A grammar of graphics: past, *present*, and future

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Past

"If any number of magnitudes are each the same multiple of the same number of other magnitudes, then the sum is that multiple of the sum."

Euclid, ~300 BC

"If any number of magnitudes are each the same multiple of the same number of other magnitudes, then the sum is that multiple of the sum."

Euclid, ~300 BC

$$m(\Sigma x) = \Sigma(mx)$$

The grammar of graphics

- An abstraction which makes thinking, reasoning and communicating graphics easier
- Developed by Leland Wilkinson, particularly in “The Grammar of Graphics” 1999/2005
- One of the cornerstones of my research (I’ll talk about the others later)

Present

ggplot

- High-level package for creating statistical graphics.
  A rich set of components + user friendly wrappers
- Inspired by "The Grammar of Graphics"
  Leland Wilkinson 1999
- John Chambers award in 2006

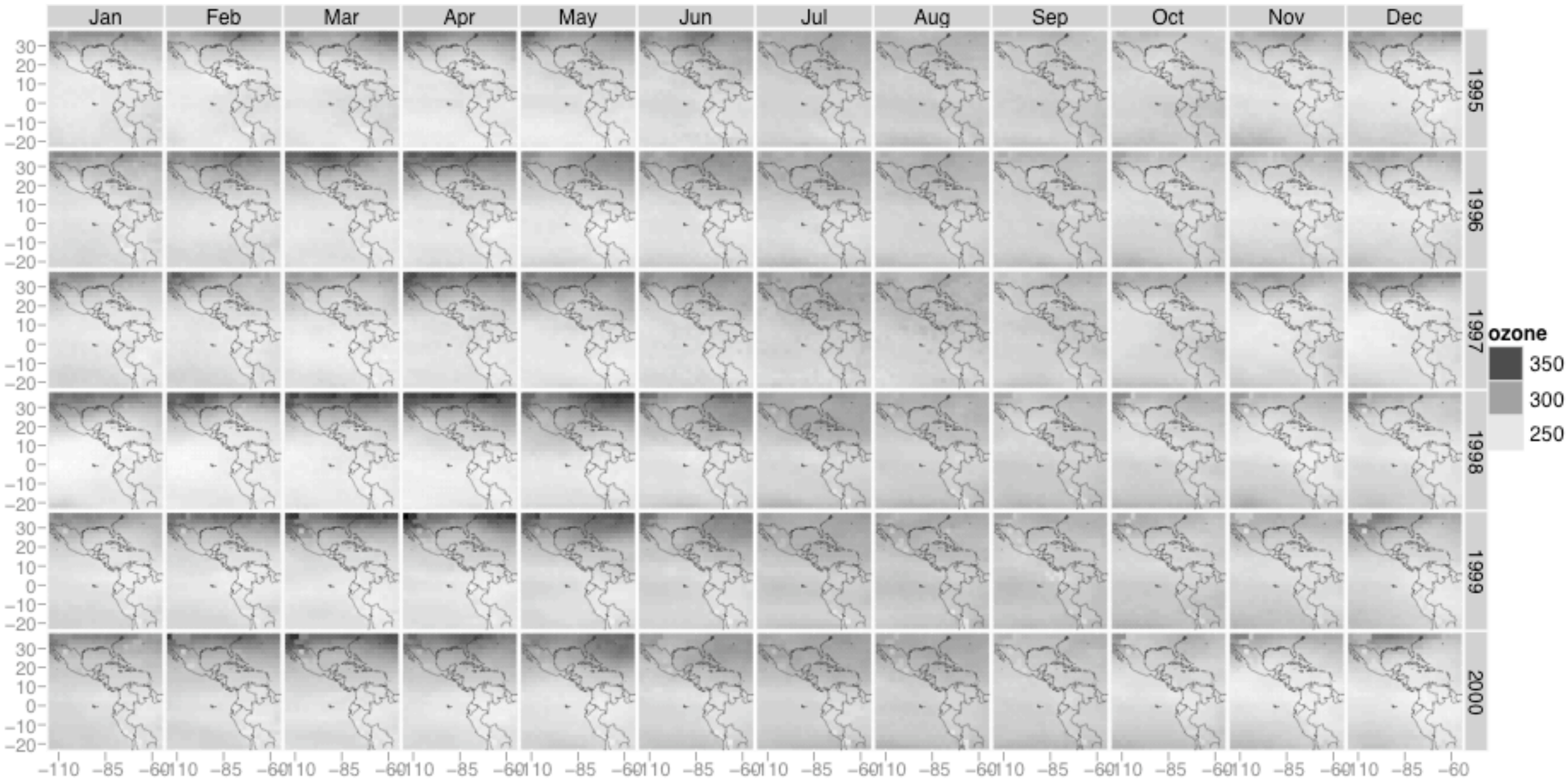
- Philosophy of ggplot
- Examples from a recent paper
- New methods facilitated by ggplot

Philosophy

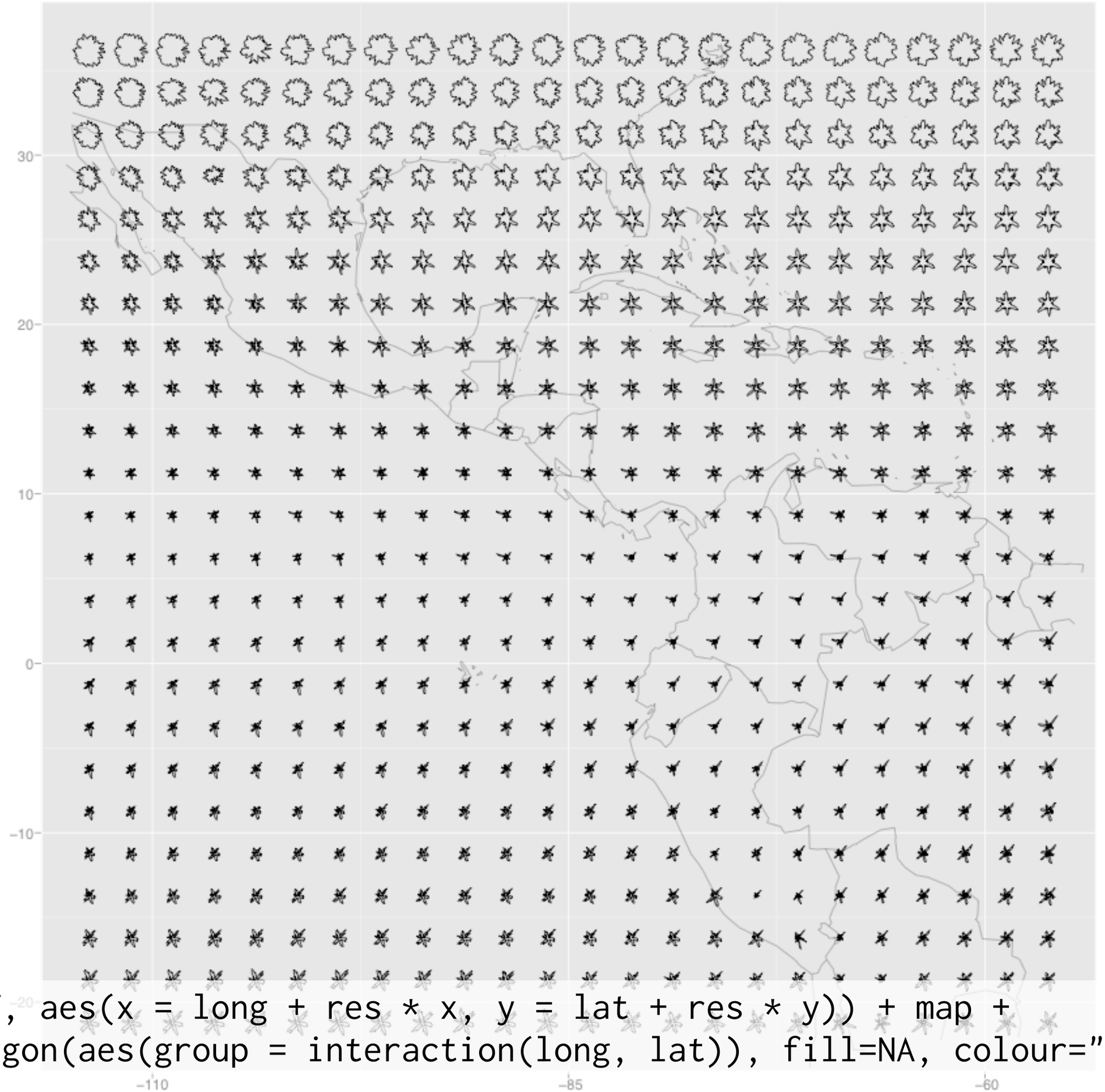
- Make graphics easier
- Use the grammar to facilitate research into new types of display
- Continuum of expertise:
  - start simple by using the results of the theory
  - grow in power by understanding the theory
  - begin to contribute new components
- Orthogonal components and minimal special cases should make learning easy(er?)

