GSOC Tests(2019)

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Test 1

Loading the required packages:

```
library(data.table)
```

```
## Warning: package 'data.table' was built under R version 3.5.2
```

```
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.5.2
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:data.table':
##
##     between, first, last
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(changepoint)
```

```
## Warning: package 'changepoint' was built under R version 3.5.2
```

```
## Loading required package: zoo
```

```
## Warning: package 'zoo' was built under R version 3.5.2
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
## Successfully loaded changepoint package version 2.2.2
##  NOTE: Predefined penalty values changed in version 2.2.  Previous penalty values with a postfix 1 i
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.5.2
```

```
library(microbenchmark)
```

```
## Warning: package 'microbenchmark' was built under R version 3.5.2
```

```
library(fpop)
```

```
## Warning: package 'fpop' was built under R version 3.5.2
```

```
## Welcome to the fpop package.
## This package implements the FPOP algorithm (http://arxiv.org/abs/1409.1842),
## see the Fpop function.
```

```
data(neuroblastoma, package="neuroblastoma")
```

Selecting one profile id and one chromosome to continue with the test.

```
selected_profile_id = "1"
selected_chromosome = "1"
```

Creating a data table for selected profile:

```
selected.profiles <- data.table(filter(neuroblastoma$profiles,
                                       profile.id == selected_profile_id,
                                       chromosome == selected_chromosome))
```

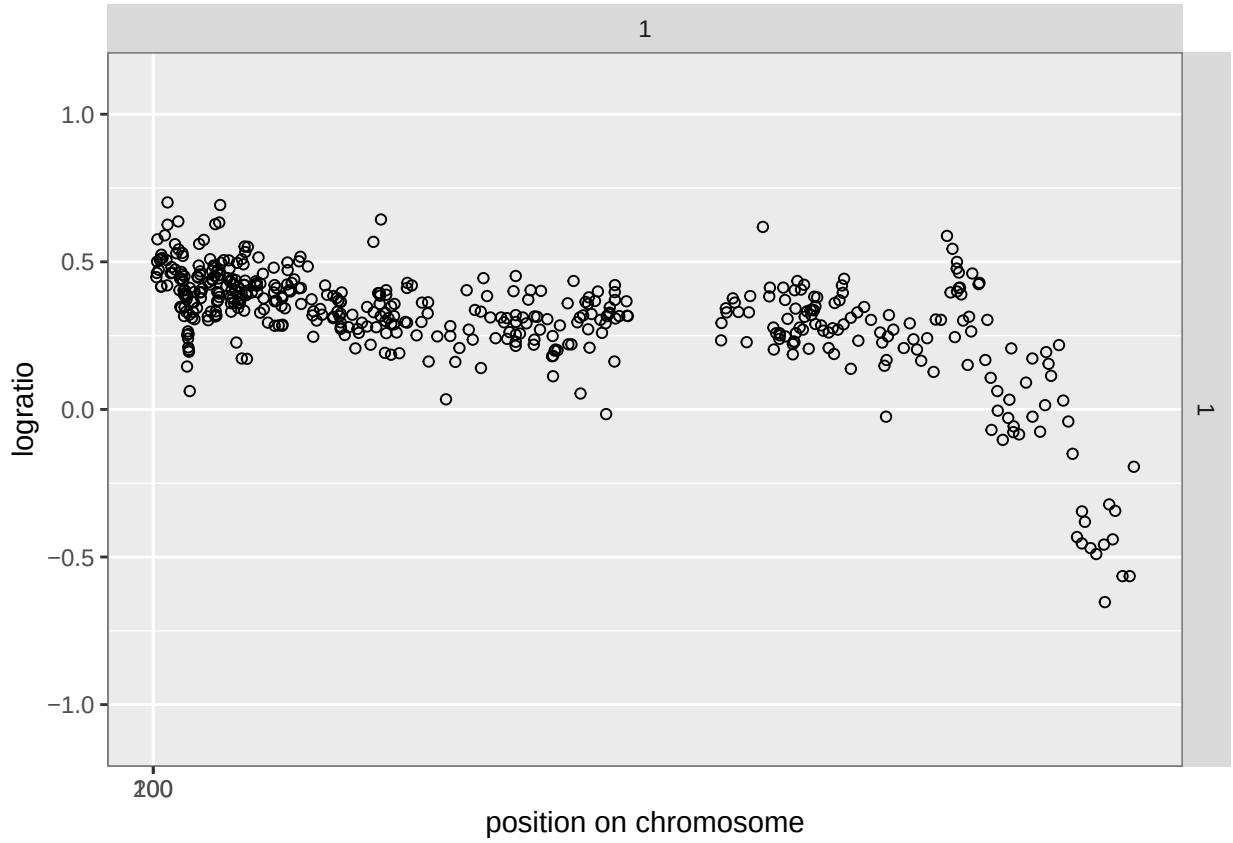
```
## Warning: package 'bindrcpp' was built under R version 3.5.2
```

