SESSION 14. PRACTICE

Personal genomes:
The differences between you and me

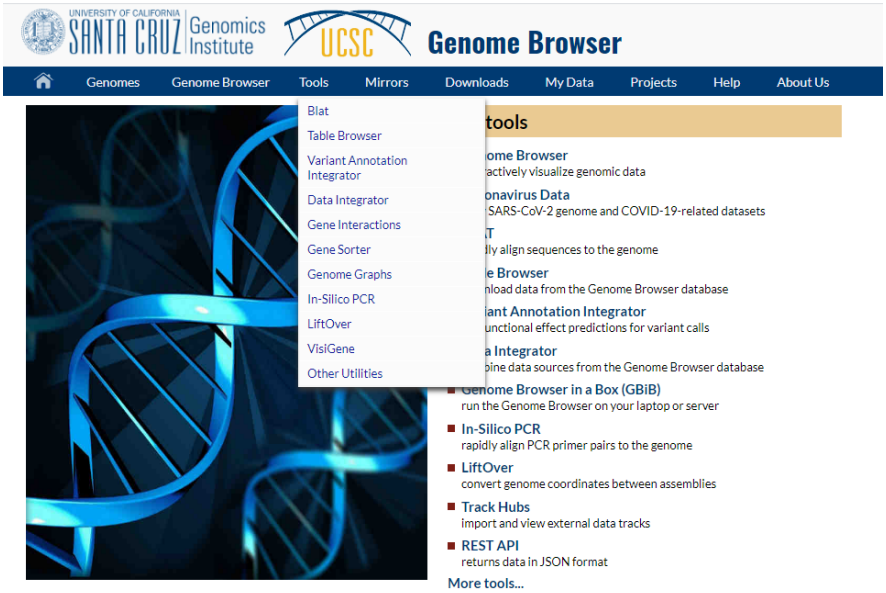
Counting SNPs

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

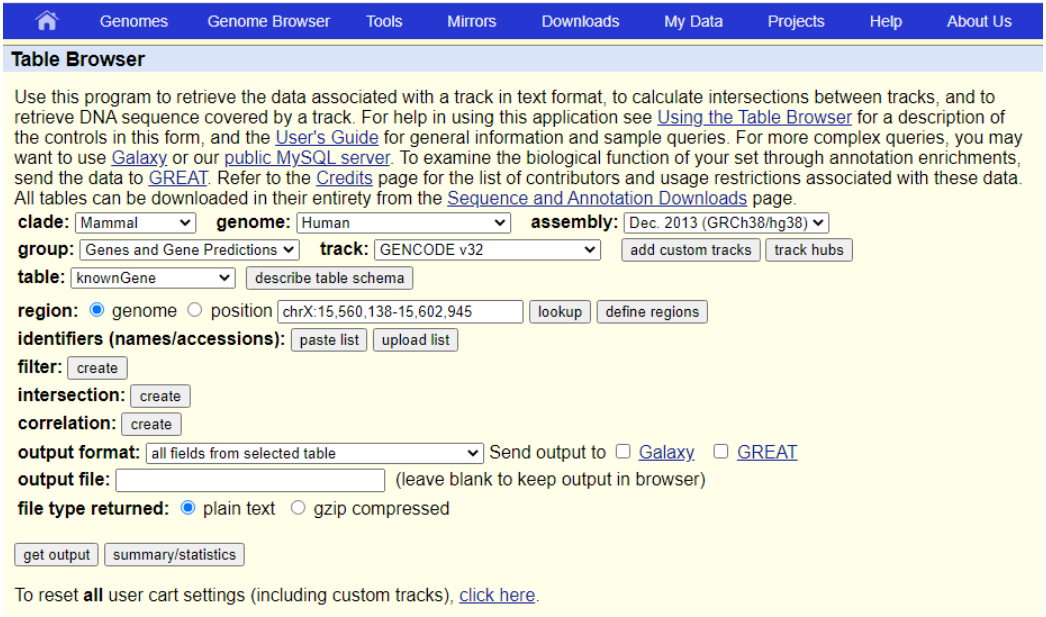
- Comparing chr4 of eight different human individuals
  (1) YanHuang (Han Chinese individual, anonymous)
  (2) Seong-Jin Kim (Korean)
  (3) James Watson
  (4) Craig Venter
  (5) YRI NA18507 (Yoruba, anonymous of the 1000 Genomes Project)
  (6) NA12891 (Central European origin, anonymous of the 1000 Genomes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

Counting SNPs

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



Counting SNPs



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
```

```
#!/usr/bin/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

```
# 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

```
# 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

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

이전 코드 부분에 있었던 print 명령어 앞에 #을 붙여서 비활성화를 꼭 시켜놓으세요!

