The uniform general signed rank test and its design sensitivity

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August 6, 2024

Abstract

A sensitivity analysis in an observational study tests whether the qualitative conclusions of an analysis would change if we were to allow for the possibility of limited bias due to confounding. The design sensitivity of a hypothesis test quantifies the asymptotic performance of the test in a sensitivity analysis against a particular alternative. We propose a new, nonasymptotic, distribution-free test, the uniform general signed rank test, for observational studies with paired data, and examine its performance under Rosenbaum’s sensitivity analysis model. Our test can be viewed as adaptively choosing from among a large underlying family of signed rank tests, and we show that the uniform test achieves design sensitivity equal to the maximum design sensitivity over the underlying family of signed rank tests. Our test thus achieves superior design sensitivity, indicating it will perform well in sensitivity analyses on large samples. We support this conclusion with simulations and a data example, showing that the advantages of our test extend to moderate sample sizes as well.

1 Introduction

In the empirical study of causal effects, the use of standard statistical hypothesis tests, along with their concomitant $p$-values and confidence intervals, accounts only for the uncertainty introduced by sampling variability. However, in an observational study where treatment assignment has not been randomized, hidden biases due to unobserved confounding can be much larger than sampling uncertainty. As such, standard hypothesis tests may fail to be convincing if they assume the study is free of hidden bias, as a randomized experiment would be. A sensitivity analysis addresses this problem by formally testing whether the qualitative conclusions of a standard procedure would change if hidden bias of a certain magnitude were present (Rosenbaum, 2002).

When an investigator plans to run a sensitivity analysis, the choice of test statistic may no longer hinge solely on traditional measures such as Pitman efficiency (Pitman, 1948; Nikitin, 2011). In particular, an investigator may seek a test statistic that is least sensitive to hidden bias, and thereby most likely to successfully distinguish treatment effects from bias, rather than one that is most likely to detect treatment effects in the absence of hidden bias. Design sensitivity is one way to quantify this idea for a particular test statistic (Rosenbaum, 2004, 2010a). Design sensitivity complements Pitman efficiency and other conventional means of comparing tests.

Rosenbaum (2010b) shows that a test statistic that focuses on a subgroup strongly affected by treatment may achieve superior design sensitivity compared to a statistic that uses all observations. Rosenbaum (2012) shows that a particular test using only the observations of largest magnitude, Noether’s test (Noether, 1973), has excellent design sensitivity but poor power against small effects. Rosenbaum then proposes an adaptive test in which the $p$-value is the minimum $p$-value from two competing test statistics, corrected for multiple testing using the joint distribution of these two test statistics. This adaptive test is shown to get the best of both worlds, good power in small samples as well as high design sensitivity. In fact, the adaptive test attains the maximum design sensitivity of its two component tests. Rosenbaum and Small (2017) similarly propose an adaptive test that chooses from the better of two test statistics, one focused on a subgroup and one examining the entire population, with correction for multiple testing.

We examine a different test for paired data that chooses adaptively from a large, highly dependent family of test statistics. We control for multiple testing using a uniform concentration bound for the stochastic process formed by this family of test statistics. This permits choosing among as many test statistics as
we have observations, while achieving nonasymptotic, distribution-free error control. Our theoretical results characterize how this test achieves excellent design sensitivity, which can be infinite against normal alternative distributions, such that no matter the strength of confounding, the test will reject the null hypothesis of no effect with probability approaching one asymptotically. We are not aware of previous discussion of such behavior.

2 Background and notation

2.1 Rosenbaum’s sensitivity analysis model for matched pairs

We focus attention on observational studies in which study subjects receiving a treatment condition are paired to similar subjects receiving a control condition for analysis. For instance, in the study of fish consumption and mercury concentration in Section 6, respondents in a nutrition survey who consume 15 servings of fish per month are each paired to a respondent who consumes two or fewer servings per month, but has similar demographic attributes and smoking habits. We assume n such pairs have been constructed. The subjects in the ith pair have control potential outcomes $R_{Cij}$, treatment potential outcomes $R_{Tij}$, and treatment indicators $Z_{ij}$ for $j = 1, 2$ and $i \in [n]$ where $[n]$ is the set $\{1, \ldots, n\}$ and where $Z_{i1} + Z_{i2} = 1$ for all pairs $i$ by construction. Let $\mathcal{F}$ be the $\sigma$-field generated by all of the potential outcomes $(R_{Cij}, R_{Tij})_{i \in [n], j \in [2]}$.

A sensitivity analysis tests whether a positive conclusion of our study, specifically a rejection of Fisher’s sharp null hypothesis of no effect of treatment for any individual, holds up under the possibility of limited confounding (Rosenbaum, 2002). To operationalize this notion, for each $\Gamma \geq 1$ we define the sensitivity analysis null hypothesis $H_0(\Gamma)$ to assert, firstly, that $R_{T11} = R_{C11}$ and $R_{T12} = R_{C12}$ for all $i \in [n]$, which is Fisher’s sharp null, and, secondly, that conditional on $\mathcal{F}$, treatment assignments are independent between pairs, and that treatment probabilities within each pair $i$ are related by the following odds ratio bounds:

$$\frac{1}{\Gamma} \leq \frac{\Pr(Z_{i1} = 1 \mid \mathcal{F})}{\Pr(Z_{i1} = 0 \mid \mathcal{F})} \leq \frac{\Pr(Z_{i2} = 1 \mid \mathcal{F})}{\Pr(Z_{i2} = 0 \mid \mathcal{F})} \leq \Gamma.$$

At $\Gamma = 1$, this specifies that, within each pair, both units have the same (conditional) probability of treatment. This is equivalent to assuming that treatments are assigned completely at random within pairs, the standard assumption that leads to valid randomization inference in the absence of unmeasured confounding variables (Rosenbaum, 2002, §3.2). When $\Gamma > 1$, treatment probabilities may differ within a pair in ways we cannot observe. If differences in treatment probabilities within pairs are correlated with differences in potential outcomes, bias will arise in estimates of the effect of treatment, although the magnitude of such bias is limited by the sensitivity parameter $\Gamma$. An equivalent model, described in Rosenbaum (2002, §4.2), assumes the presence of an unmeasured confounding variable whose relationship to treatment is limited by parameter $\Gamma$, and whose relationship to the outcome variable is unrestricted, allowing it to be arbitrarily strong. Additional assumptions about the strength of the confounder-outcome relationship can be incorporated by an amplification of the sensitivity analysis as in Rosenbaum and Silber (2009).

Write $R_{ij}^{obs} = Z_{ij}R_{Tij} + (1 - Z_{ij})R_{Cij}$ for the observed outcomes and $Y_i = (Z_{i1} - Z_{i2})(R_{ij}^{obs} - R_{ij}^{obs})$ for the observed treated-minus-control difference in the ith pair. Under the null $H_0(\Gamma)$ we know that $Y_i \in \{|R_{C11} - R_{C12}|, -|R_{C11} - R_{C12}|\}$ and

$$\frac{1}{1 + \Gamma} \leq \Pr(Y_i > 0 \mid \mathcal{F}) \leq \frac{\Gamma}{1 + \Gamma}.$$

Here and in all future statements, we implicitly condition on the event $\{Z_{i1} + Z_{i2} = 1 \text{ for all } i \in [n]\}$, omitting it from the notation, and we also assume $\Pr(Y_i = 0) = 0$ for all $i$. In words, $H_0(\Gamma)$ asserts that there is no effect of treatment for any individual, but that treatment probabilities may differ within a pair in ways we cannot observe. Again, $\Gamma = 1$ rules out unobserved confounding, since $\Pr(Y_i > 0 \mid \mathcal{F}, Z_{i1} + Z_{i2} = 1) = 1/2$; if $\Gamma > 1$ and potential outcomes are correlated with unobserved differences in treatment probabilities, bias due to confounding will be present.

This sensitivity analysis model provides a method to conduct hypothesis tests that control type I error under limited confounding, but leaves open the choice of test statistic. To judge the relative benefits of different test statistics, we calculate power for various test statistics in a test of the sensitivity analysis null $H_0(\Gamma)$. 2
As with all power calculations, we must choose a particular alternative hypothesis of interest. We define an alternative hypothesis $H_1(G)$ for a distribution $G$ over $\mathbb{R}$, motivated by the following scenario, in which we hope to reject the null hypothesis with high power. Firstly, we let $R_{Cij}$ be an independent draw from some distribution $F$, for each $i \in [n], j = 1, 2$. Secondly, we specify $R_{Tij} = R_{Cij} + \tau_i$ for all $i, j$, where $\tau_i \in \mathbb{R}$ is drawn from some fixed distribution for each $i \in [n]$, and is constant within each pair. Finally, we require $\Pr(Z_{i1} = 1, Z_{i2} = 0 \mid \mathcal{F}) = \Pr(Z_{i1} = 0, Z_{i2} = 1 \mid \mathcal{F}) = 1/2$, with treatment (conditionally) independent between pairs. In words, there is a constant treatment effect within pairs and no hidden bias due to unequal treatment probabilities. The alternative hypothesis $H_1(G)$ is characterized by the induced distribution $G$ of the independent and identically distributed pair differences $Y_i = (Z_{i1} - Z_{i2})(R_{C1i} - R_{C2i}) + \tau_i$. Because there is no hidden bias under $H_1(G)$, the mean of this distribution, when the mean exists, is the average treatment effect $E(\tau_i)$. We explore the performance of the test when $\tau_i = \tau$ is constant across pairs, so that $G$ is the distribution of $R - R' + \tau$, where $R$ and $R'$ are independent draws from $F$; this distribution is symmetric about $\tau$. We also explore performance under a rare effects model in which $\tau_i$ is zero for most pairs and equal to some large value for a small proportion of pairs. In this case, $G$ is a mixture with most mass placed on some distribution symmetric about zero, and the remaining mass on a copy of the distribution shifted to the right.

When $\Gamma$ is sufficiently small, power tends to approach one as $n$ grows large under either alternative described above, but for most test statistics there is some threshold value of $\Gamma$ above which power instead tends to zero. This threshold is known as the design sensitivity and depends not only on the alternative but on the test statistic (Rosenbaum, 2010a, §14). Test statistics with large design sensitivities are desirable because they report the presence of a treatment effect with high probability under the alternative, even allowing for large amounts of unmeasured confounding.

Rosenbaum’s sensitivity analysis model is only one of many possible approaches. Fogarty (2019) discusses the performance of the Rosenbaum procedure for a weak null hypothesis rather than a sharp null. Cornfield et al. (1959) and Ding and VanderWeele (2016) develop sensitivity bounds on a relative risk using sensitivity parameters defined by the relative risk of exposure, or outcome, in categories of an unobserved confounding variable, Gilbert et al. (2003) give an approach based on logistic modeling, and Robins et al. (2000) and Yu and Gastwirth (2005) consider methods appropriate for time-varying treatments and doses of treatment respectively.