Plotting this problem in a grid we get:

```
gg.unsupervised <- ggplot()+
  theme(
    panel.margin=grid::unit(0, "lines"),
    panel.border=element_rect(fill=NA, color="grey50")
  )+
  facet_grid(profile.id ~ chromosome, scales="free", space="free_x")+
  geom_point(aes(position, logratio),
             data=selected.profiles,
             shape=1)+
  scale_x_continuous(
    "position on chromosome",
    breaks=c(100, 200))+
  scale_y_continuous(
    "logratio",
    limits=c(-1,1)*1.1)
```

```
## Warning: `panel.margin` is deprecated. Please use `panel.spacing` property
## instead
```

```
print(gg.unsupervised)
```



Now, fitting the unsupervised change point model using the cpt.mean function and using "SIC0" as the penalty parameter we get:

```
pen.name <- "SIC0"
(models <- selected.profiles[, {
  fit.pelt <- cpt.mean(
    logratio, penalty=pen.name, method="PELT")
  end <- fit.pelt@cpts
  before.change <- end[-length(end)]
  after.change <- before.change+1L
  data.table(
    pen.name,
    pen.value=fit.pelt@pen.value,
    changes=list(as.integer((position[before.change]+position[after.change])/2)),
    before_mean=mean(logratio[1:before.change]),
    after_mean=mean(logratio[after.change:length(logratio)]),
    end_pos=position[length(position)]
    )
}, by=list(profile.id, chromosome)])
```

```
##    profile.id chromosome pen.name pen.value   changes before_mean
## 1:          1          1     SIC0  6.161207 212809180   0.3518651
##    after_mean   end_pos
## 1: -0.1539234 249063592
```

