

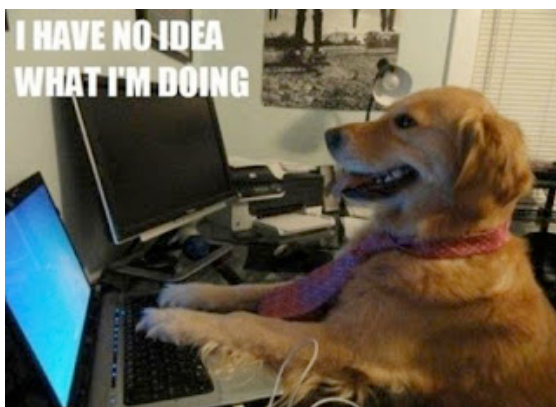
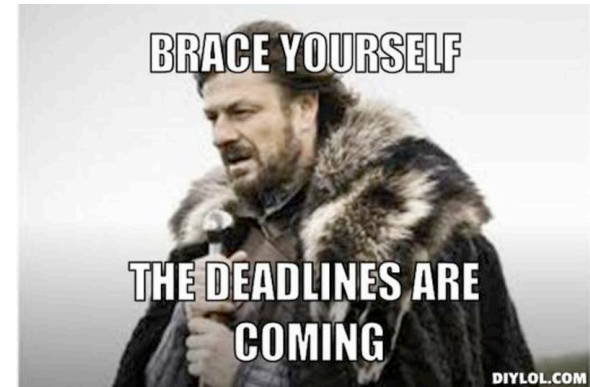
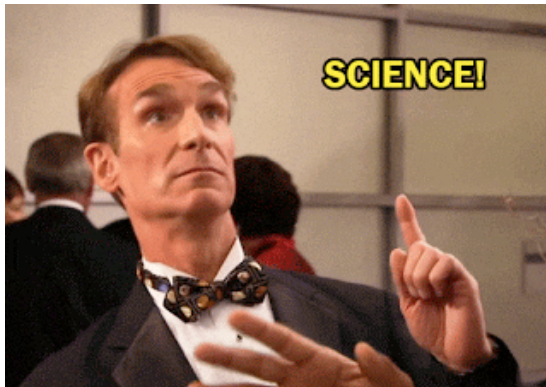
Email me your Methods homework

Thank you, Amanda Kedaigle & Prof. Ernest Fraenkel !