### 2.2 Sensitivity analysis with general signed rank statistics

Let $(Y_{(i)})$ denote the pair differences $(Y_i)$ ordered by absolute value, so that $|Y_{(1)}| \leq \cdots \leq |Y_{(n)}|$. A general signed rank statistic has the form

$$T_n = \sum_{i=1}^{n} \varphi \left( \frac{i}{n + 1} \right) 1_{Y_{(i)}>0}$$

for some score function $\varphi : (0, 1) \rightarrow [0, \infty)$. See Lehmann and Romano (2005, §6.10) and references therein for pointers to the long history of general signed rank tests; Rosenbaum (2010b) discusses their use in the context of sensitivity analysis. The score function $\varphi$ allows us to place more or less weight on pairs with relatively larger or smaller observed absolute differences. We will focus on the three score functions underlying the sign test, the Wilcoxon signed rank test, and the normal scores test, although we discuss an additional, descending score function in Appendix C. The sign test uses $\varphi(q) = 1$, so that all pairs...
contribute equally, regardless of rank. In this case $T_n$ simply counts the number of pairs in which the treated unit had a higher outcome. The Wilcoxon signed rank test is equivalent to $\varphi(q) = q$ (Rosenbaum, 2010b), so that pairs with larger effects contribute more to the test statistic. Finally, the normal scores test uses $\varphi(q) = \Phi^{-1}\{(1 + q)/2\}$, where $\Phi^{-1}$ is the standard normal quantile function, $\Pr\{Z \leq \Phi^{-1}(q)\} = q$ when $Z \sim N(0,1)$. This score function is the quantile function of the absolute value of a standard normal random variable, and this general signed rank test has high power when outcomes are drawn from a normal distribution (Lehmann and Romano, 2005, §6.9-6.10). All three score functions are illustrated in Figure 1.

The sensitivity analysis null hypothesis $H_0(\Gamma)$ does not specify a single distribution for the observables $(Y_i)$, but it does allow for easy construction of a single worst-case distribution for the test statistic $T_n$ in a one-sided test that rejects for $T_n$ sufficiently large, that is, a distribution that maximizes $\Pr\{T_n \geq a \mid F\}$ for any threshold $a$, among all distributions in $H_0(\Gamma)$. This worst-case distribution has the $n$ signs $\{1_{Y_i > 0}\}$ independent with $\Pr\{Y_i > 0 \mid F\} = \Gamma/(1 + \Gamma)$ for all $i \in [n]$ (Rosenbaum, 2002, §4.3). Write $c_{\alpha,n}(\Gamma)$ for the $1 - \alpha$ quantile of $T_n$ under this worst-case distribution, so that $c_{\alpha,n}(\Gamma)$ is the critical value of a one-sided, level-$\alpha$ sensitivity analysis testing $H_0(\Gamma)$ with test statistic $T_n$; the critical value may depend on $F$, in the case of ties. This critical value yields a valid test of the sensitivity analysis null hypothesis, and is not hard to approximate numerically or via the normal distribution. In Theorem 1 below, we build upon these ideas to define a uniform general signed rank test, deriving closed-form critical values that guarantee nonasymptotic Type I error control under the sensitivity null $H_0(\Gamma)$.

2.3 Power of a sensitivity analysis and design sensitivity

The power of a one-sided, level-$\alpha$ sensitivity analysis for a general signed rank test with statistic $T_n$ is $\Pr_1\{T_n \geq c_{\alpha,n}(\Gamma)\}$, where $\Pr_1(A)$ is the probability of an event $A$ under $H_1(G)$. The power is well-defined, since $H_1(G)$ specifies the distribution of $T_n$ completely, and depends on the level $\alpha$, the sample size $n$, the sensitivity parameter $\Gamma$, the alternative distribution $G$, and the score function $\varphi$. The design sensitivity (Rosenbaum, 2004, 2010a) of the test statistic $T_n$ is the value $\Gamma$ such that, as the sample size grows without bound, the power of a sensitivity analysis with parameter $\Gamma$ approaches one whenever $\Gamma < \Gamma$ and approaches zero whenever $\Gamma > \Gamma$:

$$\lim_{n \to \infty} \Pr_1\{T_n \geq c_{\alpha,n}(\Gamma)\} = \begin{cases} 1, & 1 \leq \Gamma < \Gamma, \\ 0, & \Gamma < \Gamma < \infty. \end{cases}$$

Formally, the design sensitivity depends on the level $\alpha$, the alternative distribution $G$ and the score function $\varphi$. In typical examples, including those considered below, the dependence on $\alpha$ vanishes; intuitively, the design sensitivity tends to delineate the point at which the worst-case mean of the test statistic under the sensitivity null $H_0(\Gamma)$ is equal to the mean under the alternative, and this is invariant to $\alpha$. It is clear from the definition that such a value is unique, if it exists, but existence must be proved as part of the derivation of design sensitivity, as in our Theorem 2. Note also that we may have $\Gamma = \infty$, which means that $\lim_{n \to \infty} \Pr_1\{T_n \geq c_{\alpha,n}(\Gamma)\} = 1$ for all $\Gamma \geq 1$; in words, the test has power approaching one against the given alternative regardless of how large a sensitivity parameter $\Gamma$ is chosen.

Proposition 2 of Rosenbaum (2010b) gives a formula for the design sensitivity of a general signed rank test whenever the score function $\varphi$ is piecewise continuous, nondecreasing and not identically zero:

$$\Gamma = \frac{\pi}{1 - \pi}, \quad \pi = \frac{\int_0^\infty \varphi \{G(y) - G(-y)\} dG(y)}{\int_0^1 \varphi(y) dy}.$$

Note that $G(y) - G(-y)$ is the CDF of $\mid Y \mid$ under $H_1(G)$. We see that the design sensitivity of a general signed rank test is determined precisely by the aspects of $\varphi$ and $G$ captured in the quantity $\pi$. In Theorem 2 and Theorem 3, we extend this result to characterize the design sensitivity of our uniform general signed rank test. Our conditions on $\varphi$, while not strictly more general, do allow for the normal score function, in contrast to Rosenbaum’s conditions.

For the sign test, $\varphi(q) \equiv 1$, we have $\int_0^1 \varphi(y) dy = 1$ and $\int_0^\infty \varphi \{G(y) - G(-y)\} dG(y)$ is exactly $\Pr(Y > 0)$ when $Y \sim G$. Hence $\pi = \Pr_1(Y > 0)$ (Rosenbaum, 2012, Proposition 1). Both $\pi$ and $\Gamma$ express the chance that a pair difference $Y$ gives evidence in favor of a positive treatment effect under the alternative with no hidden bias, as a probability and as an odds respectively.
3 A uniform general signed rank test

We now define a general class of uniform signed rank tests that operate on a family of related test statistics \( \{T_n(x)\}_{x \in (0,1)} \). Informally, our test rejects when any test statistic in the family lies above a corresponding modified critical value. These critical values are chosen to correct for multiplicity by taking advantage of the structure of the family of test statistics. The uniform nature of our test yields advantages in terms of design sensitivity, which we describe in Section 4.

For any \( \varphi : (0,1) \to [0,\infty) \), define the family of test statistics \( \{T_n(x)\}_{x \in (0,1)} \) by \( T_n(x) = 0 \) for \( x < 1/(n + 1) \), and for \( x \geq 1/(n + 1) \),

\[
T_n(x) = \sum_{i = \lceil(1-x)(n+1)\rceil}^{n} \varphi \left( \frac{i}{n + 1} \right) 1_{Y(i) > 0} = \sum_{i = \lceil(1-x)(n+1)\rceil}^{n} c_i 1_{Y(i) > 0},
\]

where we have defined \( c_i = \varphi \{i/(n + 1)\} \) for convenience. For each \( x, T_n(x) \) is a general signed rank statistic using the truncated score function \( \varphi_x(q) = \varphi(q)1_{q \geq 1 - x} \), which, roughly speaking, gives weight zero to pair differences whose absolute magnitudes lie below the \( 1 - x \) quantile. More precisely, it gives weight zero to pair differences below the \( (1 - x)(n + 1)/(n - 1) - 1/(n - 1) \) quantile, hence the condition \( T_n(x) = 0 \) for \( x < 1/(n + 1) \).

There are \( n \) distinct nontrivial test statistics in this family, \( T_n(k/(n + 1)) \) for \( k = 1, \ldots, n \), corresponding to the partial sums \( \sum_{i=k}^{n} c_i 1_{Y(i) > 0} \) for \( k = n, n - 1, \ldots, 1 \). Thus the family corresponds to a random walk with \( n \) steps and step sizes determined by the function \( \varphi(\cdot) \).

Despite the generality of our construction in terms of the score function \( \varphi \), our family always consists of truncated versions of the full test statistic. Such truncated statistics focus on subsets of the experimental sample with large observed effects \( |Y_i| \). As such, our test will tend to perform especially well against alternatives with large, rare effects.

Our uniform test will be characterized by a threshold function \( f_{\alpha,n}(x) \), the functional analogue of a critical value. Our test rejects whenever \( T_n(x) \geq f_{\alpha,n}(x) \) for any \( x \in (0,1) \). As in the fixed-sample case, there is a single worst-case distribution under \( H_0(\Gamma) \) which maximizes the probability of rejection. We defer the proof of Proposition 1 to Appendix D, along with most other proofs in this paper.

**Proposition 1.** Fix any threshold function \( f_{\alpha,n} : (0,1) \to \mathbb{R}_{>0} \). Among all distributions in \( H_0(\Gamma) \), the rejection probability \( \text{pr} \{ T_n(x) \geq f_{\alpha,n}(x) \text{ for some } x \in (0,1) \mid \mathcal{F} \} \) is maximized when \( \text{pr}(Y_i > 0 \mid \mathcal{F}) = \Gamma/(1 + \Gamma) \) for all \( i \in [n] \).

Under this worst-case distribution in \( H_0(\Gamma) \), each step of the random walk equals \( c_i \) with probability \( \rho_{\Gamma} = \Gamma/(1 + \Gamma) \) and zero otherwise; these steps are independent. The resulting mean and variance of \( T_n(x) \) are

\[
\mu_n(x) = E \{ T_n(x) \} = \rho_{\Gamma} \sum_{i = \lceil(1-x)(n+1)\rceil}^{n} c_i,
\]

\[
\sigma_n^2(x) = \text{var} \{ T_n(x) \} = \rho_{\Gamma} (1 - \rho_{\Gamma}) \sum_{i = \lceil(1-x)(n+1)\rceil}^{n} c_i^2.
\]

Our threshold function requires a tuning parameter \( x_0 > 0 \) to be fixed in advance, such that \( \sigma_n^2(x_0) > 0 \). If \( \sigma_n^2(x) = 0 \) for all \( x \), then we cannot choose a valid \( x_0 \), but in this case, \( T_n(x) = 0 \) with probability one for all \( x \) and the test statistic will be invariant to the data. We then construct the following high-probability uniform upper boundary on the random walk \( T_n(x) \):

\[
f_{\alpha,n}(x) = \frac{1}{\lambda_n} \left[ \log \left( \frac{1}{\alpha} \right) + \sum_{i = \lceil(1-x)(n+1)\rceil}^{n} \log \left( 1 + \rho_{\Gamma} (e^{c_i \lambda_n} - 1) \right) \right],
\]

where \( \lambda_n = \left( 2\log(\alpha^{-1})/\sigma_n^2(x_0) \right)^{1/2} \). For notational simplicity, we omit the dependence of \( f_{\alpha,n} \) on \( x_0 \).

**Theorem 1.** Under \( H_0(\Gamma) \), for any \( x_0 > 0 \) such that \( \sigma_n^2(x_0) > 0 \) and any \( \alpha \in (0,1) \),

\[
\text{pr} \{ T_n(x) \geq f_{\alpha,n}(x) \text{ for some } x \in (0,1) \mid \mathcal{F} \} \leq \alpha.
\]
Theorem 1 justifies rejecting the sensitivity null \( H_0(\Gamma) \) whenever \( T_n(x) \geq f_{\alpha,n}(x) \) for some \( x \in (0, 1) \), allowing us to adaptively choose a value of \( x \) after seeing the data, while retaining Type I error control at level \( \alpha \). We call this test a uniform signed rank test.

