Markdown file structure

```
---
title: "genome569"
output: html_document
---

## Course description
Programming skills and software tools for building
automated bioinformatics pipelines and computational
biology analyses. Emphasis on UNIX tools and R libraries
for distilling raw sequencing data into interpretable
results.  This course is aimed at students familiar with
UNIX and with some programming experience in python, R, or
C/C++.

## Instructional staff
* [Cole Trapnell](http://cole-trapnell-lab.github.io/)
* Teaching assistant: April Lo
```

Bulleted list. Enumerated lists also easy.