

sendplot

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sendplot creates an interactive plot with any number of decoration plots also being displayed. Although the creation of these files must be in R, R is not required for viewing output. The necessary elements for viewing an interactive plot is a web browser that has javascript capabilities. The code used to create this is a modified version of the javascript code from <http://www.onlamp.com/pub/a/onlamp/2007/07/05/writing-advanced-javascript.html> or it utilizes an open source tooltip library called wz_tooltip.js from http://www.walterzorn.com/tooltip/tooltip_e.htm Note if you are using Internet Explorer you may need to select the option allowed blocked content. Internet Explorer will initially block the scripts from running. A warning message normally appears towards the top of the browser; if you click on this warning it will give an option to allow blocked content. We will now go through an example of running this application. This example is a more advanced usage; for basic examples please see the R help files for sendplot, sendxy or sendimage; sendxy and sendimage are wrappers to the sendplot function that will create a single interactive scatterplot or image plot. We will go through the steps to make Figure 1 where the main image heatmap is interactive.

Begin by cleaning the workspace and loading the library. This example utilizes objects created with the R package aCGHplus. aCGHplus is a package designed for array comparative genomic hybridization experiments. For information on this package and objects that can be created with this package please go to the website: <http://sphhp.buffalo.edu/biostat/research/software/acghplus/index.php>. We load the aCGH object as well:

```
> rm(list = ls())
> library(sendplot)
> data("aCGHex")
```

Lets look at each argument of the sendplot function call. As a reminder the sendplot function is:

```
sendplot <- function(mat, plot.calls, x,y, mai.mat, mai.prc=FALSE,xlim=NA, ylim=NA,
                     z=NA, z.value="value",type="scatterplot", plt.extras = NA,
```

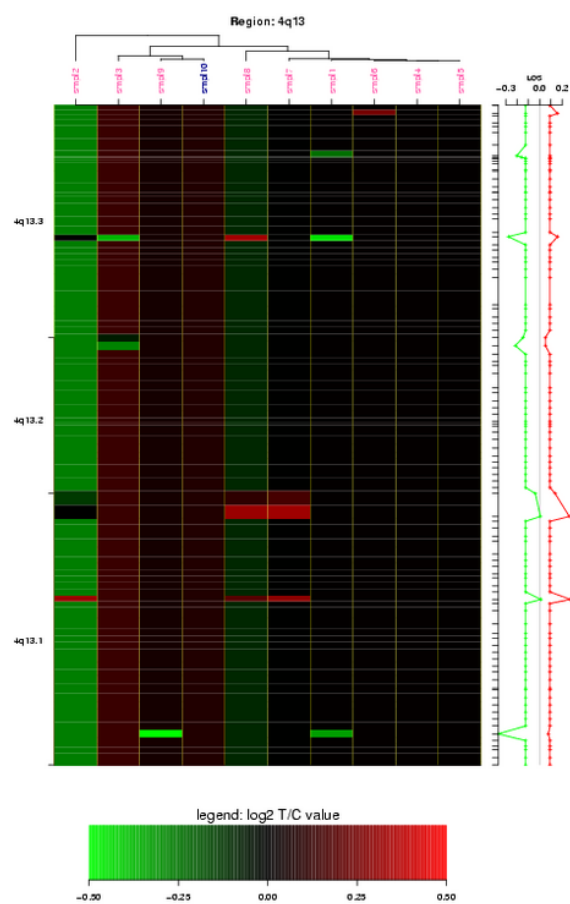


Figure 1: Interactive heatmap image

```

x.lbls=NA, y.lbls=NA, xy.lbls=NA,
bound.pt = TRUE,source.plot=NA,resize="4000x5500", ps.paper="letter",
ps.width=8,ps.height=11,fname.root="test",dir="./",header="v2",
paint=TRUE, img.prog = NA,
up.left=c(673,715),low.right=c(2874,4481),
spot.radius=10
)

```

The first argument, `mat`, is a numeric matrix that will be passed in the R graphics package function `layout`. In this case we will set up a display for four different plots.

```

> mat = matrix(c(rep(c(rep(2, 8), rep(0, 2)), 1), rep(c(rep(1,
+      8), rep(4, 2)), 14), rep(c(rep(3, 8), rep(0, 2)), 2)), ncol = 10,
+      byrow = TRUE)

```

The layout that will be used is:

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	2	2	2	2	2	2	2	2	0	0
[2,]	1	1	1	1	1	1	1	1	4	4
[3,]	1	1	1	1	1	1	1	1	4	4
[4,]	1	1	1	1	1	1	1	1	4	4
[5,]	1	1	1	1	1	1	1	1	4	4
[6,]	1	1	1	1	1	1	1	1	4	4
[7,]	1	1	1	1	1	1	1	1	4	4
[8,]	1	1	1	1	1	1	1	1	4	4
[9,]	1	1	1	1	1	1	1	1	4	4
[10,]	1	1	1	1	1	1	1	1	4	4
[11,]	1	1	1	1	1	1	1	1	4	4
[12,]	1	1	1	1	1	1	1	1	4	4
[13,]	1	1	1	1	1	1	1	1	4	4
[14,]	1	1	1	1	1	1	1	1	4	4
[15,]	1	1	1	1	1	1	1	1	4	4
[16,]	3	3	3	3	3	3	3	3	0	0
[17,]	3	3	3	3	3	3	3	3	0	0

The numbers 1-4 represent the areas that will contain four different plots. The first plot displaying in the region marked as one, the second in the region marked as two, and so on. In our final display, the first and fourth plot line up. For this reason there is a buffer region of 0 above and below the fourth plot. Zero acts as a region that no graph is displayed.

