BIOINFORMATICS SESSION 11. PRACTICE

2023-12-4

Personal genomes:

The differences between you and me

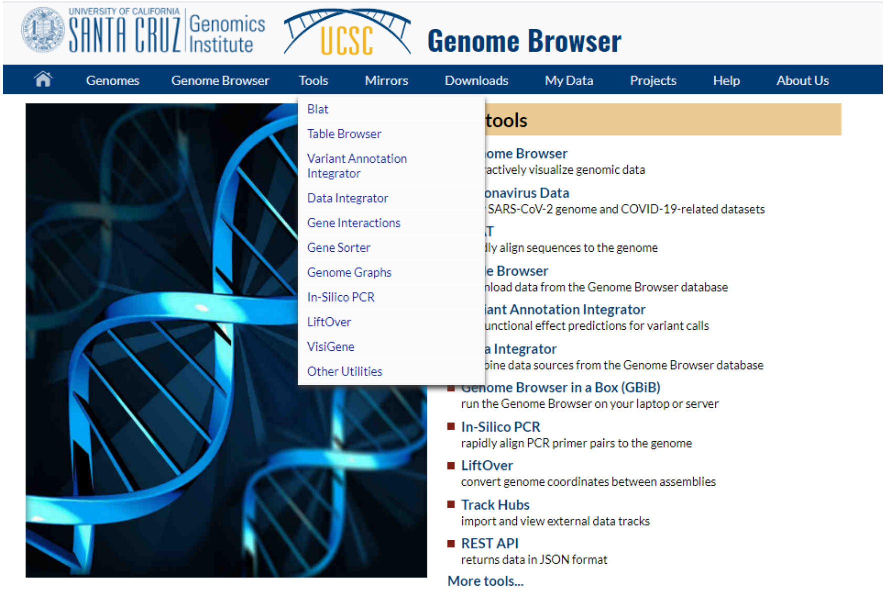
Counting SNPs

- Using the table browser at the UCSC genome database (http://genome.ucsc.edu/cgi-bin/hgTables?org=human)

- Comparing chr4 of eight different human individuals
  (1) YanHuang (Han Chinese individual, anonymous)
  (2) Seong-Jin Kim (Korean)
  (3) James Watson
  (4) Craig Venter
  (5) YRI NA18507 (Yoruba, anonymous of the 1000 Genomes Project)
  (6) NA12891 (Central European origin, anonymous of the 1000 Genomes Project)
  (7) ABT (Desmond Tutu)
  (8) KB1, Khoisan/Bushmen individual

Counting SNPs

```
http://genome.ucsc.edu/index.html
```



tools

- ome Browser
  actively visualize genomic data
- onavirus Data
  SARS-CoV-2 genome and COVID-19-related datasets
- T
  lly align sequences to the genome
- e Browser
  nload data from the Genome Browser database
- iant Annotation Integrator
  unctional effect predictions for variant calls
- a Integrator
  bine data sources from the Genome Browser database
- Genome Browser in a Box (GBiB)
  run the Genome Browser on your laptop or server
- In-Silico PCR
  rapidly align PCR primer pairs to the genome
- LiftOver
  convert genome coordinates between assemblies
- Track Hubs
  import and view external data tracks
- REST API
  returns data in JSON format

More tools...

Counting SNPs

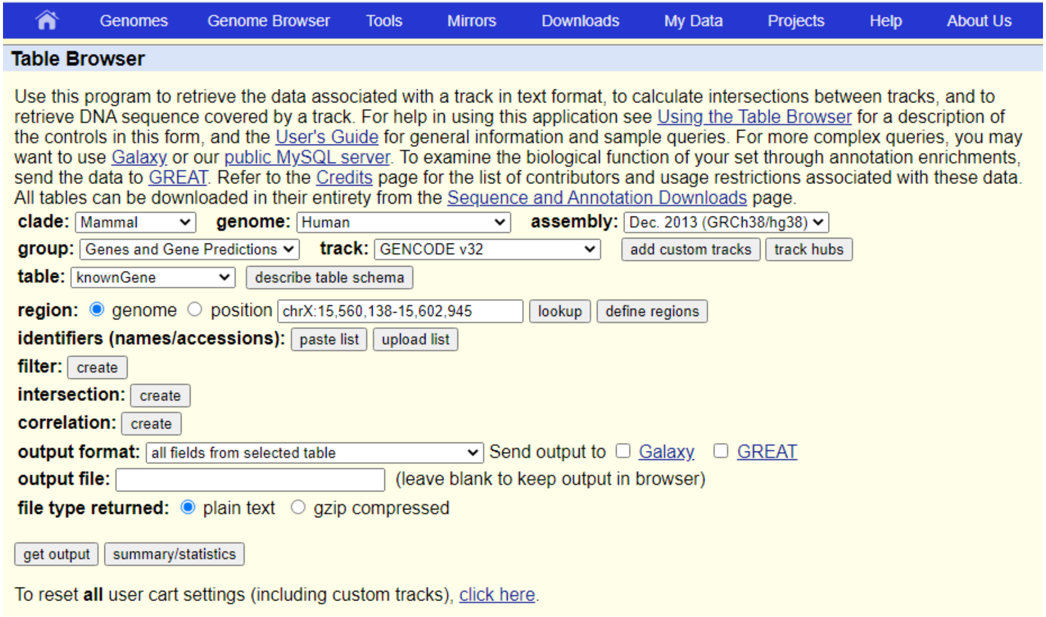


Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see Using the Table Browser for a description of the controls in this form, and the User's Guide for general information and sample queries. For more complex queries, you may want to use Galaxy or our public MySQL server. To examine the biological function of your set through annotation enrichments, send the data to GREAT. Refer to the Credits page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the Sequence and Annotation Downloads page.

