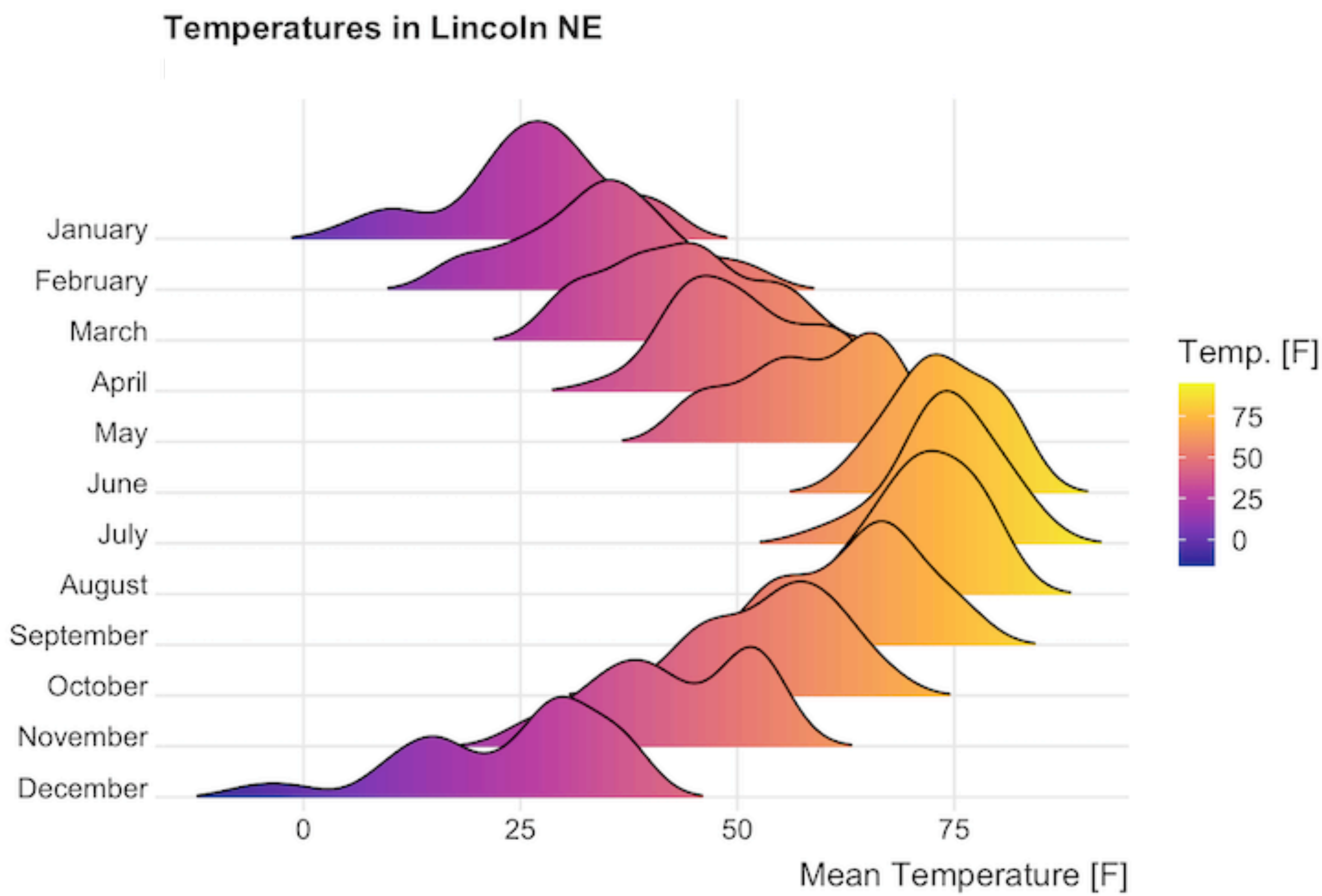

Graphics and Visualisation

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

	Vaccine Group (as Randomized)					
	BNT162b2 (30 μg) (N[a]=21669)		Placebo (N[a]=21686)			
Efficacy Endpoint Subgroup	n1[b]	Surveillance Time[c] (n2[d])	n1[b]	Surveillance Time[c] (n2[d])	VE (%)	(95% CI[e])
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).

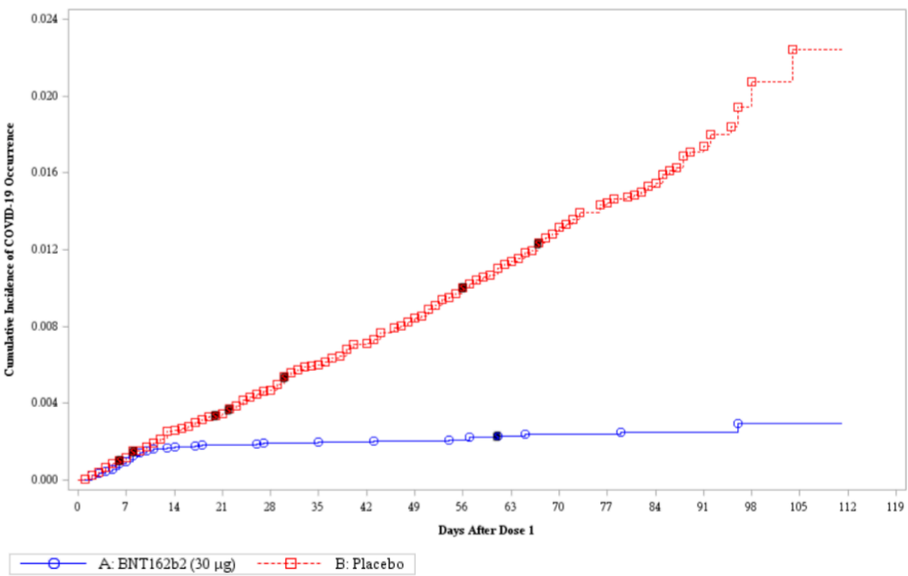

Figure 9. Cumulative Incidence Curves for the First COVID-19 Occurrence After Dose 1 – Dose 1 All-Available Efficacy Population

A picture says more than a thousand words

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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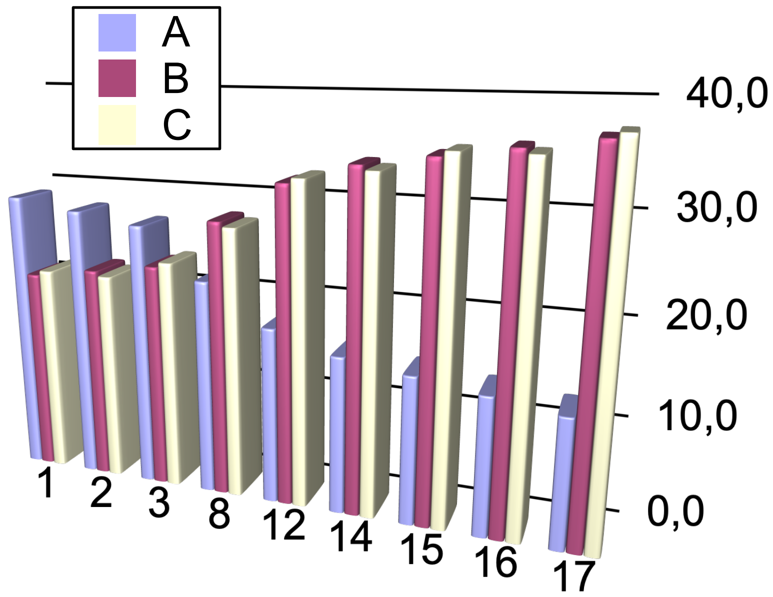

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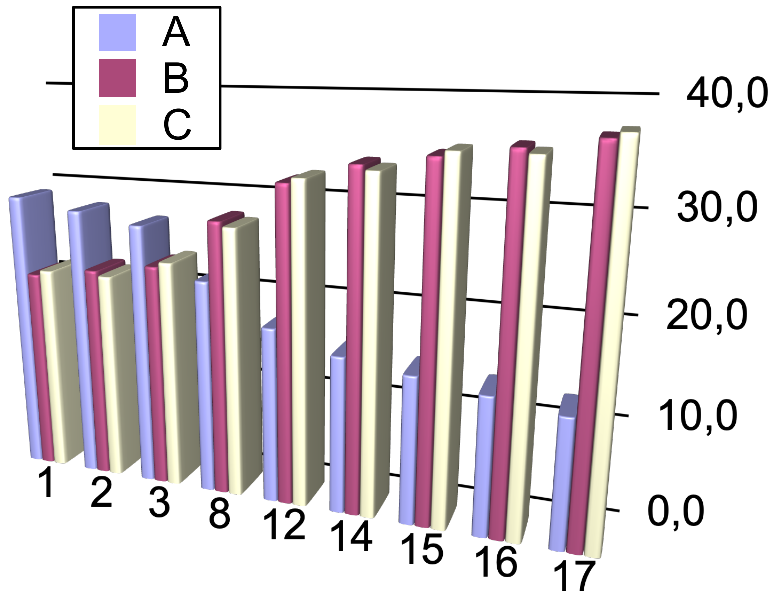
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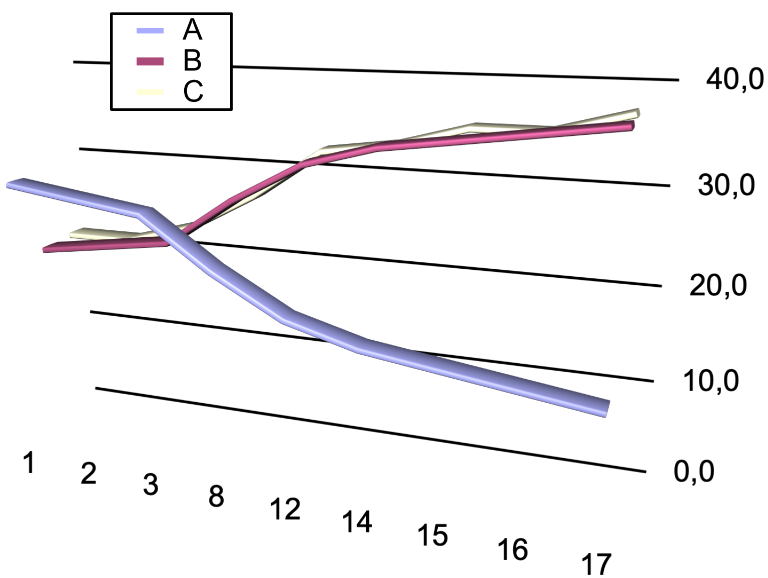
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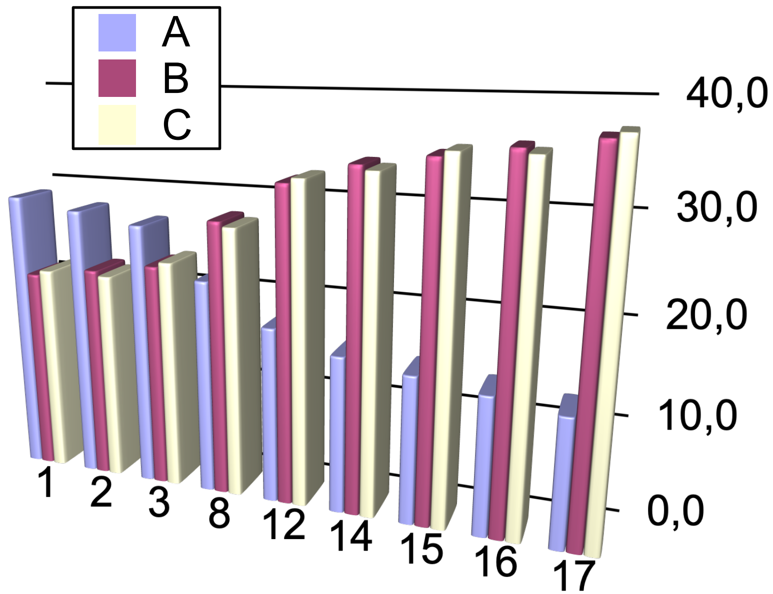
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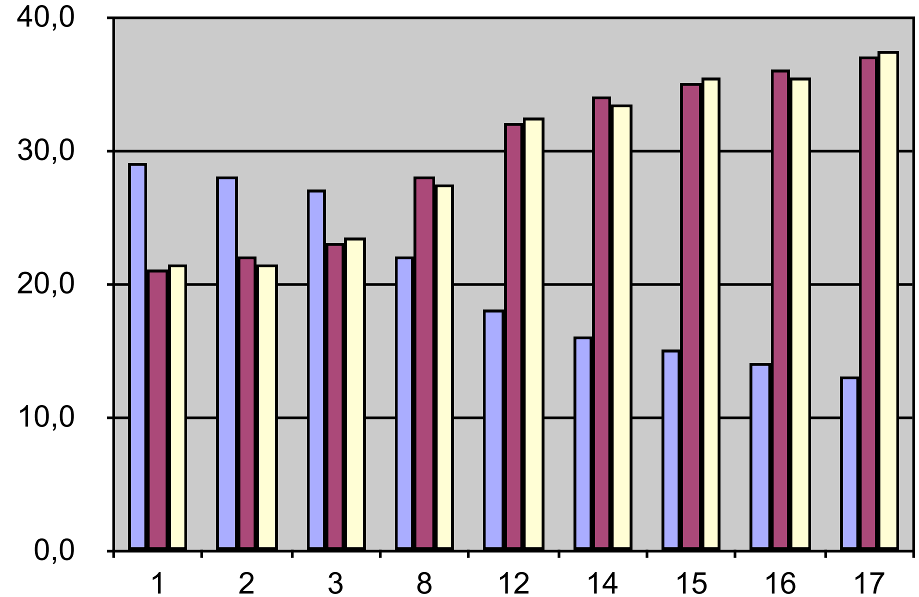
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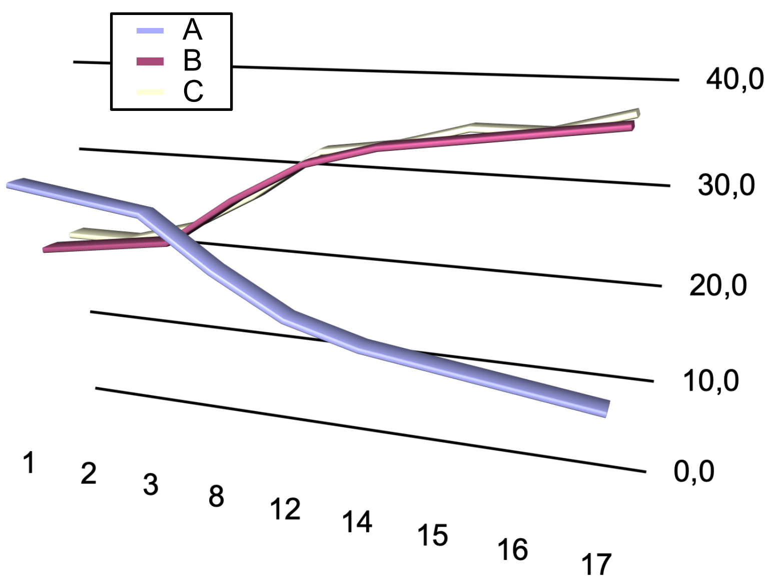
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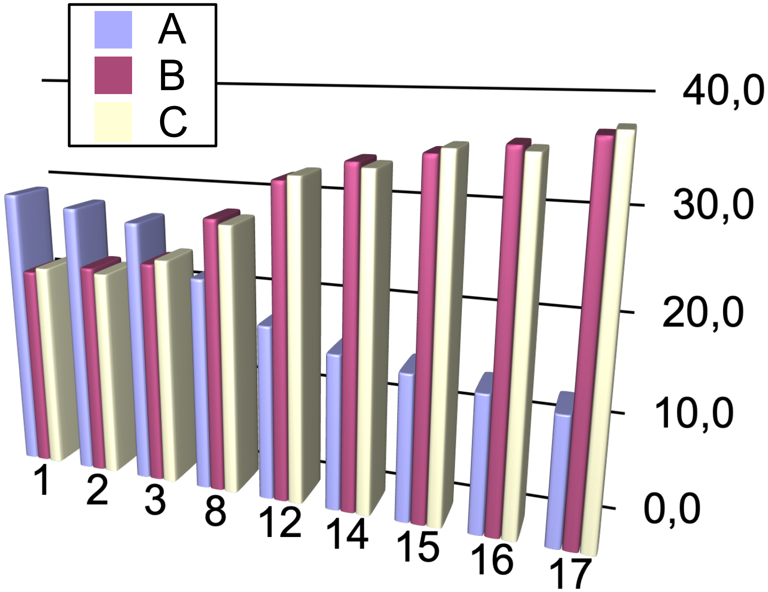
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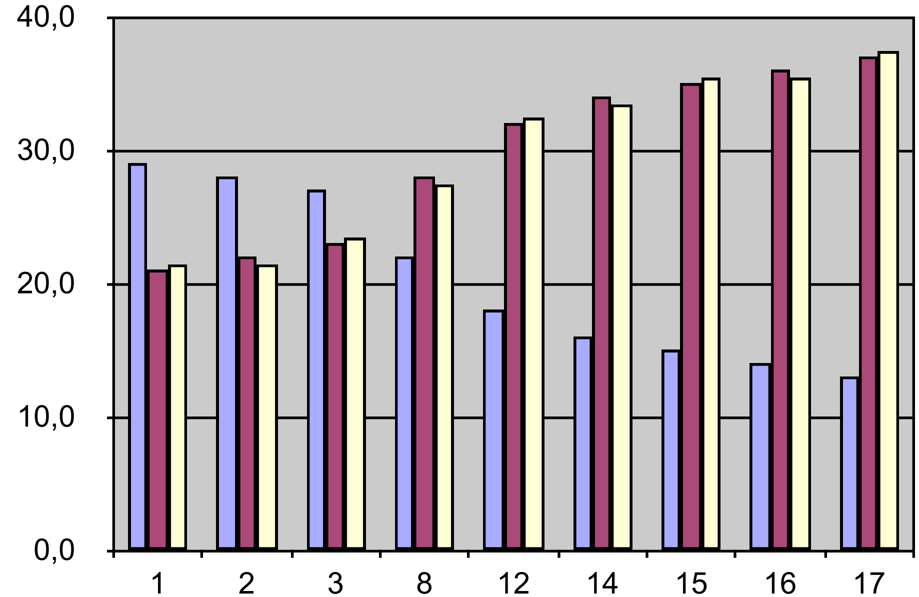
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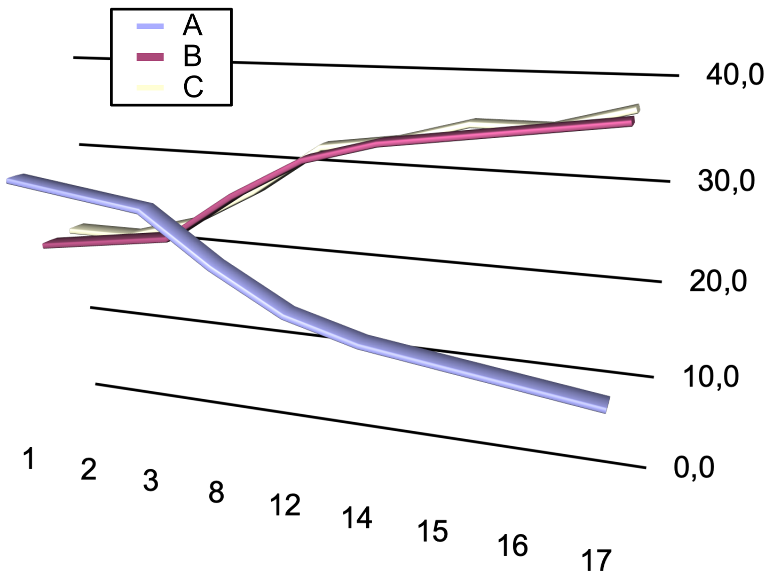
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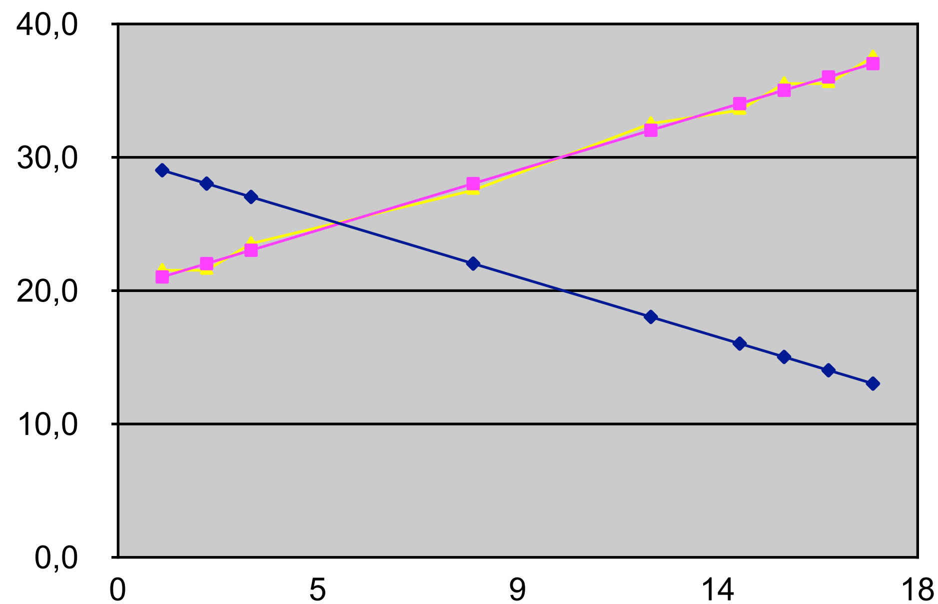
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18

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)
```

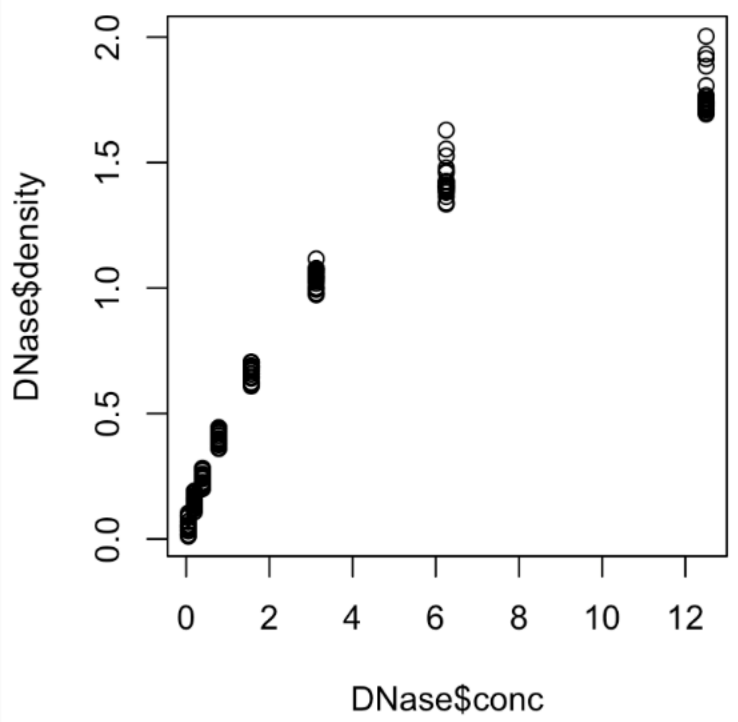


Figure 3.2: Plot of concentration vs. density for an ELISA assay of DNase.

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)
```

