A computationally efficient nonparametric approach for changepoint detection

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Abstract

In this paper we build on an approach proposed by Zou et al. (2014) for nonparametric changepoint detection. This approach defines the best segmentation for a data set as the one which minimises a penalised cost function, with the cost function defined in term of minus a non-parametric log-likelihood for data within each segment. Minimising this cost function is possible using dynamic programming, but their algorithm had a computational cost that is cubic in the length of the data set. To speed up computation, Zou et al. (2014) resorted to a screening procedure which means that the estimated segmentation is no longer guaranteed to be the global minimum of the cost function. We show that the screening procedure adversely affects the accuracy of the changepoint detection method, and show how a faster dynamic programming algorithm, Pruned Exact Linear Time, PELT (Killick et al., 2012), can be used to find the optimal segmentation with a computational cost that can be close to linear in the amount of data. PELT requires a penalty to avoid under/over-fitting the model which can have a detrimental effect on the quality of the detected changepoints. To overcome this issue we use a relatively new method, Changepoints Over a Range of PenaltieS (CROPS) (Haynes et al., 2015), which finds all of the optimal segmentations for multiple penalty values over a continuous range. We apply our method to detect changes in heart rate during physical activity.

Keywords: nonparametric maximum likelihood, PELT, CROPS, activity tracking

1 Introduction

Changepoint detection is an area of statistics broadly studied across many disciplines such as acoustics (Guarnaccia et al., 2015; Lu and Zhang, 2002), genomics (Olshen et al., 2004; Zhang and Siegmund, 2007) and oceanography (Nam et al., 2014). Whilst the changepoint literature is vast, many existing methods are parametric. For example a common approach is to introduce a model for the data within a segment, use minus the maximum of the resulting log-likelihood to define a cost for a segment, and then define a cost of a segmentation as the sum of the costs for each of its segments. See for example Yao (1988); Lavielle (2005); Killick et al. (2012); Davis et al. (2006). Finally, the segmentation of the data is obtained as the one that minimises a penalised version of this cost (see also Frick et al., 2014, for an extension of these approaches).

A second class of methods are based on tests for a single changepoint, with the tests often defined based on the type of change that is expected (such as change in mean), and the distribution of the null-statistic for each test depending on further modelling assumptions for the data (see e.g. Bai and Perron, 1998; Dette and Wied, 2015). Tests for detecting a single change can then be applied recursively to detect multiple changes, for example using binary segmentation (Scott and Knott, 1974) or its variants (e.g. Fryzlewicz, 2014). For a review of alternative approaches for change detection see Jandhyala et al. (2013) and Aue and Horvth (2013).

Much of the existing literature on nonparametric methods look at single changepoint detection (Page, 1954; Bhattacharyya and Johnson, 1968; Carlstein, 1988; Dumbgen, 1991). Several approaches are based on using rank statistics such as the Mann-Whitney test statistic (Pettitt, 1979). Ross and Adams (2012) introduce the idea of using the Kolmogorov-Smirnov and the Cramer-von Mises test statistics; both of which use the empirical distribution function. Other methods include using kernel density estimations (Baron, 2000), however these can be computationally expensive to calculate.

There is less literature on the nonparametric multiple changepoint setting. The single change-

point detection methods which have been developed using nonparametric methods do not extend easily to multiple changepoints. Within the sequential changepoint detection literature one can treat the problem as a single changepoint problem which resets every time a changepoint is detected (Ross and Adams, 2012). Lee (1996) proposed a weighted empirical measure which is simple to use but has been shown to have unsatisfactory results. Under the multivariate setting Matteson and James (2013) proposed methods, E-divisive and e-cp3o, based on clustering and probabilistic pruning respectively. The E-divisive method uses an exact test statistic with an approximate search algorithm whereas the e-cp3o method uses an approximate test statistic with an exact search algorithm. As a result e-cp3o is faster but lacks slightly in the quality for the changepoints detected.

In this article we focus on univariate changepoint detection and we are interested in the work of Zou et al. (2014) who propose a nonparametric likelihood based on the empirical distribution. They then use a dynamic programming approach, Segment Neighbourhood Search (Auger and Lawrence, 1989), which is an exact search procedure, to find multiple changepoints. Whilst this method is shown to perform well, it has a computational cost of $\mathcal{O}(Mn^2 + n^3)$ where M is the number of changepoints and n is the length of the data. This makes this method infeasible when we have large data sets, particularly in situations where the number of changepoints increases with n. To overcome this, Zou et al. (2014) propose an additional screening step that prunes many possible changepoint locations. However, as we establish in this article, this screening step can adversely affect the accuracy of the final inferred segmentation.

