sphinx-test Documentation

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First Steps with Sphinx

This document is meant to give a tutorial-like overview of all common tasks while using Sphinx.

The green arrows designate "more info" links leading to advanced sections about the described task.

1.1 Setting up the documentation sources

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The root directory of a documentation collection is called the *source directory*. This directory also contains the Sphinx configuration file *conf.py*, where you can configure all aspects of how Sphinx reads your sources and builds your documentation.

Sphinx comes with a script called *sphinx-quickstart* that sets up a source directory and creates a default *conf.py* with the most useful configuration values from a few questions it asks you. Just run

```
$ sphinx-quickstart
```

and answer its questions. (Be sure to say yes to the "autodoc" extension.)

```
library(ggplot2)
gplot(wt, mpg, data = mtcars)
```

```
theme_to_header_html <- function(theme){
  css_file = if (file.exists(theme)) theme else {
    system.file("themes", sprintf("%s.css", theme), package = "knitr")
    # css_knitr = system.file('themes', '.knitr.css', package = 'knitr')
    css_knitr <- '~/Desktop/R_Projects/knitr/inst/themes/.knitr.css'
    stringr::str_c(c(
        '<style type="text/css">',
        readLines(css_knitr),
        readLines(css_file),
        '</style>'),
        collapse = '\n')
```

Note: The default role (`content`) has no special meaning by default. You are free to use it for anything you like, e.g. variable names; use the **:confval:'default_role'** config value to set it to a known role.

Another way to highlight code is to doe the following:

```
library(ggplot2)
gplot(wt, mpg, data = mtcars)
theme_to_header_html <- function(theme){
  css_file = if (file.exists(theme)) theme else {
    system.file("themes", sprintf("%s.css", theme), package = "knitr")
    }
    # css_knitr = system.file('themes', '.knitr.css', package = 'knitr')
    css_knitr <- '~/Desktop/R_Projects/knitr/inst/themes/.knitr.css'
    stringr::str_c(c(
        '<style type="text/css">',
        readLines(css_knitr),
        readLines(css_file),
        '</style>'),
        collapse = '\n')
}
```

See also:

This is a simple **seealso** note. Other inline directive may be included (e.g., math α) but not all of them.

$$y = ax^2 + bx + c \tag{1.1}$$

$$f(x) = x^2 + 2xy + y^2 \tag{1.2}$$

We can define our hypothesis as $H_0: \mu = \mu_0, H_a: \mu = \mu_a$

Using Pandoc and knitR with Sphinx

This is a short example illustrating how to use knitr with pandoc to write a single document in markdown and have it rendered in multiple formats, especially pdf and html. For the purposes of illustration, I have chosen two code chunks, one generating a plot and the other generating a table to illustrate the power of pandoc + knitr.

We first need to tell knitr to render the output of code chunks in the gfm format, which pandoc will understand.

The chunk below is a plot chunk. You need to have the package ggplot2 installed for it to work.

```
library(ggplot2)
qplot(wt, mpg, data = mtcars)
```

The second chunk produces a table. You need to have the package ascii installed for this to work.

```
library(ascii)
x <- head(mtcars[, 1:5])
options(asciiType = "pandoc")
ascii(x)</pre>
```

	mpg	cyl	disp	hp	drat
Mazda RX4	21.00	6.00	160.00	110.00	3.90
Mazda RX4 Wag	21.00	6.00	160.00	110.00	3.90
Datsun 710	22.80	4.00	108.00	93.00	3.85
Hornet 4 Drive	21.40	6.00	258.00	110.00	3.08
Hornet Sportabout	18.70	8.00	360.00	175.00	3.15
Valiant	18.10	6.00	225.00	105.00	2.76

