




Hypothesis testing for populations of networks

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ABSTRACT

It has become an increasingly common practice in modern science and engineering to collect samples of multiple network data in which a network serves as a basic data object. The increasing prevalence of multiple network data calls for developments of models and theories that can deal with inference problems for populations of networks. In this work, we propose a general procedure for hypothesis testing of networks and in particular, for differentiating distributions of two samples of networks. We consider a very general framework which allows us to perform test on large and sparse networks. Our contribution is two-fold: (1) We propose a test statistics based on the singular value of a generalized Wigner matrix. The asymptotic null distribution of the statistics is shown to follow the Tracy–Widom distribution as the number of nodes tends to infinity. The test also yields asymptotic power guarantee with the power tending to one under the alternative; (2) The test procedure is adapted for change-point detection in dynamic networks which is proven to be consistent in detecting the change-points. In addition to theoretical guarantees, another appealing feature of this adapted procedure is that it provides a principled and simple method for selecting the threshold that is also allowed to vary with time. Extensive simulation studies and real data analyses demonstrate the superior performance of our procedure with competitors.

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1. Introduction

One of the unique features in modern data science is the increasing availability of complex data in nontraditional forms. Among the newer forms of data, network has arguably emerged as one of the most important and powerful data types. A network, an abstract object consisting of a set of nodes and edges, can be broadly used to represent interactions among a set of agents or entities and one can find its applications in virtually any scientific field. The ubiquity of network data in diverse fields ranging from biology (Chen and Yuan 2006; Cline et al., 2007), physics (Bounova and de Weck 2012; Kulig et al. 2015), social science (Hoff, Raftery, and Handcock 2002; Snijders and Baerveldt 2003) to engineering (Leonardi and Van De Ville 2013; Chen, Cao, and Bu 2010) has spurred fast

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developments in models, theories and algorithms for the field of network analysis, see e.g., Erdős and Rényi (1959); Holland, Laskey, and Leinhardt (1983); Karrer and Newman (2011); Ball, Karrer, and Newman (2011); Wolfe and Olhede (2013); Rohe, Chatterjee, and Yu (2011); Decelle et al. (2011); Amini and Levina (2018); Bickel and Chen (2009). The existing literature, however, has largely been focusing on inference of one single (often large) network. The recent advancement in technology and computer prowess has led to the increasing prevalence of network data available in multiple networks in which a network serves as the basic data object. For instance, such datasets can be found in neuroscience (Bassett et al. 2008), cancer study (Zhang et al. 2009), microbiome study (Cai et al. 2019), and social interactions (Kossinets and Watts 2006; Eagle, Pentland, and Lazer 2009). There is a strong need for development of models and theories that can deal with such data sets, and more broadly, for inference of population of networks.

One has already seen a growing effort in this direction. Ginestet et al. (2017) proposes a geometric framework for hypothesis tests of populations of networks viewing a weighted network as a point on a manifold. Along the same line, Kolaczyk et al. (2020) provides geometric characterization of space of all unlabeled networks which serve as the foundation for inference based on Fréchet mean of networks. In addition, Mukherjee, Sarkar, and Lin (2017) provides a general framework for clustering network objects. Josephs et al. (2020) proposes a Gaussian process based framework for regression and classification with network inputs. Durante, Dunson, and Vogelstein (2017) proposes a Bayesian nonparametric approach for modeling the populations of networks.

One of commonly encountered problems for inference of populations of networks is hypothesis testing which has significant applications, but remains largely understudied especially for large networks. Among the few existing work in the literature, besides Ginestet et al. (2017) as mentioned above, Tang et al. (2017) carries out hypothesis tests using random dot product graph model via adjacency spectral embedding. Ghoshdastidar et al. (2020) proposes two test statistics based on estimates of the Frobenius norm and spectral norm between link probability matrices of the two samples, the key challenge of which lies in choosing a threshold for the test statistics. Ghoshdastidar and von Luxburg (2018) uses the same statistics as Ghoshdastidar et al. (2020) and proves asymptotic normality for the statistics. Ghoshdastidar and von Luxburg (2018) further proposes a test statistics based on the extreme eigenvalues of a scaled and centralized matrix and proves that the new statistics asymptotically follows the Tracy–Widom law (Tracy and Widom 1996). Most of the literature, however, focuses on the case where the number of nodes for each network is fixed, which greatly limits the scope of inference.

The initial focus of our work is on hypothesis testing for two samples of networks including large and sparse networks. We propose a very intuitive testing statistics which yields theoretical guarantees. More specifically, we prove that its asymptotic null distribution follows the Tracy–Widom distribution and the asymptotic power tends to 1 under the alternative. One of the appealing features of our approach is that our test adopts a very general framework in which the number of the nodes are allowed to grow to infinity, while most of the existing methods assume that the number of nodes is fixed, which is not always a practical assumption since many modern networks are

often large and sparse. We then adapt our test statistics for a change-point detection procedure in dynamic networks and prove its consistency in detecting change-points. We provide a principled method for selecting the threshold level in the change-point detection procedure based on the asymptotic distribution of the testing statistics and the threshold is allowed to vary with time. This is appealing comparing to many existing change-point detection approaches which require either a cross-validation for selecting the threshold or a careful tuning of the parameters. Extensive simulation studies and two real data analyses demonstrate the superior performance of our procedure in comparing with others in both tasks.

The paper is organized as follows. In [Section 2](#), we propose a testing statistics and thoroughly study its asymptotic properties. [Section 3](#) is devoted to a change-point detection procedure for dynamic networks by adapting the testing statistics derived in [Section 2](#). Simulation studies are carried out in [Section 4](#) and real data examples are presented in [Section 5](#). Technical proofs can be found in the [supplementary material](#).

2. Two-sample hypothesis testing for networks

2.1. Notation

We first introduce some notations that will be used throughout the paper. For a set \mathcal{N} , $|\mathcal{N}|$ denotes its cardinality. TW_1 denotes the Tracy–Widom distribution with index 1. $\chi^2(n)$ denotes the Chi-squared distribution with n degrees of freedom. For a square matrix $B \in \mathbb{R}^{n \times n}$, B_{ij} denotes its (i, j) entry, B_i is the i th row of B , and $B_{\cdot i}$ is the i th column of B . For a symmetric matrix $B \in \mathbb{R}^{n \times n}$, $\lambda_j(B)$ denotes its j th largest eigenvalue, ordered as $\lambda_1(B) \geq \lambda_2(B) \geq \dots \geq \lambda_n(B)$, $\sigma_1(B)$ is the largest singular value. Write $X_n \rightsquigarrow X$ if a sequence of random variables $\{X_n\}_{n=1}^\infty$ converges in distribution to random variable X . $\lfloor x \rfloor$ denotes the largest integer but no greater than $x \in \mathbb{R}$. $I(\cdot)$ denotes indicator function. For two sequences of real numbers $\{x_n\}$ and $\{y_n\}$, we have the following notations:

$y_n = O_n(x_n)$: there exists a positive constant M such that $\lim_{n \rightarrow \infty} \left| \frac{y_n}{x_n} \right| \leq M$.

$y_n = o_n(x_n)$: $\lim_{n \rightarrow \infty} \frac{y_n}{x_n} = 0$

$y_n = o_p(x_n)$: $\lim_{n \rightarrow \infty} P\left(\left| \frac{y_n}{x_n} \right| \geq \varepsilon\right) = 0$ for any positive ε .

2.2. Problem setup and some existing tests

We consider two samples of networks with n nodes and sample sizes m_1 and m_2 respectively. More specifically, we assume one observes symmetric binary adjacency matrices $A_1^{(1)}, \dots, A_1^{(m_1)}$ that are generated from symmetric link probability matrix P_1 with $A_{1,ij}^{(k)} \sim \text{Bernoulli}(P_{1,ij})$, $k = 1, 2, \dots, m_1$, $i, j = 1, 2, \dots, n$, and another sample of adjacency matrices $A_2^{(1)}, \dots, A_2^{(m_2)}$ generated from the same model with link probability matrix P_2 . Our goal is to test whether the two samples of networks have same graph structure or not, which is equivalent to testing:

$$H_0 : P_1 = P_2 \text{ against } H_1 : P_1 \neq P_2. \quad (1)$$

For the case of $m_1 = m_2 = 1$ and a fixed n , Tang et al. (2017) focuses on random dot product graphs by applying the adjacency spectral embedding, whereas Ghoshdastidar and von Luxburg (2018) focuses on the inhomogeneous Erdős–Rényi graphs and proposes a test based on eigenvalues.