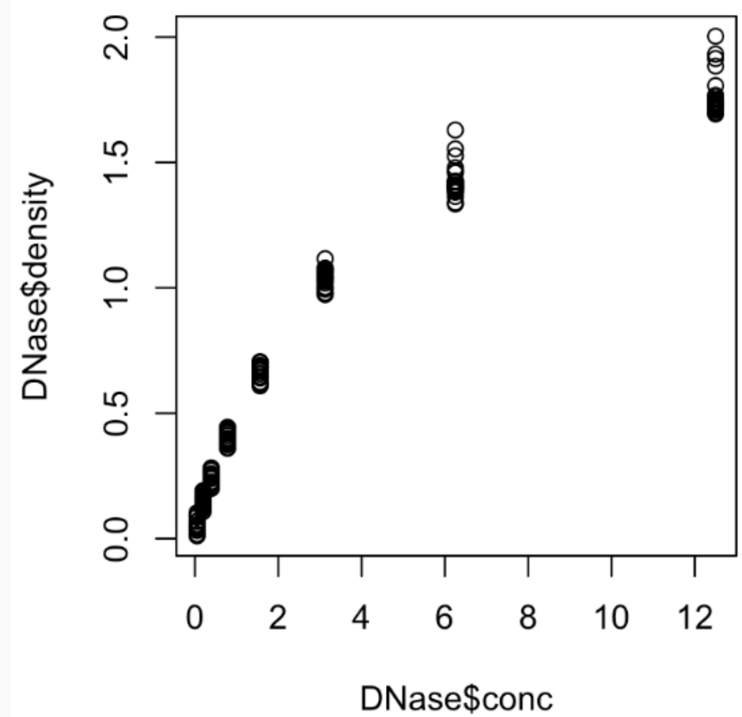
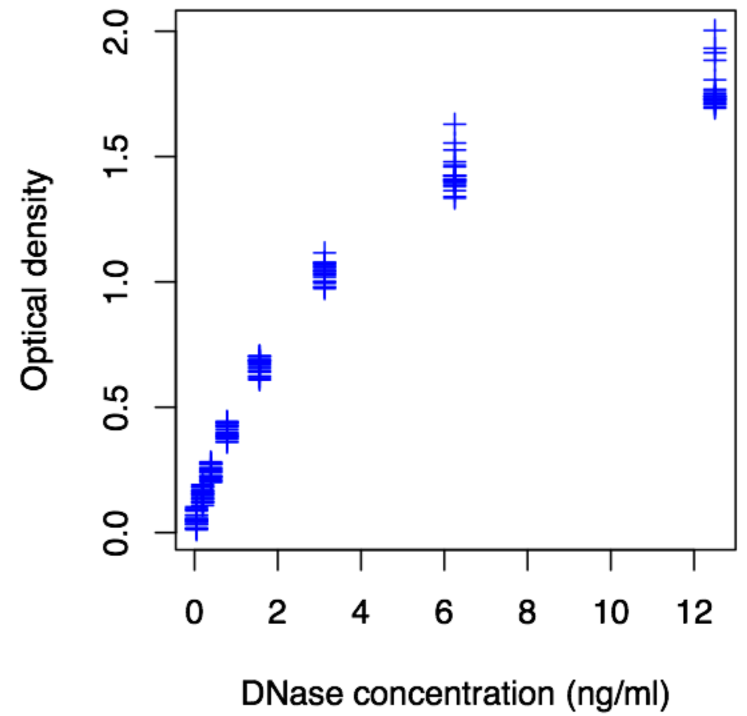


Figure 3.2: Plot of concentration vs. density for an ELISA assay of DNase.

base R plotting

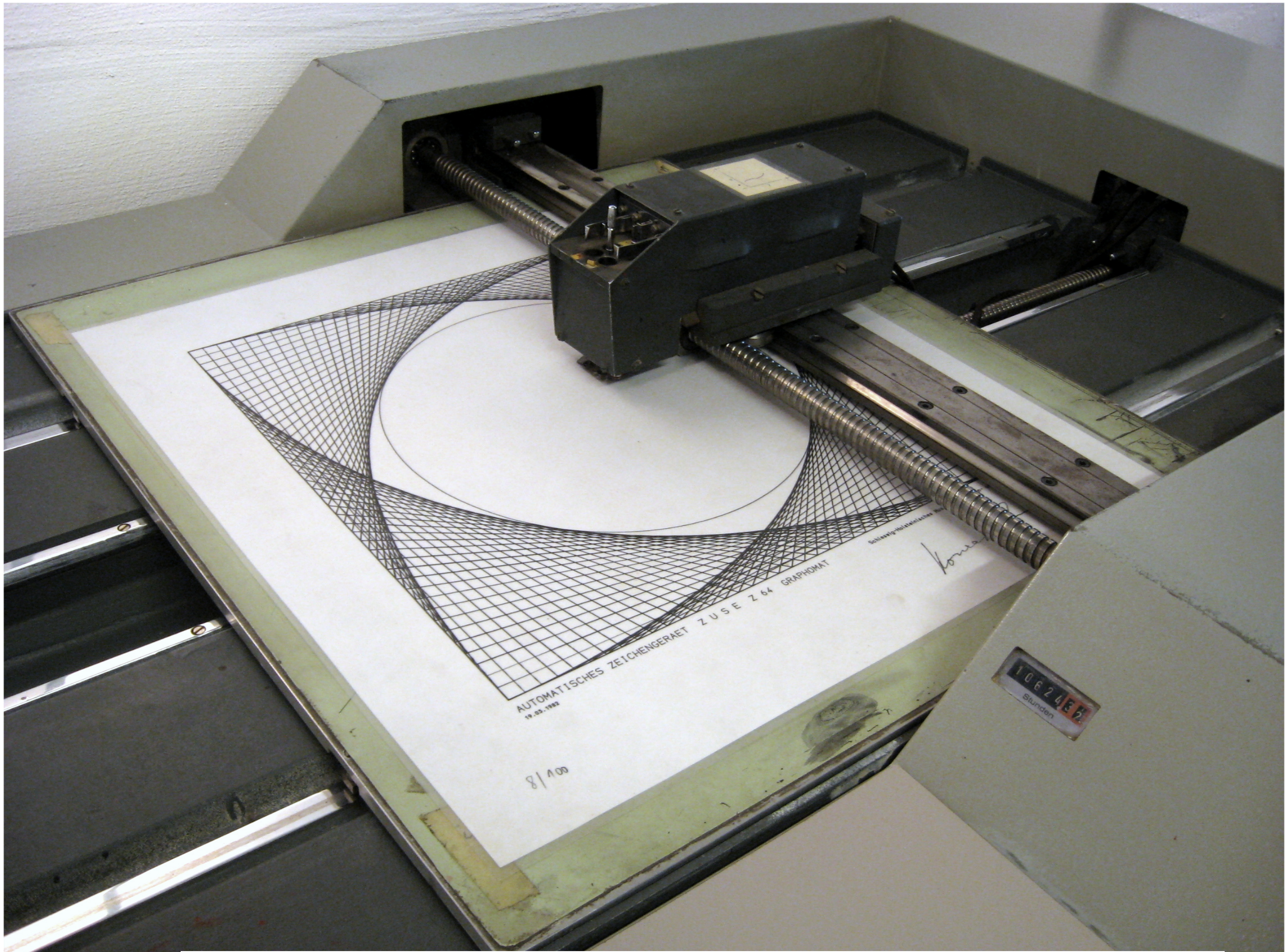
canvas model:
a series of instructions that **sequentially** fill the plotting canvas



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



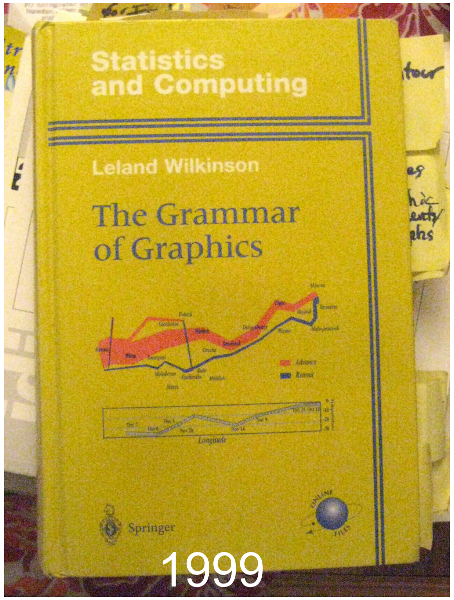
ZUSE Plotter Z64 (presented in 1961).

base R plotting

Drawbacks:

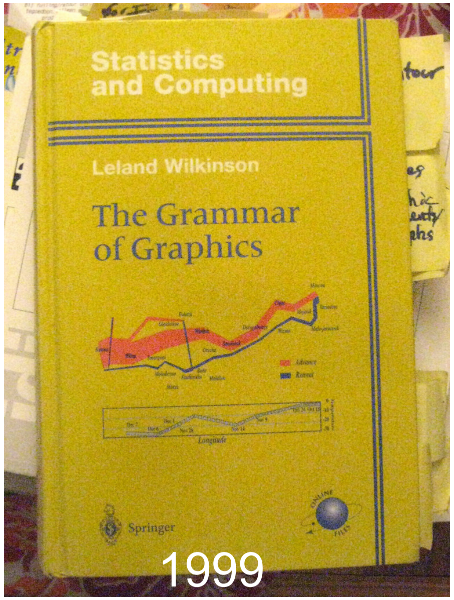
- **Layout choices have to be made at the beginning** with no overview over what may still be coming
- **Different functions for different plot types**, with different interfaces
- Routine tasks can require lots of **boilerplate code**
- **No concept of facets / lattices**
- Only a **single global coordinate**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

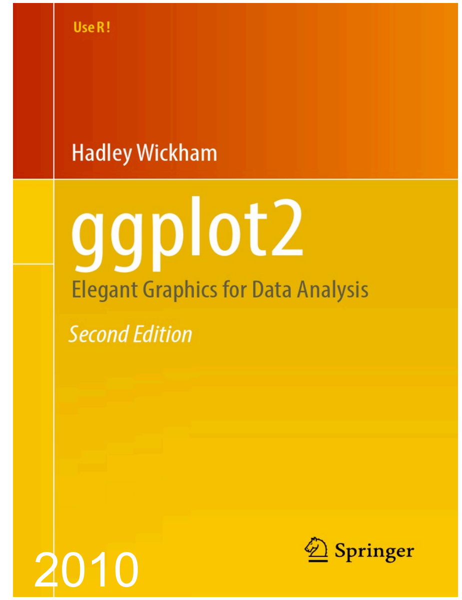
The Grammar of Graphics



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

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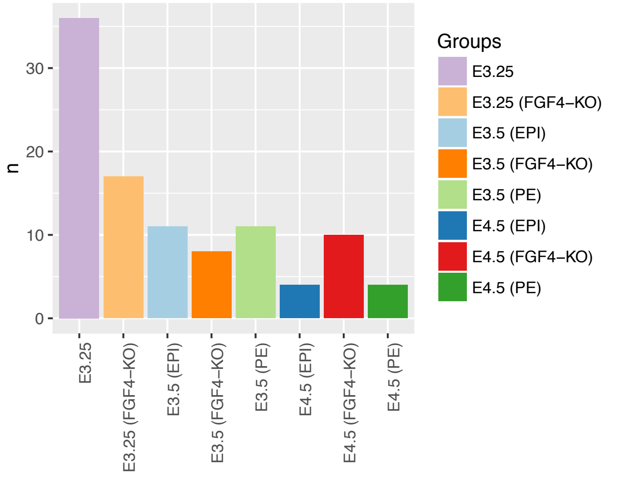
- **facets** separating subsets of data into multiple subplots,
- optional parameter settings e.g. text size, font, alignment, legend positions

```
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(Hiiragi2013)
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

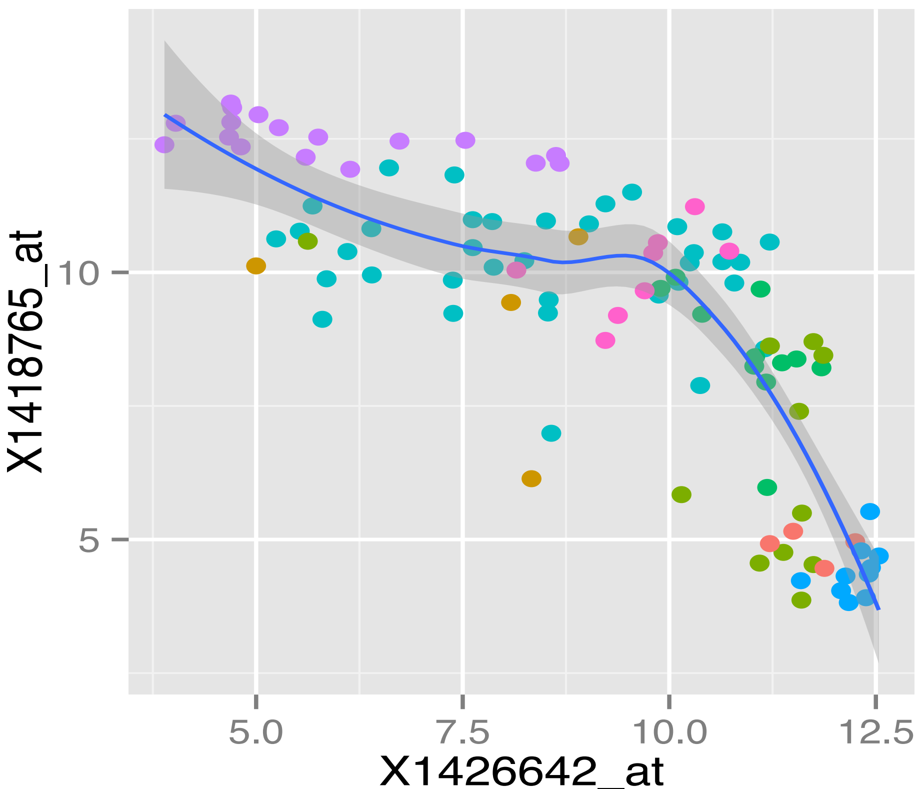
Gene expression **microarray dataset on early development of mouse embryos**

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 layers 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))
```

Using the same plot, we can easily change the coordinates

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groupSize <- table(dftx$sampleGroup)
groupSize
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```
pb <- ggplot(data.frame(
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```
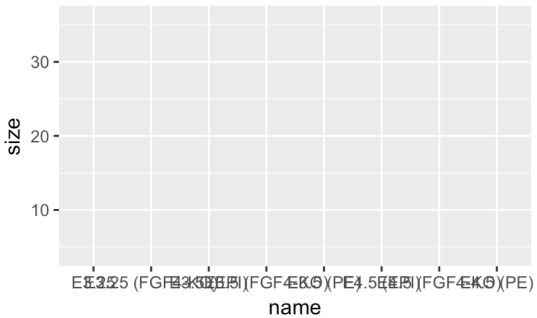

No geom defined yet!



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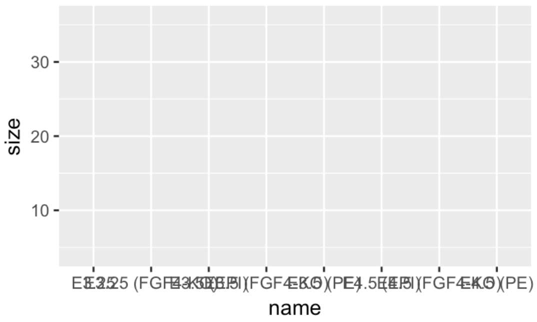


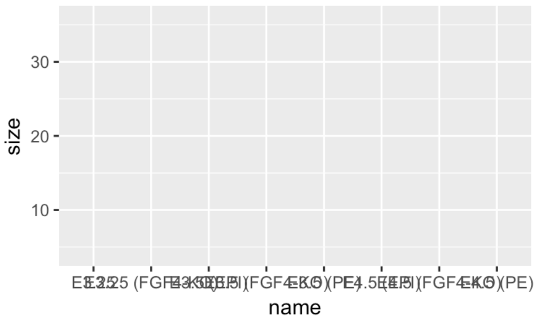

```
pb <- pb + geom_bar(stat = "identity") +
   aes(fill = name) +
   scale_fill_manual(values = groupColour, name = "Colour code") +
   theme(axis.text.x = element_text(angle = 90, hjust = 1))  +
   xlab("Groups") + ylab("Number of Samples")
```

Using the same plot, we can easily change the coordinates

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

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

No geom defined yet!

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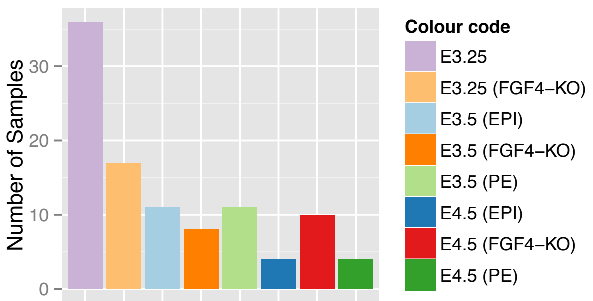

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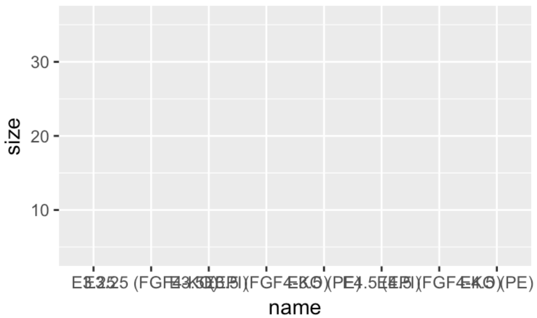


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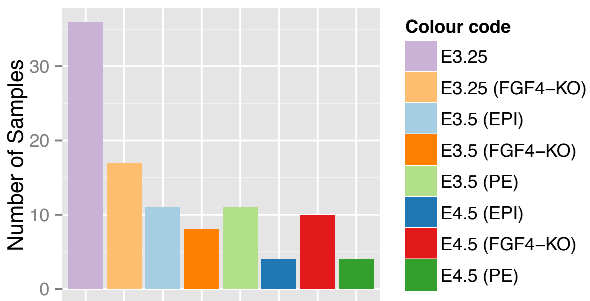


```
pb.polar <- pb + coord_polar() +
  theme(axis.text.x = element_text(angle = 0, hjust = 1),
        axis.text.y = element_blank(),
        axis.ticks = element_blank()) +
  xlab("") + ylab("")
pb.polar
```

Using the same plot, we can easily change the coordinates

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

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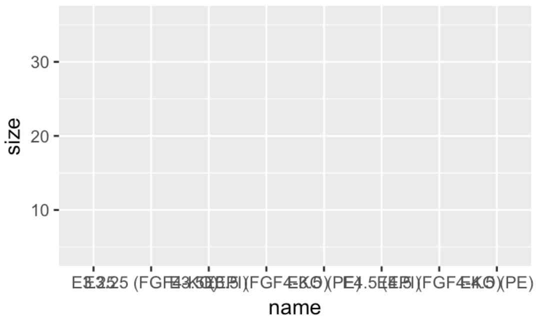

No geom defined yet!

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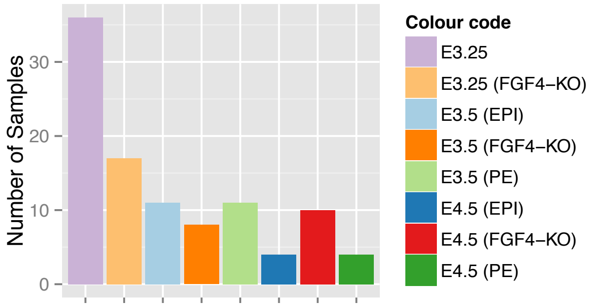
   xlab("Groups") + ylab("Number of Samples")
```

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        axis.ticks = element_blank()) +
  xlab("") + ylab("")
pb.polar
```
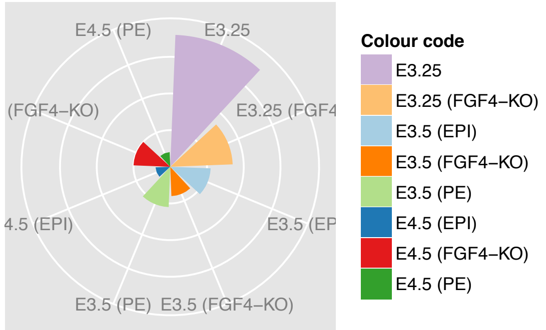
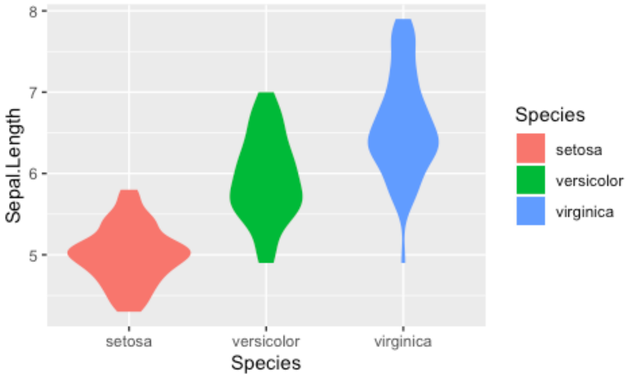



Themes can change the look

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

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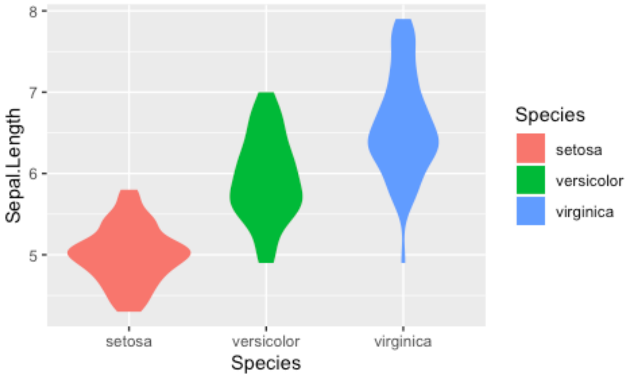
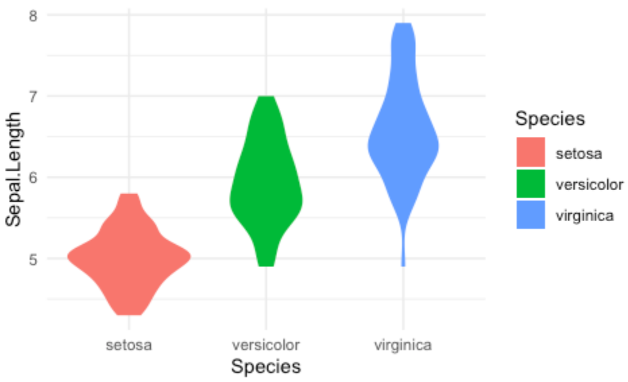




```r
g + theme_minimal()
```



Themes can change the look

```r
g = ggplot(iris,
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g
```
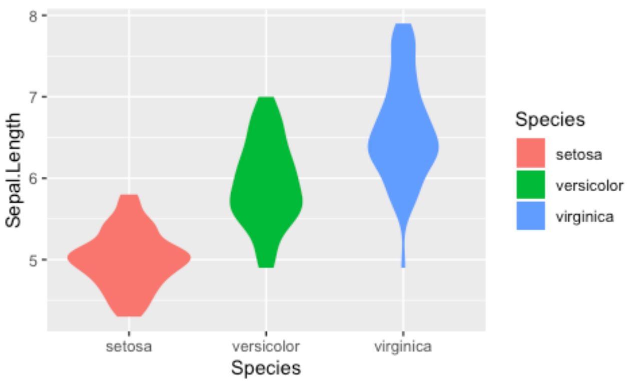
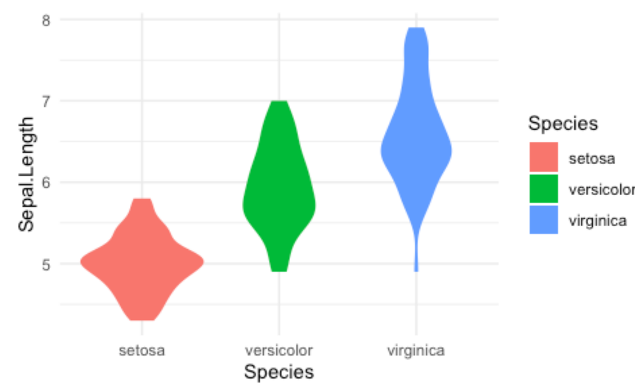
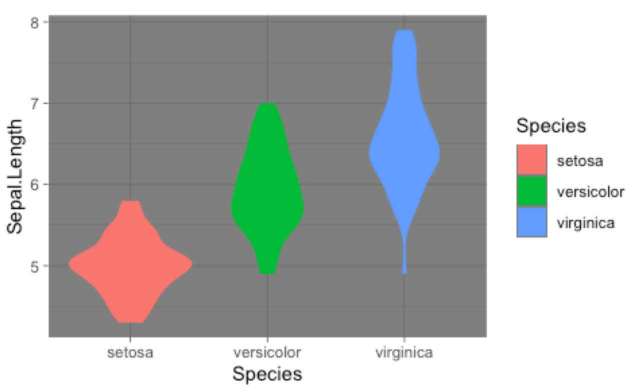




```r
g + theme_minimal()
```

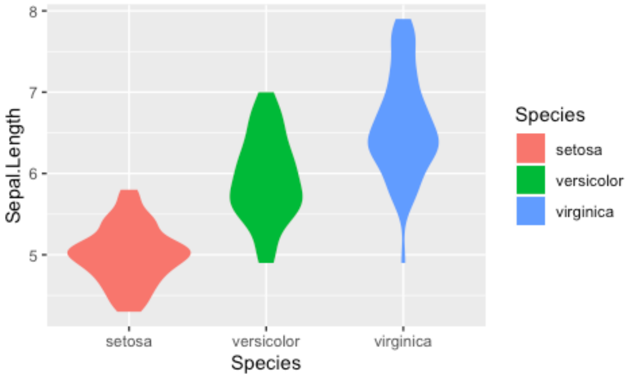



```r
g + theme_dark()
```

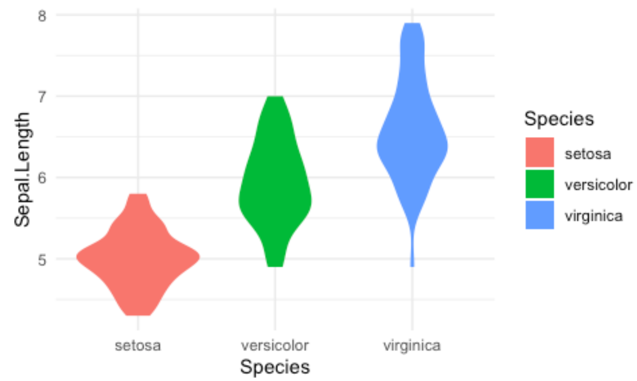


Themes can change the look

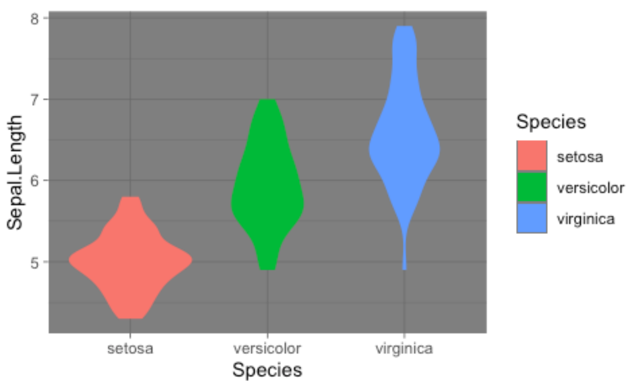
```r
g = ggplot(iris,
           aes(x = Species,
               y = Sepal.Length,
               fill = Species))+
  geom_violin(col = NA)
g
```



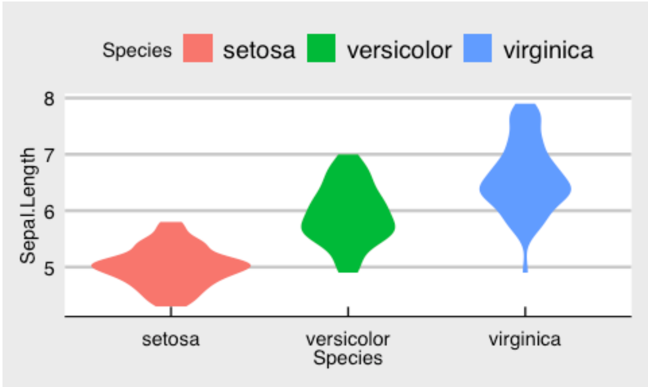

```r
g + theme_minimal()
```




```r
g + theme_dark()
```




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



BDS^ Sched BDS^ Ukrain werne MTB Entd Resea bbc d bbc

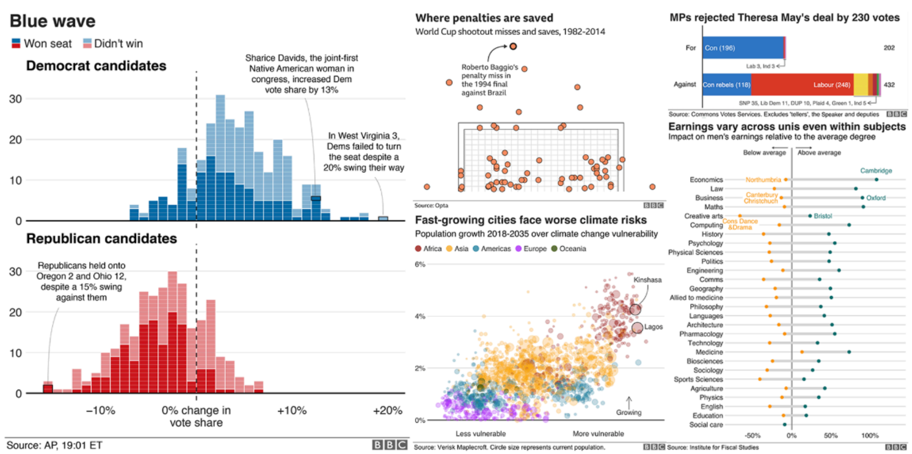
https://github.com/bbc/bbplot

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.