The next argument, `plot.calls`, is a character vector with the necessary plot calls for all graphs. In this example `plot.calls` will be of length four. The call that is included is the main chunk of the plot call or the main shell of what is plotted. Additional expressions can be evaluated on the plot through the

sendplot argument `plt.extras`. For example, you may want to graph an image as the main plot call but you may want to specify a particular axis or tick marks. The image call goes into `plot.calls` while an axis call goes into the `plt.extras` argument. We will look at `plt.extras` in more detail momentarily. The `plot.calls` argument for Figure 1 is:

```
plot.calls = c(
  "image(x=x,y=y,z=t(z),zlim=c(-0.5,0.5), ylim=range(scanLoc,na.rm=T),
    col=c(hsv(h=2/6,v=seq(1,0,length=1000)^1.15),
    hsv(h=0/6,v=seq(0,1,length=1000)^1.15)),axes=F,xlab='',ylab='')",

  "plot(DDR,axes = FALSE, xaxs = 'i', leaflab = 'none',main=ttl)",

  "image(x=seq(from=-0.5,to=0.5,length=1000),y=1,z=t(zlgnd),zlim=c(-0.5,0.5),
    col=c(hsv(h=2/6,v=seq(1,0,length=1000)^1.15),
    hsv(h=0/6,v=seq(0,1,length=1000)^1.15)),
    axes=F,xlab='',ylab='')",

  "image(x=0:1,y=0:1,z=matrix(rep(NA,4),ncol=2),xlim=range(c(W.lw,W.up),na.rm=T),
    ylim=range(scanLoc,na.rm=T),zlim=c(0,1),axes=F,xlab='',ylab='')")
```

The first plot call,

```
"image(x=x,y=y,z=t(z),zlim=c(-0.5,0.5), ylim=range(scanLoc,na.rm=T),
  col=c(hsv(h=2/6,v=seq(1,0,length=1000)^1.15),
  hsv(h=0/6,v=seq(0,1,length=1000)^1.15)),axes=F,xlab='',ylab='')",
```

creates a heatmap image that looks like Figure 2. Notice axis and additional plotting such as vertical line breaks have not yet been plotted.

The second plot call,

```
plot(DDR,axes = FALSE, xaxs = 'i', leaflab = 'none',main=ttl)
```

creates the dendrogram representation of sample clustering seen in Figure 3.

The third plot call,

```
image(x=seq(from=-0.5,to=0.5,length=1000),y=1,z=t(zlgnd),zlim=c(-0.5,0.5),
  col=c(hsv(h=2/6,v=seq(1,0,length=1000)^1.15),
  hsv(h=0/6,v=seq(0,1,length=1000)^1.15)),
  axes=F,xlab='',ylab='')
```

creates the legend image seen in Figure 4.

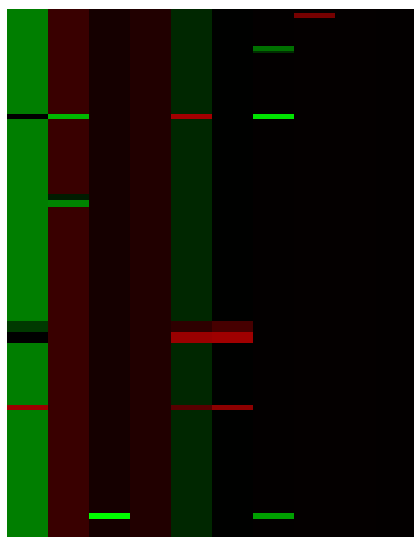


Figure 2: Initial heatmap image from executing `plot.call[1]`

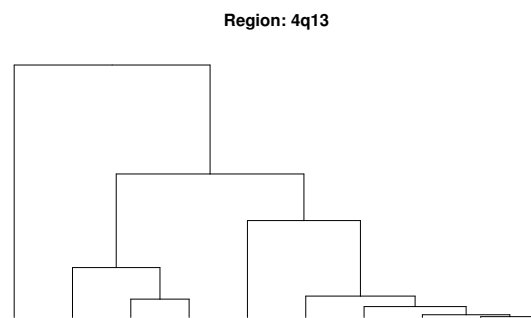


Figure 3: Dendrogram created from executing `plot.call[2]`



Figure 4: Legend created from executing `plot.call[3]`

The last plot.call,

```
image(x=0:1,y=0:1,z=matrix(rep(NA,4),ncol=2),
      xlim=range(c(W.lw,W.up),na.rm=T),
      ylim=range(scanLoc,na.rm=T),
      zlim=c(0,1),
      axes=F,xlab='',ylab='')
```