In this paper we seek to develop a computationally efficient approach to the multiple changepoint search problem in the nonparametric setting. Our approach is an extension to the method of Zou et al. (2014). This firstly involves simplifying the definition of the segment cost, so that calculating the cost for a given segment involves computation that is $O(\log n)$ rather than O(n). Secondly we apply a different dynamic programming approach, Pruned Exact Linear Time (PELT) (Killick et al., 2012), that is substantially quicker than Segment Neighbourhood Search; for many situations where the number of changepoints increases linearly with n, PELT has been proven to have a computational cost that is linear in n.

We call the new algorithm nonparametric PELT (NP-PELT). A disadvantage of NP-PELT is that it requires the user to pre-specify a value by which the addition of a changepoint is penalised. The quality of the final segmentation can be sensitive to this choice, and whilst there are default choices these do not always work well. However we show that the Changepoints for a Range of PenaltieS (CROPS) algorithm (Haynes et al., 2015) can be used with NP-PELT to explore optimal segmentations for a range of penalties.

The rest of this paper is organised as follows. In Section 2 we give details of the NMCD approach proposed by Zou et al. (2014). In Section 3 we introduce our new efficient nonparametric search approach, nonparametric PELT (NP-PELT) and show how we can substantially improve the computational cost of this method. In Section 4 we demonstrate the performance of our method on simulated data sets comparing our method with NMCD. Finally in Section 5 we include some simulations which analyse the performance of NMCD for different scenarios and then we show how a nonparametric cost function can be beneficial in situations where we do not know the underlying distribution of the data. In order to demonstrate our method we use heart rate data recorded whilst an individual is running.

2 Nonparametric Changepoint Detection

2.1 Model

The model that we refer to throughout this paper is as follows. Assume that we have data, $x_1, ..., x_n \in \mathbb{R}$, that have been ordered based on some covariate information such as time or position along a chromosome. For $v \ge u$ we denote $x_{u:v} = \{x_u, ..., x_v\}$. Throughout we let mbe the number of changepoints, and the positions be $\tau_1, ..., \tau_m$. Furthermore we assume that τ_i is an integer and that $0 = \tau_0 < \tau_1 < \tau_2 < ... < \tau_m < \tau_{m+1} = n$. Thus our m changepoints split the data into m + 1 segments, with the *i*th segment containing $x_{\tau_{i-1}+1:\tau_i}$.

As in Zou et al. (2014) we will let $F_i(t)$ be the (unknown) cumulative distribution function (CDF) for the *i*th segment, and $\hat{F}_i(t)$ the empirial CDF. In other words

$$\hat{F}_i(t) = \frac{1}{\tau_i - \tau_{i-1}} \times \left(\sum_{j=\tau_{i-1}+1}^{\tau_i} \mathbf{1}\{x_j < t\} + 0.5 \times \mathbf{1}\{x_j = t\} \right).$$
(2.1)

Finally we let $\hat{F}(t)$ be the empirical CDF for the full data set.

2.2 Nonparametric maximum likelihood

If we have n data points that are independent and identically distributed with CDF F(t), then, for a fixed value of t, the empirical CDF will satisfy $n\hat{F}(t) \sim \text{Binomial}(n, F(t))$. Hence the log-likelihood of F(t) is given by: $n\{\hat{F}(t)\log(F(t)) + (1-\hat{F}(t))\log(1-F(t))\}$. This loglikelihood is maximised by the value of the empirical CDF, $\hat{F}(t)$. We can thus use minus the maximum value of this log-likelihood as a segment cost function. So for segment *i* we have a cost that is $-\mathcal{L}_{np}(x_{\tau_{i-1}+1:\tau_i};t)$ where

$$\mathcal{L}_{np}(x_{\tau_{i-1}+1:\tau_i};t) = (\tau_i - \tau_{i-1}) \times [\hat{F}_i(t)\log\hat{F}_i(t) + (1 - \hat{F}_i(t))\log(1 - \hat{F}_i(t))].$$
(2.2)

We can then define a cost of a segmentation as the sum of the segment costs. Thus to segment the data with *m* changepoints we minimise $-\sum_{i=1}^{m+1} \mathcal{L}_{np}(x_{\tau_{i-1}+1:\tau_i};t)$.

2.3 Nonparametric multiple changepoint detection

One problem with the segment cost as defined by (2.2) is that it only uses information about the CDF evaluated at one value of t and that the choice of t can have detrimental effects on the resulting segmentations. To overcome this Zou et al. (2014) suggest defining a segment cost which integrates (2.2) over different values of t. They suggest a cost function for a segment with data $x_{u:v}$ that is

$$\int_{-\infty}^{\infty} -\mathcal{L}_{np}(x_{u:v};t)dw(t), \qquad (2.3)$$

with a weight, $dw(t) = \{F(t)(1 - F(t))\}^{-1}dF(t)$, that depends on the CDF of the full data. This weight is chosen to produce a powerful goodness of fit test (Zhang, 2002). As this is unknown they approximate it by the empirical CDF of the full data, and then further approximate the integral by a sum over the data points. This gives the following objective function

$$Q_{\text{NMCD}}(\tau_{1:m}; x_{1:n}) = -n \sum_{i=1}^{m+1} \sum_{t=1}^{n} (\tau_i - \tau_{i-1}) \times \frac{\hat{F}_i(t) \log \hat{F}_i(t) + (1 - \hat{F}_i(t)) \log(1 - \hat{F}_i(t))}{(t - 0.5)(n - t + 0.5)}.$$
(2.4)

For a fixed m this objective function is minimised to find the optimal segmentation of the data.

