Gaussian Matching

Jiaxin Hu

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1 Model Formulation

1.1 Notations

- Let the lowercase letters (e.g., a, c) denote the scalar; the bold lowercase letters (e.g, $\boldsymbol{\omega}, \boldsymbol{v}$) denote the vector; the uppercase letters with sup-script in parentheses (e.g., $P^{(m)}, Q^{(m)}$) denote the dimension-m index sets with elements in the form $(i_1, \ldots, i_m) \in \mathbb{Z}_+^m$, and drop the sup-script when $m = 1$ for simplicity; the bold uppercase letters (e.g., $\boldsymbol{P}, \boldsymbol{Q}$) denote the matrix; and the calligraphy letters (e.g., $\mathcal{A}, \mathcal{B}$) denote the tensor of order three or greater .
- For a positive integer n, let $[n]$ denote the index set $\{1, \ldots, n\}$.
- For an index set S and a positive integer m, let S^m denote the dimension-m vector space of S, where $S^m = \{(i_1, \ldots, i_m) \colon i_k \in S, \text{ for all } k \in [m]\}$.
- For two index sets S and T, we call the function $\pi \colon S \mapsto T$ *the perfect matching between S and T* if π is an one-to-one function; i.e., $\pi(i_1) = \pi(i_2)$ if and only if $i_1 = i_2$ for any $i_1, i_2 \in S$. When $T = S$, we call the π *the permutation on S*.
- For a perfect matching $\pi \colon S \mapsto T$, we call the dimension-2 index set $P^{(2)} = \{(i, \pi(i)) : i \in S\}$ *the set corresponding to* π, and we call π *the perfect matching corresponding to* $P^{(2)}$.
- For a perfect matching $\pi \colon S \mapsto T$ and an index set $S_0 \subset S$, let $\pi|_{S_0} \colon S_0 \mapsto T_0$ denote the sub-matching of π for the nodes in S_0, where $T_0 = \{\pi(i) : i \in S_0\} \subset T$.
- For a perfect matching $\pi \colon S \mapsto T$ and a dimension-m vector $\boldsymbol{v} = (v_1, \ldots, v_m) \in S^m$, let $\pi \circ \boldsymbol{v} = (\pi(v_1), \ldots, \pi(v_m)) \in T^m$ denote the permutation of the vector $\boldsymbol{v}$.
- Let $\mathcal{A} \in \mathbb{R}^{n^{\otimes m}}$ denote an order-m real tensor of dimension n on each mode. For the vector $\boldsymbol{\omega} = (\omega_1, \ldots, \omega_m) \in [n]^m$, we use $\mathcal{A}_{\boldsymbol{\omega}}$ to denote the $(\omega_1, \ldots, \omega_m)$-th entry of $\mathcal{A}$.
- We call a tensor $\mathcal{A} \in \mathbb{R}^{n^{\otimes m}}$ *super-symmetric* if for all $\boldsymbol{\omega} = (\omega_1, \ldots, \omega_m) \in [n]^m$ we have $\mathcal{A}_{\boldsymbol{\omega}} = \mathcal{A}_{\pi \circ \boldsymbol{\omega}}$ for all permutations π on the set $\{\omega_1, \ldots, \omega_m\}$.
- Let $\times_k$ denote the tensor-by-matrix multiplication on the k-th mode.
- Let $\|\cdot\|_F$ denote the Frobenius norm for tensors. Let $\langle \cdot, \cdot \rangle$ denote the inner product for tensors.

1.2 Higher-order Correlated Winger Model

Consider two random super-symmetric tensors $\mathcal{A}, \mathcal{B}' \in \mathbb{R}^{n^{\otimes m}}$. Assume that all the pairs $\{(\mathcal{A}_{\boldsymbol{\omega}}, \mathcal{B}'_{\boldsymbol{\omega}}) \colon \boldsymbol{\omega} \in [n]^m \cap \{\boldsymbol{\omega} \colon \omega_1 \leq \cdots \leq \omega_m\}\}$ follow the i.i.d. correlated multivariate zero-mean Gaussian distribution with variance 1 and correlation $\rho \in (0,1)$; i.e.,

$$\begin{pmatrix} \mathcal{A}_{\boldsymbol{\omega}} \\ \mathcal{B}'_{\boldsymbol{\omega}} \end{pmatrix} \sim \mathcal{N}\left(\mathbf{0}, \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}\right), \quad \text{and} \quad \begin{pmatrix} \mathcal{A}_{\boldsymbol{\omega}} \\ \mathcal{B}'_{\boldsymbol{\omega}} \end{pmatrix} \text{ is independent with } \begin{pmatrix} \mathcal{A}_{\boldsymbol{\omega}'} \\ \mathcal{B}'_{\boldsymbol{\omega}'} \end{pmatrix},$$

