

Visualization

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Visualization

General

- ▶ Base graphics
- ▶ *lattice*
- ▶ *ggplot2*

Accidental aRt

Bioconductor

- ▶ *Gviz*, *ggbio*
- ▶ *Rgraphviz*, *RCytoscape*,
RedeR

Interactive

- ▶ *shiny*!

Base graphics

One plot

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

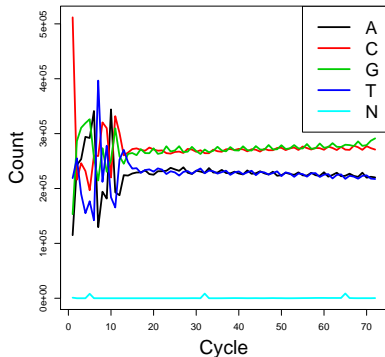
Several plots

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

Base graphics

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

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



Base graphics

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

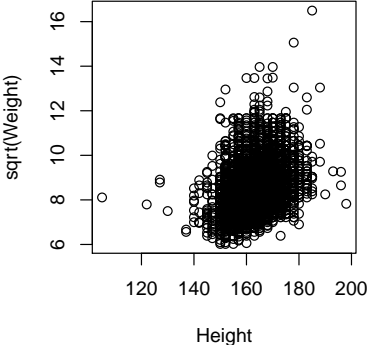
```
brfss <- read.csv(file.choose()) # 'BRFSS-subset.csv'  
brfss2010 <- brfss[brfss$Year == "2010",]
```

Plot

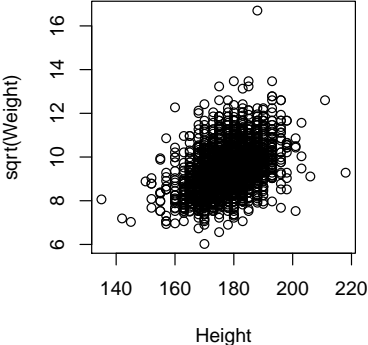
```
## set layout, capture old options  
opar <- par(mfcol=c(1, 2))  
plot(sqrt(Weight) ~ Height,  
      brfss2010[brfss2010$Sex == "Female", ],  
      main="2010, Female")  
plot(sqrt(Weight) ~ Height,  
      brfss2010[brfss2010$Sex == "Male", ],  
      main="2010, Male")  
## restore old options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

Base graphics

2010, Female



2010, Male



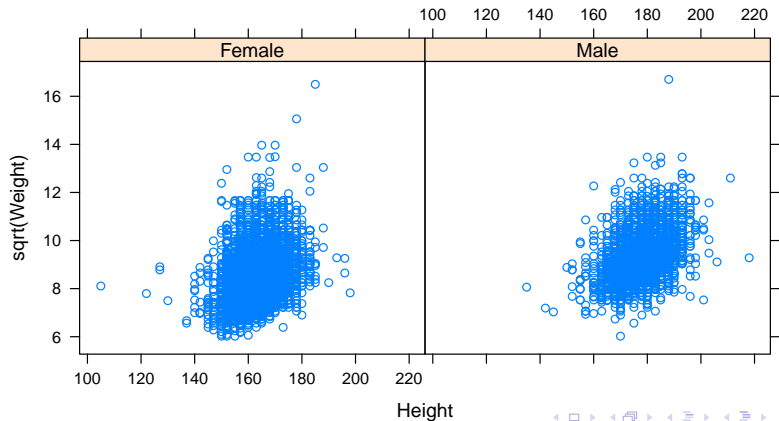
lattice graphics

- ▶ 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

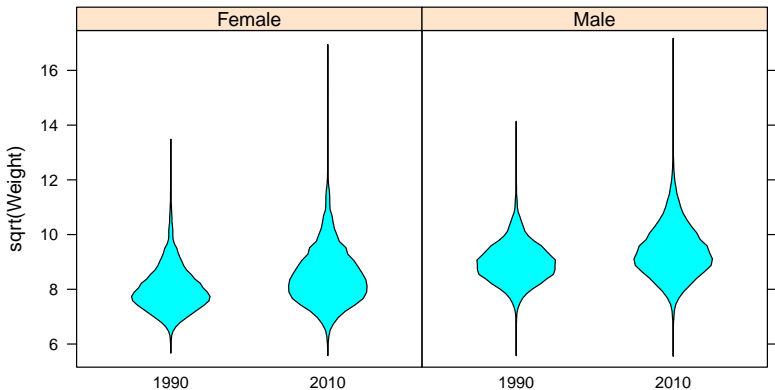
```
brfss <- read.csv(file.choose()) # 'BRFSS-subset.csv'
```

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



lattice graphics

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



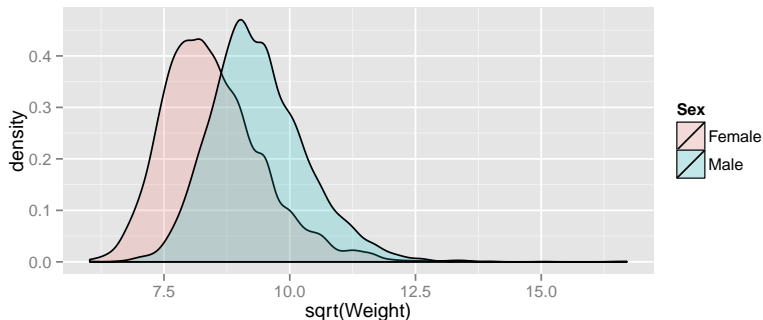
ggplot2 graphics

- ▶ 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",]
```

```
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")
```