In practice a suitable choice of m is unknown, and Zou et al. (2014) suggest estimating m using the Schwarz' Information criterion (Schwarz, 1978). That is, they minimise

SIC =
$$\min_{m;\tau_1,...,\tau_m} \{Q_{\text{NMCD}}(\tau_{1:m}; x_{1:n}) + m\xi_n\},$$
 (2.5)

where ξ_n is a sequence going to infinity.

2.4 NMCD Algorithm

To maximise the objective function (2.4), Zou et al. (2014) use the dynamic programming algorithm Segment Neighbourhood Search (Auger and Lawrence, 1989). This algorithm calculates the optimal segmentations, given a cost function, for each value of m = 1, ..., M, where M is a specified maximum number of changepoints to search for. If all the segment costs have been pre-computed then Segment Neighbourhood search has a computational cost of $\mathcal{O}(Mn^2)$. However for NMCD the segment cost involves calculating

$$\sum_{t=1}^{n} \frac{\hat{F}_i(t) \log \hat{F}_i(t) + (1 - \hat{F}_i(t)) \log(1 - \hat{F}_i(t))}{(t - 0.5)(n - t + 0.5)}$$

and thus calculating the cost for a single segment is O(n). Hence the cost of precomputing all segment costs is $O(n^3)$, and the resulting algorithm has a cost that is $O(Mn^2 + n^3)$.

To reduce the computational burden when we have long data series, Zou et al. (2014) propose a screening step. They consider overlapping windows of length $2N_I$ for some $N_I \in \mathbb{R}$. For each window they calculate the Cramér-von Mises (CvM) statistic for a changepoint at the centre of the window. They then compare these CvM statistics, each corresponding to a different changepoint location, and remove a location as a candidate changepoint if its CvM statistic is smaller than any of the CvM statistics for locations within N_I of it. The number of remaining candidate changepoint positions is normally much smaller than n and thus the computational complexity can be substantially reduced. The choice of N_I is obviously important, with larger values leading to the removal of more putative changepoint locations, but at the risk or removing true changepoint locations. In particular, the rationale for the method is based on N_I being smaller than any segment that you wish to detect. As a default, Zou et al. (2014) recommend choosing $N_I = \lceil (\log n)^{3/2}/2 \rceil$ where $\lceil x \rceil$ denotes the smallest integer which is larger than x.

3 NP-PELT

Here we develop a new, computationally efficient, way to segment data using a cost function based on (2.3). This involves firstly an alternative numerical approximation to the integral (2.3), which is more efficient to calculate. In addition we use a more efficient dynamic programming algorithm, PELT (Killick et al., 2012), to then minimise the cost function.

3.1 Improved Segment Cost

To reduce the cost of calculating the segment cost, we approximate the integral by a sum with $K \ll n$ terms. The integral in (2.3) involves a weight, and we first make a change of variables to remove this weight.

Lemma 3.1. Let $c = -\log(2n-1)$. For $x \in [-1,1]$ define $p(x) = (1 + \exp\{cx\})^{-1}$. Then

$$\int_{\frac{1}{2n}}^{\frac{2n-1}{2n}} \mathcal{L}_{np}(x_{u:v};t) \{F(t)(1-F(t))\}^{-1} dF(t) = -c \int_{-1}^{1} \mathcal{L}_{np}(x_{u:v};F^{-1}(p(x))) dx.$$
(3.1)

Proof. This follows from making the change of variable F(t) = p(x).

Using Lemma 3.1, we suggest the following approximation, based on an approximation of (3.1) using K evenly spaced x-values. Fix K, and define γ such that $K = c/\gamma$, with c defined as in Lemma 3.1. Let t_1, \ldots, t_K be such that t_k is the $(1+(2n-1)\exp\{\gamma(2k-1)\})^{-1}$ empirical quantile of the data, then we approximate (2.3) by

$$\mathcal{C}_K(x_{u:v}) = \frac{-2c}{K} \sum_{k=1}^K \mathcal{L}_{np}(x_{u:v}; t_k).$$

$$(3.2)$$

The idea is that (2.3) gives higher weight to values of t in the tail of the distribution of the data. Our approximation achieves this through a sum where each term has equal weight, but where the t_k values we choose are prefentially chosen from the tail of the distribution.

