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Optimal changepoint detection

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Workshop Plan

- What are changepoints?
- Notation
- Likelihood based changepoints
  - Change in mean
  - Change in variance
  - Change in mean & variance
- How many changes?
- Non-parametric changepoints
- Checking assumptions (if time allows)

There will be tasks throughout the sections.

What are Changepoints?

Changepoints are also known as:

- breakpoints
- segmentation
- structural breaks
- regime switching
- detecting disorder

and can be found in a wide range of literature including

- quality control
- economics
- medicine
- environment

What are changepoints?

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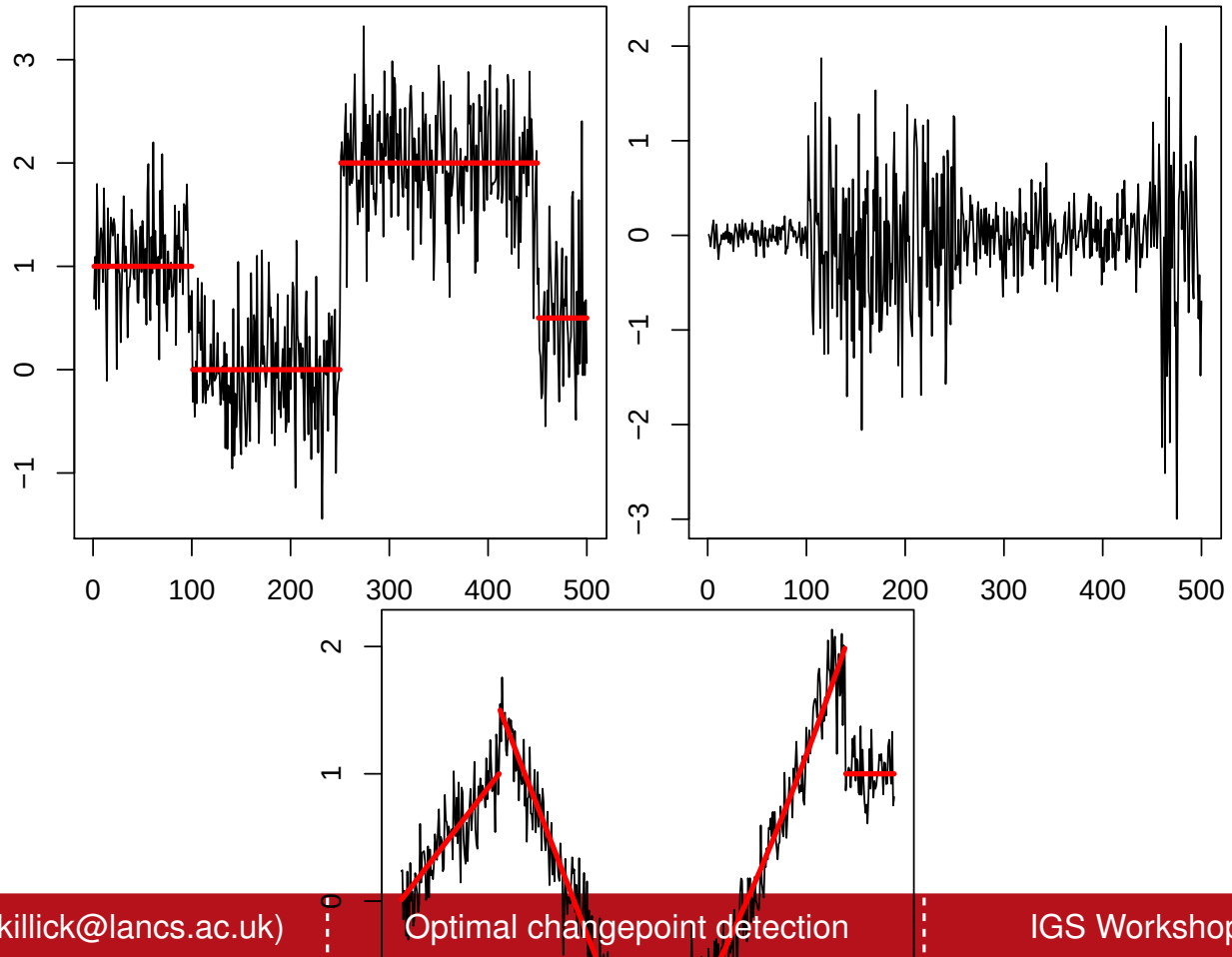
For data $y_1, \ldots, y_n$, if a changepoint exists at τ, then $y_1, \ldots, y_\tau$ differ from $y_{\tau+1}, \ldots, y_n$ in some way.

There are many different types of change.



What is the goal?

- Has a change occurred?
- If yes, where is the change?
- What is the difference between the pre and post change data?
  - Maybe this is the type of change
  - Maybe it is the parameter values before and after the change
- What is the probability that a change has occured?
- How certain are we of the changepoint location?
- How many changes have occurred (+ all the above for each change)?
- Why has there been a change?

Notation and Concepts

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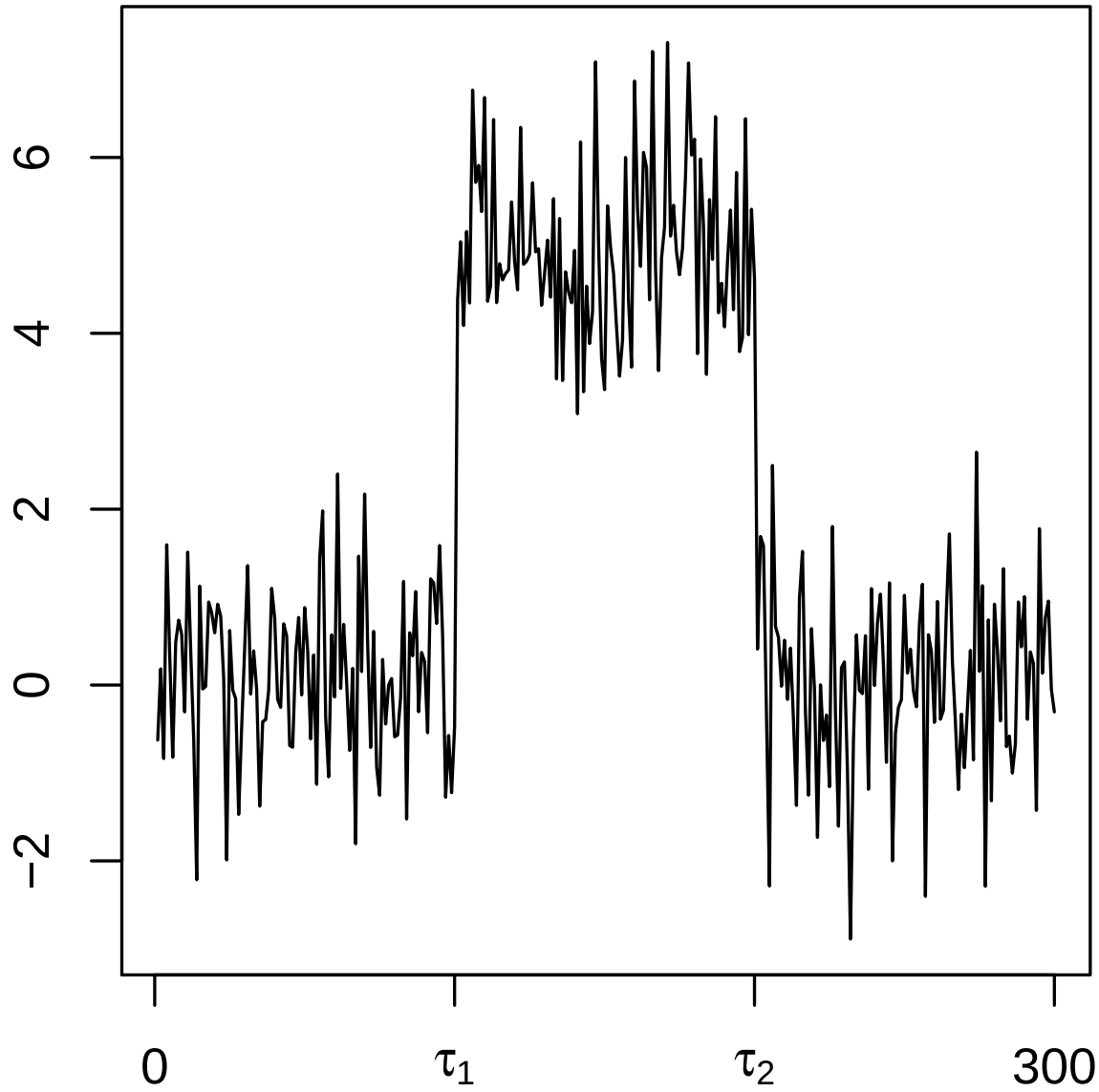
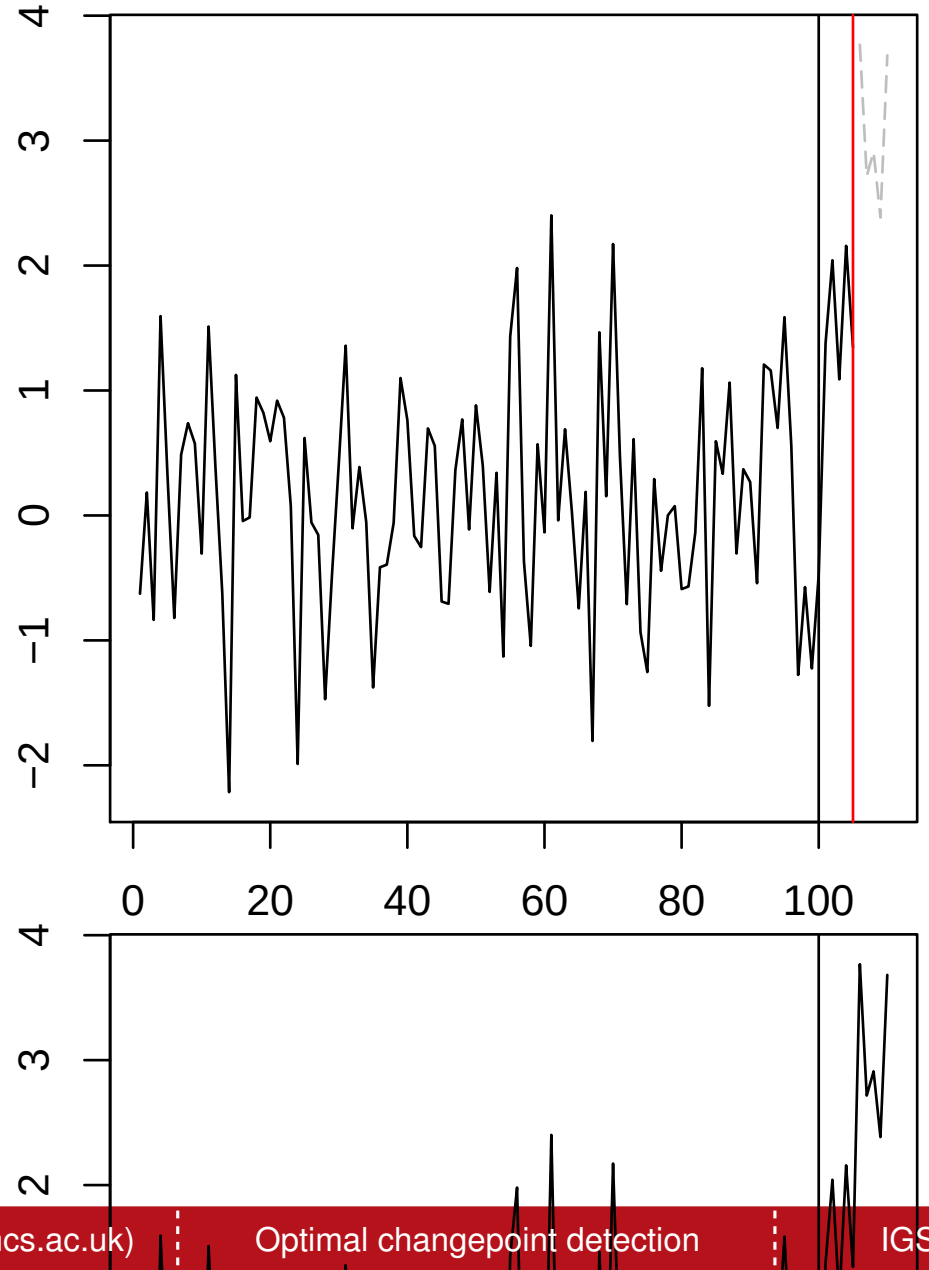


##Notation and Concepts Thus a changepoint model for a change in

Online vs Offline

- Online
  - Processes data as it arrives or in batches
  - Goal is quickest detection of a change
  - Often used in processing control, intrusion detection
- Offline
  - Processes all the data in one go
  - Goal is accurate detection of a change
  - Often used in genome analysis, audiology

Online vs Offline



Packages

Today we will use the

```
library(changepoint)
```

```
library(changepoint.np)
```

packages.

Other notable R packages are available for changepoint analysis including

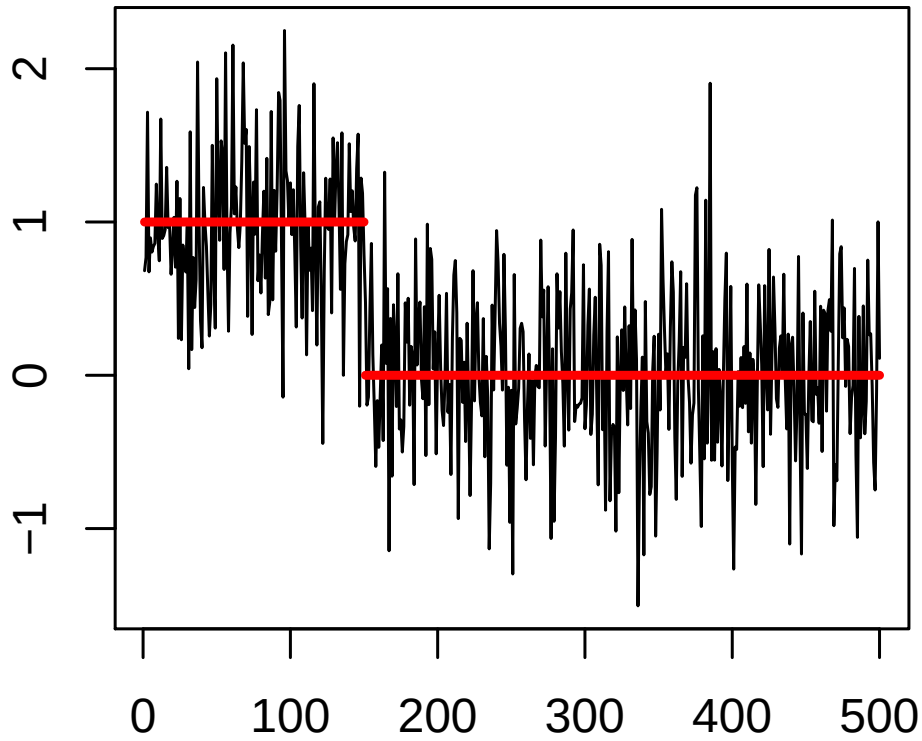
- `strucchange` - for changes in regression
- `bcp` - if you want to be Bayesian
- `cpm` - for online changes (`changepoint.online` coming soon)
- `EnvCpt` - for testing between changes in mean, trend and/or AR(1) structure

Single Changepoint

Assume we have time-series data where

$$y_t|\theta_t \sim \mathrm{N}(\theta_t, 1),$$

but where the means, θ_t, are piecewise constant through time with a single change.



