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The Binary Expansion Randomized Ensemble Test

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Abstract: The binary expansion testing framework was recently introduced to test the independence of two continuous random variables by using symmetry statistics that are complete sufficient statistics for dependence. We develop a new test based on an ensemble approach that uses the sum of squared symmetry statistics and the distance correlation. Simulation studies suggest that this method has improved power, while preserving the clear interpretation of the binary expansion testing. We extend this method to tests of independence of random vectors in an arbitrary dimension. Using random projections, the proposed binary expansion randomized ensemble test transforms the multivariate independence testing problem into a univariate problem. Simulation studies and data examples show that the proposed method provides relatively robust performance compared with that of existing methods.

Key words and phrases: Nonparametric inference, Nonparametric test of independence, Binary Expansion, Multiple testing, Multivariate analysis.

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1. Introduction

Nonparametric tests of independence are a fundamental problem in statistics and have been studied by, among others, Hoeffding (1948). This problem is garnering increased interest, owing to its important role in machine learning and big data analysis.

Numerous testing methods have been proposed, including those of Székely et al. (2007), Wang et al. (2017), and Han et al. (2017), who generalize the idea of correlation and R -squared, Shapiro and Hubert (1979), Friedman and Rafsky (1983), Azadkia and Chatterjee (2019), Deb and Sen (2019), and Deb et al. (2021), who relate dependence to graphs, Heller et al. (2012), Heller et al. (2016), and Heller and Heller (2016), who study the distance matrix of ranks, Berrett and Samworth (2019), Kim et al. (2020), and Berrett et al. (2020), who consider classical permutation-based statistics, and Gretton et al. (2008), Chwialkowski and Gretton (2014), Jitkrittum et al. (2017), Pfister et al. (2018), Zhang et al. (2018), and Chakraborty and Zhang (2019), who take advantage of the reproducing kernel Hilbert space to develop Hilbert–Schmidt independence criterion-based statistics. Other recent works include those of Weihs et al. (2018), Ke and Yin (2019), Bodnar et al. (2019), Shi et al. (2020), and Drton et al. (2018). Zhu et al. (2017) proposed a projection method related to the distance correlation

when testing independence. Excellent reviews can be found in Jaworski et al. (2010) and Josse and Holmes (2016).

An important problem in nonparametric dependence detection is that of nonuniform consistency, which means that no test can uniformly detect all forms of dependency, as described by Zhang (2019). This problem is particularly severe for nonlinear relationships, which are common in many areas of science. To avoid the power loss due to nonuniform consistency, Zhang (2019) considers the binary expansion statistics (BESat) framework, which examines dependence using a filtration approach induced by a binary expansion of the uniformly distributed variables. Zhang (2019) also proposed testing the independence of two continuous variables using the framework of maximum binary expansion testing (BET). Rather than one test of independence, this approach uses a carefully designed sequence of tests based on a filtration to achieve universality. BET also achieves uniform consistency and is minimax optimal in terms of power (see section 4.2 in Zhang (2019)). In addition, it provides clear interpretability, and can be implemented efficiently using bitwise operations.

Although BET works well for testing the independence between two variables, two crucial improvements are needed to make it more practical. The first requirement is to improve the power of BET under certain cases,

such as linear dependency. The second requirement is an extension to test the independence of random vectors. We describe a new approach that solves both problems. The first problem is addressed using a novel ensemble approach, and the second is solved by using a one-dimensional random projection. We call the new method the binary expansion randomized ensemble test (BERET). We use simulation studies to show that the proposed method has good power properties.

We use example data sets to illustrate how the proposed method provides clear interpretability, while maintaining good power properties across various dependence structures, including both linear and nonlinear relationships. In a life expectancy example, our method detects three meaningful and interpretable relationships and provides similar p-values to those of competing methods. In a mortality rate example, we show that the canonical correlation test can be interpretable, but fails to detect a nonlinear dependence structure. This is unfortunate, because the canonical correlation test is the only other method that has inherent interpretability. In contrast, our method is able to identify meaningful relationships, even when there is a nonlinear relationship. In a house price example, the mutual information test fails to reject independence because the linear relationship is not sufficiently strong. However, our method rejects independence be-

cause of its stronger sensitivity to linear relationships, and is able to detect interpretable dependence structures, including linear relationships. The canonical correlation test also works here and provides good interpretability. However, our method is the only method that can detect both linear and nonlinear relationships, as well as providing interpretable dependency structures.

The remainder of this paper is organized as follows. Section 2 describes the ensemble method and the BERET procedure. In Section 3, we present simulation studies that demonstrate the performance of the proposed method, and in Section 4, we provide three data examples. Concluding remarks are presented in Section 5. All proofs are given in the Supplementary Material.

2. Proposed Method

2.1 The BET Framework

We briefly introduce the BET and useful notation from Zhang (2019). Let $(X_1, Y_1), \dots, (X_n, Y_n)$ be a random sample from distributions of X and Y . If the marginal distributions of X and Y are known, we can use the CDF transformation so that $U = F_X(X)$ and $V = F_Y(Y)$ are each uniformly distributed over $[0, 1]$. The binary expansions of the two random variables

2.1 The BET Framework

U and V can be expressed as $U = \sum_{k=1}^{\infty} A_k/2^k$ and $V = \sum_{k=1}^{\infty} B_k/2^k$, where $A_k \stackrel{i.i.d.}{\sim} \text{Bernoulli}(1/2)$ and $B_k \stackrel{i.i.d.}{\sim} \text{Bernoulli}(1/2)$. The value of each Bernoulli distributed variable can be found using $A_{k'} = I\{U - \sum_{k=1}^{k'-1} A_k/2^k \geq 1/2^{k'}\}$ or $B_{k'} = I\{V - \sum_{k=1}^{k'-1} B_k/2^k \geq 1/2^{k'}\}$. If we truncate the expansions at depth d , then $U_d = \sum_{k=1}^d A_k/2^k$ and $V_d = \sum_{k=1}^d B_k/2^k$ are two discrete variables that can take 2^d possible values. We define the binary variables $\dot{A}_k = 2A_k - 1$ and $\dot{B}_k = 2B_k - 1$ to express the interaction between them as their products. We call any products of A_k and B_k with at least one A_k and one B_k cross-interactions. In other words, cross-interactions are defined as variables of the form $\dot{A}_{k_1} \dots \dot{A}_{k_r} \dot{B}_{k'_1} \dots \dot{B}_{k'_t}$, for some $r, t > 0$. We use the following binary integer indexing. Let $\mathbf{a}$ be a d -dimensional binary vector with ones at $k_1, \dots, k_r$ and zeros otherwise, and let $\mathbf{b}$ be a d -dimensional binary vector with ones at $k'_1, \dots, k'_t$ and zeros otherwise. Using this notation, the cross-interaction $\dot{A}_{k_1, \dots, k_r} \dot{B}_{k'_1, \dots, k'_t}$ can be written as $\dot{A}_{\mathbf{a}} \dot{B}_{\mathbf{b}}$. For example, $\dot{A}_1 \dot{A}_3 \dot{B}_2 \dot{B}_4 = \dot{A}_{\mathbf{a}} \dot{B}_{\mathbf{b}}$, where $\mathbf{a} = 1010$ and $\mathbf{b} = 0101$ when $d = 4$.