Examples

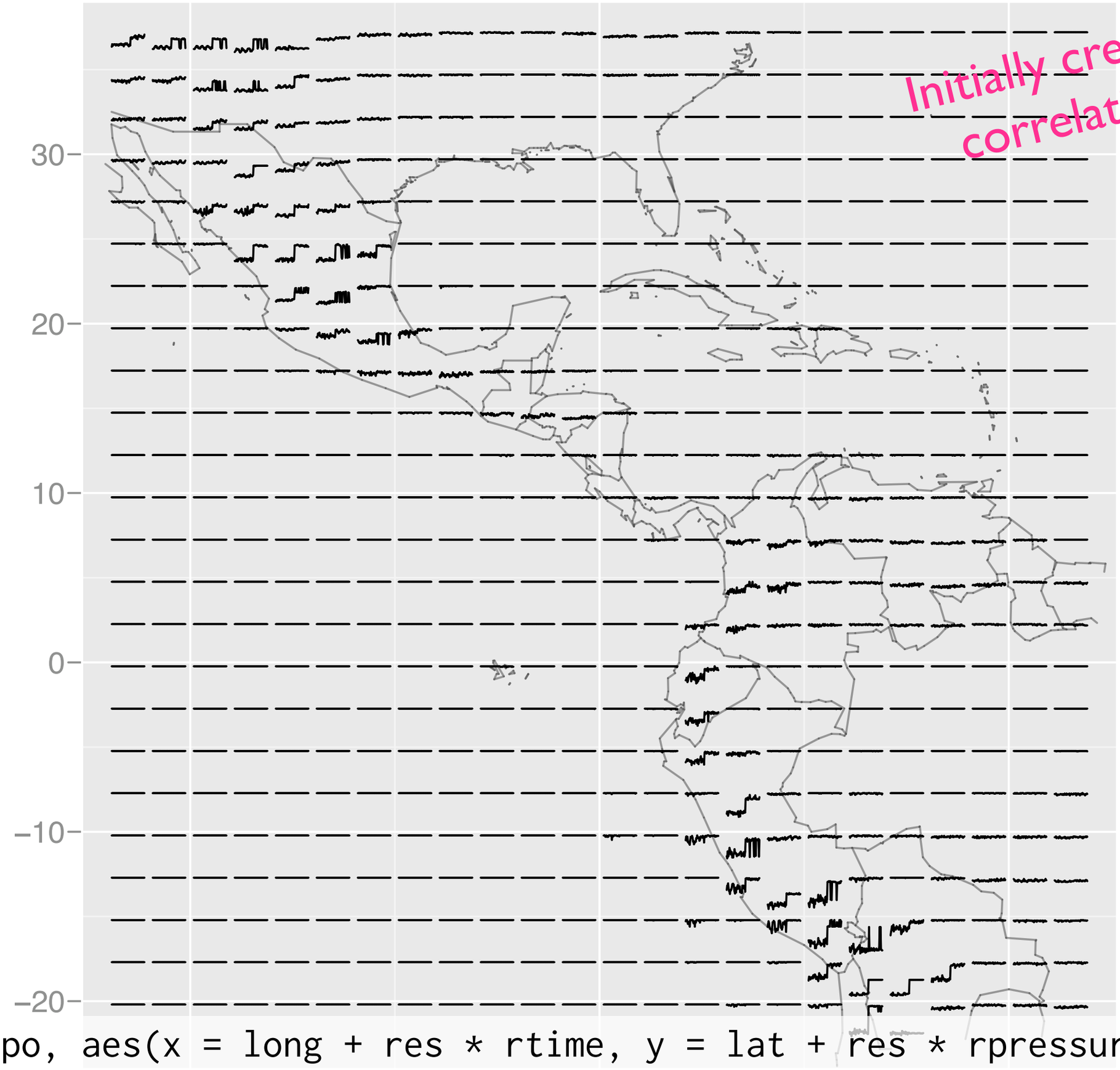
- J. Hobbs, H. Wickham, H. Hofmann, and D. Cook. **Glaciers melt as mountains warm: A graphical case study.** Computational Statistics. Special issue for ASA Statistical Computing and Graphics Data Expo 2006.
- Exploratory graphics created with GGobi, Mondrian, Manet, Gauguin and R, but needed consistent high-quality graphics that work in black and white for publication
- So... used ggplot to recreate the graphics




```
qplot(long, lat, data = expo, geom="tile", fill = ozone,
  facets = year ~ month) +
scale_fill_gradient(low="white", high="black") + map
```