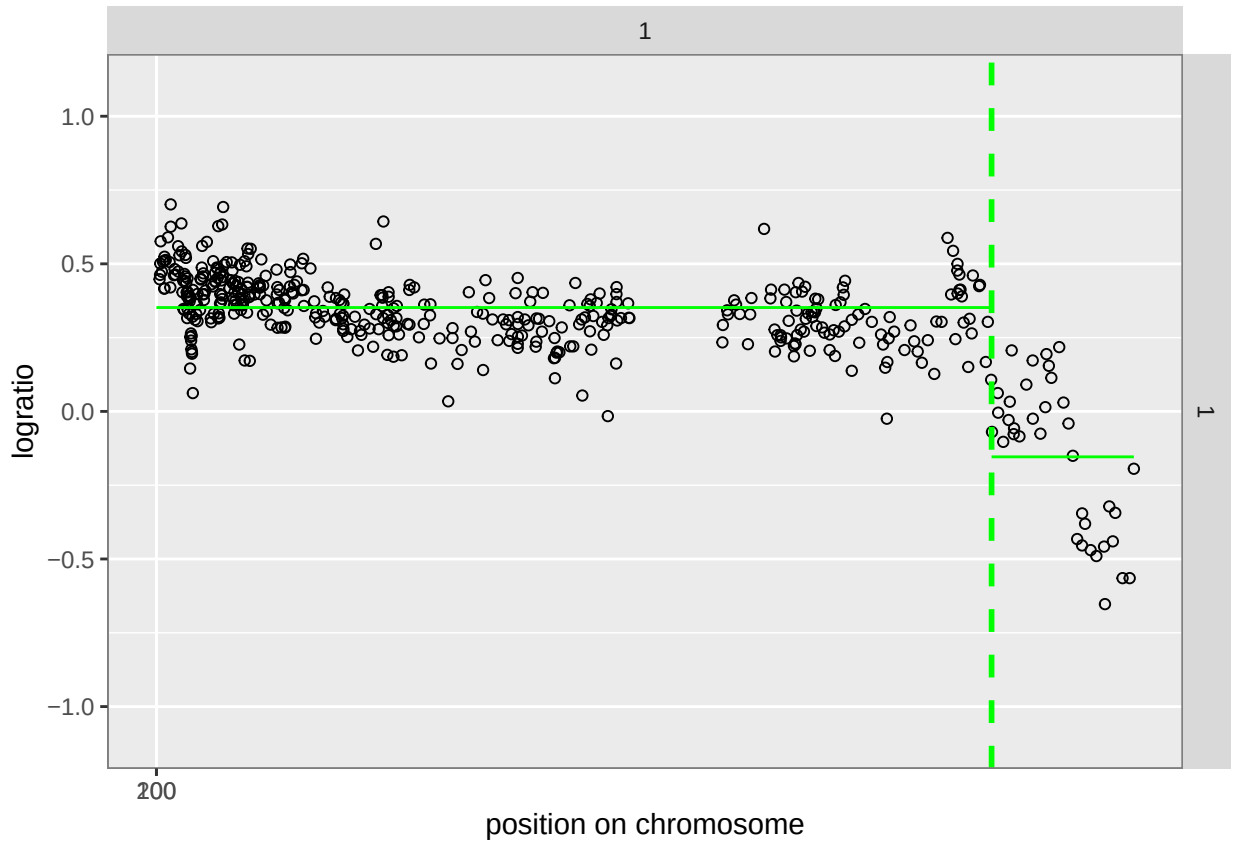
```
(changes <- models[, data.table(
  change=changes[[1]],before_mean = before_mean, after_mean = after_mean, end_pos=end_pos
), by=list(profile.id, chromosome, pen.name)])
```

```
##    profile.id chromosome pen.name    change before_mean after_mean
## 1:          1          1     SIC0 212809180   0.3518651 -0.1539234
##      end_pos
## 1: 249063592
```

```
segments.mean = NULL
segments.mean = rbind(segments.mean, c("start" = 0, "end" = changes$change,
                                       "mean" = changes$before_mean))
segments.mean = rbind(segments.mean, c("start" = changes$change,
                                       "end" = changes$end_pos,
                                       "mean" = changes$after_mean))
```

Plotting the data along with optimal segment means (green line segments) we get:

```
gg.unsupervised+
  theme(legend.box="horizontal")+
  geom_vline(aes(
    xintercept=change),
    color="green",
    size=1,
    linetype="dashed",
    data=changes)+
  geom_segment(aes(
    x = start,
    y = mean,
    xend = end,
    yend = mean,
    col = I("green")),
    data = as.data.frame(segments.mean))
```



Test 2

Seleceting 2 data sets.

```
profile1 = "1"
profile2 = "4"
chromosome1 = "1"
chromosome2 = "1"
```

Creating data table for selected profiles:

```
selected.profiles1 = filter(neuroblastoma$profiles, profile.id == profile1,
                            chromosome == chromosome1)
selected.profiles2 = filter(neuroblastoma$profiles, profile.id == profile2,
                            chromosome == chromosome2)

selected.profiles = data.table(rbind(selected.profiles1, selected.profiles2))
```

