Thesis Template using R and knitr

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Dedication

 ${\rm To}\ {\rm me}$

Abstract

Abstract goes here

Declaration

I declare that..

Acknowledgements

I want to thank...

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Chapter 1

Introduction

1.1 Introduction

I did my thesis in R, and it took me a while to get everything working the way I wanted. The example here is a skeleton that could serve as a starting point to write not only theses, but any kind of document using \LaTeX and R.

The main files have a Rnw extension and are transformed into tex files by using the knitr package. However, anything that doesn't depend on **R** can be written directly in tex files, making it flexible.

I didn't put too much effort into the layout shown here, it is only meant to serve as a starting point with some examples. Other templates can also be used.

 $^{^{1} \}verb|http://yihui.name/knitr/|$

Chapter 2

Organization

2.1 Compilation Scripts

There are two main files used for compilation: compile-linux.sh for Linux users, and compile-windows.bat for Windows users. They are both used in the same manner, so in the examples below I will simply refer to the scripts as compile.

The first thing that is needed is of course LATEX. There are many resources available on how to install it, so I will not dwell on that.

The next thing is **R** itself. Again I will not go into too much detail, just make sure that the Rscript executable is available in your path. If you have code that will use parallel computation, the default **R** package that is used is doParallel, although this can be modified in the file Thesis.R (see Section 2.2).

If you simply double click on the compile script, it will run pdflatex, bibtex and pdflatex twice (for citations to work). This will apply any changes made to any tex file, but will **not** detect any changes made in Rnw files, regardless of whether it's **R** code or not. Running the scripts from the command line with no arguments is equivalent.

The other option is to run the scripts from the command line followed by a single argument, either TRUE or FALSE; this will *knit* the main Thesis.Rnw file and apply all changes made, including R code. If you use FALSE, everything is done sequentially. With TRUE, a number of parallel workers equal to the number of detected CPU cores are registered first, so that R code can run in parallel. This is only useful if your code is specifically made to run in parallel (e.g. with the foreach package).

2.2 Main Files

If the compile scripts are called to update the R code, they basically call Rscript on Thesis.R. The latter registers the parallel workers if necessary and

calls knitr on Thesis.Rnw, which creates Thesis.tex. It also loads **R** utilities on each worker (see Section 2.2.1).

The master file is Thesis.Rnw, which contains the main tex layout as well as the defaults for knitr (more on that in Section 2.3).

2.2.1 Utilities

By "utilities" I mean the common **R** functions and libraries that will be used. I have made a basic distinction between cached and uncached utilities. This is related to **knitr**'s cache function, so you should definitely read about that first if you don't know how it works. Uncached utilities should be the ones that will be used by **knitr** itself or in the chunk options.

The files are located in the Utils folder and have obvious names...

2.3 Default Functionality

2.3.1 Knitr Cache

You can see the defaults for knitr in Thesis.Rnw. By default, all chunks are cached and hidden from the output (with echo = FALSE). Additionally, auto-dependency detection is turned on by default; this has worked well for me.

Uncached utilities are always loaded along with knitr's defaults. The rest of the used libraries and functions can be included in the cached utilities file.

Note that, if I'm not mistaken, the paths of the files are also influence the cache. So if you download these files and change folder names, you might have to re-run everything the first time you compile.

2.3.2 MD5 Hashes

I've included a function called my_md5sum that I've used in some chunk options. Since you can add any non-NULL value to chunk options in order to create its cache (again, read knitr's information on cache if you haven't), you can use MD5 hashes to create chunks that depend on specific files, so that if the files change, the chunk will be updated automatically. There is an example of this in the source code for Section 3.1.

It is a semi-custom function because the default md5sum doesn't throw an error if it doesn't find the file, in which case you might not notice if you're actually caching a valid file or not.

2.3.3 Workspace Cleaning

I also include a function called **clean_workspace** that removes everything except the uncached utilities. It can optionally reload cached utilities and ignore variables if desired.

I run this at the end of each child Rnw file. I do this because I'm not sure how knitr's auto-dependency detection works (my bad), and I wanted each child file

to be as independent as possible so that things wouldn't break in one section if I changed something from the previous section. Check the source code for the examples, and note that this cleaning is always uncached.

2.3.4 Dynamic Loading of Utilities

I was using several libraries, and it was annoying to wait for all of them to load if all I wanted to do was update content without changing any R code (recall that changes made to Rnw files won't be detected unless you re-knit everything). My solution was to use a knitr hook (see knitr's website).

The hook is a function called utils_hook, located in the uncached utilities file. If you see the defaults in Thesis.Rnw, you'll notice every chunk will run the hook by default, which loads cached utilities before actually running the chunk. Since the hooks are only executed if the chunk needs to be updated (i.e. its cache was invalidated or non-existent), utilities are only loaded whenever I actually have to re-run R code. Each chunk that needs to be updated will re-load everything, of course, but that's unimportant (e.g. re-loading a library has no effect).