Installing bbplot

`bbplot` is not on CRAN, so you will have to install it directly from Github using `devtools`.

If you do not have the `devtools` package installed, you will have to run the first line in the code below as well.

```
# install.packages('devtools')
```

Packages

No packages published

Contributors 2

nassosstylianou Nassos Stylianou

cguibourg

Languages

R 100.0%

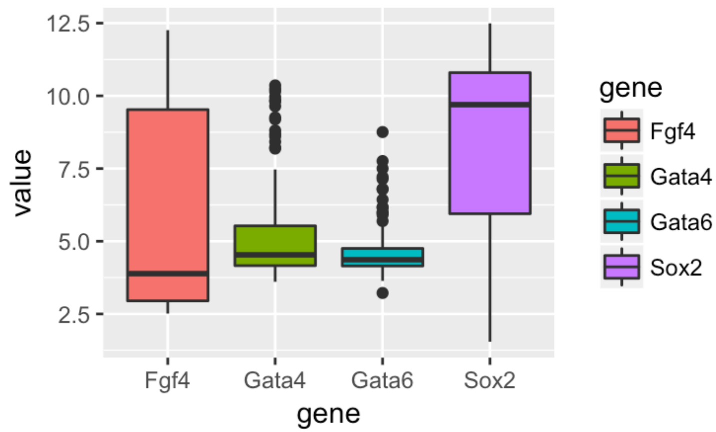
Displaying and comparing 1D distributions

Displaying and comparing 1D distributions

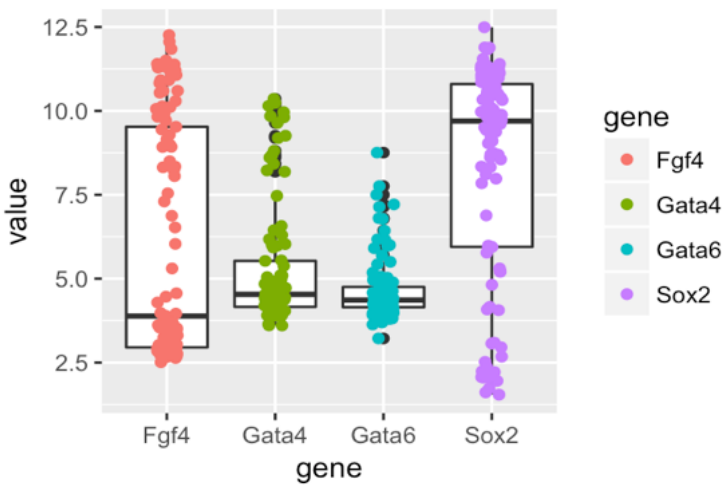
Boxplot

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))
```



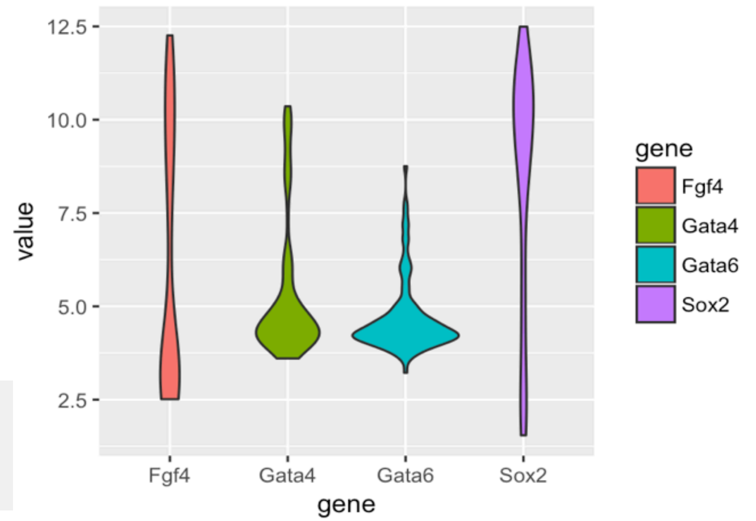

```
p + geom_boxplot() +
  geom_jitter(aes(color = gene), width = 0.1, height = 0)
```



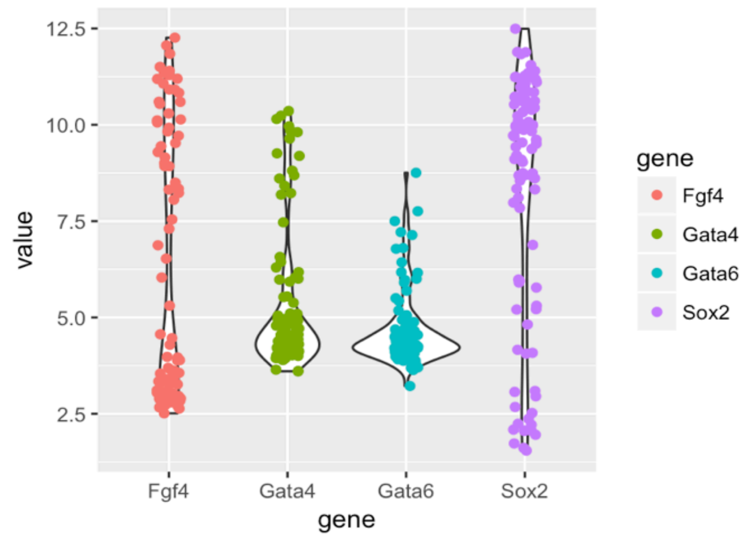
Violin Plot

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))
```

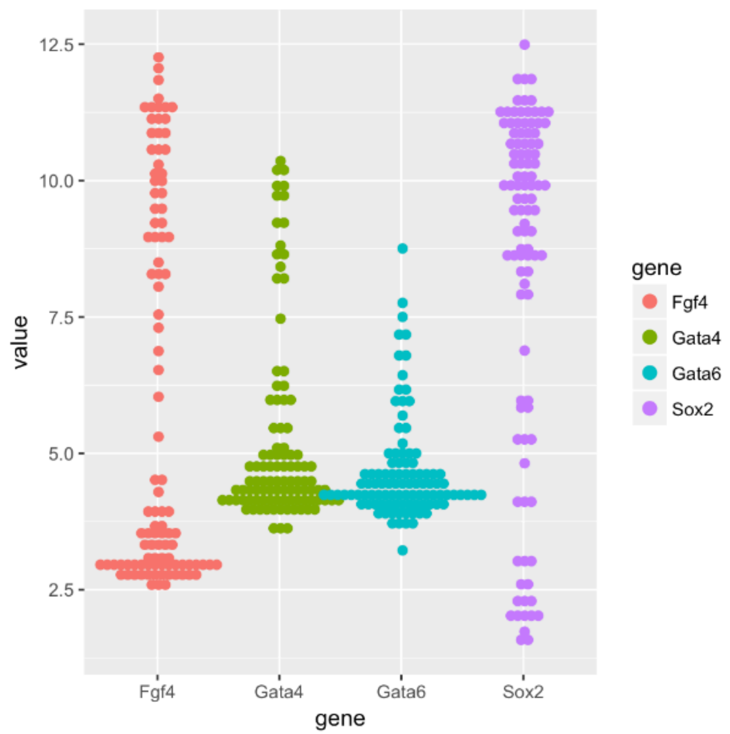


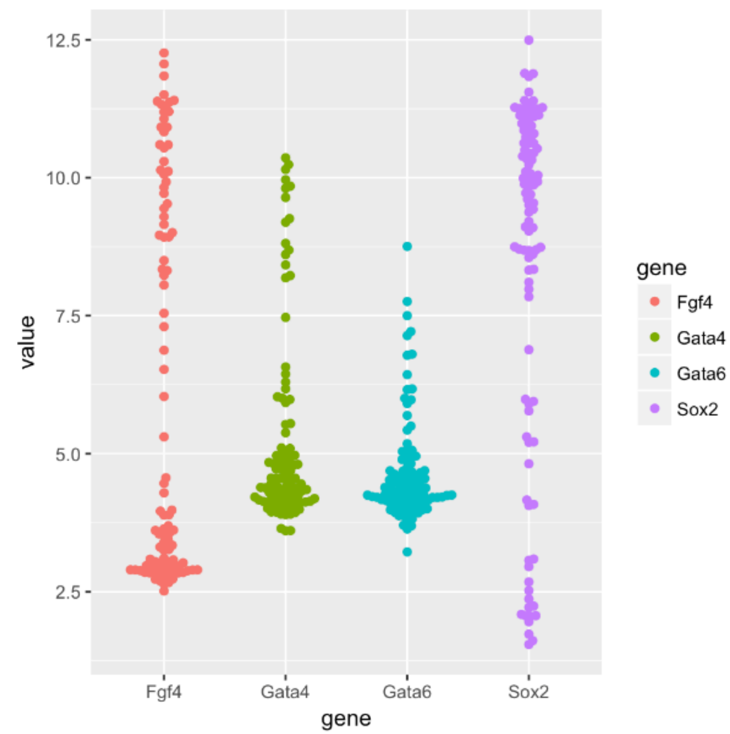

```
p + geom_boxplot() +
  geom_jitter(aes(color = gene), width = 0.1, height = 0)
```



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

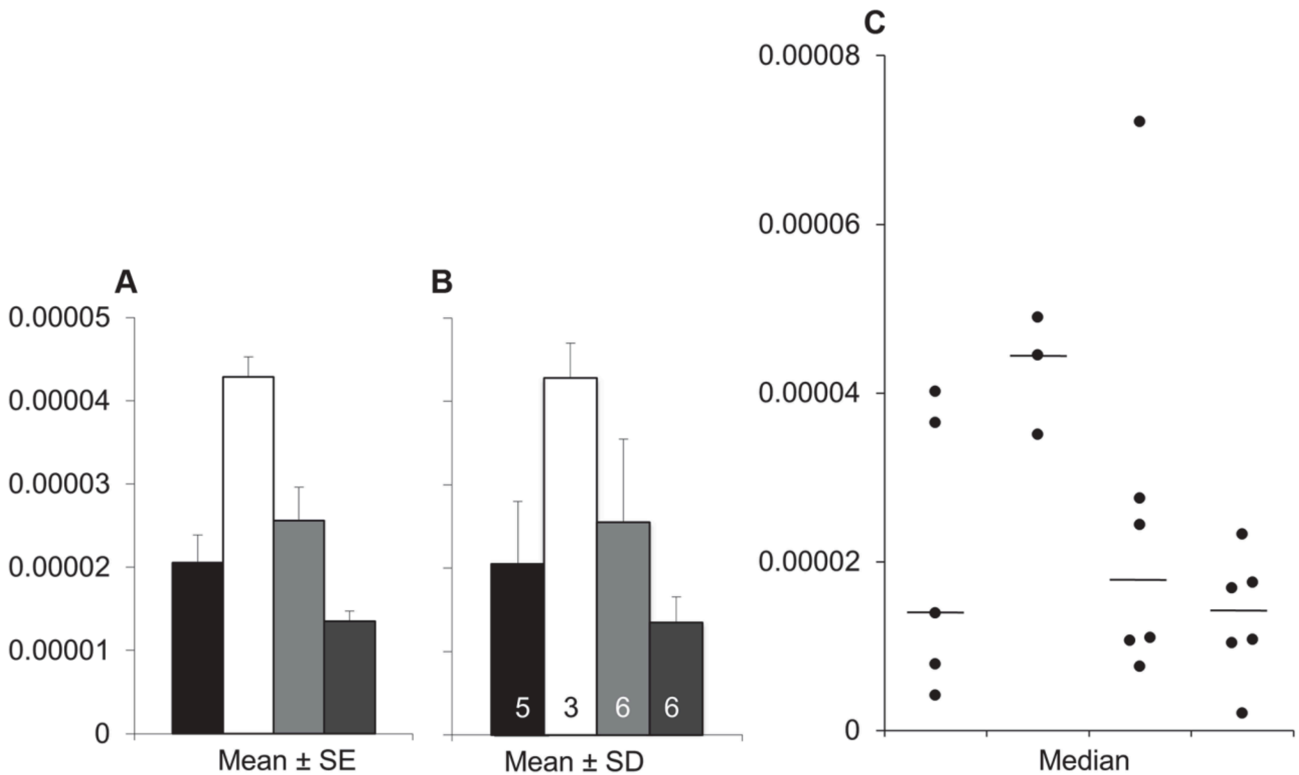


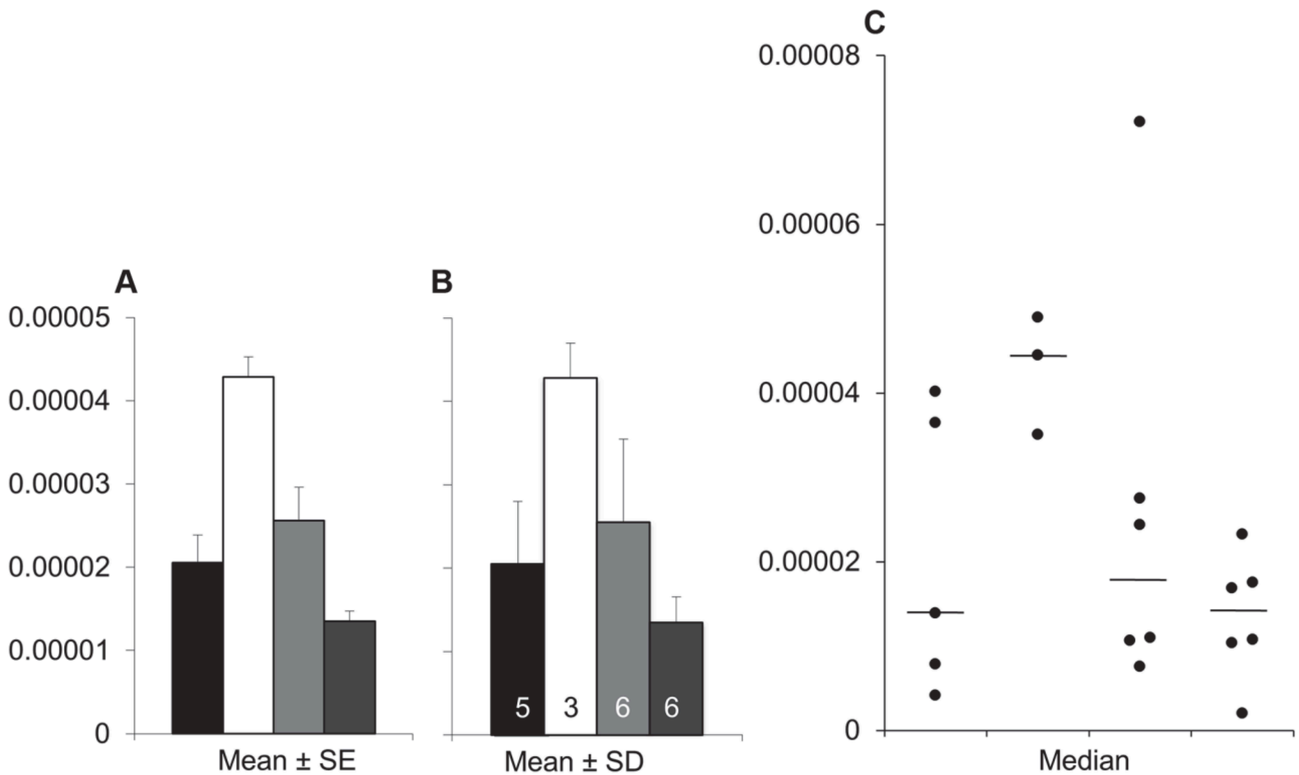
Fig 3. Bar graphs and scatterplots convey very different information. While scatterplots prompt the reader to critically evaluate the statistical tests and the authors' interpretation of the data, bar graphs discourage the reader from thinking about these issues. Placental endothelin 1 (*EDN1*) mRNA data for four different groups of participants is presented in bar graphs showing mean ± SE (Panel A), or mean ± SD (Panel B), and in a univariate scatterplot (Panel C). Panel A (mean ± SE) suggests that the second group has higher values than the remaining groups; however, Panel B (mean ± 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

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



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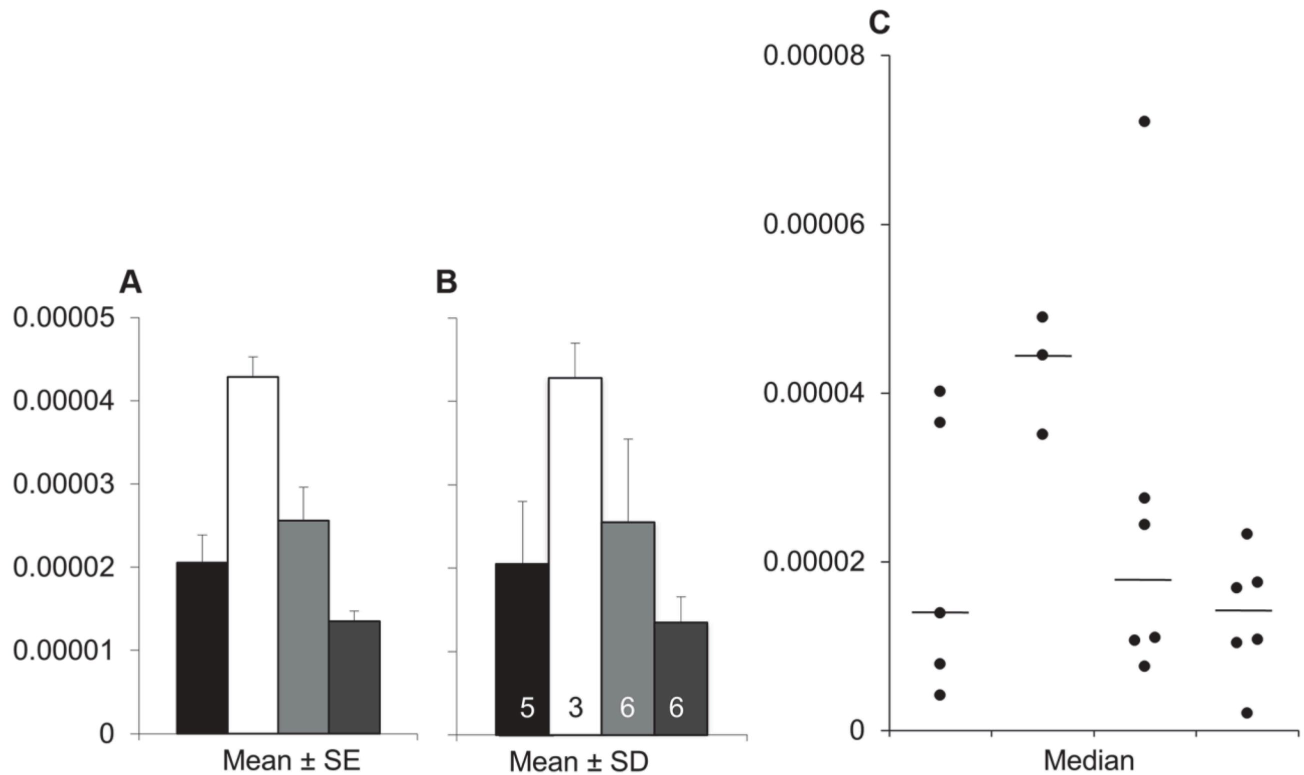

Bar charts (with error bars) **not good for showing distributions**

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

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 ± SE (Panel A), or mean ± SD (Panel B), and in a univariate scatterplot (Panel C). Panel A (mean ± SE) suggests that the second group has higher values than the remaining groups; however, Panel B (mean ± 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.