clade: Mammal **genome:** Human **assembly:** Dec. 2013 (GRCh38/hg38)

group: Genes and Gene Predictions **track:** GENCODE v32 add custom tracks track hubs

table: knownGene describe table schema

region: ● genome ○ position chrX:15,560,138-15,602,945 lookup define regions

identifiers (names/accessions): paste list upload list

filter: create

intersection: create

correlation: create

output format: all fields from selected table Send output to □ Galaxy □ GREAT

output file: (leave blank to keep output in browser)

file type returned: ● plain text ○ gzip compressed

get output summary/statistics

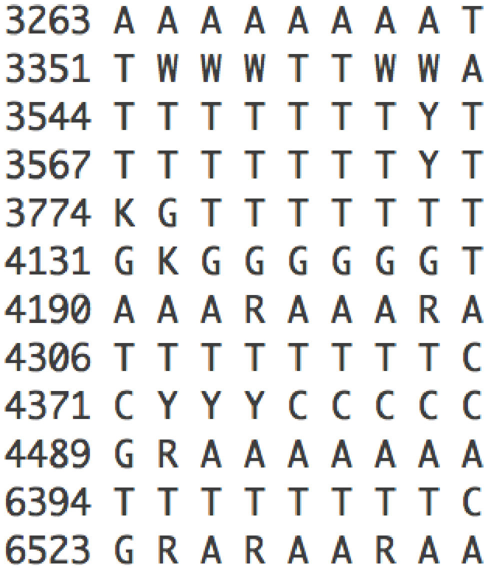
To reset **all** user cart settings (including custom tracks), click here.

Basic Shell Commands

```
$ cd [User_Folder]
$ mkdir session14
$ cd session14
```

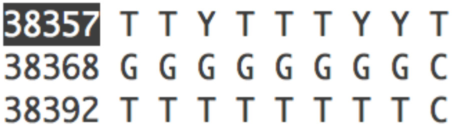
Counting SNPs

```
$ cp /home/biguser/tutor/session14/snp.txt .
$ less snp.txt
```



```
3263 A A A A A A A A T
3351 T W W W T T W W A
3544 T T T T T T T Y T
3567 T T T T T T T Y T
3774 K G T T T T T T T
4131 G K G G G G G G T
4190 A A A R A A A R A
4306 T T T T T T T T C
4371 C Y Y Y C C C C C
4489 G R A A A A A A A
6394 T T T T T T T T C
6523 G R A R A A R A A
```

Counting SNPs

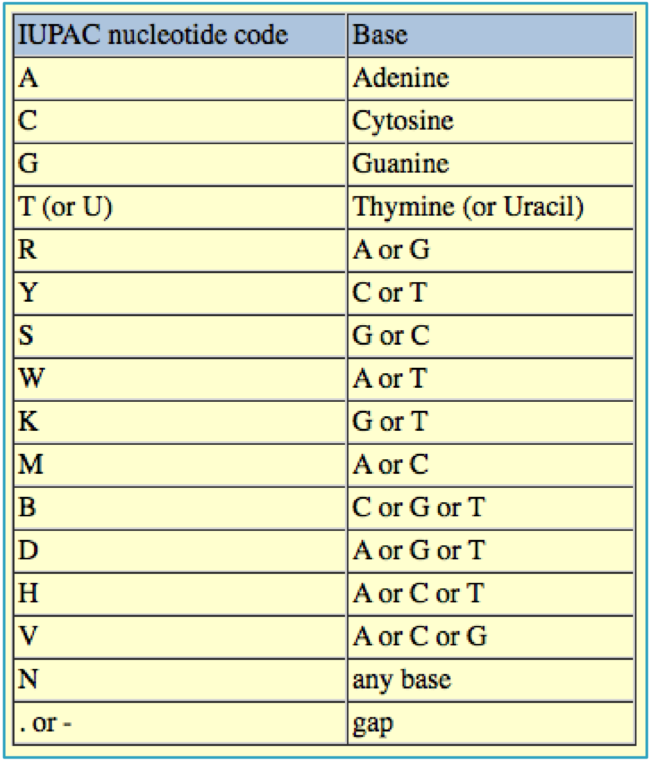


```
38357 T T Y T T T Y Y T
38368 G G G G G G G G C
38392 T T T T T T T T C
```

- The first column is position
- Nucleotides from eight individuals
- The last column is the nucleotide of chimpanzee
- Positions where at least one genome has an unknown base have been removed
- Positions containing the same nucleotide in all nine genomes have been removed

Counting SNPs

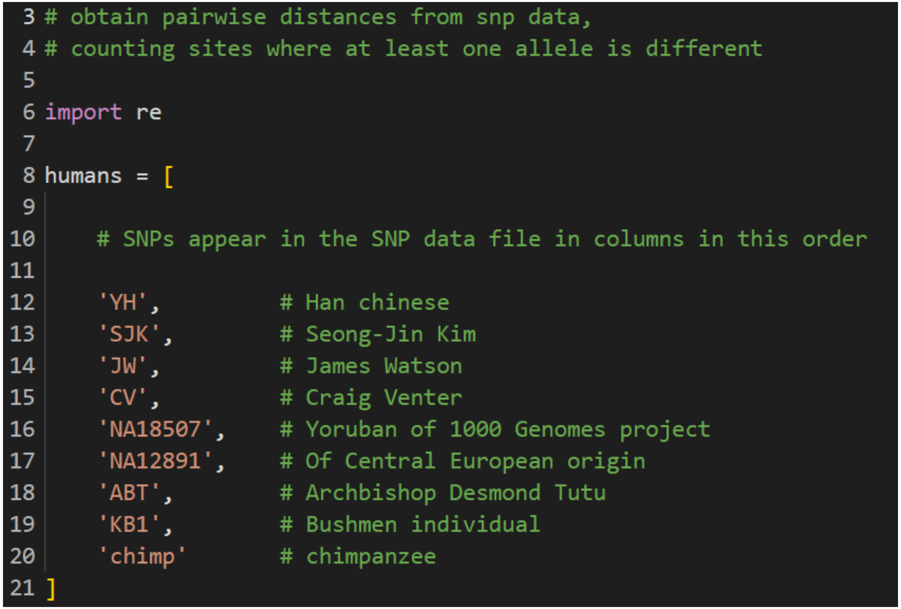
```
3263 A A A A A A A A T
3351 T W W W T T W W A
3544 T T T T T T T Y T
3567 T T T T T T T Y T
3774 K G T T T T T T T
4131 G K G G G G G G T
4190 A A A R A A A R A
4306 T T T T T T T T C
```



