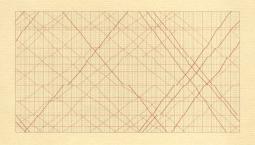
# data visualization

skimming deep waters

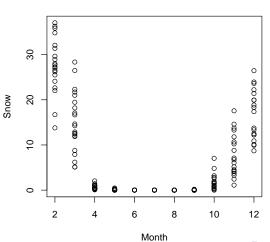




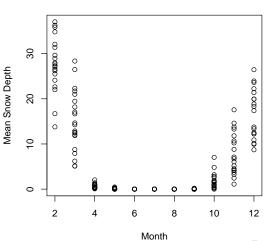
# The Visual Display of Quantitative Information

EDWARD R. TUFTE

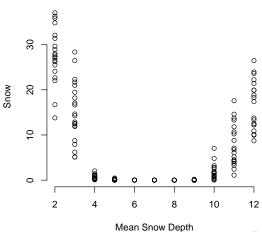
#### Show the Data



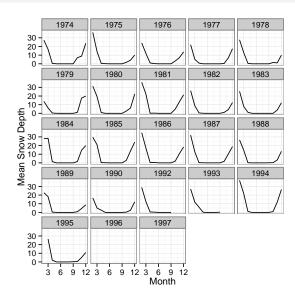
#### Minimize Distraction



#### Minimize Distraction

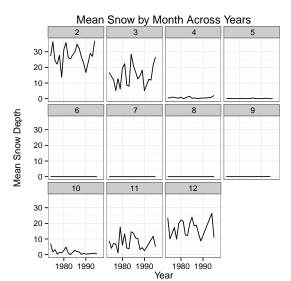


# Make Big Data Coherent



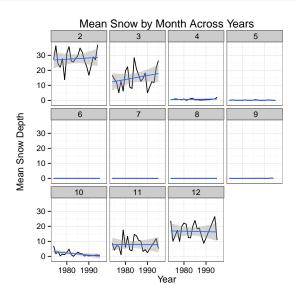


#### Reveal Several Levels of Detail





## Be Closely Integrated with Statistics

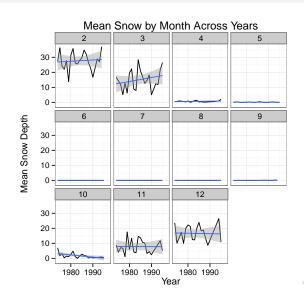




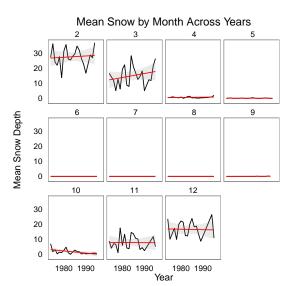
#### The Data:Ink Ratio

- 1. Above all else show data.
- 2. Maximize the data-ink ratio.
- 3. Erase non-data-ink.
- 4. Erase redundant data-ink.
- 5. Revise and edit

# Minimizing Ink

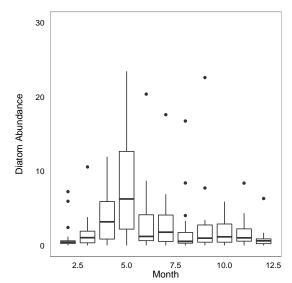


# Minimizing Ink



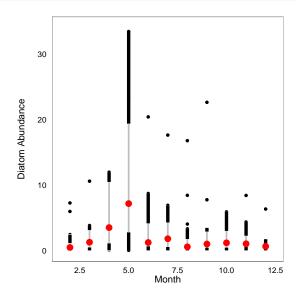


#### Extra Ink in Boxes & Lines



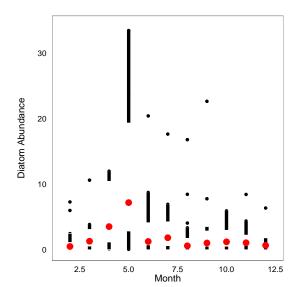


# A Cleaner Boxplot





# Pure Tufte Boxplots

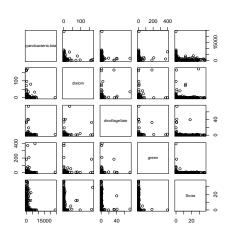




# Basic Plotting in R

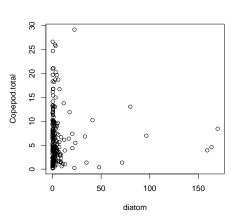
# Visualizing a Lot of the Data

pairs(plankton[, 14:18])



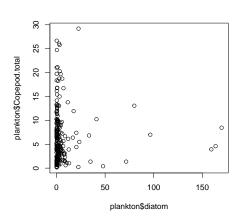
#### A Basic Bivariate Plot

plot(Copepod.total ~
 diatom, data = plankton)



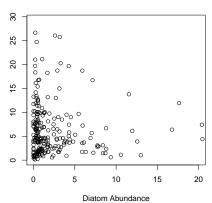
#### A Basic Bivariate Plot

plot(plankton\$diatom,
 plankton\$Copepod.total)



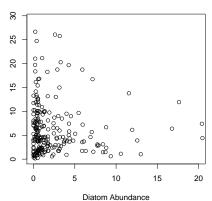
# Adding Axis Labels

```
plot(Copepod.total ~ diatom, data = plankton, xlab = "Diatom Abundance", & ded ylab = "Copepod Abundnace", & xlim = c(0, 20))
```



