

Alternative Methods to Test for Positive Assortative Mating*

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Abstract

We propose hypothesis testing methods for positive assortative mating (PAM) that use random matching as the null hypothesis, departing from existing approaches that treat PAM as the null. Our pseudo-Wald and likelihood ratio tests exploit the full sample information through closed-form expressions, avoiding numerical optimization or restrictive assumptions about specific matching cells. Monte Carlo simulations demonstrate superior performance under weak assortative mating and moderate sample sizes. Empirical applications using CPS data confirm that our methods effectively detect PAM on predicted wage.

1 Introduction

This paper proposes easy hypothesis testing methods to test for positive assortative mating (PAM). A number of empirical studies on sorting in the marriage market have investigated the intensity of assortative mating and how the strength of assortative mating has changed over time using structural (Greenwood et al., 2014; Chiappori et al., 2017; Gualdani and

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Sinha, 2023) or non-structural (Liu and Lu, 2006; Eika et al., 2019) approaches. Meanwhile, only a handful of econometric tests have been developed for testing PAM that practitioners can readily apply without specifying a structural model (Anderson and Leo, 2013; Siow, 2015).

Broadly, the literature examining PAM features two main approaches. The first constructs indices of sorting, typically by comparing observed match probabilities to counterfactual match probabilities under random pairing. This method measures the intensity of sorting without explicitly modeling individual preferences. Notable examples in this vein include Liu and Lu (2006) and Eika et al. (2019).¹ While Liu and Lu (2006) construct descriptive indices of assortative mating and Eika et al. (2019) develop indices and further examine trends and decompositions, neither study provides a formal hypothesis test or statistical inference procedure to determine the presence of positive assortative mating.²

Another strand of literature is a choice-based framework initiated by Choo and Siow (2006b). They propose a marriage matching function, which is based on the transferable utility matching framework with random preferences.^{3,4} The critical assumptions of Choo and Siow (2006b) are (a) additive separability of joint surplus, (b) a large marriage market, and (c) an extreme value distribution of the shock (Galichon and Salanié, 2021a). Choo and Siow (2006a) applied the marriage matching function to quantify the effect of the legalization of abortion on gains to marriage.

Building on the transferable utility framework, subsequent studies have extended the Choo and Siow (2006b) model in multiple directions. For instance, Chiappori et al. (2017)

¹Fernández and Rogerson (2001), Greenwood et al. (2014), and Abbott et al. (2019) apply similar ideas in the marital matching stage of their structural models.

²Researchers have developed different methods to test hypotheses related to assortative mating, although not all directly focus on assessing the positivity of assortative mating. These studies examine related but distinct questions, focusing on temporal changes in educational homogamy (Chiappori et al., 2017), peer and scale effects in matching (Mourifié and Siow, 2021), and set identification under nonparametric distributional assumptions (Gualdani and Sinha, 2023)

³See Chiappori and Salanié (2016) for the survey of the empirical marriage matching models under different assumptions: transferable utility, non-transferable utility, and imperfectly transferable utility models.

⁴See Fox (2010, 2018), and Fox et al. (2018) for an alternative method employing a maximum score approach based on the rank-order property associated with sorting. See Suen and Lui (1999) for a correlation-based test.

incorporate parental investment into a structural marriage model, embedding it in the original Choo and Siow formulation to measure changing returns to education in the U.S. marriage market. Mourifié and Siow (2021) introduce peer effects, Dupuy and Galichon (2014) adapt the framework to continuous attributes using Dagsvik’s (1994; 2000) continuous choice structure, and Galichon and Salanié (2021b) show that the extreme value assumption can be relaxed. In a related vein, Fernández and Rogerson (2001) use a search model that delivers PAM but focus on how the degree of sorting correlates with wage gaps and other economic variables. While these structural approaches are powerful for understanding matching behaviors, they often require significant effort in terms of modeling and computation.

Siow (2015) proposes a test based on maximum likelihood estimation (MLE) within the Choo and Siow (2006a) framework. He sets PAM as the null hypothesis and uses two key restrictions to test PAM: total positivity of order two (TP2) and diagonal positivity of order two (DP2). While these constraints can be effective for strong assortative matching, they often perform poorly or become overly restrictive when assortative mating is weak, and is less effective when sample size is small or moderate. Also, the associated test statistics exhibit non-standard asymptotic distributions.

We propose testing methods that set random matching as the null hypothesis, departing from existing approaches that treat PAM as the null hypothesis. Our methods offer several advantages over existing approaches for testing PAM. First, they are straightforward to implement, providing closed-form solutions that do not require numerical optimization.⁵ Second, our methods serve as a quick diagnostic tool for PAM before researchers build richer structural models for their analysis. Third, our tests exploit the full sample information, as results are not overly sensitive to the small proportion of extreme matching cells.

We first define our pseudo-Wald and Likelihood Ratio tests and investigate their distributional properties. The resulting closed-form test statistics are straightforward to implement and computationally efficient, offering strong power while maintaining ease of use. Secondly,

⁵We need not make theoretical restrictions as our test examines whether the data exhibits certain characteristics, not why it may or may not have those characteristics.

we compare our methods with the restriction-based method of Siow (2015). Our pseudo-Wald test correctly fails to detect PAM under weak assortative matching and effectively detects PAM when sample size is small ($N=500$) or moderate ($N=2,000$) and sorting is strong. For large sample size ($N = 120,000$), both tests provide support for PAM.

Finally, we provide two empirical applications of matching based on wage and matching in same-sex marriage. Our tests conclude PAM on predicted wage while tests of Siow (2015) find PAM on education. Both tests find PAM in same-sex marriage.

We explain our proposed tests in Section 2. In Section 3, we compare the performance of both approaches under varying intensities of assortative mating. Section 4 provides empirical examples. We conclude in Section 5.

2 Alternative Tests

Our tests differ from Siow (2015) in two main ways: (i) we set random matching as the null hypothesis, and (ii) we directly utilize unrestricted MLE estimates of the matching cells to evaluate test statistics. While Siow (2015) performs likelihood ratio tests under various restrictions consistent with PAM, we construct test statistics directly from unrestricted estimates. In this section, we explain these methodological differences.