Let $\dot{A}_{\mathbf{a},i}$ and $\dot{B}_{\mathbf{b},i}$ be the values of $\dot{A}_{\mathbf{a}}$ and $\dot{B}_{\mathbf{b}}$ for the i th observation. We denote the sum of the observed binary interaction variables by $S_{(\mathbf{ab})} = \sum_{i=1}^n \dot{A}_{\mathbf{a},i} \dot{B}_{\mathbf{b},i}$, with $S_{(\mathbf{00})} = n$. These are referred to as the symmetry statistics. If U_d and V_d are independent, $(S_{(\mathbf{ab})} + n)/2 \sim \text{Binomial}(n, 1/2)$, for

2.2 Univariate Independence Testing Procedure

$\mathbf{a} \neq \mathbf{0}$ and $\mathbf{b} \neq \mathbf{0}$. If the marginal distributions are unknown, we use the empirical CDF transformation, and then $(\hat{S}_{(\mathbf{ab})} + n)/4 \sim \text{Hypergeometric}(n, n/2, n/2)$, where $\hat{S}_{(\mathbf{ab})}$ is a symmetry statistic with an empirical CDF transformation.

If we truncate the expansions at depth $d = d_{\max}$, the BET procedure at depth $d_{\max}$ can be defined as follows. First, we compute all symmetry statistics with $\mathbf{a} \neq \mathbf{0}$ and $\mathbf{b} \neq \mathbf{0}$, for $d = d_{\max}$. For each depth $d = 1, \dots, d_{\max}$, we identify the symmetry statistic with the strongest asymmetry and find its p -value. Finally, we use the Bonferroni adjustment to obtain a p -value that considers the family-wise error rate.

BET has several advantages. The test is minimax optimal under certain regulatory conditions. Moreover, it provides both inferences and clear interpretations. For BET, rejecting independence implies that there is at least one significant cross-interaction. Thus, we can find a potential dependence structure in the sample by investigating the detected cross-interaction.

2.2 Univariate Independence Testing Procedure

Although BET shows good performance in many interesting dependency structures, there is room for improvement. In particular, using the maximum statistic in the BET testing procedure may introduce a loss of power when the sparsity assumption in Zhang (2019) is violated. We consider a

2.2 Univariate Independence Testing Procedure

test based on the sum of the squared symmetry statistics.

Consider a binary expansion test with specified d_{max} . For each depth $d = 1, \dots, d_{max}$, we can find a set of symmetry statistics $S_{(\mathbf{ab})}$. Let C_d be a set of corresponding $\mathbf{ab}$ indices of depth d . The sets C_d have a nested structure. Because an interaction has different $\mathbf{ab}$ indices for two different d , to avoid confusion, we use $\mathbf{ab}$ of depth d_{max} , for example, when $d_{max} = 2$, $C_1 = \{1010\}$, and $C_2 = \{0101, 0110, 0111, 1001, 1010, 1011, 1101, 1110, 1111\}$. Now, for each depth d , we introduce two measures of dependence. Suppose $X \in \mathbb{R}$ and $Y \in \mathbb{R}$ are two continuous random variables. The population measure of dependence is defined as

$$\mathcal{B}_d(X, Y) = \frac{1}{(2^d - 1)^2} \sum_{\mathbf{ab} \in C_d} E(\dot{A}_{\mathbf{a}} \dot{B}_{\mathbf{b}})^2, \quad (2.1)$$

for each depth $d = 1, \dots, d_{max}$. The joint distribution of (U_d, V_d) with a finite d is not an exact model for the joint distribution of (U, V) . Therefore, $\mathcal{B}_d(X, Y) = 0$ does not necessarily indicate independence between (U, V) . When d is large, however, we expect that the dependence in (U_d, V_d) precisely approximates that in (U, V) .

Let $\{(X_i, Y_i)\}_{i=1}^n$ be a random sample from the joint distribution of (X, Y) . The empirical measure of dependence is defined as

$$\mathcal{B}_{n,d}[\{(X_i, Y_i)\}_{i=1}^n] = \frac{1}{(2^d - 1)^2} \sum_{\mathbf{ab} \in C_d} \left(\frac{S_{(\mathbf{ab})}}{n} \right)^2, \quad (2.2)$$

2.2 Univariate Independence Testing Procedure

for each depth $d = 1, \dots, d_{max}$. The following theorem lists some properties of $\mathcal{B}_d(X, Y)$ and $\mathcal{B}_{n,d}[\{(X_i, Y_i)\}_{i=1}^n]$.

Theorem 1. *Suppose X and Y are continuous random variables. The following properties hold:*

- (i) $\mathcal{B}_d(X, Y) = 0$ if and only if U_d and V_d are independent.
- (ii) $0 \leq \mathcal{B}_d(X, Y) \leq 1$.
- (iii) $\mathcal{B}_{n,d}[\{(X_i, Y_i)\}_{i=1}^n] \xrightarrow{a.s.} \mathcal{B}_d(X, Y)$ as $n \rightarrow \infty$.
- (iv) If X and Y are independent, then $(2^d - 1)^2 n \mathcal{B}_{n,d}[\{(X_i, Y_i)\}_{i=1}^n] \xrightarrow{d} \chi_{(2^d-1)^2}^2$ as $n \rightarrow \infty$.

We define the scaled sum of the squared symmetry statistics for each depth $d = 1, \dots, d_{max}$ as

$$\xi_{n,d} = \sum_{\mathbf{ab} \in C_d} \frac{S_{(\mathbf{ab})}^2}{n}. \quad (2.3)$$

By this definition, each $\xi_{n,d}$ can be used to detect dependencies up to depth d . Consider a test that rejects H_0 : “ X and Y are independent” if at least one $\xi_{n,d}$ is greater than $\xi_{n,d,1-\alpha_d}$, the $1-\alpha_d$ quantile of $\xi_{n,d}$. Then, by Boole’s inequality, the upper bound of the type-I error is

$$Pr(\text{reject } H_0 \mid H_0 \text{ is true}) \leq \sum_{d=1}^{d_{max}} \alpha_d. \quad (2.4)$$

2.2 Univariate Independence Testing Procedure

There are many possible versions of the test based on different choices of α_d . Alternatives in C_d for smaller d reflect more global dependencies with lower resolutions. From this point of view, we propose an exponentially decaying approach for the choice of α_d . If we choose $\alpha_d = \alpha \gamma^d / \sum_{d=1}^{d_{max}} \gamma^d$, where $0 < \gamma \leq 1$, then the upper bound of the significance level is

$$Pr(reject H_0 \mid H_0 \text{ is true}) \leq \sum_{d=1}^{d_{max}} \frac{\alpha \gamma^d}{\sum_{d=1}^{d_{max}} \gamma^d} = \alpha, \quad (2.5)$$

guaranteeing a level- α test. A natural choice of γ is one:

$$Pr(reject H_0 \mid H_0 \text{ is true}) \leq \sum_{d=1}^{d_{max}} \frac{\alpha}{d_{max}} = \alpha. \quad (2.6)$$

The correct depth where the dependency may present is not known a priori. An appropriate d_{max} should reflect the desired accuracy in the approximation. However, considering $\|(U_d, V_d) - (U, V)\| = O_p(2^{-d})$, we believe that $d_{max} = 4$ provides a good approximation in practice.