For the case of large m_1, m_2 and again a fixed number of nodes n , Ginestet et al. (2017) proposes a χ^2 -type test based on a geometric characterization of the space of graph Laplacians and a notion of Fréchet means (Fréchet 1948; Bhattacharya and Lin 2017). As a simplification of the statistics in Ginestet et al. (2017), Ghoshdastidar and von Luxburg (2018) sets $m_1 = m_2 = m$ and obtains the test statistics as follows:

$$T_{\chi^2} = \sum_{i < j} \frac{(\bar{A}_{1,ij} - \bar{A}_{2,ij})^2}{\frac{1}{m(m-1)} \sum_{k=1}^m (A_{1,ij}^{(k)} - \bar{A}_{1,ij})^2 + \frac{1}{m(m-1)} \sum_{k=1}^m (A_{2,ij}^{(k)} - \bar{A}_{2,ij})^2}, \quad (2)$$

where $\bar{A}_{u,ij} = \frac{1}{m} \sum_{k=1}^m A_{u,ij}^{(k)}$ with $u = 1, 2$. Then $T_{\chi^2} \rightarrow \chi^2(\frac{n(n-1)}{2})$ as $m \rightarrow \infty$. We call this method χ^2 -type test.

The case of large n and fixed m_1 and m_2 is one of the likely scenarios in practice and is thus perhaps more interesting. Ghoshdastidar and von Luxburg (2018) uses the same statistics as Ghoshdastidar et al. (2020) as follows:

$$T_N = \frac{\sum_{i < j} \left(\sum_{k \leq m/2} A_{1,ij}^{(k)} - A_{2,ij}^{(k)} \right) \left(\sum_{k > m/2} A_{1,ij}^{(k)} - A_{2,ij}^{(k)} \right)}{\sqrt{\sum_{i < j} \left(\sum_{k \leq m/2} A_{1,ij}^{(k)} + A_{2,ij}^{(k)} \right) \left(\sum_{k > m/2} A_{1,ij}^{(k)} + A_{2,ij}^{(k)} \right)}}. \quad (3)$$

Ghoshdastidar and von Luxburg (2018) proves the asymptotic normality of T_N as $n \rightarrow \infty$. We refer this method to N -type test.

2.3. Proposed test statistics

In proposing our test statistics, we consider a very general setting in which the number of nodes can grow to infinity instead of being fixed like in most of the existing literature, and the sample sizes m_1 and m_2 grow in an appropriate rate. We first introduce the centralized and re-scaled matrix Z with entries given as follows:

$$Z_{ij} = \frac{\bar{A}_{1,ij} - \bar{A}_{2,ij}}{\sqrt{(n-1) \left[\frac{1}{m_1} P_{1,ij}(1 - P_{1,ij}) + \frac{1}{m_2} P_{2,ij}(1 - P_{2,ij}) \right]}}, \quad (4)$$

where $\bar{A}_{u,ij} = \frac{1}{m_u} \sum_{k=1}^{m_u} A_{u,ij}^{(k)}$ with $u = 1, 2$ and $i, j = 1, \dots, n$.

The matrix Z involves unknown link probability matrices P_1 and P_2 thus can not be directly used as a test statistics. As an alternative, one can choose some appropriate plugin estimates for P_1 and P_2 , and some of these estimates attain good properties for the resulting tests as we will see in the following discussions.

Denote \hat{P}_1 and \hat{P}_2 as some plugin estimators of P_1 and P_2 respectively, then the empirical standardized matrix \hat{Z} of Z can be written with entries as

$$\hat{Z}_{ij} = \frac{\bar{A}_{1,ij} - \bar{A}_{2,ij}}{\sqrt{(n-1) \left[\frac{1}{m_1} \hat{P}_{1,ij}(1 - \hat{P}_{1,ij}) + \frac{1}{m_2} \hat{P}_{2,ij}(1 - \hat{P}_{2,ij}) \right]}}, \quad i, j = 1, 2, \dots, n. \quad (5)$$

We propose to use the largest singular value of \hat{Z} , after suitable shifting and scaling, as our test statistics:

$$T_{TW_1} = n^{2/3} [\sigma_1(\hat{Z}) - 2]. \quad (6)$$

Given a significance level $\alpha \in (0, 1)$, the rejection region Q for H_0 in test (1) is

$$Q = \{T_{TW_1} | T_{TW_1} \geq \tau_{\alpha/2}\}, \quad (7)$$

where $\tau_{\alpha/2}$ is the corresponding $\alpha/2$ upper quantile of TW_1 . We then have the following results.

Theorem 2.1 (General asymptotic null distribution). *Let $A_1^{(1)}, \dots, A_1^{(m_1)}$ be a sample of networks generated from a link probability matrix P_1 with n nodes, and $A_2^{(1)}, \dots, A_2^{(m_2)}$ be another sample generated from a link probability matrix P_2 with the same number of nodes. Let \hat{Z} be given as in (5). Given some estimated matrices \hat{P}_u of $P_u, u = 1, 2$, if $\sup_{i,j} |\hat{P}_{u,ij} - P_{u,ij}| = o_p(n^{-2/3})$, then the following holds under the null hypothesis in (1):*

$$n^{2/3} [\lambda_1(\hat{Z}) - 2] \rightsquigarrow TW_1, \quad n^{2/3} [-\lambda_n(\hat{Z}) - 2] \rightsquigarrow TW_1. \quad (8)$$

Remark 2.2. Theorem 2.1 is very general in the sense that it puts no structural conditions on the networks, nor does it impose any assumption on the type of estimates for P_1 and P_2 so long as they are estimated within $o_p(n^{-2/3})$ error.

The following corollaries show asymptotic type I error control and asymptotic power for the rejection rule (7).

Corollary 2.3 (Asymptotic type I error control). *Supposing assumptions in Theorem 2.1 hold, the rejection region in (7) has size α .*

Corollary 2.4 (Asymptotic power guarantee). *Define a matrix $\tilde{Z} \in \mathbb{R}^{n \times n}$ with zero diagonal and for any $i \neq j$,*

$$\tilde{Z}_{ij} = \frac{P_{1,ij} - P_{2,ij}}{\sqrt{(n-1) \left[\frac{1}{m_1} P_{1,ij}(1 - P_{1,ij}) + \frac{1}{m_2} P_{2,ij}(1 - P_{2,ij}) \right]}}. \quad (9)$$

Under the assumptions of Theorem 2.1, if $P_{1,ij}$ and $P_{2,ij}$ are such that $n^{-2/3} [\sigma_1(\tilde{Z}) - 4]^{-1} \leq o_n(1)$, then

$$P(T_{TW_1} \geq \tau_{\alpha/2}) = 1 - o_n(1).$$

Remark 2.5. As mentioned in the introduction, in Ghoshdastidar and von Luxburg (2018), a test statistics for comparing two large graphs is proposed, and our test statistics appears to be similar in natural to theirs. However, there are some key distinctions

between our method and theirs. First, our testing statistics considers two-sample test on two populations of networks which requires exploration of the proper interplay between the asymptotics in both the sample sizes of networks and nodes number. Second, Ghoshdastidar and von Luxburg (2018) proves the asymptotic Tracy–Widom law under the true link probability matrices, while in our paper, we consider various estimates of link probability matrices (again based on multiple networks) and prove the Tracy–Widom law theoretically. We also discuss the performance of the resulting testing statistics under various estimators. Third, our testing statistics is modified for a novel and efficient change-point detection procedure and the consistency of the change-point detection is also proved.

2.4. Different estimators of link probability matrix

The testing statistics proposed in the previous section requires a plugin estimator for the link probability matrix based on a sample of networks. In this subsection, we investigate the properties of the tests corresponding to various different estimators for link probability matrix.

We first consider a different but natural and simple estimator of P_u by using the average of all the adjacency matrices in the same group. We denote this method as AVG and the link probability matrix estimator as $\hat{P}_{\text{AVG},u}$, which is actually \bar{A}_u .

It's not difficult to see that

$$\sup_{i,j} |\hat{P}_{\text{AVG},u,ij} - P_{u,ij}| = o_p(m_u^{-1/2} \log(n))$$

by applying Bernstein's inequality. To guarantee the asymptotic TW_1 in (8), it requires that $m_u = O_n(n^{4/3})$. More specifically, the sample size m_u needs to increase faster than nodes number n , so m_u will exceed n eventually as n tends to infinity. Therefore, the AVG estimator will perform well if the sample size is large enough. However, this is hard to hold in reality especially when the size of the network is large. Usually, for most practical applications, it would be more suitable to require m_u to increase slower than n .