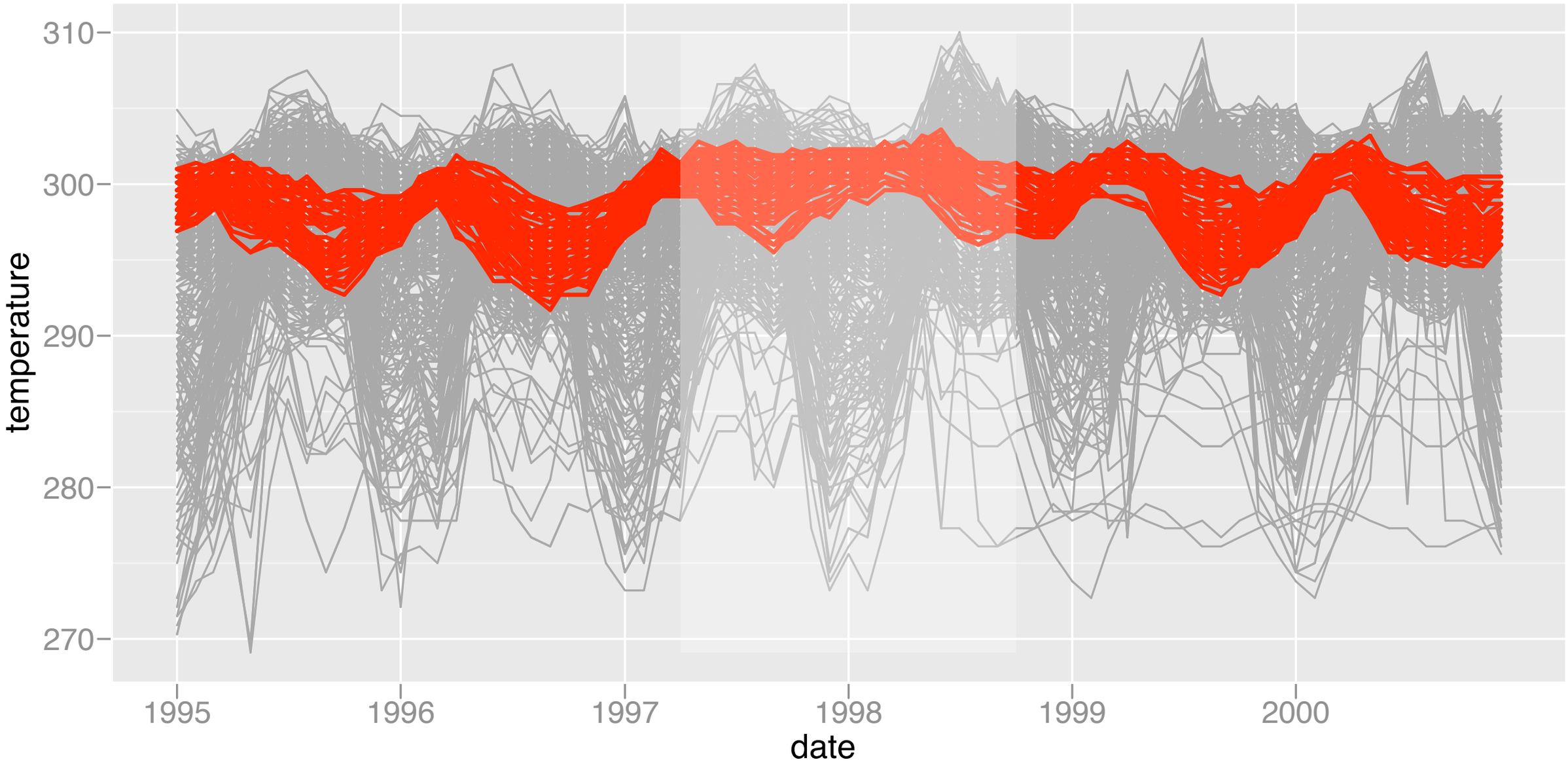

```
ggplot(df, aes(x = long + res * x, y = lat + res * y)) + map +
geom_polygon(aes(group = interaction(long, lat)), fill=NA, colour="black")
```




```
ggplot(rexpo, aes(x = long + res * rtime, y = lat + res * rpressure))
+ map + geom_line(aes(group = id))
```

```
library(maps)
outlines <- as.data.frame(map("world",xlim=-c(113.8, 56.2),ylim=c(-21.2, 36.2)))

map <- c(
  geom_path(aes(x = x, y = y), data = outlines, colour = alpha("grey20", 0.2)),
  scale_x_continuous("", limits = c(-113.8, -56.2), breaks = c(-110, -85, -60)),
  scale_y_continuous("", limits = c(-21.2, 36.2))
)
```




```
qplot(date, temperature, data=clustered, group=id, geom="line")
+ pacific + elnino(clustered$temperature)
```

```
pacific <- brush(cluster %in% c(5,6))

brush <- function(condition, background = "grey60", brush = "red") {
  cond_string <- deparse(substitute(condition), width=500)
  colour <- paste(
    "ifelse(", cond_string, ", '", brush, "', '", background, "')", sep=""
  )
  order <- paste(
    "ifelse(", cond_string, ", 2, 1)", sep=""
  )
  size <- paste(
    "ifelse(", cond_string, ", 2, 1)", sep=""
  )
  list(
    aes_string(colour = colour, order = order, size=size),
    scale_colour_identity(),
    scale_size_identity()
  )
}
```

temperature
surftemp
ozone
cloudlow
cloudmid
cloudhigh
1
2
3
4
5
30
20
10
0
−10
−20

temperature
surftemp
ozone
cloudlow
cloudmid
cloudhigh
1
2
3
4
5
30
20
10
0
−10
−20
ggplot(clustered, aes(x = long, y = lat))
+ geom_tile(aes(width = 2.5, height = 2.5,
fill = factor(cluster)))
+ facet_grid(cluster ~ .)
+ map
+ scale_fill_brewer(palette="Spectral")
qplot(date, value, data = clusterm, group = id,
geom = "line", facets = cluster ~ variable,
colour = factor(cluster))
+ scale_y_continuous("", breaks=NA)
+ scale_colour_brewer(palette="Spectral")

