Visualization

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Visualization

General

- ► Base graphics
- ► lattice
- ▶ ggplot2

Accidental aRt

Bioconductor

- ► Gviz, ggbio
- ► Rgraphviz, RCytoscape, RedeR

Interactive

► shiny!

One plot

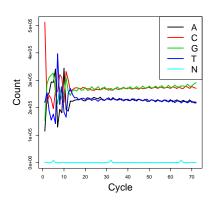
- Start a plot, matplot, hist, boxplot, ..., specifying options
- Add legend, points, ...
- ► Help: ?plot, ?par

Several plots

- ► Layout with par(mfcol=c(1, 2)), screen, ...
- Create single plots
- Restore original par settings

```
fileName <- file.choose() # 'abc.csv'
abc <- read.csv(fileName, row.names=1)</pre>
```

```
## Create a plot from a
## matrix
matplot(t(abc), type="1",
  lty=1, lwd=3,
  xlab="Cycle",
  ylab="Count",
  cex.lab=2)
## Add a legend
legend("topright",
  legend=rownames(abc),
  lty=1, lwd=3, col=1:5,
  cex=1.8)
```

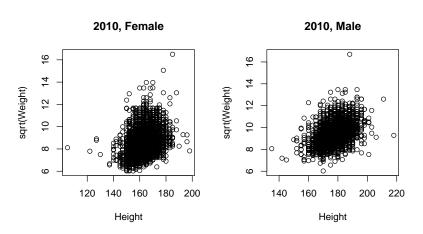


Data: US Center for Disease Control's Behavioral Risk Factor Surveillance System (BRFSS)

```
brfss <- read.csv(file.choose()) # 'BRFSS-subset.csv'
brfss2010 <- brfss[brfss$Year == "2010",]</pre>
```

Plot

```
## set layout, capture old options
opar \leftarrow par(mfcol=c(1, 2))
plot(sqrt(Weight) ~ Height,
    brfss2010[brfss2010$Sex == "Female", ],
    main="2010, Female")
plot(sqrt(Weight) ~ Height,
    brfss2010[brfss2010$Sex == "Male", ],
    main="2010, Male")
## restore old options
par(mfcol=c(1, 1))
```



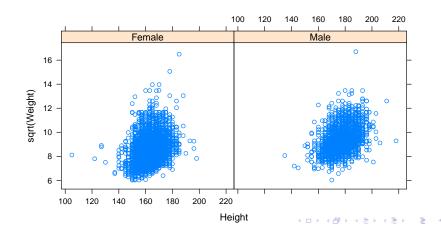
lattice graphics

- Main functions like xyplot, dotplot, contourplot
- 'Panel' functions that do the work, e.g., panel.xyplot, panel.violin
- Help: ?xyplot for working with the plot overall, ?panel.xyplot (and similar) for individual panels.

lattice graphics

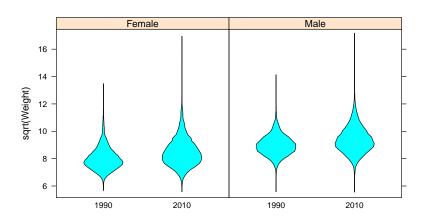
```
brfss <- read.csv(file.choose()) # 'BRFSS-subset.csv'</pre>
```

```
library(lattice)
xyplot(sqrt(Weight) ~ Height | Sex, brfss2010)
```



lattice graphics

bwplot(sqrt(Weight) ~ factor(Year) | Sex, brfss,
 panel=panel.violin)



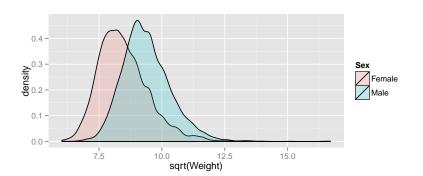
ggplot2 graphics

- ► Create a plot with ggplot
- ► Add *layers* (e.g., geom_density and *aesthetics* (e.g., aes)

ggplot2 graphics

```
brfss <- read.csv(file.choose()) # 'BRFSS-subset.csv'
brfss2010 <- brfss[brfss$Year == "2010",]</pre>
```

```
library(ggplot2)
ggplot(brfss2010) + geom_density(alpha=.2) +
    aes(sqrt(Weight), fill=Sex)
```



Genomic Visualization

- ▶ Very flexible base, *lattice*, and *ggplot2* facilities
- ► Ranges and genomes: Gviz, ggbio
- ► Graphs and networks: *Rgraphviz*, *RCytoscape*

Interactive Visualization

shiny provides an easy way to create interactive graphics. Explore the *Volcano!* application developed in class through the source code in the package.

```
system.file(package="SummerX", "shiny")
```