Single Changepoint

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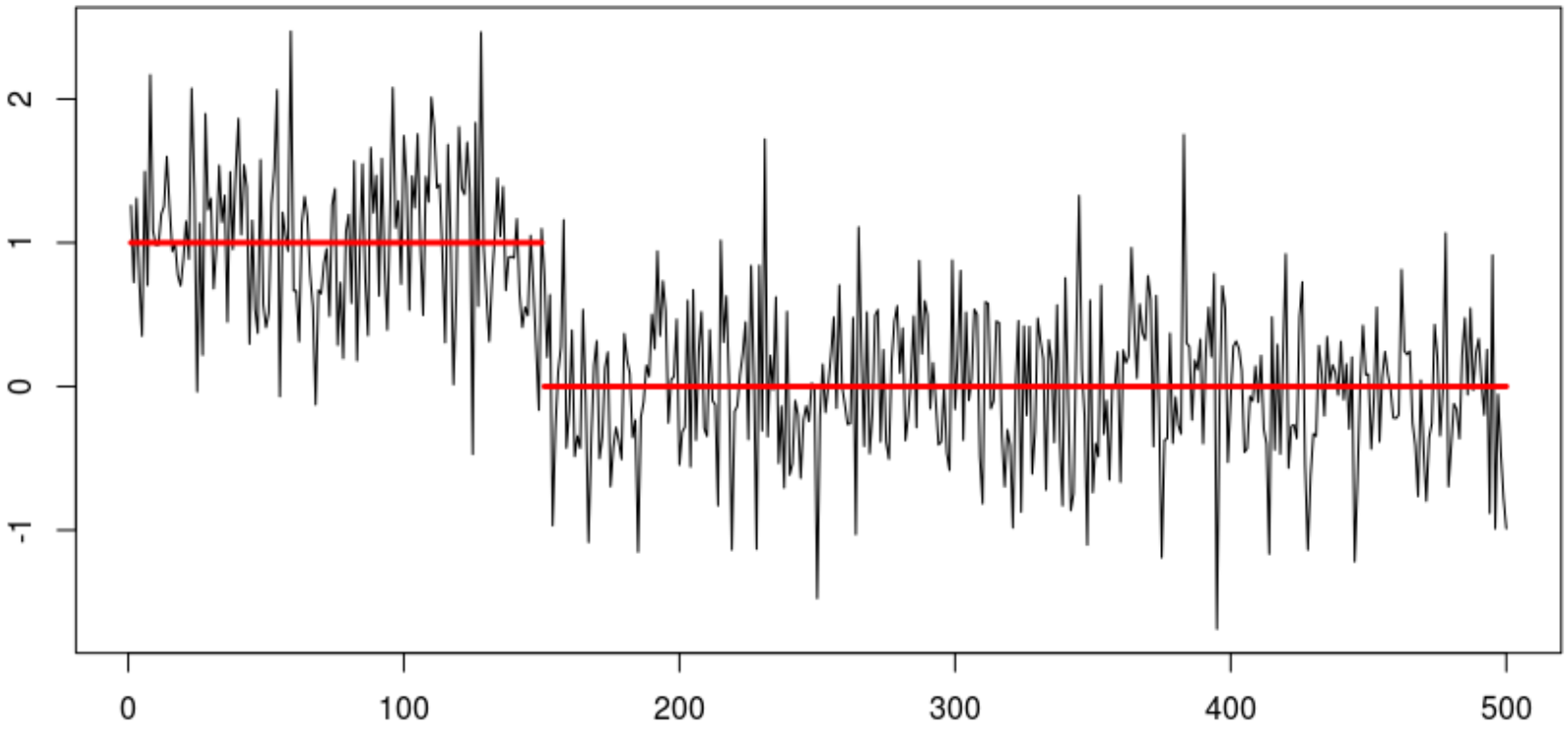
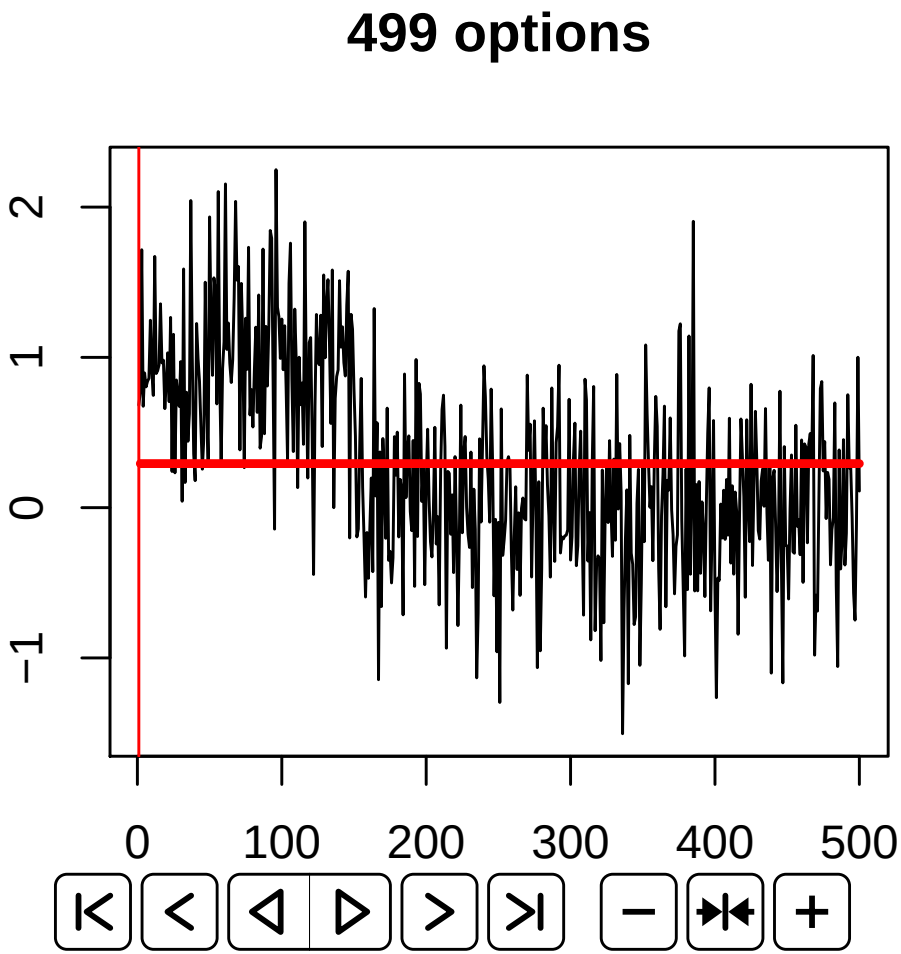
Fit for whole data

=

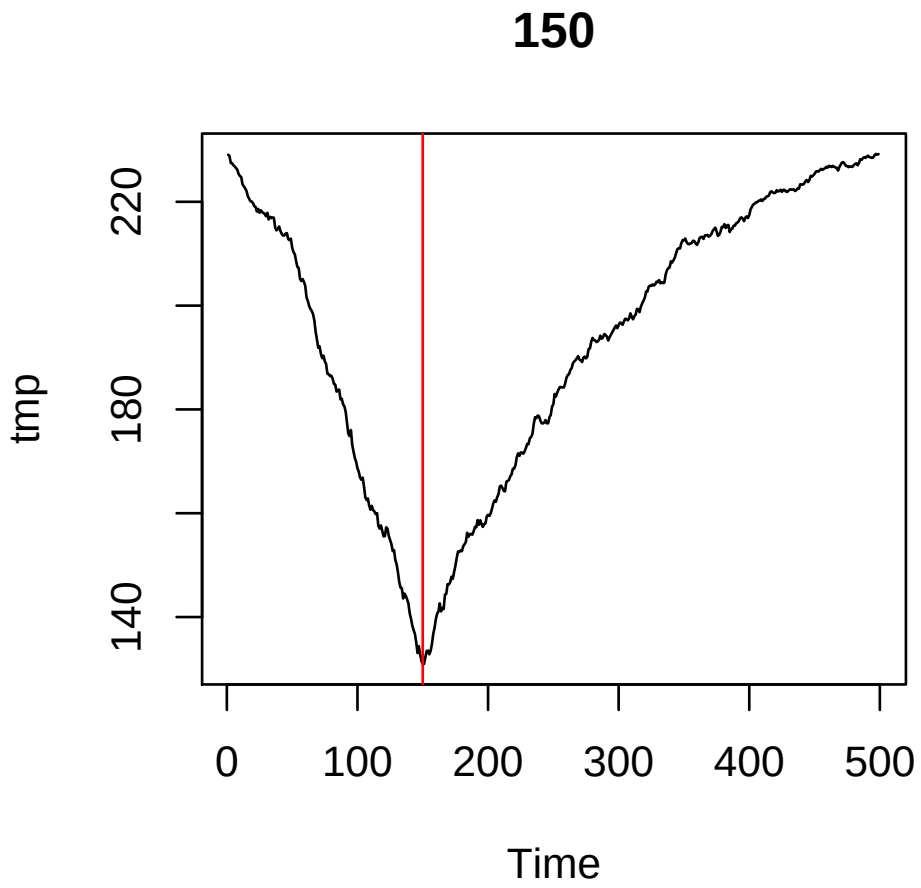
Cost of segment + Cost of segment



Finding a single change



Finding a single change



Finding a single change

How do we know if the changepoint found is “significant” or not?

- We also calculate the cost of the whole data with no change
- If the difference is **large enough** then we say there is a change

In practice **large enough** is hard to define as it is application dependent.

The default in the `changepoint` package is MBIC - a Modified Bayesian Information Criterion.

This will not be appropriate for all data sets! More later . . .

`changepoint` R package

The `changepoint` R package contains 3 wrapper functions:

- `cpt.mean` - mean only changes
- `cpt.var` - variance only changes
- `cpt.meanvar` - mean and variance changes

The package also contains:

- functions/methods for the `cpt` S4 class
- 5 data sets
- other R functions that are made available for those who know what they are doing and might want to extend/modify the package.

The `cpt` class

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- S4 class
- Slots store all the information from the analysis
  - e.g. `data.set`, `cpts`, `param.est`, `pen.value`, `ncpts.max`
- Slots are accessed via their names e.g. `cpts(x)`
- Standard methods are available for the class e.g. `plot`, `summary`
- Additional generic functions are available e.g. `seg.len`, `ncpts`
- Each core function outputs a `cpt` object

cpt.mean


```
cpt.mean(data, penalty="MBIC", pen.value=0,
method="AMOC", Q=5, test.stat="Normal", class=TRUE,
param.estimates=TRUE,minseglen=1)
```

- `data` - vector or `ts` object
- `penalty` - cut-off point, MBIC, SIC, BIC, AIC, Hannan-Quinn, Asymptotic, Manual.
- `pen.value` - Type I error for Asymptotic, number or character for manual.
- `method` - AMOC, PELT, SegNeigh, BinSeg.
- `Q` - max number of changes for SegNeigh or BinSeg.
- `test.stat` - Test statistic, Normal or CUSUM.
- `class` - return a `cpt` object or not.
- `param.estimates` - return parameter estimates or not.
- `minseglen` - minimum number of data points between changes.

Single Change in Mean


```
set.seed(1)
m1=c(rnorm(100,0,1),rnorm(100,5,1))
m1.amoc=cpt.mean(m1)
cpts(m1.amoc)
```

```
## [1] 100
```

