CSSS 569 · Visualizing Data

GRAPHICAL PROGRAMMING IN R

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Today's outline: Using R graphics functions

Review of R basics

Overview of available high-level plots

Modifying traditional graphics

R graphic devices

Next week: Writing R graphics functions

Philosophy: Start from scratch

Line & color

Annotation

Coordinate systems

General purpose graphics packages to replace base:

The `lattice` graphics package

The `grid` graphics package

The `ggplot2` graphics package*

Strategy for today

Review basics quickly

Stop and ask for clarification, elaboration, examples

Why R?

Real question: Why programming?

Non-programmers stuck with package defaults

For your substantive problem, defaults may be

- inappropriate (not quite the right model, but "close")
- unintelligible (reams of non-linear coefficients and stars)

Programming allows you to match the methods to the data & question

Get better, more easily explained results.

Why R?

Many side benefits:

1. Never forget what you did: The code can be re-run.
2. Repeating an analysis n times? Write a loop!
3. Programming makes data processing/reshaping easy.
4. Programming makes replication easy.

Why R?

R is

- free
- open source
- growing fast
- widely used
- the future for most fields

But once you learn one language, the others are much easier

Introduction to R

R is a calculator that can store lots of information in memory

R stores information as "objects"

```
> x <- 2
> print(x)
[1] 2

> y <- "hello"
> print(y)
[1] "hello"

> z <- c(15, -3, 8.2)
> print(z)
[1] 15.0 -3.0  8.2
```

Introduction to R

```
> w <- c("gdp", "pop", "income")
> print(w)
[1] "gdp"    "pop"    "income"
>
```

Note the assignment operator, <-, not =

An object in memory can be called to make new objects

```
> a <- x^2
> print(x)
[1] 2
> print(a)
[1] 4
```

```
> b <- z + 10
> print(z)
[1] 15.0 -3.0  8.2
> print(b)
[1] 25.0  7.0 18.2
```

Introduction to R

```
> c <- c(w,y)
> print(w)
[1] "gdp"    "pop"    "income"
> print(y)
[1] "hello"
> print(c)
[1] "gdp"    "pop"    "income" "hello"
```

Commands (or "functions") in R are always written `command()`

The usual way to use a command is:

```
output <- command(input)
```

We've already seen that `c()` pastes together variables.

A simple example:

```
> z <- c(15, -3, 8.2)
> mz <- mean(z)
> print(mz)
[1] 6.733333
```

Introduction to R

Some commands have multiple inputs. Separate them by commas:

`plot(var1,var2)` plots var1 against var2

Some commands have optional inputs. If omitted, they have default values.

`plot(var1)` plots var1 against the sequence {1,2,3,. . . }

Inputs can be identified by their position or by name.

`plot(x=var1,y=var2)` plots var2 against var1

Entering code

You can enter code by typing at the prompt, by cutting or pasting, or from a file

If you haven't closed the parenthesis, and hit enter, `R` let's you continue with this prompt +

You can copy and paste multiple commands at once

You can run a text file containing a program using `source()`, with the name of the file as input (ie, in "")

I prefer the `source()` approach. Leads to good habits of retaining code.

Data types

R has three important data types to learn now

Numeric	`y <- 4.3`
Character	`y <- "hello"`
Logical	`y <- TRUE`

We can always check a variable's type, and sometimes change it:

```
population <- c("1276", "562", "8903")
print(population)
is.numeric(population)
is.character(population)
```

Oops! The data have been read in as characters, or "strings". R does not know they are numbers.

```
population <- as.numeric(population)
```

Some special values

Missing data	`NA`
A “blank”	`NULL`
Infinity	`Inf`
Not a number	`NaN`

Data structures

All R objects have a data type *and* a data structure or class

Data structures can contain numeric, character, or logical entries

Important structures:

Vector

Matrix

Dataframe

List

Vectors in R

Vector is R are simply 1-dimensional lists of numbers or strings

Let's make a vector of random numbers:

```
x <- rnorm(1000)
```

x contains 1000 random normal variates drawn from a Normal distribution with mean 0 and standard deviation 1.

What if we wanted the mean of this vector?

```
mean(x)
```

What if we wanted the standard deviation?

```
sd(x)
```

Vectors in R

What if we wanted just the first element?

```
x[1]
```

or the 10th through 20th elements?

```
x[10:20]
```

what if we wanted the 10th percentile?

```
sort(x)[100]
```

Indexing a vector can be very powerful. Can apply to any vector object.

What if we want a histogram?

```
hist(x)
```

Vectors in R

Useful commands for vectors:

`seq(from, to, by)`	generates a sequence
`rep(x,times)`	repeats `x`
`sort()`	sorts a vector from least to greatest
`rev()`	reverses the order of a vector
`rev(sort())`	sorts a vector from greatest to least

Matrices in R

Vector are the standard way to store and manipulate variables in R

But usually our datasets have several variables measured on the same observations

Several variables collected together form a matrix with one row for each observation and one column for each variable

Matrices in R

Many ways to make a matrix in R

```
a <- matrix(data=NA, nrow, ncol, byrow=FALSE)
```

This makes a matrix of `nrow` $\times$ `ncol`, and fills it with missing values.

To fill it with data, substitute a vector of data for NA in the command. It will fill up the matrix column by column.

We could also paste together vectors, binding them by column or by row:

```
b <- cbind(var1, var2, var3)
c <- rbind(obs1, obs2)
```

Matrices in R

Optionally, R can remember names of the rows and columns of a matrix

To assign names, use the commands:

```
colnames(a) <- c("Var1", "Var2")
rownames(a) <- c("Case1", "Case2")
```

Substituting the actual names of your variables and observations (and making sure there is one name for each variable & observation)

Matrices in R

Matrices are indexed by row and column.

We can subset matrices into vectors or smaller matrices

`a[1,1]`	Gets the first element of a
`a[1:10,1]`	Gets the first ten rows of the first column
`a[,5]`	Gets every row of the fifth column
`a[4:6,]`	Gets every column of the 4th through 6th rows

To make a vector into a matrix, use `as.matrix()`

R defaults to treating one-dimensional arrays as vectors, not matrices

Useful matrix commands:

`nrow()`	Gives the number of rows of the matrix
`ncol()`	Gives the number of columns
`t()`	Transposes the matrix

Dataframes in R

Dataframes are a special kind of matrix used to store datasets

To turn a matrix into a dataframe (note the extra .):

```
a <- as.data.frame(a)
```

Dataframes always have columns names, and these are set or retrieved using the `names()` command

```
names(a) <- c("Var1","Var2")
```

You can access a variable from a dataframe directly using `$`:

```
a$Var1
```

Dataframes can also be "attached", which makes each column into a vector with the appropriate name

```
attach(a)
```

Loading data

There are many ways to load data to R.

I prefer using comma-separated variable files, which can be loaded with `read.csv()`

You can also check the `foreign` library for other data file types

Suppose you load a dataset using

```
data <- read.csv("mydata.csv")
```

You can check out the names of the variables using `names(data)`

And access any variables, such as `gdp`, using `data$gdp`

Benefits and dangers of `attach()`

If your data have variable names, you can also "attach" the dataset like so:

```
data <- read.csv("mydata.csv")
attach(data)
```

to access all the variables directly through newly created vectors.

Be careful! `attach()` is tricky.

1. If you attach a variable `data$x` in `data` and then modify `x`, the original `data$x` is unchanged.

2. If you have more than one dataset with the same variable names, `attach()` is a bad idea: only the first will be attached!

Sometimes `attach()` is handy, but be careful!

Missing data

When loading a dataset, you can often tell R what symbol that file uses for missing data using the option `na.strings=`

So if your dataset codes missings as ., set `na.strings="."`

If your dataset codes missings as a blank, set `na.strings=""`

If your dataset codes missings in multiple ways, you could set, e.g., `na.strings=c(".","","NA")`

Missing data

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If your dataset codes missings in multiple ways, you could set, e.g., `na.strings=c(".","","NA")`

Missing data

Many R commands will not work properly on vectors, matrices, or dataframes containing missing data (NAs)

To check if a variables contains missings, use `is.na(x)`

To create a new variable with missings listwise deleted, use `na.omit`

If we have a dataset `data` with NAs at data[15,5] and data[17,3]

```
dataomitted <- na.omit(data)
```

will create a new dataset with the 15th and 17th rows left out

Be careful! If you have a variable with lots of NAs you are not using in your analysis, remove it from the dataset *before* using `na.omit()`

Mathematical Operations

R can do all the basic math you need

Binary operators:

```
+ - * / ^
```

Binary comparisions:

```
< <= > >= == !=
```

Logical operators (and, or, and not; use parentheses!):

```
&& || !
```

Math/stat fns:

```
log exp mean median min max sd var cov cor
```

Set functions (see `help(sets)`), Trigonometry (see `help(Trig)`),

R follows the usual order of operations; if it doubt, use parentheses

An R list is a basket containing many other variables

```
> x <- list(a=1, b=c(2,15), giraffe="hello")

> x$a
[1] 1

> x$b
[1]  2 15

> x$b[2]
[1] 15

> x$giraffe
[1] "hello"

> x[3]
$giraffe
[1] "hello"

> x[["giraffe"]]
[1] "hello"
```

R lists

Things to remember about lists

- Lists can contain any number of variables of any type
- Lists can contain other lists
- Contents of a list can be accessed by name or by position
- Allow us to move lots of variables in and out of functions
- Functions often return lists (only way to have multiple outputs)

lm() basics

```
# To run a regression
res <- lm(y~x1+x2+x3,
          data,                    # A dataframe containing
                                   # y, x1, x2, etc.
          na.action="")

# To print a summary
summary(res)

# To get the coefficients
res$coefficients

# or
coef(res)

#To get residuals
res$residuals

#or

resid(res)
```

`lm()` basics

```
# To get the variance-covariance matrix of the regressors
vcov(res)

# To get the standard errors
sqrt(diag(vcov(res)))

# To get the fitted values
predict(res)

# To get expected values for a new observation or dataset
predict(res,
        newdata,                    # a dataframe with same x vars
                                    # as data, but new values
        interval = "confidence",    # alternative: "prediction"
        level = 0.95
        )
```

R lists & Object Oriented Programming

A list object in R can be given a special "class" using the `class()` function

This is just a metatag telling other R functions that this list object conforms to a certain format

For example, suppose we run a linear regression:

```
resLS <- lm(y~x1+x2+x3, data=exampledata)
```

The result `resLS` is a list object of class `‘‘lm’’`

Other functions like `plot()` and `predict()` will react to `resLS` in a special way because of this class designation

Specifically, they will run functions called `plot.lm()` and `predict.lm()`

Object-oriented programming:
a function does different things depending on class of input object

Help!

To get help on a known command `x`, type `help(x)` or `?x`

To search the help files using a keyword string `s`, type `help.search(s)`

Note that this implies to search on the word regression, you should type `help.search("regression")`

but to get help for the command `lm`, you should type `help(lm)`

Installing R on a PC

- Go to the Comprehensive R Archive Network (CRAN)
  `http://cran.r-project.org/`

- Under the heading "Download and Install R", click on "Windows"

- Click on "base"

- Download and run the R setup program.
  The name changes as R gets updated;
  the current version is "R-3.3.2-win.exe"

- Once you have R running on your computer,
  you can add new libraries from inside R by selecting
  "Install packages" from the Packages menu

Installing R on a Mac

- Go to the Comprehensive R Archive Network (CRAN)
  `http://cran.r-project.org/`

- Under the heading "Download and Install R", click on "MacOS X"

- Download and run the R setup program.
  The name changes as R gets updated;
  the current version is "R-3.3.2.pkg"

- Once you have R running on your computer,
  you can add new libraries from inside R by selecting
  "Install packages" from the Packages menu

Editing scripts

Don't use Microsoft Word to edit R code!

Word adds lots of "stuff" to text; `R` needs the script in a plain text file.

Some text editors:

- **Notepad:** Free, and comes with Windows (under Start → Programs → Accessories). Gets the job done; not powerful.
- **TextEdit:** Free, and comes with Mac OS X. Gets the job done; not powerful.
- **TINN-R:** Free and fairly powerful. Windows only.
  `http://www.sciviews.org/Tinn-R/`
- **Emacs:** Free and very powerful (my preference). Can use for R and Latex. Available for Mac and PC.

  For Mac (easy installation): `http://aquamacs.org/`

  For Windows (see the README): `http://ftp.gnu.org/gnu/emacs/windows/`

Editing data

R can load many other packages' data files

See the `foreign` library for commands

For simplicity & universality, I prefer Comma-Separated Variable (CSV) files

Microsoft Excel can edit and export CSV files (under Save As)

R can read them using `read.csv()`

OpenOffice is free alternative to Excel & makes CSV files (for all platforms):
`http://www.openoffice.org/`

My detailed guide to installing social science software on the Mac:
`http://thewastebook.com/?post=social-science-computing-for-mac`

Focus on steps 1.1 and 1.3 for now; come back later for Latex in step 1.2

What's a high-level graphics command?

Most of you probably make R graphics by calling a "high-level" command (HLC)

In R, HLCs:

- produce a standard graphic type
- fill in lots of details (axes, titles, annotation)
- have many configurable parameters
- have varied flexibility
- may respond to object class

You don't need to use HLCs to make R graphics.

Could do from scratch

Some major high-level graphics commands

The two key places to find HLCs:
the `base` graphics package, and the `lattice` package

Use different graphical primitives

Have distinctive "looks"

Lattice is really good at conditioning and EDA (coplots)

Besides these, there are many HLCs strewn through other packages

Easiest way to find them: `help.search()`

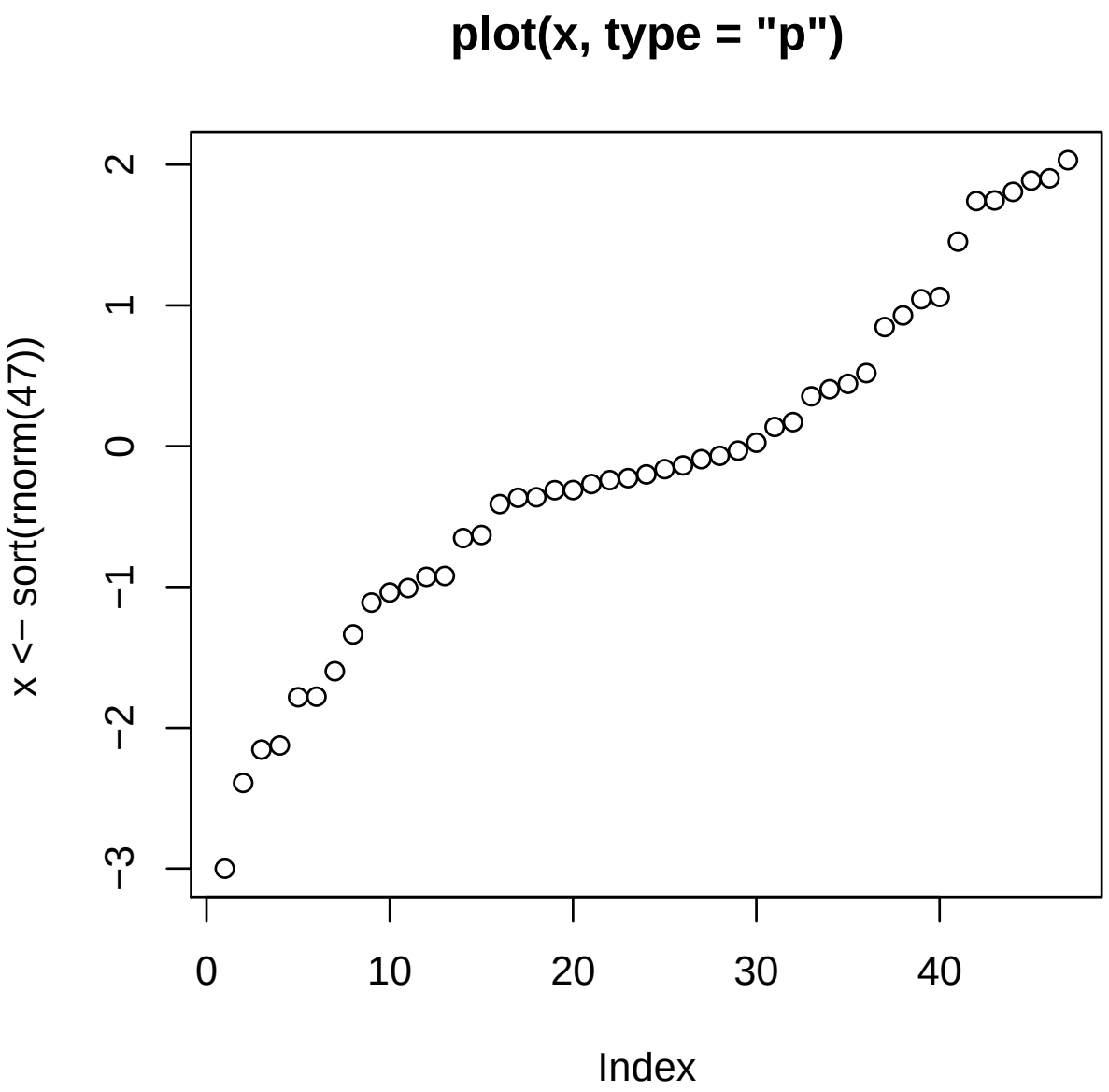
When I first wrote this lecture,
I did `help.search(''plot'')` on a full install of `R` packages

Found lots of neat plotting functions in packages I'd never heard of;
today there are many more

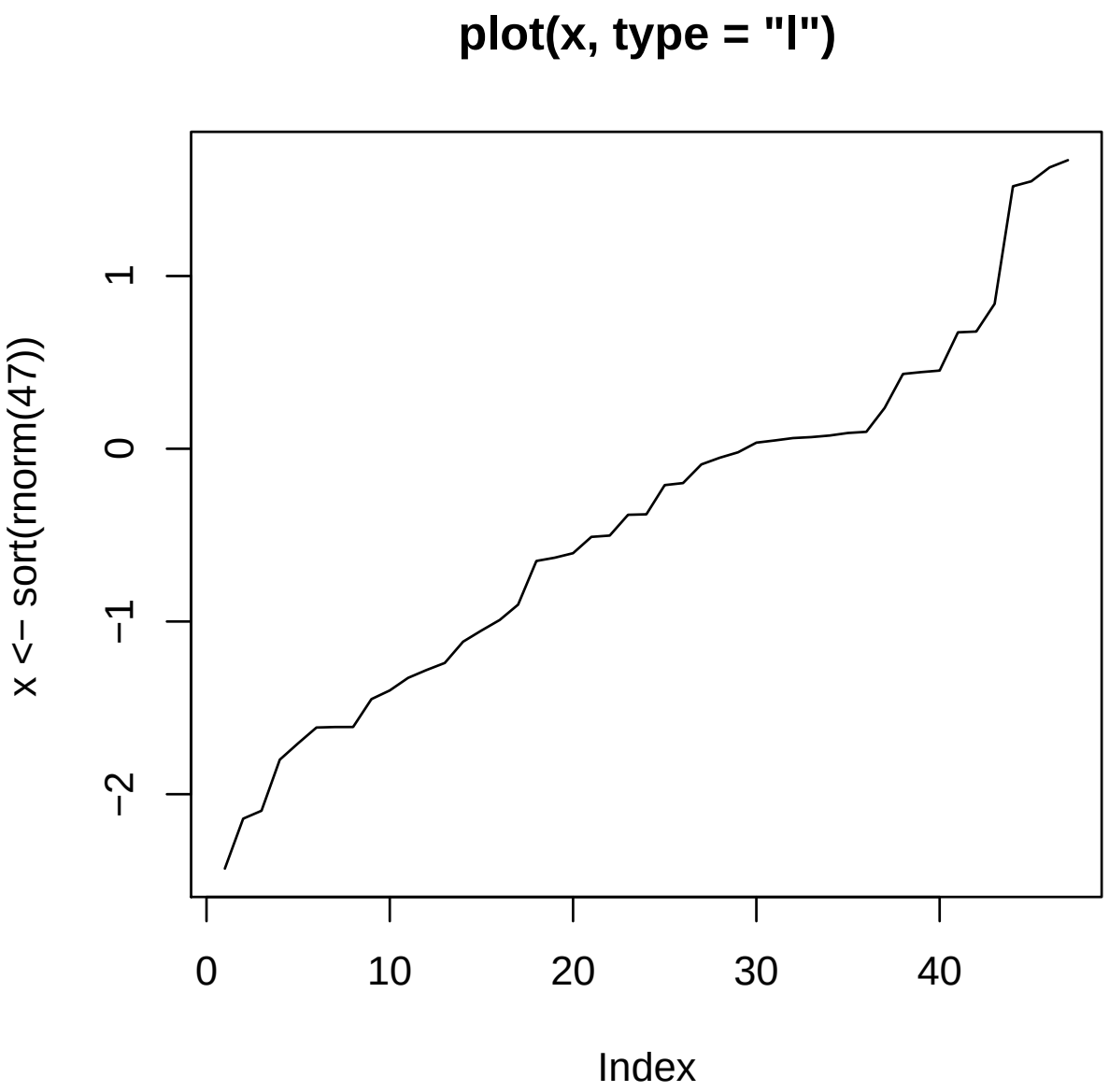
Some major high-level graphics commands

Graphic	Base command	Lattice command
scatterplot	plot()	xyplot()
line plot	plot(. . . ,type="l")	xyplot(. . . ,type="l")
Bar chart	barplot()	barchart()
Histogram	hist()	histogram()
Smoothed histograms	plot() after density()	densityplot()
boxplot	boxplot()	bwplot()
Dot plot	dotchart()	dotplot()
Contour plots	contour()	contourplot()
image plot	image()	levelplot()
3D surface	persp()	wireframe()
3D scatter	scatterplot3d()*	cloud()
conditional plots	coplot()	xyplot()
Scatterplot matrix		splom()
Parallel coordinates		parallel()
Star plot	stars()	
Stem-and-leaf plots	stem()	
ternary plot	ternaryplot() in vcd	
Mosaic plots	mosaicplot() in vcd	

