Plain text file processing in UNIX

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What are we going to learn?

- Search a pattern
- Word and line count
- Retrieve & count unique records
- String extraction & replacement
- ~~Join & paste data~~

Regular expressions

Matching string patterns according to certain rules

^A	Match A at the beginning of line
A$	Match A at the end of line
[0-9]	Match numerical character
[A-Z]	Match alphabetical character
[ATGC]	Match A,T,C or G
[^A]	Match any character but A
.	Match any character
A*	Match A 0 or more times
A{2}	Match A exactly two times
A{1,} or A+	Match A one or more times
A{1,3}	Match A 1 to 3 times
AATT|*TTAA*	Match AATT or TTAA
\s	Match whitespace

Regular expressions

Matching string patterns according to certain rules

`^ATG$`	a) AATG	b) ATGGC	c) ATG
`ATG`	a) AATG	b) ATGGC	c) ATG
`[ATGC]{6}`	a) AAAAAA	b) NATCGGCN	c) GGCT
`^[ATGC]{6}$`	a) AAAAAA	b) NATCGGCN	c) GGCT
`[^A]{3,5}`	a) AAA	b) GGG	c) CTACG
`^A*GCT`	a) GCT	b) GGCT	c) AAAGCT

Regular expressions

Matching string patterns according to certain rules

`^ATG$`	a) AATG	b) ATGGC	c) ATG
`ATG`	a) AATG	b) ATGGC	c) ATG
`[ATGC]{6}`	a) AAAAAA	b) NATCGGCN	c) GGCT
`^[ATGC]{6}$`	a) AAAAAA	b) NATCGGCN	c) GGCT
`[^A]{3,5}`	a) AAA	b) GGG	c) CTACG
`^A*GCT`	a) GCT	b) GGCT	c) AAAGCT

Pattern Search: `grep`

```
grep pattern file.txt # Returns lines matching a pattern

grep -v pattern file.txt # Returns lines not matching a pattern

grep -o pattern file.txt # Returns only matching part of lines

grep -E regex file.txt # Extended regular expressions

grep -c pattern file.txt # Returns number of lines matching a pattern

grep -B pattern file.txt # Returns number of lines before a line matching a pattern

man grep # For other options
```

Word & line count: `wc`

```
wc file.txt # Returns number of bytes, words and lines

wc -c file.txt # Returns number of bytes (i.e. number of characters incl. \n)

wc -w file.txt # Returns number of words in a file

wc -l file.txt # Returns number of lines in a file

wc -l *.txt # Returns number of lines in all TXT files by file
```

Exercise

What is the number of SNPs in the VCF file?

Retrieve & count unique records

```
cut
# Select columns
cut -f1-3 file.txt
cut -f1-3,10-
cut -d',' -f1-3 file.txt
cut --complement -f4 file.txt

sort
# Sorting data based on selected column
sort -k1,1 file.txt
sort -k1,1 -k2,2nr file.txt
sort -k1,3 file.txt

uniq
# Retrieve unique records
sort -u file.txt
< file.txt sort | uniq -c
```

Coffee Break

Exercise

What is the number of SNPs per chromosome in the VCF file??

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat \
| grep -v '^#' \
| cut -f1 \
| sort \
| uniq -c \
| sort -k1,1n
```

Exercise

Get the first six base pairs from every read and calculate prevalence of the these k-mers

```
cat *.fastq \
| grep -E "^[ACGTN]+$" \
| cut -c1-6 \
| sort \
| uniq -c \
| sort -k1,1nr \
> adapters.txt
```

Note: if you do not have data in your home directory

```
mkdir fastq
cd fastq
cp /data-shared/fastq/fastq.tar.gz .
tar -xzvf fastq.tar.gz
```

String extraction and replacement

`tr` (TRansliterate)

- Replaces or deletes **individual characters**
- Ideal for changing delimiters, removing line endings, uppercase to lowercase conversion

`sed` (text Stream Editor)

- Matches, replaces and extracts **complex patterns**
- Useful for extraction of a value according a specific tag from a gff3 or vcf file
- Can match pattern over multiple lines

`grep -o`

- Returns only matching parts of the text
- Useful for extraction of repeating patterns (e.g. microsatellites)

tr