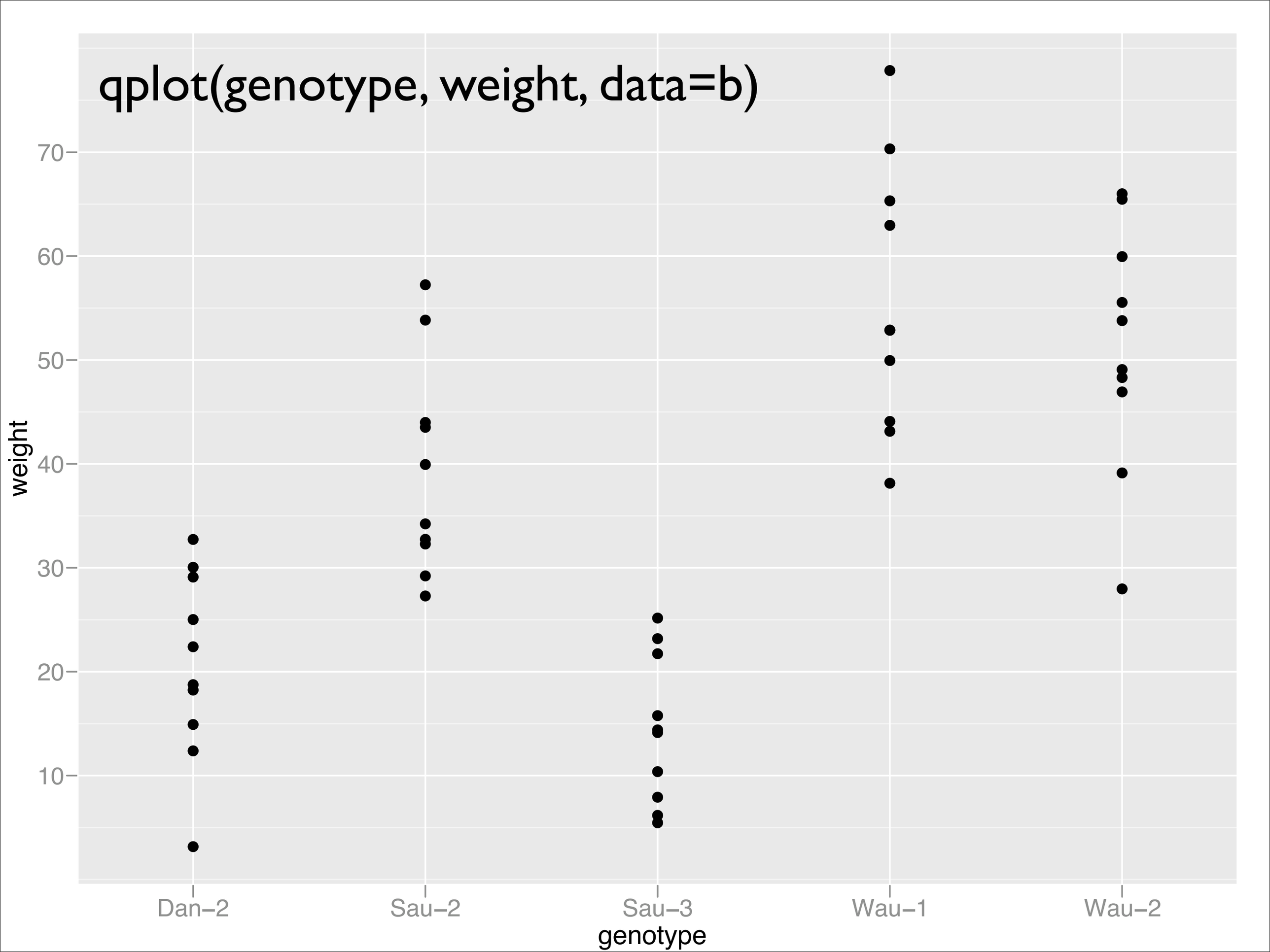
New methods

- Supplemental statistical summaries
- Iterating between graphics and models
- Tables of plots

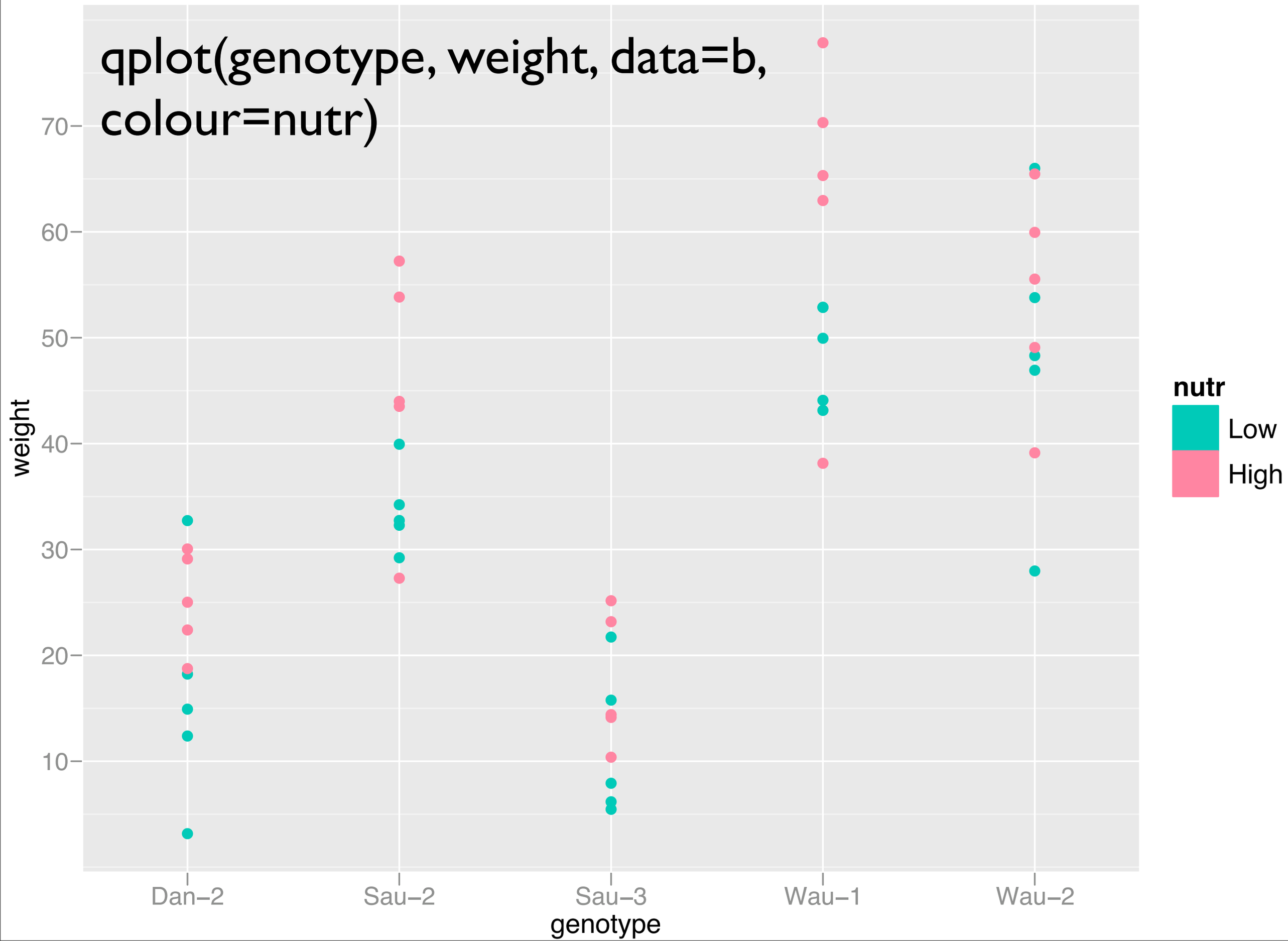
- Inspired by ideas of Tukey (and others)
- Exploratory graphics, not as pretty