We also consider an average estimator of P_u based on the stochastic block model (SBM), which is similar in spirit to the estimator in Ghoshdastidar and von Luxburg (2018) but with a different algorithm for estimating the communities. Our main idea can be summarized as follows: First, assume the graphs are SBMs, or approximate them with SBMs by a weaker version of Szemerédi's regularity lemma (see Lovász (2012)). Second, use one of the community detection algorithms such as the goodness-of-fit test proposed in Lei (2016) to estimate the number of the communities \hat{K}_u . Then perform clustering using for example the spectral clustering algorithm (see, e.g., von Luxburg (2007)) to obtain estimates of the membership vector $g_u \in \{1, \dots, \hat{K}_u\}^n$ as well as the community set $\mathcal{B}_{u,k} = \{i : 1 \leq i \leq n, g_{u,i} = k\}$, where $k = 1, 2, \dots, \hat{K}_u$ and $g_{u,i}$ is the i th element of g_u . Subsequently, P_u is approximated by a block matrix $\hat{P}_{\text{SBM},u}$ such that $\hat{P}_{\text{SBM},u,ij}$ is the mean of the submatrix of \bar{A}_u restricted to $\mathcal{B}_{u,g_{u,i}} \times \mathcal{B}_{u,g_{u,j}}$.

Under further assumption that each community has size at least proportional to n/K_u , where K_u is the true community number, it can be seen that the error of $\hat{P}_{\text{SBM}, u, ij}$ is $o_p(K_u m_u^{-1/2} n^{-1} \log n)$ (Lei 2016). This implies that only when $K_u = O_n(n^{\gamma_u})$, $\gamma_u < 1/3 + \alpha_u/2$, and $m_u = O_n(n^{\alpha_u})$, $\alpha_u \geq 0$, the error condition in Theorem 2.1 holds. For large networks in practice, the number of communities can be very large therefore such a condition might be hard to satisfy. Moreover, due to the potential double estimation in the process (in estimating the number of communities as well as the community membership), it may bring large error to the final test statistics, especially when the SBM assumption is not valid.

We now discuss another explicit method for the link probability matrix estimates that can be used as the plugging estimates in the test statistics called the modified neighborhood smoothing (MNBS) estimator. Let $\{\xi_i\}_{i=1}^n$ be a random sequence such that $\xi_i, i = 1, \dots, n$, are *i.i.d.* uniform random variables on $[0, 1]$. Conditional on this global sequence $\{\xi_i\}_{i=1}^n$, we assume all the adjacency matrices $A^{(1)}, A^{(2)}, \dots, A^{(m)}$ in the same population share the same link probability matrix $P \in \mathbb{R}^{n \times n}$, which is modeled by a graphon function $f : [0, 1]^2 \rightarrow [0, 1]$ such that

$$P_{ij} = f(\xi_i, \xi_j).$$

Therefore, we have

$$A_{ij}^{(k)} \mid \{\xi_i\}_{i=1}^n \sim \text{Bernoulli}(f(\xi_i, \xi_j)),$$

independently for all $i \leq j$ and $k = 1, \dots, m$.

We then apply MNBS method proposed in Zhao, Chen, and Lin (2019) to estimate P . The essential idea of the MNBS procedure consists of the following steps: First, for the group of adjacency matrices $A^{(1)}, A^{(2)}, \dots, A^{(m)}$ generated from P , let $\bar{A} = \sum_{k=1}^m A^{(k)}/m$, define the distance measure between nodes i and i' as $d^2(i, i') = \max_{k \neq i, i'} |\langle \bar{A}_i, \bar{A}_{i'} \rangle|$ and the neighborhood of node i as $\mathcal{N}_i = \{i' \neq i : d^2(i, i') \leq q_i(q)\}$, where $q_i(q)$ denotes the q th quantile of the distance set $\{d^2(i, i') : i' \neq i\}$. Then the parameter q is set to be $C \log n / (n^{1/2} \omega)$, where C is some positive constant and $\omega = \min\{n^{1/2}, (m \log n)^{1/2}\}$. Finally, given the neighborhood \mathcal{N}_i for each node i , the link probability P_{ij} between nodes i and j is estimated by $\tilde{P}_{ij} = \sum_{i' \in \mathcal{N}_i} \bar{A}_{i'j} / |\mathcal{N}_i|$. In comparing with the neighborhood smoothing method proposed in Zhang, Levina, and Zhu (2017), the key idea is to employ the average network information \bar{A} and simultaneously shrink the neighborhood size (from $C(\log n/n)^{1/2}$ to $C \log n / (n^{1/2} \omega)$) to obtain an estimate with an improved rate.

Based on MNBS, for the symmetric networks considered in this paper, we use symmetrized estimators of the link probability matrices $P_u, u = 1, 2$, of the two groups of graphs as

$$\hat{P}_u = \frac{\tilde{P}_u + (\tilde{P}_u)^T}{2}, \quad \text{with } \tilde{P}_{u, ij} = \frac{\sum_{i' \in \mathcal{N}_{u, i}} \bar{A}_{u, i'j}}{|\mathcal{N}_{u, i}|}, \quad (10)$$

where $\bar{A}_{u, i'j}$ is the (i', j) element of $\bar{A}_u = \sum_{k=1}^{m_u} A_u^{(k)} / m_u$ and $\mathcal{N}_{u, i}$ is the neighborhood of node i in group u .

From Lemma 9.3 in Zhao, Chen, and Lin (2019), we have

$$|\mathcal{N}_{u,i}| \geq B_u \frac{n^{1/2} \log n}{\omega_u}, \quad (11)$$

where B_u is a global positive constant and $\omega_u = \min\{n^{1/2}, (m_u \log n)^{1/2}\}$ for $u = 1, 2$.

For the MNBS, we do not provide an explicit rate on bounding the sup norm $\sup_{i,j} |\hat{P}_{u,ij} - P_{u,ij}|$ due to the difficulty in deriving the point-wise rate. From the definition of $d^2(i, i')$, it can be seen that the distance measure between nodes i and i' in the MNBS algorithm is based on the row pattern similarity instead of point-wise way. To derive an entry-wise error of P_{ij} , one can use Bernstein's inequality, but the neighbor of a node is selected by the q th quantile of the distance set, which would decrease the variance of sample in the neighbor, but this decreased variance is unknown. The extensive simulation carried out in Section 4 and Section 5 show that MNBS-based tests often yield the best performance in comparing with tests based on other estimators.

Remark 2.6. As one can see in our setup in Section 2.2, it is assumed that the edges of each network $A^{(k)}$, $k = 1, \dots, m$, in the same populations are generated *independently* from the same deterministic link probability matrix P . To fit this setup under a genuine 'graphon model', one has to assume that for each node i , the latent variable ξ_i is the same over all the samples in the same population and will not change for each sample. That is, a global latent sequence $\{\xi_i\}_{i=1}^n$ is shared across all the networks. Note that this setup does not fall under a genuine graphon model in which one first samples uniform random sequence $\{\xi_i^{(k)}\}_{i=1}^n$ for each network over k , then $A_{ij}^{(k)} | \{\xi_i^{(k)}\}_{i=1}^n \sim \text{Bernoulli}(f(\xi_i^{(k)}, \xi_j^{(k)}))$. Therefore, the entries of the adjacent matrix or network are not independent after marginalizing the latent variables.

3. Change-point detection in dynamic networks

We refer the two sample test based on asymptotic TW_1 proposed in the previous section as TW_1 -type test. In this section, we adapt the TW_1 -type test to a procedure for change-point detection in dynamic networks, which is another important learning task in statistics and has received a great deal of recent attentions. Specifically, we examine a sequence of networks whose distributions may exhibit changes at some time epochs. Then, the problem is to determine the unknown change-points based on the observed sequence of network adjacency matrices.

Assume the observed dynamic networks $\{A_t\}_{t=1}^m$ are generated by a sequence of probability matrices $\{P_t\}_{t=1}^m$ with $A_{t,ij} \sim \text{Bernoulli}(P_{t,ij})$ for time $t = 1, \dots, m$. Let $\mathcal{J} = \{\eta_j\}_{j=1}^J \subset \{1, \dots, m\}$ be a collection of change-points and $\eta_0 = 0, \eta_{J+1} = m$, ordered as $\eta_0 < \eta_1 < \dots < \eta_J < \eta_{J+1}$, such that

$$P_t = P^{(j)}, t = \eta_{j-1} + 1, \dots, \eta_j, j = 1, \dots, J + 1.$$

In other words, the change-points $\{\eta_j\}_{j=1}^J$ divide the networks into $J + 1$ groups, the networks contained in the same group follow the same link probability matrix and $P^{(j)}$

is the link probability matrix of the j th segment satisfying $P^{(j)} \neq P^{(j+1)}$. Denote $\mathcal{J} = \emptyset$ if $J = 0$.

Now we apply our TW_1 -type test to a screening and thresholding algorithm that is commonly used in change-point detection, see Niu and Zhang (2012); Zou et al. (2014); Zhao, Chen, and Lin (2019). The detection procedure is referred as TW_1 -type detection and described as follows.

