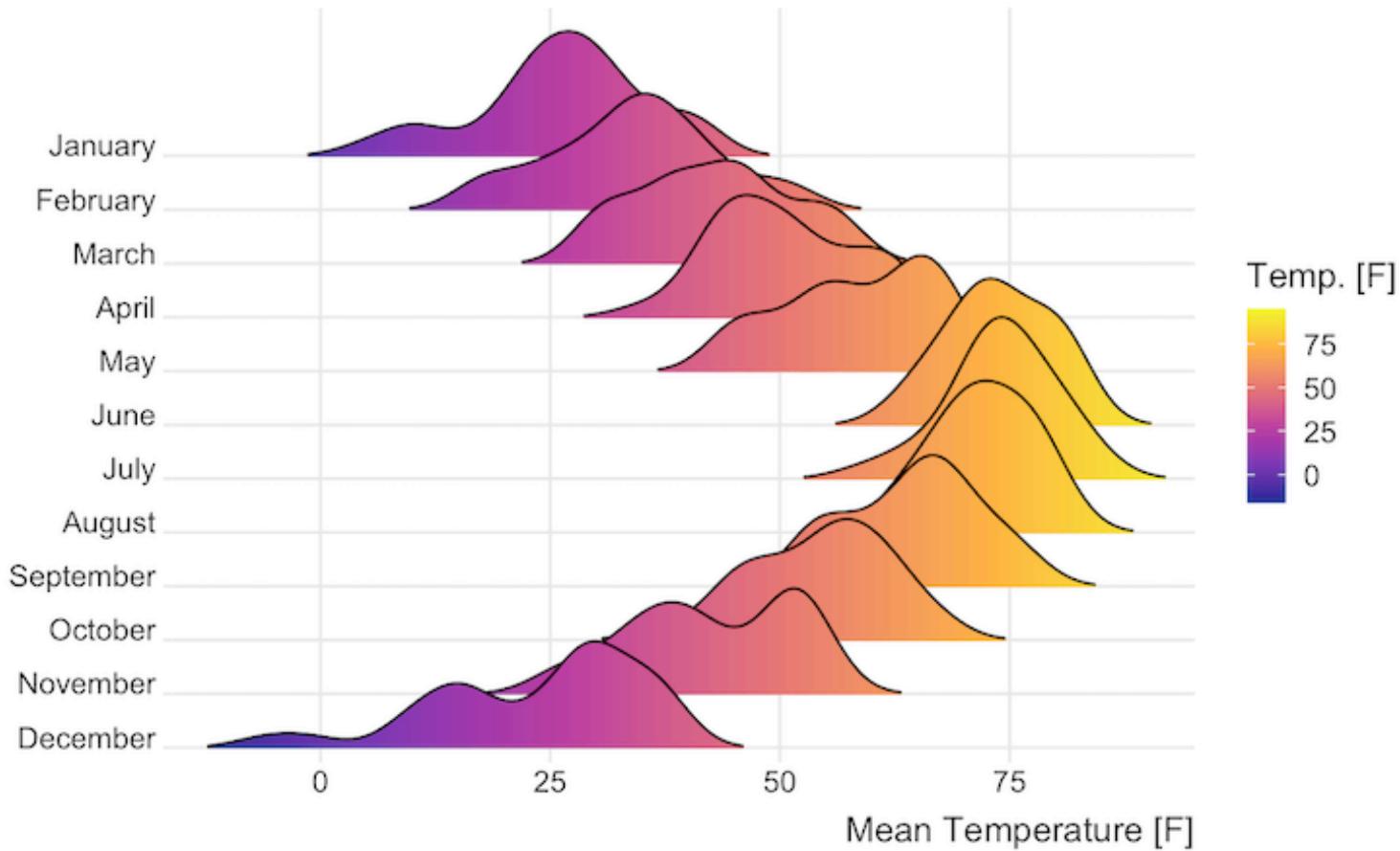


Temperatures in Lincoln NE



Graphics and Visualisation

W.Huber; some slides adapted from Laura Symul & Susan Holmes
Based on Chapter 3 of MSMB

Why?

- Explore data
- Communicate data patterns & preliminary insights with collaborators
- Display results and convince readers in a publication

Goals for this lecture

- Discuss principles of **good vs bad** data viz
- Review base R plotting
- Understand the **grammar of graphics** concept
- Look at its implementation in the `ggplot2` package
- Discuss plotting 1D, 2D, 3-5D data
- Glimpse at interactive (3D) visualization

Table 7 Vaccine Efficacy – First COVID-19 Occurrence After Dose 1 – Dose 1 All- Available Efficacy Population

Efficacy Endpoint Subgroup	Vaccine Group (as Randomized)					
	BNT162b2 (30 µg) (N=21669)		Placebo (N=21686)		VE (%)	(95% CI ^f)
	n ^b	Surveillance Time ^c (n ^d)	n ^b	Surveillance Time ^c (n ^d)		
First COVID-19 occurrence after Dose 1	50	4.015 (21314)	275	3.982 (21258)	82.0	(75.6, 86.9)
After Dose 1 to before Dose 2	39		82		52.4	(29.5, 68.4)
≥10 days after Dose 1 to before Dose 2	6		45		86.7	(68.6, 95.4)
Dose 2 to 7 days after Dose 2	2		21		90.5	(61.0, 98.9)
≥7 Days after Dose 2	9		172		94.8	(89.8, 97.6)

Abbreviations: VE = vaccine efficacy.
a. N = number of subjects in the specified group.
b. n1 = Number of subjects meeting the endpoint definition.
c. Total surveillance time in 1000 person-years for the given endpoint across all subjects within each group at risk for the endpoint. Time period for COVID-19 case accrual is from Dose 1 to the end of the surveillance period.
d. n2 = Number of subjects at risk for the endpoint.
e. Confidence interval (CI) for VE is derived based on the Clopper and Pearson method (adjusted for surveillance time for overall row).

A picture says more than a thousand words

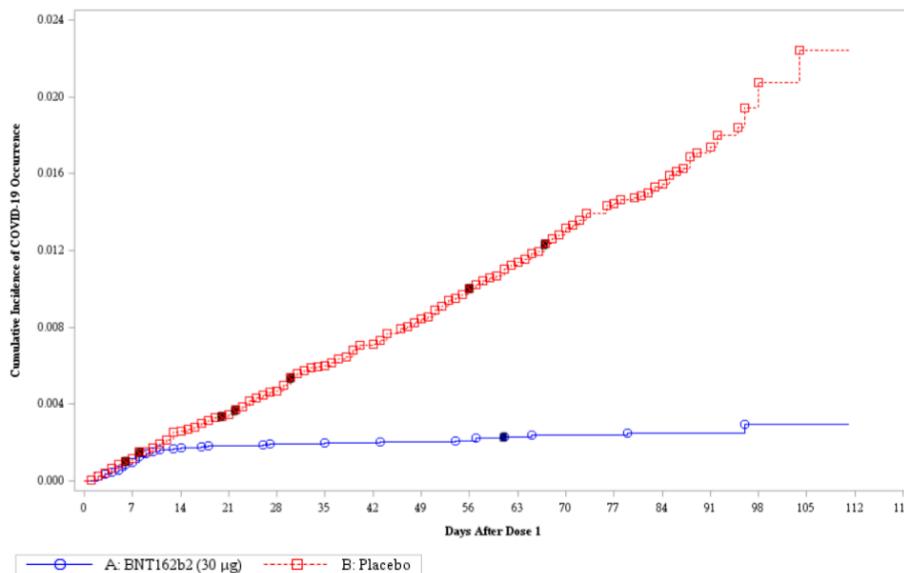
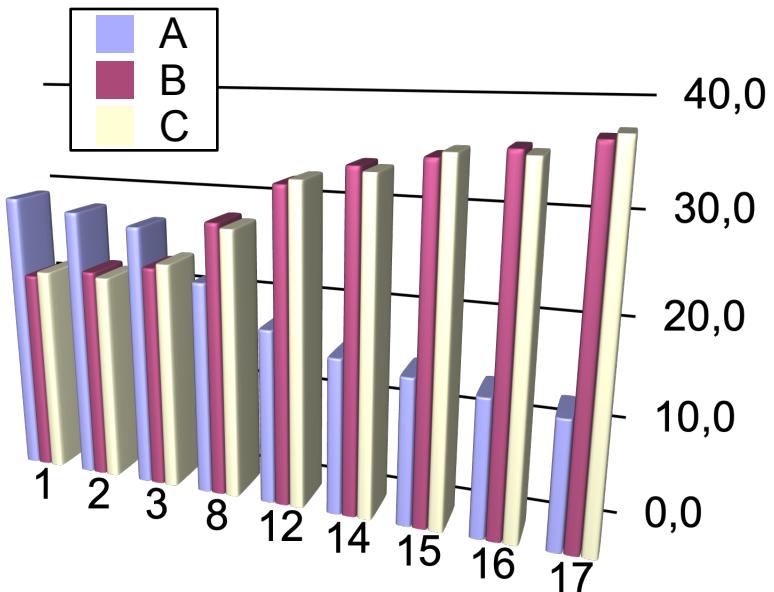
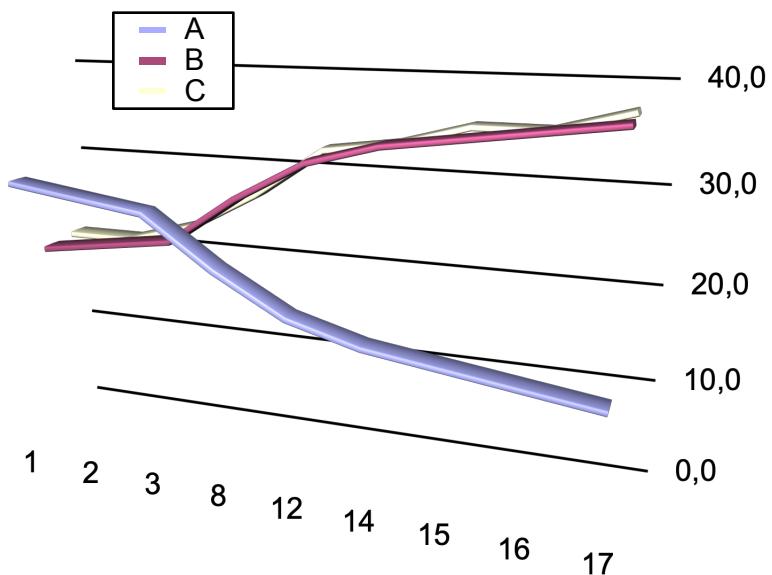
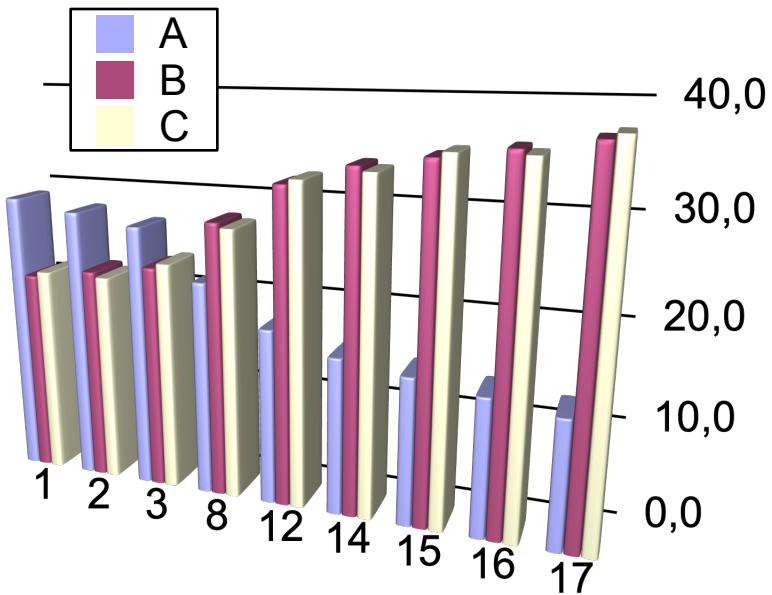


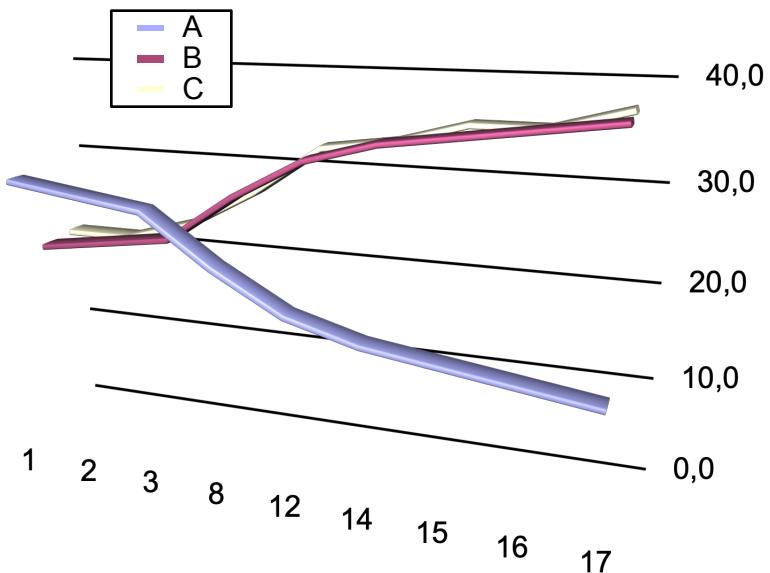
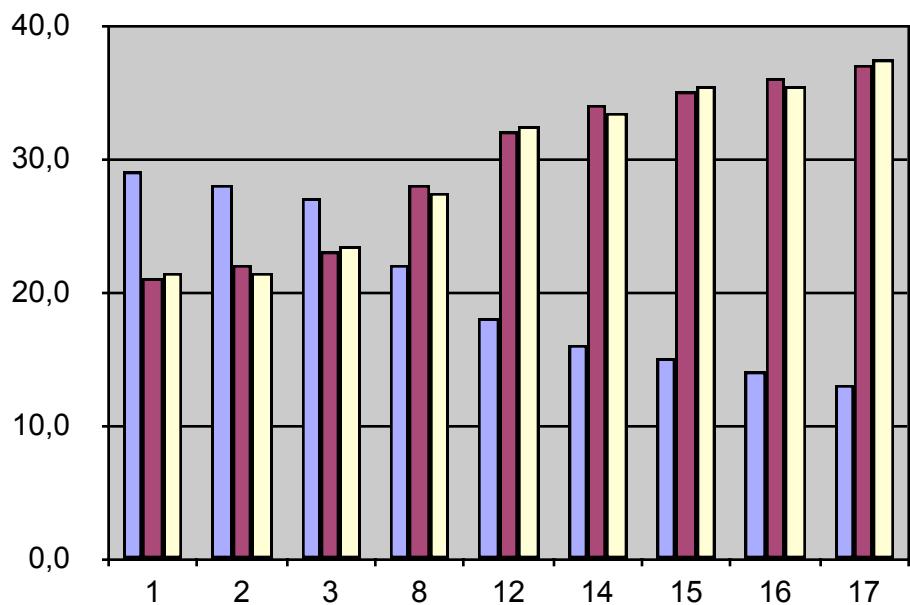
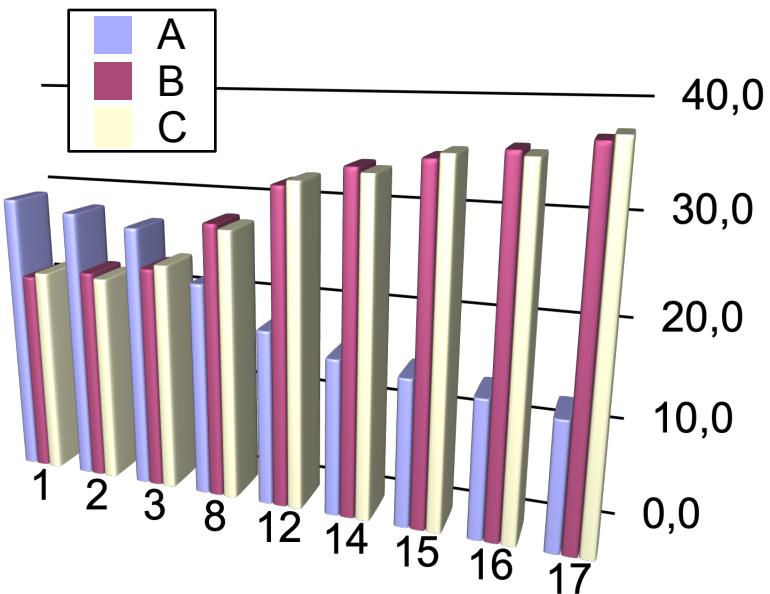
Figure 9. Cumulative Incidence Curves for the First COVID-19 Occurrence After Dose 1 – Dose 1 All-Available Efficacy Population

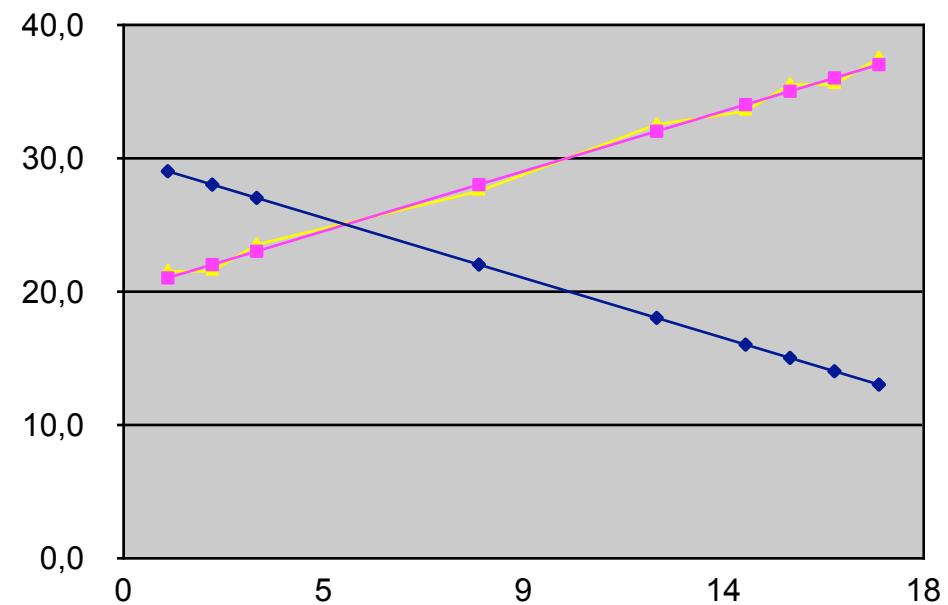
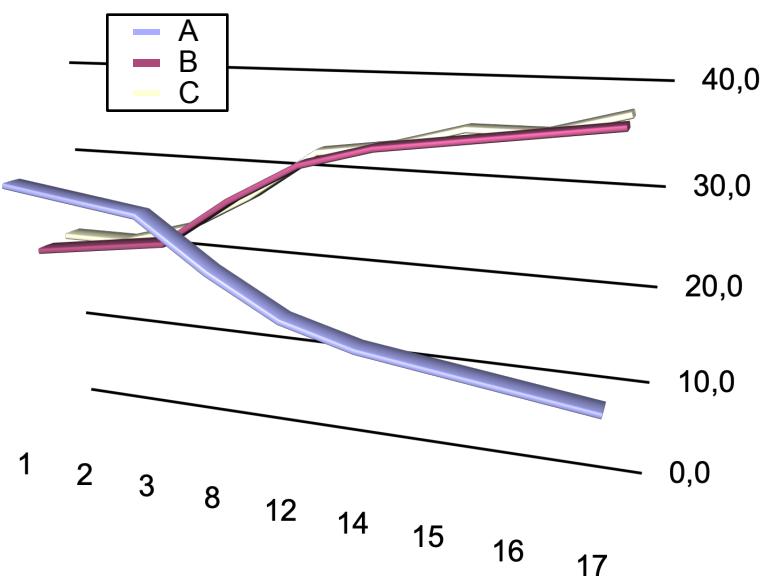
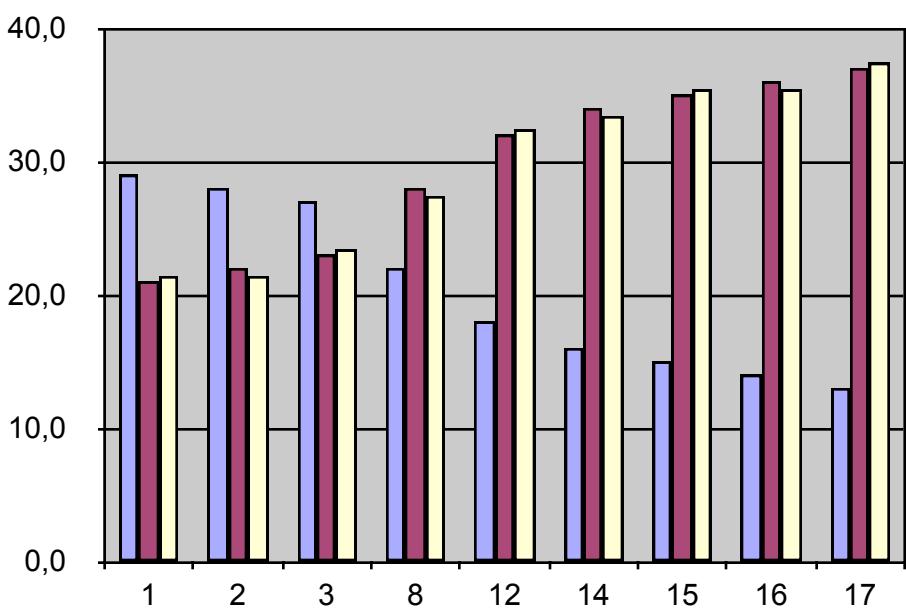
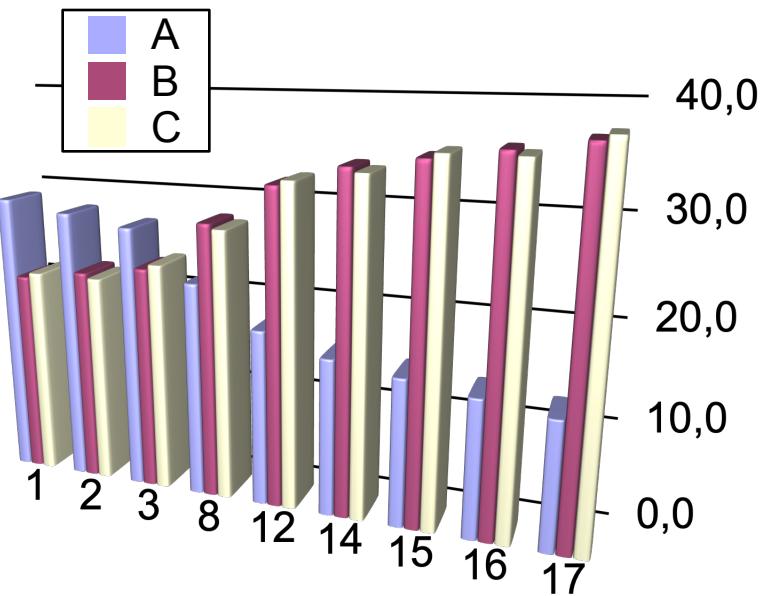
Source:
Assessment report
EMA/707383/2020
21 December 2020
Committee for Medicinal Products for Human Use (CHMP)

Comirnaty
Common name: COVID-19 mRNA vaccine (nucleoside-modified)
Procedure No.: EMEA/H/C/005735/0000
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base R plotting

canvas model:

a series of instructions that
sequentially fill the plotting
canvas

```
head(DNase)

##   Run   conc density
## 1  1 0.0488  0.017
## 2  1 0.0488  0.018
## 3  1 0.1953  0.121
## 4  1 0.1953  0.124
## 5  1 0.3906  0.206
## 6  1 0.3906  0.215
```

```
plot(DNase$conc, DNase$density)
```

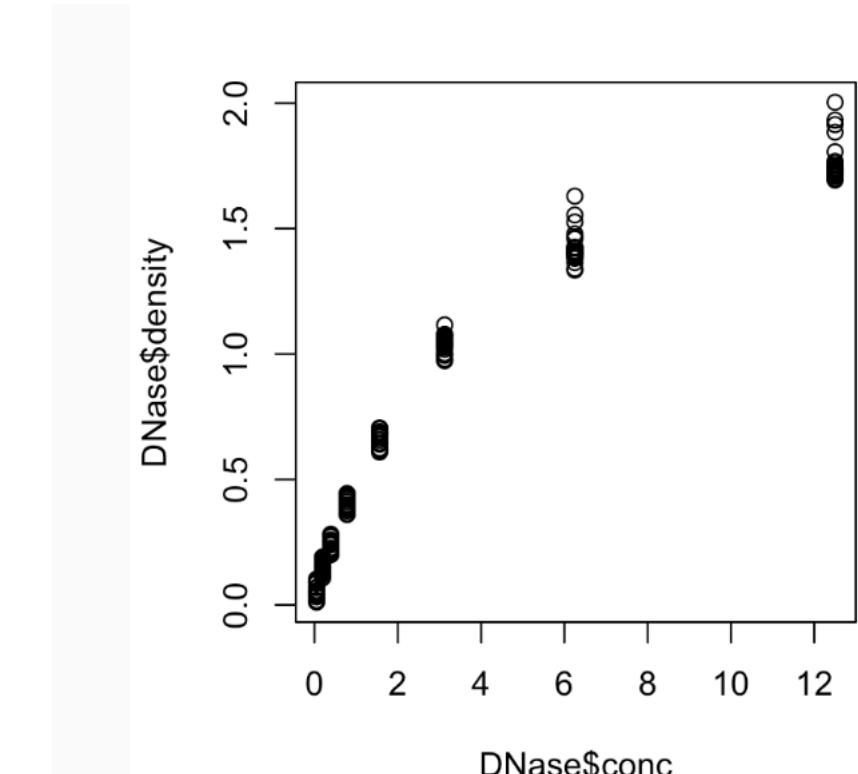


Figure 3.2: Plot of concentration vs. density for an ELISA assay of DNase.

base R plotting

canvas model:

a series of instructions that
sequentially fill the plotting
canvas

**Great for quick data
exploration!**

```
head(DNase)  
  
##   Run   conc density  
## 1  1 0.0488  0.017  
## 2  1 0.0488  0.018  
## 3  1 0.1953  0.121  
## 4  1 0.1953  0.124  
## 5  1 0.3906  0.206  
## 6  1 0.3906  0.215
```

```
plot(DNase$conc, DNase$density)
```

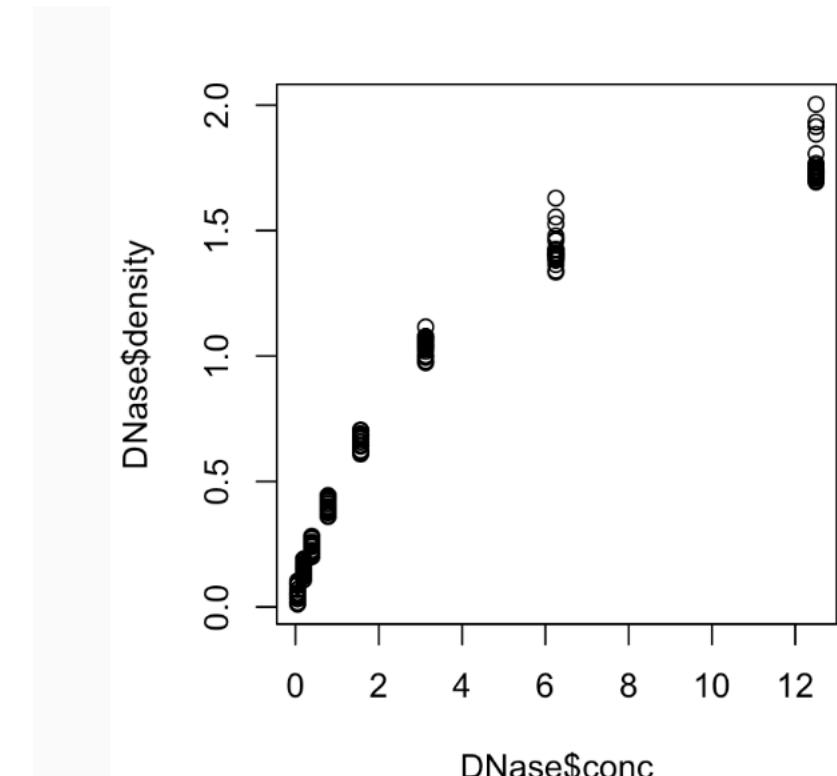


Figure 3.2: Plot of concentration vs. density for an ELISA assay of DNase.

