<https://github.com/stephenturner/oneliners>

this is required to get through mother

Untangle an interleaved paired-end FASTQ file. If a FASTQ file has paired-end reads intermingled, and you want to separate them into separate /1 and /2 files, and assuming the /1 reads precede the /2 reads:

cat interleaved.fq |paste - - - - - - - - | tee >(cut -f 1-4 | tr "\t" "\n" > deinterleaved\_1.fq) | cut -f 5-8 | tr "\t" "\n" > deinterleaved\_2.fq

transcript:

jmanast@kh16081500 MINGW64 /

$ cd

jmanast@kh16081500 MINGW64 ~

$ cd Desktop/

jmanast@kh16081500 MINGW64 ~/Desktop

$ ls

'~$ lab meeting.docx' 'final project runs'/

'~$cab and concepts..docx' 'Jupyter Notebook.lnk'\*

'~$estions on the reading for Class 13.docx' mothur.exe\*

'~$eting with Stephan 2.docx' 'New folder'/

'~$Justin Anast midterm grades.txt.xlsx' 'Not Work or School related'/

'~$My work presentation\_SSE.pptx' Papers/

'~WRL0103.tmp' 'PhD. work'/

'Anaconda Navigator.lnk'\* 'PhD. work.zip'

'Anaconda Prompt.lnk'\* Reprecilator.R

'ANS L2TP VPN Connection - Shortcut.lnk'\* RStudio.lnk\*

Atom.lnk\* Spotify.lnk\*

BCB\_545X/ Spyder.lnk\*

desktop.ini

jmanast@kh16081500 MINGW64 ~/Desktop

$ cd BCB\_545X/

jmanast@kh16081500 MINGW64 ~/Desktop/BCB\_545X

$ ls

BCB546X-Fall2017/ Final\_Project/ Python/ Readme.md

jmanast@kh16081500 MINGW64 ~/Desktop/BCB\_545X

$ cd Final\_Project/

jmanast@kh16081500 MINGW64 ~/Desktop/BCB\_545X/Final\_Project (master)

$ git pull origin

Already up-to-date.

jmanast@kh16081500 MINGW64 ~/Desktop/BCB\_545X/Final\_Project (master)

$ ls

final\_project.Rproj README.md

Final\_project\_instructions/ README.Rmd

Justin\_docs\_final\_project/ Workflow\_for\_Final\_Project.docx

jmanast@kh16081500 MINGW64 ~/Desktop/BCB\_545X/Final\_Project (master)

$ cd ../../

jmanast@kh16081500 MINGW64 ~/Desktop

$ ls

'~$ lab meeting.docx' '~$My work presentation\_SSE.pptx' Atom.lnk\* mothur.exe\* 'PhD. work.zip'

'~$cab and concepts..docx' '~WRL0103.tmp' BCB\_545X/ 'New folder'/ Reprecilator.R

'~$estions on the reading for Class 13.docx' 'Anaconda Navigator.lnk'\* desktop.ini 'Not Work or School related'/ RStudio.lnk\*

'~$eting with Stephan 2.docx' 'Anaconda Prompt.lnk'\* 'final project runs'/ Papers/ Spotify.lnk\*

'~$Justin Anast midterm grades.txt.xlsx' 'ANS L2TP VPN Connection - Shortcut.lnk'\* 'Jupyter Notebook.lnk'\* 'PhD. work'/ Spyder.lnk\*

jmanast@kh16081500 MINGW64 ~/Desktop

$ cd final\ project\ runs/

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs

$ ls

'Hospital 1 (SRX2612313)'/ 'Metro Station 1 (SRP101374)'/ 'New folder'/

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs

$ cd Hospital\ 1\ \(SRX2612313\)/

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ ls

Hospital\_01.fasta Hospital\_01.fastq

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ ho

hostid.exe hostname.exe HOSTNAME.EXE hotplug.dll HotStartUserAgent.dll

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ Hospital\_01.fastq

bash: Hospital\_01.fastq: command not found

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ Hospital\_01.fastq

bash: Hospital\_01.fastq: command not found

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ Hospital\_01.fastq head -n 15

bash: Hospital\_01.fastq: command not found

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ head -n 15 Hospital\_01.fastq

