

# PeakSegDisk usage examples

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Welcome to PeakSegDisk, an R package for optimal peak detection in very large count data sequences.

## 1 Related work

The PeakSeg R packages contain algorithms for inferring optimal segmentation models subject to the constraint that up changes must be followed by down changes, and vice versa. This ensures that the model can be interpreted in terms of peaks (after up changes) and background (after down changes).

**PeakSegDP** the historically first PeakSeg package, <https://CRAN.R-project.org/package=PeakSegDP> provides a heuristic quadratic time algorithm for computing models from 1 to  $S$  segments for a single sample. This was the original algorithm described in our ICML'15 paper, <http://jmlr.org/proceedings/papers/v37/hocking15.html>, but it is neither fast nor optimal, so in practice we recommend to use our newer packages below instead.

**PeakSegOptimal** <https://CRAN.R-project.org/package=PeakSegOptimal> provides log-linear time algorithms for computing optimal models with multiple peaks for a single sample. The algorithms are faster and more accurate than PeakSegDP, <https://arxiv.org/abs/1703.03352>

**PeakSegDisk** <https://github.com/tdhock/PeakSegDisk> provides an on-disk implementation of optimal log-linear algorithms for computing multiple peaks in a single sample. Computes same models as PeakSegOptimal but works for much larger data sets because disk is used for storage instead of memory. <https://arxiv.org/abs/1810.00117>

**PeakSegJoint** <https://CRAN.R-project.org/package=PeakSegJoint> provides a fast heuristic algorithm for computing models with a single common peak in  $0, \dots, S$  samples. <https://arxiv.org/abs/1506.01286>

**PeakSegPipeline** <https://github.com/tdhock/PeakSegPipeline> provides a pipeline for genome-wide peak calling using the other PeakSeg packages.

The remainder of this vignette is dedicated to an explanation of how to use PeakSegDisk.

## 2 Simulate a noisy integer vector with changes

The first example we will treat is detecting peaks in a vector of integer data, with possibly the same values at adjacent positions. This is an inefficient representation for large genomic data, but it is the typical output from simulation functions like `rpois`:

```

sim(seg <- function(seg.mean, size.mean=15){
  seg.size <- rpois(1, size.mean)
  rpois(seg.size, seg.mean)
})
set.seed(1)
seg.mean.vec <- c(1.5, 3.5, 0.5, 4.5, 2.5)
z.list <- lapply(seg.mean.vec, sim(seg))
(z.rep.vec <- unlist(z.list))

#> [1] 3 0 3 4 2 2 0 0 0 2 1 2 9 3 5 6 2 4 1 2 3 0 3 6 3 3 0 1 1 1 0 1 0 1 1
#> [36] 1 0 0 1 0 0 4 7 4 3 2 2 3 4 5 4 7 3 4 3 5 3 4 4 2 4 2 2 2 5 4 2 4 6 2
#> [71] 3 2 2 3 1

```

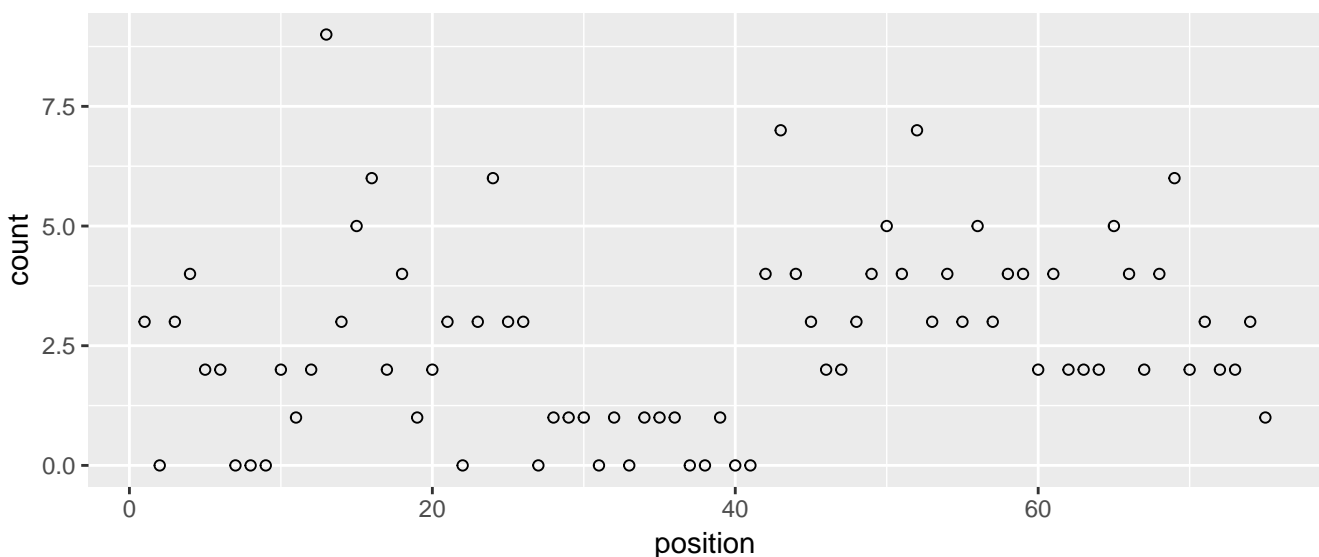
From the output above it is clear that these simulated data are integers, with some identical values at adjacent positions.

