

Package ‘FLOPART’

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Type Package

Title Functional Labeled Optimal Partitioning

Version 2024.6.19

Description Provides an efficient 'C++' code for computing an optimal segmentation model with Poisson loss, up-down constraints, and label constraints, as described by Kaufman et al. (2024) <[doi:10.1080/10618600.2023.2293216](https://doi.org/10.1080/10618600.2023.2293216)>.

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RoxygenNote 7.3.1

Suggests testthat, PeakError, knitr, markdown, ggplot2

Depends R (>= 2.10)

LinkingTo Rcpp

Imports Rcpp, data.table

VignetteBuilder knitr

NeedsCompilation yes

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Description

Main function for computing optimal segmentation model with Poisson loss, up-down constraints, and label constraints.

Usage

```
FLOPART(coverage, label, penalty)
```

Arguments

coverage	data frame of coverage
label	data frame of labels
penalty	non-negative penalty constant

Value

list with named elements: `coverage_dt` is a data table with columns `chromStart`, `chromEnd`, `count`, `weight`; `label_dt` is a data table with columns `chromStart`, `chromEnd`, `annotation`, `type`, `firstRow`, `lastRow`; `cost_mat` is a $N \times 2$ numeric matrix of optimal penalized Poisson loss values up to each data point and in each state; `intervals_mat` is a $N \times 2$ integer matrix of counts of intervals used to store the optimal cost function, useful for analyzing time/space complexity; `segments_dt` is a data table with columns `chromStart`, `chromEnd`, `status`, `mean`.

Author(s)

Toby Dylan Hocking

Examples

```
library(data.table)
data("Mono27ac.simple", package="FLOPART")
Mono27ac.simple
label.pen <- 1400
fit <- with(Mono27ac.simple, FLOPART::FLOPART(coverage, label, label.pen))
lapply(fit, head)

## Plot data and model.
ann.colors <- c(
  noPeaks="orange",
  peakStart="#efafaf",
  peakEnd="#ff4c4c")
model.color <- "blue"
(peaks.dt <- fit[["segments_dt"]][status=="peak"][, peak.y := -2][])
if(require("ggplot2")){
```

```

ggplot()+
  ggtitle("Model with label constraints (FLOPART)")+
  scale_fill_manual("label", values=ann.colors)+
  geom_rect(aes(
    xmin=chromStart, xmax=chromEnd,
    ymin=-Inf, ymax=Inf,
    fill=annotation),
    alpha=0.5,
    color="grey",
    data=Mono27ac.simple[["label"]])+
  geom_step(aes(
    chromStart, count),
    data=Mono27ac.simple[["coverage"]],
    color="grey50")+
  geom_step(aes(
    chromStart, mean),
    data=fit[["segments_dt"]],
    color=model.color)+
  geom_segment(aes(
    chromStart, peak.y,
    xend=chromEnd, yend=peak.y),
    color=model.color,
    size=1,
    data=peaks.dt)+
  geom_point(aes(
    chromEnd, peak.y),
    color=model.color,
    shape=21,
    fill="white",
    data=peaks.dt)+
  theme_bw()+
  theme(panel.spacing=grid::unit(0, "lines"))
}

## To analyze computational complexity, plot number of intervals
## stored in cost function, versus data point, for each cost status.
imat <- fit[["intervals_mat"]]
interval.dt <- data.table(
  intervals=as.integer(imat),
  status=c("peak", "background")[as.integer(col(imat))],
  data.i=as.integer(row(imat)))
if(require("ggplot2")){
  ggplot()+
    scale_fill_manual("label", values=ann.colors)+
    geom_rect(aes(
      xmin=firstRow-0.5, xmax=lastRow+0.5,
      ymin=-Inf, ymax=Inf,
      fill=annotation),
      alpha=0.5,
      color="grey",
      data=fit[["label_dt"]])+
    geom_line(aes(
      data.i, intervals, color=status),

```

```

      size=1,
      data=interval.dt)
}

```

FLOPART_data

Convert data for input to FLOPART

Description

FLOPART needs at most one label per coverage data row, which may not be the case for arbitrary coverage/labels.

Usage

```
FLOPART_data(coverage, label)
```

Arguments

coverage	data frame of coverage with columns chromStart, chromEnd, count
label	data frame of labels with with columns chromStart, chromEnd, annotation

Value

named list: coverage_dt is data table representing a run-length encoding of the input coverage data, with additional rows if there are label chromStart/chromEnd values not in the set of coverage positions; label_dt is a data table with one row per label, and additional columns firstRow/lastRow which refer to row numbers of coverage_dt, 0-based for passing to C++ code.

Author(s)

Toby Dylan Hocking

Examples

```

library(data.table)
d <- function(chromStart, chromEnd, count){
  data.table(chromStart, chromEnd, count)
}
(cov.dt <- rbind(
  d(0, 10, 53),
  d(10, 20, 124)))
l <- function(chromStart, chromEnd, annotation){
  data.table(chromStart, chromEnd, annotation)
}
lab.dt <- rbind(
  l(2, 7, "noPeaks"),
  l(8, 15, "peakStart"))
FLOPART::FLOPART_data(cov.dt)
FLOPART::FLOPART_data(cov.dt, lab.dt)

```

```
data("Mono27ac", package="FLOPART")
sapply(Mono27ac, dim)
converted <- with(Mono27ac, FLOPART::FLOPART_data(coverage, labels))
sapply(converted, dim)
```

FLOPART_interface *Interface to FLOPART C++ code*

Description

Interface to FLOPART C++ code

Usage

```
FLOPART_interface(  
  data_vec,  
  weight_vec,  
  penalty,  
  label_type_vec,  
  label_start_vec,  
  label_end_vec  
)
```

Arguments

data_vec	Integer vector of non-negative count data
weight_vec	Numeric vector of positive weights (same size as data_vec)
penalty	non-negative real-valued penalty (larger for fewer peaks)
label_type_vec	Integer vector of label types
label_start_vec	Integer vector of label starts
label_end_vec	Integer vector of label ends

Value

List with named elements: cost_mat and intervals_mat (one row for each data point, first column up, second down), segments_df (one row for each segment in the optimal model)

<code>get_label_code</code>	<i>Lookup the integer values used to represent different label types</i>
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Description

Lookup the integer values used to represent different label types

Usage

```
get_label_code()
```

Value

Integer vector with names corresponding to supported label types

Mono27ac	<i>H3K27ac ChIP-seq data from one Monocyte sample</i>
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Description

Raw coverage data and labels are provided in order to test the FLOPART algo.

Usage

```
data("Mono27ac")
```

Format

List of 2 data.tables, coverage and labels.

Source

<https://github.com/tdhock/feature-learning-benchmark>

Mono27ac.simple

Smaller H3K27ac ChIP-seq data from one Monocyte sample

Description

Raw coverage data and labels are provided in order to test the FLOPART algo.

Usage

```
data("Mono27ac.simple")
```

Format

List of two data tables, coverage and label.

Source

<https://github.com/tdhock/feature-learning-benchmark>

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