Single Change in Mean

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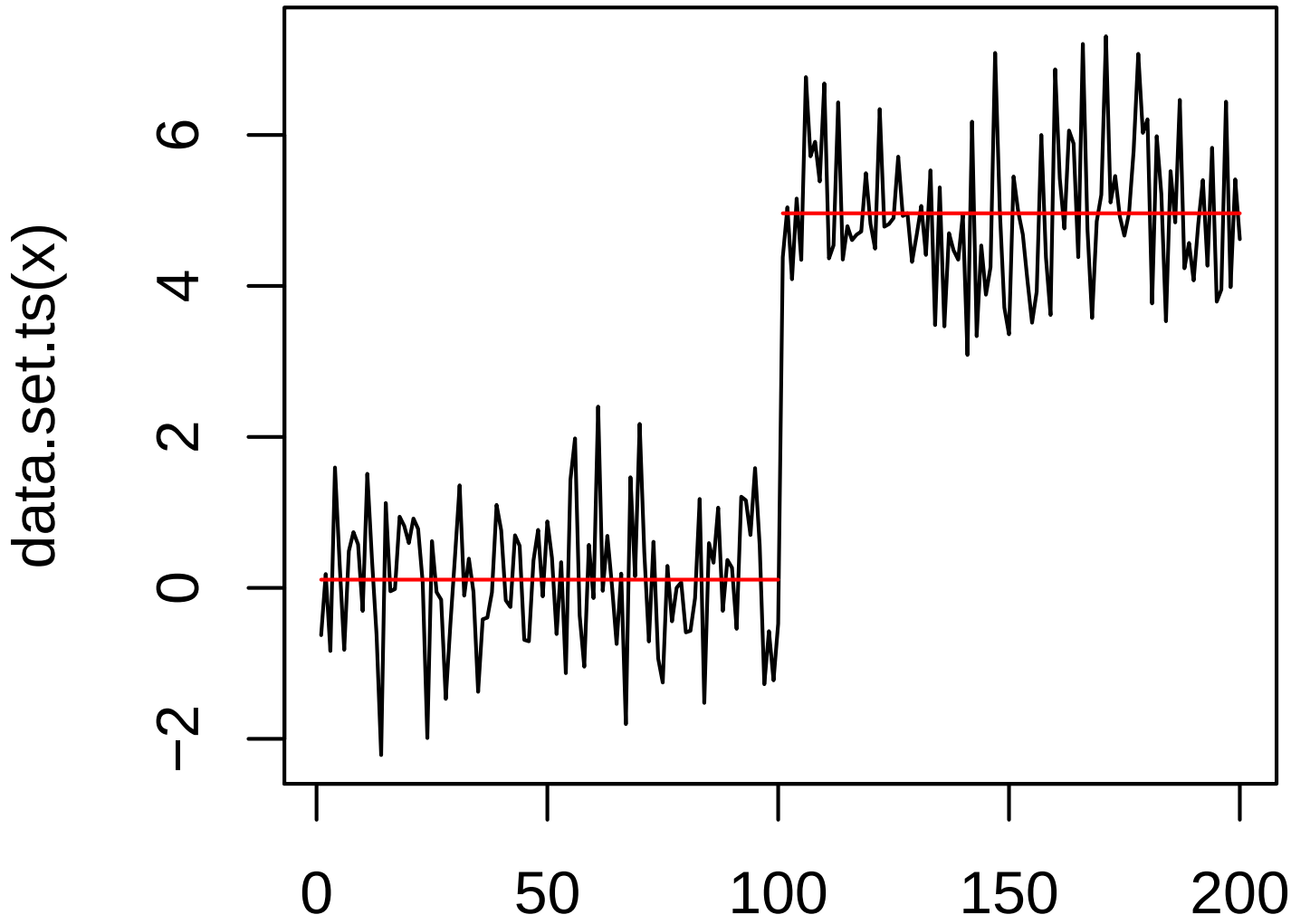
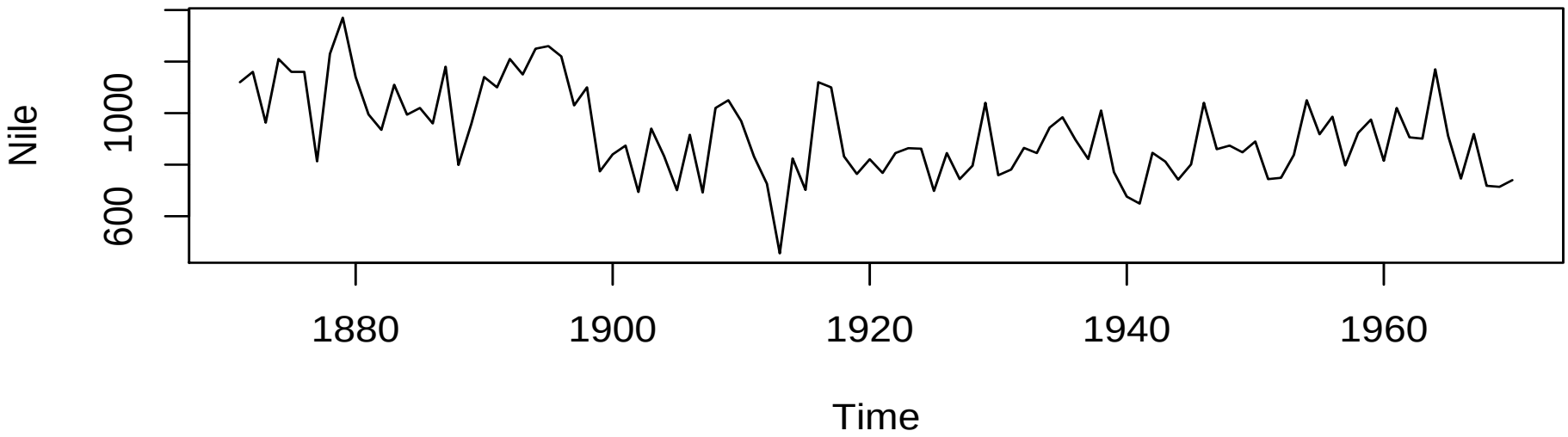
```
plot(m1.amoc)
```



Task: Nile

Data from Cobb (1978): readings of the annual flow volume of the Nile River at Aswan from 1871 to 1970.

```
data(Nile)
ts.plot(Nile)
```



Hypothesized that there was a change around the turn of the century.

Task: Nile

Use the `cpt.mean` function to see if there is evidence for a change in mean in the Nile river data.

```
data(Nile)
```

If you identify a change, where is it and what are the pre and post change means?

Don't forget to

```
library(changepoint)
```

before you start

Task: Nile

Annual flow volume of the Nile River at Aswan from 1871 to 1970 studied in Cobb(1978).

```
nile.default=cpt.mean(Nile)
cpts(nile.default)
```

```
## [1] 28
```

```
cpts.ts(nile.default)
```

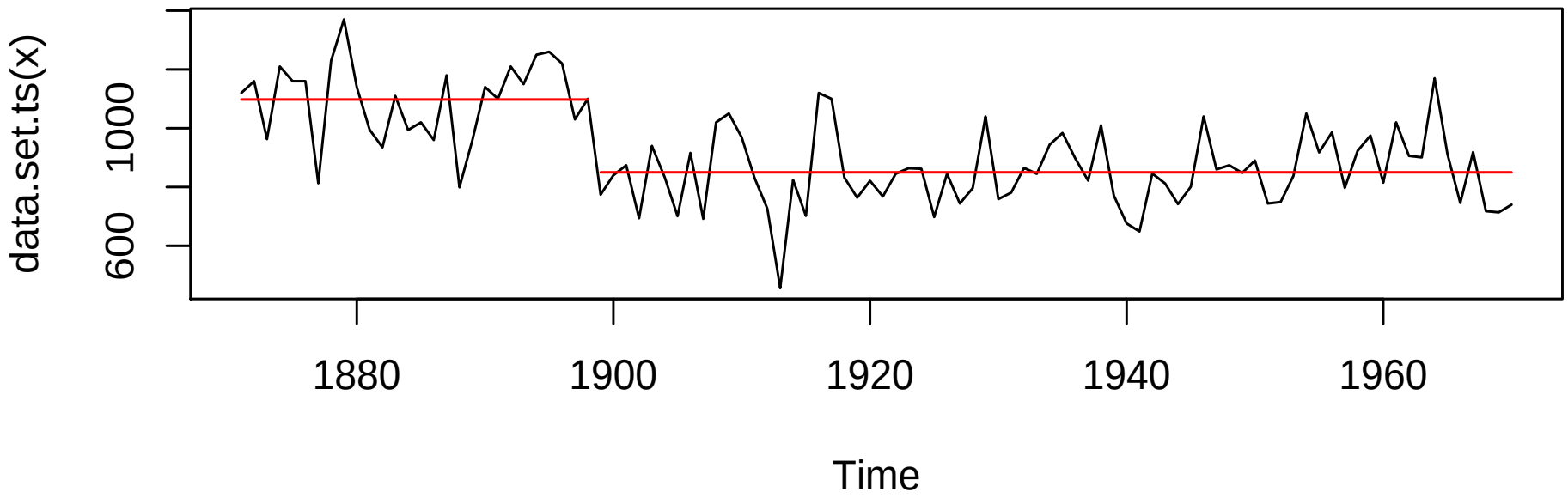
```
## [1] 1898
```

```
param.est(nile.default)
```

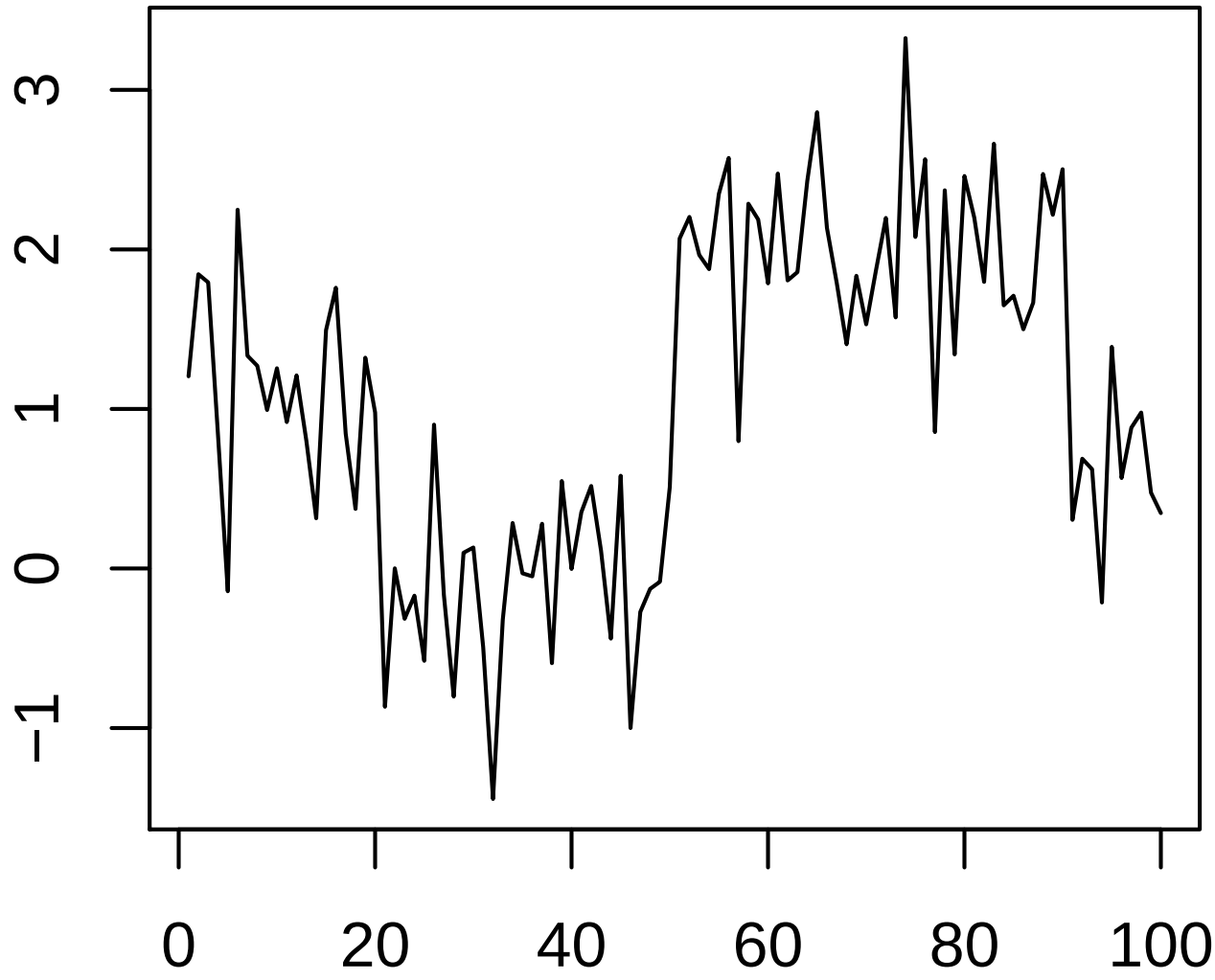
```
## $mean
## [1] 1097.7500  849.9722
```

Task: Nile

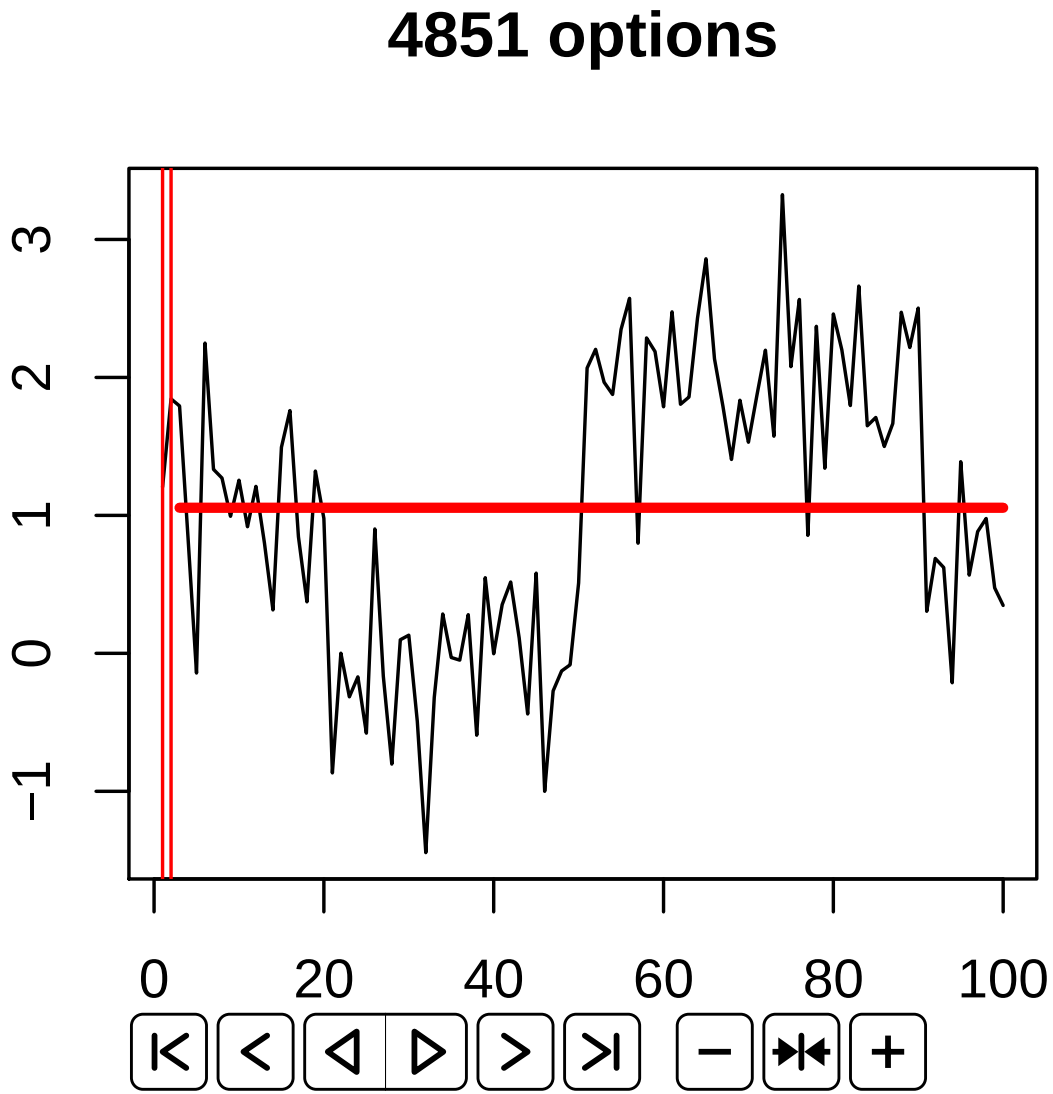

```
plot(nile.default)
```



Multiple Changepoints



Multiple Changepoints



The Challenge

- What are the values of $\tau_1, \ldots, \tau_m$?
- What is m?
- For n data points there are 2^{n-1} possible solutions
- If m is known there are still $\binom{n-1}{m}$ solutions
- If $n = 1000$ and $m = 10$, 2.607755×10^{23} solutions
- How do we search the solution space efficiently?

Methods in `changepoint`

- At Most One Change (`AMOC`)

Approximate but computationally **fast**:

- Binary Segmenation (`BinSeg`) (Scott and Knott (1974)) which is $\mathcal{O}(n \log n)$ in CPU time.

Slower but **exact**:

- Segment Neighbourhood (`SegNeigh`) (Auger and Lawrence (1989)) is $\mathcal{O}(Qn^2)$.

