Linux Operation

cp

```
cp -r whatever/ /wp2
* wp2/-
** whatever/-
*** insidewhatver/-
```

Check storage

```
du -h --max-depth=1 | sort -h
```

check and grep text

cat into file and select(cut) 3 col and chech the unique values there

```
zcat features.tsv.gz | cut -f 3 | uniq -c
## 374 Gene Expression
##     313 Gene Expression
      20 Negative Control Probe
      41 Negative Control Codeword
```

Count the values in that column

```
zcat features.tsv.gz | cut -f 3 | wc -l
 # 374
```

count the specific text in the text

```
zcat features.tsv.gz | grep "Gene Expression" | wc -l
# 313
```

replace the all `'Negative Control Codeword'` in the tect file with `Gene Expression`

```
grep -rl 'Negative Control Codeword' ./features.tsv | xargs sed -i 's
/Negative Control Codeword/Gene Expression/g'
```

gzip file into .gz

```
gzip features.tsv
# gzip features.tsv.gz
```

Duplicate the file

```
zcat features.tsv.gz > features.tsv (unzip, features.tsv is for
editting)
mv feature.tsv.gz _feature.tsv.gz (rename(keep) the original file)
```

[vi toturial](#)

soft link

```
$ln -s file1 link1
eg: ln -s ./processed_data/xenium_jul12_mask_16bit_real.tiff .
/xenium_bayor/xenium_mask0_dapi.tiff
```

Write bash script

```
# write python script
# get command line from notebook:
for i in range(0,30):
    print(f"python get_masks.py -f {i} &")
print(wait')

'''python get_masks.py -f 0 &
python get_masks.py -f 1 &
python get_masks.py -f 2 &
python get_masks.py -f 3 &'''

$nano get_masks.sh #alternative way as vi
$taskset --cpu-list 47-64 bash get_masks.sh  # select certain cpu and
run bash
```