The power of the proposed test can be improved by compromising between a distance correlation test and multiple testing over interactions. The BET framework loses power from the adverse effect of multiplicity control over depth. This loss of power is particularly severe for linear dependency. See Section 1.2 in the supplementary material of Zhang (2019) for a detailed discussion. By considering distance correlation combined with the proposed test, we can mitigate this power loss. The above test is composed of multi-

2.2 Univariate Independence Testing Procedure

ple hypothesis tests, and each test has its own set of dependence structures as its alternative hypothesis. Suppose $d_{max} = 4$. Then there is only one interaction $\dot{A}_{1000}\dot{B}_{1000}$ in $\xi_{n,1}$. The cross-interaction $\dot{A}_{1000}\dot{B}_{1000}$ falls in the first or the third quadrant of the unit square $[0, 1]^2$ when $\dot{A}_{1000}\dot{B}_{1000} = 1$, and in the second or the fourth quadrant when $\dot{A}_{1000}\dot{B}_{1000} = -1$. Therefore, $\xi_{n,1} = S_{10001000}^2/n$ represents the strength of the linear dependency. If another independence test performs better than $\xi_{n,1}$ under linear dependency, we can replace the test based on $\xi_{n,1}$ with it, while maintaining the performance of the test in other dependence structures. Because we are using a Bonferroni correction for the critical values, this replacement still maintains the targeted level of the test. We call this approach an ensemble method because it combines two testing methods. The independence test with Pearson's correlation can also be combined with the proposed test. However, we choose the distance correlation test, because it improves the power in a wider range of cases and is equivalent to Pearson's correlation under normality. The proposed procedure consists of the following steps:

Step 1 : Fix $\alpha_1, \dots, \alpha_{d_{max}}$ with $\sum_{d=1}^{d_{max}} \alpha_d = \alpha$.

Step 2 : Find the p -value for the distance correlation test.

Step 3 : For each $d = 2, \dots, d_{max}$, compute $\xi_{n,d}$ and its p -value.

2.3 Multivariate Independence Testing Procedure

Step 4 : Reject H_0 if at least one of the p -values is less than the respective α_d .

To find the p -value for each depth $d \geq 2$, we can use either a permutation approach or the asymptotic distribution given in Theorem 1, part (iv). Now, we investigate the behavior of our test in large samples.

Theorem 2. Denote the joint distribution of (U_d, V_d) by $\mathbf{P}_{(U_d, V_d)}$ and the bivariate uniform distribution over $\{\frac{0}{2^d}, \dots, \frac{2^d-1}{2^d}\}^2$ by $\mathbf{P}_{0,d}$. For any fixed $0 < \delta \leq 1/2$, denote by $\mathcal{H}_{1,d}$ the collection of distributions $\mathbf{P}_{(U_d, V_d)}$ such that $TV(\mathbf{P}_{(U_d, V_d)}, \mathbf{P}_{0,d}) \geq \delta$. Consider the testing problem,

$$H_0 : \mathbf{P}_{(U_d, V_d)} = \mathbf{P}_{0,d} \text{ v.s. } H_1 : \mathbf{P}_{(U_d, V_d)} \in \mathcal{H}_{1,d}.$$

Under H_1 , each $\xi_{n,d} \rightarrow \infty$ as $n \rightarrow \infty$.

Theorem 2 shows that our test statistics, $\xi_{n,d}$, go to infinity as the sample size increases. Moreover, the distance correlation test is known to be consistent. Therefore, the ensemble method is also statistically consistent against the collection of alternatives described in Theorem 2.

2.3 Multivariate Independence Testing Procedure

In this section, we develop a generalized independence test for random vectors. To do so, we convert the independence of the random vectors into

2.3 Multivariate Independence Testing Procedure

the independence of univariate random variables, which yields the following lemma.

Lemma 1. *Let $\mathbf{X} \in \mathbb{R}^p$ and $\mathbf{Y} \in \mathbb{R}^q$ be two random vectors. Then, $\mathbf{X}$ and $\mathbf{Y}$ are independent if and only if $\mathbf{s}^T \mathbf{X}$ and $\mathbf{t}^T \mathbf{Y}$ are independent for all $\mathbf{s} \in \mathbb{R}^p$ and $\mathbf{t} \in \mathbb{R}^q$, with $\|\mathbf{s}\| = 1$ and $\|\mathbf{t}\| = 1$.*

This result shows that to prove the independence of random vectors, it is sufficient to consider the independence of arbitrary linear combinations of the components. Therefore, the multivariate independence can be tested by checking all possible combinations of $\mathbf{s}$ and $\mathbf{t}$. However, because this cannot be implemented, we consider an approximation of the test by including a finite, but reasonably broad number of combinations. Denote the hyper unit spheres in $\mathbb{R}^p$ and $\mathbb{R}^q$ by S_p and S_q , respectively. Now, for each depth d , we propose two measures of dependence.

Suppose $\mathbf{X} \in \mathbb{R}^p$ and $\mathbf{Y} \in \mathbb{R}^q$ are two random vectors. For $\mathbf{s} \in S_p$ and $\mathbf{t} \in S_q$, we define a measure of dependence for the multivariate setting by

$$\mathcal{B}_d(\mathbf{X}, \mathbf{Y}) = \frac{1}{c_p c_q} \int_{S_q} \int_{S_p} \mathcal{B}_d(\mathbf{s}^T \mathbf{X}, \mathbf{t}^T \mathbf{Y}) d\mathbf{s} d\mathbf{t}, \quad (2.7)$$

where $c_p = \frac{2\pi^{p/2}}{\Gamma(p/2)}$ and $c_q = \frac{2\pi^{q/2}}{\Gamma(q/2)}$.

Let $\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n$ be a random sample from the joint distribution of

2.3 Multivariate Independence Testing Procedure

$(\mathbf{X}, \mathbf{Y})$. The empirical measure of dependence is defined as

$$\mathcal{B}_{n,d}[\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n] = \frac{1}{c_p c_q} \int_{S_q} \int_{S_p} \mathcal{B}_{n,d}[\{(\mathbf{s}^T \mathbf{X}_i, \mathbf{t}^T \mathbf{Y}_i)\}_{i=1}^n] d\mathbf{s} d\mathbf{t}. \quad (2.8)$$

The following theorem lists several properties of $\mathcal{B}_d(\mathbf{X}, \mathbf{Y})$ and $\mathcal{B}_{n,d}[\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n]$.

Theorem 3. *Suppose the distributions of $\mathbf{X}$ and $\mathbf{Y}$ are continuous. Let $U_d^{\mathbf{s}}$ and $V_d^{\mathbf{t}}$ be truncated binary expansions at depth d of $U^{\mathbf{s}}$ and $V^{\mathbf{t}}$, respectively, where $U^{\mathbf{s}} = F_{\mathbf{s}^T \mathbf{X}}(\mathbf{s}^T \mathbf{X})$ and $V^{\mathbf{t}} = F_{\mathbf{t}^T \mathbf{Y}}(\mathbf{t}^T \mathbf{Y})$, for $\mathbf{s} \in S_p$ and $\mathbf{t} \in S_q$. Similarity transformations consist of all Euclidean transformations and all (nonzero) scaling (Móri and Székely (2019)). The following properties hold:*

- (i) $\mathcal{B}_d(\mathbf{X}, \mathbf{Y}) = 0$ if and only if $U_d^{\mathbf{s}}$ and $V_d^{\mathbf{t}}$ are independent, for all $\mathbf{s} \in S_p$ and $\mathbf{t} \in S_q$.
- (ii) $0 \leq \mathcal{B}_d(\mathbf{X}, \mathbf{Y}) \leq 1$.
- (iii) $\mathcal{B}_d(\mathbf{X}, \mathbf{Y})$ is invariant with respect to all similarity transformations.
- (iv) $\mathcal{B}_{n,d}[\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n] \xrightarrow{a.s.} \mathcal{B}_d(\mathbf{X}, \mathbf{Y})$ as $n \rightarrow \infty$.

