Nonparametric Detection of Multiple Location-Scale Change Points via Wild Binary Segmentation

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Abstract

While parametric multiple change point detection has been widely studied, less attention has been given to the nonparametric task of detecting multiple change points in a sequence of observations when their distribution is unknown. Most existing work on this topic is either based on penalized cost functions which can suffer from false positive detections, or on binary segmentation which can fail to detect certain configurations of change points. We introduce a new approach to change point detection which adapts the recently proposed Wild Binary Segmentation (WBS) procedure to a nonparametric setting. Our approach is based on the use of rank based test statistics which are especially powerful at detecting changes in location and/or scale. We show via simulation that the resulting nonparametric WBS procedure has favorable performance compared to existing methods, particularly when it comes to detecting changes in scale. We apply our procedure to study a problem in stylometry involving change points in an author’s writing style, and provide a full implementation of our algorithm in an associated R package.

1 Introduction

The multiple change point problem involves the simultaneous estimation of the number and location of \( K \geq 0 \) change points \( \tau = \{\tau_1, \ldots, \tau_K\} \) that partition a sequence \( y = (y_1, \ldots, y_n) \) into \( K + 1 \) segments such that:

\[
S_1 = \{y_1, \ldots, y_{\tau_1}\}, \quad S_2 = \{y_{\tau_1+1}, \ldots, y_{\tau_2}\}, \quad \ldots, \quad S_{K+1} = \{y_{\tau_K+1}, \ldots, y_n\}.
\]

We will make the commonly used assumption that the \( y_i's \) are univariate observations which are independent and identically distributed between each pair of change points so that \( y_i \sim_{i.i.d.} F_j \) if \( y_i \in S_j \) for some set of unknown continuous distributions \( F_1, \ldots, F_{K+1} \). The literature on the single change point problem where \( K \in \{0, 1\} \) is vast, with an overview of traditional methods provided by Basseville and Nikiforov [1993]. For the multiple change point problem where \( K \) can be greater than 1, most existing literature has assumed that the distributional form of each \( F_j(\cdot; \theta_j) \) is known, with the change points consisting of shifts in a finite dimensional parameter \( \theta \). A recent overview of parametric techniques for multiple change point detection is provided by Niu et al. [2016] and Truong et al. [2020]. Most existing methods fall into one of four categories:

1. Sequential approaches such as the CUSUM [Page, 1954] [Moustakides, 1986] [Lai, 1995] or change point model framework [Hawkins et al., 2003] which process the sequence one observation at a time, and which are only concerned with estimating the location of the most recent change point.

2. Penalized cost function approaches which seek to find the global minimum of some appropriately chosen cost function \( C(y, \tau) \) (such as the negative log-likelihood) with a penalty.
for the number of change points. \cite{hawkins2001, killick2012, jackson2005, lavielle2005}.

3. Stepwise approaches such as binary segmentation transform the multiple change point problem into the task of recursively testing for the existence of a single change point \cite{bai1997, cho2015, oshen2014, vostrikov1981, inclan1994, fryzlewicz2014}. The key advantage of such approaches is that they allow for a strict control on the false positive rate, i.e. the probability of incorrectly concluding that at least one change point exists in the sequence when in fact none are present.

4. Various Bayesian models such as \cite{barry1992, green1995, fearnhead2006, chib1998}. Although interesting, the Bayesian paradigm takes a quite different approach to the multiple change point problem, and we will not discuss it further.

In many real world situations, it is not reasonable to expect the distributional form of each $F_j$ to be known. This has led to the development of nonparametric change point detection algorithms which do not require information about the sequence distributions. Much of the classic nonparametric literature has focused on the single change point setting \cite{carlstein1988, pettitt1979, brodsky1993, darkhovsky1993, chen2019} however the multiple change point setting is also of considerable interest. Extensions of the sequential approach to the nonparametric setting have been considered by authors such as \cite{hawkins2010, ross2011, padilla2019}, however such approaches are inefficient in a non-sequential setting since inference for a change point at time $t$ is based only on the observations $y_1, \ldots, y_{t-1}$ rather than on the whole sequence. The penalized cost function approach is limited in the nonparametric setting since there is no likelihood to act as a cost function. However, \cite{zou2014} has recently shown encouraging results using a cost function based on a nonparametric likelihood, and follow-up work by \cite{haynes2017} has rendered their approach computationally tractable even for long sequences. While this direction is promising, a limitation is the lack of control on the false positive probability which as we show in Section 3 can be very substantial.

The stepwise binary segmentation approach directly extends to the nonparametric setting, since the test for a single change point at each stage can be carried out using a nonparametric single change point test such as that based on maximized Mann-Whitney statistic as used in \cite{pettitt1979}. Such an approach was taken by \cite{matteson2014} in a multivariate context. This allows for a strict control on the false positive rate. However, binary segmentation can perform poorly in multiple change point settings due to its greedy nature which only ever searches for the best fitting single change point at each step. In some situations, which we discuss further in Section 2.2, multiple change points will mask each other which may lead to a failure to detect any of them.

Recently in an influential paper, \cite{fryzlewicz2014} proposed a modified version of binary segmentation which solves some of these problems. Their approach -- named Wild Binary Segmentation (WBS) -- is based on maximizing a test statistic over randomly sampled subsequences of $y_1, \ldots, y_n$. By considering subsequences, WBS is able to detect change points which only affect local parts of the sequence which would potentially be masked when using standard binary segmentation. Both their original paper and the subsequent literature shows a high degree of promise for WBS.

In \cite{fryzlewicz2014}, only the parametric setting of the change point problem is considered, with a focus on detecting change points in the mean of a sequence of Gaussian observations. In this work, we develop a nonparametric version of their WBS procedure which is able to detect location-scale (i.e. mean and/or variance) changes in sequences with an arbitrary and potentially unknown distribution, while maintaining strict control of the false positive rate. Our approach is based on nonparametric rank statistics which have a null distribution which is independent of the form of the $F_j$ distributions. This independence allows critical values of the test statistics to be computed in a distribution-free manner. We compute these values using large scale Monte Carlo simulation and the resulting procedure is implemented in an R package \texttt{npwbs} available at \url{https://cran.r-project.org/web/packages/npwbs/index.html}.