IUPAC nucleotide code	Base
A	Adenine
C	Cytosine
G	Guanine
T (or U)	Thymine (or Uracil)
R	A or G
Y	C or T
S	G or C
W	A or T
K	G or T
M	A or C
B	C or G or T
D	A or G or T
H	A or C or T
V	A or C or G
N	any base
. or -	gap

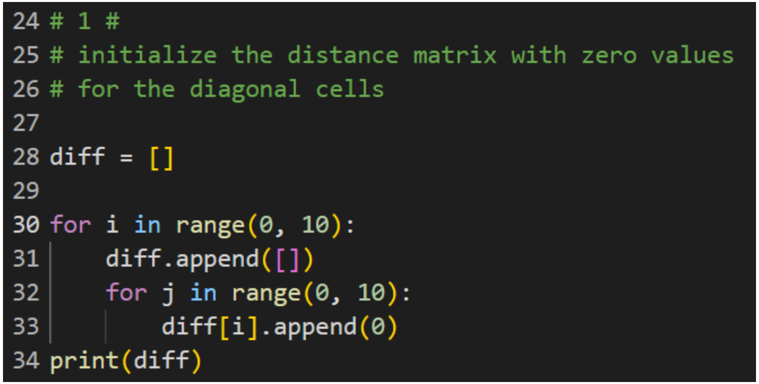
Counting SNPs

```
Create a distance matrix from SNPs of 9 genomes

$ vi snp.py
```



```python
# obtain pairwise distances from snp data,
# counting sites where at least one allele is different

import re

humans = [

    # SNPs appear in the SNP data file in columns in this order

    'YH',         # Han chinese
    'SJK',        # Seong-Jin Kim
    'JW',         # James Watson
    'CV',         # Craig Venter
    'NA18507',    # Yoruban of 1000 Genomes project
    'NA12891',    # Of Central European origin
    'ABT',        # Archbishop Desmond Tutu
    'KB1',        # Bushmen individual
    'chimp'       # chimpanzee
]
```

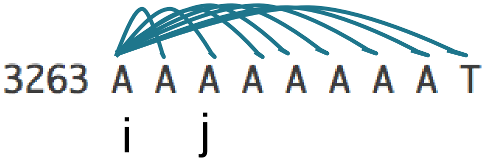
Counting SNPs



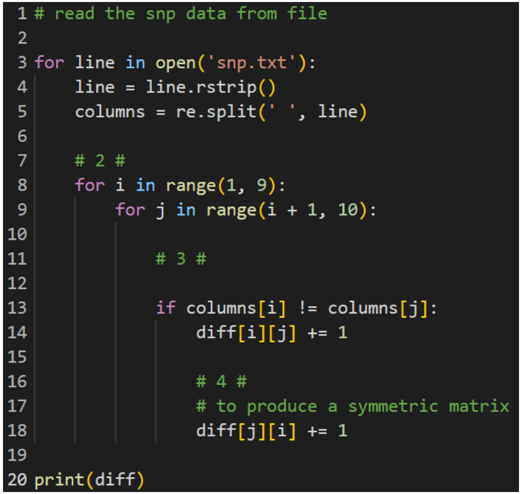
```python
# 1 #
# initialize the distance matrix with zero values
# for the diagonal cells

diff = []

for i in range(0, 10):
    diff.append([])
    for j in range(0, 10):
        diff[i].append(0)
print(diff)
```

```
$ python snp.py
```

```
[[0, 0, 0, 0, 0, 0, 0, 0, 0, 0], [0, 0, 0, 0, 0, 0, 0, 0, 0, 0],
 [0, 0, 0, 0, 0, 0, 0, 0, 0, 0], [0, 0, 0, 0, 0, 0, 0, 0, 0, 0],
 [0, 0, 0, 0, 0, 0, 0, 0, 0, 0], [0, 0, 0, 0, 0, 0, 0, 0, 0, 0],
 [0, 0, 0, 0, 0, 0, 0, 0, 0, 0], [0, 0, 0, 0, 0, 0, 0, 0, 0, 0],
 [0, 0, 0, 0, 0, 0, 0, 0, 0, 0], [0,_0, 0, 0, 0, 0, 0, 0, 0, 0]]
```