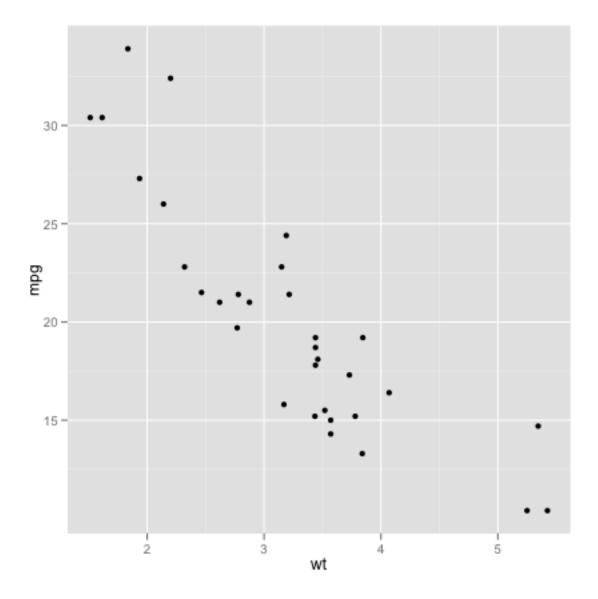


Fig. 2.1: plot of chunk plot-chunk

Statistical Computing Seminars

R is often praised for its graphics. I think R is good at graphics for the same reason it is good at anything else—it's flexible. People just like to customize graphs more than they like to customize statistical models. But as my old boss used to say, "there is no free lunch". R is powerful and flexible but using it takes time. R is, strictly speaking, not a statistical package; it is a language and environment for statistical computing. Finally, a word of advice, you will have a lot more fun if you start playing around with R when you do not need it then if you start when you need to accomplish task X by some deadline.

3.1 Graphics systems in R

Many people have outlined the differents graphics systems in R. What follows is not entirely accurate, but hopefully is a useful way to think.

Traditional ("base") Graphics

Grid Graphics

- lattice: implementation of trellis plots (William Cleveland)
- ggplot2: implementatioon of the Grammar of Graphics (Leland Wilkinson)

Other-useful-but-less-common-or-mainstream stuff

This seminar focuses on traditional graphics. It is part of a series that covers traditional, ggplot2, and lattice.

3.2 Graphs covered

This page covers a few basic graphs:

- Box Plots
- Histograms
- Density Plots
- Plots of Functions and Complex Text
- Scatter Plots
- *Bar Plots*
- *Piecharts*

I put bar plots and piecharts in italics and at the end because I belive they are overused and generally inefficient at communicating data.

3.3 Box Plots

Precise implementations vary, but essentially box plots have a box with the top being the upper quartile, the bottom being the lower quartile, a line for the median somehwere inside the box, and "whiskers" extending the range of the data. R also has the option to add "notches", these are based off the interquartile range (IQR) and are meant to be somewhat like a confidence interval around the medians. We will work with a simulated data set.

```
set.seed(1) # so this is reproducible
## data frame with variable, xn ~N(0, 1)
d <- data.frame(xn = rnorm(1000, mean = 0, sd = 1))
## basic boxplot---looks nice
boxplot(d$xn)
## with the notch
boxplot(d$xn, notch = TRUE)</pre>
```

We can see that there are a few "outliers" (the points beyond the whiskers of the boxplot), but given normal data, it looks very nice. Next we will look at a binomial distribution with 5 trials (like an in class pop quiz, with 5 true/false questions). We also add a variable, attend, that indicates whether students attended the last class.

```
d$attend <- factor(rep(0:1, each = 500), labels = c("absent",
    "present"))
## set seed to make reproducible and add to boxplot
set.seed(1)
## xb (first 500) ~ B(5, .5) and xb (last 500) ~ B(5,
# .8)
d$xb <- c(rbinom(500, 5, 0.5), rbinom(500, 5,
    0.8))
## notched box plot as before
boxplot(d$xb, notch = TRUE)
## we can also use a formula interface to get separate
# plots by attendance
boxplot(xb ~ attend, data = d)
```

3.4 Histograms

Box plots are nice and show at least 5 pieces of information for each variable, but it is not always easy to tell the distribution of a variable from them. To look at distributions, we can try a histogram. Histograms bin data by counting the number of observations falling within a certain range, and present the frequency (or probability).

```
## basic histogram
hist(d$xn)
## increase the number of bins (increases resolution)
hist(d$xn, breaks = 25)
```

Instead of plotting the frequencies, we can plot the probabilities. We will also give it better labels. Greek letters (mu and sigma) can be added by placing them in an **expression**(). This works for titles, axis labels, and text directly added

to plots.

```
hist(d$xn, breaks = 25, prob = TRUE, main = expression(paste("Histogram of ~N(",
    mu, "=0, ", sigma, "=1)")), xlab = "X")
## Now examining the 'quiz' data
hist(d$xb, main = "Pop Quiz Results", xlab = "Number Correct")
```

Looking at the histogram, 290 students got 4/5 questions correct.