2.1 Review of Siow (2015)

Suppose there are I types of men, $i = 1, 2, \dots, I$, and J types of women, $j = 1, 2, \dots, J$, where types are vertically ordered. Let n_{ij} be the number of observations where a type- i male is matched with a type- j female, and define

$$N = \sum_{i=1}^I \sum_{j=1}^J n_{ij}$$

as the total number of sampled marriages. Let p_{ij} be the probability that a randomly sampled marriage is of type ij . Following Siow (2015), consider the unrestricted likelihood problem:

$$\begin{aligned} \max_{\{p_{ij}\}} \quad & \sum_{i=1}^I \sum_{j=1}^J n_{ij} \log p_{ij} \\ \text{subject to} \quad & \sum_{i=1}^I \sum_{j=1}^J p_{ij} = 1. \end{aligned} \tag{1}$$

The unrestricted MLE of $\{p_{ij}\}$ is

$$\hat{p}^u = \{\hat{p}_{ij}^u\} \quad \text{with} \quad \hat{p}_{ij}^u = \frac{n_{ij}}{N}.$$

Siow (2015) and related work note that one way to test for PAM is to re-estimate \hat{p} under restrictions consistent with PAM, and then perform a likelihood ratio test. The main restrictions considered in Siow (2015) are total positivity of order 2 (TP2) and diagonal positivity of order 2 (DP2).⁶ Both restrictions rely on the local log-odds ratio for (i, j) , which is defined as

$$R_{ij} = \log p_{ij} + \log p_{i+1, j+1} - \log p_{i, j+1} - \log p_{i+1, j}. \tag{2}$$

Here, R_{ij} measures how strongly types i and j complement each other relative to cross-type matches $(i, j+1)$ and $(i+1, j)$.

TP2 Restriction. The TP2 condition states that *all* such local log-odds ratios are strictly positive for all matching cells:

$$R_{ij} > 0 \quad \text{for all } i = 1, 2, \dots, I-1 \text{ and } j = 1, 2, \dots, J-1, \tag{3}$$

⁶The term “order” refers to the dimension of the determinants for the matching matrix.

which is equivalent to the case that the underlying matching surplus function is supermodular (Siow, 2015).⁷

DP2 Restriction. DP2 focuses on local log-odds ratios only along the *same type* diagonal (e.g., $(i, i + 1)$), which is defined as

$$R_{ii} > 0 \quad \text{for all } i = 1, 2, \dots, \min(I, J) - 1. \quad (4)$$

In addition to the primary TP2 and DP2 constraints, Siow (2015) proposes several modifications. In particular, **TP2'** imposes the condition $R_{ij} > 0$ except for the top-right and bottom-left matchings. While this exclusion aims to mitigate the influence of extreme or sparsely populated matches, it can arbitrarily discard valuable information; moreover, outliers may arise in other corner cells not explicitly omitted by this rule.

On the one hand, it is not clear which of the restrictions in Siow (2015) are more suitable to assess PAM.⁸ For example, the log-likelihood with the TP2 restriction is rejected against the unrestricted likelihood, but the log-likelihood with the DP2 restriction is not rejected. Siow (2015) states that the rejection of the TP2 likelihood is driven by the couples whose completed education is distant. As the extreme matches account only for less than 0.2% of marriages, the TP2 restriction is arguably sensitive to such outliers.⁹

The null hypothesis in Siow (2015) is a space with positive measure, and the alternative hypothesis is a space with positive measure. To see this, consider a simple case where there are just two types of men and two types of women. The parameter space is the unit square, and the condition for PAM is

$$p_{11} + p_{22} - p_{12} - p_{21} \geq 0$$

⁷See Choo and Siow (2006b) for the descriptions of the underlying structural model.

⁸Chiappori et al. (2017) also propose a test based on their structural model that incorporates returns to parental investment. Their method requires using minimum distance of the moment conditions that come from their structural model. The main purpose of this test is to examine the changes in the intensities of educational homogamy.

⁹Anderson and Leo (2013) develop a test statistic very similar to the TP2 test in Choo and Siow (2006b).

which simplifies to

$$p_{11} + p_{22} \geq 1. \tag{5}$$

The region consistent with the null hypothesis is all values of (p_{11}, p_{22}) that satisfy equation (5), and the region consistent with the alternative hypothesis is the part of the unit square that does not satisfy equation (5). This is an uncommon problem in the literature. In comparison, the test procedure we propose in the subsequent section is standard: the null hypothesis is a point, and the alternative is a region surrounding the point.

A similar example of interest in the literature is testing a unit root hypothesis for a time series. Almost all of the literature on testing for a unit root assumes that the null hypothesis is nonstationarity. A strong reason for making this assumption instead of stationarity being the null hypothesis is that, when nonstationarity is the null hypothesis, it can be represented by a single $AR(1)$ parameter equalling 1. Thus, the situation is turned into a standard case where the null hypothesis corresponds to a point. However, from an economic point of view, the null hypothesis should be stationarity in that the model behaves better when there is stationarity (we would like to not reject the null hypothesis and then rely on the nice properties of stationary processes). Alternatively, Kwiatkowski et al. (1992), Leybourne and McCabe (1994), and Xiao (2001) all use a null hypothesis of stationarity by constructing a time series model with a random walk where the random walk is the only source of nonstationarity. The null hypothesis is then that the variance of the random walk error is equal to zero.

A second example, much closer to our problem, is to test whether the Slutsky substitution matrix is negative semidefinite. Gill and Lewbel (1992) choose a null hypothesis of semidefiniteness (which has positive measure) and show how to construct a consistent test statistic. Gill and Lewbel (1992) state that the asymptotics of this problem are very similar to that in Kodde and Palm (1986) where the null and alternative hypotheses have positive measure.¹⁰ An easier approach is to construct a Wald test, requiring only the unrestricted

¹⁰Unfortunately, Cragg and Donald (1996, 1997) show that the asymptotics for a related rank condition are incorrect, and neither paper addresses the correctness of the argument of Gill and Lewbel (1992) about testing for semidefiniteness.

estimates.¹¹ Though it does not deal with the nonstandardness of the test, it avoids the cost associated with imposing the positive assortative mating restrictions, and it allows for more general tests.