Below we put these data into a data table in order to plot them along with the model using ggplot2:

```

count.df <- data.frame(
  chrom="chrUnknown",
  chromStart=0:(length(z.rep.vec)-1),
  chromEnd=1:length(z.rep.vec),
  count=z.rep.vec)
library(ggplot2)
gg.count <- ggplot()+
  xlab("position")+
  geom_point(aes(
    chromEnd, count),
    shape=1,
    data=count.df)
gg.count

```

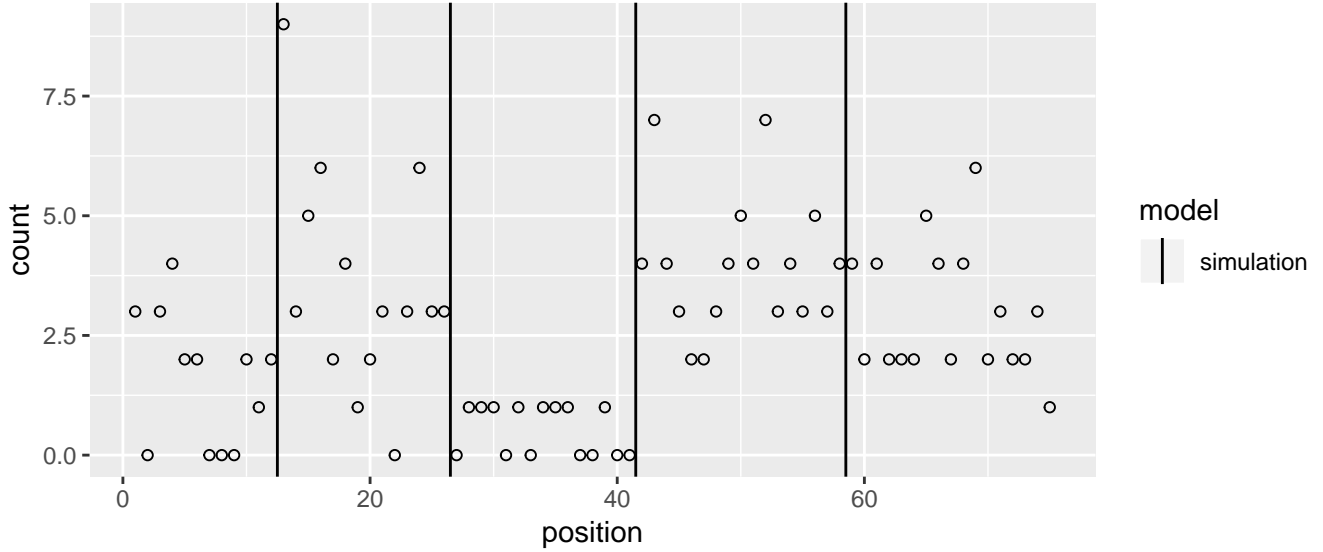


The true changepoints in the simulation are shown below.

```

n.segs <- length(seg.mean.vec)
seg.size.vec <- sapply(z.list, length)
seg.end.vec <- cumsum(seg.size.vec)
change.vec <- seg.end.vec[-n.segs]+0.5
change.df <- data.frame(
  changepoint=change.vec)
gg.change <- gg.count+
  geom_vline(aes(
    xintercept=changepoint, color=model),
    data=data.frame(change.df, model="simulation"))+
  scale_color_manual(
    values=c(
      simulation="black",
      fitted="green"))
gg.change

```



### 3 Segment a vector of integers

Let  $z_1, \dots, z_n \in \mathbb{Z}_+$  be the sequence of  $n$  non-negative count data in `z.rep.vec`, and let  $w_1 = \dots = w_n = 1$  be weights which are all 1. The peak detection algorithm computes the solution to the following optimization problem:

$$\begin{aligned}
& \underset{\substack{\mathbf{m} \in \mathbb{R}^n, \mathbf{s} \in \{0,1\}^n \\ \mathbf{c} \in \{-1,0,1\}^{n-1}}}{\text{minimize}} && \sum_{i=1}^n w_i \ell(m_i, z_i) + \lambda \sum_{i=1}^{n-1} I(c_i = 1) \\
& \text{subject to} && \text{no change: } c_i = 0 \Rightarrow m_i = m_{i+1} \text{ and } s_i = s_{i+1} \\
& && \text{go up: } c_i = 1 \Rightarrow m_i \leq m_{i+1} \text{ and } (s_i, s_{i+1}) = (0, 1), \\
& && \text{go down: } c_i = -1 \Rightarrow m_i \geq m_{i+1} \text{ and } (s_i, s_{i+1}) = (1, 0), \\
& && \text{start and end down: } s_1 = s_n = 0.
\end{aligned}$$

where  $\ell(m, z) = m - z \log m$  is the Poisson loss. The optimization variables are  $m_i$  for the segment mean,  $s_i$  for hidden state, and  $c_i$  for type of changepoint. The penalty term is proportional to the number of changepoint variables  $c_i$  which are equal to 1 (which is the same as the number of peaks in the resulting model).

