Software Manual
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fastseg

An R Package for fast segmentation

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Scope and Purpose of this Document

This document is a user manual for the R package `fastseg`. It is only meant as a gentle introduction into how to use the basic functions implemented in this package. Not all features of the R package are described in full detail. Such details can be obtained from the documentation enclosed in the R package. Further note the following: (1) this is neither an introduction to segmentation algorithms; (2) this is not an introduction to R. If you lack the background for understanding this manual, you first have to read introductory literature on these subjects.

Contents

1 Introduction

fastseg implements a very fast and efficient segmentation algorithm. It has similar functionality as DNACopy (**?**) but is considerably faster and more flexible. fastseg can segment data stemming from DNA microarrays and data stemming from next generation sequencing for example to detect copy number segments. Further it can segment data stemming from RNA microarrays like tiling arrays to identify transcripts. Most generally, it can segment data given as a matrix or as a vector. Various data formats can be used as input to fastseg like expression set objects for microarrays or GRanges for sequencing data.

The segmentation criterion of fastseg is based on a statistical test in a Bayesian framework, namely the cyber t-test (**?**). The speed-up stems from the facts, that sampling is not necessary in for fastseg and that a dynamic programming approach is used for calculation of the segments' first and higher order moments.

For further information regarding the algorithm and its assessment see the fastseg homepage at http://www.bioinf.jku.at/software/fastseg/fastseg.html

2 Getting started

To load the package, enter the following in your R session:

```
> library(fastseg)
```

2.1 Data

According to the DNAcopy package from bioconductor we selected a subset of the data set presented in (**?**). This data set will be called coriell. The data correspond to two array CGH studies of fibroblast cell strains. [1] In particular, the studies **GM05296** and **GM13330** were chosen. After selecting only the mapped data from chromosomes 1-22 and X, there are 2271 data points.

To prepare the data for our examples we execute the following code:

```
> data(coriell)
> head(coriell)
```

```
        Clone Chromosome Position Coriell.05296 Coriell.13330
1  GS1-232B23          1        1      0.000359      0.207470
2  RP11-82d16          1      469      0.008824      0.063076
3  RP11-62m23          1     2242     -0.000890      0.123881
4  RP11-60j11          1     4505      0.075875      0.154343
5 RP11-111O05          1     5441      0.017303     -0.043890
6  RP11-51b04          1     7001     -0.006770      0.094144
```

[1] http://www.nature.com/ng/journal/v29/n3/suppinfo/ng754_S1.html

```
> samplenames <- colnames(coriell)[4:5]
> data <- as.matrix(coriell[4:5])
> #data[is.na(data)] <- median(data, na.rm=TRUE)
> chrom <- coriell$Chromosome
> maploc <- coriell$Position
```

The main functions of the package are `fastseg` and `toDNAcopyObj`. The first on runs the segmentation algorithm and the latter converts the segmentation results the a DNAcopy object which will be quite helpful for plot functions.

2.2 File formats

The package can handle different file formats: GRanges, ExpressionSet objects, matrix or a vector.

2.2.1 Vector

```
> data2 <- data[, 1]
> res <- fastseg(data2)
> head(res)
```

```
GRanges object with 6 ranges and 5 metadata columns:
      seqnames       ranges strand |          ID  num.mark     seg.mean
         <Rle>    <IRanges>  <Rle> | <character> <numeric>    <numeric>
  [1]        1 [   1, 1227]      * |     sample1      1227 -0.003604316
  [2]        1 [1228, 1270]      * |     sample1        43  0.461622814
  [3]        1 [1271, 1357]      * |     sample1        87  0.004317655
  [4]        1 [1358, 1372]      * |     sample1        15 -0.651081333
  [5]        1 [1373, 2214]      * |     sample1       842  0.014980804
  [6]        1 [2215, 2271]      * |     sample1        57  0.614116421
       startRow    endRow
      <integer> <integer>
  [1]         1      1227
  [2]      1228      1270
  [3]      1271      1357
  [4]      1358      1372
  [5]      1373      2214
  [6]      2215      2271
  -------
  seqinfo: 1 sequence from an unspecified genome; no seqlengths
```

```
>
>
```