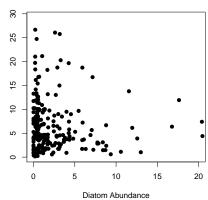
# Adding Axis Limits

```
plot(Copepod.total ~ diatom, data = plankton, xlab = "Diatom Abundance", & ded ylab = "Copepod Abundnace", & xlim = c(0, 20))
```

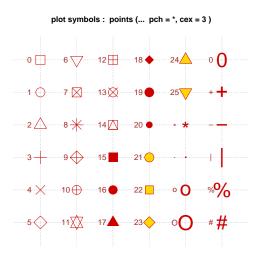


## More Point Shapes

```
plot(Copepod.total ~
    diatom, data = plankton,
    xlab = "Diatom Abundance",
    ylab = "Copepod Abundnace",
    xlim = c(0, 20),
    pch = 19)
```



#### More Point Shapes



#### cex for Size

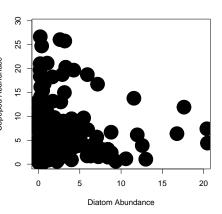
```
plot(Copepod.total ~

diatom, data = plankton,

xlab = "Diatom Abundance", pure ylab = "Copepod Abundance", ylab = "Copepod Abundance", pure ylab = c(0, 20),

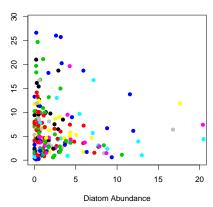
pch = 19, cex = 4)
```

See also cex.axis, cex.lab, and more.



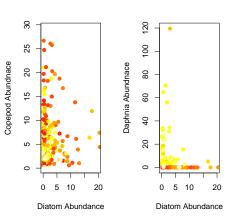
#### Add a Little Color

```
plot(Copepod.total ~ diatom, data = plankton, xlab = "Diatom Abundance", post ylab = "Copepod Abundance" xlim = c(0, 20), pch = 19, col = Month)
```



#### Panels with Par and Mfrow

par(mfrow = c(1, 2))



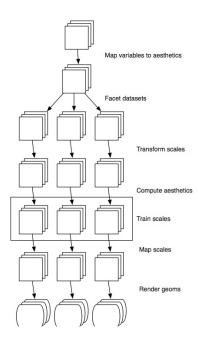
#### Lots of Other Functions that For Plots

?matplot
?lines
?axis
?title
?legend
?points
?segments

So....Explore! Plot with the data, try different par settings, or use some of these functions!

# ggplot2

or how I learned to stop worring and love http://had.co.nz/ggplot2 & http://stackoverflow.com/

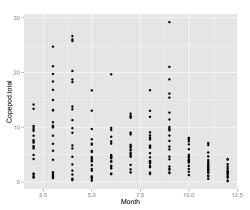


## Start with nothing...

There is no layout specified here for the data.

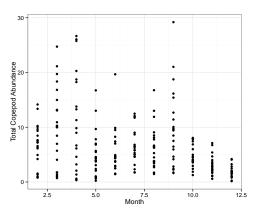
# Add a Layer

```
p <- p + geom_point()
p</pre>
```

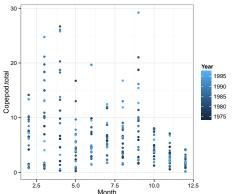


#### Format with Theme

```
p <- p + ylab("Total Copepod Abundance") + theme_bw()
p</pre>
```



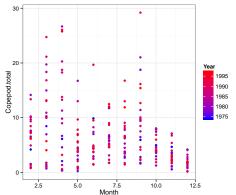
## Map a Variable to Color





#### Set Your Own Scale

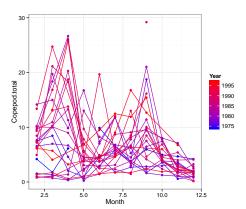
```
p2 <- p2 + scale_color_gradient(low = "blue", high = "red")
p2</pre>
```





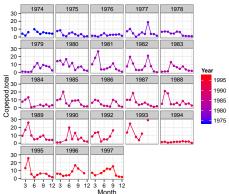
# And Maybe Add Another Layer

```
p2 <- p2 + geom_line(aes(group = Year))
p2</pre>
```



#### Facet for Easier Visualization

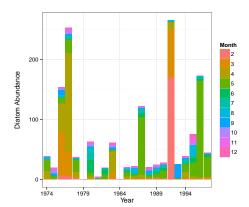
```
p2 <- p2 + facet_wrap(~Year) + scale_x_continuous(breaks = c(3,
      6, 9, 12))
p2</pre>
```





# This All Can Lead to Interesting Visualizations

```
qplot(factor(Year), diatom, geom = "bar", fill = factor(Month),
  data = plankton) + theme_bw() + xlab("Year") +
  ylab("Diatom Abundance\n") + scale_fill_discrete(name = "Month") +
  scale_x_discrete(breaks = seq(1974, 1997, 5))
```





## Lots of Layers to Add to ggplot2 Objects

```
?theme
?labs
?xlim
?facet_grid
?scale_x_log10
?geom_histogram
?geom_ribbon
?geom_linerange
?geom_freqpoly
```

So....Explore!
Also, see http://had.co.nz/ggplot2 for some examples