Note that $\mathcal{B}_{n,d}[\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n] = E_{\mathbf{S}, \mathbf{T}}(\mathcal{B}_{n,d}[\{(\mathbf{S}^T \mathbf{X}_i, \mathbf{T}^T \mathbf{Y}_i)\}_{i=1}^n] \mid \{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n)$, where $\mathbf{S}$ and $\mathbf{T}$ follow uniform distributions on S_p and S_q , respectively. This expectation can be estimated by

$$\widehat{\mathcal{B}}_{n,d}^m[\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n] = \frac{1}{m} \sum_{j=1}^m \mathcal{B}_{n,d}[\{(\mathbf{S}_j^T \mathbf{X}_i, \mathbf{T}_j^T \mathbf{Y}_i)\}_{i=1}^n], \quad (2.9)$$

2.3 Multivariate Independence Testing Procedure

where $\{(\mathbf{S}_j, \mathbf{T}_j)\}_{j=1}^m$ is a random sample generated from uniform distributions on S_p and S_q . We call this statistic the BERET measure of dependence. The following theorem shows this measure is a consistent estimator of the population measure of dependence.

Theorem 4. *Suppose $\mathbf{X}$ and $\mathbf{Y}$ are continuous random vectors. Then,*

$$\hat{\mathcal{B}}_{n,d}^m[\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n] \xrightarrow{a.s.} \mathcal{B}_d(\mathbf{X}, \mathbf{Y}) \text{ as } m, n \rightarrow \infty.$$

Now, to develop an independence test, we define the statistic

$$\zeta_{n,d}^m = n(2^d - 1)^2 \hat{\mathcal{B}}_{n,d}^m[\{(\mathbf{X}_i, \mathbf{Y}_i)\}_{i=1}^n], \quad (2.10)$$

for each depth $d = 1, \dots, d_{max}$. By computing $1 - \alpha_d$ quantiles of $\zeta_{n,d}^m$, for $d = 1, \dots, d_{max}$, we can consider the test that rejects H_0 : “ $\mathbf{X}$ and $\mathbf{Y}$ are independent” if at least one $\zeta_{n,d}^m$, for $d = 1, \dots, d_{max}$, is greater than $\zeta_{n,d,1-\alpha_d}^m$. If $\sum_{d=1}^{d_{max}} \alpha_d \leq \alpha$, this procedure provides a level- α test. To put the proposed test into practice, we estimate the asymptotic null distribution using a random permutation method.

For better performance, under possible linear dependency, we combine this procedure with the distance correlation test, as above. If the scales of the elements in the random vectors differ greatly, normalization may help to reduce the number of $\mathbf{s}$ and $\mathbf{t}$ values to be sampled when the marginal variance of each entry in the random vector cannot degenerate to zero or

2.3 Multivariate Independence Testing Procedure

diverge to infinity. The following procedure summarizes the approach:

Step 1 : Set $\alpha_1, \dots, \alpha_{d_{max}}$, with $\sum_{d=1}^{d_{max}} \alpha_d = \alpha$.

Step 2 : Normalize marginally each element of the random vectors.

Step 3 : Find the p -value for the distance correlation test.

Step 4 : Fix $m \in \mathbb{N}$ and generate the random samples $s_1, \dots, s_m$ and $t_1, \dots, t_m$ from uniform distributions on hyper spheres.

Step 5 : For each $d = 2, \dots, d_{max}$, compute $\zeta_{n,d}^m$ and its p -value using the permutation method.

Step 6 : Reject H_0 if at least one of the p -values is less than the respective α_d .

The name of the test reflects the random projection and ensemble structure. Again, we investigate the behavior of our test in large samples. Theorem 5 shows that the BERET is uniformly consistent against the alternatives in the theorem.

Theorem 5. For any fixed $0 < \delta \leq 1/2$, denote by $\mathcal{H}_{1,d}^{s,t}$ the collection of distributions $\mathbf{P}_{(U_d^s, V_d^t)}$ such that $TV(\mathbf{P}_{(U_d^s, V_d^t)}, \mathbf{P}_{0,d}) \geq \delta$. Consider the testing

2.3 Multivariate Independence Testing Procedure

problem

$$H_0 : \mathbf{P}_{(U_d^s, V_d^t)} = \mathbf{P}_{0,d} \text{ for all } \mathbf{s} \in S_p, \mathbf{t} \in S_q$$

$$\text{vs. } H_1 : \mathbf{P}_{(U_d^s, V_d^t)} \in \mathcal{H}_{1,d}^{\mathbf{s},\mathbf{t}} \text{ for some } \mathbf{s} \in S_p \text{ and } \mathbf{t} \in S_q.$$

Then, the following properties hold:

- (i) Under H_1 , $\zeta_{n,d}^m \rightarrow \infty$ as $m, n \rightarrow \infty$.
- (ii) The rejection probability of the permutation test is bounded by α under H_0 and converges to one under H_1 as $m, n \rightarrow \infty$ if $d_{max} \geq d$.

The BERET has the following advantages. First, the method achieves robust power by a compromise between the distance correlation test and multiple testing over interactions (see the simulation results in Section 3). There is also a power loss in the multivariate case owing to the multiplicity control over the depth. By considering the distance correlation result together with the proposed measure of dependence with $d \geq 2$, we can improve the power over a wide range of plausible dependencies.

The second benefit of our method is clear interpretability, which is particularly important when evaluating multivariate relationships. However, most multivariate independence tests provide only the results of the tests, with no information on potential dependence structures in the sample. In

2.3 Multivariate Independence Testing Procedure

contrast, when the proposed test rejects independence, the $\mathbf{s}$ and $\mathbf{t}$ vectors indicate the linear combinations of the vectors that have strong dependencies (see section 2.3 of the Supplementary Material). Using these vectors, we can detect possible dependence structures in the sample; see the three-dimensional double helix structure in Figure 1, in which white positive regions and gray negative regions of interactions provide the interpretation of global dependency. The double helix structure is detected by two linear combinations. Additional interesting interpretation examples are provided in Section 4.

[Figure 1 near here]

The third benefit of our method is its “invariance.” Móri and Székely (2019) introduced axioms for a measure to be a dependence measure. If a measure Δ satisfies $\Delta(f(X), g(Y)) = \Delta(X, Y)$, where f and g are similarity transformations, it is called invariant with respect to similarity transformations. Because of the random projection and the CDF transformation steps in the proposed method, translations, orthogonal linear mappings, and uniform scalings do not affect the value of the measure of dependence.

Lastly, our method provides useful exploratory information for model selection. A small entry in the unit vector $\mathbf{s}$ or $\mathbf{t}$ may indicate that the corresponding variable is not related to the other random vector; see the

data examples in Section 4 for details.

3. Simulation Studies

3.1 Univariate Independence

For comparison, we consider Hoeffding's D test (Hoeffding (1948)), the distance correlation test (Székely et al. (2007)), the mutual information test (MINTav, Berrett and Samworth (2019)), Fisher's exact scanning method (Ma and Mao (2019)), and the maximum binary expansion test (Zhang (2019)). We use the sample size $n = 128$ as a moderate sample size for the power comparison. We set the level of the tests to be 0.1, and simulate each scenario 1,000 times. We adopt $d_{max} = 4$, because this depth provides a good approximation to the true distribution; see Section 4.5 in Zhang (2019) for a detailed discussion. The p-values of the proposed method are calculated using the asymptotic distribution of Theorem 1, part (iv). Lastly, we verified that the p-value under the null hypothesis is controlled at the level 0.1.

We compare the power of the above methods using linear, parabolic, circular, sine, checkerboard, and local relationships described in Zhang (2019). At each noise level $l = 1, \dots, 10$, ϵ, ϵ' , and ϵ'' are independent $\mathcal{N}(0, (l/40)^2)$ random variables. Here, U follows the standard uniform

3.1 Univariate Independence

distribution, ϑ is a $U[-\pi, \pi]$ random variable, and W , V_1 , and V_2 follow $multi\text{-}Bern(\{1, 2, 3\}, (1/3, 1/3, 1/3))$, $Bern(\{2, 4\}, (1/2, 1/2))$, and $multi\text{-}Bern(\{1, 3, 5\}, (1/3, 1/3, 1/3))$ distributions, respectively. G_1 and G_2 are generated from $\mathcal{N}(0, 1/4)$; see Table 1. These scenarios are displayed visually in the Supplementary Material.