The cost now for calculating the segment costs is $\mathcal{O}(K)$. If we choose $K = \lceil c/\gamma \rceil$, where c is defined in Lemma 3.1, for some fixed γ then this will be $O(\log n)$. We investigate the choice of K empirically in Section 4.

3.2 Use of PELT

We now turn to consider how the PELT approach of Killick et al. (2012) can be incorporated within this framework. The PELT dynamic programming algorithm is able to solve minimisation problems of the form

$$Q_{\text{PELT}}(x_{1:n}) = \min_{m,\tau_{1:m}} \left\{ \sum_{i=1}^{m+1} [\mathcal{C}_K(x_{\tau_{i-1}+1:\tau_i}) + \xi_n] \right\}.$$

It jointly minimises over both the number and position of the changepoints, but requires the prior choice of ξ_n , the penalty value for adding a changepoint. The PELT algorithm uses the fact that $Q_{\text{PELT}}(x_{1:n})$ is the solution of the recursion, for v > 1

$$Q_{\text{PELT}}(x_{1:v}) = \min_{u < v} \left(Q_{\text{PELT}}(x_{1:u}) + \mathcal{C}_K(x_{u+1:v}) + \xi_n \right).$$
(3.3)

The interpretation of this is that the term in the brackets on the right-hand side of Equation 3.3 is the cost for segmenting $x_{1:v}$ with the most recent changepoint at u. We then optimise over the location of this most recent changepoint. Solving the resulting set of recursions leads to an $O(n^2)$ algorithm (Jackson et al., 2005), as (3.3) needs to be solved for $v = 2, \ldots, n$; and solving (3.3) for a given value of v involves a minimisation over v terms.

The idea of PELT is that we can substantially speed up solving (3.3) for a given v by reducing the set of values of u we have to minimise over. This can be done through a simple rule that enables us to detect time points u which can never be the optimal location of the most recent changepoint at any subsequent time. For our application this comes from the following result **Theorem 3.2.** If at time v, we have u < v such that

$$Q_{PELT}(x_{1:u}) + \mathcal{C}_K(x_{u+1:v}) \ge Q_{PELT}(x_{1:v}), \tag{3.4}$$

then for any future time T > v, u can never be the time of the optimal last changepoint prior to T.

Proof. This follows from Theorem 3.1 of Killick et al. (2012), providing we can show that for any u < v < T

$$\mathcal{C}_K(x_{u+1:T}) \ge \mathcal{C}_K(x_{u+1:v}) + \mathcal{C}_K(x_{v+1:T}).$$
(3.5)

As $\mathcal{C}_K(\cdot)$ is a sum of k terms, each of the form $-\mathcal{L}_{np}(\cdot; t_k)$ we need only show that for any t

$$\mathcal{L}_{np}(x_{u+1:T};t) \le \mathcal{L}_{np}(x_{u+1:v};t) + \mathcal{L}_{np}(x_{v+1:T};t).$$

Now if we introduce notation that $\hat{F}_{u,v}(t)$ is the empirical CDF for data $x_{u:v}$, we have

$$\mathcal{L}_{np}(x_{u+1:T};t) = (T-u)[\hat{F}_{u,T}(t)\log(\hat{F}_{u,T}(t)) + (1-\hat{F}_{u,T}(t))\log(1-\hat{F}_{u,T}(t))]$$

$$= \{(v-u)[\hat{F}_{u,v}(t)\log(\hat{F}_{u,T}(t)) + (1-\hat{F}_{u,v}(t))\log(1-\hat{F}_{u,T}(t))]$$

$$+ (T-v)[\hat{F}_{v,T}(t)\log(\hat{F}_{u,T}(t)) + (1-\hat{F}_{v,T}(t))\log(1-\hat{F}_{u,T}(t))]\}$$

$$\leq \mathcal{L}_{np}(x_{u+1:v};t) + \mathcal{L}_{np}(x_{v+1:T};t),$$

as required.

Thus at each time-point we can check whether (3.4) holds, and if so prune time-point u. Under certain regularity conditions, Killick et al. (2012) show that for models where the number of changepoints increases linearly with n, such substantial pruning occurs that the PELT algorithm will have an expected computational cost that is O(n). We call the resulting algorithm we obtain nonparametric PELT (NP-PELT).

4 Results

4.1 Performance of NMCD

We firstly compare the NMCD algorithm with (NMCD+) and without screening (NMCD) using the nmcdr R package (Zou and Zhange (2014)), with the default choices for N_I and ξ_n detailed in Section 2.3. We set up a similar simulation as in Zou et al. (2014). That is, we simulate data from the following three models, where $J(x) = \{1 + sgn(x)\}/2$.