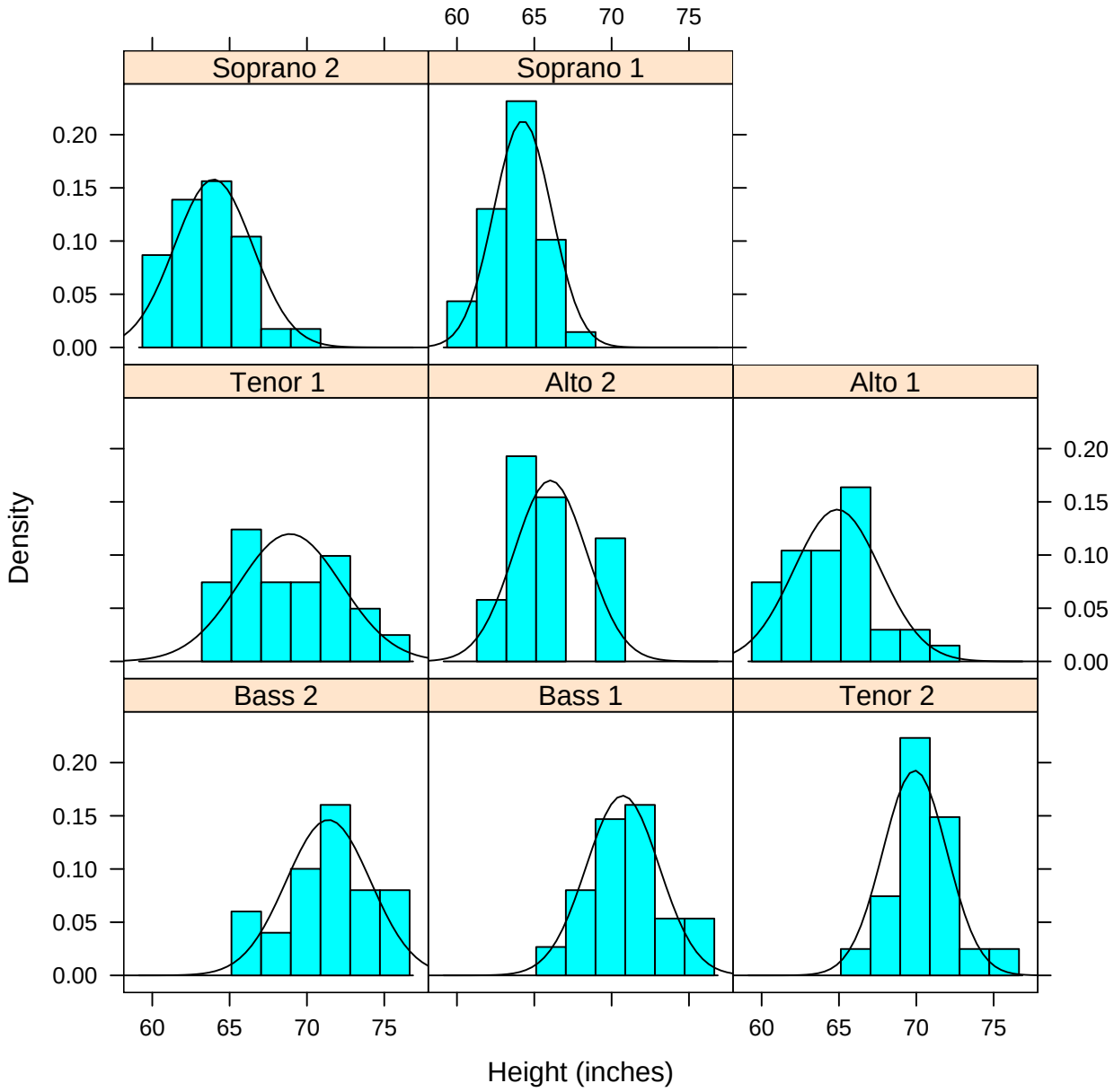
Scatterplot: `plot()`



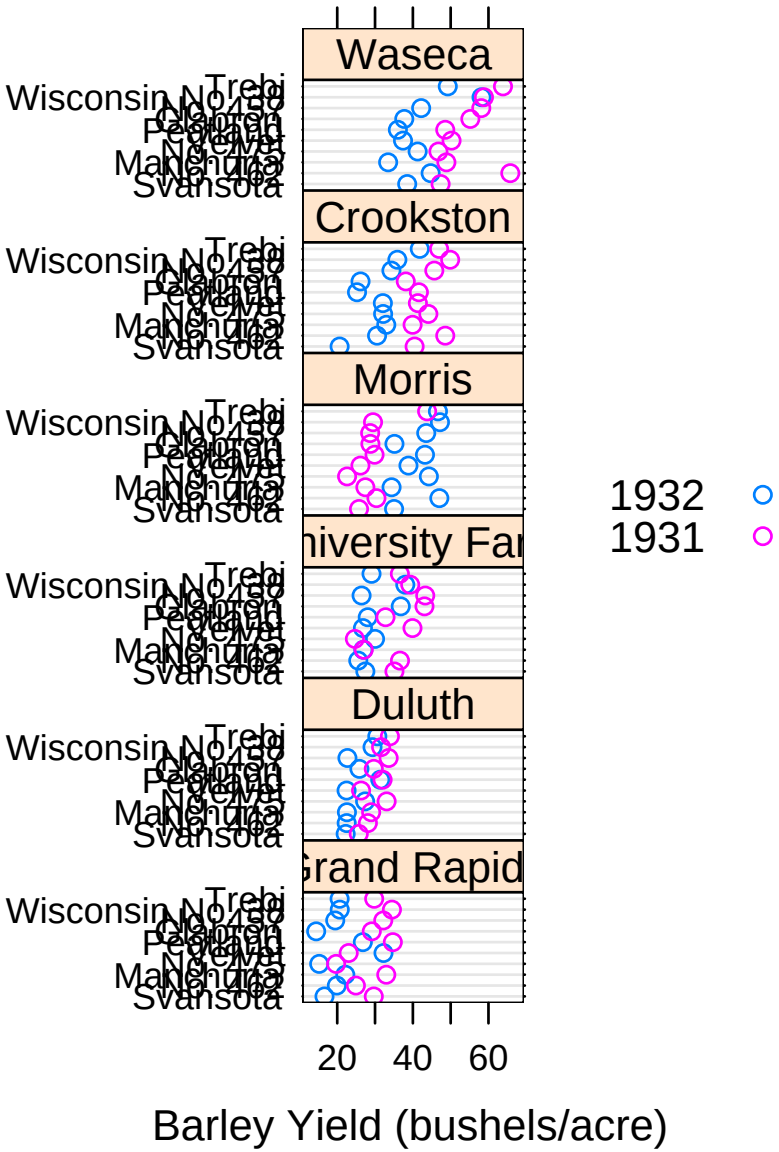
Line plot: `plot(...,type="l")`



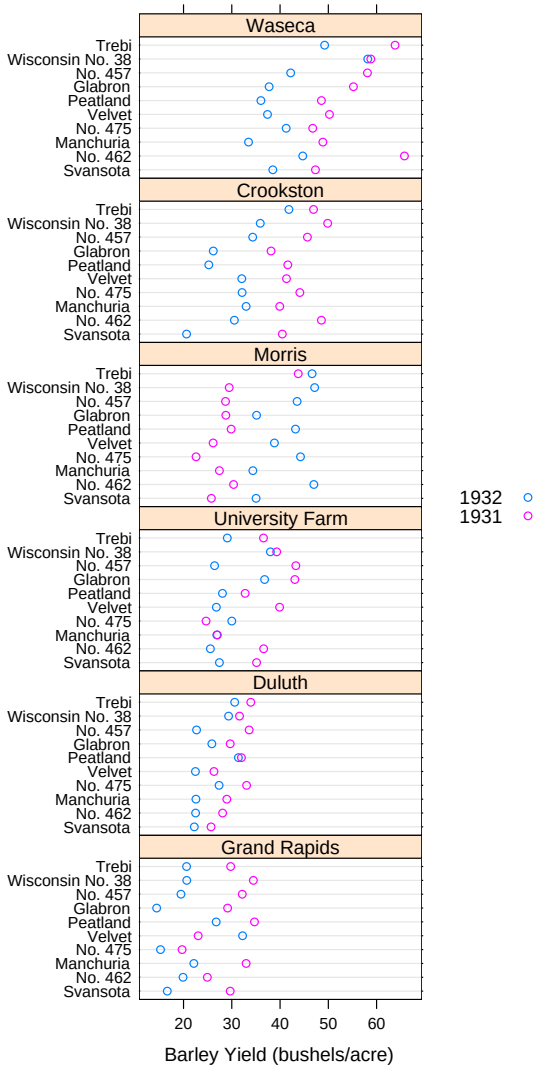
(Smoothed) Histograms: `densityplot()` & others



Dot plot: `dotplot()`



Dot plot is sensitive to device size



Dot plot has a `layout` option

Contour plot: `contour()`

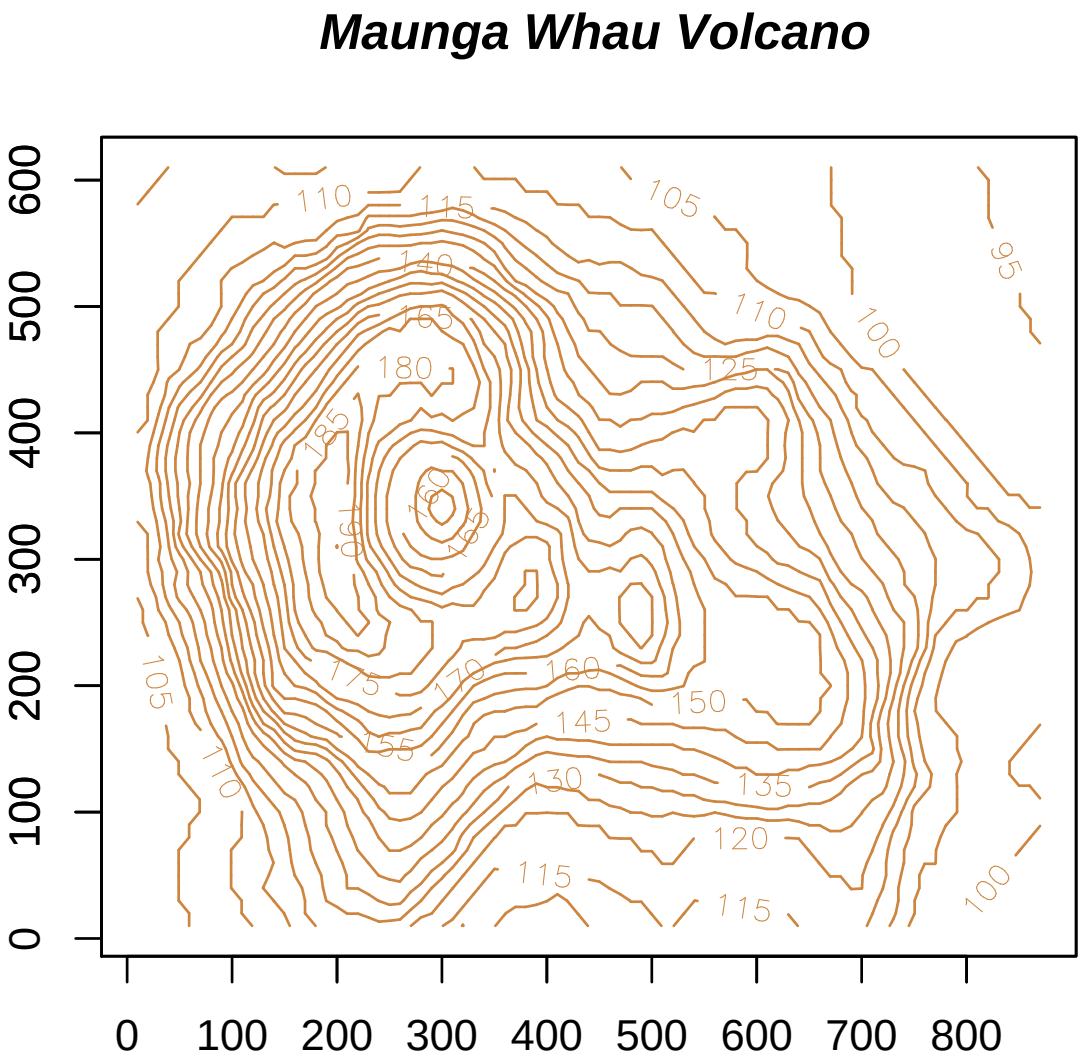


Image plot: `image()`

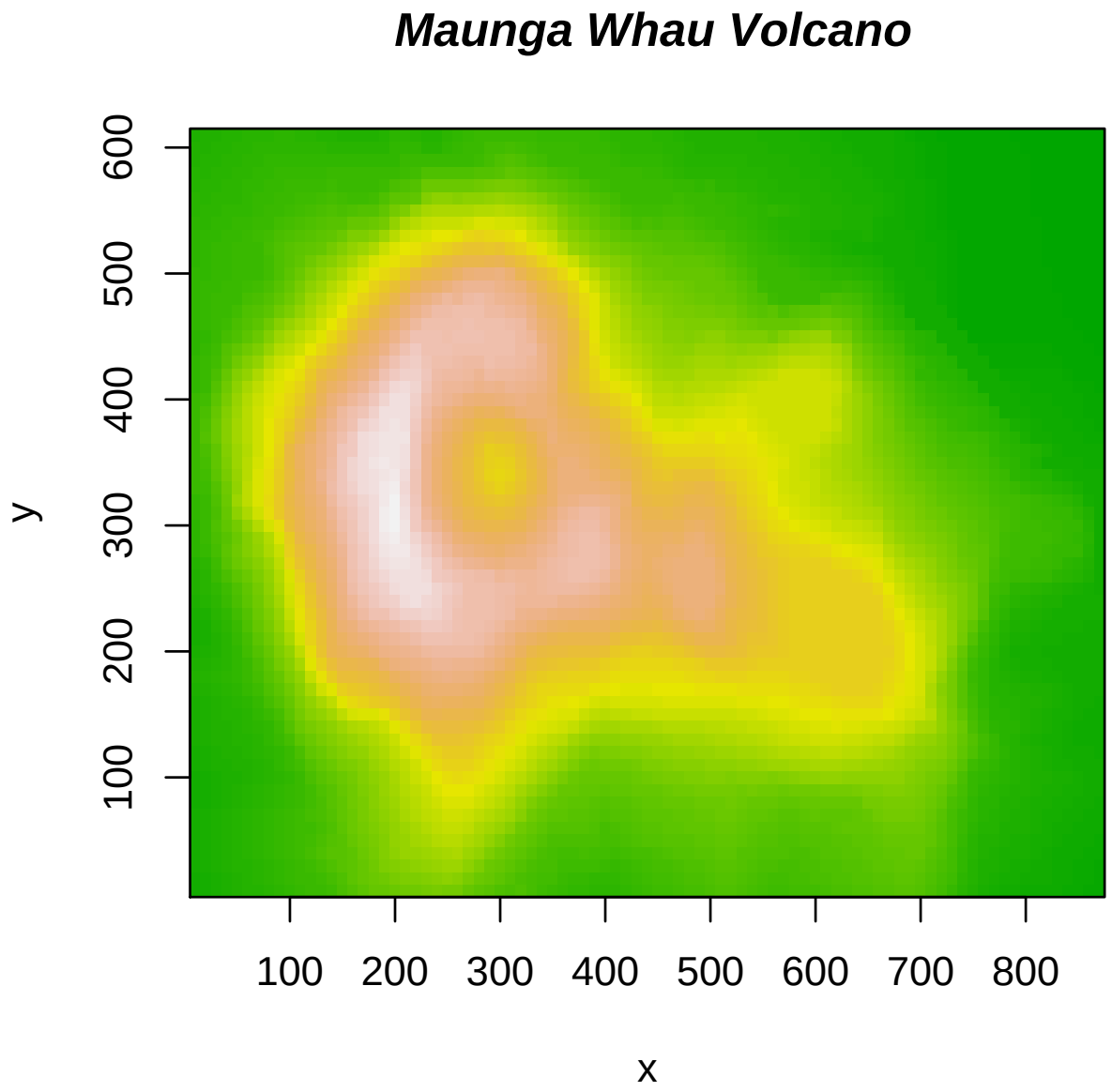
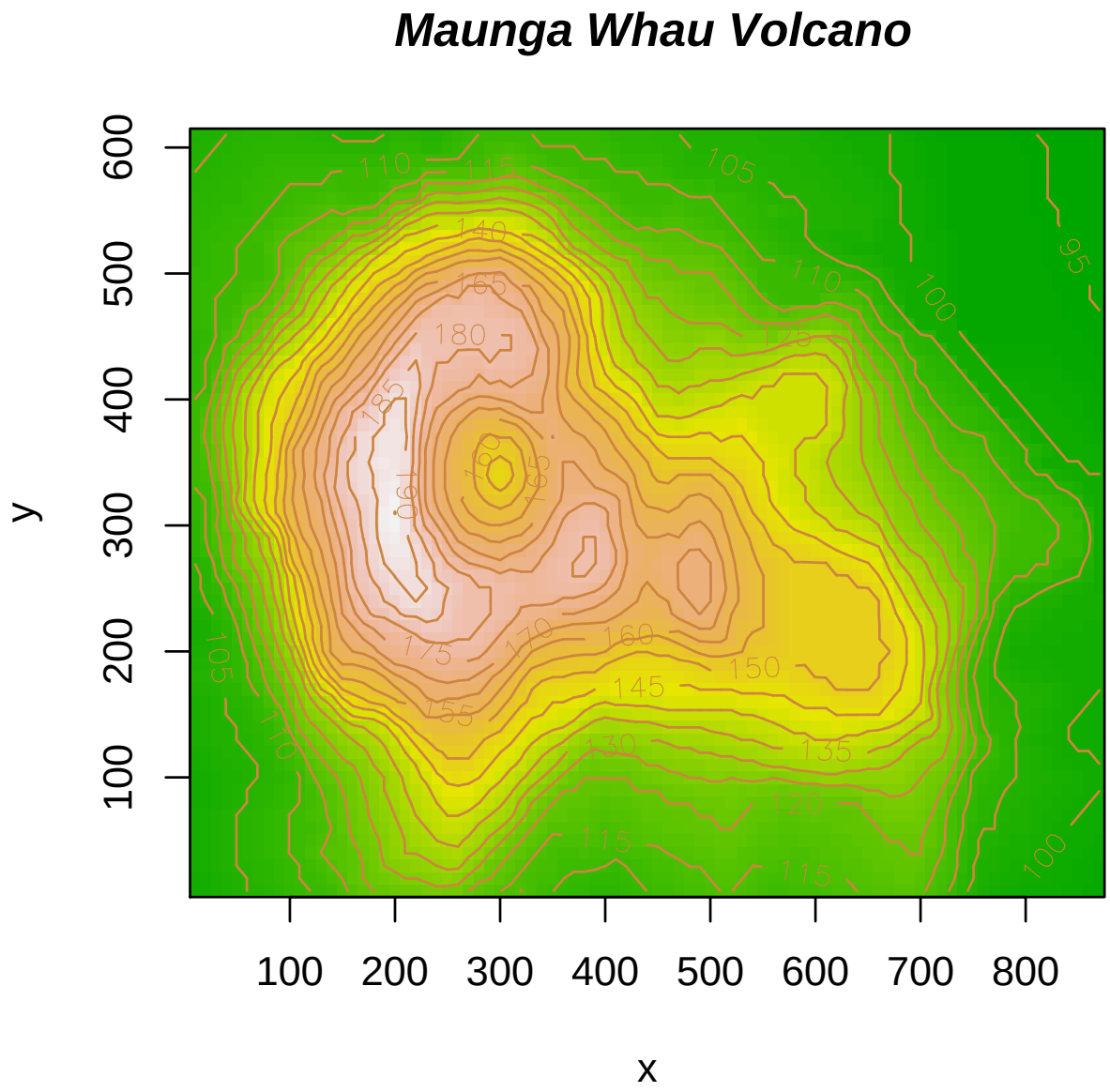
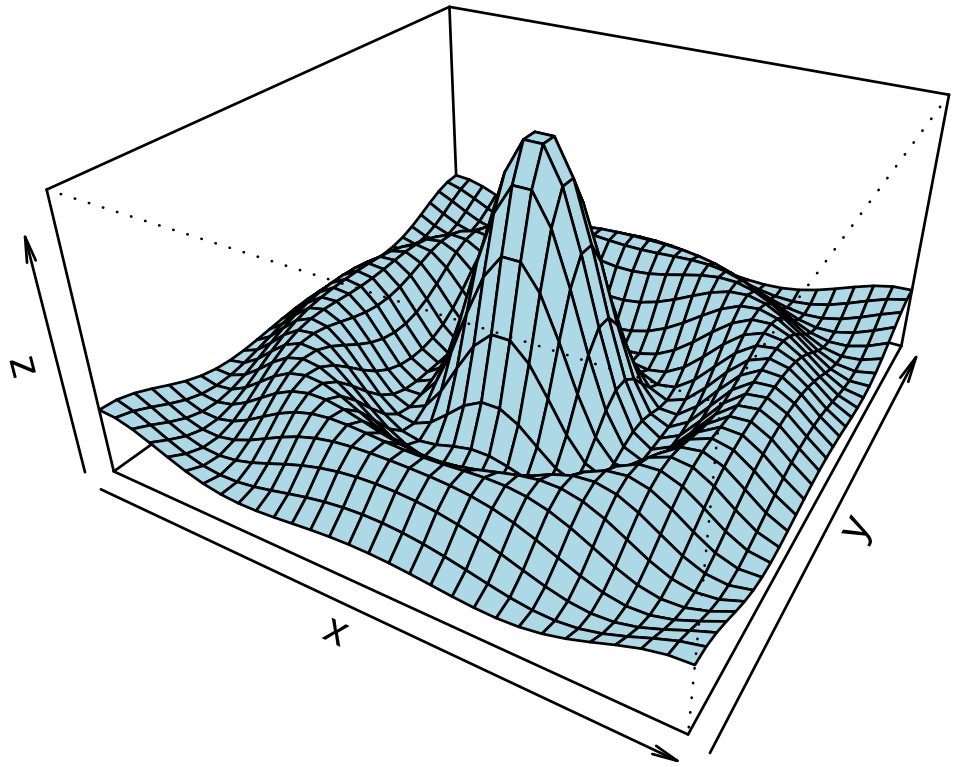