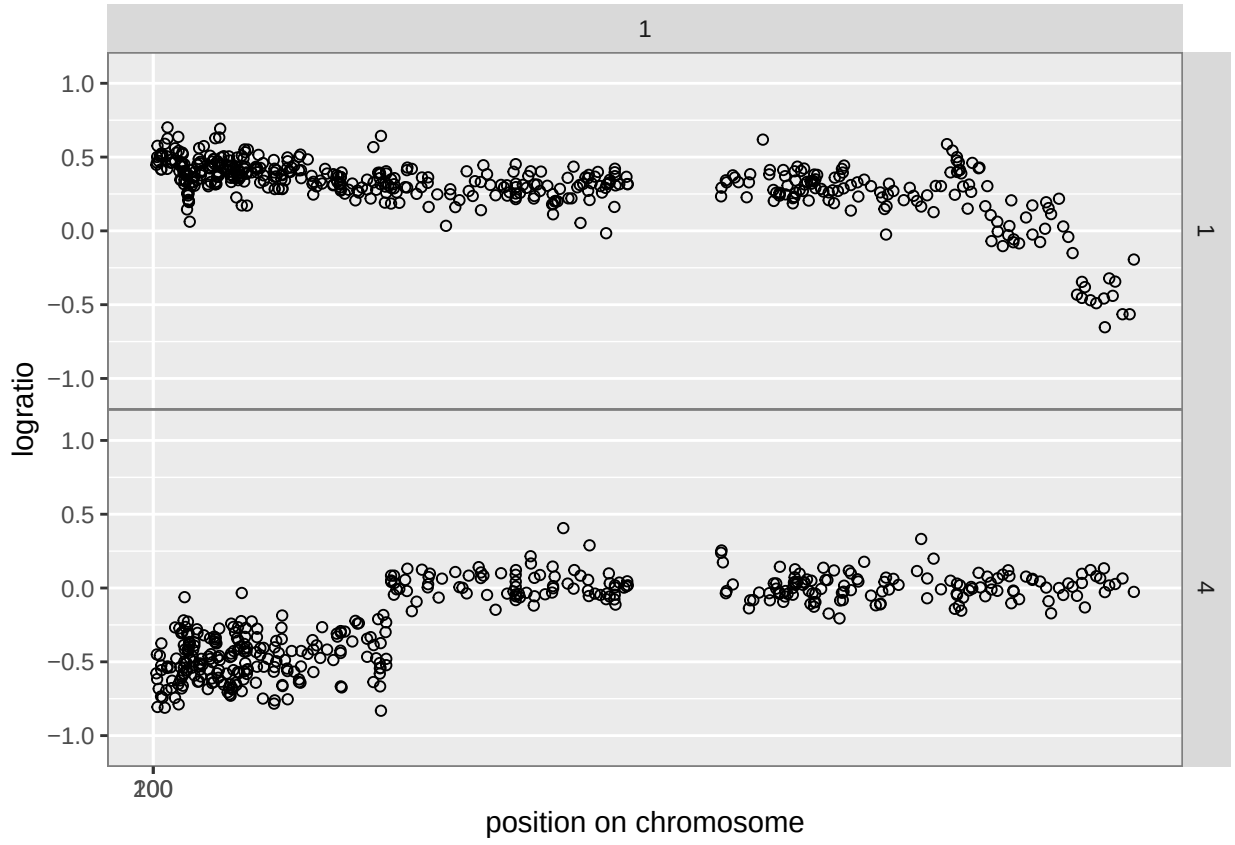
Printing the problems:

```
gg.unsupervised <- ggplot()+
  theme(
    panel.margin=grid::unit(0, "lines"),
    panel.border=element_rect(fill=NA, color="grey50")
```

```
  )+
  facet_grid(profile.id ~ chromosome, scales="free", space="free_x")+
  geom_point(aes(position, logratio),
             data=selected.profiles,
             shape=1)+
  scale_x_continuous(
    "position on chromosome",
    breaks=c(100, 200))+
  scale_y_continuous(
    "logratio",
    limits=c(-1,1)*1.1)
```

```
## Warning: `panel.margin` is deprecated. Please use `panel.spacing` property
## instead
```

```
print(gg.unsupervised)
```