The idea is illustrated well by considering the sign test score function \( \varphi(q) = 1 \) for which the resulting truncated score functions \( \varphi_x \) are exactly the score functions used in Noether's test (Noether, 1973; Rosenbaum, 2012). For this choice of \( \varphi \), each \( T_n(x) \) is the count of successes in a series of \( n(1-x) \) Bernoulli trials or coin flips, each corresponding to a particular matched pair. When \( \Gamma > 1 \), the coins may be unfair; if we consider the most extreme distribution in \( H_0(\Gamma) \) in the sense of Proposition 1, each coin has success probability \( p_0 \) and \( T_n(x) \) is binomial. Rather than waiting to observe all \( n \) coin flips, or some fixed number of coin flips, before testing the fairness of the coins, our uniform test compares the number of successes to the testing threshold \( f_{\alpha,n}(x) \) after each successive coin flip and rejects if the threshold is ever crossed. Because the probability bound in Theorem 1 holds uniformly over all \( x \), the test controls Type I error properly. More generally, we can think of the uniform rank test as simultaneously conducting general signed rank tests with truncated score functions \( \varphi_x(q) = \varphi(q)1_{q \geq 1-x} \) for all values \( x = 1/(n + 1), \ldots, n/(n + 1) \), but with modified critical values \( f_{\alpha,n}(x) \), and choosing the value of \( x \) that yields the strongest inference. The critical value \( f_{\alpha,n}(x) \) is larger than the fixed-sample exact critical value \( c_{\alpha,n}(\Gamma) \) from Section 2.2, accounting for the uniformity of our test.

To give some intuition for the bound \( f_{\alpha,n}(x) \), we show that the following function yields a good asymptotic approximation to \( f_{\alpha,n}(x) \) for large \( n \):

\[
g_{\alpha,n}(x) = \mu_n(x) + \left\{ 1 + \frac{\sigma_n^2(x)}{\sigma_n^2(x_0)} \right\} \left\{ \frac{\sigma_n^2(x_0) \log\alpha^{-1}}{2} \right\}^{1/2}.
\]  

Indeed, Proposition 3 in Appendix D.3 shows that \( f_{\alpha,n}(x) = g_{\alpha,n}(x) + O(1) \) as \( n \to \infty \). The leading term in (5), \( \mu_n(x) \), is \( O(\alpha) \) and accounts for the drift of the random walk. The next term is \( O(\sqrt{n}) \) and accounts for the deviations of the random walk about its mean. As discussed in Appendix D.3, the parameter \( x_0 \) determines the value of \( x \) for which the boundary \( g_{\alpha,n}(x) \) is optimized, and this motivates the choice of \( \lambda_n \) in the definition of \( f_{\alpha,n} \). Theorem 1 would continue to hold with any choice \( \lambda_n > 0 \), but our choice enhances interpretation by linking \( \lambda_n \) to a point \( x_0 \in (0, 1) \) at which we desire the bound to be especially small. Proposition 3 also shows that \( f_{\alpha,n}(x) \leq g_{\alpha,n}(x) \) for all \( n \) and \( x \), so that \( g_{\alpha,n}(x) \) yields a conservative threshold function with a simpler analytical form, but the resulting test has slightly less power. We prove Theorem 1 in Appendix A using a technique closely related to the classical Cramér-Chernoff method (Cramér, 1938; Chernoff, 1952; Boucheron et al., 2013, §2.2; Howard et al., 2018).

## 4 Design sensitivity of the uniform test

We have shown that the uniform test may be thought of as simultaneously conducting general signed rank tests at all values of \( x \) with modified critical values \( f_{\alpha,n}(x) \). We might equivalently think of this as adjusting the significance level \( \alpha \) downwards, and to different values for different \( x \), in computing critical values for a sequence of general signed rank tests in such a way that the familywise error rate is controlled over all the individual tests. Compared to more general methods for adjusting multiple tests to control familywise error rates, such as the Bonferroni and Holm procedures, our test is expected to achieve tighter bounds because it explicitly accounts for the strong dependence among the test statistics.

Recalling that the design sensitivity of a general signed rank test (1) does not depend on \( \alpha \), we may wonder if the uniform test has design sensitivity equal to the supremum of the design sensitivities of the test statistics \( T_n(x), x \in (0, 1) \). This conclusion is not quite trivial, since the adjusted significance levels in the uniform test vary as \( n \) grows. Nonetheless, it turns out to be true. We prove this for score functions \( \varphi : (0, 1) \to [0, \infty) \) satisfying the following properties:

**Assumption 1.** \( \int_0^1 \varphi^2(x) \, dx < \infty \).

**Assumption 2.** \( \varphi \) is discontinuous on a set of Lebesgue measure zero.

**Assumption 3.** There exists a constant \( a \in [0, 1/2) \) such that \( \varphi \) is nonincreasing on \( (0, a) \), nondecreasing on \( (1 - a, 1) \), and bounded on \( (a, 1 - a) \).

**Assumption 4.** \( \int_{1-x}^1 \varphi(y) \, dy > 0 \) for all \( x > 0 \).
Theorem 2. Suppose \( \varphi \) satisfies Assumptions 1–4 above, and \( G \) is continuous. Then the design sensitivity of the corresponding uniform general signed rank test under \( H_1(G) \) is

\[
\tilde{\Gamma}_{\varphi, \text{unif}} = \sup_{x \in (0,1)} \tilde{\Gamma}(x) = \sup_{x \in (0,1)} \frac{\pi(x)}{1 - \pi(x)}, \quad \pi(x) = \int_0^\infty \varphi\{G(y) - G(-y)\} 1_{G(y) > G(-y) \geq 1 - x} dG(y). 
\]

The quantity \( \pi(x) \) in Theorem 2 is equivalent to the quantity \( \pi \) in (1) when the score function \( \varphi \) is replaced by the truncated score function \( \varphi_{x}(q) = \varphi(q) 1_{q \geq 1 - x} \). Recall from (1) that \( \pi \) is monotonically related to the design sensitivity of the fixed-sample test by the relationship \( \Gamma = \pi/(1 - \pi) \) (Rosenbaum, 2010b). Hence \( \tilde{\Gamma}(x) = \pi(x)/(1 - \pi(x)) \) gives the design sensitivity of a fixed-sample test with a truncated score function \( \varphi_{x} \), justifyng the interpretation of Theorem 2 as showing that the design sensitivity of the uniform test is equal to the supremum of the design sensitivities of the family of fixed-sample tests with truncated score functions.

Most of the work in the proof of Theorem 2 is captured by the following pair of lemmas, both proved in Appendix D. The first characterizes the asymptotic behavior of the boundary \( f_{\alpha,n}(x) \) as \( n \to \infty \), and the second generalizes a result of Sen (1970).

Lemma 1. If \( \varphi \) satisfies Assumptions 1–3 above, then for any \( x_0 > 0 \) such that \( \sigma_x^2(x_0) > 0 \), any \( \alpha \in (0,1) \), and any \( x \in (0,1) \), we have \( n^{-1} \mu_{\alpha}(x) \to \rho_\Gamma \int_1^{1-x} \varphi(y) dy \) and \( f_{\alpha,n}(x) = \mu_{\alpha}(x) + O(\sqrt{n}) \) as \( n \to \infty \).

Lemma 2. If \( \varphi \) satisfies Assumptions 1–4, and \( Y_1, Y_2, \ldots \) are drawn independently from the same continuous distribution \( G \), then with probability one,

\[
\lim_{n \to \infty} \frac{1}{n} \sum_{i=1}^{n} \varphi\left( \frac{i}{n+1} \right) 1_{Y_i > 0} = \int_0^\infty \varphi\{H(y)\} 1_{H(y) \geq 1-x} dG(y)
\]

of Theorem 2. Let \( H(x) = G(x) - G(-x) \) denote the distribution of \( |Y| \). Fix any \( x \in (0,1) \). Applying Lemma 2 to the truncated score function \( \varphi_{x}(q) = \varphi(q) 1_{q \geq 1-x} \) yields

\[
\lim_{n \to \infty} \frac{T_n(x)}{n} = \int_0^\infty \varphi\{H(y)\} 1_{H(y) \geq 1-x} dG(y) \tag{6}
\]

with probability one. Meanwhile, Lemma 1 implies that

\[
\lim_{n \to \infty} \frac{f_{\alpha,n}(x)}{n} = \rho_\Gamma \int_1^{1-x} \varphi(y) dy. \tag{7}
\]

Combining (7) with (6), we conclude that

\[
\text{pr}\{T_n(x) \geq f_{\alpha,n}(x)\} = \text{pr}\{n^{-1} T_n(x) \geq n^{-1} f_{\alpha,n}(x)\} \to 1
\]

if

\[
\int_0^\infty \varphi\{H(y)\} 1_{H(y) \geq 1-x} dG(y) > \rho_\Gamma \int_1^{1-x} \varphi(y) dy,
\]

that is, if \( \Gamma < \pi(x)/(1 - \pi(x)) \). Since the uniform test rejects whenever \( T_n(x) \geq f_{\alpha,n}(x) \) for some \( x \), it will reject with probability approaching one whenever \( \Gamma < \pi(x)/(1 - \pi(x)) \) for some \( x \in (0,1) \). By a similar argument, \( \text{pr}\{T_n(x) \geq f_{\alpha,n}(x)\} \to 0 \) if \( \Gamma > \pi(x)/(1 - \pi(x)) \), so the uniform test will reject with probability approaching zero if \( \Gamma > \pi(x)/(1 - \pi(x)) \) for all \( x \in (0,1) \). The conclusion follows.

Compare Theorem 2 to Proposition 1 of Rosenbaum (2012). Rosenbaum constructs an adaptive test choosing between two test statistics and achieving design sensitivity equal to the maximum of the two component tests. Theorem 2 shows that this principle may be extended to an infinite family of tests, in this case because the family possesses a dependence structure that allows us to construct an appropriate uniform bound.

All of the score functions introduced in Section 2.2 satisfy Assumptions 1–4. Most of these are obvious; it suffices to show that the normal score function satisfies Assumption 1.

Proposition 2. For the normal score function, \( \varphi(q) = \Phi^{-1}\{(1 + q)/2\} \), we have \( \int_0^1 \varphi^p(x) dx < \infty \) for all \( p \geq 1 \).
Figure 2: \( \pi(x) \) from Theorem 2 for sign and Wilcoxon signed rank score functions when \( G \) is standard normal, Laplace (double exponential) or Cauchy. First two panels show alternative with \( \tau = 1/2 \). Bottom panel shows rare effects model: 90\% of pairs have no treatment effect, \( \tau = 0 \) while 10\% of pairs have a large treatment effect, \( \tau = 5 \). See Figure 6 in Appendix F for the corresponding plot with the normal score function, which has \( \pi(x) \) qualitatively similar to that for the Wilcoxon signed rank score function.