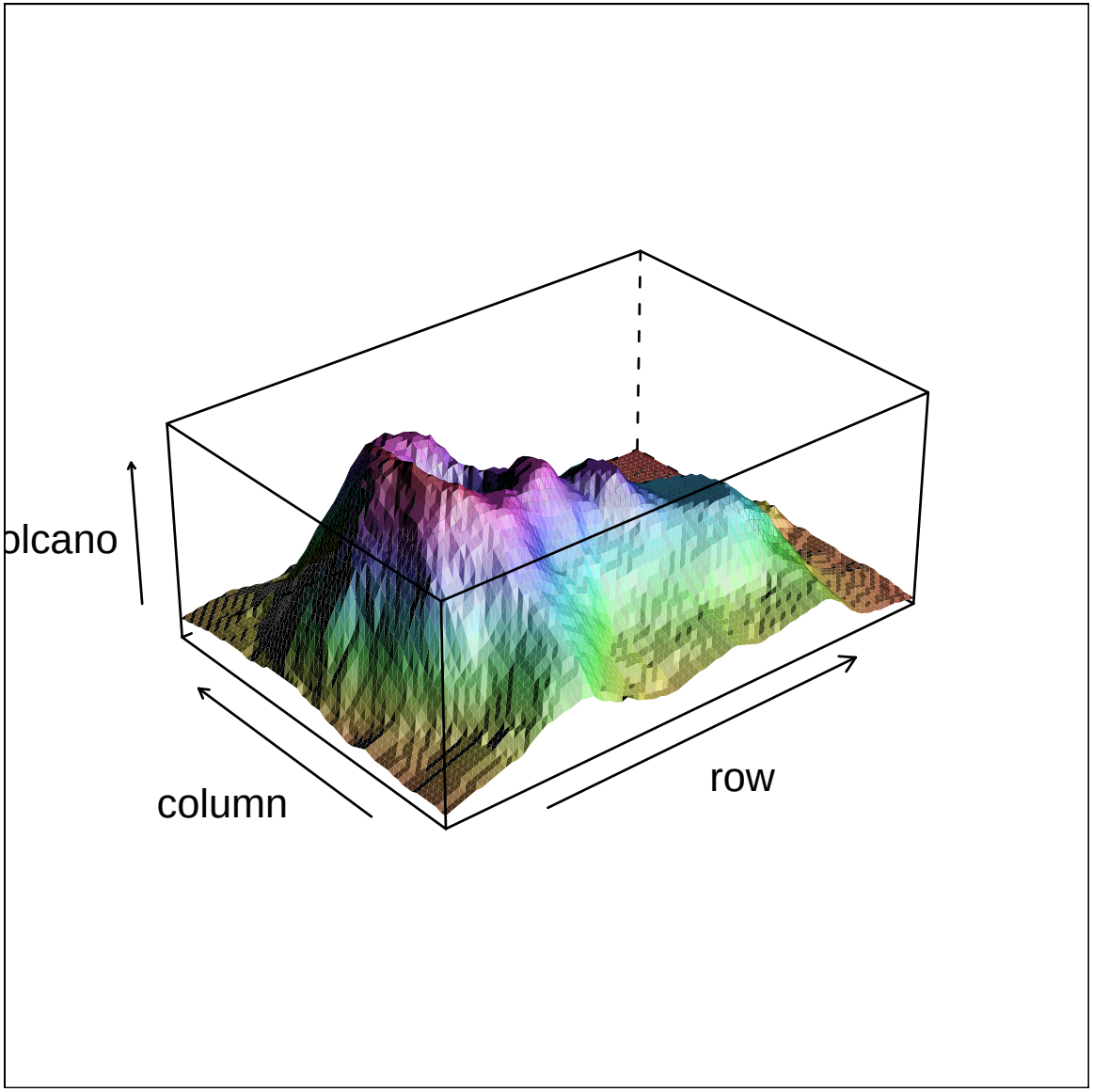
Image plot with contours: `contour(...,add=TRUE)`