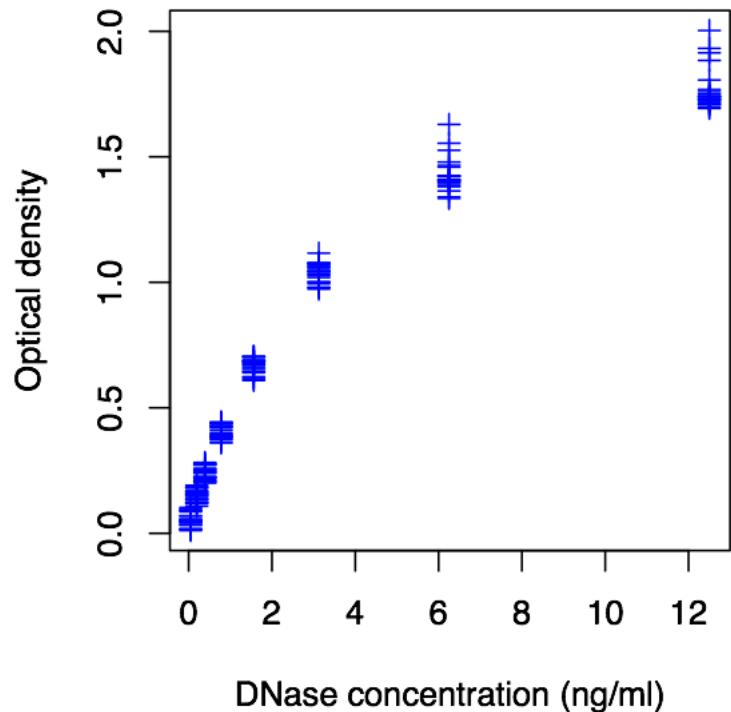
base R plotting

canvas model:

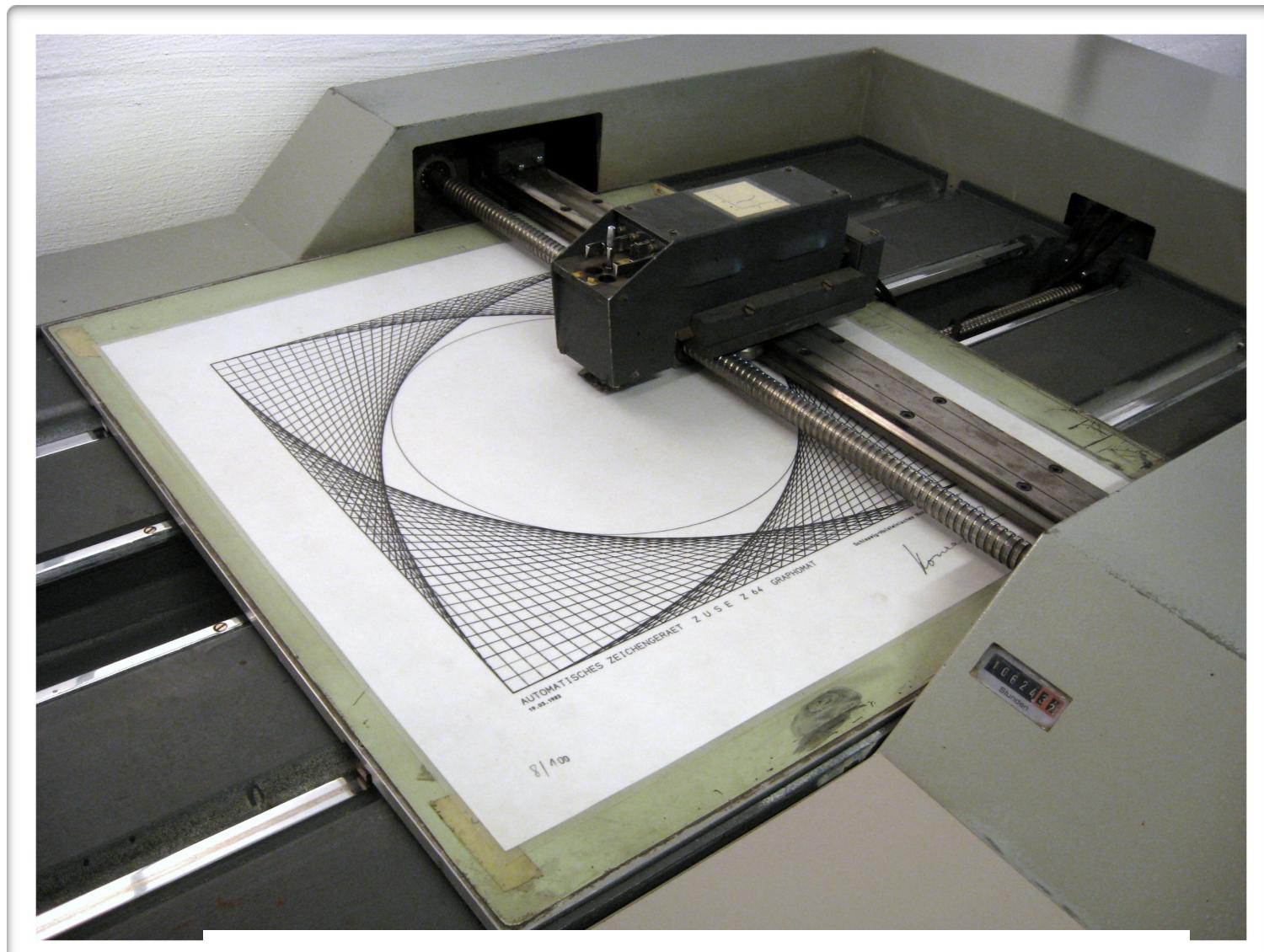
a series of instructions that
sequentially fill the plotting
canvas

**Inefficient for customization
and generating complex plots.**

```
plot(DNase$conc, DNase$density,  
ylab = attr(DNase, "labels")$y,  
xlab = paste(attr(DNase, "labels")$x, attr(DNase, "units")$x),  
pch = 3, col = "blue")
```



base R plotting



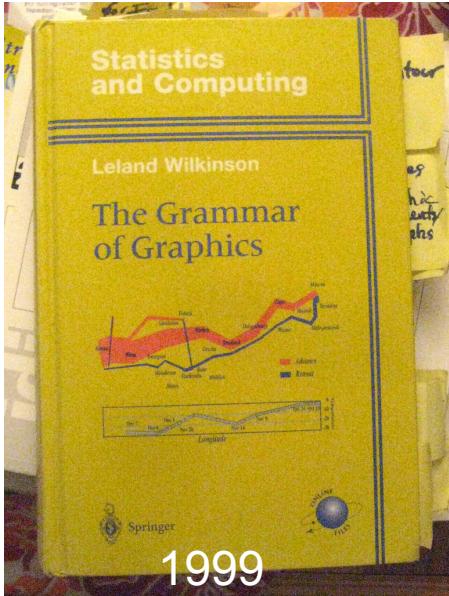
ZUSE Plotter Z64 (presented in 1961).

base R plotting

Drawbacks:

- **Layout choices have to be made at the beginning** with no overview over what may still be coming
- **Different functions for different plot types**, with different interfaces
- Routine tasks can require lots of **boilerplate code**
- **No concept of facets / lattices**
- Only a **single global coordinate system** allowed per plot
- **Poor default colours**
- **Resizing** often leads to unsatisfactory results

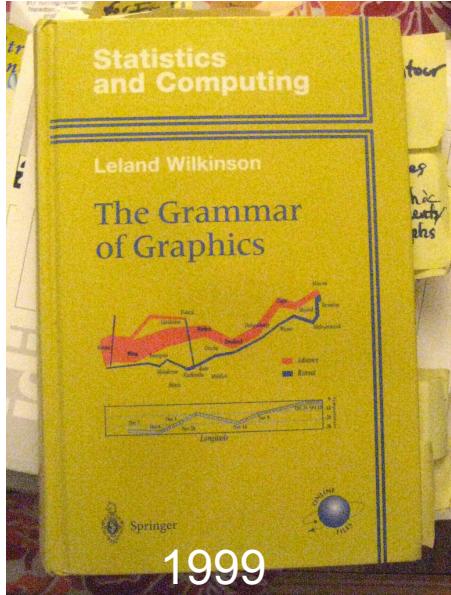
The Grammar of Graphics



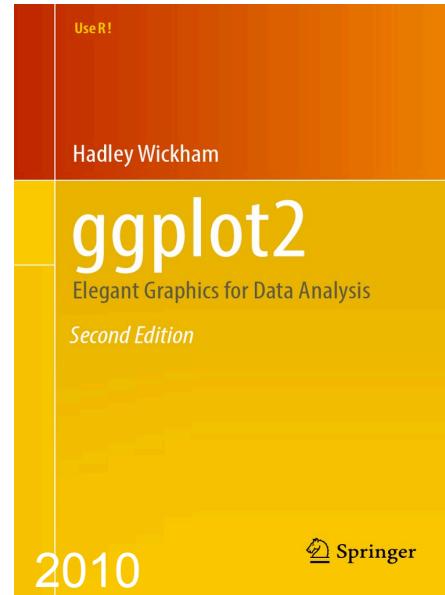
Concept **coined by**
Leland Wilkinson in
1999.

An **abstraction** which
facilitates reasoning and
communicating graphics.

The Grammar of Graphics



Concept **coined by**
Leland Wilkinson in
1999.
An **abstraction** which
facilitates reasoning and
communicating graphics.



ggplot2 is an implementation of a **layered grammar of graphics** that enables users to independently specify the building blocks of a plot and combine them to create just about any kind of graphical display.

ggplot2 grammar of graphics

The components of ggplot2's grammar of graphics are

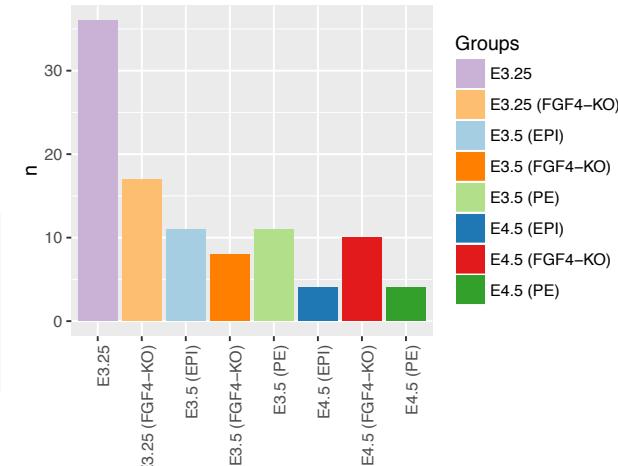
- **datasets** (*nouns*)
- **geometric objects** (*verbs*), visual representations of the data, e.g. points, lines, rectangles, contours,
- **aesthetics** (*adverbs*), instructions on how to map variables to geometric objects,
- **statistical transformation/summaries** e.g. line fitting, binning,
- **coordinate systems** and associated **scales** e.g. linear, log, rank,
- **facets** separating subsets of data into multiple subplots,
- optional parameter settings e.g. text size, font, alignment, legend positions

ggplot2 grammar of graphics

The components of ggplot2's grammar of graphics are

- **datasets** (*nouns*)
- **geometric objects** (*verbs*), visual representations of the data, e.g. points, lines, rectangles, contours,
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- **facets** separating subsets of data into multiple subplots,
- optional parameter settings e.g. text size, font, alignment, legend positions

```
ggplot(groups, aes(x = sampleGroup, y = n, fill = sampleGroup)) +  
  geom_bar(stat = "identity") +  
  scale_fill_manual(values = groupColour, name = "Groups") +  
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
```



ggplot() template

```
ggplot(data = <default data set>,
        aes(x = <default x axis variable>,
            y = <default y axis variable>,
            ... <other default aesthetic mappings>),
        ... <other plot defaults>) +
  geom_<geom type>(aes(size = <size variable for this geom>,
                        ... <other aesthetic mappings>),
                     data = <data for this point geom>,
                     stat = <statistic string or function>,
                     position = <position string or function>,
                     color = <"fixed color specification">,
                     ... <other arguments, possibly passed to the _stat_ function>) +
  scale_<aesthetic>_<type>(name = <"scale label">,
                            breaks = <where to put tick marks>,
                            labels = <labels for tick marks>,
                            ... <other options for the scale>) +
  theme(plot.background = element_rect(fill = "gray"),
        ... <other theme elements>)
```

Data must be in a tidy format

```
library(Hiragi2013)
data(x)
expression <- Biobase::exprs(x)
dftx <- data.frame(pData(x), t(expression))
head(pData(x))
```

```
##           File.name Embryonic.day Total.number.of.cells lineage genotype
## 1 E3.25    1_C32_IN       E3.25                  32      WT
## 2 E3.25    2_C32_IN       E3.25                  32      WT
## 3 E3.25    3_C32_IN       E3.25                  32      WT
## 4 E3.25    4_C32_IN       E3.25                  32      WT
## 5 E3.25    5_C32_IN       E3.25                  32      WT
## 6 E3.25    6_C32_IN       E3.25                  32      WT
```

```
##           ScanDate sampleGroup sampleColour
## 1 E3.25 2011-03-16       E3.25      #CAB2D6
## 2 E3.25 2011-03-16       E3.25      #CAB2D6
## 3 E3.25 2011-03-16       E3.25      #CAB2D6
## 4 E3.25 2011-03-16       E3.25      #CAB2D6
## 5 E3.25 2011-03-16       E3.25      #CAB2D6
## 6 E3.25 2011-03-16       E3.25      #CAB2D6
```

```
dim(expression)
```

```
## [1] 45101 101
```

ggplot()
requires input
data in form of a
tidy dataframe

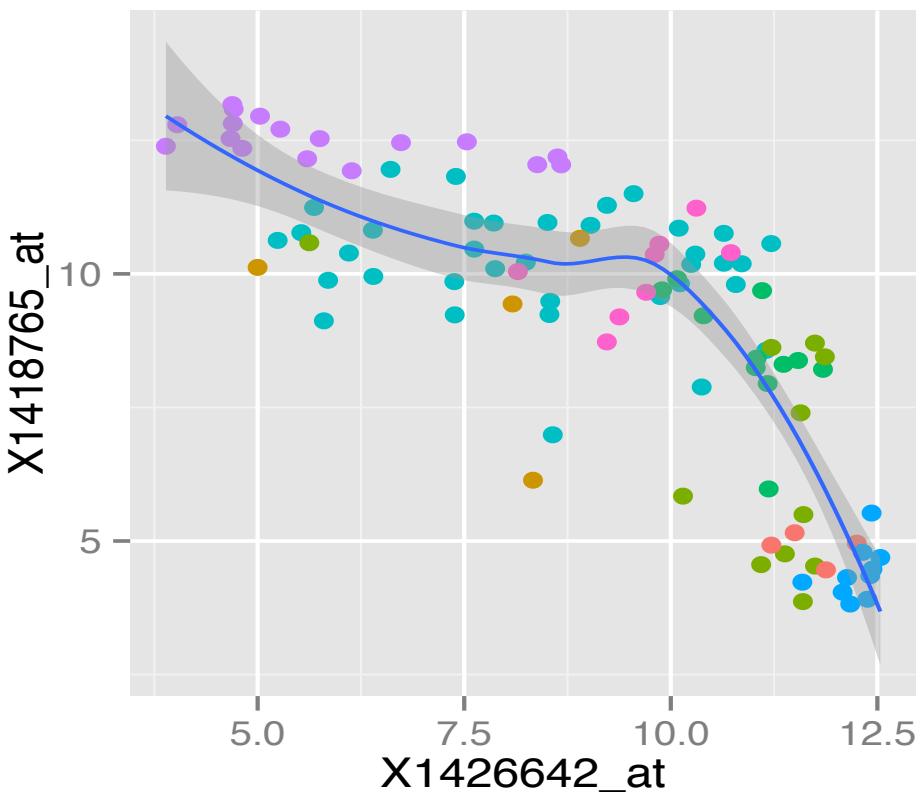
Gene expression
microarray
dataset on early
development of
mouse embryos

transcriptomes of
~100 individual
cells at different
time points in. [1]

[1] Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages by Ohnishi et al., Nature Cell Biology (2014) 16(1): 27-37. doi: 10.1038/ncb2881.

Multiple layers can be superposed

```
ggplot( dftx, aes( x = X1426642_at, y = X1418765_at ) ) +  
  geom_point( aes( colour = sampleColour), shape = 19 ) +  
  geom_smooth( method = "loess" ) +  
  scale_colour_discrete( guide = FALSE )
```



Here, the first layer holds the points, the second holds the smoothed average.

Using the same plot, we can easily change the coordinates

```
groupSize <- table(dftx$sampleGroup)  
groupSize
```

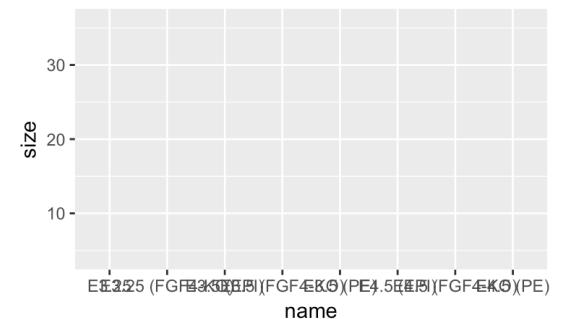
```
pb <- ggplot(data.frame(  
    name = names(groupSize),  
    size = as.vector(groupSize)),  
    aes(x = name, y = size))
```

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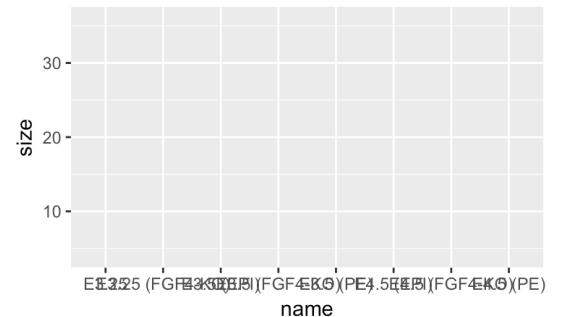
No geom defined yet!



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No geom defined yet!



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pb <- ggplot(data.frame(  
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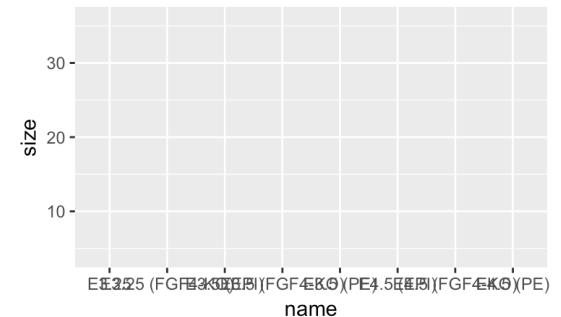
```
pb <- pb + geom_bar(stat = "identity") +  
  aes(fill = name) +  
  scale_fill_manual(values = groupColour, name = "Colour code") +  
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +  
  xlab("Groups") + ylab("Number of Samples")
```

Using the same plot, we can easily change the coordinates

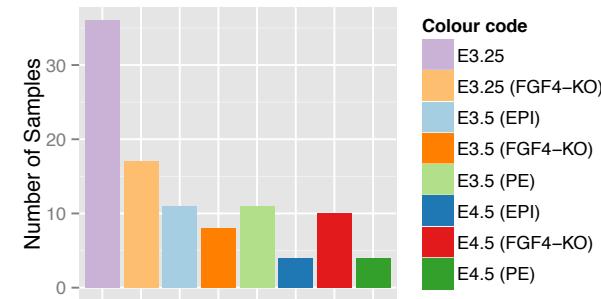
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```

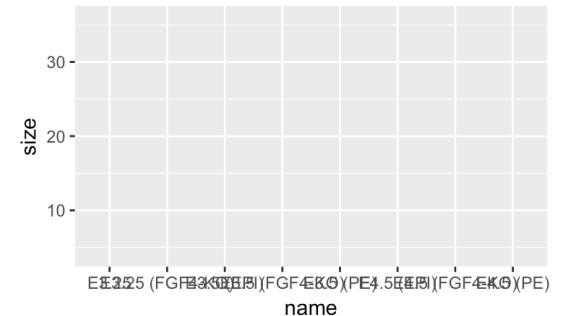


Using the same plot, we can easily change the coordinates

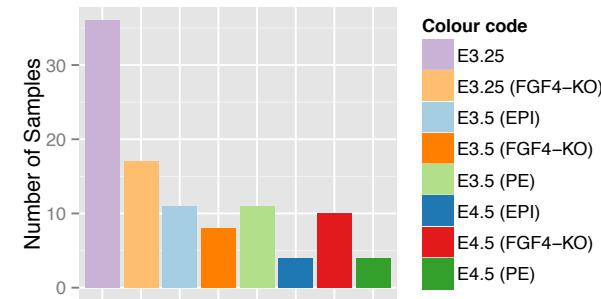
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```



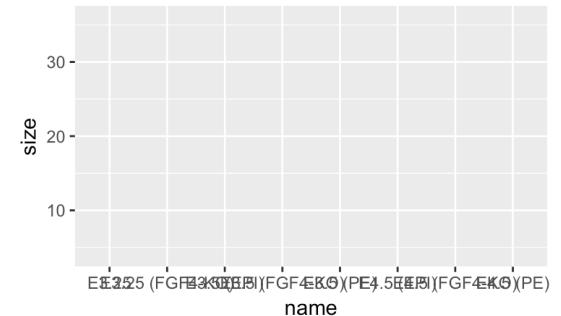
```
pb.polar <- pb + coord_polar() +  
  theme(axis.text.x = element_text(angle = 0, hjust = 1),  
        axis.text.y = element_blank(),  
        axis.ticks = element_blank()) +  
  xlab("") + ylab("")  
pb.polar
```

Using the same plot, we can easily change the coordinates

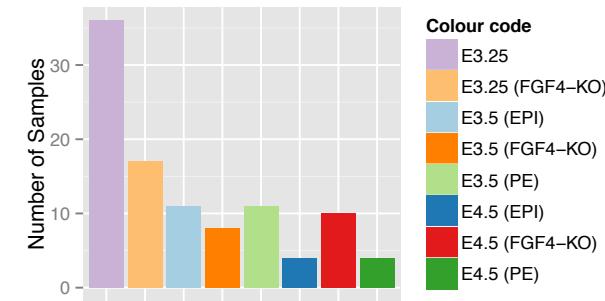
```
groupSize <- table(dftx$sampleGroup)  
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```

```
pb <- ggplot(data.frame(  
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```

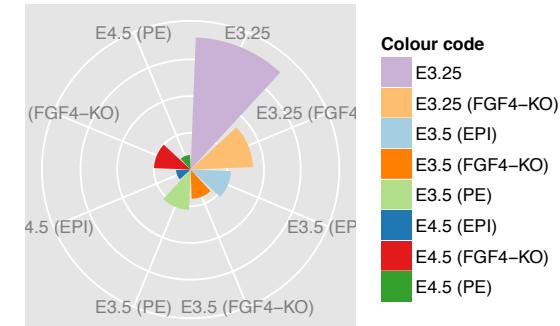
No geom defined yet!