Now, fitting the unsupervised change point model using the cpt.mean function and using 3 penalty paramters "SIC0, BIC0 and AIC0" we get:

```
pen.name <- "SIC0"
(models <- selected.profiles[, {
  fit.pelt <- changepoint::cpt.mean(
    logratio, penalty=pen.name, method="PELT")
  end <- fit.pelt@cpts
```

```
  before.change <- end[-length(end)]
  after.change <- before.change+1L
  data.table(
    pen.name,
    pen.value=fit.pelt@pen.value,
    changes=list(
    as.integer((position[before.change]+position[after.change])/2)
    ),
    before_mean=mean(logratio[1:before.change]),
    after_mean=mean(logratio[after.change:length(logratio)]),
    end_pos=position[length(position)])
}, by=list(profile.id, chromosome)])
```

```
##    profile.id chromosome pen.name pen.value   changes before_mean
## 1:          1          1     SIC0  6.161207 212809180   0.3518651
## 2:          4          1     SIC0  6.059123  59792500  -0.4800527
##     after_mean   end_pos
## 1: -0.15392338 249063592
## 2:  0.01468708 249063592
```

```
pen.name <- "BIC0"
(models1 <- selected.profiles[, {
  fit.pelt <- changepoint::cpt.mean(
    logratio, penalty=pen.name, method="PELT")
  end <- fit.pelt@cpts
  before.change <- end[-length(end)]
  after.change <- before.change+1L
  data.table(
    pen.name,
    pen.value=fit.pelt@pen.value,
    changes=list(
    as.integer((position[before.change]+position[after.change])/2)
    ),
    before_mean=mean(logratio[1:before.change]),
    after_mean=mean(logratio[after.change:length(logratio)]),
    end_pos=position[length(position)])
}, by=list(profile.id, chromosome)])
```

```
##    profile.id chromosome pen.name pen.value   changes before_mean
## 1:          1          1     BIC0  6.161207 212809180   0.3518651
## 2:          4          1     BIC0  6.059123  59792500  -0.4800527
##     after_mean   end_pos
## 1: -0.15392338 249063592
## 2:  0.01468708 249063592
```

```
models <- rbind(models, models1)


pen.name <- "AIC0"
(models2 <- selected.profiles[, {
  fit.pelt <- changepoint::cpt.mean(
    logratio, penalty=pen.name, method="PELT")
  end <- fit.pelt@cpts
  before.change <- end[-length(end)]
  after.change <- before.change+1L
```

```
  data.table(
    pen.name,
    pen.value=fit.pelt@pen.value,
    changes=list(
    as.integer((position[before.change]+position[after.change])/2)
    ),
    before_mean=mean(logratio[1:before.change]),
    after_mean=mean(logratio[after.change:length(logratio)]),
    end_pos=position[length(position)])
}, by=list(profile.id, chromosome)])
```