Define $L = \min_{1 \leq j \leq J+1} (\eta_j - \eta_{j-1})$, which is the minimum segment length. Set a screening window size $h \ll m$ and $h < L/2$. Denote $\bar{A}_1(t, h) = \frac{1}{h} \sum_{i=t-h+1}^t A_i$ and $\bar{A}_2(t, h) = \frac{1}{h} \sum_{i=t+1}^{t+h} A_i$ for each $t = h, \dots, m - h$. $\hat{P}_1(t, h)$ and $\hat{P}_2(t, h)$ are for example MNBS estimators using $\{A_i\}_{i=t-h+1}^t$ and $\{A_i\}_{i=t+1}^{t+h}$ respectively. In addition, we denote a matrix $\hat{Z}(t, h)$ with entries as follows essentially the same as in (5):

$$\hat{Z}_{ij}(t, h) = \frac{\bar{A}_{1,ij}(t, h) - \bar{A}_{2,ij}(t, h)}{\sqrt{(n-1) \left\{ \frac{1}{h} \hat{P}_{1,ij}(t, h) [1 - \hat{P}_{1,ij}(t, h)] + \frac{1}{h} \hat{P}_{2,ij}(t, h) [1 - \hat{P}_{2,ij}(t, h)] \right\}}},$$

$i, j = 1, 2, \dots, n.$

In the screening step, we calculate the scan statistics $T_{TW_1}(t, h)$ depending only on observations in a small neighborhood $[t - h + 1, t + h]$ as follows:

$$T_{TW_1}(t, h) = n^{2/3} \{ \sigma_1 [\hat{Z}(t, h)] - 2 \}.$$

Define the h -local maximizers of $T_{TW_1}(t, h)$ as $\{t : T_{TW_1}(t, h) \geq T_{TW_1}(t', h) \text{ for all } t' \in (t - h, t + h)\}$. Let \mathcal{LM} denote the set of all h -local maximizers of $T_{TW_1}(t, h)$.

In the thresholding step, we estimate the change-points by a thresholding rule to \mathcal{LM} with time t such that

$$\hat{\mathcal{J}} = \{t : t \in \mathcal{LM} \text{ and } T_{TW_1}(t, h) > \Delta_{T_{TW_1}}\}, \tag{12}$$

where $\Delta_{T_{TW_1}} = \max\{\tau_\alpha, n^{2/3}[\delta(t, h) - 4] - \tau_\alpha\}$, $\alpha = 1/2 - (1 - 1/n)^{1/(2h)}/2$, $\delta(t, h) = \sigma_1(V_1(t, h))$ is the largest singular value of matrix $V_1(t, h)$ with zero diagonal and for any $i \neq j$,

$$V_{1,ij}(t, h) = \frac{\hat{P}_{1,ij}(t, h) - \hat{P}_{2,ij}(t, h)}{\sqrt{(n-1) \left\{ \frac{1}{h} \hat{P}_{1,ij}(t, h) [1 - \hat{P}_{1,ij}(t, h)] + \frac{1}{h} \hat{P}_{2,ij}(t, h) [1 - \hat{P}_{2,ij}(t, h)] \right\}}},$$

$i, j = 1, 2, \dots, n.$

We have the following consistency result.

Theorem 3.1 (Consistency of TW_1 -type change-point detection). *Under the alternative hypothesis, assume $n^{2/3}[\sigma(t, h) - 4] \geq 2\tau_\alpha$, $\alpha = 1/2 - (1 - 1/n)^{1/(2h)}/2$, $h < L/2$, then the TW_1 -type change-point detection procedure satisfies*

$$\lim_{n \rightarrow \infty} P(\mathcal{J} = \hat{\mathcal{J}}) = 1.$$

One of the interesting findings from [Theorem 3.1](#) is that for a fixed window size h , the threshold in [\(12\)](#) is dynamic with time t instead of being a constant as in [Zhao, Chen, and Lin \(2019\)](#). By adapting the TW_1 -type test for change-point detection, we can adjust the threshold with t and still enjoy consistency of the change-point detection. From the proof of [Theorem 3.1](#), it is reflected that for a time t that does not correspond to a change-point, $T_{TW_1}(t, h) \leq \Delta_{TW_1}$ with probability 1, so it can control the type I error. However, for a change-point t , $T_{TW_1}(t, h) > \Delta_{TW_1}$ with probability 1, and hence the threshold can lead to a good performance.

The only tuning parameter of TW_1 -type change-point detection procedure is the local window size h , which is chosen according to applications with available information or artificially like set $h = \sqrt{m}$ as recommended in [Zhao, Chen, and Lin \(2019\)](#).

4. Simulation study

In this section, we illustrate the performance of TW_1 -type test and its application to change-point detection using several synthetic data examples.

We first define four graphons and an SBM, which are used for two-sample test and change-point detection in the simulation studies. The graphons are partly borrowed from [Zhang, Levina, and Zhu \(2017\)](#) and the SBM is from [Zhao, Chen, and Lin \(2019\)](#) with 2 communities. We denote the block matrix or the probability matrix of connections between blocks as Λ . More specifically, the graphons and SBM are defined as:

Graphon 1:

$$f(u, v) = \begin{cases} k/(K+1), & u, v \in ((k-1)/K, k/K), \\ 0.3/(K+1), & \text{otherwise,} \end{cases}$$

where $K = \lfloor \log n \rfloor, k = 1, 2, \dots, K$.

Graphon 2:

$$f(u, v) = (u^2 + v^2)/3 \cos[1/(u^2 + v^2)] + 0.15.$$

Graphon 3:

$$f(u, v) = \sin[5\pi(u + v - 1) + 1]/2 + 0.5.$$

Graphon 4:

$$f(u, v) = (u^2 + v^2)/10 \cos[1/(u^2 + v^2)] + 0.05.$$

SBM 1:

$$\Lambda = \begin{bmatrix} 0.6 + \theta_0 & 0.3 \\ 0.3 & 0.6 \end{bmatrix},$$

where θ_0 is a constant related to sample size m . The membership of the i th node is $M(i) = I(1 \leq i \leq \lfloor 2n/\log n \rfloor) + 2I(\lfloor 2n/\log n \rfloor + 1 \leq i \leq n)$.

To operationalize simulations related to MNBS, the quantile parameter $q = B_0(\log n)^{1/2}/(n^{1/2}h^{1/2})$ and the threshold $\Delta_D = D_0(\log n)^{1/2+\delta_0}/(n^{1/2}h^{1/2})$ with tuning parameters D_0 and δ_0 for change-point detection in Zhao, Chen, and Lin (2019) need to be specified. In the following simulations in this section and the real data analyses in Section 5, we set the related parameters $h = \sqrt{m}$, $B_0 = 3$, $\delta_0 = 0.1$, $D_0 = 0.25$ as recommended in Zhao, Chen, and Lin (2019) unless otherwise indicated.

4.1. Two-sample test with simulated data

To examine the performance of the two-sample test (1), we present our results by TW_1 -type tests based on MNBS (TW_1 -MNBS), AVG (TW_1 -AVG), and SBM (TW_1 -SBM) discussed in subsection 2.4, χ^2 -type test with statistics (2), and N -type test with statistics (3). We measure the performance in terms of the Attained Significance Level (ASL) which is the probability of observing a statistics far away from the true value under the null hypothesis, and the Attained Power (AP), the probability of correctly rejecting the null hypothesis when the alternative hypothesis is true.

We conduct two experiments using Graphon 1 and Graphon 2 respectively. In the first experiment, we generate two groups of networks $\{A_1^{(k)}\}_{k=1}^{m_1}$ and $\{A_2^{(k)}\}_{k=1}^{m_2}$. We vary the number of nodes n growing from 100 to 1000 in a step of 100 with sample sizes $m_1 = m_2 = 30, 200$, and set significance level at $\alpha = 0.05$. $\{A_1^{(k)}\}_{k=1}^{m_1}$ are generated from Graphon 1. Under the null hypothesis, $\{A_2^{(k)}\}_{k=1}^{m_2}$ are also generated from the Graphon 1 and hence $P_1 = P_2$. Under the alternative hypothesis, randomly choose $\lfloor \log n \rfloor$ -element subset $S \subset \{1, 2, \dots, n\}$, generate $\{A_2^{(k)}\}_{k=1}^{m_2}$ from P_2 by setting $P_{2,ij} = P_{1,ij} + \theta_1$ with $\theta_1 = 0.05$ for $m_1 = m_2 = 30$ ($\theta_1 = 0.02$ for $m_1 = m_2 = 200$) if $i, j \in S$, and $\theta_1 = 0$ otherwise. Using TW_1 -MNBS, TW_1 -AVG, TW_1 -SBM tests, χ^2 -type test and N -type test, we run 1000 Monte Carlo simulations for the experiment to estimate the ASLs and APs of test (1).

The second experiment is conducted similarly but using Graphon 2. The only difference is that for a better visualization of comparisons, under the alternative hypothesis, we set $P_{2,ij} = P_{1,ij} + \theta_2$ with $\theta_2 = 0.2$ for $m_1 = m_2 = 30$ ($\theta_2 = 0.17$ for $m_1 = m_2 = 200$) if $i, j \in S$ and $\theta_2 = 0$ otherwise. The rates of rejecting the null hypothesis for these two experiments are summarized in Figures 1 and 2 respectively.