```
tr ";" "\t" file.txt # Replace delimiter

tr -d "\n" file.txt # Remove line ending character

tr "ATGCN" "atgcn" file.txt # Uppercase to lowercase
```

Exercise

Extract list of samples from a VCF file:

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat \
| grep -v "^##" \
| cut -f10- \
| tr "\t" "\n"
```

sed

```
sed 's/pattern/replacement/'

# Replaces first 6 characters (A,C,G,T,N) with Ns
sed 's/^[ACGTN]\{6\}/NNNNNN/'

# The same thing using extended regular expressions
sed -r 's/^[ACGTN]{6}/NNNNNN/'

echo 'AAATTTCCCGGG' | sed -r 's/A+(T+)C+(G+)/\1\2/'
# The result would be 'TTTGGG'
```

Exercise

Replace "chr" in the CHROM column in a VCF file:

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
sed -r 's/^chr//'
```

Exercise

Retrieve an overall read depth from a VCF file:

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat \
| grep -v "^#" \
| sed -r 's/^.+DP=([^;]+).+$/\1/'
```

Exercise

Retrieve an overall read depth from a VCF file:

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat \
| grep -v "^#" \
| sed -r 's/^.+DP=([0-9]+);.+$/\1/'
```

grep -o

```
# Match AT di-nucleotide twice or more times
grep -o -E "(AT){2,}"

# Match GTC tri-nucleotide twice or more times
grep -o -E "(GTC){2,}"

# Match any repeating pattern
grep -o -E "([ATGC]{1,})\1+"
```

Exercise

Retrieve an overall read depth from a VCF file with `grep -o`*:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E 'DP=([^;]+)' |
sed 's/DP=//'
```

Exercise

Retrieve an overall read depth from a VCF file with `grep -o`*:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E 'DP=([^;]+)' |
sed 's/DP=//'
```

create FILE variable containing absolute path to compressed VCF file

Exercise

Retrieve an overall read depth from a VCF file with `grep -o`*:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E 'DP=([^;]+)' |
sed 's/DP=//'
```

use newly created FILE variable an input to zcat to decompress

Exercise

Retrieve an overall read depth from a VCF file with `grep -o`*:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E 'DP=([^;]+)' |
sed 's/DP=//'
```

Extract sequence depth, e.i. skip all lines with # or ##. Output only text specified by regular expression, not the rest of the line.

Exercise

Retrieve an overall read depth from a VCF file with `grep -o`*:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E 'DP=([^;]+)' |
sed 's/DP=//'
```

Get rid of DP= and just output numbers

Exercise

What is the number of SNPs per chromosome in the VCF file??

...without using `cut` *command:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E '^chr[Z0-9]+' |
sort |
uniq -c |
sort -k1,1nr
```

Exercise

What is the number of SNPs per chromosome in the VCF file??

...without using `cut` *command:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E '^chr[Z0-9]+' |
sort |
uniq -c |
sort -k1,1nr
```

create FILE variable containing absolute path to compressed VCF file

Exercise

What is the number of SNPs per chromosome in the VCF file??

...without using `cut` *command:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E '^chr[Z0-9]
sort |
uniq -c |
sort -k1,1nr
```

use newly created FILE variable an input to zcat to decompress

Exercise

What is the number of SNPs per chromosome in the VCF file??

...without using `cut` *command:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E '^chr[Z0-9]+' |
sort |
uniq -c |
sort -k1,1nr
```

Extract chromosomes names only, e.i. skip all lines with # or ## and all other columns

Exercise

What is the number of SNPs per chromosome in the VCF file??

...without using `cut` *command:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E '^chr[Z0-9]+' |
sort |
uniq -c |
sort -k1,1nr
```

Sort chromosomes

Exercise

What is the number of SNPs per chromosome in the VCF file??

...without using `cut` *command:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E '^chr[Z0-9]+' |
sort |
uniq -c |
sort -k1,1nr
```

Count occurrence for each chromosome

Exercise

What is the number of SNPs per chromosome in the VCF file??

...without using `cut` *command:*

```
FILE=/data-shared/vcf_examples/luscinia_vars_flags.vcf.gz

< $FILE zcat |
grep -o -E '^chr[Z0-9]+' |
sort |
uniq -c |
sort -k1,1nr
```