2.2.2 Matrix

```
> data2 <- data[1:400, ]
> res <- fastseg(data2)
> head(res)
```

```
GRanges object with 6 ranges and 5 metadata columns:
      seqnames     ranges strand |            ID  num.mark     seg.mean
         <Rle>  <IRanges>  <Rle> |   <character> <numeric>    <numeric>
  [1]        1 [  1,  80]      * | Coriell.05296        80  0.016815675
  [2]        1 [ 81,  84]      * | Coriell.05296         4  0.134374750
  [3]        1 [ 85, 400]      * | Coriell.05296       316  0.003267547
  [4]        1 [  1,  91]      * | Coriell.13330        91  0.016150637
  [5]        1 [ 92, 140]      * | Coriell.13330        49  0.485243673
  [6]        1 [141, 400]      * | Coriell.13330       260 -0.032339504
       startRow    endRow
      <integer> <integer>
  [1]         1        80
  [2]        81        84
  [3]        85       400
  [4]         1        91
  [5]        92       140
  [6]       141       400
  -------
  seqinfo: 1 sequence from an unspecified genome; no seqlengths
```

2.2.3 GRanges objects

```
> library("GenomicRanges")
> ## with both individuals
> gr <- GRanges(seqnames=chrom,
+         ranges=IRanges(maploc, end=maploc))
> mcols(gr) <- data
> colnames(mcols(gr)) <- samplenames
> res <- fastseg(gr)
> head(res)
```

```
GRanges object with 6 ranges and 5 metadata columns:
      seqnames           ranges strand |            ID  num.mark    seg.mean
         <Rle>        <IRanges>  <Rle> |   <character> <integer>   <numeric>
  [1]        1 [     1, 240001]      * | Coriell.05296       141  0.01973119
  [2]       10 [     1,  65001]      * | Coriell.05296        57 -0.01061286
  [3]       10 [ 66906, 108904]      * | Coriell.05296        43  0.45160927
  [4]       10 [110001, 142001]      * | Coriell.05296        34  0.00403140
  [5]       11 [     1,  34421]      * | Coriell.05296        52  0.01163838
  [6]       11 [ 35417,  39624]      * | Coriell.05296        14 -0.65108133
```

```
       startRow    endRow
      <integer> <integer>
  [1]         1       142
  [2]         1        58
  [3]        59       102
  [4]       103       137
  [5]         1        53
  [6]        54        68
  -------
  seqinfo: 23 sequences from an unspecified genome; no seqlengths

> ## with one individual
> gr2 <- gr
> data2 <- as.matrix(data[, 1])
> colnames(data2) <- "sample1"
> mcols(gr2) <- data2
> res <- fastseg(gr2)
> head(res)

GRanges object with 6 ranges and 5 metadata columns:
      seqnames            ranges strand |          ID  num.mark    seg.mean
         <Rle>         <IRanges>  <Rle> | <character> <integer>   <numeric>
  [1]        1 [     1, 240001]      * |     sample1       141  0.01973119
  [2]       10 [     1,  65001]      * |     sample1        57 -0.01061286
  [3]       10 [ 66906, 108904]      * |     sample1        43  0.45160927
  [4]       10 [110001, 142001]      * |     sample1        34  0.00403140
  [5]       11 [     1,  34421]      * |     sample1        52  0.01163838
  [6]       11 [ 35417,  39624]      * |     sample1        14 -0.65108133
       startRow    endRow
      <integer> <integer>
  [1]         1       142
  [2]         1        58
  [3]        59       102
  [4]       103       137
  [5]         1        53
  [6]        54        68
  -------
  seqinfo: 23 sequences from an unspecified genome; no seqlengths

>
```

2.2.4 ExpressionSet objects

```
> library(oligo)
> eSet <- new("ExpressionSet")
```

```
> assayData(eSet) <- list(intensity=data)
> featureData(eSet) <- new("AnnotatedDataFrame",
+         data=data.frame(
+                 chrom = paste("chr",chrom,sep=""),
+                 start = maploc,
+                 end   = maploc,stringsAsFactors=FALSE))
> phenoData(eSet) <- new("AnnotatedDataFrame",
+         data=data.frame(samples=samplenames))
> sampleNames(eSet) <- samplenames
> res <- fastseg(eSet)
> head(res)

GRanges object with 6 ranges and 5 metadata columns:
      seqnames           ranges strand |            ID  num.mark    seg.mean
         <Rle>        <IRanges>  <Rle> |   <character> <integer>   <numeric>
  [1]     chr1 [     1, 240001]      * | Coriell.05296       141  0.01973119
  [2]    chr10 [     1,  65001]      * | Coriell.05296        57 -0.01061286
  [3]    chr10 [ 66906, 108904]      * | Coriell.05296        43  0.45160927
  [4]    chr10 [110001, 142001]      * | Coriell.05296        34  0.00403140
  [5]    chr11 [     1,  34421]      * | Coriell.05296        52  0.01163838
  [6]    chr11 [ 35417,  39624]      * | Coriell.05296        14 -0.65108133
       startRow    endRow
      <integer> <integer>
  [1]         1       142
  [2]         1        58
  [3]        59       102
  [4]       103       137
  [5]         1        53
  [6]        54        68
  -------
  seqinfo: 23 sequences from an unspecified genome; no seqlengths
```