The remainder of this paper proceeds as follows: In Section 2.1 we discuss the single change point problem where $K \in \{0, 1\}$. Section 2.2 generalizes this to the multiple change point problem via binary segmentation, and explains the problems that this procedure can suffer from. In Section 2.3 we introduce our nonparametric multiple change point detection procedure using Wild Binary Segmentation, with further implementation details discussed in Sections 2.4 and 2.5. Section 3 compares its performance to several existing nonparametric change point methods. This includes the
We first consider the task of testing for the existence of a single change point \( \tau \) which we write \( T^\tau \). Let \( T_{1,n}^\tau \) denote a two sample test statistic that has been chosen with regards to the type of change that we wish to detect. To make the notation clear, we write \( T_{p,q}^{k} \) to denote a two sample test statistic for the samples \( y_1 = (y_p, y_{p+1}, \ldots, y_k) \) and \( y_2 = (y_{k+1}, \ldots, y_q) \). In the parametric case where the functional forms of \( F_0 \), \( F_1 \), \( F_2 \) are all known with only their parameters unknown, a statistic based on the generalised likelihood ratio test is a common choice \( \text{Basseville and Nikiforov} \ [1993] \). Now suppose that \( k \) is unknown and requires estimation. In this case, the null hypothesis is the same as above but the alternative hypothesis becomes:

\[
H_1 : \exists k : y_1, \ldots, y_k \sim_{i.i.d} F_1, y_{k+1}, \ldots, y_n \sim_{i.i.d} F_2, F_1 \neq F_2
\]

The test statistic can be chosen as the maximal value of \( T_{1,n}^{k} \) over all possible \( k \), i.e.:

\[
T_{1,n} = \max_{1 \leq k < n} |T_{1,n}^{k}|
\]

The null hypothesis of no change is rejected if \( T_{1,n} > \gamma \) for some appropriately chosen threshold \( \gamma(n) \), where we write . In the case where the null distribution of \( T_{1,n} \) is known and where \( \gamma \) is chosen to be equal to its \( 1 - \alpha \)th percentile then this leads to a control of the false positive rate at level \( \alpha \), i.e. if the null hypothesis of no change is true, then the probability of incorrectly detecting a change is less than \( \alpha \).

If the null hypothesis is rejected then an estimate of \( \tau \) is given by \( \hat{\tau} = \hat{k} \) where \( \hat{k} \) is the value of \( k \) for which \( |T_{1,n}^{k}| \) is maximal. There is a vast literature studying the theoretical properties of this change detection procedure in a parametric context, including derivations of the (usually asymptotic) null distribution of \( T_{1,n} \) under various choices of the test statistic \( T_{1,n}^{k} \), along with the construction of confidence bands for the estimate of \( \tau \).

The extension of this procedure to a nonparametric setting is straightforward: simply choose \( T_{1,n}^{k} \) to be a test statistic with a null distribution that does not depend on the underlying distribution of \( y_i \). One way to achieve this is to take \( T_{1,n}^{k} \) to be a statistic associated with a nonparametric test based on sample ranks \( \text{Pettitt} \ [1979] \; \text{Brodsky and Darkhovsky} \ [1993] \). In this case, the null distribution of \( T_{1,n} \) will not depend on the distribution of the \( y_i \) observations and the false positive rate can hence be controlled without requiring distributional information about \( y_i \).

2.2 Binary Segmentation for Detecting Multiple Change Points

Next suppose that there are an unknown number \( K \geq 0 \) of change-points \( \tau = \{ \tau_1, \ldots, \tau_K \} \) and the task is to estimate both \( K \) and \( \tau \). The above procedure could be directly extended by replacing the maximal test statistic \( T_{1,n} \) with one that is maximized over every possible configuration of change points for every value \( K \in \{ 1, 2, \ldots, n - 1 \} \). While finding the configuration which maximizes \( T_{1,n} \) might appear challenging, it can often be achieved in a computationally efficient manner through the use of dynamic programming \( \text{Killick et al.} \ [2012] \). However, determining the null distribution of
Figure 1: Example of a sequence with 3 change points (dotted lines) at locations \( \tau = \{100, 110, 120\} \) where binary segmentation will struggle to detect any changes due to the masking effect.

the resulting \( T_{1,n} \) is a substantially more difficult task. This has led to the development of step-wise procedures which avoid this direct maximization and instead recursively apply hypothesis tests based on the single change point alternative. Specifically, consider again the single change point hypothesis test:

\[
0 : y_1, \ldots, y_n \sim_{i.i.d} F_0 \\
H_1 : \exists k : y_1, \ldots, y_k \sim_{i.i.d} F_1, \quad y_{k+1}, \ldots, y_n \sim_{i.i.d} F_2, \quad F_1 \neq F_2
\]  

Let \( T_{1,n} = \max_{1 \leq k < n} |T_{k,n}^1| \) for an appropriate \( T_{k,n}^1 \) be defined as above. Again, the null hypothesis of no change is rejected if \( T_{1,n} > \gamma(n) \) where we choose \( \gamma \) as a function of the sample size for reasons that will be discussed below. Suppose the null hypothesis is rejected and let \( \hat{k} \) be the estimated change point location. The binary segmentation procedure consists of performing a further hypothesis test to check for a change in the observations \( y_1, \ldots, y_{\hat{k}} \) to the left of the change point. This is carried out in the same manner as was done for the original sequence, i.e. by computing \( T_{1,\hat{k}} = \max_{1 \leq k < \hat{k}} |T_{k,\hat{k}}^1| \). If this \( T_{1,\hat{k}} > \gamma(\hat{k}) \) then we deduce that there is a second change point in the observations \( y_1, \ldots, y_{\hat{k}} \). This procedure is then applied recursively, with the segment \( y_1, \ldots, y_{\hat{k}} \) split into two pieces around this second point, and both segments tested for further change points and so on, until no more change points are found. The same procedure is applied to the observations \( y_{\hat{k}+1}, \ldots, y_n \) to the right of the original change point, with a further change point in this segment detected if \( T_{\hat{k}+1,n} = \max_{\hat{k}+1 \leq k < n} |T_{k+1,n}^1| > \gamma(n - \hat{k}) \). The final output of this procedure is an estimate \( \hat{K} \) of the number of change points and their locations \( \hat{\tau} = (\hat{\tau}_1, \ldots, \hat{\tau}_{\hat{K}}) \).

The binary segmentation procedure was first introduced by Vostrikov [1981] and has been widely used since Inclan and Tiao [1994], Fryzlewicz [2014]. It is sometimes claimed that the main advantage of binary segmentation is computational since it avoids searching through every possible change point configuration [Niu et al., 2016]. While this is true, another major advantage is that it allows the false positive rate to be strictly controlled in the case where the sequence does not contain any change points which is not typically the case with multiple change point methods which are based on optimizing a penalized cost function.