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  scale_fill_manual(values = groupColour, name = "Colour code") +  
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  xlab("Groups") + ylab("Number of Samples")
```



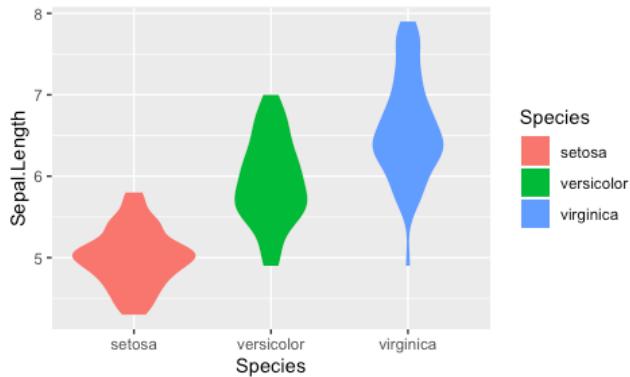
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  xlab("") + ylab("")  
pb.polar
```



Themes can change the look

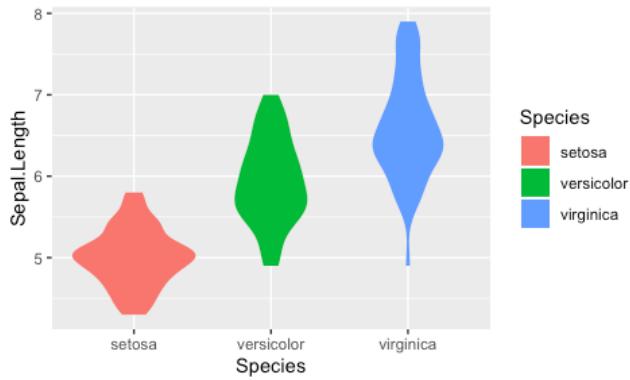
Themes can change the look

```
g = ggplot(iris,  
           aes(x = Species,  
                 y = Sepal.Length,  
                 fill = Species))+  
  geom_violin(col = NA)  
g
```

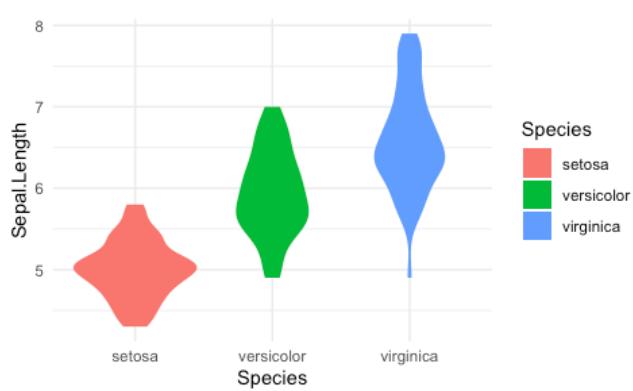


Themes can change the look

```
g = ggplot(iris,  
           aes(x = Species,  
                 y = Sepal.Length,  
                 fill = Species))+  
  geom_violin(col = NA)  
g
```

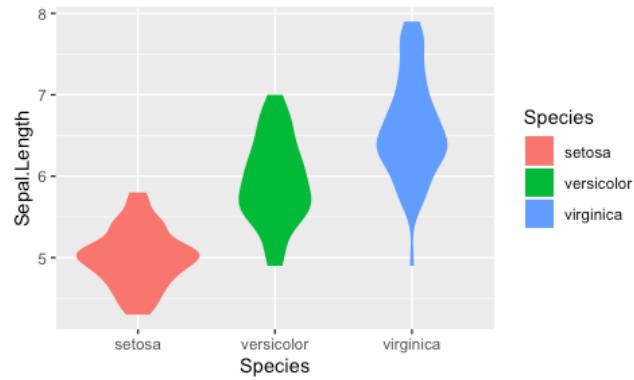


```
g + theme_minimal()
```

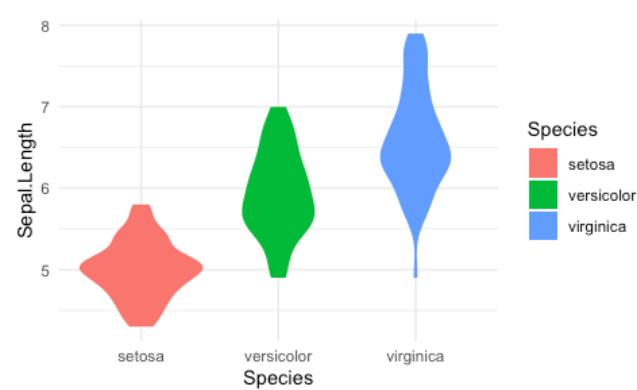


Themes can change the look

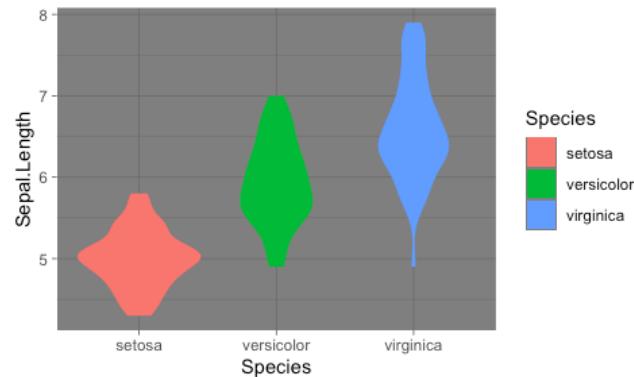
```
g = ggplot(iris,  
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                 fill = Species))+  
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```
g + theme_minimal()
```

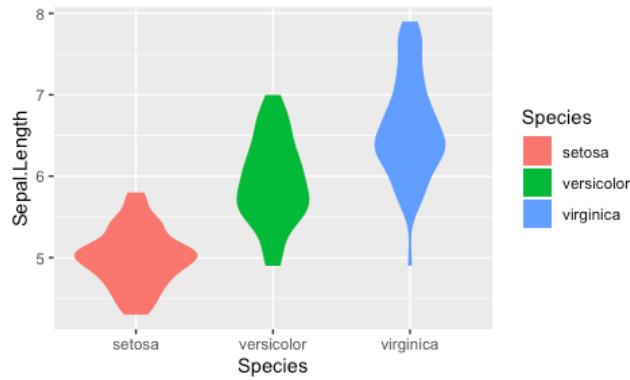


```
g + theme_dark()
```

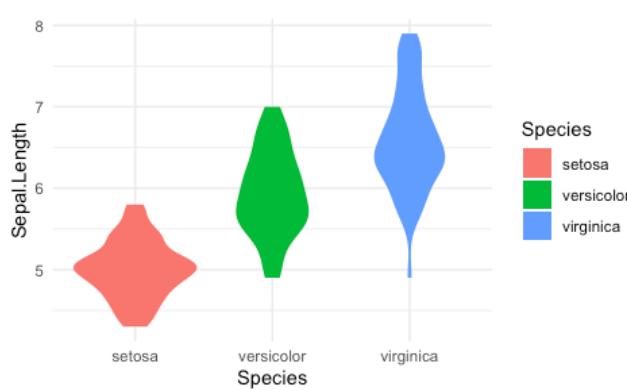


Themes can change the look

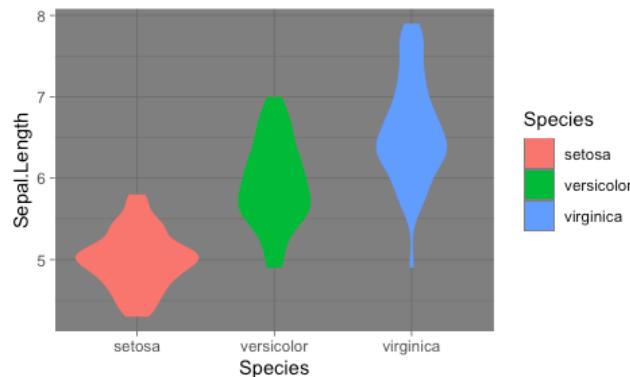
```
g = ggplot(iris,  
           aes(x = Species,  
                 y = Sepal.Length,  
                 fill = Species))+  
  geom_violin(col = NA)  
g
```



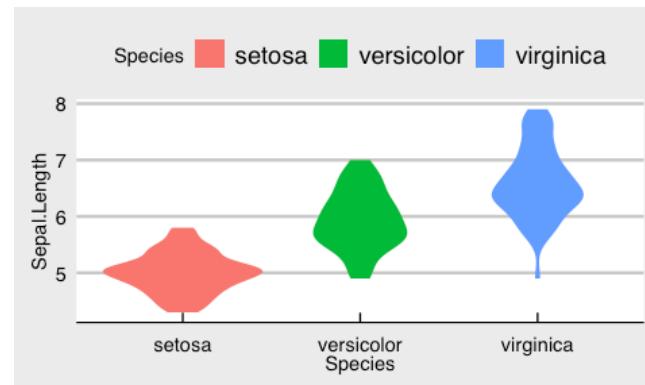
```
g + theme_minimal()
```



```
g + theme_dark()
```



```
library(ggthemes)  
g + theme_economist_white()
```



bbplot.Rproj pushes repo to Github 5 years ago

README.md

BBPLOT

This repo contains the functions of the `bbplot` package, which once installed locally, provides helpful functions for creating and exporting graphics made in ggplot in the style used by the BBC News data team.

Packages

No packages published

Contributors

nassosstylianou Nassos Stylianou
cguibourg

Languages

R 100.0%

`# install.packages('devtools')`

Displaying and comparing 1D distributions



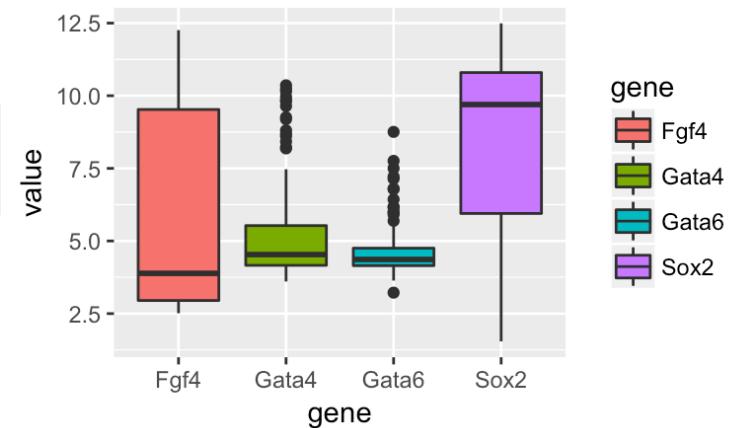
Displaying and comparing 1D distributions



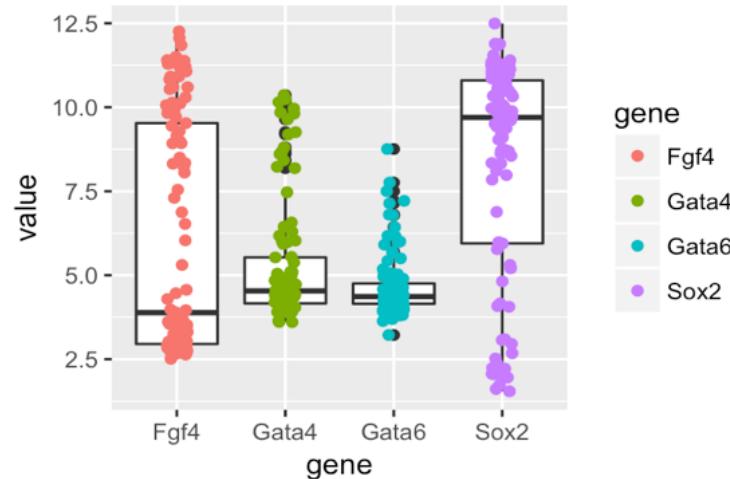
Boxplot

Boxplots are good for plotting summary of 1D continuous data; they enable you to **compare quantiles of data distributions**.

```
p = ggplot(genes, aes(x = gene, y = value))  
p + geom_boxplot(aes(fill = gene))
```



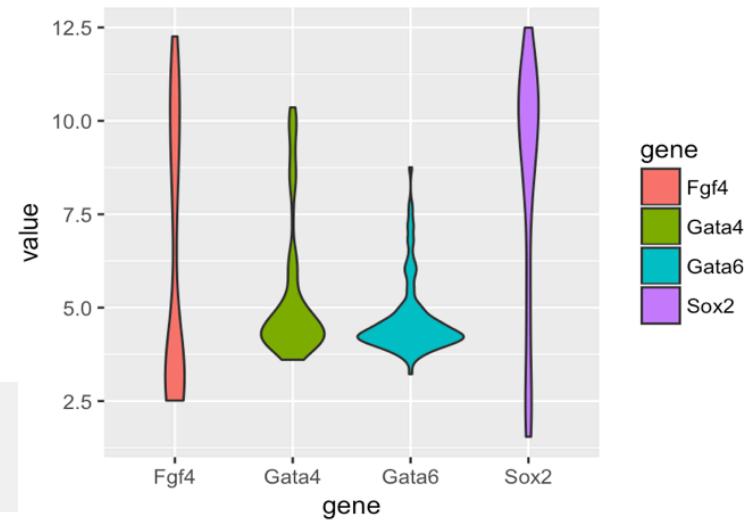
```
p + geom_boxplot() +  
  geom_jitter(aes(color = gene), width = 0.1, height = 0)
```



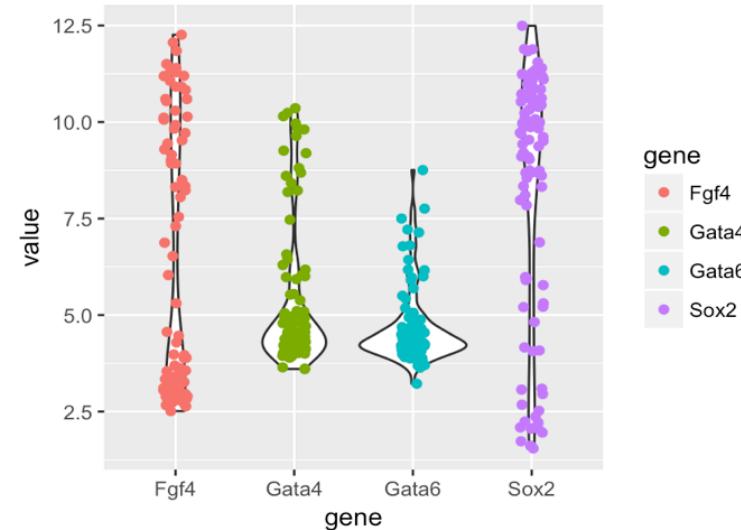
Violin Plot

If there are many observations in the dataset, we can **show the estimated distribution with violin plots.**

```
p = ggplot(genes, aes( x = gene, y = value))  
p + geom_violin(aes(fill = gene))
```

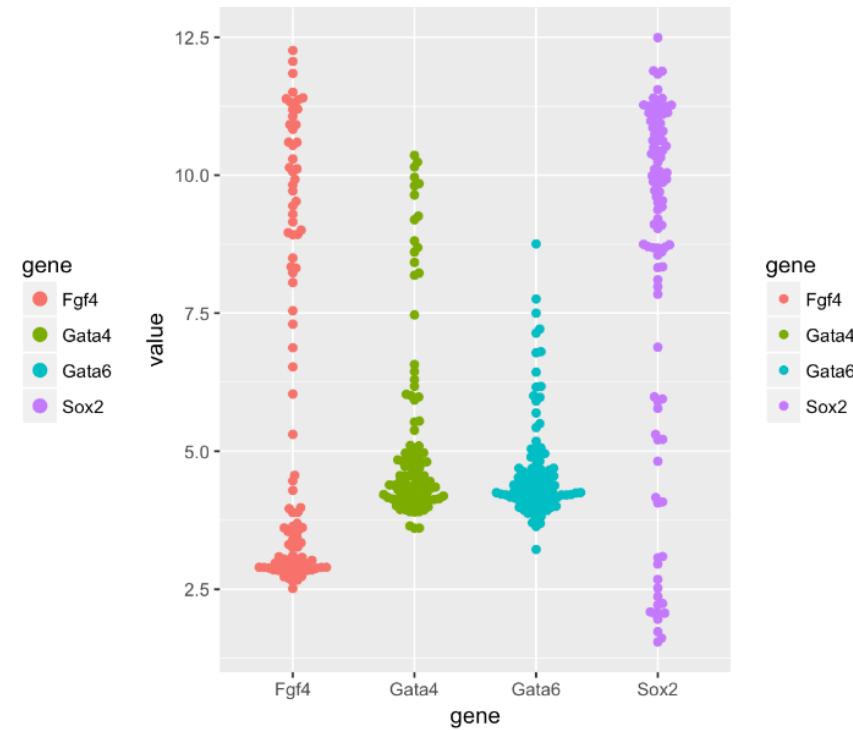
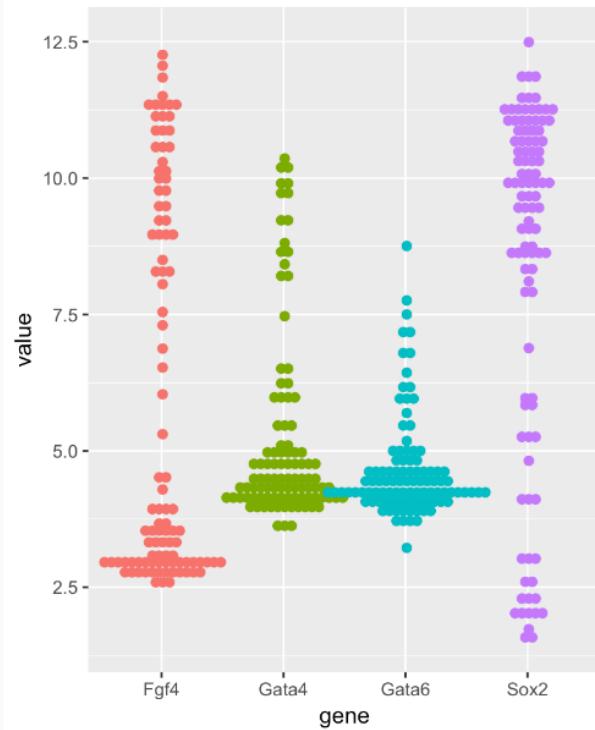


```
p + geom_boxplot() +  
  geom_jitter(aes(color = gene), width = 0.1, height = 0)
```



Dot & Beeswarm Plot

```
p + geom_dotplot(binaxis = "y", binwidth = 1/6,  
                  stackdir = "center", stackratio = 0.75,  
                  aes(color = gene))  
  
library("ggbeeswarm")  
p + geom_beeswarm(aes(color = gene))
```



Bar charts with error bars

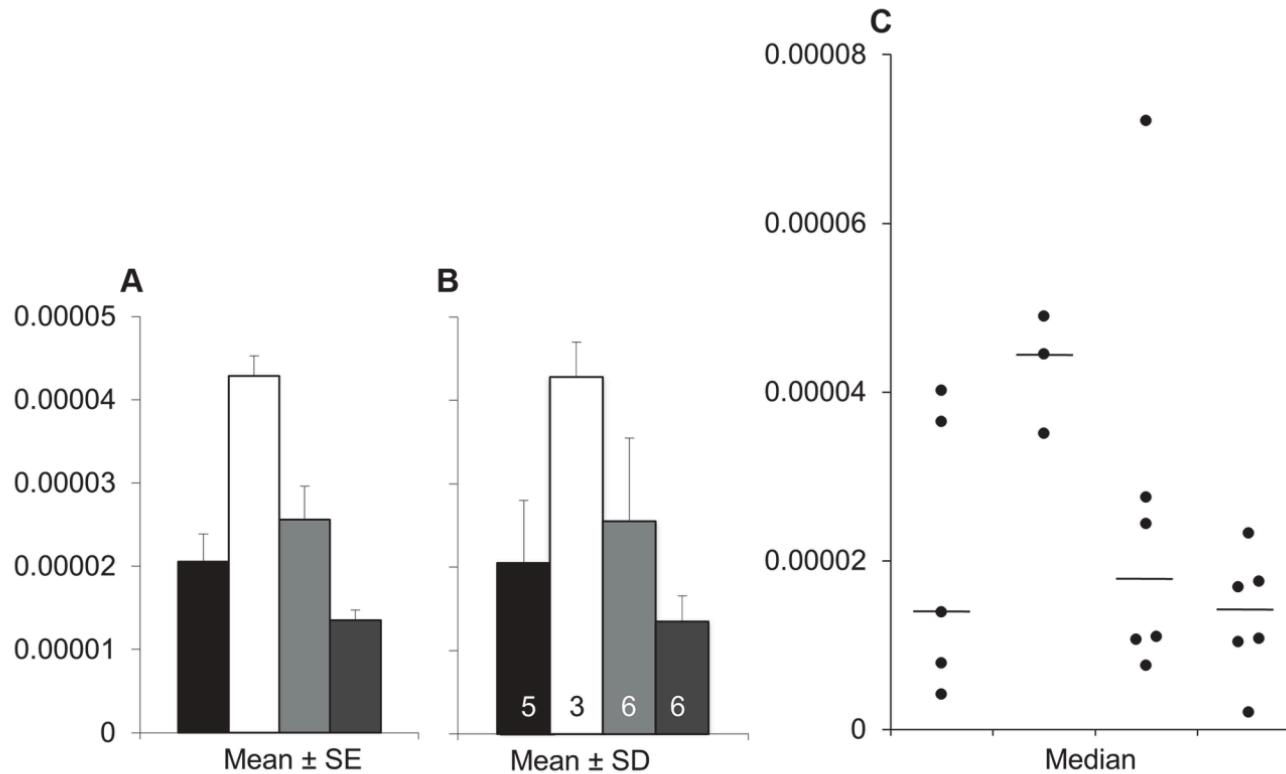


Fig 3. Bar graphs and scatterplots convey very different information. While scatterplots prompt the reader to critically evaluate the statistical tests and the authors' interpretation of the data, bar graphs discourage the reader from thinking about these issues. Placental endothelin 1 (*EDN1*) mRNA data for four different groups of participants is presented in bar graphs showing mean \pm SE (Panel A), or mean \pm SD (Panel B), and in a univariate scatterplot (Panel C). Panel A (mean \pm SE) suggests that the second group has higher values than the remaining groups; however, Panel B (mean \pm SD) reveals that there is considerable overlap between groups. Showing SE rather than SD magnifies the apparent visual differences between groups, and this is exacerbated by the fact that SE obscures any effect of unequal sample size. The scatterplot (Panel C) clearly shows that the sample sizes are small, group one has a much larger variance than the other groups, and there is an outlier in group three. These problems are not apparent in the bar graphs shown in Panels A and B.

Bar charts with error bars

What is wrong with {bar charts + error bars} ?

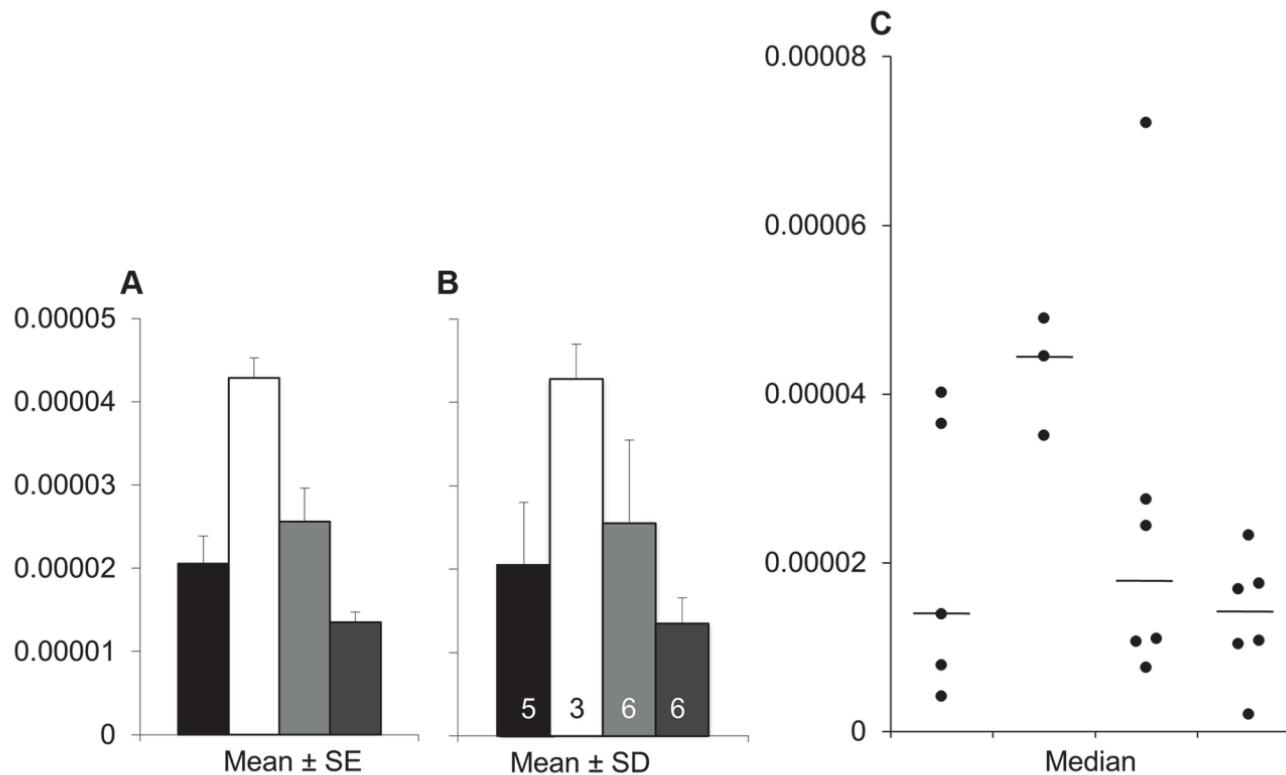


Fig 3. Bar graphs and scatterplots convey very different information. While scatterplots prompt the reader to critically evaluate the statistical tests and the authors' interpretation of the data, bar graphs discourage the reader from thinking about these issues. Placental endothelin 1 (*EDN1*) mRNA data for four different groups of participants is presented in bar graphs showing mean \pm SE (Panel A), or mean \pm SD (Panel B), and in a univariate scatterplot (Panel C). Panel A (mean \pm SE) suggests that the second group has higher values than the remaining groups; however, Panel B (mean \pm SD) reveals that there is considerable overlap between groups. Showing SE rather than SD magnifies the apparent visual differences between groups, and this is exacerbated by the fact that SE obscures any effect of unequal sample size. The scatterplot (Panel C) clearly shows that the sample sizes are small, group one has a much larger variance than the other groups, and there is an outlier in group three. These problems are not apparent in the bar graphs shown in Panels A and B.