Model 1: $x_i = \sum_{j=1}^M h_j J(nt_i - \tau_j) + \sigma \xi_i$, where

$$\{\tau_j/n\} = \{0.1, 0.13, 0.15, 0.23, 0.25, 0.40, 0.44, 0.65, 0.76, 0.78, 0.81\},\$$

$$\{h_j\} = \{2.01, -2.51, 1.51, -2.01, 2.51, -2.11, 1.05, 2.16, -1.56, 2.56, -2.11\},\$$

and there are n equally spaced t_i in [0, 1].

Model 2:
$$x_i = \sum_{j=1}^M h_i J(nt_i - \tau_j) + \sigma \xi_i \prod_{j=1}^{\sum_{j=1}^M J(nt_i - \tau_j)} v_j$$
, where
 $\{\tau_j/n\} = \{0.20, 0.40, 0.65, 0.85\}, \{h_j\} = \{3, 0, -2, 0\}, \text{ and } \{v_j\} = \{1, 5, 1, 0.25\}.$

Model 3: $x_i \sim F_j(x)$, where $\tau_j/n = \{0.20, 0.50, 0.75\}$, j = 1, 2, 3, 4, and $F_1(x), ..., F_4(x)$ corresponds to the standard normal, the standardized $\chi^2_{(3)}$ (with zero mean and unit variance), the standardized $\chi^2_{(1)}$ and the standard normal distribution respectively.

The first model has M = 11 changepoints, all of which are changes in location. Model 2 has both changes in location and in scale and model 3 has changes in skewness and in kurtosis. For the first two models we also consider three distributions for the error, ξ_i : N(0, 1), Student's tdistribution with 3 degrees of freedom and the standardised chi-square distribution with one degree of freedom, $\chi^2_{(1)}$.

To compare both the NMCD and NMCD+ we look at the proportion of true positive change-

		$\xi(\mathbf{C} \hat{\mathbf{C}})$			$\xi(\hat{\mathbf{C}} \mathbf{C})$			TIME	
(I)	NMCD+	NMCD	NPPELT+	NMCD+	NMCD	NPPELT+	NMCD+(s)	NMCD(min)	NPPPELT+(s)
N(0, 1)	0.91(0.08)	0.93(0.07)	0.92(0.07)	0.09(0.08)	0.07(0.07)	0.08(0.07)	1.89(1.08)	19.57(1.08)	1.49(0.02)
$t_{(3)}$	0.76(0.13)	0.81(0.12)	0.79(0.12)	0.24(0.13)	0.23(0.12)	0.21(0.12)	2.00(0.36)	20.91(0.36)	1.62(0.07)
$\chi^{2}_{(3)}$	0.83(0.10)	0.91(0.08)	0.90(0.09)	0.17(0.10)	0.10(0.09)	0.10(0.09)	2.43(0.26)	19.4(0.26)	1.57(0.02)
(II)									
N(0, 1)	0.39(0.17)	0.58(0.22)	0.57(0.22)	0.63(0.17)	0.45(0.21)	0.43(0.22)	1.92(1.25)	19.38(1.24)	3.16(0.19)
$t_{(3)}$	0.33(0.16)	0.48(0.21)	0.50(0.21)	0.69(0.16)	0.57(0.20)	0.50(0.21)	1.92(0.25)	19.77(0.25)	3.92(0.43)
$\chi^{2}_{(3)}$	0.35(0.17)	0.49(0.21)	0.48(0.22)	0.66(0.17)	0.51(0.21)	0.52(0.22)	1.90(0.31)	21.76(0.31)	3.48(0.20)
(III)									
	0.36(0.24)	0.48(0.26)	0.45(0.24)	0.64(0.24)	0.53(0.26)	0.55(0.24)	0.06(0.28)	30.90(1.09)	3.34(0.12)

Table 1: Comparison of NCMD and NMCD+ methods. Values in the table are mean (standard deviation in parentheses) for 100 replications.

points, $\xi(\mathbf{C}||\hat{\mathbf{C}})$, and false positive changepoints, $\xi(\hat{\mathbf{C}}||\mathbf{C})$, i.e.,

$$\xi(\mathbf{C}||\hat{\mathbf{C}}) = \frac{\#\mathbf{C} \in \hat{\mathbf{C}}}{n_{\mathbf{C}}} \text{ and } \xi(\hat{\mathbf{C}}||\mathbf{C}) = \frac{\#\hat{\mathbf{C}} \notin \mathbf{C}}{n_{\hat{\mathbf{C}}}}, \tag{4.1}$$

where $\hat{\mathbf{C}}$ are the estimated changepoints; \mathbf{C} are the true changepoints; $n_{\hat{\mathbf{C}}}$ is the length of the estimated changepoint set and $n_{\mathbf{C}}$ is the length of the true changepoint set. In addition we also compare the computational time taken to run both of these methods. The results can be seen in Table 1.