Sort chromosomes based on number of SNPs per chromosome in descending order

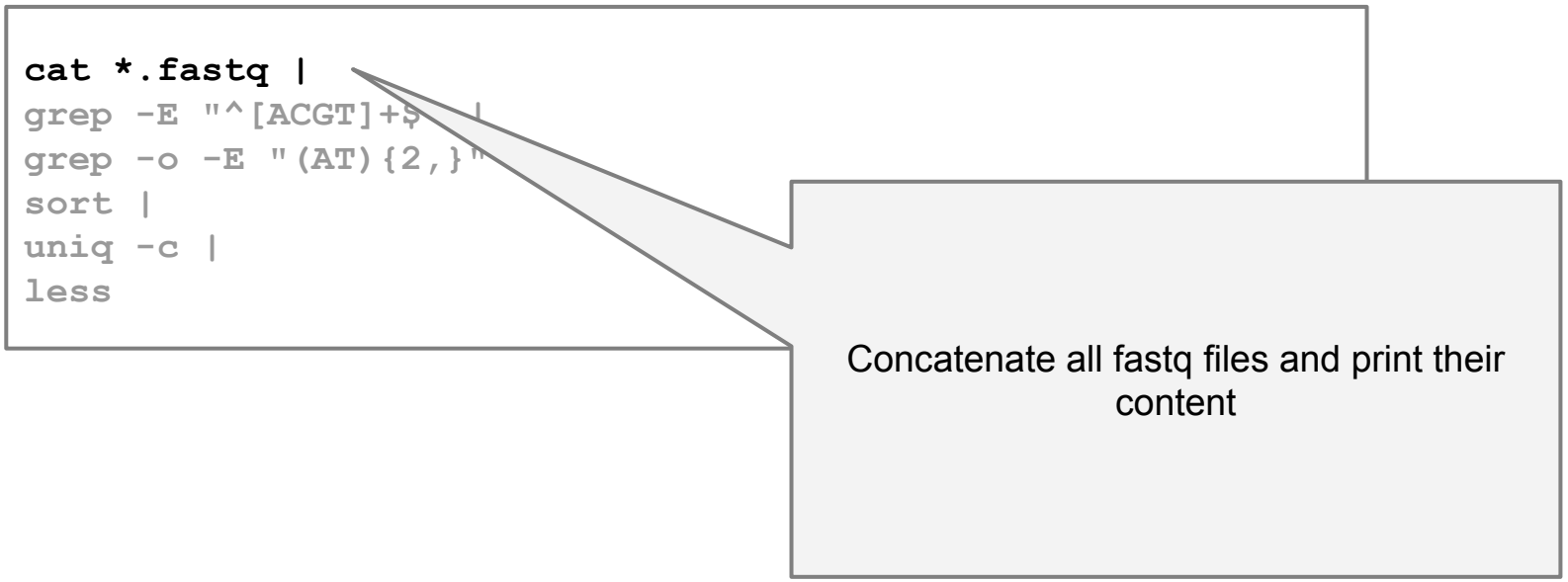
Exercise

Microsatellites statistics: Extract all AT dinucleotides repeating at least twice and calculate their frequency distribution in the whole dataset.

```
cat *.fastq |
grep -E "^[ACGT]+$" |
grep -o -E "(AT){2,}" |
sort |
uniq -c |
less
```

Exercise

Microsatellites statistics: Extract all AT dinucleotides repeating at least twice and calculate their frequency distribution in the whole dataset.



Exercise

Microsatellites statistics: Extract all AT dinucleotides repeating at least twice and calculate their frequency distribution in the whole dataset.

```
cat *.fastq |
grep -E "^[ACGT]+$" |
grep -o -E "(AT){2,}" |
sort |
uniq -c |
less
```