Despite this, binary segmentation suffers from a major limitation. At each stage in the recursive segmentation process, a decision is taken whether the segment under consideration contains exactly 0 or 1 change points. This may result in a failure to detect change in the case where two or more change points mask each other. Consider the sequence shown in Figure 1. In this case, there are three change points in the sequence mean that are easily visible to the eye. However there is no obvious location for a single change point that would split this sequence into two segments with substantially different means. As such, performing the hypothesis test in Equation 2 based on a single change point alternative may fail to reject the null hypothesis, in which case the estimate of the number of change points will be \( \hat{K} = 0 \). To solve this problem, Fryzlewicz [2014] introduced Wild Binary Segmentation which replaces the above test statistic with one based on maximizing over random length subsequences of \( y_1, \ldots, y_n \). We will now discuss this procedure along with its nonparametric extension.
2.3 Nonparametric Wild Binary Segmentation

Our goal is the nonparametric detection of multiple location-scale change points in a univariate sequence of continuous valued observations. Following the above discussion, we use a hypothesis testing framework with a nonparametric two-sample test statistic that is sensitive to changes in both location and scale. A natural choice would be an omnibus statistic such as the Kolmogorov-Smirnov or Cramer-von-Mises which can detect arbitrary distributional changes. However these statistics can be underpowered for detecting location-scale changes compared to other statistics which are more specialized towards these alternatives. Instead, we will consider a Lepage-like statistic which is based on a linear combination of standardized Mann-Whitney and Mood test statistics [Lepage, 1971; Ross et al., 2011].

Let \( y_1 = (y_1, \ldots, y_k) \) and \( y_2 = (y_{k+1}, \ldots, y_n) \) denote two samples of independent observations and consider a test for distributional equality where the null hypothesis is that both samples have identical distributions. For each observation \( y_i \), let \( r_i \) denote its rank in the combined sample, i.e. \( r_i = \sum_{j=1}^{k} I(y_i \geq y_j) \) so that smallest observation has rank 1, the second smallest has rank 2 and so on. The Mann-Whitney test [Mann and Whitney, 1947] is a two sample rank test for the alternative hypothesis that the distribution of the two samples differs in location. It is defined as:

\[
U_{1,n}^k = \sum_{i=1}^{k} r_i - \frac{k(k+1)}{2}
\]

Since this statistic depends on the observations only through their ranks, it is easy to show that its distribution under the null hypothesis is independent of the distribution of the observations. Specifically, its mean and variance under the null are [Mann and Whitney, 1947]:

\[
E[U_{1,n}^k] = \frac{k(n-k)}{2}, \quad Var[U_{1,n}^k] = \frac{k(n-k)(n+1)}{12}
\]

While the Mann-Whitney test will reject the null hypothesis if \( y_1 \) and \( y_2 \) come from distributions with different locations, it will generally not reject it if the distributions differ only in scale. For this purpose an alternative test statistic should be used. Our choice is the Mood statistic [Mood, 1954], defined as:

\[
M_{1,n}^k = \sum_{i=1}^{k} \left( r_i - \frac{n+1}{2} \right)^2
\]

Like the Mann-Whitney test, the distribution of the Mood statistic under the null hypothesis is independent of the distribution of the observations. Its mean and variance under the null hypothesis are Mood [1954]:

\[
E[M_{1,n}^k] = \frac{k(n^2-1)}{12}, \quad Var[M_{1,n}^k] = \frac{k(n-k)(n+1)(n^2-4)}{180}
\]

In cases where the distribution of the two samples can differ in either location or scale, a test statistic which is sensitive to both possibilities can be defined by combining the Mann-Whitney and Mood statistics together. Specifically, we use a Lepage-type statistic similar to Lepage [1971] that is based on the sum of squared standardized versions of these statistics, i.e:

\[
T_{1,n}^k = \left( \frac{U_{1,n}^k - E[U_{1,n}^k]}{\sqrt{Var[U_{1,n}^k]}} \right)^2 + \left( \frac{M_{1,n}^k - E[M_{1,n}^k]}{\sqrt{Var[M_{1,n}^k]}} \right)^2
\]

Note that the original Lepage statistic defined in Lepage [1971] use an Ansari-Bradley test statistic rather than the Mood test statistic for detecting in scale. Our decision to use the Mood is based on some empirical results suggesting it has favorable power [Duran, 1976] although we did not find a substantial difference between the two.
Now suppose that we wish to test the hypothesis in Equation 2 for a single change point alternative in the sequence $y_1, \ldots, y_n$. Due to the concerns discussed in the above section, the previous maximized test statistic $T_{1,n}^{\text{WBS}} = \max_k |T_{1,n}^k|$ may fail to detect a change in the case where multiple change points mask each other. Our WBS procedure avoids this problem by randomly selecting subsequences of $y_1, \ldots, y_n$ and computing the maximized single change point Lepage statistic on each of these subsequences. The statistic used to test the hypothesis in Equation 2 is then the maximum of these subsequence statistics. The intuition behind this procedure can be seen in Figure 1. The failure of standard binary segmentation in this situation comes from the fact that there is no single location which would divide the sequence into two segments with substantially different means. However, there are subsequences within which a change point will be very apparent, for example the subsequence $y_{95}, \ldots, y_{105}$ which will contain the first change point located at $\gamma_1 = 100$. As such, the value of the Lepage statistic would be substantially higher when evaluated only on this subsequence rather than on the sequence as a whole.