Fast and **exact**:

- Pruned Exact Linear Time (`PELT`) (Killick et al. (2012)) At worst $\mathcal{O}(n^2)$. For linear penalties , scaling changes, $\mathcal{O}(n)$.

cpt.var


```
cpt.var(data, penalty, pen.value, know.mean=FALSE, mu=NA,
method, Q, test.stat="Normal", class, param.estimates,
minseglen=2)
```

Majority of arguments are the same as for `cpt.mean`

- `know.mean` - if known we don't count it as an estimated parameter when calculating penalties.
- `mu` - Mean if known.
- `test.stat` - Normal or CSS (cumulative sums of squares)
- `minseglen` - Default is 2

Changes in Variance

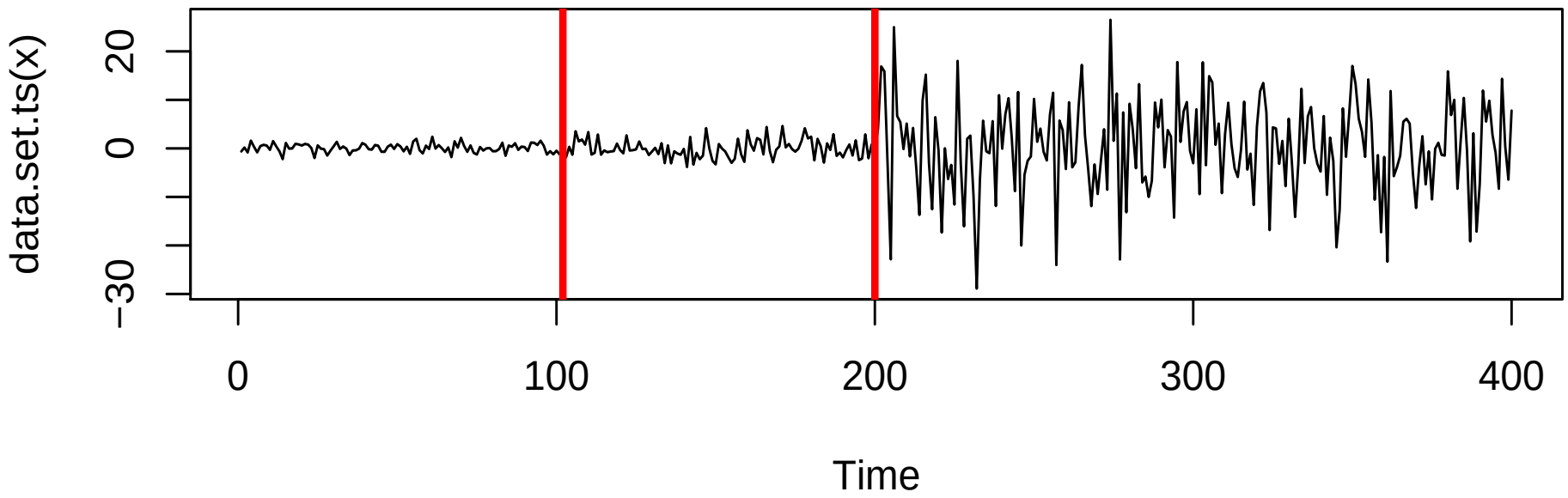

```
set.seed(1)
v1=c(rnorm(100,0,1),rnorm(100,0,2),rnorm(100,0,10),
     rnorm(100,0,9))
v1.man=cpt.var(v1,method='PELT',penalty='Manual',
     pen.value='2*log(n)')
cpts(v1.man)
param.est(v1.man)
```

```
## [1] 102 200
## $variance
## [1]  0.8007158  3.6933616 92.3876410
##
## $mean
## [1] 0.1986058
```

Changes in Variance

Ratios of true variances (4, 25, 0.81)

```
plot(v1.man,cpt.width=3)
```



cpt.meanvar


```
cpt.meanvar(data, penalty, pen.value, method, Q,
test.stat="Normal", class, param.estimates,
shape=1,minseglen=2)
```

Again the same underlying structure as `cpt.mean`.

- `test.stat` - choice of Normal, Gamma, Exponential, Poisson.
- `shape` - assumed shape parameter for Gamma.
- `minseglen` - minimum segment length of 2

Mean & Variance


```
set.seed(1)
mv1=c(rexp(50,rate=1),rexp(50,5),rexp(50,2),rexp(50,7))
mv1.pelt=cpt.meanvar(mv1,test.stat='Exponential',
      method='BinSeg',Q=10,penalty="SIC")
cpts(mv1.pelt)
```

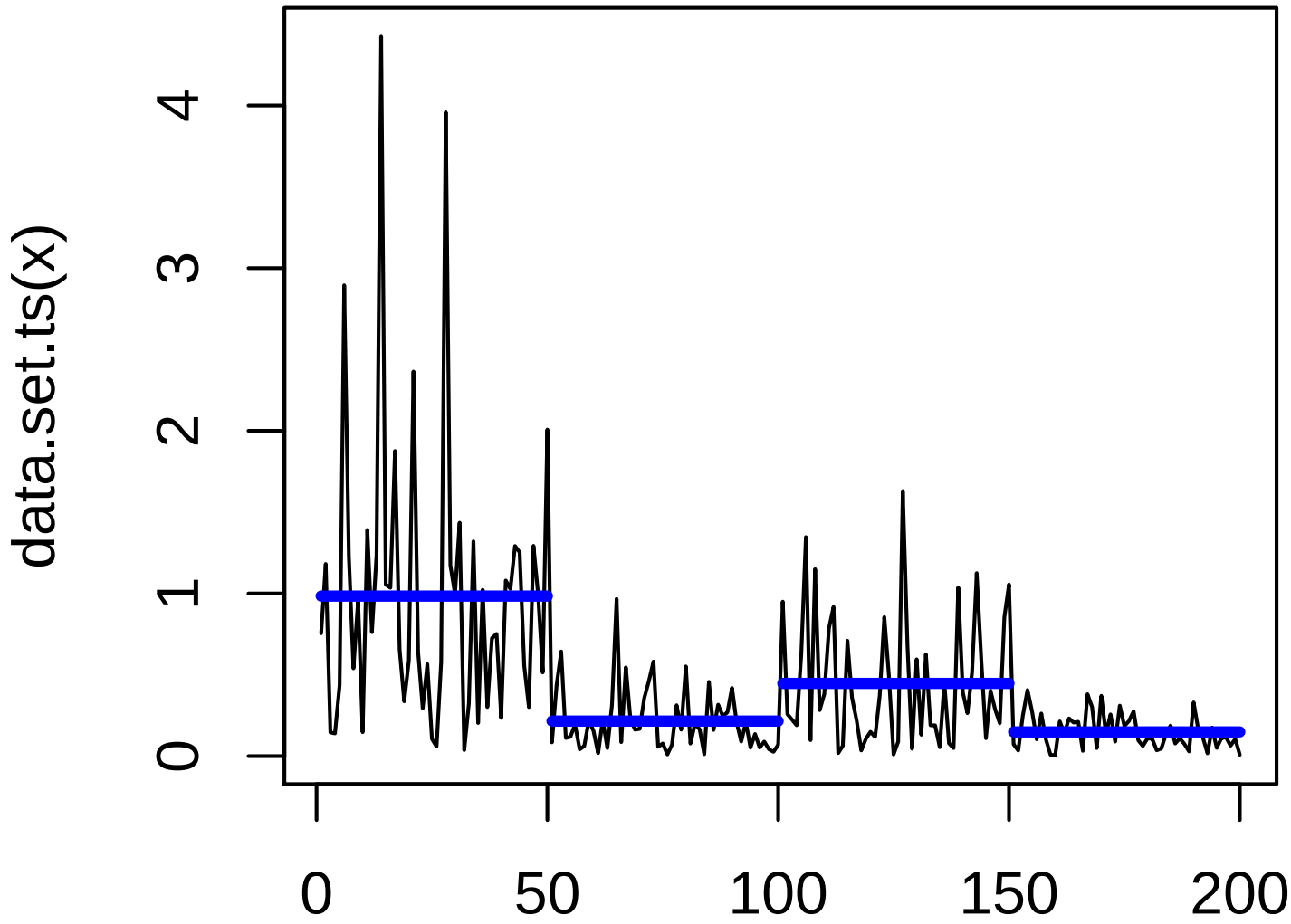
```
## [1]  50 100 150
```

```
param.est(mv1.pelt)
```

```
## $rate
## [1] 1.016217 4.641184 2.235431 6.705612
```

Mean & Variance


```
plot(mv1.pelt,cpt.width=3,cpt.col='blue')
```

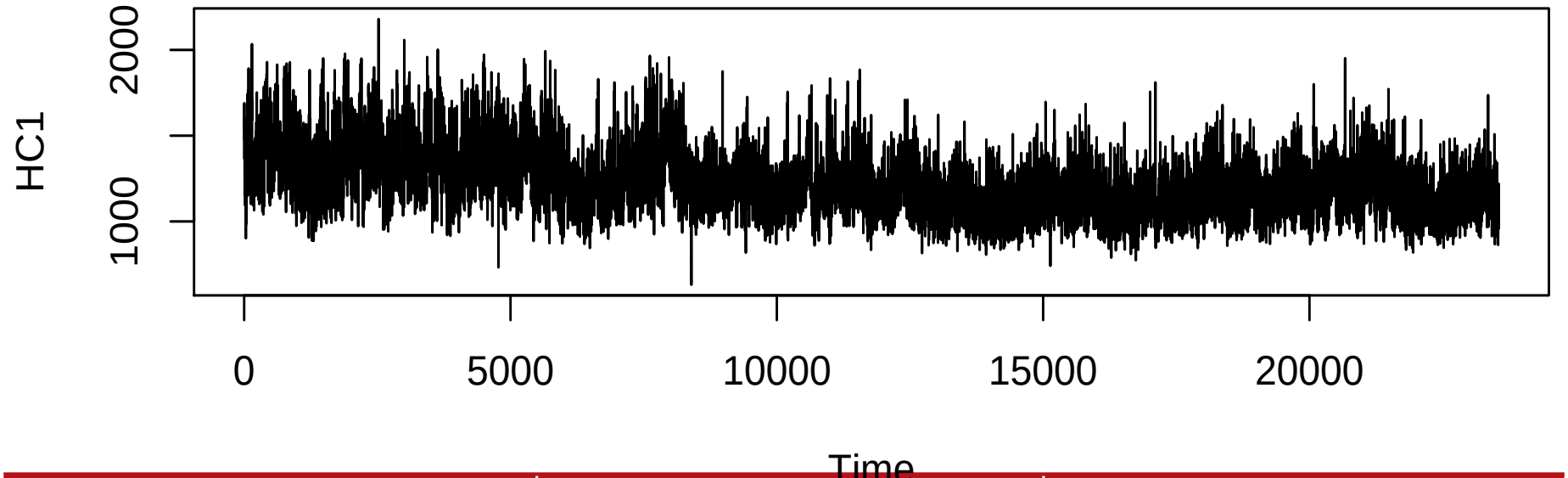


Task HC1

G+C content within part of Human Chromosome 1, data from NCBI. 3kb windows along the Human Chromosome from 10Mb to 33Mb.

Use the `cpt.meanvar` function to identify regions with different C+G content.

```
data(HC1)
ts.plot(HC1)
```



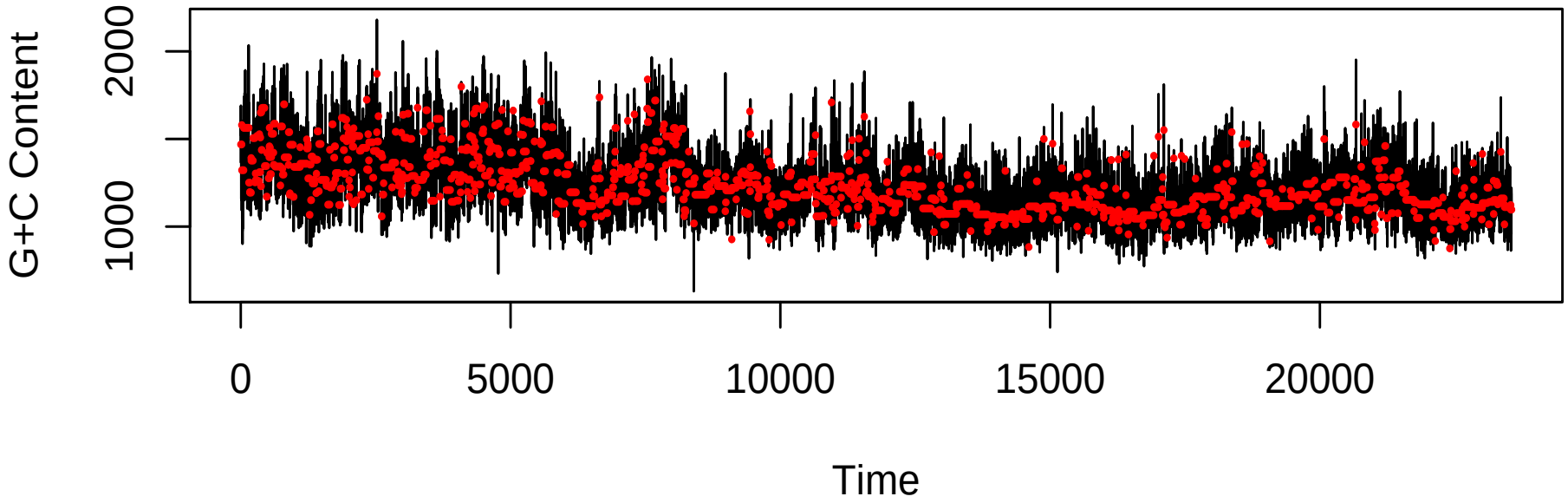
A solution: HC1


```
data(HC1)
hc1.pelt=cpt.meanvar(HC1,method='PELT',penalty='Manual',
         pen.value=14)
ncpts(hc1.pelt)
```

```
## [1] 805
```

A solution: HC1

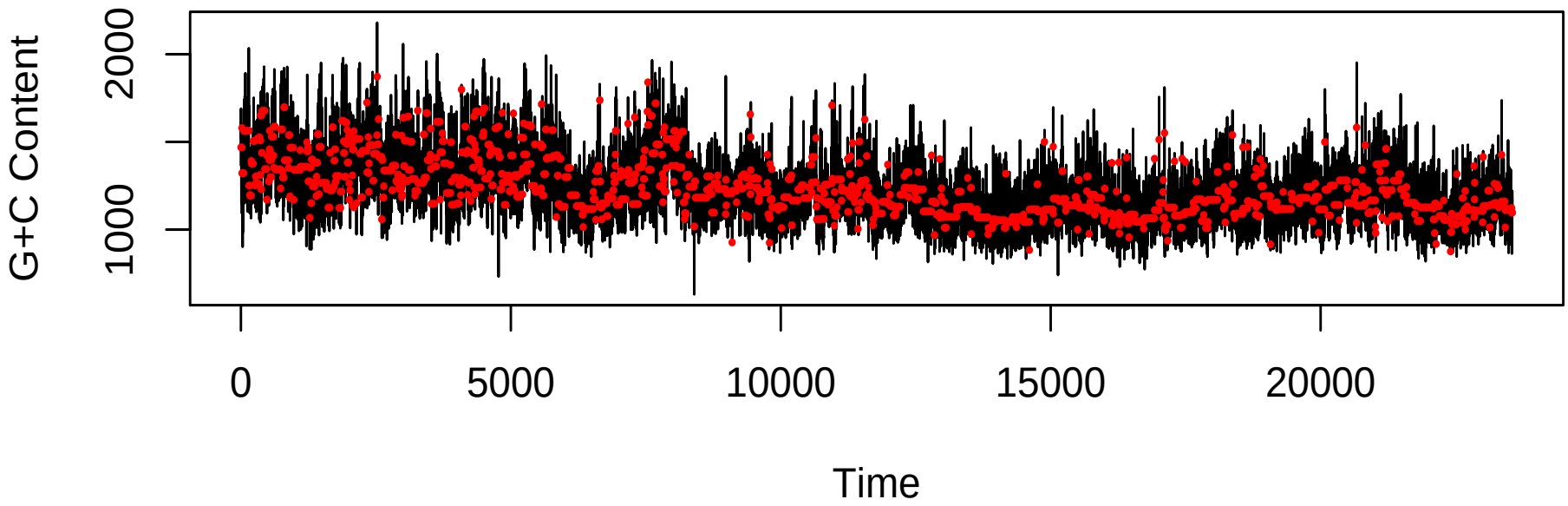

```
plot(hc1.pelt,ylab='G+C Content',cpt.width=3)
```



Number of changes?

