

# Medium Test

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```
library(dplyr)
library(ggplot2)
library(reshape2)
library(changepoint)
data(neuroblastoma, package = "neuroblastoma")
```

## cpt\_segments()

```
# Put cpt changepoint intervals in plottable format.
cpt_segments <- function(data, penalty) {

  # Calculate changepoints using changepoint library.
  cpt <- cpt.mean(data, penalty=penalty,
                  method="PELT", pen.value=0.5)

  # Get the starts and ends of each changepoint interval.
  end <- cpt@cpts
  start <- c(1, end[1:length(end)-1])

  # Get mean over each changepoint interval.
  seg_mean <- vector(length=length(end))
  for(i in 1:length(start)) {
    seg_mean[i] <- mean(data[start[i]:end[i]])
  }

  # We use NA to avoid jumps in plot.
  seg <- c(rep(seg_mean, times=(end-start)), NA)
  seg[start] <- NA

  return(seg)
}
```

## Get relevant data

```
# Desired id and chromosome to examine.
id <- c("2", "4")
chr <- c("1", "2")

# Filter data for only specified id and chromosome.
prof1 <- filter(neuroblastoma$profiles,
                profile.id == id[1],
                chromosome == chr[1])

prof2 <- filter(neuroblastoma$profiles,
                profile.id == id[2],
                chromosome == chr[2])
```

```
profile <- rbind(as.data.frame(prof1),
                 as.data.frame(prof2))
```

## Calculate changepoints for different penalties

```
# Different penalty parameters to try.
penalties <- c("AIC", "MBIC", "Manual")

# Get plottable changepoint interval for each
# profile and add to profile data frame.
for(penalty in penalties) {
  profile[penalty] <-
    c(cpt_segments(prof1$logratio, penalty),
      cpt_segments(prof2$logratio, penalty))
}
```

## Plot results

```
molten_profile <- melt(profile,
                       measure.vars=penalties,
                       value.name="cpts", variable.name="penalty")

ggplot(data=molten_profile) +
  geom_point(mapping=aes(x=position, y=logratio)) +
  geom_line(mapping=aes(x=position, y=cpts, col="green")) +
  facet_grid(penalty ~ profile.id + chromosome)
```