Figure 2 plots \( \pi(x) \) as defined in Theorem 2, showing how the design sensitivity of a fixed-sample test varies with the truncation level \( x \). Recall that \( \pi(x) = \Gamma(x)/[1 + \Gamma(x)] \), so \( \pi(x) \) indicates design sensitivity on a \([0,1]\) scale rather than a \([0,\infty)\) scale. Each panel includes three alternative distributions \( G \) : normal with unit variance, Laplace (double exponential) with unit scale, and Cauchy with unit scale. In the first two panels, each distribution is centered at \( \tau = 1/2 \). The bottom panel shows a rare effects model in which \( G \) is a mixture of two of the given base distributions, one centered at zero receiving 90\% of the total mass, and the other centered at \( \tau = 5 \) receiving 10\% of the total mass. This simulates a situation in which 90\% of pairs have no treatment effect, while the remaining 10\% of pairs have a large constant treatment effect, so that the average treatment effect remains equal to 1/2.

The first two panels of Figure 2 show \( \pi(x) \) for the sign and Wilcoxon signed rank score functions introduced in Section 2.2; Figure 6 in Appendix F plots \( \pi(x) \) for the normal score function, which is qualitatively similar to \( \pi(x) \) for the Wilcoxon signed rank score function. For the sign test, \( \pi(x) \) is maximized at some value \( x < 1 \) under all distributions, although the increase is modest for the Laplace and Cauchy alternatives. This illustrates the benefits of truncation with the sign test. With the Wilcoxon signed rank test, we still see dramatic gains under a normal alternative, and indeed \( \pi(x) \uparrow 1 \) as \( x \downarrow 0 \) for all of our score functions under a normal alternative. This indicates we can achieve infinite design sensitivity under normal tails, a fact that we prove in Corollary 1. Under the Laplace or Cauchy alternatives, however, we do not see substantial gains in \( \pi(x) \) as \( x \) decreases from one for the Wilcoxon signed rank test; the same holds true for the normal score function. Under the heavier-tailed Laplace and Cauchy alternatives, it seems, score functions that place more weight on larger outcomes do not benefit from narrowing attention to a subset of pairs with the largest absolute differences. Informally speaking, the higher likelihood of large outliers means less information is present in the tails.

The \( \pi(x) \) functions in the bottom panel, computed under a rare effects model, tells a different story. Here, a uniform Wilcoxon signed rank test benefits from narrowing attention to a subset of pairs with large absolute differences regardless of the alternative distribution, although gains are still more modest for the Cauchy alternative than for the others. This confirms that, when effects are large and rare, a test which restricts attention accordingly will retain high power under more adversarial conditions and achieve a larger design sensitivity than a less-focused test.

Figure 2 makes it clear that the best choice of \( x \) depends on the alternative distribution \( G \) and the score function.
function in a complicated manner. The advantage of our uniform test is that it can adapt to the alternative at hand without prior knowledge, achieving performance equivalent to the oracle choice of \( x \) in terms of design sensitivity. It is also notable that all four score functions exhibit identical behavior near \( x = 0 \). The following result makes this observation precise whenever \( G \) is continuous with infinite support. We show that the limiting behavior of \( \pi(x) \) as \( x \downarrow 0 \) is often determined by the tails of \( G \) alone, not by the score function \( \phi \), and this may be used to bound the design sensitivity from below over a broad class of score functions.

**Theorem 3.** Suppose \( \phi \) satisfies Assumptions 1–4 above, and suppose \( G \) has positive density \( g(x) \) with respect to Lebesgue measure for all \( x \in \mathbb{R} \). Then

\[
\tilde{\Gamma}_{\phi, \text{unif}} \geq \liminf_{q \to \infty} \frac{g(q)}{g(-q)}.
\]

Plugging the normal density into Theorem 3 for \( g(x) \) confirms the fact suggested by Figure 2:

**Corollary 1.** If \( G = \mathcal{N}(\tau, \sigma^2) \), then \( \tilde{\Gamma}_{\phi, \text{unif}} = \infty \). That is, no matter what value of \( \Gamma \) is used in a sensitivity analysis with a uniform general signed rank test, the power under \( H_1(G) \) tends to one as \( n \to \infty \).

As also suggested by Figure 2, the uniform test does not achieve infinite design sensitivity for other distributions. The limit (8) is equal to \( \exp(2\mu/s) \) for the Laplace distribution with mean \( \mu \) and scale \( s \), while it is equal to one for the Cauchy distribution, hence Theorem 3 offers no meaningful guarantee for the Cauchy distribution.

### 5 Simulations

Figure 3 illustrates Theorem 2 with simulations under standard normal, Laplace and Cauchy alternatives; in each case \( \tau = 1/2 \), except for the rare effects panels in Figure 3, which uses the rare effects model described in Section 4. We simulate both fixed-sample tests and uniform tests based on Theorem 1 with the three score functions introduced in Section 2.2. All tests are run with level \( \alpha = 0.05 \) and plots are based on 10,000 replications.

Our results show that the improvements in performance for uniform tests expected from Figure 2 are in many cases realized in moderately-sized finite samples. Figure 3 compares power for each uniform test to the corresponding fixed-sample test based on the same score function, for a variety of different sample sizes. In the normal case, the uniform test does not indicate finite design sensitivity, as we expect from Corollary 1, and all uniform tests show substantial gains over their fixed-sample counterparts for \( n \geq 1,000 \). In the Laplace and Cauchy cases, the uniform sign test still shows gains, but uniform tests based on other score functions often fail to outperform their fixed-sample counterparts, as we expect from Figure 2; only at the very largest sample sizes do the uniform tests remain competitive in nearly all cases. However, in the rare effects case each uniform test improves substantially on its fixed-sample counterpart for \( n \geq 1,000 \), even with Cauchy noise. Though not shown here, the gains for normal and Laplace noise under the rare effects model are even more dramatic. Figure 7 in Appendix F gives additional power comparisons, while Appendix E contains simulation results under the null, illustrating the true Type I error rates of our uniform test in some representative settings.

Overall, the uniform sign test shows considerable promise for use in practice. It is competitive in all cases and is the strongest performer of the four tests considered here in a number of cases. This is particularly interesting since the fixed-sample sign test is arguably the least attractive among the fixed-sample tests we have considered. It seems the landscape of uniform general signed rank tests is qualitatively different from that of their fixed-sample counterparts.

### 6 Application: impact of fish consumption on mercury concentration

Mercury can be harmful to human health when concentrated too heavily in the bloodstream, and evidence suggests that consuming large amounts of fish can lead to elevated levels of mercury in the blood (Mahaffey
Figure 3: Comparison of simulated power for fixed-sample tests (dashed lines) vs. uniform tests (solid lines), based on 10,000 replications. Cauchy rare effects panels show the rare effects alternative model based on Cauchy distribution, as described in Section 4. Other panels show alternative model $H_1(G)$ with distribution $G$ as indicated, having center $1/2$ and unit scale. All tests use $\alpha = 0.05$. 
et al., 2004). To study the impact of a high-fish diet on mercury concentration we use data from the National Health and Nutrition Examination Survey (Centers for Disease Control and Prevention (CDC) National Center for Health Statistics (NCHS), 2017), which records information about respondents’ diets as well as analysis of blood samples, including a measure of total mercury concentration. Each of the 1,672 respondents from 2007 to 2016 who consumed an average of 15 or more servings of fish monthly was matched to a similar respondent consuming two or fewer servings per month. Respondents were matched within the same two-year period, and pairs were chosen by optimal matching on a robust Mahalanobis distance (Rosenbaum, 2010a, §8.3) computed from respondent age, household income, gender, ethnicity, cigarettes smoked per day, and indicators for high school graduation, missing high school graduation status, and smoking more than 7 cigarettes per day. A propensity score was fit to these same variables, and matches were required to obey a propensity score caliper of 0.2 standard deviations (Rosenbaum and Rubin, 1985). The final matched sample of 1,672 pairs achieved close balance on covariates; see Table 2 in Appendix F. For matching, we used R packages rcbalance and optmatch with package cobalt used for balance checking (Pimentel, 2016; Hansen and Klopfer, 2006; Greifer, 2018). For more discussion on the optimal construction of matched samples see Rosenbaum (1989), Hansen (2004), Zubizarreta et al. (2014), and Pimentel et al. (2015).

Although the balance on observed variables in Table Table 2 is very close, individuals with high-fish diets may differ from individuals with low-fish diets on many unobserved attributes correlated with mercury levels. Accordingly, we are interested not only in whether a test assuming an absence of unobserved confounders rejects the null hypothesis, but in how sensitive such a result is to potential bias from unobserved confounders.

In each of the 1,672 pairs formed, we computed the difference in total mercury concentration, in micrograms per mole, between the respondent with the high-fish diet and the respondent with the low-fish diet. The average concentrations for matched individuals with high-fish diets and low-fish diets were 3.76 and 1.02 respectively, yielding an average pair difference of 2.73 micrograms per mole. We next tested the sharp null of no effect of treatment in any pair. Mercury measurements were rounded to two decimal places leading to some ties, so for each test we used a minor modification of our procedure described in Appendix B to account for ties. We set $x_0 = 1/3$ for the uniform bound. Setting $x_0$ too large leads to slight conservatism, as shown in Figure 5 in Appendix E, while setting $x_0$ too small optimizes for a test using only a small fraction of the data. Our choice simply balances between these two extremes. In other settings, prior information about the distribution of outcomes and treatment effects may inform the choice of $x_0$ (see, e.g., Figure 2). The methods and data used for this analysis will be made available to readers via the R package uniformrank.

The first three columns of Table 1 show the results of sensitivity analysis in the matched data for the three general signed rank tests considered in this paper. For each of these test statistics, the naïve test with $\Gamma = 1$ produces results highly significant at the 0.05 level. The numbers in the table describe the smallest amount of unmeasured bias necessary to explain the observed effects assuming there is no true effect of treatment, that is, the minimum value of $\Gamma$ at which we fail to reject the sensitivity analysis null. For example, the fixed-sample sign test ceases to reject the null when we allow for an unobserved confounder that increases the odds of a high-fish diet by a factor of $\Gamma = 4.82$; in contrast, the uniform sign test requires an unobserved confounder that increases the odds of a high fish diet by $\Gamma = 10.51$ before it ceases to reject.

| Score function | 1,672 pairs | 190 pairs |
|----------------|------------|-----------|
|                | Fixed-sample | Uniform | Fixed-sample | Uniform |
| Sign           | 4.82       | 10.51    | 3.72        | 8.29    |
| Wilcoxon Signed Rank | 8.06       | 10.47    | 6.04        | 8.09    |
| Normal Scores  | 8.55       | 10.36    | 6.52        | 7.95    |

Table 1: Sensitivity analysis for matched data. Each cell of the table represents a different test statistic for testing the null of no effect of a fish diet on mercury concentration; the first two columns give results for the full matched sample of 1,672 pairs, while the third and fourth columns give results for the smaller sample from 2015-2016 alone. The number in each cell is the smallest degree of unmeasured confounding $\Gamma$ necessary in the sensitivity analysis model before the test no longer rejects at the $\alpha = 0.05$ level.

Repeating the same test many times with different test statistics, as in Table 1, may lead to problems with Type I error control. In practice one should select a single test statistic in advance, possibly based on a pilot sample (Heller et al., 2009). We show the results of several tests here to illustrate the impact of the choice of test statistic and complement the discussion in Section 5.

Several interesting patterns are clear in the full-sample results of Table 1. First, regardless of the score function used, the uniform version of the test is less sensitive to bias from unmeasured confounding than the
fixed-sample version. This pattern is consistent with Theorem 2, which tells us that in large samples the uniform test should perform at least as well as any fixed-sample test it incorporates. Second, the performance of the uniform test across score functions varies much less than the performance of the fixed-sample version across score functions. In particular, the sign test performs substantially worse than any other test examined in the fixed-sample case, but is comparable to the other score functions in the uniform setting, corroborating the evidence from simulations in Section 5. In this dataset, as in the simulations, adapting over many different truncated statistics appears to compensate for the deficiencies of the fixed-sample sign test.