It is clear from Table 1 that using the screening step (NMCD+) significantly improves the computational cost for this method. However using this screening step comes at a cost of not correctly detecting the true changepoints. It can be seen that in all cases NMCD+ detects fewer true positives and more false positives than NMCD.

We now turn to consider the choice of the screening window N_I further. Using Model 1 with normal errors we can compare the results for different values of N_I . The default value for this data is $N_I = 10$, but we now repeat the analysis using $N_I \in \{1, ..., 12\}$. Figure 1a shows a bar plot of the number of times (in 100 simulations) that the window size resulted in the same changepoints as using NMCD without screening. Similarly Figure 1b looks at the number of true and false positives found using the different window lengths in the screening step. Figure 1c shows the computational time taken for NMCD+ with varying window lengths N_I . We found similar results for the other models.



Figure 1: (a) The number of replications out of 100 in which using NMCD+ with varying N_I results in the same results as NMCD without screening. (b) The proportion of true (black) and 1-False (red) changepoints detected with varying window size N_I . (c) The computational time (secs) for NMCD+ with increasing window size N_I .

It is clear that whilst in the majority of the cases NMCD+ with the different N_I gives the same result as NMCD but with an improved computational speed, there is a reasonable proportion of data sets where NMCD+ does not find the optimal segmentation. As a result the segmentations it obtains are less accurate.

The NMCD method also requires us to choose a penalty value in order to pick the best segmentation. The default choice appears to work reasonably well, but resulted in slight over-estimates of the number of changepoints for our three simulation scenarios. These overestimates suggest that the penalty value has been too small.

4.2 Comparison to NMCD

To compare NP-PELT to NMCD we initially used the same 3 models as above and again looked at the accuracy of the methods and the computational time. As before, to implement NMCD we used the nmcdr R package Zou and Zhange (2014) which has the bulk of the code in FORTRAN and we used R code to run NP-PELT. As R code is slower than FORTRAN, this means that the raw CPU timings we give will favour NMCD.

Firstly we investigate the speed up obtained by using the PELT pruning. We implement PELT with the same segment costs as NMCD, and call this NP-PELT. We found that NP-PELT was at least 60 times faster than NMCD to run, but that NP-PELT is still an order



Figure 2: (a) The proportion of true positive changepoints for a range of quantiles, K, in NP-PELT+ (solid) in comparison to NP-PELT (dashed). Black: n = 500, red: n = 1000, blue: n = 2000 and grey: n = 5000. (b) Relative speed of using NP-PELT+ compared to using NP-PELT. with varying number of quantiles, K. Black: n = 500, red: n = 1000, blue: n = 2000 and grey: n = 5000.

of magnitude slower than NMCD+.

4.3 Choice of *K* in NP-PELT

In order to use the improvement suggested in Section 3.1 for NP-PELT we first of all need to decide on an appropriate value for K. We use Model 1 again to assess the performance of NP-PELT using only K quantiles of the data (NP-PELT+), for a range of values of K, in comparison to NP-PELT using the full data set. Here we only look at the model with normal errors and simulate data-series with lengths n = (500, 1000, 2000, 5000). Further simulations using different error terms gave similar results. In order to assess performance we look at the proportion of true positives detected using both methods and also the computational cost. Again we use 100 replications. The results for the accuracy can be seen in Figure 2a.

We can see from Figure 2a that as the number of quantiles increases the proportion of true change points detected using NP-PELT+ converges to the same result as NP-PELT. As the

length of the data increases this convergence appears to happen more slowly, this can be seen from the grey lines in Figure 2a, which represent data of length 5000. We suggest using $K = \lceil 4 \log(n) \rceil$ in order to conserve as much accuracy as possible. This choice corresponds to K = 25, 28, 31 and 35 for n = 500, 1000, 2000 and 5000 respectively.

In addition to the accuracy we also look at the relative speed up of NP-PELT+ with various K values in comparison to NP-PELT, i.e.,

$\frac{(\text{speed of NP-PELT}+)}{\text{speed of NP-PELT}}.$

The results of this analysis can be seen in Figure 2b. Clearly as the number of quantiles increases the relative speed up decreases. This is expected since the number of quantiles is converging to the whole data set which is used in NP-PELT. We can also see that the relative speed up of NP-PELT+ increases with increasing data length.

4.4 Comparison of NMCD and NP-PELT+

We next compare NP-PELT+ with $K = 4 \log(n)$ to NMCD as above. For this we perform an equivalent analysis to that of Section 4.2. The results for NP-PELT+ can be found in Table 1. In terms of accuracy we can see that NP-PELT+ is comparable to NMCD and is significantly faster to run. In comparison to NMCD+, in Models 2 and 3 NP-PELT+ is slightly slower. This is to be expected however as the results of Killick et al. (2012) imply that the cost of PELT will tend to be lower in situations with more changepoints. In the first model there are 11 changepoints in data sets of length 1000, however in Models 2 and 3 there are only 4 changepoints. Despite this method being slower than NMCD+ it is more accurate.