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~~Bar charts with error bars~~

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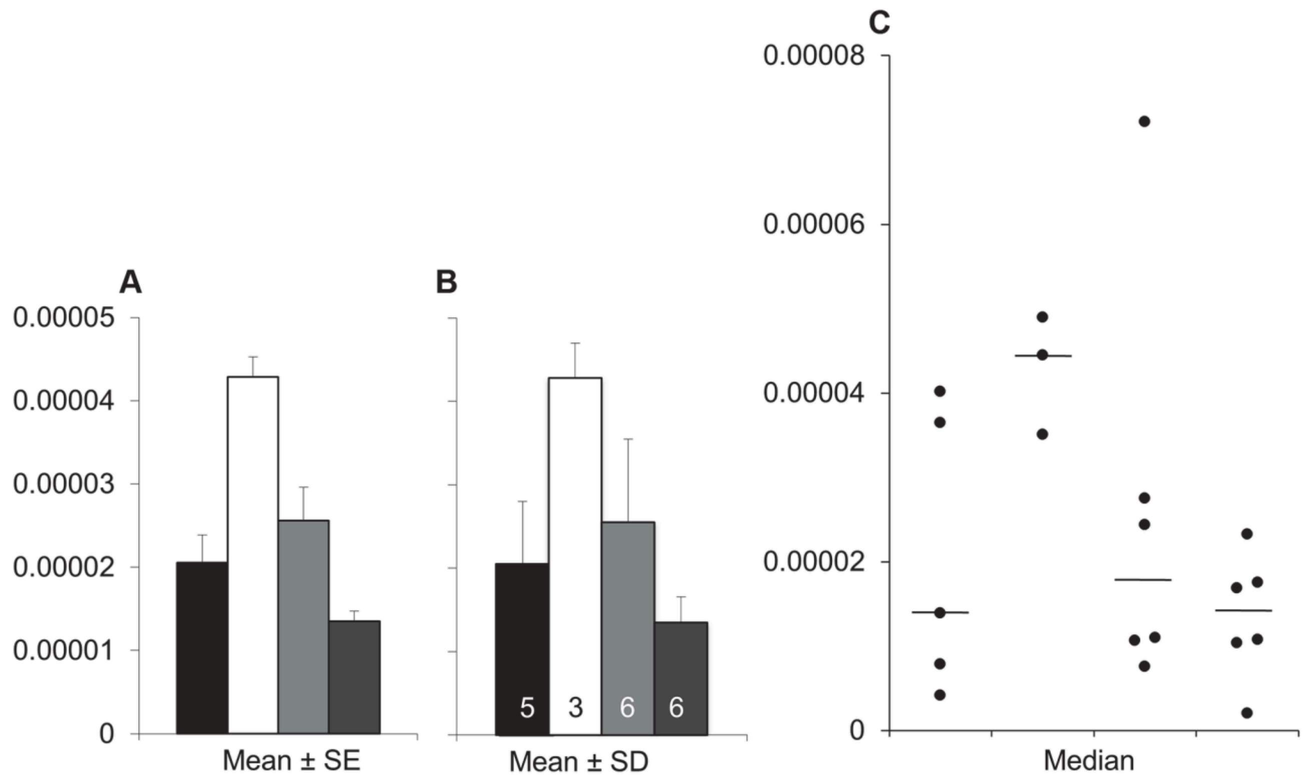

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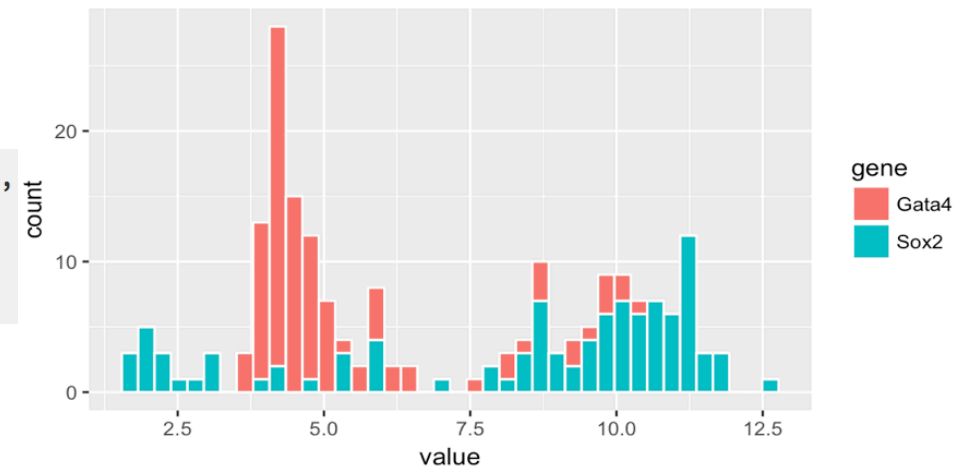
Bar charts (with error bars) **not good for showing distributions**

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

Histograms

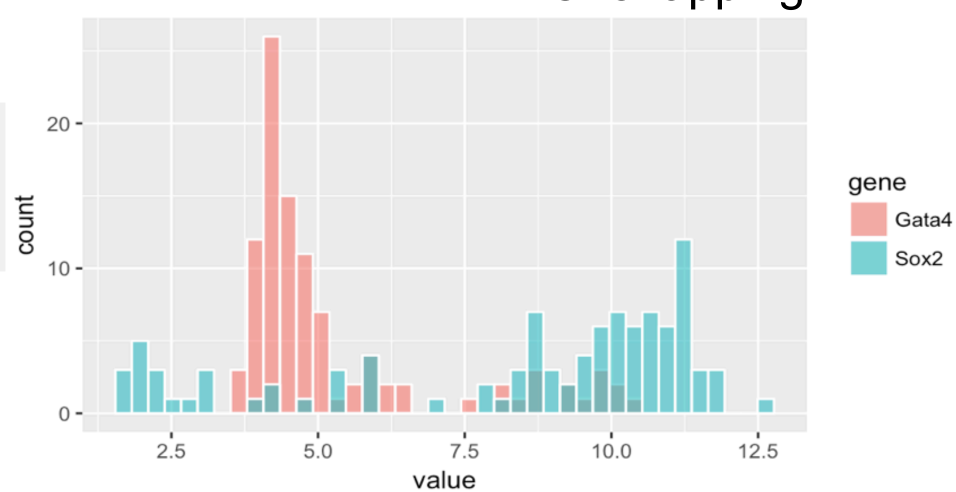
```
p = ggplot(genes %>% filter(gene %in% c("Gata4", "Sox2")),
           aes(x = value))
p + geom_histogram(aes(fill = gene),
                   color = "white", bins = 40)
```

Stacked



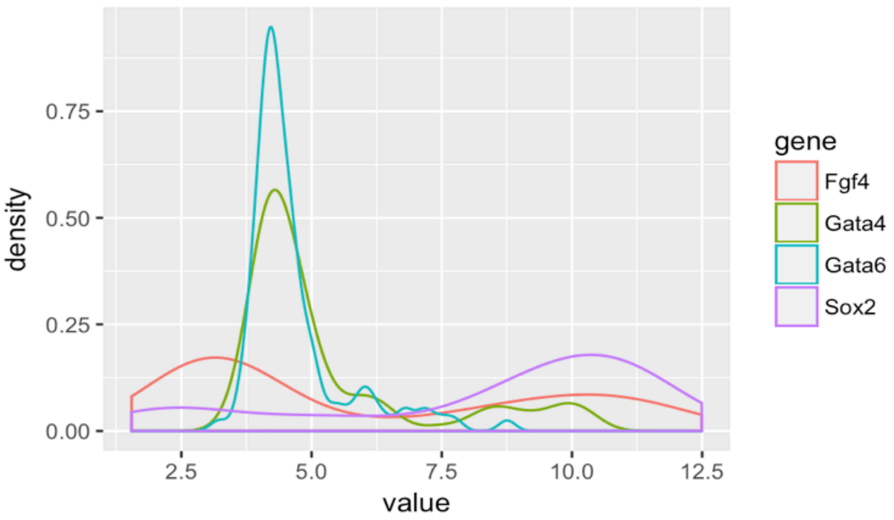

```
p + geom_histogram(
  aes(fill = gene), color="white", alpha=0.6,
  bins = 40, position = "identity")
```

Overlapping

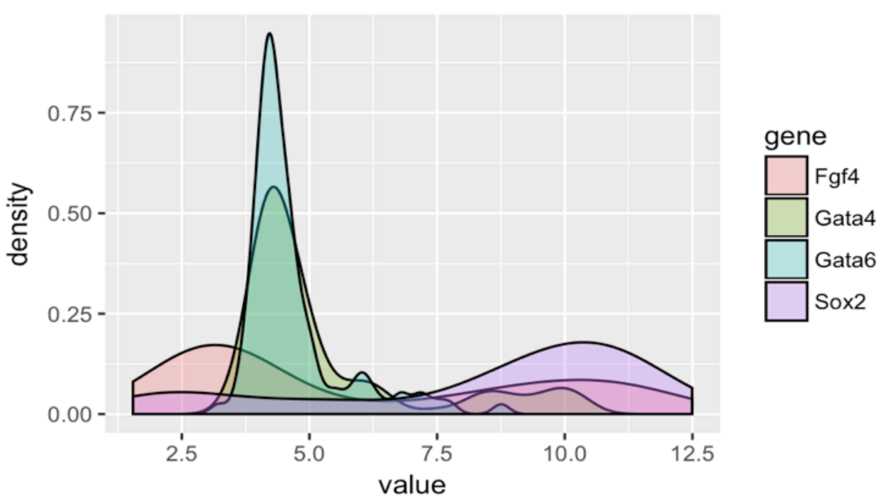


Density plots

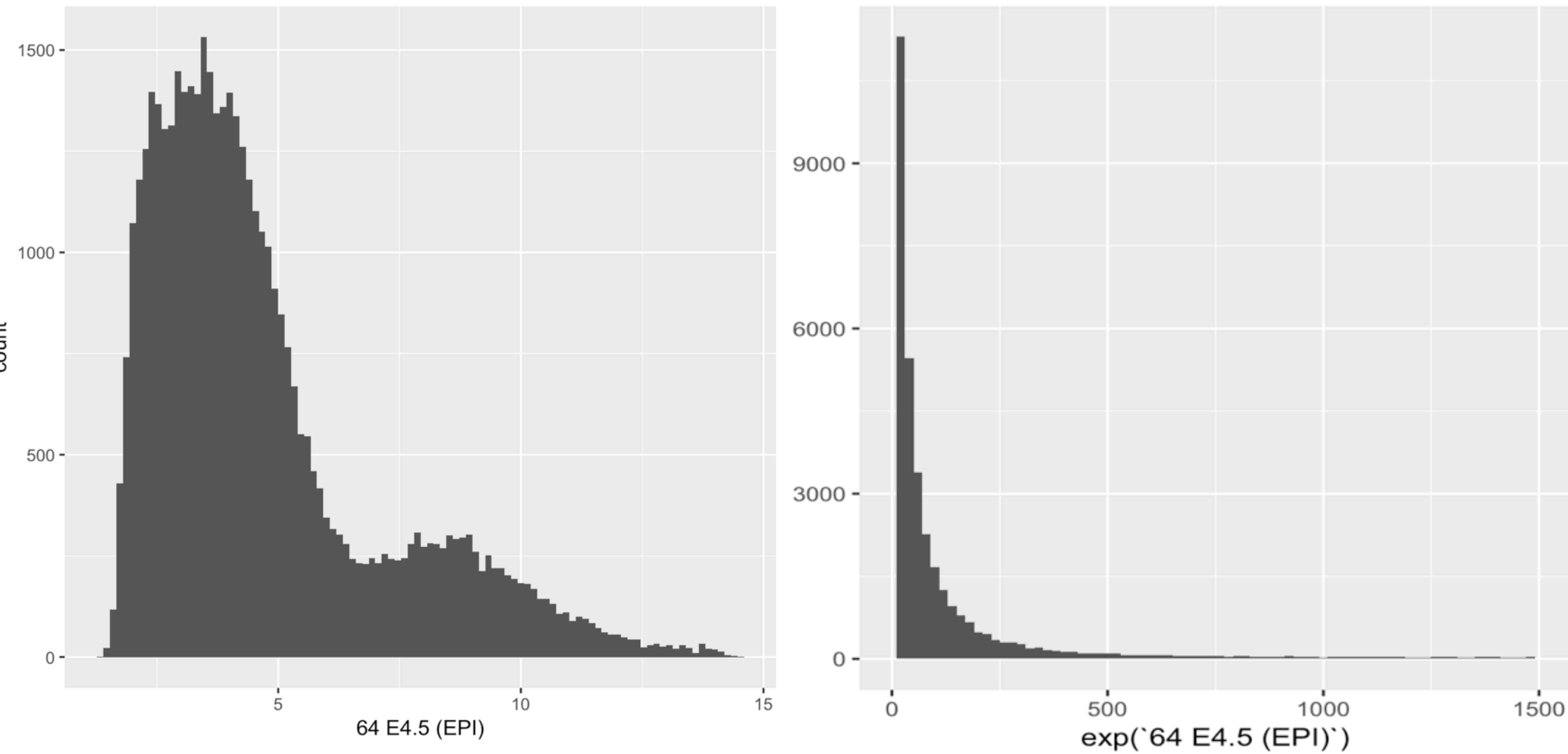
```r
p = ggplot(genes, aes( x = value, color = gene))
p + geom_density()
```




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



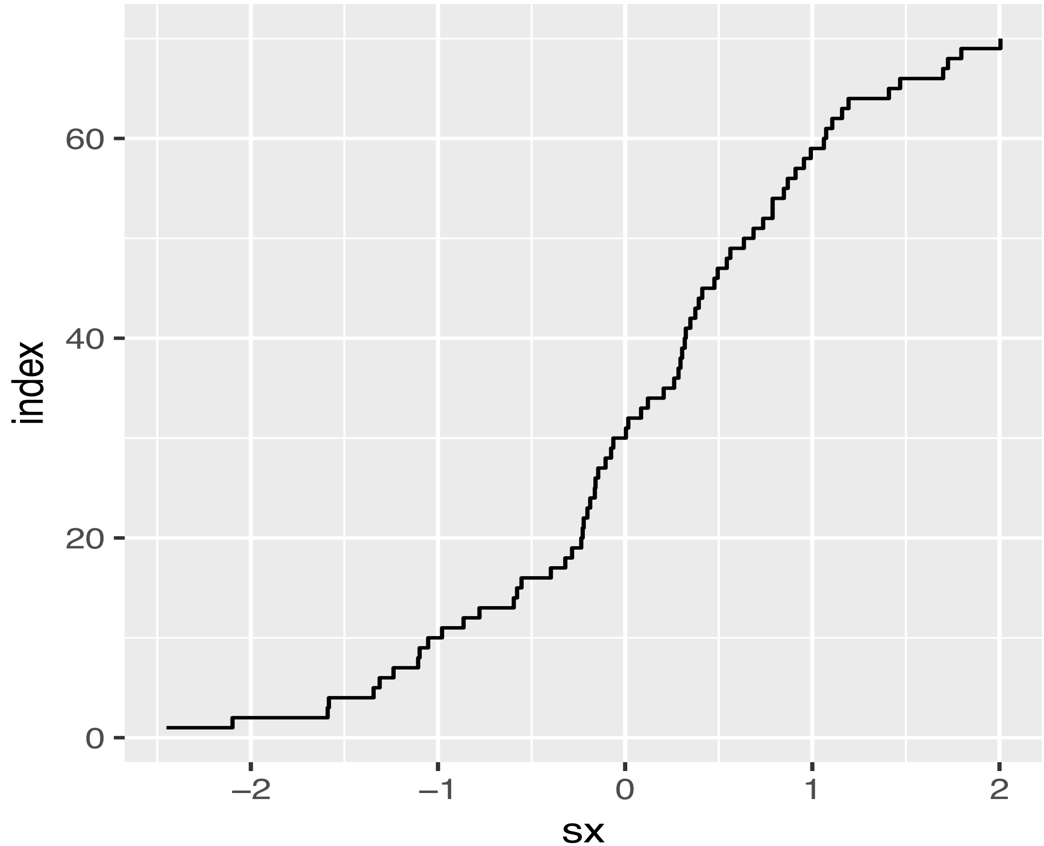
Non-linear transformations change the shape of a density



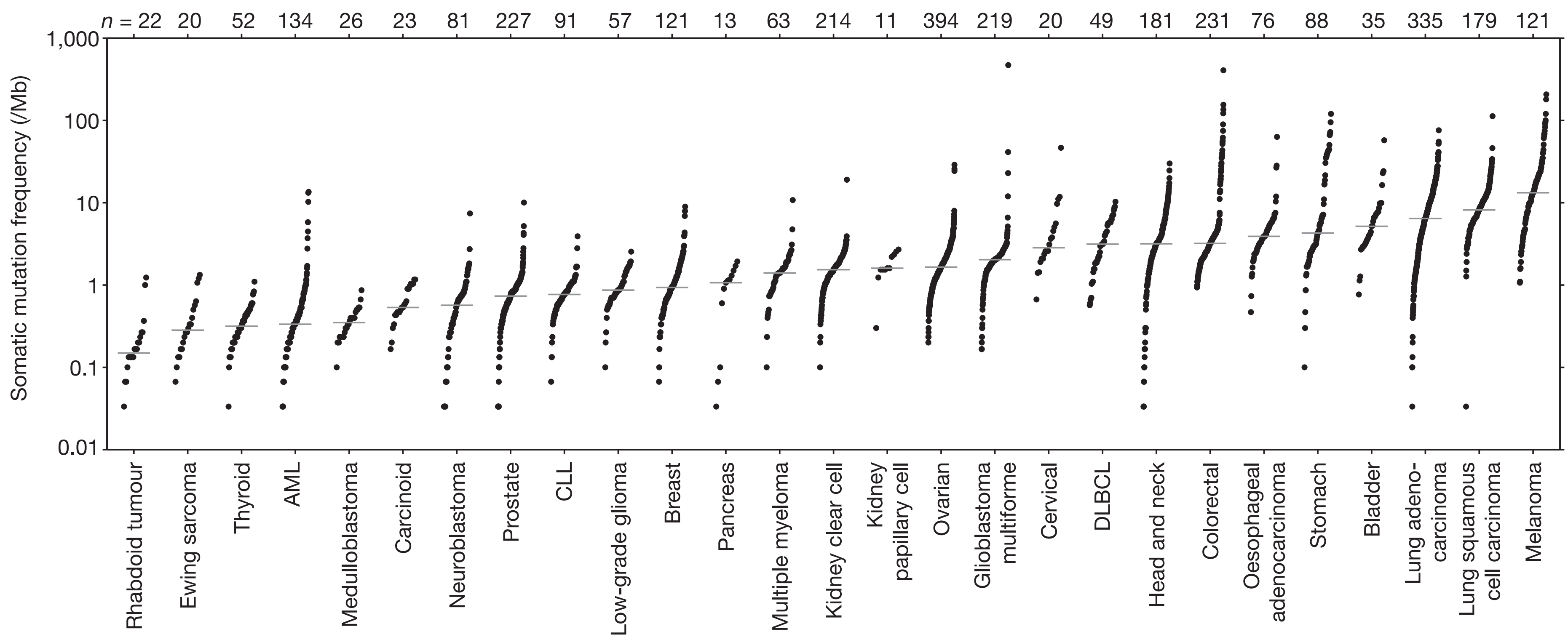
- The **mode** of a distribution is an **infinitesimal concept**.
- Need either an infinite amount of data or choose smoothing / binning bandwidth
- **Number of modes (let alone their positions) can change under non-linear data transformations**