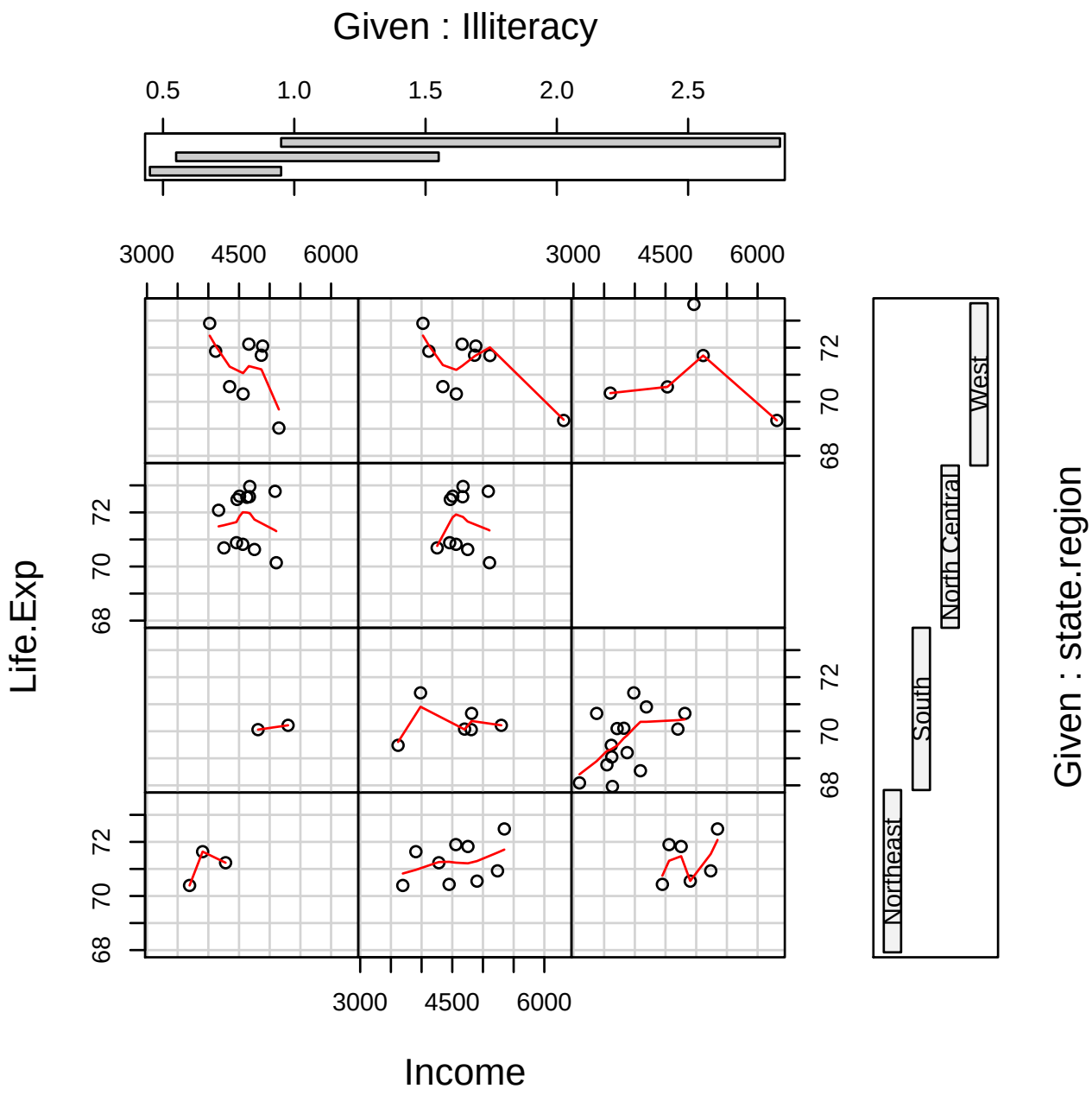
3D surface: `persp()`



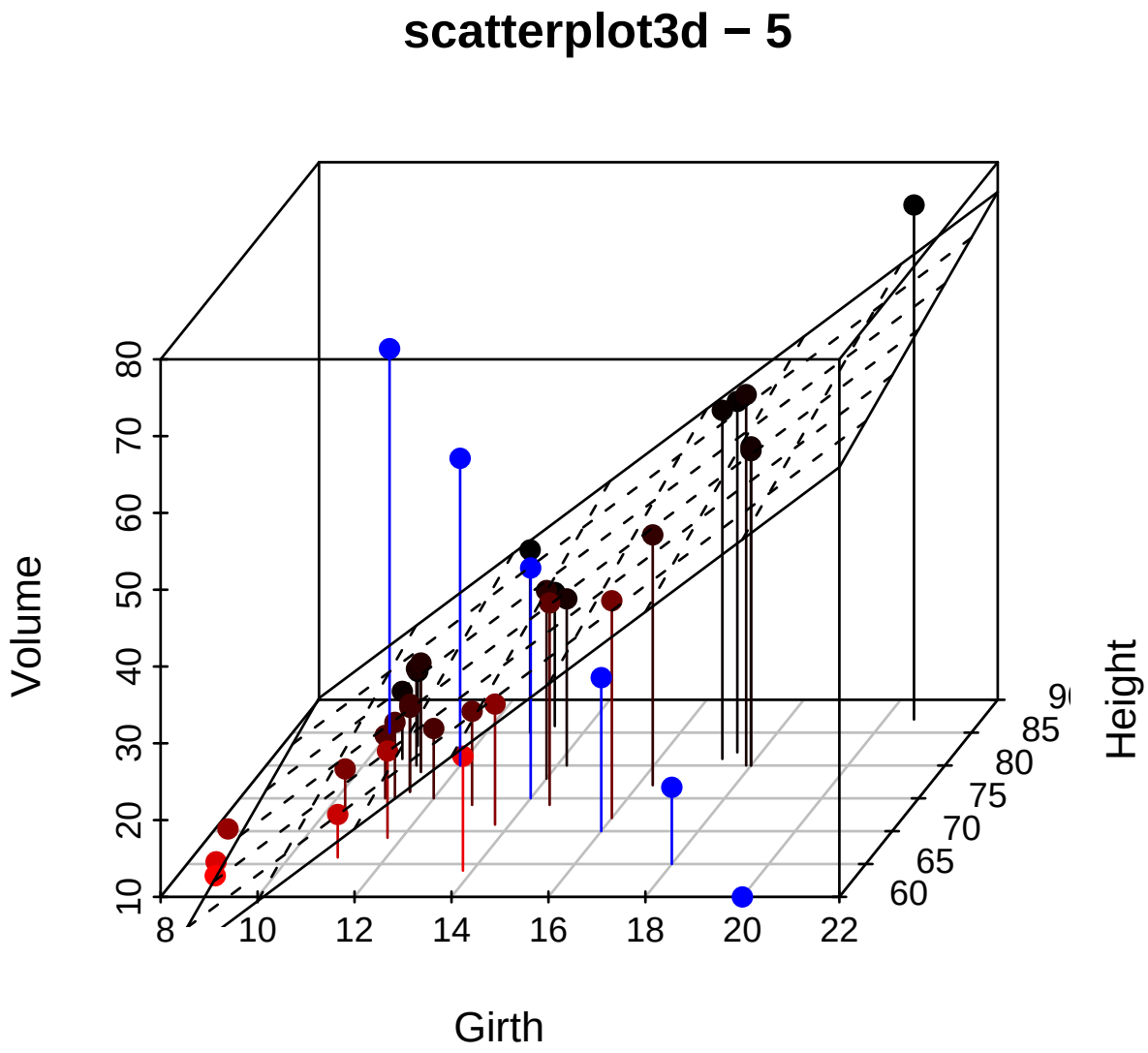
3D surface: `wireframe()`



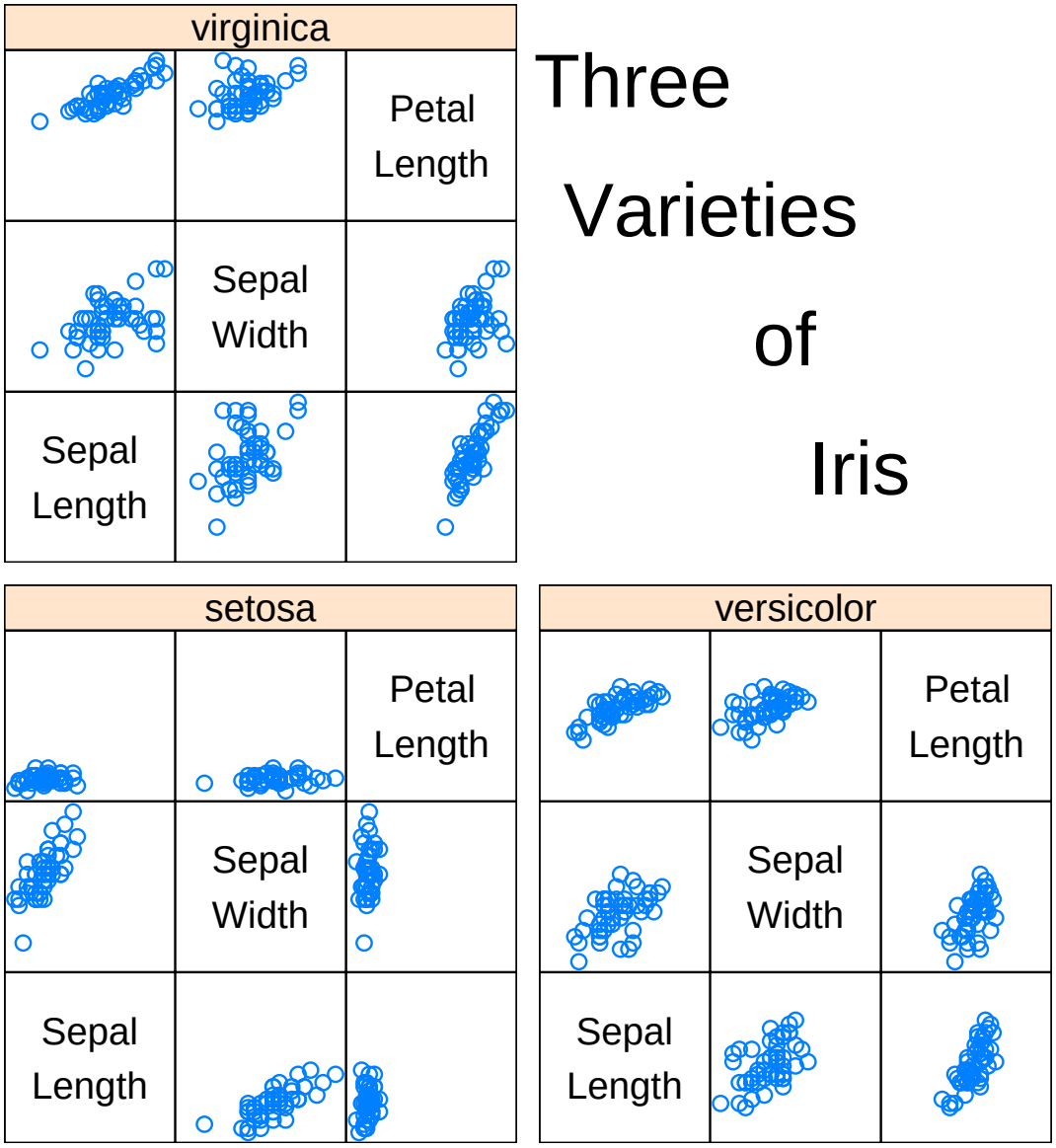
Conditional plots: `coplot()`



3D scatter: `scatterplot3d()` in own library



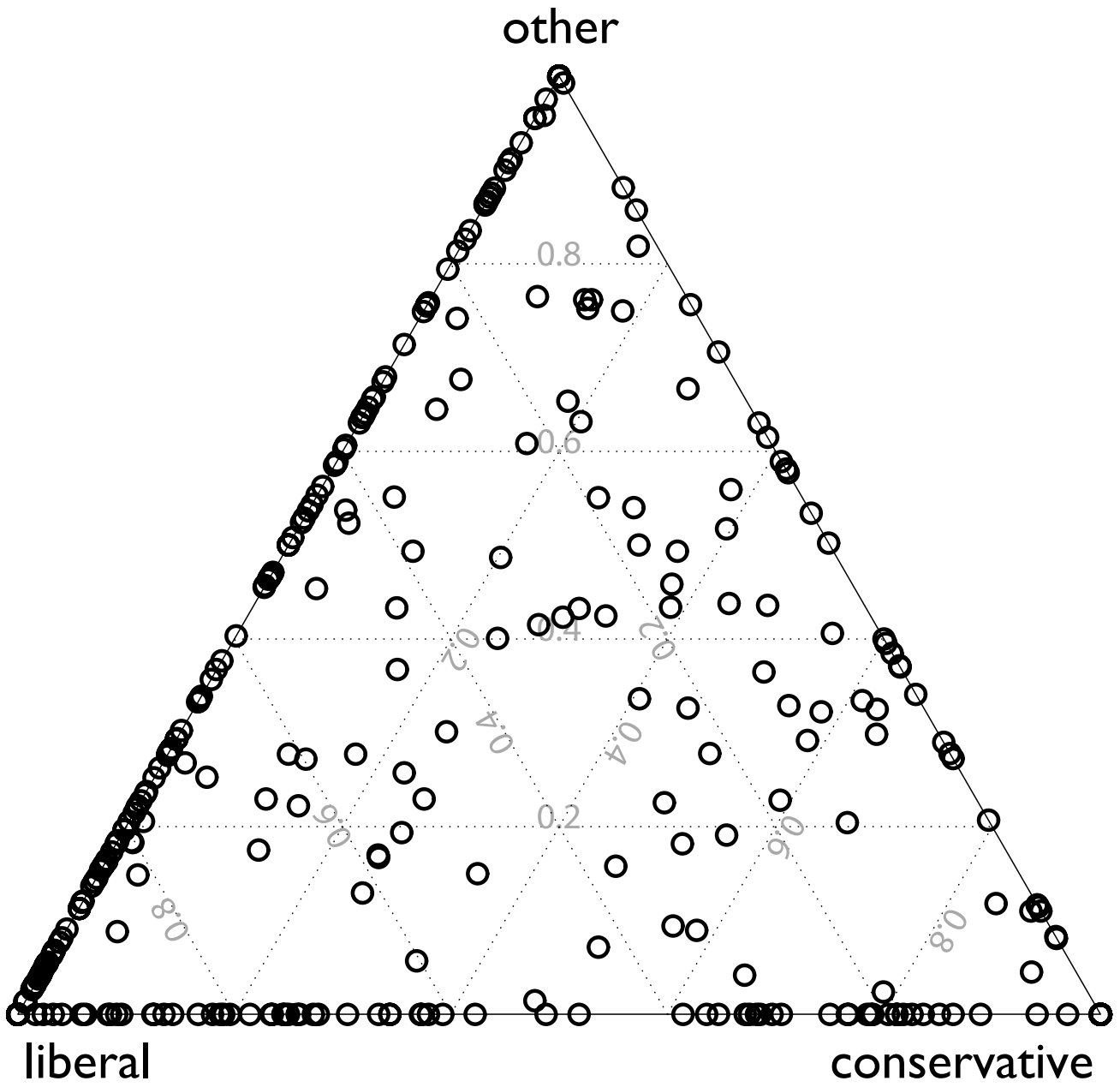
Scatterplot matrix: `splom()`



Three Varieties of Iris

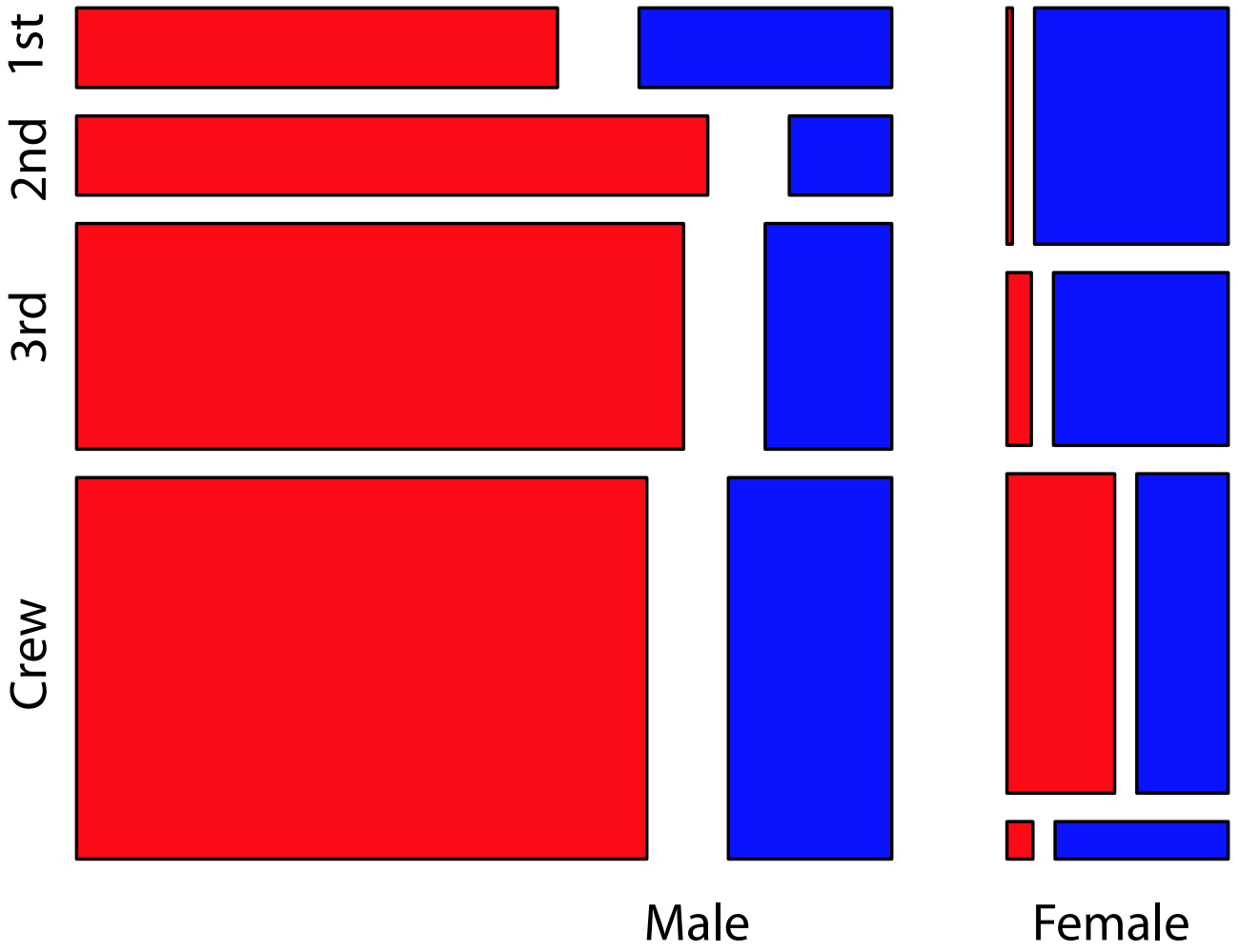
Scatter Plot Matrix

Ternary plot: `ternaryplot()` in `vcd`



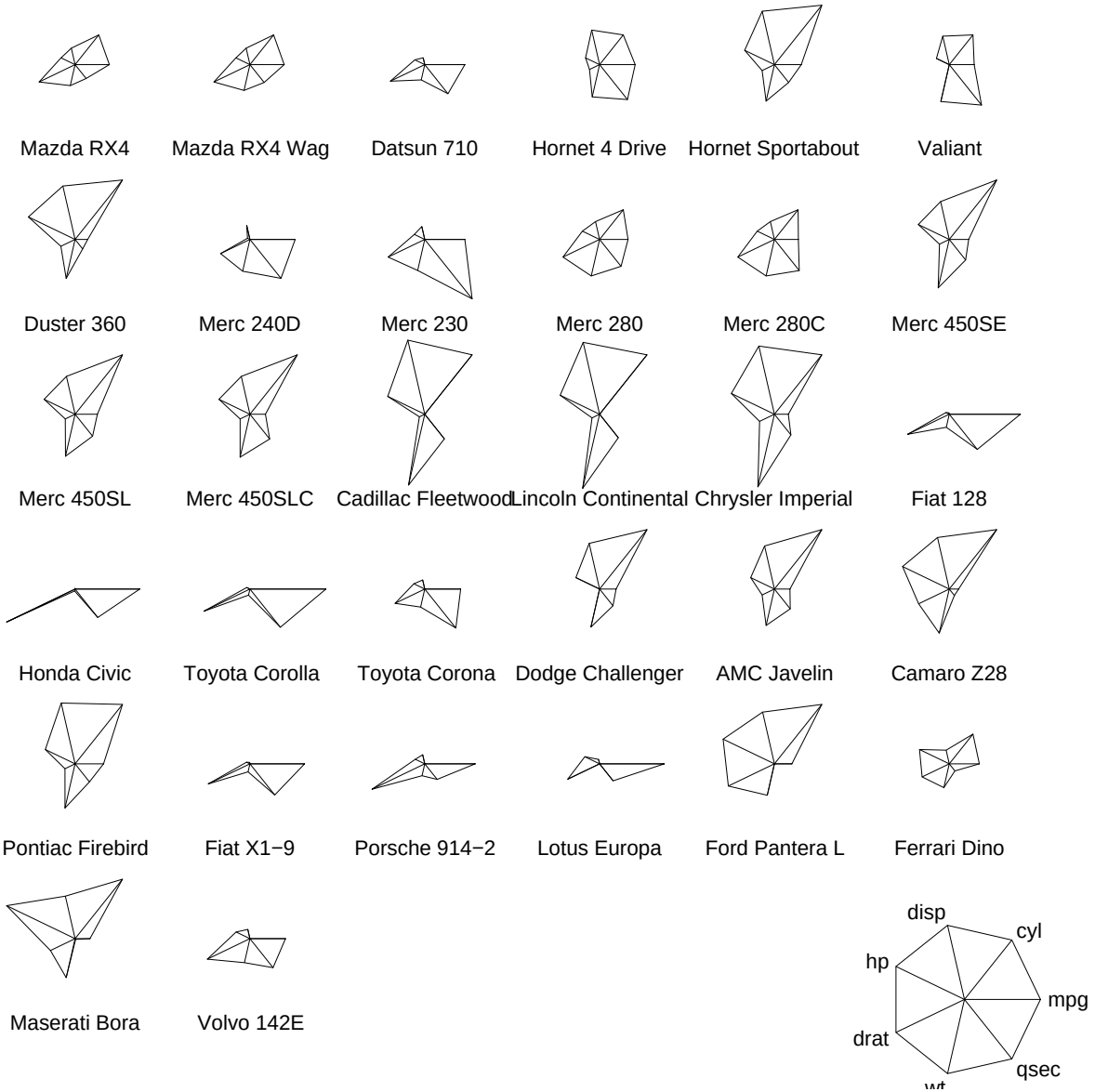
Mosaic plot: `mosaic()` in `vcd`

Titanic Survival Proportions: Deaths vs Survivors



Star plot: `stars()`

Motor Trend Cars : full stars()



Some major high-level graphics commands

```
stem> stem(log10(islands))

  The decimal point is at the |

  1 | 1111112222233444
  1 | 5555556666667899999
  2 | 3344
  2 | 59
  3 |
  3 | 5678
  4 | 012
```

Some major high-level graphics commands

Graphic	Base command	Lattice command
scatterplot	plot()	xyplot()
line plot	plot(. . . ,type="l")	xyplot(. . . ,type="l")
Bar chart	barplot()	barchart()
Histogram	hist()	histogram()
Smoothed histograms	plot() after density()	densityplot()
boxplot	boxplot()	bwplot()
Dot plot	dotchart()	dotplot()
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image plot	image()	levelplot()
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conditional plots	coplot()	xyplot()
Scatterplot matrix		splom()
Parallel coordinates		parallel()
Star plot	stars()	
Stem-and-leaf plots	stem()	
ternary plot	ternaryplot() in vcd	
Fourfold plot	fourfoldplot() in vcd	
Mosaic plots	mosaicplot() in vcd	

Basic customization

For any given high-level plotting command, there are many options listed in help

```
barplot(height, width = 1, space = NULL,
        names.arg = NULL, legend.text = NULL, beside = FALSE,
        horiz = FALSE, density = NULL, angle = 45,
        col = NULL, border = par("fg"),
        main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
        xlim = NULL, ylim = NULL, xpd = TRUE,
        axes = TRUE, axisnames = TRUE,
        cex.axis = par("cex.axis"), cex.names = par("cex.axis"),
        inside = TRUE, plot = TRUE, axis.lty = 0, offset = 0, ...)
```

Just the tip of the iceberg: notice the `...`

This means you can pass other, unspecified commands through `barplot`

Basic customization

The most important (semi-) documented parameters to send through `...` are settings to `par()`

Most base (traditional) graphics options are set through `par()`

`par()` has no effect on grid graphics (e.g., lattice, tile)

If you never have, consult `help(par)` now!

Some key examples, grouped functionally

`par()` settings

Customizing text size:

cex	Text size (a multiplier)
cex.axis	Text size of tick numbers
cex.lab	Text size of axes labels
cex.main	Text size of plot title
cex.sub	Text size of plot subtitle

note the latter will multiply off the basic `cex`

`par()` settings

More text specific formatting

font	Font face (bold, italic)
font.axis	etc
srt	Rotation of text in plot (degrees)
las	Rotation of text in margin (degrees)

Note the distinction between text in the plot and outside.

Text in the plot is plotted with `text()`

Text outside the plot is plotted with `mtext()`, which was designed to put on titles, etc.

Aside on margins

`mtext()` expects to be told which side of the plot & how many margin lines away the text is

This is kind of hopeless

A work-around to get stuff in the margins:

1. Turn off "clipping", the function that keeps data outside the plotting region from showing up in the margin.

   We do this by setting `par(xpd=TRUE)` for the current plot

2. Then plot your text using the usual `text()` command, but with coordinates outside the plot region

3. Now, if you want to rotate, use `par(srt)` as normal

4. You could turn clipping on and off to get only certain marginal data plotted.

`grid` offers a much better way

More `par()` settings

Formatting for most any object

bg	background color
col	Color of lines, symbols in plot
col.axis	Color of tick numbers, etc

Want to color the axes? You'll need to draw them yourself (next time)

Aside: Colors in R

Three ways to specify a color to an R function (for all R graphics tools):

1. color names, like `''red''` or `''lightblue''`
   (see `colors()` for a list of hundreds of color names)

Aside: Colors in R

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2. numerical color codes from `rgb()`, `hsv()`, or `hcl()`

   (`hcl()` gives CIEluv equal perceptual changes for unit changes in chroma, value, or brightness)

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   Also useful: `col2rgb()`, `rgb2hsv()`, etc. for conversions among these functions

3. numerical color codes offered by packages for selecting cognitively valid palattes, optimized to your required number of colors and level of measurement (categorical, ordered, interval):

Package	Key function(s)
`RColorBrewer`	`brewer.pal()`
`colorspace`	`sequential_hcl()` and `diverge_hcl()`

`RColorBrewer` is fast and easy; `colorspace` is very powerful

More `par()` settings

Formatting for lines and symbols

lty	Line type (solid, dashed, etc)
lwd	Line width (default too large; try really small, e.g., 0)
pch	Data symbol type; see `example(points)`

`lty` can take complex inputs, see the help for `par()`

You will very often need to set the above

More `par()` settings

Formatting for axes

lab	Number of ticks
xaxp	Number of ticks for xaxis
tck,tcl	Length of ticks relative to plot/text
mgp	Axis spacing: axis title, tick labels, axis line

These may seem trivial, but affect the aesthetics of the plot & effective use of space

`R` defaults to excessive mgp, which looks ugly & wastes space

Most HLCs forget to rotate the y-axis labels. This is a bit harder to fix

More `par()` settings

More formating for axes

The following commands are special:
they are primitives in `par()` that can't be set inside the `...` of high-level commands

You must set them with `par()` first

usr	Ranges of axes: c(xmin, xmax, ymin, ymax)
xlog	Log scale for x axis?
ylog	Log scale for y axis?

Getting math on plots

Getting mathematics on the plots is sometimes possible

See `example(text)` for ideas

The key command is `expression()`

For example,

`expression(bar(x))`	$\bar{x}$
`expression(x[i])`	x_i
`expression(x^{-2})`	x^{-2}
etc	

Vaguely Latex-like, but less powerful

Give up and use Illustrator and/or Latex?

R graphics devices

Everything you draw in R must be drawn on a canvas

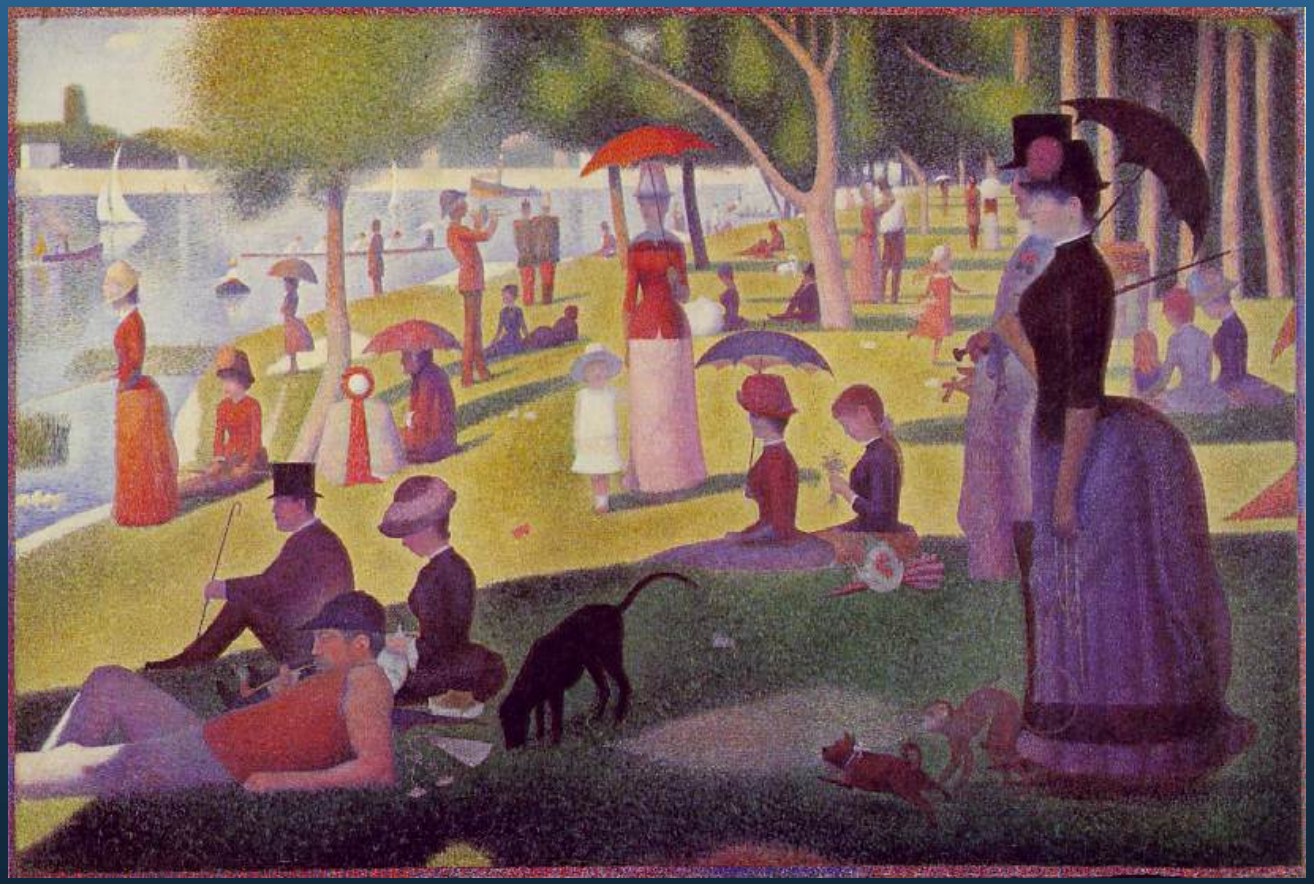
Must create the canvas before you draw anything

Computer canvases are **devices** you draw to

Devices save graphical input in different ways

Most important distinction: raster vs. vector devices

Vector vs. raster



Pointalism = raster graphics. Plot each pixel on an n by m grid.

Vector vs. raster

Pixel = Point = Raster

Good for pictures. Bad for drawings/graphics/cartoons.

(Puzzle: isn't everything raster? In display, yes. Not in storage)

Advantages of vector:

- Easily manipulable/modifiable groupings of objects
- Easy to scale objects larger or smaller/ Arbitrary precision
- Much smaller file sizes
- Can always convert to raster (but not the other way round, at least not well)

Disadvantages:

- A photograph would be really hard to show (and huge file size)
- Not web accessible. Convert to PNG or PDF.

Some common graphics file formats

	Lossy	Lossless
Raster	.gif, .jpeg	.wmf, .png, .bmp
Vector	—	.ps, .eps, .pdf, .ai, .wmf

Lossy means during file compression, some data is (intentionally) lost

Avoid lossy formats whenever possible

Avoid copy-and-paste on PC: rasterizes vector graphics in lossy way!

Some common graphics file formats

In `R`, have access to several formats:

win.metafile()	wmf, Windows media file
pdf()	pdf, Adobe portable data file
postscript()	postscript file (printer language)

x11()	opens a screen; all computers
windows()	opens a screen; PC only
quartz()	opens a screen; Mac only

Latex, Mac or Unix users can't use wmf

`windows(record=TRUE)` let's you cycle thru old graphs with arrow keys

Best to make final graphics directly through pdf() or postscript()

Avoids rasterization

R from the Ground Up: Outline

Coordinate systems

Line & color

The grid graphics system

Using lattice

Approach

What I'm giving you today:

More readings from the dictionary. . .

Lots of sample code

Random bits of advice I wish someone had told me

Knowledge I consider most useful for graphical programming

I may gloss over something important

Stop me with questions

Initial minimalism

Always start with a blank screen.

```
filename <- "example.pdf"   # Name of output file
width <- 4                  # width of output
height <- 4.5               # height of output
pdf(filename=filename,
    width=width,
    height=height
    )
    # Other pdf options to consider:
    #  family, fontsize, bg, fg

plot.new()                  # Start the plot

# Do some graphics

dev.off()                   # Save the plot to disk and end
```

Initial minimalism

A good motto is to add nothing without thinking about why it needs to be added

This approach

- eliminates chartjunk
- casts aside convention for creativity
- gives you complete control

Before we ask

What to put on that screen?

we should ask:

Where to put it?

Coordinate systems

Computer graphics can *always* be though of as occurring on a 2D plane.

Convenient to treat the bottom left of screen as 0,0 and the top-right as 1,1.

Let's us put objects on screen w/ easy reference to relative position.

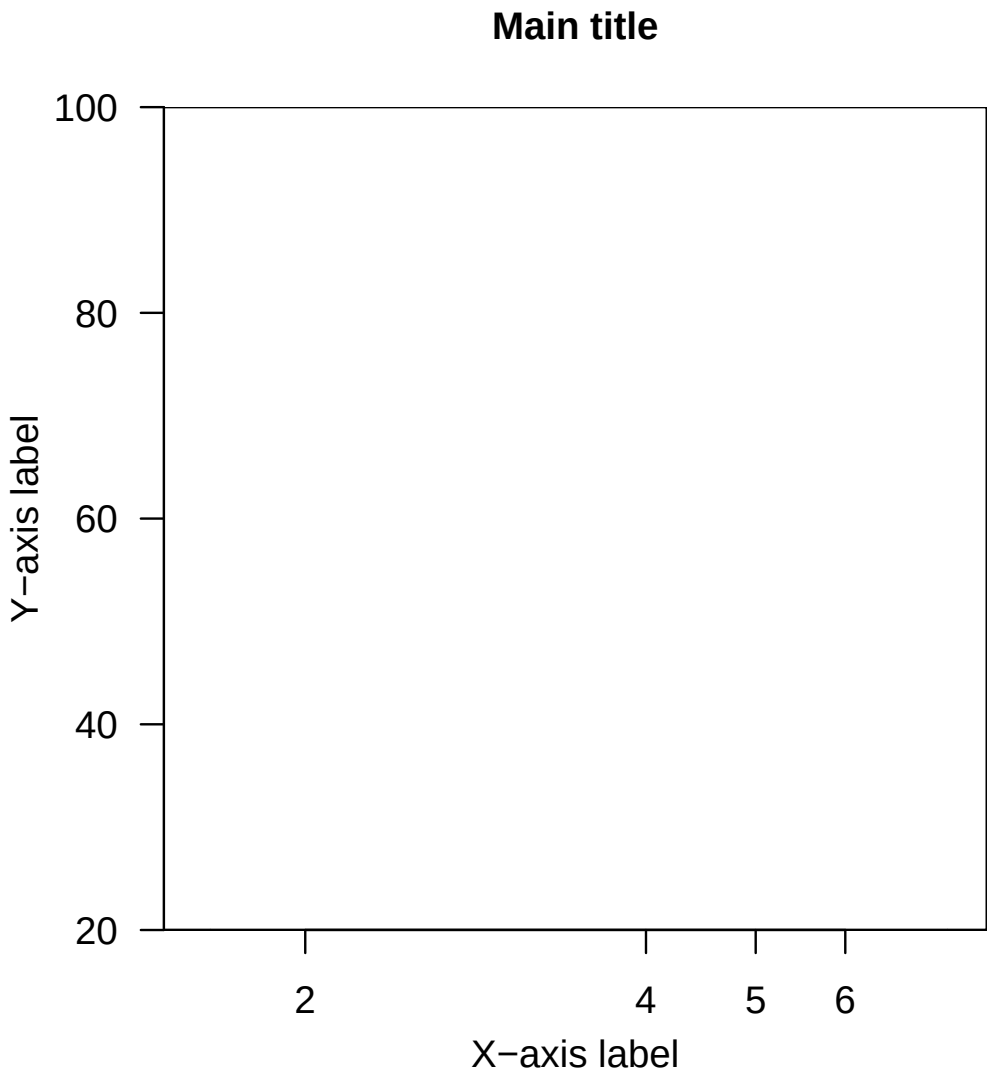
Note this is not an "axis system".

We have drawn no axes.

If we wanted to draw axes denoting this coordinate space, they would lie off the screen by definition, because the coordinate system is the screen

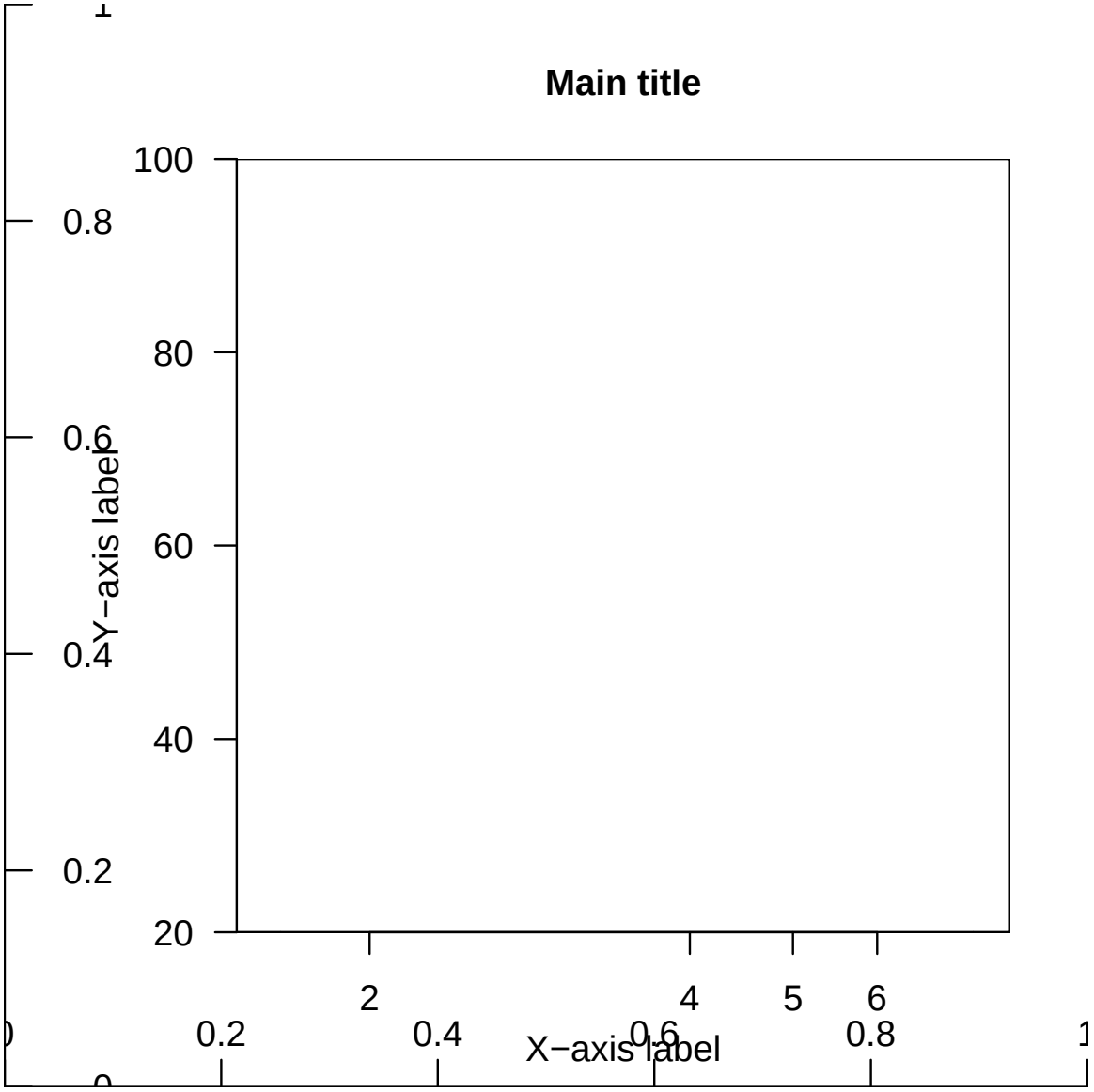
This coordinate system complete not just for 2D images, but for representing "3D" images (ie 2D with false perspective), or for showing movies, or for interactive displays.