creates a blank image. We choose to use image as a base instead of plot to ensure ratios and buffers would be equivalent between the first and fourth plots. There are many features that have not been included with the main plot calls in the plot.calls argument. These will be added by the plt.extras argument. If you look closely at the plot calls, you will notice that they use many variables we have yet to define. Any variables that are used in plotting calls should be in local R memory at the time of execution. The following are variables needed for plot calls:

```
# index of genome - we want to look at region 4q13
# the aCGHplus object has already been subset for this region for 10 samples
scanDX = 1:dim(aCGH$mapping.info)[1]
bioDX = scanDX
scanLoc=aCGH$mapping.info$loc.genome[scanDX]
scanLoc[which(diff(scanLoc)<=0)]=scanLoc[which(diff(scanLoc)<=0)]-0.001
# add sample names to index of log2 data
colnames(aCGH$log2.ratios.fitted)=aCGH$inventory$sample.ID
# perform a sample clustering and create dendrogram
ManDist=dist(t(aCGH$log2.ratios.fitted),method = "manhattan")
hc=hclust(ManDist,method="ward")
ddr=as.dendrogram(hc)
# useful sample information
nsmpl = aCGH$data.info$nsmpl
smplDX = 1:nsmpl
ttl = "Region: 4q13"
# creates legend scale for log2 ratios from -.5 to .5
zlgn=array(seq(from=-0.5,to=0.5,length=1000),dim=c(1,1000))
# x values = samples
x = 1:length(smplDX)
# y values = genomic location
y = scanLoc
# z values = log 2 ratios that have been fitted
# by circular binary segmentation - min and max cutoffs applied
z.value="log2.ratios.fitted"
z = aCGH$log2.ratios.fitted[,hc$order]
z.raw = z
z[z>0.5]=0.5
z[z<(-0.5)]=-0.5
# sorts log2 values and splits into low region and high region
```



```
# to create fourth plot of avg. means
rowSort=function(i,x) sort(x[i,])
z.sort=t(mapply(rowSort,1:(dim(z.raw)[1]),MoreArgs=list(x=z.raw)))
lwDX=1:ceiling(nsmpl/4)
upDX=(floor((3/4)*nsmpl)+1):nsmpl
W.up=rowMeans(z.sort[,upDX],na.rm=T)
W.lw=rowMeans(z.sort[,lwDX],na.rm=T)
```

We now return to the arguments of `sendplot`. We have defined the `mat` and the `plot.calls` arguments for our example. The next argument is `mai.mat`. This perhaps is the hardest for a user to define. `mai.mat` is a matrix that holds the arguments for each plots' margins. Each row is a different `mai` vector. These values will be passed into the R graphics package `par(mai=)` command. The matrix is `n` by four, where `n` is the number of plot calls. The four columns represent the margins bottom, left, top, and right as defined by the R graphics package function `par`. If the figure margins are set too large an error will occur when plotting. If the user gets an Error figure margins too large, decrease the values in `mai.mat`. The `mai.mat` for our example is created with the following code:

```
> mai.mat = matrix(0, ncol = 4, nrow = 4, byrow = TRUE)
> mai.mat[1, ] = c(0.5, 0, 0.5, 0)
> mai.mat[2, ] = c(0, 0, 0.3, 0)
> mai.mat[3, ] = c(0.4, 0.4, 0.2, 0.4)
> mai.mat[4, ] = c(0.5, 0.2, 0.5, 0.2)
```

The first row, `mai.mat[1,]`, indicates the figure margins for the first plot. The heatmap plot will have a bottom and top margin of .5, while the left and right will have no margin. The second row, `mai.mat[2,]`, indicates the figure margins for the second plot. The dendrogram plot will have no left or right margin so that it will line up with the heatmap width, no bottom margin, but a top margin of .3. The others follow accordingly. The `mai.mat` values may also be a percentage of the default margins rather than hard coded values. If the values in `mai.mat` are percentages an argument `mai.prc` should be tripped to `TRUE`.

The `x`, `y`, and `z` arguments of the `sendplot` function have already been defined. The `x` argument is the `x` values that will be used for graphing the first plot. The `y` argument is the `y` values that will be used for graphing the first plot. These need to be specified again separately from the plot calls in order to accurately make the first plot's points interactive. If the first plot is an image, the `z` argument is the `z` values used in the first plot's image call. If the first plot is a scatterplot `z` will be left as `NA`. We have already defined `x`, `y`, and `z` in local memory. `z.value` is the label for what is being displayed by the `z` values. This label will be used in the interactive window display. It should not contain any spaces. The data being used as `z` values for our example is `log2ratios` that have been fitted by circular binary segmentation. We will call our `z.value` `log2ratios.fitted`.

```

> z.value = "log2ratios.fitted"
> xlim = NA
> ylim = NA
> type = "image"

```

In the above code we have set three more of the `sendplot` function's arguments: `xlim`, `ylim`, and `type`. `xlim` and `ylim` only need to be specified if the type is scatterplot. `xlim` and `ylim` help define the range of the data for accurate display of information when the points of a scatterplot are interactive. The `xlim` and `ylim` should be defined as the appropriate minimum and maximum value to use for the plot axis. If the type is scatterplot and the `xlim` or `ylim` is left as `NA`, the range of the `x` values and range of `y` values are used. Our example is a heatmap which is plotted by `image`. `xlim` and `ylim` therefore remain `NA`. The `xlim` and `ylim` values will be generated from the `image` call. `Type` indicates the type of graph that the first, main plot of the `plot.calls` is. Currently supported types are scatterplot or `image`. Our first plot is generated with an `image` call, and therefore is of type `image`.