Counting SNPs

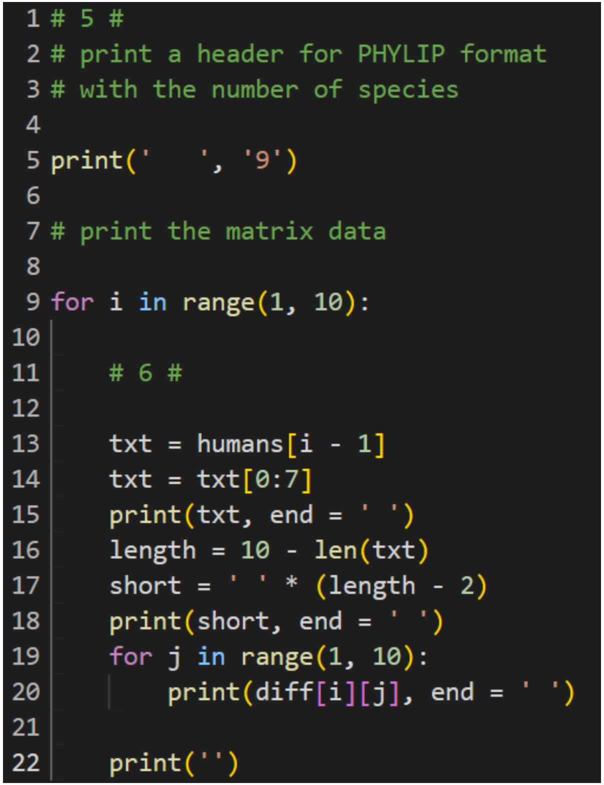


```python
# read the snp data from file

for line in open('snp.txt'):
    line = line.rstrip()
    columns = re.split(' ', line)

    # 2 #
    for i in range(1, 9):
        for j in range(i + 1, 10):

            # 3 #

            if columns[i] != columns[j]:
                diff[i][j] += 1

                # 4 #
                # to produce a symmetric matrix
                diff[j][i] += 1

print(diff)
```

```
$ python snp.py
```

```
[[0, 0, 0, 0, 0, 0, 0, 0, 0, 0], [0, 0, 44597, 53594, 53913, 67914, 53710, 68837, 77272, 593367],
 [0, 44597, 0, 54192, 54537, 68826, 55281, 69404, 76929, 593496], [0, 53594, 54192, 0, 50859, 702
84, 51260, 70256, 77590, 592751], [0, 53913, 54537, 50859, 0, 70149, 51009, 69659, 77369, 592632]
, [0, 67914, 68826, 70284, 70149, 0, 69245, 70057, 79508, 599102], [0, 53710, 55281, 51260, 51009
, 69245, 0, 69941, 78130, 594831], [0, 68837, 69404, 70256, 69659, 70057, 69941, 0, 77707, 599292
], [0, 77272, 76929, 77590, 77369, 79508, 78130, 77707, 0, 600776], [0, 593367, 593496, 592751, 5
92632, 599102, 594831, 599292, 600776, 0]]
```

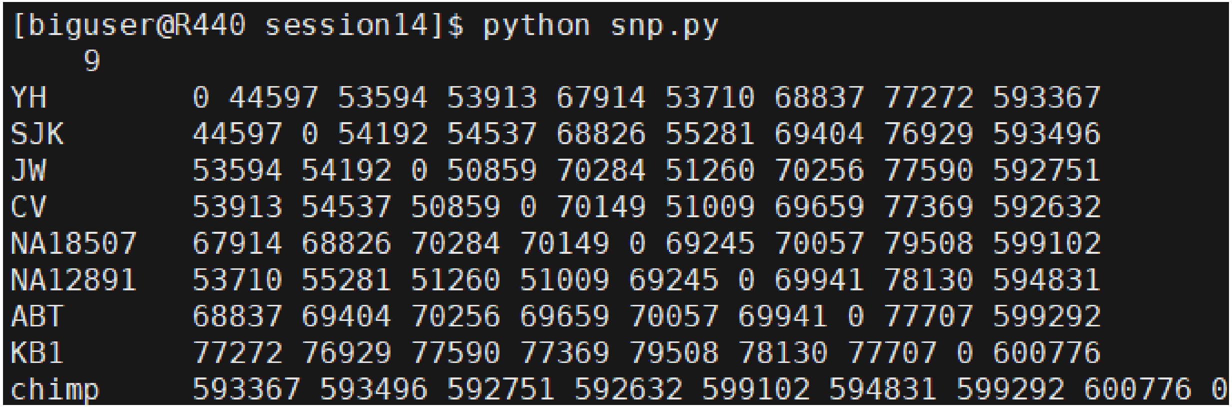
Counting SNPs



```python
# 5 #
# print a header for PHYLIP format
# with the number of species

print('   ', '9')

# print the matrix data

for i in range(1, 10):

    # 6 #

    txt = humans[i - 1]
    txt = txt[0:7]
    print(txt, end = ' ')
    length = 10 - len(txt)
    short = ' ' * (length - 2)
    print(short, end = ' ')
    for j in range(1, 10):
        print(diff[i][j], end = ' ')

    print('')
```

Counting SNPs

```
$ python snp.py
```

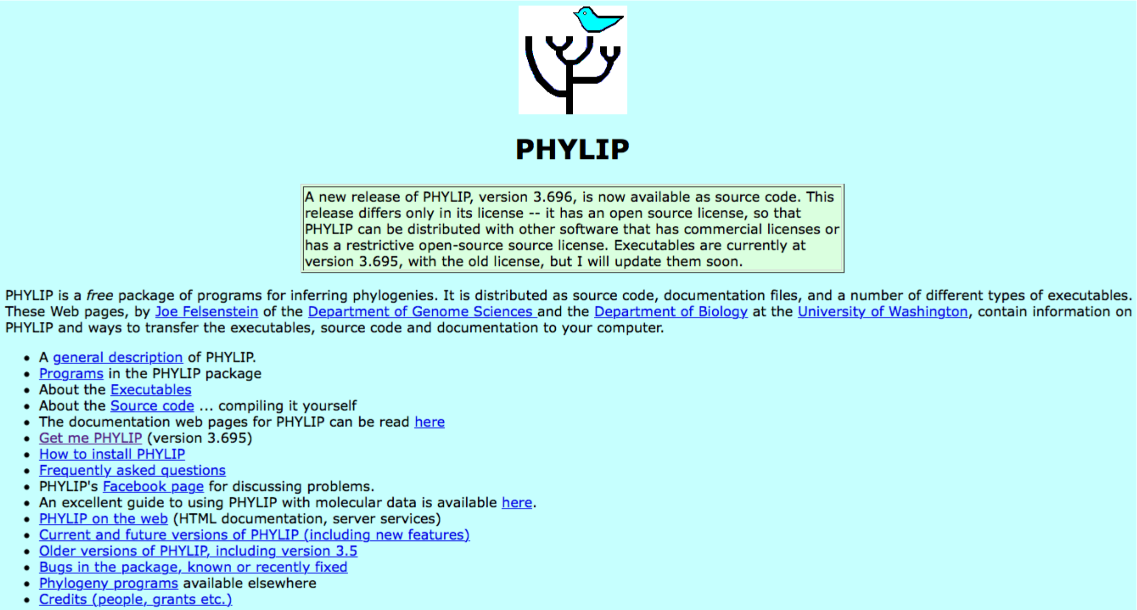


```
[biguser@R440 session14]$ python snp.py
    9
YH        0 44597 53594 53913 67914 53710 68837 77272 593367
SJK       44597 0 54192 54537 68826 55281 69404 76929 593496
JW        53594 54192 0 50859 70284 51260 70256 77590 592751
CV        53913 54537 50859 0 70149 51009 69659 77369 592632
NA18507   67914 68826 70284 70149 0 69245 70057 79508 599102
NA12891   53710 55281 51260 51009 69245 0 69941 78130 594831
ABT       68837 69404 70256 69659 70057 69941 0 77707 599292
KB1       77272 76929 77590 77369 79508 78130 77707 0 600776
chimp     593367 593496 592751 592632 599102 594831 599292 600776 0
```

```
$ python snp.py > snp.out
```