Does the number of changes appear reasonable?

```
plot(hc1.pelt,ylab='G+C Content',cpt.width=3)
```



CROPS

Changepoints for a **r**ange **o**f **p**enalti**es**

Use `penalty='CROPS'` with `method='PELT'` to get all segmentations for a range of penalty values.

```
v1.crops=cpt.var(v1,method="PELT",penalty="CROPS",
                 pen.value=c(5,500))
```

```
## [1] "Maximum number of runs of algorithm = 10"
## [1] "Completed runs = 2"
## [1] "Completed runs = 3"
## [1] "Completed runs = 4"
## [1] "Completed runs = 5"
## [1] "Completed runs = 6"
## [1] "Completed runs = 8"
## [1] "Completed runs = 9"
```

CROPS


```
cpts.full(v1.crops)
```

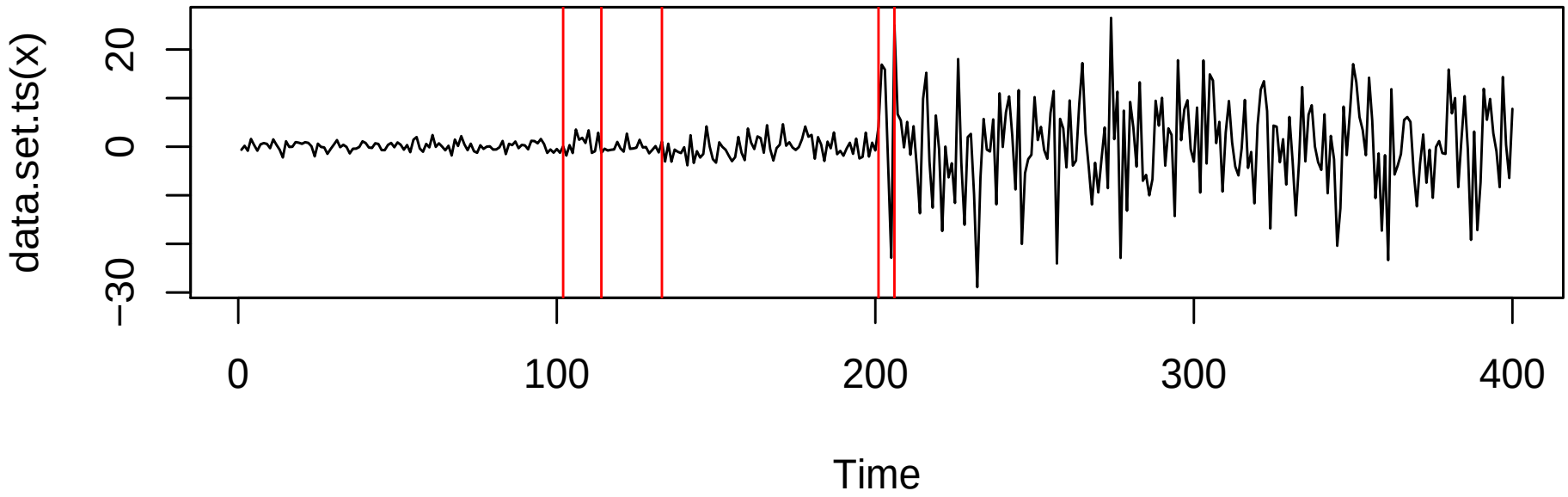
```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
## [1,]  102  114  133  201  206  213  375  379
## [2,]  102  114  133  201  206  375  379   NA
## [3,]  102  114  133  201  206   NA   NA   NA
## [4,]   96  133  201  206   NA   NA   NA   NA
## [5,]  102  201  206   NA   NA   NA   NA   NA
## [6,]  102  200   NA   NA   NA   NA   NA   NA
## [7,]  200   NA   NA   NA   NA   NA   NA   NA
## [8,]   NA   NA   NA   NA   NA   NA   NA   NA
```

CROPS


```
pen.value.full(v1.crops)
```

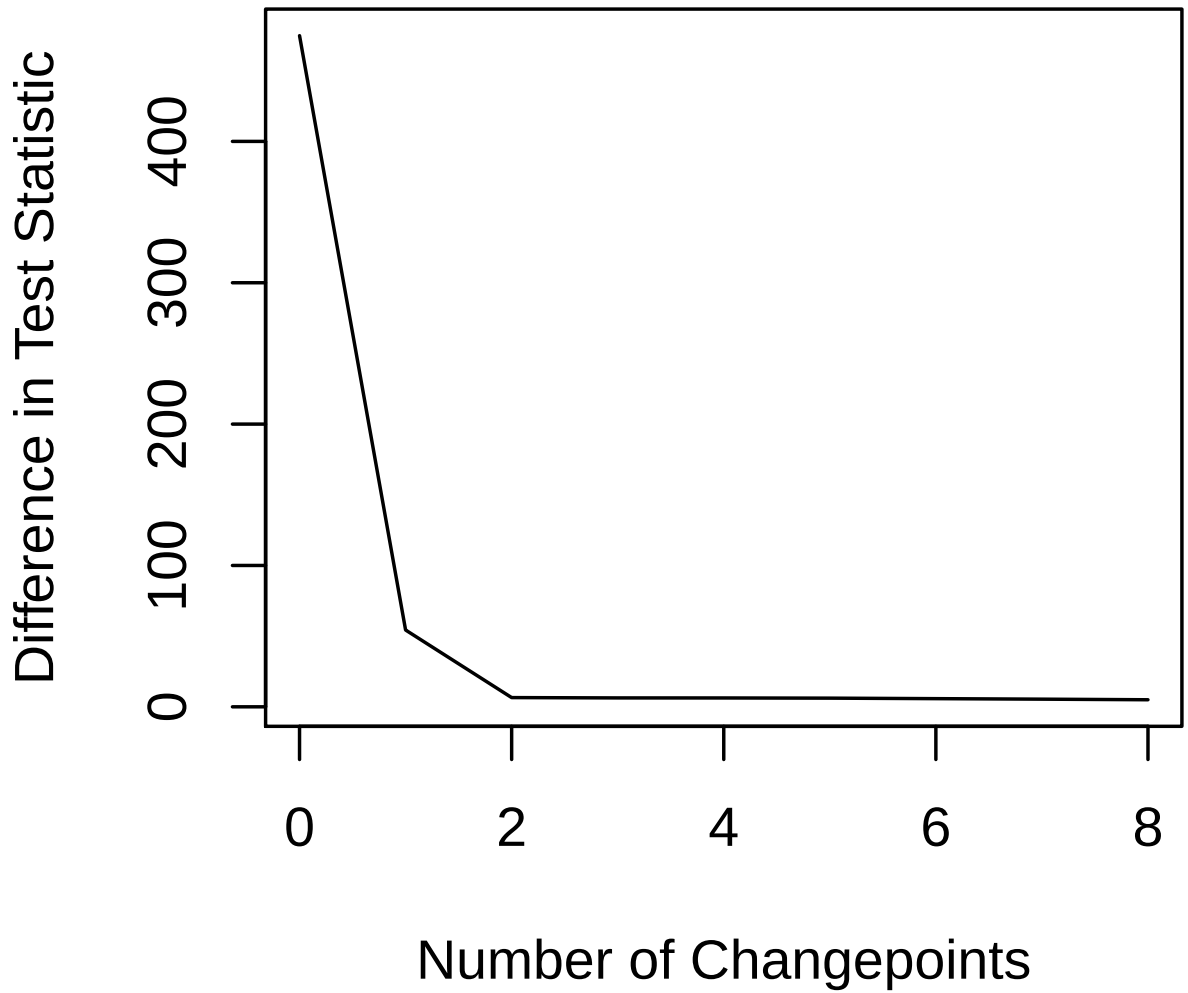
```
## [1]   5.000000   5.431360   6.151053   6.270164   6.314013
## [8] 474.797364
```

```
plot(v1.crops,ncpts=5)
```



CROPS


```
plot(v1.crops,diagnostic=TRUE)
```



cpt.np


```
cpt.np(data, penalty, pen.value, method,
test.stat="empirical_distribution", class, minseglen=1,
nquantiles=10)
```

Again the same underlying structure as `cpt.mean`.

- `test.stat` - choice of empirical_distribution
- `minseglen` - minimum segment length of 1
- `nquantiles` - number of quantiles to use

Example


```
set.seed(12)
J <- function(x){(1+sign(x))/2}
n <- 1000
tau <- c(0.1,0.13,0.15,0.23,0.25,0.4,0.44,0.65,0.76,0.78,
      0.81)*n
h <- c(2.01, -2.51, 1.51, -2.01, 2.51, -2.11, 1.05, 2.16,
      -1.56, 2.56, -2.11)
sigma <- 0.5
t <- seq(0,1,length.out = n)
data <- array()
for (i in 1:n){
   data[i] <- sum(h*J(n*t[i] - tau)) + (sigma * rnorm(1))
}
```

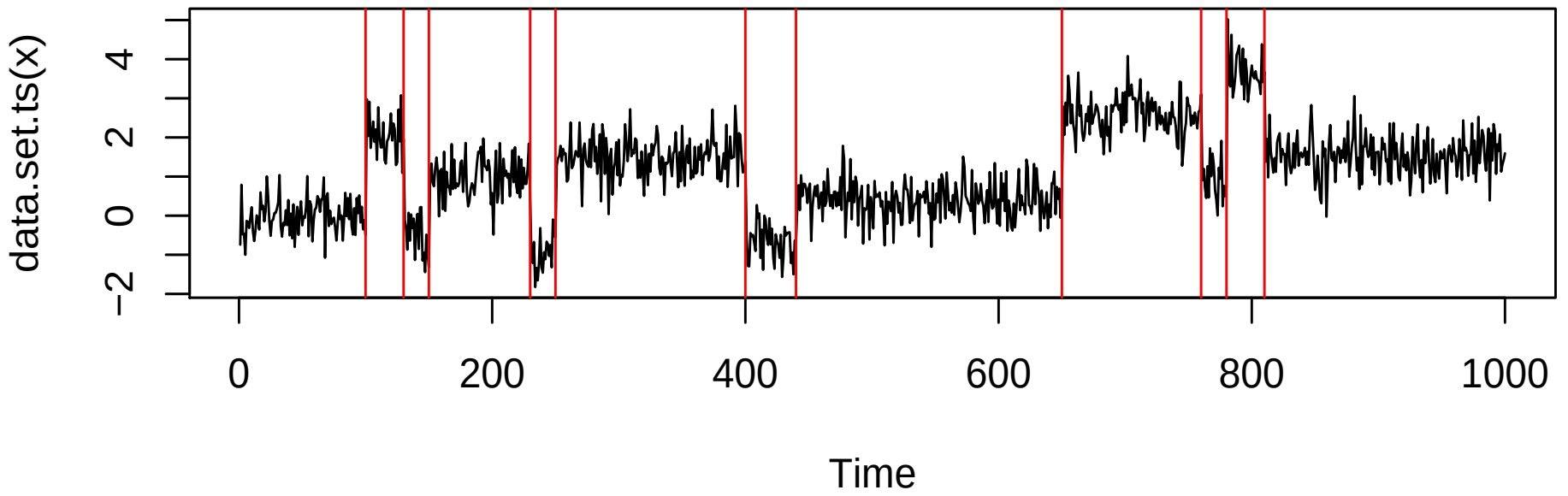
Example


```
out <- cpt.np(data, method="PELT",minseglen=2,
        nquantiles =4*log(length(data)))
cpts(out)
```

```
##  [1] 100 130 150 230 250 400 440 650 760 780 810
```

Example


```
plot(out)
```



Task: Sea Ice

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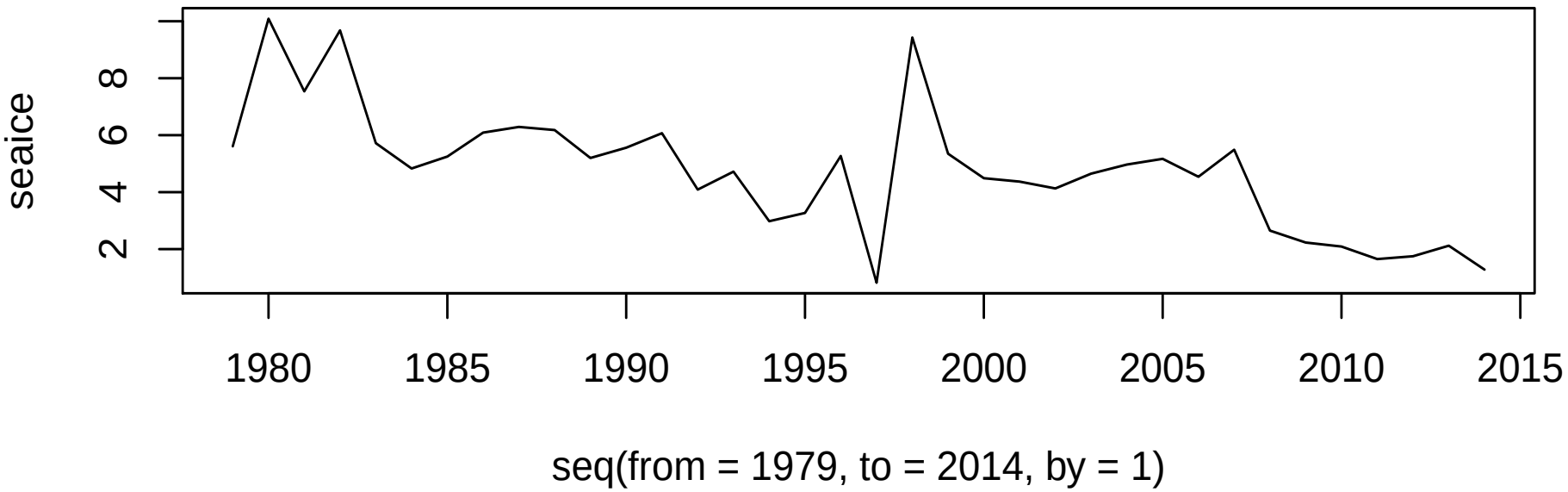
Yearly Sea Ice measurements for July-Sept for Barents from 1979 until 2014.