We now return to the `plt.extras` argument. `plt.extras` is a list of length equal to the number of `plot.calls`. In our example, `plt.extras` should be of length four. Each argument of the list is also a list, which we will refer to as a sublist. Each sublist contains character vectors with additional plot calls for the plot created with the `plot.call` of the location of the sublist in the `plt.extras`. For example, the sublist `test` has two calls and we want them to be graphed on the second plot or `plot.calls[2]` while there are no additional plot calls for the first plot:

```

plt.extras = list()
plt.extras$plot1 = NA
test = list()
test[1] = "abline(v=0, col='gray77', lwd=1)"
test[2] = "title(main='mytest')"
plt.extras$plot2 = test

```

If we look back at Figure 2 compared with Figure 1, we see we want to add an axis to the left and top of the plot with labels, and vertical lines to separate `x` values. The following code will achieve this:

```

plot1 = list()
plt1.ind = 1

nlbl=50
eval.js("sample.colors=as.character(aCGH$inventory$sex)")
colorSet =c("hotpink","darkblue", "green")
lev = levels(factor(sample.colors))
for(i in 1:length(lev)){
  sample.colors[sample.colors==lev[i]] = colorSet[i]
}

```

```

count.arm=sum((aCGH$Band.Aid$Regions[[2]]$Upper>=min(scanLoc,na.rm=T))
&(aCGH$Band.Aid$Regions[[2]]$Lower<=max(scanLoc,na.rm=T)))
count.broadband=sum((aCGH$Band.Aid$Regions[[3]]$Upper>=min(scanLoc,na.rm=T))
&(aCGH$Band.Aid$Regions[[3]]$Lower<=max(scanLoc,na.rm=T)))
count.finband=sum((aCGH$Band.Aid$Regions[[4]]$Upper>=min(scanLoc,na.rm=T))
&(aCGH$Band.Aid$Regions[[4]]$Lower<=max(scanLoc,na.rm=T)))
cat("label counts:",count.arm,count.broadband,count.finband,fill=T)
cat("target number=",nlbl,fill=T)
ilbl=order(abs(c(count.arm,count.broadband,count.finband,length(scanDX))-nlbl))[1]
cat("ilbl=",ilbl,fill=T)
if(ilbl<=3){
  if(ilbl==1) bandDX=1:40
  if(ilbl==2) bandDX=(
    (sum(aCGH$Band.Aid$Regions[[3]]$Upper<=min(scanLoc,na.rm=T),na.rm=T)+1)
    : (sum(aCGH$Band.Aid$Regions[[3]]$Lower<=max(scanLoc,na.rm=T),na.rm=T)))
  if(ilbl==3) bandDX=(
    (sum(aCGH$Band.Aid$Regions[[4]]$Upper<=min(scanLoc,na.rm=T),na.rm=T)+1)
    : (sum(aCGH$Band.Aid$Regions[[4]]$Lower<=max(scanLoc,na.rm=T),na.rm=T)))
  lbls=paste(aCGH$Band.Aid$Regions[[ilbl+1]]$Chrom[bandDX],
    aCGH$Band.Aid$Regions[[ilbl+1]]$Label[bandDX],sep="")

  plot1[plt1.ind] = "axis(2,aCGH$Band.Aid$Regions[[ilbl+1]]$Center[bandDX],
    tick=F,labels=lbls,las=2,cex.axis=1)"

  plt1.ind = plt1.ind + 1
  plot1[plt1.ind] = "axis(2,aCGH$Band.Aid$Regions[[ilbl+1]]$Lower[bandDX], labels=F)"
  plt1.ind = plt1.ind + 1
}
if(ilbl==4){
  lbls=as.character(aCGH$mapping.info$spot.ID[scanDX])

  plot1[plt1.ind] = "axis(2,aCGH$mapping.info$loc.genome[scanDX],tick=F,
    labels=lbls, las=2,cex.axis=1)"
  plt1.ind = plt1.ind + 1
}

plot1[plt1.ind] = "abline(v=(0:nsmpl)+1/2,col=7,lty=1,lwd=1/3)"
plt1.ind = plt1.ind + 1

if(length(sample.colors)==1){
  plot1[plt1.ind] = "axis(3,1:length(smplDX),cex.axis=1,las=2,
    labels=aCGHsub$inventory$sample.ID[hc$order])"
  plt1.ind = plt1.ind + 1
}

```

```

}
if(length(sample.colors)!=1){
  unq.colors=unique(sample.colors[hc$order])
  lbls2=aCGH$inventory$sample.ID[hc$order]
  col.labs=sample.colors[hc$order]
  for(j in 1:length(unq.colors)){
    iclr = unq.colors[j]
    cat("eye color=",iclr,fill=T)
    nm = paste("adx",j,sep="")
    eval.js(paste(nm, "which(col.labs==iclr)",sep=""))

    plot1[plt1.ind] = paste("axis(3,\"nm\",labels=lbls2[\"nm\"],
      cex.axis=1,las=2,col.axis='\",iclr,\"')", sep="")
    plt1.ind = plt1.ind +1
  }
}

