

Using Rmarkdown and Github for reproducible and collaborative research

Jinliang Yang

November 5, 2014

Setup your project

- ▶ using **github** do the version control
- ▶ using **packrat** do the R package dependency management
- ▶ using **ProjectTemplate** to layout the directories

```
#install.packages('ProjectTemplate')  
library('ProjectTemplate')  
create.project('temp')  
system("mv temp/* .")  
system("rm -r temp/")
```

Or simply just copy your directory system everything here!

Setup your project

- project/
 - cache/
 - config/
 - data/
 - diagnostics/
 - 1.R
 - doc/
 - graphs/
 - lib/
 - helpers.R
 - logs/
 - munge/
 - profiling/
 - 1.R
 - reports/
 - src/
 - tests/
 - 1.R
 - README
 - TODO

Figure: Minor allele frequency and missing rate of the about 14 million SNR on founder lines

R Markdown

This is an R Markdown presentation. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document.

Slide with Bullets

- ▶ Bullet 1
- ▶ Bullet 2
- ▶ Bullet 3

Slide with R Code and Output

```
summary(cars)
```

##	speed	dist
##	Min. : 4.0	Min. : 2.00
##	1st Qu.:12.0	1st Qu.: 26.00
##	Median :15.0	Median : 36.00
##	Mean :15.4	Mean : 42.98
##	3rd Qu.:19.0	3rd Qu.: 56.00
##	Max. :25.0	Max. :120.00

Slide with Plot

