


Bio 720 - Assignment 01

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September 11, 2018

EMAIL ▾	NAME ▾	COURSES COMPLETED ▾	CHAPTERS COMPLETED ▾	XP POINTS ▾
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- 1.
2. `scp lucy@info.mcmaster.ca:/home/brian/720example* ~`
3. `mkdir myFirstDir`
`touch file.{a..c}{a..c}{a..c}`
4. `mkdir my{Second,Third,Fourth}Dir`
`cp file.a* mySecondDir`
`cp file.b* myThirdDir`
`cp file.c* myFourthDir`
5. `cp file.*b* ~`
6. (a) `mkdir myFifthDir && touch myFifthDir/file.{1..20}`
(b) `mv myFifthDir/file.{5..15} myFirstDir`
7. `scp lucy@info.mcmaster.ca:/home/brian/720example.fasta 720example_fasta.doc /home/lucy`
more can only display plaintext files, it crashes because it doesn't know how to read the Word document encoding.
8. `mv 720example_fasta.doc 720example\ fasta.doc`
output:

`720example.fasta`
`720example fasta.doc`
9. Use a monospace font like Courier New or Lucida Console
10. (a) the `.fasta` file only contains the sequence reads while the `.fastq` file contains the sequence reads as well as the quality (Phred score) of each read.
(b) '-' is a quality score of 12 in the new Illumina format, it corresponds to the p-error of 0.06310, which means there is a 6.3% chance that the base call is inaccurate.