AlignFix:
A Seed and Extend Aligner

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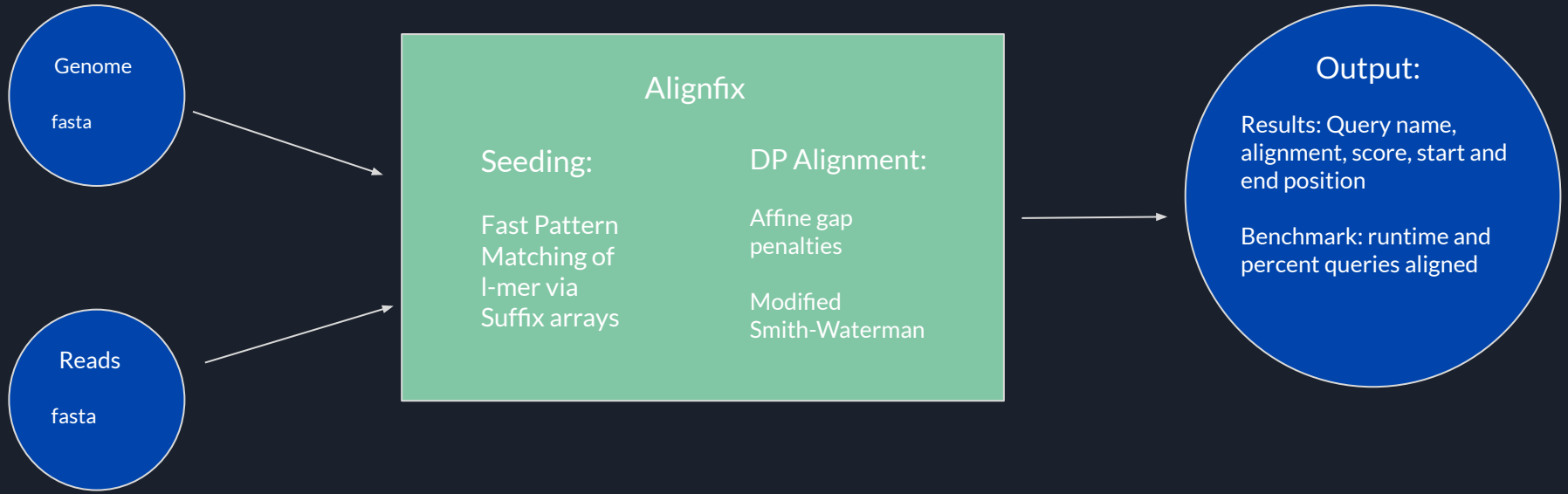
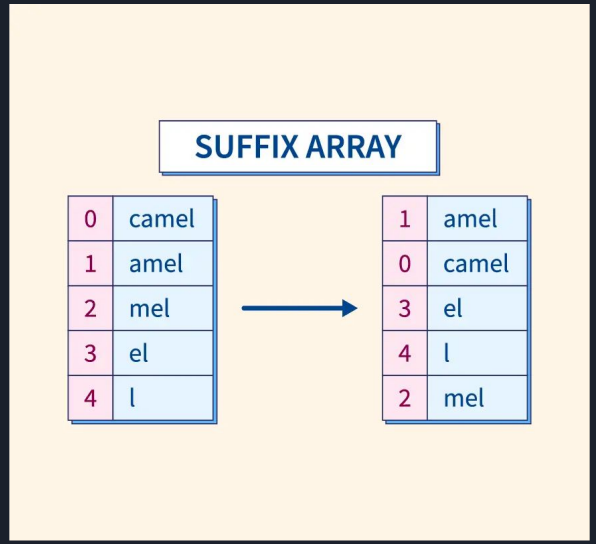
Overview of AlignFix