Use the `cpt.meanvar` function and CROPS to identify the number of changes.

```
plot(seq(from=1979,to=2014,by=1),seaice,type='l')
```



Task: `cpt.np`

Look at the `HeartRate` data from the `changepoint.np` package. Use one of the non-parametric functions to see if there is evidence for changes in heart rate.

```
data(HeartRate)
```

A solution: Sea Ice


```
seaice.crops=cpt.meanvar(seaice,method="PELT",
      penalty="CROPS",pen.value=c(1,100))
```

```
## [1] "Maximum number of runs of algorithm = 17"
## [1] "Completed runs = 2"
## [1] "Completed runs = 3"
## [1] "Completed runs = 5"
## [1] "Completed runs = 9"
## [1] "Completed runs = 12"
## [1] "Completed runs = 15"
## [1] "Completed runs = 16"
```

A solution: Sea Ice

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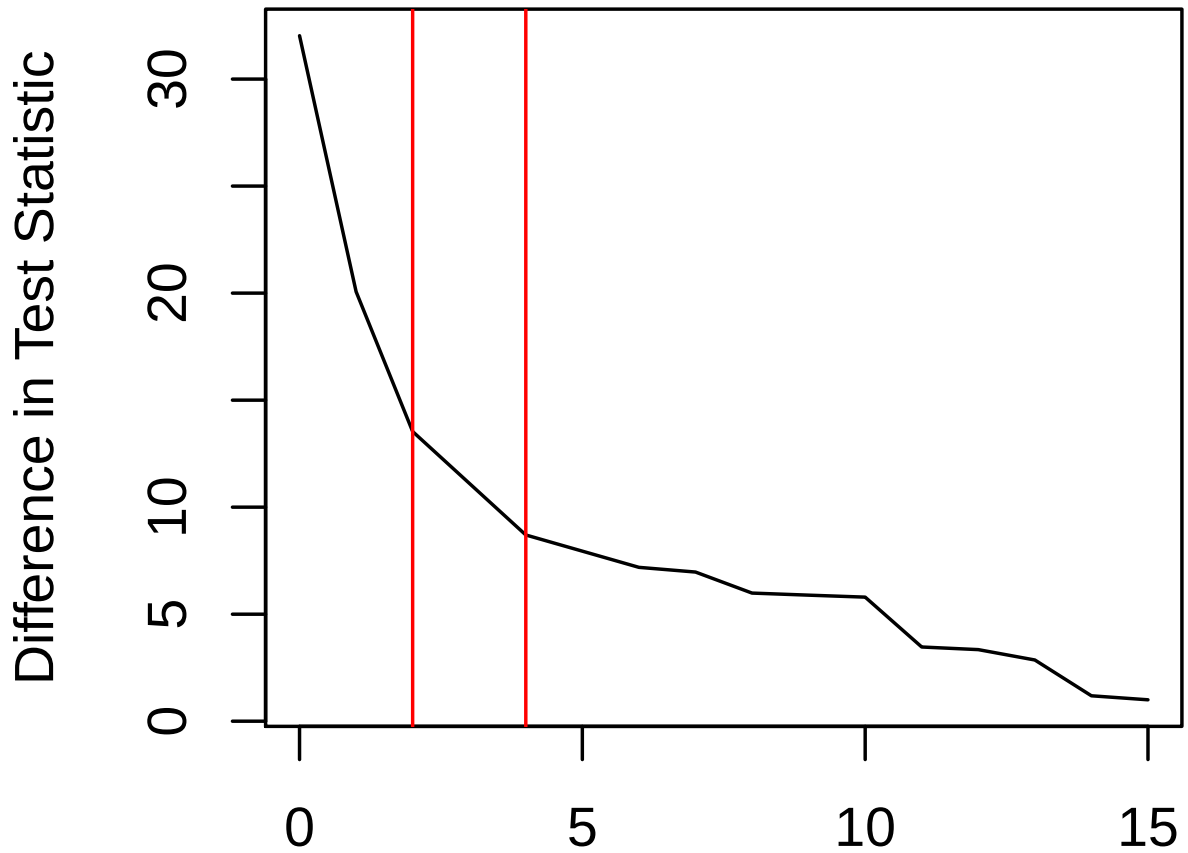
```
plot(seaice.crops,diagnostic=TRUE)
abline(v=2,col='red')
abline(v=4,col='red')
```



A solution: Sea Ice

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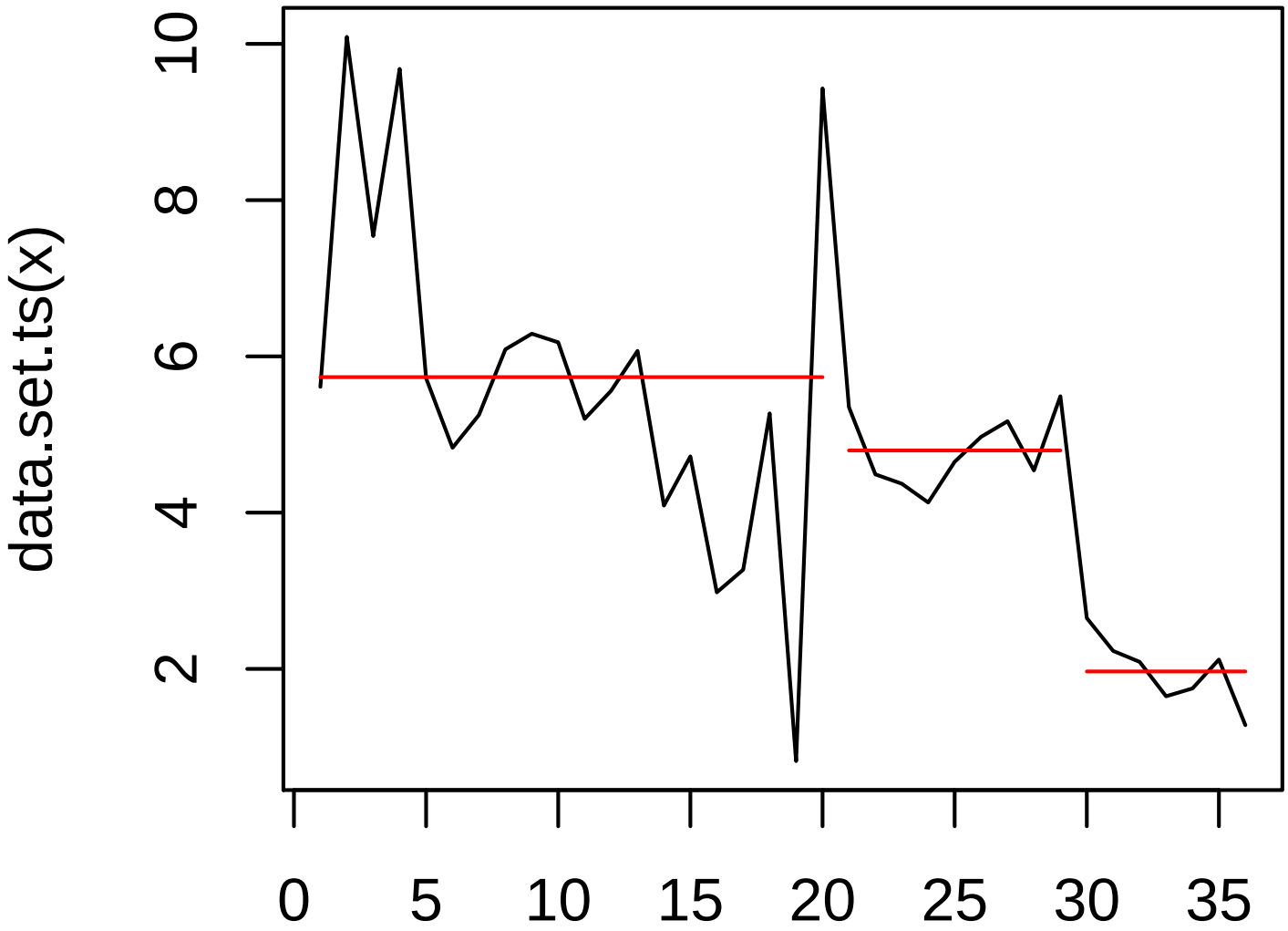
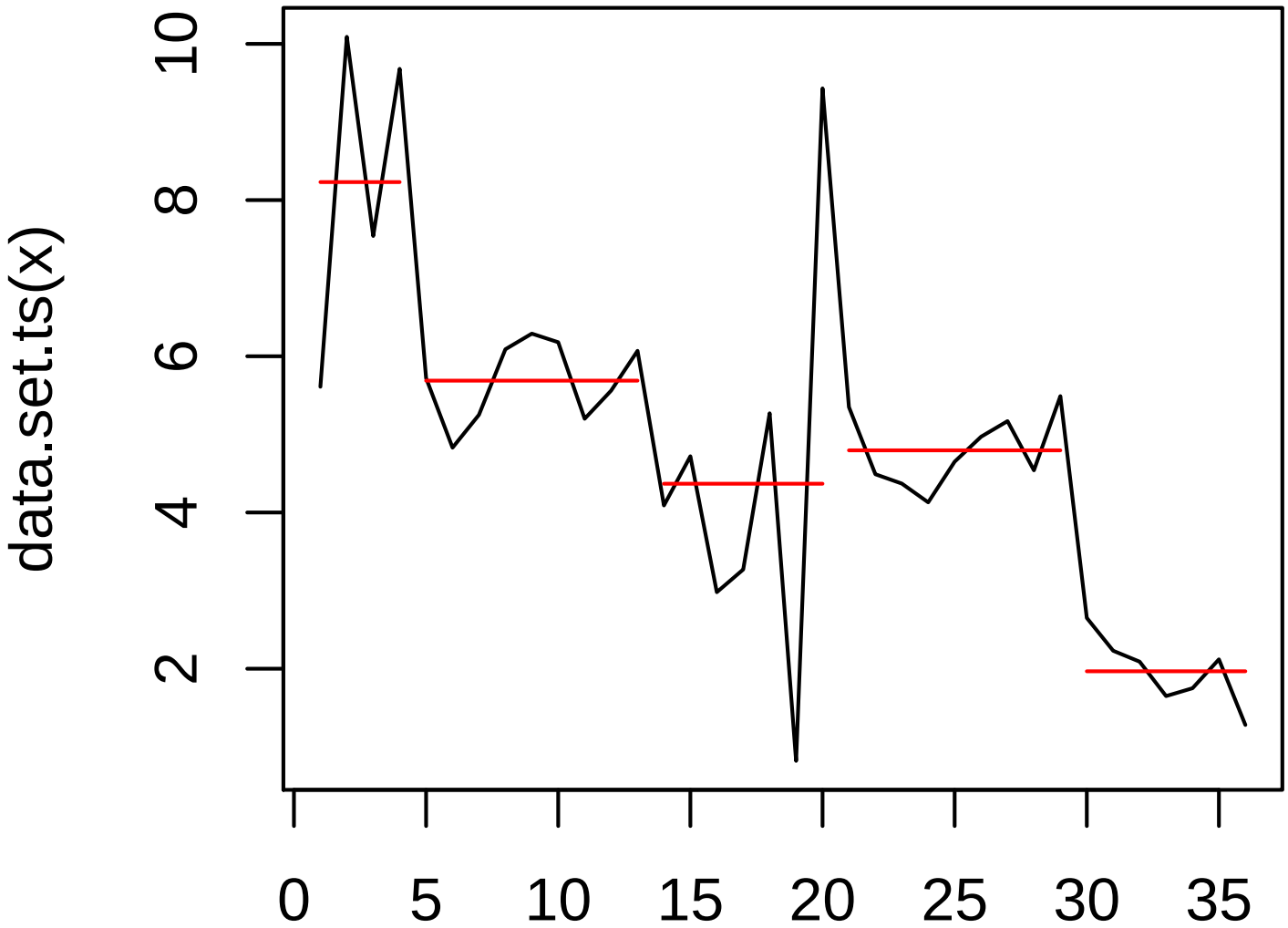
```
plot(seaice.crops,ncpts=2)
```



A solution: Sea Ice


```
plot(seaice.crops,ncpts=4)
```



A solution: HeartRate

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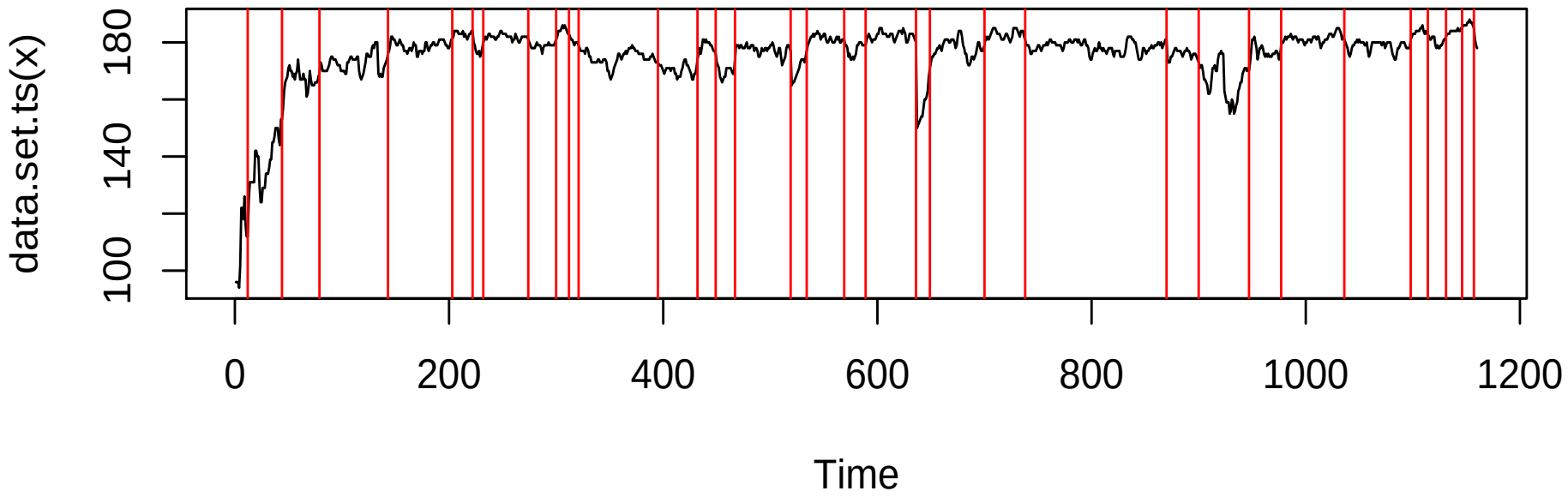
```
HR.pelt=cpt.np(HeartRate,method='PELT',
               nquantiles=4*log(length(HeartRate)))
ncpts(HR.pelt)
```

```
## [1] 33
```

