

# CAD Laboratory

Jan 30th, 2009

structural variation

copy number

aCGH

oligonucleotide  
chip

reference

tumor



```
graph TD; reference --- tumor; tumor --> chip;
```

chip

$\log_2$  ratio

$\log_2$  ratio

positive

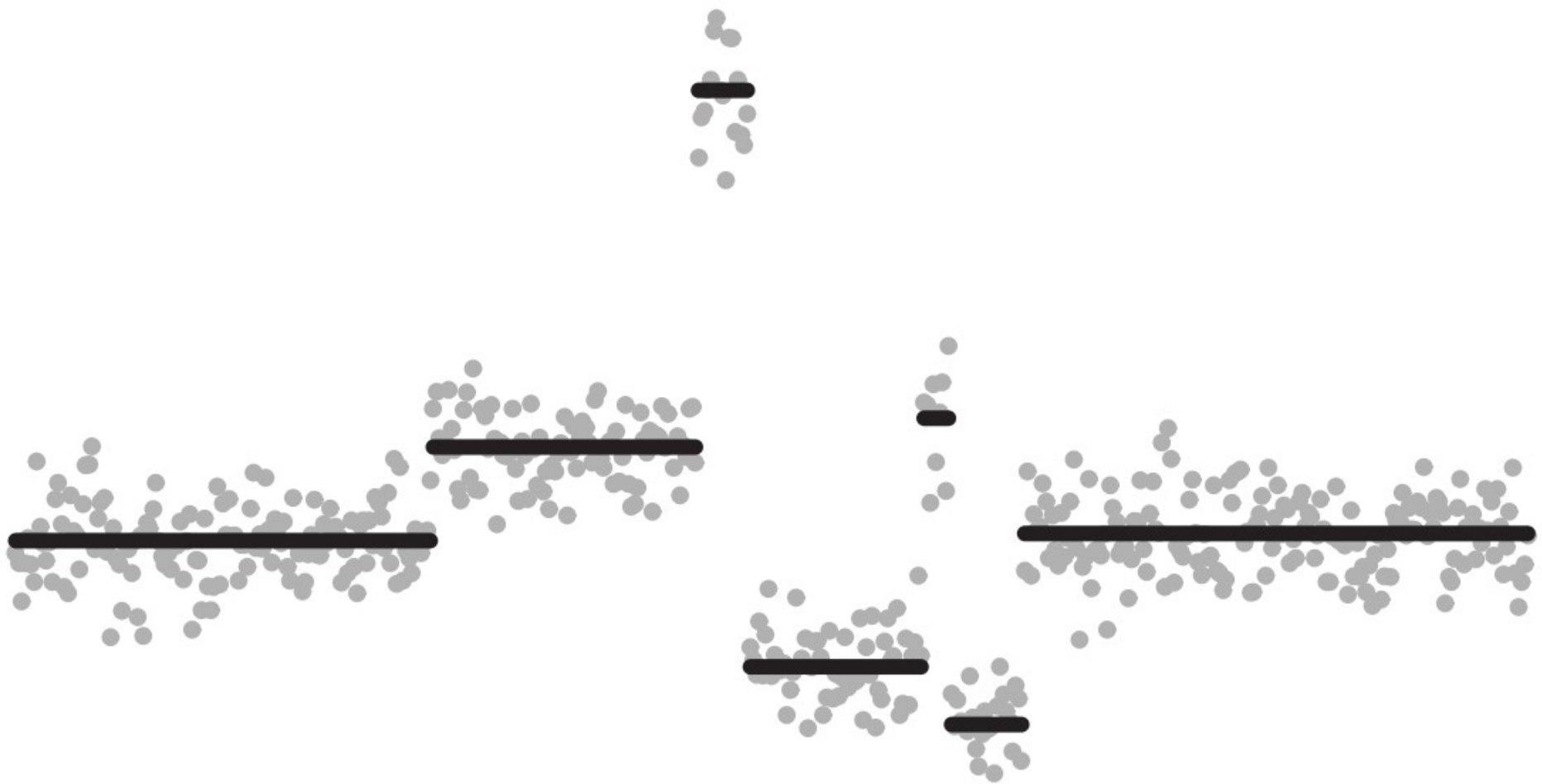
$\log_2$  ratio

negative

$\log_2$  ratio

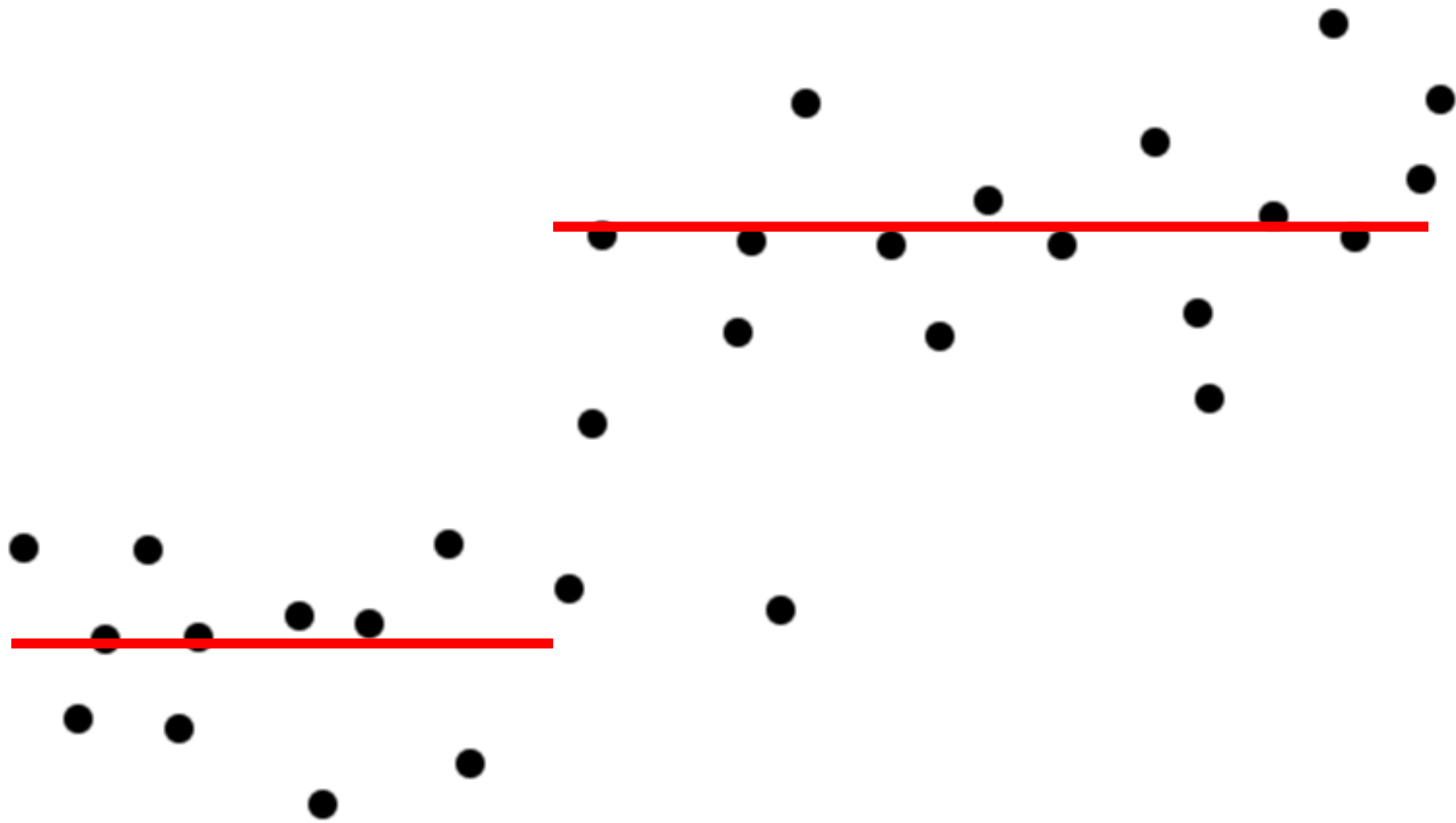
zero

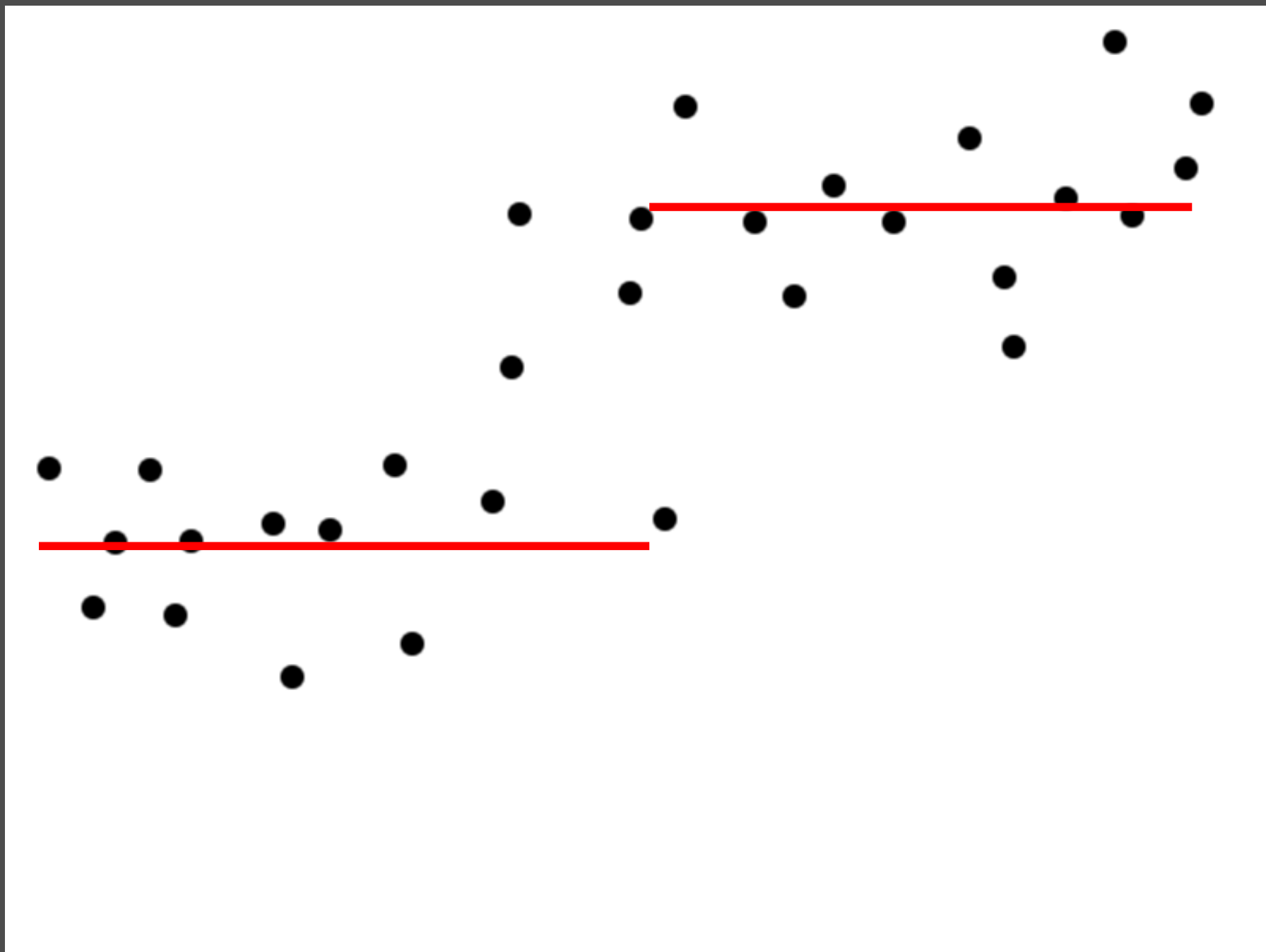
segmentation

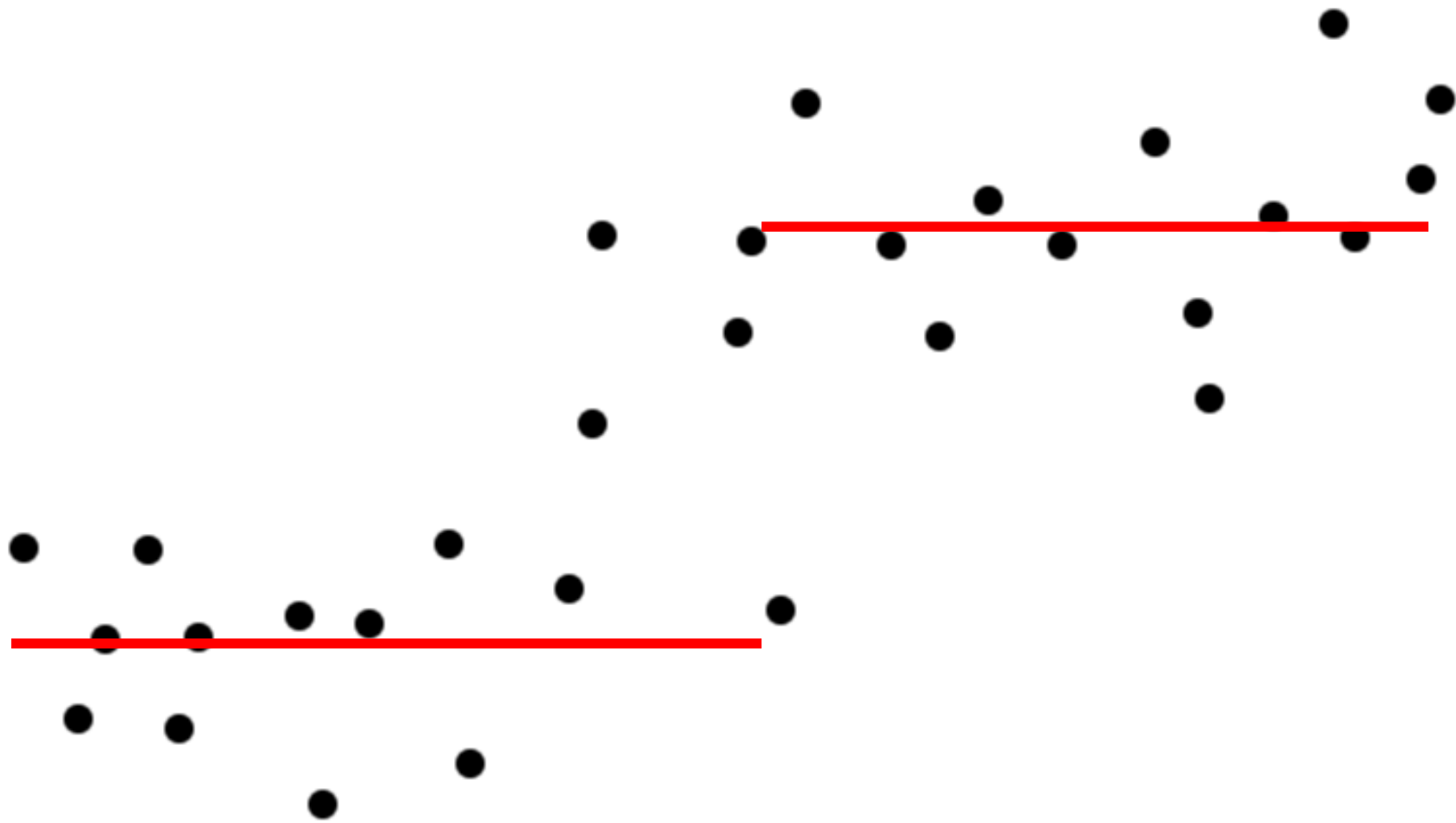


circular binary  
segmentation

change-points







100 kb

tools

segmentation tool

Group	camiller_sandbox
Database	CAD test
Select Tool	8) Segmentation Tool

## Segmentation Tool

This tool uses the DNACopy R library to divide the given data into segments of equal copy number, based on the  $\log_2$  ratio assumed to be in the score field. This is useful for taking noisy array data and converting it into regions of gain and loss.

