Smooth2D Spot Location Viewer

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Contents

This application allows the user to view spot location on the chip image to its log2.ratio value and location on a genomic profile of any of the samples for a spot and its replicate. Plots of other zoomed in versions of graphs with highlight spot and spot replicates, a graph of the global loess correction, and a graph of the values before and after different corrections are also plotted.

1 Running Application

This application requires an aCGH object. Please see aCGHplus user manual for more information on creating this object. We have provided an example with the aCGHplus package. We begin by loading the package, loading the example, and loading the provided object.

```
library(aCGHplus)
Write.aCGH.ex2()
load("RData/aCGH.RData")
```

The following function call activates this application:

```
DiagPlot.Smooth2D(aCGH,
        ismpl=1,
        heatMats.object.labels=c(
                "array.images$smooth2D$LambdaList$Mxy.original.list[[1]]",
                "array.images$smooth2D$LambdaList$Mxy.loess.list[[1]]",
                "array.images$smooth2D$LambdaList$MxyFit.loess.list[[1]]",
                "array.images$smooth2D$LambdaList$Axy.original.list[[1]]",
                "array.images$matrix$cy5$Signal.Mean",
                "array.images$matrix$cy3$Signal.Mean",
                "array.images$matrix$cy5$Background.Mean",
                "array.images$matrix$cy3$Background.Mean",
                "array.images$matrix$cy5$Signal.Stdev",
                "array.images$matrix$cy3$Signal.Stdev",
                "array.images$matrix$cy5$Background.Stdev",
```

```
                "array.images$matrix$cy3$Background.Stdev"),
        heatMatsLbls=c("raw log2(T/C) values",
                "loess corrected log2(T/C) values",
                "fitted loess log2(T/C) values",
                "yprod",
                "cy5mat",
                "cy3mat",
                "Back.cy5mat",
                "Backcy3mat",
                "sd.cy5mat",
                "sd.cy3mat",
                "sd.Back.cy5mat",
                "sd.Back.cy3mat"),
        Mxy.original.label="array.images$smooth2D$LambdaList$Mxy.original.list[[1]]",
        Axy.original.label="array.images$smooth2D$LambdaList$Axy.original.list[[1]]",
        FlagMat.label="array.images$matrix$cy3$Flag",
        MxyFit.loess.label="array.images$smooth2D$LambdaList$MxyFit.loess.list[[1]]",
        Mxy.loess.label="array.images$smooth2D$LambdaList$Mxy.loess.list[[1]]",
        Mxy.noDesign.label="array.images$smooth2D$LambdaList$Mxy.noDesign.list[[1]]",
        Mxy.Smooth2D.label="array.images$smooth2D$LambdaList$Mxy.smooth.list[[1]]",
        GridMat.label="array.images$matrix$Grid",
        dbg=TRUE)
```

```
or if all these default values are used
```

```
DiagPlot.Smooth2D(aCGH)
```

The only required arugment is an aCGH object. The other arguments may be specified if the user desires setting other than the default.

- ismpl: numeric; index of the initial aCGH sample values to use for chip images and genomic profile. It is possible to change the sample by an increment of one within the application.

- heatMats.object.labels: character array; list of paths to matricies of values for different chip images to view.

- heatMatsLbls: character array; should be of length equal to previous heat-Mats.object.labels argument call; list of plot title names corresponding to each of the chip images listed in the heatMats.object.labels.

- Mxy.original.label: character; path to the matrix of raw log2 Tumor/Control values

- Axy.original.label: character; path to the matrix of yprod set of values

- FlagMat.label: character; path to the matrix of spot flags for bad quality or failed chip spots

- MxyFit.loess.label: character; path to the matrix of fitted loess log2 tumore/control values

- Mxy.loess.label: character; path to the matrix of loess corrected log2 tumor/control values

- Mxy.noDesign.label: character; path to the matrix of values that have no been corrected for design patterns

- Mxy.Smooth2D.label: character; path to the matrix of values that have been corrected for design or values to be used as final smoothing step

- GridMat.label: character; path to the matrix of Grid locations to map chip images to matricies

- dbg: logical; indicates if status messages for windows should be plotted; originally designed as part of a debug

2   Brief Widow Descriptions

There are three windows that appear: detailed smoothing plot, genomic profile plot, and chip image plot.

