

Clone the “hello world” repo

Click on this link: <https://classroom.github.com/a/qXxea7q1>

```
$ git clone git@github.com:colettrapnell-teaching/hello-world-<your_github_id>.git
```

```
Cloning into 'hello-world'...
Warning: Permanently added the RSA host key for IP address '192.30.255.112' to the list of known hosts.
remote: Enumerating objects: 3, done.
remote: Counting objects: 100% (3/3), done.
remote: Total 3 (delta 0), reused 0 (delta 0), pack-reused 0
Receiving objects: 100% (3/3), done.
```



README.md

1 README.md x xxx.txt Untitled-1

Volumes > GoogleDrive > My Drive > Teaching > GENOME5XX > website > README.md > ...

```
1 <meta charset="utf-8"/>
2 <script type="text/x-mathjax-config">
3   MathJax.Hub.Config({
4     // Don't process any delimiters, only <script type="math/tex">
5     // tags generated by kramdown from $$...$$ in source.
6     // (Could also avoid loading tex preprocessor – only need
7     // tex input jax – but not worth the trouble.)
8     tex2jax: {
9       inlineMath: [],
10      displayMath: [],
11    }
12  });
13 </script>
14 <script src="https://cdnjs.cloudflare.com/ajax/libs/mathjax/2.7.0/MathJax.js?
15   config=TeX-AMS_HTML"></script>
16
17 ## Course description
18 Programming skills and software tools for building automated bioinformatics pipelines and
19 computational biology analyses. Emphasis on UNIX tools and R libraries for distilling raw
20 sequencing data into interpretable results. This course is aimed at students familiar with
21 UNIX and with some programming experience in python, R, or C/C++.
```

Ln 14, Col 108 Spaces: 2 UTF-8 LF Markdown