Optionally, this data can then be filtered so that only segments that exceed a certain mean log-ratio threshold or that is a certain number of standard deviations from the global mean log-ratio will be output. To output all segments, set the threshold condition to '0'

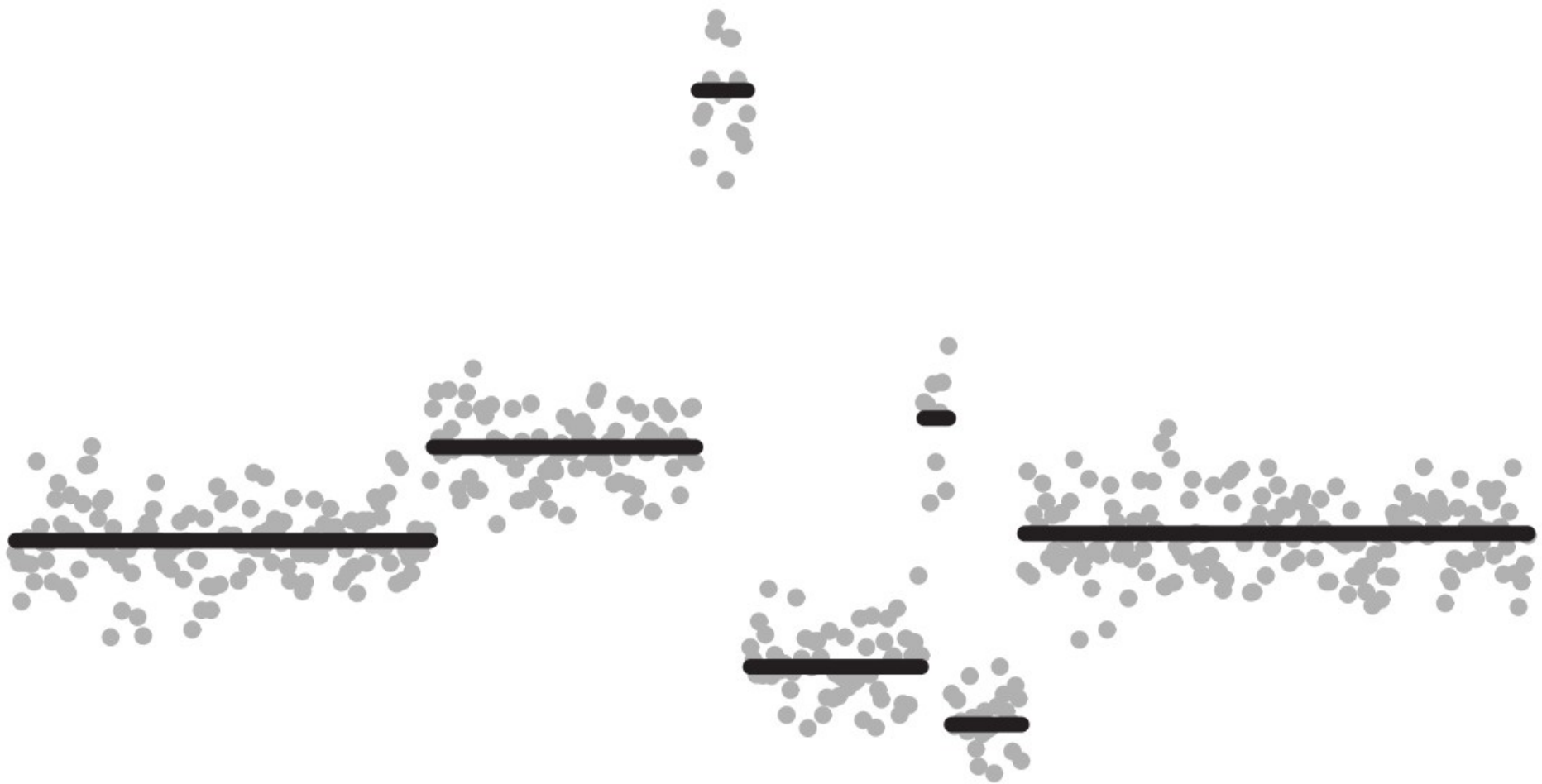
(For more information on the circular binary segmentation algorithm used, see: *Olshen, et al. Circular binary segmentation for the analysis of array-based DNA copy number data. Biostatistics. 2004 Oct;5(4):557-72.*)