2.2 A Pseudo–Wald Test

Our pseudo-Wald test adopts random matching as a null hypothesis, in contrast to Siow (2015) using the PAM criteria (such as TP2 or DP2) as a null. Conceptually, random matching serves as a natural null because it is the outcome we want to rule out. This aligns with frequentist practice of choosing “undesirable” nulls to control Type I error. In particular, we test the null of random matching,

$$H_0 : R_{ij} = 0 \quad \text{for all } 1 \leq i \leq I-1, 1 \leq j \leq J-1, \quad (6)$$

against the alternative of assortative matching.

Define the stacked vector $\widehat{\mathbf{R}} = (\widehat{R}_{1,1}, \dots, \widehat{R}_{I-1,1} \mid \widehat{R}_{1,2}, \dots, \widehat{R}_{I-1,2} \mid \dots \mid \widehat{R}_{1,J-1}, \dots, \widehat{R}_{I-1,J-1})^\top$, which has length $K = (I-1)(J-1)$.

Asymptotics. Recall that each local log–odds is a fixed linear combination of four log cell probabilities,

$$R_{ij} = \log \hat{p}_{ij} + \log \hat{p}_{i+1,j+1} - \log \hat{p}_{i+1,j} - \log \hat{p}_{i,j+1}.$$

By the multinomial CLT applied to \hat{p}_{ij} and the delta method applied to $\log \hat{p}_{ij}$,

$$\sqrt{N} (\widehat{\mathbf{R}} - \mathbf{R}) \xrightarrow{d} \mathcal{N}(0, C(\mathbf{R})), \quad (7)$$

where $C(R)$ is the $((I-1)(J-1) \times (I-1)(J-1))$ asymptotic covariance matrix whose elements are given by the $Var(R_{ij})$ and $Cov(R_{ij}, R_{kl})$ formulas (see Appendix A).

¹¹It is not clear which should be considered the restricted model and which the alternative.

Test statistic. Under the null of random matching, we can estimate cell probabilities by independence, $\hat{p}_{ij}^0 = \hat{x}_i \hat{y}_j$ with $\hat{x}_i = \sum_j n_{ij}/N$ and $\hat{y}_j = \sum_i n_{ij}/N$, and form a plug-in covariance \hat{C}_0 by substituting \hat{p}_{ij}^0 into the closed-form Var/Cov expressions. The pseudo-Wald statistic is

$$T_W = N \hat{\mathbf{R}}^\top \hat{C}_0^{-1} \hat{\mathbf{R}} \xrightarrow{d} \chi_{(I-1)(J-1)}^2. \quad (8)$$

Our pseudo-Wald statistic aggregates all local log-odds ratios $\{\hat{R}_{ij}\}$ in a single summation which allows us to exploit *all* information in the sample simultaneously without discarding thinly populated cells or imposing stronger global restrictions. When some matching cells are close to zero and others are far from zero, the pseudo-Wald test statistic captures the net effect—i.e., whether the overall “signal” of PAM outweighs zero assortative matching in certain subgroups. Also, the covariance matrix captures the dependence between the matching cells, which accounts for the equilibrium spillover in the marriage market.

2.3 Likelihood Ratio Test and Lagrange Multiplier Test

Also note that the MLE of p under the restriction of random mating is $\hat{p}^r = \{\hat{p}_{ij}^r\}$ where

$$\hat{p}_{ij}^r = \hat{x}_i \hat{y}_j, \quad \hat{x}_i = \frac{\sum_j n_{ij}}{N}, \quad \hat{y}_j = \frac{\sum_i n_{ij}}{N}.$$

Thus, one can test the null hypothesis of random mating against a general alternative with a likelihood ratio (LR) test,

$$\begin{aligned} T_{LR} &= 2 \left[\sum_{i,j} n_{ij} \log \hat{p}_{ij}^u - \sum_{i,j} n_{ij} \log \hat{p}_{ij}^r \right] \\ &= 2 \left[\sum_{i,j} n_{ij} \log \frac{\hat{p}_{ij}^u}{\hat{p}_{ij}^r} \right] \\ &= 2 \left[\sum_{i,j} n_{ij} \log \frac{\hat{p}_{ij}^u}{(\sum_k \hat{p}_{ik}^u)(\sum_k \hat{p}_{kj}^u)} \right] \sim \chi_K^2 \end{aligned}$$

(which requires only estimation of \widehat{p}^u) with

$$K = (I - 1)(J - 1)$$

which is identical with the degrees of freedom in for the Wald test.¹²

Alternatively, one can construct a Lagrange Multiplier (LM) test. Let

$$L = \sum_{i,j} n_{ij} \log p_{ij}.$$

Then,

$$\begin{aligned} \frac{\partial L}{\partial p_{ij}} \bigg|_{p_{ij}=\widehat{p}_{ij}} &= \frac{n_{ij}}{\widehat{p}_{ij}} \\ &= \frac{n_{ij}}{\frac{\sum_k n_{ik}}{N} \frac{\sum_k n_{kj}}{N}} \\ &= \frac{N \widehat{p}_{ij}^u}{(\sum_k \widehat{p}_{ik}^u) (\sum_k \widehat{p}_{kj}^u)} \end{aligned}$$

implying that the LM has the same form and the same distribution as the LR test.

3 Properties of the Proposed Tests

We provide a simulation-based analysis of the finite-sample properties of the proposed tests to corroborate the asymptotic theory stated above. The empirical distributions generated by simulations show that the proposed tests follow $\chi^2_{(I-1)(J-1)}$ reasonably well and power increases with both the sample size and the strength of assortativeness.