3.5 Density plots

Density plots are great to follow histograms because you can actually plot them right on top of a histogram if it is of porbabilities instead of frequencies. Density plots use a smoothing kernel (typically gaussian).

```
## default density plot
plot (density(d$xn))

## plot a histogram and add density plot on top
## setting a smaller bandwidth (.1) than before
## makes it more 'jagged'
hist(d$xn, breaks = 30, prob = TRUE)
lines(density(d$xn, bw = 0.1))

## bandwidth of .4
hist(d$xn, breaks = 30, prob = TRUE)
lines(density(d$xn, bw = 0.4))
```

The bandwidths determine the degree of smoothing being done. Higher bandwidths will be "less true" to the data, but creating smoother density plots. Next we show the quiz data and also demonstrate the use of the **with** function, to avoid having to keep typing the dataset name.

```
with(d, {
    hist(xb, breaks = 30, prob = TRUE, main = "Histogram of Quiz Scores",
        xlab = "Number of Questions Correct")
    lines(density(xb, bw = 0.2), lwd = 2, lty = 1)
    lines(density(xb, bw = 1), lwd = 2, lty = 2)
})
```

With discrete data like this, the smoothing is not very effective as it does little to help us understand the data. The trend is better shown with just the bars. To end our demonstrations of graphs for distributions, we will add a "rug" to the histograms and density plots. The rug is simply a verticle line for every observation—very true to the data, but imposible to see multiple observations with the same value. The rug is nice to get insight about the more rare values in the extremes.

```
with(d, {
    hist(xn, prob = TRUE, main = "Histogram with Density and Rug")
    lines(density(xn, bw = 0.1), lwd = 2, lty = 1)
    lines(density(xn, bw = 0.5), lwd = 2, lty = 2)
    rug(xn)
})
```

3.6 Plots of functions and complex text

Sometimes it is nice to plot a function directly. Particular for instructional purposes. Using the **curve** function in R, you can plot arbitrary functions evaluated over a range of values, as long as the function takes a vector, x, and returns a vector the same length as x. Two common examples in statistics are probability density functions and cumulative distribution functions. When you are plotting a function, it also makes sense to show the formula being plotted. This section shows how to plot functions and how to add complex text (formulae) to a plot.

The builtin function **dnorm** is plotted from -3 to 3. The interesting part is adding the **text**. The first argument is the location on the x axis, the second the location on the y axis. Next is the text to be plotted. In this case, it is an expression. Plotting math in R is similar to using LaTeX. **frac** takes two arguments, the first is the top of the fraction, the second is the bottom. Greek letter names are automatically converted to their symbol form. Finally, the text is made 1.2 times bigger using the **cex** (character expansion) argument.

```
## plot the function from -3 to 3
curve(dnorm, from = -3, to = 3, n = 1000, xlab = "x",
    ylab = expression(P(x)), main = "Normal Probability Density Function")
## add the formula to the plot
text(-2, 0.3, expression(P(x) == paste(frac(1,
    sqrt(2 * pi * sigma^2)), " ", e^{{
    frac(-(x - mu)^2, 2 * sigma^2)
})), cex = 1.2)
```

Here is another example where we first define a function to plot the cumulative percent of normal density of x. This is used in **curve** to create the plot. This formula demonstrates how to add infinity as well as integrals.

```
## define the function
normCDF <- function(x) {
    x <- dnorm(x)
    cumsum(x)/sum(x)
}
## plot the function from -3 to 3
curve(normCDF, from = -3, to = 3, n = 1000, type = "1",
    col = "blue", xlab = "x", ylab = expression(phi(x)),
    main = "Standard Normal Cumulative Distribution Function")
## add the formula to the plot
text(-1.5, 0.7, expression(phi(x) == paste(frac(1,
    sqrt(2 * pi)), " ", integral(e^(-t^2/2) * dt, -infinity,
    x))), cex = 1.2)</pre>
```

3.7 Scatter plots

Scatter plots may be the most common way to plot the relationship between two variables. In R, scatter plots are made using the **plot** function, which has a lot of options. We will only scratch the surface now, but you can find out more from the documentation, **?plot** and **?plot.default**.

```
## what happens if you only plot one variable?
plot(d$xn) # index on the x axis
## create some data correlated with xn
set.seed(2)
d$xnr <- 0.4 * d$xn + rnorm(1000, 0, 1)
plot(x = d$xn, y = d$xnr)</pre>
```

