libs <- c('ggplot2', 'latticeExtra', 'gridExtra', 'MASS', 'colorspace', 'plyr', 'Hmisc', 'scales')

lapply(libs, require, character.only = T)

zebrafishdata <- read.table("GenesLists.txt",fill =TRUE, h=T)

str(zebrafishdata)

scatter.lattice <- xyplot(GeneID ~ Size, data = zebrafishdata)

scatter.lattice #produces scatterplot

my.theme <- trellis.par.get() my.theme$strip.background$col <- "grey80" my.theme$plot.symbol$pch <- 16 my.theme$plot.symbol$col <- "grey60" my.theme$plot.polygon$col <- "grey90" l.sc <- update(scatter.lattice, par.settings = my.theme, layout = c(3, 2), between = list(x = 0.3, y = 0.3)) print(l.sc)

scatter.lattice <- xyplot(GeneID ~ Size | Organism,

data = zebrafishdata,

panel = function(x, y, ...) {

panel.xyplot(x, y, ...)

lm1 <- lm(y ~ x)

lm1sum <- summary(lm1)

r2 <- lm1sum$adj.r.squared

panel.text(labels =

bquote(italic(R)^2 ==

.(format(r2,

digits = 3))),

x = 4, y = 1000)

panel.smoother(x, y, method = "lm",

col = "black",

col.se = "black",

alpha.se = 0.3)

},

xscale.components = xscale.components.subticks,

yscale.components = yscale.components.subticks,

as.table = TRUE)

l.sc <- update(scatter.lattice, par.settings = my.theme)

print(l.sc)

scatter.ggplot <- ggplot(aes(x = Size, y = GeneID), data = zebrafishdata)

g.sc <- scatter.ggplot + geom\_point()

print(g.sc)

hist(zebrafishdata) #creates multiple graphs for data

my.theme <- trellis.par.get() my.theme$strip.background$col <- "grey80" my.theme$plot.symbol$pch <- 16 my.theme$plot.symbol$col <- "grey60" my.theme$plot.polygon$col <- "grey90"

dens.lattice <- densityplot(~ GeneID | Size + TFBindingSite,

l.den <- useOuterStrips(dens.lattice)

data = zebrafishdata,

as.table = TRUE,

par.settings = my.theme,

plot.points = FALSE,

between = list(x = 0.2, y = 0.2),

scales = list(x = list(rot = 45)))

l.den <- useOuterStrips(dens.lattice)

dens.lattice <- densityplot(~ Organism | TFBindingSite + GeneID,

data = zebrafishdata,

as.table = TRUE,

par.settings = my.theme,

plot.points = TRUE,

between = list(x = 0.2, y = 0.2),

scales = list(x = list(rot = 45)))

l.den <- useOuterStrips(dens.lattice)

print(l.den)

library(karyoploteR)

regions <- createRandomRegions(nregions=**10000**, length.mean = **1e6**, mask=**NA**)

kp <- plotKaryotype()

kpPlotDensity(kp, data=regions)

#generates a karyotype density plot using human chromosomes

my.theme <- trellis.par.get() my.theme$strip.background$col <- "grey80" my.theme$plot.symbol$pch <- 16 my.theme$plot.symbol$col <- "grey60" my.theme$plot.polygon$col <- "grey90"