Hw1

Question 1

Using given files, make a table with the following information per species:

- Question 1.1. Total genome size
- Question 1.2. Number of chromosomes
- Question 1.3. Largest chromosome size and name
- Question 1.4. Smallest chromosome size and name
- Question 1.5. Mean chromosome length

Answer:

	TAIR10	zm4	ecoli	dm6	hg38	rice	ce10	yeast
Total genome size	119146348	2106338117	4639211	137547960	3088269832	373245519	100286070	12157105
Number of chromosomes	5	10	1	7	24	12	7	17
Largest chromosome size and name	Chr1: 30427671	1: 307041717	Ecoli: 4639211	chr3R: 32079311	chr1: 248956422	Chr1: 43270923	chrV: 20924149	chrIV: 1531933
Smallest chromosome size and name	Chr4: 18585056	10: 150982314	Ecoli: 4639211	chr4: 1348131	chr21: 46709983	Chr9: 23012720	chrM: 13794	chrM: 85779
Mean chromosome length	23829369.6	210633811.7	4639211.0	19649708.6	128677909.7	31103793.2	14326581.4	715123.8

Codes are shown here:

```
#!/usr/bin/env python3
import sys
f = sys.stdin
line = f.readline()
dic = {}
while line != '':
    line = line.strip().rstrip('\n').split()
    dic[line[0]]=int(line[1])
     ###int is really really really important!!!!
    line = f.readline()
f.close()
print('number of chromosomes:',len(dic))

n = 0
for i in dic:
    n += int(dic[i])
print('total length:',n)

b = max(dic.values())   # largest size
c = list(dic.keys())[list(dic.values()).index(b)]   #coresponding name
print('largest chromosome size and name: %s %s'%(c,b))

b = min(dic.values())   # smallest size
```

```
c = list(dic.keys())[list(dic.values()).index(b)]       #coresponding name
print('smallest chromosome size and name: %s %s'%(c,b))

print('mean chromosome length:',format(n/len(dic),'.1f'))
```