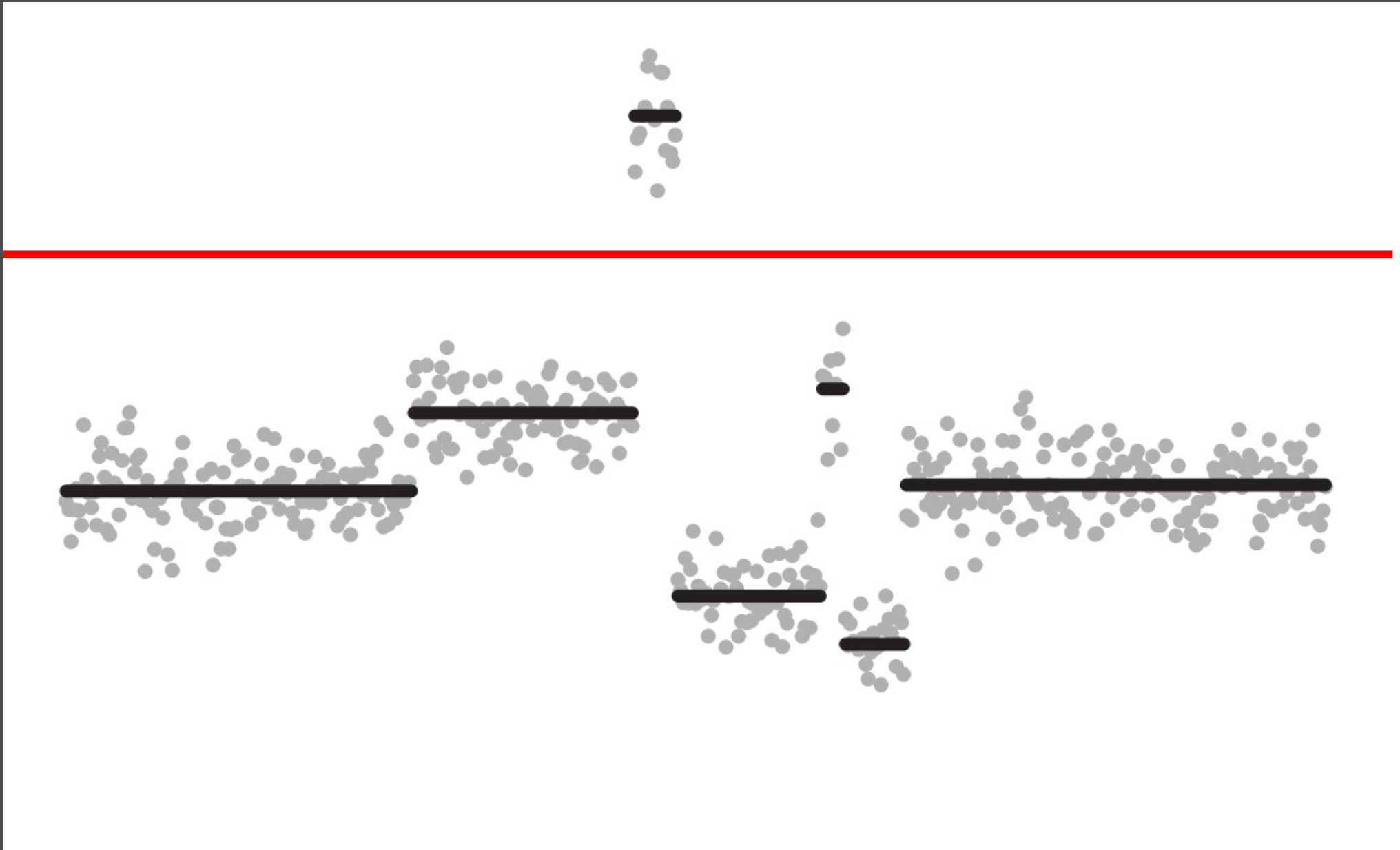
**Note:** This tool requires that the score field of the track be a set of  $\log_2$ -ratio scores.