- detailed smoothing plot: This window is design to depict details concerning smoothing.
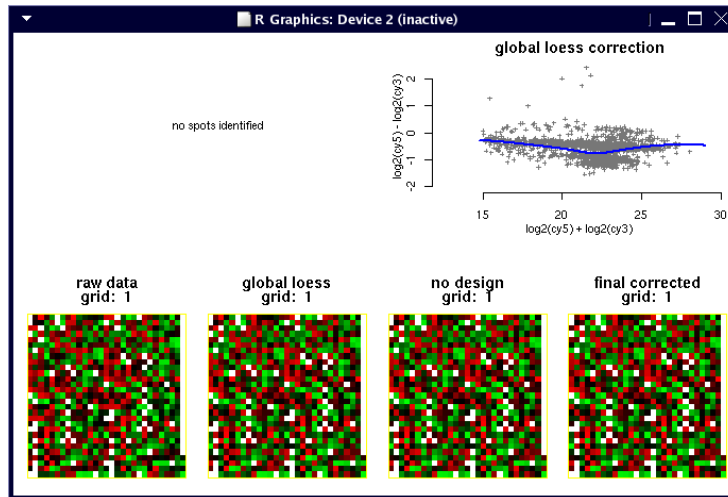
There are four zoomed in regions of a chip image. These initial views are of the lower left grid block of a chip. When a spot or BAC is selected it will show a zoomed in version of the chip block where the spot and its replicate reside. This window also displays the global loess correction graph. Initially, a third section of the window is blank with a message no spots identified. This region will eventually show a plot of how the values change through different smoothing functions.

