

# ggplot2: Going further in the tidyverse

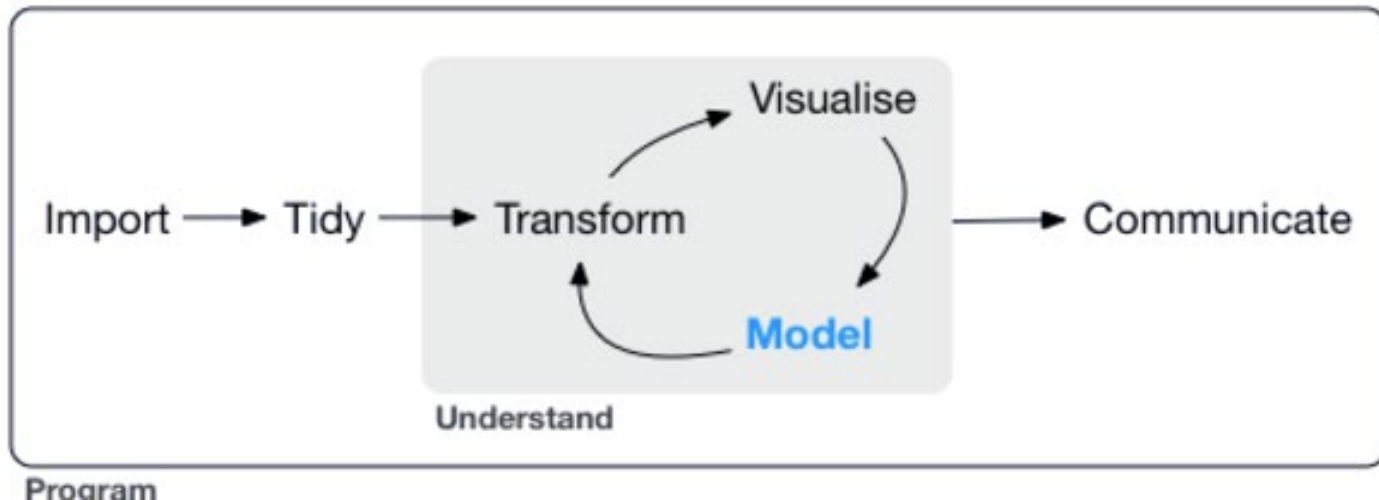
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Psych 6135

<https://friendly.github.io/6135/>

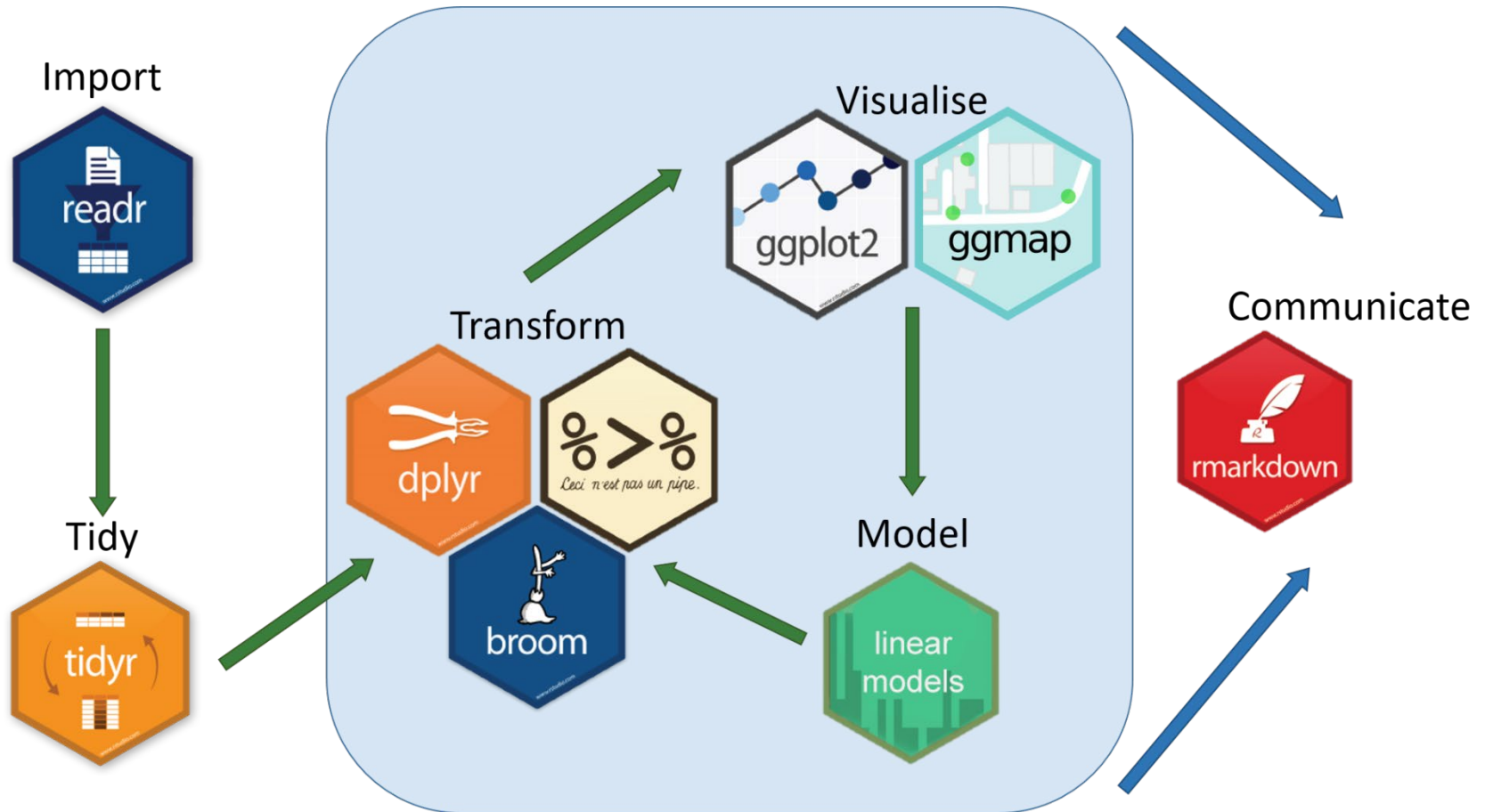
# A larger view: Data science

- Data science treats statistics & data visualization as parts of a larger process
  - Data import: text files, data bases, web scraping, ...
  - Data cleaning → “tidy data”
  - Model building & visualization
  - Reproducible report writing

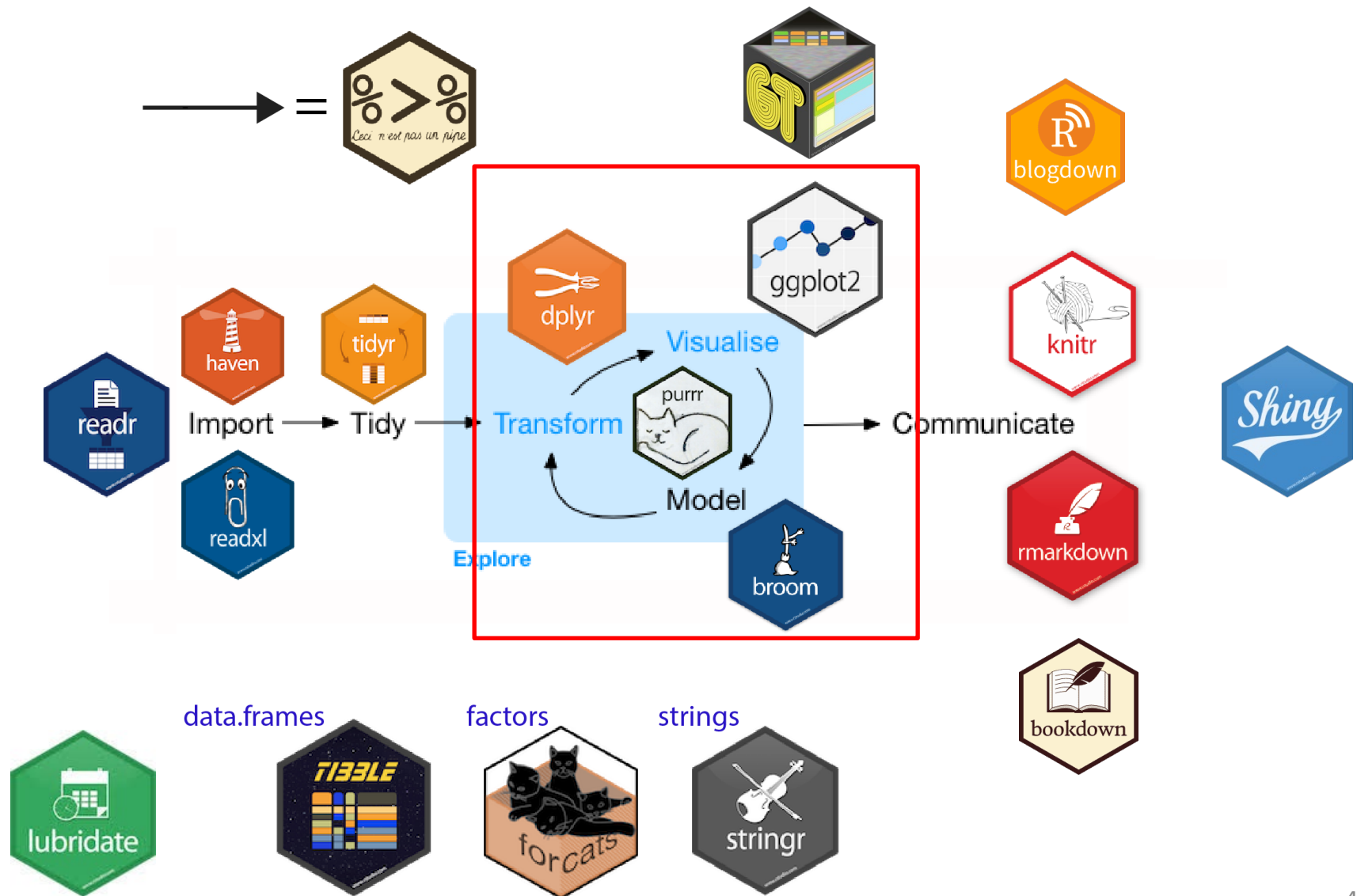




# The tidyverse of R packages

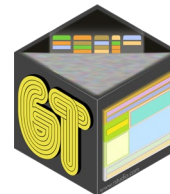
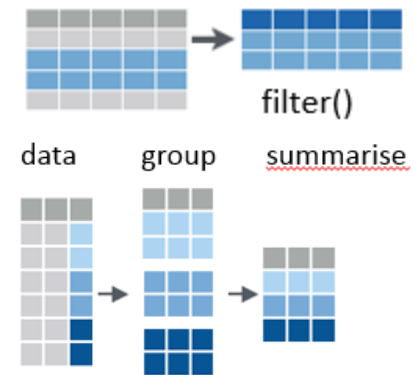


# The tidyverse expands



# Topics

- Data import / export
- Data wrangling: getting your data into shape
  - dplyr & tidyr
  - pipes: %>%
  - grouping & summarizing
  - Example: NASA data on solar radiation
- Working with models: broom
  - Example: gapminder data
- Nice tables in R
- Bootstrapping



# Ready for some heavy lifting?



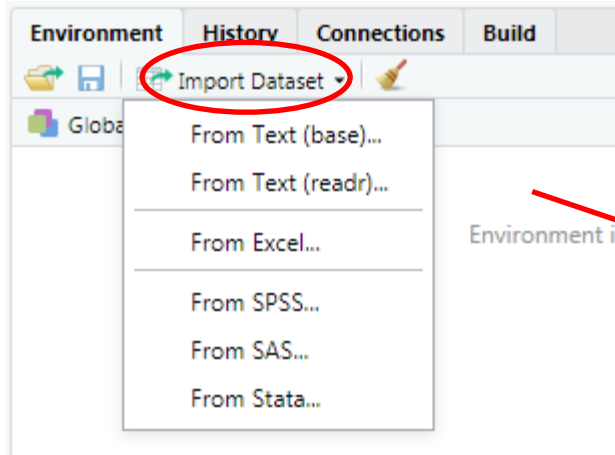
# Data Import / Export

- The readr package is the modern, tidy way to import and export data
  - Tabular data:
    - comma delimited (read.csv)
    - any other delimiters (“;” = read.csv2; <tab> = read\_tsv)
  - Data types:
    - specify column types or let functions guess
- Other data formats



package	Data types
haven	SAS, SPSS, Stata
readxl	Excel files (.xls and .xlsx)
DBI	Databases (SQL, ...)
rvest	HTML (web scraping)

# Data Import: RStudio



file:

Import Text Data

File/URL:  
C:/Users/friendly/Dropbox/Documents/6135/R/drugs.txt

Data Preview:

subject (character)	drug1 (double)	drug2 (double)	drug3 (double)	drug4 (double)
subj1	20	34	38	44
subj2	16	28	30	34
subj3	14	28	26	30
subj4	18	20	24	30
subj5	10	18	14	22

options:

Import Options:

Name: drugs  
Skip: 0

☒ First Row as Names  
☒ Trim Spaces  
☒ Open Data Viewer

Delimiter: **Whitespace**  
Quotes: Default  
Locale: Configure...