Finally, we consider the role of sample size by analyzing the subset of the matched dataset consisting of respondents from the final two-year period (2015-2016), a total of 190 pairs. The final two columns of Table 1 repeat the analysis for this smaller dataset. The same pattern of results is observed, with the uniform test outperforming the fixed-sample test for each score function, and the sign test performing best among uniform tests. Although the benefits of uniform testing articulated in Theorem 2 relate to asymptotic performance in large samples, uniform tests may also offer substantial improvement in datasets of only moderate size.

7 Conclusion and future work

We have focused on continuous outcomes, although minor modifications, described in Appendix B, can handle cases when ties are present but rare as in Section 6. However, outcomes with relatively few unique values require alternative methodology. In such cases, the random walk $\{T^*_n(x)\}_{x \in (0,1)}$ for tied data defined in Appendix B will have few steps, at most the number of unique values of the outcome, with each step comprised of many individual observations, namely all those pairs with absolute outcome equal to a given value. In the sequential analysis literature, such random walks are handled well by group sequential designs (Pocock, 1977; O’Brien and Fleming, 1979; Lan and DeMets, 1983; Jennison and Turnbull, 2000). An application to uniform general signed rank tests may yield promising future results.

Another interesting avenue is theoretical properties besides design sensitivity for uniform general signed rank tests. Rosenbaum (2015) characterizes the Bahadur efficiency of sensitivity analyses based on signed rank tests, allowing comparison of asymptotic performance for different test statistics at values of $\Gamma$ strictly smaller than the design sensitivity. Deriving Bahadur slopes for uniform signed rank tests would shed light on their relative performance at small values of $\Gamma$. Additionally, Lehmann and Romano (2005, §6) discuss the locally most powerful property of general signed rank tests against particular families of alternatives determined by the function $\varphi$. The uniform test chooses adaptively from among a family of related $\varphi$ functions, and the implications for local optimality in the sense discussed by Lehmann and Romano deserve attention.

8 Acknowledgments

We thank Eli Ben-Michael for the conversation that sparked this project. Howard thanks Office Of Naval Research (ONR) Grant N00014-15-1-2367.

This is a pre-copyedited, author-produced version of an article accepted for publication in Biometrika following peer review. The version of record:

Howard, S.R., and Pimentel, S.D. (2021). The uniform general signed rank test and its design sensitivity. Biometrika 108, 381-396.

is available online at: https://academic.oup.com/biomet/article-abstract/108/2/381/5911093.

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A Proof of Theorem 1

Throughout the proof we condition on $\mathcal{F}$ implicitly in probability statements. Let $S_i = 1_{Y_{(i)}>0}$ for $i \in [n]$, so that $T_n(k/(n+1)) = \sum_{i=n+1-k}^{n} c_i S_i$ for each $k \in [n]$. By Proposition 1, under the worst-case distribution in $H_0(\Gamma)$, $(S_i)_{i \in [n]}$ are distributed as $n$ i.i.d. Bernoulli($\rho_{T}$) random variables. The moment-generating function of $c_i S_i$ is

$$E(e^{\lambda c_i S_i}) = 1 + \rho_{T}(e^{\lambda} - 1)$$

(9)

for all $\lambda \in \mathbb{R}$. Now define $(L_k)_{k=0}^{n}$ by $L_0 = 1$ and, for $k \in [n]$,

$$L_k = \exp\left[\lambda_n T_n\left(\frac{k}{n+1}\right) - \sum_{i=n+1-k}^{n} \log\left(1 + \rho_{T}(e^{\lambda_i} - 1)\right)\right] = \prod_{i=n+1-k}^{n} \frac{e^{\lambda_i c_i S_i}}{1 + \rho_{T}(e^{\lambda_i} - 1)}.$$  

(10)

From (9) and (10) we see that $E(L_k | S_n, S_{n-1}, \ldots, S_{n+2-k}) = L_{k-1}$, so $L_k$ is a nonnegative martingale with respect to the natural filtration defined by $S_n, S_{n-1}, \ldots, S_1$. By Ville’s maximal inequality for nonnegative supermartingales (Ville, 1939; Durrett, 2013, Exercise 5.7.1),

$$\alpha \geq \text{pr}\{L_k \geq \alpha^{-1} \text{ for some } k \in [n]\} = \text{pr}\left\{T_n\left(\frac{k}{n+1}\right) \geq f_{\alpha,n}\left(\frac{k}{n+1}\right) \text{ for some } k \in [n]\right\}$$

$$= \text{pr}\left\{T_n(x) \geq f_{\alpha,n}(x) \text{ for some } x \in \left\{\frac{1}{n+1}, \frac{2}{n+1}, \ldots, \frac{n}{n+1}\right\}\right\}$$

$$= \text{pr}\{T_n(x) \geq f_{\alpha,n}(x) \text{ for some } x \in (0,1]\}.$$  

The final equality follows since values $x = 1/(n+1), 2/(n+1), \ldots, n/(n+1)$ capture all distinct values of both $T_n(x)$ and $f_{\alpha,n}(x)$ for $x \geq 1/(n+1)$; adding the region $0 < x < 1/(n+1)$ does not change the overall probability since $T_n(x) = 0$ here and $f_{\alpha,n}(x)$ is strictly positive.
B  Handling ties

Under the assumption that outcomes are drawn from a continuous distribution, ties among outcome observations occur with probability zero. In practice however, tied outcome data may arise in a variety of settings. In this section we discuss how to adapt the results of the paper to the setting of ties.

Let \( Y_{(1)}, \ldots, Y_{(n)} \) be the outcome data ordered in any way so that \( |Y_{(1)}| \leq |Y_{(2)}| \leq \ldots |Y_{(n)}| \). This ordering is not unique when ties are present; in such cases, choose one such ordering arbitrarily. We may still apply the methods described in the paper directly to conduct a test. The test statistic and the uniform bound are clearly defined given our chosen ordering of outcomes, and Theorem 1 holds since no aspect of its proof depends on the absence of ties. We remark that it is reasonable to expect \( \text{pr}(Y_i = 0) > 0 \) in the presence of ties; however, this only reduces \( \text{pr}(Y_i > 0 | \mathcal{F}) \), so Proposition 1 and Theorem 1 continue to hold.

However, the version of our uniform test in Theorem 1 depends on the ordering we choose, perhaps arbitrarily, for \( (Y_{(i)}) \). To remove this undesirable feature of the procedure, we may instead use a generalization of \( T_n(x) \) that is invariant to the specific choice of ordering in the tied setting. We write \( T_n^*(x) \) for this new test statistic. The intuition for \( T_n^* \) comes from recognizing that when ties are present, one or more test statistics in the family \( \{T_n(x)\}_{x \in (0,1)} \) are partial sums that include some terms with a particular absolute value but exclude others with the same absolute value, and that the scores associated with these terms may be different from one another. We obtain the family \( \{T_n^*(x)\}_{x \in (0,1)} \) by replacing the score for each tied value by the average of scores for all indices involved in the tie, and by adding all these terms together to the partial sum rather than allowing partial sums that contain some terms but not all.

Formally, define \( J_i = \{ j \in [n] : |Y_{(j)}| = |Y_{(i)}| \} \), the set of ranks with equal absolute pair differences to the \( i \)th ranked pair. Let \( m(i) = \min J_i \), the lowest rank within the tied group containing the \( i \)th ranked pair. Now define the test statistic

\[
T_n^*(x) = \sum_{i: m(i) \geq (1-x)(n+1)} c_i^* 1_{Y_{(i)}>0}, \quad c_i^* = |J_i|^{-1} \sum_{j \in J_i} \varphi \left( \frac{j}{n+1} \right).
\]

When a group of pairs share the same absolute outcome value, this test statistic treats all these pairs as a single unit, including either all or none of them in the partial sum, and assigning each a score equal to the average score across all members in the tied set. If there are only \( k < n \) distinct absolute outcome values, there are only \( k \) distinct nontrivial values for \( T_n^*(x) \); however, if no ties are present, \( T_n^* \) is identical to \( T_n \).

We obtain a uniform boundary for \( T_n^*(x) \) by substituting \( c_i^* \) for \( c_i \) in (3) and (4), yielding new quantities \( \sigma_n^*, f_{\alpha,n}^* \) and \( f_{\alpha,n}^* \). In the absence of ties, the quantities \( \sigma_n^*, f_{\alpha,n}^* \) coincide with the original quantities \( \sigma_n^*, f_{\alpha,n} \). However, the quantities \( (c_i^*)_{i=1}^n \) are random, unlike \( (c_i) \), hence \( \sigma_n^* \) and \( f_{\alpha,n}^* \) are random as well. This requires no real change to the analysis, since these quantities are \( \mathcal{F} \)-measurable and we condition on \( \mathcal{F} \) throughout the proof of Theorem 1. As the reader may expect, the new boundary \( f_{\alpha,n}^* \) yields a valid uniform test of the sensitivity null \( H_0(\Gamma) \) using the order-invariant test statistic \( T_n^* \).

**Theorem 4.** Under \( H_0(\Gamma) \), for any \( \mathcal{F} \)-measurable \( x_0 > 0 \) such that \( \sigma_n^2 \) \( x_0 > 0 \) a.s., and any \( \alpha \in (0,1) \), we have \( \text{pr}\{ T_n^*(x) \geq f_{\alpha,n}^* (x) \text{ for some } x \in (0,1) \mid \mathcal{F} \} \leq \alpha \).

**Proof.** Write \( \bar{T}_n(x) = \sum_{i=\lceil (1-x)(n+1) \rceil}^{n} c_i^* 1_{Y_{(i)}>0}; \) this is the same as \( T_n(x) \) with \( c_i^* \) substituted for \( c_i \). Repeating the proof of Theorem 1 with \( \sigma_n^* \) and \( f_{\alpha,n}^* \) in place of their unstarred counterparts, we obtain

\[
\text{pr}\{ \bar{T}_n(x) \geq f_{\alpha,n}^* (x) \text{ for some } x \in (0,1) \mid \mathcal{F} \} \leq \alpha. \tag{11}
\]

Since \( m(i) \leq i \) and \( c_i \geq 0 \) for all \( i \), we have \( T_n^*(x) \leq \bar{T}_n(x) \) for all \( x \), which implies the result together with (11).

\[\square\]

C  The redescending score function

In this section we discuss an additional, redescending score function, defined as follows in terms of three positive integer parameters \( m \leq l \leq m \):

\[
\varphi(q) = \sum_{l=m}^{\infty} \frac{1}{m} \binom{m}{l} q^{l-1} (1-q)^{m-l}.
\]
The function’s name reflects its shape: it rises as \( q \) increases from zero, as with the Wilcoxon signed rank score and normal score functions do, but falls back to zero as \( q \) approaches one, unlike the score functions in the main manuscript. The resulting statistic puts more weight on pairs with larger absolute differences, but excludes the most extreme outlying observations. In some cases it may be preferable to remove potential outliers from the data in advance rather than to use a redescending score function; for more discussion, see Huber and Ronchetti (2009).