To run the peak detection algorithm a numeric penalty parameter  $\lambda \geq 0$  must be specified by the user. The smallest value is 0 which yields max peaks, and the largest value is Inf which yields no peaks. The code below runs the peak detection algorithm on this count data vector, using the penalty parameter  $\lambda = 10.5$ :

```
fit <- list()
(fit$vec <- PeakSegDisk::PeakSegFPOP_vec(z.rep.vec, 10.5))

#> $segments
#>      chrom chromStart chromEnd      status      mean
#> 1: chrUnknown      69      75 background 2.166670
#> 2: chrUnknown      41      69      peak 3.714290
#> 3: chrUnknown      26      41 background 0.533333
#> 4: chrUnknown      12      26      peak 3.571430
#> 5: chrUnknown       0      12 background 1.583330
#>
#> $loss
#>      penalty segments peaks bases bedGraph.lines mean.pen.cost total.loss
#> 1:      10.5       5     2   75              60    0.01507491  -19.86938
#>      equality.constraints mean.intervals max.intervals  megabytes seconds
#> 1:              0              4.6              8 0.02745438    0.003
#>
#> $data
#>      chrom chromStart chromEnd count
#> 1: chrUnknown       0       1     3
#> 2: chrUnknown       1       2     0
#> 3: chrUnknown       2       3     3
#> 4: chrUnknown       3       4     4
#> 5: chrUnknown       4       6     2
#> 6: chrUnknown       6       9     0
#> 7: chrUnknown       9      10     2
#> 8: chrUnknown      10      11     1
#> 9: chrUnknown      11      12     2
#> 10: chrUnknown     12      13     9
#> 11: chrUnknown     13      14     3
#> 12: chrUnknown     14      15     5
#> 13: chrUnknown     15      16     6
#> 14: chrUnknown     16      17     2
#> 15: chrUnknown     17      18     4
#> 16: chrUnknown     18      19     1
#> 17: chrUnknown     19      20     2
#> 18: chrUnknown     20      21     3
#> 19: chrUnknown     21      22     0
```

```

#> 20: chrUnknown      22      23      3
#> 21: chrUnknown      23      24      6
#> 22: chrUnknown      24      26      3
#> 23: chrUnknown      26      27      0
#> 24: chrUnknown      27      30      1
#> 25: chrUnknown      30      31      0
#> 26: chrUnknown      31      32      1
#> 27: chrUnknown      32      33      0
#> 28: chrUnknown      33      36      1
#> 29: chrUnknown      36      38      0
#> 30: chrUnknown      38      39      1
#> 31: chrUnknown      39      41      0
#> 32: chrUnknown      41      42      4
#> 33: chrUnknown      42      43      7
#> 34: chrUnknown      43      44      4
#> 35: chrUnknown      44      45      3
#> 36: chrUnknown      45      47      2
#> 37: chrUnknown      47      48      3
#> 38: chrUnknown      48      49      4
#> 39: chrUnknown      49      50      5
#> 40: chrUnknown      50      51      4
#> 41: chrUnknown      51      52      7
#> 42: chrUnknown      52      53      3
#> 43: chrUnknown      53      54      4
#> 44: chrUnknown      54      55      3
#> 45: chrUnknown      55      56      5
#> 46: chrUnknown      56      57      3
#> 47: chrUnknown      57      59      4
#> 48: chrUnknown      59      60      2
#> 49: chrUnknown      60      61      4
#> 50: chrUnknown      61      64      2
#> 51: chrUnknown      64      65      5
#> 52: chrUnknown      65      66      4
#> 53: chrUnknown      66      67      2
#> 54: chrUnknown      67      68      4
#> 55: chrUnknown      68      69      6
#> 56: chrUnknown      69      70      2
#> 57: chrUnknown      70      71      3
#> 58: chrUnknown      71      73      2
#> 59: chrUnknown      73      74      3
#> 60: chrUnknown      74      75      1
#>      chrom chromStart chromEnd count
#>
#> attr(,"class")
#> [1] "PeakSegFPOP_df" "PeakSegFPOP_dir" "list"

```

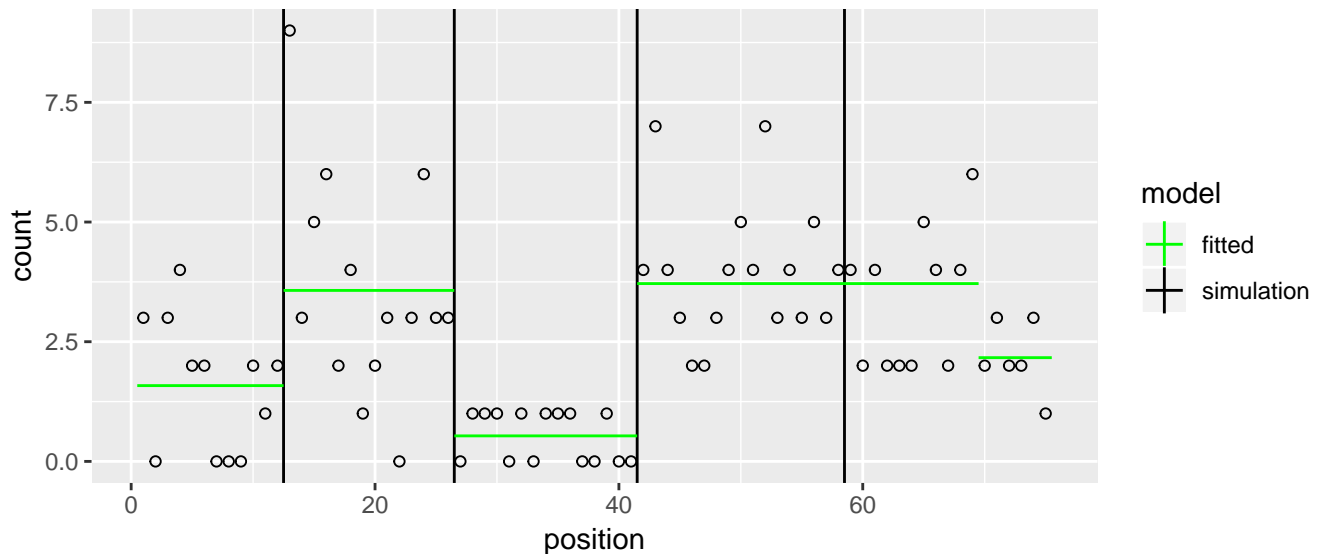
The model output list above includes **segments**, a data table with one row for each segment mean,

and loss, a data table with one row that reports the model meta-data. Of interest are:

- `penalty`, the user-provided penalty value,
- `segments`, the number of segments,
- `peaks`, the number of peaks (even-numbered segments),
- `bases`, the number of data points in repetitive form (not run-length encoding),
- `bedGraph.lines`, the number of data points in run-length encoding form,
- `mean.pen.cost`, the optimal mean loss plus `penalty*peaks`,
- `total.loss`, the optimal total Poisson loss over all data points,
- `equality.constraints`, the number of adjacent segment means that are equal in the optimal solution. Note that when this number is greater than 0, then there are some active equality constraints, and the optimal model is therefore not feasible for the strict inequality constraints, which implies that the optimum of the problem with strict inequality constraints is undefined, i.e. for any sub-optimal solution that satisfies the strict inequality constraints, we can find a lower cost solution that satisfies the strict inequality constraints (but is still sub-optimal), by getting closer to the solution with active equality constraints.
- `megabytes`, the storage space on disk used by the solver,
- `seconds`, the amount of time used by the solver,
- `mean.intervals`, `max.intervals`, statistics over all intervals (candidate changepoints) computed by the functional pruning algorithm, useful for analyzing computational complexity, which is linear in the number of intervals.

Note in particular that `PeakSegFPOP_vec` internally uses `rle` to construct a run-length encoding, which is passed to the solver to save time/storage. In this case the repetitive integer data vector contains 75 elements but the `coverage.bedGraph` data file contains only 60 lines. In real genomic data sets the difference is typically much larger.

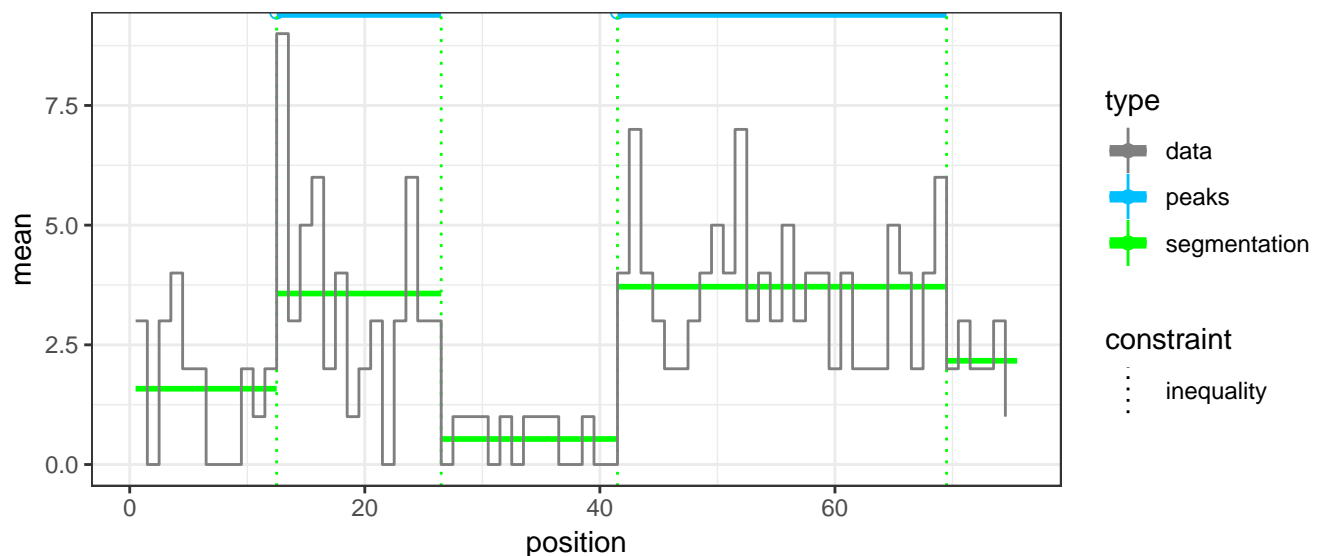
```
gg.change+
  geom_segment(aes(
    chromStart+0.5, mean, xend=chromEnd+0.5, yend=mean, color=model),
    data=data.frame(fit$vec$segments, model="fitted"))
```



It is clear from the plot above that the first three changepoints are estimated exactly and the last one is a bit over-estimated.

