

Sharing Scripts & Data

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Overview

1 Goals

2 Gitting

- Fetch, Commit, Push & Pull

3 Data

- Commandline Tools
- SRA

Today's Goals

- Set up a group git

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 - `wget`, `curl`, `sratoolkit`

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- To decide who gets which paper we'll do another guessing game:

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- Or the buttons on the SourceTree or github

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- e.g. - `/work/cc216/490S/<your folder>`

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- We’ll talk about how to get data from each of these places

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- curl
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- Each is useful in different situations

curl

- Downloads a given url site

```
Usage:  curl [options...] <url>
```

- Options include username & password
- Useful for sftp servers
- An example:

```
curl -o ESPNfrontpage.html http://www.espn.com/
```

- saved as ESPNfrontpage.html

wget

- Downloads a given url site

Usage: `wget [OPTION]... [URL]...`

- Same options as curl
- An example:

```
wget http://www.bzip.org/1.0.6/bzip2-1.0.6.tar.gz
```

- Often used for downloading software (you'll see later...)

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- Use SRA Toolkit to access the files

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- You should be able to follow the paper’s methodology to separate the data into samples (if it wasn’t kept that way on SRA)

- So, how do we download the data?

- How do we get the software onto the cluster?

- How do we use this file?

SRA Toolkit

- How do we use the toolkit?
- What is the toolkit (file, command, etc)?

Group Work

Group steps

- 1 Pick a group ID/Name
 - 2 Make a group folder with that name within:
 - 3 `duke-bio490s/projects/<group name here>`
- This is where you'll keep scripts to download, trim, etc data

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 - Once your output looks correct THEN submit to the cluster
 - This will save a lot of headaches and waiting
 - And most importantly:
DON'T write data to the git repo

The End