More formally, let $F^M_n$ be a set of $M$ randomly chosen intervals where the start and end points of each interval have been sampled uniformly from the set $\{1, 2, \ldots, n\}$. For each such interval $[s_m, e_m] \in F^M_n$, let $T^k_{s_m, e_m}$ denote the value of the Lepage statistic for the two sample hypothesis test where $y_1 = (y_{s_m}, \ldots, y_k)$ and $y_2 = (y_{k+1}, \ldots, y_{e_m})$ and let $T^k_{s_m, e_m} = \max_{s_m \leq k < e_m} |T^k_{s_m, e_m}|$ be the maximal value of the test statistic on this subsequence. The test statistic used in the WBS procedure is then:

$$ T_{1,n}^{\text{WBS}} = \max_{m: [s_m, e_m] \in F^M_n} T^k_{s_m, e_m} $$

The null hypothesis of no change is rejected if $T_{1,n}^{\text{WBS}} > \gamma(n)$ where $\gamma$ is again a function of the number of observations and will be discussed in the next section. If rejection occurs then let $(s_0, e_0) = \arg \max_{m} T^k_{s_m, e_m}$ be the interval for which the Lepage statistic was maximal. The estimate of the change point is then $\hat{\tau} = \hat{k}$ where $\hat{k} = \arg \max_{k} T^k_{s_0, e_0}$. The WBS procedure then finds additional change points in a recursive manner, using the same procedure as binary segmentation above. First, the observations $y_1, \ldots, y_k$ are tested for a change point by maximizing the Lepage statistic over $M$ randomly chosen subsequences of $y_1, \ldots, y_k$ and comparing it to a threshold $\gamma(\hat{k})$. The observations $y_{k+1}, \ldots, y_n$ to the right of the $\hat{k}$ are tested for further change points in a similar way. If any further change points are found, the sequence is again split into two segments and both are tested for additional change points, until no further change points are found. A full description of the procedure is given in Algorithm 1.

### 2.4 Threshold Determination

We next turn our attention to choosing appropriate values of the thresholds $\gamma(n)$ used in the WBS-Lepage procedure. In order to control the false positive rate, we will choose $\gamma(n)$ to be the $1 - \alpha^{th}$ percentile of the null distribution of $T_{1,n}^{\text{WBS}}$ in which case the false positive rate will be controlled at level $\alpha$. For example, if we choose $\gamma(n)$ to be equal to the 95\textsuperscript{th} percentile then the probability of incorrectly detecting a change when none exists will be less than 0.05. Note that this is a different approach to that taken by [Fryzlewicz 2014] who instead used an information criteria based method to determine the number of change points, which does not give any direct control over the false positive rate.

Due to the nonparametric nature of the Lepage test statistics, the null distribution of $T_{1,n}^{\text{WBS}}$ does not depend on the distribution of the $y_i$ observations. As such, Monte Carlo simulation can be used to find the required percentiles of the null distribution. While this requires a substantial amount of computation, it only needs to be done a single time and the resulting percentiles will hold for any length $n$ sequence of independent continuous observations regardless of their distribution.

We implemented this computation as follows: for each $n \in \{10, 11, 12, \ldots, 99, 100\}$ we simulated 1,000 sequences of length $n$ from a $N(0,1)$ distribution and computed $T_{1,n}^{\text{WBS}}$ for each sequence. For each $n$, the resulting $T_{1,n}^{\text{WBS}}$ statistics were ranked from smallest to largest, with the 50\textsuperscript{th} largest being an estimate of the 95\textsuperscript{th} percentile of $T_{1,n}^{\text{WBS}}$. Since the distribution of $T_{1,n}^{\text{WBS}}$ does not depend on the distribution of the data, this will also be a valid estimate of its 95\textsuperscript{th} percentile for any other choice of sequence distribution, not just $N(0,1)$. 

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The same procedure was then carried out for each $n \in \{105, 110, \ldots, 995, 1000\}$, for each $n \in \{1100, 1200, \ldots, 5000\}$, then for each $n \in \{6000, 7000, \ldots, 10000\}$. Linear interpolation based on these values was then used to produce thresholds for every $n \leq 10,000$. Figure 2 shows a plot of the resulting thresholds $\gamma(n)$ for significance level $\alpha = 0.05$. We also carried out a similar procedure to find thresholds corresponding to a significance level of $0.01$, which may be useful in cases where there is even greater desire to avoid false positives.

These thresholds provide the values of $\gamma(n)$ which are used to test for an initial change point in $y_1, \ldots, y_n$. Suppose a change point is found a location $\tilde{k}$. When the test for the next change point is applied to observations $y_1, \ldots, y_{\tilde{k}}$ we use the threshold that corresponds to the length of this segment, i.e. $\gamma(\tilde{k})$. This procedure is then repeated at each stage of the segmentation, with $\gamma(\cdot)$ always chosen to be the value corresponding to the length of the segment being tested for a change point. The full procedure for our nonparametric WBS algorithm is provided in Algorithm 1. This algorithm is implemented in the npwbs R package Ross [2021] which also contains the precomputed values of $\gamma(n)$ above for both $\alpha = 0.05$ and $\alpha = 0.01$.

The following two points should be noted:

1. Since our procedure only detects a change point if the observed value $T_{p,q}^{WBS}$ is greater than its 95th (or 99th) null percentile, it may not be possible to detect a change point if the segment under consideration is too short. This is because our use of rank-based test statistics means that the distribution of $T_{p,q}^{WBS}$ is highly discrete when $q - p$ is small. For example, suppose we attempt to detect changes in a sequence of length 3, so the observations are $y_1, y_2, y_3$. Regardless of the observed values of the $y_i$'s, there are only 6 possible sequences that can be obtained once the observations are converted to ranks: (1,2,3), (1,3,2), (2,1,3), (2,3,1), (3,1,2), (3,2,1). As such, it is clear that the number of unique values of $\max_k |T_{1,3}^k|$ must be less than 6 (it will not be exactly equal to 6, since several of these rank sequences will produce identical values of the test statistic). As such, it will not be possible to choose a threshold $\gamma$ such that the false positive probability is controlled at level $\alpha = 0.05$ and where it is also possible for $\max_k |T_{1,3}^k|$ to be greater than this value. In general for the Lepage test statistic, it can be shown that the minimum number of observations required for both these conditions to hold is 10. As such when we compute thresholds and subsample sequences, we restrict the minimum length of the sequences considered to be 10. Note that this does not mean that we require change points to be at separated by at least 10 observations in order to be detectable, since a detected change point in such a sequence of 10 observations will segment it into two sequences of smaller length.

