digital™

LIVE FREE OR DIE

UNIX

Registered TM of UNIX System Laboratories,

A wholly owned subsidiary of Novell, Inc.
What computers can run Unix?
What computers can run Unix?

Apple OS X Macs
What computers can run Unix?

Apple OS X Macs

Wireless internet routers
What computers can run Unix?

- Apple OS X Macs
- Google’s Android phones
- Wireless internet routers
What computers can run Unix?

- Apple OS X Macs
- Wireless internet routers
- Google’s Android phones
- Airplane entertainment systems
The Terminal Window
The Terminal Window
The Terminal Window
The Terminal Window

the shell, the prompt, the command line
The Terminal Window
The Terminal Window

Make it comfortable to work in:

• Resize the window
• Change your font size
• Open multiple terminal windows
Obtain a cheat sheet

google “unix commands”
In UNIX everything is a file organized in a hierarchy
/home/catchen/working
Create a series of directories

```
ubuntu@ip-10-4-193-188:~$ mkdir shell
ubuntu@ip-10-4-193-188:~$ cd shell
ubuntu@ip-10-4-193-188:~$/shell$ mkdir research
ubuntu@ip-10-4-193-188:~$/shell$ ls
research
ubuntu@ip-10-4-193-188:~$/shell$ cd research/
ubuntu@ip-10-4-193-188:~$/shell/research$ mkdir seq
ubuntu@ip-10-4-193-188:~$/shell/research$ ls
seq
ubuntu@ip-10-4-193-188:~$/shell/research$ cd seq/
ubuntu@ip-10-4-193-188:~$/shell/research/seq$ mkdir radtags
ubuntu@ip-10-4-193-188:~$/shell/research/seq$ ls -la
total 8
drwxrwxr-x 2 ubuntu ubuntu 4096 2012-03-06 23:08 .
drwxrwxr-x 3 ubuntu ubuntu 4096 2012-03-06 23:08 ..
ubuntu@ip-10-4-193-188:~$/shell/research/seq/radtags$ pwd
/home/ubuntu/shell/research/seq/radtags
ubuntu@ip-10-4-193-188:~$/shell/research/seq/radtags$ 
```
Create a series of directories

```bash
% mkdir shell
% cd shell
% mkdir research
% ls
research
% cd research/
% mkdir seq
% ls
seq
% cd seq/
% mkdir radtags
% ls
radtags
% ls -la
total 8
drwxrwxr-x 2 ubuntu ubuntu 4096 2012-03-06 23:08 ..
drwxrwxr-x 3 ubuntu ubuntu 4096 2012-03-06 23:08 .
% pwd
/home/ubuntu/shell/research/seq/radtags
% ls
```

% mkdir shell       % cd shell       % ls
Paths, cont

This shell view of the nested directories
shell, research, seq, and radtags.....

.... is equivalent to this GUI view of the
same directories

And the **radtags** directory is uniquely identified by its path:
/home/ubuntu/shell/research/seq/radtags
Absolute and relative paths

How do I get to the Hotel Zlaty Andel?
Absolute and relative paths

How do I get to the Hotel Zlaty Andel?
Absolute and relative paths

How do I get to the Hotel Zlaty Andel?
Absolute Path

/home/catchen/working
Relative Path?

```
/home/usr/bin/...
cresko/catchen/lib/bin/...
working/research/...
```
Special files -- ‘dot’

```
/  
  ├── root
  │   └── ...  
  ├── home
  │   └── ...  
  ├── usr
  │   └── ...  
  └── bin
      └── ...  
```

```
  ├── cresko
  │   └── ...  
  ├── catchen
  │   └── ...  
  ├── lib
  │   └── ...  
  └── bin
      └── ...  
```

```
  └── working
      └── ...  
```

```
  └── research
      └── ...  
```

Special files -- ‘dot’
Special files -- ‘dot dot’
Special files -- ‘dot dot’
Relative Path
Relative Path