We first specify an auxiliary model of assortative mating, which we use to (i) simulate the distribution of our test statistics and (ii) compare our test methods with the tests of Siow (2015). Define a male as having an integer value of x_i between 1 and 5, and define a

¹²This is because x_i for $i = 1, 2, \dots, I - 1$ and $j = 1, \dots, J - 1$ are the sufficient parameters estimate the whole p_{ij} matching cells under the null.

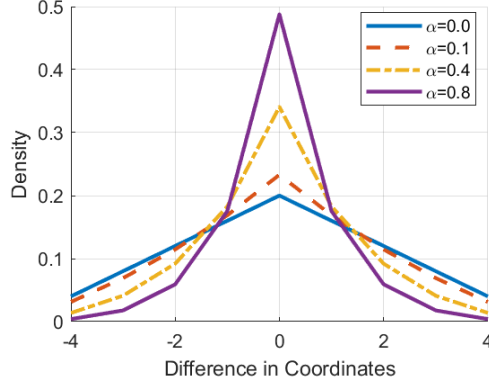


Figure 1: Density from 1 to M (F)

female as having an integer value of x_j between 1 and 5. Assume that the density of matches in an economy is

$$f(x_i, x_j) = \frac{\exp\{-\alpha|x_i - x_j| + \varepsilon_{i,j}\}}{\sum_{x'_i=1}^I \sum_{x'_j=1}^J \exp\{-\alpha|x'_i - x'_j| + \varepsilon_{i,j}\}} \quad (9)$$

where $\varepsilon_{i,j} \sim N(0, \sigma^2)$.^{13,14} We first analyze the distribution of test statistics.¹⁵ Then, we empirically compare the performance of our tests with the tests in Siow (2015).

3.1 Distribution of Test Statistics

Figure 1 shows the contour of $f(x_i, x_j)$ as (x_i, x_j) moves from (1, 5) to (5, 1) for $\alpha = 0, 0.1, 0.4$, and 0.8 . As α increases, assortative mating becomes stronger, with increased density along the diagonal where the difference in coordinates is 0.

Figure 2 shows the distributions of the pseudo-Wald test statistics for samples of 500, 2,000, and 10,000 when $\alpha = 0$, along with the χ^2_{16} distribution.¹⁶ The χ^2_{16} distribution shows little difference compared to the pseudo-Wald test statistics for samples of at least 2,000, but it stochastically dominates the pseudo-Wald test statistic distribution for a sample of 500.

¹³Note that $\sum_{x_i=1}^I \sum_{x_j=1}^J f(x_i, x_j) = 1$.

¹⁴Also, note that this is somewhat like a triangle kernel function with $\alpha = b^{-1}$ where b is the bandwidth (Kokonendji and Zocchi, 2010).

¹⁵We fix $\varepsilon_{i,j} = 0$ when analyzing the distribution.

¹⁶The degrees of freedom are $(M-1)(F-1)$.

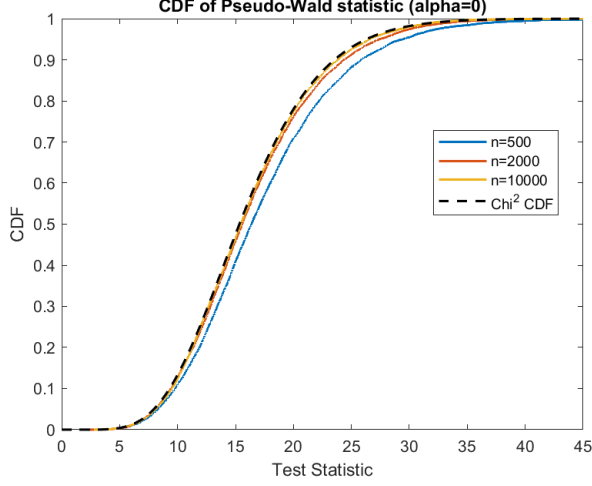


Figure 2: Distribution of Pseudo-Wald Test Statistic for $\alpha = 0$ (under the null)

The 5% critical value for the χ_{16}^2 distribution shows a small difference from the simulated Wald test statistic with a sample size greater than 2,000, but it is off by a meaningful amount relative to the simulated Wald test statistic distribution with a sample size of 500. The 5% critical value for a test statistic with a χ_{16}^2 distribution is 26.3, while the pseudo-Wald test statistics with sample sizes 500, 2,000, and 10,000 are 29.29, 27.03, and 26.39, respectively. These discrepancies arise because the χ_{16}^2 curve is an asymptotic approximation, while the simulated distribution reflects the finite-sample distribution of the pseudo-Wald statistic. In practice, this mismatch is a minor issue, since researchers can bootstrap the test's null distribution and use those empirical critical values instead of the χ_{16}^2 . In our empirical applications, we report p-values using bootstrap throughout our exercises. However, computing p-values using χ_k^2 with k degrees of freedom does not alter the conclusions.¹⁷

Figure 3 shows the distributions of the LR test statistic for samples of 500, 2,000, and 10,000 when $\alpha = 0$, along with the χ_{16}^2 distribution. The χ_{16}^2 distribution is almost identical to the LR test statistic distributions for all three sample sizes. The 5% critical value for a test statistic with a χ_{16}^2 distribution is 26.3, while, for the LR test statistic distributions with sample sizes 500, 2,000, and 10,000, they are 26.39, 26.35, and 26.36, respectively.

¹⁷We report results of the tests with χ^2 in Appendix D.