The results of the first experiment using Graphon 1, an SBM set up, are plotted in Figure 1. It reveals undesirable behaviors of χ^2 -type test and TW_1 -AVG test since with increasing number of nodes n , the ASLs of both tests grow quickly close to 1, which is too large to be used in practice. We can also see that the N -type test is not efficient as both ASLs and APs of the test are 0 for both cases of $m_1 = m_2 = 30, 200$. Its poor performance in APs is partly due to the small difference between $\{A_1^{(k)}\}_{k=1}^{m_1}$ and $\{A_2^{(k)}\}_{k=1}^{m_2}$ we set. However, the performance of TW_1 -SBM test and TW_1 -MNBS test are much better, ASLs of both tests are stable and close to the significance level of $\alpha = 0.05$, while APs improve to 1 as n grows. It is also found that when n is not that large, TW_1 -SBM test is slightly more powerful in terms of AP than TW_1 -MNBS test. This is not surprising because the networks generated from Graphon 1 are endowed with an SBM structure.

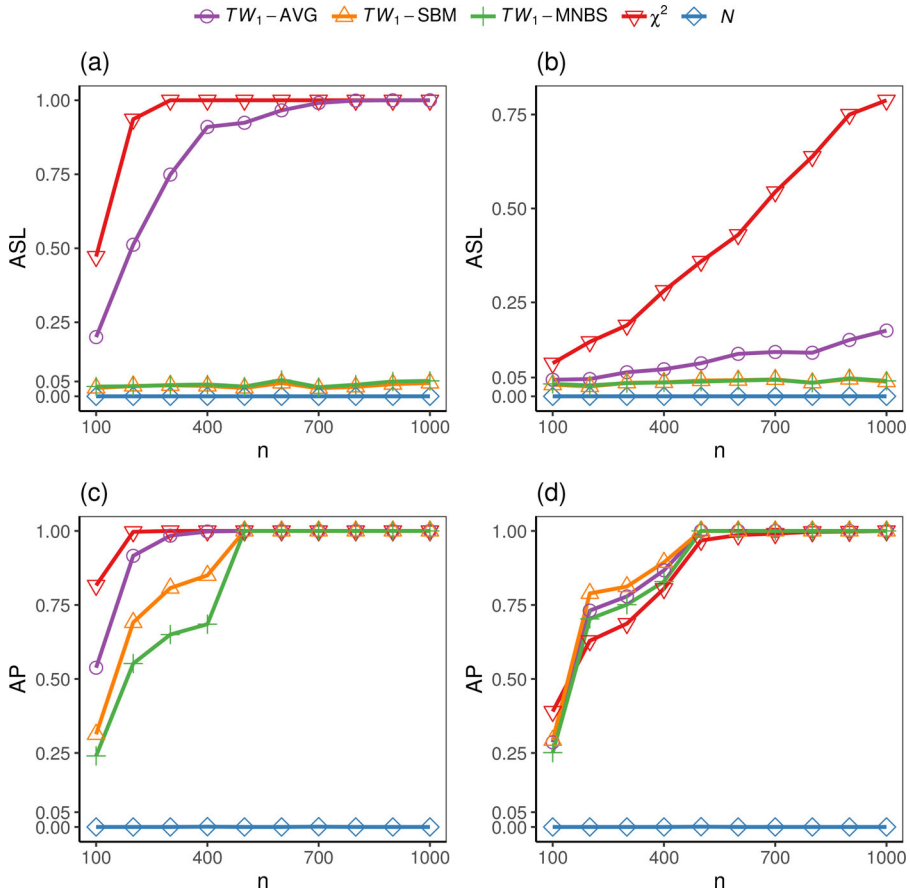


Figure 1. ASLs and APs of tests using Graphon 1 for different values of nodes number n , sample sizes m_1 and m_2 . $m_1 = m_2 = 30$ for (a) and (c) and $m_1 = m_2 = 200$ for (b) and (d).

The results of the second experiment using Graphon 2, which is not an SBM, are given in Figure 2. It indicates that the behaviors of TW_1 -AVG test, χ^2 -type test and N -type test are similar to those in the first experiment using Graphon 1 and the performance is poor. On the other hand, TW_1 -MNBS test has a superior performance than TW_1 -SBM in both ASL and AP. Specifically, ASLs of TW_1 -SBM test are away from 0.05, whereas TW_1 -MNBS test still performs well on both ASL and AP. Moreover, this also indicates that TW_1 -SBM test is sensitive to the network structure especially deviation from an SBM. Hence, TW_1 -MNBS test is more robust to the network structure whereas TW_1 -SBM test is preferable for SBM networks.

4.2. Change-point detection in dynamic networks

To assess the performance of TW_1 -type change-point detection in dynamic networks, we compare its performance based on MNBS, AVG, and SBM estimators (referred as CP-TWMNBS, CP-TWAVG, CP-TWSBM respectively) to the graph-based nonparametric testing procedure in Chen and Zhang (2015) referred as CP-GRA detection, and the

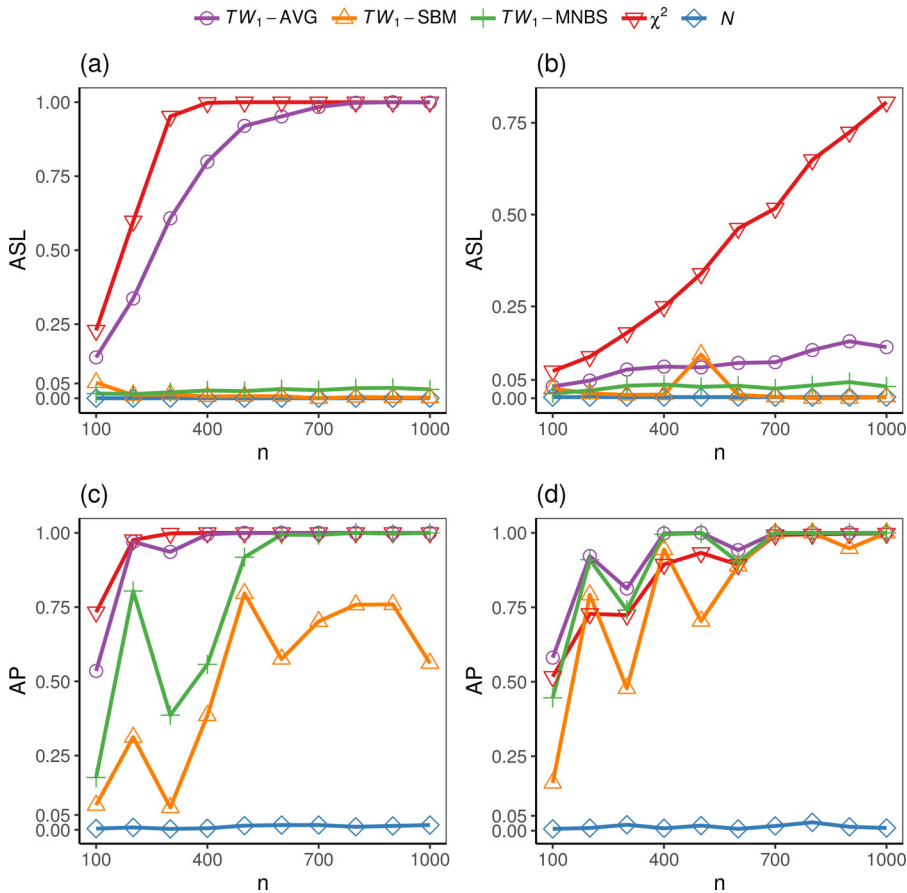


Figure 2. ASLs and APs of tests using Graphon 2 for different values of nodes number n , sample sizes m_1 and m_2 . $m_1 = m_2 = 30$ for (a) and (c) and $m_1 = m_2 = 200$ for (b) and (d).

(a) HC

(b) SCZ

MNBS-based change-point detect procedure in Zhao, Chen, and Lin (2019) referred as CP-DMNBS detection.

Specifically, using all the above five methods, we conduct change-point detection experiments under three different scenarios with zero, one, and three change-points respectively. For all the experiments, we vary the nodes number and the sample size at $n = 100, 200, 300, m = 100, 200$, and set the significance $\alpha = 0.05$. For each combination of the sample size, nodes number, and the network model, we run 100 Monte Carlo trials. Simultaneously, we also explore the effect of network sparsity on the performance of change-point detection. For this, we consider the above setting, but scale the link probability P as ρP by a factor $\rho = 1, 0.25$, where $\rho = 1$ is exactly the same as the above setting while $\rho = 0.25$ corresponds to sparser graphs.