@SRR5312489.1.1 1 length=101

NCATTGAGATCGGTCAAGTGCGTCGGATAGTCGCCCGTGAAGTAATGGTCGGTGAATTGCGGGGACTGGGCATTGCGCTTCTCTCCCCCAACTGCCTCCTA

+SRR5312489.1.1 1 length=101

#<<BBFFFB/BFFFFFFFFFFFFFFFFFFFFFFF/FFFF<<FFFFFFFFFFFFFFFFFBB<FBFF</FFFFFFFBFFFBFFFFFFFFFFF<FFFFFFF/<7

@SRR5312489.1.2 1 length=101

CTTGCCAATCAATATGCCGATCTGGACGCAATGTGTCGGTTCATCGGTGCGGATTCGTTGGCTTTCCTCTCCATCGATGGACTTTATGAGGCAGTTGGGGG

+SRR5312489.1.2 1 length=101

BBBBBFFBFFFFFFFFFFFFFFFFF<FFFFFFFFFFFFFFFBFFFFFFFFFFFBFFFFFFFFFFFFBFFFFFFFFFFFF/BB/FFFFFFFF/FBFFB/<<B

@SRR5312489.2.1 2 length=101

GGCGTGACGACCGACGAGGTCGACCGGATCGGCCACGAGTTCCTGCTCGACCCCGGCGCCTACCCCTCGACCCTGGGCTACCGCGGCTTCCCCAAGTCGCT

+SRR5312489.2.1 2 length=101

BBBBB<<<<BBFFFFFF/7<FF/<F<//F/7<B/7FF/<7/<<FFF/FF/F<//B/B<<BBFBFBFF<FFFFFFFB7B<77/BBB<FF/BBF/B//7F/B<

@SRR5312489.2.2 2 length=101

CTCGTTGATCGAGGTGCACAGCGACTTGGGGAAGCCGCGGTAGCCCAGGGTCGAGGGGGAGGCGCCGTGGTCGAGCAGGAACTCGTGGCCGATCCGGTCGA

+SRR5312489.2.2 2 length=101

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ ^C

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ help grep

bash: help: no help topics match `grep'. Try `help help' or `man -k grep' or `info grep'.

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ ?grep

bash: ?grep: command not found

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ help(grep)

bash: syntax error near unexpected token `grep'

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ head -n 30 Hospital\_01.fastq