Up until now, we have not really made too many changes to the default settings. Now we will show many different ways to customize graphs. Although these are shown for scatter plots, many of the same arguments can be used for other plotting functions. The pch argument adjusts the p**lotting **ch**character. The **col**our argument adjusts the point colour. **xlim**its controls the lower and upper limit of the X axis (often +/- a twiddle value). **xlab**el sets the label for the X axis. **xaxt controls the style or turns off (n) the X **ax**is **t**icks.

```
plot(x = d$xn, y = d$xnr, pch = 18, col = "blue",
    xlim = c(-4, 4), ylim = c(-2, 2), xlab = "Variable 1",
    ylab = "Variable 2", main = "The Main Plot Title", sub = "A Subtitle",
    xaxt = "n", yaxt = "n")
```

Arguments that accept single values (e.g., **pch**) also often accept vectors that are the same length as the data. We can take advantage of this to adjust the plotting character and colour depending on attendance. The trick is to convert the "absent", "present" data into numbers for the plotting character and colours. There are many ways to accomplish this. **ifelse** is one way. Attend is a factor and its levels are automatically used to select two colours (by default black and then red). We also show how this can be customized in various ways.

3.8 Bar plots

Bar plots, are typically information impoverished. They use a lot of space to present a few values, probably easier to report exactly in a table or in text. Most often, barplots are anchored at 0, and the height of the bar indicates the mean of a variable.

```
## first example
barplot(mean(d$xb), ylab = "Quiz Grade", xlab = "Overall Class")
## mean broken down by attendance
g <- tapply(d$xb, d$attend, FUN = mean)
## now create the bar plot
barplot(g, ylim = c(0, 5))</pre>
```

What do these graphs really tell us? Just that the mean of the absent group is 2.47 and the mean of the present group is 3.958. An equivalent presentation would be:

```
## cex (character expansion) makes the points larger plot(x = g, pch = 18, cex = 2, ylim = c(0, 5))
```

Without all the pointless shading for the bars (remember, only the tops of the bars convey information), the plot looks sparse. What are the alternatives? Well, for one, the boxplots we looked at earlier. Alternately, plot the real points and add the means. Because the outcome is discrete, we use **jitter** to add a some noise to get a better sense of the distribution.

```
with(d, {
    plot(jitter(as.numeric(attend)), xb, xaxt = "n", col = "blue",
        xlab = "Attendance", ylab = "Quiz Score")
    points(x = c(1, 2), y = g, col = "black", pch = 18, cex = 4)
    axis(1, at = c(1, 2), labels = names(g))
})
```

This is probably not the visual display I would choose for these data, but at least you can see not only the means, but that there are people in the absent group who score 5 and people in the present that score 0, etc. Along the way, we used the **points** function to add points (the means) on top of an existing plot and added our own X axis to get the labels we wanted.

3.9 Piecharts

Pie charts are another problematic type of graph. Why? The human perceptual system is lousy at accurately quantifying area.

```
g <- 1:4
names(g) <- letters[1:4]
## How are a, b, c, d growing?
pie(g)
barplot(g)</pre>
```

Our visual systems are able to detect small differences in lengths of lines, and we can quickly see from the bars that the difference between each bar is about equal. Similarly, in the graphs below, it is easy to tell that "b" is twice as high as "a", but difficult to tell "b" has twice the area of "a".

pie(c(a = 2, b = 4))
barplot(c(a = 2, b = 4))

3.10 Summary

We looked at how to make plots in R using **boxplot**, **hist**, **density**, **plot**, **barplot**, **pie**, as wella s how to customize the colours, shapes, and labels. We briefly saw how to set our own axes. The next installment of this series will explore how to really customize plots from tweaking aspects of one plot like adding a legend to including multiple subplots in one bigger plot.

```
Built on: 2012-03-20 Under: R Under development (unstable) (2012-02-22 r58461) With: knitr 0.4
```

Types of smooths

Although points and lines of raw data can be helpful for exploring and understanding data, it can be difficult to tell what the overall trend or patterns are. Adding data summaries can make it much easier to see. When working with two or more variables, rather than raw summaries such as means, we can use conditional means or expected values of one variable based on some model. To demonstrate this, we will use a data set that is built into \mathbf{R} , the '**mtcars**' data. Specifically, we will look at the relationship between miles per gallon (**mpg**) and horsepower (**hp**). in 32 different cars.

head(mtcars)

