Population Problem)

Assume Assumptions 1-3 and other regularity condition holds. Then, with the oracle version of the proposed method, network weights optimization has the unique solution $\tilde{\delta} = \delta^*$, and

$$\tilde{\mathbf{P}}_G^{(1)} = \mathbf{P}_G^{(1)}$$

Large Sample Theory

Uniform Consistency

Additional Assumption 4 (smoothness and other regularity conditions):

(i) Ensure every ξ has enough, but not too many, neighbors for denoising and matching

(ii) Individuals with similar ξ have similar neighborhood in terms of link probabilities

(iii) No two distinct ξ look the same from the target network G's perspective

▸ Detailed Assumption 4

Theorem 2 (Uniform consistency)

Let Assumptions 1-4 hold, together with other regularity conditions. As $N_{\min} := \min_{g \in [G]} N_g \to \infty$,

$$\|\hat{P}_G^{(1)} - P_G^{(1)}\|_{\max} = o_p(1)$$

Max Norm Rate of Convergence

Additional Assumption 5 (target network structure and cross network relation):

(i) Uniform comonotonicity for further quantifying the relation between g and G

(ii) Any reassignment of ξ that substantially changes them must also distort G's geometry

▸ Detailed Assumption 5

Theorem 3 (Max norm rate of convergence)

Let Assumptions 1-5 hold, together with other regularity conditions. As $N_{\min} := \min_{g \in [G]} N_g \to \infty$,

$$\|\hat{P}_G^{(1)} - P_G^{(1)}\|_{\max} = O_p\left([\log(N_{\min})]^{3/2(d_\xi+2)} N_{\min}^{-1/\max\{d_\xi,2\}(d_\xi+2)} \right)$$

Simulation

Compare SCN with Five Benchmark Procedures

- **Nearest GW source:** select by the smallest pre-treatment GW distance

$$\hat{g}_{\mathrm{GW}} = \arg\min_{g<G} \hat{\mathrm{GW}}(g, G)$$

- **Best single projected source:** select by the smallest projected pre-treatment fitting error

$$\hat{g}_{\mathrm{single}} = \arg\min_{g<G} \left\| \hat{P}_G^{(0)} - \hat{Q}_g^{(0)} \right\|_F^2$$

- **Uniform GW barycenter:** average the same GW projections with weights $1/(G-1)$
- **Degree alignment:** align pre-treatment degree quantiles, then refit the synthetic weights
  - (i) Compute each individual's normalized pre-treatment degree: $\hat{\mathrm{deg}}_{g,i}^{(0)} = \frac{1}{N_g - 1} \sum_{j \neq i} \hat{P}_{g,i,j}^{(0)}$
  - (ii) Rank individuals within each network from lowest to highest degree
  - (iii) Match source and target individuals by their degree quantiles
- **No change:** use the target's pre-treatment estimate as its post-treatment prediction

Simulation Design 1: Mixing Homophily and Popularity

Individual characteristics and network-specific effects

- All networks have the same individual characteristics distribution

$$\xi_{g,i} \overset{\text{i.i.d.}}{\sim} \text{Uniform}[0,1] \quad \forall i \in [N_g] \quad \forall g \in [G]$$

- Network specific effects vary across networks with $\gamma_G = \sum_{g<G} \delta_g^* \gamma_g$
  - $G = 10$, and true weights δ_g^* only concentrate on a few source network

Simulation Design 1: Mixing Homophily and Popularity

Individual characteristics and network-specific effects

- All networks have the same individual characteristics distribution

$$\xi_{g,i} \overset{\text{i.i.d.}}{\sim} \text{Uniform}[0,1] \quad \forall i \in [N_g] \quad \forall g \in [G]$$

- Network specific effects vary across networks with $\gamma_G = \sum_{g<G} \delta_g^* \gamma_g$
  - $G = 10$, and true weights δ_g^* only concentrate on a few source network