Escape: None  
Comment: Default  
NA: Default




code:

```
library(readr)
drugs <- read_table2("R/drugs.txt")
view(drugs)
```



# Data transformation tools

Some common data types can be messy when imported. Tidy tools are there to help

dates/times	lubridate	read dates/times in various formats; extract components	
factors	forcats	Change order of levels, drop levels, combine levels	
strings	stringr	detect matches, subset, replace	



# lubridate: Dates & times

## PARSE DATE-TIMES (Convert strings or numbers to date-times)

1. Identify the order of the year (**y**), month (**m**), day (**d**), hour (**h**), minute (**m**) and second (**s**) elements in your data.
2. Use the function below whose name replicates the order. Each accepts a wide variety of input formats.

**2017-11-28T14:02:00**    **ymd\_hms()**, **ymd\_hm()**, **ymd\_h()**.  
*ymd\_hms("2017-11-28T14:02:00")*

**2017-22-12 10:00:00**    **ydm\_hms()**, **ydm\_hm()**, **ydm\_h()**.  
*ydm\_hms("2017-22-12 10:00:00")*

**11/28/2017 1:02:03**    **mdy\_hms()**, **mdy\_hm()**, **mdy\_h()**.  
*mdy\_hms("11/28/2017 1:02:03")*

**1 Jan 2017 23:59:59**    **dmy\_hms()**, **dmy\_hm()**, **dmy\_h()**.  
*dmy\_hms("1 Jan 2017 23:59:59")*

**20170131**    **ymd()**, **ydm()**. *ymd(20170131)*

**July 4th, 2000**    **mdy()**, **myd()**. *mdy("July 4th, 2000")*

**4th of July '99**    **dmy()**, **dym()**. *dmy("4th of July '99")*

**2001: Q3**    **yq()** Q for quarter. *yq("2001: Q3")*

**2:01**    **hms::hms()** Also lubridate:**hms()**,  
**hm()** and **ms()**, which return  
periods.\* *hms::hms(sec = 0, min = 1,  
hours = 2)*

## # parse dates in various formats

```
ymd("20210604")  
#> [1] "2021-06-04"  
mdy("06-04-2021")  
#> [1] "2021-06-04"  
dmy("04/06/2021")  
#> [1] "2021-06-04"
```

## # extract date components

```
minard_bday <- ymd("1781-03-27")  
year(minard_bday)  
#> [1] 1781  
month.name[month(minard_bday)]  
#> [1] "March"
```

## # date arithmetic: how old is Minard?

```
year(today()) - year(minard_bday)  
#> [1] 241
```



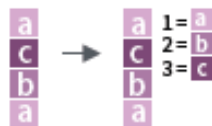
# forcats: Working with factors

R represents categorical variables as factors, useful for analysis (e.g., ANOVA)  
In graphics, we often want to recode levels or reorder them

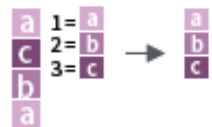
## Factors

R represents categorical data with factors. A **factor** is an integer vector with a **levels** attribute that stores a set of mappings between integers and categorical values. When you view a factor, R displays not the integers, but the values associated with them.

	integer vector	stored	displayed
	1	1 = a	a
	3	2 = b	b
	2	3 = c	c
levels	1		a



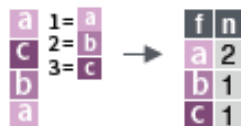
Create a factor with `factor()`  
**factor**(x = character(), levels, labels = levels, exclude = NA, ordered = is.ordered(x), nmax = NA) Convert a vector to a factor. Also **as\_factor**.  
`f <- factor(c("a", "c", "b", "a"), levels = c("a", "b", "c"))`



Return its levels with `levels()`  
**levels**(x) Return/set the levels of a factor. `levels(f)`; `levels(f) <- c("x", "y", "z")`

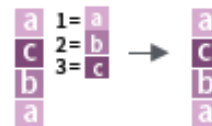
Use `unclass()` to see its structure

## Inspect Factors

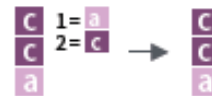


**fct\_count**(f, sort = FALSE)  
Count the number of values with each level. `fct_count(f)`

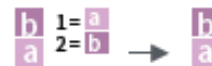
## Change the order of levels



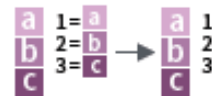
**fct\_relevel**(f, ..., after = 0L)  
Manually reorder factor levels.  
`fct_relevel(f, c("b", "c", "a"))`



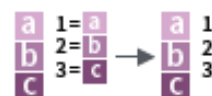
**fct\_infreq**(f, ordered = NA)  
Reorder levels by the frequency in which they appear in the data (highest frequency first).  
`f3 <- factor(c("c", "c", "a"))`  
`fct_infreq(f3)`



**fct\_inorder**(f, ordered = NA)  
Reorder levels by order in which they appear in the data.  
`fct_inorder(f2)`



**fct\_rev**(f) Reverse level order.  
`f4 <- factor(c("a", "b", "c"))`  
`fct_rev(f4)`



**fct\_shift**(f) Shift levels to left or right, wrapping around end.  
`fct_shift(f4)`

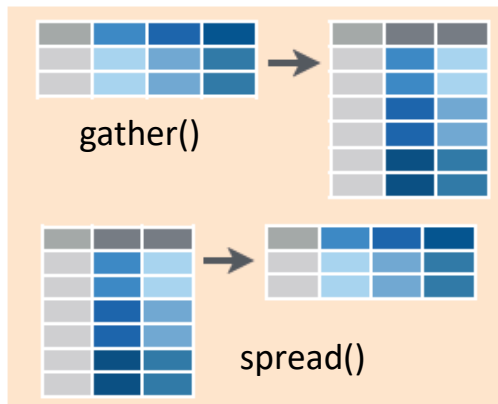
# Tidy tools: overview



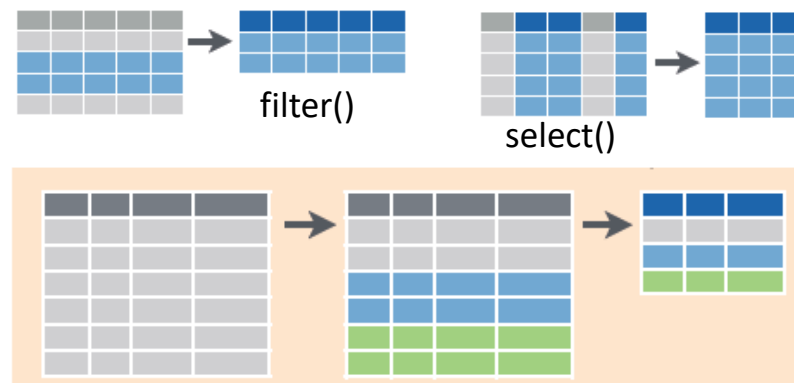
**tidyr**

**pipes**

**dplyr**



$\%>\%$

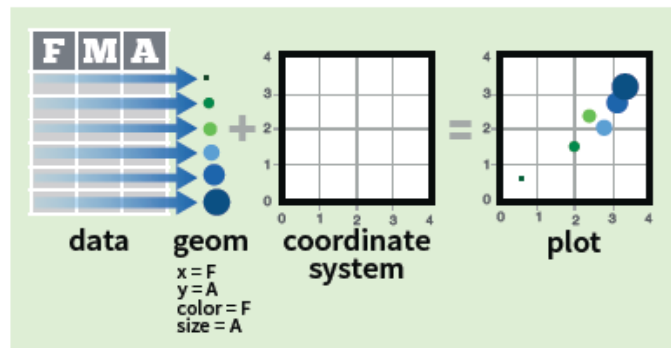


Reshape data to be tidy

Manipulate & summarize tidy data



**ggplot2**



Visualize me!

# Tidy operations

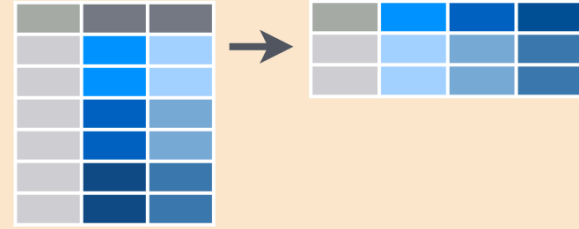
Reshape wide to long  
synonym: **tidyr::pivot\_longer()**



**tidyr::gather(cases, "year", "n", 2:4)**

Gather columns into rows.

Reshape long to wide  
synonym: **tidyr::pivot\_longer()**



**tidyr::spread(pollution, size, amount)**

Spread rows into columns.



**tidyr::separate(storms, date, c("y", "m", "d"))**

Separate one column into several.



**tidyr::unite(data, col, ..., sep)**

Unite several columns into one.

Separate parts of a value into  
several variables

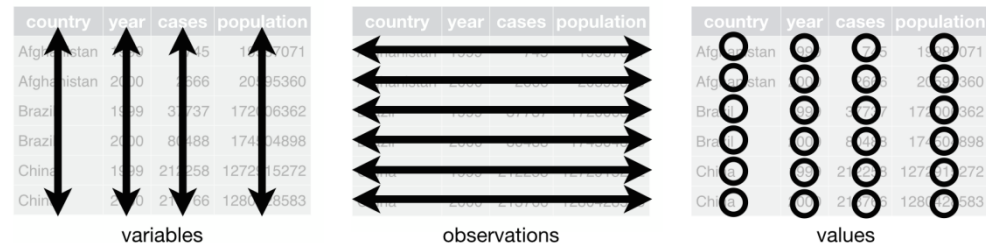
Join related variables into one

# Data wrangling with dplyr & tidyr

## What is Tidy Data?

A dataset is said to be tidy if:

- observations are in **rows**
- variables are in **columns**
- each value is in its own **cell**.



A “messy” dataset: Survey of income by religion from Pew Research

- Values of **income** are in separate columns, not one variable
- Column headers are **values**, not variable names
- Cell values are frequencies--- **implicit**, not explicit

religion	<\$10k	\$10-20k	\$20-30k	\$30-40k	\$40-50k	\$50-75k
Agnostic	27	34	60	81	76	137
Atheist	12	27	37	52	35	70
Buddhist	27	21	30	34	33	58
Catholic	418	617	732	670	638	1116

This organization is easy in Excel

But, this makes data analysis and graphing hard

# Tidying: reshaping wide to long

We can tidy the data by reshaping from wide to long format using **tidyr::gather()**

```
> pew <- read.delim(
  file = "http://stat405.had.co.nz/data/pew.txt",
  header = TRUE,
  stringsAsFactors = FALSE, check.names = FALSE)

> (pew1 <- pew[1:4, 1:6]) # small subset
```

	religion	<\$10k	\$10-20k	\$20-30k	\$30-40k	\$40-50k
1	Agnostic	27	34	60	81	76
2	Atheist	12	27	37	52	35
3	Buddhist	27	21	30	34	33
4	Catholic	418	617	732	670	638

Another solution, using **reshape2::melt()**

```
> library(reshape2)
> pew_tidy <- melt(
  data = pew1,
  id = "religion",
  variable.name = "income",
  value.name = "frequency"
)
```

key      value      columns

↓      ↓      ↓

```
> library(tidyr)
> gather(pew1, "income", "frequency", 2:6)
```

	religion	income	frequency
1	Agnostic	<\$10k	27
2	Atheist	<\$10k	12
3	Buddhist	<\$10k	27
4	Catholic	<\$10k	418
5	Agnostic	\$10-20k	34
6	Atheist	\$10-20k	27
7	Buddhist	\$10-20k	21
8	Catholic	\$10-20k	617
9	Agnostic	\$20-30k	60
10	Atheist	\$20-30k	37
11	Buddhist	\$20-30k	30
12	Catholic	\$20-30k	732
13	Agnostic	\$30-40k	81
14	Atheist	\$30-40k	52
15	Buddhist	\$30-40k	34
16	Catholic	\$30-40k	670
...	...	...	...

