Homework/Review

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Programming for Scientists

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Homework



- Download file
- Open/parse it
- Analyse it

FastQ Format



According to Wikipedia, we get a sequence every four lines:

- Header
- DNA sequence
- \bullet + line
- Qualities

```
ifile = open('hw-HeLa.fg')
while True:
    header = ifile.readline().strip()
    seq = ifile.readline().strip()
   _ = ifile.readline().strip()
    qualities = ifile.readline().strip()
    if not len (qualities):
        break
```

(This is not the only way to structure this)

Converting Qualities



- We have read it as a string
- We have a sequence of characters
- Now, we want to get the numeric value

We will look it up.

Continuing



```
import numpy as np . . . while True: . . . .  \text{qualities} = \left[ \left( \text{ord} \left( q \right) \text{ - 64} \right) \text{ for } q \text{ in } \text{qualities} \right]   \text{qualities} = \text{np.array} \left( \text{qualities} \right)
```

Let us compute the averages



```
import numpy as np
from matplotlib import pyplot as plt
allqs = []
ifile = open('hw-HeLa.fq')
while True:
    header = ifile.readline().strip()
    seq = ifile.readline().strip()
    = ifile.readline().strip()
    qualities = ifile.readline().strip()
    if not len (qualities):
        break
    qualities = [(ord(q) - 64) for q in qualities]
    qualities = np.array(qualities)
    allgs.append(qualities)
allqs = np.array(allqs)
```

Continuing...



Now we have an array named allqs with all the qualities

```
mean = allqs.mean(0)
std = allqs.std(0)
```

Continuing...



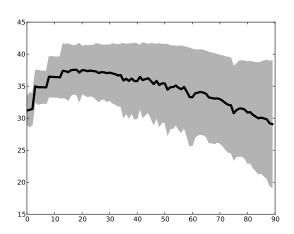
Now we have an array named allqs with all the qualities

```
mean = allqs.mean(0)
std = allqs.std(0)

gray = (.7,.7,.7)
plt.fill_between(
    np.arange(allqs.shape[1]),
    mean-std,
    mean+std,
    color=gray)
plt.plot(mean, color='k', lw=4)
plt.show()
```

Output





Minor Improvements



- So far, as I said, I used the file after unzipping
- Can we use the file as is?
- For that, we need to open a gzipped file.
- Let us look it up...

gzip Module

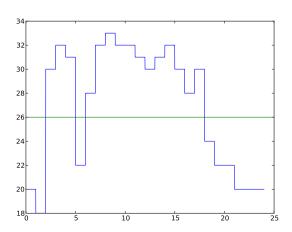


Replace

```
ifile = open('hw-HeLa.fq')
by
import gzip
ifile = gzip.open('hw-HeLa.fq.gz')
```

Trimming





Algorithm



- We look from left to right.
- 2 Remember the longest substring we have seen.
- When we are done, the longest substring will be it.



```
def trim (qs, thresh):
    bestlen = 0
    startcur = 0
    for i in xrange (len(qs)+1):
        if i >= len(qs) or qs[i] < thresh:
            curlen = i - startcur
            if curlen > bestlen:
                 bestlen = curlen
                 best = (startcur, i)
            startcur = (i+1)
    s, e = best
    return s,e
```

Putting it Together



Let us look at the source code...

Improvements



• Do it in one pass