Bar charts with error bars

What is wrong with {bar charts + error bars} ?

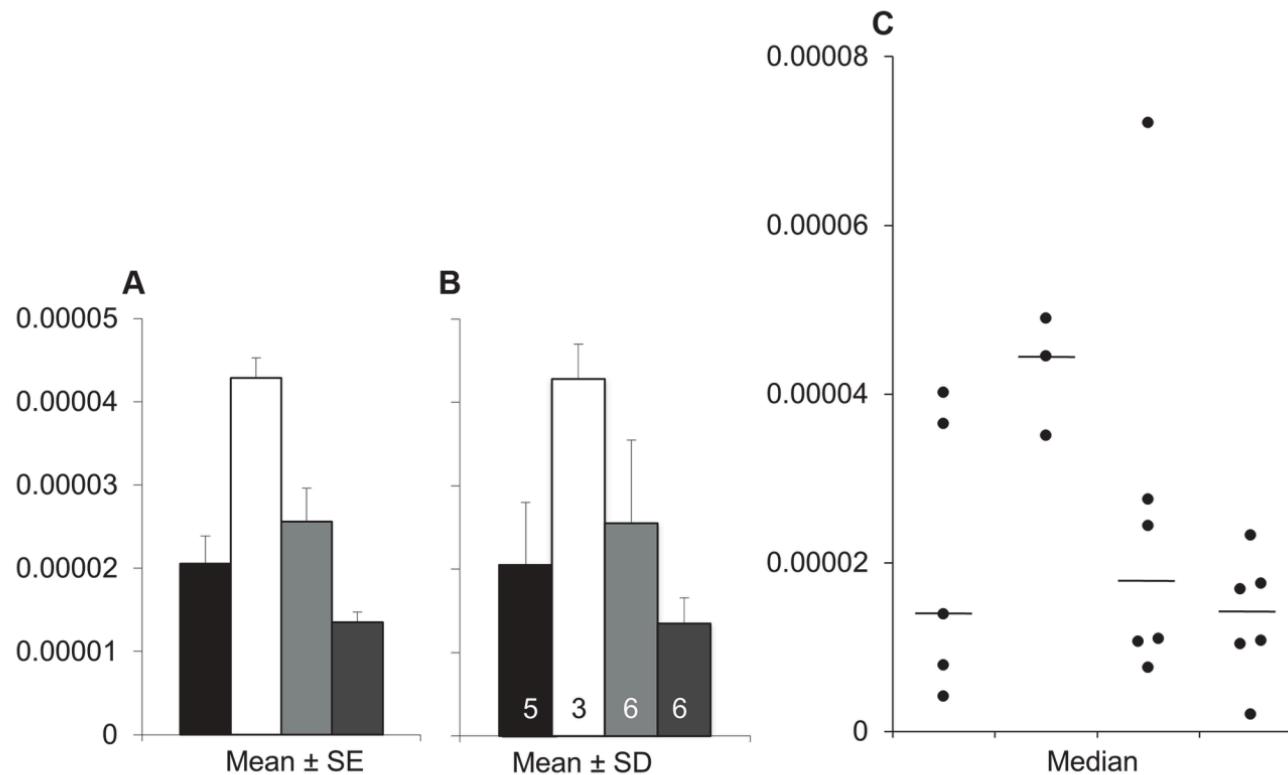


Fig 3. Bar graphs and scatterplots convey very different information. While scatterplots prompt the reader to critically evaluate the statistical tests and the authors' interpretation of the data, bar graphs discourage the reader from thinking about these issues. Placental endothelin 1 (*EDN1*) mRNA data for four different groups of participants is presented in bar graphs showing mean \pm SE (Panel A), or mean \pm SD (Panel B), and in a univariate scatterplot (Panel C). Panel A (mean \pm SE) suggests that the second group has higher values than the remaining groups; however, Panel B (mean \pm SD) reveals that there is considerable overlap between groups. Showing SE rather than SD magnifies the apparent visual differences between groups, and this is exacerbated by the fact that SE obscures any effect of unequal sample size. The scatterplot (Panel C) clearly shows that the sample sizes are small, group one has a much larger variance than the other groups, and there is an outlier in group three. These problems are not apparent in the bar graphs shown in Panels A and B.

Bar charts
(with error
bars)
**not good for
showing
distributions**

Use bar charts
**only to show
class counts.**

Bar charts with error bars

What is wrong with {bar charts + error bars} ?

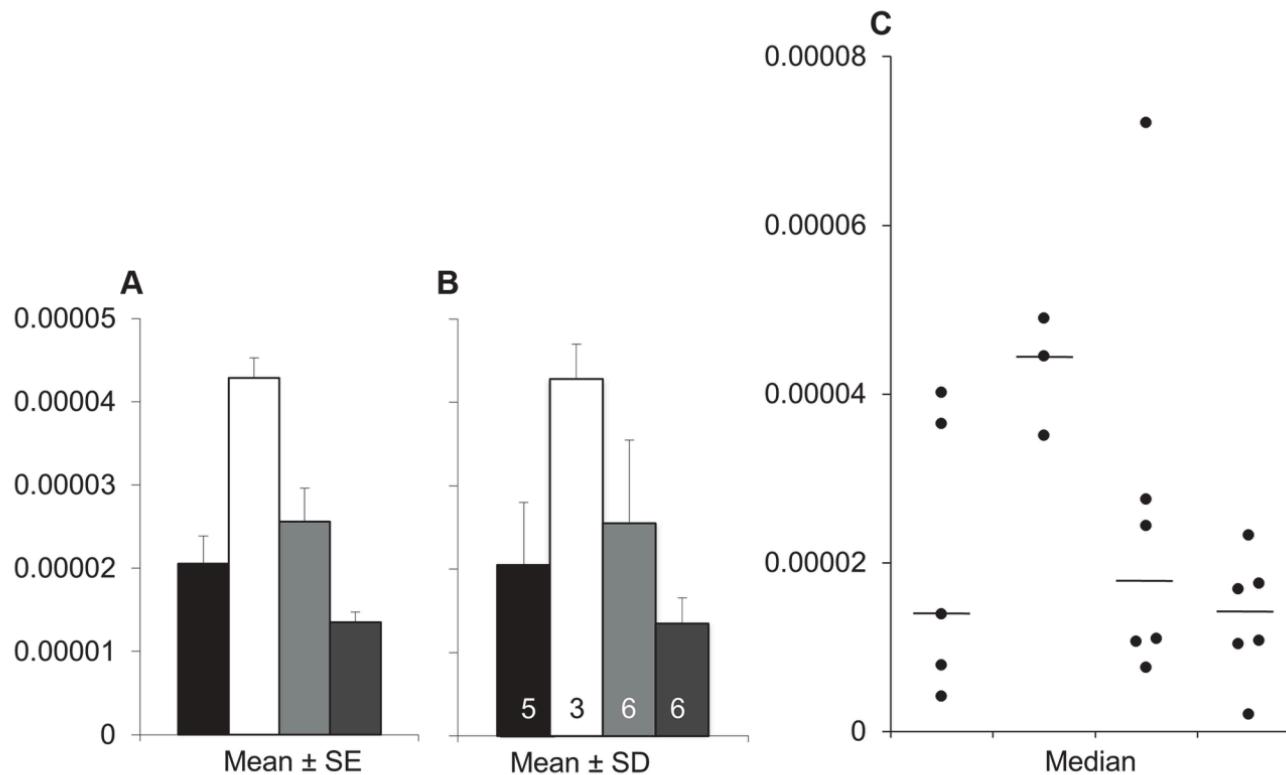


Fig 3. Bar graphs and scatterplots convey very different information. While scatterplots prompt the reader to critically evaluate the statistical tests and the authors' interpretation of the data, bar graphs discourage the reader from thinking about these issues. Placental endothelin 1 (*EDN1*) mRNA data for four different groups of participants is presented in bar graphs showing mean \pm SE (Panel A), or mean \pm SD (Panel B), and in a univariate scatterplot (Panel C). Panel A (mean \pm SE) suggests that the second group has higher values than the remaining groups; however, Panel B (mean \pm SD) reveals that there is considerable overlap between groups. Showing SE rather than SD magnifies the apparent visual differences between groups, and this is exacerbated by the fact that SE obscures any effect of unequal sample size. The scatterplot (Panel C) clearly shows that the sample sizes are small, group one has a much larger variance than the other groups, and there is an outlier in group three. These problems are not apparent in the bar graphs shown in Panels A and B.

doi:10.1371/journal.pbio.1002128.g003

Weissgerber TL, et al. (2015) Beyond Bar and Line Graphs: Time for a New Data Presentation Paradigm. PLOS Biology 13(4): e1002128.

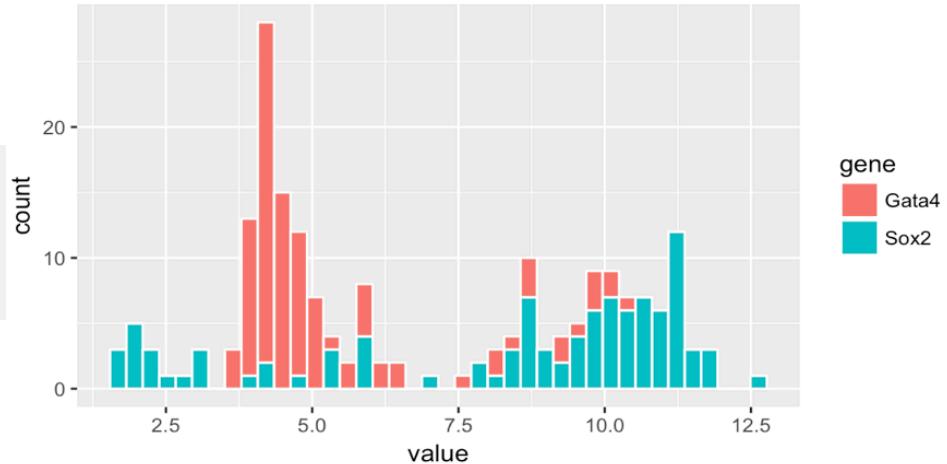
Bar charts
(with error
bars)
**not good for
showing
distributions**

Use bar charts
**only to show
class counts.**

Histograms

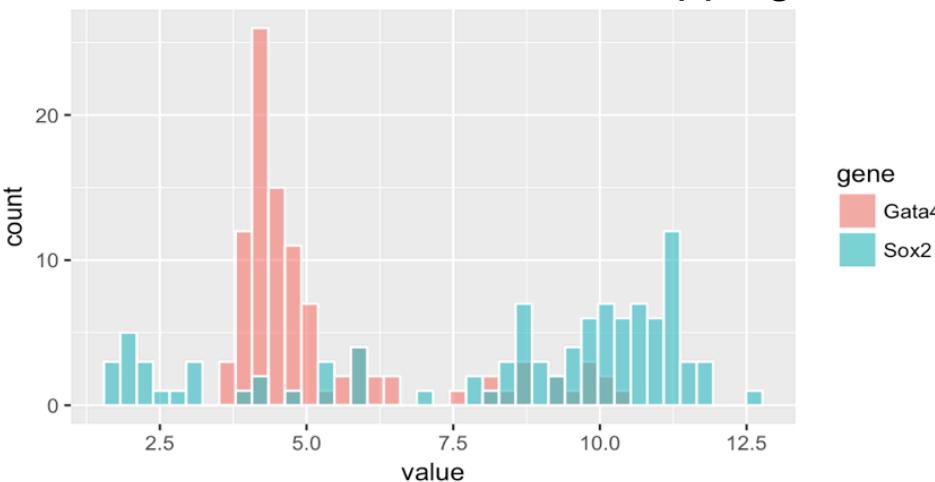
Stacked

```
p = ggplot(genes %>% filter(gene %in% c("Gata4", "Sox2")),
            aes(x = value))
p + geom_histogram(aes(fill = gene),
                   color = "white", bins = 40)
```



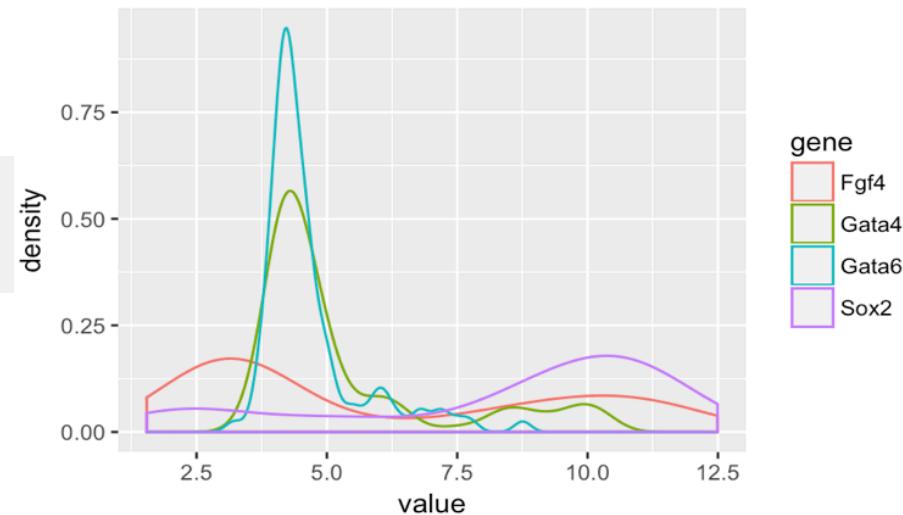
```
p + geom_histogram(
  aes(fill = gene), color="white", alpha=0.6,
  bins = 40, position = "identity")
```

Overlapping

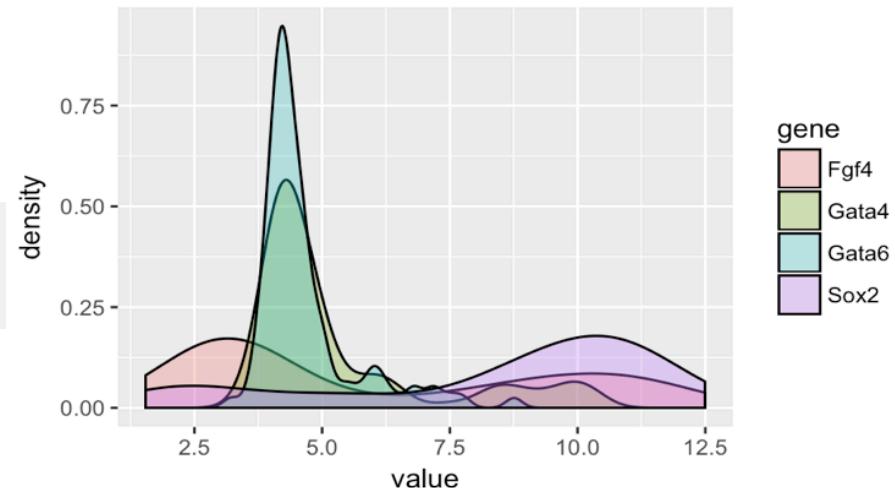


Density plots

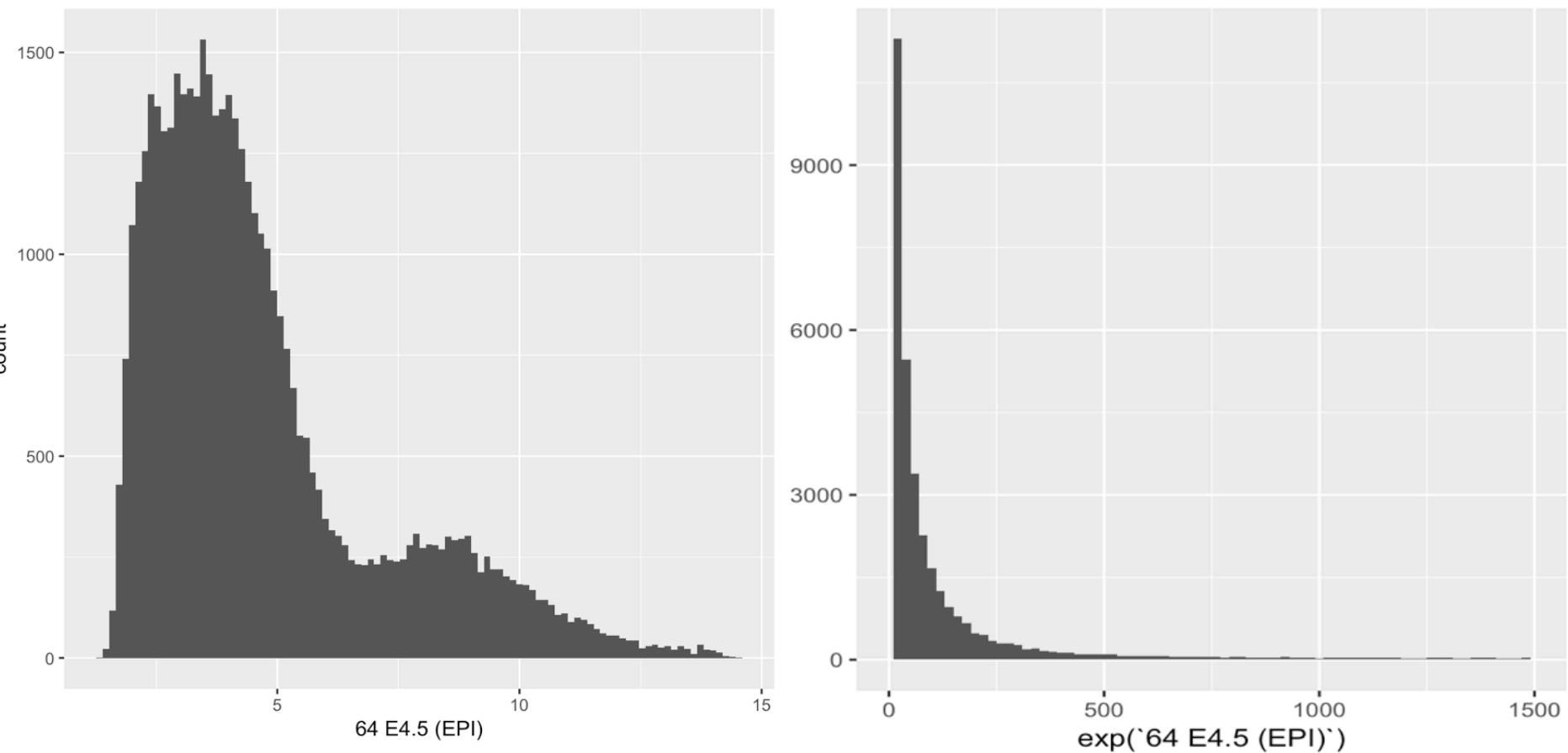
```
p = ggplot(genes, aes( x = value, color = gene))  
p + geom_density()
```



```
p = ggplot(genes, aes( x = value, fill = gene))  
p + geom_density(alpha = 0.3)
```



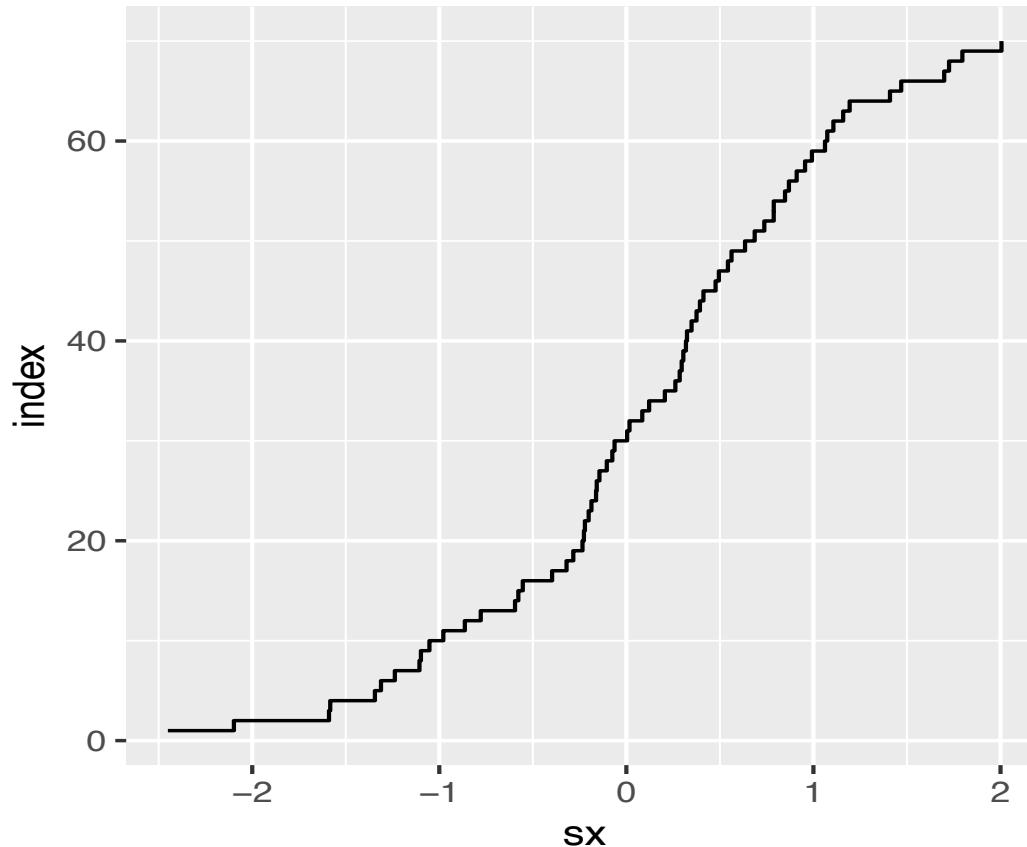
Non-linear transformations change the shape of a density



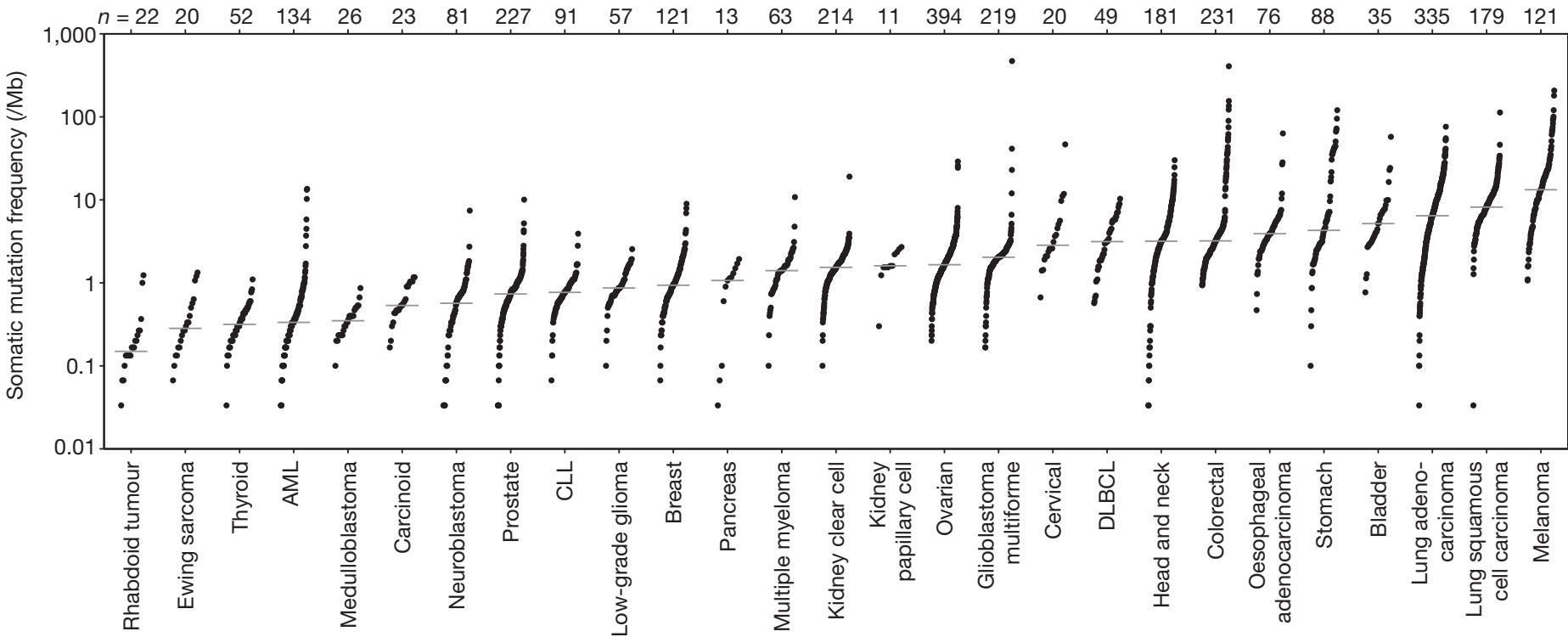
- The **mode** of a distribution is an **infinitesimal concept**.
- Need either an infinite amount of data or choose smoothing / binning bandwidth
- **Number of modes (let alone their positions) can change under non-linear data transformations**

The empirical cumulative distribution

$$F_n(x) = \frac{\text{number of } i \text{ for which } x_i \leq x}{n} = \frac{1}{n} \sum_{i=1}^n \mathbb{1}(x \leq x_i)$$



```
simdata = rnorm(70)
simdf <- data.frame(index = seq(along = simdata), sx = sort(simdata))
ggplot(simdf, aes(x = sx, y = index)) + geom_step()
```