NB: income is a **character** variable; we might want to create an **ordered factor** or **numeric** version



# Using pipes: %>%

- R is a functional language
  - This means that  $f(x)$  returns a value, as in  $y \leftarrow f(x)$
  - That value can be passed to another function:  $g(f(x))$
  - And so on:  $h(g(f(x)))$

```
> x <- c(0.109, 0.359, 0.63, 0.996, 0.515, 0.142)
> exp(diff(log(x)))
[1] 3.29 1.75 1.58 0.52 0.28
```

- This gets messy and hard to read, unless you break it down step by step

```
> # Compute the logarithm of `x`, calculate lagged differences,
> # return the exponential function of the result
> log(x)
[1] -2.216 -1.024 -0.462 -0.004 -0.664 -1.952
> diff(log(x))          #calculate lagged diffs
[1] 1.19 0.56 0.46 -0.66 -1.29
> exp(diff(log(x)))     # convert back to original scale
[1] 3.29 1.75 1.58 0.52 0.28
```



# Using pipes: %>%

- Pipes (%>%) change the syntax to make this easier

```
> # use pipes
> x %>% log() %>% diff() %>% exp()
[1] 3.29 1.75 1.58 0.52 0.28
```

- Basic rules

- $x \%>\% f()$  passes object on left hand side as first argument (or . argument) of function on right hand side
  - $x \%>\% f()$  is the same as  $f(x)$
  - $x \%>\% f(y)$  is the same as  $f(x, y)$
  - $y \%>\% f(x, ., z)$  is the same as  $f(x, y, z)$
- $x \%<>\% f()$  does the same, but assigns the result to x
  - Shortcut for  $x \leftarrow x \%>\% f()$



# Using pipes: %>% ggplot()



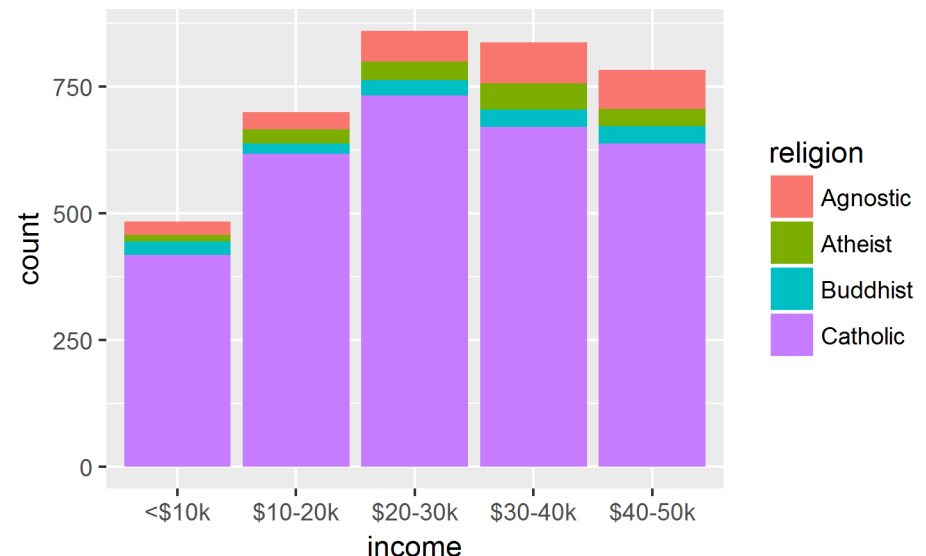
For the Pew data, mutate income → ordered factor and make a ggplot

```
pew1 %>%  
  gather("income", "frequency", 2:6) %>%  
  mutate(income = ordered(income, levels=unique(income))) %>%  
  ggplot(aes(x=income, fill=religion)) +  
    geom_bar(aes(weight=frequency))
```

# reshape  
# make ordered  
# plot  
# as freq bars

mutate() calculates or transforms  
column variables  
ordered(income) levels are now ordered  
appropriately.

The result is piped to ggplot()



# Tidying: separate() and unite()

It sometimes happens that several variables are crammed into one column, or parts of one variable are split across multiple columns



`tidyr::separate(storms, date, c("y", "m", "d"))`

Separate one column into several.



`tidyr::unite(data, col, ..., sep)`

Unite several columns into one.

For example, for the pew data, we might want separate income into low & high

```
pew_long %>%  
  mutate(inc = gsub("[\\$k]", "", income)) %>%  
  mutate(inc = gsub("<", "0-", inc)) %>%  
  separate(inc, c("low", "high"), "-") %>%  
  head()
```

	religion	income	frequency	low	high
1	Agnostic	<\$10k	27	0	10
2	Atheist	<\$10k	12	0	10
3	Buddhist	<\$10k	27	0	10
4	Catholic	<\$10k	418	0	10
5	Agnostic	\$10-20k	34	10	20
6	Atheist	\$10-20k	27	10	20

# dplyr: Subset observations (rows)

dplyr implements a variety of verbs to select a subset of observations from a dataset



In a pipe expression, omit the dataset name

**dplyr::filter(iris, Sepal.Length > 7)**

Extract rows that meet logical criteria.

**dplyr::distinct(iris)**

Remove duplicate rows.

**dplyr::sample\_frac(iris, 0.5, replace = TRUE)**

Randomly select fraction of rows.

**dplyr::sample\_n(iris, 10, replace = TRUE)**

Randomly select n rows.

**dplyr::slice(iris, 10:15)**

Select rows by position.

**dplyr::top\_n(storms, 2, date)**

Select and order top n entries (by group if grouped data).

```
iris %>% filter(Sepal.Length > 7)
iris %>% filter(Species == "setosa")
```

```
iris %>% sample_n(10)
iris %>% slice(1:50) # setosa
```

# dplyr: Subset variables (columns)



**dplyr::select(iris, Sepal.Width, Petal.Length, Species)**

Select columns by name or helper function.

Many helper functions in dplyr allow selection by a **function** of variable names:

**select(iris, contains("."))**

Select columns whose name contains a character string.

**select(iris, ends\_with("Length"))**

Select columns whose name ends with a character string.

**select(iris, everything())**

Select every column.

**select(iris, matches(".t."))**

Select columns whose name matches a regular expression.

**select(iris, num\_range("x", 1:5))**

Select columns named x1, x2, x3, x4, x5.

**select(iris, one\_of(c("Species", "Genus")))**

Select columns whose names are in a group of names.

**select(iris, starts\_with("Sepal"))**

Select columns whose name starts with a character string.

**select(iris, Sepal.Length:Petal.Width)**

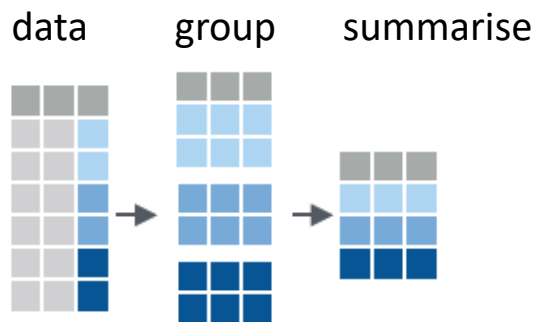
Select all columns between Sepal.Length and Petal.Width (inclusive).

**select(iris, -Species)**

Select all columns except Species.

# dplyr: group\_by() and summarise()

- Fundamental operations in data munging are:
  - grouping** a dataset by one or more variables
  - calculating one or more **summary** measures
  - ungrouping**: expand to an ungrouped copy, if needed



```
mtcars %>%  
  group_by(cyl) %>%  
  summarise(avg=mean(mpg))
```



```
mtcars %>%  
  group_by(cyl) %>%  
  summarise(avg=mean(mpg)) %>%  
  ungroup()
```

# Example: NASA data on solar radiation



## Surface meteorology and Solar Energy

*A renewable energy resource web site (release 6.0)*

sponsored by [NASA's Applied Science Program](#) in the Science Mission Directorate  
developed by [POWER](#): Prediction of Worldwide Energy Resource Project

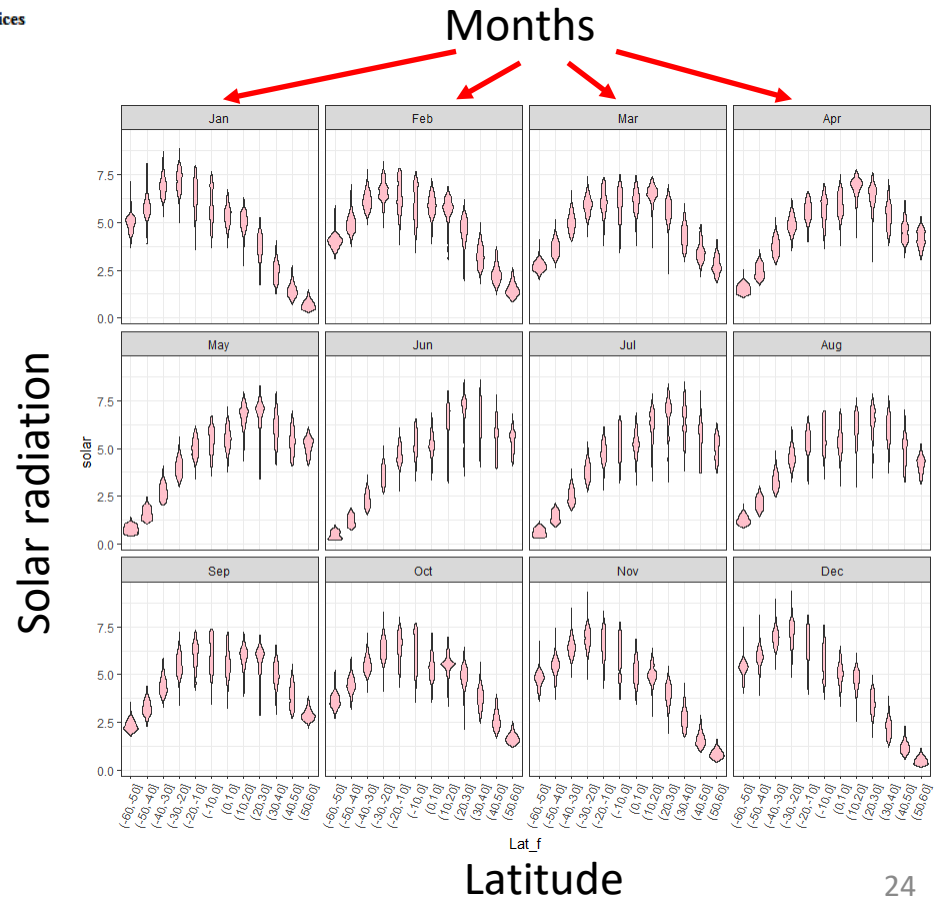


- over 200 satellite-derived meteorology and solar energy parameters
- monthly averaged from 22 years of data
- data tables for a particular location
- GIS Web Mapping Application & Services

How does solar radiation vary with latitude, over months of the year?

How to make this plot?

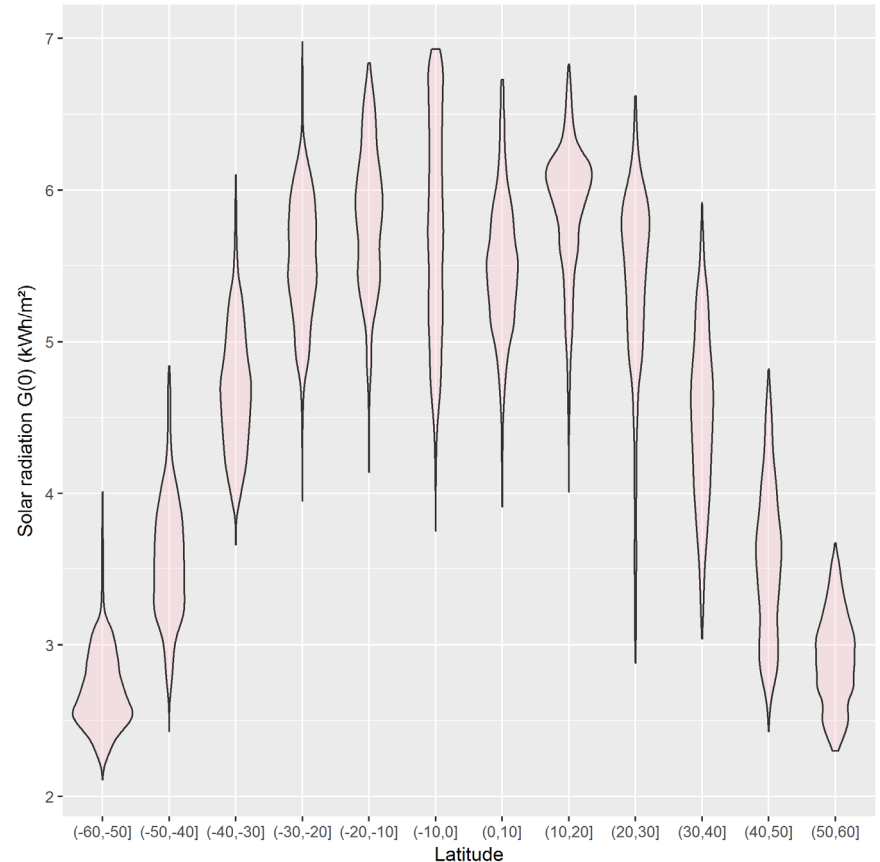
Q:  
what are the basic plot elements?



