Genomic Sequencing Analysis Parallelization

CS205 - Computing Foundations for Computational Science - Spring 2018 Final Project

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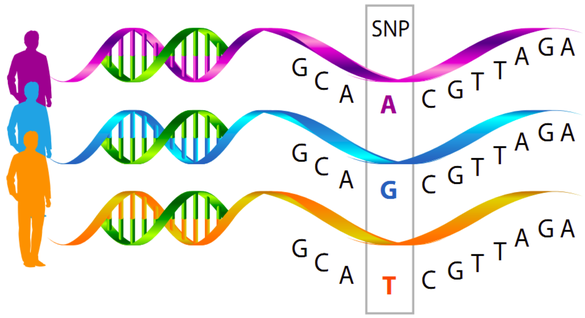
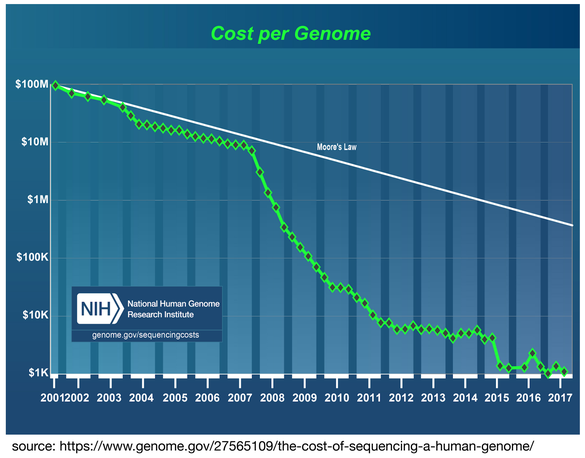
Introduction

Project Goal

To speed up the identification of single nucleotide polymorphisms (SNP) in DNA and RNA through big data and high throughput parallelization techniques.



- SNPs are the differences between people and can identify diseases, disorders, or medication responses
- The cost of sequencing has dramatically decreased in the last decade
- The primary overhead is now computation



source: https://www.genome.gov/27565109/the-cost-of-sequencing-a-human-genome/

- SNP algorithms are not easy to parallelize
- Some analyses take more than 1 week
- Too slow for timely clinical diagnostics

Tools & Infrastructure

SAMtools

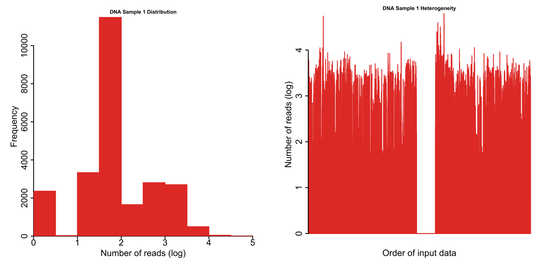
- Suite of programs for interacting with high-throughput sequencing data
- Open-source

HARVARD MEDICAL SCHOOL

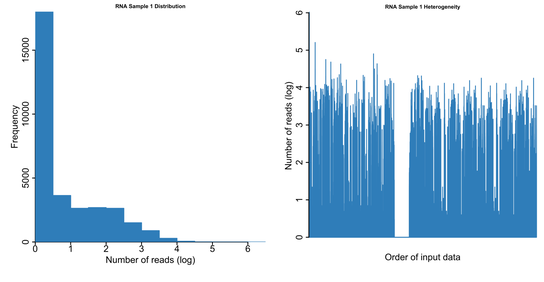
- HMS Research Computing cluster
- 8000 cores with several PB network storage

Data

- DNA, RNA alignments for 2 people (1000 Genomes Project)
- .bam (~10GB each), .bai (~5MB each)