```

The second plot of the dendrogram does not require any additional plotting and therefore will be NA. The legend created by the third plot call requires a title and a bottom axis. This will be achieved by setting up the following:

```

> plot3 = list()
> plt3.ind = 1
> plot3[plt3.ind] = "mtext('legend: log2 T/C value',side=3,cex=1,line=1/4)"
> plt3.ind = plt3.ind + 1
> plot3[plt3.ind] = "axis(1,seq(from=-0.5,to=0.5,length=5),line=0)"
> plt3.ind = plt3.ind + 1

```

The entire fourth graph still needs to be generated since we only set up an image shell. The following calls will achieve this:

```

> plot4 = list()
> plt4.ind = 1
> plot4[plt4.ind] = "abline(v=0,col='gray77',lwd=1)"
> plt4.ind = plt4.ind + 1
> plot4[plt4.ind] = "points(W.lw,scanLoc,col='green',pch=3,cex=0.5)"
> plt4.ind = plt4.ind + 1
> plot4[plt4.ind] = "points(W.up,scanLoc,col='red',pch=3,cex=0.5)"
> plt4.ind = plt4.ind + 1
> plot4[plt4.ind] = "lines(W.lw,scanLoc,col='green',pch=3,cex=0.5)"
> plt4.ind = plt4.ind + 1
> plot4[plt4.ind] = "lines(W.up,scanLoc,col='red',pch=3,cex=0.5)"
> plt4.ind = plt4.ind + 1
> plot4[plt4.ind] = "axis(3)"
> plt4.ind = plt4.ind + 1
> plot4[plt4.ind] = "mtext(text='LOS',side=3,line=2,cex=0.5)"
> plt4.ind = plt4.ind + 1

```

```
> plot4[plt4.ind] = "axis(2,at=scanLoc,labels=F)"
> plt4.ind = plt4.ind + 1
```

The above code generates all the sublists of the plt.extras list. The following will put all the sublists in the plt.extras list object:

```
> plt.extras = list()
> plt.extras$plot1 = plot1
> plt.extras$plot2 = NA
> plt.extras$plot3 = plot3
> plt.extras$plot4 = plot4
```

The plt.extras argument has now been generated for our example. Notice how this argument will add any additional plot calls to the original plot. Our plt.extras is of length four which is consistent with the length of our plot.calls argument. The sublist for the first plot of the heatmap image, plot1, has five additional plot arguments: one call generating vertical lines at all x boundaries, two calls generating axis, one for the top and one for the left, and two calls generating tick labels for the axis.

```
> plot1

[[1]]
[1] "axis(2,aCGH$Band.Aid$Regions[[ilbl+1]]$Center[bandDX],tick=F,labels=lbls,las=2,cex.axis

[[2]]
[1] "axis(2,aCGH$Band.Aid$Regions[[ilbl+1]]$Lower[bandDX], labels=F)"

[[3]]
[1] "abline(v=(0:nsmpl)+1/2,col=7,lty=1,lwd=1/3)"

[[4]]
[1] "axis(3,adx1,labels=lbls2[adx1],cex.axis=1,las=2,col.axis='hotpink')"

[[5]]
[1] "axis(3,adx2,labels=lbls2[adx2],cex.axis=1,las=2,col.axis='darkblue')"
```

The sublist for the second plot of the dendrogram, plot2, is NA because there is no additional graphing needed. The legend is the third plot, plot3, which has two additional calls: one to make the title of the image and one to make the axis.

```
> plot3

[[1]]
[1] "mtext('legend: log2 T/C value',side=3,cex=1,line=1/4)"

[[2]]
[1] "axis(1,seq(from=-0.5,to=0.5,length=5),line=0)"
```

The fourth plot consists of eight different additional plotting calls which make axis, add labels, and add points and lines.

```
> plot4

[[1]]
[1] "abline(v=0,col='gray77',lwd=1)"

[[2]]
[1] "points(W.lw,scanLoc,col='green',pch=3,cex=0.5)"

[[3]]
[1] "points(W.up,scanLoc,col='red',pch=3,cex=0.5)"

[[4]]
[1] "lines(W.lw,scanLoc,col='green',pch=3,cex=0.5)"

[[5]]
[1] "lines(W.up,scanLoc,col='red',pch=3,cex=0.5)"

[[6]]
[1] "axis(3)"

[[7]]
[1] "mtext(text='LOS',side=3,line=2,cex=0.5)"

[[8]]
[1] "axis(2,at=scanLoc,labels=F)"
```

It is worth noting that some of the `plt.extras` arguments can be included in the `plot.calls` argument. This is achieved by separating any calls for the same plot with a semicolon. For example, the third plot.call for the heatmap legend, originally is

```
"image(x=seq(from=-0.5,to=0.5,length=1000),y=1,z=t(zlgnd),zlim=c(-0.5,0.5),
        col=c(hsv(h=2/6,v=seq(1,0,length=1000)^1.15),
              hsv(h=0/6,v=seq(0,1,length=1000)^1.15)),
        axes=F,xlab='',ylab=''),"
```

and the `plt.extras` calls were

```
"mtext('legend: log2 T/C value',side=3,cex=1,line=1/4)"

and

"axis(1,seq(from=-0.5,to=0.5,length=5),line=0)"
```