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()
```



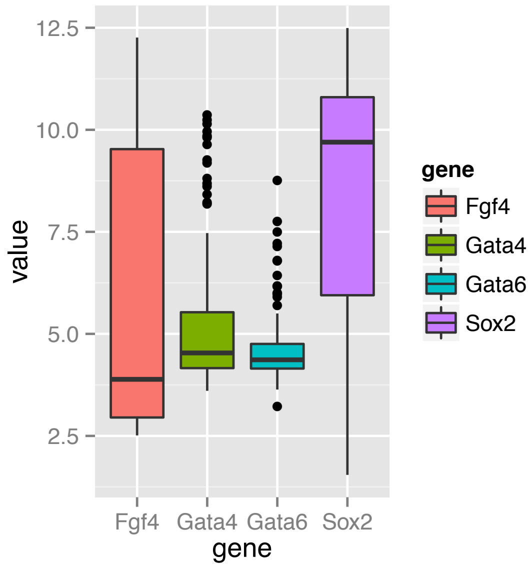
LETTER

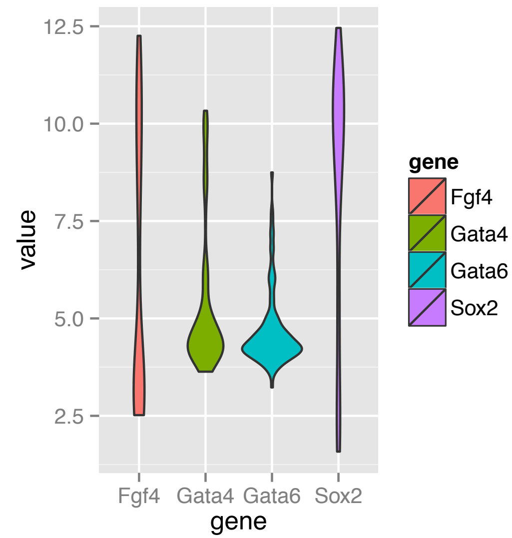
doi:10.1038/nature12213

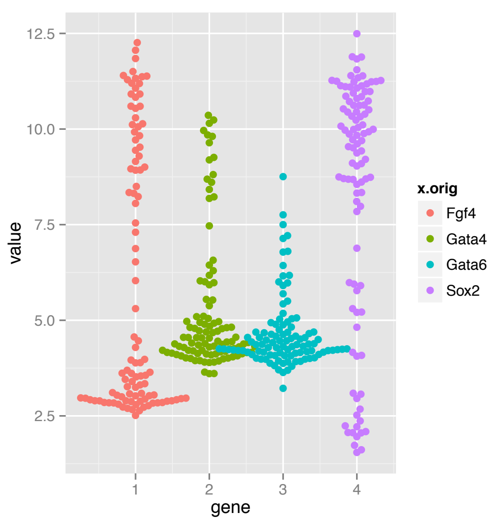
Mutational heterogeneity in cancer and the search for new cancer-associated genes

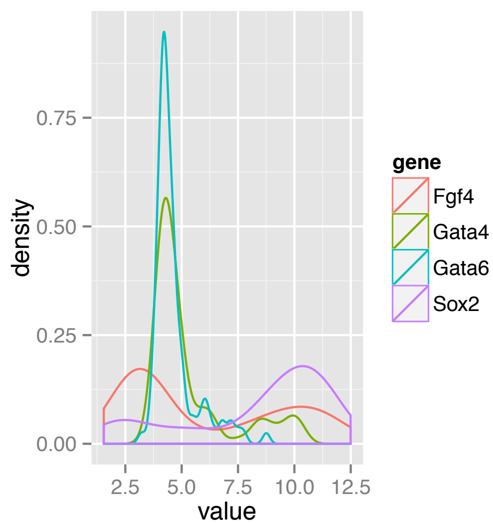
Michael S. Lawrence[1]*, Petar Stojanov[1,2]*, Paz Polak[1,3,4]*, Gregory V. Kryukov[1,3,4], Kristian Cibulskis[1], Andrey Sivachenko[1], Scott L. Carter[1], Chip Stewart[1], Craig H. Mermel[1,5], Steven A. Roberts[6], Adam Kiezun[1], Peter S. Hammerman[1,2], Aaron McKenna[1,7], Yotam Drier[1,3,5,8], Lihua Zou[1], Alex H. Ramos[1], Trevor J. Pugh[1,2,3], Nicolas Stransky[1,9], Elena Helman[1,10], Jaegil Kim[1], Carrie Sougnez[1], Lauren Ambrogio[1], Elizabeth Nickerson[1], Erica Shefler[1], Maria L. Cortés[1], Daniel Auclair[1], Gordon Saksena[1], Douglas Voet[1], Michael Noble[1], Daniel DiCara[1], Pei Lin[1], Lee Lichtenstein[1], David I. Heiman[1], Timothy Fennell[1], Marcin Imielinski[1,5], Bryan Hernandez[1], Eran Hodis[1,2], Sylvan Baca[1,2], Austin M. Dulak[1,2], Jens Lohr[1,2], Dan-Avi Landau[1,2,11], Catherine J. Wu[2,3], Jorge Melendez-Zajgla[12], Alfredo Hidalgo-Miranda[12], Amnon Koren[1,3], Steven A. McCarroll[1,3], Jaume Mora[13], Ryan S. Lee[2,3,14], Brian Crompton[2,14], Robert Onofrio[1], Melissa Parkin[1], Wendy Winckler[1], Kristin Ardlie[1], Stacey B. Gabriel[1], Charles W. M. Roberts[2,3,14], Jaclyn A. Biegel[15], 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. Gordenin[6], Shamil Sunyaev[1,3,4], Eric S. Lander[1,3,10] & Gad Getz[1,5]

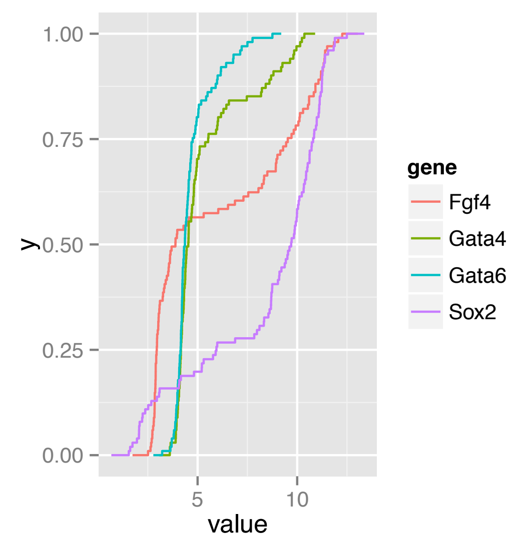
Summary: Visualizing distributions in 1D











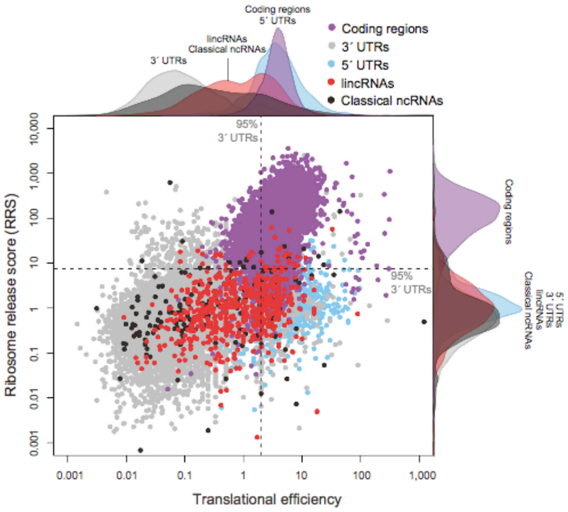
2D data plots

2D data plots

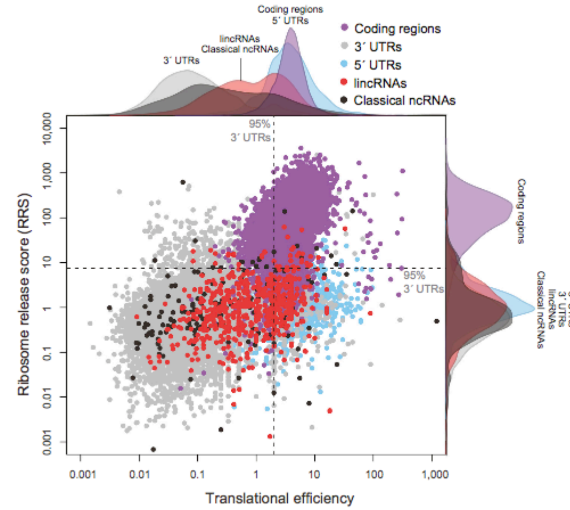
Scatterplots (x,y)-point plots

2D data plots

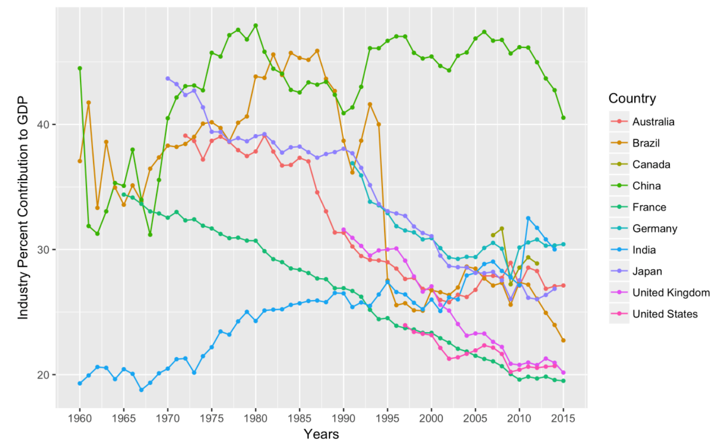
Scatterplots (x,y)-point plots



2D data plots

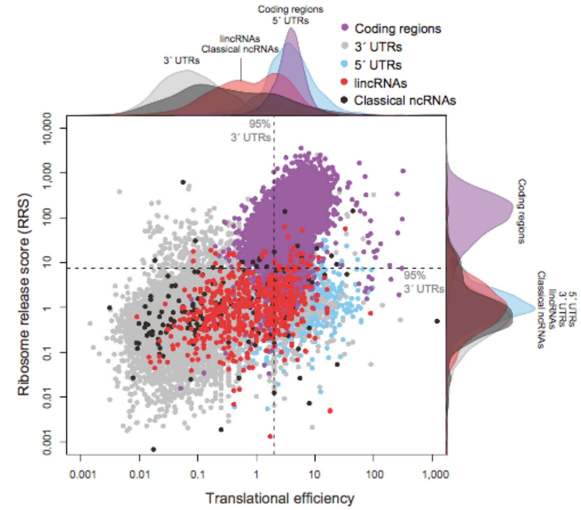


Scatterplots (x,y)-point plots

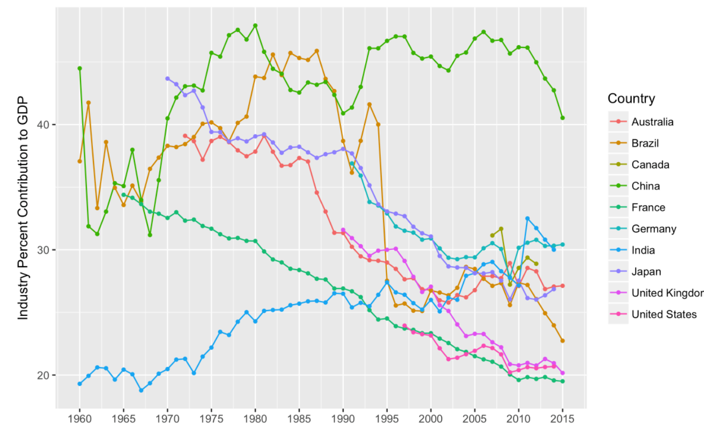


Line plots (x,y)-line plots

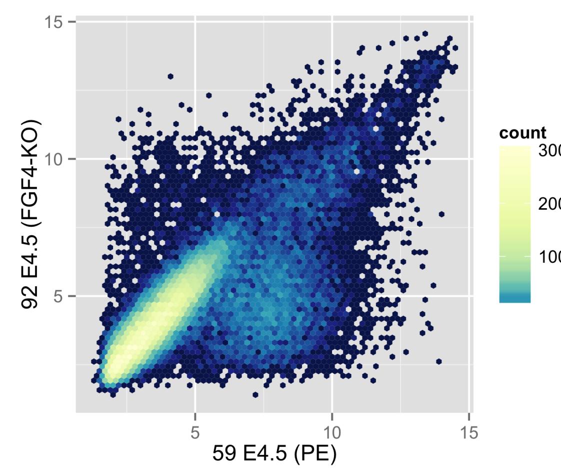
2D data plots



Scatterplots (x,y)-point plots



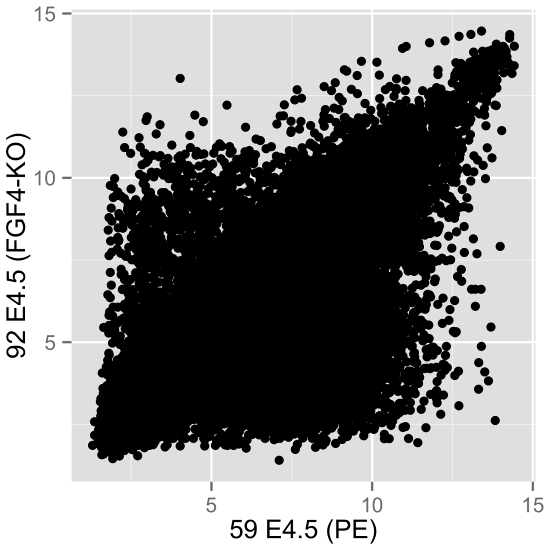
Line plots (x,y)-line plots



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

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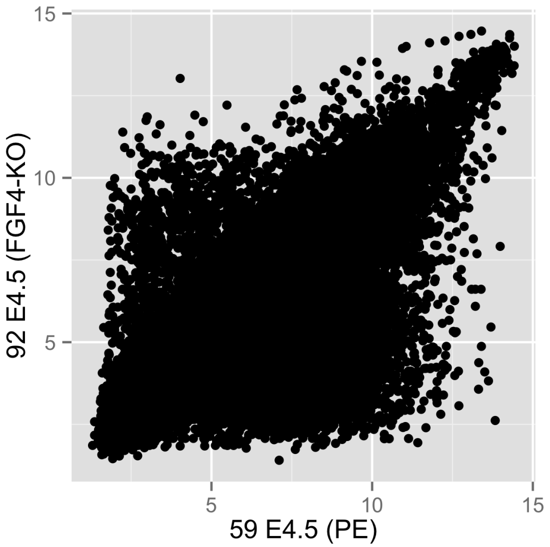
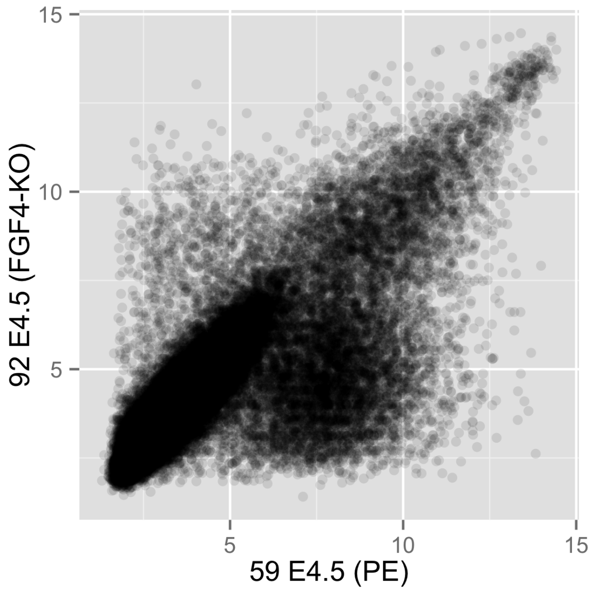
```




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



Showing distributions in 2D

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scp + geom_point()
```

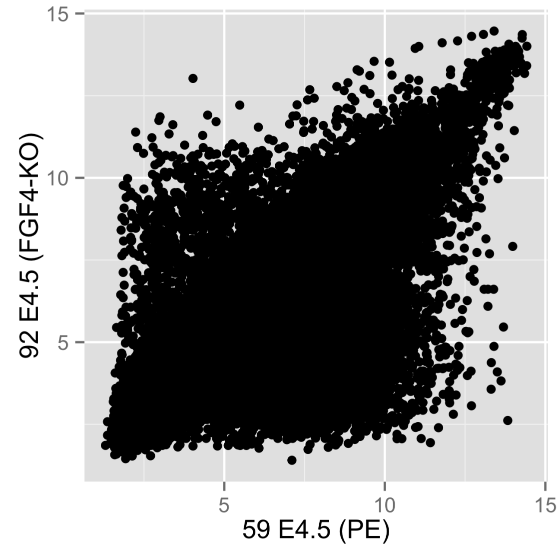


```
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```
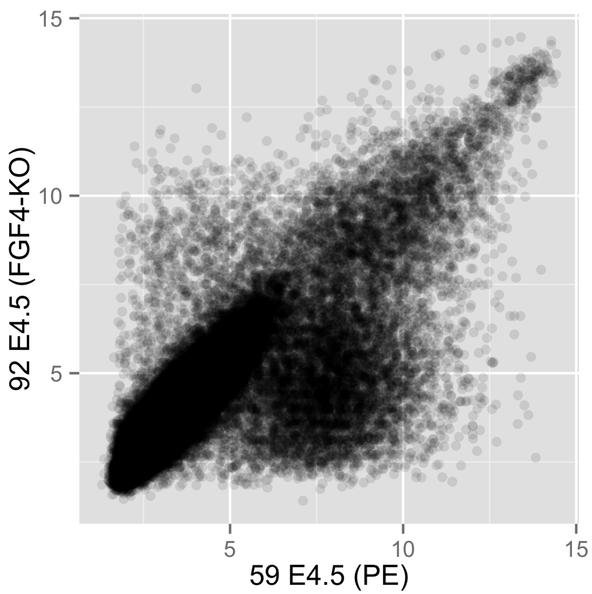
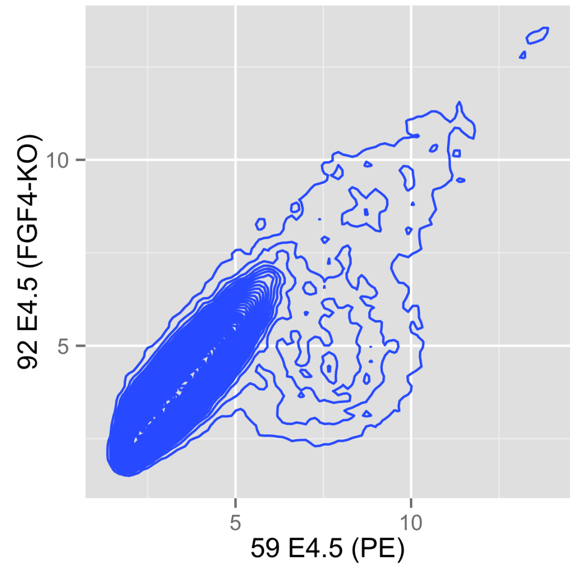
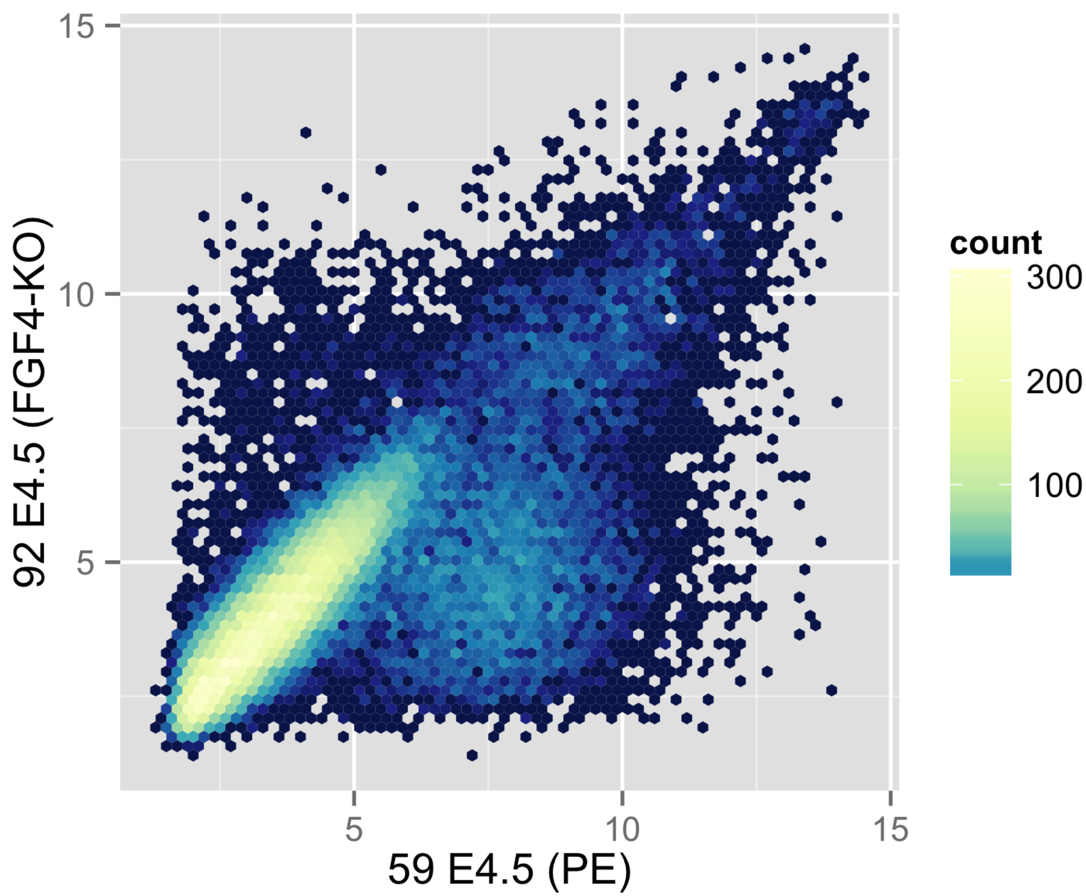




```
scp + geom_density2d(h = 0.5, bins = 60)
```



`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

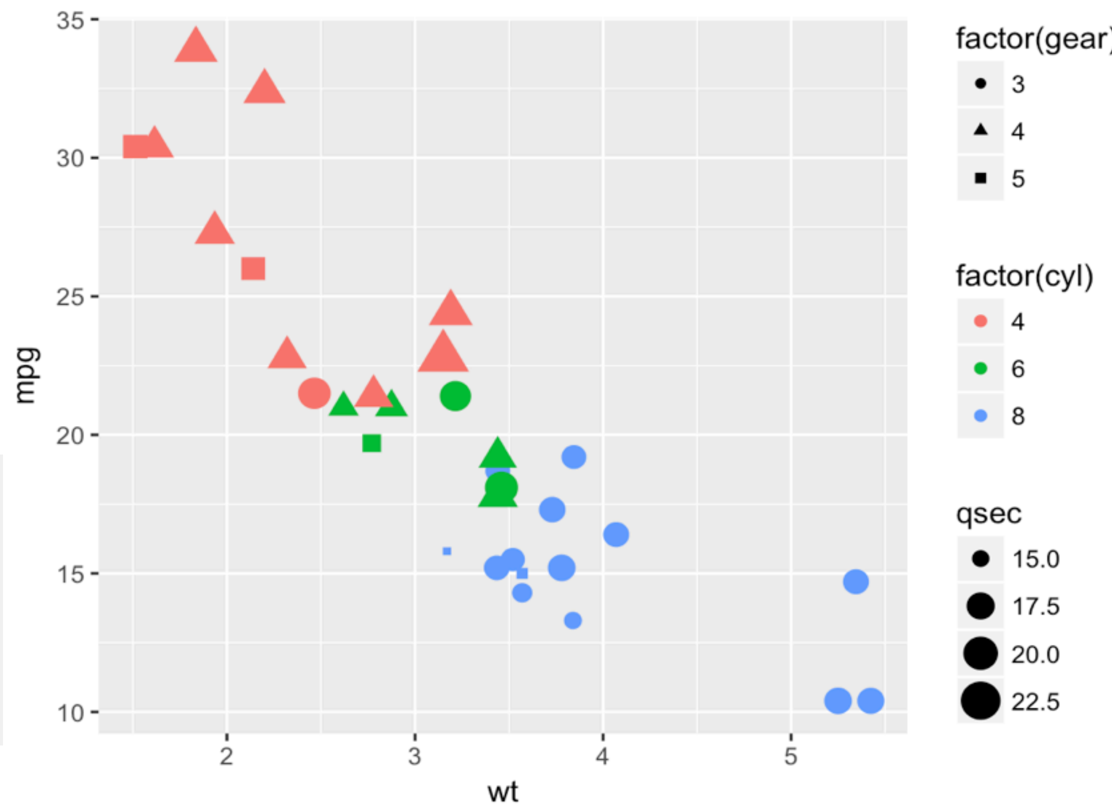
(apart from x and y):

- 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
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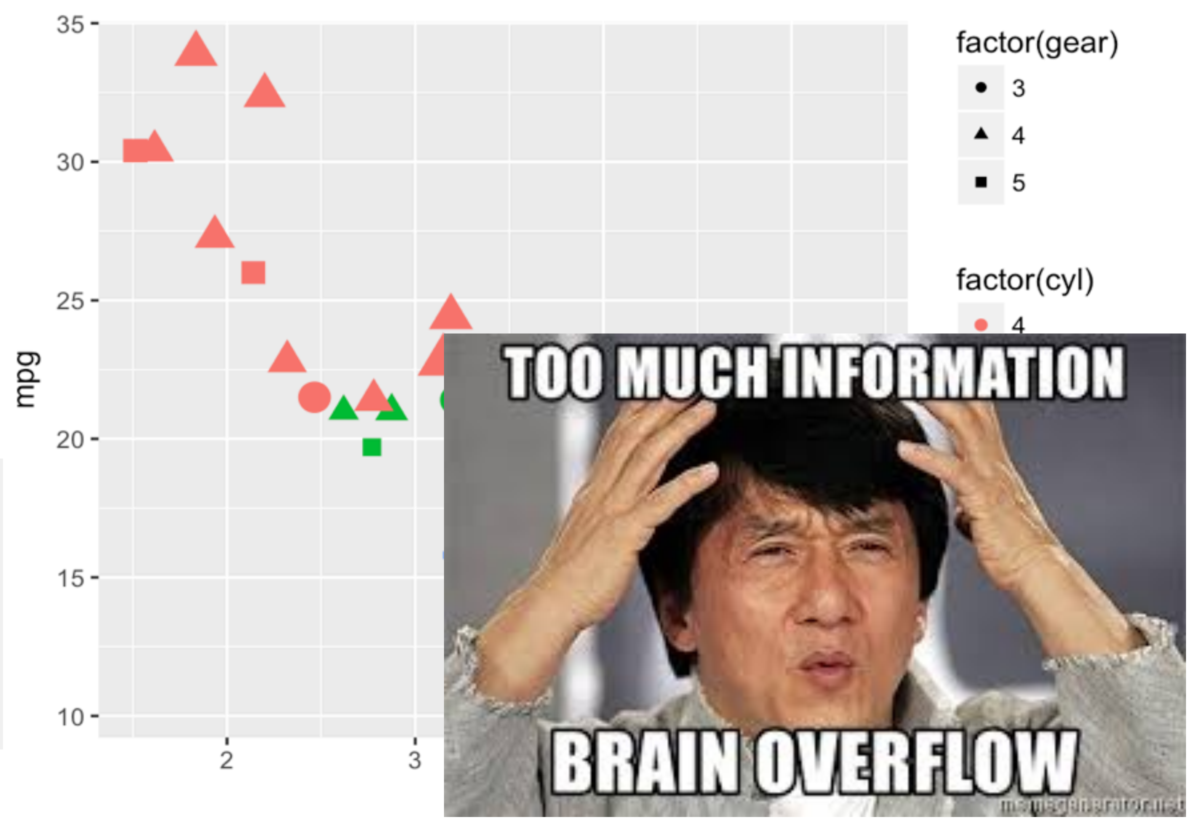
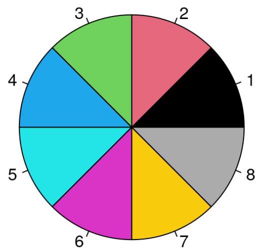


Color Usage

Default color scheme in base R plot:

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



Color Usage

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```
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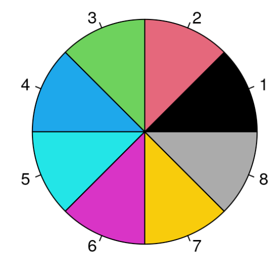
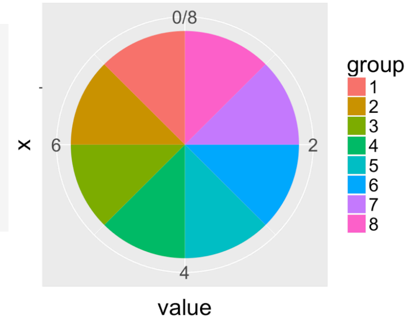


Default color scheme in ggplot:

```
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))
```



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Default color scheme in base R plot:

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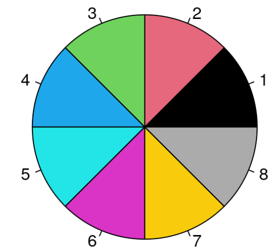