2. An alternative to this pre-computing procedure would be to adaptively generate each $\gamma(\cdot)$ in real-time during the segmentation procedure using a permutation test, as was done in a CUSUM context by Olshen et al. [2014]. A potential advantage of this approach is that it allows the choice of each $\gamma$ to be sensitive to the previous split points, and would also (e.g.) allow the threshold level $\alpha$ to be changed adaptively, perhaps gradually lowering it after
Algorithm 1 WBS-Lepage

1: Choose a value for $\alpha$ on which the $\gamma$ thresholds are based
2: **Initialization:** Call WBS-LP($y$, 1, $n$) to find all change points in $y = (y_1, \ldots, y_n)$
3: 
4: **procedure** WBS-LP($y$, $p$, $q$)
5: For each $y_i$ where $p \leq i \leq q$, replace $y_i$ with its rank $r_i = \sum_{j=p}^{q} I(y_i \geq y_j)$
6: Compute $T_{p,q}^{WBS}$ from Equation [5]
7: Let $\gamma(q-p)$ be the precomputed threshold corresponding to $\alpha$.
8: if $T_{p,q}^{WBS} > \gamma(q-p)$ then
9: Let $(s_0, e_0) = \arg \max_{m} T_{s_0,e_0}^{WBS}$
10: Let $\hat{k} = \arg \max_{k} T_{s_0,e_0}^{k}$
11: Return $\bigcup \{\{WBS-LP(y, p, \hat{k})\}, \{\hat{k}\}, \{WBS-LP(y, \hat{k}+1, q)\}\}$
12: else
13: Return $\{\emptyset\}$
14: Prune the resulting change points as described in Section 2.5

2.5 Pruning

A potential issue when using WBS is that, like binary segmentation, the location of each change point is estimated in a greedy manner and is not adjusted based on additional change points that are found at later stages in the segmentation procedure. This can sometimes result in an overestimation of the number of change points if a single change point ends up getting detected twice. Suppose that when WBS is used on a sequence, the first change point is estimated to occur at location $\hat{k}_1$. The sequence is then split into two segments, and WBS is applied recursively to each. Suppose this results in two further change points being found at locations $\hat{k}_0$ and $\hat{k}_2$ such that $\hat{k}_0 < \hat{k}_1 < \hat{k}_2$. It may be the case that given $\hat{k}_0$ and $\hat{k}_2$, the change point at $\hat{k}_1$ is not needed, i.e. that the observations between $\hat{k}_0$ and $\hat{k}_2$ are identically distributed.

This issue was noticed as far back as Inclan and Tiao [1994] but hasn’t always been taken into account in the subsequent literature. We will use a procedure similar to that discussed in Inclan and Tiao [1994] to prune the change points found by WBS via a post-processing step. Suppose that the WBS-Lepage algorithm finds $K$ change points that have been estimated to occur at locations $\hat{\tau}_1 < \ldots < \hat{\tau}_K$. For notational convenience we write $\hat{\tau}_0 = 0$ and $\hat{\tau}_{K+1} = n$. For each $k \in 1, \ldots, K$ we will make a decision whether $\hat{\tau}_k$ should be pruned. This is done by performing the following hypothesis test, which tests whether the observations between $\hat{\tau}_{k-1}$ and $\hat{\tau}_{k+1}$ are identically distributed:

$$H_0 : y_{\tau_{k-1}+1}, \ldots, y_{\tau_{k+1}} \sim_{i.i.d} F_0$$

$$H_1 : \exists k : y_{\tau_{k-1}+1}, \ldots, y_k \sim_{i.i.d} F_1, \quad y_{k+1}, \ldots, y_{\tau_{k+1}} \sim_{i.i.d} F_2, \quad F_1 \neq F_2$$

This is carried out using the same WBS procedure described above, i.e. we compute the maximized Lepage statistic over $\hat{M}$ randomly chosen subsequences of $y_{\tau_{k-1}+1}, \ldots, y_{\tau_{k+1}}$ to form $T_{\tau_{k-1}+1, \tau_{k+1}}^{WBS}$ and compare this to the threshold $\gamma(\hat{\tau}_{k+1} - \hat{\tau}_{k-1})$. If the null hypothesis is not rejected, then we delete $\hat{\tau}_k$ from the list of change points. Note that since this post-processing step only involves the removal of change points rather than the creation of new ones, it cannot increase the false positive rate of tests used in the WBS procedure. The improvement in performance that comes from this pruning step will be studied in Section 3.3.
3 Experiments

We now investigate the performance of our proposed WBS-Lepage method for detecting location-scale changes. We will compare its performance to three other recently proposed methods for nonparametric change detection. The first is the divisive partitioning approach from Matteson and James [2014] which is implemented in the ecp R package [James and Matteson, 2015]. This uses a type of binary segmentation to perform change detection in multivariate sequences, but is also applicable in our univariate setting. The second method is that of [Zou et al., 2014] which estimates change points using a penalized cost function approach. Specifically, they utilize a nonparametric maximum likelihood estimate, penalized by a BIC-type penalty. While their approach is computationally demanding, an extension using the PELT (Pruned Linear Exact Time [Killick et al., 2012]) algorithm was introduced by Haynes et al. [2017] which has been implemented in the changepoint.np R package [Haynes et al., 2021] and we use this version. The third method we compare to is the PYWR method from [Padilla et al., 2021] which also uses a WBS-type approach although with different test statistics and thresholding than ours. We use the R implementation which they provide alongside their paper. For our own WBS-Lepage procedure, we choose $\gamma(\cdot)$ such that the false positive rate is controlled at the level of $\alpha = 0.05$, and utilize the pruning step described in Section 2.5.

3.1 False Positives

In many situations it will not be known in advance whether the sequence being studied contains any change points at all. In this case, it is desirable for a change point detection algorithm to avoid false positive detections, and to correctly estimate that no change points have occurred.

Due to the way the thresholds were constructed in Section 2.4 our WBS algorithm is guaranteed to control the false positive rate at the desired level (such as $\alpha = 0.05$). The ECP algorithm is also based around hypothesis testing and hence offers a similar guarantee. However approaches such as PELT which are based only on optimizing a penalized cost function offer no such guarantees. This is not necessarily a flaw, since the guaranteed control of false positives reflects a strongly frequentist attitude to statistical inference which is not universally accepted. Nonetheless, a change detection algorithm which is highly likely to find that change points have occurred when in fact they have not, will have limited practical utility in some situations.

To explore this further, we carry out the following simulation: we independently simulated 50,000 sequences from each from the following three distributions: 1) Normal(0,1), 2) Student-t(3), and 3) Lognormal(1,1/2). The latter two are examples of a heavy-tailed and a skewed distribution respectively. Each of these 50,000 sequences consists of 100 independent observations, and does not contain any change points. The WBS, ECP and PELT algorithms were then applied to each sequence. Since there are no change points in any of the sequences, any detected change points will be false positives. For both WBS and ECP we set the false positive rate to be $\alpha = 0.05$. For PELT, we tried a variety of cost functions implemented in the changepoint.np package, specifically the Bayesian Information Criterion (BIC), the Modified BIC (MBIC) and the Strengthened Information Criterion (SIC). For PYWR we used the default parameter settings in the authors code.