Coordinate systems



Are the axes controlling the plot? Or just added ornamentation?

Coordinate systems



Axes don't control anything. Like everything else, axes are drawn on the canvas

Everything is line and color

What can we to plot? Last time we saw dozens of options

But really, there are just two: line and color

We can build anything from these elements

- Drawing lines:

  `lines(x,y,...)`

  Note `...` can include `col`, `lty`, `lwd`, etc.

  Can even alter the style of the line endings

Everything is line and color

- Drawing filled shapes: `polygon(x,y,col="red",border=NA,...)`

  This draws a red polygon with vertices at (x, y).

  Need to set the `col` and `border` as above to get a plain shape

  If we were hardcore, that would be enough. we could draw anything, even letters and glyphs from `lines()` and `polygon()`

  But that would be a real pain.

Add two more primitive commands

- Drawing glyphs:

  `points(x,y,...)`

  Note that `...` can include `col`, `pch`, etc.

- Drawing text: `text(x,y,labels,...)`

  Note `...` can include `col`, `xpd`, `srt`, etc.

  Useful: `offset` moves the label a set amount (to position under a glyph)

Programming tips

The best programs are:

- stand-alone functions
- use clear, consistent variable names
- generalized. variables should be allowed to vary

Justify to yourself any numerical constants or strings hard-coded.

Programming tips

```
#Don't do this:
example <- function(x,
                    y) {
 points(x=x,
        y=y,
        col="blue"
       )
}

#Do this:
example <- function(x,
                    y,
                    col="blue") {
 points(x=x,
        y=y,
        col=col
       )
}
```

Programming tips

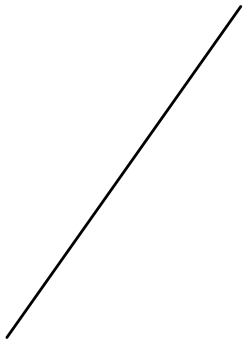
More advice:

- Comment on blocks or lines of code
- Think about making your code extensible (hard)
- Think about how your code will interact with other code (hard)
- Be realistic:
  do *just* enough programming to make yourself most efficient as a scientist

The base system: Example

```
# Building traditional R graphics from primitives
x11()          # Opens a graphics window (technically, a device)
plot.new()     # Clears the graphics screen

# Let's draw a line
lines( x=c(0,0.25), y=c(0,0.5) )

# We connected the points (0,0) and (0.25,0.5)
```

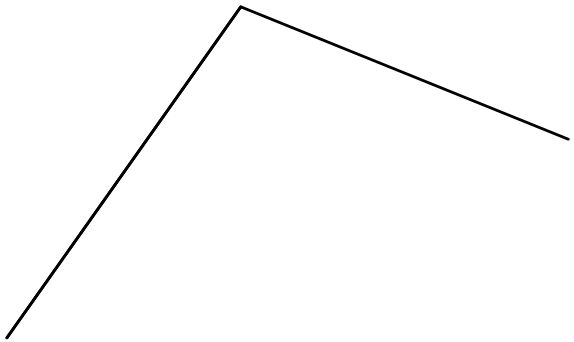
The plot so far



The base system: Example

```
# Okay, now let's draw a kinky line
lines( x=c(0,0.25,0.6), y=c(0,0.5,0.3) )
```

The plot so far

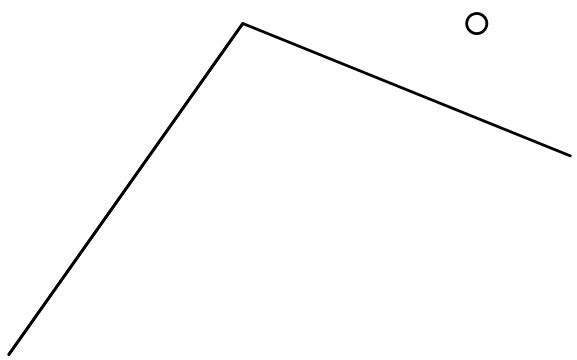


We connected the points (0,0), (0.25,0.5), and (0.6,0.3)
Using lines() we can draw any shape

The base system: Example

```
# What if we want a point?
points(x=0.5, y =0.5)
```

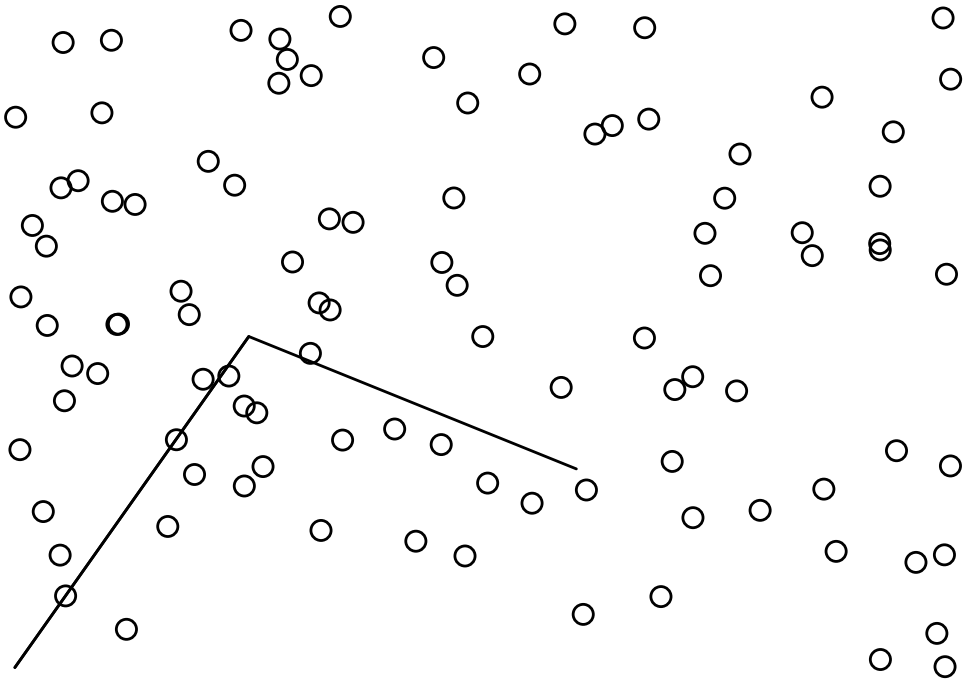
The plot so far



The base system: Example

```
# Or a lot of points?
points(x = runif(100), y = runif(100) )
```

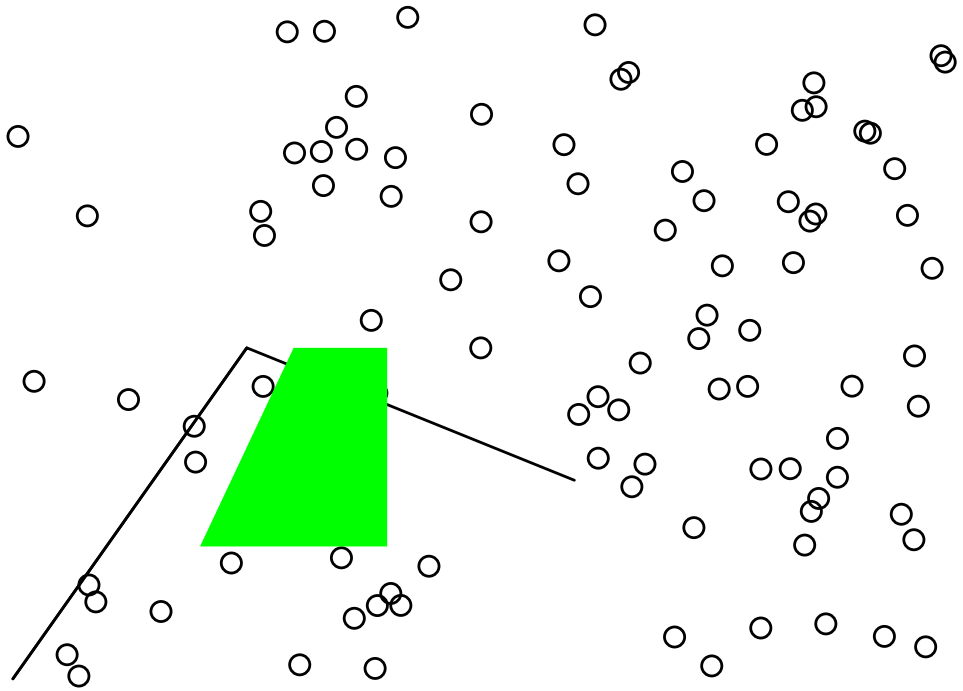
The plot so far



The base system: Example

```
# Or a polygon?

xpoly <- c(0.2,0.4,0.4,0.3)
ypoly <- c(0.2,0.2,0.5,0.5)

polygon(x=xpoly,
        y=ypoly,
        col="green",
        border=NA
        )
```

The plot so far

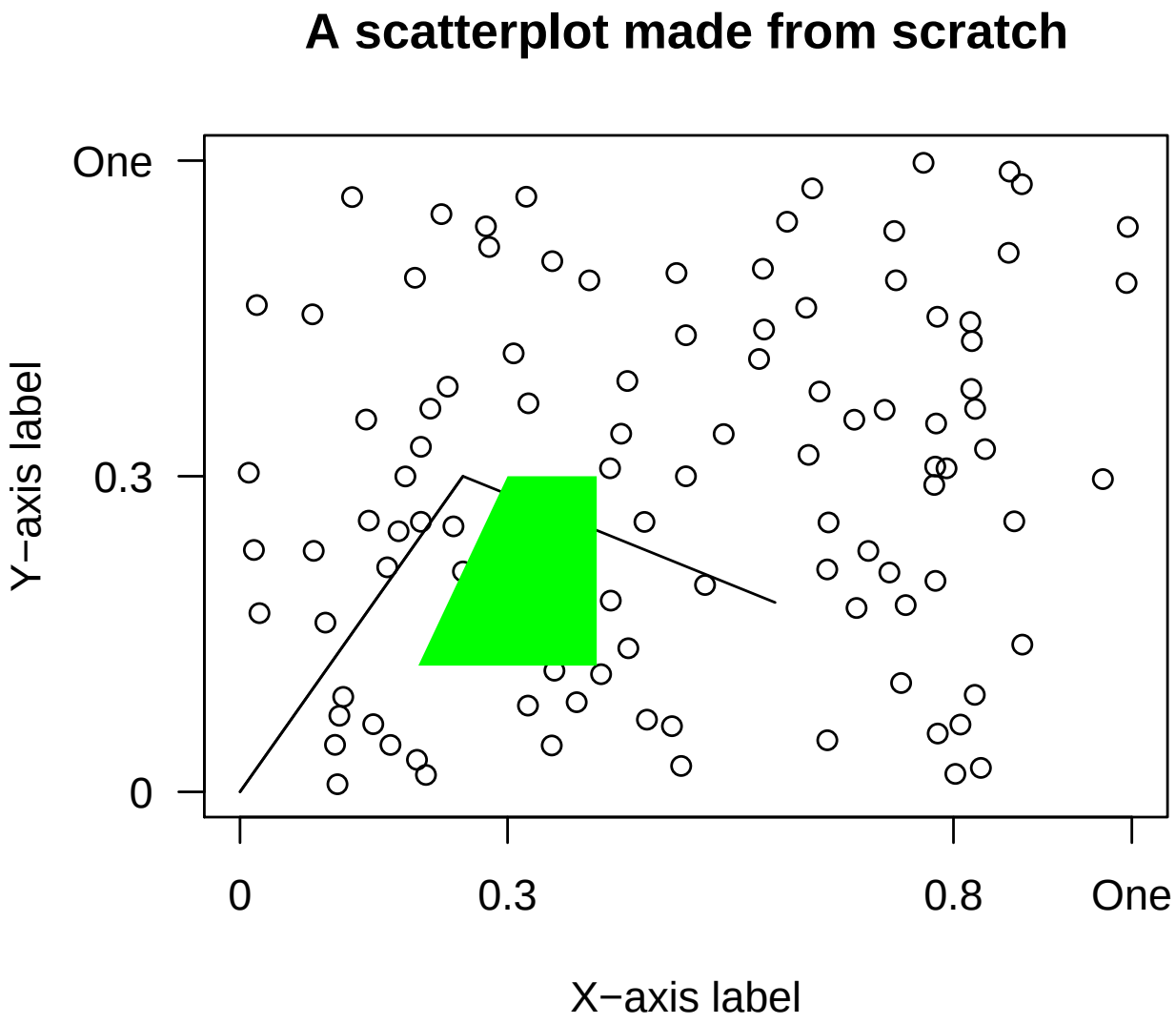


Notice that it covers everything else. R is "Painter-style"
Plot polygons first. May use alpha transparency (pdf only)

The base system: Example

```
# We can draw the axes at any time
axis(side=1,                        # 1 = x.  Lovely
     at=c(0,0.3,0.8,1),             # Where the ticks are
     labels=c(0,0.3,0.8,"One")      # What the ticks say
     )

axis(side=2,                        # 2 = y.  Obviously
     at=c(0,0.5,1),
     labels=c(0,0.3,"One"),
     las=1                          # rotate labels
     )

title(main = "A scatterplot made from scratch",
      xlab = "X-axis label",
      ylab = "Y-axis label"
      )

box()
```

The final plot



The grid system

"Traditional" R Graphics are fairly powerful

. . . As long as you only want to make one graphic, with a single coordinate system

Plotting multiple graphs, or plotting "in the margin" is difficult

Workarounds exist, but a package with powerful low level control of multiple plotting regions would be better

If you are planning to develop new graphical software in R, I recommend using grid as your toolkit

The `grid` system

3 things to remember:

- You can create a "plotting region" (with implicit coordinates & axes) anywhere on the canvas
- You can nest these plotting regions, producing a hierarchical graphical object
- You can reference (and plot to) points with respect to any plotting region using any system of measurement

Viewports

A grid plotting region is called a viewport

Some key commands:

`pushViewport()`, `upViewport()`, `downViewport`

What can you do with viewports?

- Create separate plotting regions: Grids of plots
- Fine control of margins
- Plots inside plots
- Even plots inside of plotting symbols

Units in the `grid` system

`grid` needs to be told the unit of things it plots

Instead of `points(x = 0.5, y = 0.25)` use

```
grid.points( x = unit(0.5, "native"), y = unit(0.25, "native") )
```

Some units available:

`native`	Based on the current x, y scales (e.g., your data)
`npc`	Treats the current viewport as (0,0) to (1,1)
`inches`	This and other physical unit available, given device
`strwidth`	Multiples of the width of a given string
`strheight`	Multiples of the height of a given string
`null`	In layouts, any remaining space is divided among nulls

The last three are very powerful

`unit( 1, "strwidth", "this string" )` creates a unit as wide as the text "this string"

Can't `c()` on `unit()` terms. Use `unit.c()` instead

Primitives in the `grid` system

Plot as usual.

Except you need to use the grid packages commands.

Traditional graphics commands don't work in grid!

Use instead

```
grid.lines()
grid.polygon()
grid.points()
grid.text()
etc
```

Primitives in the `grid` system

Let's look at an example and an alternative:

```
grid.points(x, y,
            pch = 1,
            size = unit(1, "char"),
            default.units = "native",
            name = NULL,
            gp=gpar(),
            draw = TRUE,
            vp = NULL)

x <- pointsGrob(x, y,
                pch = 1,
                size = unit(1, "char"),
                default.units = "native",
                name = NULL,
                gp=gpar(),
                vp = NULL)
```

`grid` graphics parameters

Grid replaces `par` with `gpar`

Near complete list (from `help(gpar)`):

col	Colour for lines and borders.
fill	Colour for filling rectangles, polygons, ...
alpha	Alpha channel for transparency
lty	Line type
lwd	Line width
cex	Multiplier applied to fontsize
lineend	Line end style (round, butt, square)
linejoin	Line join style (round, mitre, bevel)
linemitre	Line mitre limit (number greater than 1)
fontsize	The size of text (in points)
fontfamily	The font family
fontface	The font face (bold, italic, ...)
lineheight	The height of a line as a multiple of the size of text

Other important `grid` commands

layout	Makes a layout of viewports
editGrob	Edits an existing graphical object
unit.length	Returns the length of a unit

Let's use grid to plot a regression line with a shaded confidence region

grid is really meant for designing totally new graphics,
and especially for building functions for end-users

Although you wouldn't normally write a plot from scratch in grid,
it's the best way to learn how grid works

Let's use grid to plot a regression line with a shaded confidence region

grid is really meant for designing totally new graphics,
and especially for building functions for end-users

Although you wouldn't normally write a plot from scratch in grid,
it's the best way to learn how grid works

We begin by loading libraries and helper functions...

```
# Clear memory of all objects
rm(list=ls())

# Load libraries
library(RColorBrewer)       # For nice colors
library(grid)               # For graphics
```

```
# MM-estimator fitting
mmest.fit <- function(y, x, ci, quiet=TRUE) {
    require(MASS)
    y <- y[order(x)]
    x <- x[order(x)]
    result <- rlm(y~x, method="MM")
    if (!quiet) print(result)
    fit <- list(x=x)
    fit$y <- result$fitted.values
    fit$lower <- fit$upper <- NULL
    if (length(na.omit(ci))>0)
        for (i in 1:length(ci)) {
            pred <- predict(result, interval="confidence", level=ci[i])
            fit$lower <- cbind(fit$lower, pred[,2])
            fit$upper <- cbind(fit$upper, pred[,3])
        }
    fit
}
```

```
# Here's an effort at a color lightener (could use work)
lighten <- function(col,
                    pct=0.75,
                    alpha=1){
    if (abs(pct)>1) {
        warning("invalid pct in lighten(); must be between 0 and 1.")
        pcol <- col2rgb(col)/255
    } else {
        col <- col2rgb(col)/255
        if (pct>0) {
            pcol <- col + pct*(1-col)
        } else {
            pcol <- col*pct
        }
    }
    rgb(pcol[1], pcol[2], pcol[3], alpha)
}
```

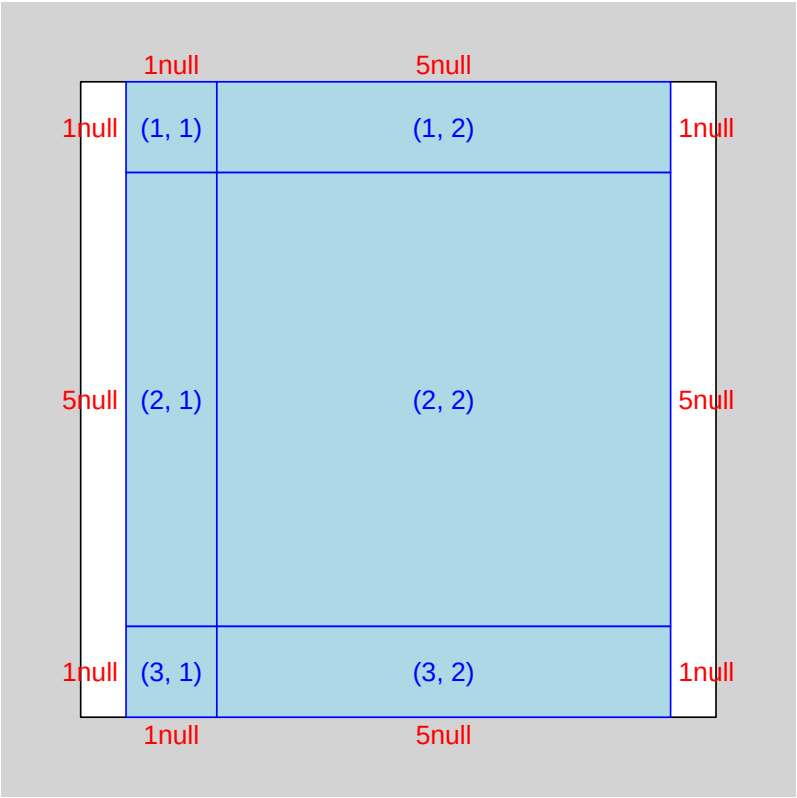
Build a graphic using `grid` — *Initialize device & make layout*

```
# Open a new pdf device
pdf("testgrid.pdf", width=5, height=5)

# Set up plot limits (used later)
limits <- c(log(1.5), log(8), 20, 100)

# Set up tick locations (used later)
yat <- c(20, 40, 60, 80, 100)
xat <- c(2, 3, 4, 5, 6, 7)

# Establishing limits and tick locations
# up front makes them easier to change
# -- otherwise, you need to make lots of edits
```