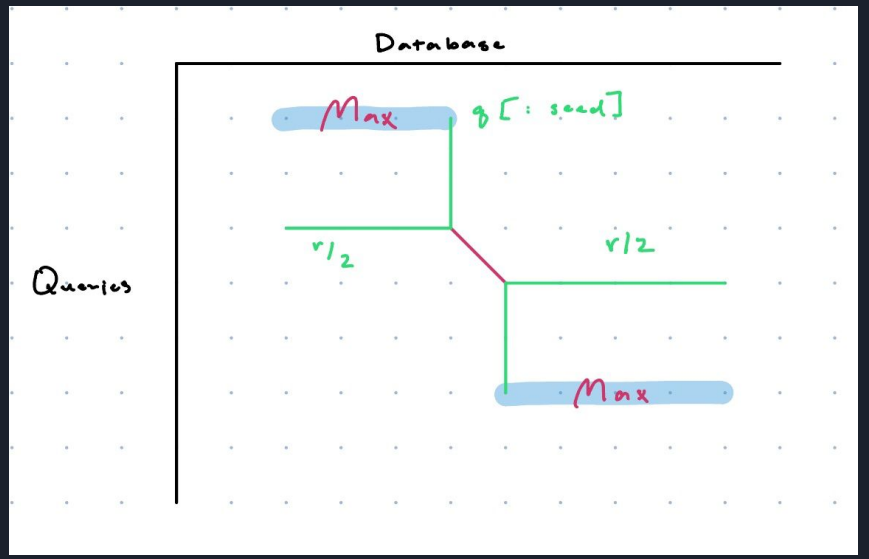
Implementation Details and Algorithms

Suffix Arrays



Given a keyword, you can apply binary search
We stored indices in the database

Alignment



Seed length -> 15
r -> length of the query * 2

For the top, we reverse the strings and compute the alignment

Finally, we start backtracking from the max of the bottom row

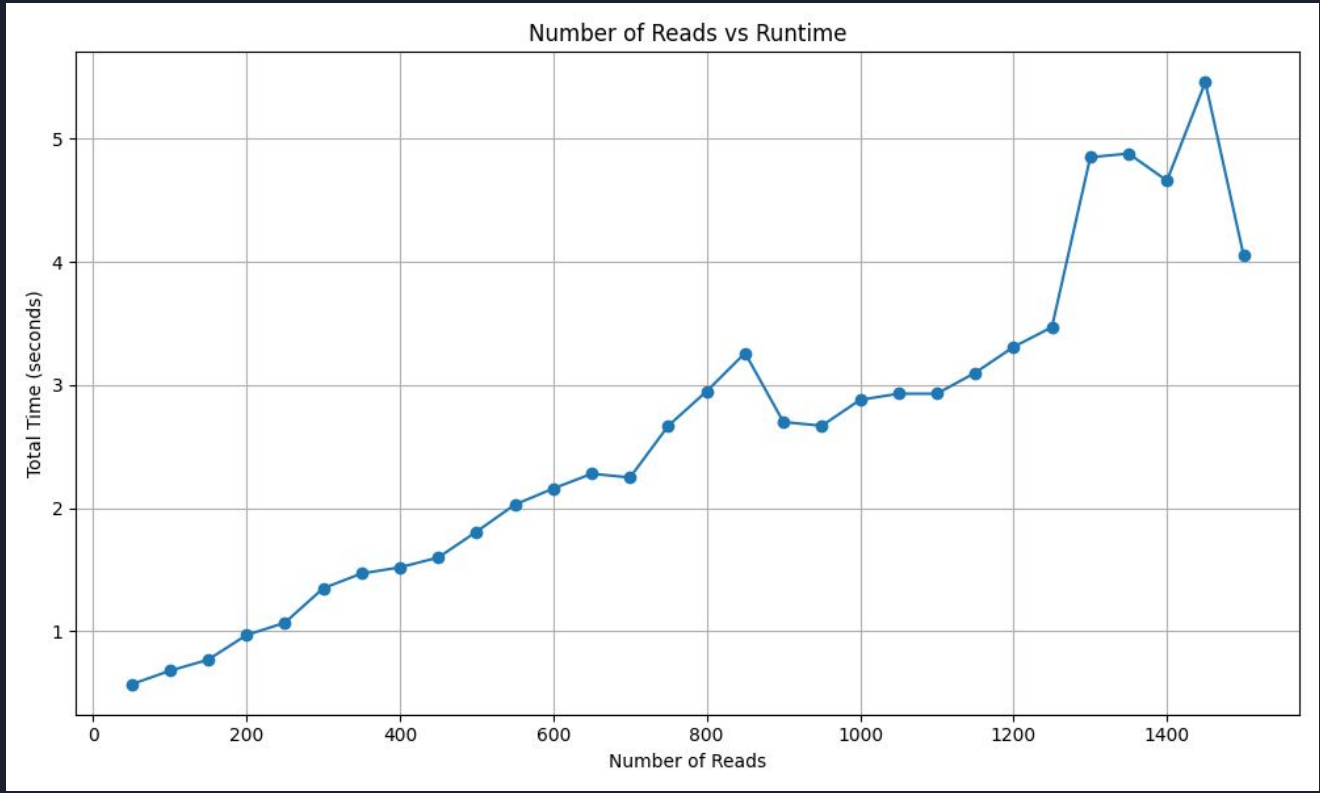
Alignment

- Way of generating a score of the best alignment possible through a 2D matrix
- Backtracks from the best score to get the alignment
- Uses affine gap penalties: minimizes penalties for increasing the gap between nucleotides
- Together, an alignment is generated