2.2.5 Vector

```
> data2 <- data[, 1]
> res <- fastseg(data2)
> head(res)

GRanges object with 6 ranges and 5 metadata columns:
      seqnames       ranges strand |          ID  num.mark     seg.mean
         <Rle>    <IRanges>  <Rle> | <character> <numeric>    <numeric>
  [1]        1 [   1, 1227]      * |     sample1      1227 -0.003604316
  [2]        1 [1228, 1270]      * |     sample1        43  0.461622814
  [3]        1 [1271, 1357]      * |     sample1        87  0.004317655
  [4]        1 [1358, 1372]      * |     sample1        15 -0.651081333
  [5]        1 [1373, 2214]      * |     sample1       842  0.014980804
```

```
  [6]        1 [2215, 2271]      * |     sample1        57  0.614116421
       startRow    endRow
      <integer> <integer>
  [1]         1      1227
  [2]      1228      1270
  [3]      1271      1357
  [4]      1358      1372
  [5]      1373      2214
  [6]      2215      2271
  -------
  seqinfo: 1 sequence from an unspecified genome; no seqlengths

>
>
```

2.2.6 Matrix

```
> data2 <- data[1:400, ]
> res <- fastseg(data2)
> head(res)
```

```
GRanges object with 6 ranges and 5 metadata columns:
      seqnames     ranges strand |            ID  num.mark     seg.mean
         <Rle>  <IRanges>  <Rle> |   <character> <numeric>    <numeric>
  [1]        1 [  1,  80]      * | Coriell.05296        80  0.016815675
  [2]        1 [ 81,  84]      * | Coriell.05296         4  0.134374750
  [3]        1 [ 85, 400]      * | Coriell.05296       316  0.003267547
  [4]        1 [  1,  91]      * | Coriell.13330        91  0.016150637
  [5]        1 [ 92, 140]      * | Coriell.13330        49  0.485243673
  [6]        1 [141, 400]      * | Coriell.13330       260 -0.032339504
       startRow    endRow
      <integer> <integer>
  [1]         1        80
  [2]        81        84
  [3]        85       400
  [4]         1        91
  [5]        92       140
  [6]       141       400
  -------
  seqinfo: 1 sequence from an unspecified genome; no seqlengths
```

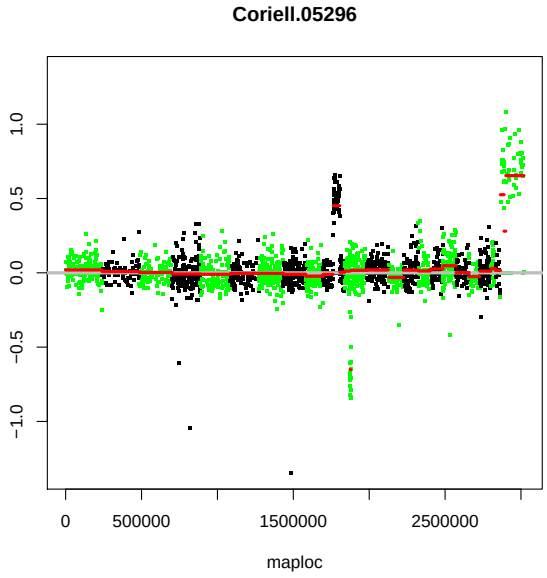
2.3 Plotting the segmentation results

For plotting the data we have to generate an `DNAcopy` object out of the segmentation results:

```
> ## with both individuals
> gr <- GRanges(seqnames=chrom,
+         ranges=IRanges(maploc, end=maploc))
> mcols(gr) <- data
> colnames(mcols(gr)) <- samplenames
> res <- fastseg(gr,segMedianT=0.2)
```