# NASA data: solar radiation

This is easy to do for the total **Annual** solar radiation, a column in the data

```
> str(nasa)
'data.frame': 64800 obs. of 15 variables:
 $ Lat: int -90 -90 -90 -90 -90 -90 -90 -90 -90 -90 ...
 $ Lon: int -180 -179 -178 -177 -176 -175 -174 -173 -172 -171 ...
 $ Jan: num 9.63 9.63 9.63 9.63 9.63 9.63 9.63 9.63 9.63 9.63 ...
 $ Feb: num 5.28 5.28 5.28 5.28 5.28 5.28 5.28 5.28 5.28 5.28 ...
 $ Mar: num 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 ...
 $ Apr: num 0 0 0 0 0 0 0 0 0 0 ...
 $ May: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Jun: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Jul: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Aug: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Sep: num 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 ...
 $ Oct: num 3.24 3.24 3.24 3.24 3.24 3.24 3.24 3.24 3.24 3.24 ...
 $ Nov: num 8.28 8.28 8.28 8.28 8.28 8.28 8.28 8.28 8.28 8.28 ...
 $ Dec: num 11 11 11 11 11 ...
 $ Ann: num 3.19 3.19 3.19 3.19 3.19 3.19 3.19 3.19 3.19 3.19 ...
```



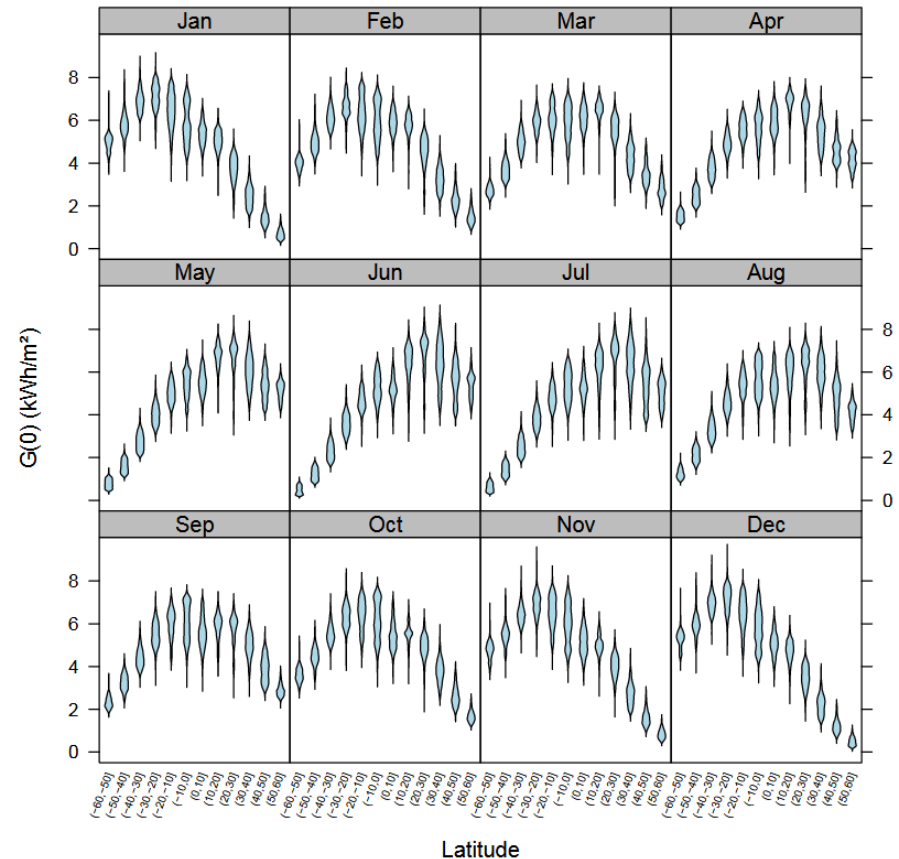
```
nasa %>%
  filter(abs(Lat) < 60) %>%
  mutate(Latf = cut(Lat, pretty(Lat, n=10))) %>%
  ggplot(aes(x=Latf, y=Ann)) +
    geom_violin(fill="pink", alpha=0.3) +
    labs(x="Latitude", y="Solar radiation G(0) (kWh/m²)")
```



# Faceting & tidy data

This is complicated to do for the separate months, because the data structure is **untidy**--- months were in separate variables (wide format)

```
> str(nasa)
'data.frame': 64800 obs. of 15 variables:
 $ Lat: int -90 -90 -90 -90 -90 -90 -90 -90 -90 ...
 $ Lon: int -180 -179 -178 -177 -176 -175 -174 -173 -172 -171 ...
 $ Jan: num 9.63 9.63 9.63 9.63 9.63 9.63 9.63 9.63 9.63 9.63 ...
 $ Feb: num 5.28 5.28 5.28 5.28 5.28 5.28 5.28 5.28 5.28 5.28 ...
 $ Mar: num 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 0.75 ...
 $ Apr: num 0 0 0 0 0 0 0 0 0 0 ...
 $ May: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Jun: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Jul: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Aug: num 0 0 0 0 0 0 0 0 0 0 ...
 $ Sep: num 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 ...
 $ Oct: num 3.24 3.24 3.24 3.24 3.24 3.24 3.24 3.24 3.24 3.24 ...
 $ Nov: num 8.28 8.28 8.28 8.28 8.28 8.28 8.28 8.28 8.28 8.28 ...
 $ Dec: num 11 11 11 11 11 ...
 $ Ann: num 3.19 3.19 3.19 3.19 3.19 3.19 3.19 3.19 3.19 3.19 ...
```



# tidying the data

To plot solar radiation against latitude by month (separate panels), we need to:

- remove the Ann column
- reshape the data to long format, so solar is all in one column

```
library(tidyr)
library(dplyr)
library(ggplot2)

nasa_long <- nasa %>%
  select(-Ann) %>%
  gather(month, solar, Jan:Dec, factor_key=TRUE) %>%
  filter( abs(Lat) < 60 ) %>%
  mutate( Lat_f = cut(Lat, pretty(Lat, 12)))
```

%>% “pipes” data to the next stage

**select()** extracts or drops columns

**gather()** collapses columns into key-value pairs

**filter()** subsets observations

**mutate()** creates new variables

# tidying the data

```
> str(nasa_long)
'data.frame': 514080 obs. of 5 variables:
 $ Lat : int -59 -59 -59 -59 -59 -59 -59 -59 -59 -59 ...
 $ Lon : int -180 -179 -178 -177 -176 -175 -174 -173 -172 -171 ...
 $ month: Factor w/ 12 levels "Jan","Feb","Mar",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ solar: num 5.19 5.19 5.25 5.25 5.17 5.17 5.15 5.15 5.15 5.15 ...
 $ Lat_f: Factor w/ 12 levels "(-60,-50]", "(-50,-40]", ...: 1 1 1 1 1 1 1 1 1 1 ...
```

For ease of plotting, I created a factor version of Lat with 12 levels

```
> head(nasa_long)
  Lat Lon month solar  Lat_f
1 -59 -180  Jan  5.19 (-60,-50]
2 -59 -179  Jan  5.19 (-60,-50]
3 -59 -178  Jan  5.25 (-60,-50]
4 -59 -177  Jan  5.25 (-60,-50]
5 -59 -176  Jan  5.17 (-60,-50]
6 -59 -175  Jan  5.17 (-60,-50]
```

The data are now in a form where I can plot solar against Lat or Lat\_f and facet by month

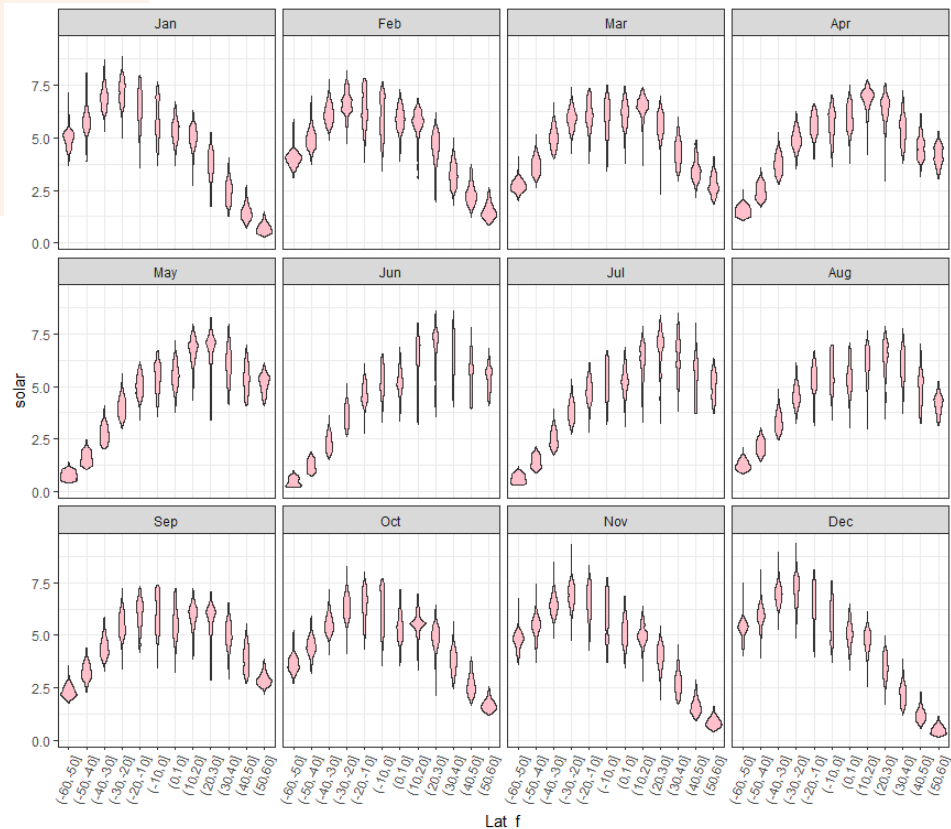
# plotting the tidy data

Using `geom_violin()` shows the shapes of the distributions for levels of `Lat_f`

```
ggplot(nasa_long, aes(x=Lat_f, y=solar)) +  
  geom_violin(fill="pink") +  
  facet_wrap(~ month) +  
  theme_bw() +  
  theme(axis.text.x =  
    element_text(angle = 70,  
                  hjust = 1))
```