Table 1 shows the proportion of sequences in which a change point was detected. For the WBS-Lepage and ECP procedures, the false positive rate is correctly bounded by $\alpha = 0.05$ regardless of the data distribution, i.e. there is less than a 5% probability of incorrectly flagging that at least one change point has occurred, when the sequence actually contains no change points. This reflects their nonparametric nature and allows the false positive rate to be controlled regardless of the sequence distribution. While the PYWR algorithm does not provide any guaranteed control of the false positive rate, it does in practice also incur only a low number of false positive detections. However the PELT approach suffers from a severely high rate of false positives, with the BIC and SIC penalties incorrectly flagging that a change has occurred in 99% of sequences, regardless of the data distribution. The MBIC penalty does slightly better and only flags in around 40% of cases. This makes the PELT approach questionable in situations where it reasonable to expect that the sequence may not contain any change points.
We now explore how our method performs on a number of simulated data sets. Specifically, we use two metrics. The first assesses whether the change detection algorithm can correctly recover the true number of change points. The second assesses whether the change point:

3.2 Change Detection Performance

We now explore how our method performs on a number of simulated data sets. Specifically, we consider the following four data models which have previously been studied in the change point literature:

- **fms data**, previously studied by Fryzlewicz [2014], Frick et al. [2014]. This data consists of 497 observations with $K = 6$ change points at locations $\tau = \{39, 226, 243, 300, 309, 333\}$. The sequence means in each segment are respectively 0.18, 0.08, 1.07, $-0.53, 0.16, -0.69, -0.16$ and the standard deviation $\sigma = 0.3$ is constant.

- **mix data**, previously studied by Fryzlewicz [2014]. This consists of 560 observations with $K = 13$ change points at locations $\tau = \{11, 21, 41, 61, 91, 121, 161, 201, 251, 301, 361, 421, 491\}$. The sequence means in each segment are respectively 7, $-7, 6, -6, 5, -5, 4, -4, 3, -3, 2, -2, 1, -1$ and the standard deviation $\sigma = 4$ is constant.

- **dhk data**, previously studied by Davies et al. [2012]. This consists of 1000 observations with $K = 9$ change points at locations $\tau = \{100, 200, 300, 400, 500, 600, 700, 800, 900\}$. The sequence standard deviations in each segment are respectively 2.5, 1, 2.5, 1, 2.5, 1, 2.5, 1 and the sequence mean $\mu = 0$ is constant.

- **kfe data**, previously studied by Killick et al. [2012]. This consists of 1000 observations with $K = 5$ change points. Unlike the other data models, these change points are not fixed, and are randomly generated from a uniform distribution on [30, 970] with the constraint that they must be at least 30 observations in each segment. The mean of the sequence $\mu = 0$ is constant, and the sequence standard deviations are randomly generated from a Lognormal(0, log(10/2)) distribution. Note that in the original version of this data studied by Killick et al. [2012] there were 10 change points; we have reduced the number to 5 since the nonparametric version of the segmentation task is substantially more challenging than the parametric version which they consider.

The first two data modes represent shifts in location, while the latter two are shifts in scale. We also consider a fifth data model which has not been previously studied and is intended to represent a short-duration location change inside a longer sequence: which is precisely the situation in which classic binary segmentation algorithms struggle since there is no obvious location to place a single change point:

- **interval data**. This data consists of 1000 observations with $K = 2$ change points at locations $\tau = \{490, 510\}$. The sequence means in each segment are respectively 0, 2, 0 and the standard deviation $\sigma = 1$ is constant.

For each of the five data models, we will consider the case where the error distribution is 1) Normal, 2) Student-t with 3 degrees of freedom, and 3) Lognormal(1, 1/2), giving 15 data models in total. The latter two distributions represent heavy-tailed and skewed distributions respectively. For each of these 15 types of data, 100 independent sequences were simulated. Figure 3 shows a typical sequence in each of these 15 data sets.

To measure performance, we use two metrics. The first assesses whether the change detection algorithm can correctly recover the true number of change points. The second assesses whether the
Algorithm can correctly identify their locations. For a particular data model, let $K$ denote the true number of change points and $\hat{K}_i$ denote the estimated number of change points in the $i^{th}$ simulated data set where $i \in \{1, 2, \ldots, 100\}$. Similarly, let $\tau = \{\tau_1, \ldots, \tau_K\}$ denote the true location of the change points, and $\hat{\tau}_i = \{\hat{\tau}_{i,1}, \ldots, \hat{\tau}_{i,K}\}$ be their estimated locations in the $i^{th}$ data set. The two metrics are:

1. $\frac{1}{100} \sum_{i=1}^{100} |K - \hat{K}_i|$, i.e. the average absolute error in the estimated number of change points

2. $\frac{1}{100K} \sum_{i=1}^{100} \sum_{k=1}^{K} I(\tau_k \in \hat{\tau}_i)$, i.e. the proportion of true change points which are estimated to be in the correct location.

The second metric only counts a change point as being correctly detected if its location is predicted with exact accuracy. Since this is fairly challenging for sequences where the changes are not of a
| Data | Method  | Normal | Student-t(3) | LNorm(1,1/2) |
|------|---------|--------|-------------|--------------|
| fms  | WBS-LP  | 0.32   | 0.37        | 0.19         |
|      | ECP     | 0.09   | 0.11        | 0.06         |
|      | PELT-MBIC | 0.12   | 0.45        | 0.22         |
|      | PYWR    | 1.92   | 1.31        | 1.43         |
| mix  | WBS-LP  | 1.44   | 1.02        | 0.77         |
|      | ECP     | 0.95   | 0.25        | 0.55         |
|      | PELT-MBIC | 1.17   | 0.86        | 0.74         |
|      | PYWR    | 5.60   | 4.29        | 4.72         |
| interval | WBS-LP | 0.21   | 0.31        | 0.15         |
|       | ECP     | 0.10   | 0.18        | 0.13         |
|       | PELT-MBIC | 1.30   | 1.88        | 1.96         |
|       | PYWR    | 2.21   | 2.36        | 2.11         |
| dhk  | WBS-LP  | 0.45   | 0.52        | 0.34         |
|      | ECP     | 7.10   | 7.84        | 0.38         |
|      | PELT-MBIC | 1.78   | 1.85        | 1.71         |
|      | PYWR    | 8.55   | 8.80        | 4.41         |
| kfe  | WBS-LP  | 0.97   | 1.34        | 1.08         |
|      | ECP     | 2.64   | 2.75        | 2.78         |
|      | PELT-MBIC | 1.35   | 1.57        | 1.52         |
|      | PYWR    | 3.18   | 3.03        | 3.03         |

