Parallel decompression of `gzip`-compressed files

and random access to DNA sequences

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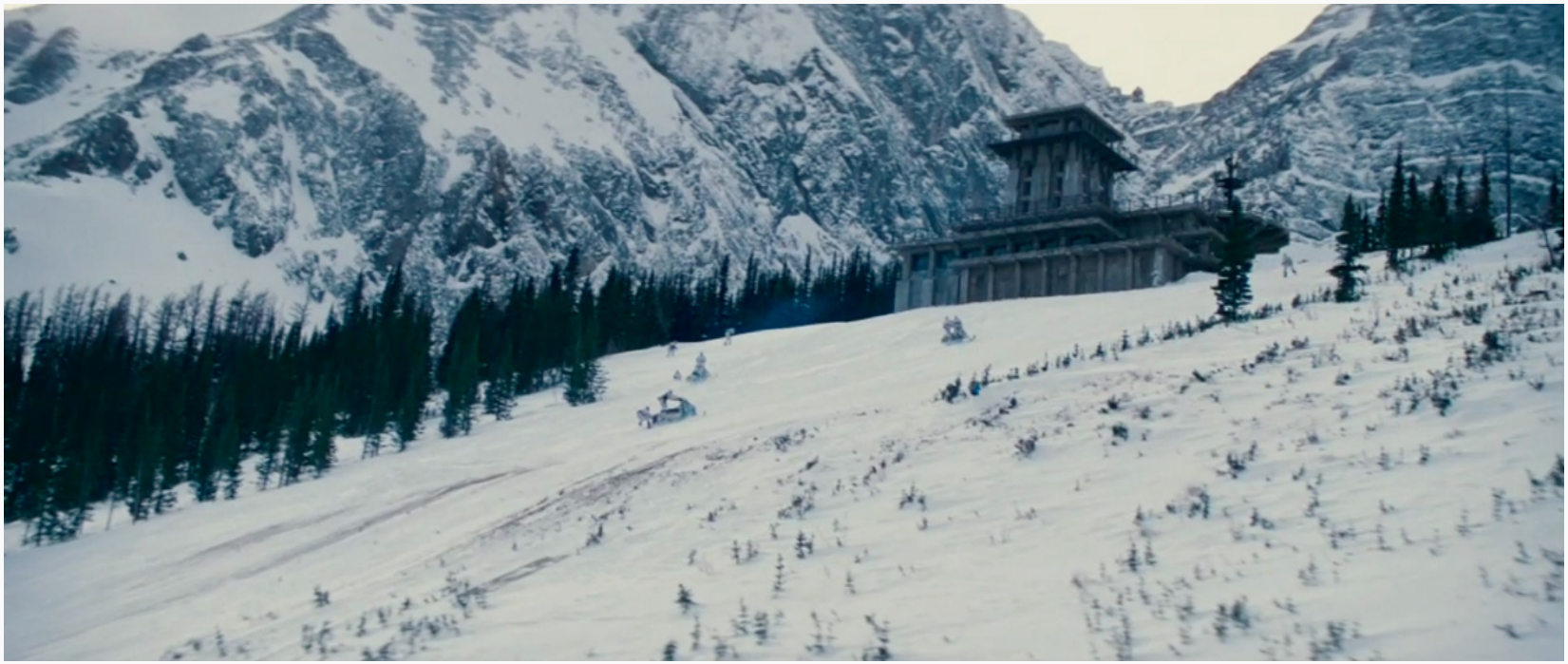
Motivation



Not so long ago, in a French research center..

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So please find a way to decompress gzip files in parallel

That's impossible 

because.. 

`gzip` format

. . . of the nature of `gzip` files.

But first:

`gzip` is the software (v0.1 in 1992)

`zlib` is the library

`DEFLATE` is the algorithm (1989)

`DEFLATE` compression has essentially two components:

- LZ77
- Huffman coding

Huffman coding (1952)

- Frequent symbols are encoded into fewer bits
- No code word is a prefix of another

No need to understand Huffman coding to follow this talk.