`facet_wrap(~month)` does the  
right thing

I had to adjust the x-axis labels for  
`Lat_f` to avoid overplotting



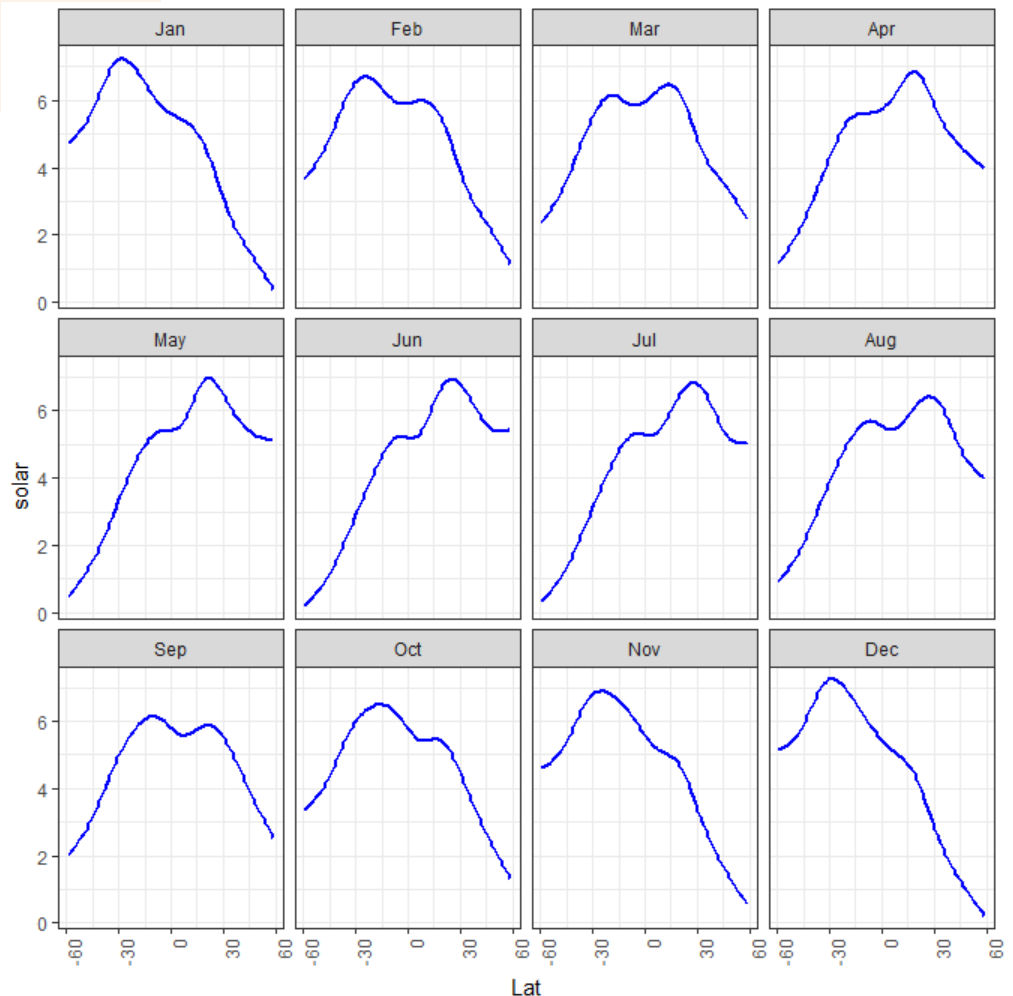
# plotting the tidy data: smoothing

```
ggplot(nasa_long, aes(x=Lat, y=solar)) +  
  geom_smooth(color="blue" ) +  
  facet_wrap(~ month) +  
  theme_bw()
```

Here we treat Lat as quantitative.  
`geom_smooth()` uses `method = "gam"` here because of large  $n$

The variation in the smoothed trends over the year suggest quite lawful behavior

Can we express this as a statistical model ?



# build a model

What we saw in the plot suggests a **generalized additive model**, with a smooth,  $s(\text{Lat})$

```
library(mgcv)
nasa.gam <- gam(solar ~ Lon + month + s(Lat), data=nasa_long)
summary(nasa.gam)
```

Family: gaussian  
Link function: identity

Formula:  
 $\text{solar} \sim \text{Lon} + \text{month} + s(\text{Lat})$

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.691e+00	6.833e-03	686.409	< 2e-16 ***
Lon	-1.713e-04	1.898e-05	-9.022	< 2e-16 ***
monthFeb	1.195e-01	9.664e-03	12.364	< 2e-16 ***
...	...	...	...	...
monthDec	-8.046e-02	9.664e-03	-8.326	< 2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

The violin plots suggest that variance is not constant. I'm ignoring this here by using the default gaussian model.

Model terms:

- Lon wasn't included before
- month is a factor, for the plots
- $s(\text{Lat})$  fits a **smoothed term** in latitude, averaged over other factors

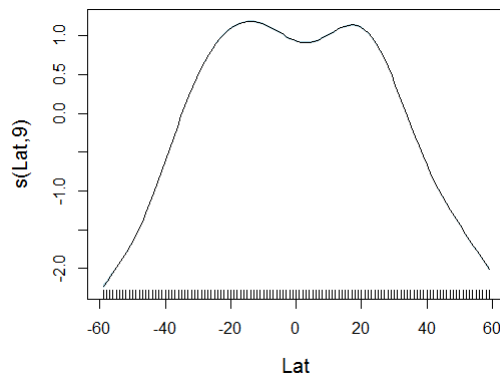
There are other model choices, but it is useful to visualize what we have done so far

# visualize the model

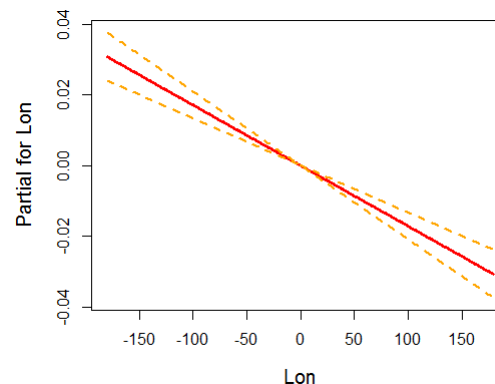
Effect plots show the fitted relationship between the response and model terms, averaged over other predictors.

The {mgcv} package has its own versions of these.

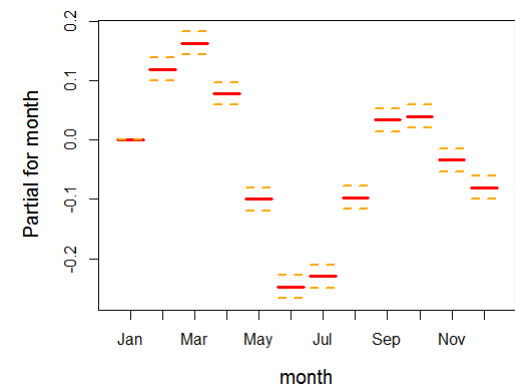
```
plot(nasa.gam, cex.lab=1.25)
termplot(nasa.gam, terms="month", se=TRUE, lwd.term=3, lwd.se=2, cex.lab=1.25)
termplot(nasa.gam, terms="Lon", se=TRUE, lwd.term=3, lwd.se=2, cex.lab=1.25)
```



why the dip at the equator?



effect of longitude is very small, but maybe interpretable



month should be modeled as a cyclic time variable

# Visualizing models

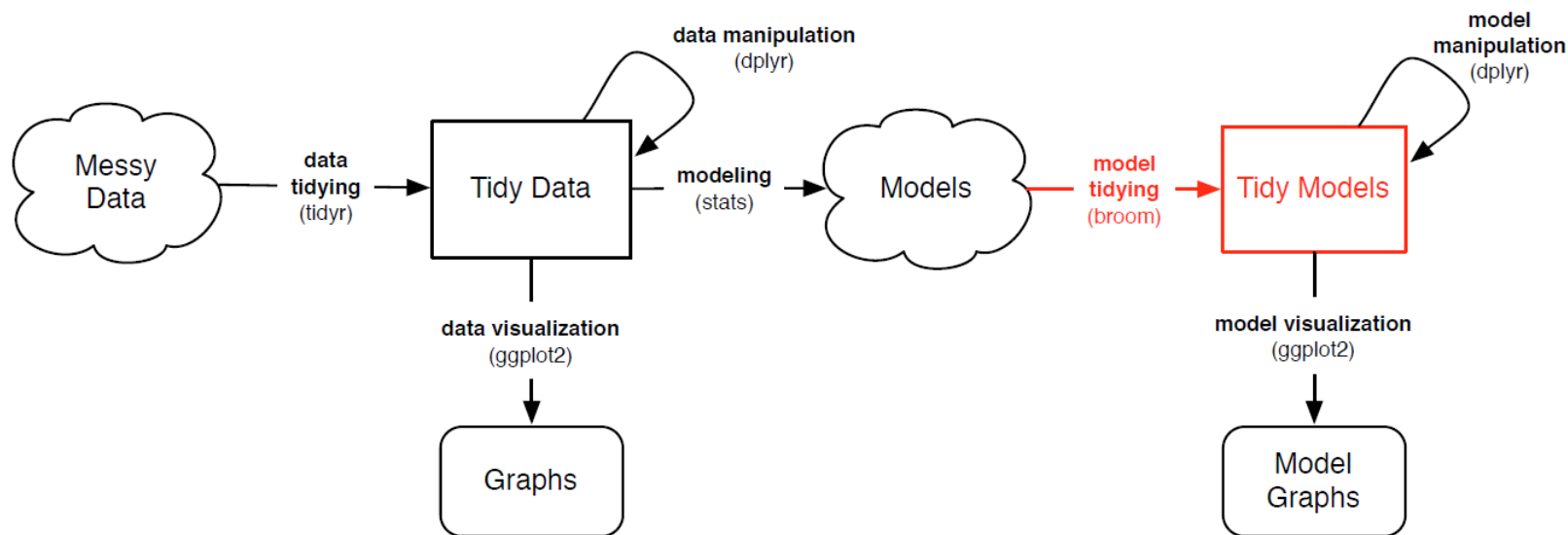
- R modeling functions [`lm()`, `glm()`, ...] return model objects, but these are “messy”
  - extracting coefficients takes several steps: `data.frame(coef(mymod))`
  - some info ( $R^2$ ,  $F$ ,  $p.value$ ) is computed in `print()` method, not stored
  - can't easily combine models
- Some have associated plotting functions
  - `plot(model)`: diagnostic plots
  - `car` package: many model plot methods
  - `effects` package: plot effects for model terms
- But what if you want to:
  - make a table of model summary statistics
  - fit a **collection** of models, compare, summarize or visualize them?





# broom: manipulating models

- The broom package turns model objects into tidy data frames
  - **glance**(models) extracts model-level summary statistics ( $R^2$ , df, AIC, BIC)
  - **tidy**(models) extracts coefficients, SE, p-values
  - **augment**(models) extracts observation-level info (residuals, ...)



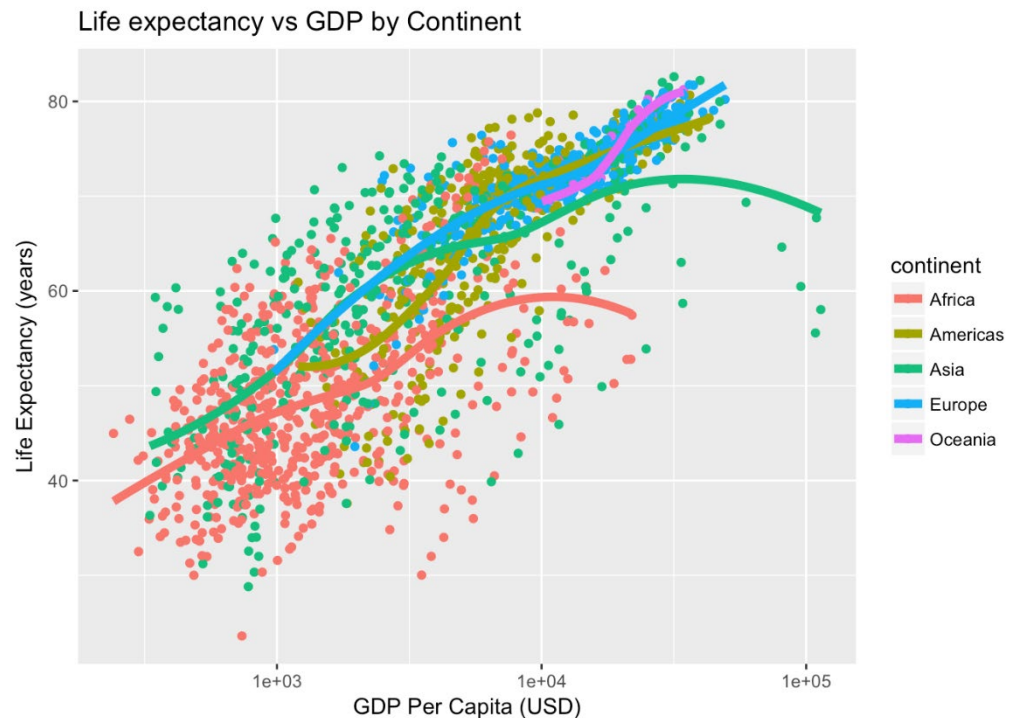
# Example: gapminder data

```
ggplot(aes(x = log(gdpPercap), y=lifeExp, color=continent), data=gapminder) +  
  geom_point() +  
  geom_smooth(method = "loess")
```

How to model this?

How to extract & plot model statistics?

How to fit & display multiple models for subsets?