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

require(ggplot2)
require(methods)
p <- ggplot(mtcars, aes(x = hp, y = mpg)) + geom_point()
print(p)</pre>

Fig. 4.1: plot of chunk mtcars

One thing to notice is that into the ' \mathbf{p} ' object, we saved both the basic plot setup and the request to add points. This saves typing down the road if we know we always want points plotted in our graph. A quick visual of the data indicates the relationship may not be linear. This is confirmed when we look at a linear smooth. The fit is poor at the extremes.

p + stat_smooth(method = "lm", formula = y ~ x, size = 1)

Fig. 4.2: plot of chunk linear-fit

To get a sense of something like the mean miles per gallon at every level of horsepower, we can instead use a locally weighted regression.

```
p + stat_smooth(method = "loess", formula = y ~
x, size = 1)
```

Looking at the fit, it seems a quadratic function might be a good approximation. We can go back to a linear model, but change the formula to include a squared term for x (which is horse power here).

Fig. 4.3: plot of chunk local-wt-reg

p + stat_smooth(method = "lm", formula = y ~ x + $I(x^2)$, size = 1)

Fig. 4.4: plot of chunk quad-fun-approx

We could achieve the same results using orthogonal polynomials, in this case with a second order (quadratic) polynomial. The advantage is that the poly() function can easily fit polynomials of arbitrary degree

p + stat_smooth(method = "lm", formula = y ~ poly(x, 2), size = 1)

Fig. 4.5: plot of chunk polynomial-fit

Another flexible aspect of the smooths is that it can use many different modelling functions as long as they follow some common conventions. This opens up access to many R packages to fit very specialized models. For the sake of demonstration, we will try a generalized additive model (GAM) from the '**mgcv**' package with a smooth on the x predictor variable. First we load the required package, and then show how it is easily used inside our graph.

```
require(mgcv)
p + stat_smooth(method = "gam", formula = y ~
    s(x), size = 1)
```

The GAM with a smooth seems to fit the data better than the straight line did. We could also customize the basis dimension. Arbitrarily, we choose 3.

```
p + stat_smooth(method = "gam", formula = y ~ s(x, k = 3), size = 1)
```

If we wanted to directly compare, we could add multiple smooths and colour them to see which we like best. By default each smooth would include shaded standard errors, which would be messy so we turn them off.

```
p + stat_smooth(method = "lm", formula = y ~ x,
size = 1, se = FALSE, colour = "black") + stat_smooth(method = "lm",
formula = y ~ x + I(x^2), size = 1, se = FALSE, colour = "blue") +
stat_smooth(method = "loess", formula = y ~ x, size = 1,
se = FALSE, colour = "red") + stat_smooth(method = "gam",
formula = y ~ s(x), size = 1, se = FALSE, colour = "green") +
stat_smooth(method = "gam", formula = y ~ s(x, k = 3),
size = 1, se = FALSE, colour = "violet")
```

It is clear in this case that all the models except the strictly linear fit the data similarly. To distinguish which was "best" any further would likely require comparing model fit statistics.

Smooths can also be fit separately by levels of another variable. This allows a sort of examination of 'interactions' in the data.

```
ggplot(mtcars, aes(x = hp, y = mpg, colour = factor(vs))) +
geom_point() + stat_smooth(method = "lm", formula = y ~
x, se = FALSE)
```

```
ggplot(mtcars, aes(x = hp, y = mpg, colour = factor(vs))) +
geom_point() + stat_smooth(aes(group = 1), method = "lm",
formula = y ~ x, se = FALSE)
```

Fig. 4.6: plot of chunk gams

Fig. 4.7: plot of chunk custom-gam

ggplot(mtcars, aes(x = hp, y = mpg)) + geom_point(aes(colour = factor(vs))) +
stat_smooth(method = "lm", formula = y ~ x, se = FALSE)

Fig. 4.9: plot of chunk by-levels

Fig. 4.10: plot of chunk by-levels

Fig. 4.11: plot of chunk by-levels

Summary

Smoothed, conditional summaries are easy to add to plots in ggplot2. This makes it easy to see overall trends and explore visually how different models fit the data. Many of the examples were redundant or clearly a poor choice for this particular data; the purpose was to demonstrate the capabilities of ggplot2 and show what options are available. Each example may be more or less appropriate for exploring a particular set of data.

CHAPTER 6

Indices and tables

- genindex
- modindex
- search