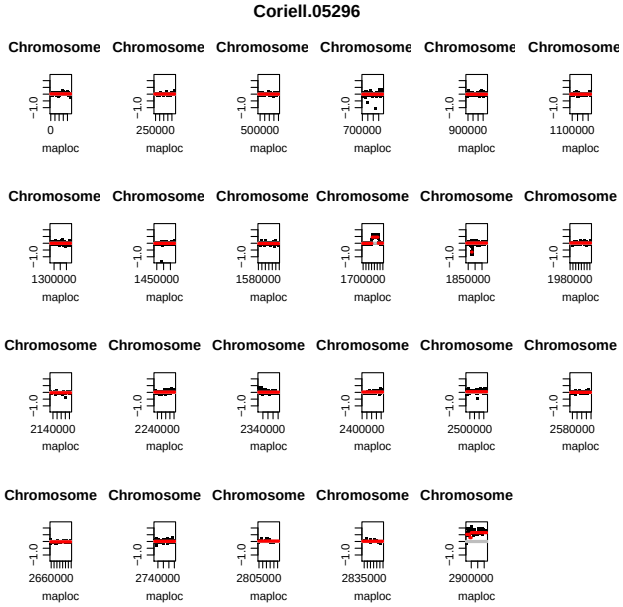
The plotting is done via the `plot` function of `DNAcopy`:

```
> segPlot(gr,res, plot.type="w")
```



Or alternatively:

```
> segPlot(gr,res, plot.type="s")
```



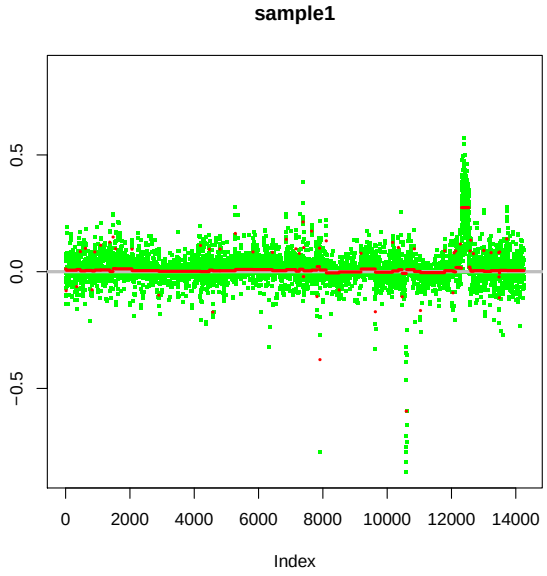
2.4 Performance of the method

Here we show that `fastseg` outperforms `DNAcopy` with respect to computational time on summarized microarray data. The quality of the segmentation result of both `fastseg` and `DNAcopy` depends strongly on the methods' parameters.
The data is a small subset of copy number calls which were produced by the `cn.farms` algorithm **?** from an Affymetrix SNP microarray experiment of a HapMap sample.

```
> data(fastsegData)
> system.time(res <- fastseg(fastsegData))
```

```
   user  system elapsed
  0.141   0.001   0.142
```

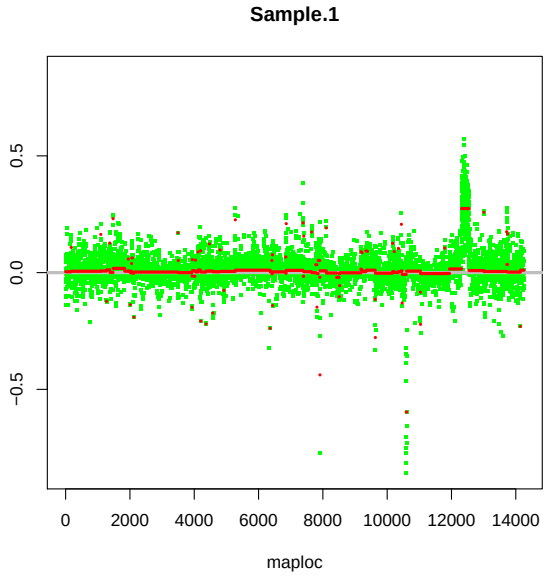
```
> segPlot(fastsegData,res, plot.type="w")
```




```
> library(DNAcopy)
> cna <- DNAcopy::CNA(fastsegData,chrom="chr1",maploc=1:length(fastsegData))
> system.time(res2 <- DNAcopy::segment(cna))

Analyzing: Sample.1
   user  system elapsed
  4.701   0.003   4.705

> plot(res2, plot.type="w", xmaploc=TRUE)
```



3 Future Extensions

We are planning to program a parallelized version of this package. Furthermore we will enhance the plot functions by our own.

4 How to cite this package

If you use this package for research that is published later, you are kindly asked to cite it as follows: (**?**).

To obtain BibTEX entries of the two references, you can enter the following into your R session:

```
> toBibtex(citation("fastseg"))
```