Table 2: Average absolute discrepancy \( \frac{1}{100} \sum_{i=1}^{100} |K - K_i| \) for each change point method computed over 100 realizations of each of the 15 data models. Lower numbers indicate better performance. The best method for each data model is highlighted in bold text.

large magnitude, we also consider a third metric which counts a change point as being correctly detected if it is estimated to have occurred within 2 observations (inclusive) on either side, i.e.:

3. \[ \frac{1}{100K} \sum_{i=1}^{100} \sum_{k=1}^{K} I(\exists \hat{\tau}_{i,j} \in \hat{\tau}_i \text{ such that } |\tau_k - \hat{\tau}_{i,j}| \leq 2), \]

We compare performance of nonparametric WBS to the ecp, changepoint.np (PELT) and PYWR methods discussed above. We use the MBIC version of PELT due to its lower false positive rate discussed above. Tables 2, 3 and 4 show the results of all these methods evaluated over the simulated data. We can draw the following conclusions:

1. When it comes to the identifying the correct number of change points, the WBS method performs the best when it comes to scale changes, while ECP is superior for location changes. However the extent to which ECP struggles with scale changes is notable, with it often failing to detect even a single change point on the dhk data despite it containing 9 change points.

2. The PYWR method performs relatively poorly on essentially every data set under all performance metrics.

3. The PELT method generally performs well for location changes although it somewhat struggles on the interval data, and consistently overestimates the number of change points. This is due to its tendency to incur false positive when faced with a long segment of observations which does not contain any change points.

4. When it comes to identifying the correct location of the change points, the ECP method performs very poorly. Its performance improves drastically when performance is judged on estimating the change point to within two observations of its true location. This suggests that it not a preferred approach when absolute accuracy is necessary. The performance of WBS and PELT is very similar when it comes to identifying the location of change points that correspond to location changes, with WBS being superior for scale changes.

In summary, these results show a strong performance by the WBS algorithm which tends to be the best at detecting scale shifts, while also performing reasonably well at detecting location shifts. While it is not the best method in every situation, it did not perform extremely badly in any situation either. The very poor performance of ECP in some of the scale shift settings means that ECP cannot be
recommended in these settings, and PYWR generally does not perform well. However it should be noted that an advantage of ECP is its ability to also detect changes in multivariate data, for which our WBS approach would not be appropriate. The difference between WBS and PELT is less drastic, with both giving similar performances for detecting location changes, with WBS being better for scale changes. However PELT’s tendency to flag for false positive detections in situations where there are no change points is a potential handicap in situations where there may not be any changes at all, or where the number of change points is small compared to the length of the sequence, as in the interval data.

3.3 The Impact of Pruning

In Section 2.5 we mentioned that Wild Binary Segmentation can still suffer from overestimating the number of change points due to its greedy nature, and recommended a pruning strategy to combat this. The above results utilized this pruning technique. It is potentially interesting to compare the extent to which pruning actually improves performance. To this end, Table 5 compares the performance of the pruned and unpruned version of the algorithm, according to the mean absolute discrepancy performance metric. It can be seen that pruning results in consistent and noticeable improvements in performance across most of the data sets. As such, its use can generally be recommended in practice compared to the unpruned version.

4 Real Data

We conclude with a real data example drawn from the field of stylometry, where statistical methods are used to answer literary authorship questions. Specifically we consider the case of Sir Terry Pratchett, a celebrated British author who wrote the Discworld series of fantasy novels, which consists of 41 books written over a 32 year period from 1983 to 2015. During 2007, Pratchett was diagnosed with Alzheimer’s disease [BBC News, 2015], although he continued to write for several years after this diagnosis. In [Ross, 2020] the authors developed a multivariate parametric change point model to analyse whether there was a detectable change in Pratchett’s writing style following this diagnosis. We reanalyze their dataset in a nonparametric manner.

In stylometry, it is common to represent texts as vectors containing the counts of frequently occurring words. Specifically, let \( w_1, \ldots, w_{200} \) denote the 200 most commonly occurring words across the whole corpus of Discworld books. Each of the 41 books can then be written as a vector \( y_i = (c_{i,1}, \ldots, c_{i,200}) \) where \( c_{i,j} \) denotes the number of times that word \( w_j \) appeared in book \( i \), with the books arranged in temporal order so that the first Discworld novel corresponds to vector \( y_1 \) and the last corresponds to vector \( y_{41} \). A 201st element \( c_{i,201} \) is also appended to each vector to count the number of words in the book which were not one of the 200 common words, so that the elements of each vector sum to the total number of words in the corresponding book. For reference, the list of the 200 most common words in the corpus is shown in Figure 4, reproduced from [Ross, 2020].

Given this data representation, [Ross 2020] developed a change point model using the Dirichlet-Multinomial distribution to test for a change point in the sequence of books \( y_1, \ldots, y_{41} \), to investigate whether Alzheimer’s may cause a detectable change in writing style that would show up in the usage pattern of these common words. This hypothesis is based on a substantial volume of stylometric evidence which has found that literary writing style can be effectively characterized through the use of commonly occurring words [Argamon and Levitan 2005]. The change point approach taken in [Ross 2020] is multivariate and explicitly treats each book as a 201 element vector. Since our WBS method is univariate, we will use a lower dimensional representation of this dataset. Specifically we project the 43x201 matrix of word counts down onto the principal components of its associated correlation matrix. We found that the first principal component did not reveal much useful information. However the second principal is shown in Figure 5 and displays evidence of structural change towards both the beginning and end of the sequence.

We deployed our WBS-Lepage method on this univariate sequence of 41 observations. Two change points were detected at locations \( i = 8 \) and \( i = 35 \) and are shown on Figure 5. The first change point most likely corresponds to a maturation of writing style from Pratchett’s early books into his main body of writing. The second change point immediately follows the release of his novel ‘Wintersmith’ in the year 2006. The next Discworld novel to be written after this change point was titled ‘Making Money’ and released in 2007. Since Pratchett’s Alzheimer’s diagnosis was publicly announced in the
Figure 4: List of the 200 most common words in the Discword corpus of 41 novels.