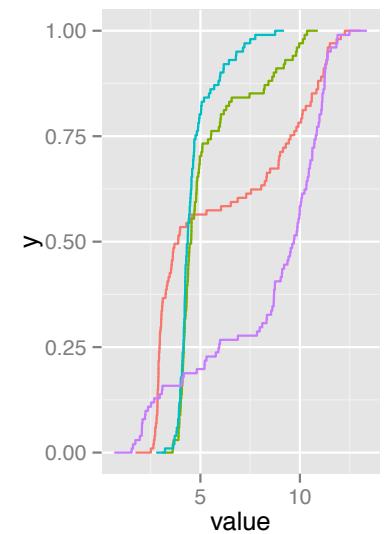
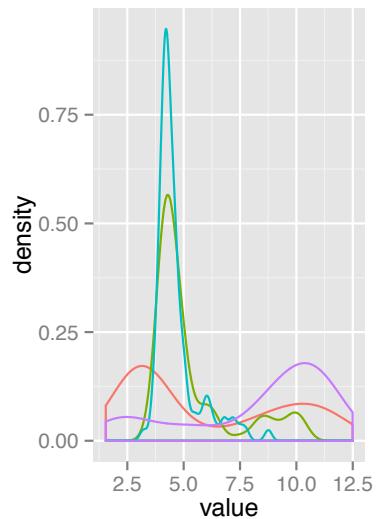
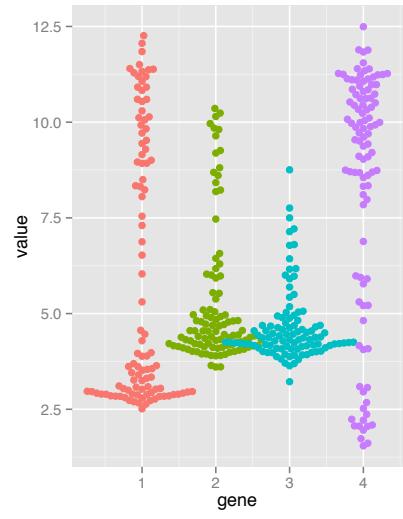
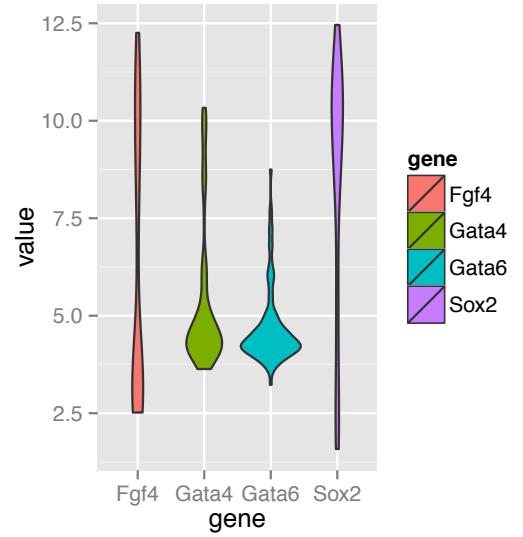
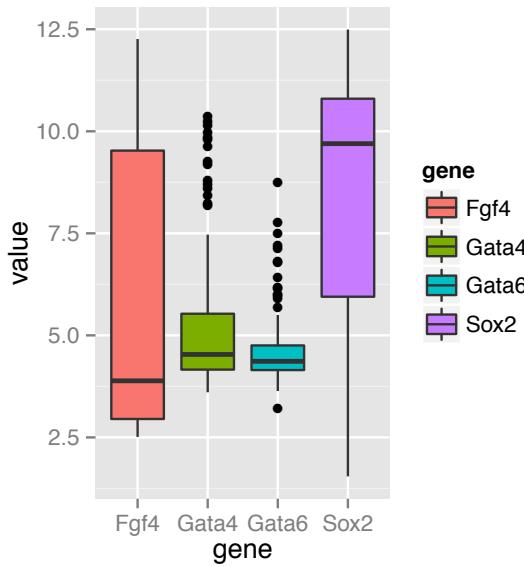
LETTER

doi:10.1038/nature12213

Mutational heterogeneity in cancer and the search for new cancer-associated genes

Michael S. Lawrence^{1*}, Petar Stojanov^{1,2*}, Paz Polak^{1,3,4*}, Gregory V. Kryukov^{1,3,4}, Kristian Cibulskis¹, Andrey Sivachenko¹, Scott L. Carter¹, Chip Stewart¹, Craig H. Mermel^{1,5}, Steven A. Roberts⁶, Adam Kiezun¹, Peter S. Hammerman^{1,2}, Aaron McKenna^{1,7}, Yotam Drier^{1,3,5,8}, Lihua Zou¹, Alex H. Ramos¹, Trevor J. Pugh^{1,2,3}, Nicolas Stransky^{1,9}, Elena Helman^{1,10}, Jaegil Kim¹, Carrie Sougnez¹, Lauren Ambrogio¹, Elizabeth Nickerson¹, Erica Shefler¹, Maria L. Cortes¹, Daniel Auclair¹, Gordon Saksena¹, Douglas Voet¹, Michael Noble¹, Daniel DiCara¹, Pei Lin¹, Lee Lichtenstein¹, David I. Heiman¹, Timothy Fennell¹, Marcin Imitielinski^{1,5}, Bryan Hernandez¹, Eran Hodis^{1,2}, Sylvan Bacq^{1,2}, Austin M. Dulak^{1,2}, Jens Lohr^{1,2}, Dan-Avi Landau^{1,2,11}, Catherine J. Wu^{2,3}, Jorge Melendez-Zajgla¹², Alfredo Hidalgo-Miranda¹², Amnon Koren^{1,3}, Steven A. McCarroll^{1,3}, Jaume Mora¹³, Ryan S. Lee^{2,3,14}, Brian Crompton^{2,14}, Robert Onofrio¹, Melissa Parkin¹, Wendy Winckler¹, Kristin Ardlie¹, Stacey B. Gabriel¹, Charles W. M. Roberts^{2,3,14}, Jaclyn A. Biegel¹⁵, Kimberly Stegmaier^{1,2,14}, Adam J. Bass^{1,2,3}, Levi A. Garraway^{1,2,3}, Matthew Meyerson^{1,2,3}, Todd R. Golub^{1,2,3,8}, Dmitry A. Gordenin⁶, Shamil Sunyaev^{1,3,4}, Eric S. Lander^{1,3,10} & Gad Getz^{1,5}

Summary: Visualizing distributions in 1D



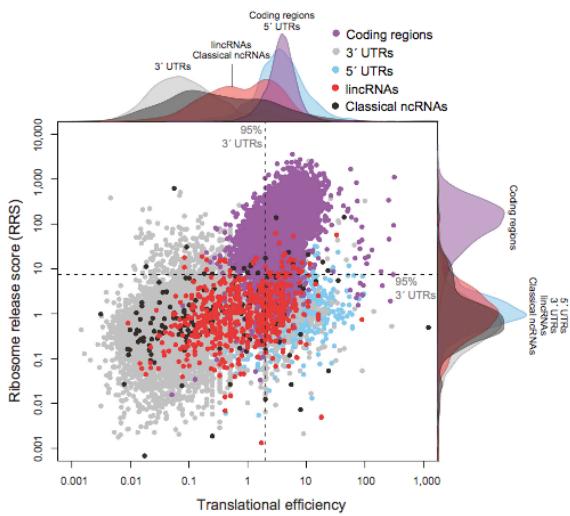
2D data plots

2D data plots

Scatterplots (x,y)-point plots

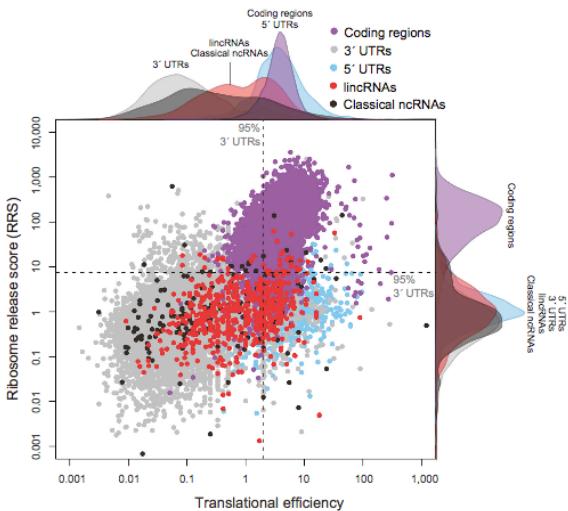
2D data plots

Scatterplots (x,y)-point plots

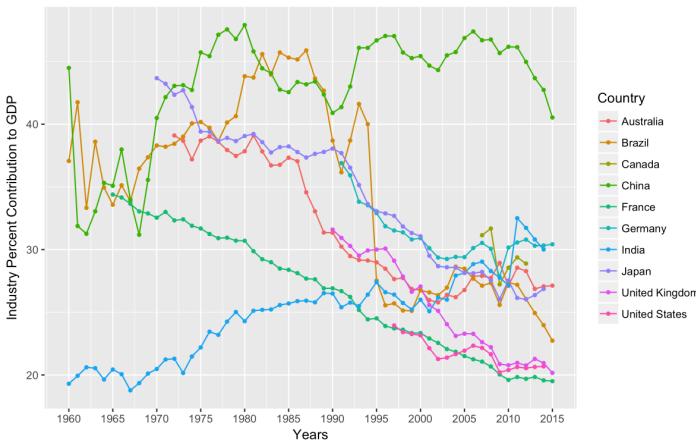


2D data plots

Scatterplots (x,y)-point plots

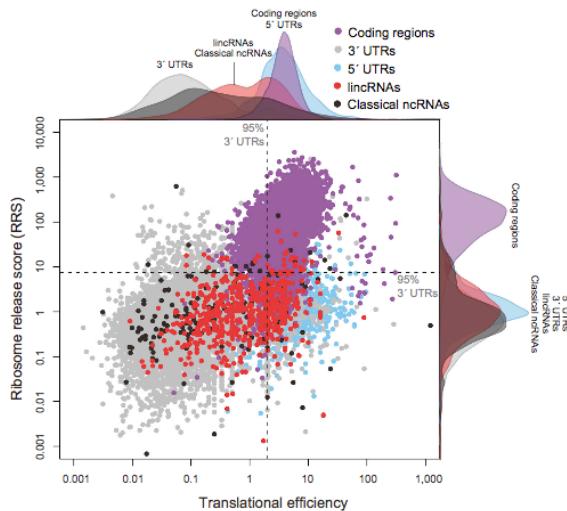


Line plots (x,y)-line plots

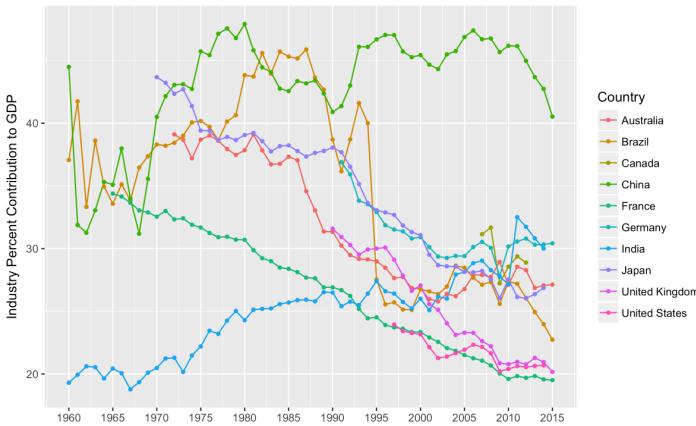


2D data plots

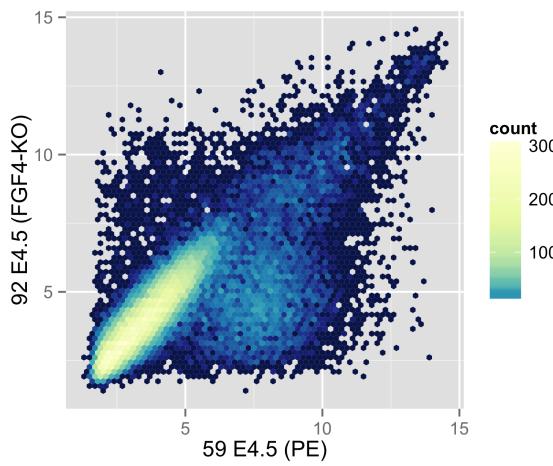
Scatterplots (x,y)-point plots



Line plots (x,y)-line plots

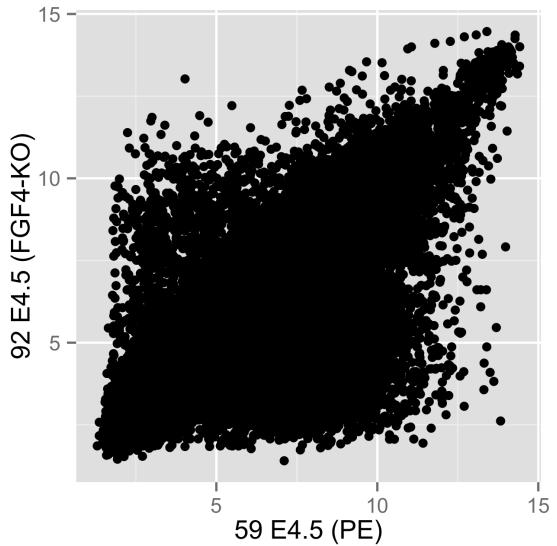


2D density requires the choice of bandwidth; obscures the sample size (i.e. the uncertainty of the estimate)



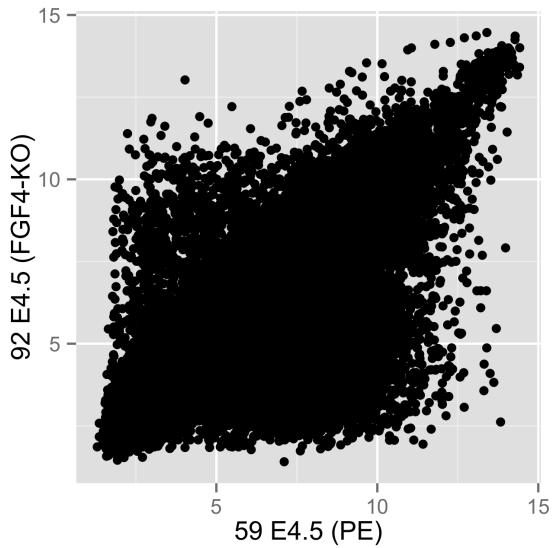
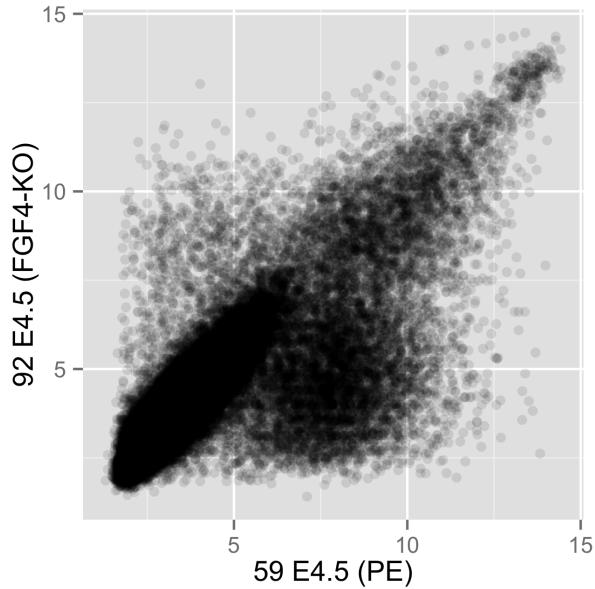
Showing distributions in 2D

```
scp <- ggplot(dfx, aes( x = '59 E4.5 (PE)' ,  
                      y = '92 E4.5 (FGF4-KO)' ))  
scp + geom_point()
```



Showing distributions in 2D

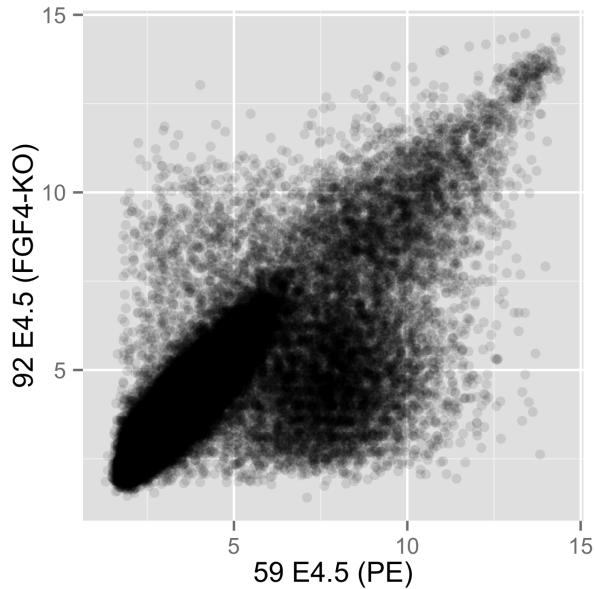
```
scp <- ggplot(dfx, aes( x = '59 E4.5 (PE)' ,  
y = '92 E4.5 (FGF4-KO)' ))  
scp + geom_point()
```



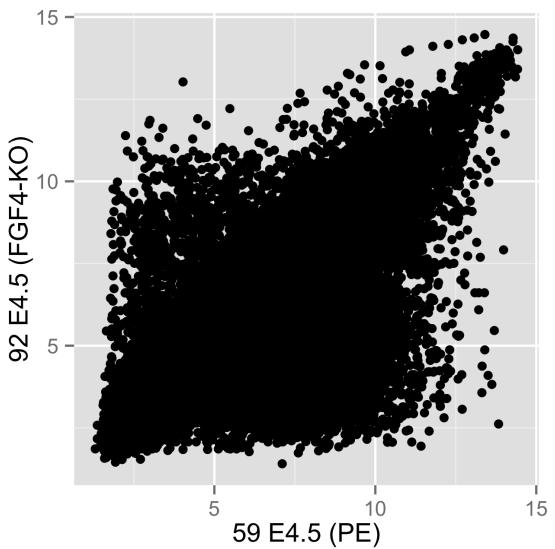
```
scp + geom_point(alpha = 0.1)
```

Showing distributions in 2D

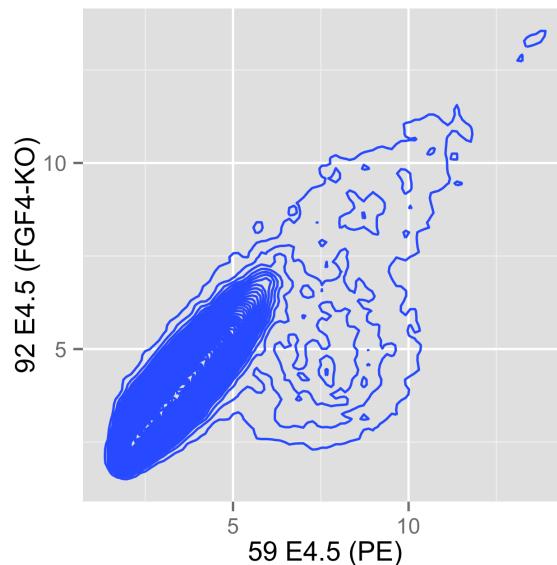
```
scp <- ggplot(dfx, aes( x = '59 E4.5 (PE)' ,  
y = '92 E4.5 (FGF4-KO)' ))  
scp + geom_point()
```



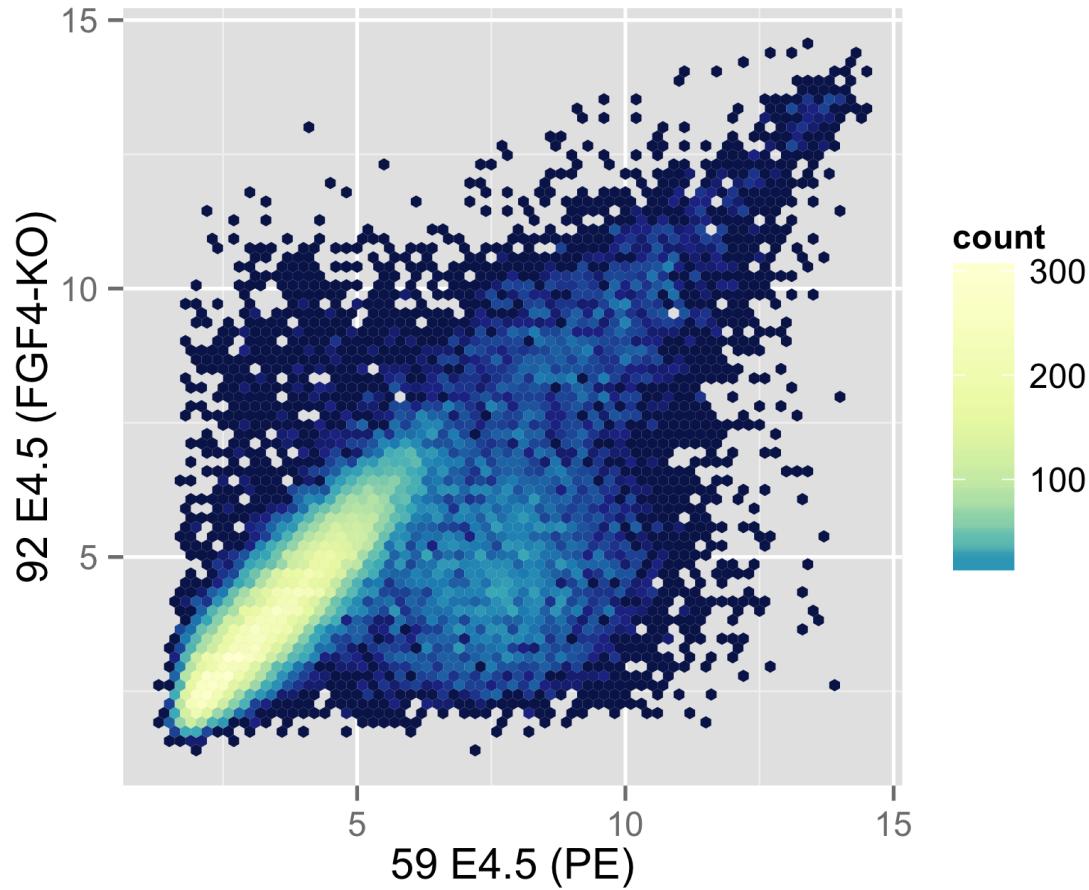
```
scp + geom_point(alpha = 0.1)
```



```
scp + geom_density2d(h = 0.5, bins = 60)
```



binhex is a good, easy to read, option to show 2D density



```
scp + stat_binhex(binwidth = c(0.2, 0.2)) + colourscale +  
coord_fixed()
```

How to show
more than 2D?