		A	C	A	T	A	G
	0	0	0	0	0	0	0
A	0	1	0	1	0	1	0
A	0	1	0	1	0	1	0
T	0	0	0	0	2	1	0
G	0	0	1	0	1	1	2

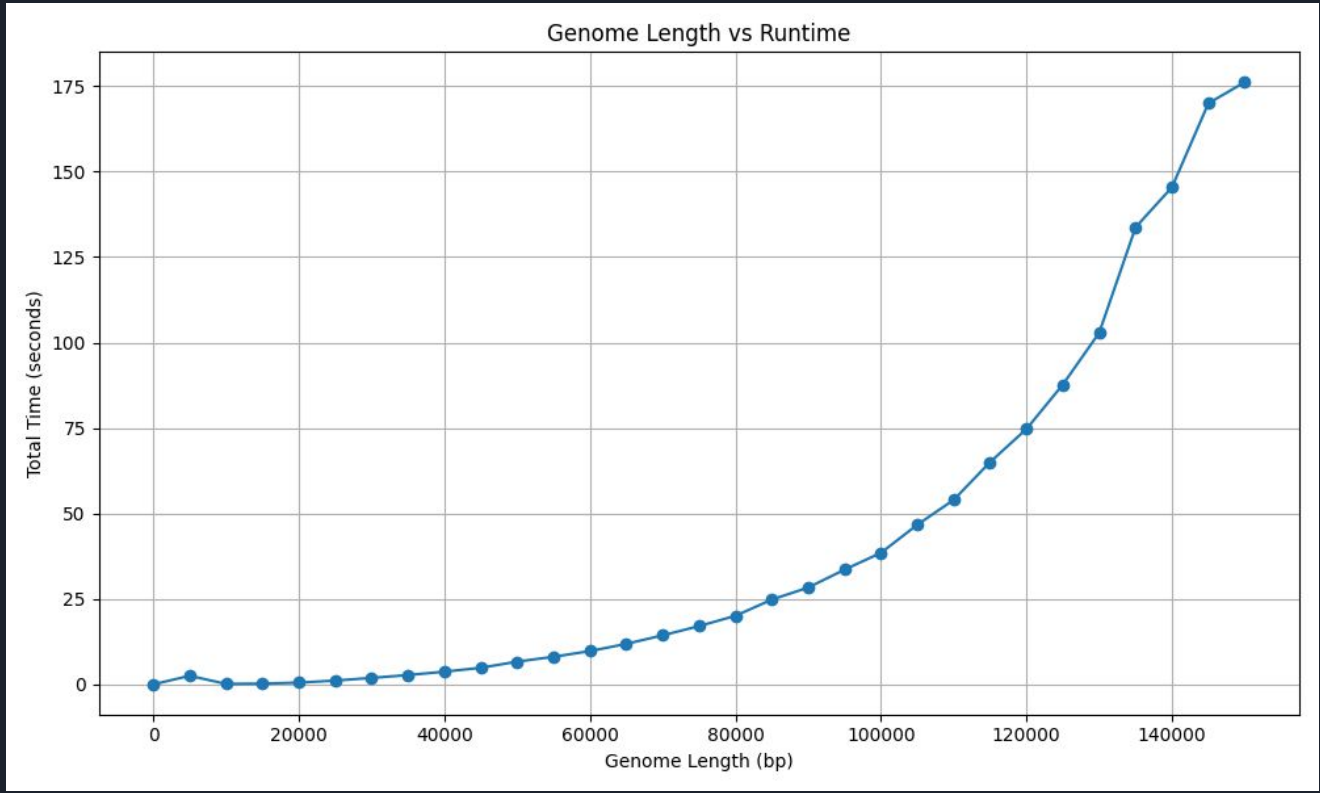
Benchmarking

The graph shows approximately a linear relationship between the number of reads and runtime.