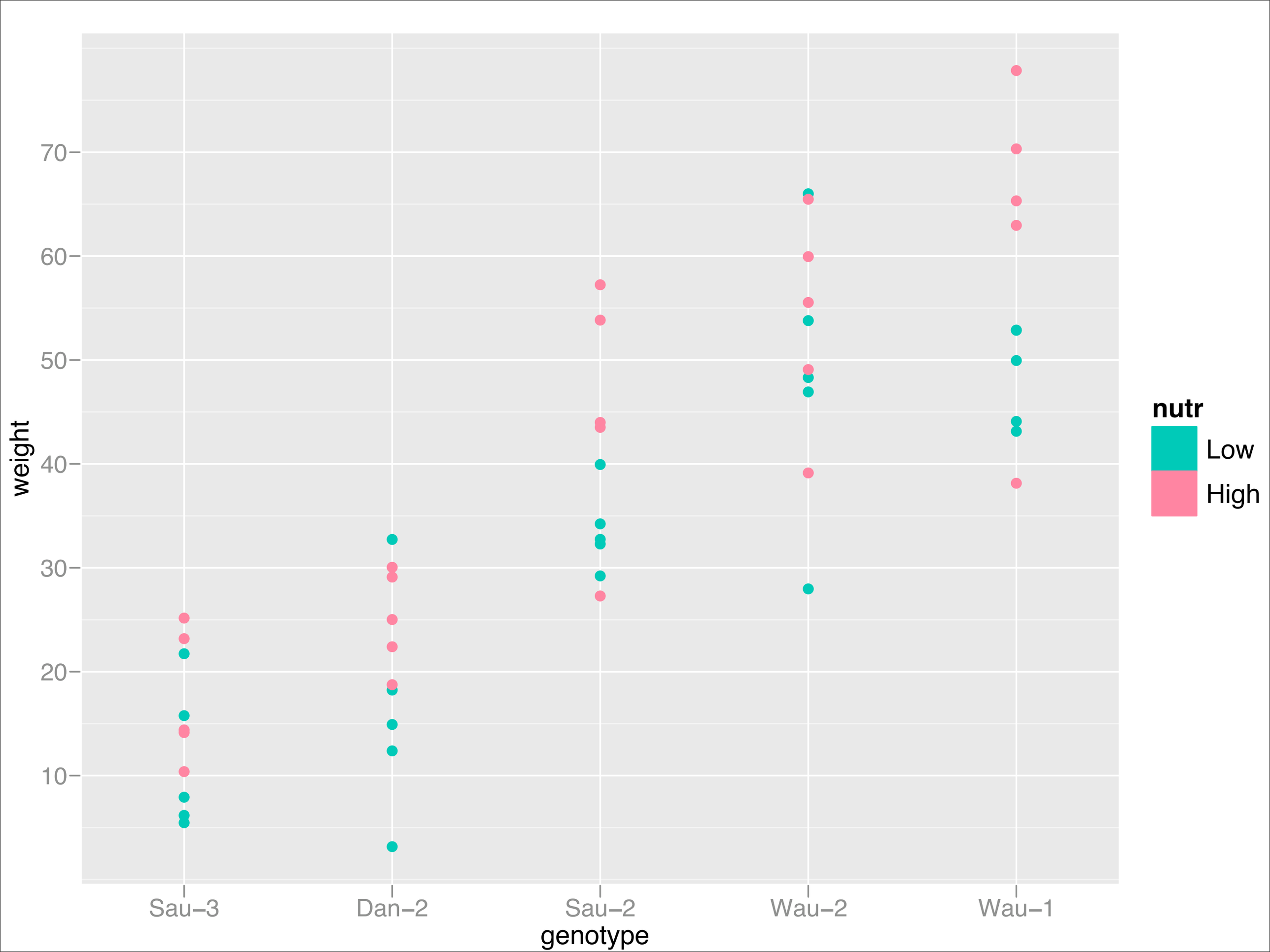
Intro to data

- Response of trees to gypsy moth attack
- 5 genotypes of tree: Dan-2, Sau-2, Sau-3, Wau-1, Wau-2
- 2 treatments: NGM / GM
- 2 nutrient levels: low / high
- 5 reps
- Measured: weight, N, tannin, salicylates


qplot(genotype, weight, data=b)
weight
70
60
50
40
30
20
10
Dan–2
Sau–2
Sau–3
Wau–1
Wau–2
genotype

qplot(genotype, weight, data=b, colour=nutr)




weight
70
60
50
40
30
20
10
Sau–3
Dan–2
Sau–2
Wau–2
Wau–1
genotype
nutr
Low
High

Comparing means

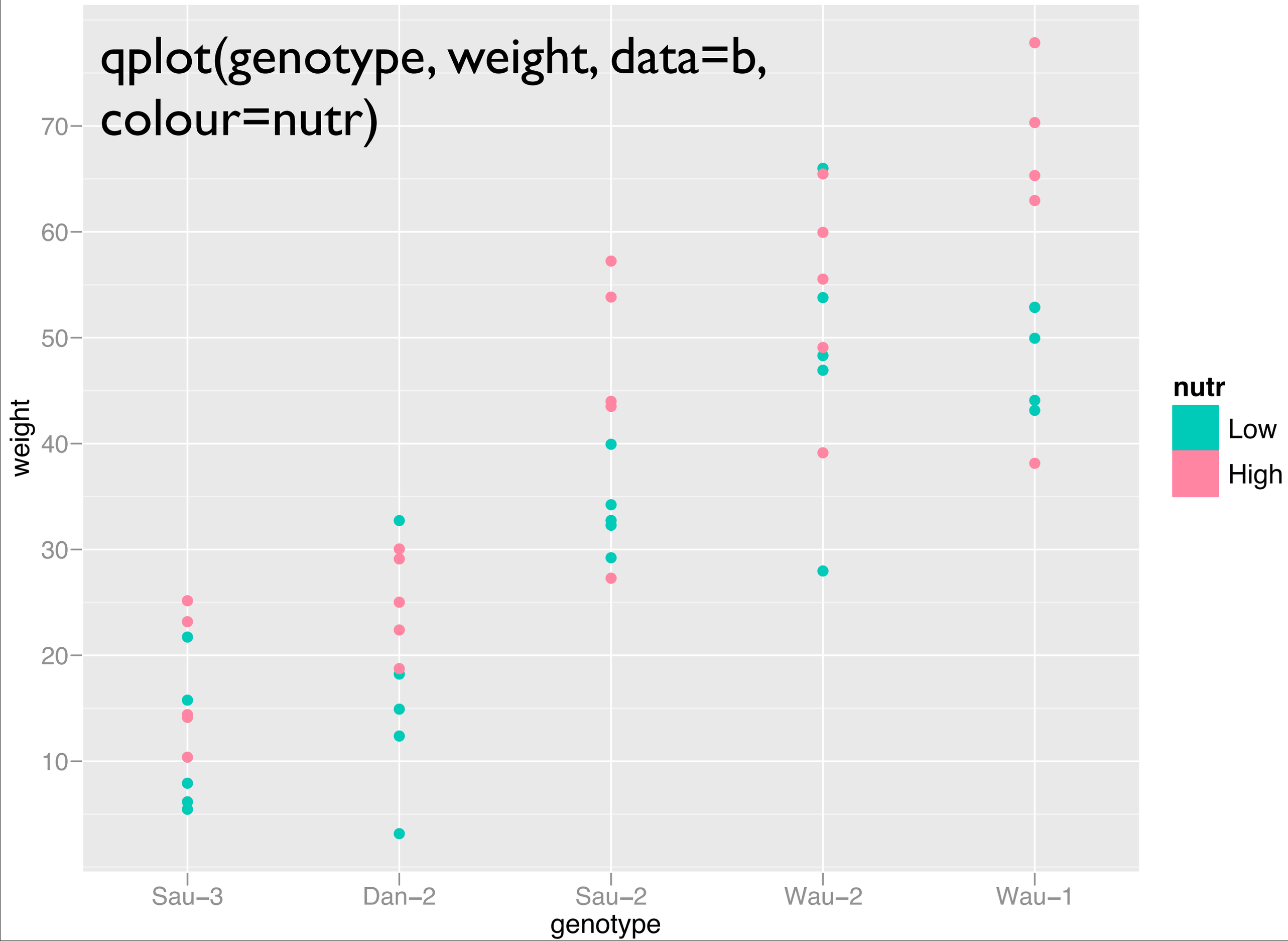
- For inference, interested in comparing the means of the groups
- But hard to do visually - eyes naturally compare ranges
- What can we do? - Visual ANOVA