.. working
Absolute Path:  /home/catchen/working/foo
Relative Path:  ../../../working/foo
Absolute Path: /home/catchen/working/foo
Relative Path: ../working/foo
Absolute Path:
Absolute Path:
Absolute Path:
Absolute Path:
Absolute Path: /home/catchen/working/foo
Absolute Path:
Absolute Path: `/home/catchen/working/foo`

Absolute Path:
Absolute Path: /home/catchen/working/foo
Absolute Path: /home/catchen/research/foo
Relative Path:
Relative Path:
Relative Path: 

`../working/foo`
Relative Path: `../working/foo`
Relative Path: `./working/f`
Relative Path:   ../working/foo
Relative Path:   ./foo
Absolute and relative paths

```
$ mkdir shell
$ cd shell
$ mkdir research
$ ls

$ cd research/
$ mkdir seq
$ ls

$ cd seq/
$ mkdir radtags
$ ls

$ cd radtags/
$ ls

$ ls -la

total 8
```

```
$ pwd
/home/ubuntu/shell/research/seq/radtags
```
Absolute and relative paths

```bash
# mkdir shell
# cd shell
# mkdir research
# ls

# cd research/
# mkdir seq
# ls

# cd seq/
# mkdir radtags
# ls

# cd radtags/
# ls

# pwd
```

Special Files
- `dot`
- `dot dot`

```bash
% ls .
% ls..
% ls ../../../
```
Binary programs - ls, cp, mkdir, etc.

Diagram:

- Root
  - Home
    - Cresko
    - Catchen
    - Lib
    - Bin
    - Working
    - Research
  - Usr
    - Bin
    - ...
Binary programs - `ls`, `cp`, `mkdir`, etc.

```
% ls /bin
```

```
bash  csh  
bunzip2 dash  
busybox date  
bzcat  dbus-clean-up-sockets  
bzcmp  dbus-daemon  
bzdiff  dbus-uuidgen  
bzegrep  dd  
bzexe  df  
bzfgrep  dir  
bzgrep  dmesg  
bzgrep  dnsdomainname  
bzgrep2recover  domainname  
bzless  dumpkeys  
bzmore  echo  
cat  ed  
chacl  egrep  
chgrp  false  
chmod  fgconsole  
chown  fgrep  
chvt  findmnt  
cp  fuser  
cpio  fusermount  
```
Relative and absolute paths

A shortcut to your ‘home’, tilde:

~

Moving through the filesystem:

cd

Knowing where you are:

pwd

% ls ~/
% cd ~/
% cd
% pwd
Relative and absolute paths

/home/tgac/shell/research/seq/radtags
Relative and absolute paths

```
/home/tgac/shell/research/seq/radtags
```

```
% ls .
% ls ..
% ls ../../../
```
Relative and absolute paths

```
% ls .
% ls ..
% cd ~/
% cd shell/research
% pwd
/home/tgac/shell/research/seq/radtags
```
Are you typing? You’re doing it wrong.

Tab-completion:

• Tab once to complete uniquely
• Tab twice to see all possible completions

Up-arrow:

• Previous commands can be found by pressing “up-arrow”

‘history’
Are you typing? You’re doing it wrong.

Tab-completion:

- Tab once to complete uniquely
- Tab twice to see all possible completions

Up-arrow:

- Previous commands can be found by pressing “up-arrow”

‘history’

% ls c <tab>
% ls c <tab><tab>
Are you typing? You’re doing it wrong.