3-5D: aesthetics allow to show more than 2D

geom_point's

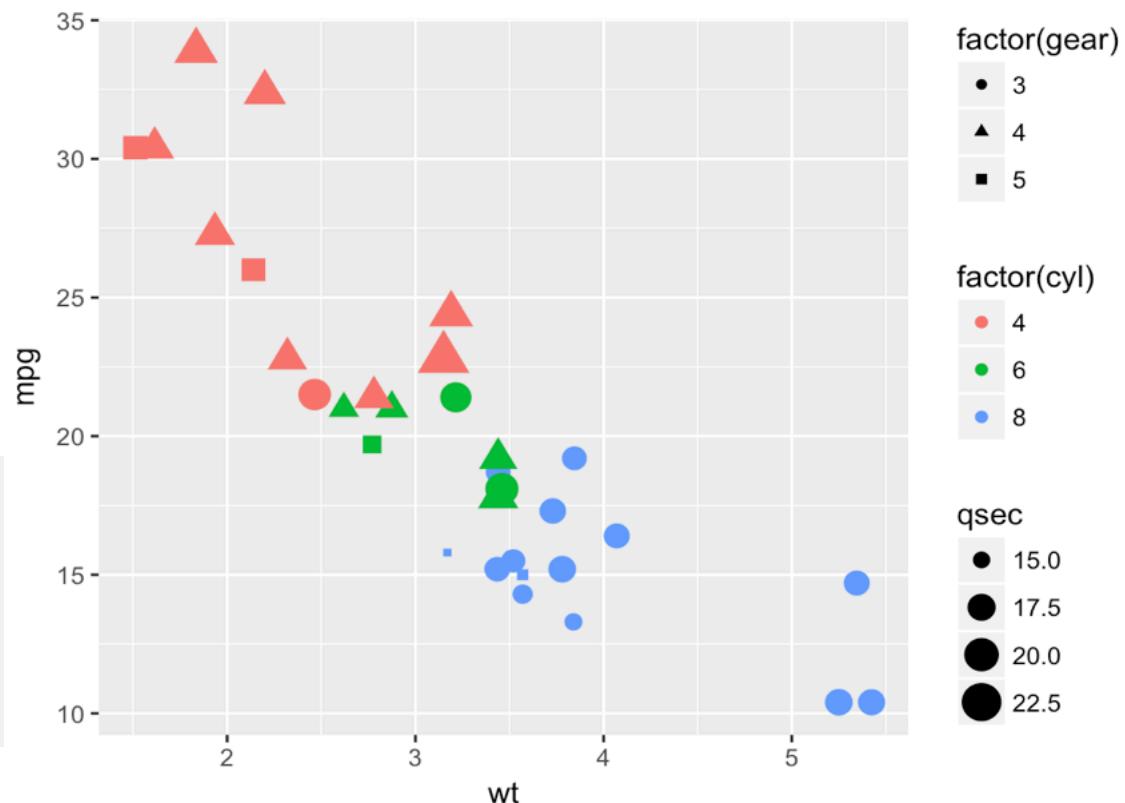
aesthetics

(apart from x and y):

- fill / color
- shape
- size
- alpha

```
ggplot(data = mtcars) +  
  geom_point(  
    aes(x = wt, y = mpg,  
        shape = factor(gear),  
        color = factor(cyl),  
        size = qsec))
```

```
head(mtcars)  
##          mpg cyl disp  hp drat    wt  qsec vs am gear carb  
## Mazda RX4   21.0   6 160 110 3.90 2.620 16.46  0  1    4    4  
## Mazda RX4 Wag 21.0   6 160 110 3.90 2.875 17.02  0  1    4    4  
## Datsun 710   22.8   4 108  93 3.85 2.320 18.61  1  1    4    1  
## Hornet 4 Drive 21.4   6 258 110 3.08 3.215 19.44  1  0    3    1  
## Hornet Sportabout 18.7   8 360 175 3.15 3.440 17.02  0  0    3    2  
## Valiant     18.1   6 225 105 2.76 3.460 20.22  1  0    3    1
```



3-5D: aesthetics allow to show more than 2D

geom_point's

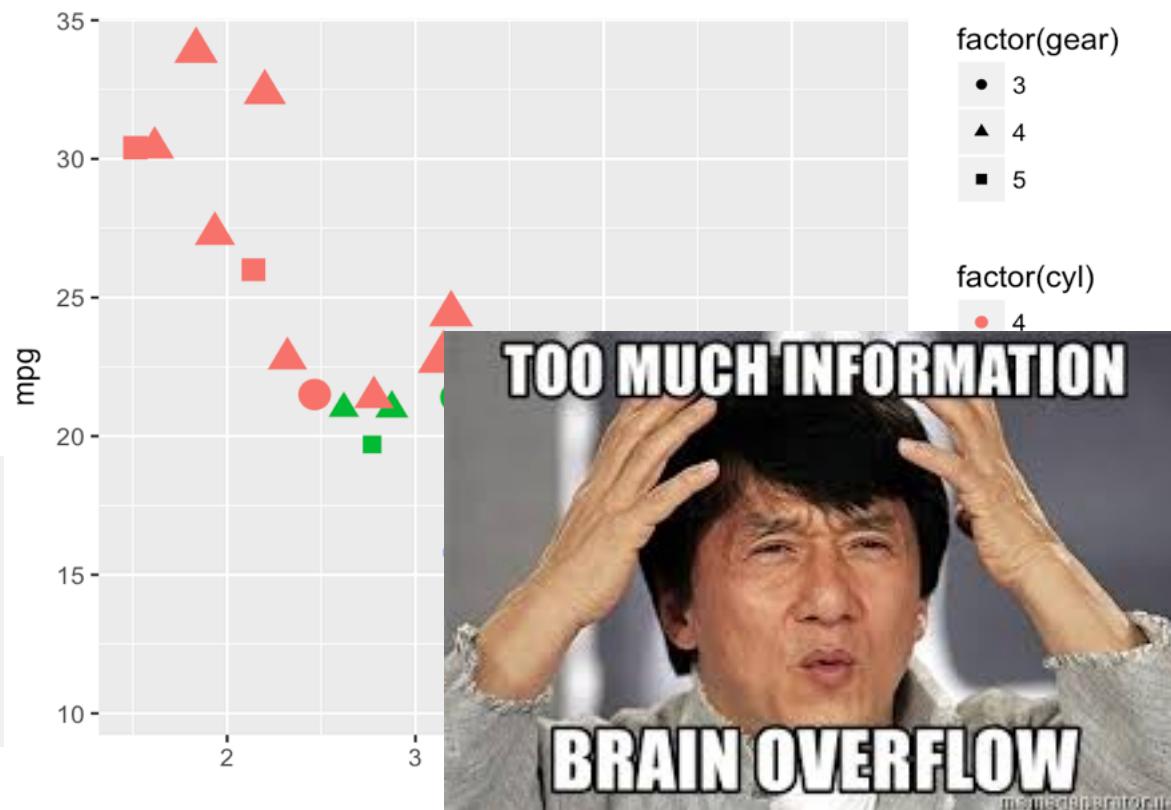
aesthetics

(apart from x and y):

- fill / color
- shape
- size
- alpha

```
ggplot(data = mtcars) +  
  geom_point(  
    aes(x = wt, y = mpg,  
        shape = factor(gear),  
        color = factor(cyl),  
        size = qsec))
```

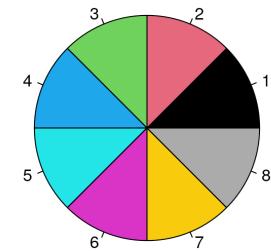
```
head(mtcars)  
##          mpg cyl disp  hp drat    wt  qsec vs am gear carb  
## Mazda RX4   21.0   6 160 110 3.90 2.620 16.46  0  1    4    4  
## Mazda RX4 Wag 21.0   6 160 110 3.90 2.875 17.02  0  1    4    4  
## Datsun 710   22.8   4 108  93 3.85 2.320 18.61  1  1    4    1  
## Hornet 4 Drive 21.4   6 258 110 3.08 3.215 19.44  1  0    3    1  
## Hornet Sportabout 18.7   8 360 175 3.15 3.440 17.02  0  0    3    2  
## Valiant     18.1   6 225 105 2.76 3.460 20.22  1  0    3    1
```



Color Usage

Default color scheme in base R plot:

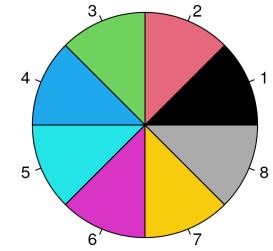
```
pie(rep(1, 8), col=1:8)
```



Color Usage

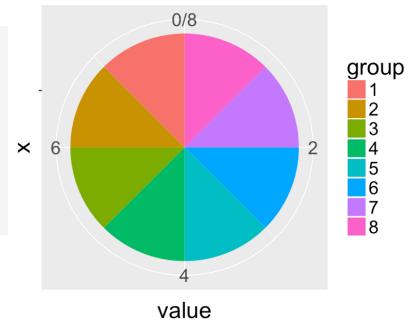
Default color scheme in base R plot:

```
pie(rep(1, 8), col=1:8)
```



Default color scheme in ggplot:

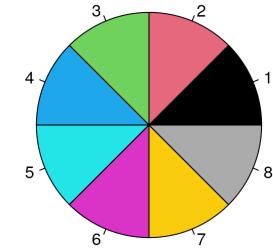
```
ggplot(data.frame(group = factor(seq_len(8)), value = rep(1, 8)),
       aes(x="", y=value, fill=group)) +
  geom_bar(width = 1, stat = "identity") +
  coord_polar("y", start=0) +
  theme(text = element_text(size = 20))
```



Color Usage

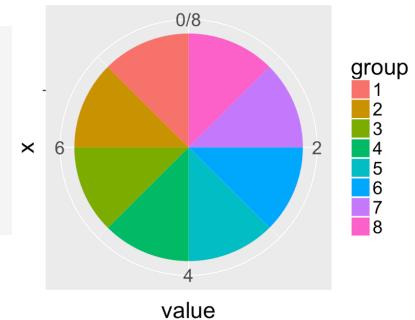
Default color scheme in base R plot:

```
pie(rep(1, 8), col=1:8)
```



Default color scheme in ggplot:

```
ggplot(data.frame(group = factor(seq_len(8)), value = rep(1, 8)),
       aes(x="", y=value, fill=group)) +
  geom_bar(width = 1, stat = "identity") +
  coord_polar("y", start=0) +
  theme(text = element_text(size = 20))
```



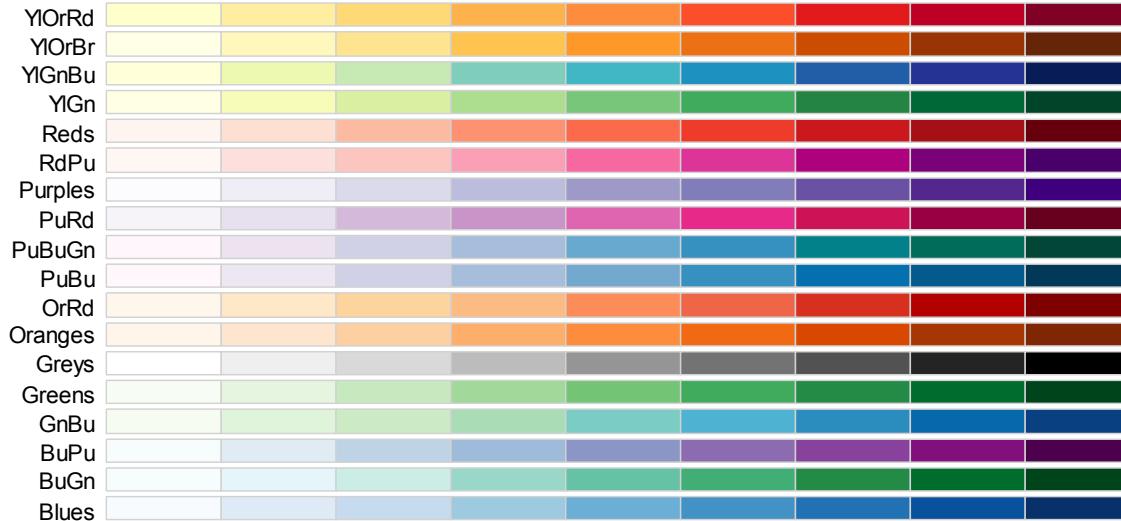
When choosing a coloring scheme, consider these:

- Different requirements for line & area colors
- Many people are **red-green color-blind**
- Lighter colors tend to make areas look larger than darker colors
→ **use colors of equal luminance for filled areas.**

RColorBrewer

```
display.brewer.all()
```

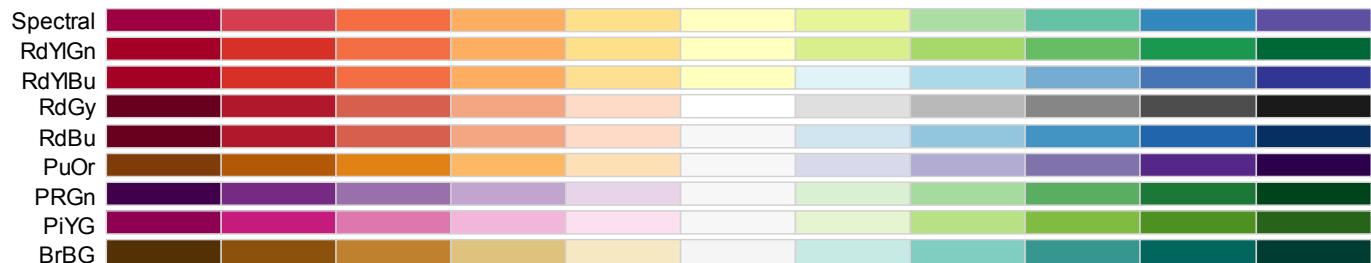
sequential



qualitative



diverging



Viridis Palettes

```
install.packages("viridis")
library(viridis)
```

Simply add: `scale_color_viridis()`
`scale_fill_viridis()`.

to your plot

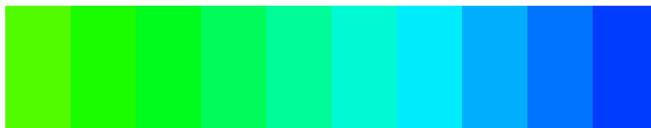


Viridis Palettes

Color scales are designed to be:

- **Colorful and Pretty**, spanning as wide a palette as possible so as to make differences easy to see,
- **Perceptually uniform**, the perceived difference between two colors is proportional to the Euclidian distance within the color space
- **Robust to colorblindness**, looks good in grey scale and to people with common forms of colorblindness

You can hear more about the science behind creating these color scales, on Walt and Smith's [talk at SciPy 2015](#).

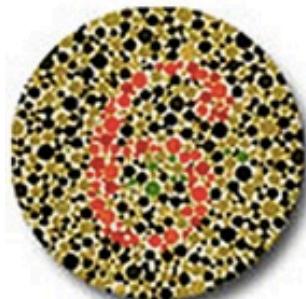


not perceptually uniform

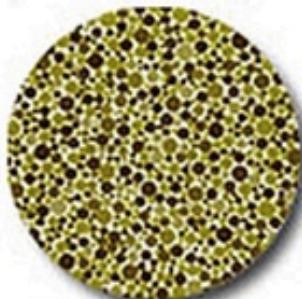


perceptually uniform

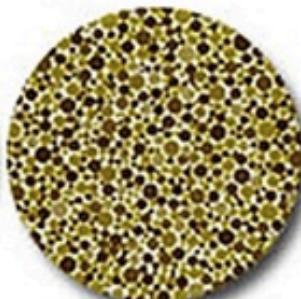
Be kind to colorblind people



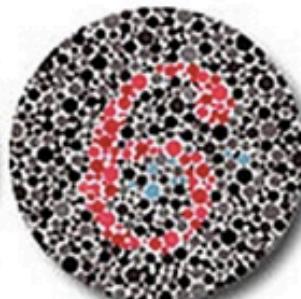
Normal Vision



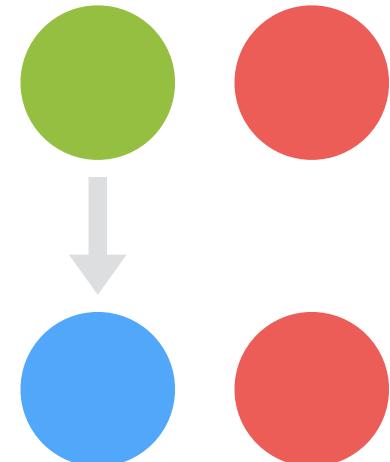
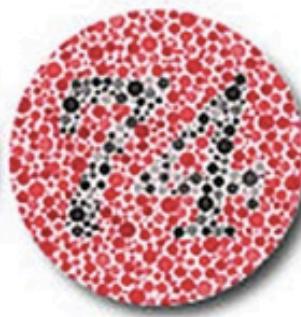
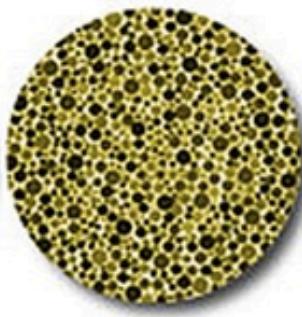
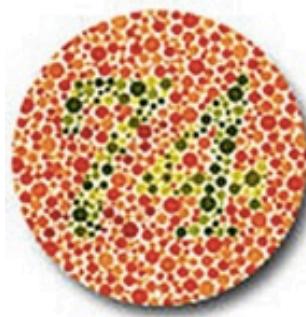
Protanope Vision



Deuteranope Vision



Tritanope Vision

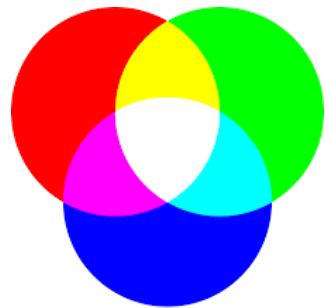


Simple solution: replace greens by blues.

Blues also display better on most monitors than greens.

Colour models

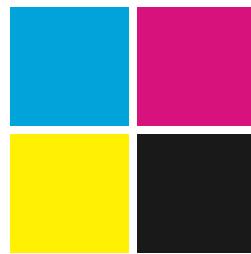
How are colours defined?



RGB

Light emitting screens

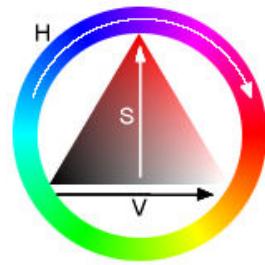
Red **G**reen **B**lue
additive



CMYK

Printing, ink

Cyan **M**agenta **Y**ellow **B**lack
subtractive



HSV
HSB

coordinates in
human perception
space

Faceting is useful to show more dimensions without overcrowding the graph

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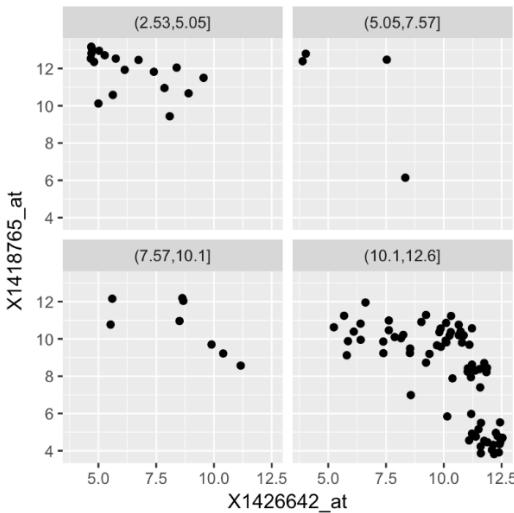


Figure 3.33: Faceting: the same data as in Figure 3.9, split by the continuous variable X1450989_at and arranged by facet_wrap.

Trellis — chart that uses multiple instances of the same chart

facet_wrap

```
ggplot(mutate(dftx, Tdgf1 = cut(X1450989_at, breaks = 4)),  
       aes( x = X1426642_at, y = X1418765_at)) + geom_point() +  
       facet_wrap( ~ Tdgf1, ncol = 2 )
```

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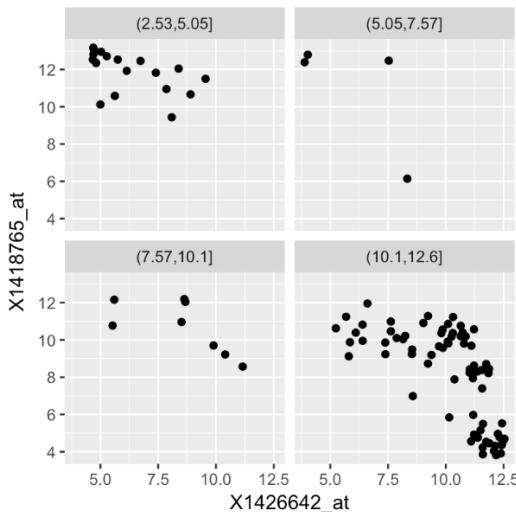


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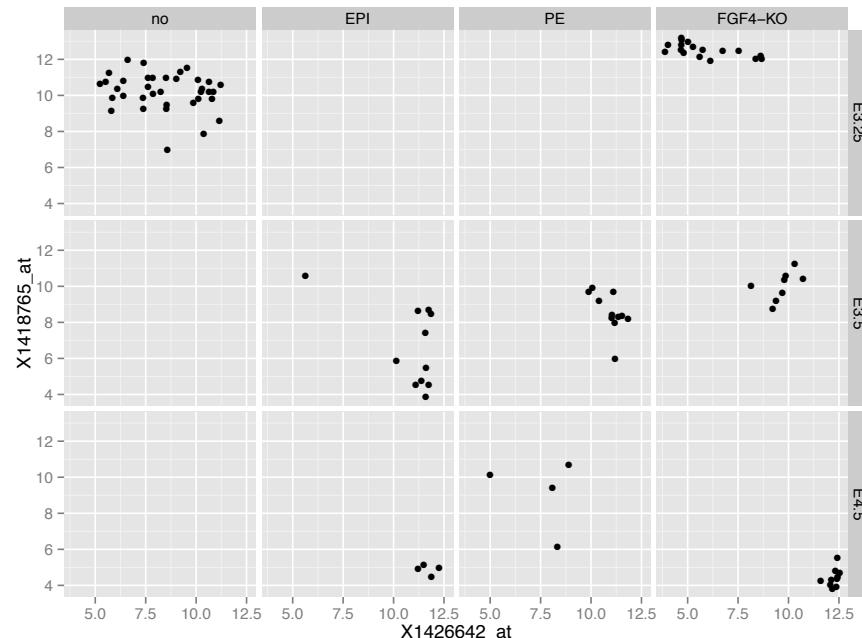
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facet_grid

```
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```



Faceting is useful to show more dimensions without overcrowding the graph

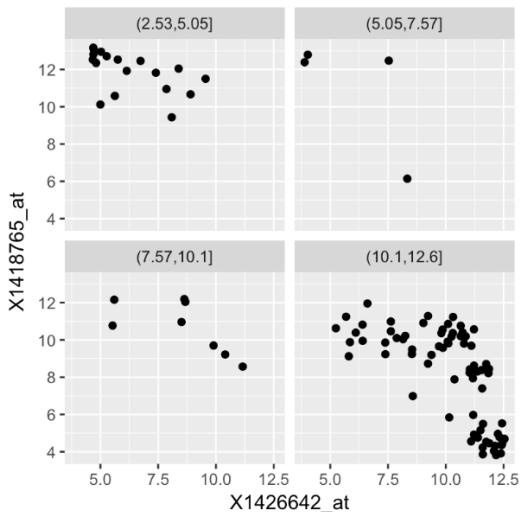


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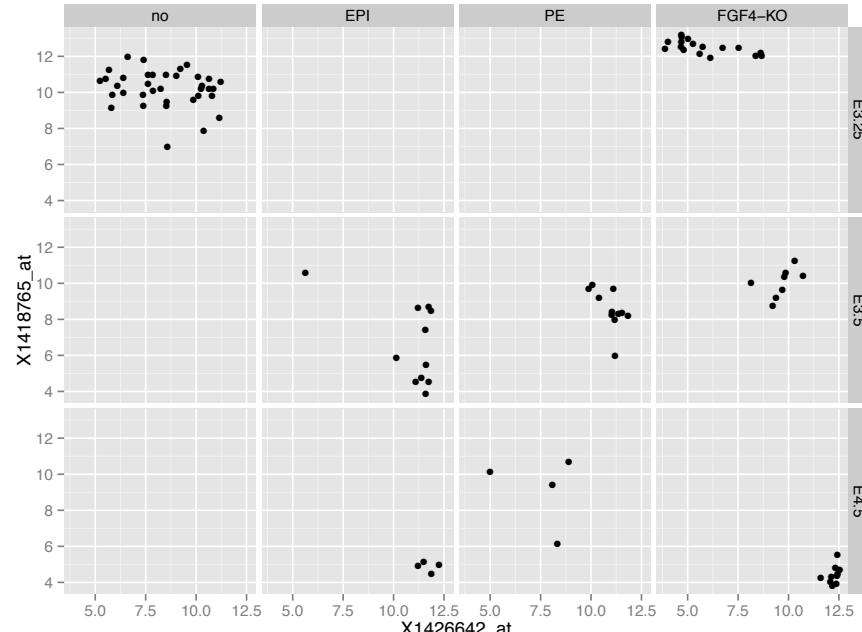
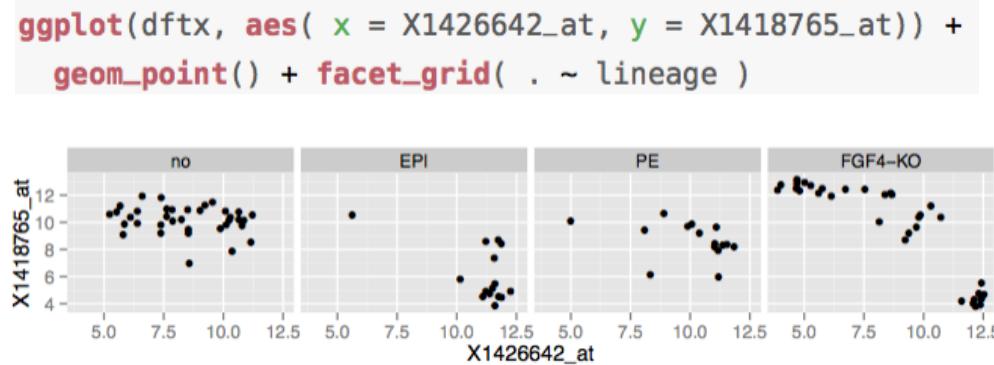
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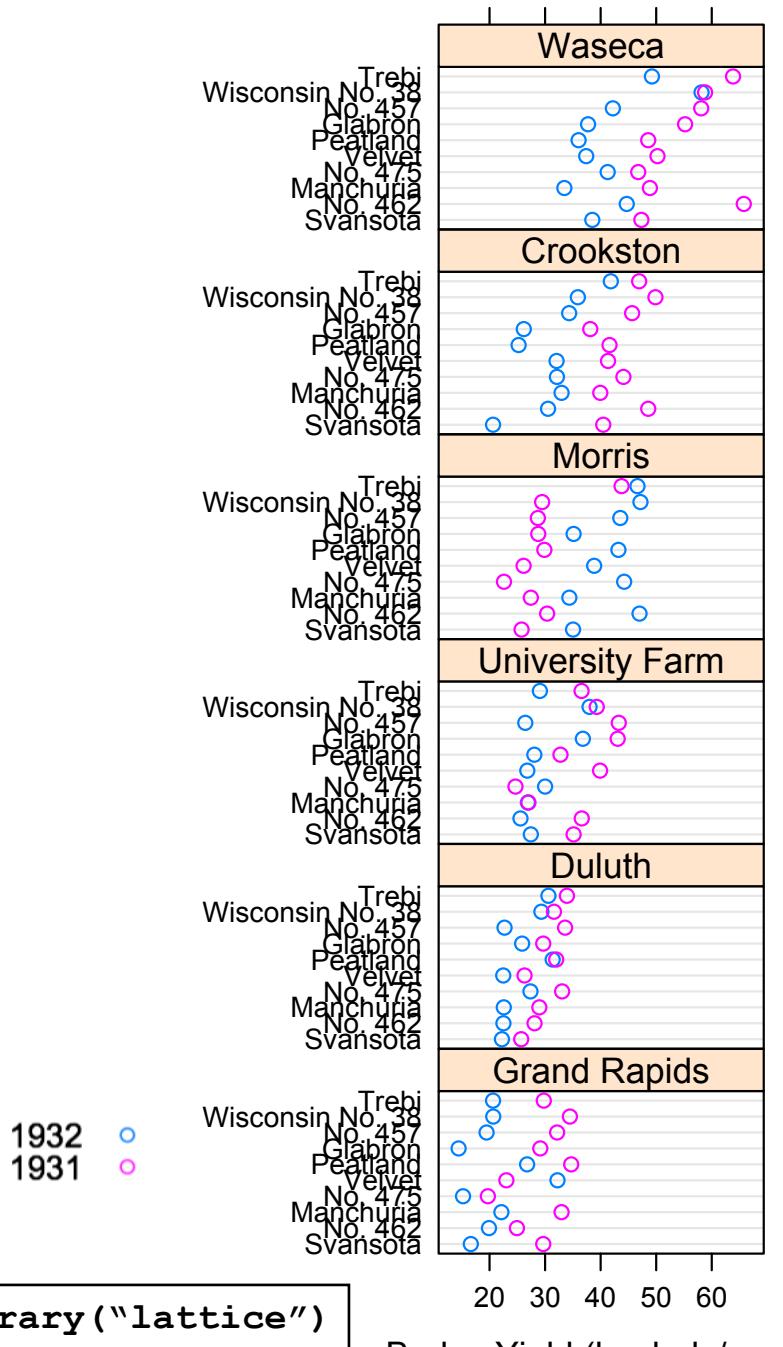
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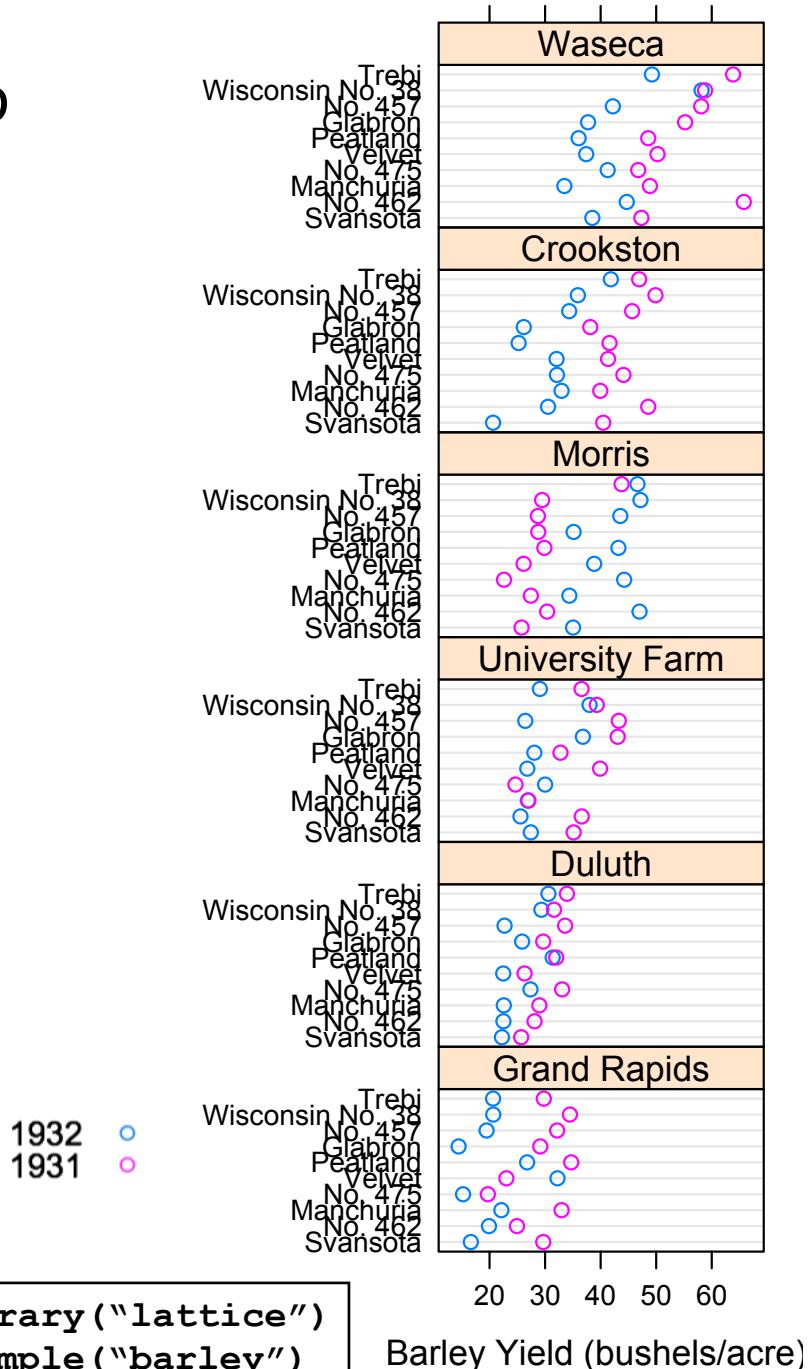
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```
library("lattice")
example("barley")
```