4.2.1. No change-point detection

To study the performance with respect to false positives, we simulate two kinds of dynamic networks $\{A_t\}_{t=1}^m$ with no change-point from Graphon 3 and SMB 1 with

Table 1. Average estimated change-points number \hat{J} under no change-point scenarios through Graphon 3.

m	n	ρ	CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS
100	100	1	0.00	0.00	0.00	0.04	3.75
		0.25	0.00	0.00	0.00	0.03	2.04
100	200	1	0.00	0.00	0.00	0.11	0.15
		0.25	0.00	0.00	0.00	0.07	0.3
100	300	1	0.00	0.00	0.00	0.04	0.02
		0.25	0.00	0.00	0.00	0.04	0.02
200	100	1	0.00	0.00	0.00	0.02	2.02
		0.25	0.00	0.00	0.00	0.08	5.16
200	200	1	0.00	0.00	0.00	0.08	0.21
		0.25	0.00	0.00	0.00	0.03	0.35
200	300	1	0.00	0.00	0.00	0.05	0.01
		0.25	0.00	0.00	0.00	0.08	0.01

Table 2. Average estimated change-points number \hat{J} under no change-point scenarios through SBM 1.

m	n	ρ	CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS
100	100	1	4.19	0.02	0.02	0.10	0.00
		0.25	0.06	0.02	0.02	0.02	0.00
100	200	1	4.21	0.00	0.00	0.04	0.00
		0.25	0.16	0.00	0.03	0.03	0.00
100	300	1	4.09	0.01	0.01	0.04	0.00
		0.25	0.17	0.02	0.03	0.01	0.00
200	100	1	5.74	0.02	0.02	0.08	0.00
		0.25	0.42	0.02	0.07	0.04	0.00
200	200	1	6.34	0.03	0.03	0.07	0.00
		0.25	1.13	0.02	0.02	0.01	0.00
200	300	1	6.26	0.02	0.02	0.03	0.00
		0.25	2.30	0.01	0.01	0.02	0.00

$\theta_0 = 0$ respectively. Tables 1 and 2 report the average number of estimated change-points by using the five methods.

As one can see, the performance of CP-TWSBM, CP-TWMNBS, and CP-GRA detections perform reasonably well and improves as n increases. CP-TWAVG detect method performs well in the case of Graphon 3 while experiences heavy inflated levels in the case of SBM 1. As for CP-DMNBS detection, the empirical type I error is completely controlled at the target level 0.05 for SBM 1, but there are some false positives in the case of Graphon 3.

4.2.2. Single change-point detection

We now assess the accuracy of our proposed TW_1 -type change-point estimators in different scenarios. The dynamic networks $\{A_t\}_{t=1}^m$ are designed as follows. For $t = 1, 2, \dots, m/2$, A_t is generated from link probability matrix P_1 by SBM 1 with $\theta_0 = 0$. For $t = m/2 + 1, \dots, m$, A_t is generated from P_2 by SBM 1 with $\theta_0 = -m^{-1/4}$.

We adopt Boysen distance suggested in Boysen et al. (2009) as a measurement in the change-point estimation. Specifically, calculate the distances between the estimated change-point set $\hat{\mathcal{J}}$ and the true change-point set \mathcal{J} as $\varepsilon(\hat{\mathcal{J}}|\mathcal{J}) = \max_{b \in \mathcal{J}} \min_{a \in \hat{\mathcal{J}}} |a - b|$ and $\varepsilon(\mathcal{J}|\hat{\mathcal{J}}) = \max_{b \in \hat{\mathcal{J}}} \min_{a \in \mathcal{J}} |a - b|$.

Utilizing CP-TWMNBS, CP-TWAVG, CP-TWSBM, CP-GRA, and CP-DMNBS detections, we estimate the efficient detect rate (the rate at least one change-point is detected over 100 simulations), the average change-point number over the efficient detections, and the average Boysen distances over the efficient detections. The corresponding results are listed in Tables 3–5.

Results provided in Tables 3–5 show that CP-TWSBM and CP-TWMNBS detections yield reliable estimates of the number of change-points and their locations. When $\rho = 1$, CP-TWAVG over-estimates the number of change-points, but it's interesting that it performs well for sparser case of $\rho = 0.25$. A possible explanation is that the sparser structure overcomes its inflated behavior to some extent. As for CP-GRA and CP-DMNBS detections, the performances of both methods are reasonable in dense scenarios, especially CP-DMNBS. However, they are unable to detect any change-point for the sparser setting $\rho = 0.25$ in this example.

4.2.3. Three change-points detection

To assess the robustness of our method for change-point detection, we further construct a model with three change-points in the networks. We first design three types of link probability matrix changes, which we use to build dynamic networks later. Given a link probability matrix P , define a changed link probability matrix initialized as $P' = P$. For two given sets $\mathcal{M}_1, \mathcal{M}_2 \subset \{1, 2, \dots, n\}$, for any $i \in \mathcal{M}_1$ and $j \in \mathcal{M}_2$, the different types of link probability matrix changes are defined as follows:

1. Community switching: $P'_{i,\cdot} = P_{j,\cdot}, P'_{\cdot,i} = P_{\cdot,j}, P'_{j,\cdot} = P_{i,\cdot}, P'_{\cdot,j} = P_{\cdot,i}$.
2. Community merging: $P'_{i,\cdot} = P_{j,\cdot}, P'_{\cdot,i} = P_{\cdot,j}$.
3. Community changing: Regenerate $P'_{i,j}$ from Graphon 4.

Then the dynamic networks $\{A_t\}_{t=1}^m$ for multiple change-points are designed as follows. \mathcal{M}_1 and \mathcal{M}_2 are two sets with $\lfloor n/3 \rfloor$ nodes randomly chosen from $\{1, 2, \dots, n\}$. For $t = 1, 2, \dots, m/4$, A_t is generated from P_1 by Graphon 2. For $t = m/4 + 1, \dots, m/2$, A_t is generated from P_2 changed from P_1 by community switching. For $t = m/2 + 1, \dots, 3m/4$, A_t is generated from P_3 changed from P_2 by community merging. For $t = 3m/4 + 1, \dots, m$, A_t is generated from P_4 changed from P_3 by community changing. The results are illustrated in Tables 6–8.

The reports suggest that CP-TWMNBS performs the best in terms of the number, efficiency and accuracy of change-point estimation. CP-TWSBM enjoys reasonably good behavior when $m = 100$ while encounters some false positives when m increases to 200. As for CP-TWAVG, although the estimated change-points number $\hat{\mathcal{J}}$ in Table 6 are not far away from real value 3 and the efficient detect rates in Table 7 are all equal to 1, the Boysen distances in Table 8 are sometimes too large to be accepted, i.e., the location error can not be controlled stably.

On the other hand, CP-GRA detection suffers greatly under-estimating the change-points, especially when $\rho = 0.25$, there is no change-point detected in all cases. It happens similarly to CP-DMNBS detection when $\rho = 0.25$, so CP-DMNBS is also not the ideal for this scenario even though it is powerful when the networks are dense.

Table 3. Average estimated change-points number \hat{J} under single change-point scenarios through SBM 1.

m	n	ρ	CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS
100	100	1	3.43	1.01	1.01	1.07	1.00
		0.25	1.02	0.95	0.98	0.00	0.00
100	200	1	3.50	1.01	1.01	1.09	1.00
		0.25	1.04	1.00	1.01	0.00	0.00
100	300	1	3.49	1.01	1.01	1.11	1.00
		0.25	1.04	1.00	1.01	0.00	0.00
200	100	1	5.09	1.00	1.00	1.06	1.00
		0.25	1.05	0.66	0.73	0.04	0.00
200	200	1	5.52	1.03	1.03	1.11	1.00
		0.25	1.51	1.00	1.01	0.00	0.00
200	300	1	5.34	1.00	1.01	1.06	1.00
		0.25	2.19	1.00	1.00	0.00	0.00

Table 4. Average efficient detect rate under single change-point scenarios through SBM 1.

m	n	ρ	CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS
100	100	1	1.00	1.00	1.00	1.00	1.00
		0.25	0.97	0.94	0.95	0.00	0.00
100	200	1	1.00	1.00	1.00	1.00	1.00
		0.25	1.00	1.00	1.00	0.00	0.00
100	300	1	1.00	1.00	1.00	1.00	1.00
		0.25	1.00	1.00	1.00	0.00	0.00
200	100	1	1.00	1.00	1.00	1.00	1.00
		0.25	0.88	0.65	0.70	0.03	0.00
200	200	1	1.00	1.00	1.00	1.00	1.00
		0.25	1.00	1.00	1.00	0.00	0.00
200	300	1	1.00	1.00	1.00	1.00	1.00
		0.25	1.00	1.00	1.00	0.00	0.00

Table 5. Average Boysen distances $\varepsilon_1, \varepsilon_2$ under single change-point scenarios through SBM 1.

