```
Script started on Mon Sep 19 23:19:05 2016
 ^[]01ib501_stud12@compute-0-18:-/shell'G^[[71034h^[[01;31m^B23:19:08 ^[[01;32m^Bib501_stud12 ^[[02;36m^Bcompute-0-18 ^[[01;34m^B/home/a-m/ib501_stud12/shell ^[[00;33m^B^[[00m
 $ cat fs^Gt_tally.py
#!/usr/bin/python
 in_file = '/home/a-m/ib501_stud12/shell/fst/batch_2.fst_1-2.Chr_only.tsv'
fst_total = 0.0
  # Create a dictionary of chromosomes
  fh = open(in_file, 'r')
  next(fh)
  # Iterate over each line in the file
  for line in fh:
          # Remove new lines
           line = line.strip('\n')
          # We can split TSV files
         parts = line.split('\t')
          # print the fst value
         count = count + 1
fst_total = float(parts[8]) + float(fst_total)
           # save chromosomes number with count number
          chrom[count] = parts[4]
 print "printing avg fst:", float(fst_total) / float(count)
  # print uniq chromosomes
  chrom_uniq = list()
 for i in chrom.values():
if i in chrom_uniq:
                  continue
          else:
                   chrom_uniq.append(i)
  print "here the list of uniq chromosomes:", chrom_uniq
 ^[]0;ib501_stud12@compute-0-18:~/shell^G^[[01;31m^B23:19:15 ^[[01;32m^Bib501_stud12 ^[[02;36m^Bcompute-0-18 ^[[01;34m^B/home/a-m/ib501 stud12/shell ^[[00;33m^b^[[00m
$ cat ~/shell/fst/batch_2.fst_1-2.Chr_only.tsv | sed 1d | cut -f 9 | awk '{total_lines=total_lines+$1} END {print total_
 | State - | Shell-| | Shell - | Shel
  groupI
groupII
  groupIII
 groupIV
groupIX
 groupV
groupVI
  groupVII
  groupVIII
  groupX
  groupXI
  groupXII
  groupXIII
 groupXIV
groupXIX
  groupXV
  groupXVI
  groupXVII
  groupXVIII
  groupXX
 groupXII
groupXII
^[]01;3501_stud12@compute-0-18:~/shell^G^[[01;31m^B23:20:08 ^[[01;32m^Bib501_stud12 ^[[02;36m^Bcompute-0-18 ^[[01;34m^B/home/a-m/ib501_stud12/shel1 ^[[00;33m^p^[[00m
  $ exit
  exit
  Script done on Mon Sep 19 23:20:22 2016
```