M2D6: Intro to R Clustering

04/04/2017

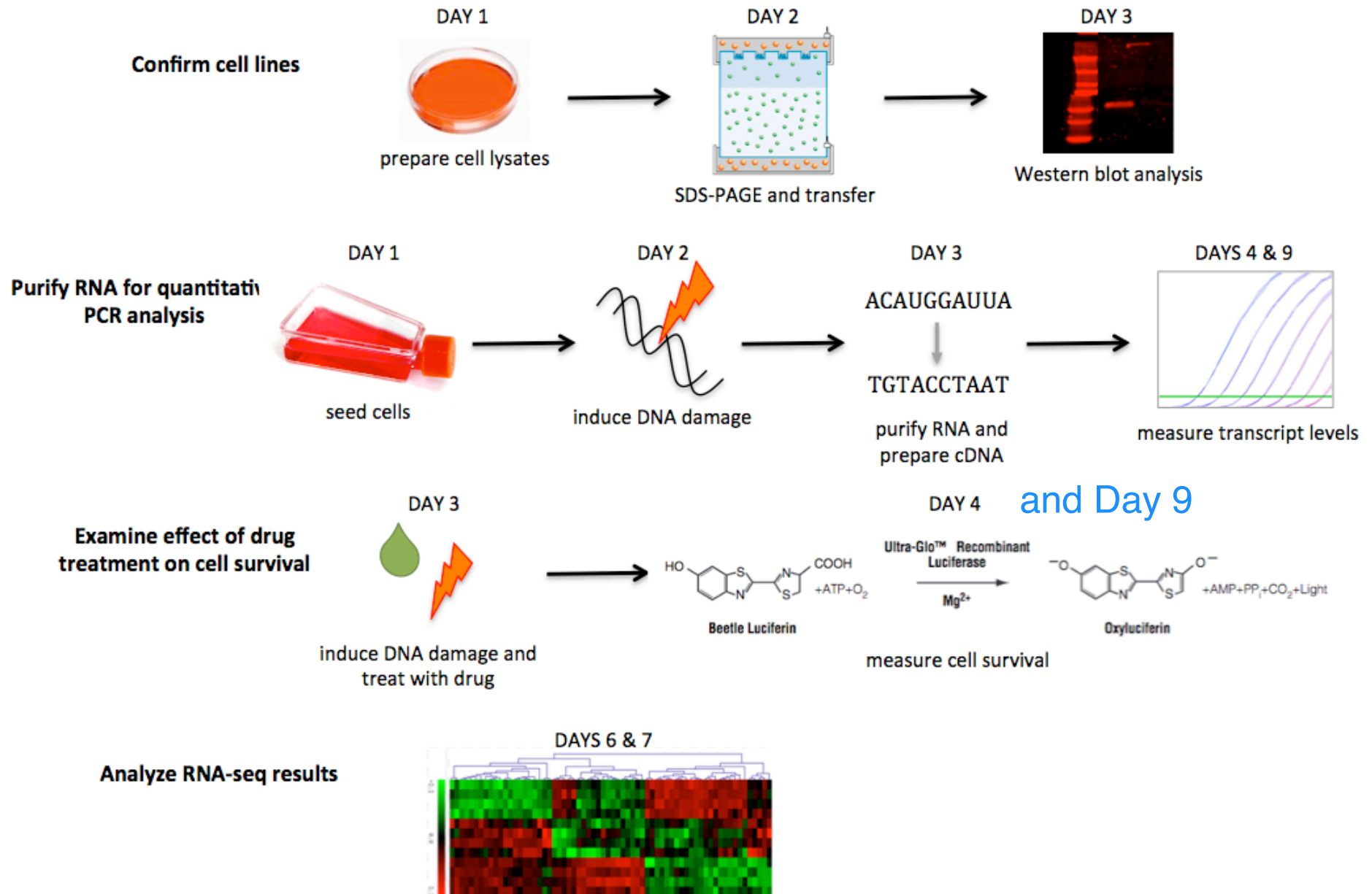




I enjoyed reading
your blog posts!

Grades and feedback on M1 Data Summary
revision will be email at the end of this week.