# Example: gapminder data

Predict life expectancy from year, population, GDP and continent:

```
gapmod <- lm(lifeExp ~ year + pop + log(gdpPercap) + continent, data=gapminder)
summary(gapmod)
```

Call:

```
lm(formula = lifeExp ~ year + pop + log(gdpPercap) + continent, data = gapminder)
```

Residuals:

Min	1Q	Median	3Q	Max
-24.928	-3.285	0.314	3.699	15.221

observation level

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-4.58e+02	1.67e+01	-27.43	< 2e-16 ***
year	2.38e-01	8.61e-03	27.58	< 2e-16 ***
pop	5.40e-09	1.38e-09	3.91	9.5e-05 ***
log(gdpPercap)	5.10e+00	1.60e-01	31.88	< 2e-16 ***
continentAmericas	8.74e+00	4.63e-01	18.86	< 2e-16 ***
continentAsia	6.64e+00	4.09e-01	16.22	< 2e-16 ***
continentEurope	1.23e+01	5.10e-01	24.11	< 2e-16 ***
continentOceania	1.26e+01	1.27e+00	9.88	< 2e-16 ***

component level  
(coefficients)

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.79 on 1696 degrees of freedom

Multiple R-squared: 0.8, Adjusted R-squared: 0.799

F-statistic: 969 on 7 and 1696 DF, p-value: <2e-16

model level

**glance()** gives the **model level** summary statistics

```
> glance(gapmod)
  r.squared adj.r.squared sigma statistic p.value df logLik   AIC    BIC deviance df.residual
1      0.8      0.7992 5.789      969      0   8  -5406 10830 10879    56835         1696
```

**tidy()** gives the **model component** (term) statistics

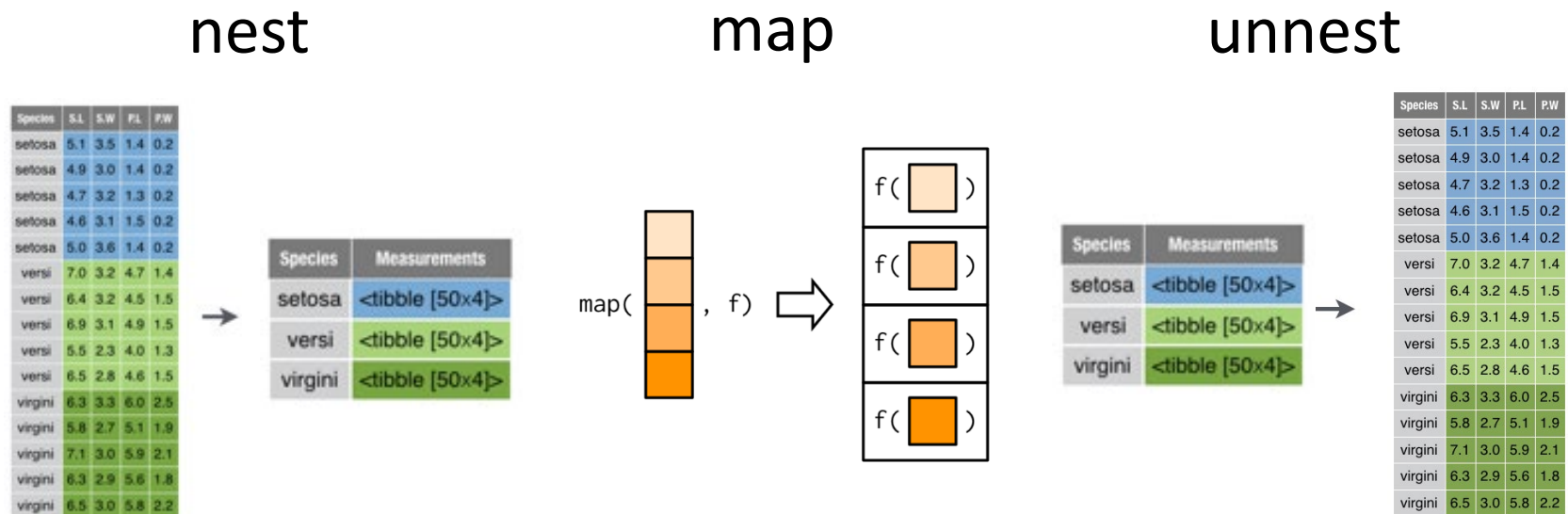
```
> tidy(gapmod)
  term      estimate std.error statistic    p.value
1 (Intercept) -4.585e+02 1.671e+01   -27.433 1.982e-137
2      year      2.376e-01 8.613e-03    27.584 1.122e-138
3      pop       5.403e-09 1.381e-09     3.912 9.496e-05
4 log(gdpPercap)  5.103e+00 1.601e-01    31.876 4.096e-175
5 continentAmericas 8.739e+00 4.635e-01    18.856 3.758e-72
6  continentAsia    6.635e+00 4.091e-01    16.219 4.167e-55
7  continentEurope  1.230e+01 5.102e-01    24.113 1.044e-110
8  continentOceania 1.256e+01 1.270e+00     9.884 1.943e-22
```

**augment()** gives the **observation level** statistics

```
> augment(gapmod) %>% slice(1:5)
# A tibble: 5 x 12
  lifeExp  year      pop log.gdpPercap. continent .fitted .se.fit .resid      .hat .sigma
  <dbl> <int>    <int>      <dbl> <fct>      <dbl>    <dbl> <dbl>    <dbl> <dbl>
1   28.8  1952  8425333      6.66 Asia      46.0    0.408  -17.1  0.00496  5.78
2   30.3  1957  9240934      6.71 Asia      47.4    0.390  -17.1  0.00454  5.78
3   32.0  1962 10267083      6.75 Asia      48.8    0.376  -16.8  0.00423  5.78
4   34.0  1967 11537966      6.73 Asia      49.9    0.372  -15.9  0.00413  5.78
5   36.1  1972 13079460      6.61 Asia      50.5    0.382  -14.4  0.00435  5.78
# ... with 2 more variables: .cooksd <dbl>, .std.resid <dbl>
```

# tidyr:: “nest – map – unnest” trick

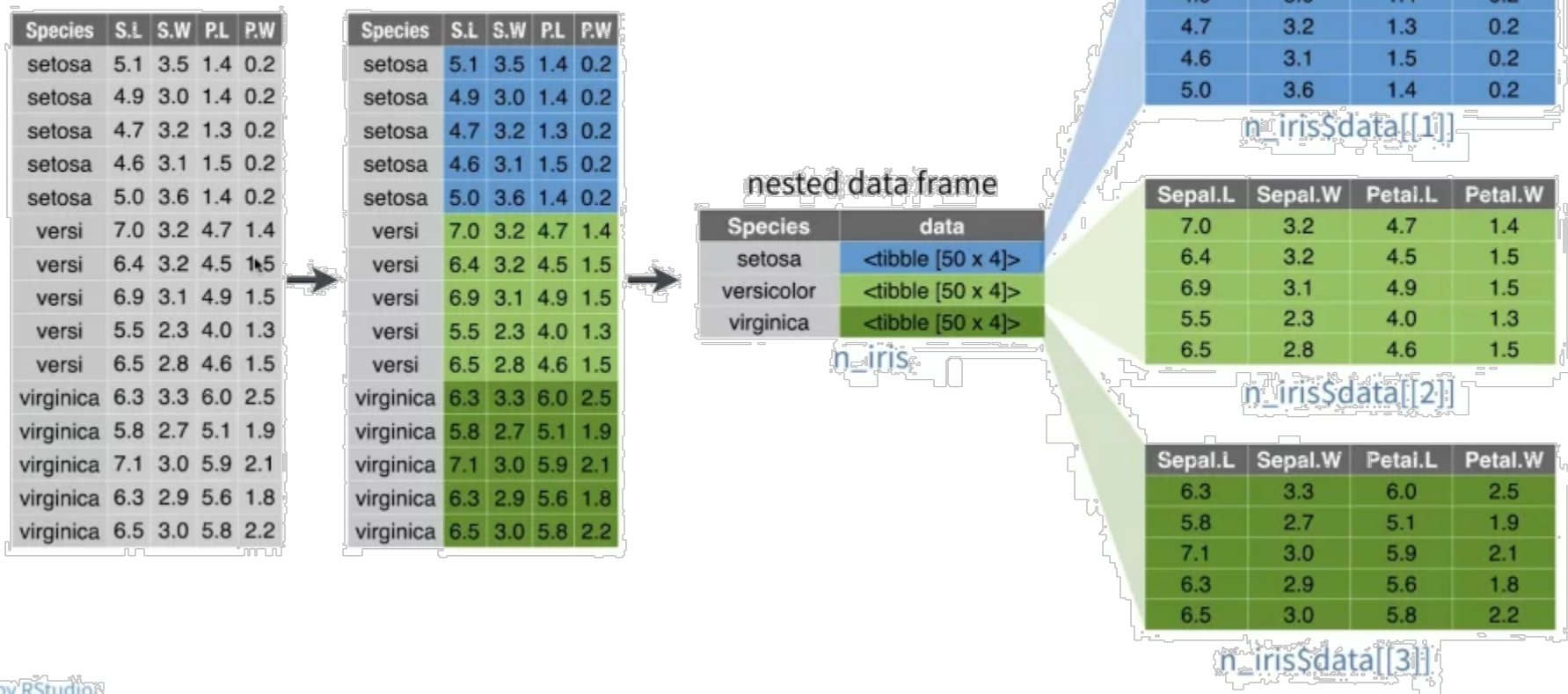
- In many cases, we want to perform analysis for each subset of a dataset defined by one or more variables
  - dplyr::group\_by(), summarise(), ungroup() is one way
- tidyr::nest(), purrr::map(), tidyr::unnest() is more general



See: [https://cran.r-project.org/web/packages/broom/vignettes/broom\\_and\\_dplyr.html](https://cran.r-project.org/web/packages/broom/vignettes/broom_and_dplyr.html)

```
n_iris <- iris %>% group_by(Species) %>% nest()    # group by Species, then nest
n_iris <- iris %>% nest(-Species)                 # nest all other cols
```

## tidyr nest()



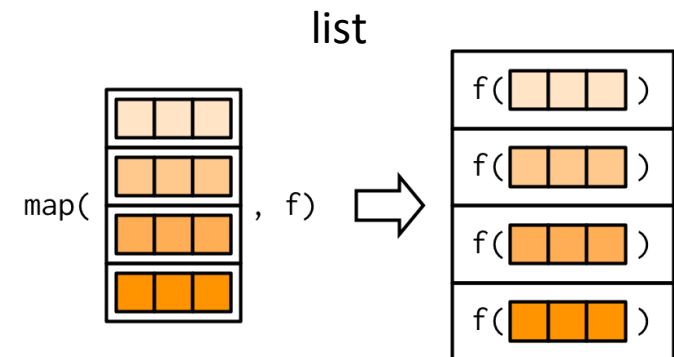
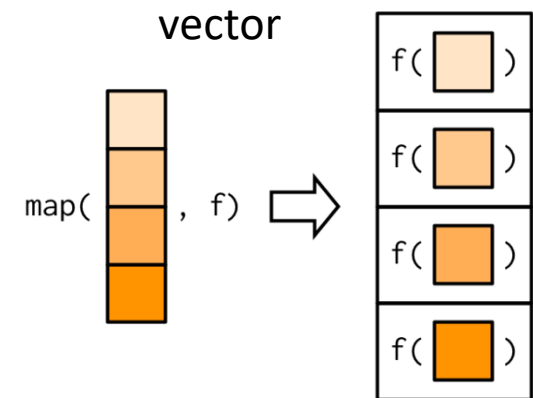
# purrr::map() & friends



A fundamental operation is doing something,  $f()$ , to each element of a vector, list, or column of a data.frame

`map(1:3, log)`  $\longleftrightarrow$  `list(log(1), log(2), log(3))`

`map(x, f)` returns a **list** of  $f()$  applied to each of  $x$   
Other variants, `map_{dbl, int, chr}` return **vectors**



data\_frame : df

a	b
1	10
2	20
3	30
4	40



list : return

`mean(` `)`  
`mean(` `)`

`map(df, mean)`

# tidyr: fitting multiple models

There may be different effects by continent ( GDP x continent interaction)

- What if want to fit (and visualize) a separate model for each continent?
- → nest by continent, then {fit, tidy, glance, augment}

```
models <- gapminder %>%  
  filter(continent != "Oceania") %>%           # only two countries  
  nest(data = -continent) %>%  
  mutate(  
    fit = map(data, ~ lm(lifeExp ~ year + pop + log(gdpPercap), data = .x)),  
    tidied = map(fit, tidy),  
    glanced = map(fit, glance),  
    augmented = map(fit, augment)  
  )
```

What's in this object?

```
names(models)
```

```
[1] "continent" "data"      "fit"       "tidied"    "glanced"   "augmented"
```