Also note that a default plot method is defined for these objects:

```
plot(fit$vec)
```



## 4 Segment a data frame

Another interface that can be used on a data.frame with  $n$  rows and exactly 4 columns (chrom, chromStart, chromEnd, count) is `PeakSegFPOP_df`. For each row  $i \in \{1, \dots, n\}$ , let  $z_i \in \mathbb{Z}_+$  be the non-negative count data (count column), and let  $w_i > 0$  be the weight (equal to the number of bases,  $\text{chromEnd} - \text{chromStart}$ ). The optimization problem we solve is the same as before. Note that this function does not perform run-length encoding for you:

```
(fit$ddf <- PeakSegDisk::PeakSegFPOP_df(count.df, 10.5))

#> $segments
#>      chrom chromStart chromEnd      status      mean
#> 1: chrUnknown      69      75 background 2.166670
#> 2: chrUnknown      41      69      peak 3.714290
#> 3: chrUnknown      26      41 background 0.533333
#> 4: chrUnknown      12      26      peak 3.571430
#> 5: chrUnknown       0      12 background 1.583330
#>
#> $loss
#>      penalty segments peaks bases bedGraph.lines mean.pen.cost total.loss
#> 1:      10.5      5      2      75      75      0.01507491 -19.86938
#>      equality.constraints mean.intervals max.intervals megabytes seconds
#> 1:              0      4.633333      8 0.0344162      0.004
#>
#> $data
#>      chrom chromStart chromEnd count
#> 1: chrUnknown      0      1      3
#> 2: chrUnknown      1      2      0
#> 3: chrUnknown      2      3      3
#> 4: chrUnknown      3      4      4
#> 5: chrUnknown      4      5      2
#> 6: chrUnknown      5      6      2
#> 7: chrUnknown      6      7      0
#> 8: chrUnknown      7      8      0
#> 9: chrUnknown      8      9      0
#> 10: chrUnknown      9     10      2
#> 11: chrUnknown     10     11      1
#> 12: chrUnknown     11     12      2
#> 13: chrUnknown     12     13      9
#> 14: chrUnknown     13     14      3
#> 15: chrUnknown     14     15      5
#> 16: chrUnknown     15     16      6
#> 17: chrUnknown     16     17      2
#> 18: chrUnknown     17     18      4
#> 19: chrUnknown     18     19      1
#> 20: chrUnknown     19     20      2
#> 21: chrUnknown     20     21      3
#> 22: chrUnknown     21     22      0
#> 23: chrUnknown     22     23      3
#> 24: chrUnknown     23     24      6
#> 25: chrUnknown     24     25      3
#> 26: chrUnknown     25     26      3
#> 27: chrUnknown     26     27      0
#> 28: chrUnknown     27     28      1
#> 29: chrUnknown     28     29      1
```