Data from an agricultural field trial to study the crop barley.

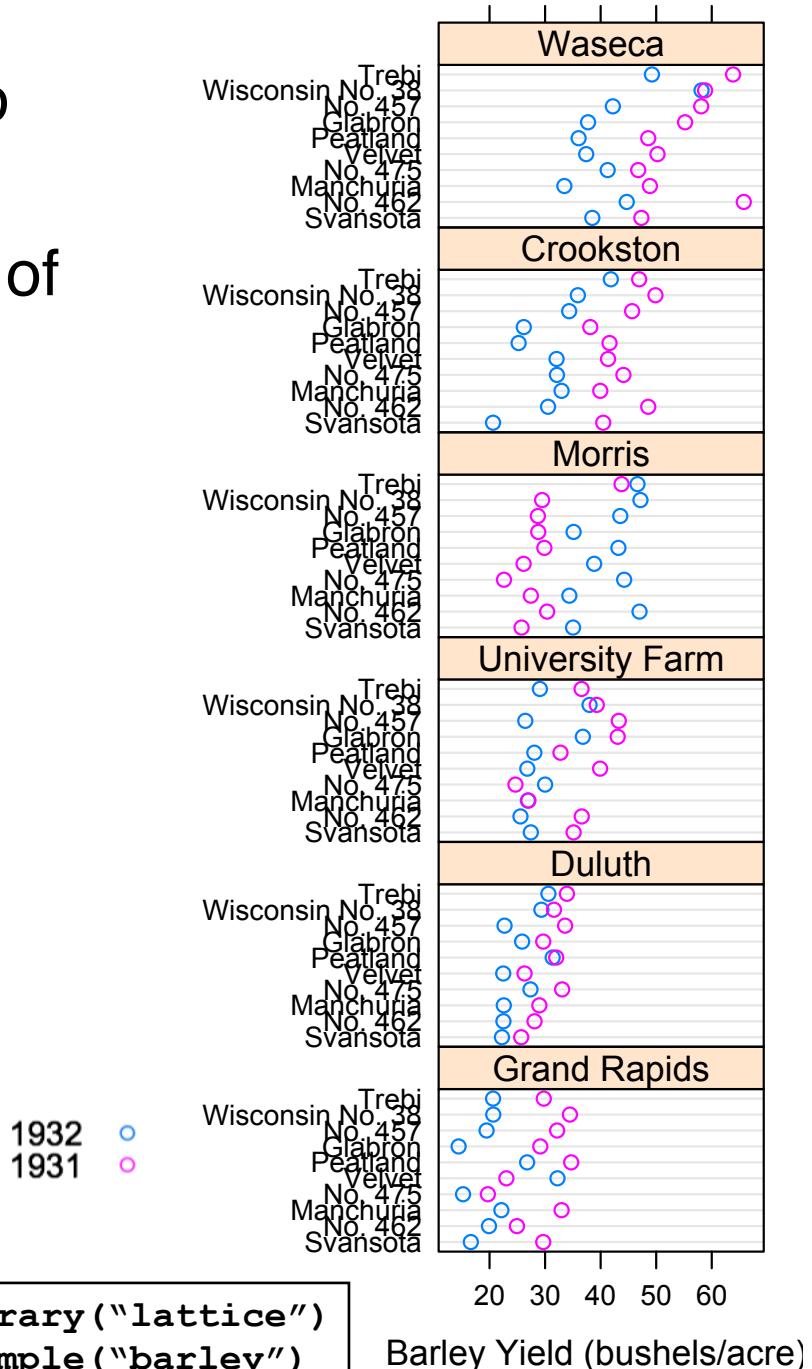


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Barley Yield (bushels/acre)

Data from an agricultural field trial to study the crop barley.

At 6 sites in Minnesota, 10 varieties of barley were grown in each of two years.



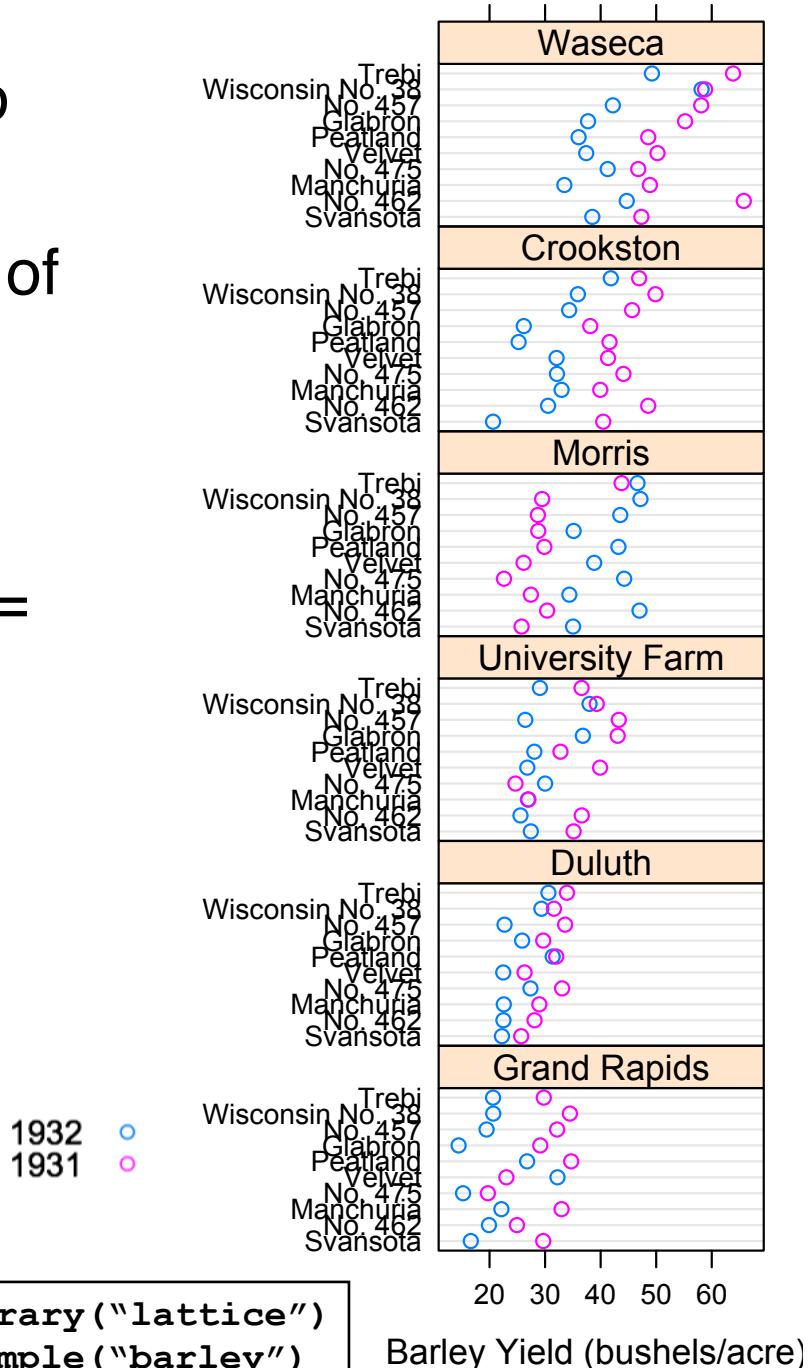
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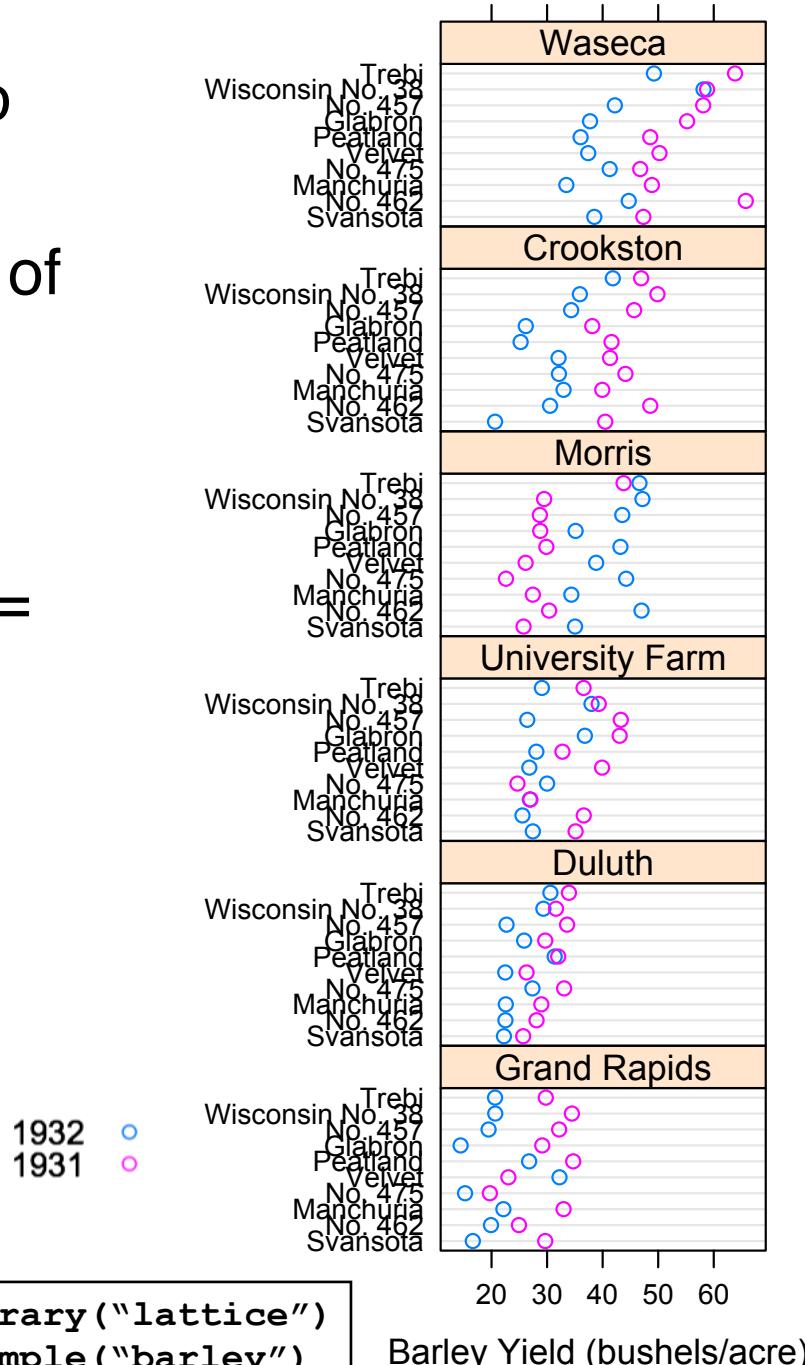
Data: yield, for all combinations of site, variety, and year ($6 \times 10 \times 2 = 120$ observations)



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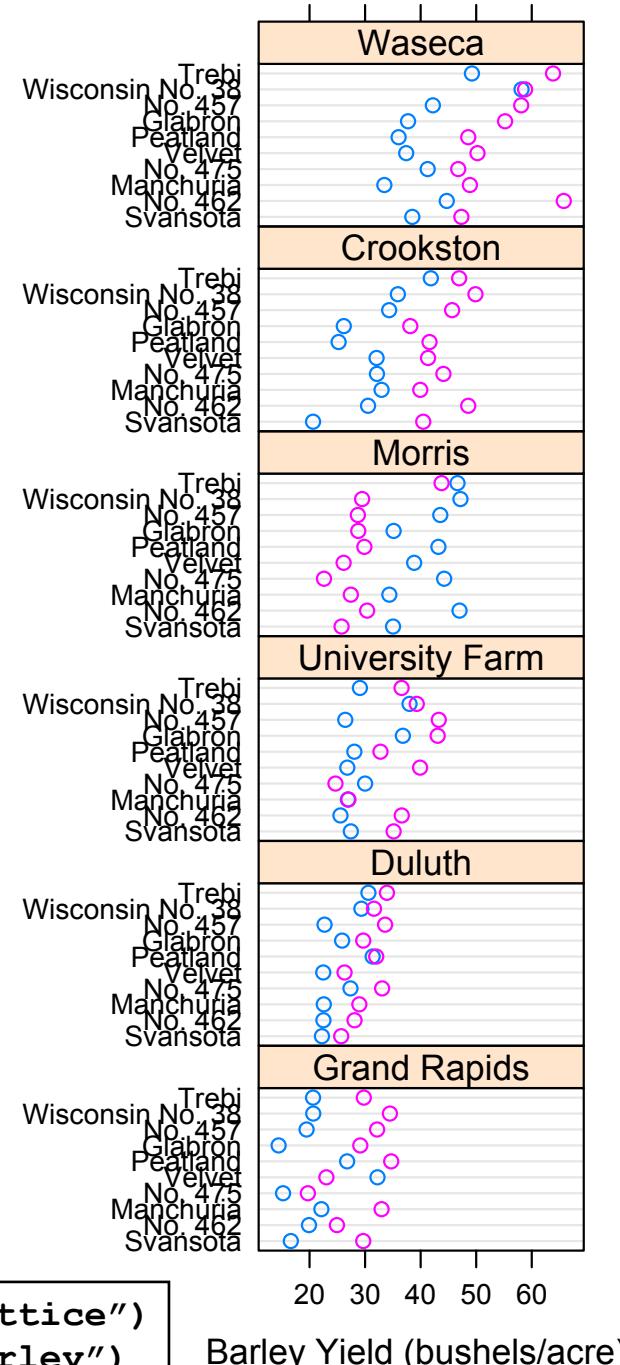
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Note the data for **Morris** - reanalysis in the 1990s using Trellis revealed that the years had been flipped!

1932 ○
1931 ●



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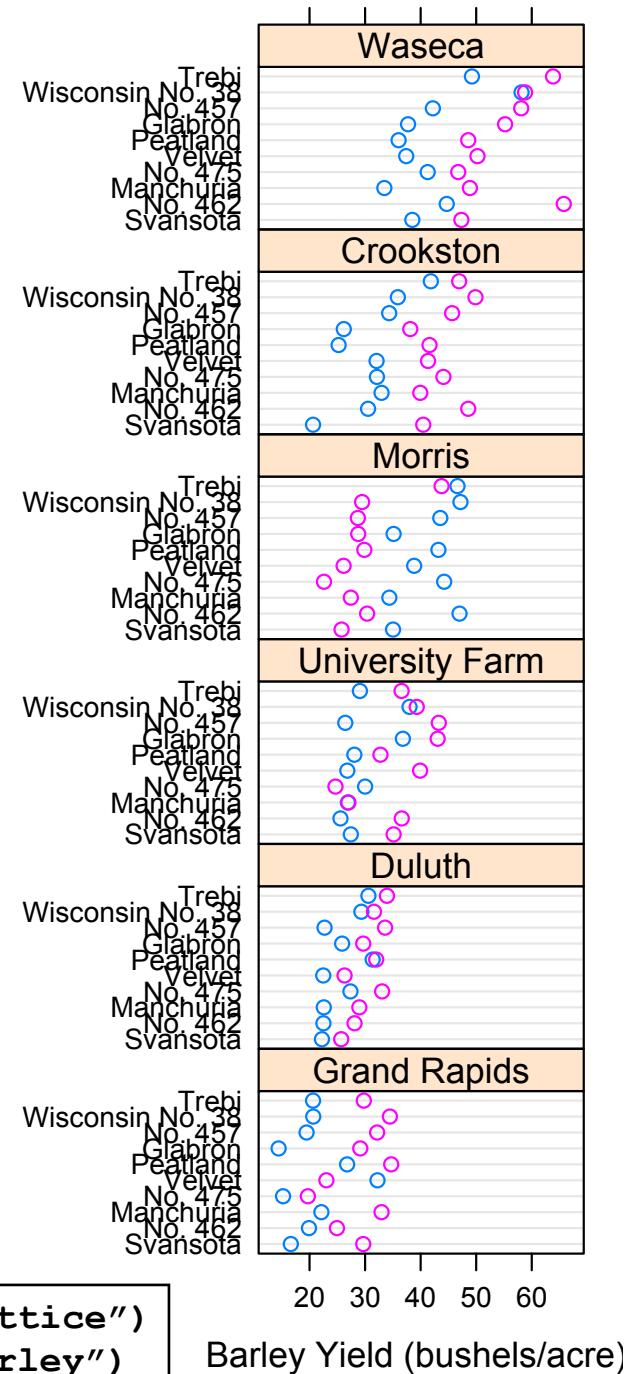
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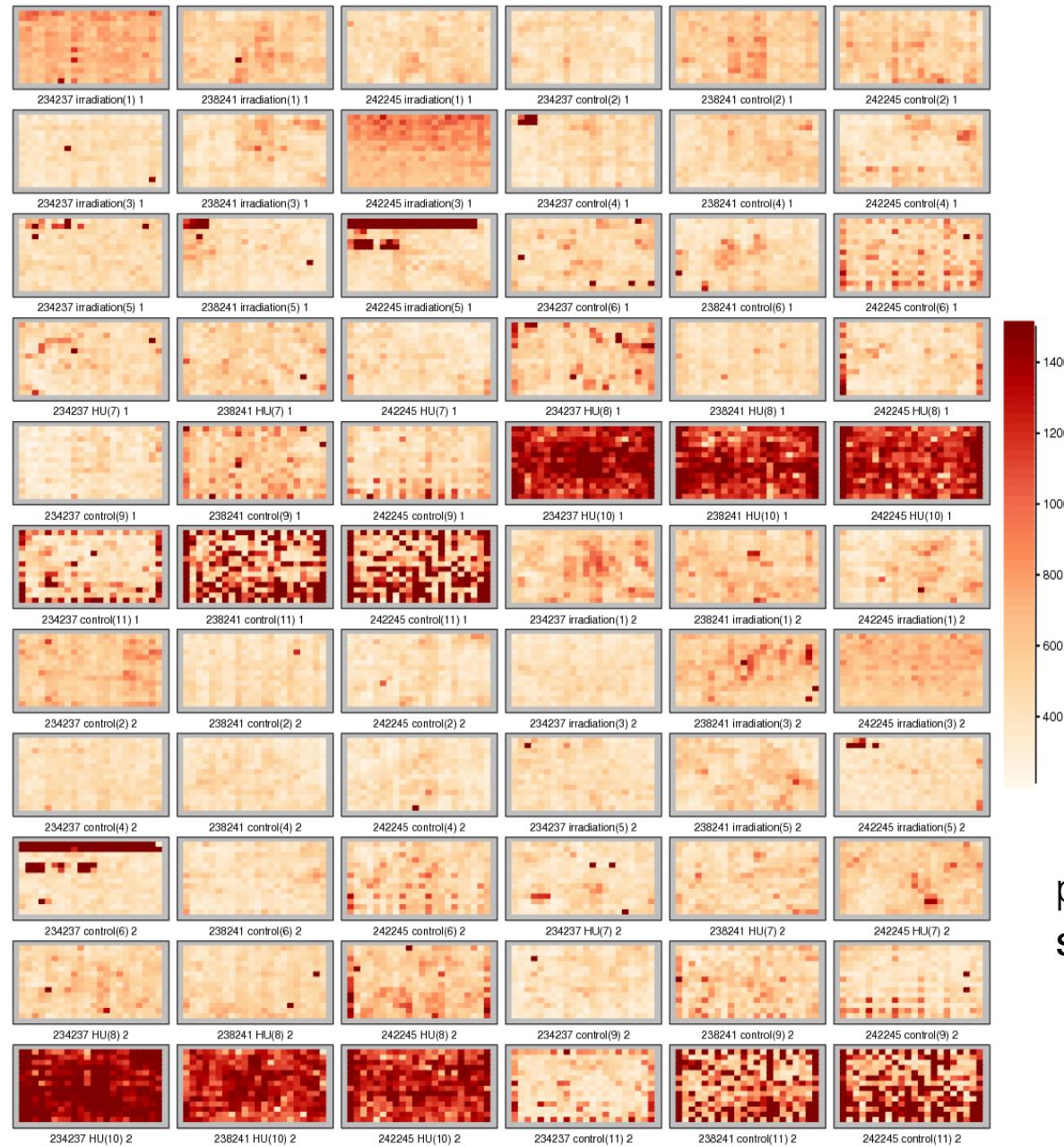
1932 ○
1931 ●

How could you quickly check for potential batch effects?

```
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example("barley")
```