for all $\boldsymbol{\omega}' \neq \boldsymbol{\omega}$ and $\boldsymbol{\omega}' \in [n]^m \cap \{\boldsymbol{\omega} \colon \omega_1 \leq \cdots \leq \omega_m\}$. The tensors $\mathcal{A}, \mathcal{B}'$ are two correlated Winger tensors. Let π^* be a permutation on $[n]$, and $\Pi^* \in \{0,1\}^{n \times n}$ denote the corresponding permutation matrix with entries $\Pi^*_{ij} = 1$ if $j = \pi^*(i)$ and $\Pi^*_{ij} = 0$, otherwise. Consider the permuted tensor $\mathcal{B}$ such that for all $\boldsymbol{\omega} \in [n]^m$

$$\mathcal{B}_{\boldsymbol{\omega}} = \mathcal{B}'_{\pi^* \circ \boldsymbol{\omega}}, \quad \text{or equivalently} \quad \mathcal{B} = \mathcal{B}' \times_1 \Pi^* \times_2 \cdots \times_m \Pi^*.$$

We call the pair $(i,k) \in [n]^2$ as a *true pair* if $k = \pi^*(i)$, and (i,k) is a *fake pair*, otherwise. We also call the observation $(\mathcal{A}, \mathcal{B})$ follow the *permuted higher-order correlated Winger model (pHCWM) with parameter* π^* *and* ρ, denoted as $(\mathcal{A}, \mathcal{B}) \sim pHCWM_{n,m}(\pi^*, \rho)$.

Our goal is to recover π^* (or equivalently Π^*) observing $\mathcal{A}, \mathcal{B}$.

1.3 Maximum Likelihood Estimate

Theorem 1.1 (MLE for Higher-order correlated Winger model)**.** *Suppose that the order-m tensor observation $(\mathcal{A}, \mathcal{B}) \sim pHCWM_{n,m}(\pi^*, \rho^*)$. The MLE of the true permutation π^*, denoted $\hat{\pi}$ satisfies*

$$\hat{\Pi} = \underset{\Pi \in \mathcal{P}_n}{\arg\max} \left\langle \mathcal{A} \times_1 \Pi \times_2 \cdots \times_m \Pi, \mathcal{B} \right\rangle,$$

where $\hat{\Pi}$ is the permutation matrix corresponding to $\hat{\pi}$, and $\mathcal{P}_n$ is the collection for all possible permutation matrices on $[n]$.

Proof of Theorem 1.1. Let Σ denote the covariance matrix $\begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}$ with inverse $\Sigma^{-1} = \frac{1}{1-\rho^2} \begin{pmatrix} 1 & -\rho \\ -\rho & 1 \end{pmatrix}$. With given (π, ρ), the pHCWM assumes that pairs $(\mathcal{A}_{\pi \circ \boldsymbol{\omega}}, \mathcal{B}_{\boldsymbol{\omega}}) \sim \mathcal{N}(\mathbf{0}, \Sigma)$ for all $\boldsymbol{\omega} \in [n]^m$ and $(\mathcal{A}_{\pi \circ \boldsymbol{\omega}}, \mathcal{B}_{\boldsymbol{\omega}})$ are independent with $(\mathcal{A}_{\pi \circ \boldsymbol{\omega}'}, \mathcal{B}_{\boldsymbol{\omega}'})$ for all $\boldsymbol{\omega} \neq \boldsymbol{\omega}'$. Hence, we have the likelihood for the higher-order correlated Winger model

$$\begin{aligned}
\mathcal{L}(\Pi, \rho | \mathcal{A}, \mathcal{B}) &= \frac{1}{[2\pi \det(\Sigma)]^{n^m/2}} \exp\left(-\frac{1}{2} \sum_{\boldsymbol{\omega} \in [n]^m} (\mathcal{A}_{\pi \circ \boldsymbol{\omega}}, \mathcal{B}_{\boldsymbol{\omega}}) \Sigma^{-1} (\mathcal{A}_{\pi \circ \boldsymbol{\omega}}, \mathcal{B}_{\boldsymbol{\omega}})^T \right) \\
&= \frac{1}{[2\pi \det(\Sigma)]^{n^m/2}} \exp\left(-\frac{1}{2(1-\rho^2)} \left[\|\mathcal{A}\|_F^2 + \|\mathcal{B}\|_F^2 - 2\rho \left\langle \mathcal{A} \times_1 \Pi \times_2 \cdots \times_m \Pi, \mathcal{B} \right\rangle \right] \right).
\end{aligned}$$