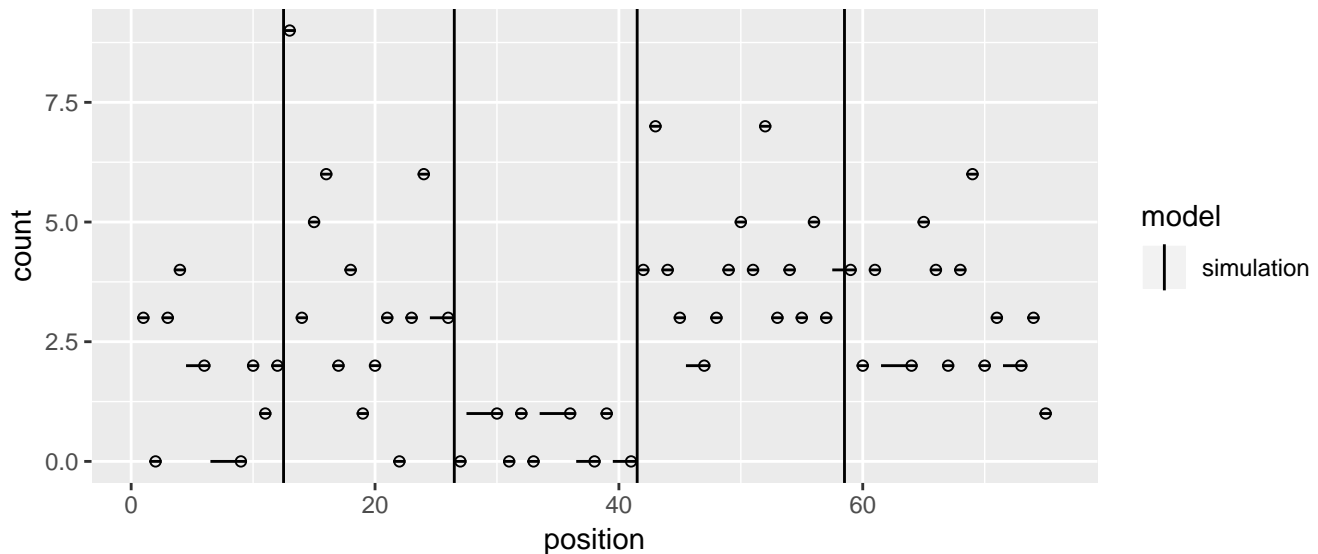


#> 30: chrUnknown	29	30	1
#> 31: chrUnknown	30	31	0
#> 32: chrUnknown	31	32	1
#> 33: chrUnknown	32	33	0
#> 34: chrUnknown	33	34	1
#> 35: chrUnknown	34	35	1
#> 36: chrUnknown	35	36	1
#> 37: chrUnknown	36	37	0
#> 38: chrUnknown	37	38	0
#> 39: chrUnknown	38	39	1
#> 40: chrUnknown	39	40	0
#> 41: chrUnknown	40	41	0
#> 42: chrUnknown	41	42	4
#> 43: chrUnknown	42	43	7
#> 44: chrUnknown	43	44	4
#> 45: chrUnknown	44	45	3
#> 46: chrUnknown	45	46	2
#> 47: chrUnknown	46	47	2
#> 48: chrUnknown	47	48	3
#> 49: chrUnknown	48	49	4
#> 50: chrUnknown	49	50	5
#> 51: chrUnknown	50	51	4
#> 52: chrUnknown	51	52	7
#> 53: chrUnknown	52	53	3
#> 54: chrUnknown	53	54	4
#> 55: chrUnknown	54	55	3
#> 56: chrUnknown	55	56	5
#> 57: chrUnknown	56	57	3
#> 58: chrUnknown	57	58	4
#> 59: chrUnknown	58	59	4
#> 60: chrUnknown	59	60	2
#> 61: chrUnknown	60	61	4
#> 62: chrUnknown	61	62	2
#> 63: chrUnknown	62	63	2
#> 64: chrUnknown	63	64	2
#> 65: chrUnknown	64	65	5
#> 66: chrUnknown	65	66	4
#> 67: chrUnknown	66	67	2
#> 68: chrUnknown	67	68	4
#> 69: chrUnknown	68	69	6
#> 70: chrUnknown	69	70	2
#> 71: chrUnknown	70	71	3
#> 72: chrUnknown	71	72	2
#> 73: chrUnknown	72	73	2
#> 74: chrUnknown	73	74	3
#> 75: chrUnknown	74	75	1

```
#>      chrom chromStart chromEnd count
#>
#> attr(,"class")
#> [1] "PeakSegFPOP_df" "PeakSegFPOP_dir" "list"
```

Note how `bedGraph.lines` is now the same size as `bases`, 75. The time/storage complexity is log-linear in the number of `bedGraph.lines`, so it is more efficient to use the run-length encoding. This can be easily done in R:

```
z.rle.vec <- rle(z.rep.vec)
chromEnd <- cumsum(z.rle.vec$lengths)
rle.df <- data.frame(
  chrom="chrUnknown",
  chromStart=c(0L, chromEnd[-length(chromEnd)]),
  chromEnd,
  count=z.rle.vec$values)
gg.rle <- ggplot()+
  geom_segment(aes(
    chromStart+0.5, count, xend=chromEnd+0.5, yend=count),
  data=rle.df)+
  geom_point(aes(
    chromEnd, count),
  shape=1,
  data=rle.df)+
  geom_vline(aes(
    xintercept=changepoint, color=model),
  data=data.frame(changepoint, model="simulation"))+
  scale_color_manual(
    values=c(
      simulation="black",
      fitted="green"))+
  xlab("position")
gg.rle
```



The plot above shows the run-length encoded data, with a `geom_point` for the last position in each run, and a `geom_segment` extending left to the first position. These data can be segmented as above:

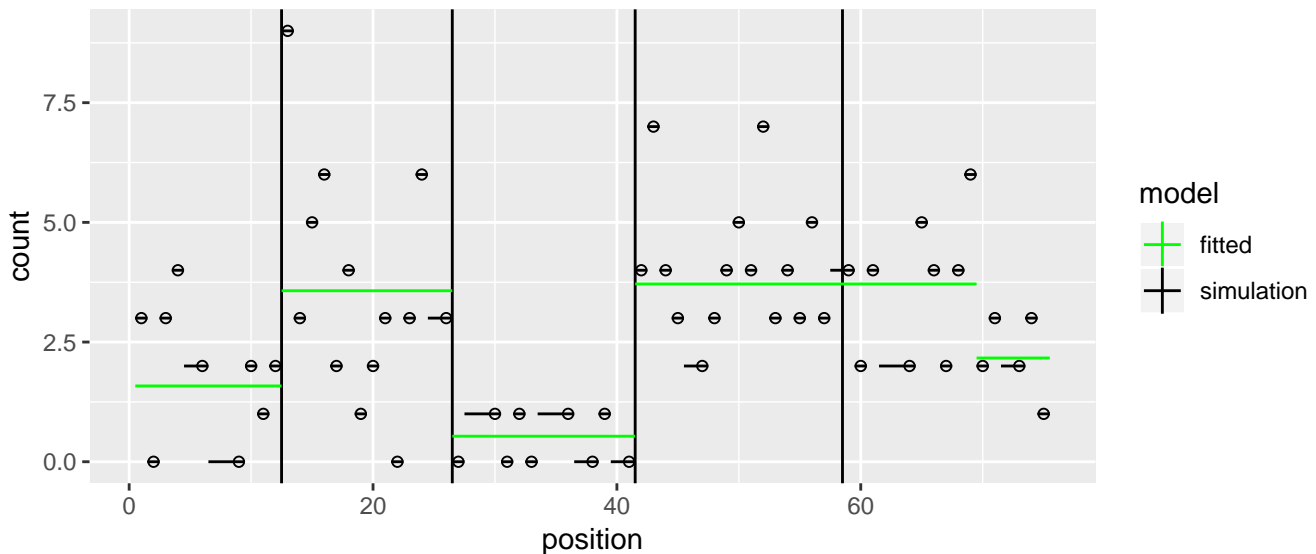
```
(fit$rle <- PeakSegDisk::PeakSegFPOP_df(rle.df, 10.5))

#> $segments
#>      chrom chromStart chromEnd  status    mean
#> 1: chrUnknown      69      75 background 2.166670
#> 2: chrUnknown      41      69      peak 3.714290
#> 3: chrUnknown      26      41 background 0.533333
#> 4: chrUnknown      12      26      peak 3.571430
#> 5: chrUnknown       0      12 background 1.583330
#>
#> $loss
#>  penalty segments peaks bases bedGraph.lines mean.pen.cost total.loss
#> 1:    10.5         5    2    75              60    0.01507491 -19.86938
#>  equality.constraints mean.intervals max.intervals  megabytes seconds
#> 1:              0              4.6              8 0.02745438   0.003
#>
#> $data
#>      chrom chromStart chromEnd count
#> 1: chrUnknown       0        1     3
#> 2: chrUnknown       1        2     0
#> 3: chrUnknown       2        3     3
#> 4: chrUnknown       3        4     4
#> 5: chrUnknown       4        6     2
#> 6: chrUnknown       6        9     0
#> 7: chrUnknown       9       10     2
#> 8: chrUnknown      10       11     1
#> 9: chrUnknown      11       12     2
#> 10: chrUnknown     12       13     9
#> 11: chrUnknown     13       14     3
```