m	n	ρ		CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS
100	100	1	ε_1	35.16	0.39	0.39	1.53	0.03
			ε_2	0.00	0.00	0.00	0.00	0.03
		0.25	ε_1	1.62	0.39	0.92	-	-
			ε_2	0.13	0.12	0.12	-	-
100	200	1	ε_1	36.09	0.39	0.39	1.80	0.00
			ε_2	0.00	0.00	0.00	0.00	0.00
		0.25	ε_1	0.91	0.00	0.19	-	-
			ε_2	0.00	0.00	0.00	-	-
100	300	1	ε_1	35.83	0.31	0.31	2.18	0.00
			ε_2	0.00	0.00	0.00	0.00	0.00
		0.25	ε_1	0.93	0.00	0.36	-	-
			ε_2	0.00	0.00	0.00	-	-
200	100	1	ε_1	78.46	0.00	0.00	3.22	0.08
			ε_2	0.00	0.00	0.00	0.06	0.08
		0.25	ε_1	11.51	1.35	3.60	38.00	-
			ε_2	1.34	0.34	1.31	27.33	-
200	200	1	ε_1	80.86	1.60	1.60	3.88	0.00
			ε_2	0.00	0.00	0.00	0.00	0.00
		0.25	ε_1	23.31	0.01	0.41	-	-
			ε_2	0.01	0.01	0.01	-	-
200	300	1	ε_1	78.86	0.00	0.45	2.78	0.00
			ε_2	0.00	0.00	0.00	0.00	0.00
		0.25	ε_1	48.20	0.00	0.00	-	-
			ε_2	0.00	0.00	0.00	-	-

Note: the dash “-” means there is no change-points detected.

Table 6. Average estimated change-points number \hat{J} under three change-points scenarios.

m	n	ρ	CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS
100	100	1	3.00	3.00	3.00	0.31	3.00
		0.25	1.92	3.40	2.99	0.00	0.02
100	200	1	3.00	3.00	3.00	2.10	3.00
		0.25	3.00	3.03	3.00	0.00	0.15
100	300	1	3.00	3.00	3.00	0.00	3.00
		0.25	3.00	3.00	3.00	0.00	1.52
200	100	1	3.16	3.00	3.00	2.29	3.02
		0.25	2.20	5.35	2.96	0.00	0.07
200	200	1	3.37	3.00	3.00	1.06	3.01
		0.25	3.00	4.57	3.01	0.00	1.62
200	300	1	3.57	3.01	3.00	0.11	3.00
		0.25	3.00	4.55	3.00	0.00	1.95

Table 7. Average efficient detect rate under three change-points scenarios.

m	n	ρ	CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS
100	100	1	1.00	1.00	1.00	0.13	1.00
		0.25	1.00	1.00	1.00	0.00	0.02
100	200	1	1.00	1.00	1.00	1.00	1.00
		0.25	1.00	1.00	1.00	0.00	0.15
100	300	1	1.00	1.00	1.00	0.00	1.00
		0.25	1.00	1.00	1.00	0.00	0.96
200	100	1	1.00	1.00	1.00	0.81	1.00
		0.25	1.00	1.00	1.00	0.00	0.07
200	200	1	1.00	1.00	1.00	0.39	1.00
		0.25	1.00	1.00	1.00	0.00	0.98
200	300	1	1.00	1.00	1.00	0.06	1.00
		0.25	1.00	1.00	1.00	0.00	1.00

Table 8. Average Boysen distances $\varepsilon_1, \varepsilon_2$ under three change-points scenarios.

m	n	ρ		CP-TWAVG	CP-TWSBM	CP-TWMNBS	CP-GRA	CP-DMNBS		
100	100	1	ε_1	0.00	0.01	0.00	8.69	0.02		
			ε_2	0.00	0.01	0.00	34.31	0.02		
		0.25	ε_1	0.06	5.50	0.15	–	0.00		
			ε_2	26.99	0.39	0.40	–	50.00		
		100	200	1	ε_1	0.00	0.00	0.00	1.17	0.00
					ε_2	0.00	0.00	0.00	25.10	0.00
0.25	ε_1			0.00	0.45	0.00	–	0.07		
	ε_2			0.00	0.00	0.00	–	50.07		
100	300			1	ε_1	0.00	0.00	0.00	–	0.00
					ε_2	0.00	0.00	0.00	–	0.00
		0.25	ε_1	0.00	0.00	0.00	–	0.03		
			ε_2	0.00	0.00	0.00	–	34.90		
		200	100	1	ε_1	4.70	0.00	0.00	14.72	0.69
					ε_2	0.00	0.00	0.00	53.96	0.16
0.25	ε_1			0.08	29.51	0.67	–	0.43		
	ε_2			40.01	0.51	3.30	–	79.00		
200	200			1	ε_1	11.27	0.00	0.00	15.72	0.35
					ε_2	0.00	0.00	0.00	61.03	0.04
		0.25	ε_1	0.00	27.64	0.30	–	0.04		
			ε_2	0.00	0.03	0.00	–	65.83		
		200	300	1	ε_1	17.05	0.33	0.00	11.17	0.00
					ε_2	0.00	0.00	0.00	89.33	0.00
0.25	ε_1			0.00	27.85	0.00	–	0.07		
	ε_2			0.00	0.02	0.00	–	52.47		

Note: the dash “–” means there is no change-points detected.

Overall, the numerical experiments clearly demonstrate the superior performance of CP-TWMNBS detection over other detect methods for all simulation scenarios with CP-TWSBM method coming in second. CP-TWMNBS detection provides robust and stable performance across all experiments with more accurate $\hat{\mathcal{J}}$, higher efficient detection and smaller Boysen distances.

5. Data analysis

In this section, we analyze the performance of the proposed TW_1 -type method for two-sample test and TW_1 -type change-point detection using two real datasets. The first dataset used for the two-sample test comes from the Centers of Biomedical Research Excellence (COBRE) and the second dataset used for change-point detection is from MIT Reality Mining (RM) (Eagle, Pentland, and Lazer 2009).

5.1. Two-sample test with real data example

Raw anatomical and functional scans from 146 subjects of 72 patients with schizophrenia (SCZ) and 74 healthy controls (HCs) can be downloaded from a public database (http://fcon_1000.projects.nitrc.org/indi/retro/cobre.html). In this paper, we use the processed connectomics dataset in Reli3n et al. (2019). After a series of pre-processing steps, Reli3n et al. (2019) keeps 54 SCZ and 70 HC subjects for analysis and chooses 264 brain regions of interest as the nodes. For each of the 263 nodes with every other node, they applies Fisher's R-to-Z transformation to the cross-correlation matrix of Pearson r -values.

In our study, we perform the Z-to-R inverse transformation to their dataset to get the original cross-correlation matrix of Pearson r -values, which is denoted as R . To analyze graphical properties of these brain functional networks, we need to create an adjacency matrix A from R . We set A_{ij} to be 1 if R_{ij} exceeds a threshold T and A_{ij} to be 0 otherwise. There is no generally accepted way to identify an optimal threshold for this graph construction procedure, we decide to set T varied between 0.3 and 0.7 with step of 0.05.

For each threshold T , two situations are considered for the two-sample test. In the first situation, we randomly divide HC into 2 groups with sample sizes $m_1 = m_2 = 35$ and calculate the average null hypothesis reject rates of TW_1 -MNBS test, TW_1 -AVG test, TW_1 -SBM test, χ^2 -type test, and N -type test through 100 repeated simulations. In the second situation, we apply the same test methods above to two groups of SCZ and HC directly and compare their average null hypothesis reject rates. In both cases, the significance level is set to be 0.05. The results are shown in Tables 9 and 10 respectively.

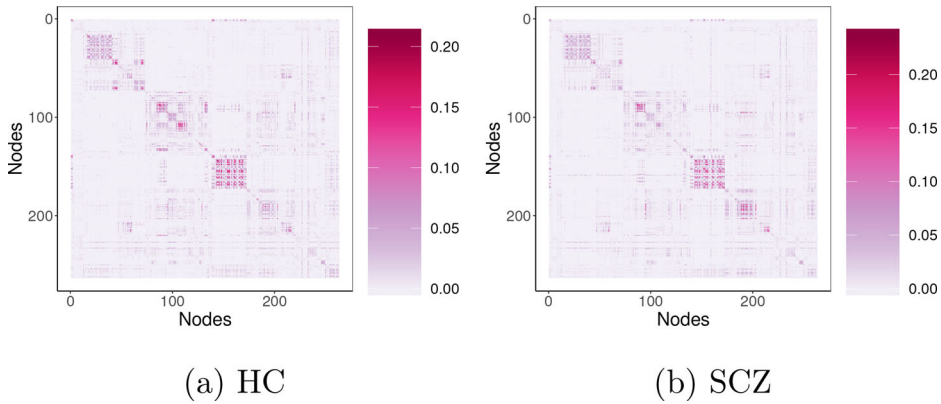
To investigate the performance of the tests, we need to compare the type I error in Table 9 and the power result in Table 10 together. Table 9 shows that TW_1 -type tests based on SBM and AVG have poor performance for the test over HC group because the reject rates all exceed 0.05 and even equal to 1. From Table 10, it is found that χ^2 -type test loses power for the test over SCZ and HC groups, where the reject rates are all 0. Only TW_1 -type test based on MNBS when $T = 0.55, 0.60$ and N -type test when

Table 9. Average H_0 reject rate of test over HC group over 100 simulations.