Note that $\max_{\Pi, \rho} \mathcal{L}(\Pi, \rho | \mathcal{A}, \mathcal{B}) = \max_\rho \max_\Pi \mathcal{L}(\Pi | \rho, \mathcal{A}, \mathcal{B})$. Then for any $\rho \in (0,1)$, we consider the estimator

$$\hat{\Pi}(\rho) = \underset{\Pi}{\arg\max}\, \mathcal{L}(\Pi | \rho, \mathcal{A}, \mathcal{B}) = \underset{\Pi}{\arg\max} \left\langle \mathcal{A} \times_1 \Pi \times_2 \cdots \times_m \Pi, \mathcal{B} \right\rangle.$$

Note that $\hat{\Pi}(\rho)$ is independent with ρ. Therefore, we let $\hat{\Pi}$ denote the estimator $\hat{\Pi}(\rho)$, and $\hat{\Pi}$ is the MLE of Π^*. The permutation $\hat{\pi}$ corresponding to $\hat{\Pi}$ is the MLE of π^*.

$\square$

2 Algorithm

2.1 Matching via Empirical Distributions

We describe each node by the slice empirical distribution and adapt the sup-norm distance for distributions as the similarity measure to construct the mapping. Specifically, we define the sup-norm distance for all pairs $(i,k) \in [n]^2$ as

$$d_{ik} = \sup_{t\in\mathbb{R}} |F_n^i(t) - G_n^k(t)|, \tag{1}$$

where for all $t \in \mathbb{R}$

$$F_n^i(t) = \frac{1}{n^{m-1}} \sum_{\boldsymbol{\omega}\in[n]^{m-1}} \mathbb{1}\{\mathcal{A}_{i,\boldsymbol{\omega}} \le t\}, \quad G_n^k(t) = \frac{1}{n^{m-1}} \sum_{\boldsymbol{\omega}\in[n]^{m-1}} \mathbb{1}\{\mathcal{B}_{k,\boldsymbol{\omega}} \le t\}$$

are slice empirical distributions for node i with observation $\mathcal{A}$ and node k with observation $\mathcal{B}$, respectively. The sup-norm distance d_{ik} is smaller when F_n^i are G_n^k are more correlated, which motivates our Algorithm 1 for Gaussian tensor matching.

Algorithm 1 Gaussian tensor matching via empirical distribution

Input: Gaussian tensors $\mathcal{A}, \mathcal{B} \in \mathbb{R}^{n^{\otimes m}}$.

1: Calculate the sup-norm distance matrix $D = [\![d_{ik}]\!] \in \mathbb{R}^{n\times n}$, where d_{ik} is defined in (1).

2: Obtain the estimated permutation $\hat{\pi}$ on $[n]$ such that

$$\hat{\pi} = \mathop{\arg\max}_{\pi \text{ is a permutation on [n]}} \sum_{i\in[n]} d_{i\pi(i)}.$$

Output: Estimated permutation $\hat{\pi}$.

Following theorem shows the guarantee for Algorithm 1 to exactly recover true permutation π^*.

Theorem 2.1 (Guarantee for Algorithm 1)**.** *Let $\sigma^2 = \sqrt{1-\rho^2}$. Suppose $\sigma \le c\log^{-2} n$ for some sufficiently small positive constant c. Algorithm 1 exactly recovers the true permutation π^* with probability tends to 1 as $n \to \infty$.*

Remark 1. The condition $\sigma \lesssim \log^{-2} n$ is stricter than Ding's condition $\sigma \lesssim \log^{-1} n$. The current unideal tail bound for the sup-norm distance in note 0403 leads to the decrement.

2.2 Improved Matching with Seeded Algorithm

We improve the Algorithm 1 with seeded algorithm. Our seeded algorithm involves three steps: (1) generating seeds that reveals the true permutation π^* for a subset of nodes; (2) recovering the full permutation with the seed; (3) refining the estimated permutation in (2) to achieve exact recovery.