PDF output is blank so far:
Nothing plotted yet

Build a graphic using `grid` — *Initialize device & make layout*

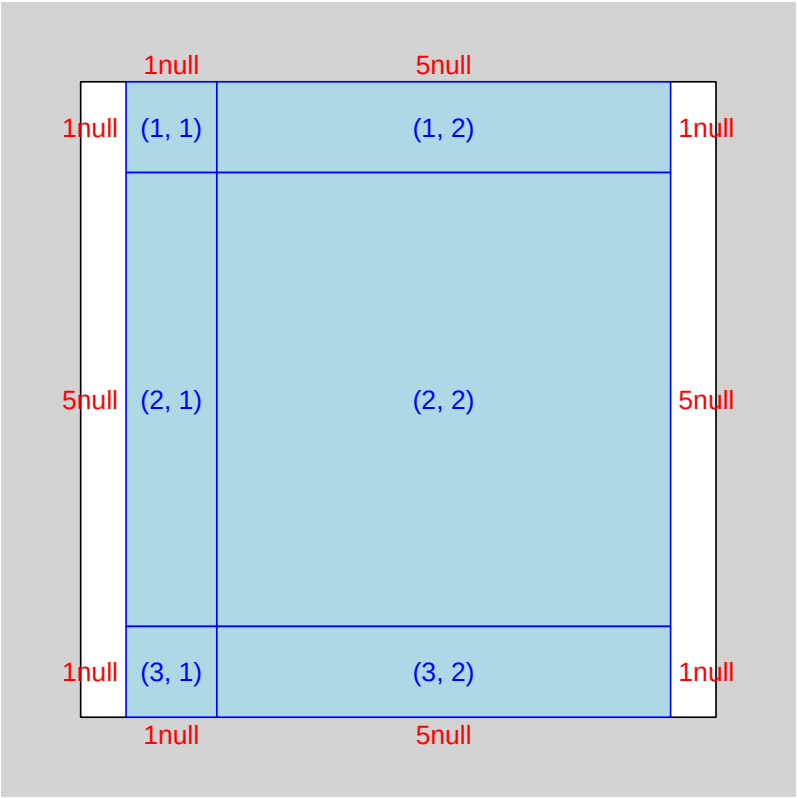
```
# Create layout
overlay <- grid.layout(nrow=3,
                       ncol=2,
                       widths=c(1, 5),
                       heights=c(1, 5, 1),
                       respect=TRUE)

# Display layout
grid.show.layout(overlay)
```



Diagnostic plot of `overlay` layout

Build a graphic using `grid` — *Initialize device & make layout*

```
# Create layout
overlay <- grid.layout(nrow=3,
                       ncol=2,
                       widths=c(1, 5),
                       heights=c(1, 5, 1),
                       respect=TRUE)

## Display layout
#grid.show.layout(overlay)

# "Push" layout to create initial viewport
pushViewport(viewport(layout=overlay))
```

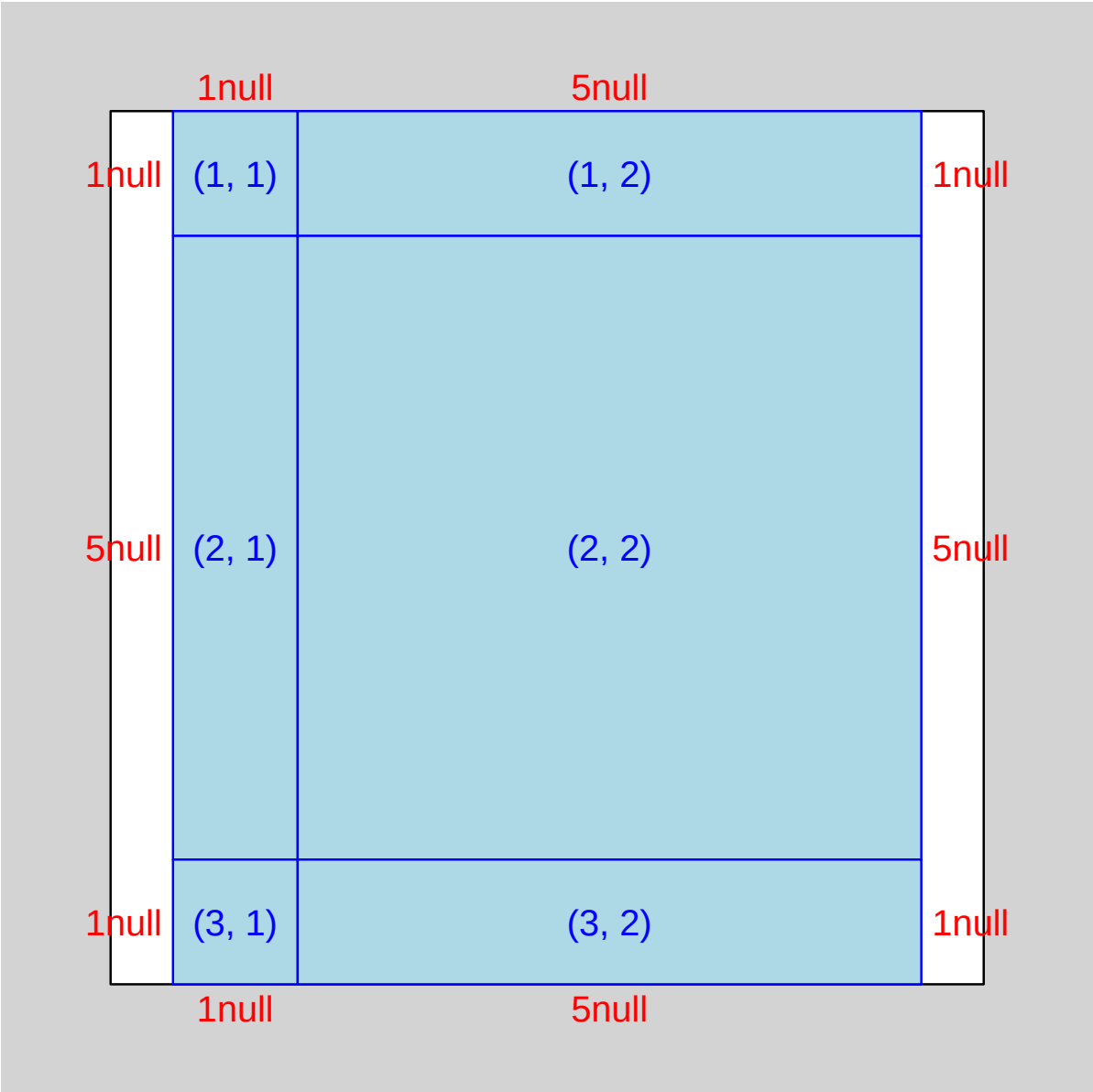


Diagnostic plot of `overlay` layout

If you make a `grid.layout()` you can take a look at it with `grid.show.layout()`

Don't confuse `grid.layout()` with the base command `layout()`!

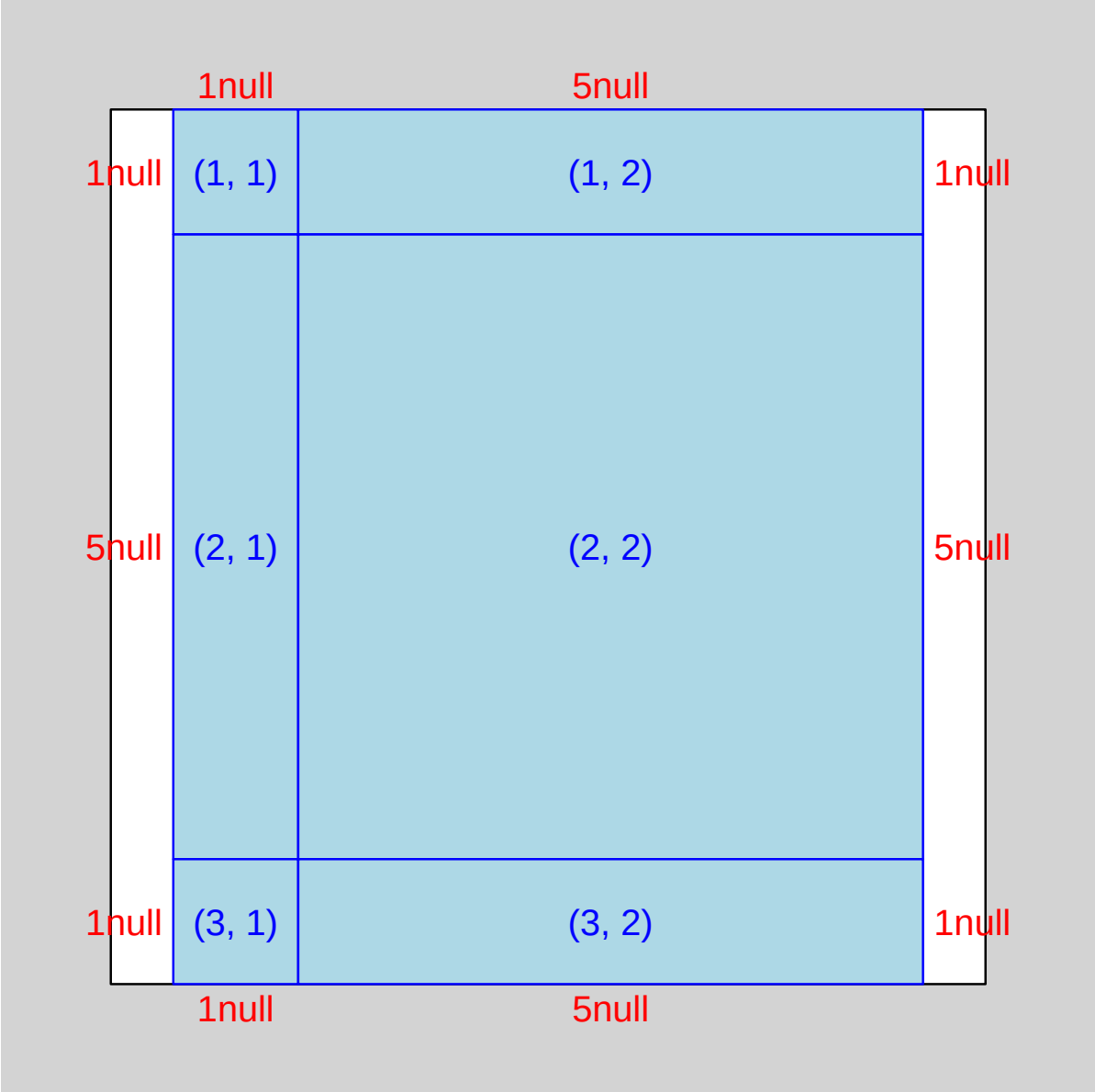
Let's use this diagnostic plot to understand `null` units better...



This graphic is 7 `null`'s high and 6 `null`'s wide

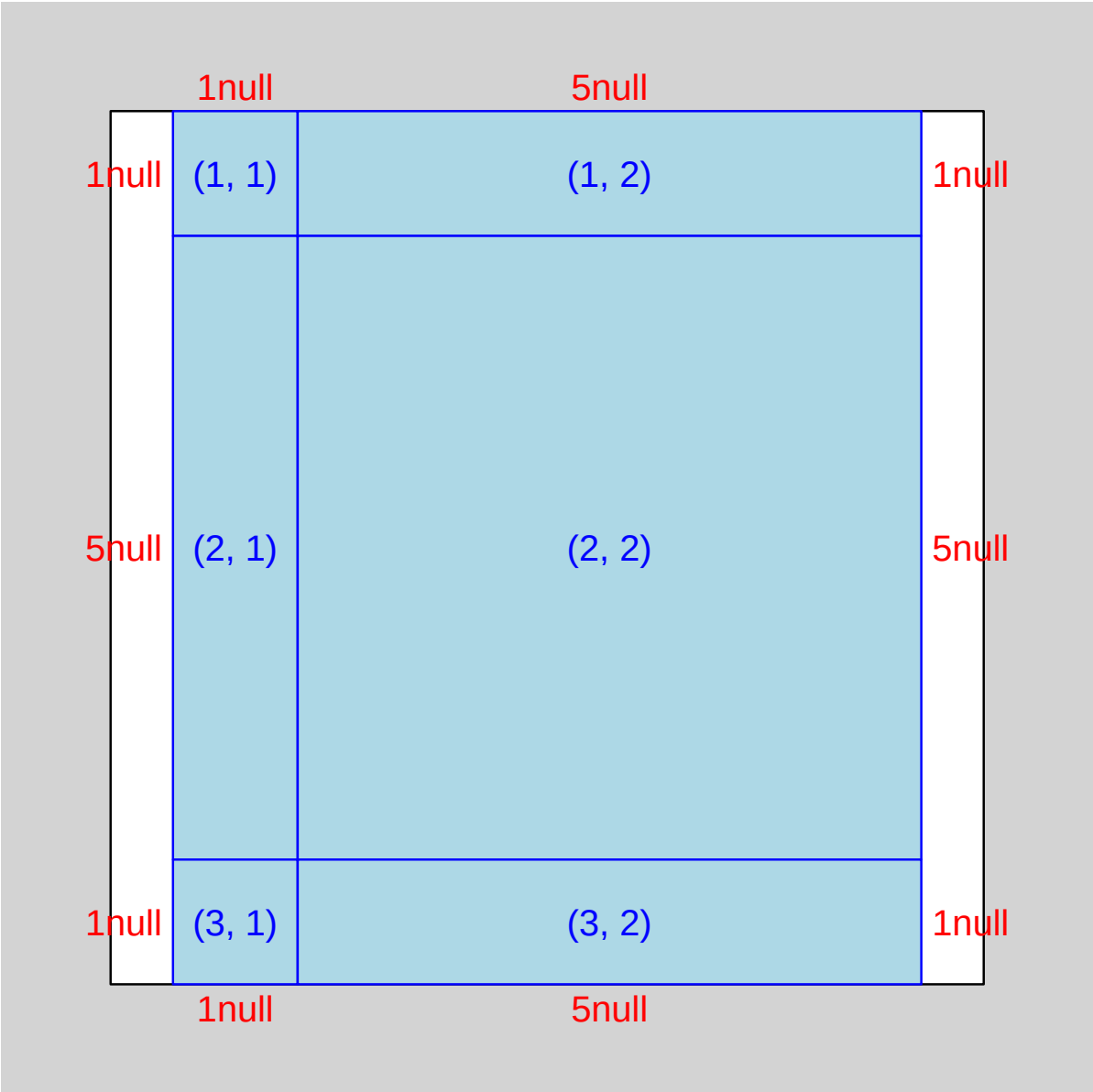
After allocating any fixed units (like `inches`), grid will assign remaining space to `null`

Thus the size of 1 `null` varies based on the fixed content of the graph



Recall this graphic exists in a pdf device that is 5 inches $\times$ 5 inches

So how big is a null in inches?

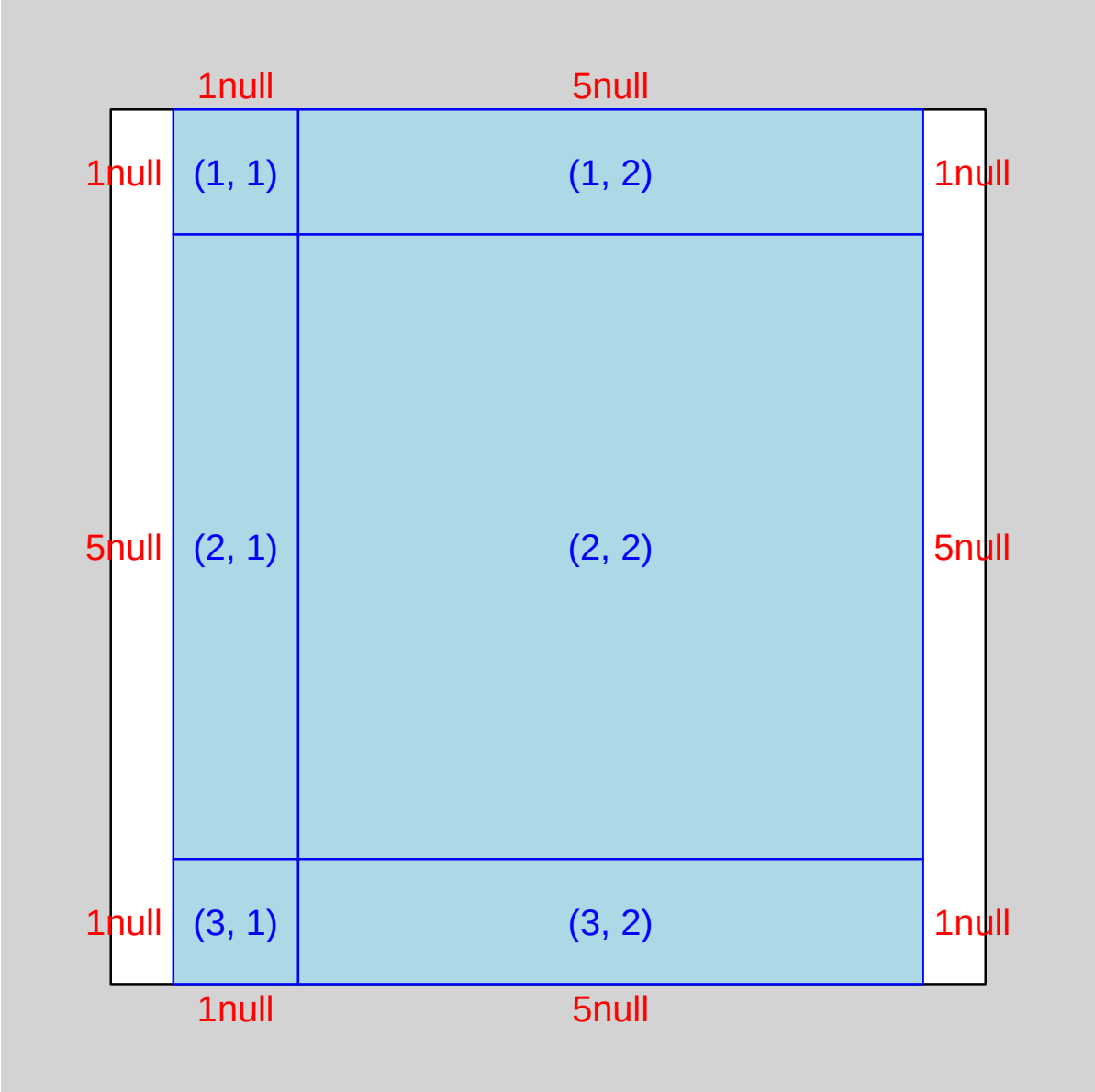


Recall this graphic exists in a pdf device that is 5 inches $\times$ 5 inches

So how big is a null in inches?

The graph is 7 null's tall, so 7 null = 5 inches

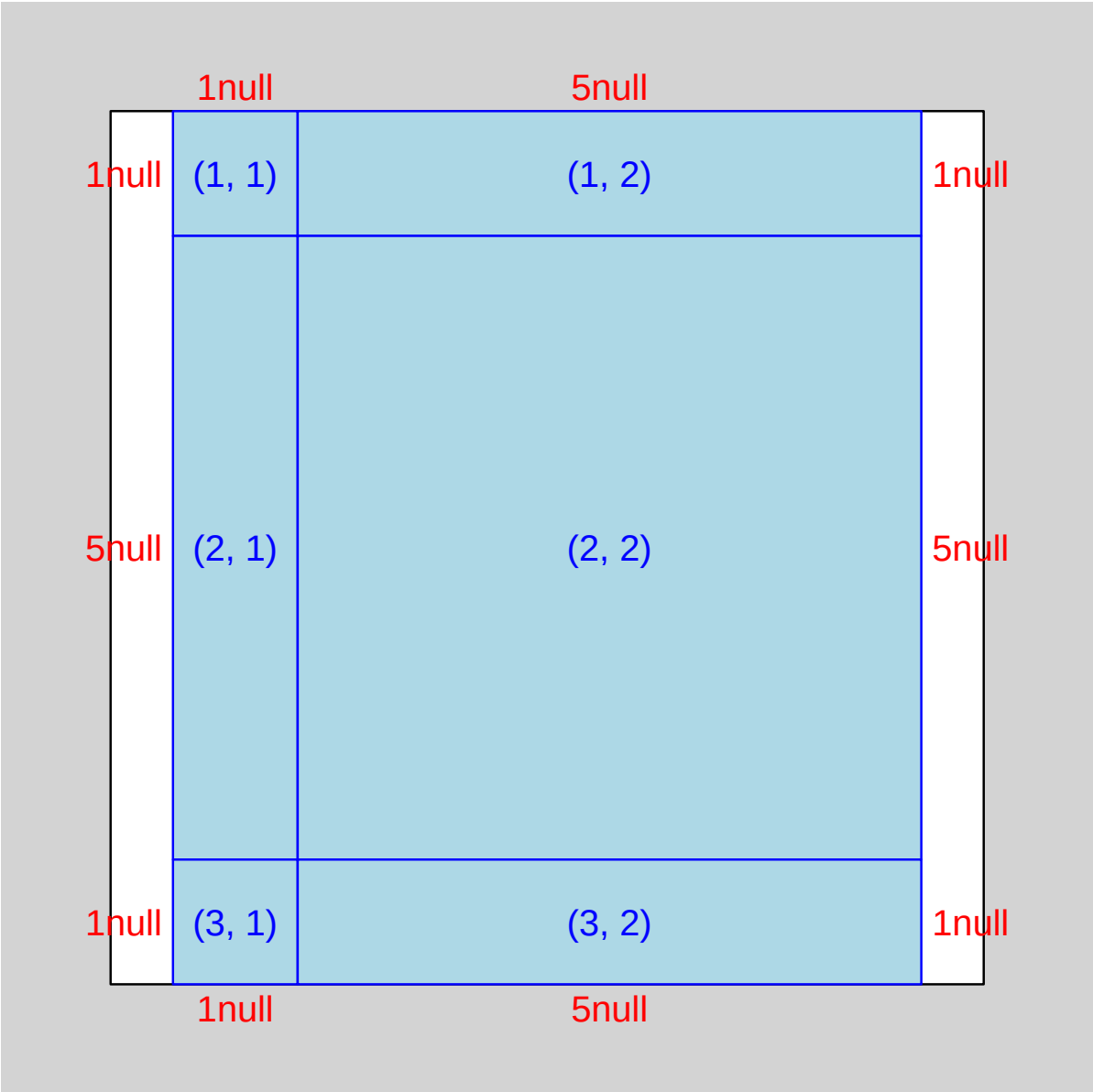
Thus 1 null = 5/7 inches ($\approx$0.714 inches)



Why didn't we set the width of 6 nulls equal to 5 inches?