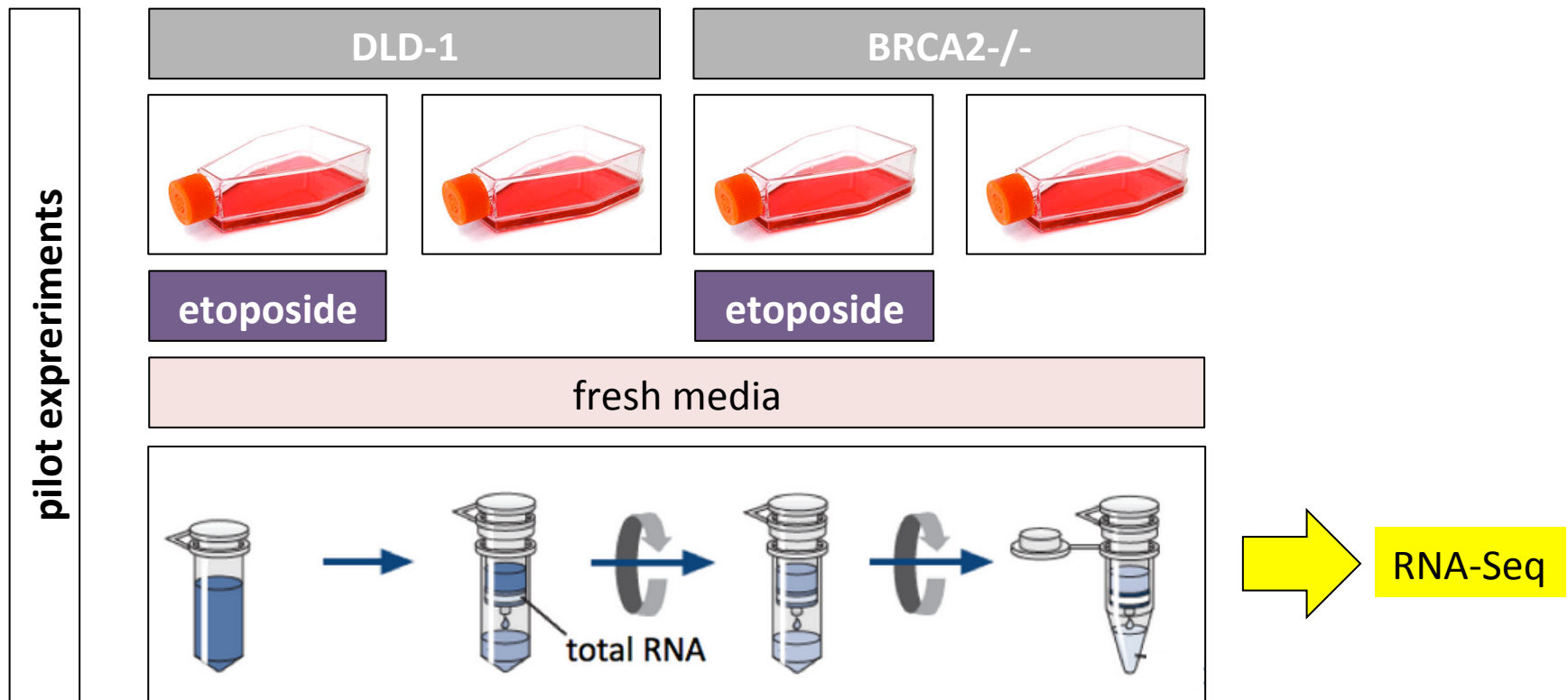
M2: Experimental overview





Let's analyze RNA-Seq data

- With qPCR, you looked at p21 transcript levels (norm. to GAPDH)
- With RNA-Seq, we'll peek into the entire transcriptome



First things first: programming language R

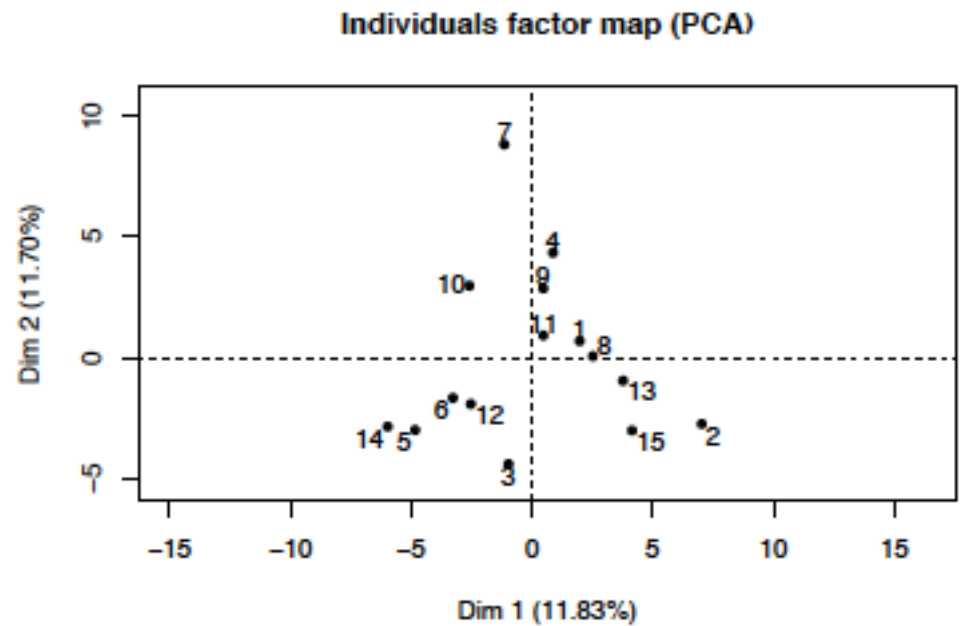
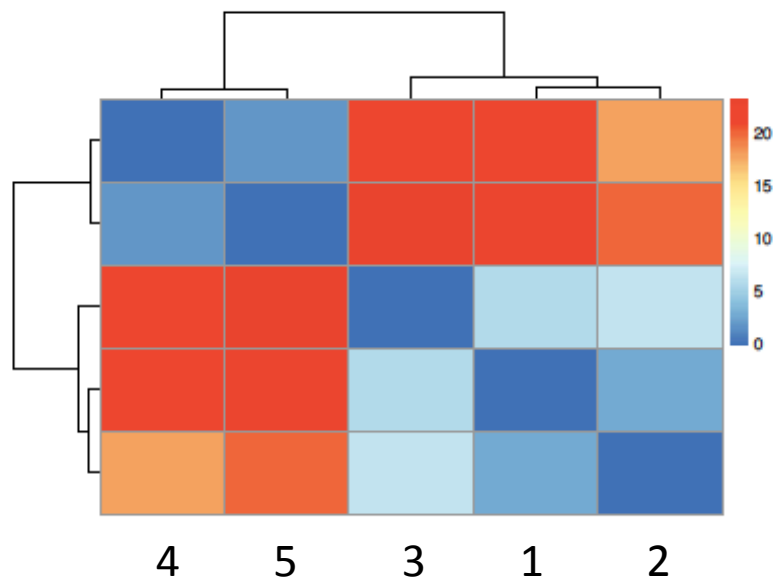
The image shows the RStudio application window with four main panels highlighted by blue boxes and labeled with white text:

- editor**: The top-left panel showing an R Markdown file named `20.109_RNAseq_Analysis_Day6.Rmd`. The code includes a YAML header with title, author, date, and output, followed by a Knitr chunk setup and an introduction to R.
- workspace**: The top-right panel showing the **Environment** tab with the **Global Environment**. It displays a variable `b` of type `num [1:3]` with values `3 4 5`.
- console**: The bottom-left panel showing the R console output. It displays the download of the `ph heatmap` package (1.0.8.tgz) and the execution of the following R code:

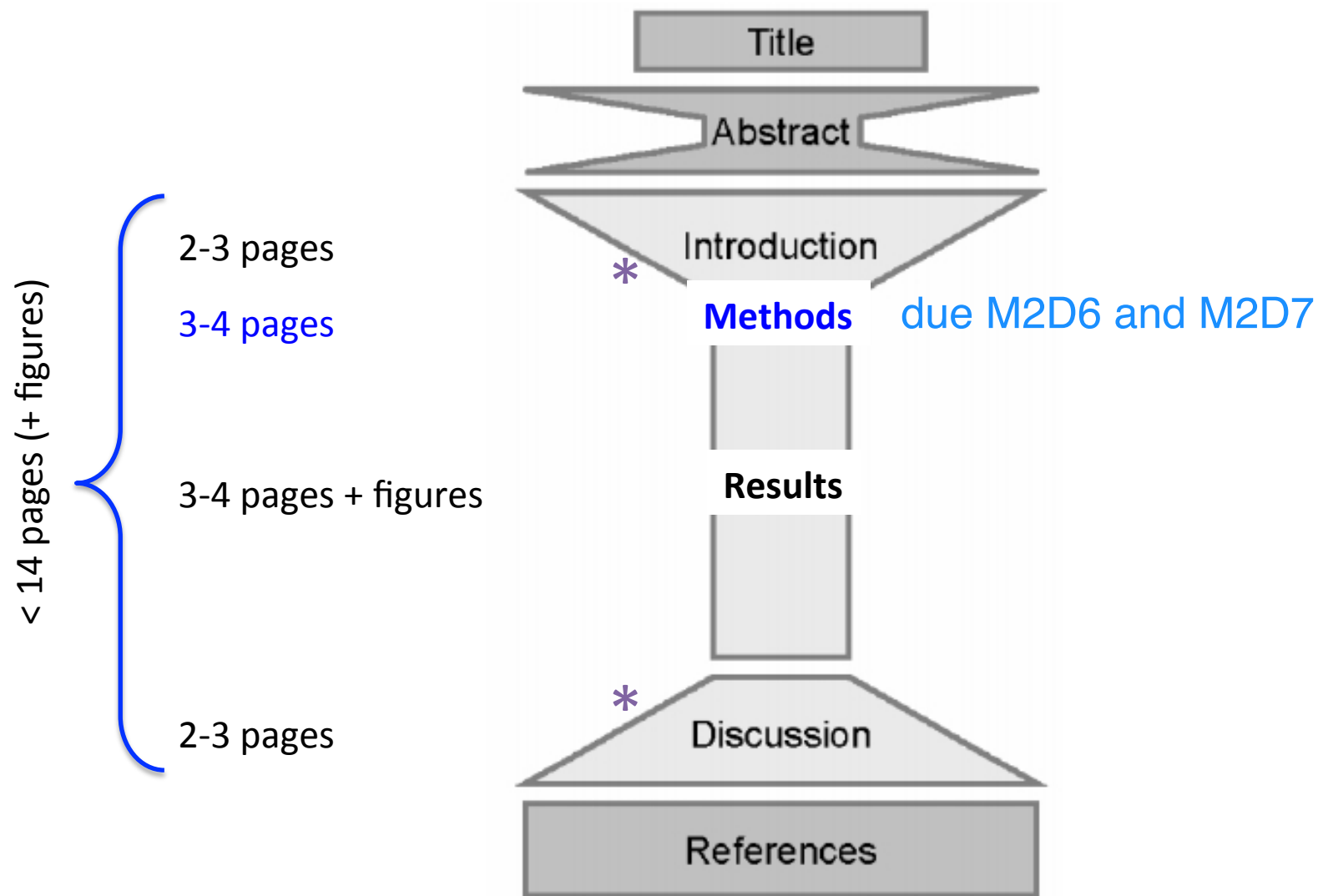
```
> library("ph heatmap", lib.loc = "~/Library/R/3.3/library")
> b = c(3, 4, 5)
> |
```
- packages, plots, help**: The bottom-right panel showing the **Packages** tab. It lists installed and available packages with their descriptions and versions. The `ph heatmap` package is checked and highlighted.