- genomic profile plot: This plot will show the genomic profile of the current sample for a specific chromosome. Initially it depeicts the first chromosome, however it will be updated to show the chromosome containing the spots chosen on the chip image if the chip image plot is active. It is possible to change the chromosome view up or down a single chromosome by using the Chrom Up and Chrom Down options on the menu (see details on menu).
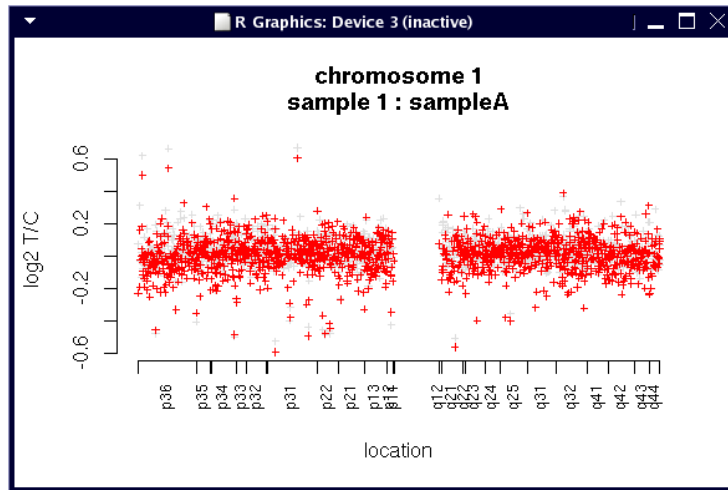
- chip image plot: The chip image plot depicts the chip images listed in the arguments heatMats.object.labels. The first item in the argument list is the initial image that will be displayed for the current sample. This window is the initial user interactive window. It is possible to scroll through the chip images given as arguemnts by choosing toggle HeatMap on the menu. This will go through the images in the order of the list in the argument.
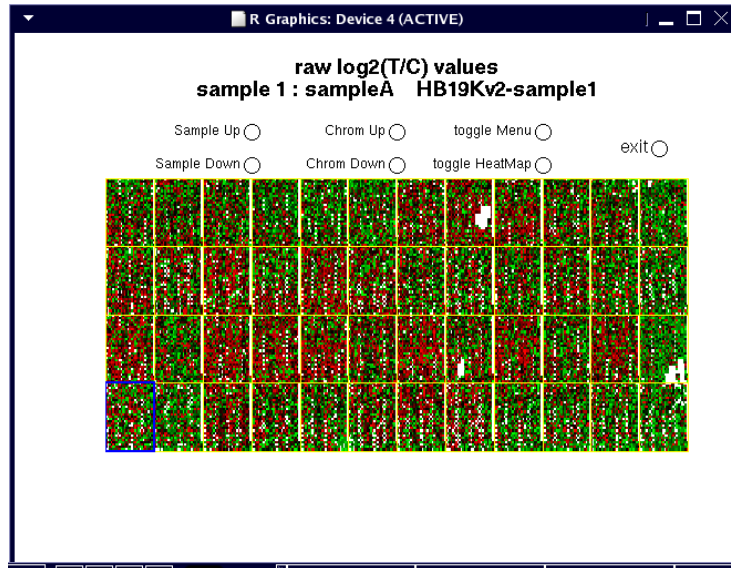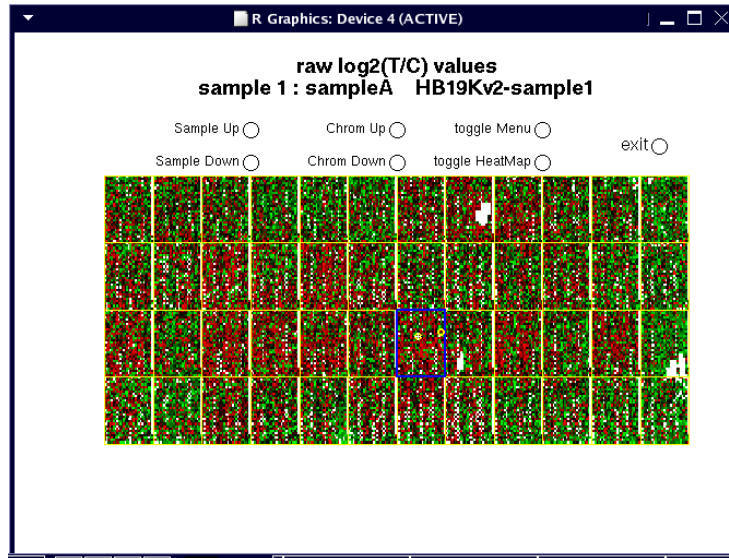
The menu choice option will be located on the current active window which will either be the chip image or the genomic profile. This menu has seven options:
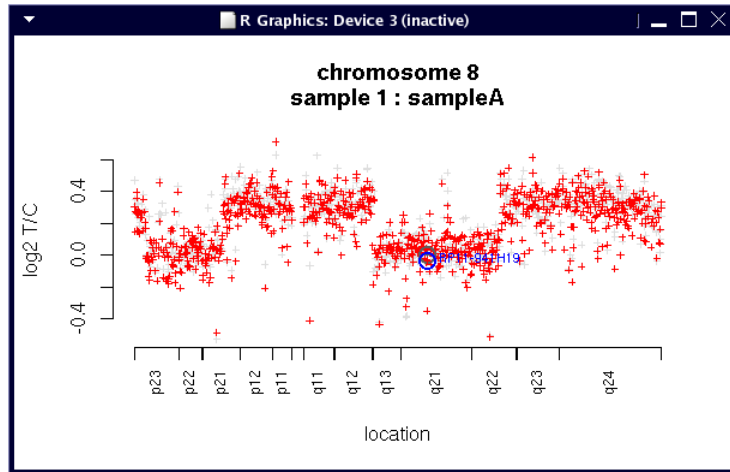
Sample Up ◯   Chrom Up ◯   toggle Menu ◯

exit ◯

Sample Down ◯   Chrom Down ◯   toggle HeatMap ◯

1. Sample Up: Choosing this option will change the sample to the next
   sample in the aCGH object. It will cycle around to the first sample when
   it has reached the last available sample and work upwards. All three
   windows will be updated with the new sample's information.