Phylip package - neighbor

- Phylip package (https://phylipweb.github.io/phylip/)



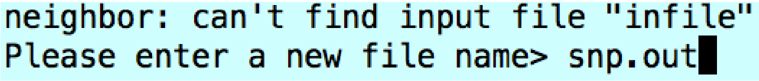
PHYLIP

A new release of PHYLIP, version 3.696, is now available as source code. This release differs only in its license -- it has an open source license, so that PHYLIP can be distributed with other software that has commercial licenses or has a restrictive open-source source license. Executables are currently at version 3.695, with the old license, but I will update them soon.

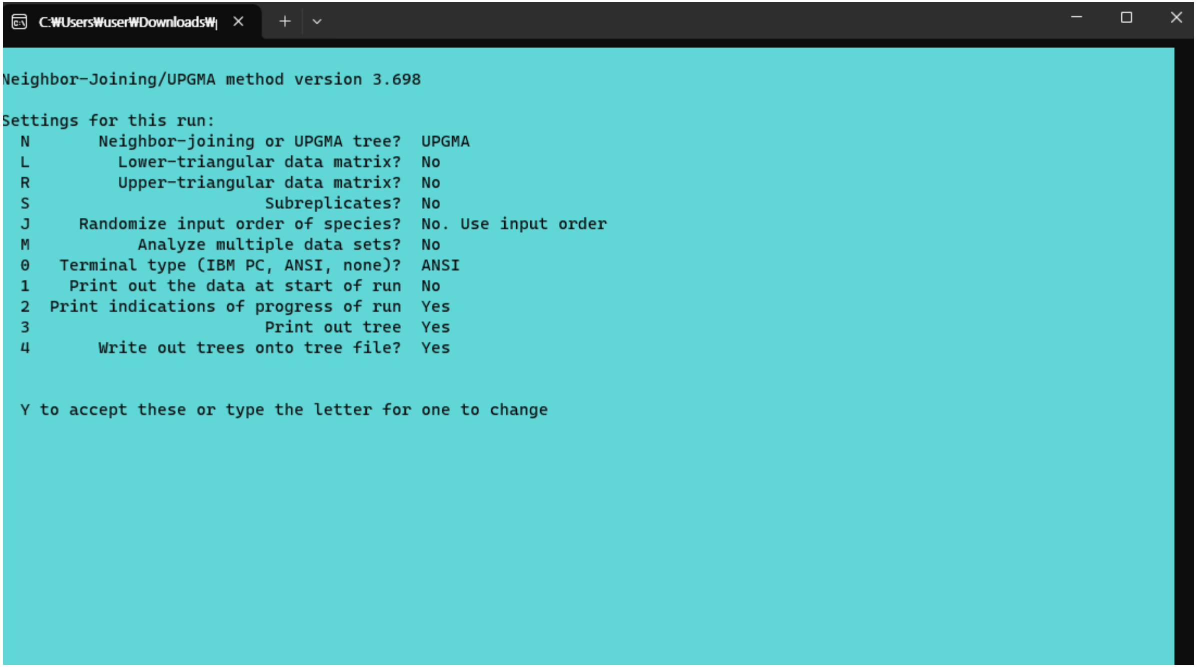
PHYLIP is a *free* package of programs for inferring phylogenies. It is distributed as source code, documentation files, and a number of different types of executables. These Web pages, by Joe Felsenstein of the Department of Genome Sciences and the Department of Biology at the University of Washington, contain information on PHYLIP and ways to transfer the executables, source code and documentation to your computer.

- A general description of PHYLIP.
- Programs in the PHYLIP package
- About the Executables
- About the Source code ... compiling it yourself
- The documentation web pages for PHYLIP can be read here
- Get me PHYLIP (version 3.695)
- How to install PHYLIP
- Frequently asked questions
- PHYLIP's Facebook page for discussing problems.
- An excellent guide to using PHYLIP with molecular data is available here.
- PHYLIP on the web (HTML documentation, server services)
- Current and future versions of PHYLIP (including new features)
- Older versions of PHYLIP, including version 3.5
- Bugs in the package, known or recently fixed
- Phylogeny programs available elsewhere
- Credits (people, grants etc.)