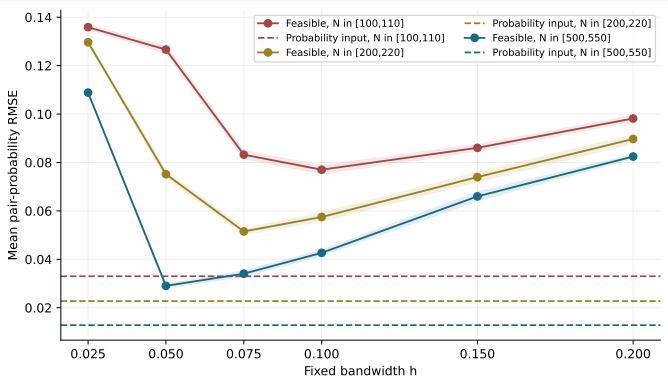
Graphon function: Mixing (i) homophily, (ii) popularity, and (iii) baseline density

$$f^{(w)}(\xi, \xi', \gamma) = \sum_{k=1}^{3} \psi_k^{(w)}(\gamma) \phi_k(\xi, \xi')$$

$$\begin{cases} \phi_1(\xi, \xi') = \exp\left[-\frac{(\xi-\xi')^2}{2(0.12)^2}\right] \\ \phi_2(\xi, \xi') = \xi \xi' \\ \phi_3(\xi, \xi') = 0.35 \end{cases} \qquad \begin{aligned} \psi^{(0)}(\gamma) &= (1-\gamma)\begin{pmatrix} 0.75 \\ 0.05 \\ 0.20 \end{pmatrix} + \gamma \begin{pmatrix} 0.30 \\ 0.55 \\ 0.15 \end{pmatrix} \\ \psi^{(1)}(\gamma) &= (1-\gamma)\begin{pmatrix} 0.15 \\ 0.55 \\ 0.30 \end{pmatrix} + \gamma \begin{pmatrix} 0.05 \\ 0.75 \\ 0.20 \end{pmatrix} \end{aligned}$$

- Treatment reduces homophily and increases popularity in every network
- The relative importance of these components varies across networks

Simulation Design 1: Bandwidth Sensitivity for Denoising Step



Solid curves: means over 500 replications with pointwise 95% Monte Carlo intervals.

Dashed lines: bandwidth-independent oracle means.

- Very small bandwidths leave too few neighbors
- Lowest SCN RMSE on the grid occurs at $h = 0.10$, 0.075, and 0.05 as sizes increase

Simulation Design 1: Feasible Implementation ($N_g \in [500, 550], h = 0.05$)

Method	RMSE	MedAE	Q95	Direction	Degree	Triangle
SCN	0.0290	0.0185	0.0571	95.0%	0.0117	0.0021
	(0.0004)	(0.0003)	(0.0007)	(0.0004)	(0.0003)	(0.0001)
Nearest GW source	0.0652	0.0419	0.1294	89.5%	0.0274	0.0028
	(0.0027)	(0.0020)	(0.0052)	(0.0038)	(0.0018)	(0.0001)
Best single source	0.0448	0.0273	0.0905	92.3%	0.0138	0.0024
	(0.0001)	(0.0001)	(0.0002)	(0.0006)	(0.0001)	(0.0001)
Uniform GW barycenter	0.0509	0.0345	0.0983	93.1%	0.0274	0.0045
	(0.0017)	(0.0012)	(0.0032)	(0.0018)	(0.0011)	(0.0001)
Degree alignment	0.0798	0.0311	0.1657	93.7%	0.0221	0.0027
	(0.0007)	(0.0003)	(0.0016)	(0.0004)	(0.0002)	(0.0001)
No change	0.1506	0.0946	0.3124	0.0%	0.0435	0.0021
	(0.0006)	(0.0004)	(0.0013)	(0.0000)	(0.0003)	(0.0001)

Entries are Monte Carlo means over 500 replications. Standard errors are in parentheses.

