

Direct to project1 folder

```
[guest@centos6] cd project1
```

Extract files

```
[guest@centos6 project1]$ gunzip
```

```
gencommand_proj1_data.tar.gz
```

```
[guest@centos6 project1]$ tar -xf gencommand_proj1_data.tar
```

Direct to gencommand_proj1_data folder

```
[guest@centos6 project1]$ cd gencommand_proj1_data
```

```
[guest@centos6 gencommand_proj1_data]$ ls
```

Question1: How many chromosomes are there in the genome?

```
[guest@centos6 gencommand_proj1_data]$ grep -c ">"
```

```
apple.genome
```

Question2: How many genes and transcript variants?

```
[guest@centos6 gencommand_proj1_data]$ cut -f1 apple.genes |  
uniq | wc -l (or cut -f1 apple.genes | sort -u | wc -l)
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f2 apple.genes |  
uniq | wc -l (or cut -f2 apple.genes | sort -u | wc -l)
```

Question3: How many genes have a single splice variant?

```
[guest@centos6 gencommand_proj1_data]$ cut -f1 apple.genes |  
uniq -c | grep " 1 " | wc -l
```

Question4: How many genes have 2 or more splice variants?

```
[guest@centos6 gencommand_proj1_data]$ cut -f1 apple.genes |  
uniq -c | grep -v " 1 " | wc -l
```

Question5: How many genes are there on the '+' and '-' strands, respectively?

```
[guest@centos6 gencommand_proj1_data]$ cut -f1,4 apple.genes  
| grep "+" | uniq | wc -l
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f1,4 apple.genes  
| grep "-" | uniq | wc -l
```

Question6: How many genes are there on each chromosome?
List them in the order in which they are listed in the genome, i.e.
genes on chr1, chr2, etc.

```
[guest@centos6 gencommand_proj1_data]$ cut -f1,3 apple.genes  
| grep "chr1" | uniq | wc -l
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f1,3 apple.genes  
| grep "chr2" | uniq | wc -l
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f1,3 apple.genes  
| grep "chr3" | uniq | wc -l
```

Question7: How many transcripts are there on each chromosome? Follow instructions above.

```
[guest@centos6 gencommand_proj1_data]$ cut -f2,3 apple.genes  
| grep "chr1" | uniq | wc -l
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f2,3 apple.genes  
| grep "chr2" | uniq | wc -l
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f2,3 apple.genes  
| grep "chr3" | uniq | wc -l
```

Question8: How many genes are in common between condition A and condition B?

```
[guest@centos6 gencommand_proj1_data]$ cut -f1  
apple.conditionA | sort -u > conditionA
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f1  
apple.conditionB | sort -u > conditionB
```

```
[guest@centos6 gencommand_proj1_data]$ comm -1 -2  
conditionA conditionB | wc -l
```

Question9: How many genes are specific to condition A? How many genes are specific to condition B?

```
[guest@centos6 gencommand_proj1_data]$ comm -2 -3  
conditionA conditionB | wc -l
```

```
[guest@centos6 gencommand_proj1_data]$ comm -1 -3  
conditionA conditionB | wc -l
```

Question10: How many genes are in common to all three conditions?

```
[guest@centos6 gencommand_proj1_data]$ comm -1 -2  
conditionA conditionB > conditionAB
```

```
[guest@centos6 gencommand_proj1_data]$ cut -f1  
apple.conditionC | sort -u > conditionC
```

```
[guest@centos6 gencommand_proj1_data]$ comm -1 -2
```

conditionAB conditionC | wc -l