A solution: HeartRate


```
plot(HR.pelt)
```



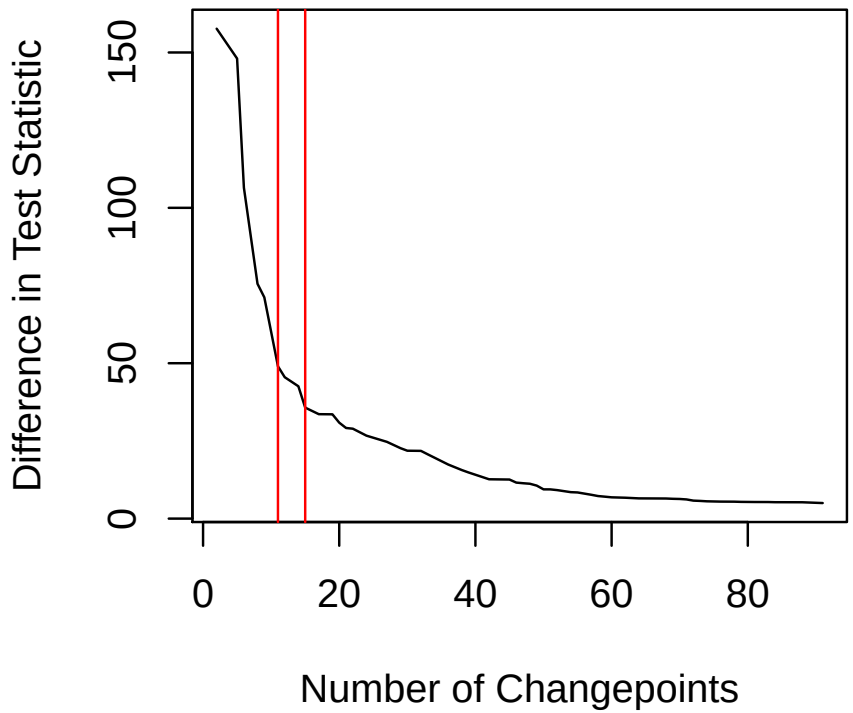
A solution: HeartRate


```
HR.crops=cpt.np(HeartRate, penalty = "CROPS",
        pen.value = c(5,200), method="PELT",minseglen=2,
        nquantiles =4*log(length(HeartRate)))
```

```
## [1] "Maximum number of runs of algorithm = 91"
## [1] "Completed runs = 2"
## [1] "Completed runs = 3"
## [1] "Completed runs = 5"
## [1] "Completed runs = 9"
## [1] "Completed runs = 17"
## [1] "Completed runs = 32"
## [1] "Completed runs = 52"
## [1] "Completed runs = 75"
## [1] "Completed runs = 84"
```

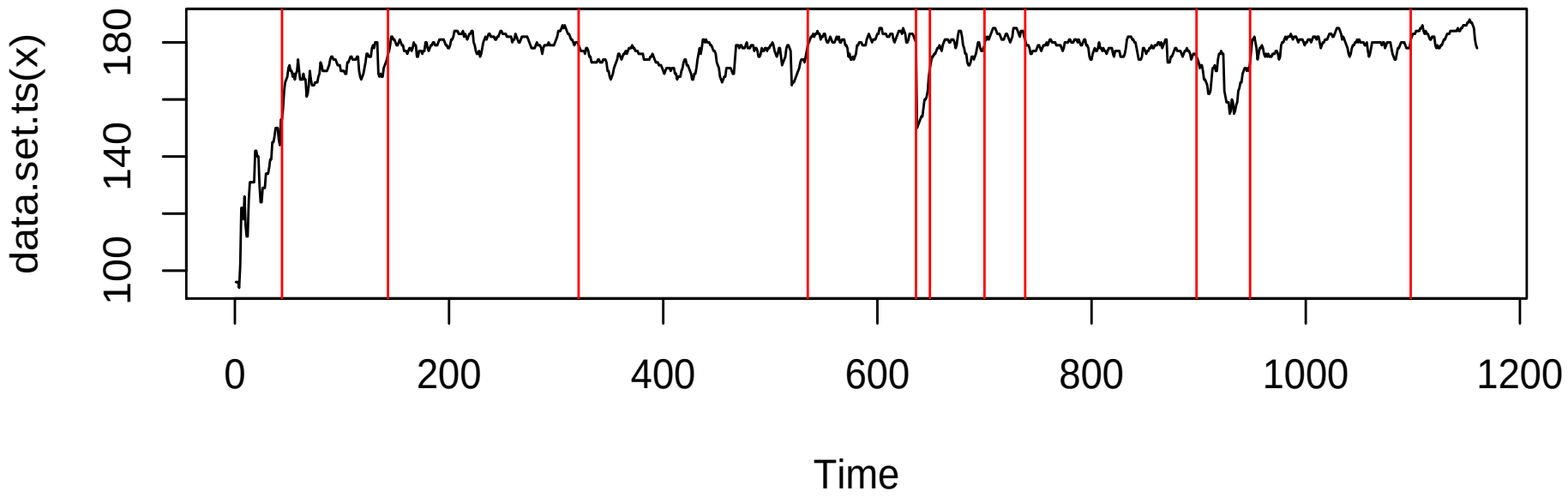
A solution: HeartRate


```
plot(HR.crops, diagnostic = TRUE)
abline(v=11,col='red')
abline(v=15,col='red')
```



A solution: HeartRate


```
plot(HR.crops, ncpts = 11)
```



A solution: HeartRate

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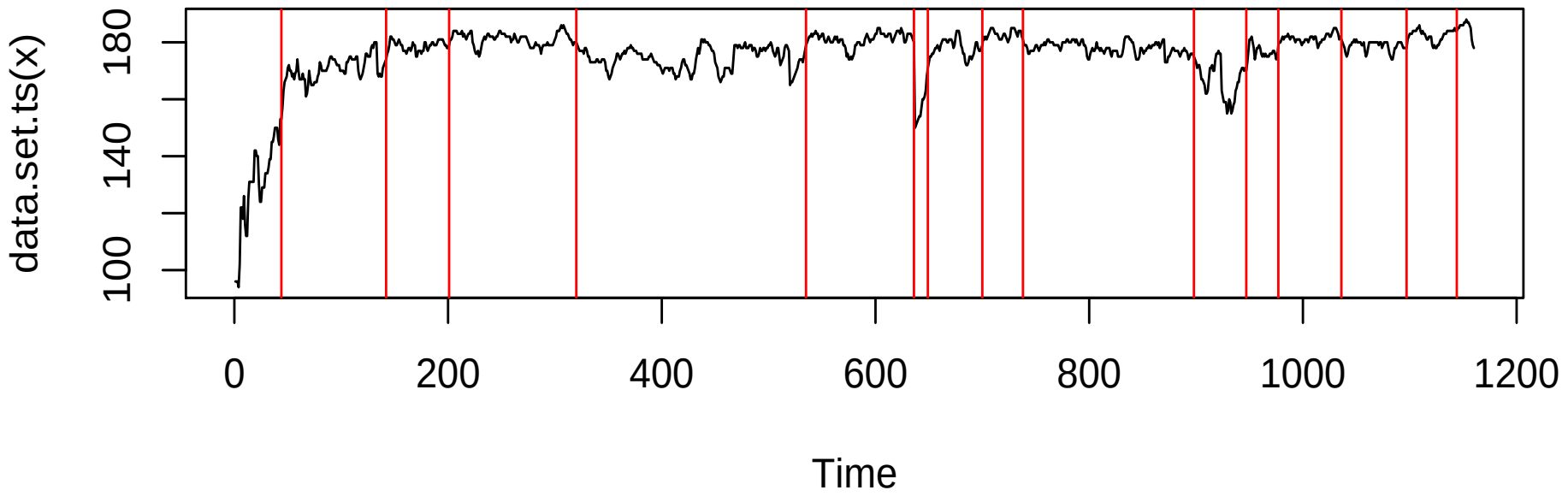
```
plot(HR.crops, ncpts = 15)
```



EnvCpt

EnvCpt automatically fits 8 different models to your data:

- Flat mean (+AR1, +Change, +AR1+Change)
- Trend mean (+AR1, +Change, +AR1+Change)

AR1= autoregressive of order 1 = current data point is strongly related to the last data point.

BONUS: Can see which model is best

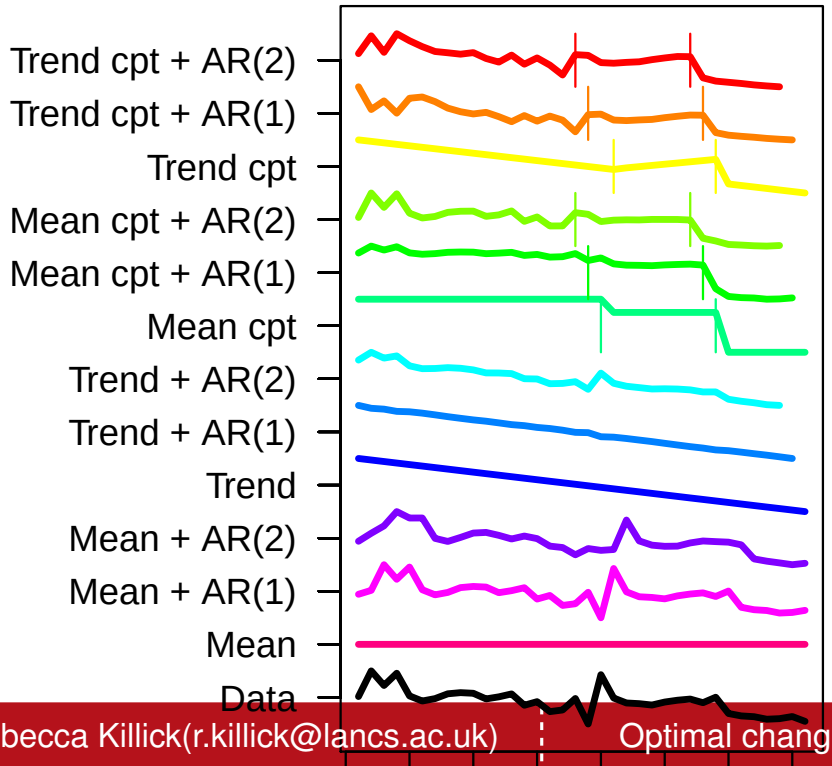
PITFALL: Might be best to use another model which isn't checked - always look at the fit!

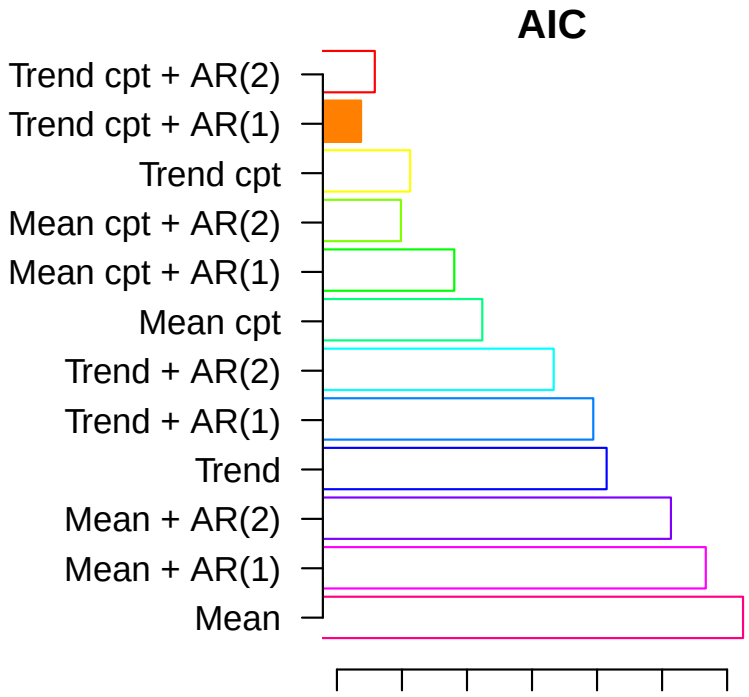
EnvCpt: Sea Ice


```
## Loading required package: EnvCpt

## Loading required package: MASS
```

```
seaice.envcpt=envcpt(seaice,verbose=FALSE)
plot(seaice.envcpt)
plot(seaice.envcpt,type='aic')
```



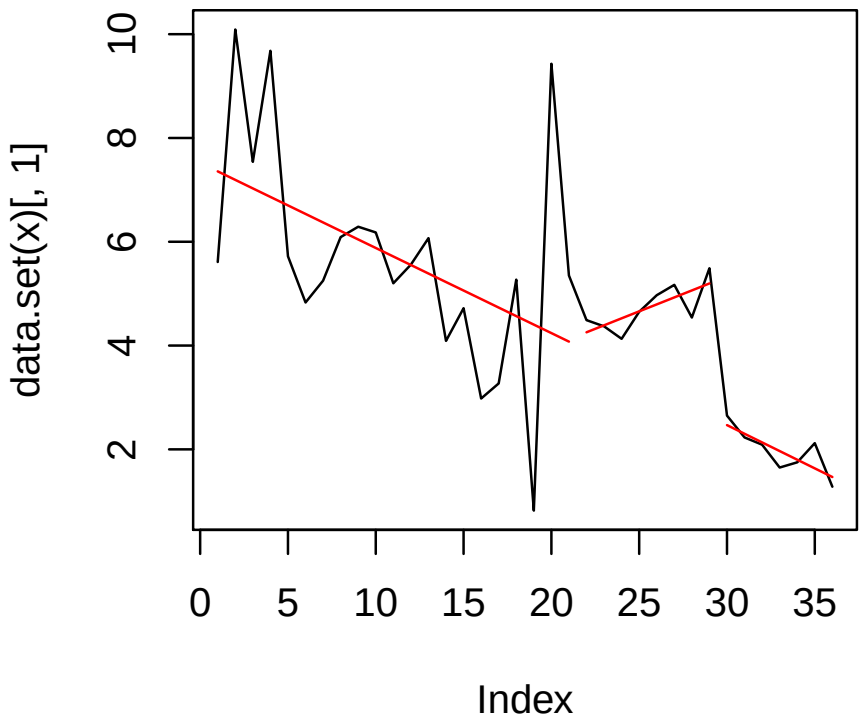


EnvCpt: Sea Ice


```
cpts(seaice.envcpt[[9]])
```

```
## [1] 21 29
```

```
plot(seaice.envcpt[[9]])
```



