Data Wrangling and Processing for Genomics - Parte 3

Evidencia:

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estuardo8u14@LAPTOP-5IN4BIR3:~/dc workshop/data/untrimmed fastq$ cp ~/src/Trimmomatic-0.38/ada
pters/NexteraPE-PE.fa .
estuardo8u14@LAPTOP-5IN4BIR3:~/dc workshop/data/untrimmed fastq$ trimmomatic PE SRR2589044 1.f
astq.gz SRR2589044 2.fastq.gz \
                   SRR2589044 1.trim.fastq.gz SRR2589044 1un.trim.fastq.gz \
                   SRR2589044_2.trim.fastq.gz SRR2589044_2un.trim.fastq.gz \
                   SLIDINGWINDOW:4:20 MINLEN:25 ILLUMINACLIP:NexteraPE-PE.fa:2:40:15
trimmomatic: command not found
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ java -jar ~/src/Trimmomatic-0
 .38/trimmomatic-0.38.jar PE SRR2589044 1.fastq.gz SRR2589044 2.fastq.gz
                                                                       SRR2589044 2.trim.fastq.gz S
9044 1.trim.fastq.gz SRR2589044 1un.trim.fastq.gz
RR2589044 2un.trim.fastq.gz
                                               SLIDINGWINDOW:4:20 MINLEN:25 ILLUMINACLIP:NexteraP
E-PE.fa:2:40:15
TrimmomaticPE: Started with arguments:
 SRR2589044_1.fastq.gz SRR2589044_2.fastq.gz SRR2589044_1.trim.fastq.gz SRR2589044_1un.trim.fa
stq.gz SRR2589044 2.trim.fastq.gz SRR2589044 2un.trim.fastq.gz SLIDINGWINDOW:4:20 MINLEN:25 IL
LUMINACLIP:NexteraPE-PE.fa:2:40:15
Multiple cores found: Using 4 threads
Using PrefixPair: 'AGATGTGTATAAGAGACAG' and 'AGATGTGTATAAGAGACAG'
Using Long Clipping Sequence: 'GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG'
Using Long Clipping Sequence: 'TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG'
Using Long Clipping Sequence: 'CTGTCTCTTATACACATCTCCGAGCCCACGAGAC'
Using Long Clipping Sequence: 'CTGTCTCTTATACACATCTGACGCTGCCGACGA'
ILLUMINACLIP: Using 1 prefix pairs, 4 forward/reverse sequences, 0 forward only sequences, 0 r
everse only sequences
Exception in thread "main" java.io.FileNotFoundException: SRR2589044 2.fastq.gz (No such file
or directory)
         at java.base/java.io.FileInputStream.open0(Native Method)
         at java.base/java.io.FileInputStream.open(FileInputStream.java:219)
         at java.base/java.io.FileInputStream.init>(FileInputStream.java:157)
         at org.usadellab.trimmomatic.fastq.FastqParser.parse(FastqParser.java:135)
         at org.usadellab.trimmomatic.TrimmomaticPE.process(TrimmomaticPE.java:268)
         at org.usadellab.trimmomatic.TrimmomaticPE.run(TrimmomaticPE.java:555)
         at org.usadellab.trimmomatic.Trimmomatic.main(Trimmomatic.java:80)
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ |
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Se puede ver una Excepción y tuve que bajar de nuevo UNA sola secuencia que al parecer no se descargó con el curl, talvez por no poner el comando sudo al inicio.

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estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ java -jar ~/src/Trimmomatic-0
 .38/trimmomatic-0.38.jar PE SRR2589044_1.fastq.gz SRR2589044_2.fastq.gz SRR2589044_1.trim.fast
 q.gz SRR2589044 1un.trim.fastq.gz SRR2589044 2.trim.fastq.gz SRR2589044 2un.trim.fastq.gz SLID
 INGWINDOW:4:20 MINLEN:25 ILLUMINACLIP:NexteraPE-PE.fa:2:40:15
 TrimmomaticPE: Started with arguments:
    SRR2589044 1.fastq.gz SRR2589044 2.fastq.gz SRR2589044 1.trim.fastq.gz SRR2589044 1un.trim.fa
 stq.gz SRR2589044_2.trim.fastq.gz SRR2589044_2un.trim.fastq.gz SLIDINGWINDOW:4:20 MINLEN:25 IL
LUMINACLIP:NexteraPE-PE.fa:2:40:15
Multiple cores found: Using 4 threads
Using PrefixPair: 'AGATGTGTATAAGAGACAG' and 'AGATGTGTATAAGAGACAG'
Using Long Clipping Sequence: 'GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG' Using Long Clipping Sequence: 'TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG'
Using Long Clipping Sequence: 'CTGTCTCTTATACACATCTCCGAGCCCACGAGAC'
Using Long Clipping Sequence: 'CTGTCTCTTATACACATCTGACGCTGCCGACGA'
ILLUMINACLIP: Using 1 prefix pairs, 4 forward/reverse sequences, 0 forward only sequences, 0 r
everse only sequences
Quality encoding detected as phred33
 Input Read Pairs: 1107090 Both Surviving: 885220 (79.96%) Forward Only Surviving: 216472 (19.5
 5%) Reverse Only Surviving: 2850 (0.26%) Dropped: 2548 (0.23%)
 TrimmomaticPE: Completed successfully
    StuardoBuld@LAPTOP-SIMMBIR3:-/de_workshop/data/untrimmed_fastq$ for infile in *_1.fastq.gz; do base=$(basename $(infile) _1.fastq.gz); java -jar -/src/Trimmomatic=0.38/trimmomatic=0.38.jar PE ${base}_1.trim.fastq.gz ${base}_1.trim.fastq.gz ${base}_1.trim.fastq.gz ${base}_2.trim.fastq.gz ${base
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Y los movemos a una capeta nueva de ya trimado:

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TrimmomaticPE: Completed successfully
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ ls
NexteraPE-PE.fa SRR2584866_1.fastq.gz SRR2589044_1.trim.fastq.gz
SRR2584863_1.fastq.gz SRR2584866_1.trim.fastq.gz SRR2589044_2.fastq.gz
SRR2584863_1.trim.fastq.gz SRR2584866_1.un.trim.fastq.gz SRR2589044_2.fastq.gz
SRR2584863_1.un.trim.fastq.gz SRR2584866_2.fastq.gz SRR2589044_2.trim.fastq.gz
SRR2584863_2.fastq.gz SRR2584866_2.trim.fastq.gz SRR2589044_2.trim.fastq.gz
SRR2584863_2.trim.fastq.gz SRR2584866_2.un.trim.fastq.gz
SRR2584863_2.un.trim.fastq.gz SRR2589044_1.fastq.gz
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ cd ~/dc_workshop/data/untrimmed_fastq
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ mkdir ../trimmed_fastq
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ cd ../trimmed_fastq
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ cd ../trimmed_fastq
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/untrimmed_fastq$ cd ../trimmed_fastq
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/trimmed_fastq$ cd ../trimmed_fastq
estuardo8u14@LAPTOP-5IN4BIR3:~/dc_workshop/data/trimmed_fastq$ SRR2589044_1.trim.fastq.gz
SRR2584863_1.trim.fastq.gz SRR2584866_1.trim.fastq.gz SRR2589044_1.trim.fastq.gz
SRR2584863_2.trim.fastq.gz SRR2584866_2.trim.fastq.gz SRR2589044_2.trim.fastq.gz
```