

VISUALISING DATA: INTERACTIVE REPORTS WITH KNITR

National Workshop
Accra, Ghana

Outline

1. Report writing with interactive graphs
2. Application to the HIES data



1. Report writing with interactive graphs

Data analysis reports

- Figures/tables
- Static Word document
- knitr + Markdown → Web page

- What if the data change?
- What if you used the wrong version of the data?

knitr code chunks

- Input to knitr:

We see that this is an intercross with ``r nind(sug)`` individuals. There are ``r nphe(sug)`` phenotypes, and genotype data at ``r totmar(sug)`` markers across the ``r nchr(sug)`` autosomes. The genotype data is quite complete.

```
```${r summary_plot , fig.height=8}  
plot(sug)
```
```

- Output from knitr:

We see that this is an intercross with 163 individuals. There are 6 phenotypes, and genotype data at 93 markers across the 19 autosomes. The genotype data is quite complete.

```
```${r  
plot(sug)
```
```

```
![plot of chunk summary_plot](RmdFigs/summary_plot.png)
```

html

```
<!DOCTYPE html>
<html>
<head>
<meta charset=utf-8"/>
<title>Example html file</title>
</head>

<body>
<h1>Markdown example </h1>
<p>Use a bit of <strong>bold</strong> or <em>italics </em>. Use
backticks to indicate <code>code</code> that will be rendered
in monospace.</p>
<ul>
<li>This is part of a list</li>
<li>another item</li>
</ul>
</body>
</html>
```

Markdown

Markdown example

Use a bit of **bold** or *italics*. Use backticks to indicate `code` that will be rendered in monospace.

- This is part of a list
- another item

Include blocks of code using three backticks:

```
```\n\nx <- rnorm(100)\n\n```\n
```

Or indent four spaces:

```
mean(x)\nsd(x)\n
```

And it's easy to create links, like to

[Markdown](<http://daringfireball.net/projects/markdown/>).



# R Markdown

- R Markdown is a variant of Markdown, developed at RStudio.com
- Markdown + knitr + extras
- A few extra marks
- LATEX equations
- Bundle images into the final html file

# Code chunks, again

```
``{r knitr_options , include=FALSE}
knitr::opts_chunk$set(fig.width=12, fig.height=4,
fig.path='Figs/', warning=FALSE ,
message=FALSE)
set.seed (53079239)
...

Preliminaries
Load the R/qtl package using the `library` function:
``{r load_qtl}
library(qtl)
...

To get help on the read.cross function in R, type the
following:
``{r help , eval=FALSE}
?read.cross
...

```

# Chunk options

- `echo=FALSE` Don't include the code
- `results="hide"` Don't include the output
- `include=FALSE` Don't show code or output
- `eval=FALSE` Don't evaluate the code at all
- `warning=FALSE` Don't show R warnings
- `message=FALSE` Don't show R messages
- `fig.width=#` Width of figure
- `fig.height=#` Height of figure
- `fig.path="Figs/"` Path for figure files

There are [lots of chunk options](#).

# Global chunk options

```
``{r knitr_options , include=FALSE}
knitr::opts_chunk$set(fig.width=12, fig.height=4,
fig.path='Figs/', warning=FALSE ,
message=FALSE , include=FALSE ,
echo=FALSE)
set.seed (53079239)
``

``{r make_plot , fig.width=8, include=TRUE}
x <- rnorm (100)
y <- 2*x + rnorm (100)
plot(x, y)
``
```

- Use global chunk options rather than repeat the same options over and over.
- You can override the global values in specific chunks.

# In-line code

We see that this is an intercross with ``r nind(sug)`` individuals. There are ``r nphe(sug)`` phenotypes, and genotype data at ``r totmar(sug)`` markers across the ``r nchr(sug)`` autosomes. The genotype data is quite complete.

- Each bit of in-line code needs to be within one line; they can't span across lines.
- I'll often precede a paragraph with a code chunk with `include=FALSE`, defining various variables, to simplify the in-line code.
- Never hard-code a result or summary statistic again!

# YAML header

```

title: "knitr/R Markdown example"
author: "Thilo Klein"
date: "2 November 2015"
output: html_document