Phylip package - neighbor

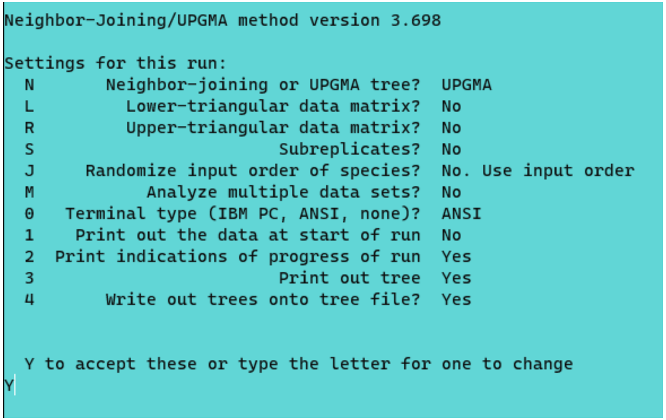


```
neighbor: can't find input file "infile"
Please enter a new file name> snp.out
```

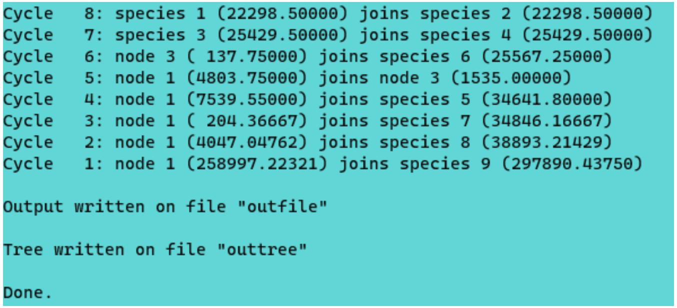


```
Neighbor-Joining/UPGMA method version 3.698

Settings for this run:
  N       Neighbor-joining or UPGMA tree?  UPGMA
  L         Lower-triangular data matrix?  No
  R         Upper-triangular data matrix?  No
  S                        Subreplicates?  No
  J     Randomize input order of species?  No. Use input order
  M           Analyze multiple data sets?  No
  0   Terminal type (IBM PC, ANSI, none)?  ANSI
  1    Print out the data at start of run  No
  2  Print indications of progress of run  Yes
  3                        Print out tree  Yes
  4       Write out trees onto tree file?  Yes


  Y to accept these or type the letter for one to change
```

Phylip package - neighbor

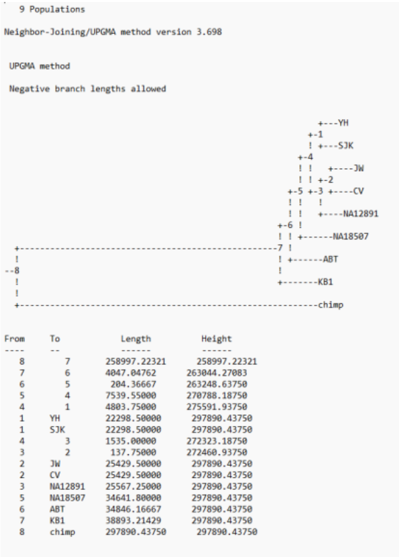


```
Neighbor-Joining/UPGMA method version 3.698

Settings for this run:
  N       Neighbor-joining or UPGMA tree?  UPGMA
  L         Lower-triangular data matrix?  No
  R         Upper-triangular data matrix?  No
  S                        Subreplicates?  No
  J     Randomize input order of species?  No. Use input order
  M           Analyze multiple data sets?  No
  0   Terminal type (IBM PC, ANSI, none)?  ANSI
  1    Print out the data at start of run  No
  2  Print indications of progress of run  Yes
  3                        Print out tree  Yes
  4       Write out trees onto tree file?  Yes


  Y to accept these or type the letter for one to change
Y
```



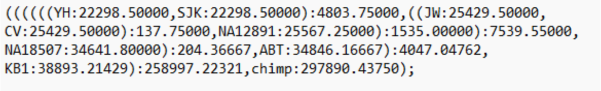
```
Cycle   8: species 1 (22298.50000) joins species 2 (22298.50000)
Cycle   7: species 3 (25429.50000) joins species 4 (25429.50000)
Cycle   6: node 3 ( 137.75000) joins species 6 (25567.25000)
Cycle   5: node 1 (4803.75000) joins node 3 (1535.00000)
Cycle   4: node 1 (7539.55000) joins species 5 (34641.80000)
Cycle   3: node 1 ( 204.36667) joins species 7 (34846.16667)
Cycle   2: node 1 (4047.04762) joins species 8 (38893.21429)
Cycle   1: node 1 (258997.22321) joins species 9 (297890.43750)

Output written on file "outfile"

Tree written on file "outtree"

Done.
```

outfile



```
   9 Populations

Neighbor-Joining/UPGMA method version 3.698


 UPGMA method

 Negative branch lengths allowed


                                                              +---YH
                                                            +-1
                                                            ! +---SJK
                                                          +-4
                                                          ! !   +----JW
                                                          ! ! +-2
                                                        +-5 +-3 +----CV
                                                        ! !   !
                                                        ! !   +----NA12891
                                                      +-6 !
                                                      ! ! +------NA18507
  +--------------------------------------------------7 !
  !                                                   ! +------ABT
--8                                                   !
  !                                                   +-------KB1
  !
  +-----------------------------------------------------------chimp


From     To             Length          Height
----     --             ------          ------
   8        7       258997.22321       258997.22321
   7        6       4047.04762     263044.27083
   6        5        204.36667     263248.63750
   5        4       7539.55000     270788.18750
   4        1       4803.75000     275591.93750
   1     YH         22298.50000     297890.43750
   1     SJK        22298.50000     297890.43750
   4        3       1535.00000     272323.18750
   3        2        137.75000     272460.93750
   2     JW         25429.50000     297890.43750
   2     CV         25429.50000     297890.43750
   3     NA12891    25567.25000     297890.43750
   5     NA18507    34641.80000     297890.43750
   6     ABT        34846.16667     297890.43750
   7     KB1        38893.21429     297890.43750
   8     chimp      297890.43750       297890.43750
```

