Project – Sequence Alignment with Bowtie2

Background

- Sequence alignment
  - Compare and align sequence data (reads) to reference to identify regions of similarity (e.g. genes)
- Bowtie2
  - A multi-threaded tool for aligning sequencing reads to long reference sequences

```
Read:       GACTGGGCGATCTCGACTTCG

            | | | | |   | | | | | | | | |   | | |

Reference:  GACTG--CGATCTCGACATCG
```

Tasks

- Run bowtie2 with 1, 2, 4 and 8 threads
  - Record the wall clock time and memory usage
- Use Python (or any method you prefer) to estimate wall clock time and memory usage for the cases with 16 and 32 threads
- Run bowtie2 again with 16 and 32 threads
  - Again, record the wall clock time and memory usage
  - Compare them to the estimated values

Step 1: Get Files

- List of files
  - Reference yeast genome: `yeast_ref.fa`
  - Read file: `read1.fastq`
- How to get them
  - Create a directory in your work directory and cd to it

    ```
    mkdir /work/<user name>/bowtie2_yeast
    cd /work/<user name>/bowtie2_yeat
    ```
  - Copy files over

    ```
    cp /work/lyan1/Bootcamp2018/yeast/yeast_ref.fa ./
    ```
  -
    ```
    cp /work/lyan1/Bootcamp2018/yeast/read1.fastq ./
    ```

```
[lyan1@shelob002 Bootcamp2018]$ cp /work/lyan1/Bootcamp2018/yeast/yeast_ref.fa .
[lyan1@shelob002 Bootcamp2018]$ cp /work/lyan1/Bootcamp2018/yeast/s1.fastq .
[lyan1@shelob002 Bootcamp2018]$ ls -l
total 2038788
-rw-r--r-- 1 lyan1 Admins 2080972366 May 23 14:17 s1.fastq
-rw-r--r-- 1 lyan1 Admins   12400379 May 23 14:17 yeast_ref.fa
[lyan1@shelob002 Bootcamp2018]$ 
```

Step 2: Run Bowtie2

- ## Run bowtie2 with 1, 2, 4 and 8 threads
  - ### Command:

```
time bowtie2 --threads <number of threads> -x yeast_ref -U read1.fastq -S yeast1.sam
```

  - ### Ex: with 2 threads

```
time bowtie2 --threads 2 -x yeast_ref -U read1.fastq -S yeast1.sam
```

Thread	Time (seconds)	Memory (MB)
1		
2		
4		
8		

Step 3: Estimate

- Use Python (or any method you prefer) to estimate wall clock time and memory usage for the cases with 16 and 32 threads

Thread	Time (seconds)	Memory (MB)
1		
2		
4		
8		
16		
32		

Step 4: Run Bowtie2 Again

- Run bowtie2 again with 16 and 32 threads
- Compare the observed data with your estimates

Thread	Time (seconds)		Memory (MB)	
1				
2				
4				
8				
16	Estimate	Measured	Estimate	Measured
32	Estimate	Measured	Estimate	Measured

Step 5: What Do You Learn?