Tab-completion:

- Tab once to complete uniquely
- Tab twice to see all possible completions

Up-arrow:

- Previous commands can be found by pressing “up-arrow”

`history`

```
% cd /etc
% ls c <tab>
% pwd
% ls c <tab><tab>
```
<table>
<thead>
<tr>
<th>Command</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ls -l</code></td>
<td>Provides a long listing</td>
</tr>
<tr>
<td><code>ls -la</code></td>
<td>Includes all files, even hidden files</td>
</tr>
<tr>
<td><code>ls -lh</code></td>
<td>Displays file sizes in human readable numbers</td>
</tr>
<tr>
<td></td>
<td>more</td>
</tr>
<tr>
<td>--------</td>
<td>-------------------------------------------</td>
</tr>
<tr>
<td>view a text file one screen full at a time</td>
<td>view the top 15 lines of a file</td>
</tr>
<tr>
<td>space-bar: scroll q: quit</td>
<td>-n num controls the number of lines</td>
</tr>
</tbody>
</table>
Explore the file hierarchy

1. Move to the directory /etc
   - What is the first line of the file ‘hosts’ in the directory /etc?
   - What is the relative file path to get to /var/log from here?
   - What is the absolute path?

2. Move to the directory /var/log/
   - What is the contents on line 73 of the dmesg file?
   - Without changing directories, what is the second line of the cpuinfo file in the proc directory?
     - What is the command to read this file with a relative path?
     - An absolute path?

3. Move back to the root, what directories do you see?

4. Move back home, what are three ways to move home from the root?
Copy example files

Return to the directory in your home called ‘shell’.

TSV file:
~/workshop_data/unix/batch_1.genotypes_1.loc.gz

FASTQ file:
~/workshop_data/unix/s_1_sequence.txt.gz

Tar Archive:
~/workshop_data/unix/samples.tar.gz
What is a tar archive?

tar = tape archive
Compress / Decompress

gzip / gunzip

batch_1.genotypes_1.loc.gz

s_1_sequence.txt.gz

Gzipped Tar archive

tar xvfz

samples.tar.gz

Tar archive

tar xvf

samples.tar
Sequencing on Illumina’s Flow cell
Sequencing on Illumina’s Flow cell, ctd.
Sequencing on Illumina’s Flow cell, ctd.

Sequencing on Illumina’s Flow cell, ctd.

Phred Quality Score

\[ Q = -10 \log_{10} p \]
Phred Quality Score

\[ Q = -10 \log_{10} p \]

<table>
<thead>
<tr>
<th>Phred Quality Score</th>
<th>Probability of incorrect base call</th>
<th>Base call accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>1 in 10</td>
<td>90%</td>
</tr>
<tr>
<td>20</td>
<td>1 in 100</td>
<td>99%</td>
</tr>
<tr>
<td>30</td>
<td>1 in 1000</td>
<td>99.9%</td>
</tr>
<tr>
<td>40</td>
<td>1 in 10000</td>
<td>99.99%</td>
</tr>
<tr>
<td>50</td>
<td>1 in 100000</td>
<td>99.999%</td>
</tr>
</tbody>
</table>
The FASTQ File Format

**FASTA**

>chromosome7
TTTGCTCTGCAAGGGGACACGTCAAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATT
ACATACTGCAGGTCAGGGATTATATCTCTGAGCCTGCTGTAACCCCTGATTCTTCATCCTTT
CCTAAGTGCAGGAGCTGGAGTCTGAGGATCTTGATGACAAAGACATATGCAGGGCTCAATTGGGATATA

**FASTQ**

@Sequence_137
TTTGCTCTGCAAGGGGACACGTCAAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATT
+Sequence_137
<?@DDDDHDFHHFBB@GGIACFHGGHBBHGCDBEAHACHE=CH.=7AACHHADDECDBCC66 (6>@C>5@CACCA
The FASTQ File Format

FASTA

>chromosome7
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
ACATACTGCAGGGTCAGGAGGATTATCTCCTCTGCAAGGTAACCGCTGCTGTAACCGTTGTTCTTCATCCTTT
CTAACTGCAGGGCTGTCTTGTCAGGTCTGACAAGACATATGCAGGGCTCAATTTGAGATAATTTGCTCAATATA

FASTQ

@Sequence_137
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
+Sequence_137
<?@DDDDDFHFFHB@GGIACFHGGHBGGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA

@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGTCTGCAGGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGATTTT
+?
<?@DDDDDFHFFHB@GGIACFHGGHBGGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA
ASCII Code