5 Activity Tracking

In this section we apply NP-PELT+ to try to detect changes in heart rate during a run. Wearable activity trackers are becoming increasingly popular devices used to record step count, distances (based on the step count), sleep patterns and in some of the newer devices, such as the Fitbit change HR (Fitbit Inc., San Francisco, CA), heart rate. The idea behind these devices is that the ability to monitor your activity should help you lead a fit and active lifestyle. Changepoint detection can be used in daily activity tracking data to segment the day into periods of activity, rest and sleep.

Similarly, many keen athletes, both professional and amateur, also use GPS sports watches which have the additional features of recording distance and speed which can be very beneficial in training, especially in sports such as running and cycling. Heart rate monitoring during training can help make sure you are training hard enough without over training and burning out. Heart rate is the number of heart beats per unit time, normally we express this as beats per minute (bpm).

5.1 Changepoints in heart rate data

In the changepoint and signal processing literature many authors have looked at heart rate monitoring in different scenarios (see for example Khalfa et al. (2012); Galway et al. (2011); Billat et al. (2009); Staudacher et al. (2005)). Aubert et al. (2003) give a detailed review of the influence of heart rate variability in athletes. They highlight the difficulty of analysing heart rate measurements during exercise since no steady state is obtained due to the heart rate variability increasing according to the intensity of the exercise. They note that one possible solution is to pre-process the data to remove the trend.

In this section we apply NP-PELT+ to see whether changes can be detected in the raw heart rate time series without having to initially pre-process the data. We use a nonparametric approach since heart rate is a stochastic time dependent series and thus does not satisfy the conditions for an IID Normal model. However we will compare the performance had we assumed that the data was Normal in Section 5.3. The aim is to develop a method which can be used on data recorded from commercially available devices without the need to pre-process the data.

5.2 Range of Penalties

One disadvantage of NP-PELT+ over NMCD is that NP-PELT+ produces a single segmentation, which is optimal for the pre-chosen penalty value ξ_n . By comparison, NCMD finds a range of segmentations, one for each of m = 1, ..., M changepoints (though, in practice, the nmcdr package only outputs a single segmentation). Whilst there are default choices for ξ_n , these do not always work well, and there are advantages to being able to compare segmentations with different number of changepoints.

Haynes et al. (2015) propose a method, Changepoints over a Range Of PenaltieS (CROPS), which efficiently finds all the optimal segmentations for penalty values across a continuous range. This involves an iterative procedure which chooses values of ξ_n to run NP-PELT on, based on the segmentations obtained from previous runs of NP-PELT for different penalty values. Assume we have a given range $[\xi_{\min}, \xi_{\max}]$ for the penalty value, and the optimal segmentations at ξ_{\min} and ξ_{\max} have m_{\min} and m_{\max} changepoints respectively. Then CROPS requires at most $m_{\min} - m_{\max} + 2$ runs of NP-PELT to be guaranteed to find all optimal segmentations for $\xi_n \in [\xi_{\min}, \xi_{\max}]$. Furthermore, it is possible to recycle many of the calculations from early runs of NP-PELT to speed up the later runs.

5.2.1 Nonparametric Changepoint Detection

An example data set is given in Figure 4, where we show heart-rate, speed and elevation recorded during a 10 mile run. We will aim to segment this data using the heart-rate data only, but include the other two series in order that we may assess how well the segmentation of the heart-rate data relates to the obvious different phases of the run. In training many people use heart rate as an indicator of how hard they are working. There are different heart rate zones that you can train in each of which enhances different aspects of your fitness (BrainMacSportsCoach, 2015). The training zones are defined in terms of percentages of a maximum heart-rate: peak (90-100%), anaerobic (80-90%), aerobic (70-80%) and recovery (< 70%).

This example looks at detecting changes in heart rate over a long undulating run. We use CROPS with NP-PELT+ with $\xi_{min} = 25$, $\xi_{max} = 200$ and $K = 4 \log(n)$ (the results are similar for different K). In order to choose the best segmentation we use the approach



Figure 3: The cost vs number of changepoints plotted for (a) NP-PELT+ and (b) Change in slope. the red lines indicate the elbow and the blue circle highlights the point that we use as being the centre of the elbow.

suggested by Lavielle (2005). This involves plotting the segmentation cost against the number of changepoints and then looking for an "elbow" in the plot. The points on the "elbow" are then suggested to be the most feasible segmentations. The intuition for this method is that as more true changepoints are detected the cost will decrease however as we detect more changepoints we are likely to be detecting false positives and as such the cost will not decrease as much. The plot of the "elbow" for this example can be seen in Figure 3a. The elbow is not always obvious therefore the choice can be subjective however this gives us a method for roughly choosing the best segmentations which we can then explore further. We have highlighted the points on the "elbow" as the points which are between the two red lines. We decided from this plot that the segmentations with 9, 10, 12 and 13 changepoints are the best. We illustrate the segmentation with 10 changepoints, the number of changepoints at the centre of the elbow in Figure 3a indicated by the blue circle, in Figure 4. The segments have been colour coded based on the average heart-rate in each segment. That is red: peak, orange: anaerobic, yellow: aerobic and green: recovery. Alternative segmentations from the number of changepoints on the elbow can be found in the supplementary material.