In our layout, we set `respect=TRUE`, which forces `null` widths and `null` heights to be equal

Where nulls might differ, this forces the tightest dimension to "bind" them both to the smaller of the two possible lengths

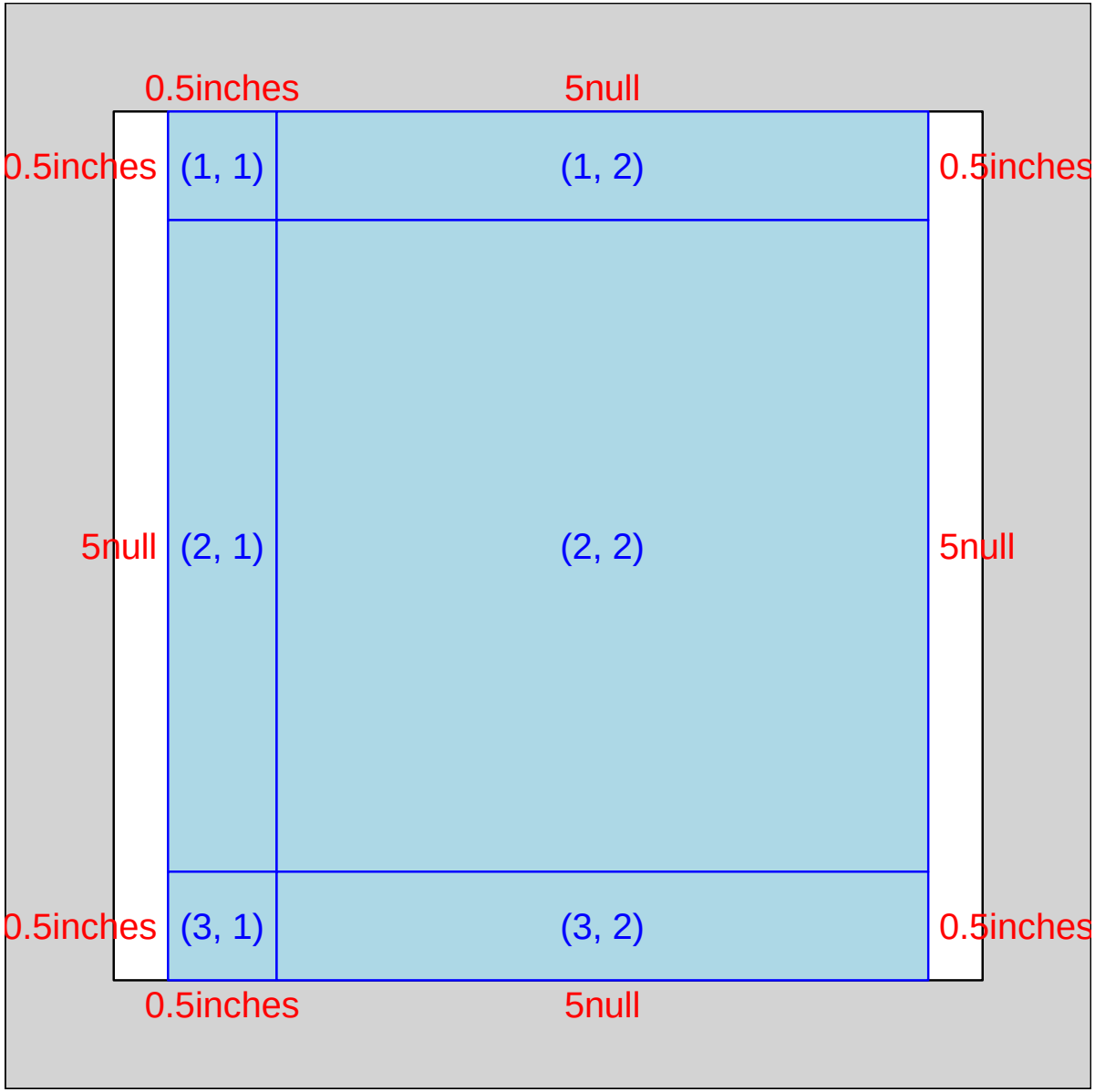


To understand `null`'s better, let's change the layout so the first column is 0.5 inches wide...

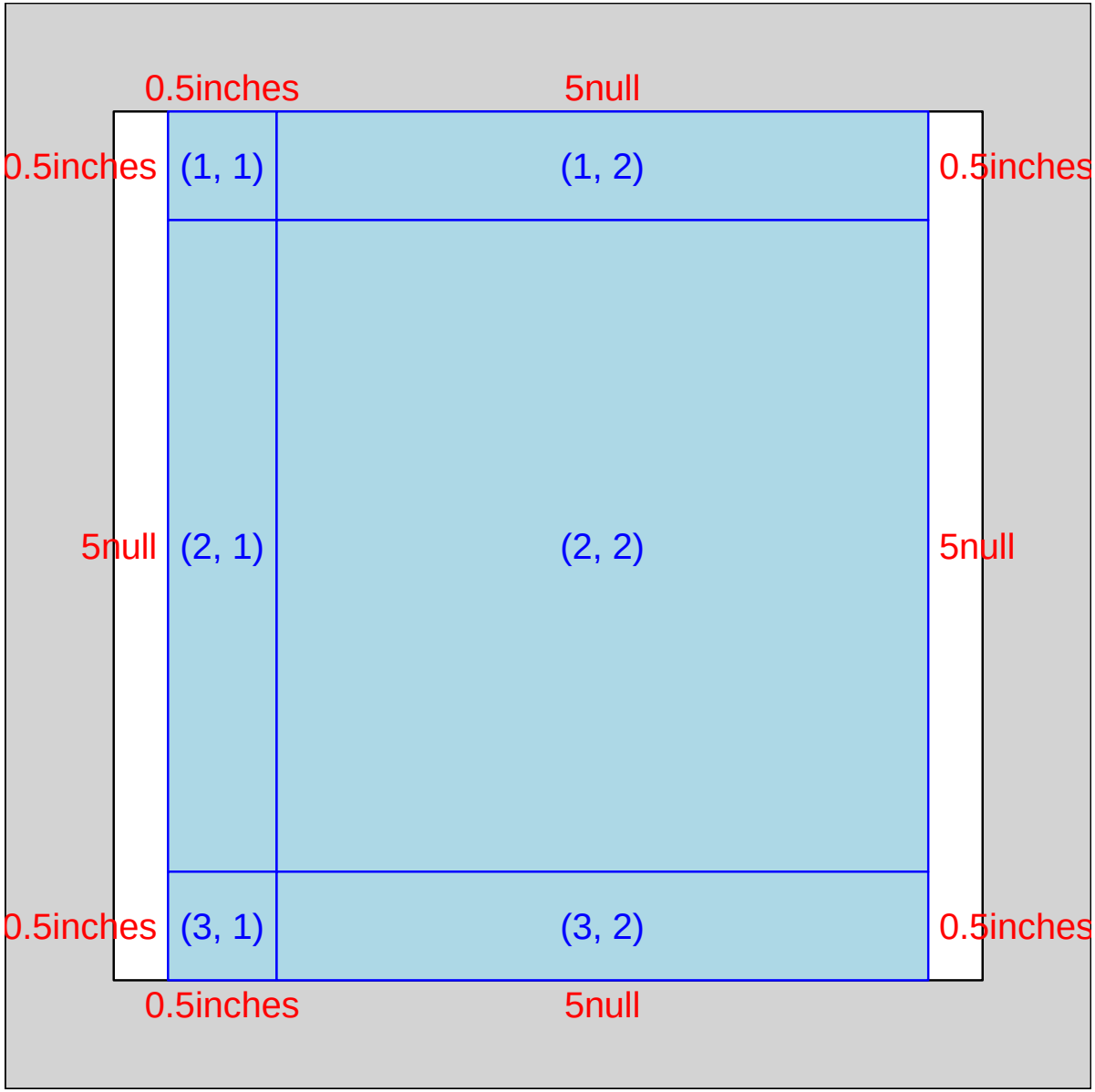
...and the first and last rows are 0.5 inches tall

Why? Because these are spaces for text labels

Fixing to 0.5 inch is one (inelegant) way to ensure they're readable & not too big



What is the size of a `null` in inches now?



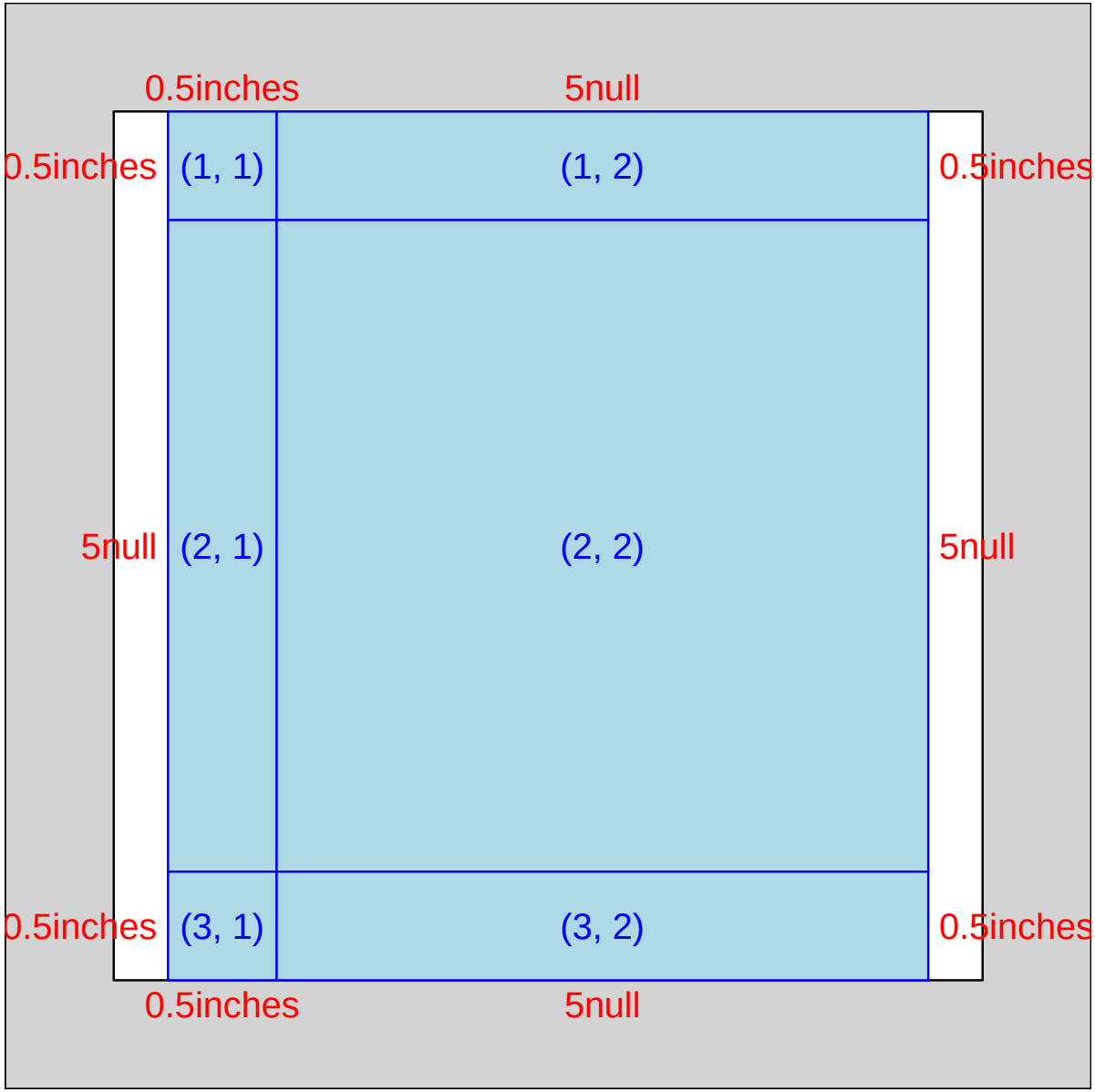
What is the size of a `null` in inches now?

Height is still the binding dimension

Layout is 1 inch and 5 `null`'s tall, and must fit a 5 inch tall pdf

This leaves 4 inches to devote to `null`'s,
so 4 inches = 5 null

A `null` is now 4/5 inches (0.8 in), increasing the space of our graphic devoted to data

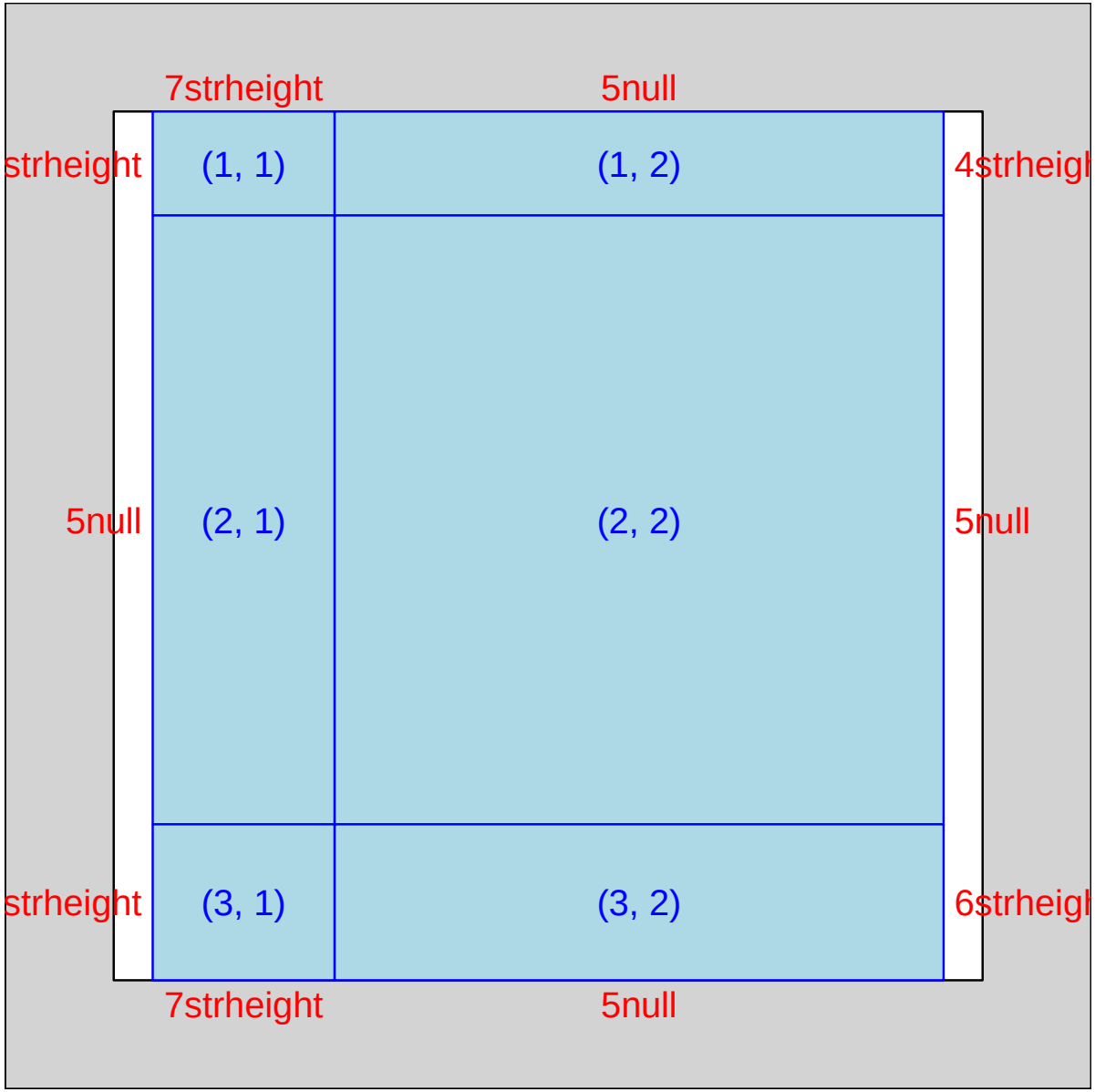


A still more powerful grid unit allows us to tile layouts to the heights and widths of specific strings

We can snugly fit text areas around the text as plotted in the device

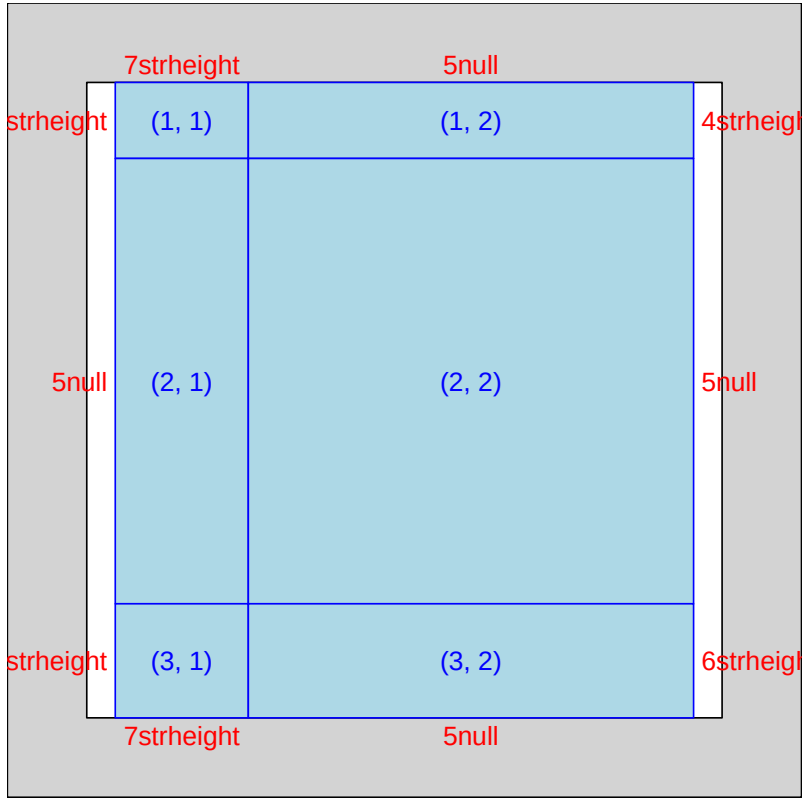
...Leaving the maximum possible space for the graphic

Critical for tiling small multiples effectively – why base R does this badly



Build a graphic using `grid` — *Initialize device & make layout*

```
# Strings for titles
mainTitle <- "Avoid plot titles, except for small multiples"
yaxisTitle <- "Poverty Reduction"
xaxisTitle <- "Effective Number of Parties"

# Set up layout widths
wd <- unit.c(unit(7,"strheight", yaxisTitle),
             unit(5,"null"))

# Set up layout heights
ht <- unit.c(unit(4,"strheight", mainTitle),
             unit(5,"null"),
             unit(6,"strheight", xaxisTitle))

# Create layout
overlay <- grid.layout(nrow=3,  ncol=2,
                       widths=wd,  heights=ht,
                       respect=TRUE)

# "Push" layout to create initial viewport
pushViewport(viewport(layout=overlay))
```



Diagnostic plot of *revised* layout

Build a graphic using grid

Plot the main title

```
# Push the main title viewport
pushViewport(viewport(layout.pos.col=2,
                      layout.pos.row=1,
                      xscale=c(0,1),
                      yscale=c(0,1),
                      gp=gpar(fontsize=12),
                      name="maintitle",
                      clip="on"
                      ))

# Note the use of a grid primitive
grid.text(mainTitle,
          x=unit(0.5,"npc"), # Why NPC?
          y=unit(0.5,"npc"),
          gp=gpar(fontface="bold")
          )

# Go back up to the top level Viewport
upViewport(1)
```

Avoid plot titles, except for small multiples

Our plot so far...

Build a graphic using `grid` — *Plot the Y-axis title*

```
# Push the Y-axis title viewport
pushViewport(viewport(layout.pos.col=1,
                      layout.pos.row=2,
                      xscale=c(0, 1),
                      yscale=c(0, 1),
                      gp=gpar(fontsize=12),
                      name="ytitle",
                      clip="on"
                      ))

grid.text(yaxisTitle,
          x=unit(0.15, "npc"),
          y=unit(0.5, "npc"),
          rot=90
          )

upViewport(1)
```

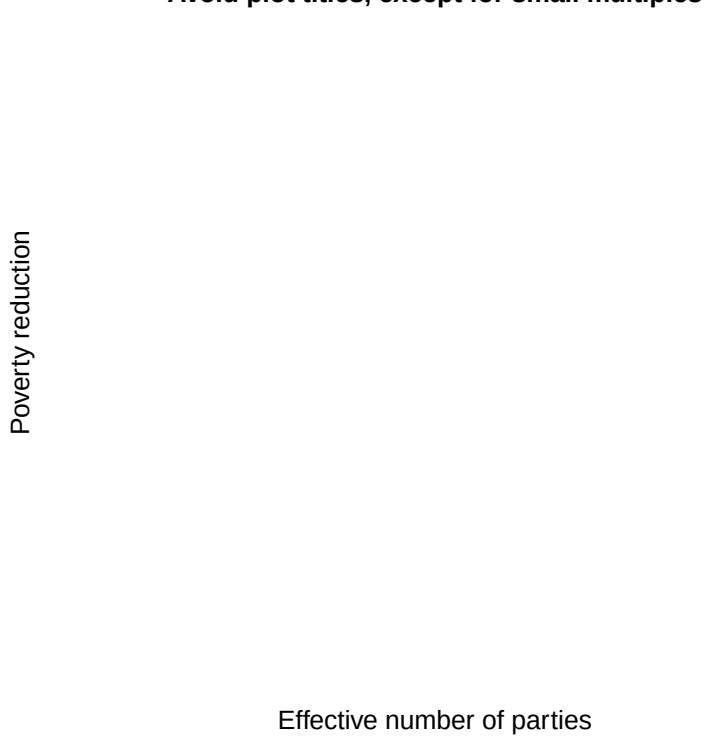
Avoid plot titles, except for small multiples

Poverty reduction

Our plot so far...

Build a graphic using `grid` — *Plot the X-axis title*

```
# Push the X-axis title viewport
pushViewport(viewport(layout.pos.col=2,
                      layout.pos.row=3,
                      xscale=c(0, 1),
                      yscale=c(0, 1),
                      gp=gpar(fontsize=12),
                      name="xtitle",
                      clip="on"
                      ))

grid.text(xaxisTitle,
          x=unit(0.5, "npc"),
          y=unit(0.25, "npc")
          )

upViewport(1)
```



Our plot so far...