@SRR5312489.1.1 1 length=101

NCATTGAGATCGGTCAAGTGCGTCGGATAGTCGCCCGTGAAGTAATGGTCGGTGAATTGCGGGGACTGGGCATTGCGCTTCTCTCCCCCAACTGCCTCCTA

+SRR5312489.1.1 1 length=101

#<<BBFFFB/BFFFFFFFFFFFFFFFFFFFFFFF/FFFF<<FFFFFFFFFFFFFFFFFBB<FBFF</FFFFFFFBFFFBFFFFFFFFFFF<FFFFFFF/<7

@SRR5312489.1.2 1 length=101

CTTGCCAATCAATATGCCGATCTGGACGCAATGTGTCGGTTCATCGGTGCGGATTCGTTGGCTTTCCTCTCCATCGATGGACTTTATGAGGCAGTTGGGGG

+SRR5312489.1.2 1 length=101

BBBBBFFBFFFFFFFFFFFFFFFFF<FFFFFFFFFFFFFFFBFFFFFFFFFFFBFFFFFFFFFFFFBFFFFFFFFFFFF/BB/FFFFFFFF/FBFFB/<<B

@SRR5312489.2.1 2 length=101

GGCGTGACGACCGACGAGGTCGACCGGATCGGCCACGAGTTCCTGCTCGACCCCGGCGCCTACCCCTCGACCCTGGGCTACCGCGGCTTCCCCAAGTCGCT

+SRR5312489.2.1 2 length=101

BBBBB<<<<BBFFFFFF/7<FF/<F<//F/7<B/7FF/<7/<<FFF/FF/F<//B/B<<BBFBFBFF<FFFFFFFB7B<77/BBB<FF/BBF/B//7F/B<

@SRR5312489.2.2 2 length=101

CTCGTTGATCGAGGTGCACAGCGACTTGGGGAAGCCGCGGTAGCCCAGGGTCGAGGGGGAGGCGCCGTGGTCGAGCAGGAACTCGTGGCCGATCCGGTCGA

+SRR5312489.2.2 2 length=101

BBBBBFFF<<//<F<F<FFBBFB//7/<F/BF/7B/<<F/F/</<</<</BBB/BF/</</7<BFFBFB77/B/<F/FF/B/77B7BFBB/BF7BB</77/

@SRR5312489.3.1 3 length=101

NGCATGCACATAAAAACACAAACATGGTACATGTCATTTTTTCAGGAATACATTGAAGGAATTCCATGAGAAGCCATTAAAGACATTGGTAAAGAAAAAAC

+SRR5312489.3.1 3 length=101

#<<<BFFFFFFFFFFFFFF<FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFB/FFBFFFFFFFFBFFFFFFFF/FFFFFFFBFFFFF<BFFBF/<

@SRR5312489.3.2 3 length=101

GTGGAGGATGAACATGTCTGATCTGGAGTCTCTAGACAGGTAAAATGGTTTTTCTTTACCAATGTCTTTAATGGCTTCTCATGGAATTCCTTCAATGTATT

+SRR5312489.3.2 3 length=101

BBBBBFFFFFFFFFFFFFFFBFFFFFFFFFFFFFFFFFFF<FBFFFFFF<FFFFFBFFFFFFFFFBFFFFFF<FFFFFFBFFFF<FFFFFFFFFFFFFBBF

@SRR5312489.4.1 4 length=101

NCTTCCAGCCTCTAAAACTGTGAGAAAATAAATCTCTGTTGTTTAAGCTGCCCAGTCTGTGGCCTTAGTTATAGCAGTCCTAGAAAATTGATATACTCTGT

+SRR5312489.4.1 4 length=101

#<<BBFFFFFFFFFFFFFFFFFFFBFFFFFFFFFFFFFFFFFFFFFFFFFFFFBBFFFFFFFFFFFFFFFFFFFFFFFFFF<<BFFFFFFFFFFFFFFFFF

@SRR5312489.4.2 4 length=101

ACTTAGAGTCTACTTGGAGCCAATTTTTTTGTAAAAGCCTGCGTTGTTTTGTTTTGTTTTAAGATACAGAGTATATCAATTTTCTAGGACTGCTATAACTA

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ man grep

bash: man: command not found

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ ls

Hospital\_01.fasta Hospital\_01.fastq

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ $ cat Hospital\_01.fastqHo |paste - - - - - - - - | tee >(cut -f 1-4 | tr "\t" "\n" > deinterleaved\_1.fq) | cut -f 5-8 | tr "\t" "\n" > deinterleaved\_2.fq

bash: $: command not found

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ cat interleaved.fq |paste - - - - - - - - | tee >(cut -f 1-4 | tr "\t" "\n" > deinterleaved\_1.fq) | cut -f 5-8 | tr "\t" "\n" > deinterleaved\_2.fq

cat: interleaved.fq: No such file or directory

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ cat interleaved.fq |paste - - - - - - - - | tee >(cut -f 1-4 | tr "\t" "\n" > deinterleaved\_1.fq) | cut -f 5-8 | tr "\t" "\n" > deinterleaved\_2.fq

cat: interleaved.fq: No such file or directory

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ cat Hospital\_01.fastq |paste - - - - - - - - | tee >(cut -f 1-4 | tr "\t" "\n" > Hospital\_deinterleaved1\_01.fastq) | cut -f 5-8 | tr "\t" "\n" > Hospital\_deinterleaved2\_01.fastq) bash: syntax error near unexpected token `)'

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ cat Hospital\_01.fastq |paste - - - - - - - - | tee >(cut -f 1-4 | tr "\t" "\n" > Hospital\_deinterleaved1\_01.fastq) | cut -f 5-8 | tr "\t" "\n" > Hospital\_deinterleaved2\_01.fastq

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ ls

deinterleaved\_1.fq deinterleaved\_2.fq Hospital\_01.fasta Hospital\_01.fastq Hospital\_deinterleaved1\_01.fastq Hospital\_deinterleaved2\_01.fastq

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ head -n 30 Hospital\_deinterleaved1\_01.fastq