#> 12: chrUnknown	14	15	5
#> 13: chrUnknown	15	16	6
#> 14: chrUnknown	16	17	2
#> 15: chrUnknown	17	18	4
#> 16: chrUnknown	18	19	1
#> 17: chrUnknown	19	20	2
#> 18: chrUnknown	20	21	3
#> 19: chrUnknown	21	22	0
#> 20: chrUnknown	22	23	3
#> 21: chrUnknown	23	24	6
#> 22: chrUnknown	24	26	3
#> 23: chrUnknown	26	27	0
#> 24: chrUnknown	27	30	1
#> 25: chrUnknown	30	31	0
#> 26: chrUnknown	31	32	1
#> 27: chrUnknown	32	33	0
#> 28: chrUnknown	33	36	1
#> 29: chrUnknown	36	38	0
#> 30: chrUnknown	38	39	1
#> 31: chrUnknown	39	41	0
#> 32: chrUnknown	41	42	4
#> 33: chrUnknown	42	43	7
#> 34: chrUnknown	43	44	4
#> 35: chrUnknown	44	45	3
#> 36: chrUnknown	45	47	2
#> 37: chrUnknown	47	48	3
#> 38: chrUnknown	48	49	4
#> 39: chrUnknown	49	50	5
#> 40: chrUnknown	50	51	4
#> 41: chrUnknown	51	52	7
#> 42: chrUnknown	52	53	3
#> 43: chrUnknown	53	54	4
#> 44: chrUnknown	54	55	3
#> 45: chrUnknown	55	56	5
#> 46: chrUnknown	56	57	3
#> 47: chrUnknown	57	59	4
#> 48: chrUnknown	59	60	2
#> 49: chrUnknown	60	61	4
#> 50: chrUnknown	61	64	2
#> 51: chrUnknown	64	65	5
#> 52: chrUnknown	65	66	4
#> 53: chrUnknown	66	67	2
#> 54: chrUnknown	67	68	4
#> 55: chrUnknown	68	69	6
#> 56: chrUnknown	69	70	2
#> 57: chrUnknown	70	71	3

```
#> 58: chrUnknown      71      73      2
#> 59: chrUnknown      73      74      3
#> 60: chrUnknown      74      75      1
#>      chrom chromStart chromEnd count
#>
#> attr("class")
#> [1] "PeakSegFPOP_df" "PeakSegFPOP_dir" "list"

gg.rle+
geom_segment(aes(
  chromStart+0.5, mean, xend=chromEnd+0.5, yend=mean, color=model),
  data=data.frame(fit$rle$segments, model="fitted"))
```



## 5 Write the file yourself

The interfaces discussed in the previous sections are perhaps the most intuitive for useRs, but they are also the least efficient, so they are not recommended for large data.

In this section we introduce the most efficient way of using PeakSegDisk, which involves:

- creating a “problem” directory for each segmentation problem (sample and genome subset),
- saving the data to `coverage.bedGraph` in that directory,
- and then running `PeakSegFPOP_dir`.

The reason why this method is recommended for large data is because `PeakSegFPOP_dir` saves its results to the “problem” directory. So if a certain result has already been computed, these result files are used as a cache, and are read instead of doing computations, which saves a lot of time. The file system is used as the interface in order to support very large data sets with very little memory usage.

To use `PeakSegFPOP_dir` the data should be saved to a `chrXX-start-end/coverage.bedGraph` file, where the problem directory “chrXX-start-end” should be named using a genome position string:

- chrXX is the chromosome (which is irrelevant to the algorithm),
- start is the 0-based first position of the region to segment (the smallest possible value is 0),
- end is the 1-based end position (the smallest possible value is 1).

```
data.dir <- file.path(
  tempfile(),
  with(rle.df, sprintf(
    "%s-%d-%d", chrom[1], min(chromStart), max(chromEnd))))
dir.create(data.dir, showWarnings=FALSE, recursive=TRUE)
coverage.bedGraph <- file.path(data.dir, "coverage.bedGraph")
write.table(
  rle.df, coverage.bedGraph,
  sep="\t", row.names=FALSE, col.names=FALSE)
```

The next step is to run the main solver,

```
(fit$dir <- PeakSegDisk::PeakSegFPOP_dir(data.dir, 10.5))

#> $segments
#>      chrom chromStart chromEnd      status      mean
#> 1: chrUnknown      69      75 background 2.166670
#> 2: chrUnknown      41      69      peak 3.714290
#> 3: chrUnknown      26      41 background 0.533333
#> 4: chrUnknown      12      26      peak 3.571430
#> 5: chrUnknown       0      12 background 1.583330
#>
#> $loss
#>      penalty segments peaks bases bedGraph.lines mean.pen.cost total.loss
#> 1:    10.5         5     2   75              60    0.01507491 -19.86938
#>      equality.constraints mean.intervals max.intervals  megabytes seconds
#> 1:                  0              4.6              8 0.02745438   0.004
#>
#> attr("class")
#> [1] "PeakSegFPOP_dir" "list"
```

The underlying C++ code creates penalty-specific files such as

chrXX-start-end/coverage.bedGraph\_penalty=0.1\_loss.tsv which are used to store/cache the results. If the files already exist (and are consistent) then `PeakSegFPOP_dir` just reads them; otherwise it runs the dynamic programming C++ code in order to create those files, which are then read into R.