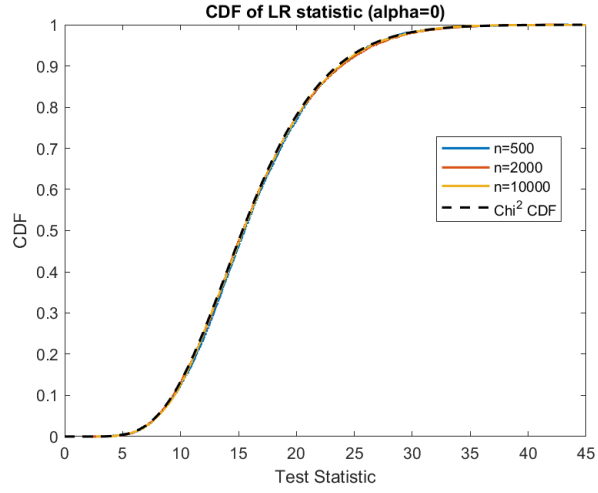


Figure 3: Distribution of LR Test Statistic for $\alpha = 0$ (under the null)

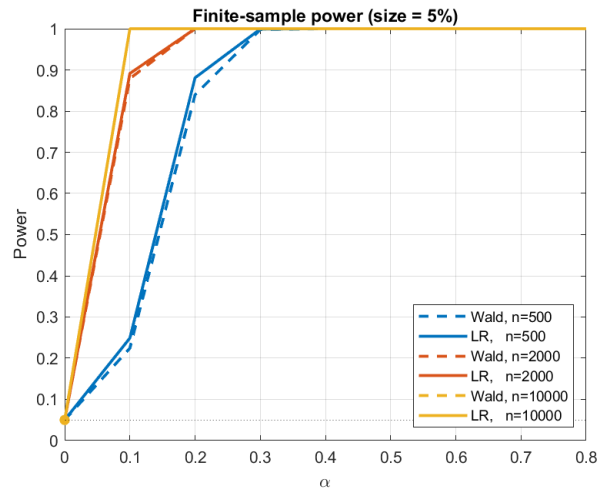


Figure 4: Power for Proposed Tests

Figure 4 shows the power functions for both test statistics for different values of α using the 5% critical values under the null hypothesis of $\alpha = 0$. Both test statistics have relatively weaker power for a small sample size of $N = 500$, but quickly gain power with a moderate sample size ($N = 2,000$).

3.2 Performance of the Tests with different α and n

We compare our Wald and Likelihood Ratio (LR) tests with the TP2 and DP2 tests in Siow (2015). The purpose of this exercise is to investigate whether each test can effectively reject PAM when assortative mating is sufficiently weak and whether each test can detect PAM when assortative mating is present.

The estimated assortative mating intensity α (defined in equation (9)) for the 2000 Census dataset is $0.798 \approx 0.8$.¹⁸ Starting from this value, we simulate the DGP and generate synthetic datasets with weaker assortative mating of $\alpha = 0.4, 0.1$, and 0. We use three levels of sample size: 500, 2,000, and 120,000. In this exercise, we fix σ_ε to 0.1. Then, we apply each of the four tests and compare their performance in testing PAM.

Table 1: Verdict for Positive Assortative Mating (PAM) by Four Methods

n	$\alpha = 0$				$\alpha = 0.1$				$\alpha = 0.4$				$\alpha = 0.8$			
	Wald	LR	TP2	DP2	Wald	LR	TP2	DP2	Wald	LR	TP2	DP2	Wald	LR	TP2	DP2
500	N	N	P	P	N	N	P	P	P	P	P	P	P	P	P	P
2,000	N	N	P	P	P	P	P	P	P	P	P	P	P	P	P	P
120,000	P	P	N	P	P	P	N	P	P	P	N	P	P	P	N	P

Notes: Wald and LR refer to the proposed Pseudo-Wald and Likelihood Ratio Tests, respectively. TP2 and DP2 refer to tests by Siow (2015). “P” indicates PAM, and “N” indicates no PAM.

Table 1 presents the results of applying our Wald and LR tests and the TP2 and DP2 of Siow (2015). N indicates no support for PAM, and P indicates the support for PAM. Since rejection of our tests versus Siow’s tests implies opposite conclusions about PAM, this notation is introduced to alleviate confusion. Table 2 reports the detailed results. It is

¹⁸We use the same data that is used in the empirical application of Siow (2015).

worth noting that $(\alpha, n) = (0.8, 120,000)$ closely matches the application of Siow (2015). Our exercise using the comparable (α, n) pair replicate their results: TP2 is rejected while DP2 is not rejected under the parameter/sample-size pair.

For weak assortative mating of $\alpha = 0$ and 0.1, the tests yield opposite results. Our proposed pseudo-Wald and LR tests fail to reject random matching for sample sizes of 500 and 2,000. On the other hand, TP2 and DP2 of Siow (2015) fail to reject their PAM restrictions (supporting PAM). The results suggest that under moderate sample sizes, our tests correctly do not find evidence for PAM when assortative mating intensity is weak ($\alpha=0.1$) or absent ($\alpha=0$). For large sample sizes, our Wald and LR tests reject random matching (supporting PAM), as does DP2 of Siow (2015).

All tests consistently support PAM when $\alpha = 0.4$ and $\alpha = 0.8$. This is consistent with findings of previous papers analyzing PAM around 2,000 (Greenwood et al., 2014; Chiappori et al., 2017). At the same time, when the sample size is very large, all four tests produce consistent results. Our Wald and LR tests reject the zero assortative mating. For Siow (2015), DP2, as a criteria for PAM, is not rejected, thus support PAM. TP2 is rejected, but again, this is consistent with their original results.

4 Empirical Applications

4.1 Assortative Mating on Predicted Wage

We test PAM using predicted wages based on within-gender wage quintiles from the CPS March 2000 sample ($N = 12,497$ married households). Compared with discrete measures, using wage provides a finer, continuous metric of assortative mating. Also, the rank measure is scale-invariant and robust to outliers.¹⁹ We employ a two-step estimation procedure

¹⁹Several studies have employed income rank as the measure of assortative mating (Fagereng et al., 2022; Holmlund, 2022; Almås et al., 2023).