[Table 1 near here]

Figure 2 shows the performance of the six methods. With the exception of the proposed test, the other methods all show the lowest power in at least one scenario. The ensemble approach and the BET show similar power across the scenarios, except for the linear and local dependency. The ensemble approach improves the power considerably in the linear and local dependency scenarios. As discussed previously, the ensemble approach uses the information on dependence remaining in the symmetry statistics that is not reflected in the calculation of the maximum BET. Therefore, small asymmetries in many symmetry statistics can be combined to provide a significant result in the ensemble approach when the sparsity assumption is violated. This result is related to the second finding that the ensemble approach outperforms Fisher’s exact scanning in terms of both global and local dependence structures. Zhang (2019) reported that the maximum BET provides better power for global dependence structures, whereas

3.2 Multivariate Independence

Fisher's exact scanning performs better for local dependence structures. The simulation results suggest that the ensemble approach works better than Fisher's exact scanning, even in the local dependency scenario.

[Figure 2 near here]

3.2 Multivariate Independence

Although the proposed method can be applied to arbitrary p and q , we choose $p = 2$ and $q = 1$ for better illustration. We compare the proposed method with the distance correlation test (Székely et al. (2007)), Heller–Heller–Gorfine test (Heller et al. (2012)), d-variable Hilbert–Schmidt independence criterion (Gretton et al. (2008)), and mutual information test (MINTav, Berrett and Samworth (2019)). We again use the sample size $n = 128$. We set the level of the tests to be 0.1, and simulate each scenario 1,000 times. For our method, we adopt $m = 30$, because there is no considerable difference in performance compared with larger m , such as $m = 360$. We also use a permutation method with 1,000 replicates to calculate the p-values of the proposed approach. We verified that the p-value under the null hypothesis is controlled at the level 0.1.

We compare the power of the methods over linear, parabolic, spherical, sine, and local dependence structures. These scenarios are generalized

3.2 Multivariate Independence

from the univariate dependence simulations. In addition, we include an additional interesting relationship, namely, the double helix structure. At each noise level $l = 1, \dots, 10$, ϵ , ϵ' , and ϵ'' are independent $\mathcal{N}(0, (l/40)^2)$ random variables, U_1 and U_2 follow the standard uniform distribution, ϑ follows $U[0, 4\pi]$, G_1 , G_2 , and G_3 are independent $\mathcal{N}(0, 1/4)$ random variables, and I follows the Rademacher distribution; see Table 2. These three-dimensional scenarios are provided in the Supplementary Material.

[Table 2 near here]

Before we compare the statistical performance of the methods, we report the computation time of 100 runs for each method in Table 3.

[Table 3 near here]

Figure 3 shows the simulation results. The BERET provides the best power in more complex dependency structures, such as the sine and double helix dependencies, and it outperforms the distance correlation test and the d -variable Hilbert–Schmidt independence criterion in at least five scenarios. Moreover, our method provides stable results across the scenarios considered. It ranks at least third in all scenarios. The mutual information test performs best in the highest number of scenarios. In linear and

sine relationships, however, there is a significant loss of power in the mutual information test compared with the proposed method. Note that our method provides additional insight. Other methods provide only test results of independence, whereas our method also provides potential dependence structures. The simulation results show that BERET provides competitive performance, while providing a much clearer interpretation.

[Figure 3 near here]

4. Data Examples

4.1 Life Expectancy

We use the proposed method to test the independence between geographic location and life expectancy, and compare its performance with that of the distance correlation test (dCor), Heller–Heller–Gorfine test (HHG), mutual information test (MINT), and canonical correlation test (CC). We include the canonical correlation test because it provides some insight on the dependence structure, as does the proposed method. For the proposed method, we set $d_{max} = 4$ and $m = 30$. The p-value of the test is calculated using a permutation method with 1,000 replicates. The data set is obtained from the life expectancy report released by the World Health Organization in 2016, and includes males and females and total life expectancy for 189

4.1 Life Expectancy

countries and special administrative regions estimated in 2015. We use the latitude (X_1), longitude (X_2), and total life expectancy (Y) in the analysis. Table 4 presents the testing results for the five methods. All five tests provide p-values close to zero, indicating a significant dependence between geographic location and life expectancy.

[Table 4 near here]

To identify the dependence structure, we investigate the symmetry statistics. Figure 4 shows the three largest symmetry statistics and the corresponding $\mathbf{s}$ in each case. The most asymmetric result is shown in the first row, that is, $\dot{A}_2\dot{B}_1$, with $\mathbf{s} = (0.516, 0.857)^T$. The horizontal axis is the empirical cumulative distribution function transformation of $0.516X_1 + 0.857X_2$, wherein a smaller value implies that the country is located in the southwest, and a larger value implies that it is located in the northeast. There are four groups. Each gray cell represents a specific region, namely, America, Africa, Europe, and Asia, from left to right. The countries in America and Europe show a higher life expectancy than do countries in Africa and Asia. The four points in the top-right corner are Hong Kong, Japan, Macau, and South Korea. These can be interpreted as potential outliers distinct from the global pattern.

4.1 Life Expectancy

[Figure 4 near here]

The second row shows that there is a positive relationship between latitude and life expectancy. That is, countries in North America, Europe, and Northeast Asia have a higher life expectancy than do countries in Africa, South America, and the other parts of Asia. The last row shows that a circular dependency can exist, indicating that countries in America and Asia have a medium life expectancy, whereas countries around the prime meridian have different life expectancies, higher in Europe and lower in Africa. These findings prove clearly that our method detects the dependence structures between geographic location and life expectancy.

A canonical correlation analysis can also be used to find information on the dependence structure. The canonical correlation is 0.43, and it is calculated using $0.991X_1 - 0.137X_2$ and Y . The coefficients of X_1 and X_2 are similar to the elements of $\mathbf{s}$ in the result of the proposed method in the second row. However, a canonical correlation provides information only on the linear dependence structure, whereas our method provides richer information by considering various nonlinear dependence structures.

4.2 Mortality Rate

In this section, we investigate the relationship between mortality rate, birth rate, and income level. We use the Central Intelligence Agency's world fact data, estimated in 2018. The data set includes the income level (X_1), birth rate (X_2), and mortality rate (Y) of 224 countries and special administrative regions. The p-values of the five methods are presented in Table 4. Once again, the proposed method and two other methods provide p-values close to zero, thus rejecting the null hypothesis, whereas the mutual information test and canonical correlation fail to reject it. The poor performance of the canonical correlation can be explained by investigating the results of our method. The strongest asymmetry is in Figure 5, which shows a strong quadratic relationship. This relationship explains the failure of the canonical correlation for these data. Although the canonical correlation test provides both an inference and information on the dependence structure, it performs poorly in nonlinear dependency settings.

[Figure 5 near here]

Two conflicting phenomena explain the observed quadratic relationship. First, developed countries have low birth rates, but high mortality rates, owing to population aging. However, developing countries have high birth

4.3 House Price

rates because of a lack of family planning, and high mortality rates because of insufficient public health. Thus, mortality rates are high in countries with low or high birth rates. The BERET detects an interesting structure that can be explained by widely recognized relationships between mortality rate and birth rate.