8 bits = $2^8$ combinations = 256

$$0 \times 2^7 + 1 \times 2^6 + 1 \times 2^5 + 1 \times 2^4 + 1 \times 2^3 + 0 \times 2^2 + 0 \times 2^1 + 1 \times 2^0 = 121 = y$$

$$1 \times 10^2 + 2 \times 10^1 + 1 \times 10^0 = 121 = y$$
The FASTQ File Format, ctd

@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGCTGAGGGGACACGTCAAGTCAACGCAGAGGTGTATGTCCAGTGATCTTTTGTATTTTT+
@?@DDDDDFHFFHHFBB@GGIACFHGGHBGGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA

Quality Scores

<table>
<thead>
<tr>
<th>S - Sanger</th>
<th>Phred+33, raw reads typically (0, 40)</th>
</tr>
</thead>
<tbody>
<tr>
<td>X - Solexa</td>
<td>Solexa+64, raw reads typically (-5, 40)</td>
</tr>
<tr>
<td>I - Illumina 1.3+</td>
<td>Phred+64, raw reads typically (0, 40)</td>
</tr>
<tr>
<td>J - Illumina 1.5+</td>
<td>Phred+64, raw reads typically (3, 40)</td>
</tr>
<tr>
<td></td>
<td>with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)</td>
</tr>
<tr>
<td></td>
<td>(Note: See discussion above).</td>
</tr>
<tr>
<td>L - Illumina 1.8+</td>
<td>Phred+33, raw reads typically (0, 41)</td>
</tr>
</tbody>
</table>

ASCII values 33 - 73 = 0 - 40

http://en.wikipedia.org/wiki/FASTQ_format
The FASTQ File Format, ctd

@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGTCTGCAAGGGGACACGTCAAAGGTCAGGGCAAGTTGGTTATGTCCAGTGGATCTTTTGATT
+
<?@DDDDHFHHFBB@GGIACFHHGGBHGBHCDHBEAHACHI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA

Quality Scores

<table>
<thead>
<tr>
<th>ASCII values</th>
<th>S - Sanger</th>
<th>Phred+33, raw reads typically (0, 40)</th>
</tr>
</thead>
<tbody>
<tr>
<td>33</td>
<td>59</td>
<td>64</td>
</tr>
<tr>
<td>73</td>
<td>104</td>
<td>126</td>
</tr>
</tbody>
</table>

X - Solexa  Solexa+64, raw reads typically (-5, 40)
I - Illumina 1.3+ Phred+64, raw reads typically (0, 40)
J - Illumina 1.5+ Phred+64, raw reads typically (3, 40)
   with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)
   (Note: See discussion above).
L - Illumina 1.8+ Phred+33, raw reads typically (0, 41)

ASCII values $33 - 73 = 0 - 40$
‘F’ = 70

http://en.wikipedia.org/wiki/FASTQ_format
Quality Scores

<table>
<thead>
<tr>
<th>S</th>
<th>Sanger</th>
<th>Phred+33, raw reads typically (0, 40)</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>Solexa</td>
<td>Solexa+64, raw reads typically (-5, 40)</td>
</tr>
<tr>
<td>I</td>
<td>Illumina 1.3+</td>
<td>Phred+64, raw reads typically (0, 40)</td>
</tr>
<tr>
<td>J</td>
<td>Illumina 1.5+</td>
<td>Phred+64, raw reads typically (3, 40)</td>
</tr>
<tr>
<td></td>
<td>with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(Note: See discussion above).</td>
<td></td>
</tr>
<tr>
<td>L</td>
<td>Illumina 1.8+</td>
<td>Phred+33, raw reads typically (0, 41)</td>
</tr>
</tbody>
</table>