## # view model summaries

```
models %>%  
  select(continent, glanced) %>%  
  unnest(glanced)
```

Model summary  
statistics

```
# A tibble: 4 x 13  
  continent r.squared adj.r.squared sigma statistic  p.value    df logLik   AIC  
  <fct>      <dbl>      <dbl> <dbl>    <dbl>    <dbl> <dbl> <dbl> <dbl>  
1 Asia      0.696      0.694  6.56    299. 5.27e-101    3 -1305. 2620.  
2 Europe    0.797      0.795  2.46    466. 7.42e-123    3 -833. 1675.  
3 Africa    0.500      0.498  6.48    207. 5.90e- 93    3 -2050. 4110.  
4 Americas  0.720      0.718  4.97    254. 1.39e- 81    3 -904. 1819.  
# ... with 4 more variables: BIC <dbl>, deviance <dbl>, df.residual <int>,
```

## # model coefficients & tests

```
models %>%  
  select(continent, tidied) %>%  
  unnest(tidied)
```

Coefficients

```
# A tibble: 16 x 6  
  continent term          estimate std.error statistic  p.value  
  <fct>      <chr>          <dbl>    <dbl>    <dbl>    <dbl>  
1 Asia      (Intercept) -6.20e+2  4.00e+1  -15.5    1.34e-42  
2 Asia      year          3.23e-1  2.06e-2   15.7    2.41e-43  
3 Asia      pop           5.13e-9  1.66e-9    3.09    2.15e- 3  
4 Asia      log(gdpPercap) 5.04e+0  2.76e-1   18.3    2.25e-54  
5 Europe    (Intercept) -1.72e+2  1.72e+1  -10.0    4.51e-21  
# ...
```

## # observation-level statistics

```
models %>%
  select(continent, augmented) %>%
  unnest(augmented)
```

```
# A tibble: 1,680 x 10
  continent lifeExp year      pop `log(gdpPercap)` .fitted  .hat .sigma .cooksd
  <fct>      <dbl> <int>   <int>          <dbl>   <dbl>  <dbl> <dbl>  <dbl>
1 Asia      28.8  1952  8425333      6.66    43.7  0.0101  6.53  0.0133
2 Asia      30.3  1957  9240934      6.71    45.6  0.00822  6.53  0.0113
3 Asia      32.0  1962 10267083      6.75    47.4  0.00685  6.53  0.00957
4 Asia      34.0  1967 11537966      6.73    48.9  0.00616  6.53  0.00805
5 Asia      36.1  1972 13079460      6.61    49.9  0.00645  6.54  0.00727
6 Asia      38.4  1977 14880372      6.67    51.9  0.00640  6.54  0.00678
7 Asia      39.9  1982 12881816      6.89    54.6  0.00607  6.53  0.00771
8 Asia      40.8  1987 13867957      6.75    55.5  0.00795  6.53  0.0101
9 Asia      41.7  1992 16317921      6.48    55.8  0.0114  6.53  0.0134
10 Asia     41.8  1997 22227415      6.45    57.3  0.0138  6.53  0.0198
# ... with 1,670 more rows, and 1 more variable: .std.resid <dbl>
```

y

predictors

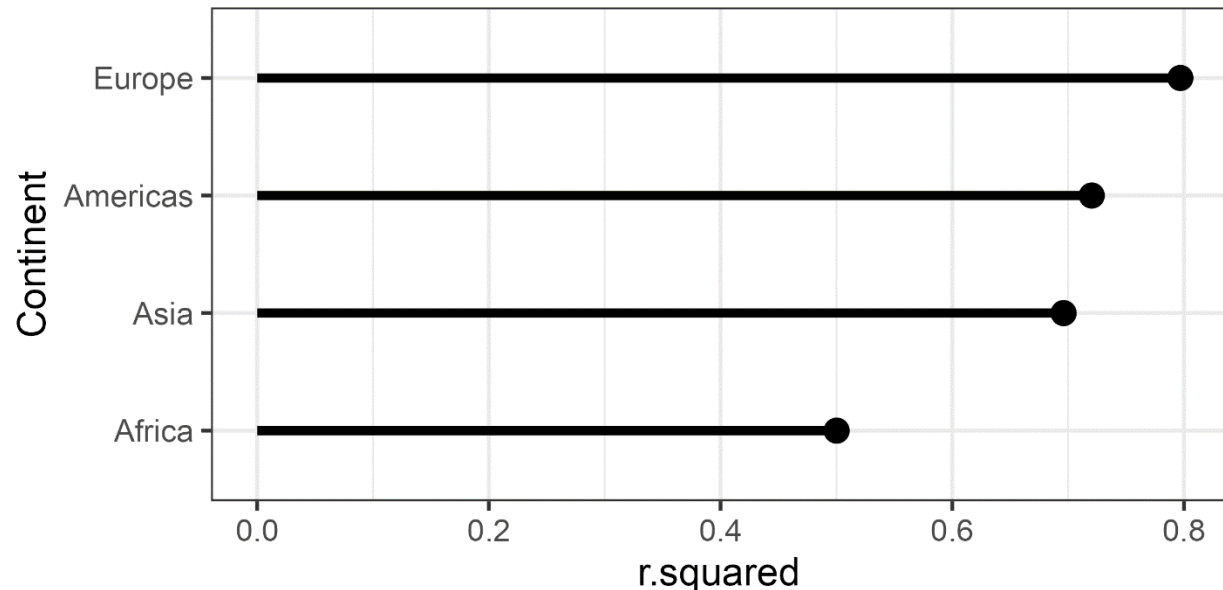
y

diagnostics

# Visualizing multiple models

One visual summary might be a plot of  $R^2$  values, ordered by continent

```
models %>%  
  select(continent, glanced) %>% unnest(glanced) %>%  
  ggplot(aes(r.squared, reorder(continent, r.squared))) +  
    geom_point(size=4) +  
    geom_segment(aes(xend = 0, yend = ..y..)) +  
    ylab("Continent")
```



# Visualizing coefficients

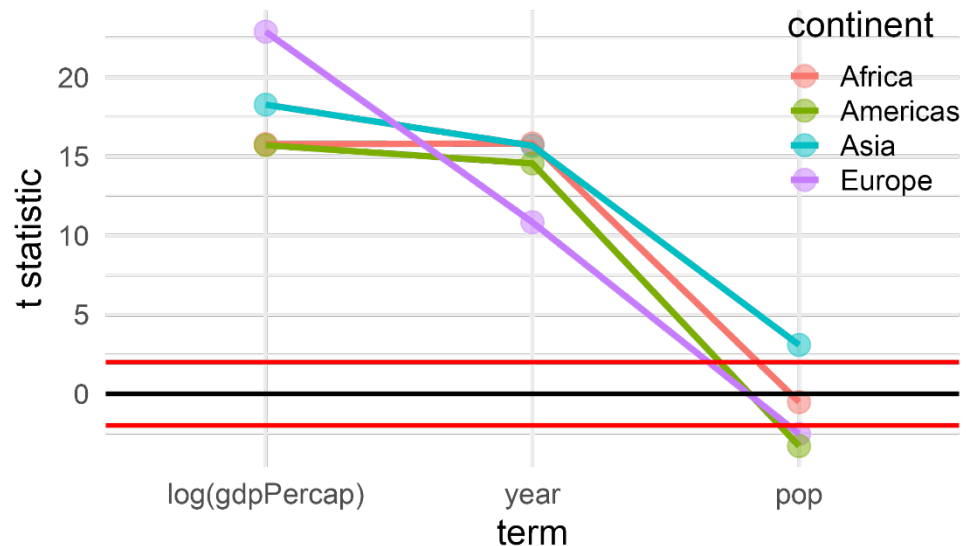
Coefficient plots are often useful, but these are on different scales.

```
models %>% select(continent, tidied) %>% unnest(tidied)
  filter(term != "(Intercept)") %>%
  mutate(term=factor(term, levels=c("log(gdpPercap)", "year", "pop"))) %>%
  ggplot(aes(x=term, y=statistic, color=continent, group=continent)) +
    geom_point(size=5, alpha=0.5) +
    geom_line(size=1.5) +
    geom_hline(yintercept=c(-2, 0, 2), color = c("red", "black", "red")) +
    ylab("t statistic") +
    theme_minimal() + theme(legend.position=c(0.9, 0.8))
```

# get model stats  
# ignore the intercept  
# reorder terms sensibly  
  
# hlines for non-significance

Here, I plot the  $t$ -statistics,  
 $t = b_{ij} / se(b_{ij})$  for all terms in  
all models.

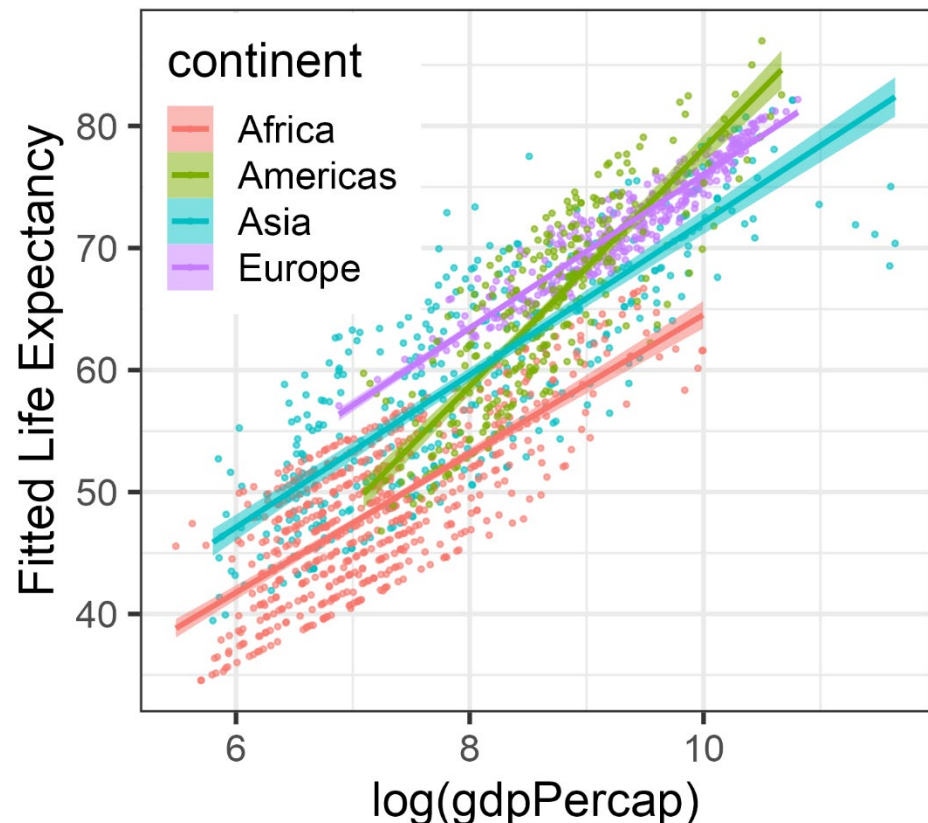
Any values outside  $\sim \pm 2$  are  
significant,  $p < 0.5$ !