4.3 House Price

The third data example is based on the market historical data set of real estate from the University of California, Irvine machine learning repository. The data include 414 transactions from the Xindan district of Taipei between August 2012 and July 2013. We use these data to detect the relationship between geographic location and house price. The p-values of the five methods are presented in Table 4. All methods except the mutual information test provide p-values close to zero, which is consistent with the commonly assumed relationship between location and house price in a city. The mutual information test fails to reject the independence. Figure 6 presents the two strongest dependencies identified by the proposed method.

[Figure 6 near here]

The symmetry statistic with the strongest asymmetry is $\dot{A}_1\dot{B}_1$, which means there may be a linear relationship between geographic location and

house price. The corresponding $\mathbf{s}$ for the horizontal axis is $(0.964, 0.268)$. That is, houses have higher values in the north and lower values in the south. This is because the central part of Taipei is above the Xindan district. The symmetry statistic with the second strongest asymmetry is $\dot{A}_1\dot{A}_2\dot{B}_1$. The corresponding $\mathbf{s}$ for the horizontal axis is $(0.215, 0.977)^T$. That is, house prices are high at the center of the district, where two main roads intersect, and decrease toward the periphery. These results accord closely with the general characteristics of real estate prices in a city. Therefore, we conclude that the proposed method properly detects the relationship between house price and geographic location.

5. Conclusion

Detecting dependence in a distribution-free setting is an important problem in statistics. Existing methods find it difficult to detect complicated dependence structures. For example, in our simulations, the distance correlation test does not detect circular dependency well, but does provide good power in linear, parabolic, and sine settings. The BET procedure in Zhang (2019) suggests a novel way of solving this problem. However, it is limited to the independence test of two random variables, and there is room to enhance the power when the sparsity assumption is violated.

We have introduced an ensemble approach and a binary expansion randomized ensemble test. The ensemble approach uses both the sum of the squared symmetric statistics and the distance correlation test. It shows better power in linear and local settings, while maintaining power for other dependence structures. Moreover, it can be easily generalized to an independence test for the multivariate setting, the binary expansion randomized ensemble test. Using random projections, the BERET transforms the multivariate independence testing problem into a univariate testing problem. The BERET also maintains the clear interpretability of the maximum BET.

Simulation studies suggest that the BERET is more powerful than several competitors considered in meaningful dependence structures. Three data examples show that the BERET reveals hidden dependence structures in the data, while maintaining a level of power similar to that of the best of the competing methods.

Several improvements are worth considering for future work. For instance, there may be a different method of combining the symmetry statistics that offers better performance. It would also be useful to derive the limiting null distribution of the test statistic for the multivariate setting to avoid a permutation method.

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Supplementary Material

The online Supplementary Material provides technical details and proofs.

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Table 1: Simulation scenarios for the univariate independence test

Scenario	Generation of X	Generation of Y
Linear	$X = U$	$Y = X + 6\epsilon$
Parabolic	$X = U$	$Y = (X - 0.5)^2 + 1.5\epsilon$
Circular	$X = \cos \vartheta + 2\epsilon$	$Y = \sin \vartheta + 2\epsilon'$
Sine	$X = U$	$Y = \sin(4\pi X) + 8\epsilon$
Checkerboard	$X = W + \epsilon$	$Y = \begin{cases} V_1 + 4\epsilon' & \text{if } W = 2 \\ V_2 + 4\epsilon'' & \text{otherwise} \end{cases}$
Local	$X = G_1$	$Y = \begin{cases} X + \epsilon & \text{if } 0 \leq G_1 \leq 1 \text{ and } 0 \leq G_2 \leq 1 \\ G_2 & \text{otherwise} \end{cases}$

Table 2: Simulation scenarios for multivariate independence testing

Scenario	Generation of X	Generation of Y
Linear	$\mathbf{X} = \begin{pmatrix} U_1 \\ U_2 \end{pmatrix}$	$\mathbf{Y} = X_1 + X_2 + 7\epsilon$
Parabolic	$\mathbf{X} = \begin{pmatrix} U_1 \\ U_2 \end{pmatrix}$	$\mathbf{Y} = (X_1 - 0.5)^2 + (X_2 - 0.5)^2 + 1.5\epsilon$
Spherical	$\mathbf{X} = \begin{pmatrix} \frac{G_1}{\sqrt{G_1^2 + G_2^2 + G_3^2}} \\ \frac{G_2}{\sqrt{G_1^2 + G_2^2 + G_3^2}} \end{pmatrix}$	$\mathbf{Y} = \frac{G_3}{\sqrt{G_1^2 + G_2^2 + G_3^2}} + 3\epsilon$
Sine	$\mathbf{X} = \begin{pmatrix} U_1 \\ U_2 \end{pmatrix}$	$\mathbf{Y} = \sin(5\pi X_1) + 4\epsilon$
Double helix	$\mathbf{X} = \begin{pmatrix} Icos(\vartheta) + 1.5\epsilon \\ Isin(\vartheta) + 1.5\epsilon' \end{pmatrix}$	$\mathbf{Y} = \frac{\vartheta}{2} + 2\epsilon''$
Local	$\mathbf{X} = \begin{pmatrix} G_1 \\ G_2 \end{pmatrix}$	$\mathbf{Y} = \begin{cases} \frac{X_1}{\sqrt{2}} + \frac{X_2}{\sqrt{2}} + \frac{\epsilon}{2}, & \text{if } 0 \leq G_1 + G_2 \leq 2 \text{ and } 0 \leq G_3 \leq 1. \\ G_3, & \text{otherwise.} \end{cases}$

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Table 3: Computing time (in seconds) of each method for 100 runs

	BERET	dCor	HHG	d-HSIC	MINT
CPU Time (seconds)	74.89	0.17	510.42	16.96	65.19

Table 4: p-values from five tests of independence

	BERET	dCor	HHG	MINT	CC
Life expectancy	<0.0001	<0.0001	0.0010	0.0010	<0.0001
Mortality rate	0.0040	0.0050	0.0010	0.3077	0.4303
House price	<0.0001	<0.0001	0.0010	0.6204	<0.0001

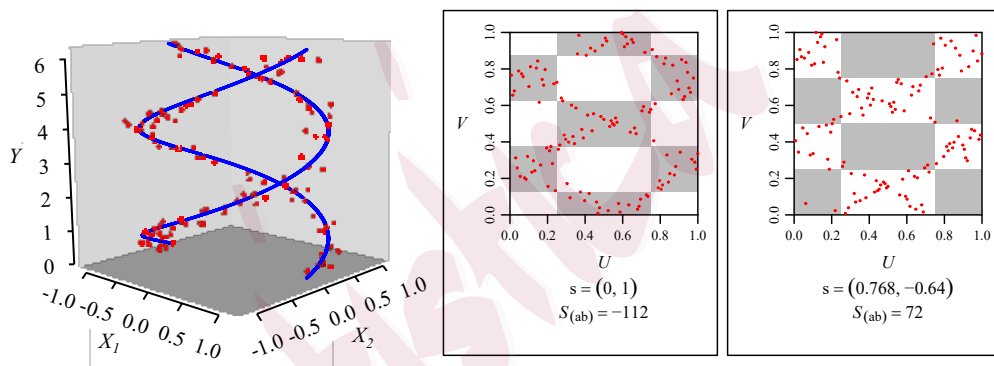


Figure 1: The first plot shows a sample with a double helix dependency between a random vector $(X_1 \ X_2)^T$ and a random variable Y with $n = 128$. The second and third plots show the linear combinations of X_1 and X_2 with the strongest asymmetries and the corresponding symmetry statistics $(S_{(ab)})$. Positive regions $(\dot{A}_{\mathbf{a}}\dot{B}_{\mathbf{b}} = 1)$ are in white, and negative regions $(\dot{A}_{\mathbf{a}}\dot{B}_{\mathbf{b}} = -1)$ are in gray.