- SCN has the smallest mean RMSE, MedAE, and Q95
- SCN recovers change directions for 95.0% of evaluated pairs
- No change has a similar triangle error despite much larger pair and degree errors

Simulation Design 1: Oracle Implementation ($N_g \in [500, 550], h = 0.05$)

Method	RMSE	MedAE	Q95	Direction	Degree	Triangle
SCN	0.0128	0.0080	0.0234	99.7%	0.0073	0.0016
	(0.0004)	(0.0003)	(0.0008)	(0.0003)	(0.0003)	(0.0001)
Nearest GW source	0.0232	0.0157	0.0433	98.6%	0.0144	0.0028
	(0.0019)	(0.0014)	(0.0037)	(0.0028)	(0.0012)	(0.0001)
Best single source	0.0133	0.0083	0.0244	99.8%	0.0076	0.0021
	(0.0002)	(0.0002)	(0.0004)	(0.0001)	(0.0002)	(0.0001)
Uniform GW barycenter	0.0279	0.0193	0.0528	98.4%	0.0171	0.0033
	(0.0013)	(0.0010)	(0.0026)	(0.0015)	(0.0008)	(0.0001)
Degree alignment	0.0640	0.0174	0.1218	97.1%	0.0138	0.0022
	(0.0010)	(0.0004)	(0.0022)	(0.0006)	(0.0003)	(0.0001)
No change	0.1519	0.0954	0.3250	0.0%	0.0442	0.0020
	(0.0006)	(0.0004)	(0.0012)	(0.0000)	(0.0003)	(0.0001)

Means over 500 replications, with Monte Carlo standard errors in parentheses. Oracle results do not depend on h.

- Oracle SCN has RMSE 0.0128, compared with 0.0290 for feasible SCN
- The best single source is close in RMSE (0.0133) and slightly higher in direction accuracy

Simulation Design 2: Complex Mixing

Individual characteristics and network-specific effects

- Network specific effects vary across networks with $\gamma_G = \sum_{g<G} \delta_g^* \gamma_g$
  - $G = 10$, and true weights δ_g^* only concentrate on a few source network
- Individual characteristics distributions are now different across different networks

$$\xi_{g,i} \overset{\text{i.i.d.}}{\sim} \text{Beta}\left(1+4\gamma_g,\, 1+4(1-\gamma_g)\right)$$

Simulation Design 2: Complex Mixing

Individual characteristics and network-specific effects

- Network specific effects vary across networks with $\gamma_G = \sum_{g<G} \delta_g^* \gamma_g$
  - $G = 10$, and true weights δ_g^* only concentrate on a few source network
- Individual characteristics distributions are now different across different networks

$$\xi_{g,i} \overset{\text{i.i.d.}}{\sim} \text{Beta}\left(1+4\gamma_g,\, 1+4(1-\gamma_g)\right)$$

Graphon function: Mixing (i) block, (ii) smooth oscillatory, (iii) homophily, and (iv) non-smooth

$$f^{(w)}(\xi,\xi',\gamma) = \sum_{k=1}^{4} \psi_k^{(w)}(\gamma)\phi_k(\xi,\xi')$$

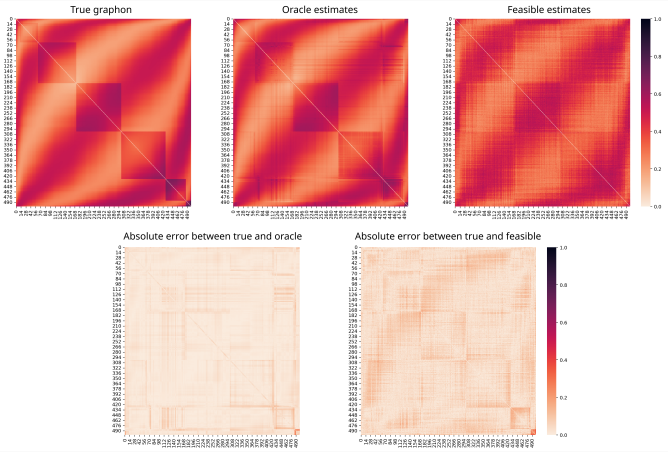
$$\begin{cases} \phi_1(\xi,\xi') = \begin{cases} k/8, & \xi,\xi' \in I_k, \quad k=1,\ldots,7 \\ 0.3/8, & \text{otherwise} \end{cases} \\ \phi_2(\xi,\xi') = 0.5 + 0.5\sin\{5\pi(\xi+\xi'-1)+1\} \\ \phi_3(\xi,\xi') = 1 - \left[1+\exp\{15(0.8|\xi-\xi'|)^{4/5} - 0.1\}\right]^{-1} \\ \phi_4(\xi,\xi') = 0.15 + \frac{1}{3}(\xi^2+\xi'^2)\cos\{1/(\xi^2+\xi'^2)\} \end{cases}$$