ASCII values 33 - 73 = 0 - 40

‘F’ = 70

70 - 33 = 37

http://en.wikipedia.org/wiki/FASTQ_format
The FASTQ File Format, ctd

@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGCTGTCCAGGGGACACGTCAGTCGTCAAGTAGCAGGCAAGTTTGTGTATGTCCAGTTGATTTTGATTTT
+
<?@DDDDHFHHFBB@GGIACFHHGHBHGGCDHBEAHHACI=@CH.=7ACAHHADECDBCC66(6>@C>5@CACCA

http://en.wikipedia.org/wiki/Phred_quality_score
The FASTQ File Format, ctd

@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTTGTCTGCAGGGGACACGTCAAAGTCAAACGCAGGCAAGTTTGTGTTTATGTCCAGTGATCTTTTGATTTT
+
<?@DDDDDFHHFBBGGAFCFHGGHGBGHGCDHBHACHIC=CH.7ACAHHADECDBCC66(6>C>5CACCA

70 - 33 = 37

http://en.wikipedia.org/wiki/Phred_quality_score
The FASTQ File Format, ctd

@HWI-ST0747:162:C03AJACXX:3:1108:19763:106771 1:N:0:
TTGTCTGAGGGGACACGTCAAAGTCAGGCAAGTTTGTGTTTATGTCCAGTGGATCTTTTGTGTTT
+
<?@DDDDDHFHFHHFBB@GGIACFHGGHBGHGCDHBEAHACHI=@CH.=7ACAHHADECDBCC66 (6)>C>5@CACCA

70 - 33 = 37

<table>
<thead>
<tr>
<th>Phred Quality Score</th>
<th>Probability of incorrect base call</th>
<th>Base call accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>1 in 10</td>
<td>90%</td>
</tr>
<tr>
<td>20</td>
<td>1 in 100</td>
<td>99%</td>
</tr>
<tr>
<td>30</td>
<td>1 in 1000</td>
<td>99.9%</td>
</tr>
<tr>
<td>40</td>
<td>1 in 10000</td>
<td>99.99%</td>
</tr>
<tr>
<td>50</td>
<td>1 in 100000</td>
<td>99.999%</td>
</tr>
</tbody>
</table>

Count raw reads:

```
wc -l s_1_sequence.txt
```

```
grep "@" s_1_sequence.txt
grep -c "@" s_1_sequence.txt
```

```
grep -v "@" s_1_sequence.txt
grep -v -c "@" s_1_sequence.txt
```

Count reads with barcode:

```
grep -c "^CGATA" s_1_sequence.txt
```
Special Files

STDIN, STDOUT, STDERR

The Shell’s Killer App: Pipes

Leci n’est pas une pipe.
The Shell’s Killer App: Pipes, ctd.
The Shell’s Killer App: **Pipes**, ctd.
The Shell’s Killer App: **Pipes**, ctd.
The Shell’s Killer App: Pipes, ctd.
The Shell’s Killer App: *Pipes*, ctd.

So what is the purpose of the program *cat*?
cut

cut -f 10 batch_1.genotypes_1.loc

cut, capture the output

cut -f 1-10 batch_1.genotypes_1.loc > genos

cut, pipe the output to grep

cut -f 2 batch_1.genotypes_1.loc | grep -c "nnxnp"

cut -f 1-10,15,17 batch_1.genotypes_1.loc | grep "nnxnp" > genos2

Examine a marker, translating the output

cat batch_1.genotypes_1.loc | tr " " "," | grep "^96053"
ls
gunzip
man
more
cat
wc
head
cut
grep
sort
uniq
>
|
s_1_sequence.txt.gz

Decompress the file

1. Count the number of raw reads (250,000)
2. Count the number of reads with barcode CGATA (19,501)
3. Capture all FASTQ records for ACCAT into a file called sample_01.fq (you should get 18352 records, 73408 lines)
4. Determine the count of all barcodes in the file

```
286 CTAGT
7900 TCAGA
10659 ACTGC
10931 TGACC
11536 GAGAT
11871 CTGAA
14409 CGGCG
14508 TGGTT
18226 GAAGC
18352 ACCAT
18375 TCGAG
19501 CGATA
23012 AATTT
26336 GCATT
31136 CTAGG
```