The score function for general \((m, m, \overline{m})\) is due originally to Rosenbaum (2011), who introduced a family of test statistics defined by three positive integers \(m \leq \overline{m} \leq m\) where \(m\) is no greater than the overall sample size \(n\). Each statistic takes a sum over all size-\(m\) subsets of observations; within each subset, observations are ranked by absolute magnitude and the number of positive differences among observations with ranks \(m\) through \(\overline{m}\) inclusive is added to the sum. This family includes the sign statistic \((m = m = \overline{m} = 1)\) and a close approximation to the Wilcoxon signed rank statistic \((m = m = \overline{m} = 2)\) as special cases. These statistics are general signed rank statistics, and although their exact score functions may be computationally intensive and depend on sample size in general, Rosenbaum gives (12) as a convenient asymptotic approximation to the scores. The redescending behavior described above occurs whenever \(\overline{m} < m\), and Rosenbaum (2014) studied the specific setting \((m, m, \overline{m}) = (20, 12, 19)\).

Using the redescending score function within the uniform general signed rank test as we have defined it in (2) is not problematic from a technical perspective, but the resulting test runs contrary to the goal of the redescending function. In particular, the truncated score functions \(\phi(q) 1_{q \geq 1-x}\) will eventually restrict attention to the most extreme pair differences, which the redescending score function is designed to emphasize less relative to other observations; this is in contrast to the other score functions discussed in the manuscript, which are all nondecreasing. A more natural generalization of the truncation idea in the redescending case is to truncate regions of the domain associated with lower score \(\varphi(x)\) first. We now show how to generalize the test statistic to truncate in this manner.

Let \(D\) be a mapping between real numbers in the closed unit interval and subsets of the unit interval such that \(D(0) = \{\}\), \(D(1) = [0, 1]\), and \(D(x_1) \subseteq D(x_2)\) whenever \(x_1 < x_2\). We now reformulate the test statistic and the uniform bound as functions of both \(x\) and \(D\):

\[
T_n(x; D) = \sum_{\{i: i/(n+1) \in D(x)\}} \varphi\left(\frac{-i}{n+1}\right) 1_{p_i > 0}, \tag{13}
\]

\[
f_{\alpha,n}(x; D) = \frac{1}{\lambda_n} \left[ \log \left(\frac{1}{\alpha}\right) + \sum_{\{i: i/(n+1) \in D(x)\}} \log \{1 + \rho_T(e^{c_i \lambda_n} - 1)\} \right], \tag{14}
\]

with a similar modification to the sum in \(\sigma_n^2(x_i)\) which appears in the definition of \(\lambda_n\). Intuitively, \(D(x)\) defines an order of truncation for the \(n\) observed ranks. Definitions (2) and (4) are special cases obtained by choosing \(D(x) = [1 - x, 1]\), which corresponds to truncating the observations with smallest absolute ranks first. For bounded redescending score functions such as (12), we suggest the following alternative choice of \(D\):

\[
D(x) = \left\{ q : \varphi(q) > (1 - x) \max_{0 < q < 1} \varphi(q) \right\}.
\]

This \(D\)-function specifies that observations with the lowest scores will be trimmed first. For redescending score functions, this means specifically that the largest observations will be trimmed before certain intermediate observations, a desirable property in cases where the extreme observations may be unreliable.

We now discuss how to generalize the theory in the main manuscript to give results for test statistic (13) and boundary (14). For any given sample, function \(D(x)\) defines a specific order of truncation among the \(n\) observations. Taking any \(i, j \in [n]\), \(i \neq j\), we say that \(i <_D j\), or \(i\) is truncated later than \(j\), if there exists some \(x \in (0, 1)\) such that \(i \in D(x)\) and \(j \notin D(x)\). Note that \(i <_D j\) and \(j <_D i\) cannot both hold since \(D(x_1) \subseteq D(x_2)\) for any \(x_1 < x_2\). If neither \(i <_D j\) nor \(j <_D i\) then \(i \sim_D j\), meaning that \(i\) and \(j\) lie in the same equivalence class with respect to truncation.

Generalizing Theorem 1 to hold for \(T_n(x; D)\) and \(f_{\alpha,n}(x; D)\) in place of \(T_n(x)\) and \(f_{\alpha,n}(x)\) is straightforward. In fact, if no pair of observations \(i, j \in [n]\) lies in the same equivalence class with respect to truncation, so that either \(i <_D j\) or \(j <_D i\) in all cases, then the arguments require no changes except for substituting the more general definitions, since \(T_n(x; D)\), like \(T_n(x)\), is a random walk with \(n\) distinct partial sums.
If there exist one or more pairs of observations $i, j \in [n]$ such that $i \sim_D j$, then $T_n(x; D)$ does not have $n$ distinct partial sums; since some observations are always truncated together, there will only be $k$ distinct partial sums for some $k < n$. Since the proof of Theorem 1 relies on a random walk with $n$ distinct partial sums, we construct a new random walk with $n$ distinct partial sums, $k$ of which are the partial sums of $T_n(x; D)$. Let $\pi : [n] \to [n]$ be a permutation of the indices such that $\pi(i) < \pi(j)$ whenever $i <_D j$. Define

$$T_n(j; D) = \sum_{\{i: \pi(i) \leq \pi(j)\}} \varphi\left(\frac{i}{n+1}\right) 1_{Y_{(i)} > 0},$$

$$f_{\alpha,n}(j; D) = \frac{1}{\lambda_n} \left[ \log\left(\frac{1}{\alpha}\right) + \sum_{\{i: \pi(i) \leq \pi(j)\}} \log \{1 + \rho(\exp^{\alpha/n} - 1)\} \right].$$

The dependence on $D$ here is through the restriction that the ordering $\pi$ respect the ordering given by $\prec_D$. Consider the set $I = \{i \in [n] : \pi(i) < \pi(j) \text{ or } j <_D i \text{ for all } j \in [n] \setminus i\}$. Set $I$ contains exactly one observation from each of the $k$ equivalence classes, choosing the first element by ordering $\pi$ in equivalence classes with more than one element, and the values $\{T_n(i; D) : i \in I\}$ are exactly the $k$ distinct partial sums of $T_n(x; D)$. Thus the partial sums of $T_n(x; D)$ form a subset of the partial sums $\{T_n(j; D) : j \in [n]\}$. In addition, the values $\{f_{\alpha,n}(i; D) : i \in I\}$ capture all distinct values of $f_{\alpha,n}(x; D)$.

To finish the proof, it suffices to repeat our previous arguments for Theorem 1 replacing $T_n(x)$ and $f_{\alpha,n}(x)$ with $T_n(j; D)$ and $f_{\alpha,n}(j; D)$. Because the individual tests performed by $T_n(j; D)$ at different values $j$ are a superset of the individual tests performed by $T_n(x; D)$ at different values $x$, the rejection event for the latter uniform test is a subset of the rejection event for the former, and control of Type I error for the latter guarantees control of Type I error for the former.

Finally we comment on adaptations needed to generalize Theorem 3 for statistic (13) and (14). We modify Assumptions 2–4 to impose conditions on $D$ as follows:

**Assumption 6.** For all $x \in (0, 1]$, $q \mapsto \varphi(q) 1_{q \in D(x)}$ is discontinuous on a set of Lebesgue measure zero.

**Assumption 7.** For all $x \in (0, 1)$, there exists a constant $a_x \in [0, 1/2]$ such that $q \mapsto \varphi(q) 1_{q \in D(x)}$ is nonincreasing on $(0, a_x)$, nondecreasing on $(1 - a_x, 1)$, and bounded on $(a_x, 1 - a_x)$.

**Assumption 8.** $\int_{D(x)} \varphi(y) \, dy > 0$ for all $x > 0$.

Under these conditions, the design sensitivity of the uniform test based on (13) and (14) is now the supremum of $\pi(x; D)/(1 - \pi(x; D))$ over $x \in (0, 1)$, where

$$\pi(x; D) = \frac{\int_0^\infty \varphi(G(y) - G(-y)) 1_{G(y) - G(-y) \in D(x)} \, dG(y)}{\int_D \varphi(y) \, dy}.$$  

The proof of this result is largely the same as the argument for Theorem 2 with appropriate substitutions. Assumptions 6 and 7 are needed when applying Lemma 2 to test statistic $T_n(x; D)$ to ensure that the regularity conditions needed for convergence apply to the truncated score function, and Assumption 8 is needed to ensure $\pi(x; D)$ has a nonzero denominator.

### D Additional proofs

**D.1 Proof of Proposition 1**

Throughout the proof, we condition on $\mathcal{F}$, dropping it from the notation for simplicity. For each $i \in [n]$, write $S_i = 1_{Y_{(i)} > 0}$, $X_i = T_n(i/(n+1)) = \sum_{j=n-i+1}^n c_j S_j$, and $a_i = f_{\alpha,n}(i/(n+1))$. Under $H_0(\Gamma)$, the $(S_i)$ are independent with $1/(1 + \Gamma) \leq \Pr(S_i = 1) \leq \Gamma/(1 + \Gamma)$. Let $p_i = \Pr(S_i = 1)$. We wish to show that the rejection probability $\Pr(X_i \geq a_i)$ for some $i \in [n]$ is maximized when $p_i = \Gamma/(1 + \Gamma)$ for all $i \in [n]$.

Write $S = (S_1, \ldots, S_n)^T$, a random vector in $\{0, 1\}^n$. For $s \in \{0, 1\}^n$, $\Pr(S = s) = \prod_{i=1}^n p_i^{s_i}(1 - p_i)^{1-s_i}$. Let $R = \left\{s \in \{0, 1\}^n : \sum_{j=n-i+1}^n c_j s_j \geq a_i \text{ for some } i \in [n]\right\}$. This set represents the rejection event, in the
sense that the test rejects if and only if \( S \in \mathcal{R} \). We will show that \( \Pr(S \in \mathcal{R}) \) is increasing in \( p_i \) for each \( i \in [n] \), from which it follows that the rejection probability is maximized when \( p_i \) is maximized for each \( i \).

We claim that if \( s \in \mathcal{R} \) and \( s' \geq s \) elementwise, then \( s' \in \mathcal{R} \). To see this, observe that \( s \in \mathcal{R} \) implies that we can choose \( i \in [n] \) such that \( \sum_{j=n-i+1} a_j s_j \geq a_i \). Then \( \sum_{j=n-i+1} a_j s'_j \geq \sum_{j=n-i+1} a_j s_j \geq a_i \), so \( s' \in \mathcal{R} \).

Now write \( \Pr(S \in \mathcal{R}) = \sum_{s \in \mathcal{R}} \prod_{i=1}^n p_i^{s_i} (1 - p_i)^{1-s_i} \), and differentiate with respect to \( p_k \) for any \( k \in [n] \):

\[
\frac{d}{dp_k} \Pr(S \in \mathcal{R}) = \sum_{s \in \mathcal{R}} \left( (2s_k - 1) \prod_{i \neq k} \frac{p_i^{s_i} (1 - p_i)^{1-s_i}}{p_k^{s_k}} \right)
\]

where \( \pi^{(k)}(s) = \prod_{i \neq k} p_i^{s_i} (1 - p_i)^{1-s_i} \). For each \( s \in \mathcal{R} \) with \( s_k = 0 \), there corresponds an \( s' \) that is identical except for \( s'_k = 1 \), i.e., \( s'_i = s_i 1_{i \neq k} + 1_{i=k} \), and this \( s' \in \mathcal{R} \) by the claim above. Also, \( \pi^{(k)}(s) = \pi^{(k)}(s') \). Hence each term in the second sum of (15) is canceled by a term in the first sum. We conclude \( \frac{d}{dp_k} \Pr(S \in \mathcal{R}) \geq 0 \) as desired, completing the proof.