$$\psi^{(0)}(\gamma) = (1-\gamma)\begin{pmatrix}0.45\\0.20\\0.20\\0.15\end{pmatrix} + \gamma\begin{pmatrix}0.15\\0.45\\0.15\\0.25\end{pmatrix}$$

$$\psi^{(1)}(\gamma) = (1-\gamma)\begin{pmatrix}0.15\\0.45\\0.20\\0.20\end{pmatrix} + \gamma\begin{pmatrix}0.35\\0.15\\0.15\\0.35\end{pmatrix}$$

- These four graphon templates are from Zhang et al. (2017)

Simulation Design 2: True, Oracle, and Feasible Probability Matrices



First replication among 500 Monte Carlo replications with $N_g \in [500, 550]$ and $h = 0.05$.

- Most of the performance loss is coming from the denoising step

Simulation Design 2: Feasible Implementation ($N_g \in [500, 550], h = 0.05$)

Method	RMSE	MedAE	Q95	Direction	Degree	Triangle
SCN	0.0634	0.0422	0.1239	64.4%	0.0135	0.0022
	(0.0002)	(0.0001)	(0.0003)	(0.0024)	(0.0002)	(0.0001)
Nearest GW source	0.0972	0.0609	0.1940	63.0%	0.0172	0.0017
	(0.0003)	(0.0002)	(0.0006)	(0.0024)	(0.0001)	(0.0001)
Best single source	0.0946	0.0592	0.1891	61.8%	0.0176	0.0024
	(0.0003)	(0.0002)	(0.0006)	(0.0023)	(0.0001)	(0.0001)
Uniform GW barycenter	0.0662	0.0452	0.1280	62.2%	0.0160	0.0030
	(0.0002)	(0.0002)	(0.0004)	(0.0027)	(0.0002)	(0.0001)
Degree alignment	0.1223	0.1012	0.2135	68.0%	0.0148	0.0032
	(0.0004)	(0.0005)	(0.0005)	(0.0086)	(0.0001)	(0.0001)
No change	0.0905	0.0575	0.1793	0.0%	0.0196	0.0072
	(0.0005)	(0.0004)	(0.0011)	(0.0000)	(0.0003)	(0.0002)

Entries are Monte Carlo means over 500 replications. Standard errors are in parentheses.

- SCN has the smallest mean RMSE, MedAE, Q95, and degree error
- In other measures, SCN is still very competitive

Simulation Design 2: Oracle Implementation ($N_g \in [500, 550], h = 0.05$)

Method	RMSE	MedAE	Q95	Direction	Degree	Triangle
SCN	0.0277 (0.0002)	0.0137 (0.0002)	0.0572 (0.0005)	89.7% (0.0023)	0.0058 (0.0001)	0.0012 (0.0000)
Nearest GW source	0.0380 (0.0004)	0.0157 (0.0003)	0.0809 (0.0009)	87.3% (0.0029)	0.0064 (0.0002)	0.0014 (0.0001)
Best single source	0.0367 (0.0003)	0.0149 (0.0002)	0.0778 (0.0009)	87.7% (0.0029)	0.0062 (0.0001)	0.0014 (0.0001)
Uniform GW barycenter	0.0393 (0.0004)	0.0264 (0.0003)	0.0757 (0.0007)	77.4% (0.0039)	0.0129 (0.0002)	0.0031 (0.0001)
Degree alignment	0.1159 (0.0005)	0.0919 (0.0006)	0.2088 (0.0007)	72.8% (0.0109)	0.0088 (0.0002)	0.0030 (0.0001)
No change	0.0280 (0.0006)	0.0197 (0.0004)	0.0518 (0.0010)	0.0% (0.0000)	0.0163 (0.0005)	0.0070 (0.0002)

Means over 500 replications, with Monte Carlo standard errors in parentheses. Oracle results do not depend on h.