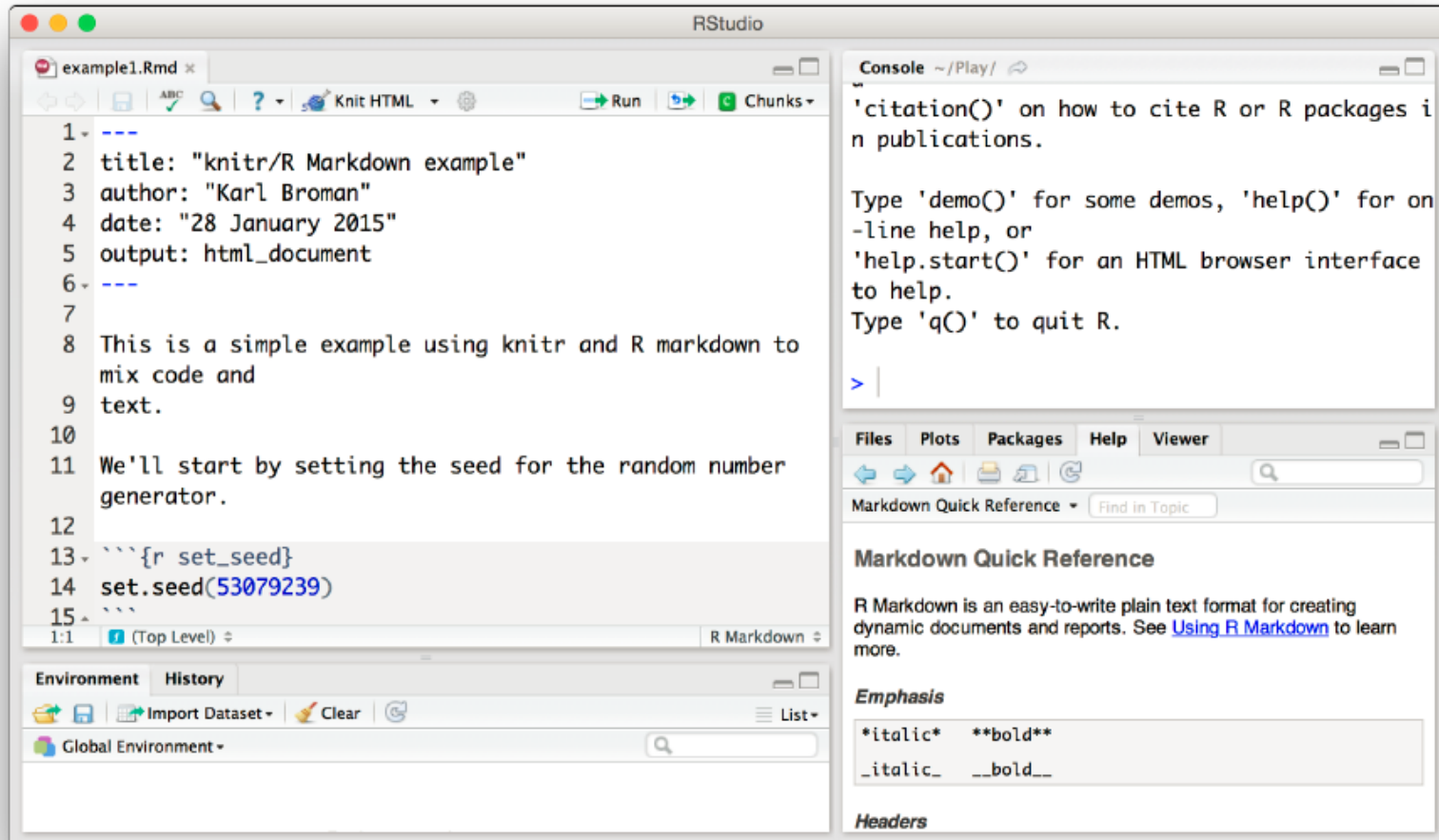
```

```

title: "Another knitr/R Markdown example"
author: "[Thilo Klein](http://klein.uk)"
date: "`r Sys.Date()`"
output: word_document

```

# R Markdown -> html, in RStudio



The screenshot shows the RStudio interface with a file named 'example1.Rmd' open. The editor contains the following R Markdown code:

```
1 ---
2 title: "knitr/R Markdown example"
3 author: "Karl Broman"
4 date: "28 January 2015"
5 output: html_document
6 ---
7
8 This is a simple example using knitr and R markdown to
9 mix code and
10 text.
11 We'll start by setting the seed for the random number
12 generator.
13 ```{r set_seed}
14 set.seed(53079239)
15 ```
```

The console on the right shows the following output:

```
'citation()' on how to cite R or R packages in
publications.

Type 'demo()' for some demos, 'help()' for on-
line help, or
'help.start()' for an HTML browser interface
to help.
Type 'q()' to quit R.

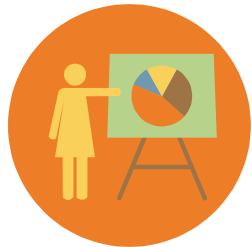
> |
```

The bottom right pane displays the 'Markdown Quick Reference' section, which includes the following content:

**Emphasis**

<i>*italic*</i>	<b>**bold**</b>
<u>_italic_</u>	<u>__bold__</u>

**Headers**



## 2. Application to the HIES data



# A worked example

- check folder: `\project\permanent\4_Report\`