5. Use `head` when building a command, `cat` once the command is working
6. Look at the `-n` option for the `head` command, the `-l` option for `wc`
7. The “^” character means “must occur at beginning of line” in a `grep` search
8. Look at the `grep` options: `-c`, `-v`, `-A`, `-B`
9. Read the man pages for `sort` and `uniq` to learn how to combine them
## Problem Set #1

### Danger Is. #04 vs Middleton Is. #16 Fst

<table>
<thead>
<tr>
<th>#</th>
<th>Batch ID</th>
<th>Locus ID</th>
<th>Pop 1 ID</th>
<th>Pop 2 ID</th>
<th>Chr</th>
<th>BP</th>
<th>Column</th>
<th>Overall Pi</th>
<th>Fst</th>
<th>Fisher's P</th>
<th>Odds Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>7894</td>
<td>2</td>
<td>3</td>
<td>groupI</td>
<td>11832</td>
<td>19</td>
<td>0.428182</td>
<td>-0.0076252913</td>
<td>0.191294</td>
<td>0.687192</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7896</td>
<td>2</td>
<td>3</td>
<td>groupI</td>
<td>11900</td>
<td>83</td>
<td>0.328622</td>
<td>0.1775694587</td>
<td>4.35747e-08</td>
<td>5.44667</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>9611</td>
<td>2</td>
<td>3</td>
<td>groupI</td>
<td>49756</td>
<td>48</td>
<td>0.090426</td>
<td>-0.1127451906</td>
<td>0.00109115</td>
<td>0.0898072</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>9611</td>
<td>2</td>
<td>3</td>
<td>groupI</td>
<td>49765</td>
<td>57</td>
<td>0.0132887</td>
<td>-0.1522407447</td>
<td>0.518395</td>
<td>0.493113</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>9611</td>
<td>2</td>
<td>3</td>
<td>groupI</td>
<td>49766</td>
<td>58</td>
<td>0.0133776</td>
<td>-0.1563725438</td>
<td>0.520033</td>
<td>0.501401</td>
<td></td>
</tr>
<tr>
<td>...</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7083</td>
<td>2</td>
<td>3</td>
<td>groupIX</td>
<td>20172984</td>
<td>57</td>
<td>0.0480227</td>
<td>-0.1249752728</td>
<td>0.0230205</td>
<td>0.152263</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7083</td>
<td>2</td>
<td>3</td>
<td>groupIX</td>
<td>20173004</td>
<td>77</td>
<td>0.0181808</td>
<td>-0.1405892833</td>
<td>0.27288</td>
<td>0.355556</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7083</td>
<td>2</td>
<td>3</td>
<td>groupIX</td>
<td>20173016</td>
<td>89</td>
<td>0.0424072</td>
<td>-0.1243625038</td>
<td>0.0442229</td>
<td>0.17037</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7083</td>
<td>2</td>
<td>3</td>
<td>groupIX</td>
<td>20173018</td>
<td>91</td>
<td>0.148072</td>
<td>0.2305903127</td>
<td>2.24832e-07</td>
<td>13.2936</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7084</td>
<td>2</td>
<td>3</td>
<td>groupIX</td>
<td>20172960</td>
<td>29</td>
<td>0.388239</td>
<td>-0.0102170169</td>
<td>0.307185</td>
<td>0.758001</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7084</td>
<td>2</td>
<td>3</td>
<td>groupIX</td>
<td>20172995</td>
<td>64</td>
<td>0.368259</td>
<td>-0.0130602425</td>
<td>0.233889</td>
<td>0.70084</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>7084</td>
<td>2</td>
<td>3</td>
<td>groupIX</td>
<td>20173013</td>
<td>82</td>
<td>0.0121578</td>
<td>-0.1359057575</td>
<td>0.51309</td>
<td>0.46472</td>
<td></td>
</tr>
</tbody>
</table>