- Oracle SCN has RMSE 0.0277 (compared with 0.0634 for feasible SCN) and direction accuracy 89.7% (compared with 64.4% for feasible SCN)
- Most of the performance loss comes from the denoising step

Empirical Illustration

Empirical Illustration: Informal Risk-Sharing Networks

Household network data from Banerjee et al. (2024)

- 75 villages in Karnataka, India: 43 exposed to microfinance (MF) and 32 untreated
- Use the 43 treated villages for the placebo exercise
- Nodes represent households, with binary connections before and after MF exposure
  - Baseline household counts range from 114 to 356
  - Mean approximately 223, with standard deviation approximately 56

Empirical Illustration: Leave-One-Out Placebo Study

Each of the 43 treated village takes a turn as target G

1. Withhold the target's post-treatment network $A_G^{(1)}$ and use the other 42 villages as sources
2. Fit the GW optimal couplings and synthetic weights using pre-treatment networks
3. Project the source post-treatment networks and impute the held-out target:

$$\hat{P}_G^{(1)} = \sum_{g<G} \hat{\delta}_g \hat{Q}_g^{(1)}$$

4. Compare the imputation with the denoised held-out network $\hat{P}_G^{(1),\text{obs}}$

Empirical Illustration: Leave-One-Out Placebo Study

Each of the 43 treated village takes a turn as target G

1. Withhold the target's post-treatment network $A_G^{(1)}$ and use the other 42 villages as sources
2. Fit the GW optimal couplings and synthetic weights using pre-treatment networks
3. Project the source post-treatment networks and impute the held-out target:

$$\hat{P}_G^{(1)} = \sum_{g<G} \hat{\delta}_g \hat{Q}_g^{(1)}$$

4. Compare the imputation with the denoised held-out network $\hat{P}_G^{(1),\text{obs}}$

This leave-one-out placebo study serves as an imputation exercise

- The causal effect of microfinance is not being further investigated

Empirical Illustration: Placebo Results ($h = 0.20$)

Method	RMSE	MedAE	Q95	Direction	Degree	Triangle($\times 10^4$)
SCN	0.0238	0.0139	0.0483	0.806	0.0102	1.155
Nearest GW source	0.0300	0.0178	0.0607	0.701	0.0137	1.486
Best single source	0.0310	0.0181	0.0635	0.725	0.0140	1.679
Uniform GW barycenter	0.0255	0.0163	0.0502	0.778	0.0140	1.588
Degree alignment	0.0239	0.0138	0.0485	0.807	0.0101	1.156
No change	0.0257	0.0160	0.0511	0.000	0.0135	1.416

Unweighted means of village-level statistics against denoised held-out networks; triangle errors are multiplied by 10^4.

- SCN has the smallest mean RMSE and upper-tail pair error
- SCN achieves the direction accuracy of 80.6%, and is competitive in all other measures

Conclusion

- With Gromov-Wasserstein OT, the **Synthetic Counterfactual Network** method recovers **entire counterfactual networks**, while still **keep track of each individual pair**
- Handles **unequal network sizes** and **disentangles the two heterogeneities**:
  - GW alignment tackle the difference in individual characteristics distribution
  - Optimized weights δ combine the network specific effects
- In the population problem, we derive the required conditions for the identification
- We further establish the uniform consistency and derive the max norm rate of convergence

References

Abadie, A. (2021). Using synthetic controls: Feasibility, data requirements, and methodological aspects. *Journal of Economic Literature*, 59(2):391–425.

Abadie, A., Diamond, A., and Hainmueller, J. (2010). Synthetic control methods for comparative case studies: Estimating the effect of california's tobacco control program. *Journal of the American statistical Association*, 105(490):493–505.

Auerbach, E. and Cai, Y. (2025). Identifying socially disruptive policies. Working paper, arXiv version 3, July 29, 2025; first circulated in 2023 under this title.