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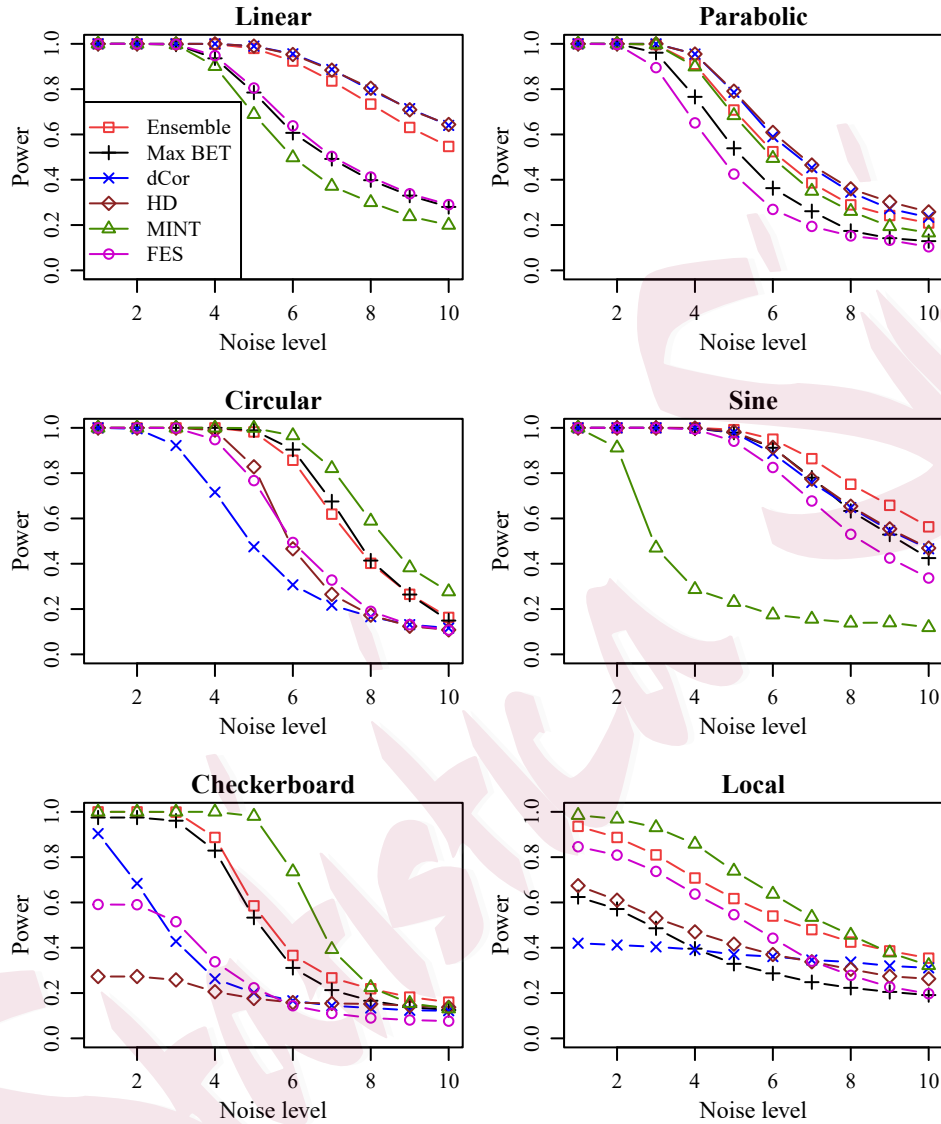


Figure 2: Comparison of the power of six tests of independence: the binary expansion randomized ensemble test with $d_{max} = 4$ (square), the maximum binary expansion test with $d_{max} = 4$ (plus sign), the distance correlation test (cross), Hoeffding's D (diamond), the mutual information test (triangle), and Fisher exact scanning (circle).

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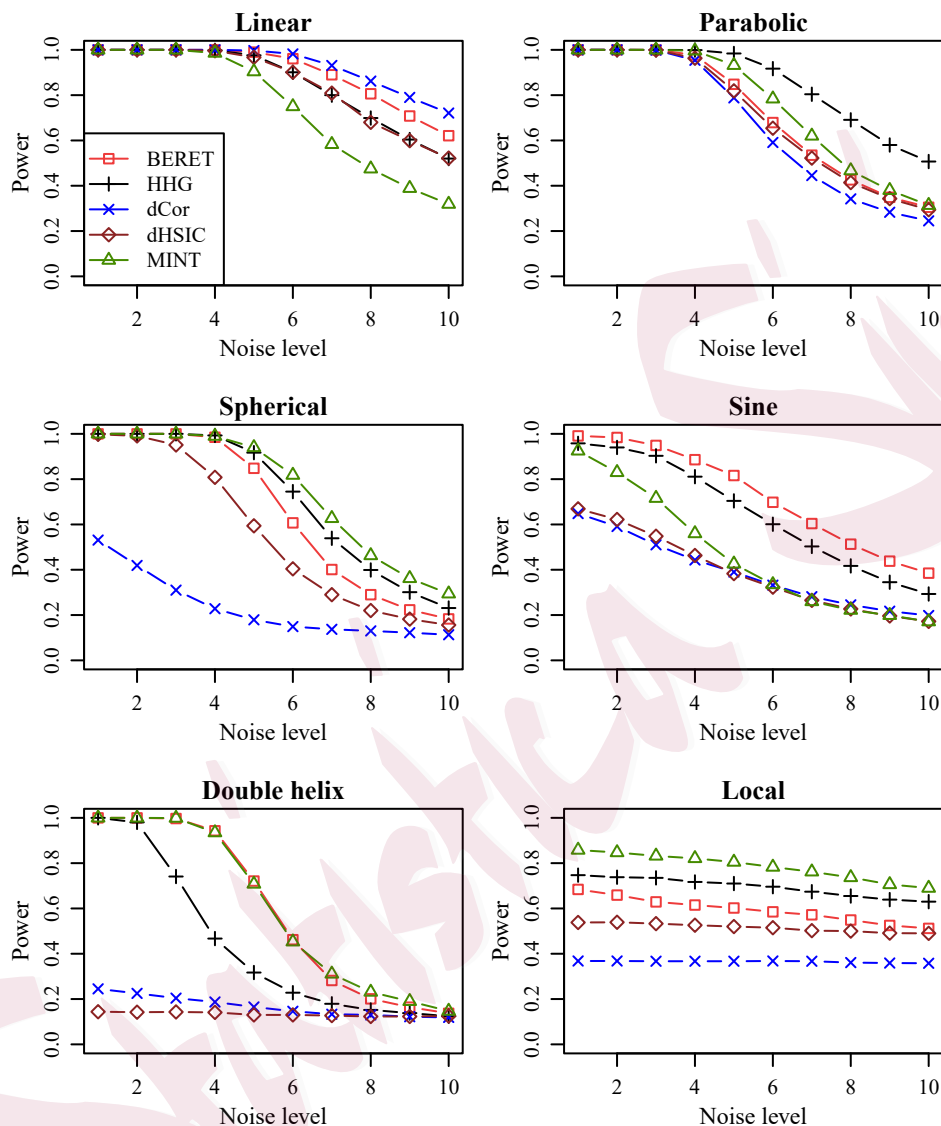


Figure 3: Comparison of the power of five tests of independence: the binary expansion randomized ensemble test with $d_{max} = 4$ (square), the Heller–Heller–Gorfine test (plus sign), the distance correlation test (cross), the d -variable Hilbert–Schmidt independence criterion (diamond), and the mutual information test (triangle).

