Server Scince how to stop typing manually? Samples

During the work with biological data on server I recognized that I had a problem:

I need to type a code in a terminal <u>manually</u> for each sample of my data.

<u>AWFUL!</u>

feel free to smile)

Let's meet with my brilliant idea

PLAN

my script should do the following things:

find all samples in a directory

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for each sample:

- 1) <u>find a pair</u> of the sample (difference between them is _R1_ or _R2_ in the names)
- 2) <u>change the names</u> of my _R1_ and _R2_ samples for output of a program for paired and unpaired reads

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indicate the program for terminal

Let's Try!



os path for rglob

from pathlib import Path import os

for el in Path('/scratch/mshumilova/filtered_by_tile/').rglob('*'):

for each sample:

1) <u>find a pair</u> of the sample (difference between them is _R1_ or _R2_ in the names)

```
from pathlib import Path
import os

pairname = ''

for el in Path('/scratch/mshumilova/filtered_by_tile/').rglob('*'):
    if '_R1_' not in str(el):
        continue
    pairname = str(el).replace('_R1_', '_R2_')
```

for each sample:

2) <u>change the names</u> of my _R1_ and _R2_ samples for output of a program for paired and unpaired reads

```
from pathlib import Path
import os
pairname = ' '
out1_paired = "
out1_unpaired = "
out2_paired = "
out2_unpaired = "
for el in Path('/scratch/mshumilova/filtered_by_tile/').rglob('*'):
    if '_R1_' not in str(el):
        continue
    pairname = str(el).replace('_R1_', '_R2_')
    out1_paired = str(el).replace('/filtered_by_tile/', '/trimm/')
    out1_paired = out1_paired.replace('.fq.gz', '.trimm_20_paired_1.fq.gz')
    out1_unpaired = out1_paired.replace('_paired', '_unpaired')
     out2_paired = pairname.replace('/filtered_by_tile/', '/trimm/')
     out2_paired = pairname.replace('.fq.gz', '.trimm_20_paired_2.fq.gz')
     out2_unpaired = out2_paired.replace('_paired', '_unpaired')
```

08 **cmd**

indicate the program for terminal

```
from pathlib import Path
import os
pairname = ' '
out1_paired = "
out1_unpaired = "
out2_paired = "
out2_unpaired = "
for el in Path('/scratch/mshumilova/filtered_by_tile/').rglob('*'):
    if '_R1_' not in str(el):
        continue
    pairname = str(el).replace('_R1_', '_R2_')
    out1_paired = str(el).replace('/filtered_by_tile/', '/trimm/')
    out1_paired = out1_paired.replace('.fq.gz', '.trimm_20_paired_1.fq.gz')
    out1_unpaired = out1_paired.replace('_paired', '_unpaired')
    out2_paired = pairname.replace('/filtered_by_tile/', '/trimm/')
    out2_paired = pairname.replace('.fq.gz', '.trimm_20_paired_2.fq.gz')
    out2_unpaired = out2_paired.replace('_paired', '_unpaired')
    cmd = f'java -jar Trimmomatic-0.39/trimmomatic-0.39.jar PE -phred33
   {str(el)} {pairname} {out1_paired} {out1_unpaired} {out2_paired}
   {out2_unpaired} LEADING:20 TRAILING:20 SLIDINGWINDOW:5:20 MINLEN:60'
   os.system(cmd)
```

What does our output look like?

Let's see

OUTPUT

java -jar Trimmomatic-0.39/trimmomatic-0.39.jar PE -phred33
/scratch/mshumilova/filtered_by_tile/FL865_S10_L001_R1_001.fq.gz
/scratch/mshumilova/filtered_by_tile/FL865_S10_L001_R2_001.fq.gz
/scratch/mshumilova/trimm/FL865_S10_L001_R1_001.trim_20_paired_1.fq.gz
/scratch/mshumilova/trimm/FL865_S10_L001_R1_001.trim_20_unpaired_1.fq.gz
/scratch/mshumilova/trimm/FL865_S10_L001_R2_001.trim_20_paired_1.fq.gz
/scratch/mshumilova/trimm/FL865_S10_L001_R2_001.trim_20_unpaired_1.fq.gz
LEADING:20 TRAILING:20 SLIDINGWINDOW:5:20 MINLEN:60

program part

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pair of samples (_R1_, _R2_)

output of the program (_R1_, paired, unpaired)

output of the program (_R2_, paired, unpaired)

program part

*Thank you for your attention.

I wish you to have a factastic day!*

l've solved my "manual" problem and use the script above for my tasks. I'm happy)

P.s. recently I found one more problem. to be continued...