**NOTE:** This is a new service. If you encounter any problems, please contact [brl\\_admin@bcm.tmc.edu](mailto:brl_admin@bcm.tmc.edu).

Job Name:	<input type="text"/>	?
Input Track:	Select a Track	?
Condition:	Minimum number of probes to comprise a segment: <input type="text" value="2"/> Keep segments that have a mean log-ratio value greater than: <input type="text" value="2.0"/> <input checked="" type="radio"/> as how many standard deviations from the global average log-ratio the segment must be OR <input type="radio"/> as an absolute threshold the mean log-ratio must exceed	?
Output Track:	Class: <input type="text" value="Segment"/> Type: <input type="text"/> Subtype: <input type="text"/>	?

Submit





annotation selector

Job Name:

Source Tracks:

- All: Segments
- chr12: gains
- recurr: genes
- RefSeq: Blocked
- Sample: 0001
- seg: 0001

Annotation Selection Criteria: ?

Match **All** of the conditions. + -

Attribute	Data Type	Operation	Values
<b>Anno. Chrom.</b> ▼	<b>text</b> ▼	<b>=</b> ▼	<b>chr1</b> <input type="checkbox"/> Case Sensitive
<b>Anno. Score</b> ▼	<b>number</b> ▼	<b>&gt;</b> ▼	<b>500</b>

+ -

Output Track: "Class"  "Type":  "Subtype":  ?

attribute lifter

attribute-value pair

```
gender=male;
```

gender=male; sampleId=97A;

Track 1: Regions

Track 2: Genes

Job Name:	<input type="text"/>	?
First Track:	Select a Track <input type="button" value="v"/> Intersecting annotations must be within <input type="text" value="0"/> bp of these annotations.	?
Condition:	<input type="checkbox"/> Only output annotations that intersect 1+ annotations from the following tracks:	?
Second Track(s):	<input checked="" type="checkbox"/> All: Segments <b>Select attributes to copy from this track to the new track:</b> <input type="checkbox"/> ALL ATTRIBUTES <input type="checkbox"/> Anno. Class <input checked="" type="checkbox"/> Anno. Name as <input type="text" value="sampleName"/> <input type="checkbox"/> Anno. Type <input type="checkbox"/> Anno. Subtype <input type="checkbox"/> Anno. Chrom <input type="checkbox"/> Anno. Start <input type="checkbox"/> Anno. Stop <input type="checkbox"/> Anno. Strand <input type="checkbox"/> Anno. Phase <input type="checkbox"/> Anno. Score <input type="checkbox"/> Anno. Qstart <input type="checkbox"/> Anno. Qstop <input type="checkbox"/> Anno. Sequence <input type="checkbox"/> Anno. Free Comments <input type="checkbox"/> length <input type="checkbox"/> sample <input type="checkbox"/> chr12: gains <input type="checkbox"/> recurr: genes <input type="checkbox"/> RefSeq: Blocked <input type="checkbox"/> Sample: 0001 <input type="checkbox"/> seg: 0001	?
Output Track:	Class: <input type="text" value="AttrsLifted"/> Type: <input type="text"/> Subtype: <input type="text"/> <input type="text"/>	?

```
intGenes=ERBB2, MET, KRAS;
```

tabular view

R

```
> a -> c(1, 2, 3, 2, 1, 2, 1)
```

```
> b -> c(2, 3, 1, 2, 1, 1, 1)
```

```
> t.test(a, b)
```

rsruby

```
> a = [1, 2, 3, 2, 1, 2, 1]
```

```
> b = [2, 3, 1, 2, 1, 1, 1]
```

```
> r.t_test(a,b)
```

`cran.r-project.org`

```
> gem install rsruby
```

assignment

glioblastoma

1 year

TGCA

186 tumors

matched normals

structrual variants

data munging

segment

recurrence

genes

expression

correlation

Feb 13th

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