Figure 5: The left hand plot shows the 41 Discworld books projected onto the second principal component of the corpus. The right hand plot shows the same data with the two detected change-points superimposed as vertical lines.

year 2007, this provides some evidence that the change in writing style may indeed be connected to the diagnosis. These results are consistent with the findings of [Ross, 2020] who detected a similar change point using their Dirichlet-Multnomial approach.

5 Conclusion

The task of detecting multiple change points in a nonparametric setting has been under-explored, however recent developments have produced methods such as nonparametric maximum likelihood [Zou et al., 2014] and binary segmentation [Matteson and James, 2014] which are well-suited to this purpose. We have presented an alternative approach that combines wild binary segmentation with rank based hypothesis testing that competes extremely well with these existing methods on a variety of simulated data sets. Compared to the nonparametric maximum likelihood approach, our method is substantially better for detecting changes in scale, while being almost as effective as detecting changes in location. It also allows for the control of the false positive rate, which can be important in situations where the sequence does not contain any change points, or when the number of change points is small compared to the number of observations. In this situation, we find that the nonparametric maximum likelihood approach tends to overestimate the number of change points, which may not be desirable. A drawback of our method is the amount of computational time required to simulate from the null distribution of the test statistic in order to generate the $\gamma(n)$ thresholds. As such, we have provided an R implementation of our method in the npwbs package which contains our algorithm using these precomputed thresholds.
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Table 3: Percentage of change points which were estimated to be in their correct location, for each detector, averaged over 100 realizations of each of the 15 data models. Higher numbers indicate better performance. The best method for each data model is highlighted in bold text.

| Data | Method   | Normal | Student-t(3) | LNorm(1,1/2) |
|------|----------|--------|--------------|--------------|
| fms  | WBS-LP   | 0.63   | 0.73         | 0.70         |
|      | ECP      | 0.12   | 0.13         | 0.14         |
|      | PELT-MBIC| **0.64** | **0.74**     | **0.76**     |
|      | PYWR     | 0.14   | 0.15         | 0.18         |
| mix  | WBS-LP   | 0.48   | **0.62**     | 0.60         |
|      | ECP      | 0.09   | 0.06         | 0.07         |
|      | PELT-MBIC| **0.51** | 0.61         | **0.62**     |
|      | PYWR     | 0.00   | 0.00         | 0.00         |
| interval | WBS-LP | **0.57** | **0.75** | 0.70         |
|      | ECP      | 0.11   | 0.10         | 0.08         |
|      | PELT-MBIC| 0.57   | 0.74         | **0.71**     |
|      | PYWR     | 0.28   | 0.61         | 0.56         |
| dhk  | WBS-LP   | **0.29** | **0.21**     | 0.24         |
|      | ECP      | 0.02   | 0.01         | 0.10         |
|      | PELT-MBIC| **0.28** | 0.15         | **0.25**     |
|      | PYWR     | 0.01   | 0.00         | 0.12         |
| kfe  | WBS-LP   | **0.31** | 0.30         | **0.34**     |
|      | ECP      | 0.04   | 0.05         | 0.04         |
|      | PELT-MBIC| **0.31** | 0.24         | 0.31         |
|      | PYWR     | 0.04   | 0.04         | 0.06         |

Table 4: Percentage of change points which were estimated to be within 2 observations of their correct location, for each detector, averaged over 100 realizations of each of the 15 data models. Higher numbers indicate better performance. The best method for each data model is highlighted in bold text.

| Data | Method   | Normal | Student-t(3) | LNorm(1,1/2) |
|------|----------|--------|--------------|--------------|
| fms  | WBS-LP   | 0.90   | **0.95**     | 0.93         |
|      | ECP      | 0.88   | 0.94         | 0.94         |
|      | PELT-MBIC| **0.91** | 0.94         | **0.96**     |
|      | PYWR     | 0.57   | 0.66         | 0.62         |
| mix  | WBS-LP   | 0.76   | 0.88         | **0.86**     |
|      | ECP      | 0.82   | **0.90**     | 0.85         |
|      | PELT-MBIC| 0.79   | 0.86         | **0.86**     |
|      | PYWR     | 0.42   | 0.56         | 0.52         |
| interval | WBS-LP | **0.95** | **0.99** | **0.96**     |
|      | ECP      | 0.93   | 0.98         | 0.97         |
|      | PELT-MBIC| 0.93   | **0.99**     | 0.94         |
|      | PYWR     | 0.41   | 0.77         | 0.70         |
| dhk  | WBS-LP   | **0.70** | **0.58**     | 0.64         |
|      | ECP      | 0.09   | 0.04         | 0.57         |
|      | PELT-MBIC| **0.70** | 0.43         | **0.65**     |
|      | PYWR     | 0.02   | 0.00         | 0.23         |
| kfe  | WBS-LP   | **0.59** | **0.56**     | **0.62**     |
|      | ECP      | 0.38   | 0.35         | 0.35         |
|      | PELT-MBIC| 0.57   | 0.49         | 0.57         |
|      | PYWR     | 0.15   | 0.17         | 0.19         |
\begin{table}[h]
\centering
\begin{tabular}{|c|c|c|c|}
\hline
Data & Method & Normal & Student-t(3) & LNorm(1,1/2) \\
\hline
fms & WBS-Unpruned & 0.48 & 0.52 & 0.41 \\
    & WBS-Pruned & 0.32 & 0.37 & 0.19 \\
\hline
mix & WBS-Unpruned & 1.34 & 1.04 & 1.16 \\
    & WBS-Pruned & 1.44 & 1.02 & 0.77 \\
\hline
interval & WBS-Unpruned & 0.24 & 0.31 & 0.20 \\
    & WBS-Pruned & 0.21 & 0.71 & 0.15 \\
\hline
dnk & WBS-Unpruned & 0.62 & 0.71 & 0.60 \\
    & WBS-Pruned & 0.45 & 0.52 & 0.34 \\
\hline
kfe & WBS-Unpruned & 1.10 & 1.39 & 1.05 \\
    & WBS-Pruned & 1.07 & 1.38 & 1.05 \\
\hline
\end{tabular}
\caption{Average discrepancy $\frac{1}{100} \sum_{i=1}^{100} (K - K_i)$ for the pruned and unpruned version of the WBS method across each data set. Lower numbers indicate better performance.}
\end{table}