Notice that chunks that are manually uncached should set the load.utils hook option to NULL to avoid loading things unnecessarily. See the source code for workspace cleaning chunks for examples.

2.3.5 Tables

I used the xtable package to create tables from data frames. I created a (cached) function called make_table that has some defaults so that I didn't need to write everything every time. You can see the defaults in the source code and note that any default can be overridden via the ellipsis.

The results chunk option should be set to "asis" so that everything is detected correctly. See the source code for Section 3.3.

2.4 Considerations

2.4.1 Random Seeds

If you're doing things that depend on randomness, you probably care about reproducibility. Some of you might now that knitr can be configured to detect changes in random seed to update chunks, but this doesn't play very well with its cache functionality, so I ended up specifying a random seed for **each** chunk that required it.

2.4.2 File Paths

Be careful with paths, for example you should specify the correct figure path in both knitr and LATEX options; see the source code for Section 3.2.

Additionally, you should know that each child Rnw file is run with its own directory as the working directory. However, the paths you give to knitr or the ones used in chunk options are always with respect to the root directory, i.e. where Thesis.Rnw is located. See the source code for Section 3.1 for an example.

2.4.3 Chunk Names

I think all chunk names need to be unique.

Chapter 3

Examples

3.1 Basics

The caret package is one that can take of parallel execution. Below, I train a random forest on a sample dataset [Lichman(2013)].

Using a random forest with the Chess dataset and OOB error estimate, best value of mtry was 13 with an accuracy of 0.995.

Try changing the seed (to invalidate the chunk's cache) and compiling the thesis with/without parallel support to see the difference in run time.

If you don't specify a seed, you might lose reproducibility. For example, the code below might give a different result each time you recompile if you add code before it and *after* the cache for the previous chunk has been created. This is because the previous chunk will no longer set the seed unless its cache is invalidated and the chunk is thus updated.

```
rnorm(1)
## [1] 0.1699193
```

3.2 Figures

Plots can be created directly in R and the results are added automatically to the tex file. See Fig. 3.1 for an example of a single plot.

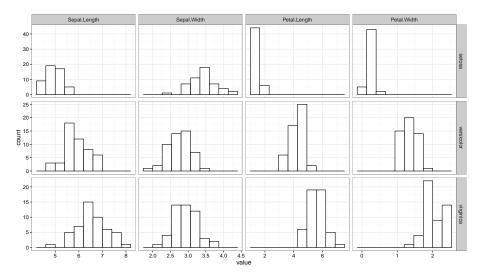


Fig. 3.1: Histograms for the iris dataset. Look at the list of figures to see difference between short and long captions.

You can create several plots per chunk and have them in the same main figure. See Fig. 3.2 for an example of two plots: Fig. 3.2a and Fig. 3.2b.

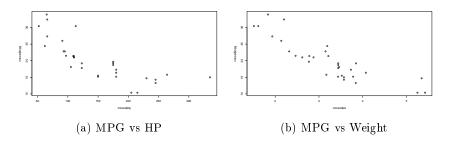


Fig. 3.2: Plots using mtcars dataset.

3.3 Tables

Tables can also be created in **R** and inserted automatically. Check Table 3.1. Something Useful I found was that you can use the LATEX package makecell to insert linebreaks in table headers. See the source code for Table 3.2.

Table 3.1: First rows of the CO2 dataset. Look at the list of tables to see the difference between short and long table caption.

	Plant	Туре	${ m Treatment}$	conc	uptake
1	Qn1	\mathbf{Quebec}	nonchilled	95.00	16.00
2	Qn1	$_{ m Quebec}$	$\operatorname{nonchilled}$	175.00	30.40
3	Qn1	Quebec	$\operatorname{nonchilled}$	250.00	34.80
4	Qn1	Quebec	$\operatorname{nonchilled}$	350.00	37.20
5	Qn1	Quebec	$\operatorname{nonchilled}$	500.00	35.30
6	Qn1	$_{ m Quebec}$	$\operatorname{nonchilled}$	675.00	39.20

Table 3.2: Same table as before but with linebreaks.

Plant Something	Type Yes	Treatment No	conc whatever	uptake ok
Qn1	Quebec	${ m nonchilled}$	95.00	16.00
Qn1	$_{ m Quebec}$	${ m nonchilled}$	175.00	30.40
Qn1	Quebec	$\operatorname{nonchilled}$	250.00	34.80
Qn1	$_{ m Quebec}$	${ m nonchilled}$	350.00	37.20
Qn1	$_{ m Quebec}$	$\operatorname{nonchilled}$	500.00	35.30
Qn1	$\overline{\text{Quebec}}$	${\rm nonchilled}$	675.00	39.20

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Appendix A

First Appendix

In case it's needed.