2. Sample Down: Choosing this option will change the sample to the previous
   sample in the aCGH object. If it cycles around to the first sample, it will
   advance from the last available sample and work downwards. All three
   windows will be updated with the new sample's information.

3. Chrom Up: This option will advance the genomic profile view to the
   next chromosome. It will move upwards and cycle back down to the first
   chromosome once the final one is reached.

4. Chrom Down: This option will advance the genomic profile view to the
   previous chromosome. It will move downwards and cycle back up to the
   last chromosome once the first one is reached.

5. toggle Menu: This option changes the active window and how points/spots
   are selected. The menu location determines the active window; it may
   either be the chip image window or the genomic profile window. The
   toggle will move the menu from one window the the other. If the chip
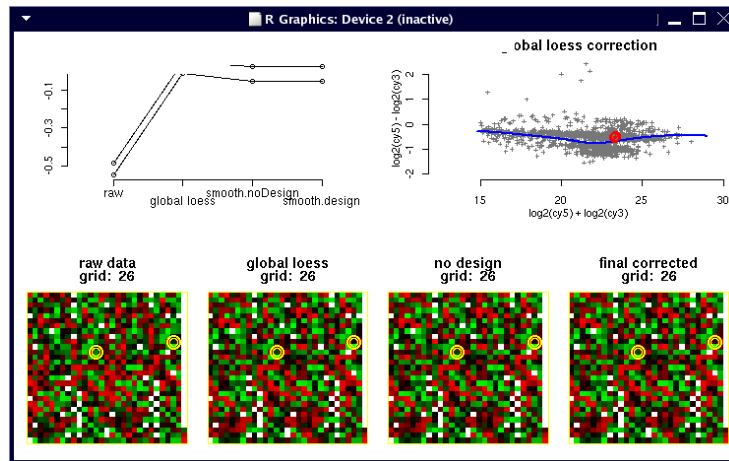   image window is active, the user may select any point within the chip

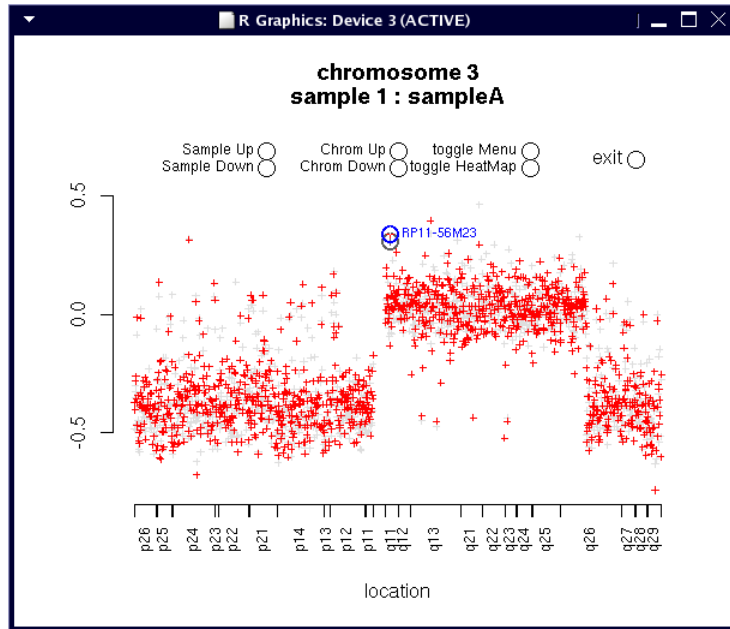image. The spot and its replicate are circled in yellow and the grid block is highlighted in blue.