We superimpose the changepoints detected in the heart rate onto the plots for speed and elevation to see if we can explain any of the changepoints. The first segment captures the "warm-up" where the heart-rate is on average in the recovery zone but is rising to the



Figure 4: Segmentations using NP-PELT+ with 10 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery.

anaerobic zone. The heart-rate in the second segment is in the anaerobic zone but changes to the peak zone in segment three. This change initially corresponds to an increase in speed and then it is because of the steep incline. The third changepoint matches up to the top of the elevation which is the start of the fourth segment where the heart-rate drops into the anaerobic zone whilst running downhill. The fifth segment is red which might be as a result of both the speed being slightly higher than the previous segment and consistent, and a slight incline in elevation. This is followed by a brief time in the aerobic zone which could be due to a drop in speed. The heart-rate in the next three segments stays in the anaerobic zone. The changepoints that split this section into three segments relate to the dip in speed around 75 minutes. In the final segment the heart-rate is in the peak zone which corresponds to an increase in elevation and an increase in speed (a sprint finish).

5.3 Piece-wise linear model

For comparison we look at estimating the changepoints based on a penalised likelihood approach that assumes the data is normally distributed with a mean that is piecewise linear within each segment. To find the best segmentation we use PELT with a segment cost proportional to minus the log-likelihood of our model:

$$C(y_{s:t}) = \min_{\theta_1, \theta_2} \sum_{u=s}^{t} (y_u - \theta_1 - u\theta_2)^2,$$
(5.1)

where θ_1 and θ_2 and the estimates of the segment intercept and slope, respectively. We use CROPS to find the best segmentation under this criteria for a range of penalties. The resulting elbow plot can be seen in Figure 3b. We can see that the number of changepoints for the feasible segmentations is similar to the number of changepoints for using NP-PELT+. Figure 5 shows the segmentation with 9 changepoints which we have deduced to being the number of changepoints in the centre of the elbow in Figure 3b. Alternative segmentations from the number of changepoints on the elbow can be found in the supplementary material.

It is obvious from the first look at Figure 5 that the change in slope method has not detected segments where the average heart-rate is different to the surrounding segments. The majority

of the plot is coloured orange with only changes in the first and last segments. The change in slope method splits the "warm-up" period into two segments whereas having this as one segment appears more appropriate. Unlike NP-PELT+ the change in slope does not detect changes which correspond to the change in elevation and thus NP-PELT+ appears to split the heart-rate data into more appropriate segments which relate to different phases of the run.

6 Conclusion

We have developed a new algorithm, NP-PELT, to detect changes in data series where we do not know the underlying distribution. This method is an adaption of the NMCD method proposed by Zou et al. (2014). The main advantage of NP-PELT over NMCD is that it is orders of magnitude faster. We initially reduced the time to calculate the cost of a segment from $\mathcal{O}(n)$ to $\mathcal{O}(\log n)$ by simplifying the definition of the segment cost. Zou et al. (2014) use a screening step to improve the computational time and even though this is slightly faster than NP-PELT we show that it isn't as accurate. We have also shown that non-parametric changepoint detection, using NP-PELT, holds promise for segmenting data from activity trackers. We were able to segment heart-rate data recorded during a run into meaningful segments that correspond to different phases of the run, and can be related to different regimes of heart-rate activity.

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Figure 5: Segmentations using change in slope with 9 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery. The solid black line in the top plot is the best fit for the mean within each segment.

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Figure 1: Segmentations using NP-PELT+ with 13 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery.



Figure 2: Segmentations using NP-PELT+ with 12 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery.



Figure 3: Segmentations using NP-PELT+ with 9 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery.





Figure 4: Segmentations using change in slope with 12 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery. The solid black line in the top plot is the best fit for the mean within each segment.



Figure 5: Segmentations using change in slope with 10 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery. The solid black line in the top plot is the best fit for the mean within each segment.



Figure 6: Segmentations using change in slope with 8 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery. The solid black line in the top plot is the best fit for the mean within each segment.



Figure 7: Segmentations using change in slope with 7 changepoints. We have colour coded the line based on the average heart-rate of each segment where red: peak, orange: anaerobic, yellow: aerobic and green: recovery. The solid black line in the top plot is the best fit for the mean within each segment.