Extract only sequence lines, e.i. not sequence ID or sequence quality

Exercise

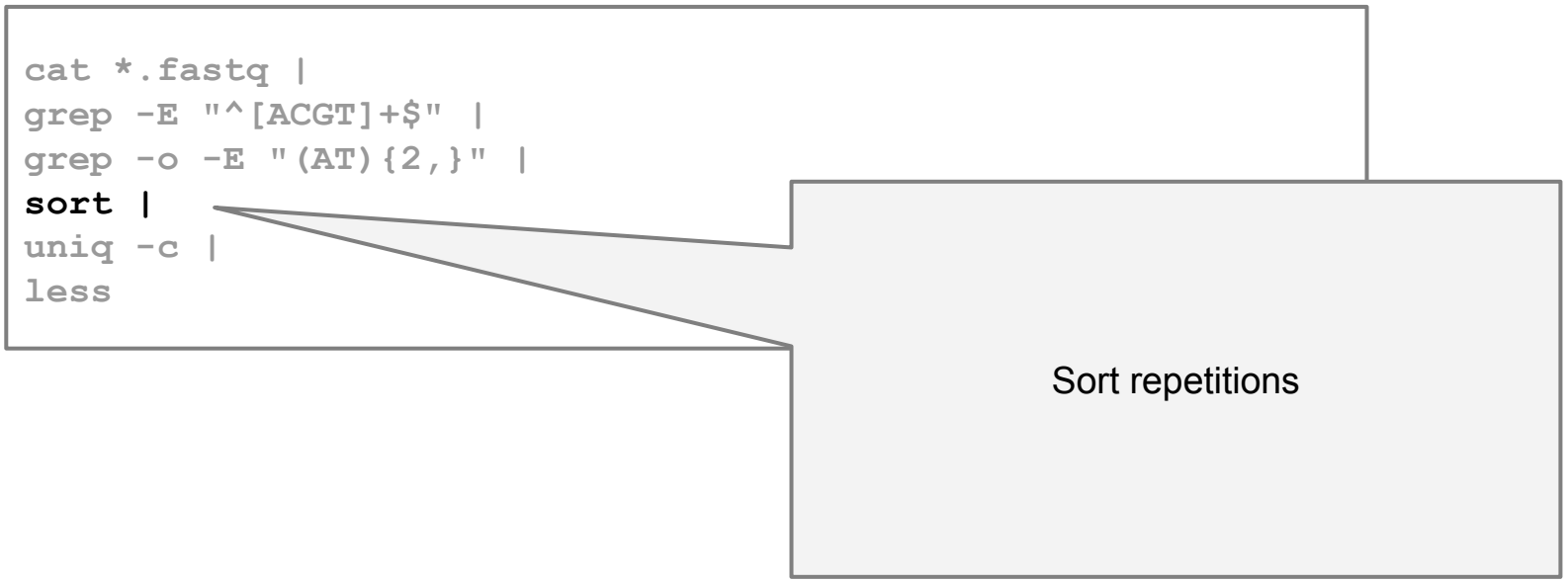
Microsatellites statistics: Extract all AT dinucleotides repeating at least twice and calculate their frequency distribution in the whole dataset.

```
cat *.fastq |
grep -E "^[ACGT]+$" |
grep -o -E "(AT){2,}" |
sort |
uniq -c |
less
```

Extract AT repetitions (2 or more)

Exercise

Microsatellites statistics: Extract all AT dinucleotides repeating at least twice and calculate their frequency distribution in the whole dataset.



Exercise

Microsatellites statistics: Extract all AT dinucleotides repeating at least twice and calculate their frequency distribution in the whole dataset.

```
cat *.fastq |
grep -E "^[ACGT]+$" |
grep -o -E "(AT){2,}" |
sort |
uniq -c |
less
```

Count repetitions occurrence

Exercise

Microsatellites statistics: Extract all AT dinucleotides repeating at least twice and calculate their frequency distribution in the whole dataset.

```
cat *.fastq |
grep -E "^[ACGT]+$" |
grep -o -E "(AT){2,}" |
sort |
uniq -c |
less
```

Look into data

What have we learned today?

- Search a pattern (`grep` and regular expressions)
- Word and line count (`wc`)
- Retrieve & count unique records (`cut`, `sort`, `uniq`)
- String extraction & replacement (`tr`, `sed`)

Lunch, Lunch!!

Join and paste data

`join`

- *Joining two files based on a specific key column*
- *Corresponds to JOIN in SQL language*

`paste`

- *Simply aligns files by column*
- *No key column is needed*
- *Assumes one to one correspondence between the two datasets*

join

```
# Join file1.txt and file2.txt based on 2nd and 3rd column
sort -k2,2 file1.txt > file1.tmp
sort -k3,3 file2.txt > file2.tmp
join -12 -23 file1.tmp file2.tmp > joined-file.txt
```

paste

```
# Merge vertically two files
paste file1.txt file2.txt > file-merged.txt
```

file1.txt		file2.txt		file-merged.txt
ID1		AATG		ID1 AATG
ID2	+	CAAG	=	ID2 CAAG
ID3		ATCG		ID3 ATCG
ID4		GTTG		ID4 GTTG

paste

```
# Transpose file
< filte.txt paste - -
```

file1.txt

item-line1
item-line2
item-line3
item-line4

=

item-line1 item-line2
item-line3 item-line4

Exercise

Convert FASTQ file to TAB separated file with each read on one line

```
cat *.fastq |
paste - - - - |
cut --complement -f3 \
> reads.tab
```