@SRR5312489.1.1 1 length=101

NCATTGAGATCGGTCAAGTGCGTCGGATAGTCGCCCGTGAAGTAATGGTCGGTGAATTGCGGGGACTGGGCATTGCGCTTCTCTCCCCCAACTGCCTCCTA

+SRR5312489.1.1 1 length=101

#<<BBFFFB/BFFFFFFFFFFFFFFFFFFFFFFF/FFFF<<FFFFFFFFFFFFFFFFFBB<FBFF</FFFFFFFBFFFBFFFFFFFFFFF<FFFFFFF/<7

@SRR5312489.2.1 2 length=101

GGCGTGACGACCGACGAGGTCGACCGGATCGGCCACGAGTTCCTGCTCGACCCCGGCGCCTACCCCTCGACCCTGGGCTACCGCGGCTTCCCCAAGTCGCT

+SRR5312489.2.1 2 length=101

BBBBB<<<<BBFFFFFF/7<FF/<F<//F/7<B/7FF/<7/<<FFF/FF/F<//B/B<<BBFBFBFF<FFFFFFFB7B<77/BBB<FF/BBF/B//7F/B<

@SRR5312489.3.1 3 length=101

NGCATGCACATAAAAACACAAACATGGTACATGTCATTTTTTCAGGAATACATTGAAGGAATTCCATGAGAAGCCATTAAAGACATTGGTAAAGAAAAAAC

+SRR5312489.3.1 3 length=101

#<<<BFFFFFFFFFFFFFF<FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFB/FFBFFFFFFFFBFFFFFFFF/FFFFFFFBFFFFF<BFFBF/<

@SRR5312489.4.1 4 length=101

NCTTCCAGCCTCTAAAACTGTGAGAAAATAAATCTCTGTTGTTTAAGCTGCCCAGTCTGTGGCCTTAGTTATAGCAGTCCTAGAAAATTGATATACTCTGT

+SRR5312489.4.1 4 length=101

#<<BBFFFFFFFFFFFFFFFFFFFBFFFFFFFFFFFFFFFFFFFFFFFFFFFFBBFFFFFFFFFFFFFFFFFFFFFFFFFF<<BFFFFFFFFFFFFFFFFF

@SRR5312489.5.1 5 length=101

CATCACCGAAGCTGTTGATCTGCAAAATATAAGTTGCCGCAGGTTTTGCAGCCTGAATGCTAGCAGTACCTGCGCCTGCATTATTGGTGGACGTATTATTG

+SRR5312489.5.1 5 length=101

BBBBBB/BBFFFFFFFFFFFFFFBBFF/<FFBFFB<FFFB<FFF/<F<FBFFFFFB/<FFFFFFFFFFFFFFFFFFF<FFBB//<FFFFBBFFFFFFFFFB

@SRR5312489.6.1 6 length=101

NCCCGCTCGGGATTCTGAGTGCGATCGCCGTGGTCGGTGCCGTCTTCGTGATCCTCGGGTTCTGTGCGCTGTGGGGCATGGACGGACAGGAGACCAACGCA

+SRR5312489.6.1 6 length=101

#<<BBFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF<BFFFFFFFFFFFFFFFFFFFFBFFFBFFFF/BFFFBFFFF7

@SRR5312489.7.1 7 length=101

AGAATGATTTTAAATTCTATTCTGGATTTTACTGGAAGCCAATGCAAAGAAGCTAAAACGGGAGAAATATGATCTCTTTTCCTGGTTCCTGTCAGAACACG

+SRR5312489.7.1 7 length=101

BBBBBBFFFFFFFFFFFFBFFFFFFFFFFFFFFFFFFFFFFFFBFFFFFFFFFFFBFFF<FFFFFFFFFFFFFFFFFFFFFFFFBFFFFFFFFFFBFFFFF

@SRR5312489.8.1 8 length=101

GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATCAGATCTCGTATGCCGTCTTCTGCTTGAAAAAAAAAAAACATGCGCGTGCCGACGTATGGGATGG

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ head -n 30 Hospital\_deinterleaved2\_01.fastq