Table 2: Test Statistics by N and α

N	$\alpha = 0.0$	$\alpha = 0.1$	$\alpha = 0.4$	$\alpha = 0.8$
Panel A: Proposed Pseudo-Wald				
500	20.36	27.94	119.54***	394.66***
2,000	29.30	52.40**	384.78***	1454.82***
120,000	786.10***	2195.02***	21350.92***	81096.90***
Panel B: Proposed LR Test				
500	19.23	25.99	110.31***	310.02***
2000	28.71	52.00***	382.76***	1219.64***
120000	782.29***	2225.41***	21820.48***	71478.45***
Panel C: TP2 of Siow (2015)				
500	15.69	11.21	9.17	8.63
2000	23.33	16.76	11.94	10.98
120000	638.38***	401.57***	333.50***	238.77***
Panel D: DP2 of Siow (2015)				
500	2.07	1.24	0.02	$7.8e-7$
2000	3.55	1.06	$9.8e-5$	$1.2e-6$
120000	92.21*	20.35	$1.3e-5$	$3.4e-5$

Note: * $p \leq 0.10$, ** $p \leq 0.05$, *** $p \leq 0.01$. In computing p , we use parametric bootstrap.

(Heckman, 1979) and use predicted log wages to construct our predicted wage measures.²⁰

Table 3 presents the contingency tables by (a) education and (b) predicted wage quintiles.²¹ Compared to the five-category education matrix, the wage-rank table exhibits greater dispersion from the main diagonal, reflecting within-education variation captured by rank measures. The diagonal components in the education matching table (Table 3 (a)) sum to 0.508, but those in the wage-rank matching table (Table 3 (b)) sum to only 0.339, indicating greater dispersion in the predicted wage matching table.

Table 5 reports the results of the four tests using predicted wage quintiles. The pseudo-Wald and likelihood-ratio (LR) statistics strongly reject the null of no assortative mating ($p < 0.001$), consistent with the strong PAM found in the literature (Greenwood et al., 2014;

²⁰We explain the procedure in Appendix C. See Carroll et al. (2021) for the more detailed explanations and the results of the estimation.

²¹While the literature often employs deciles (Fagereng et al., 2022), we use quintiles for fair comparison with educational assortative mating, which usually has five discrete measures. The results of our tests are robust to the number of matching indices.

Table 3: CPS 2000 Matching Table

(a) Matching Table by Education

Male Education	Female Education				
	Below High	High	Some Col	Bachelor	Graduate
Below High	0.101	0.048	0.018	0.003	0.001
High	0.040	0.191	0.075	0.021	0.004
Some Col	0.014	0.079	0.118	0.032	0.007
Bachelor	0.002	0.032	0.048	0.073	0.014
Graduate	0.001	0.008	0.016	0.033	0.025

(b) Matching Table by Predicted Wage Quintiles

Male Wage Quintile	Female Wage Quintile				
	Q1	Q2	Q3	Q4	Q5
Q1	0.101	0.050	0.034	0.011	0.004
Q2	0.054	0.040	0.060	0.030	0.016
Q3	0.028	0.042	0.047	0.056	0.027
Q4	0.013	0.039	0.030	0.058	0.060
Q5	0.005	0.029	0.029	0.044	0.093

Notes: Entries are matching probabilities. Rows denote male spouse’s category, and columns denote female spouse’s category.

Table 5: Comparison of Predicted Wage Quintile Example

Test	Statistic	p -value	Assortative Mating
Kang–Stern (pseudo-Wald)	6712.95	< 0.001	P
Kang–Stern (LR)	4420.734	< 0.001	P
Siow TP2	67.031	< 0.001	N
Siow DP2	13.101	< 0.001	N
Sample Size: 12,497			

Note: For proposed methods, the null hypothesis is zero assortative mating. For Siow’s methods, the null hypothesis implies PAM. In computing p , we use parametric bootstrap.

Chiappori et al., 2017). Siow’s TP2 and DP2 statistics reject the null of PAM, presumably because its restriction based methods are sensitive to the off-diagonal elements.

4.2 Assortative Mating in Same-Sex Marriage

Finally, we analyze same-sex married couples using the 2019 Census data. Table 6 presents the results. The sample size for same-sex married couples is 1,645, consisting of 695 male couples and 950 female couples. Our test supports PAM in the aggregated, male, and female samples. Both pseudo-Wald and LR tests strongly reject the null of zero assortative mating. Interestingly, Siow’s DP2 results indicate PAM only for male same-sex couples.²²

These results provide evidence of strong positive assortative mating in same-sex marriages. The simulation evidence in Section 3.2 demonstrates that our tests maintain appropriate size under the null and correctly fail to reject random matching when PAM is weak ($\alpha=0.1$) at comparable sample sizes ($n=500$ to $2,000$). The fact that our tests strongly reject random matching for same-sex couples (test statistics of 473.21 and 726.24, compared to critical values around 26-29) indicates that the intensity of educational sorting in same-sex marriages substantially exceeds weak PAM, suggesting educational homogamy patterns similar to or stronger than those observed in opposite-sex marriages (where $\alpha \approx 0.8$ from Section 3.2).

5 Conclusion

We develop empirical tests for PAM that are straightforward to implement and outperform existing methods. By adopting random matching as the null hypothesis, our approach aligns with the convention that the null represents an undesirable benchmark. Our tests provide a convenient diagnostic for PAM before researchers build richer structural models. Our pseudo-Wald test performs well, particularly when assortative mating is weaker and sample

²²In contrast, Ciscato et al. (2020) find weaker assortative mating for male same-sex couples using California samples between 2008-2012.

Table 6: Positive Assortative Mating for Same-Sex Married Couples

Sample	Test	Statistic	p -value	Assortative Mating
Both	pseudo-Wald	1237.40	0.001	P
Both	LR	676.64	<0.001	P
Both	TP2	3.62	0.507	P
Both	DP2	0	0.447	P
Both Sample Size: 1,645				
Male	pseudo-Wald	473.21	0.001	P
Male	LR	286.52	<0.001	P
Male	TP2	14.39	0.018	N
Male	DP2	4.2e-6	0.244	P
Male Sample Size: 695				
Female	pseudo-Wald	726.24	0.001	P
Female	LR	410.13	<0.001	P
Female	TP2	1.64	0.611	P
Female	DP2	1.7e-5	0.018	N
Female Sample Size: 950				

Note: For proposed methods, the null hypothesis is zero assortative mating. For Siow's methods, the null hypothesis implies PAM. In computing p , we use parametric bootstrap. For DP2 results of both samples, the statistic is less than the machine precision, so we report as 0.

sizes are moderate, providing advantages over existing tests. Empirical applications using CPS and Census data confirm that our methods effectively detect PAM on wage, confirming their practical value.