We could have placed both of the `plt.extra` calls in the `plot.calls` argument and changed the `plt.extra` call to NA. The `plot.call` for the third graph would become the following:

```
"image(x=seq(from=-0.5,to=0.5,length=1000),y=1,z=t(zlgnd),zlim=c(-0.5,0.5),
      col=c(hsv(h=2/6,v=seq(1,0,length=1000)^1.15),
            hsv(h=0/6,v=seq(0,1,length=1000)^1.15)),
      axes=F,xlab='',ylab=''); mtext('legend: log2 T/C value',side=3,cex=1,line=1/4);
      axis(1,seq(from=-0.5,to=0.5,length=5),line=0)"
```

Notice how the three separate calls are separated by a semicolon but are all considered part of the first `plot.call` because of the placement of the quotation markers. Either is acceptable but we wanted the user to recognize this option.

The next few arguments, `x.lbls`, `y.lbls`, and `xy.lbls`, control what is displayed in the interactive window when the user hovers the mouse over points or regions of the first, main, plot. `x.lbls` refers to data that is specific to the x value of the data point or region in question, likewise `y.lbls` refers to the data that is specific to the y value of the data point or region in question. `xy.lbls` refers to data that is specific to both x and y location. In the case of a scatterplot, `x.lbls`, `y.lbls`, and `xy.lbls` refer to the same position; it therefore is only necessary to use either `x.lbls` or `y.lbls`. `x.lbls` and `y.lbls` are data.frames. `x.lbls` is of the dimension n by m where n is equal to the length of x. Each row of the `x.lbl` is specific to a certain x.value. The row should be ordered to correspond with the order of the graph. Each column of the data frame is a unique piece of data. The names of the columns will be used as the label in the interactive display window. In our example x values are samples. We have 43 x values and therefore 43 rows in the `x.lbls` data.frame. We wish to display the information for sample.ID and sex which are sample specific data. The `aCGH` object contains a data.frame that holds information about the samples: the first column of that data frame holds the sample.ID information and the eighth column holds the sex data. Earlier we ordered the samples by clustering. The `x.lbls` data frame therefore may be attained with the following:

```
> x.lbls = aCGH$inventory[hc$order, c(1, 8)]
> y.lbls = aCGH$mapping.info[scanDX, c(5, 6, 8, 10, 12)]
```

In our example the y values are BACs of specific genomic location. We selected a specific range of BACs by setting `scanDX`. There are 98 different y value locations and therefore `y.lbls` will have 98 rows. The `y.lbls` data frame is similar to the `x.lbls` data frame in that it is of the dimension n by m where n is equal to the length of y. Each row of the `y.lbl` is specific to a certain y value and the rows should be ordered to correspond with the ordering of the graph. Each column of the `y.lbls` data frame is a unique piece of data. We wish to display the information for genomic location, chromosome, arm, broad.band, and fine.band location in the interactive display. The `aCGH` object contains a data.frame that holds information about the BACs; The corresponding columns in that data.frame are 5, 6, 8, 10, and 12.

The `xy.lbls` argument is a little different because it is specific to both the selected `x` value and `y` value. The `xy.lbls` argument is therefore a list of matrices; Each matrix is of the dimension `n` by `m` where `n` is equal to the length of `y` and `m` is equal to the length of `x`. For our example the only `xy` specific data we have are raw `log2` ratios and the `log2` ratios that have been fitted by circular binary segmentation. Since we have used the fitted `log 2` ratios as the `z` value to create the heatmap, these values are included automatically in the interactive display. Our example therefore has one matrix in the `xy.lbls` list.

```
> xy.lbls = list()
> log2.ratio = as.matrix(aCGH$log2.ratios[, hc$order])
> xy.lbls$log2.ratio = log2.ratio
```

The `source.plot` argument controls what file formats are created. The interactive html file requires a `.png` file. There are two possible scenerios for making a `png` file: the `png` file may be made directly, or a `postscript` file may be made first and then converted into a `png` file. `source.plot` will be `ps` if the `postscript` file should be created and will be `png` if the `png` file should be made directly. If `NA`, `source.plot` will be determined by the operating system. We recommend making the `postscript` file and converting to the `png` file because we feel it maintains better clarity and quality. There is a `convert` call that is automatically executed on `linux/unix` machines to convert a `postscript` file into a `png` file. This `convert` call is not available for `windows` users. If a `windows` or `mac` user decides to go to `postscript` first, it is up to the user to convert the file into the appropriate, readable `.png` file. For this reason if `source.plot` is left `NA`, for `linux/unix` the default is `ps` and for `windows/mac` the default is `png`. If a `postscript` file is used the `sendplot` arguments `ps.paper`, `ps.width`, and `ps.height` are passed into the `postscript` call for `paper`, `width`, and `height`.