The genomic profile is updated to show the chromosome on which the spots are located. It highlights the spot, both raw and fit log2 ratio values, and adds the spot label.
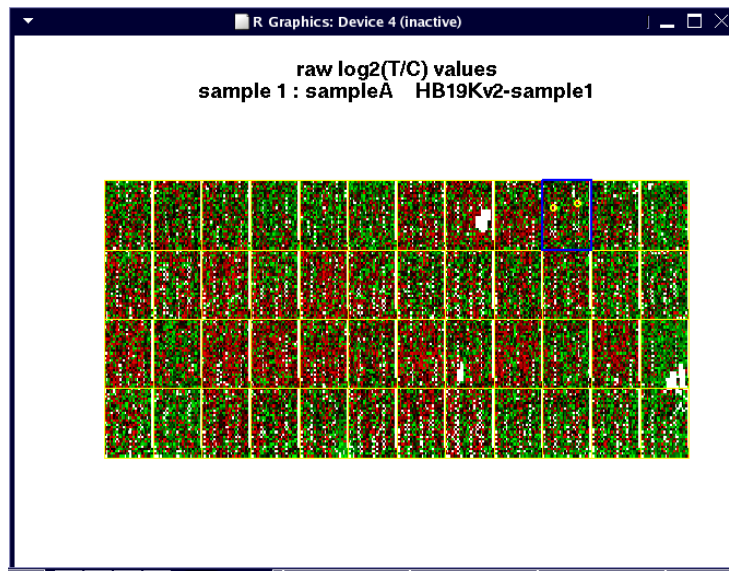
The smooth descriptive window will update the four zoomed chip images to display the highlighted block from the chip image window with the spot and its replicate highlighted in yellow.
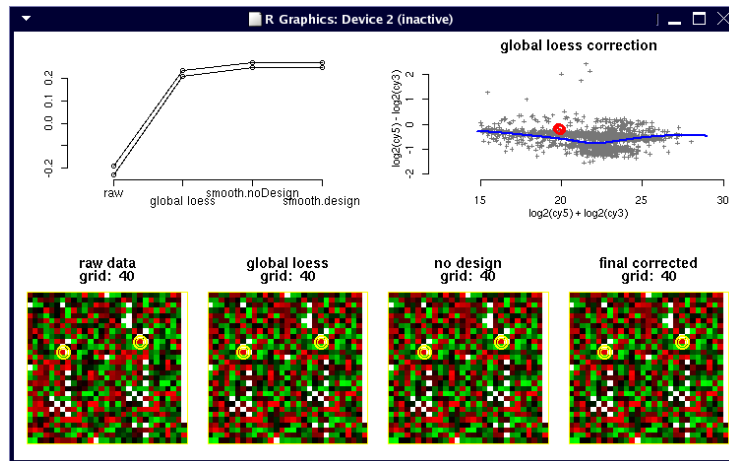
If the genomic profile window is active, the user may select any of the log2 ratios, raw or fitted. The points, raw and fit value will be highlighted and the spot label is added.

The chip image is updated to highlight where the spot and replicate occured. It is highlighted in yellow and the grid block is highlighted in blue.

The smooth descriptive window will update the four zoomed chip images to display the highlighted block from the chip image window with the spot and its replicate highlighted in yellow.
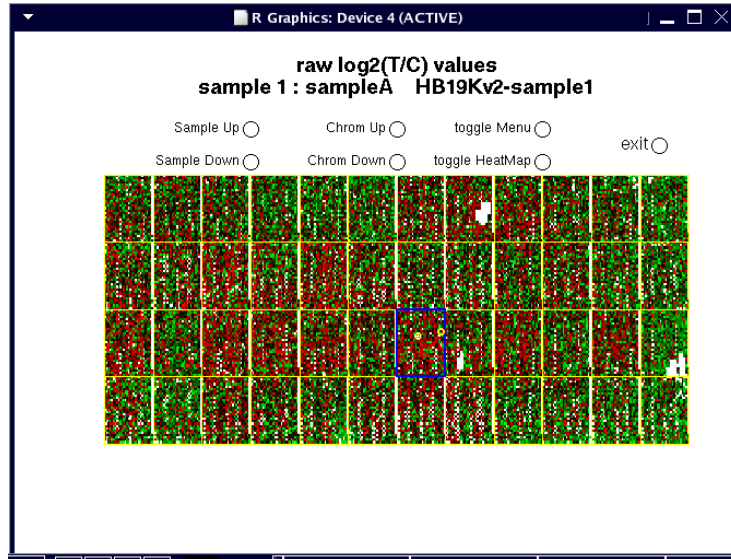
6. toggle Heatmap: This option will change the display in the chip image window. This option allows the user to cycle through any chip image that was listed as part of the function argument heatMats.object.labels. It will cycle through in the order they appear in the argument and begin again once the last image is reached.