@SRR5312489.1.2 1 length=101

CTTGCCAATCAATATGCCGATCTGGACGCAATGTGTCGGTTCATCGGTGCGGATTCGTTGGCTTTCCTCTCCATCGATGGACTTTATGAGGCAGTTGGGGG

+SRR5312489.1.2 1 length=101

BBBBBFFBFFFFFFFFFFFFFFFFF<FFFFFFFFFFFFFFFBFFFFFFFFFFFBFFFFFFFFFFFFBFFFFFFFFFFFF/BB/FFFFFFFF/FBFFB/<<B

@SRR5312489.2.2 2 length=101

CTCGTTGATCGAGGTGCACAGCGACTTGGGGAAGCCGCGGTAGCCCAGGGTCGAGGGGGAGGCGCCGTGGTCGAGCAGGAACTCGTGGCCGATCCGGTCGA

+SRR5312489.2.2 2 length=101

BBBBBFFF<<//<F<F<FFBBFB//7/<F/BF/7B/<<F/F/</<</<</BBB/BF/</</7<BFFBFB77/B/<F/FF/B/77B7BFBB/BF7BB</77/

@SRR5312489.3.2 3 length=101

GTGGAGGATGAACATGTCTGATCTGGAGTCTCTAGACAGGTAAAATGGTTTTTCTTTACCAATGTCTTTAATGGCTTCTCATGGAATTCCTTCAATGTATT

+SRR5312489.3.2 3 length=101

BBBBBFFFFFFFFFFFFFFFBFFFFFFFFFFFFFFFFFFF<FBFFFFFF<FFFFFBFFFFFFFFFBFFFFFF<FFFFFFBFFFF<FFFFFFFFFFFFFBBF

@SRR5312489.4.2 4 length=101

ACTTAGAGTCTACTTGGAGCCAATTTTTTTGTAAAAGCCTGCGTTGTTTTGTTTTGTTTTAAGATACAGAGTATATCAATTTTCTAGGACTGCTATAACTA

+SRR5312489.4.2 4 length=101

BBBBBFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFBFFFFB/</BFFF<BBB<FFFFFFFFFFFF</FBFFFFFFFFFFFB

@SRR5312489.5.2 5 length=101

AATAACGCTGCTACCAGTAATAGCGGCGATGACATTGTGATCGTTGAAGAAGACGCGACCTATGATGGATCGACGCCTGCTAGTAGCAATAATACGTCCAC

+SRR5312489.5.2 5 length=101

BBBBBFFFFFFFFFFFFF<FFFFFFFFFFFFFFFFBFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF<FFFBFFFFFFFFFFFFFFF/BFFFFFFFFFFF

@SRR5312489.6.2 6 length=101

GGAGTATGCGTTGGTCTCCTGTCCGTCCATGCCCCACAGCGCACAGAACCCGAGGATCACGAAGACGGCACCGACCACGGCGATCGCACTCAGAATCCCGA

+SRR5312489.6.2 6 length=101

BBBBBFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFBFFFFFFFFFFFFFBFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF/

@SRR5312489.7.2 7 length=101

CAGAATGCTGCAGCACGTGTTCTGACAGGAACCAGGAAAAGAGATCATATTTCTCCCGTTTTAGCTTCTTTGCATTGGCTTCCAGTAAAATCCAGAATAGA

+SRR5312489.7.2 7 length=101

BBBBBFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFBFFF<F

@SRR5312489.8.2 8 length=101

GATCGGAAGAGCGTCGTGTAGGGGAAGAGTGTAGATTTCGGTGGGCGCCGTATCCTTAAAAAAAAAAAAAAGACGAACAGTGCGCTCGGGCAGCAGCCCCA

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ ls

deinterleaved\_1.fq deinterleaved\_2.fq Hospital\_01.fasta Hospital\_01.fastq Hospital\_deinterleaved1\_01.fastq Hospital\_deinterleaved2\_01.fastq

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Hospital 1 (SRX2612313)

$ cd ../

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs

$ cd Metro\ Station\ 1\ \(SRP101374\)/

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Metro Station 1 (SRP101374)

$ ls

Metrostation\_01.fasta Metrostation\_01.fastq

jmanast@kh16081500 MINGW64 ~/Desktop/final project runs/Metro Station 1 (SRP101374)

$ cat Metrostation\_01.fastq |paste - - - - - - - - | tee >(cut -f 1-4 | tr "\t" "\n" > Metrostation\_deinterleaved1\_01.fastq) | cut -f 5-8 | tr "\t" "\n" > Metrostation\_deinterleaved2\_01.fastq