Name	Description	Version
<input type="checkbox"/> memoise	Memoisation of Functions	1.0.0
<input type="checkbox"/> mime	Map File Names to MIME Types	0.5
<input type="checkbox"/> munsell	Utilities for Using Munsell Colours	0.4.3
<input type="checkbox"/> org.Hs.eg.db	Genome wide annotation for human	3.4.0
<input checked="" type="checkbox"/> ph heatmap	Pretty Heatmaps	1.0.8
<input type="checkbox"/> plogr	The 'plogr' C++ Logging Library	0.1-1
<input type="checkbox"/> plyr	Tools for Splitting, Applying and Combining Data	1.8.4
<input type="checkbox"/> RColorBrewer	ColorBrewer Palettes	1.1-2
<input type="checkbox"/> Rcpp	Seamless R and C++ Integration	0.12.10
<input type="checkbox"/> RcppArmadillo	'Rcpp' integration for the 'Armadillo' Template Linear Algebra library	0.7.700.0
<input type="checkbox"/> RCurl	General Network (HTTP/FTP/...) Client Interface for R	1.95-4.8
<input type="checkbox"/> reshape2	Flexibly Reshape Data: A Reboot of the Reshape Package	1.4.2
<input type="checkbox"/> RSQLite	'SQLite' Interface for R	1.1-2
<input type="checkbox"/> S4Vectors	S4 implementation of vectors and	0.12.2

First things first: clustering



M2 research article is due Saturday, April 22



What goes into the Introduction?

- General background: motivation
- Specific background: focused context
 - minimal essential information
 - define all key terms
- Knowledge gap, central question
- [State hypothesis](#)
- Preview of results [Here we show](#)
- ... and of implications
- Don't forget references



The meat of your paper

- Figures and captions
 - Decide on these first
 - Use subpanels
 - Text: limited on figure, explicit in caption
 - reasonable size
 - descriptive title
 - caption purely descriptive of image
 - intro sentence in caption
- Results
 - title + topic sentence
 - What you did: experiments and expectations, including controls
 - What you found:
 - transition

What goes into the Discussion?

- Recapitulate the results
- Interpret
- Put in context: how does this fit with other studies?
- Highlight significance: how might this impact this/other field?
- Discuss controversial or surprising results
- Describes caveats and suggest remedy
- Conjecture (one layer only!) implications
- Propose future work, identify new questions that arise
- Follow same order as in Figures/Results
- Make sure you come back to big picture introduced in intro
- Don't overreach / overpromise!