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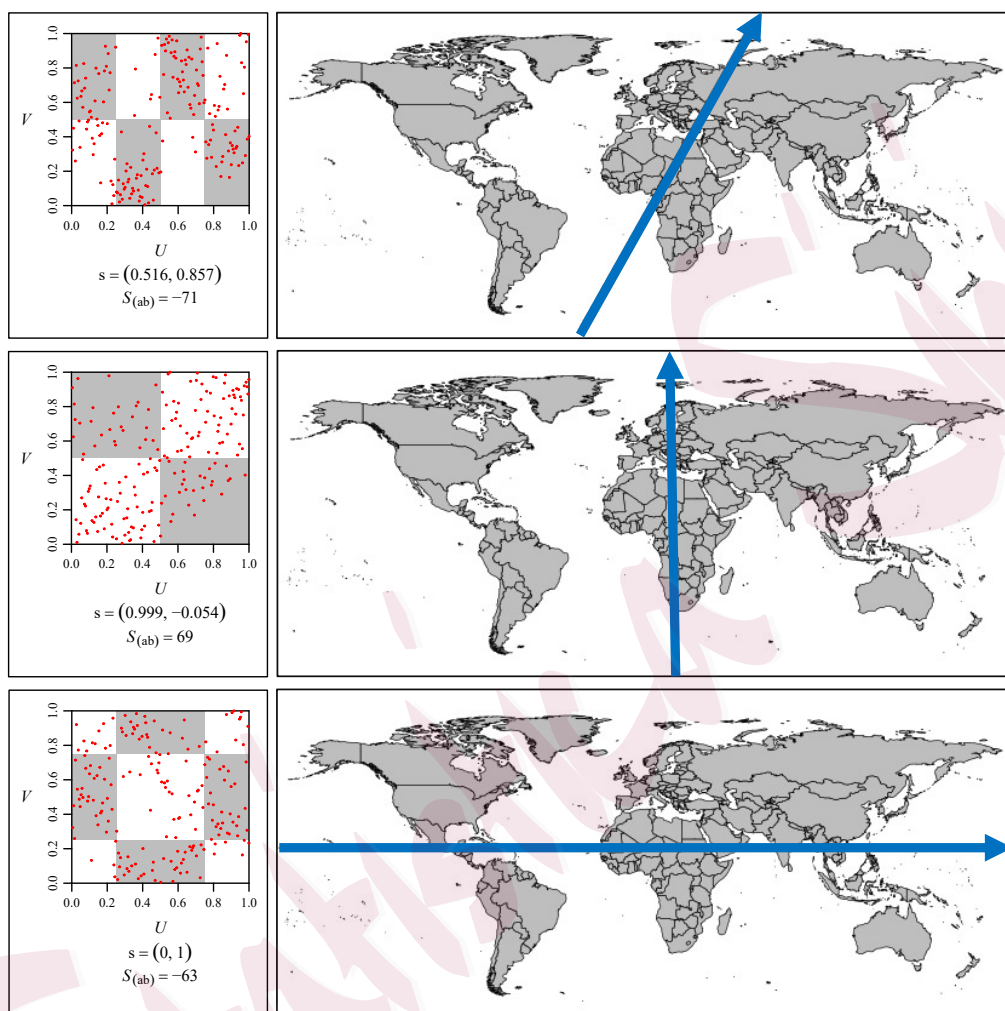


Figure 4: The three strongest dependency structures between geographic location and life expectancy, as well as the corresponding values of the symmetry statistics ($S_{(ab)}$) and the coefficients of linear combination (s) of X_1 and X_2 . The arrows in the world maps represent the horizontal axes in the scatterplots.

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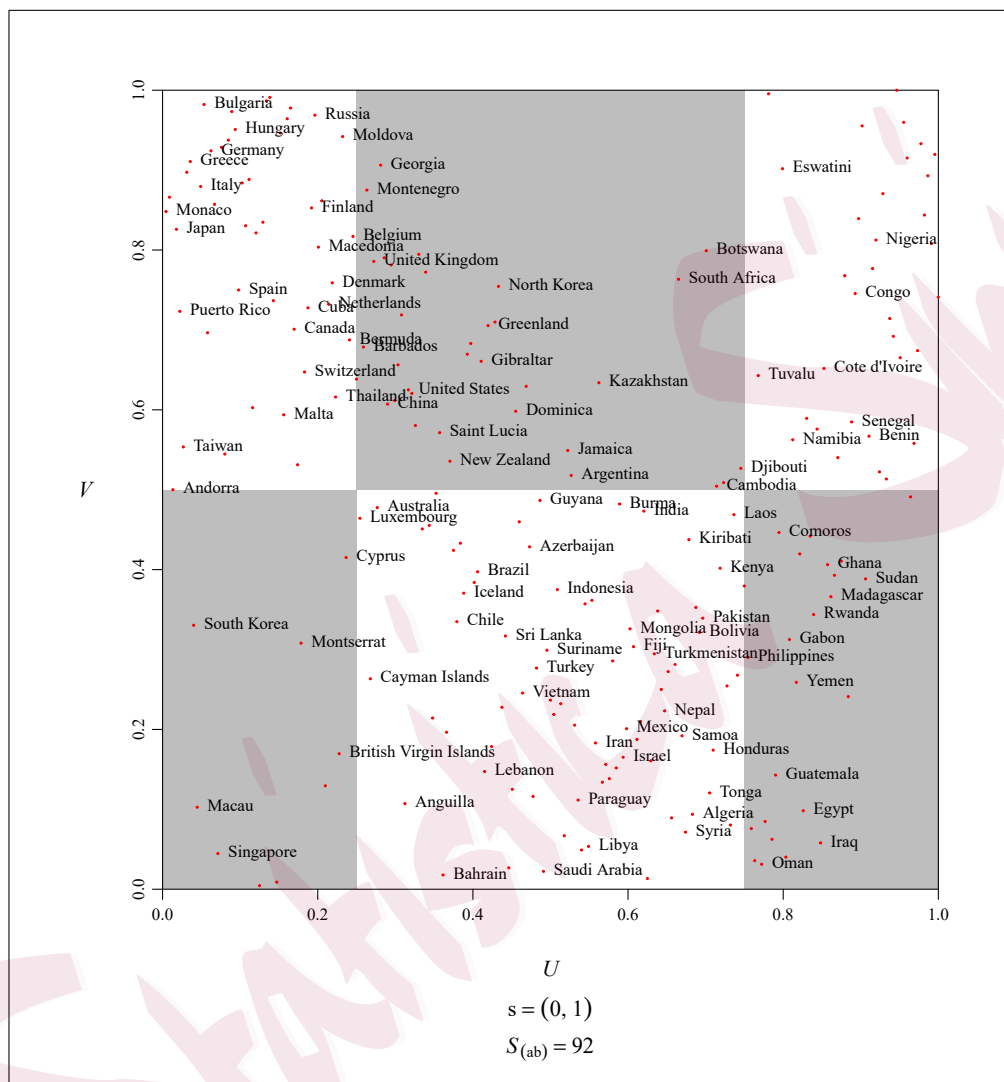


Figure 5: The plot shows the strongest dependency structure between birth rate, income level, and mortality rate, as well as the corresponding value of the symmetry statistic ($S_{(ab)}$) and the coefficients of the linear combination (s) of X_1 and X_2 .

REFERENCES



Figure 6: The plots show the two strongest dependency structures between geographic location and house price. The plots also present the symmetry statistics ($S_{(ab)}$) and the coefficients in the linear combinations $\mathbf{s}$ and $\mathbf{t}$. The arrows in the map represent the horizontal axes in the scatterplots.