We remark that an alternative proof could use Holley’s inequality for distributions over finite distributive lattices (Rosenbaum, 2002, Sections 2.10, 4.7.2). We have opted for the direct proof above to keep the paper more self-contained.

### D.2 Proof of Lemma 1

The following result ensures convergence of certain Riemann sums for some unbounded functions, and is necessary to analyze the asymptotic behavior of \( f_{\alpha,n} \).

**Lemma 3.** Suppose \( \varphi : (0, 1) \to [0, \infty) \) is discontinuous on a set of measure zero, \( \int_0^1 \varphi(x) \, dx < \infty \), and there exists a constant \( a \in [0, 1/2] \) such that \( \varphi \) is nonincreasing on \((0, a)\), nondecreasing on \((1 - a, 1)\), and bounded on \((a, 1 - a)\). Then

\[
\lim_{n \to \infty} \frac{1}{n} \sum_{i=1}^n \varphi \left( \frac{i}{n+1} \right) = \int_0^1 \varphi(x) \, dx.
\]

**Proof.** Write \( \varphi = \varphi_1 + \varphi_2 + \varphi_3 \) where \( \varphi_1(x) = \varphi(x)1_{x < a} \), \( \varphi_2(x) = \varphi(x)1_{a \leq x \leq 1 - a} \), and \( \varphi_3(x) = \varphi(x)1_{x > a} \). Since \( \varphi_2 \) is bounded, it is Riemann integrable, so \( n^{-1} \sum_{i=1}^n \varphi_2(i/(n+1)) \to \int_0^1 \varphi_2(x) \, dx \) by standard Riemann integration theory, noting that \( i/(n+1) \to ((i-1)/n, i/n) \) for each \( i \in [n] \). For \( \varphi_1 \) and \( \varphi_3 \), we appeal to Lemma 4 below to conclude that \( n^{-1} \sum_{i=1}^n \varphi_k(i/(n+1)) \to \int_0^1 \varphi_k(x) \, dx \) for \( k = 1, 3 \). The result follows by linearity. \( \square \)

**Lemma 4.** Suppose \( \varphi : (0, 1) \to [0, \infty) \) is monotone and \( \int_0^1 \varphi(x) \, dx < \infty \). Then

\[
\lim_{n \to \infty} \frac{1}{n} \sum_{i=1}^n \varphi \left( \frac{i}{n+1} \right) = \int_0^1 \varphi(x) \, dx.
\]

**Proof.** Suppose first that \( \varphi \) is nondecreasing, and for each \( n \in \mathbb{N} \) define \( \varphi_n(x) = \varphi(i/(n+1)) \) for \( i/(n+1) \leq x < (i+1)/(n+1) \), \( i = 1, \ldots, n \), and \( \varphi_n(x) = 0 \) for \( x \leq 1/(n+1) \). Then \( |\varphi_n| \leq |\varphi| \) for all \( n \) by construction, since \( \varphi \) is nonnegative and nondecreasing. Furthermore, since \( \varphi \) is monotone, it is discontinuous at a countable number of points (Knapp, 2007, p. 344), so \( \varphi_n(x) \to \varphi(x) \) pointwise almost everywhere. So the dominated convergence theorem implies

\[
\lim_{n \to \infty} \frac{1}{n+1} \sum_{i=1}^n \varphi \left( \frac{i}{n+1} \right) = \lim_{n \to \infty} \int_0^1 \varphi_n(x) \, dx = \int_0^1 \varphi(x) \, dx.
\]

The conclusion follows since \( (n+1)/n \to 1 \) as \( n \to \infty \). If \( \varphi \) is instead nonincreasing, apply the above argument to \( x \mapsto \varphi(1-x) \). \( \square \)
Before proving Lemma 1 we require one more technical lemma. For \( \rho \in [1/2, 1) \), define
\[
h_\rho(x) = e^x / \{1 + \rho(e^x - 1)\}^2 \quad \text{on } x \geq 0.
\] (16)

**Lemma 5.** For any \( \rho \in [1/2, 1) \), \( 0 \leq h_\rho(x) \leq 1 \) for all \( x \geq 0 \).

**Proof.** That \( h_\rho(x) \geq 0 \) for all \( x \geq 0 \) is clear from the definition. To see that \( h_\rho(x) \leq 1 \), observe
\[
h'_\rho(x) = e^x \left[ \frac{1 - \rho(1 + e^x)}{(1 + \rho(e^x - 1))^2} \right].
\]
Now the inequality \( e^x \geq 1 + x \) implies \( 1 - \rho(1 + e^x) \leq 1 - 2\rho \leq 0 \) by our assumption \( \rho \geq 1/2 \), while \( 1 + \rho(e^x - 1) \geq 1 > 0 \). Hence \( h'_\rho(x) \leq 0 \) for all \( x \geq 0 \). Together with \( h_\rho(0) = 1 \), the conclusion follows. \( \square \)

We are now ready to prove Lemma 1.

**Proof of Lemma 1.** The limit \( n^{-1}\mu_n(x) \to \rho_T \int_{1-x}^1 \varphi(y) \, dy \) follows directly from Lemma 3 applied to the function \( q \mapsto \varphi(1-q)1_{q \leq x} \). The bulk of the work is in proving that \( f_{\alpha,n}(x) = \mu_n(x) + O(\sqrt{n}) \). For this, we start with first-order application of Taylor’s theorem about \( \lambda = 0 \), which yields, for any \( c \geq 0 \), \( \lambda \geq 0 \),
\[
\log \{1 + \rho_T(e^{\lambda} - 1)\} = \rho_T c \lambda + \frac{\rho_T(1 - \rho_T)h_{\rho_T}(\xi)c^2\lambda^2}{2},
\] (17)
for some \( \xi \in [0, c\lambda] \). So combining the definition (4) of \( f_{\alpha,n} \) with the expansion (17), we have
\[
f_{\alpha,n}(x) = \frac{\log \alpha^{-1}}{\lambda_n} + \mu_n(x) + \frac{\rho_T(1 - \rho_T)\lambda_n}{2} \sum_{i = [1-x](n+1)}^n h_{\rho_T}(\xi_i)c_i^2,
\]
where \( \xi_i \in [0, c_i\lambda_n] \) for each \( i = 1, \ldots, n \). Since \( \Gamma \geq 1 \), we are assured \( \rho_T \in [1/2, 1) \), so Lemma 5 implies
\[
0 \leq \rho_T(1 - \rho_T)\lambda_n \sum_{i = [1-x](n+1)}^n h_{\rho_T}(\xi_i)c_i^2 \leq \frac{\lambda_n\sigma_n^2(x)}{2},
\]
so that
\[
0 \leq f_{\alpha,n}(x) - \mu_n(x) \leq \frac{\log \alpha^{-1}}{\lambda_n} + \frac{\lambda_n\sigma_n^2(x)}{2}.
\]
Applying Lemma 3 to the function \( q \mapsto \varphi^2(1-q)1_{q \leq x} \), which is integrable by Assumption 1, we see that \( n^{-1}\sigma_n^2(x) = O(1) \) for each \( x \in (0, 1) \). Together with the definition of \( \lambda_n \) just below (4), we conclude
\[
0 \leq \frac{f_{\alpha,n}(x) - \mu_n(x)}{\sqrt{n}} = \frac{1}{\sqrt{n}} \left( \frac{\log \alpha^{-1}}{\lambda_n} + \frac{\lambda_n\sigma_n^2(x)}{2} \right) = \sqrt{\frac{\sigma_n^2(x)0}{2n}} + \sqrt{\frac{2n\log \alpha^{-1}}{\sigma_n^2(x)0}} \cdot \frac{\sigma_n^2(x)}{n} = O(1),
\] (18)
as desired. \( \square \)

**D.3 Asymptotic approximation of \( f_{\alpha,n} \)**

The following result formalizes the second-order expansion mentioned in Section 3; recall the definition of \( g_{\alpha,n} \) from (5).

**Proposition 3.** If \( \varphi \) satisfies Assumptions 1–4, and furthermore \( \int_0^1 \varphi^3(x) \, dx < \infty \), then for all \( x \in (0, 1) \), we have \( f_{\alpha,n}(x) \leq g_{\alpha,n}(x) \) for all \( n \) and \( f_{\alpha,n}(x) = g_{\alpha,n}(x) + O(1) \) as \( n \to \infty \).
Proof. We follow an analogous argument to the proof of Lemma 1, starting from
\[
\log \left\{ 1 + \rho(e^{c \lambda} - 1) \right\} = \rho c \lambda + \frac{\rho(1 - \rho)c^2\lambda^2}{2} - \frac{\rho(1 - \rho)h_2(\xi)e^3\lambda^3}{6},
\]
for some \( \xi \in [0, e \lambda] \), where
\[
h_2(x) = e^x \frac{\rho (1 + e^x - 1)}{(1 + \rho(e^x - 1))^3}
\]
satisfies 0 \( \leq h_2(x) \leq 1 \) for all \( x \geq 0 \). By the same argument that led from (17) to (18), we find
\[
0 \leq \frac{\log \alpha^{-1}}{\lambda_n} + \mu_n(x) + \frac{\lambda_n \sigma_n^2(x)}{2} - f_{\alpha,n}(x) \leq \frac{\rho \alpha (1 - \rho \alpha) \lambda_n^2}{6} \sum_{i=\lfloor (1-x)/(n+1) \rfloor}^n c_i^2 = O(1) \tag{19}
\]
Substituting the choice \( \lambda_n = \left( 2 \log(\alpha^{-1})/\sigma_n^2(x_0) \right)^{1/2} \) shows that
\[
\frac{\log \alpha^{-1}}{\lambda_n} + \mu_n(x) + \frac{\lambda_n \sigma_n^2(x)}{2} = \mu_n(x) + \left( \frac{\sigma_n^2(x)}{\sigma_n^2(x_0)} \right) \sqrt{\frac{\sigma_n^2(x_0) \log \alpha^{-1}}{2}} = g_{\alpha,n}(x) \tag{20}
\]
so that (19) reads 0 \( \leq g_{\alpha,n}(x) - f_{\alpha,n}(x) = O(1) \) as desired. \hfill \Box

The chosen value of \( \lambda_n \) is the minimizer of the left-hand side of (20) when \( x = x_0 \), justifying the claim that \( \lambda_n \) is chosen to optimize the bound \( g_{\alpha,n}(x) \) at \( x = x_0 \).

D.4 Proof of Lemma 2

Let \( H(x) = G(x) - G(-x) \). Fix any \( \epsilon > 0 \). Because bounded, continuous functions with compact support are dense in \( L^p \) (Hewitt and Stromberg, 1965, Theorem 13.21), we can find a continuous function \( \varphi_c : [0,1] \to [0,\infty) \) such that \( \int_0^1 |\varphi(x) - \varphi_c(x)| \, dx < \epsilon \), and \( \varphi_c(x) = 0 \) for all \( x \in [0,b) \cup (1-b,1] \) for some \( 0 < b < a \). Now write
\[
\tau = \int_0^\infty \varphi \{ H(x) \} \, dG(x), \quad \tau_c = \int_0^\infty \varphi_c \{ H(x) \} \, dG(x).
\]
We will show the following three relations hold:
\[
\Pr \left\{ \limsup_{n \to \infty} \frac{1}{n} \sum_{i=1}^n \varphi \left( \frac{i}{n+1} \right) 1_{Y(i) > 0} - \sum_{i=1}^n \varphi_c \left( \frac{i}{n+1} \right) 1_{Y(i) > 0} \right\} < \epsilon \right\} = 1, \tag{21}
\]
\[
\Pr \left\{ \lim_{n \to \infty} \frac{1}{n} \sum_{i=1}^n \varphi_c \left( \frac{i}{n+1} \right) 1_{Y(i) > 0} = \tau_c \right\} = 1, \tag{22}
\]
\[
|\tau_c - \tau| < \epsilon. \tag{23}
\]
From this we conclude \( \limsup_{n \to \infty} \left| n^{-1} \sum_{i=1}^n \varphi \left( \frac{i}{n+1} \right) 1_{Y(i) > 0} - \tau \right| < 2\epsilon \) with probability one. Since \( \epsilon \) was arbitrary, the conclusion follows.