EDA for finding batch effects



package
splots

Tidying data to use columns as aesthetics

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Data.frame in R can be in:

wide format

```
##           X1420085_at X1418863_at X1425463_at X1416967_at  
## 1 E3.25      3.027715    4.843137    5.500618    1.731217  
## 2 E3.25      9.293016    5.530016    6.160900    9.697038  
## 3 E3.25      2.940142    4.418059    4.584961    4.161240  
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To switch wide ↔ long: pivot_longer, pivot_wider

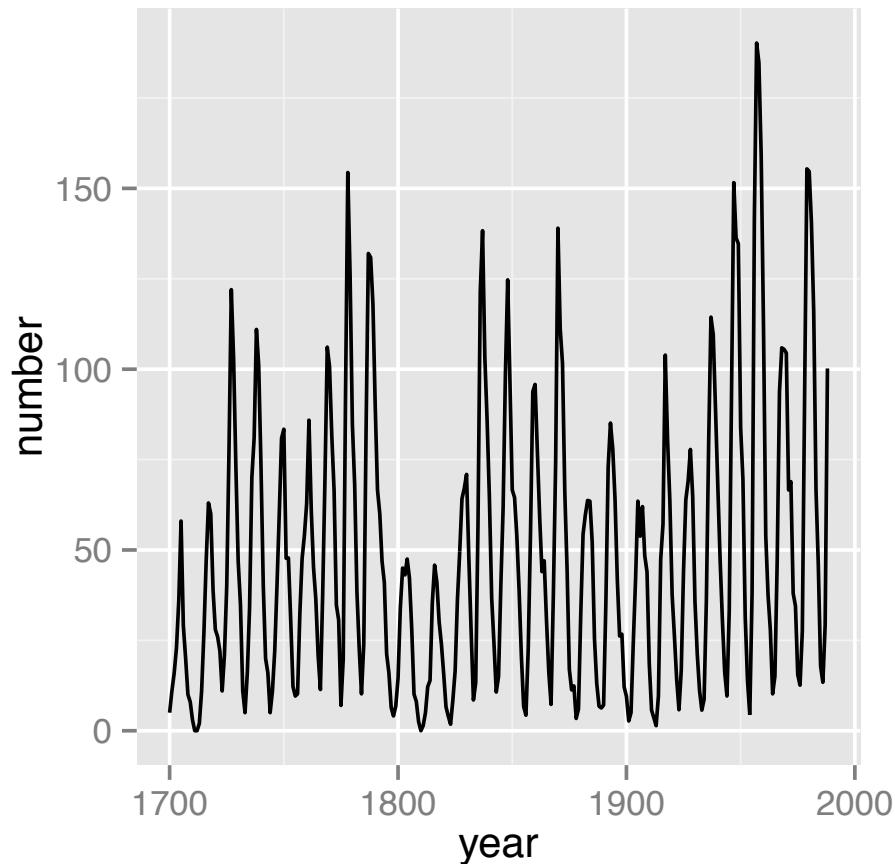
Choose aspect ratio so that banking = 45%

Yearly sunspot numbers 1849-1924 - changes in amplitude

Banking to 45 degrees:

Choose aspect ratio so that the median absolute slope is 1, i.e. at 45 degrees angle.

Sawtooth: Sunspot cycles typically rise more rapidly than they fall — steep rise and slow decline.



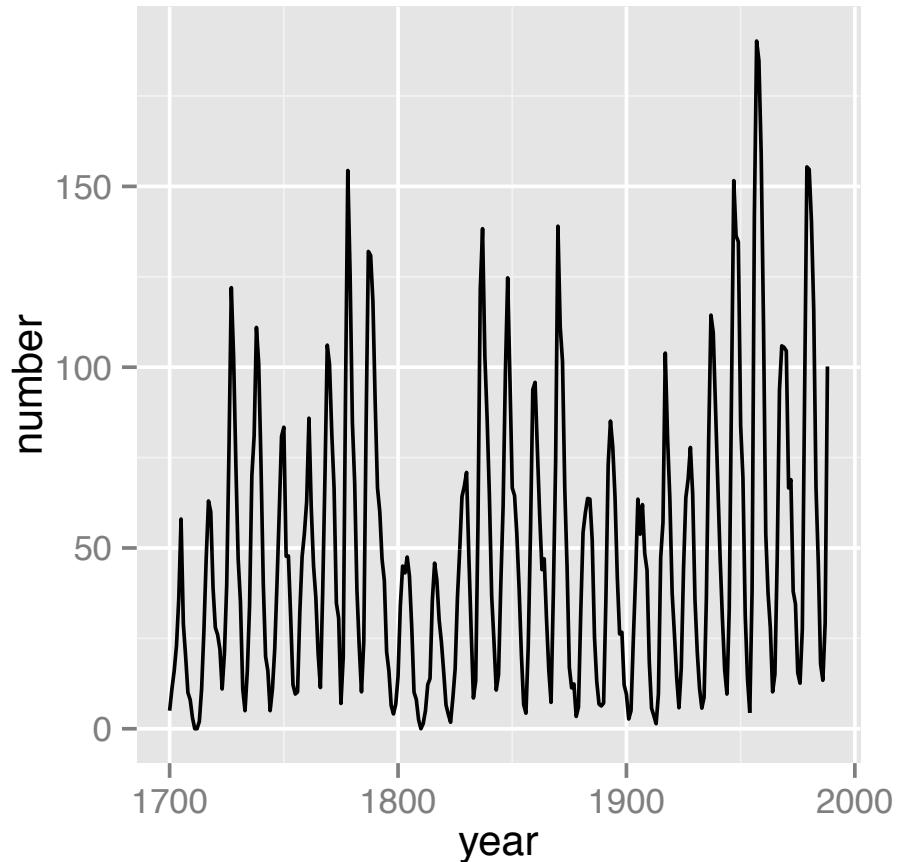
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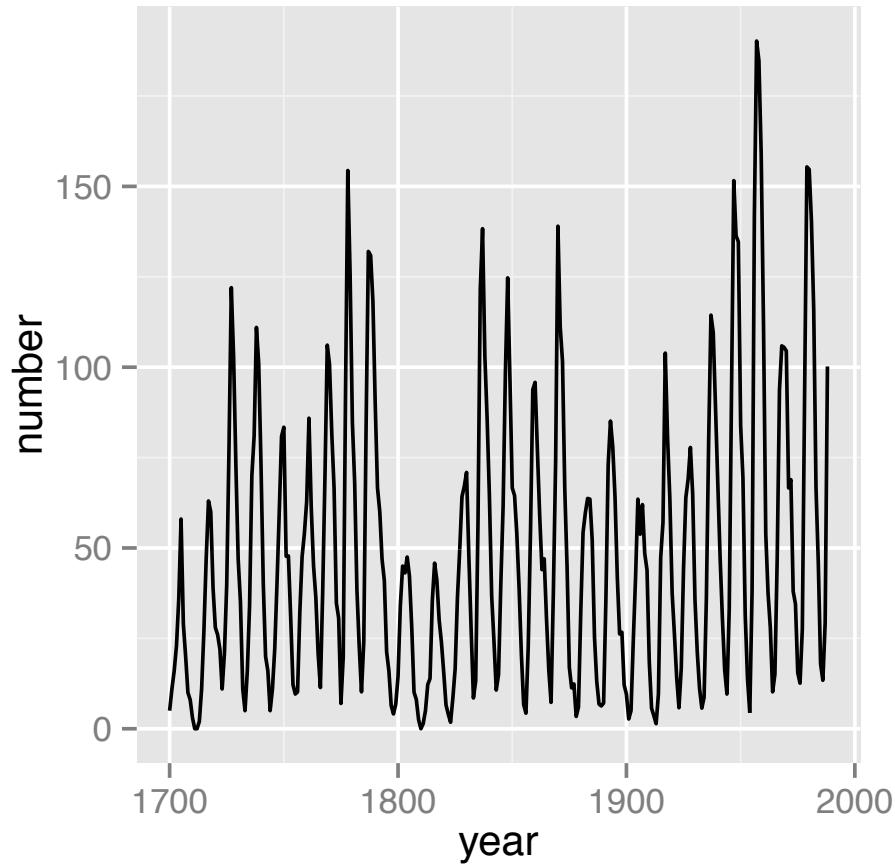
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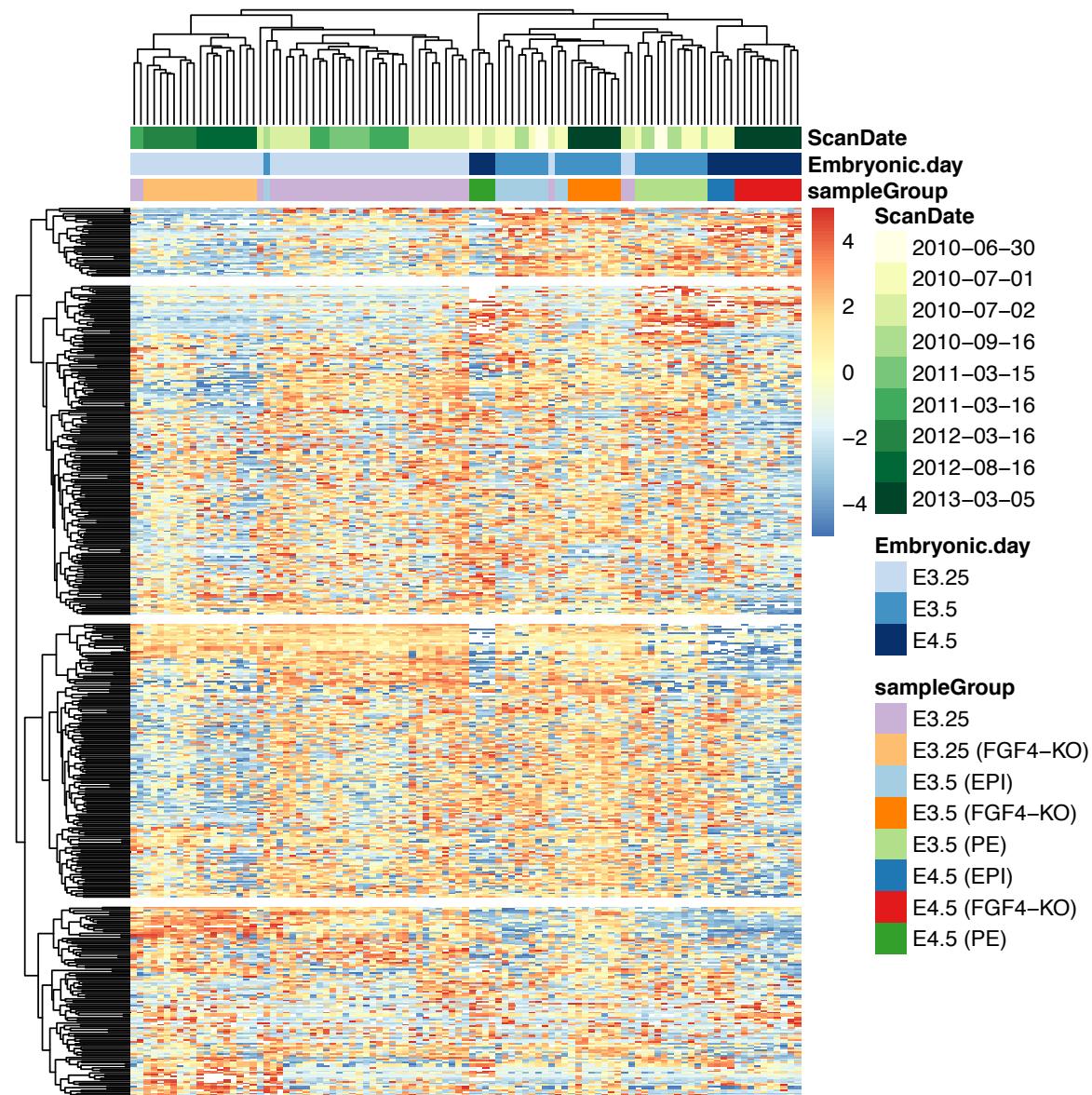


For plots where x- and y-axis have same units:
use 1:1 aspect ratio

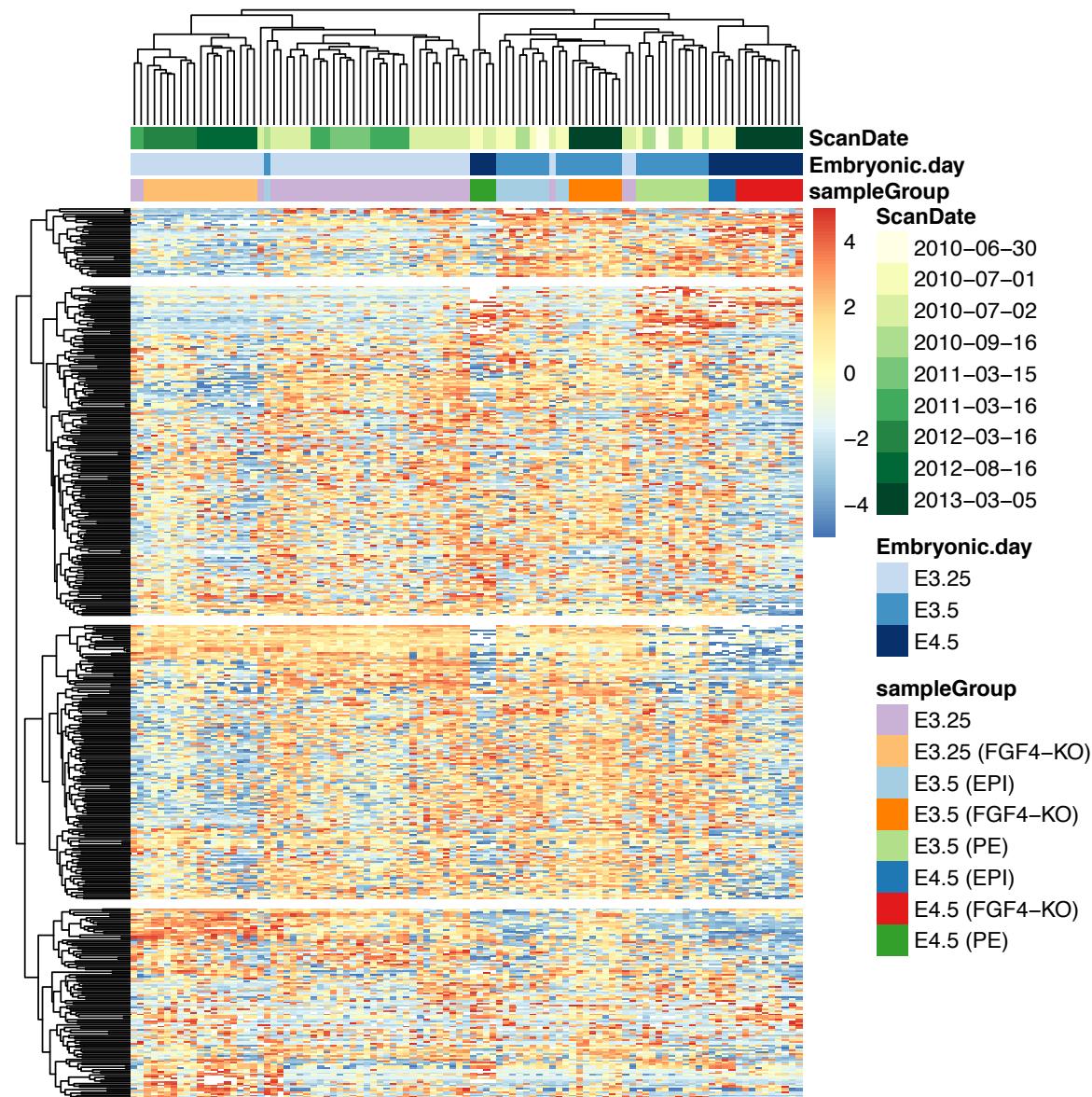


Heatmaps for visualizing large matrices

Heatmaps for visualizing large matrices



Heatmaps for visualizing large matrices



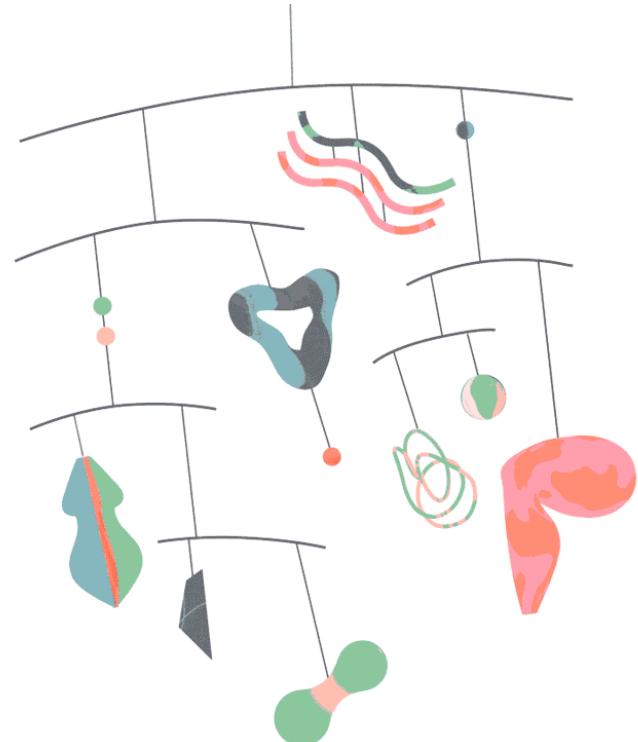
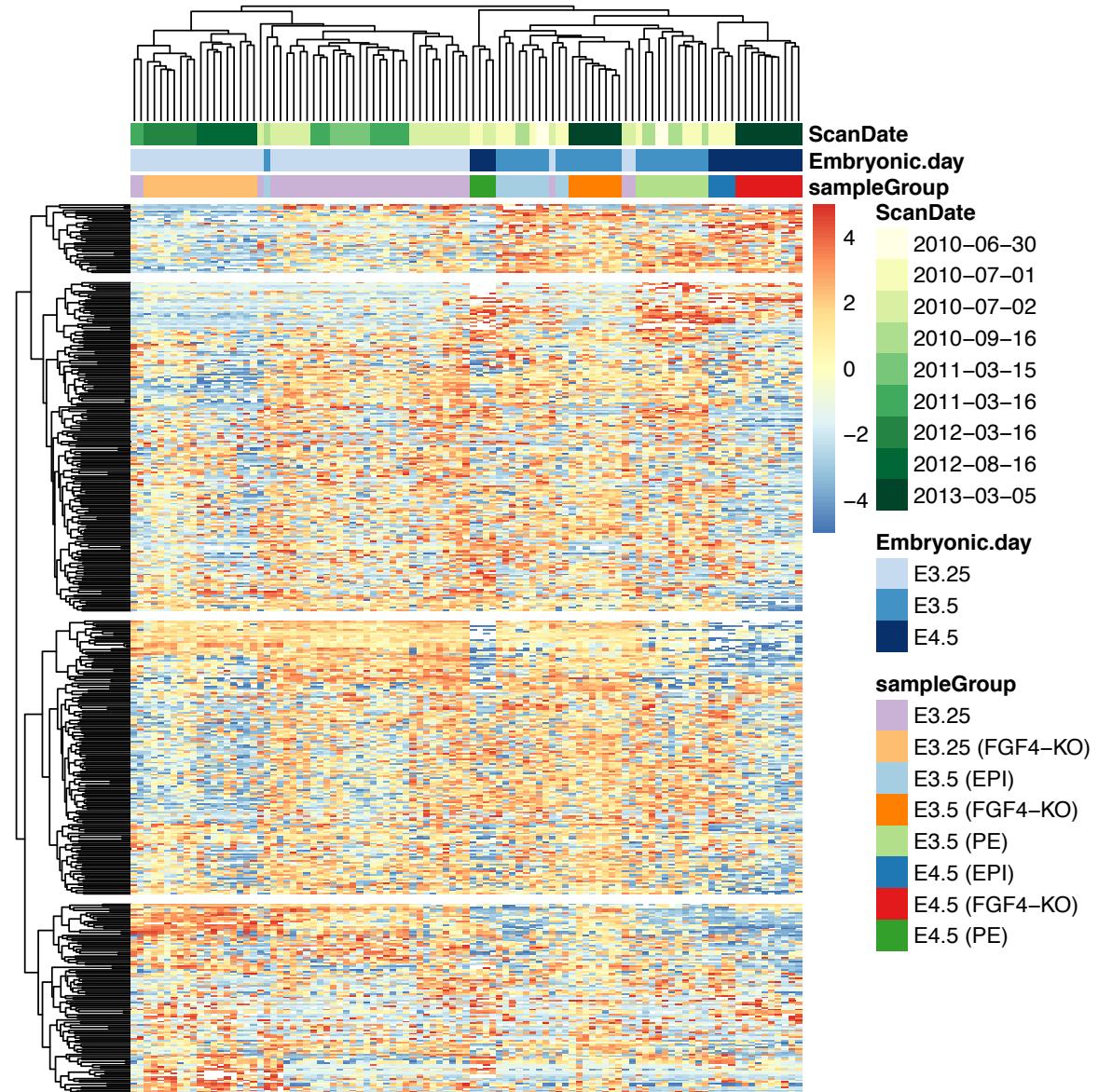
pheatmap

- many “reasonable” defaults
- easy to add column and row ‘metadata’ at the sides

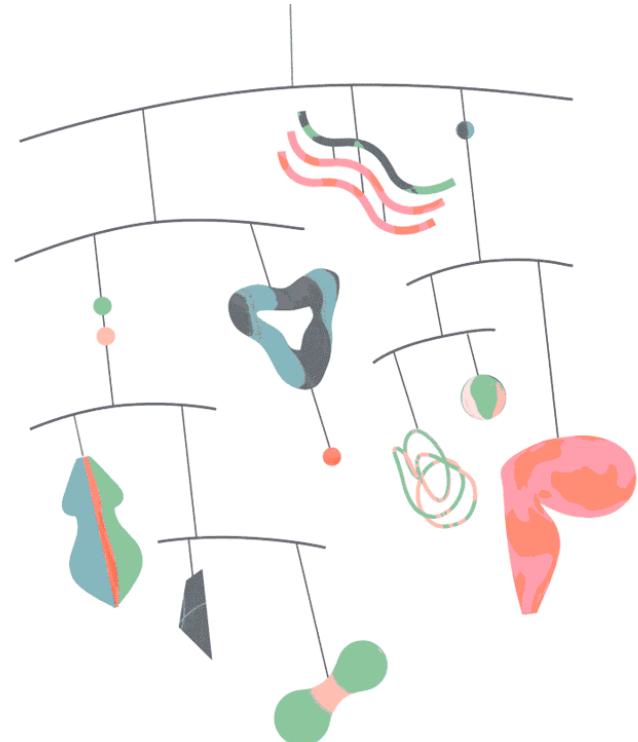
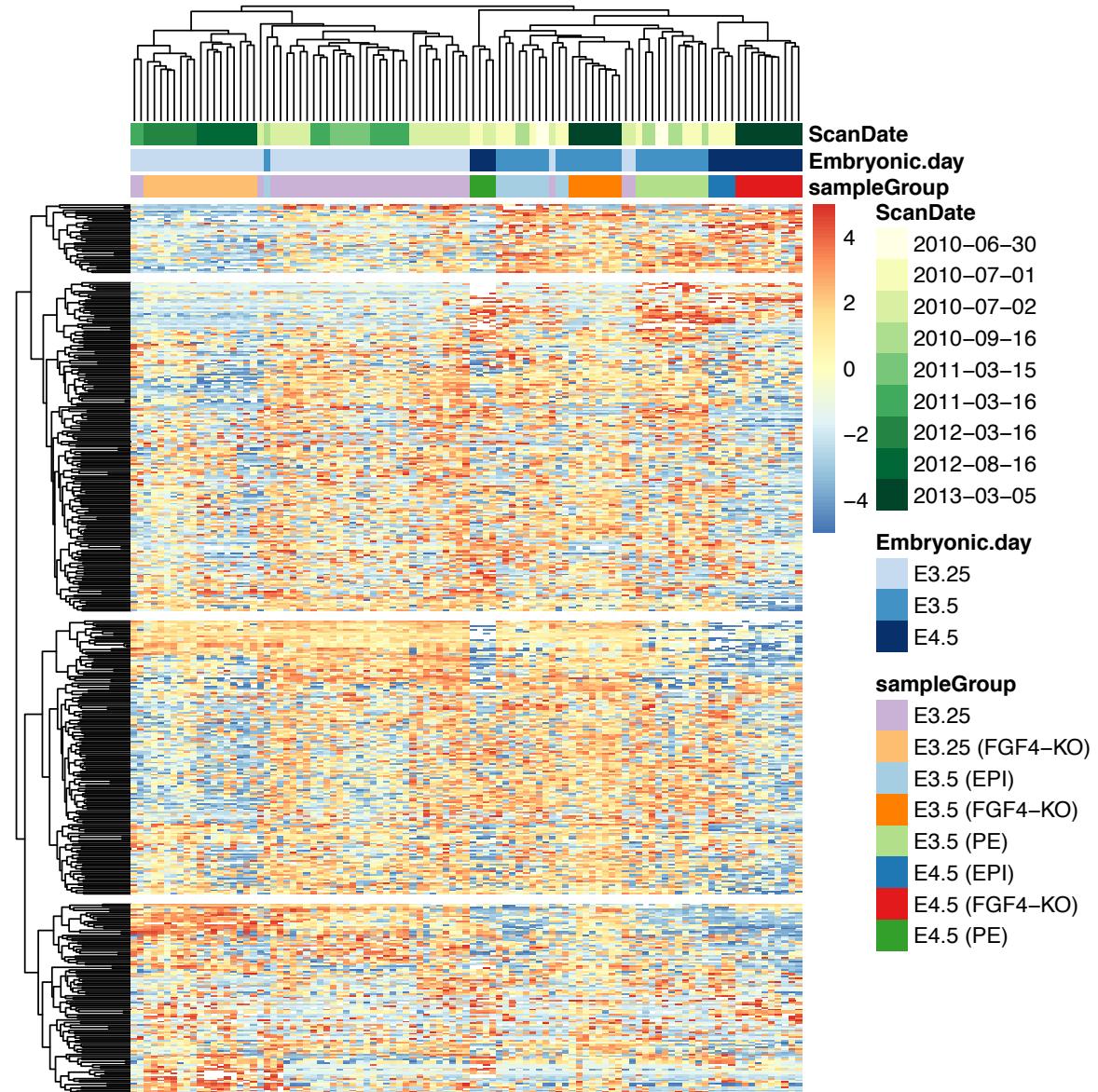
See also

ComplexHeatmap
package

The order of dendrogram branches is not unique



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Interactivity

Use shiny or plotly

<https://shiny.rstudio.com/gallery/genome-browser.html>

Animations (time-dependent plots):

<https://gganimate.com>

Linked Charts

<https://anders-biostat.github.io/linked-charts/>

plotly interactive graphics

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More on plotly e.g. at <https://plotly-book.cpsievert.me/>

plotly interactive graphics demos

<https://chart-studio.plotly.com/~demos#/>

Further links

Advanced Data Visualization - Going Deeper with R

<https://rfortherestofus.github.io/going-deeper/slides/slides-data-visualization.html#1>

<https://ggplot2.tidyverse.org/>

Modern Statistics for Modern Biology

<https://www.huber.embl.de/msmb/03-chap.html>

Acknowledgements

Susan Holmes

Laura Marie J Symul

Hadley Wickham

Lan Huong Nguyen