## 6 Computing the model with a given number of peaks

The `sequentialSearch_dir` function can be used to compute the optimal model with a certain number of peaks:

```

if(interactive() && requireNamespace("future"))future::plan("multiprocess")
(fit$search <- PeakSegDisk::sequentialSearch_dir(data.dir, 2L, verbose=1))

#> Loading required namespace: future.apply

#> Next = 0, Inf
#> Next = 2.20991803112367
#> Next = 7.11950550040458
#> $segments
#>      chrom chromStart chromEnd      status      mean
#> 1: chrUnknown      69      75 background 2.166670
#> 2: chrUnknown      41      69      peak 3.714290
#> 3: chrUnknown      26      41 background 0.533333
#> 4: chrUnknown      12      26      peak 3.571430
#> 5: chrUnknown       0      12 background 1.583330
#>
#> $loss
#>      penalty segments peaks bases bedGraph.lines mean.pen.cost total.loss
#> 1: 7.119506         5      2      75             60 -0.07507161 -19.86938
#>      equality.constraints mean.intervals max.intervals  megabytes seconds
#> 1:                  0      4.558333             9 0.02735901  0.002
#>      iteration under over
#> 1:          3      0      6
#>
#> $others
#>      penalty segments peaks bases bedGraph.lines mean.pen.cost total.loss
#> 1: 0.000000      53      26      75             60 -0.63772877 -47.829658
#> 2:      Inf         1       0      75             60  0.12837615  9.628211
#> 3: 2.209918      13       6      75             60 -0.26439085 -33.088822
#> 4: 7.119506         5       2      75             60 -0.07507161 -19.869382
#>      equality.constraints mean.intervals max.intervals  megabytes seconds
#> 1:                  5      2.550000             4 0.02276230  0.003
#> 2:                  0      0.000000             0 0.00000000  0.001
#> 3:                  0      4.708333             9 0.02770233  0.003
#> 4:                  0      4.558333             9 0.02735901  0.002
#>      iteration under over
#> 1:          1     NA     NA
#> 2:          1     NA     NA
#> 3:          2      0     26
#> 4:          3      0      6
#>
#> attr(,"class")
#> [1] "PeakSegFPOP_dir" "list"

```

The algorithm must evaluate several penalty values to compute the optimal model with a certain number of peaks. The **others** component of the model list above shows that

- the search starts with penalty values 0 and Inf, which result in models with 26 and 0 peaks,

respectively.

- the next penalty evaluated is 2.21, which results in 6 peaks.
- the final penalty evaluated is 7.12, which results in 2 peaks.

At each step (except the first) the new penalties are computed based on the loss values found in the previous step. If present with a registered parallel future plan, the `future.apply` package is used to run the first step (penalties 0,  $\infty$ ) in parallel.

Note how the number of peaks and `total.loss` of this model is the same as the other models computed above,

```
lossDF <- function(L)data.frame(L$loss)[, names(fit$dir$loss)]
do.call(rbind, lapply(fit, lossDF))

#>      penalty segments peaks bases bedGraph.lines mean.pen.cost
#> vec      10.500000      5     2    75           60  0.01507491
#> df       10.500000      5     2    75           75  0.01507491
#> rle      10.500000      5     2    75           60  0.01507491
#> dir      10.500000      5     2    75           60  0.01507491
#> search   7.119506      5     2    75           60 -0.07507161
#>      total.loss equality.constraints mean.intervals max.intervals
#> vec      -19.86938              0      4.600000      8
#> df       -19.86938              0      4.633333      8
#> rle      -19.86938              0      4.600000      8
#> dir      -19.86938              0      4.600000      8
#> search   -19.86938              0      4.558333      9
#>      megabytes seconds
#> vec      0.02745438  0.003
#> df       0.03441620  0.004
#> rle      0.02745438  0.003
#> dir      0.02745438  0.004
#> search   0.02735901  0.002
```

Finally we demonstrate how the filesystem caching is especially useful for the sequential search. In the code below we ask the sequential search algorithm to compute the optimal model with four peaks:

```
four.peaks <- PeakSegDisk::sequentialSearch_dir(data.dir, 4L)
#> Loading required namespace: future.apply
four.peaks$others[, .(iteration, penalty, peaks)]

#>   iteration  penalty peaks
#> 1:         1 0.000000    26
#> 2:         1      Inf     0
#> 3:         2 2.209918     6
#> 4:         3 7.119506     2
#> 5:         4 3.304860     3
#> 6:         5 2.830674     5
#> 7:         6 3.107790     4
```



Looking at the output above, we see that the first three iterations of the sequential search require computing models with 26, 0, 6, 2 peaks. Since all of these have been previously computed (and saved to disk), the dynamic programming algorithm does not need to be re-run, and instead the model results are simply read from the files. After that the dynamic programming is run for the subsequent iterations 4-6. In this particular example the savings in computation time is not extraordinary, but in real genomic data, this can result in substantial speed-ups.