T	0.30	0.35	0.40	0.45	0.50	0.55	0.60	0.65	0.70
TW_{γ} -AVG	1	1	1	1	0.80	0.67	0.57	0.50	0.44
TW_{γ} -SBM	1	1	1	1	1	1	1	1	1
TW_{γ} -MNBS	1	1	1	1	1	0	0	1	1
χ^2 -type	1	1	0	0	0	0	0	0	0
N -type	1	1	1	0	0	0	0	0	0

Table 10. Average H_0 reject rate of test over SCZ and HC groups.

T	0.30	0.35	0.40	0.45	0.50	0.55	0.60	0.65	0.70
TW_{γ} -AVG	1	1	1	1	1	0	0	0	0
TW_{γ} -SBM	1	1	1	1	1	1	1	1	1
TW_{γ} -MNBS	1	1	1	1	1	1	1	1	1
χ^2 -type	0	0	0	0	0	0	0	0	0
N -type	1	1	1	1	1	1	1	1	1

**Figure 3.** Adjacency matrices estimated by MNBS for HC and SCZ groups.

$T \geq 0.45$ can perform well in both situations. In addition, applying MNBS, we illustrate the adjacency matrices of subject-specific networks of HC and SCZ groups when $T=0.60$ in Figure 3. One can find that the two groups do have differences in the network structure.

5.2. Change-point detection in dynamic networks

In this section, we apply CP-TWMNBS, CP-TWAVG, CP-TWSBM, CP-GRA, and CP-DMNBS detections to perform change-point detection for a phone-call network data extracted from RM dataset. The data is collected through an experiment conducted by the MIT Media Laboratory following 106 MIT students and staff using mobile phones with preinstalled software that can record and send call logs from 2004 to 2005 academic year. Note that this is different from the MIT proximity network data considered in Zhao, Chen, and Lin (2019) which is based on the bluetooth scans instead of phone calls. In this analysis, we are interested in whether phone call patterns changed during this time, which may reflect a change in relationship among these subjects. 94 of the 106 RM subjects completed the survey, we remain records only within these participants and filter records before 07/20/2004 due to the extreme scarcity of sample before that

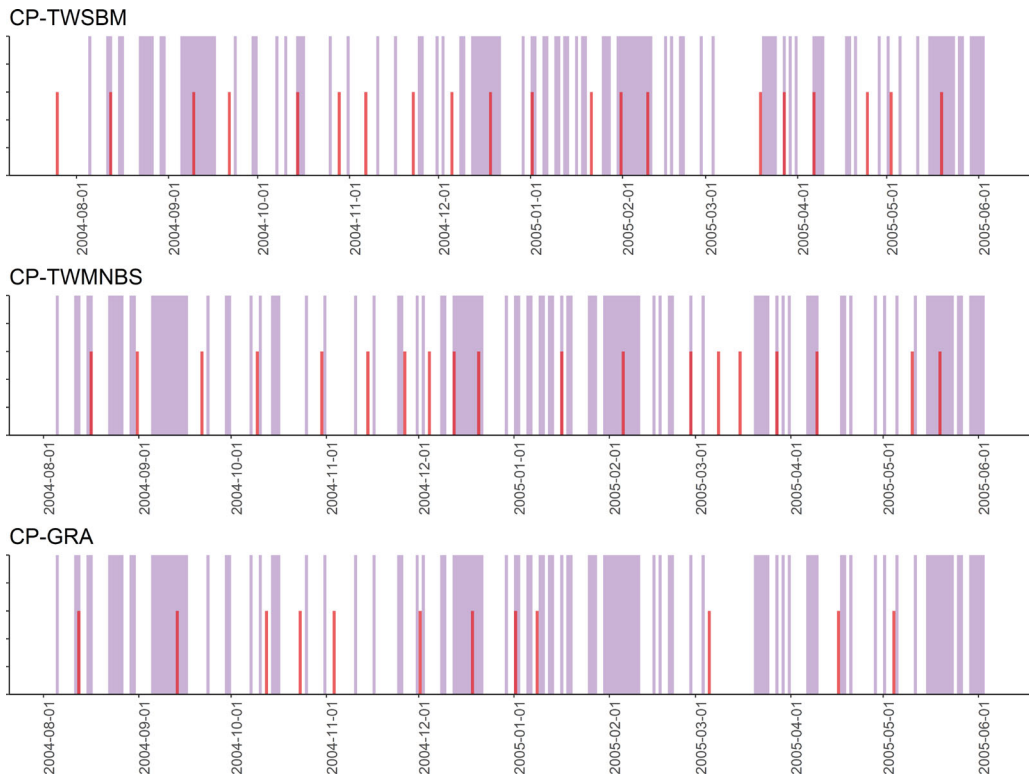


Figure 4. Calendar time intervals of events and estimated change-points.

time. Then there remains 81 subjects left and we construct dynamic networks among these subjects by day. For each day, construct a network with the subjects as nodes and a link between two subjects if they had at least one call on that day. We encode the network of each day by an adjacency matrix, with 1 for element (i, j) if there is an edge between subject i and subject j , and 0 otherwise. Thus, there are in total 310 days from 07/20/2004 to 06/14/2005. The calendar of events is included in the [supplementary material](#). We claim that an estimated change-point is reasonable if it is at most three days away from the real dates the event lasts.

We first choose $h=7$ and [Figure 4](#) plots the results of different methods on the dynamic networks. The purple shadow areas mark time intervals from the beginning to the end of events continue on MIT academic calendar 2004–2005, which can be used as references for the estimated change-points’ occurrences. The red lines in [Figure 4](#) are the estimated change-points applying different detect methods.

It turns out that CP-TWAVG and CP-DMNBS detections either do not work well or detect no change-point. CP-TWSBM method detects 20 change-points, CP-TWMNBS method detects 19 change-points, while CP-GRA detection detects 12 change-points. When comparing the estimated change-points to intervals of calendar events, we see that they align each other the best by using CP-TWMNBS detection and then CP-TWSBM detection, whereas there are more estimated change-points by CP-GRA detection that can not be explained.

Table 11. Estimated change-points by different methods for MIT phone data.

CP-TWSBM	02/08/2004 23/03/2005	08/09/2004 03/05/2005	12/10/2004	15/11/2004	27/12/2004	03/02/2005	19/02/2005
CP-TWMNBS	10/08/2004 10/04/2005	27/09/2004 04/05/2005	17/10/2004	20/11/2004	05/12/2004	24/12/2004	13/02/2005
CP-GRA	13/08/2004 02/12/2004	01/09/2004 19/12/2004	14/09/2004 09/01/2005	28/09/2004 06/03/2005	13/10/2004 17/04/2005	04/11/2004 05/05/2005	18/11/2004

However, it's observed that some of the change-points detected by CP-TWSBM and CP-TWMNBS methods can be a little trivial. For example, CP-TWMNBS detected a change-point occurred at around 01/09/2004, which is near event “English Evaluate Test for International Students” in the calendar. To ignore the less significant events, we only consider the seemingly major events displayed in bold in the calendar as possible reasons for estimated change-points and set $h = 14$, which corresponds to 2 weeks. The details are reported in Table 11. The CP-TWMNBS and CP-TWSBM methods detect 9 change-points, CP-GRA method detects 13 change-points. Notably CP-GRA method still labels more trivial change-points away from the important events. Based on the results, it is most likely valid in saying that CP-TWSBM and CP-TWMNBS detections are more reliable.

6. Conclusion

We consider the problem of hypothesis testing on whether two populations of networks defined on a common vertex set are from the same distribution. Two-sample testing on populations of networks is a challenging task especially when the the number of nodes is large. We propose a general TW_1 -type test (which is later adapted to a change-point detection procedure in dynamic networks), derive its asymptotic distribution and asymptotic power. The test statistics utilizes some plugin estimates for the link probability matrices and properties of the resulting tests with various estimates are discussed by evaluating and comparing TW_1 -type tests based on MNBS, AVG, SBM theoretically, and numerically with both simulated and real data. From the simulation study, we see that the proposed TW_1 -type test based on MNBS performs the best and yields robust results even when the structure is sparse. In addition, we provide a significant modification of the two-sample network test for change-point detection in dynamic networks. Simulation and real data analyses show that the procedure is consistent, principled and practically viable.

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