Heatmaps

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## The two steps are to combine two datasets and make a heatmap. The code below will combine two of the expression sets. If batch effects are present there should be 'clusters' of different shades of color. If there is a lack of batch effects most of the data will have a similar coloration and should look like a near unified shade.

## The code below will establish what each eset looks like.

library(Biobase)  
heatmap(exprs(var.feset1[1:40]))

heatmap(exprs(var.feset2[1:96]))  
  
heatmap(exprs(var.feset3[1:50]))

## Combine two expression sets (var.functioneset1, var.feset2) then make a heatmap.

var.feset1.2<-combine(var.feset1,var.feset2)

heatmapvar.feset1.2<-heatmap(exprs(var.feset1.2[1:136]))

## Repeat steps for the other esets paired with eset1.

var.feset1.3<-combine(var.feset1,var.feset3)

heatmapvar.feset1.3<-heatmap(exprs(var.feset1.3[1:90]))

## Pair up esets 2 and 3.

var.feset2.3<-combine(var.feset2,var.feset3)

heatmapvar.feset2.3<-heatmap(exprs(var.feset2.3[1:146]))

## The heatmaps should show up on the left under 'plots' and can be coverted to an image or pda. The batch effects should be very clear in the heatmaps.