Supplemental summaries

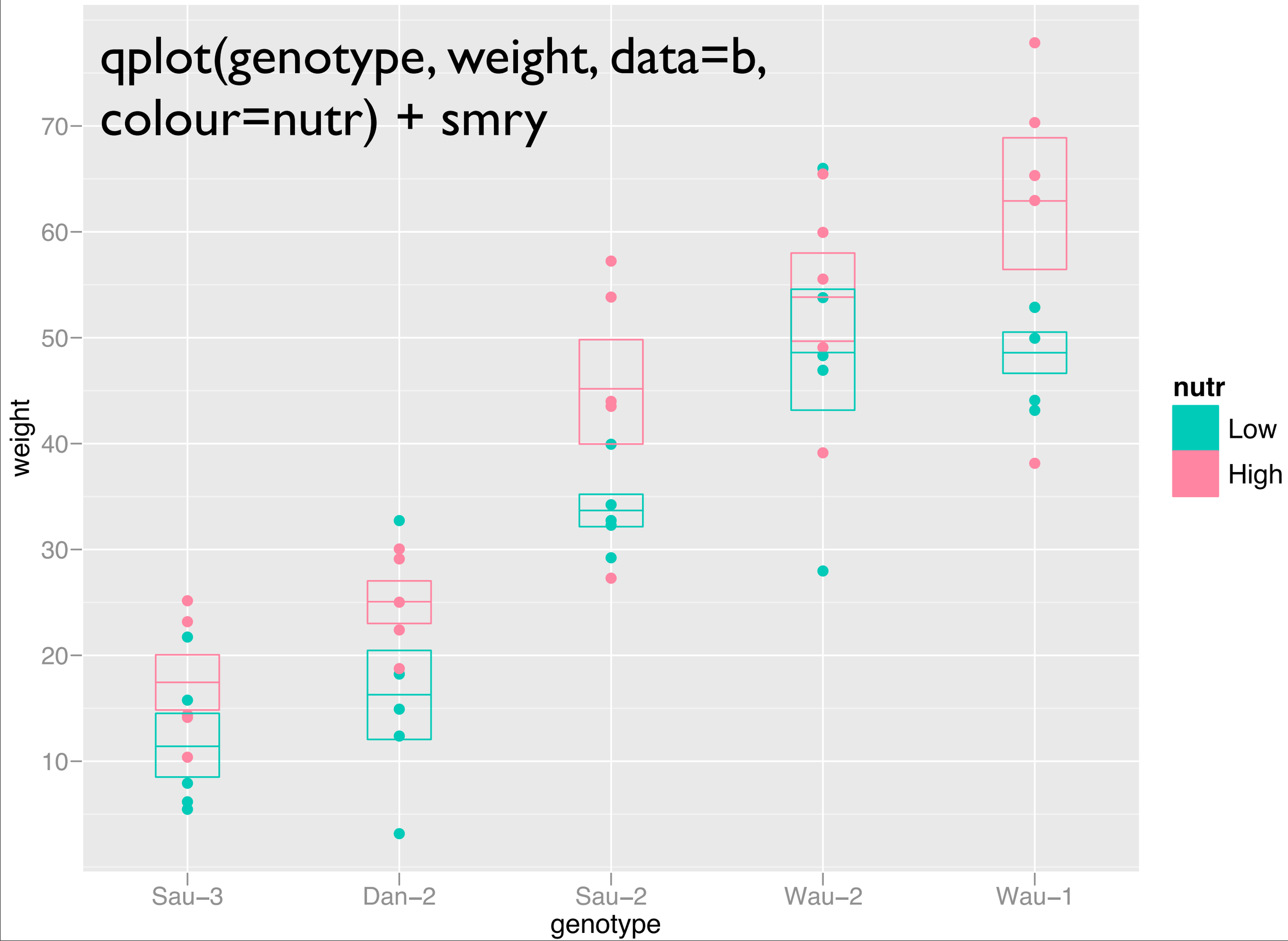
From Hmisc

- ```
  smry <- stat_summary(
    fun="mean_cl_boot", conf.int=0.68,
    geom="crossbar", width=0.3
  )
  ```
- Adds another layer with summary statistics: mean + bootstrap estimate of standard error
- Motivation: still exploratory, so minimise distributional assumptions, will model explicitly later
  ```

qplot(genotype, weight, data=b, colour=nutr)



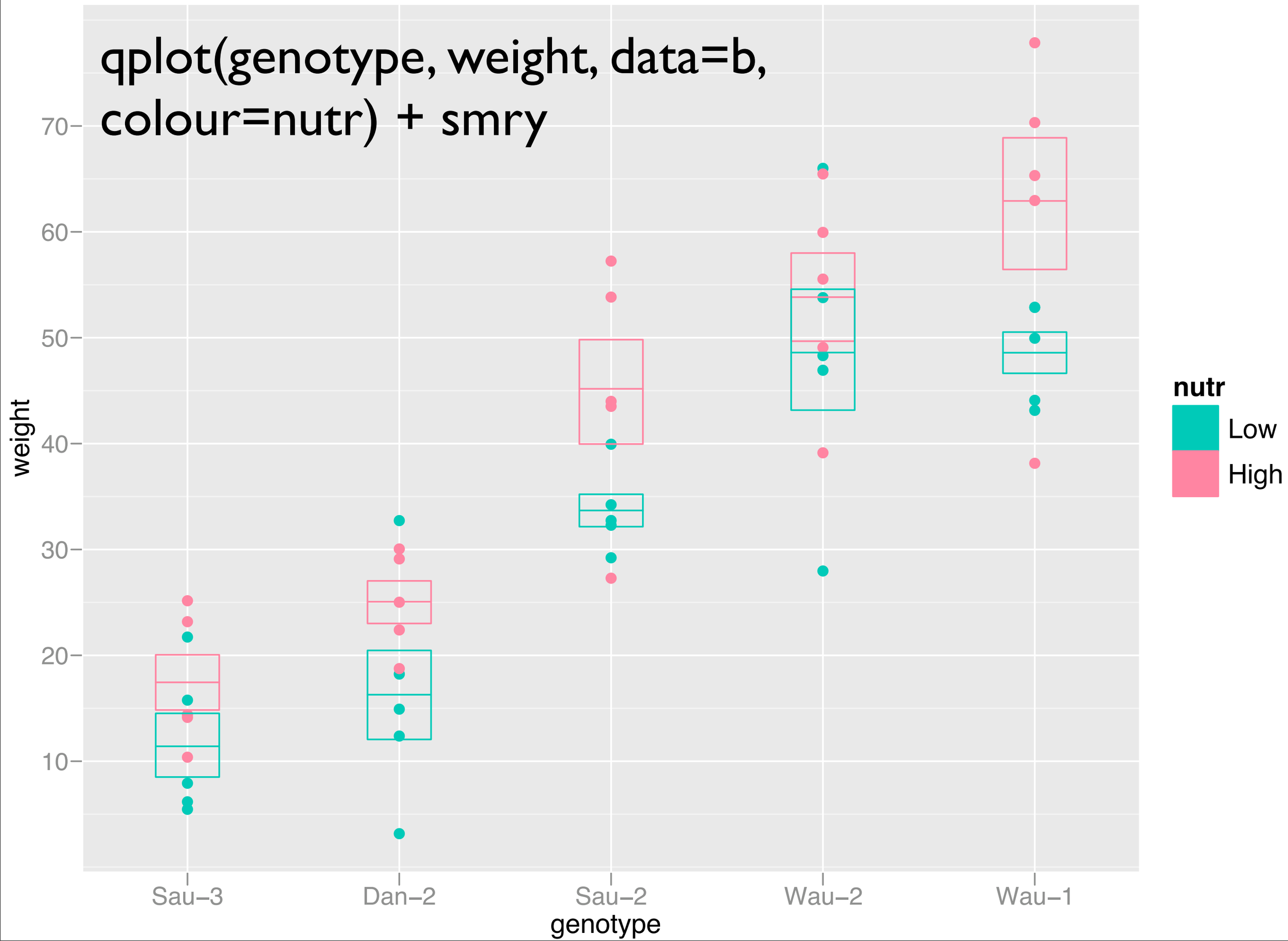
qplot(genotype, weight, data=b, colour=nutr) + smry



Iterating graphics and modelling

- Clearly strong genotype effect. Is there a nutr effect? Is there a nutr-genotype interaction?
- Hard to see from this plot - what if we remove the genotype main effect? What if we remove the nutr main effect?
- How does this compare an ANOVA?

qplot(genotype, weight, data=b, colour=nutr) + smry