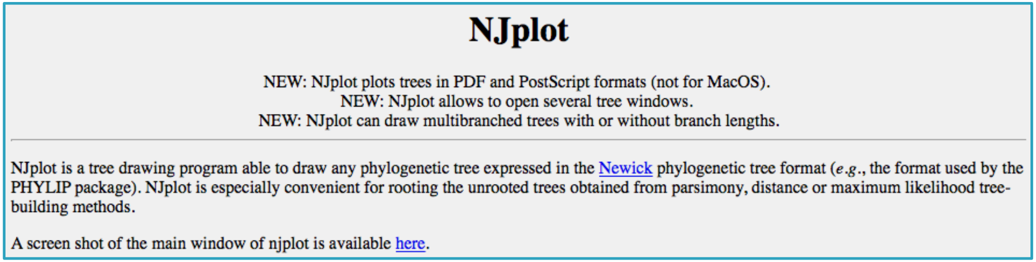
outtree



```
((((((YH:22298.50000,SJK:22298.50000):4803.75000,((JW:25429.50000,
CV:25429.50000):137.75000,NA12891:25567.25000):1535.00000):7539.55000,
NA18507:34641.80000):204.36667,ABT:34846.16667):4047.04762,
KB1:38893.21429):258997.22321,chimp:297890.43750);
```

NJplot

- NJplot (http://doua.prabi.fr/software/njplot)

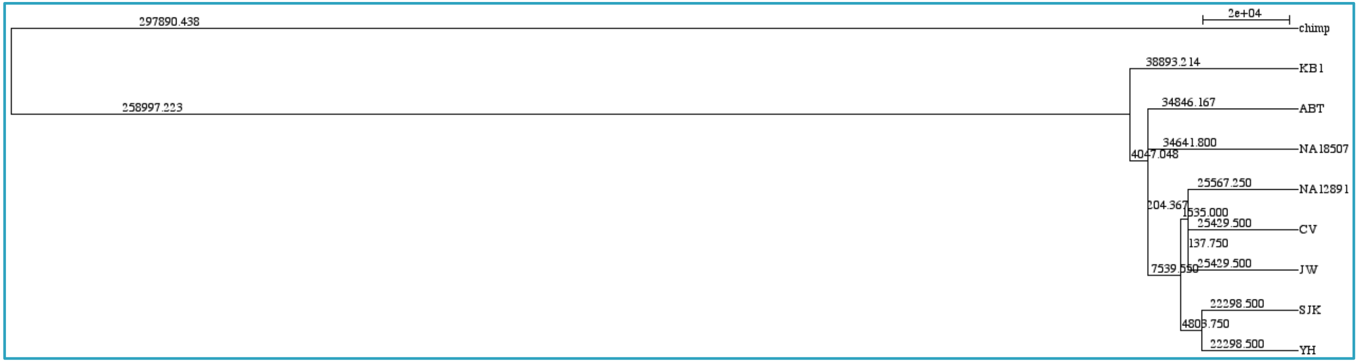


NJplot

NEW: NJplot plots trees in PDF and PostScript formats (not for MacOS).
NEW: NJplot allows to open several tree windows.
NEW: NJplot can draw multibranched trees with or without branch lengths.

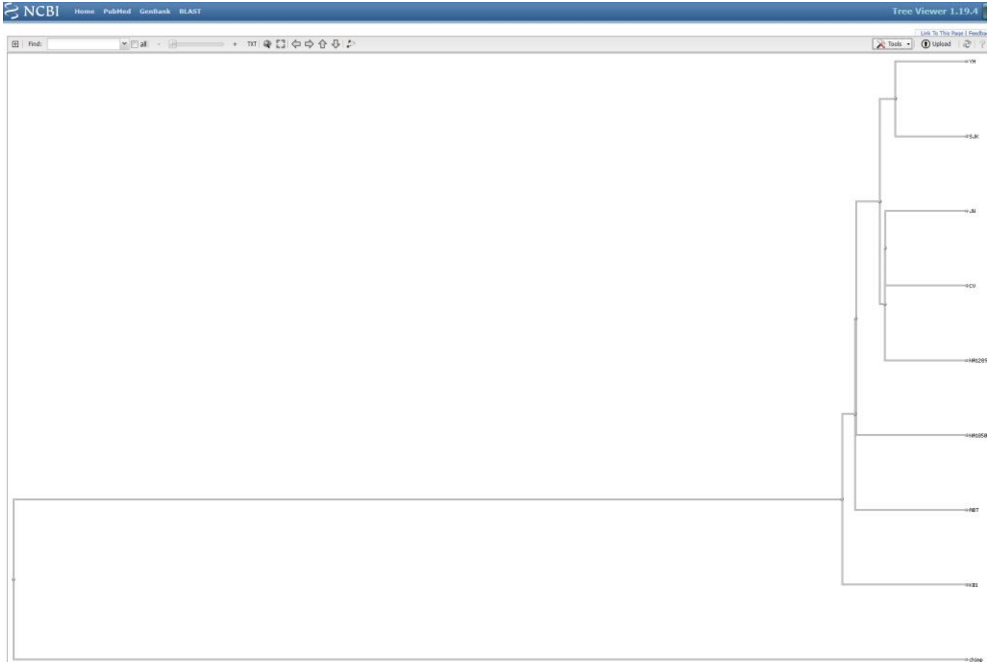
NJplot is a tree drawing program able to draw any phylogenetic tree expressed in the Newick phylogenetic tree format (*e.g.*, the format used by the PHYLIP package). NJplot is especially convenient for rooting the unrooted trees obtained from parsimony, distance or maximum likelihood tree-building methods.

A screen shot of the main window of njplot is available here.