Checking Assumptions

The main assumptions for a Normal likelihood ratio test for a change in mean are:

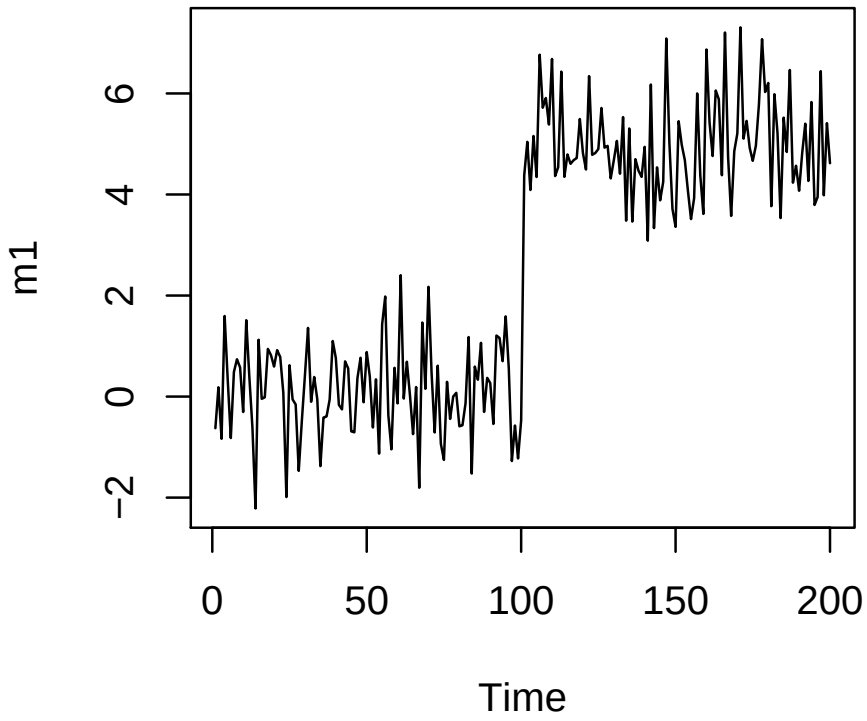
- Independent data points;
- Normal distributed points pre and post change;
- Constant variance across the data.

How can we check these?

Checking Assumptions

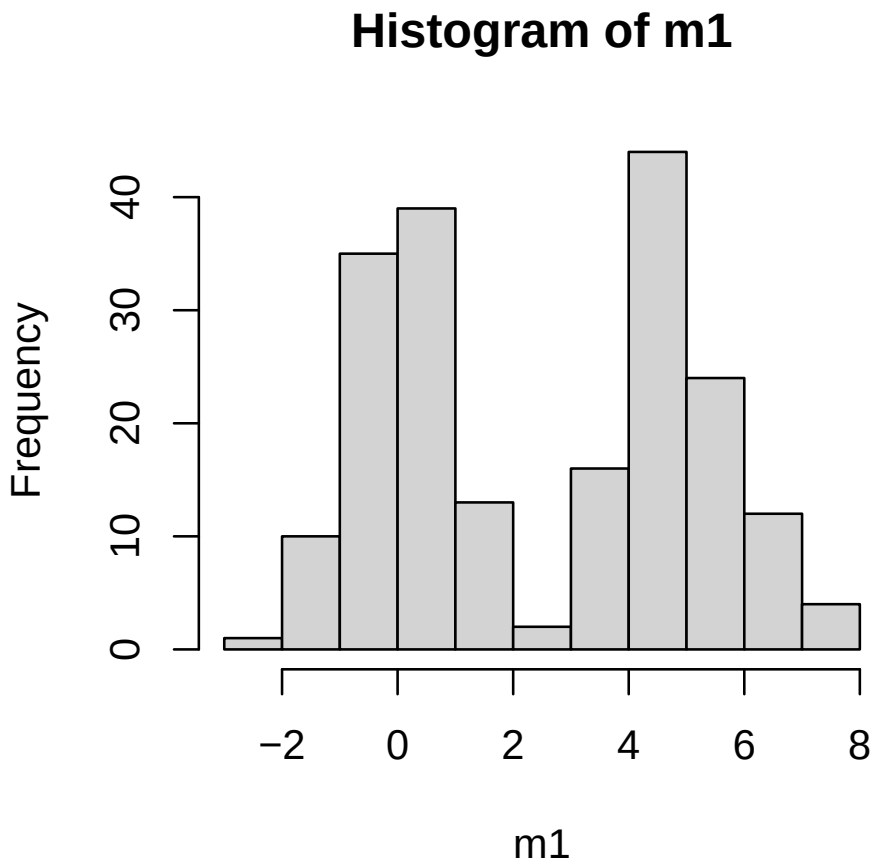
In reality we can't check assumptions prior to analysis.

```
ts.plot(m1)
```



Checking Assumptions


```
hist(m1)
```



Checking Assumptions


```
shapiro.test(m1)
```

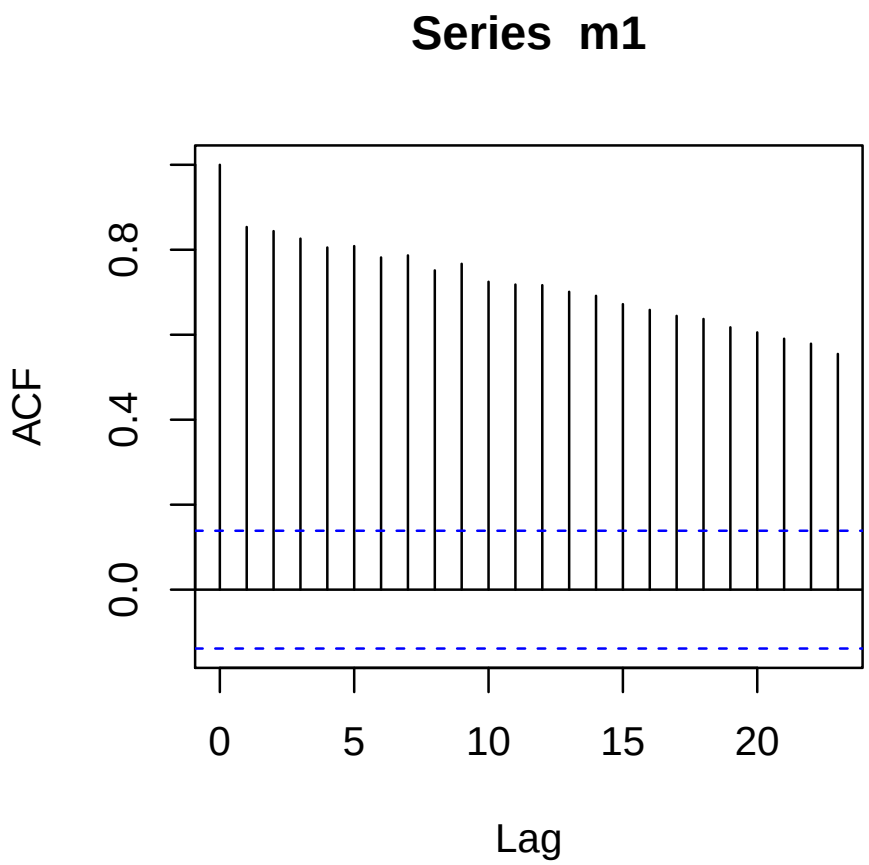
```
##
##  Shapiro-Wilk normality test
##
## data:  m1
## W = 0.91086, p-value = 1.31e-09
```

```
ks.test(m1,pnorm,mean=mean(m1),sd=sd(m1))
```

```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  m1
## D = 0.15491, p-value = 0.0001355
## alternative hypothesis: two-sided
```

Checking Assumptions


```
acf(m1)
```



How to check

- Check the residuals

```
means=param.est(m1.amoc)$mean
m1.resid=m1-rep(means,seg.len(m1.amoc))
shapiro.test(m1.resid)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  m1.resid
## W = 0.99228, p-value = 0.3721
```

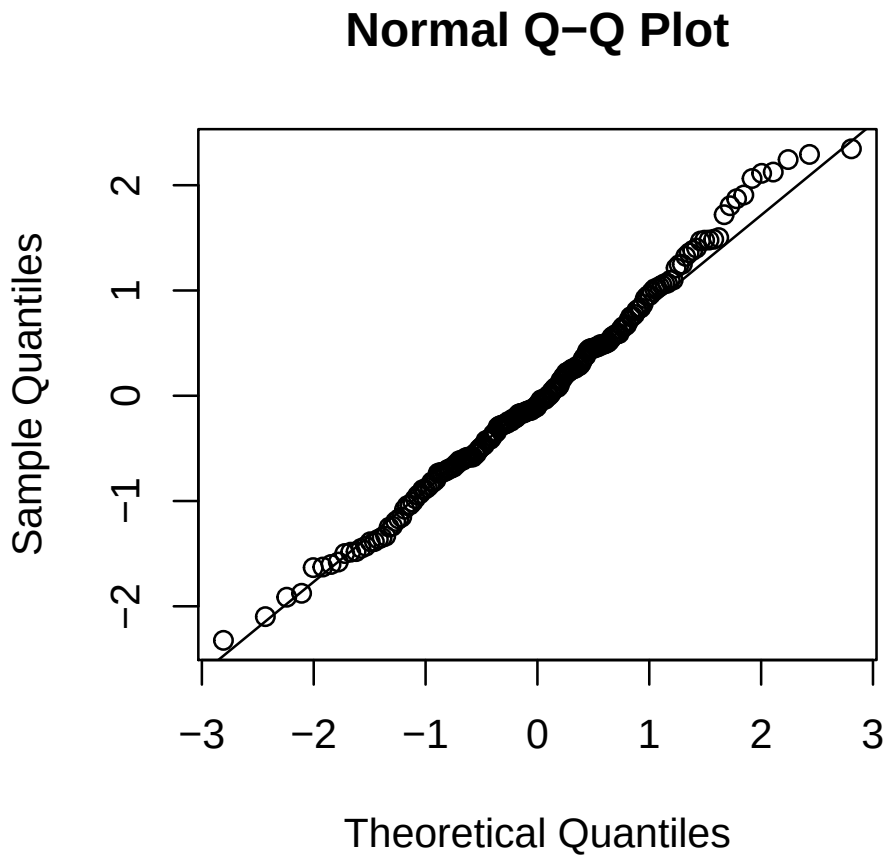
Residual Check


```
ks.test(m1.resid,pnorm,mean=mean(m1.resid),sd=sd(m1.resid))

##
##  One-sample Kolmogorov-Smirnov test
##
## data:  m1.resid
## D = 0.045812, p-value = 0.7953
## alternative hypothesis: two-sided
```

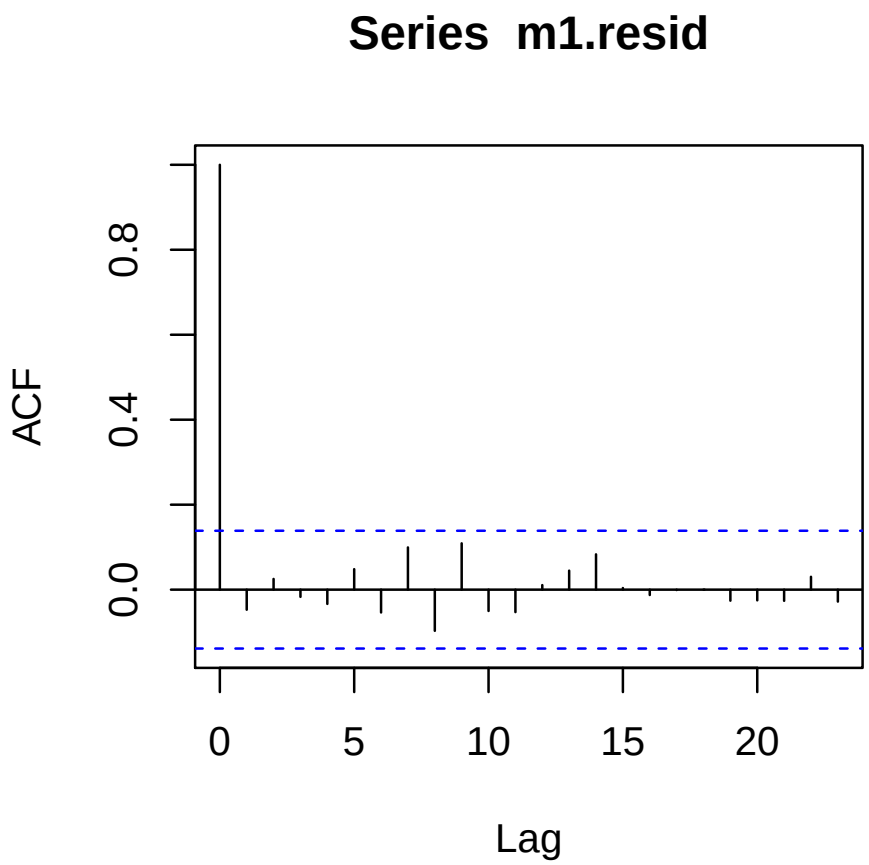
Residual Check


```
qqnorm(m1.resid)
qqline(m1.resid)
```



Residual Check


```
acf(m1.resid)
```



Task

Check the assumptions you have made on the simulated, Nile, Air Temps and HeartRate data using either the segment or residual check.

What effect might any invalid assumptions have on the inference?

Consolidating Task

Download the ratings for the following TV shows from the IMDB and analyze the series using some of the techniques you have learnt from today. For each series, do you identify any changes? Are the assumptions you are making valid? What effect might any invalid assumptions have on the inference?

- Doctor Who
- Grey's Anaytomy
- Mistresses
- The Simpsons
- Top Gear

(Understandably IMBD does not allow screen scraping nor downloads of information for redistribution so you will have to copy and paste the table into Excel, or equivalent, yourself in order to get the ratings data into R.)

Bonus

Just from looking at the data, can you predict which shows have been cancelled?

References

JSS: Killick, Eckley (2014)
PELT: Killick, Fearnhead, Eckley (2012)
CROPS: Kaynes, Eckley, Fearnhead (2015)
cpt.np: Haynes, Fearnhead, Eckley (2016)

Coming soon

. . . to a changepoint package near you

- Robust changepoint detection (GH)
- Join-pin regression
- FPOP (faster than binary segmentation but exact, GH)
- Online PELT
- Multivariate changepoints
- Long memory or changepoint?