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  coord_polar("y", start=0) +
  theme(text = element_text(size = 20))
```
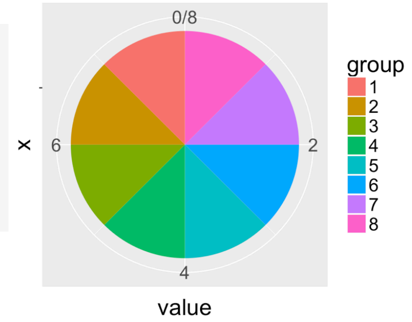



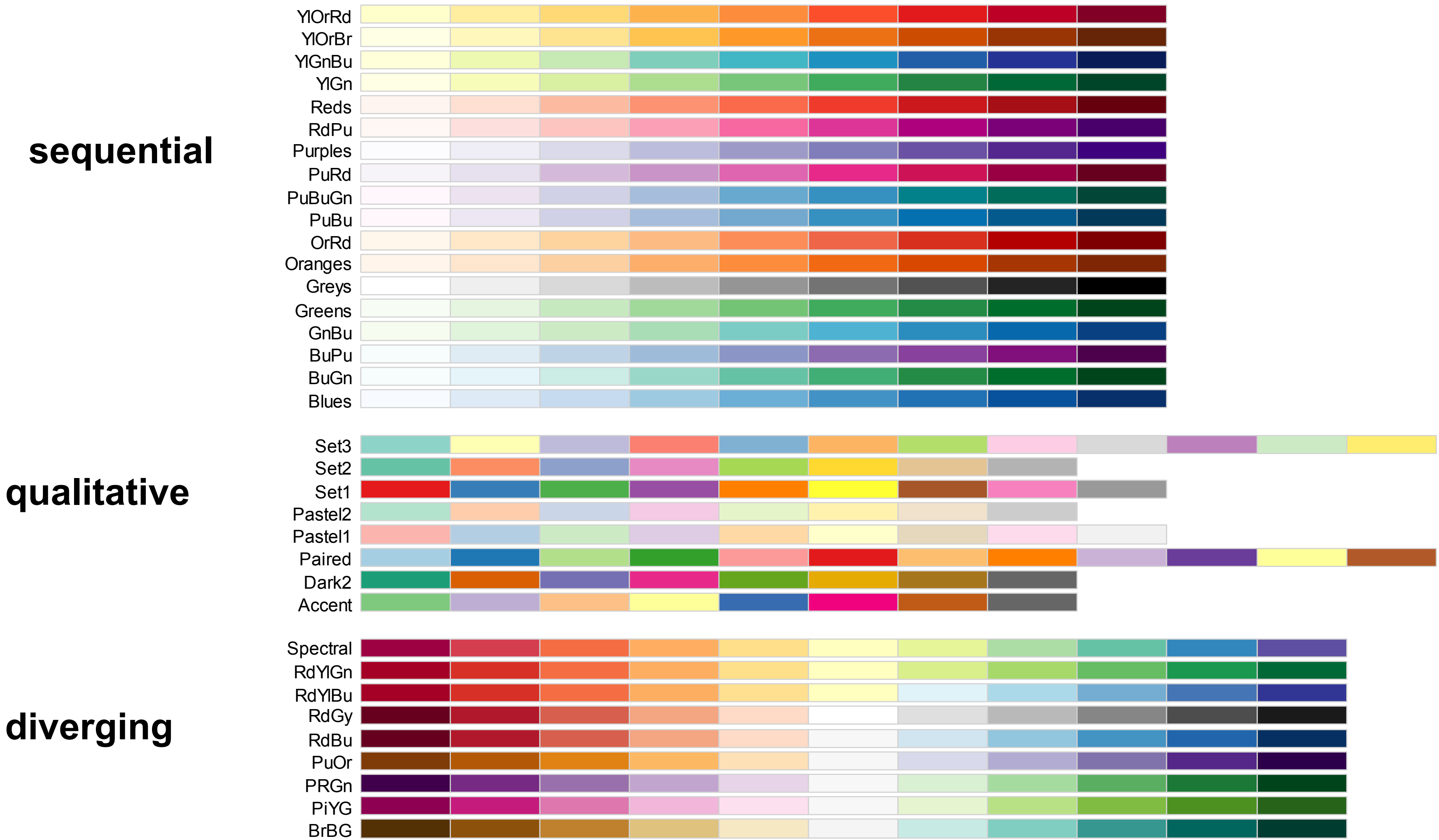
When choosing a coloring scheme, consider these:

- 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

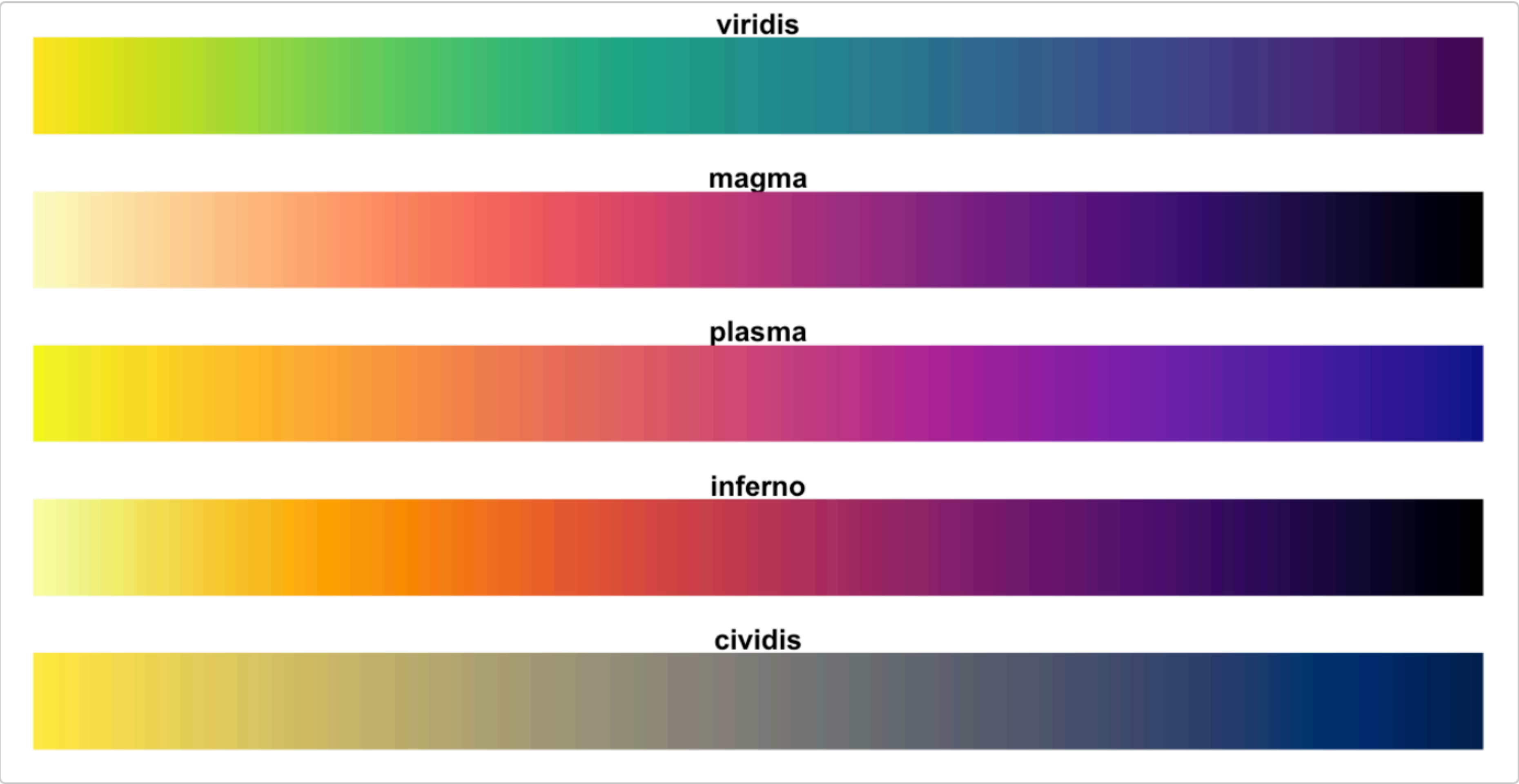
```
display.brewer.all()
```



Viridis Palettes

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

Simply add: `scale_color_viridis()` `scale_fill_viridis()`. to your plot

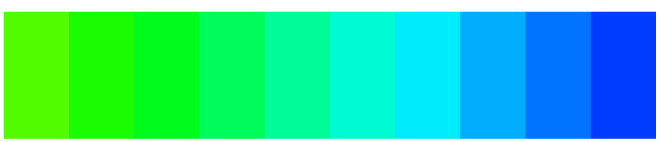


Viridis Palettes

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

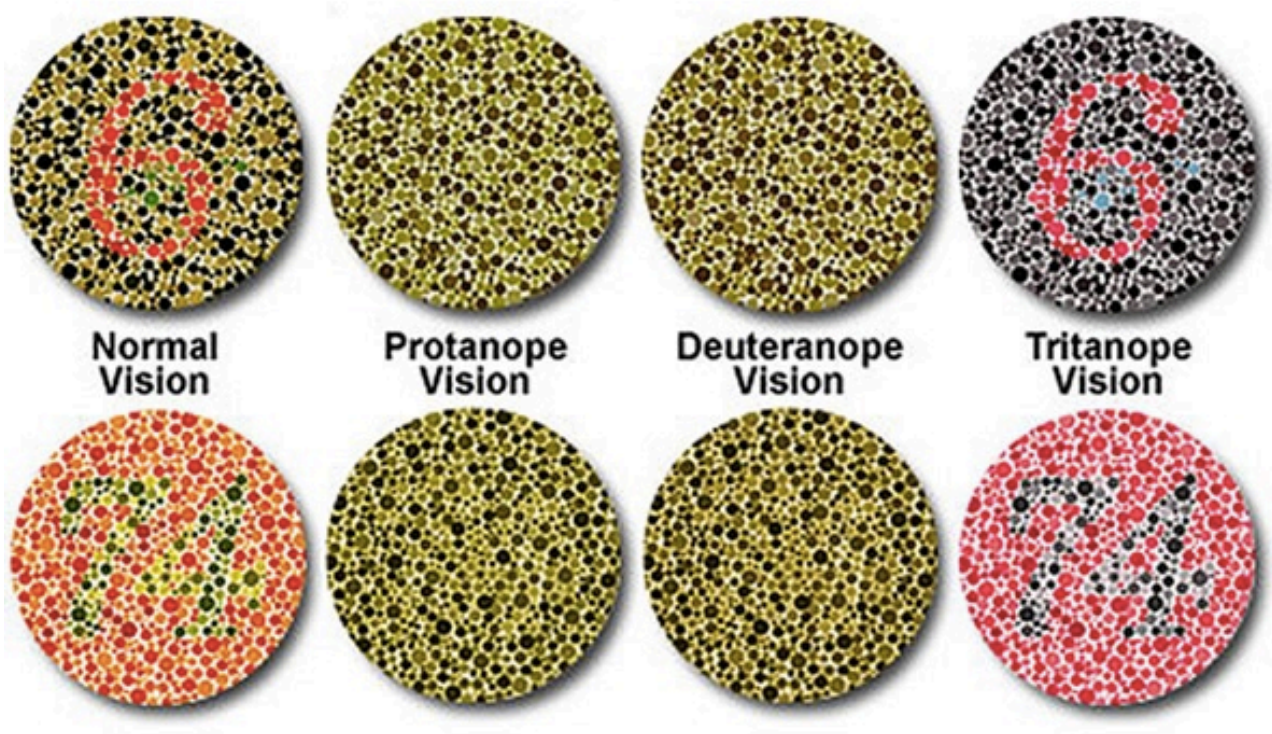
You can hear more about the science behind creating these color scales, on Walt and Smith's talk at SciPy 2015.

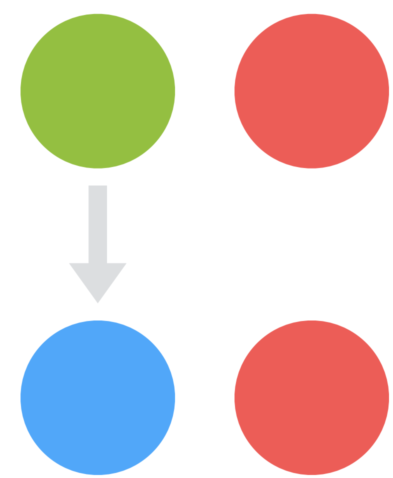


not perceptually uniform

perceptually uniform

Be kind to colorblind people





Simple solution: replace greens by blues.
Blues also display better on most monitors than greens.

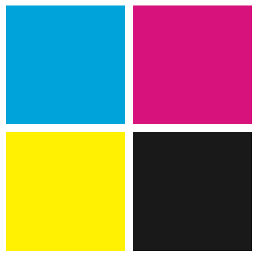
Colour models

How are colours defined?

RGB

Light emitting screens

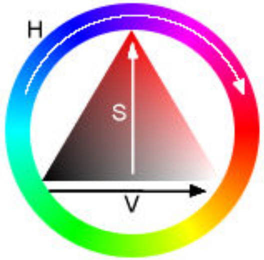
Red **G**reen **B**lue
additive



CMYK

Printing, ink

Cyan **M**agenta **Y**ellow Blac**k**
subtractive



HSV
HSB

coordinates in human perception space

Faceting is useful to show more dimensions without overcrowding the graph

Faceting is useful to show more dimensions without overcrowding the graph

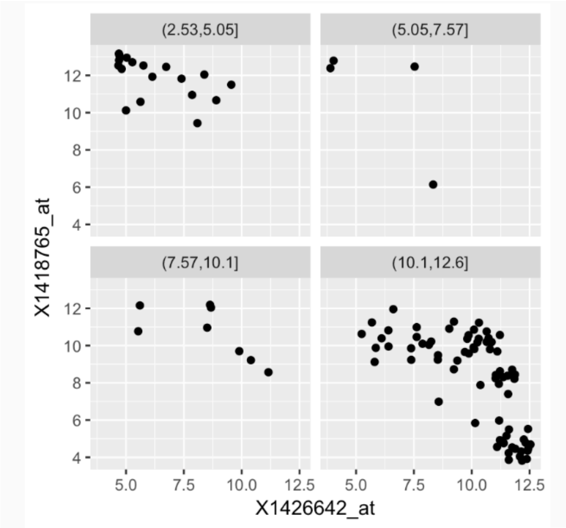


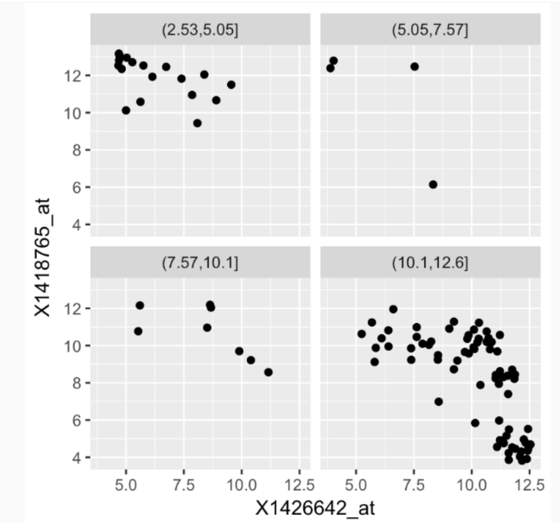
Figure 3.33: **Faceting**: the same data as in Figure 3.9, split by the continuous variable `X1450989_at` and arranged by `facet_wrap`.

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 )
```

Faceting is useful to show more dimensions without overcrowding the graph



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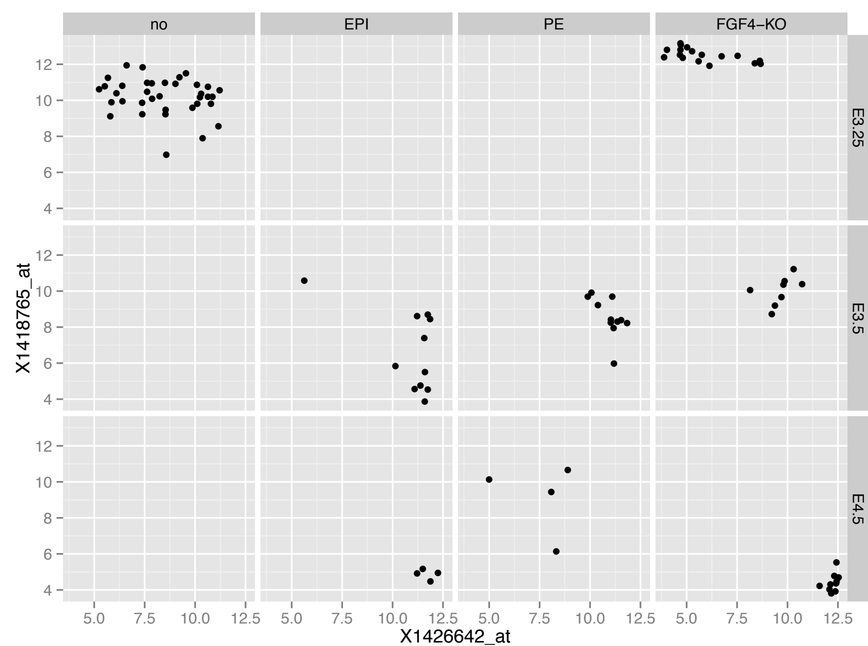
   facet_wrap( ~ Tdgf1, ncol = 2 )
```

facet_grid

```
ggplot( dftx,
  aes( x = X1426642_at, y = X1418765_at)) + geom_point() +
   facet_grid( Embryonic.day ~ lineage )
```



Faceting is useful to show more dimensions without overcrowding the graph

Trellis — chart that uses multiple instances of the same chart

facet_wrap

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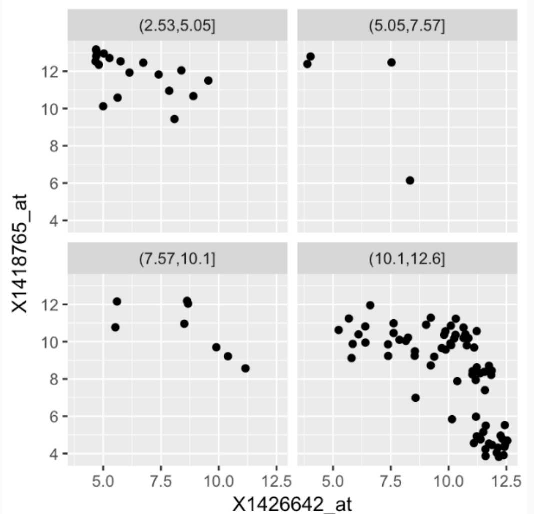
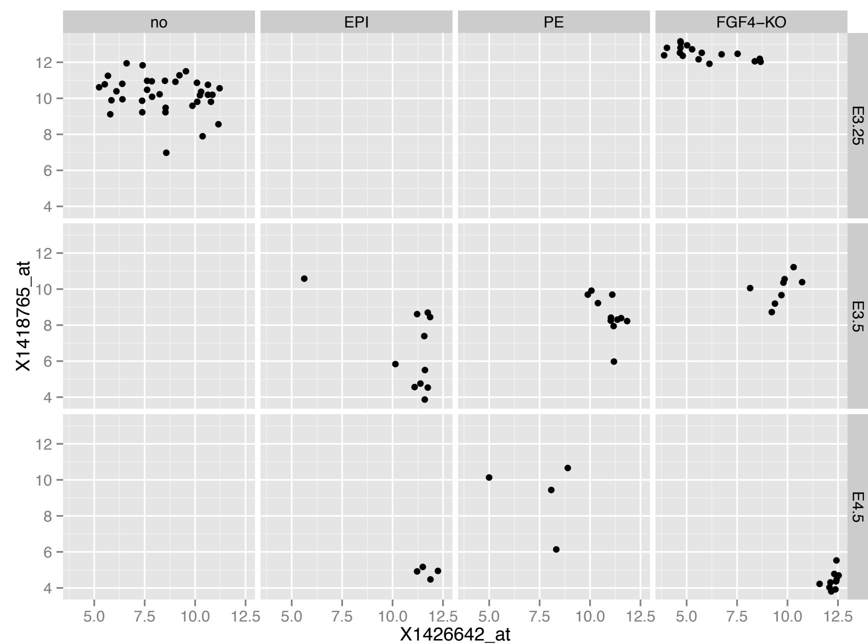


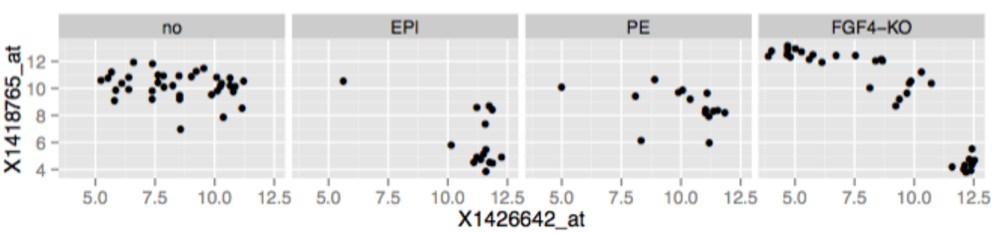
Figure 3.33: Faceting: the same data as in Figure 3.9, split by the continuous variable `X1450989_at` and arranged by `facet_wrap`.

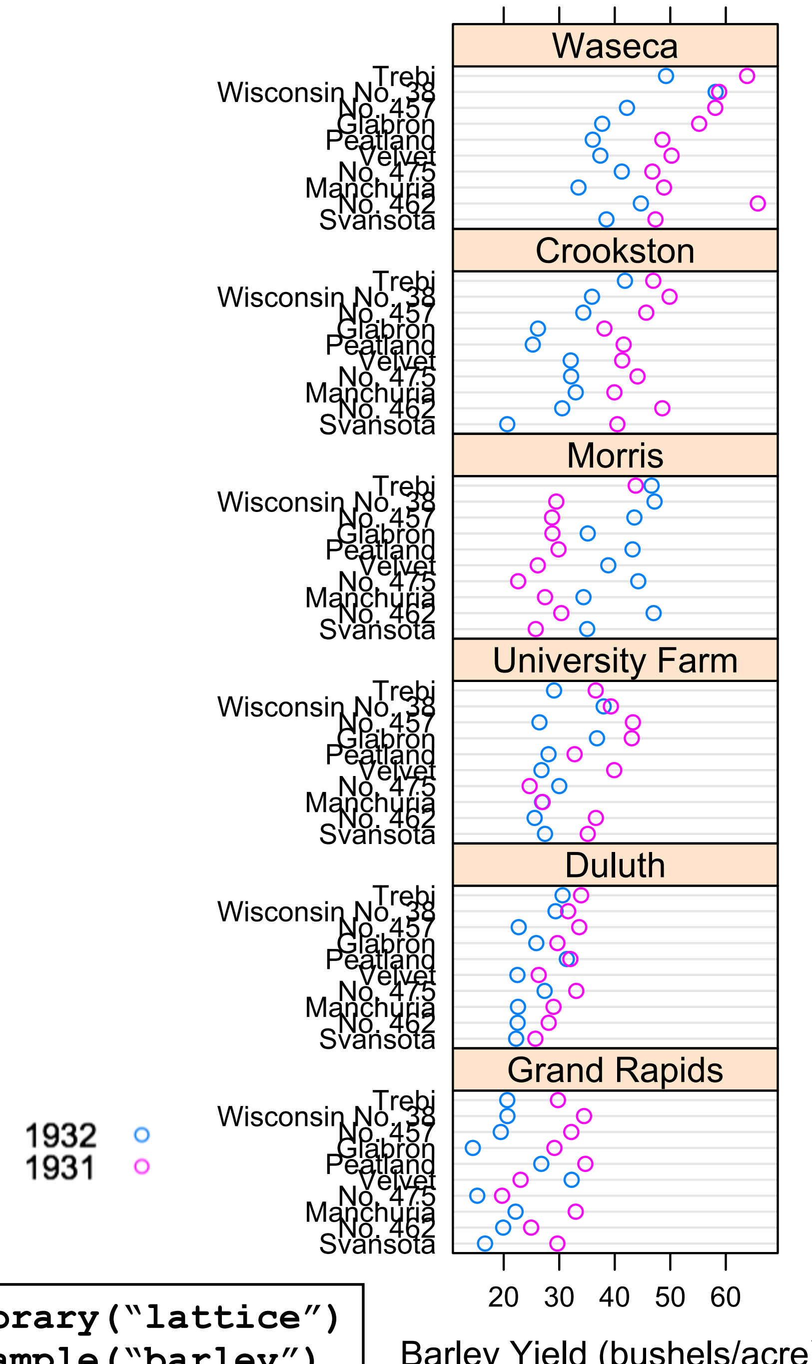
facet_grid

```
ggplot( dftx,
  aes( x = X1426642_at, y = X1418765_at)) + geom_point() +
   facet_grid( Embryonic.day ~ lineage )
```



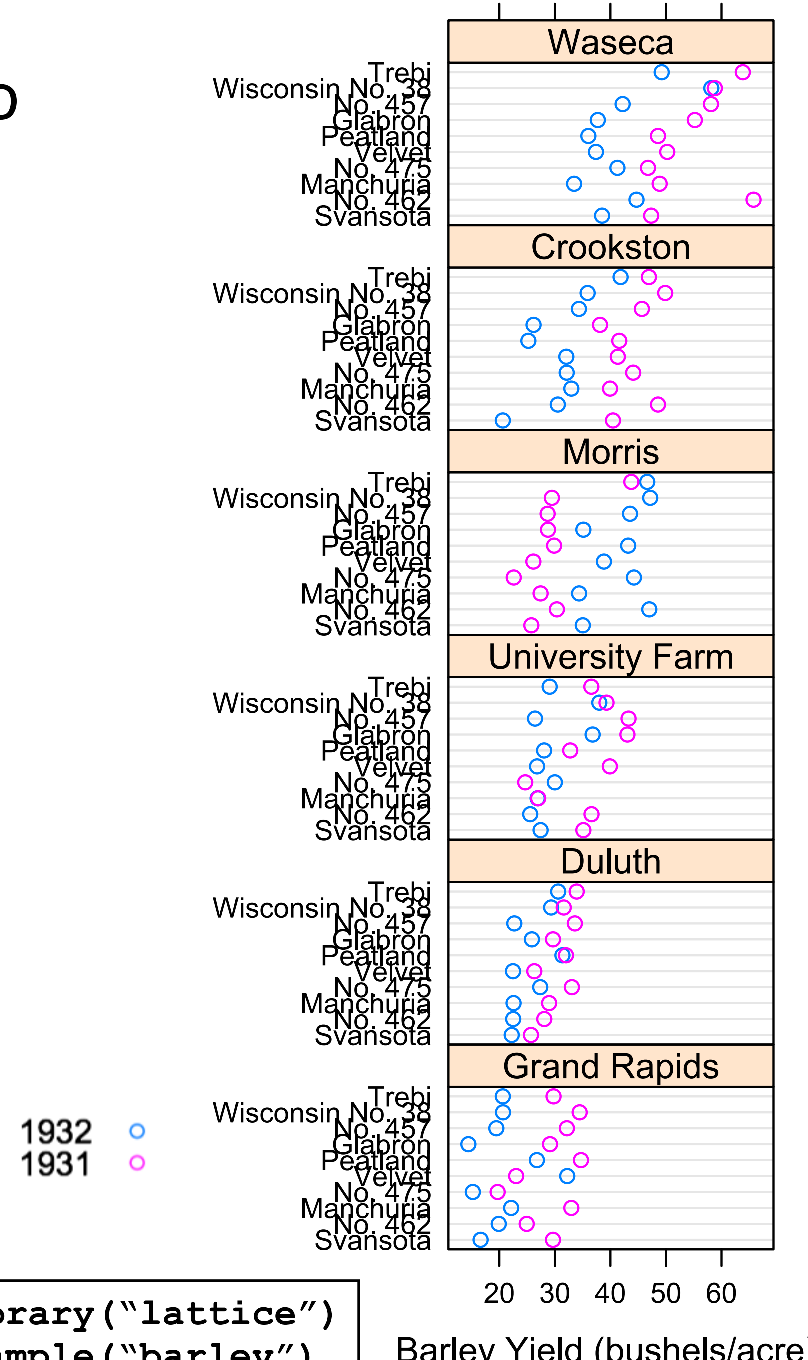