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Appendix

A Wald Test Derivations

In this appendix, we derive the formula to compute the elements of $\widehat{C(R)}$ in equation (8).

A.1 Variance of Local Log-Odds Ratios

Starting by $\log(\widehat{p}_{ij}^u)$, a first order Taylor series approximation for $\log \widehat{p}_{ij}^u$ is

$$\log \widehat{p}_{ij}^u \approx \log(p_{ij}) + \frac{\widehat{p}_{ij}^u - p_{ij}}{p_{ij}}.$$

Then, using the approximation,

$$\begin{aligned} \text{plim}(\log \widehat{p}_{ij}^u) &= \log p_{ij}, \\ n\text{Var}(\log \widehat{p}_{ij}^u) &= \frac{1 - p_{ij}}{p_{ij}}, \\ n\text{Cov}(\log \widehat{p}_{ij}^u, \log \widehat{p}_{kl}^u) &= -1 \quad \text{for } (i, j) \neq (k, l). \end{aligned}$$

Hence,

$$\begin{aligned} n\text{Var}(\widehat{R}_{ij}) &= n\text{Var}\left((\log \widehat{p}_{ij}^u + \log \widehat{p}_{i+1,j+1}^u) - (\log \widehat{p}_{i+1,j}^u + \log \widehat{p}_{i,j+1}^u) \right) \\ &= n\text{Var}(\log \widehat{p}_{ij}^u) + n\text{Var}(\log \widehat{p}_{i+1,j+1}^u) + n\text{Var}(\log \widehat{p}_{i+1,j}^u) + n\text{Var}(\log \widehat{p}_{i,j+1}^u) \\ &\quad + 2 \left[\text{Cov}(\log \widehat{p}_{ij}^u, \log \widehat{p}_{i+1,j+1}^u) - \text{Cov}(\log \widehat{p}_{ij}^u, \log \widehat{p}_{i+1,j}^u) \right. \\ &\quad \left. - \text{Cov}(\log \widehat{p}_{ij}^u, \log \widehat{p}_{i,j+1}^u) - \text{Cov}(\log \widehat{p}_{i+1,j+1}^u, \log \widehat{p}_{i+1,j}^u) \right. \\ &\quad \left. - \text{Cov}(\log \widehat{p}_{i+1,j+1}^u, \log \widehat{p}_{i,j+1}^u) + \text{Cov}(\log \widehat{p}_{i+1,j}^u, \log \widehat{p}_{i,j+1}^u) \right] \\ &= n\text{Var}(\log \widehat{p}_{ij}^u) + n\text{Var}(\log \widehat{p}_{i+1,j+1}^u) + n\text{Var}(\log \widehat{p}_{i+1,j}^u) + n\text{Var}(\log \widehat{p}_{i,j+1}^u) + 4 \\ &= \left(\frac{1 - p_{ij}}{p_{ij}} + \frac{1 - p_{i+1,j+1}}{p_{i+1,j+1}} + \frac{1 - p_{i+1,j}}{p_{i+1,j}} + \frac{1 - p_{i,j+1}}{p_{i,j+1}} \right) + 4 \\ &= \frac{1}{p_{ij}} + \frac{1}{p_{i+1,j}} + \frac{1}{p_{i,j+1}} + \frac{1}{p_{i+1,j+1}}. \end{aligned}$$

A.2 Covariance of Local Log-Odds Ratios

Recall the local log-odds ratio

$$R_{ij} = \log \hat{p}_{ij} + \log \hat{p}_{i+1,j+1} - \log \hat{p}_{i+1,j} - \log \hat{p}_{i,j+1}.$$

We now derive $\text{Cov}(R_{ij}, R_{i+1,j+1})$ by direct expansion. Using bilinearity of $\text{Cov}(\cdot, \cdot)$, write

$$\begin{aligned} \text{Cov}(R_{ij}, R_{i+1,j+1}) &= \text{Cov}\left(\underbrace{\log \hat{p}_{ij} + \log \hat{p}_{i+1,j+1} - \log \hat{p}_{i+1,j} - \log \hat{p}_{i,j+1}}_{R_{ij}}, \underbrace{\log \hat{p}_{i+1,j+1} + \log \hat{p}_{i+2,j+2} - \log \hat{p}_{i+2,j+1} - \log \hat{p}_{i+1,j+2}}_{R_{i+1,j+1}}\right) \\ &= \text{Cov}(\log \hat{p}_{ij}, \log \hat{p}_{i+1,j+1}) + \text{Cov}(\log \hat{p}_{ij}, \log \hat{p}_{i+2,j+2}) \\ &\quad - \text{Cov}(\log \hat{p}_{ij}, \log \hat{p}_{i+2,j+1}) - \text{Cov}(\log \hat{p}_{ij}, \log \hat{p}_{i+1,j+2}) \\ &\quad + \text{Cov}(\log \hat{p}_{i+1,j+1}, \log \hat{p}_{i+1,j+1}) + \text{Cov}(\log \hat{p}_{i+1,j+1}, \log \hat{p}_{i+2,j+2}) \\ &\quad - \text{Cov}(\log \hat{p}_{i+1,j+1}, \log \hat{p}_{i+2,j+1}) - \text{Cov}(\log \hat{p}_{i+1,j+1}, \log \hat{p}_{i+1,j+2}) \\ &\quad - \text{Cov}(\log \hat{p}_{i+1,j}, \log \hat{p}_{i+1,j+1}) - \text{Cov}(\log \hat{p}_{i+1,j}, \log \hat{p}_{i+2,j+2}) \\ &\quad + \text{Cov}(\log \hat{p}_{i+1,j}, \log \hat{p}_{i+2,j+1}) + \text{Cov}(\log \hat{p}_{i+1,j}, \log \hat{p}_{i+1,j+2}) \\ &\quad - \text{Cov}(\log \hat{p}_{i,j+1}, \log \hat{p}_{i+1,j+1}) - \text{Cov}(\log \hat{p}_{i,j+1}, \log \hat{p}_{i+2,j+2}) \\ &\quad + \text{Cov}(\log \hat{p}_{i,j+1}, \log \hat{p}_{i+2,j+1}) + \text{Cov}(\log \hat{p}_{i,j+1}, \log \hat{p}_{i+1,j+2}). \end{aligned}$$