Banerjee, A., Breza, E., Chandrasekhar, A. G., Duflo, E., Jackson, M. O., and Kinnan, C. (2024). Changes in social network structure in response to exposure to formal credit markets. *Review of Economic Studies*, 91(3):1331–1372.

Cai, Y. (2026). Linear regression with centrality measures.

Chowdhury, S. and Needham, T. (2020). Gromov-wasserstein averaging in a riemannian framework. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition Workshops*, pages 842–843.

Deaner, B., Hsiang, C.-W., and Zeleneev, A. (2025). Simple specification-free causal inference in large panels. *Working paper*.

Gunsilius, F. F. (2023). Distributional synthetic controls. *Econometrica*, 91(3):1105–1117.

Kurisu, D., Zhou, Y., Otsu, T., and Müller, H.-G. (2025). Geodesic synthetic control methods for random objects and functional data.

Lin, C. (2025). Functional synthetic control. *Working Paper*.

Martín, R. D., Medri, I. V., and Murphy, J. M. (2026). Gromov-wasserstein barycenters: The analysis problem. *arXiv preprint arXiv:2507.09865*.

Mémoli, F. (2011). Gromov–wasserstein distances and the metric approach to object matching. *Foundations of computational mathematics*, 11(4):417–487.

Peyré, G., Cuturi, M., and Solomon, J. (2016). Gromov-wasserstein averaging of kernel and distance matrices. In *International conference on machine learning*, pages 2664–2672. PMLR.

Zeleneev, A. (2020). Identification and estimation of network models with nonparametric unobserved heterogeneity. *arXiv preprint arXiv:2602.06885*.

Zhang, Y., Levina, E., and Zhu, J. (2017). Estimating network edge probabilities by neighbourhood smoothing. *Biometrika*, 104(4):771–783.

Zhang, Z., Goldfeld, Z., Mroueh, Y., and Sriperumbudur, B. K. (2024). Gromov–wasserstein distances: Entropic regularization, duality and sample complexity. *The Annals of Statistics*, 52(4):1616–1645.

Reference Space and Reference Measure

To study how matching works, we introduced an imaginary common auxiliary space

Definition (Reference space and reference measure)

A reference space is a pair $(\breve{\Xi}, \breve{\mu})$ consisting of

- an uncountable Polish space $\breve{\Xi}$, and
- a **non-atomic** Borel probability measure $\breve{\mu}$ on it

With such reference measure $\breve{\mu}$, there exists $\rho_g : \breve{\Xi} \to \Xi$ such that $(\rho_g)_{\#}\breve{\mu} = \mu_g$

Toy example: Assume $\Xi =$ age where μ_g is skewed toward young vs μ_G is skewed toward old

- A reference space can be
  - Unit interval $[0, 1]$ with uniform distribution, in which case a reference point $\breve{\xi}$ is age rank
  - The concept of young-to-old age line, equipped with any non-atomic reference distribution
- With such auxiliary space, same $\breve{\xi}$ from $(\breve{\Xi}, \breve{\mu})$ can represent young in g and old in G

Back

Alignment Maps

Extending the toy example: Assume $\Xi = \{\text{Age}, \text{Income}\}$, $\breve{\Xi} = \text{socioeconomic index}$, and

$$\rho_g(\breve{\xi}) = \left(20 + 60\,\breve{\xi}^2,\ 20 + 100\,\breve{\xi}^2\right) \qquad \text{and} \qquad \rho_G(\breve{\xi}) = \left(20 + 60\sqrt{\breve{\xi}},\ 20 + 100\sqrt{\breve{\xi}}\right)$$

- Village g is young and poor, and village G is old and rich
- The pushforward maps produce two skewed populations
- A **role** $\breve{\xi}$ here is interpreted as within-village socioeconomic rank, not the value of ξ
- There is no restriction on the dimension of the reference space

Under our assumptions, proposed method aligns individuals with similar roles

Back

Assumption 3

Assumption 3 (Rigidity of the target structure)

(i) For every $g \in [G-1]$, one of the following holds:

- The law of d_g^2 under $\mu \otimes \mu$ is non-atomic
- There exists a Borel $b_g : [0,\infty) \to [0,1]$ with $d_G^2 = b_g \circ d_g^2$ $\mu \otimes \mu$-a.e.