Build a graphic using `grid` *Plot the data*

```
# Push the main plot Viewport. Note the scales
pushViewport(viewport(layout.pos.col=2,
                      layout.pos.row=2,
                xscale=c(limits[1], limits[2]),
                yscale=c(limits[3], limits[4]),
                      gp=gpar(fontsize=12),
                      name="mainplot",
                      clip="on"
                      )
             )

# get the fit from the data
fit <- mmest.fit(y=data$povertyReduction,
                 x=log(data$effectiveParties),
                 ci=0.95)
```

Avoid plot titles, except for small multiples

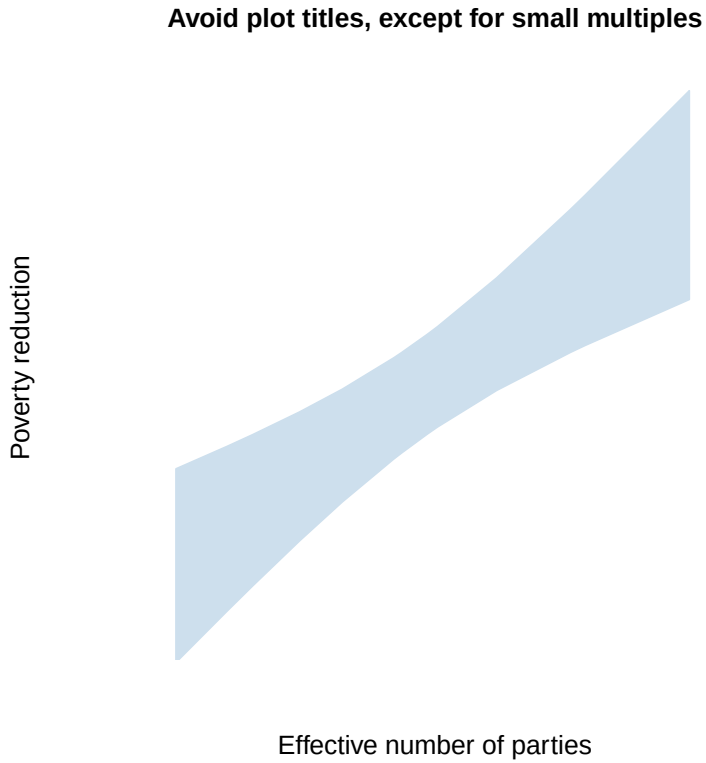
Poverty reduction

Effective number of parties

Our plot so far...

Build a graphic using `grid` *Plot the data*

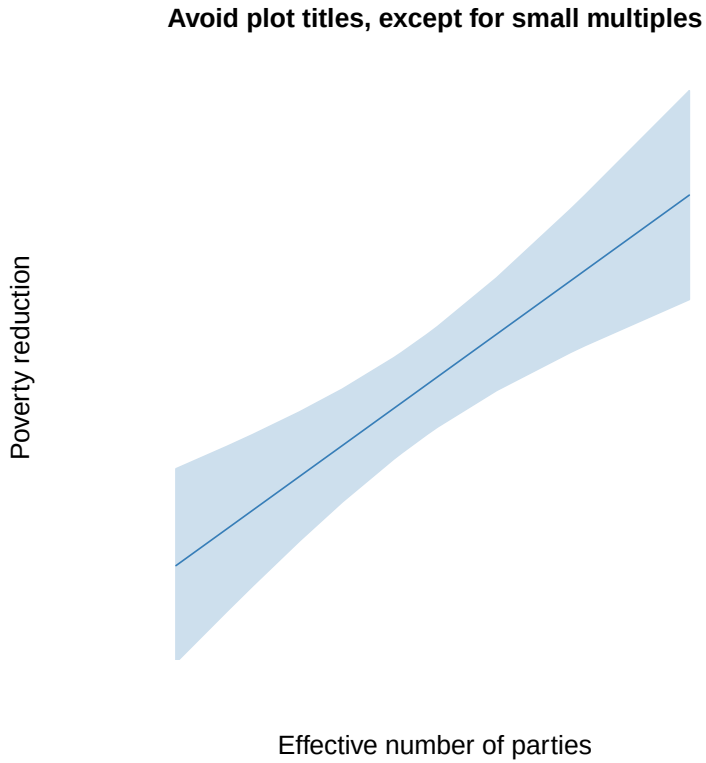
```
# Make the x-coord of a CI polygon
xpoly <- c(fit$x,  rev(fit$x),  fit$x[1])

# Make the y-coord of a CI polygon
ypoly <- c(fit$lower, rev(fit$upper), fit$lower[1])

# Pick a nice blue
niceblue <- brewer.pal(3,"Set1")[2]

# Choose a pastel color for the polygon
pastelblue <- lighten("blue")

# Plot the polygon first
grid.polygon(x=xpoly,
             y=ypoly,
             gp=gpar(col=pastelblue,
                 border=FALSE,
                 fill=pastelblue),
             default.units="native")
```



Our plot so far...

Build a graphic using `grid` *Plot the data*

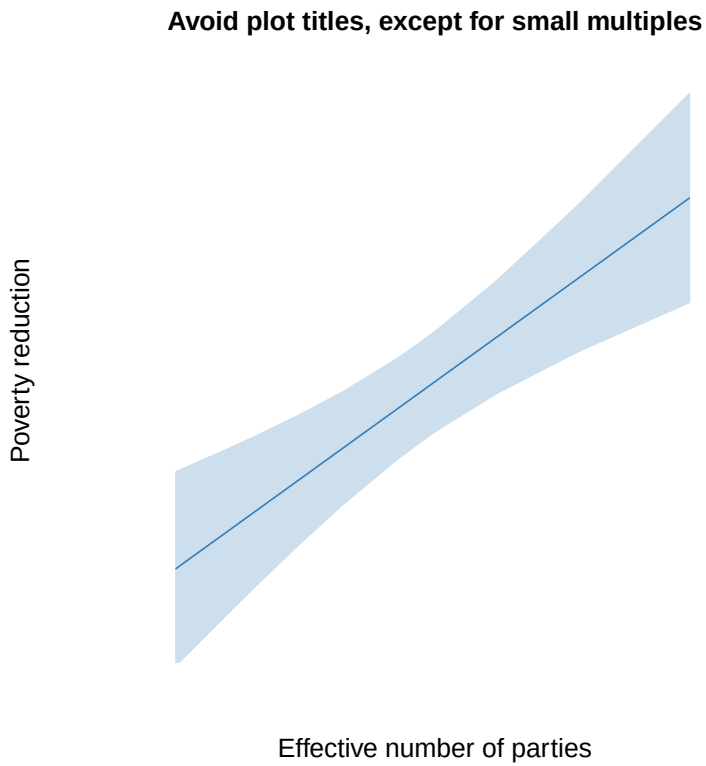
```
# Then plot the line
grid.lines(x=fit$x,
           y=fit$y,
           gp=gpar(lty="solid",
               col=niceblue),
           default.units="native")

# If you want a box around the graph,
# now's the time to plot it
#grid.rect(gp=gpar(linejoin="round"))

# Return to layout level
upViewport(1)
```



Our plot so far...

Build a graphic using `grid` *Add the axes*

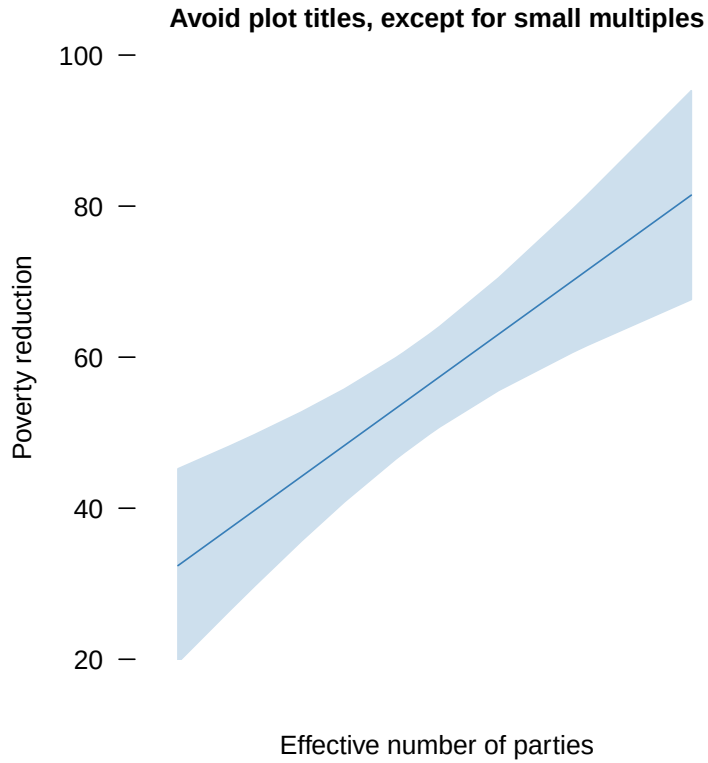
```
# Wait! We haven't made axes!
# Axes plot facing out of the Viewport
pushViewport(viewport(layout.pos.col=2,
                      layout.pos.row=2,
                xscale=c(limits[1], limits[2]),
                yscale=c(limits[3], limits[4]),
                      gp=gpar(fontsize=12),
                      name="mainplot",
                      clip="off"
                      ))

# Make axis as a "grob" (graphical object),
# but don't plot yet
yaxis <- yaxisGrob(at = yat,    # Where to put ticks
             label = TRUE, # Only takes logical values!
             main = TRUE   # Top (TRUE) or bottom (FALSE)
                    )
```



Our plot so far...

Build a graphic using grid — *Add the axes*

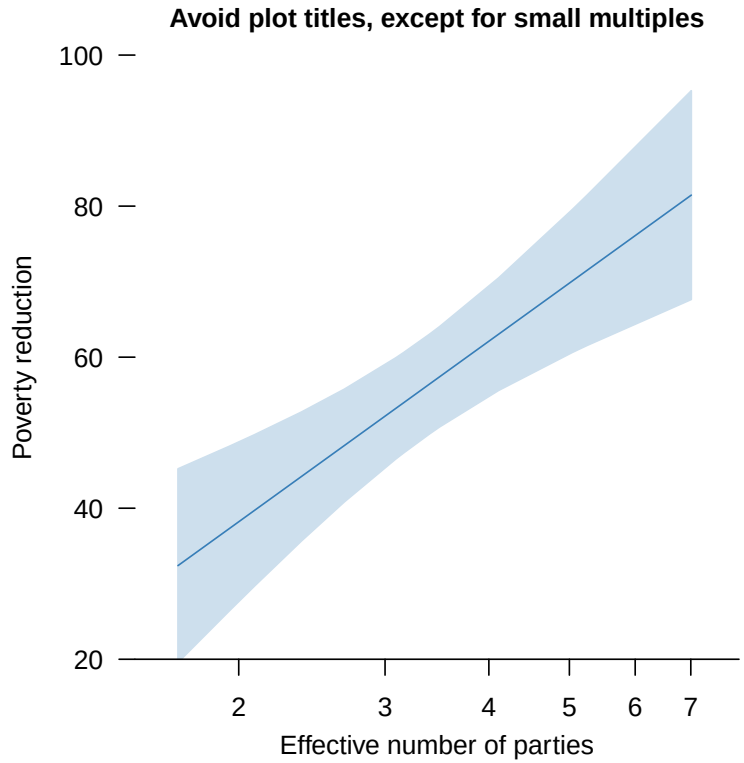
```
# Edit the y-axis to remove the major line
yaxis <- editGrob(yaxis,
                  gPath("major"),
                  major=FALSE
                  )

# Edit the y-axis to remove the major line
yaxis <- removeGrob(yaxis, gPath("major"))

# Draw the y-axis grob
grid.draw(yaxis)
```



Our plot so far...

Build a graphic using `grid` *Add the axes*

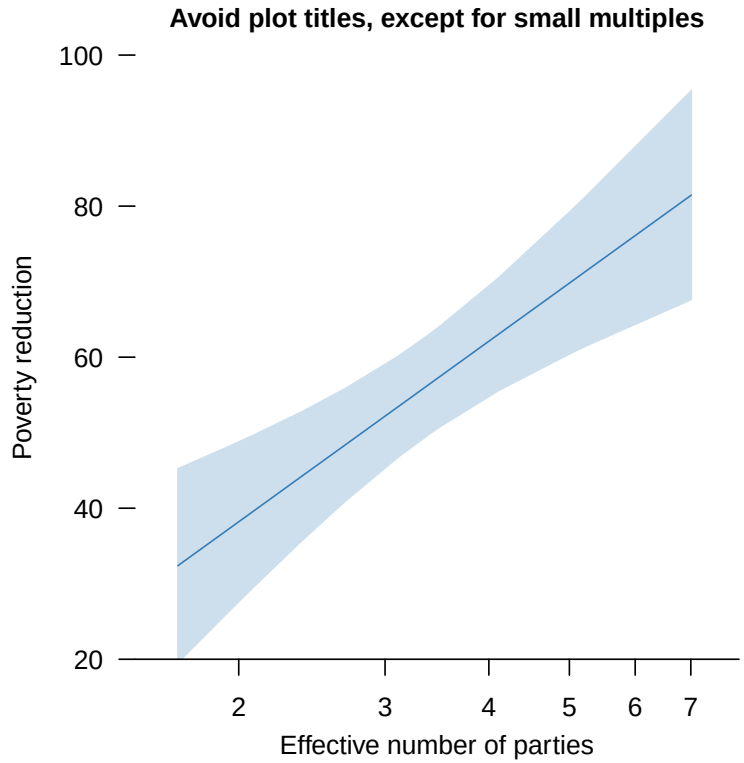
```
# Recall that our tick locations are:
# xat <- c(2, 3, 4, 5, 6, 7)

# Make an x-axis as a "grob"
xaxis <- xaxisGrob(at = log(xat),
          label = TRUE,
          main = TRUE)

# Edit the x-axis to show unlogged units
xaxis <- editGrob(xaxis,
                  gPath("labels"),
                  label = xat)

# Edit the x-axis to fit the plot
xaxis <- editGrob(xaxis,
                  gPath("major"),
                  x=unit(c(0, 1), "npc")
                  )

# Draw the x-axis grob
grid.draw(xaxis)
```



Our plot so far...

Build a graphic using `grid` — *Save the graphic*

```
# Return to layout viewport
upViewport(1)

# Save the graph!
dev.off()
```



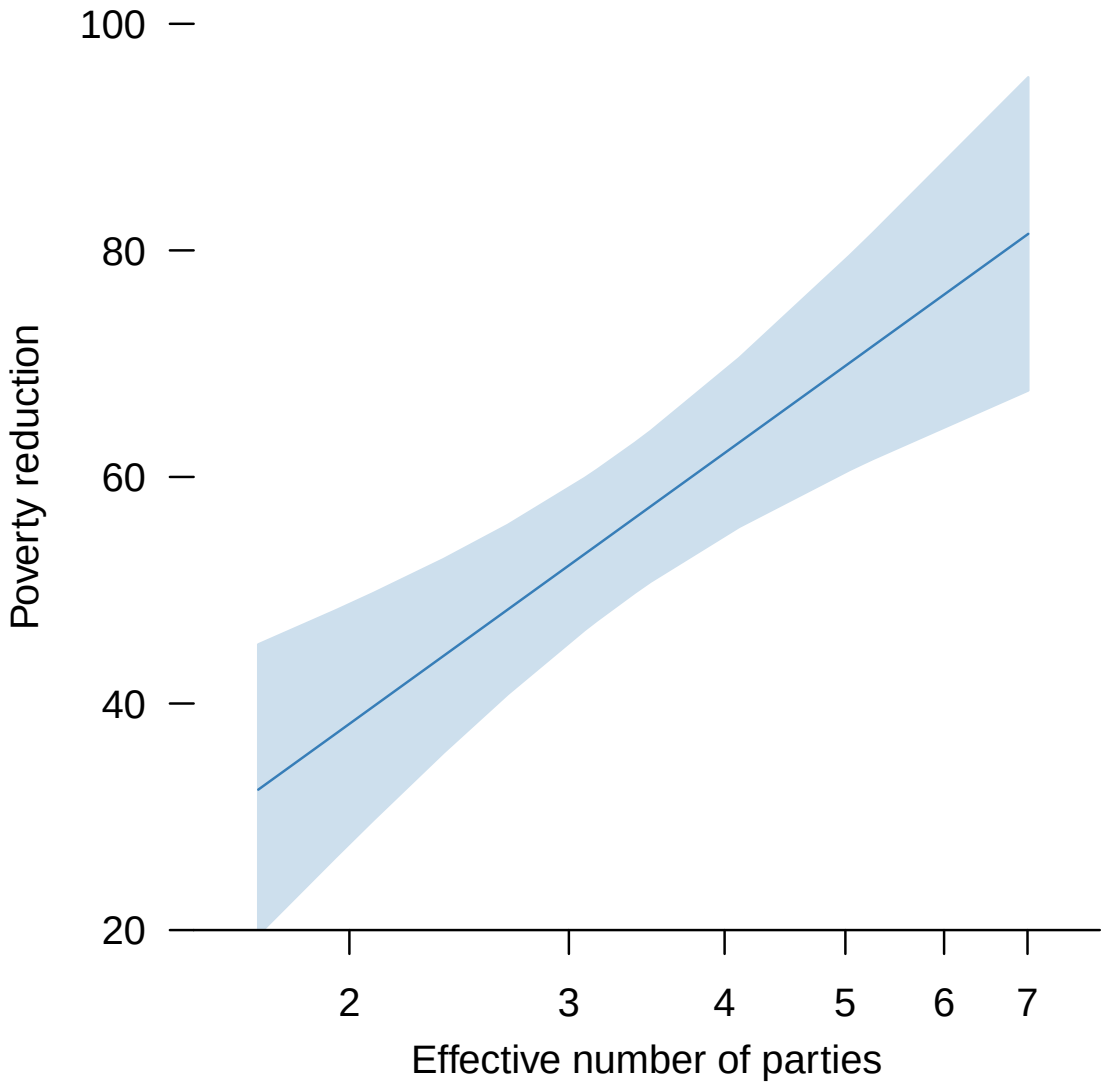
Our plot so far...

`grid` provides detailed control over coordinates, plotting elements, layout, spacing, alignment, etc.

Essential for legible small multiples

Vastly more powerful than base graphics

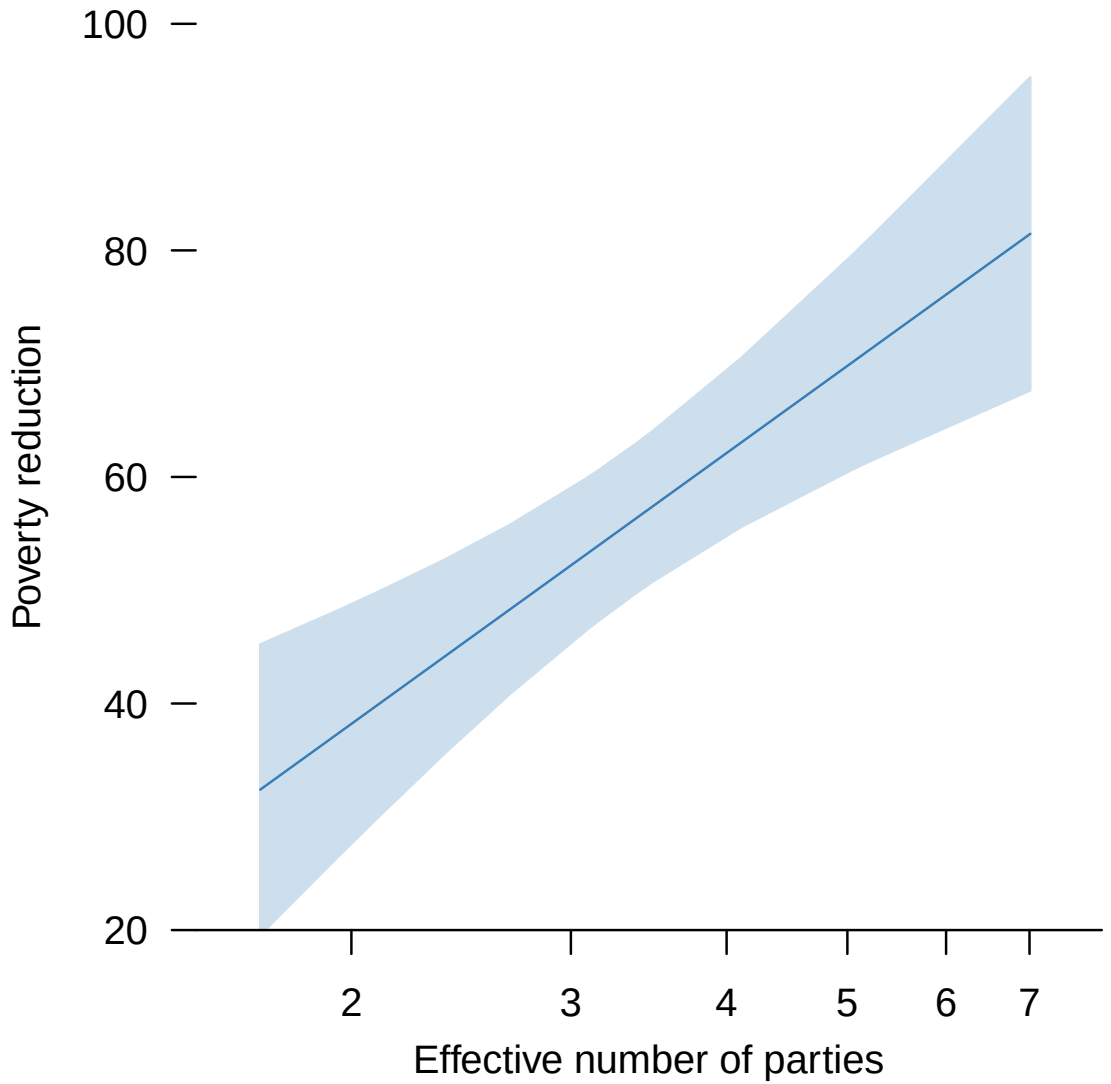
And vastly more time consuming to make



`grid` is the workhouse behind powerful but easier to use graphics packages:

- `lattice`
- `ggplot2`
- `tile`

If you are writing a new graphics *function*, write it using either `grid` primitives or a package based on `grid`



Suppose we wanted to add more features to the plot, such as replacing the y ticks with thin gridlines?

Turns out to be a lot of work! (Code on course site)

My package `tile` provides users *easy* ways to make these sorts of changes, but only because `grid` is in the background doing the lifting