Counting SNPs

```
$ python snp.py
```

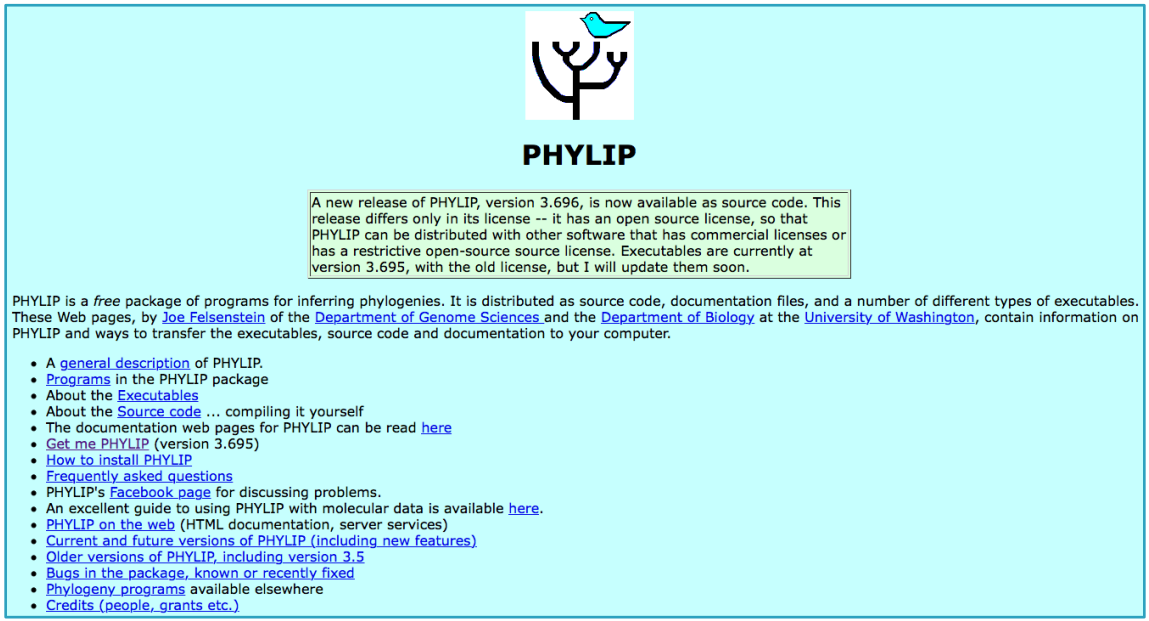
YH SJK JW CV NA18507 NA12891 ABT KB1 chimp

```
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 (http://evolution.genetics.washington.edu/phylip.html)



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 3.695

Settings for this run:
  N       Neighbor-joining or UPGMA tree?  Neighbor-joining
  O                       Outgroup root?  No, use as outgroup species  1
  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
N
```

Phylip package - neighbor

```
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.
```

outtree

```
((((((YH:22298.50000,SJK:
22298.50000):4803.75000,
((JW:25429.50000,
CV:25429.50000):
137.75000,NA12891:25567.2
5000):1535.00000):
7539.55000,
NA18507:34641.80000):
204.36667,ABT:
34846.16667):4047.04762,
KB1:38893.21429):
258997.22321,chimp:
297890.43750);
```

NJplot

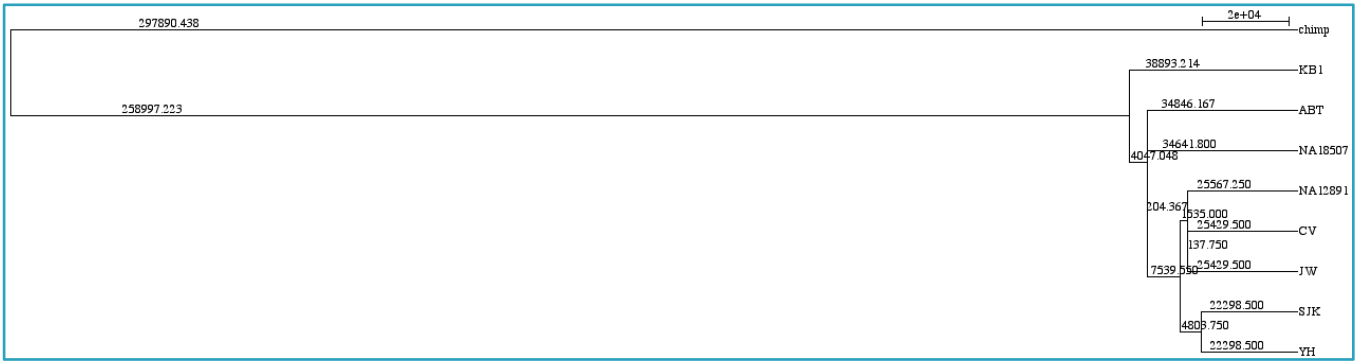
- NJplot
  (http://doua.prabi.fr/software/njplot)

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.



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 들을 snp.txt에 없는 position을 출력 할 거!

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():
        columns = line.split(' ')
        pos = columns[0]
        snppos[pos] = ''
infile1.close()

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

```
191262559
191262569
191262593
191262622
191262626
191262659
191262699
191262724
191262788
191262790
191262826
191262846
191262860
```