Specifically, we consider the seed that involves high-similarity and high-degree pairs in step (1). We measure the similarity by the sup-norm distance defined in (1). The "degree" of node i in $\mathcal{A}$ and node k in $\mathcal{B}$ for all $i, k \in [n]$ are represented as

$$a_i = \frac{1}{n^{(m-1)/2}} \sum_{\boldsymbol{\omega} \in [n]^{m-1}} \mathcal{A}_{i,\boldsymbol{\omega}}, \quad \text{and} \quad b_k = \frac{1}{n^{(m-1)/2}} \sum_{\boldsymbol{\omega} \in [n]^{m-1}} \mathcal{B}_{k,\boldsymbol{\omega}}. \tag{2}$$

Hence, we consider the following seed set $Q^{(2)}$ with given thresholds ξ, ζ

$$Q^{(2)} = \{(i,k) \in [n]^2 \colon a_i, b_k \geq \xi, d_{ik} \leq \zeta\}. \tag{3}$$

The $Q^{(2)}$ contains more seeds with a smaller ξ and larger ζ. As our proof shows later, the set $Q^{(2)}$ with proper thresholds ξ and ζ contains only true pairs with high probability. Suppose that there exists a perfect matching $\pi_0 : S \mapsto T$ corresponding to $Q^{(2)}$, where S and T are two subsets of $[n]$. Then, we solve the rest permutations by transferring the multiway tensor matching to a bipartite matching problem with π_0. Detail procedures are in Algorithm 2.

Following theorem shows the guarantee for Algorithm 2 to exactly recover true permutation π^*.

Theorem 2.2 (Guarantee for Algorithm 2)**.** *Let $\sigma^2 = \sqrt{1-\rho^2}$. Suppose $\sigma \leq c \log^{-1/3(m-1)} n$ for some sufficiently small positive constant c. Choose thresholds $\xi \geq c_1 \sqrt{\log^{1/(m-1)} n}$ and $\zeta \leq c_2 \sqrt{\sigma / n^{m-1}}$ for some positive constants c_1, c_2. Algorithm 2 exactly recovers the true permutation π^* with probability tends to 1 as $n \to \infty$.*

References

Algorithm 2 **Improved Gaussian tensor matching with seeded algorithm**

Step 1: Seeds generation

Input: Gaussian tensors $\mathcal{A}, \mathcal{B} \in \mathbb{R}^{n^{\otimes m}}$, thresholds ξ and ζ.

Calculate the sup-norm distances d_{ik} as (1) for all pairs $(i,k) \in [n]^2$ and the degrees a_i and b_i as (2) for all $i \in [n]$.

Obtain the seed set $Q^{(2)}$ as (3) with ξ and ζ.

if there exists a perfect matching $\pi_0 : S \mapsto T$ corresponding to $Q^{(2)}$ **then**

    Output π_0.

else

    Stop the entire Algorithm 2 immediately and output error.

end if

Output: Perfect matching π_0 or error.

Step 2: Seeded matching

Input: Gaussian tensors $\mathcal{A}, \mathcal{B} \in \mathbb{R}^{n^{\otimes m}}$ and the perfect matching $\pi_0 : S \mapsto T$ from **Step 1**.

Calculate the analogy of sample covariance H_{ik} for all pairs (i,k) such that $i \in S^c$ and $k \in T^c$, where $S^c = [n]/S, T^c = [n]/T$, and

$$H_{ik} = \sum_{\boldsymbol{\omega} \in S^{m-1}} \mathcal{A}_{i,\boldsymbol{\omega}} \mathcal{B}_{k,\pi_0 \circ \boldsymbol{\omega}}.$$

Find the optimal perfect matching $\tilde{\pi}_1 \colon S^c \mapsto T^c$ such that

$$\tilde{\pi}_1 = \underset{\pi \colon S^c \mapsto T^c}{\arg\max} \sum_{i \in S^c} H_{i\pi(i)}.$$

Concatenate the matching π_0 and $\tilde{\pi}_1$ to a permutation π_1 on $[n]$ such that $\pi_1|_S = \pi_0$ and $\pi_1|_{S^c} = \tilde{\pi}_1$.

Output: Estimated permutation π_1.

Step 3: Non-iterative clean-up

Input: Gaussian tensors $\mathcal{A}, \mathcal{B} \in \mathbb{R}^{n^{\otimes m}}$ and the permutation π_1 on $[n]$ from **Step 2**.

Calculate $W_{ik} = \sum_{\boldsymbol{\omega} \in [n]^{m-1}} \mathcal{A}_{i,\boldsymbol{\omega}} \mathcal{B}_{k,\pi_1 \circ \boldsymbol{\omega}}$ for all pairs $(i,k) \in [n]^2$.

Obtain the set $P^{(2)} = \{(i,k) \in [n]^2 \colon W_{ik}$ is no smaller than the n-th largest $W_{ik}\}$.

if there exists a permutation on $[n]$, $\hat{\pi}$, corresponding to the set $P^{(2)}$ **then**

    Output $\hat{\pi}$.

else

    Output error.

end if

Output: Estimated permutation $\hat{\pi}$ or error.