```
b$weight2 <- resid(lm(weight ~ genotype, data=b))
qplot(genotype, weight2, data=b, colour=nutr) + smry
```


```
b$weight3 <- resid(lm(weight ~ genotype + nutr, data=b))
qplot(genotype, weight3, data=b, colour=nutr) + smry
```

```
               Df Sum Sq Mean Sq F value  Pr(>F)
genotype        4  13331    3333   36.22 8.4e-13 ***
nutr            1   1053    1053   11.44  0.0016 **
genotype:nutr   4    144      36    0.39  0.8141
Residuals      40   3681      92
```

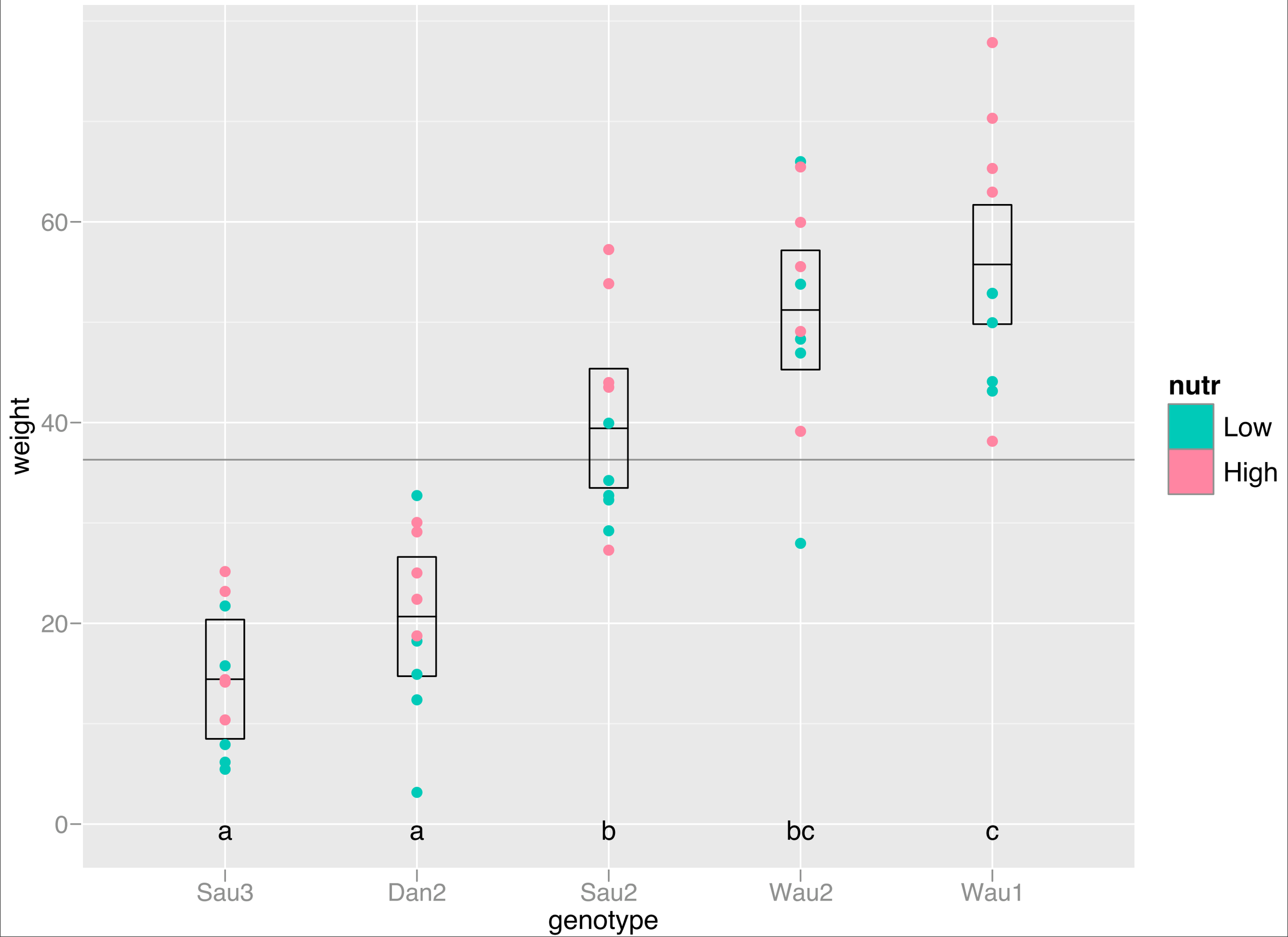
```
anova(lm(weight ~ genotype * nutr, data=b))
```

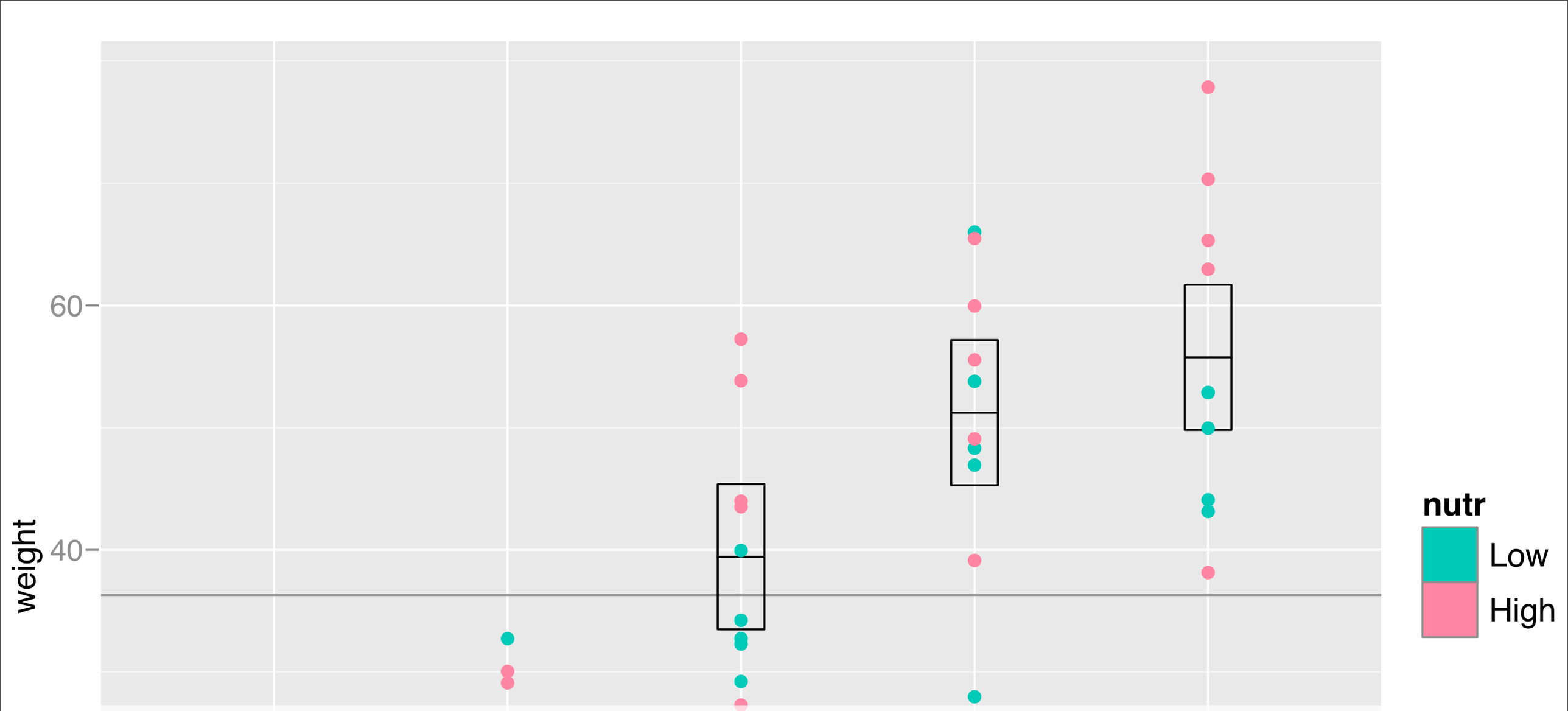
Graphics → Model

- In the previous example, we used graphics to iteratively build up a model - a la stepwise regression!
- But: here interested in gestalt, not accurate prediction, and must remember that this is just one possible model
- What about model → graphics?

Model ➔ Graphics

- If we model first, we need graphical tools to summarise model results, e.g. post-hoc comparison of levels
- We can do better than SAS! But it's hard work: effects, multComp and multCompView
- Rich research area


60
40
20
0
weight
a
a
b
bc
c
Sau3
Dan2
Sau2
Wau2
Wau1
genotype
nutr
Low
High