```
ggplot(dftx, aes( x = X1426642_at, y = X1418765_at)) +
  geom_point() + facet_grid( . ~ lineage )
```






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

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

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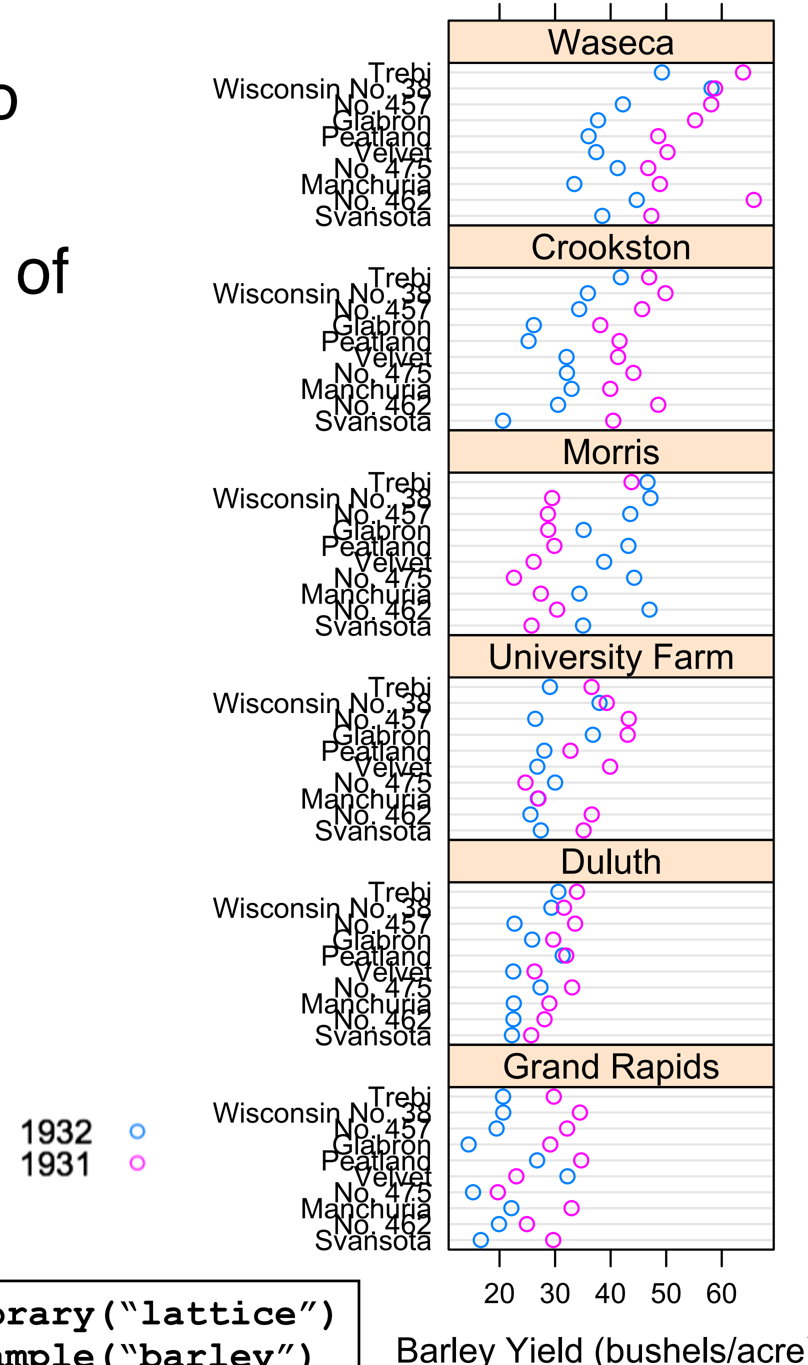
Data from an agricultural field trial to study the crop barley.

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

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example("barley")
```

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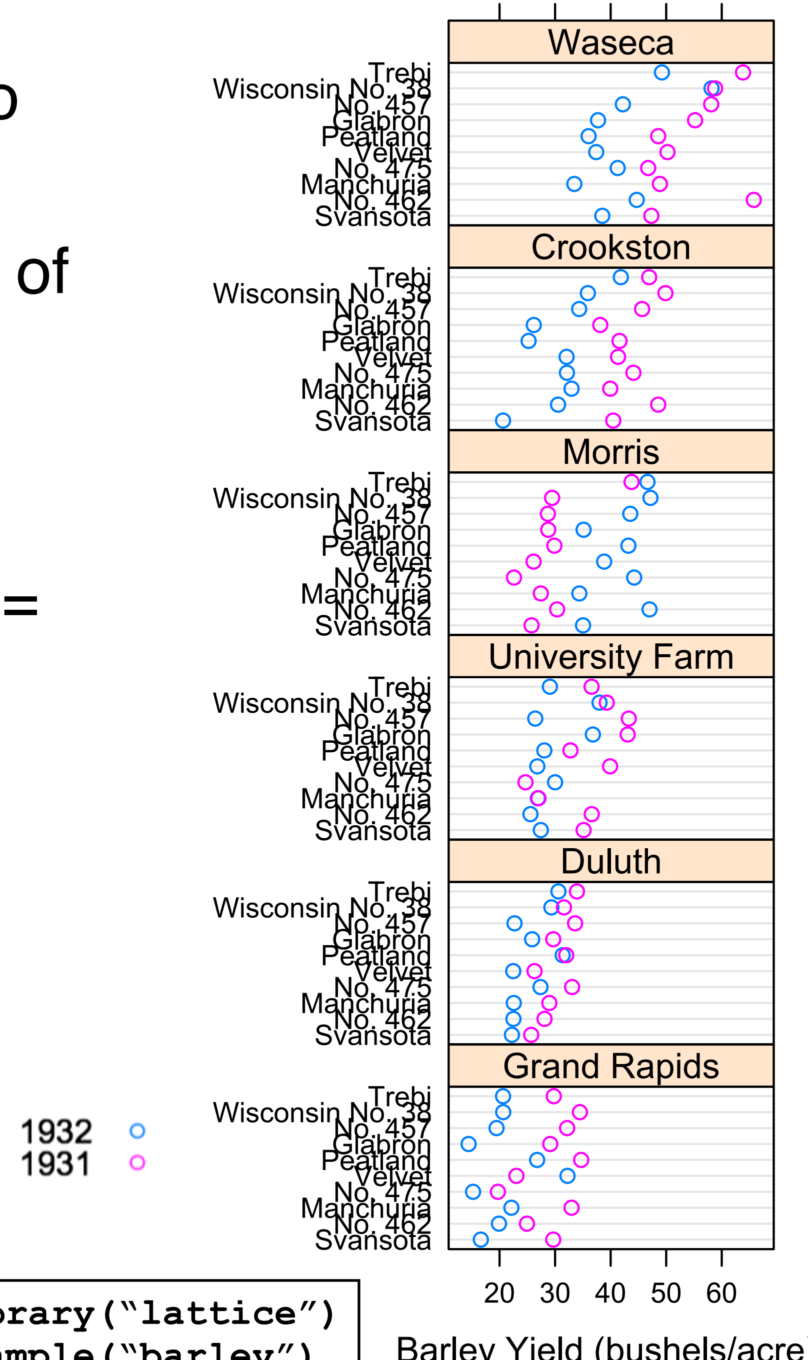
- Data: yield, for all combinations of site, variety, and year (6 x 10 x 2 = 120 observations)




```
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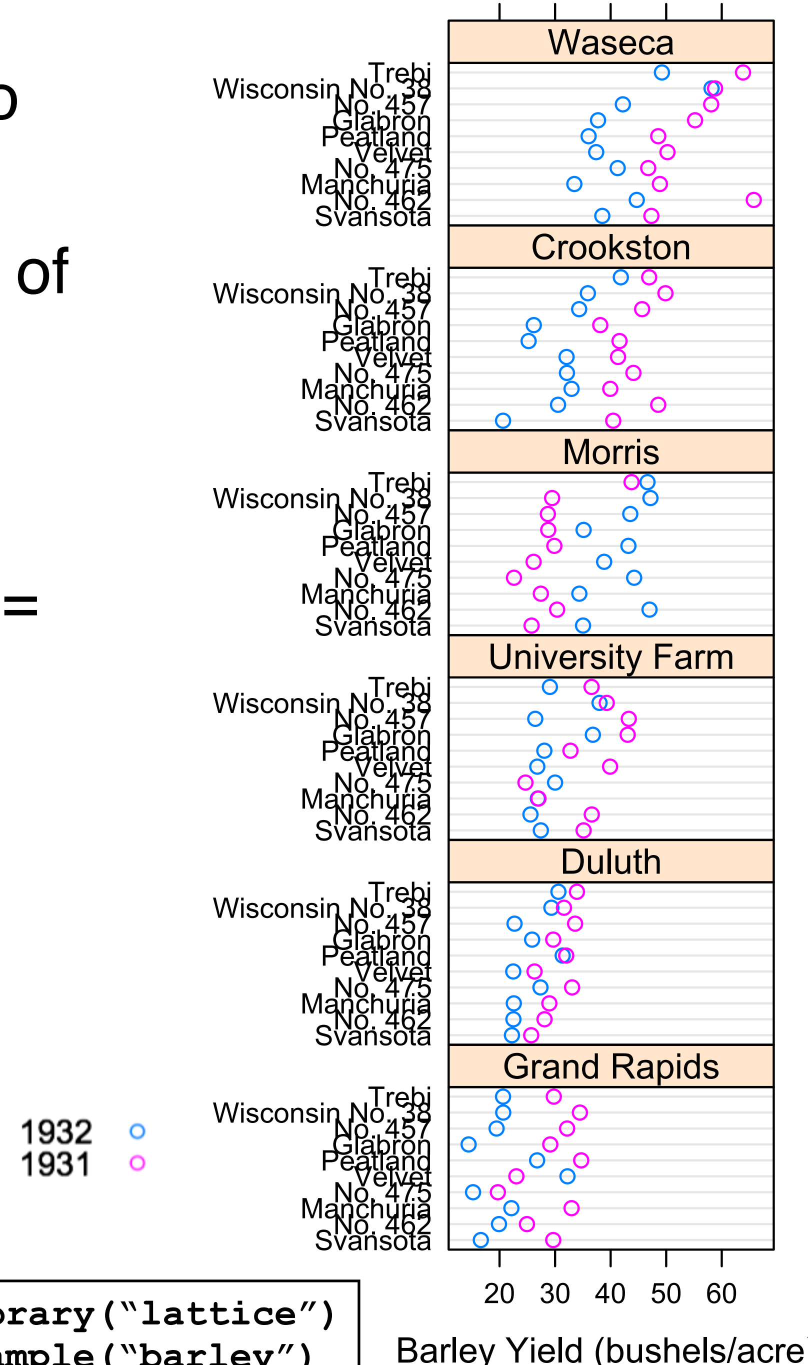


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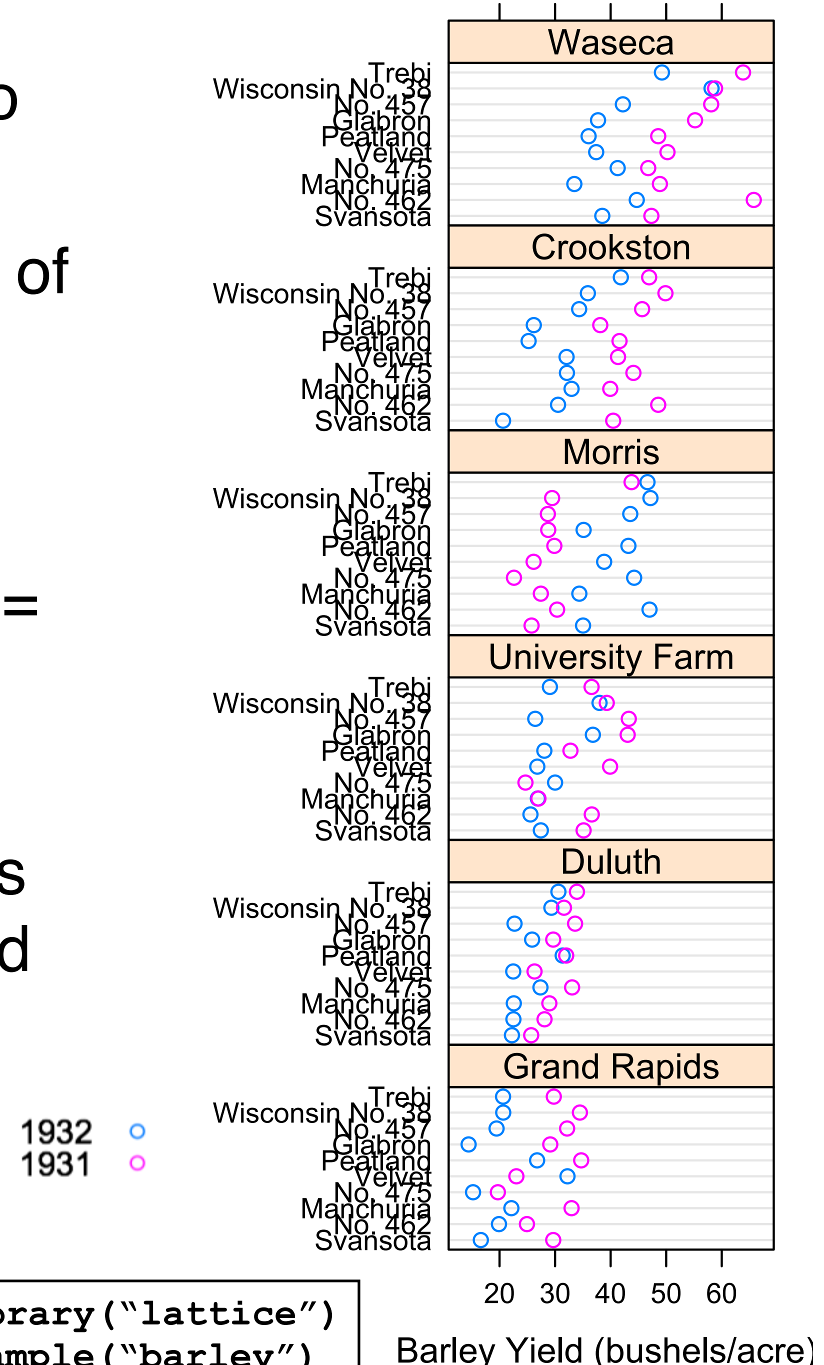
Note the data for **Morris** - reanalysis in the 1990s using Trellis revealed that the years had been flipped!

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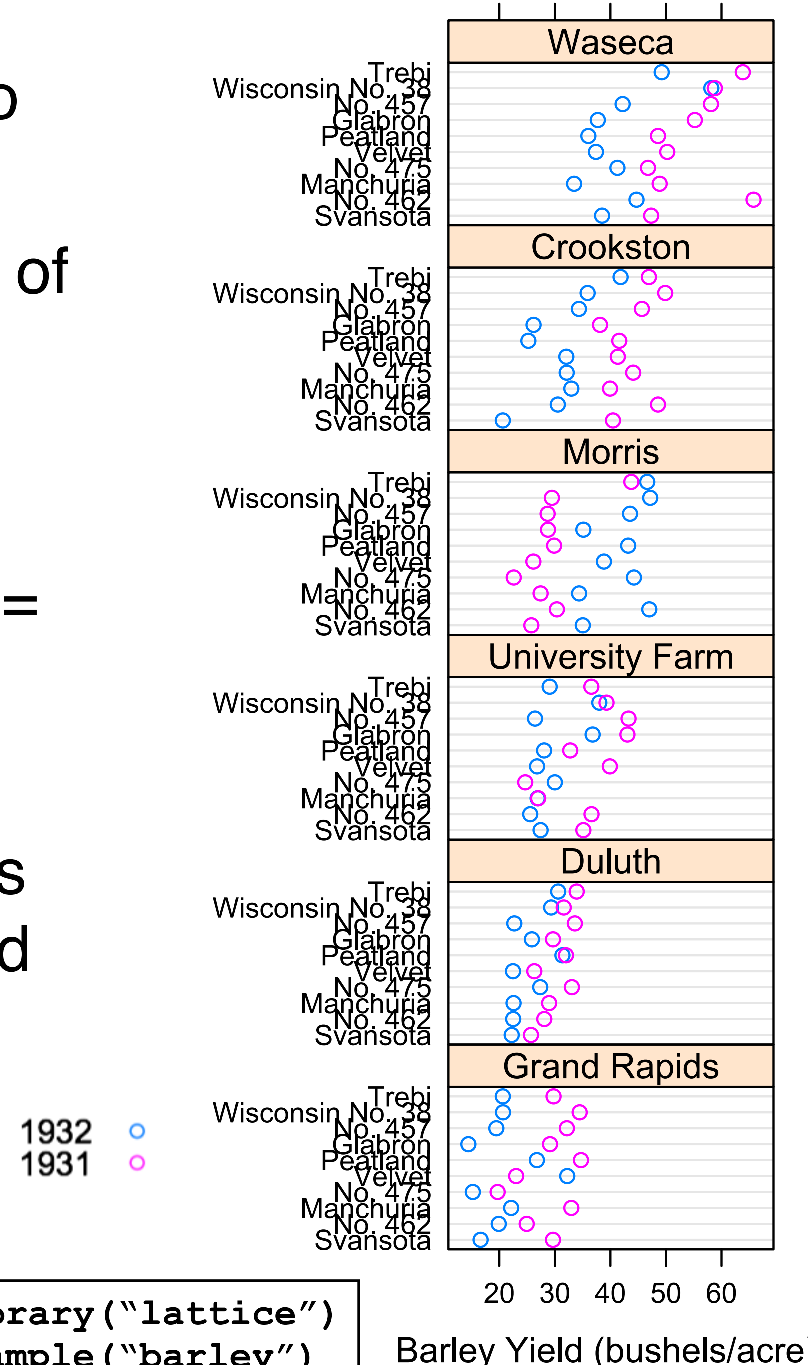
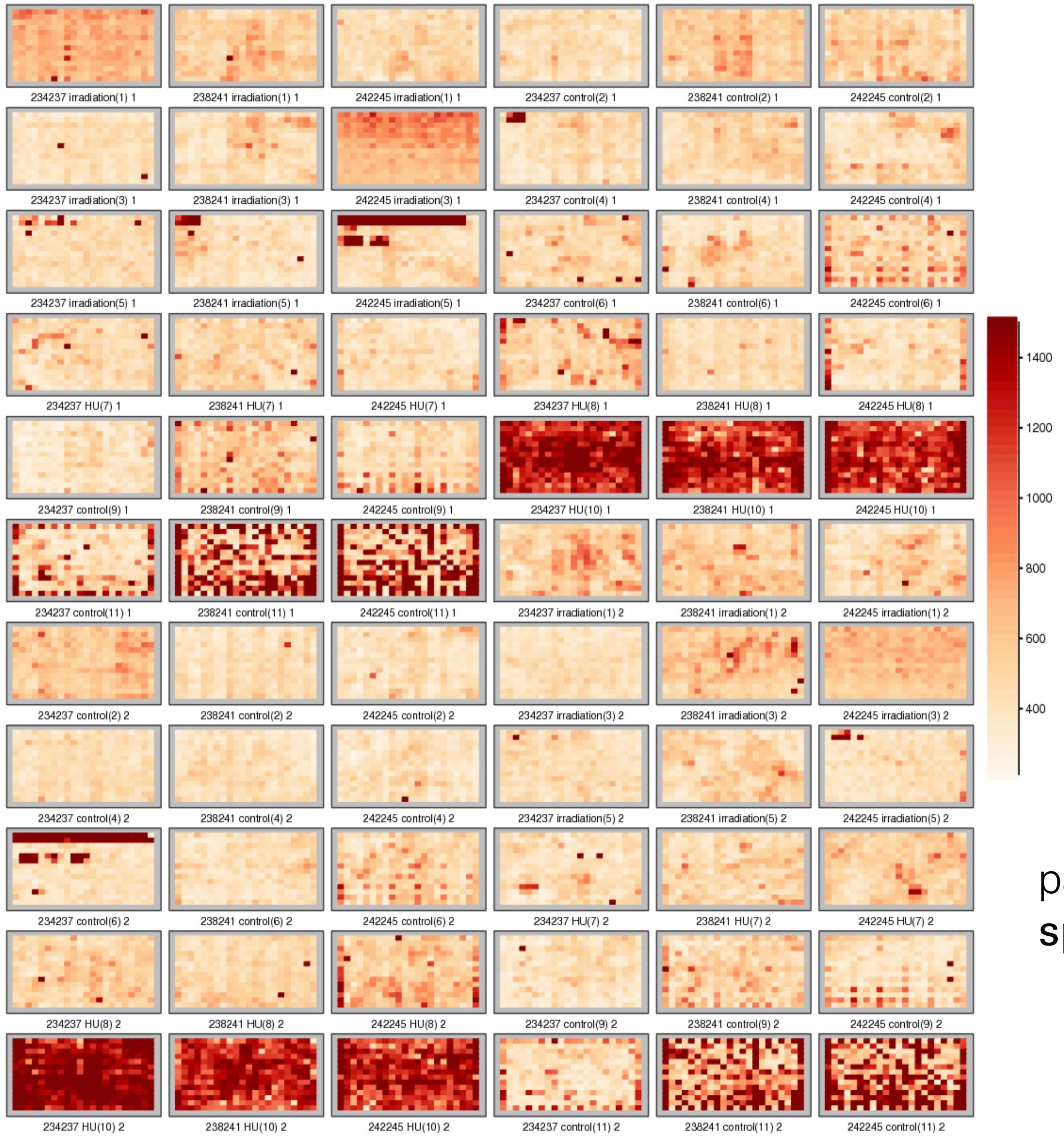


How could you quickly check for potential batch effects?

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

EDA for finding batch effects



package
splots

Tidying data to use columns as aesthetics

```
ggplot( dftx,
  aes( x = X1426642_at, y = X1418765_at)) + geom_point() +
   facet_grid( Embryonic.day ~ lineage )
```

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Data.frame in R can be in:

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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
## 4 E3.25     9.715243    5.982314    4.753439    9.540123
## 5 E3.25     8.924228    4.923580    4.629728    8.705340
## 6 E3.25    11.325952    4.068520    4.165692    8.696228
```

e.g. a expression matrix with each raw containing
a gene expression for all samples

