



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 Excel or your eyeballs) 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

```
[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:

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

Ex: with 2 threads

[lyan1@shelob002 yeast]\$ time bowtie2 --threads 2 -x yeast_ref -U s1.fastq -S yeast1.sam



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Step 3: Estimate

 Use Python (or Excel or your eyeballs) to estimate wall clock time and memory usage for the cases with 16 and 32 threads

Phread	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?