(ii) Every $\pi \in \Pi(\mu,\mu)$ with $d_G^2(\zeta,\zeta') = d_G^2(\xi,\xi')$ for $\pi \otimes \pi$-a.e. pairs satisfies $f_g^{(w)}(\zeta,\zeta') = f_g^{(w)}(\xi,\xi')$ for $\pi \otimes \pi$-a.e. pairs, for every g and both $w \in \{0,1\}$

Back

Assumption 4

Assumption 4 (Regularity on reference representation and smoothness conditions)

For every g, $\rho_g : \check{\Xi} \to \mathrm{supp}(\mu_g)$ is a Borel bijection. With this, the following conditions hold:

(i) $\check{\Xi} \subseteq \mathbb{R}^{d_\xi}$ is compact and convex

(ii) Assume $\mathrm{supp}(\check{\mu}) = \check{\Xi}$. There exists $0 < \underline{c}_\mu \le \bar{c}_\mu < \infty$ and $r_\mu > 0$ such that

$$\underline{c}_\mu r^{d_\xi} \le \check{\mu}\left(B(x,r) \cap \check{\Xi}\right) \le \bar{c}_\mu r^{d_\xi}, \qquad x \in \check{\Xi}, \quad 0 < r \le r_\mu$$

(iii) Every $\check{f}_g^{(w)}$ is symmetric, locates in $[0,1]$, and Lipschitz in each argument:

(iv) If $\check{d}_G(\check{\xi}, \check{\xi}') = 0$, then $\check{\xi} = \check{\xi}'$ for all $\check{\xi}, \check{\xi}' \in \check{\Xi}$

(i) Two roles in the reference space can be connected by a path lying within the reference space

(ii) Ensure every roles $\check{\xi}$ has enough, but not too many, neighbors for denoising and matching

(iii) Individuals with similar roles $\check{\xi}$ have similar neighborhood in terms of link probabilities

(iv) No two distinct roles look the same from the target network G's perspective

Assumption 5

Assumption 5 (Target network structure and cross network relation)

(i) For fixed $0 < \underline{c}_b \leq \bar{c}_b < \infty$, every source $g \in \{1, \ldots, G-1\}$, and all $(\check{\xi}, \check{\xi}'), (\check{\zeta}, \check{\zeta}') \in \check{\Xi} \times \check{\Xi}$,

$$\underline{c}_b \left| \check{d}_g^2 \left((\check{\xi}, \check{\xi}') \right) - \check{d}_g^2 \left((\check{\zeta}, \check{\zeta}') \right) \right| \leq \left| \check{d}_G^2 \left((\check{\xi}, \check{\xi}') \right) - \check{d}_G^2 \left((\check{\zeta}, \check{\zeta}') \right) \right| \leq \bar{c}_b \left| \check{d}_g^2 \left((\check{\xi}, \check{\xi}') \right) - \check{d}_g^2 \left((\check{\zeta}, \check{\zeta}') \right) \right|$$

(ii) Let $\mathcal{T}$ be the set of symmetries of the target, that is, Borel bijections $T : \check{\Xi} \to \check{\Xi}$ with $T_{\#}\check{\mu} = \check{\mu}$ and $\check{d}_G(T\check{\xi}, T\check{\xi}') = \check{d}_G(\check{\xi}, \check{\xi}')$ for all $\check{\xi}, \check{\xi}'$. Then there exists $\kappa > 0$, such that, for every coupling $\check{\pi} \in \Pi(\check{\mu}, \check{\mu})$ of the reference measure with itself,

$$GW_{\check{d}_G^2, \check{d}_G^2}(\check{\pi}) \geq \kappa \inf_{T \in \mathcal{T}} \int_{\check{\Xi} \times \check{\Xi}} \|T\check{\xi} - \check{\xi}'\|^2 \mathrm{d}\check{\pi}(\check{\xi}, \check{\xi}').$$

(i) Further quantifies the relation between g and G that Assumptions 2 & 3 already deliver

(ii) Any reassignment of roles that substantially changes them must also distort G's geometry

Back