The `resize` argument used different ways depending if `source.plot` is `ps` or `png`. If `source.plot` is `ps`, `resize` is passed as part of a system `convert` command to convert the `postscript` to the `.png`. The original image is resized to this dimension. This helps expand condensed looking images, or visa versa. If `source.plot` is `png`, the argument is parsed and the dimensions are passed into the `R` `grDevices` package function `png` as the `width` and `height` arguments. For our example plot we wish to `resize` making the final image smaller in both `width` and `height`.

```
> resize = "600x900"
```

The arguments `fname.root` and `dir` define the name and path of the `postscript`, `png`, and `html` files created. `dir` is the path of the directory that the files should be created in. The default directory is the currently working directory. `fname.root` is the base name of the files. The `postscript`, `png`, and `html` file will all have the same name with different extensions. For example, if `fname.root = "test"` then the files generated will be `test.ps`, `test.png`, and `test.html`.

The next argument `header` refers to which `java` tooltip is used in the `html` file. Older versions of the package utilized a tooltip that worked well with `firefox` but would not work on `internet explorer` web browsers. `header` may either be `vlör`

v2: The more recent default tooltip works on multiple web browsers; however if the user wishes to use the original version for firefox, the first version, v1, may be specified.

The key to the interactive html is correct mappings of the x and y values in R to pixel locations of the .png. The function will automatically generate this mapping, however the information in up.left and low.right must be accurate. up.left and low.right refer to the upper left hand corner and lower right hand corner of the first, main plot generated. If this is an image it is the corners of the image generated. If this is a scatterplot, it is the corners of the bounding box generated. The sendplot function may need to be run twice to get the finalized interactive version. Consider running our example with the default up.left = (673, 715) and low.right=c(2874,4481). The mappings for the data points will not be correct and the interactive html file will appear not to work correctly. If the correct pixel locations are not known, the png file must be opened in some viewer that will tell pixel locations. We have provided a options to open the png file in default applications or a given application call. This is controlled by the sendplot argument paint. If paint is TRUE, the .png file is opened by the call given by img.prog. If img.prog is NA, the application is determined by the operating system. If unix/linux the kolourpaint application (img.prog=kolourpaint) is used. In windows the microsoft paint application (img.prog=mspaint) is used. Other application may be specified but the user should make sure img.prog is the command line call to execute the application. If paint is TRUE, the png file will open automatically in the appropriate program; we will consider kolourpaint and mspaint for our example. As stated before, for an image the corners of the image should be used. A scatterplot however is more challenging. A buffer is added to the plot so the bounding box is not clear. When the bounding box location is not known the sendplot argument bound.pt should be TRUE. This will add two red points where the pixel locations should be recorded. (NOTE: blue points are added to an image). If bound.pt is TRUE only the ps and/or png image is created, not the interactive html file since the mapping would be incorrect. Figure 5 is a snapshot of the sendplot help function example for scatterplot opened in kolourpaint:

Notice the mouse is over the upper left red point for the up.left bounding box. The pixel location is shown on the bottom of the window in the second box from the left. It shows a location of 188, 200. The sendplot function used to created this figure should be rerun with bound.pt=FALSE and up.left=c(188,200). Lets look at the code that will open our example in kolourpaint. This function does not have correct up.left or low.right entries.

```
sendplot(mat=mat, plot.calls=plot.calls, mai.mat=mai.mat,
         x=x,y=y,z=z,xlim=NA,ylim=NA, z.value=z.value, type="image",
         plt.extras=plt.extras, x.lbls=x.lbls, y.lbls=y.lbls,xy.lbls=xy.lbls,
         spot.radius=3,up.left=c(673,715),low.right=c(2874,4481),
```

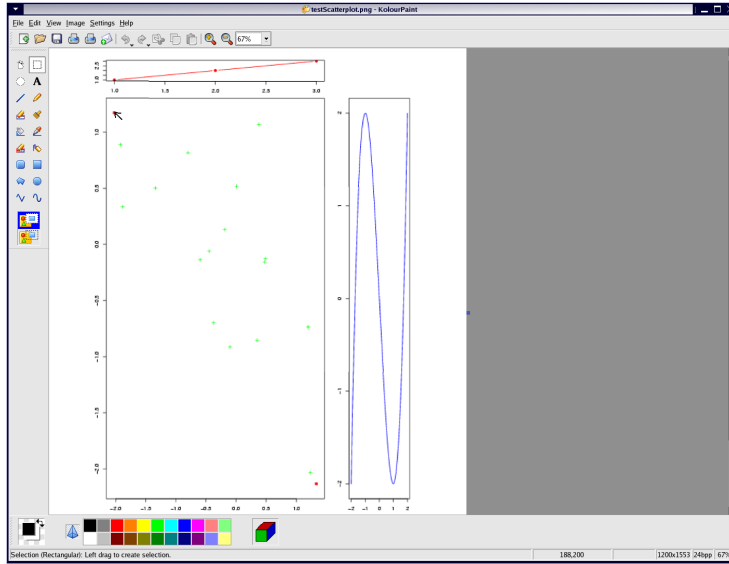


Figure 5: scatterplot opened in kolourpaint, showing additional red points to aid in locating boundaries. Notice where pixel location can be found

```
source.plot=NA, img.prog=TRUE,
resize=resize, bound.pt=TRUE, paint=TRUE)
```

