Command Line Options for Transferring Files

Because MacOS Catalina is too secure

Secure File Transfer Protocol (SFTP)

This logs you into the server, similarly to `ssh` so you can look around and navigate the filesystem, and allows to upload and download files. In addition to what I show below, there's a helpful list of commands at the link https://www.uppmax.uu.se/support/user-guides/basic-sftp-commands/

Logging In

To get started, log in to the server using `sftp` instead of `ssh`

```
### log in using sftp instead of ssh
sftp kkeith@10.1.105.13
```

Downloading

To transfer stuff from your local (personal) computer to the server, use the command `get`. This is what you'll primarily need to do for the rest of the experience.

```
### EXAMPLE: tranfer stuff from the server to your machine
# look around on the server
sftp> ls
data            rnaseq_practice
# go to the folder you want to grab stuff from
sftp> cd rnaseq_practice/data/fastqc
sftp> ls
ls
dac1_chr21_R1_fastqc.html  dac1_chr21_R1_fastqc.zip   dac1_chr21_R2_fastq
c.html  dac1_chr21_R2_fastqc.zip
dac2_chr21_R1_fastqc.html  dac2_chr21_R1_fastqc.zip   dac2_chr21_R2_fastq
c.html  dac2_chr21_R2_fastqc.zip
dac3_chr21_R1_fastqc.html  dac3_chr21_R1_fastqc.zip   dac3_chr21_R2_fastq
```

```
c.html  dac3_chr21_R2_fastqc.zip
siC1_chr21_R1_fastqc.html  siC1_chr21_R1_fastqc.zip   siC1_chr21_R2_fastq
c.html  siC1_chr21_R2_fastqc.zip
siC2_chr21_R1_fastqc.html  siC2_chr21_R1_fastqc.zip   siC2_chr21_R2_fastq
c.html  siC2_chr21_R2_fastqc.zip
siC3_chr21_R1_fastqc.html  siC3_chr21_R1_fastqc.zip   siC3_chr21_R2_fastq
c.html  siC3_chr21_R2_fastqc.zip
# download all the html files
sftp> get *.html
Fetching /home/kkeith/rnaseq_practice/data/fastqc/dac1_chr21_R1_fastqc.ht
ml to dac1_chr21_R1_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/dac1_chr21_R1_fastqc.html
  100%  243KB  33.0MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/dac1_chr21_R2_fastqc.ht
ml to dac1_chr21_R2_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/dac1_chr21_R2_fastqc.html
  100%  238KB  42.4MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/dac2_chr21_R1_fastqc.ht
ml to dac2_chr21_R1_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/dac2_chr21_R1_fastqc.html
  100%  234KB  42.3MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/dac2_chr21_R2_fastqc.ht
ml to dac2_chr21_R2_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/dac2_chr21_R2_fastqc.html
  100%  232KB  46.3MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/dac3_chr21_R1_fastqc.ht
ml to dac3_chr21_R1_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/dac3_chr21_R1_fastqc.html
  100%  237KB  51.6MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/dac3_chr21_R2_fastqc.ht
ml to dac3_chr21_R2_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/dac3_chr21_R2_fastqc.html
  100%  234KB  53.7MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/siC1_chr21_R1_fastqc.ht
ml to siC1_chr21_R1_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/siC1_chr21_R1_fastqc.html
  100%  243KB  53.1MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/siC1_chr21_R2_fastqc.ht
ml to siC1_chr21_R2_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/siC1_chr21_R2_fastqc.html
  100%  234KB  55.8MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/siC2_chr21_R1_fastqc.ht
ml to siC2_chr21_R1_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/siC2_chr21_R1_fastqc.html
  100%  240KB  56.6MB/s   00:00
```

```
Fetching /home/kkeith/rnaseq_practice/data/fastqc/siC2_chr21_R2_fastqc.ht
ml to siC2_chr21_R2_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/siC2_chr21_R2_fastqc.html
   100%  233KB  59.4MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/siC3_chr21_R1_fastqc.ht
ml to siC3_chr21_R1_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/siC3_chr21_R1_fastqc.html
   100%  236KB  60.9MB/s   00:00
Fetching /home/kkeith/rnaseq_practice/data/fastqc/siC3_chr21_R2_fastqc.ht
ml to siC3_chr21_R2_fastqc.html
/home/kkeith/rnaseq_practice/data/fastqc/siC3_chr21_R2_fastqc.html
   100%  233KB  63.4MB/s   00:00
```

Uploading

To upload to the server from your local (personal) computer, use the command `put` .

```
### upload files to the server
### Generally, to run commands to see stuff on your local (personal compu
ter), put an l in front fo the command
# check your local (personal computer) location
sftp> lpwd
Local working directory: /Users/kelsey/Documents/2020_bioinformatics_rese
arch_experience/rnaseq-demo
# list the files  on your local (personal computer) location; for example
 I can see the FastQC html reports I just downloaded
sftp> llls
README.md             dac3_chr21_R1_fastqc.html    siC2_chr21_R2_fastqc.html
dac1_chr21_R1_fastqc.html    dac3_chr21_R2_fastqc.html    siC3_chr21_R1_fas
tqc.html
dac1_chr21_R2_fastqc.html    siC1_chr21_R1_fastqc.html    siC3_chr21_R2_fas
tqc.html
dac2_chr21_R1_fastqc.html    siC1_chr21_R2_fastqc.html
dac2_chr21_R2_fastqc.html    siC2_chr21_R1_fastqc.html
# If I want to upload my README file with my documentation for the projec
t to the main rnaseq_practice directory, use put and specify the file pat
h
sftp> put README.md ../../
# show that it's where you expect
sftp> cd ../../
sftp> pwd
Remote working directory: /home/kkeith/rnaseq_practice
sftp> ls
README.md    analysis    data
```