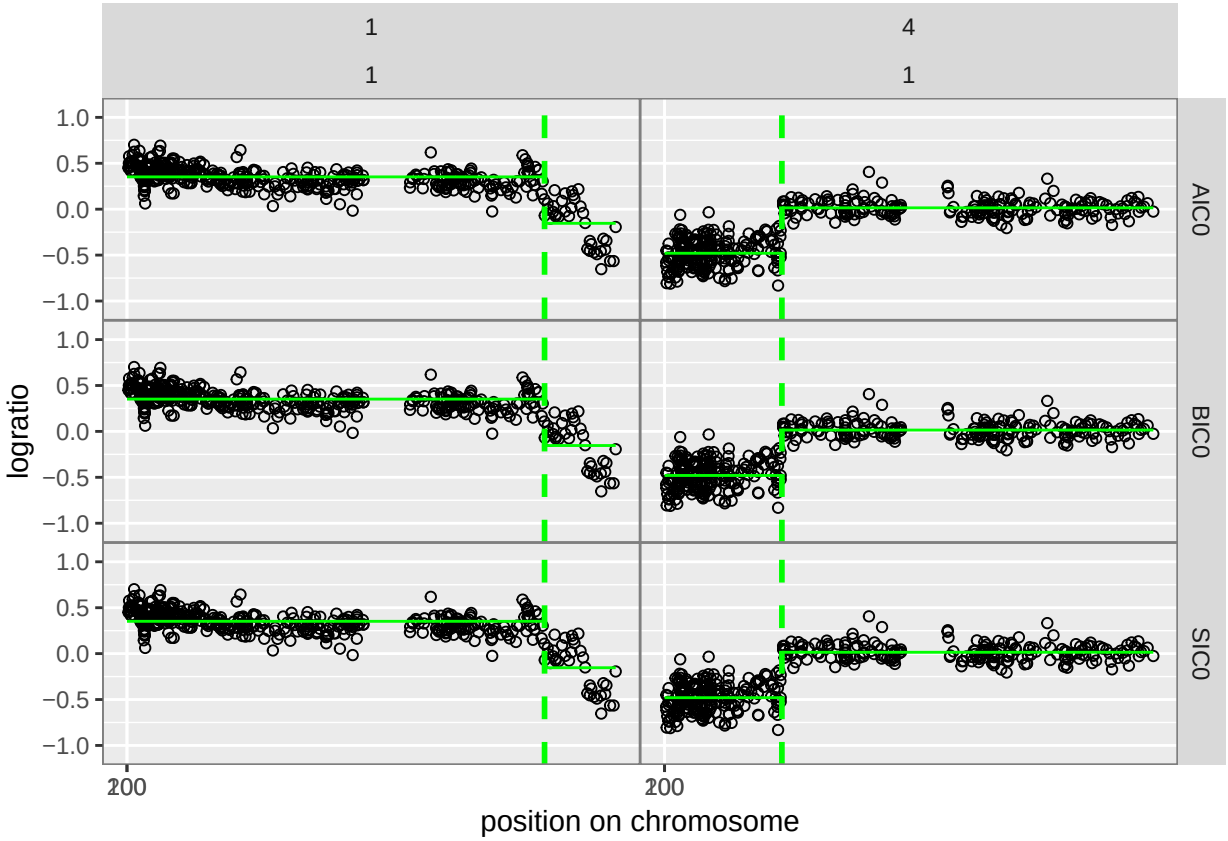
```
##    profile.id chromosome pen.name pen.value   changes before_mean
## 1:          1          1     AIC0         2 212809180   0.3518651
## 2:          4          1     AIC0         2  59792500  -0.4800527
##     after_mean   end_pos
## 1: -0.15392338 249063592
## 2:  0.01468708 249063592
```

```
models <- rbind(models, models2)


changes <- models[, data.table(
  change=changes[[1]],before_mean = before_mean,
  after_mean = after_mean, end_pos=end_pos,
  start = 0, end = changes[[1]], mean = before_mean
), by=list(profile.id, chromosome, pen.name)]

segments <- changes[, data.table(
  change=change,before_mean = before_mean,
  after_mean = after_mean, end_pos=end_pos,
  start = change, end = end_pos, mean = after_mean
), by=list(profile.id, chromosome, pen.name)]

segments = rbind(changes, segments)
```

Plotting the data along with optimal segment means (green line segments) we get:

```
gg.unsupervised+
  facet_grid(pen.name ~ profile.id + chromosome, scales="free", space="free_x")+
  theme(legend.box="horizontal")+
  geom_vline(aes(
    xintercept=change),
    color="green",
    size=1,
    linetype="dashed",
    data=segments)+
  geom_segment(aes(
    x = start,
    y = mean,
    xend = end,
    yend = mean),
    col = I("green"),
```

```
    data = segments
  )
```



Test 3

Performing test on all chromosomes for profile ids in [1 100].

```
num_tests = 100
#selected_data = filter(neuroblastoma$profiles, chromosome == sel_chromosome)
selected_ids = unique(neuroblastoma$profiles$profile.id)[1:num_tests]
selected_data = filter(neuroblastoma$profiles, profile.id %in% selected_ids)
```

Performing the test:

```
timing_list <- list()
n = 1
while(n <= num_tests){
  current_id = selected_ids[n]
  current_data = filter(selected_data, profile.id == current_id)
  length = length(current_data$logratio)
  timing <- microbenchmark(
    "cpt_mean"={
        cpt.mean(current_data$logratio, method="PELT", pen.value = 1)
    },
  "fpop"={
      Fpop(current_data$logratio, 1)
    }, times=5)
```

```
  timing_list[[paste(n)]] <- data.table(length, timing)
  n = n + 1
}

timing.dt <- do.call(rbind, timing_list)

ggplot(data = timing.dt, aes(x = log(timing.dt$length), y = log(timing.dt$time), col = timing.dt$expr))+
  geom_smooth()+
  labs(x="log(size)", y="log(time)", col="method")
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```