To obtain (21), use the triangle inequality to write
\[
\frac{1}{n} \sum_{i=1}^n \left\{ \varphi \left( \frac{i}{n+1} \right) - \sum_{i=1}^n \varphi_c \left( \frac{i}{n+1} \right) \right\} 1_{Y(i) > 0} \leq \frac{1}{n} \sum_{i=1}^n |\varphi - \varphi_c| \left( \frac{i}{n+1} \right) \leq \frac{1}{n} \sum_{i=1}^{n+1} |\varphi - \varphi_c| \left( \frac{i}{n+1} \right) - |\varphi - \varphi_c| (1) \frac{1}{n} \to \int_0^1 |\varphi - \varphi_c| (x) \, dx < \epsilon,
\]
where the limit uses Lemma 3, noting that \( |\varphi - \varphi_c| \) is bounded on \([b,1-b]\) and monotone elsewhere, and final inequality follows from our choice of \( \varphi_c \).

The second step (22) follows from Theorem 1 of Sen (1970) applied to \( \varphi_c \), which we partially restate. See Appendix D.7 below for an explanation of why our statement differs from Sen’s.
Lemma 6 (Sen, 1970, Theorem 1). Suppose \( \varphi_c \in L^1(0,1) \) is bounded and continuous, and suppose \( Y_1, Y_2, \ldots \) are drawn i.i.d. from a continuous distribution \( G \). Then

\[
\frac{1}{n} \sum_{i=1}^{n} \varphi_c \left( \frac{i}{n+1} \right) 1_{Y(i) \geq 0} \xrightarrow{a.s.} \int_0^\infty \varphi_c \{ H(x) \} \, dG(x).
\]

Finally, to see (23), use the triangle inequality to write

\[
|\tau_c - \tau| \leq \int_0^\infty |\varphi_c - \varphi| \{ H(y) \} \, dG(y)
\]

\[
\leq \int_0^\infty |\varphi_c - \varphi| \{ H(y) \} \, dH(y),
\]

since \( H'(y) = G'(y) + G'(-y) \geq G'(y) \) and the integrand is nonnegative. From this we conclude

\[
|\tau_c - \tau| \leq \int_0^1 |\varphi_c - \varphi| (u) \, du < \epsilon,
\]

by our choice of \( \varphi_c \). The proof is complete.

D.5 Proof of Theorem 3

Write \( q_x \) for the \( x \)-quantile of \( |Y| \) when \( Y \sim G \), so that \( q_x \) is defined by the equation \( G(q_x) - G(-q_x) = x \). We shall require the derivative of \( q_x \) below, which we find by implicit differentiation:

\[
\frac{d q_x}{dx} = \frac{1}{g(q_x) + g(-q_x)}. \tag{24}
\]

Now observe that, using the definition of \( q_x \), we may write \( \pi(x) \) from Theorem 2 as

\[
\pi(x) = \frac{\int_{q_{1-x}}^{\infty} \varphi \{ G(y) - G(-y) \} \, dG(y)}{\int_{1-x}^{1} \varphi(y) \, dy}. \tag{25}
\]

We apply the generalized form of L'Hôpital's rule, which says that \( \limsup f/g \geq \liminf f'/g' \) when \( \lim f = \lim g = 0 \), to the formula (25) for \( \pi(x) \) to find

\[
\limsup_{x \downarrow 0} \pi(x) \geq \liminf_{x \downarrow 0} \frac{\frac{d}{dx} \int_{q_{1-x}}^{\infty} \varphi \{ G(y) - G(-y) \} \, dG(y)}{\frac{d}{dx} \int_{1-x}^{1} \varphi(y) \, dy}
\]

\[
= \liminf_{x \downarrow 0} \frac{\varphi(1-x) g(q_{1-x})}{\varphi(1-x) g(q_{1-x}) + g(-q_{1-x})},
\]

where the equality uses the fundamental theorem of calculus and (24). Assumption 4 on \( \varphi \) implies \( \varphi(q) \) must be positive on a neighborhood \( q \in (1-\epsilon, 1) \) for some \( \epsilon > 0 \), which ensures the limit is well-defined. Reparametrizing in terms of \( q = q_{1-x} \), and noting that \( q_{1-x} \uparrow \infty \) as \( x \downarrow 0 \) since \( g \) is positive throughout \( \mathbb{R} \), we have

\[
\limsup_{x \downarrow 0} \pi(x) \geq \liminf_{q \uparrow \infty} \frac{1}{1 + \frac{g(-q)}{g(q)}}.
\]

Hence \( \limsup_{x \downarrow 0} \pi(x) \geq \liminf_{q \uparrow \infty} \frac{g(q)}{g(q)+g(-q)} \). The conclusion follows from Theorem 2.

D.6 Proof of Proposition 2

Fix any \( p \geq 1 \). A standard Cramér-Chernoff tail bound for the normal distribution (Boucheron et al., 2013, Section 2.2) gives \( 1 - \Phi(x) \leq e^{-x^2/2} \), which implies \( \Phi^{-1}(q) \leq \sqrt{2 \log(1-q)}^{-1} \). Hence

\[
\int_0^1 |\varphi(q)|^p \, dq \leq 2^{p/2} \int_0^1 [\log\{2/(1-q)\}]^{p/2} \, dq
\]

\[
= 2^{1+p/2} \int_{\log 2}^{\infty} y^{p/2} e^{-y} \, dy
\]

using the substitution \( y = \log\{2/(1-q)\} \). The final integral is upper bounded by \( \Gamma(1 + p/2) \), using the definition of the Gamma function and non-negativity of the integrand, which completes the proof.
Figure 4: Simulated Type I error rate of uniform sign rank tests versus sample size, based on one million replications. Solid lines show $$\Gamma = 1$$ while dashed lines show $$\Gamma = 5$$. All tests use $$x_0 = 1/3$$ and nominal level $$\alpha = 0.05$$.

### D.7 A remark on Theorem 1 from Sen (1970)

Sen (1970) assumes only that $$\varphi \in L^1(0,1)$$ is continuous. Denoting $$\varphi_n(x) = \varphi\{i/(n + 1)\}$$ for $$(i - 1)/n < x \leq i/n$$, $$i = 1, \ldots, n$$, their proof (p. 2141) claims that

$$\lim_{n \to \infty} \int_0^1 |\varphi_n(x)| \, dx = \int_0^1 |\varphi(x)| \, dx. \tag{26}$$

The conclusion (26) is not true for all continuous $$\varphi \in L^1(0,1)$$, as the counterexample below shows. However, noting that $$\int_0^1 \varphi_n(x) \, dx = n^{-1} \sum_{i=1}^n \varphi\{i/(n + 1)\}$$, our Lemma 3 shows that (26) is true under stronger conditions, and in particular is true for bounded $$\varphi$$. This is the reason we require boundedness in our restatement of Sen’s result, Lemma 6.

Let $$\varphi(x) = n$$ for $$1/(n+1) \leq x \leq 1/(n+1) + 1/(n^2n+1)$$, $$n \in \mathbb{N}$$. Then $$\int_0^1 \varphi(x) \, dx = \sum_{n=1}^{\infty} 2^{-n-1} = 1/2$$, hence $$\varphi(x) \in L^1$$. But $$n^{-1} \sum_{i=1}^n \varphi\{i/(n + 1)\} \geq n^{-1} \varphi\{1/(n + 1)\} = 1$$ for all $$n$$, so $$\lim \inf_{n \to \infty} n^{-1} \sum_{i=1}^n \varphi\{i/(n + 1)\} \geq 1 > 1/2 = \int_0^1 \varphi(x) \, dx$$, showing (26) does not hold. This $$\varphi$$ is not continuous, but may be replaced with a continuous approximation by standard arguments.

### E Simulations of Type I error rate

Theorem 1 shows that the uniform general signed rank test has size no larger than the nominal level $$\alpha$$, while the simulations in Section 5 illustrate the realized power of the test under various alternatives. Neither tells us how close the true size of the test is to the nominal level $$\alpha$$, that is, how close the inequality in Theorem 1 is to an equality. Figures 4 and 5 present simulation results under the null $$H_0(\Gamma)$$ to illustrate the size of some uniform tests. These simulations use the worst-case distribution within $$H_0(\Gamma)$$ defined by Proposition 1.

The simulations reveal several interesting patterns. Size appears to increase towards a limit as sample size grows, but this limit is not equal to $$\alpha$$ in general. For larger $$\Gamma$$, the test becomes more conservative at small sample sizes, but the effect is negligible at large sample sizes. As $$x_0$$ approaches zero, the asymptotic size approaches $$\alpha$$. Finally, the sign score function yields the least conservative uniform test, followed by the Wilcoxon score function and then the normal score function.

### F Additional plots and tables

Table 2 shows covariate balance between treated and control groups for the constructed pairs used in the data example of Section 6. Figure 6 plots $$\pi(x)$$ as defined in Theorem 2 for additional score functions not
Figure 5: Simulated Type I error rate of uniform sign rank tests versus tuning parameter $x_0$ at sample size $n = 10^5$ when $\Gamma = 1$, based on one million replications. All tests use nominal level $\alpha = 0.05$.

Table 2: Balance table for 1,672 matched pairs formed from NHANES data. Each pair contains one individual who consumed $\geq 15$ servings of fish in the previous month, and one who consumed no more than two. The first two columns give the sample means in the matched samples for various attributes of interest, and the third gives the standardized difference, which is computed by dividing the difference in group sample means by the pooled standard deviation estimate from the full dataset before matching.

Figure 7 complements Figure 3 by comparing power between uniform tests with different score functions. Tests tend to perform similarly with small sample sizes, but clear distinctions emerge with large sample sizes. In the normal case, the normal scores test dominates while the redescending score function substantially underperforms. As we have seen, under normal noise the outliers contain the most information, and a score function that places more weight upon pairs with large absolute differences will attain higher power as a result. Conversely, in the Cauchy case, the normal scores tests performs the worst, while the sign test performs the best. Here the extreme tails yield less information, as indicated by Figure 2. The Laplace case is a middle ground in which the tails yield no more or less information than most of the rest of the distribution, as we have seen in Figure 2. Here the choice of score function makes little difference.
Figure 6: $\pi(x)$ from Theorem 2 for the normal score function when $G$ is standard normal, Laplace (double exponential) or Cauchy, and $\tau = 1/2$.

Figure 7: Comparison of simulated power for uniform tests using different score functions, based on 10,000 replications under alternative model $H_1(G)$ with $G$ as indicated, having center 1/2 and unit scale. All tests use $\alpha = 0.05$. 