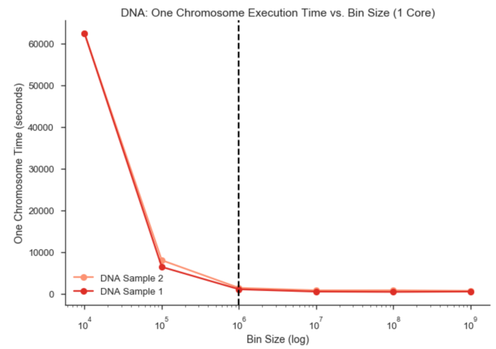


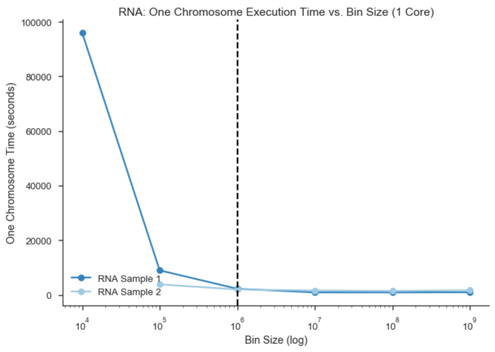
- Uneven input data chunk sizes
- Unpredictable sizing in index file



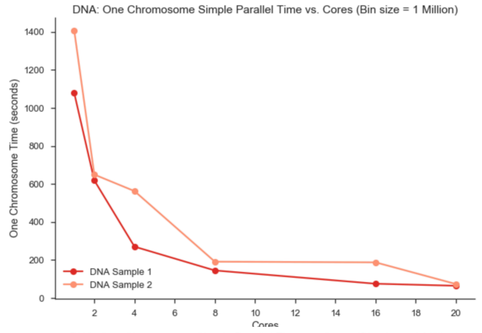
Binning

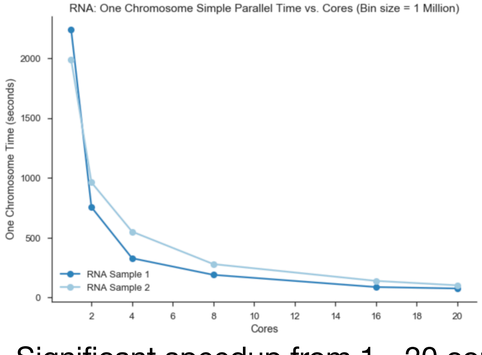
- Distribute DNA & RNA reads (sequence strings) into “bins” amongst cores





- Best bin size: at least 1,000,000 chromosome positions





- Significant speedup from 1 - 20 cores

Profiling

- **gprof** profiler on 10,000,000 read DNAsample

```
Each sample counts as 0.01 seconds.
%           cumulative       self              self     total
time        seconds  seconds calls  s/call  s/call  name
51.10       1.16     1.16    1     1.16    2.27  mpileup
18.06       1.57     0.41    4519010  0.00    0.00  bam_plp_next
12.11       1.85     0.28    26195998 0.00    0.00  pileup_seq
9.69        2.07     0.22    26896170 0.00    0.00  resolve_cigar2
5.73        2.20     0.13    4213250  0.00    0.00  bam_mplp_auto
0.44        2.21     0.01    353719   0.00    0.00  kh_get_olap_hash
0.44        2.22     0.01    330015   0.00    0.00  bam_read1
0.44        2.23     0.01    305760   0.00    0.00  mp_free
0.44        2.24     0.01    305760   0.00    0.00  mplp_func
0.44        2.25     0.01    305759   0.00    0.00  bam_copy1
0.44        2.26     0.01    17474    0.00    0.00  tweak_overlap_quality
0.44        2.27     0.01    2670     0.00    0.00  printw
0.22        2.27     0.01    4213249  0.00    0.00  mplp_get_ref
```

OpenMP

- Shared-memory technique to reduce execution
- **mpileup** identified in profiling (above) as primary function to focus parallelization
- 457 lines, 22 for/while loops

MPI

- Distributed-memory technique to reduce execution
- Requires wrapper around SAMtools to scale up to 640 nodes on HMSRC cluster
- Currently limited to 20 cores with binning and OpenMP

Load Balancing

- Read the index (.bai) file
- Apply sorting algorithm to bin by size rather than index in current binning method

Desired Outcome

- Ultimate goal to combine binning, OpenMP, MPI to achieve maximum possible speedup
- Scale to ~200GB (whole genome)