Exploring cDNA data

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The following exercise will show you some possibilities to load data from spotted cDNA microarrays

Histogram of log2(x$CH1I)

Figure 1:

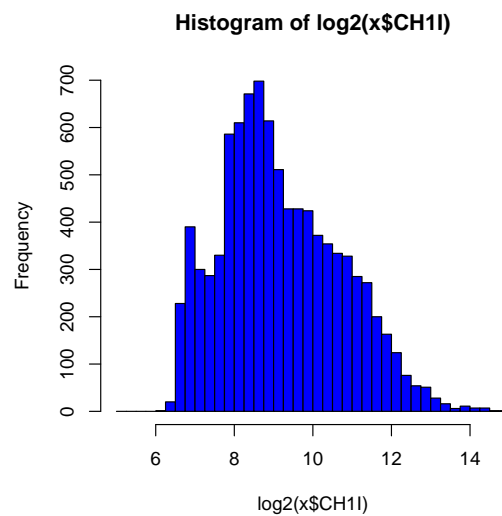```
> rankedbg1 <- spatialLayout(value = rank(x$CH1B), row = x$ROW,
+   col = x$COL, block = x$GRID)
> plot(rankedbg1)
> fg1 <- spatialLayout(value = x$CH1I, row = x$ROW, col = x$COL,
+   block = x$GRID)
> plot(log(fg1))
```
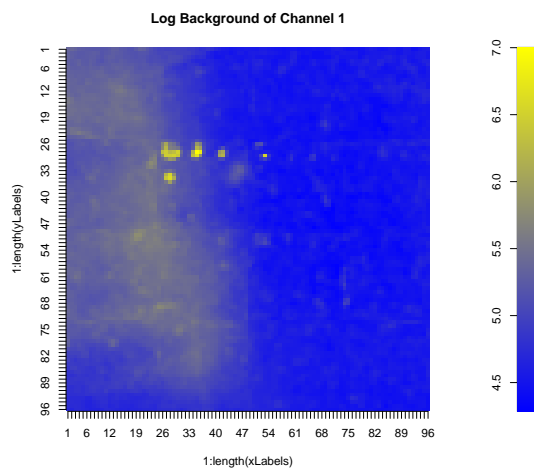
**Log Background of Channel 1**



Figure 2:

c. Save one of the plots as PDF, and as Windows metafile. Copy and paste it into an MS-O ce application.

**4.) Calibration and variance stabilization.**

a. Subtract the background intensities CH1B, CH2B from the foreground intensities CH1I, CH2I,

```
> y = cbind(x$CH1I - x$CH1B, x$CH2I - x$CH2B)
```

b. What does the function cbind do? Use the R online help to find out.

c. Now we can use the function vsn to calibrate and transform the data, and plot the result (Fig. 3).

```
> ny <- vsn(y)
```

```
vsn: 9216 x 2 matrix (1 stratum). Please wait for 10 dots: ..........
```

```
> plot(exprs(ny), pch = ".")
```

a. Look at the built-in function `t.test`, and at `mt.teststat` from the package `multtest`. Here, we use `mt.teststat` to calculate the *t*-test statistic for the comparison. The package `multtest` provides extensive functionality to calculate multiple-testing adjustments.

```
> classlabel = c(0, 0, 0, 0, 1, 1, 1, 1)
> tStat = mt.teststat(M[, , 1], classlabel)
> summary(tStat)
    Min.  1st Qu.   Median    Mean  3rd Qu.     Max.
-24.3400  -1.0330   0.1861  0.1832   1.3670  28.1000
> hist(tStat, breaks = 100, col = "#fb6090")
```