Tidying data to use columns as aesthetics

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e.g. a expression matrix with each raw containing a gene expression for all samples

long format

```
##     sample       probe     value
## 1 1 E3.25 X1420085_at  3.027715
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```

e.g. a collapsed expression data with each row corresponding to a gene-sample pair

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e.g. a collapsed expression data with each row corresponding to a gene-sample pair

Each **row** corresponds to a **sample** and each **column** to a **feature** (or vice versa).

Tidying data to use columns as aesthetics

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## 4 4 E3.25 X1420085_at  9.715243
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e.g. a collapsed expression data with each row corresponding to a gene-sample pair

Feature and **sample** information is stored separately for each measurement in data columns.

Tidying data to use columns as aesthetics

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e.g. a collapsed expression data with each row corresponding to a gene-sample pair

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To switch wide ↔ long: pivot_longer, pivot_wider

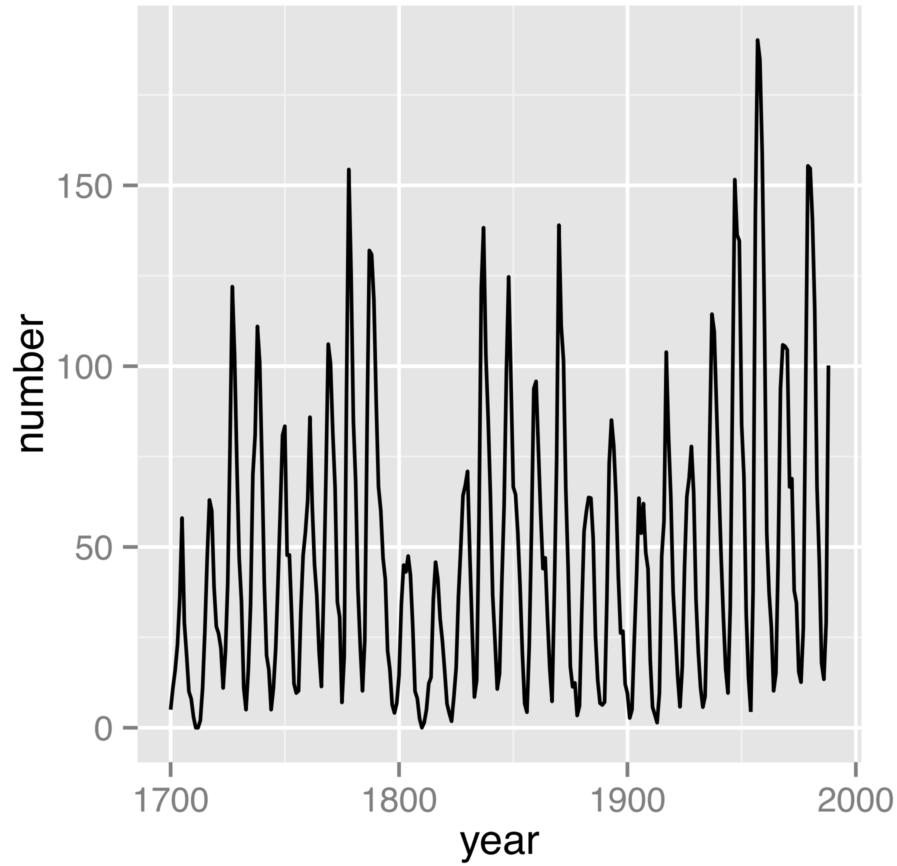
Choose **aspect ratio** so that banking = 45%

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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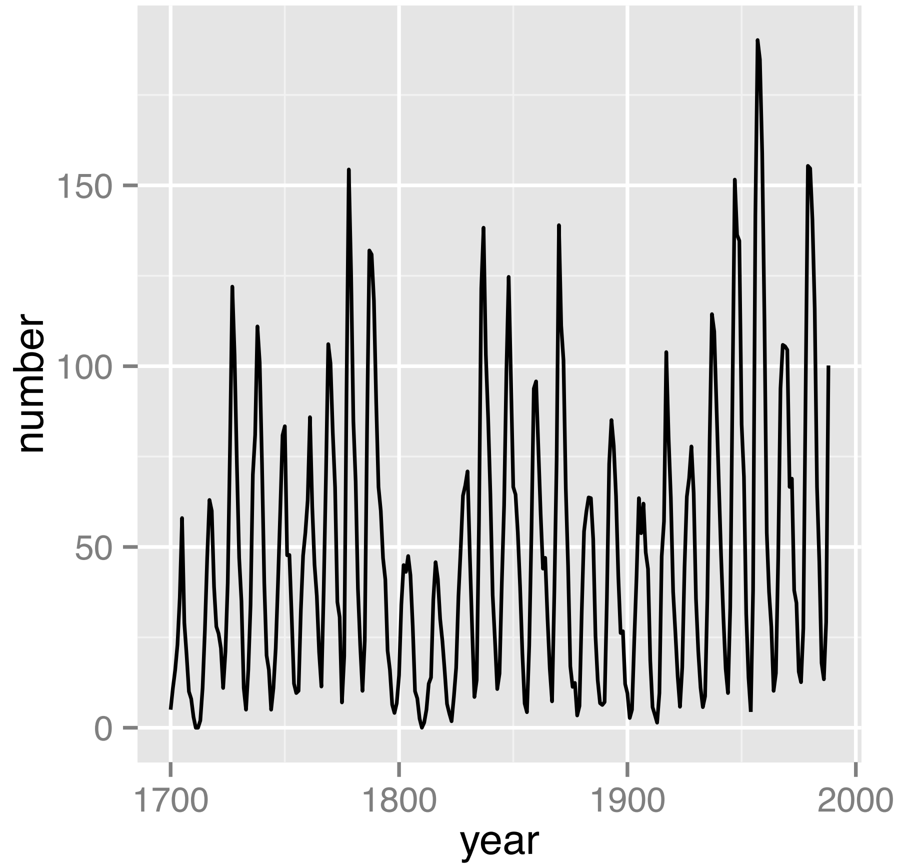
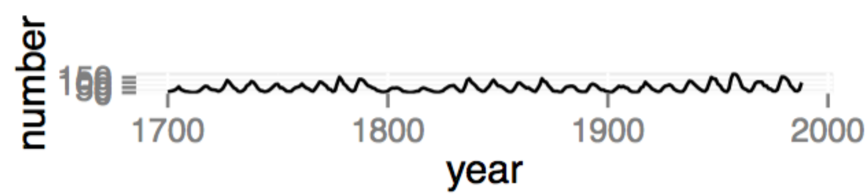
Yearly sunspot numbers 1849-1924 - changes in amplitude

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.





Choose **aspect ratio** so that banking = 45%

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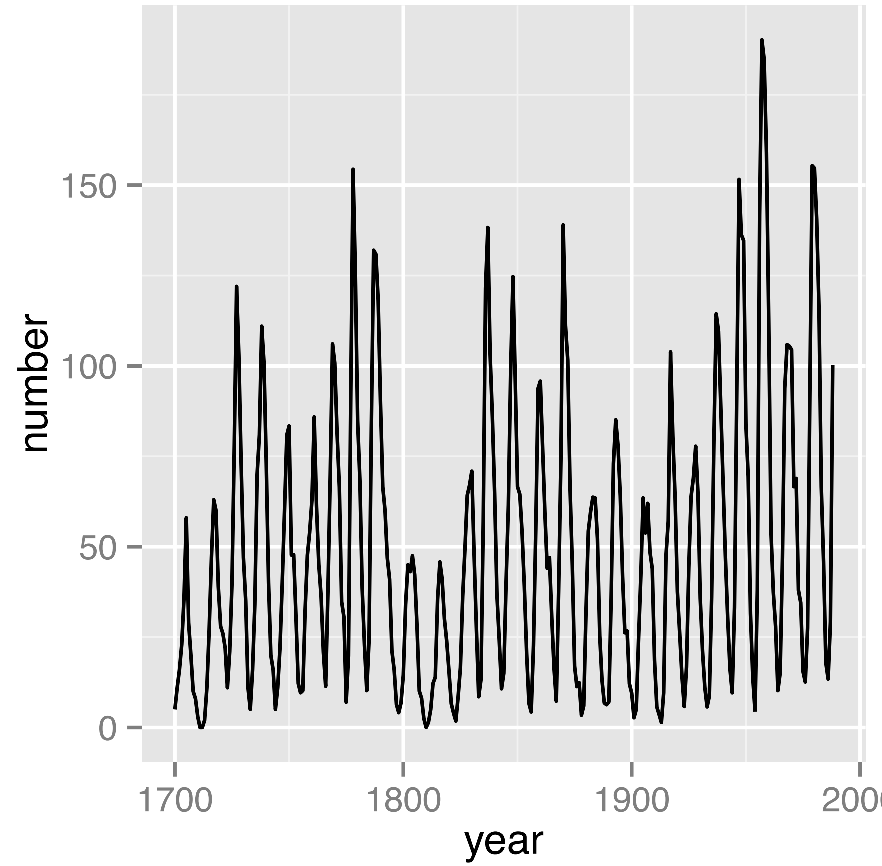
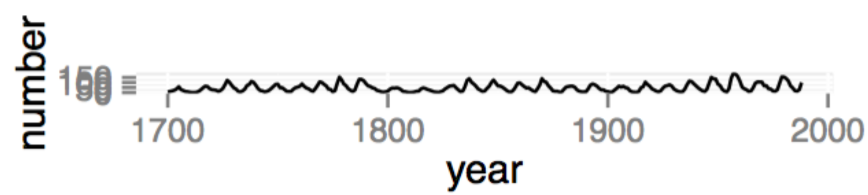


For plots where x- and y-axis have same units: use 1:1 aspect ratio



Heatmaps for visualizing large matrices

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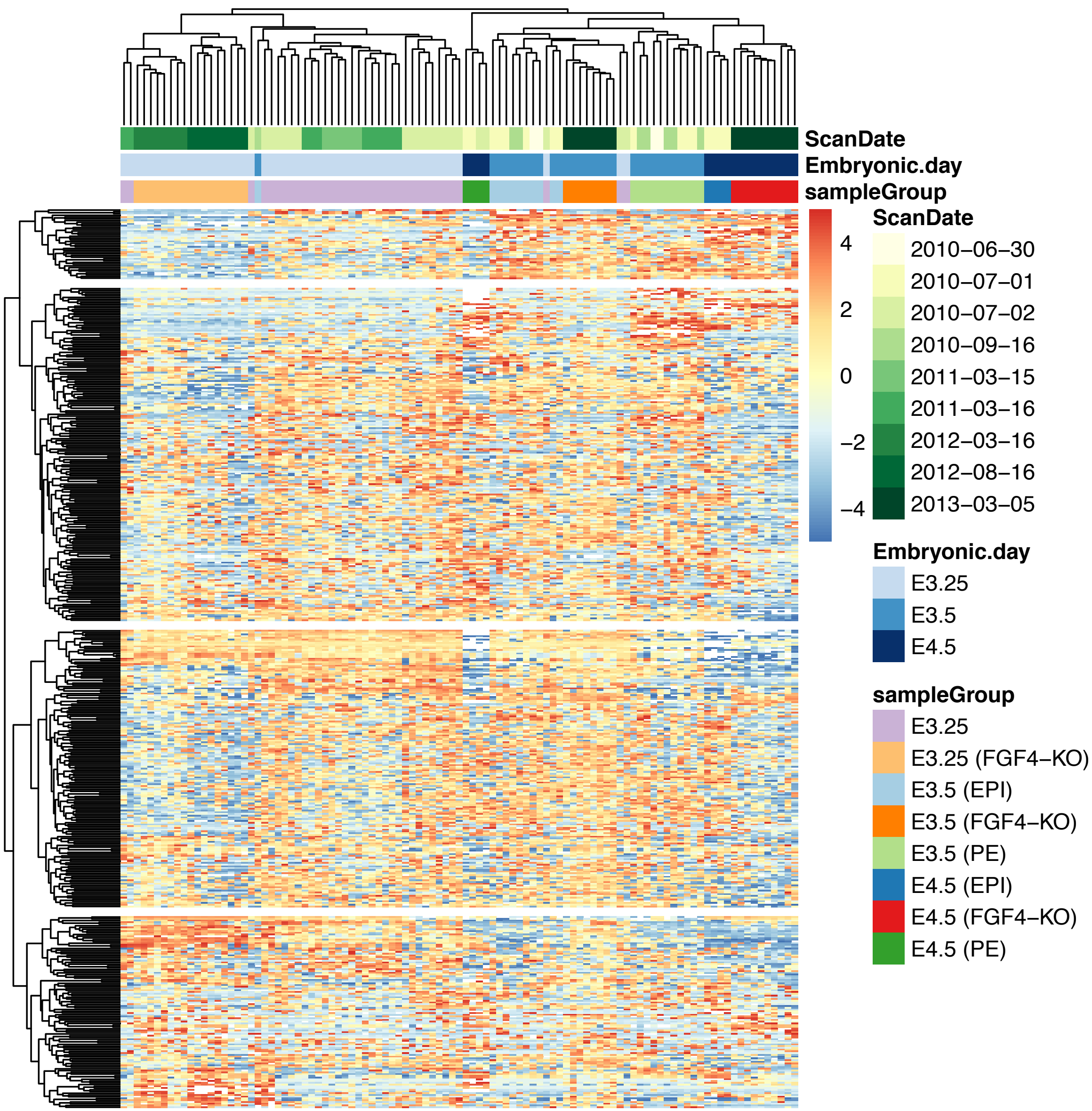

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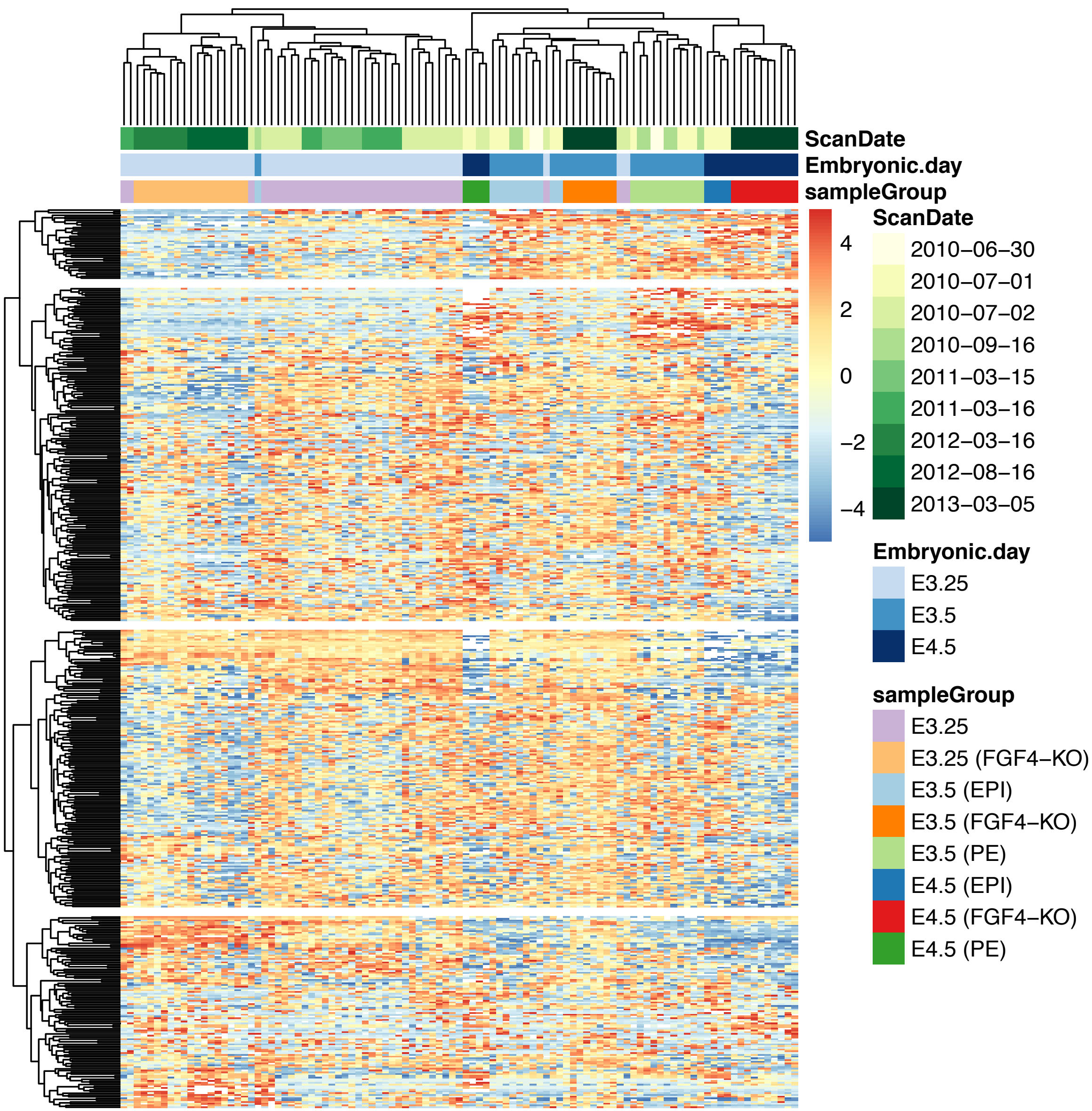
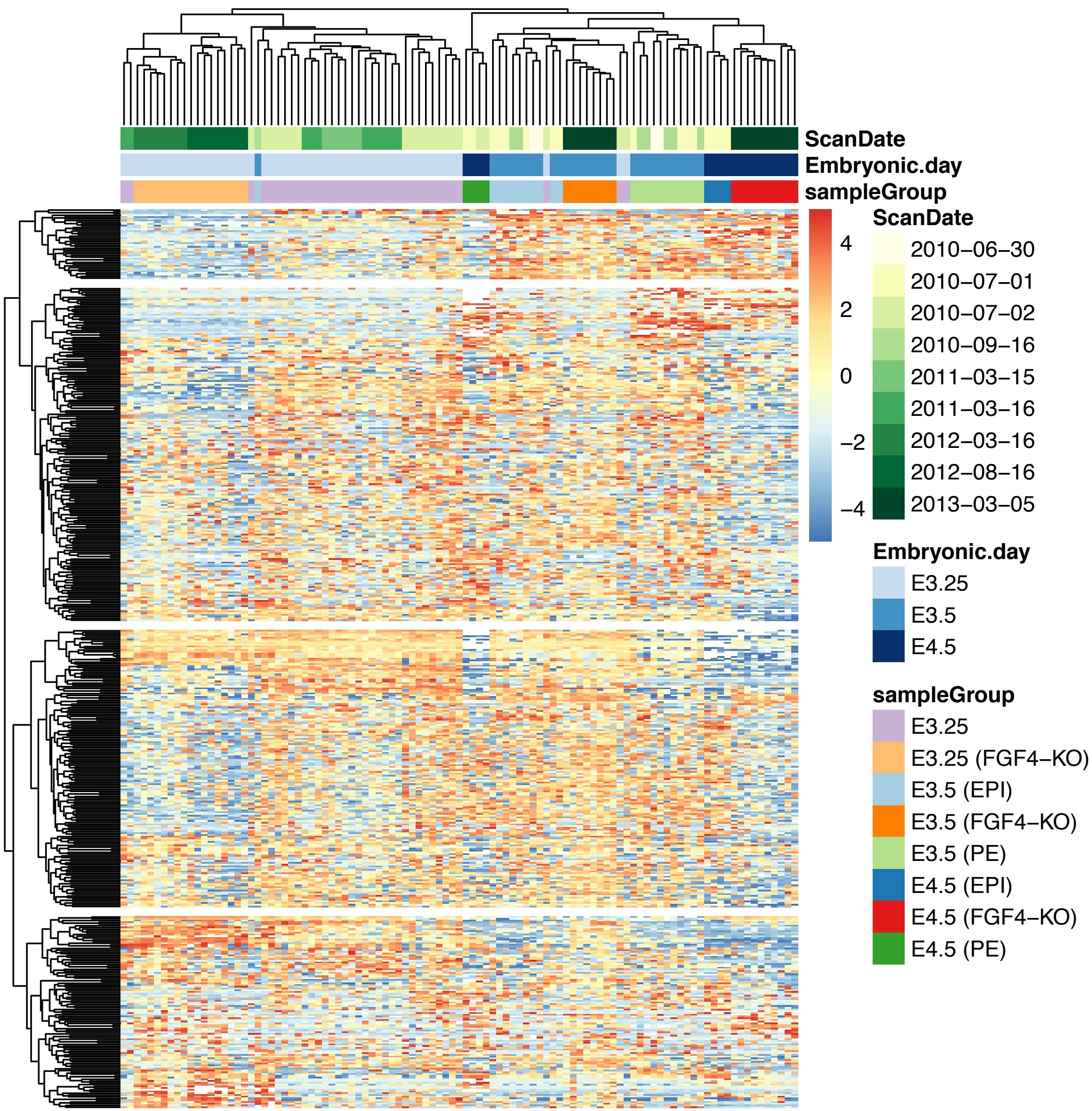


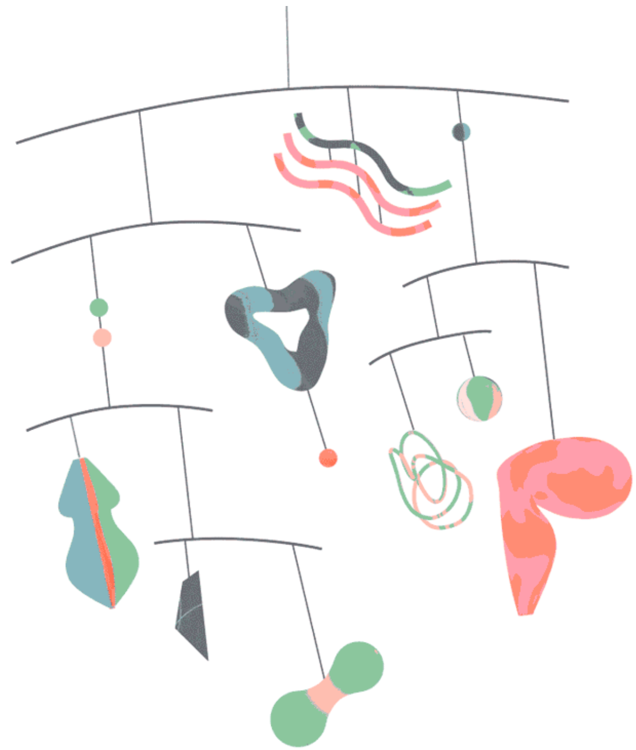
pheatmap

- 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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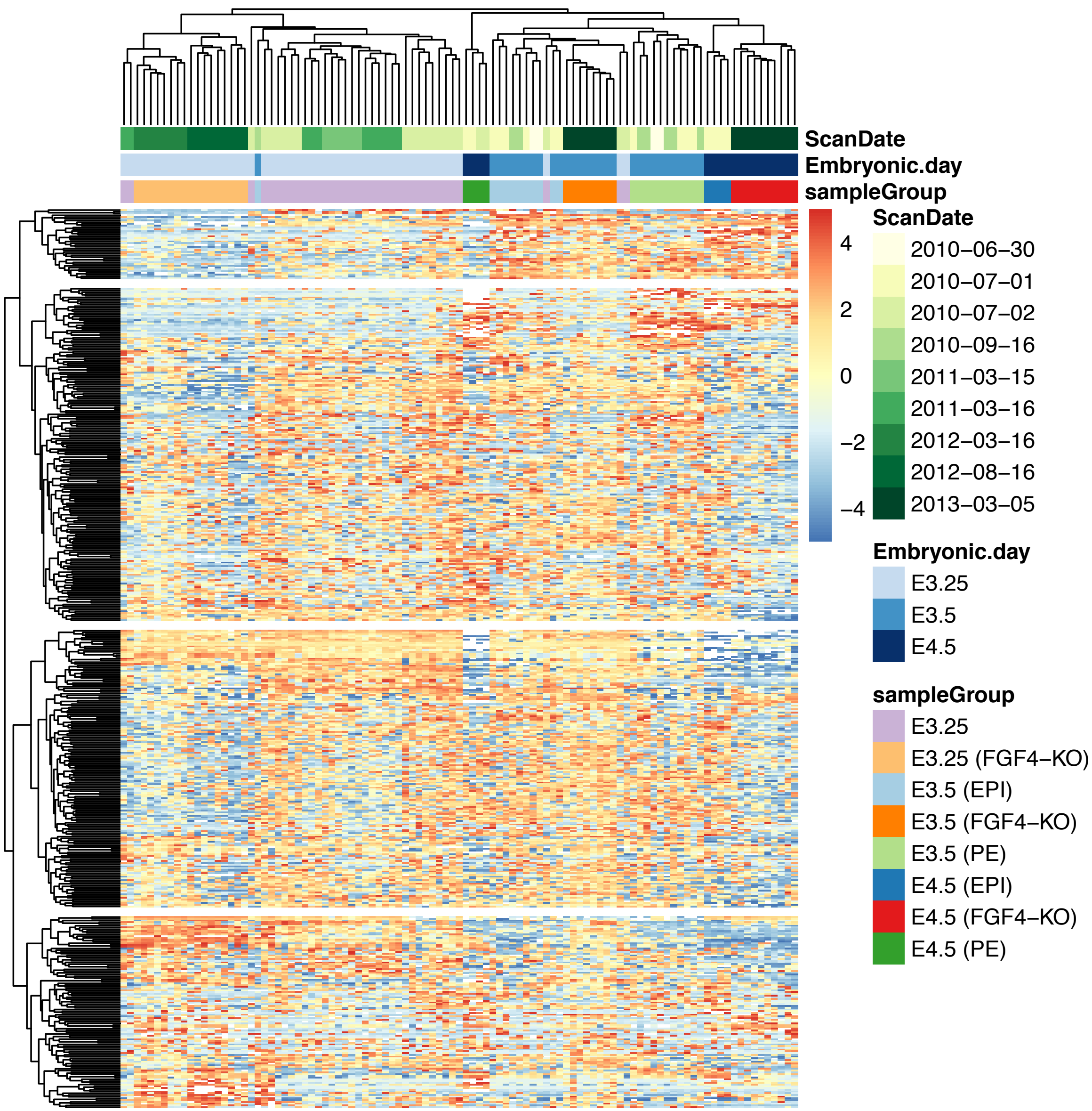

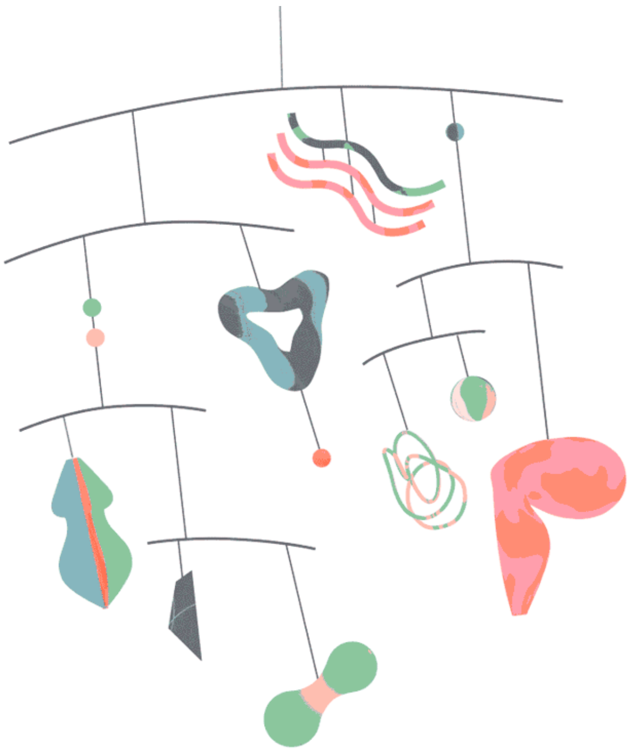

Interactivity

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/

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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

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