# Visualizing model fits

```
models %>% select(continent, augmented) %>% unnest(augmented) %>%  
  ggplot(aes(x=`log(gdpPercap)`, y=.fitted, color=continent, fill=continent)) +  
  geom_point(size = 0.8, alpha=0.5) +  
  geom_smooth(method = "lm", alpha=0.5) +  
  ylab("Fitted Life Expectancy")
```

The slope for the Americas  
is noticeably larger than for  
other continents



# Nice tables in R

- Not a ggplot topic, but it is useful to know that you can also produce beautiful tables in R
- There are many packages for this: See the CRAN Task View on Reproducible Research, <https://cran.r-project.org/web/views/ReproducibleResearch.html>
  - xtable: Exports tables to LaTeX or HTML, with lots of control
  - gt: the ggplot of tables!
  - flextable: similar to gt, but with themes
  - stargazer: Well-formatted model summary tables, side-by-side
  - apaStyle: Generate APA Tables for MS Word

# Tables in R: xtable

Just a few examples, stolen from xtable: vignette(“xtableGallery.pdf”)

```
fm1 <- aov(tlimth ~ sex + ethnicity + grade + disadvg, data = tli)
xtable(fm1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
sex	1	75.37	75.37	0.38	0.5417
ethnicity	3	2572.15	857.38	4.27	0.0072
grade	1	36.31	36.31	0.18	0.6717
disadvg	1	59.30	59.30	0.30	0.5882
Residuals	93	18682.87	200.89		

```
fm3 <- glm(disadvg ~ ethnicity*grade, data = tli, family = binomial)
xtable(fm3)
```

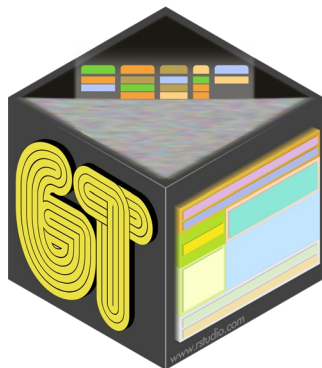
	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	3.1888	1.5966	2.00	0.0458
ethnicityHISPANIC	-0.2848	2.4808	-0.11	0.9086
ethnicityOTHER	212.1701	22122.7093	0.01	0.9923
ethnicityWHITE	-8.8150	3.3355	-2.64	0.0082
grade	-0.5308	0.2892	-1.84	0.0665
ethnicityHISPANIC:grade	0.2448	0.4357	0.56	0.5742
ethnicityOTHER:grade	-32.6014	3393.4687	-0.01	0.9923
ethnicityWHITE:grade	1.0171	0.5185	1.96	0.0498

Too many decimals are used here, but you can control all that

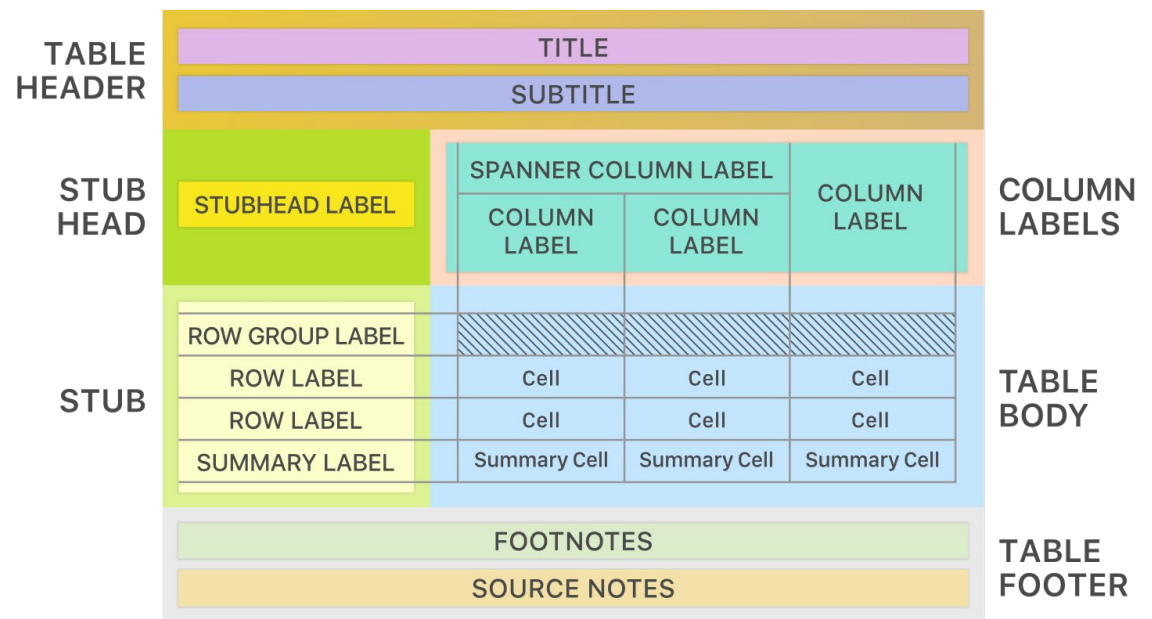
# Tables with {gt}

- The {gt} package aims to provide a grammar of tables just as ggplot2 does for graphs
  - Designed to be simple to use, yet powerful

```
iris %>% gt()
```



## The Parts of a gt Table



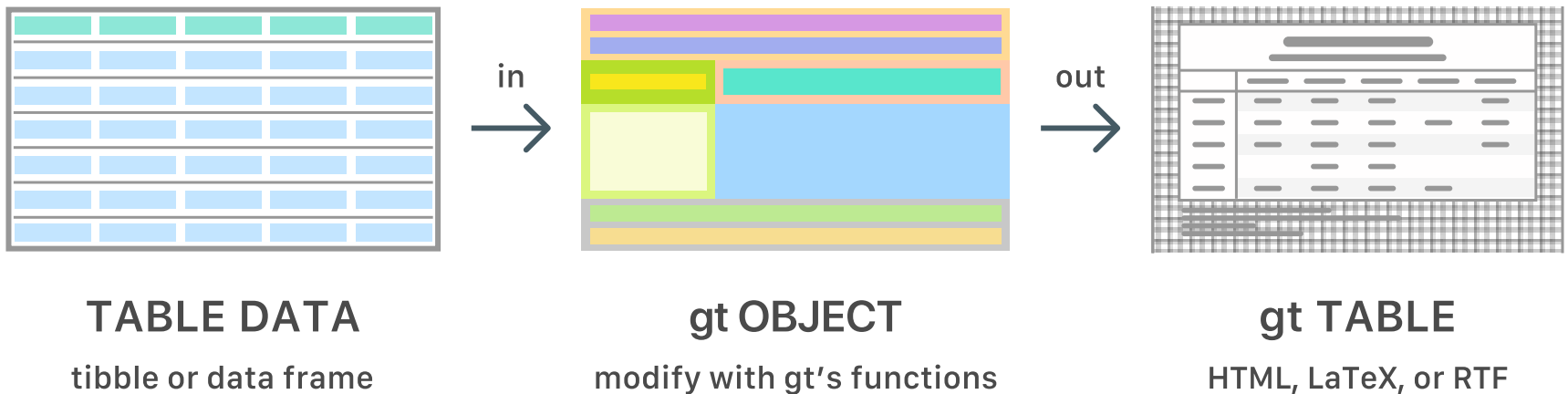


# {gt} workflow

- Data table -> gt\_tbl object

```
iris %>% gt() %>%  
  tab_header(...) %>%  
  tab_options(...) %>% gtsave()
```

## A Typical gt Workflow



```
iris_tab <-
iris %>%
  slice(1:5) %>%
  gt() %>%
  tab_header(
    title = "Anderson's Iris Data",
    subtitle = "(Collected in ...)")
```

Sample 5 rows  
pipe to gt()

add header

Anderson's Iris Data				
(Collected in the Gaspé Peninsula)				
Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
6.4	3.1	5.5	1.8	virginica
6.9	3.1	5.4	2.1	virginica
4.4	3.2	1.3	0.2	setosa
7.7	2.8	6.7	2.0	virginica
5.0	2.3	3.3	1.0	versicolor

```
iris_tab <-
iris %>%
  slice(1:5) %>%
  gt() %>%
  tab_header(
    title = "Anderson's Iris Data",
    subtitle = "(Collected in ...)")
```

```
iris_tab <-
iris_tab %>%
  tab_spanner(
    label = "Sepal",
    columns = c(Sepal.Length,
                 Sepal.Width)) %>%
  tab_spanner(
    label = "Petal",
    columns = c(Petal.Length,
                 Petal.Width)) %>%
```

Add table column spanning headers

Anderson's Iris Data				
(Collected in the Gaspé Peninsula)				
Sepal		Petal		Species
Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	
6.4	3.1	5.5	1.8	virginica
6.9	3.1	5.4	2.1	virginica
4.4	3.2	1.3	0.2	setosa
7.7	2.8	6.7	2.0	virginica
5.0	2.3	3.3	1.0	versicolor

```
iris_tab <-
iris %>%
  slice(1:5) %>%
  gt() %>%
  tab_header(
    title = "Anderson's Iris Data",
    subtitle = "(Collected in ...)")
```

```
iris_tab <-
  iris_tab %>%
  tab_spanner(
    label = "Sepal",
    columns = c(Sepal.Length,
                 Sepal.Width)) %>%
  tab_spanner(
    label = "Petal",
    columns = c(Petal.Length,
                 Petal.Width)) %>%
```

```
iris_tab <- iris_tab %>%
  cols_label(
    Sepal.Length = "Length",
    Sepal.Width = "Width",
    Petal.Length = "Length",
    Petal.Width = "Width") %>%
  tab_options(
    heading.background.color = "#c6dbef",
    column_labels.background.color = "#edf8fb")
```

Re-label columns

Colorize headings

Anderson's Iris Data				
(Collected in the Gaspé Peninsula)				
Sepal		Petal		Species
Length	Width	Length	Width	
6.4	3.1	5.5	1.8	virginica
6.9	3.1	5.4	2.1	virginica
4.4	3.2	1.3	0.2	setosa
7.7	2.8	6.7	2.0	virginica
5.0	2.3	3.3	1.0	versicolor

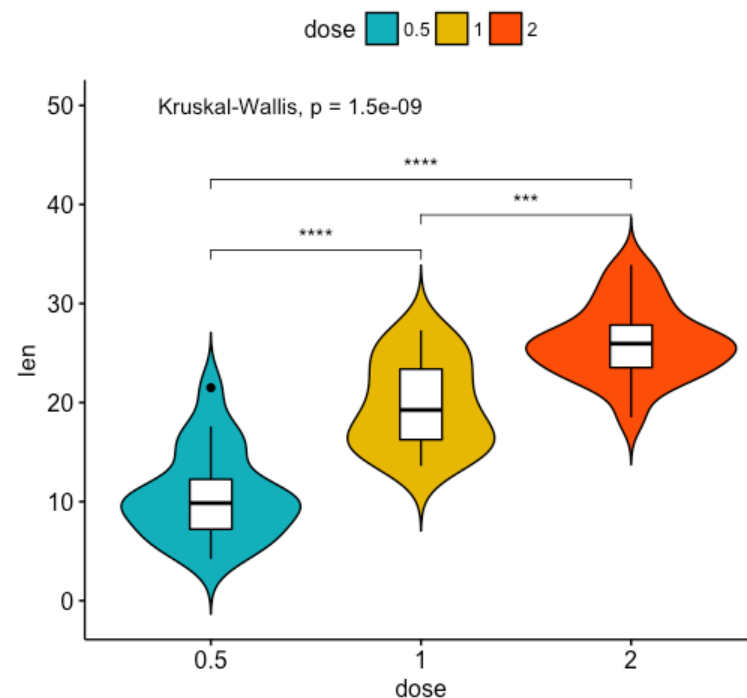
# ggpubr

The **ggpubr** package provides some easy-to-use functions for creating and customizing publication ready plots.

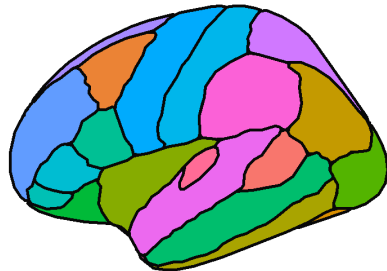
```
ggviolin(df, x = "dose", y = "len", fill = "dose",  
  palette = c("#00AFBB", "#E7B800", "#FC4E07"),  
  add = "boxplot", add.params = list(fill = "white")) +  
  stat_compare_means(comparisons = my_comparisons, label = "p.signif") +  
  stat_compare_means(label.y = 50)
```

see the examples at

<http://www.sthda.com/english/rpkgs/ggpubr/>



# ggseg: plotting brain atlases



left  
hemisphere

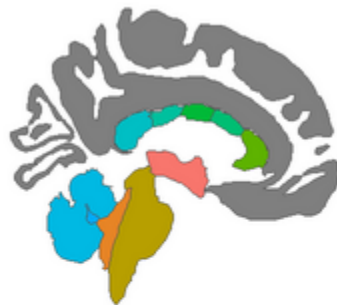
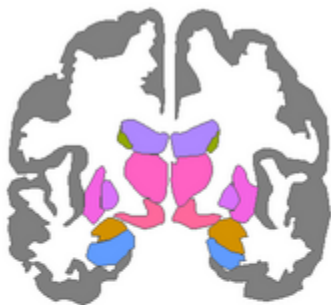





axial



sagittal

side



rd ventricle		CC anterior		cerebellum cortex		putame
th ventricle		CC central		cerebellum white matter		thalam
mygdala		CC mid anterior		hippocampus		ventral
rain stem		CC mid posterior		lateral ventricle		NA
audate		CC posterior		pallidum		

```
# install.packages("remotes")
# remotes::install_github("LCBC-UiO/ggseg")
library(ggseg)
# install.packages("ggplot2")
library(ggplot2)

ggplot() +
  geom_brain(atlas = aseg) +
  theme_void() +
  theme(legend.position = "bottom",
        legend.text = element_text(size = 8)) +
  guides(fill = guide_legend(ncol = 4))
```