7. exit: This will end the interactive application. All windows will remain open and must be manual closed by the user.
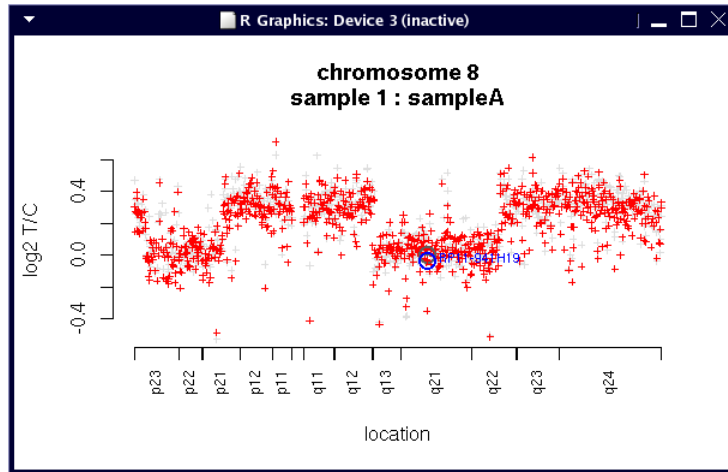
The user chooses the menu option by clicking in the circle to the right of the desired selection. The following would select Chrom Up:
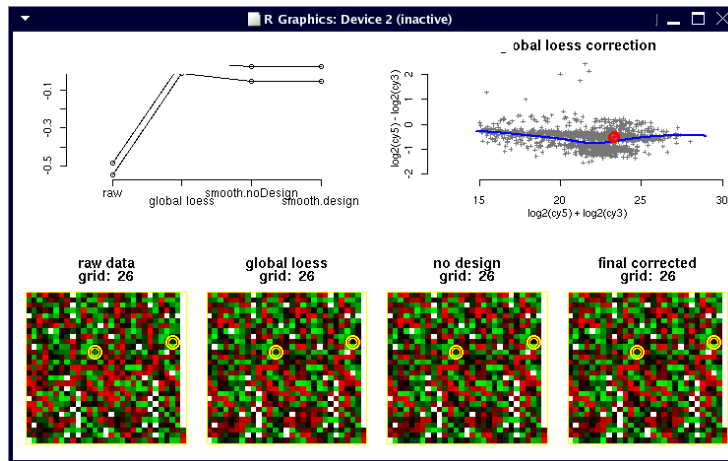
Sample Up ◯   Chrom Up ⊕   toggle Menu ◯

Sample Down ◯   Chrom Down ◯   toggle HeatMap ◯   exit ◯

3   Review On User Interaction

The menu location determines the active user interactive window; it may either be the chip image window or the genomic profile window. If the chip image window is active, the user may select any point within the chip image. The spot and its replicate are circled in yellow and the grid block is highlighted in blue. The genomic profile is updated to show the chromosome on which the spots are located. It highlights the spot, both raw and fit log2 ratio values, and adds the spot label. The smooth descriptive window will update the four zoomed chip images to display the highlighted block from the chip image window with the spot and its replicate highlighted in yellow.

If the genomic profile window is active, the user may select any of the log2 ratios, raw or fitted. The points, raw and fit value will be highlighted and the spot label is added. The chip image is updated to highlight where the spot and replicate occured. It is highlighted in yellow and the grid block is highlighted in blue. The smooth descriptive window will update the four zoomed chip images to display the highlighted block from the chip image window with the spot and its replicate highlighted in yellow.