NCBI tree viewer

- NCBI tree viewer (https://www.ncbi.nlm.nih.gov/projects/treeview/)

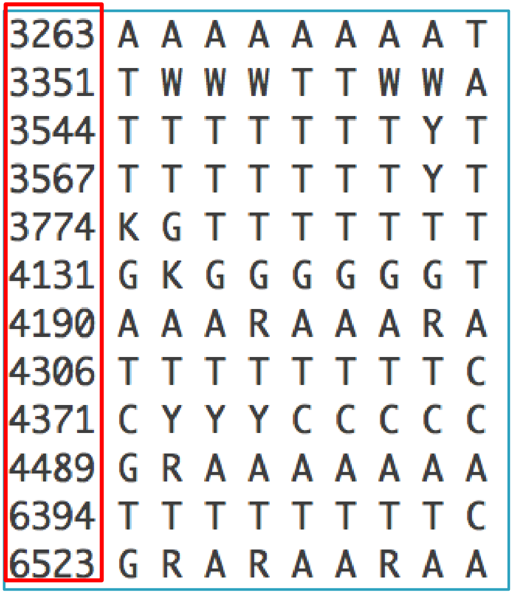


Exercise

- The file ‘chr4snp.txt’ is a list of SNPs in the human chromosome 4, according to dbSNP build 130. Write a Python script that will list the SNPs (positions) that are present in this file but that are not found in the file ‘snp.txt’. The file ‘chr4snp.txt’ uses ‘zero-based’ numbering. From a practical point of view, this means that the third column positions in that file are comparable to the position numbers in ‘snp.txt’.

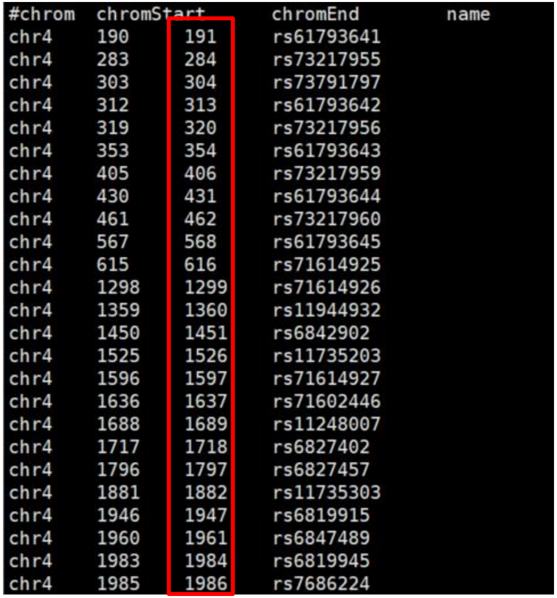
```
cp /home/biguser/tutor/session14/chr4snp.txt .
```

Exercise



```
3263 A A A A A A A A T
3351 T W W W T T W W A
3544 T T T T T T T Y T
3567 T T T T T T T Y T
3774 K G T T T T T T T
4131 G K G G G G G G T
4190 A A A R A A A R A
4306 T T T T T T T T C
4371 C Y Y Y C C C C C
4489 G R A A A A A A A
6394 T T T T T T T T C
6523 G R A R A A R A A
```

Snp.txt

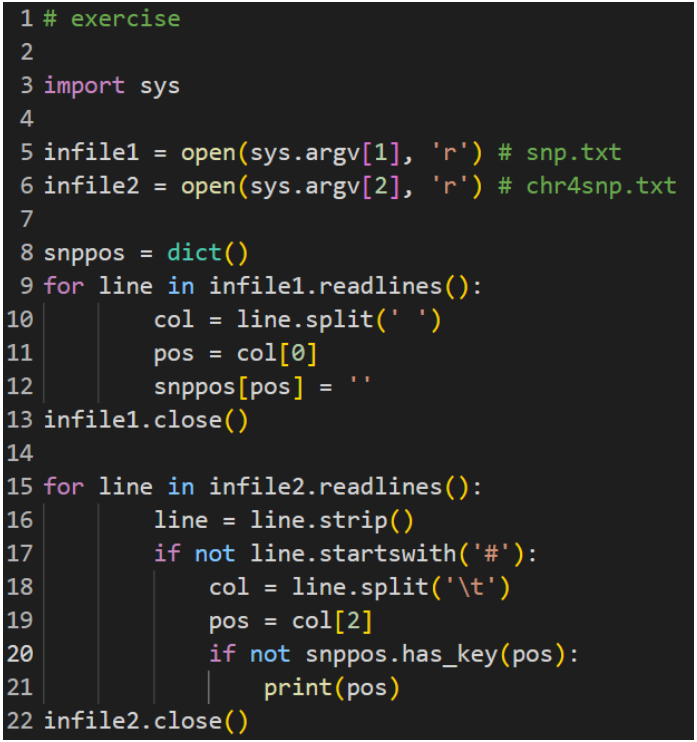


```
#chrom  chromStart      chromEnd        name
chr4    190     191     rs61793641
chr4    283     284     rs73217955
chr4    303     304     rs73791797
chr4    312     313     rs61793642
chr4    319     320     rs73217956
chr4    353     354     rs61793643
chr4    405     406     rs73217959
chr4    430     431     rs61793644
chr4    461     462     rs73217960
chr4    567     568     rs61793645
chr4    615     616     rs71614925
chr4    1298    1299    rs71614926
chr4    1359    1360    rs11944932
chr4    1450    1451    rs6842902
chr4    1525    1526    rs11735203
chr4    1596    1597    rs71614927
chr4    1636    1637    rs71602446
chr4    1688    1689    rs11248007
chr4    1717    1718    rs6827402
chr4    1796    1797    rs6827457
chr4    1881    1882    rs11735303
chr4    1946    1947    rs6819915
chr4    1960    1961    rs6847489
chr4    1983    1984    rs6819945
chr4    1985    1986    rs7686224
```

실제 position chr4snp.txt

Chr4snp.txt 에 있는 snp 들중 snp.txt에 없는 position을 출력 할 것!

Exercise



```
# exercise

import sys

infile1 = open(sys.argv[1], 'r') # snp.txt
infile2 = open(sys.argv[2], 'r') # chr4snp.txt

snppos = dict()
for line in infile1.readlines():
        col = line.split(' ')
        pos = col[0]
        snppos[pos] = ''
infile1.close()

for line in infile2.readlines():
        line = line.strip()
        if not line.startswith('#'):
            col = line.split('\t')
            pos = col[2]
            if not snppos.has_key(pos):
                print(pos)
infile2.close()
```