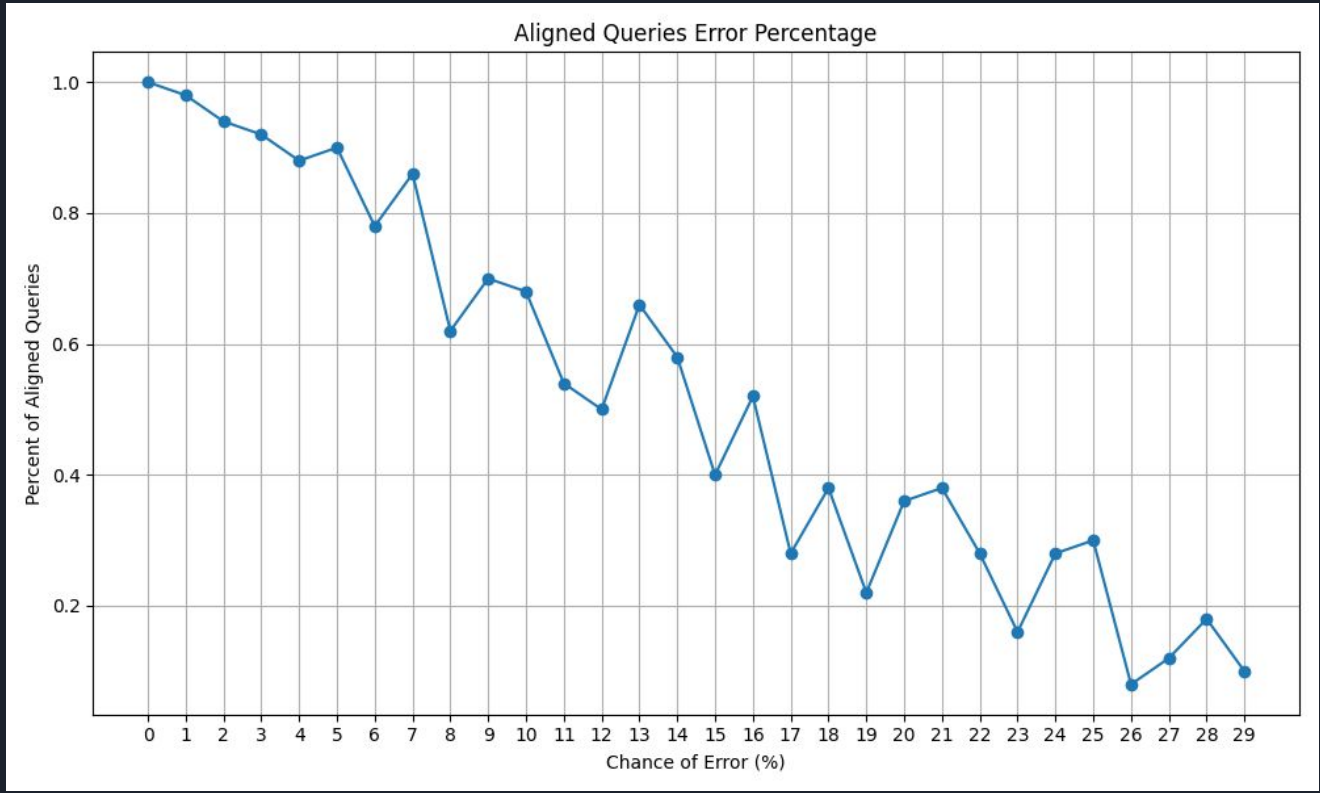
Benchmarking

The graph shows approximately a quadratic relationship between genome length and runtime.



Benchmarking

The graph shows approximately a linear relationship between the chance of error and percent of aligned queries.



BWA MEM vs AlignFix

These results were taken based on the real world data.

Categories	AlignFix	BWA MEM
Time To Align	152.93 seconds	0.289 seconds
Percent of Queries Aligned	83%	99.93%

Challenges

- Figuring out affine gap penalties
  - needs three matrices to keep track of
- Figuring out how pip install could be used to download AlignFix
  - Creating a package that can be used by the user

Sources

- Altschul, S.F., Gish, W., Miller, W., Myers, E.W., Lipman, D.J. (1990) “Basic local alignment search tool.” J. Mol. Biol. 215:403-410
- Heng Li, Richard Durbin, Fast and accurate short read alignment with Burrows–Wheeler transform, Bioinformatics, Volume 25, Issue 14, July 2009, Pages 1754–1760, https://doi.org/10.1093/bioinformatics/btp324