```
ggplot(b, aes(x=genotype, y=weight))
+ geom_hline(intercept = mean(b$weight))
+ geom_crossbar(aes(y=fit, min=lower,max=upper),
  data=geffect)
+ geom_point(aes(colour = nutr))
+ geom_text(aes(label = group), data=geffect)
```

Tables of plots

- Often interested in marginal, as well as conditional, relationships
- Or comparing one subset to the whole, rather than to other subsets
- Like in contingency table, we often want to see margins as well

Dan–2
Sau–2
Sau–3
Wau–1
Wau–2
High
Low
n
4.5
4.0
3.5
3.0
2.5
2.0
GM
NGM
trt
trt
NGM
GM

Dan–2
Sau–2
Sau–3
Wau–1
Wau–2
(all)
High
Low
(all)
n
4.5
4.0
3.5
3.0
2.5
2.0
GM
NGM
trt
trt
NGM
GM

Arranging plots

- Facilitate comparisons of interest
- Small differences need to be closer together (big differences can be far apart)
- Connections to model?

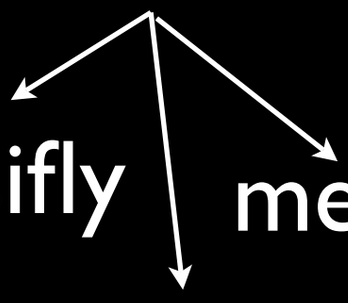
Summary

- Need to move beyond canned statistical graphics to experimenting with new graphical methods
- Strong links between graphics and models, how can we best use them?
- Static graphics often aren't enough

Future

GGobi

rggobi



classifly

meifly

clusterfly

faceoff

geozoo

ggplot2

reshape

fda

hints

localmds

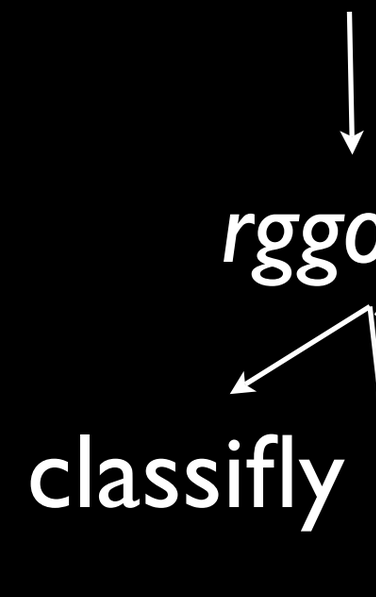
lvboxplot

scagnostics

DescribeDisplay

Bio- and bibliographic tools for statistics

GGobi



rggobi

classifly

meifly

clusterfly

faceoff

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ggplot2

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fda

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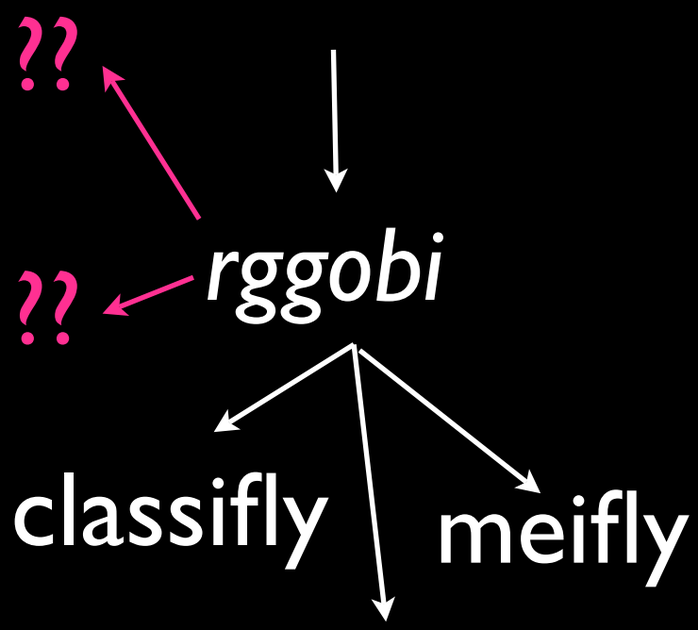
DescribeDisplay

New methods

Foundations of statistical graphics

Dissemination and outreach

GGobi



faceoff *geozoo*

ggplot2

A grammar of interactive graphics

A grammar of graphics for categorical data

reshape2

fda

hints

localmds

lvboxplot

scagnostics

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Questions?