Now use the multinomial-delta identity

$$\text{Cov}(\log \hat{p}_{ab}, \log \hat{p}_{cd}) = \frac{1}{N} \left(\frac{\mathbf{1}\{(ab) = (cd)\}}{p_{ab}} - 1 \right).$$

There is exactly one shared pair, $(ab) = (cd) = (i+1, j+1)$, contributing

$$\frac{1}{N} \left(\frac{1}{p_{i+1,j+1}} - 1 \right).$$

All other 15 pairs have $(ab) \neq (cd)$ and contribute $\pm \frac{1}{N}(-1)$ with the signs shown above. The sum

of those signs equals +1. Therefore,

$$\text{Cov}(R_{ij}, R_{i+1,j+1}) = \frac{1}{N} \left(\frac{1}{p_{i+1,j+1}} - 1 \right) + \frac{1}{N} = \frac{1}{N} \cdot \frac{1}{p_{i+1,j+1}}.$$

Other Results (i) With similar procedures,

$$N \text{Cov}(R_{ij}, R_{i,j+1}) = - \left(\frac{1}{p_{i,j+1}} + \frac{1}{p_{i+1,j+1}} \right), \quad N \text{Cov}(R_{ij}, R_{i+1,j}) = - \left(\frac{1}{p_{i+1,j}} + \frac{1}{p_{i+1,j+1}} \right),$$

and

$$\text{Cov}(R_{ij}, R_{i+1,j+1}) = \frac{1}{N} \cdot \frac{1}{p_{i+1,j+1}}.$$

B Data

2019 Current Population Survey (CPS) ASEC

We use 2000 and 2019 CPS for the wage and the same-sex marriage analysis, respectively. The working sample is defined by the following sequential selection rules:

1. **Age.** Keep only households in which both spouses are aged 16–64. This removes roughly 7–13 % of observations, depending on year
2. **Marital status.** Retain legally married couples; exclude widowed, divorced, never-married and co-habiting pairs This step eliminates about one-half of the raw sample in recent years.
3. **Employment class.** Exclude households in which either spouse is self-employed, works for government, or is on active military duty, following Siow (2015). The rule removes 10–15 % of couples each year
4. **Missing or implausible data.** Drop observations with missing schooling, race, region, or hours/weeks information and discard hourly wages below the year-specific real federal minimum wage

2000 Census

We replicate the selection rules used by Siow (2015). Because identical filters are applied, our Census contingency tables are identical to those in Siow (2015).

C Heckman Two-Step Wage Prediction

First, for each gender and year we estimate a probit

$$y_{ij}^* = X_{ij}\beta + \varepsilon_{ij}, \quad y_{ij} = 1\{y_{ij}^* > 0\},$$

where X_{ij} includes a quadratic in age, race dummies, four education dummies, region, metro status and, for women, an indicator of at least one child under 5 years old.

Second, on the working subsample we estimate

$$w_{ij} = Z_{ij}\gamma + \sigma_u \rho \lambda_{ij} + u_{ij},$$

where $Z_{ij} = X_{ij}$ excluding the young-child variable (an exclusion restriction) and $\lambda_{ij} = \varphi(X_{ij}\hat{\beta})/\Phi(X_{ij}\hat{\beta})$ is the inverse Mills ratio. Then, We compute

$$\tilde{w}_{ij} = \begin{cases} Z_{ij}\hat{\gamma} + \hat{\sigma}_u \hat{\rho} \lambda_{ij}, & \text{if } y_{ij} = 1, \\ Z_{ij}\hat{\gamma} - \hat{\sigma}_u \hat{\rho} \lambda_{ij}, & \text{if } y_{ij} = 0, \end{cases}$$

and use \tilde{w}_{ij} to generate quintiles of wage.

D Results of the Tests with $\chi^2_{(I-1)(J-1)}$

Table D.1: Predicted Wage Quintile Example with Chi-square Standard Errors

Test	Statistic	p -value	Assortative Mating
Kang–Stern (pseudo-Wald)	6712.95	< 0.001	P
Kang–Stern (LR)	4420.734	< 0.001	P
Siow TP2	67.031	< 0.001	N
Siow DP2	13.101	< 0.001	N
Sample Size: 12,497			

Note: For proposed methods, the null hypothesis is zero assortative mating. For Siow’s methods, the null hypothesis implies PAM. In computing p , we use parametric bootstrap for TP2 and DP2, but use chi-square p -values for pseudo-Wald and LR tests.

Table D.2: Positive Assortative Mating for Same-Sex Married Couples with Chi-square Standard Errors

Sample	Test	Statistic	p -value	Assortative Mating
Both	pseudo-Wald	1237.4	< 0.001	P
Both	LR	676.64	< 0.001	P
Both	TP2	3.62	0.507	P
Both	DP2	0	0.447	P
Both Sample Size: 1,645				
Male	pseudo-Wald	473.21	< 0.001	P
Male	LR	286.52	< 0.001	P
Male	TP2	14.39	0.018	N
Male	DP2	4.2e-6	0.244	P
Male Sample Size: 695				
Female	pseudo-Wald	726.24	< 0.001	P
Female	LR	410.13	< 0.001	P
Female	TP2	1.64	0.611	P
Female	DP2	1.7e-5	0.018	N
Female Sample Size: 950				

Note: For proposed methods, the null hypothesis is zero assortative mating. For Siow’s methods, the null hypothesis implies PAM. In computing p , we use parametric bootstrap for TP2 and DP2, but use chi-square p -values for pseudo-Wald and LR tests. For DP2 results of both samples, the statistic is less than the machine precision, so we report as 0.