In Figure 6, We have circled the mouse location in blue to aid in viewing. Your mouse will not have the blue circle surrounding it. The pixel location at this location is 83,97. This therefore should be used as the up.left location. The lower right pixel location is 430, 635. After these values are determined, the sendplot function call should be run again, changing only the up.left, up.right, paint, and bound.pt argument. up.left and low.right should be updated accordingly. paint and bound.pt should be tripped to FALSE. (NOTE: these are the correct up.left and low.right boundaries when the png is created from the postscript in linux/unix environment. If the png file was generated directly, like when in a windows environment, the up.left and low.right values of this example may be slightly different). The following will make the correct interactive plot.

```
> sendplot(mat = mat, plot.calls = plot.calls, mai.mat = mai.mat,
+   x = x, y = y, z = z, xlim = NA, ylim = NA, z.value = z.value,
+   type = "image", plt.extras = plt.extras, x.lbls = x.lbls,
+   y.lbls = y.lbls, xy.lbls = xy.lbls, spot.radius = 3, up.left = c(83,
+   97), low.right = c(430, 635), source.plot = NA, img.prog = TRUE,
+   resize = resize, bound.pt = FALSE, paint = FALSE)
```

The resulting html file may be opened in any web browser that is capable of running javascript. We recommend using mozilla firefox; Internet Explorer

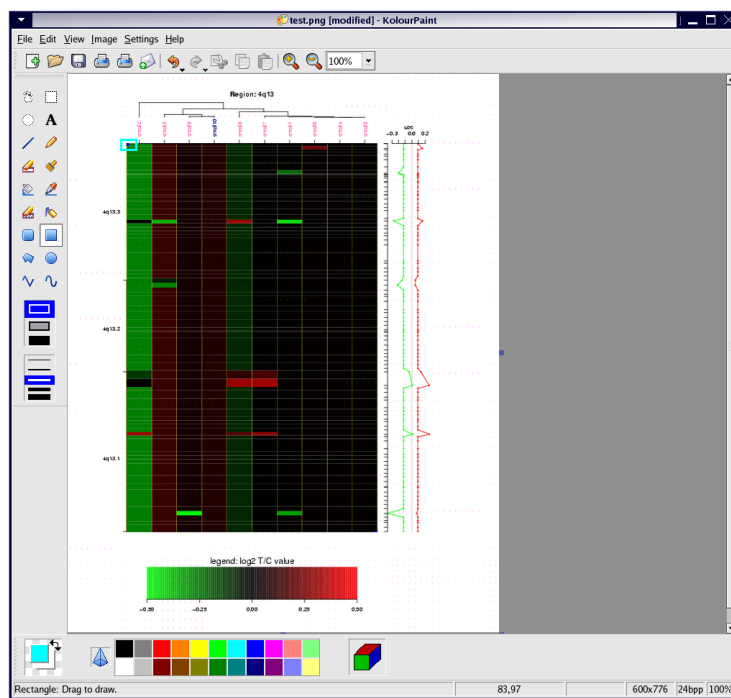


Figure 6: our example image opened in kolourpaint. The boundaries of the image is where the pixel location should be taken.

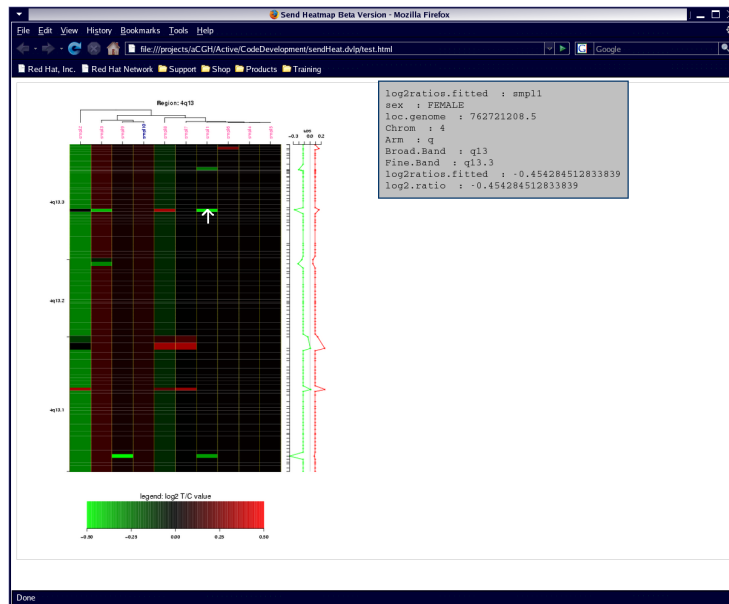


Figure 7: snapshot of our example html file opened in firefox. The information is displayed for the region under the white arrow.

currently is not supported. Figure 7 shows a snapshot of the final graph opened in firefox. Notice how the appropriate information for the region located under the white arrow is displayed in the information box.

Briefly, the `spot.radius` argument controls how large an area will be active when the mouse is scrolled over. If the user selects a larger region, some spot locations may overlap and be lost. If the user selects a low region, the interactive application is very sensitive.