Lempel-Ziv 1977 (DEFLATE variant)

Encodes a string as a **sequence** of either:

- a **literal** (raw character), or
- a **back-reference** to a previous substring

Original text: **abcdeabcfbc**

LZ77 encoding: **abcde**`[-5,3]`**f**`[-3,2]`

literals

back-references
[offset, length]

-32KB ≤ offset ≤ 0
(i.e. sliding window)

`gzip` in bioinformatics

- Text files everywhere
- **gzip** is a natural choice:
  - **ASCII**: $>$ 12% space reduction (every 8th bit is always 0)
  - **FASTQ**: encodes ACTG's in $\approx$2 bits/character
- Not best in class in neither **speed** nor **ratio** (see brotli, Zstd)
- However, **ubiquitous** and **fast** (note: `gzip -1` is 7x faster than default)
- **Default** compression format of `bcl2fastq` (Illumina)

`gzip` decompression speed

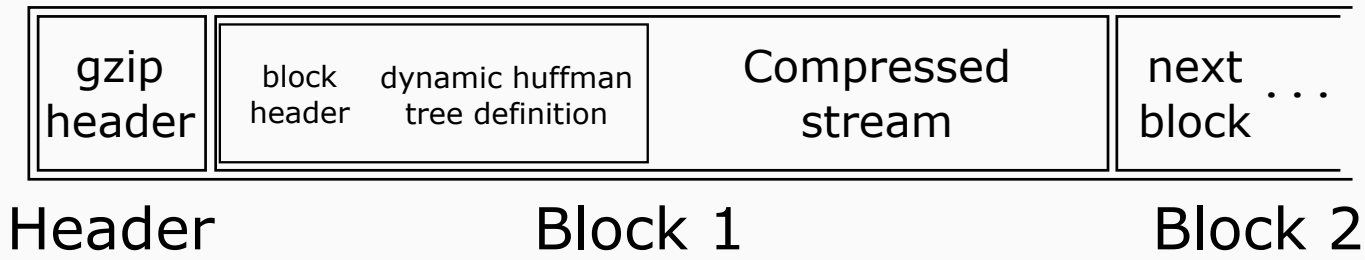
- `gunzip` decompresses at **30** MB/s (input read speed)
- Hard drives read at **100 – 200** MB/s
- SSDs read at **0.5 – 3** GB/s

→ reading compressed data can slow down programs, up to 30x

Parallelism in gzip

`pigz` only does parallel **compression** because parallel decompression is difficult.

Anatomy of a `.gz` file:



Obstacles:

- Positions of **start of blocks** are unknown
- Blocks contain **back-references** to previous blocks

Common solutions

`zran.c` / `BGZF` / `BAM`

- Keep an index of block start positions
- Avoid back-references across blocks

A fine solution, but:

- Not a widely deployed format
- $<$ 50% of the SRA had indexed `.fastq.gz`'s in 2018
- Although new `bcl2fastq` indexes by default
- Slightly worse compression ratio

Our work

In **regular** `.fastq.gz` files:

- Quickly **guess** block positions
- See if we can perform random access

Our work

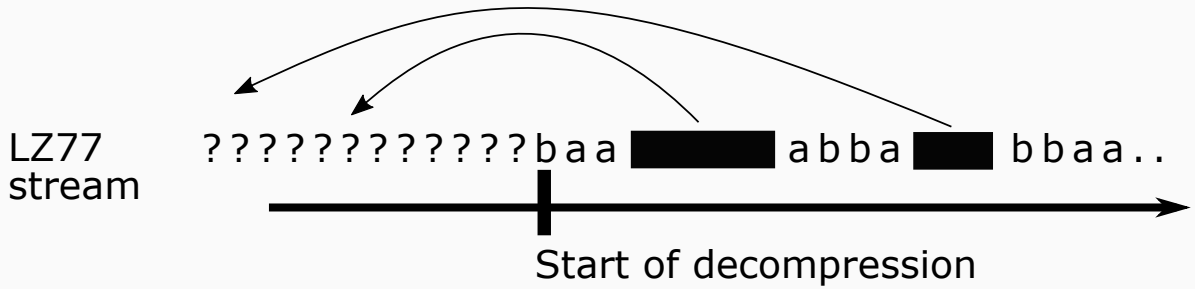
In **regular** `.fastq.gz` files:

- Quickly **guess** block positions
- See if we can perform random access
- We could, but only at low compression levels
- Failed to do it reliably at higher levels
- Found another way to do parallel decompression, without random access

Random access in gzip stream

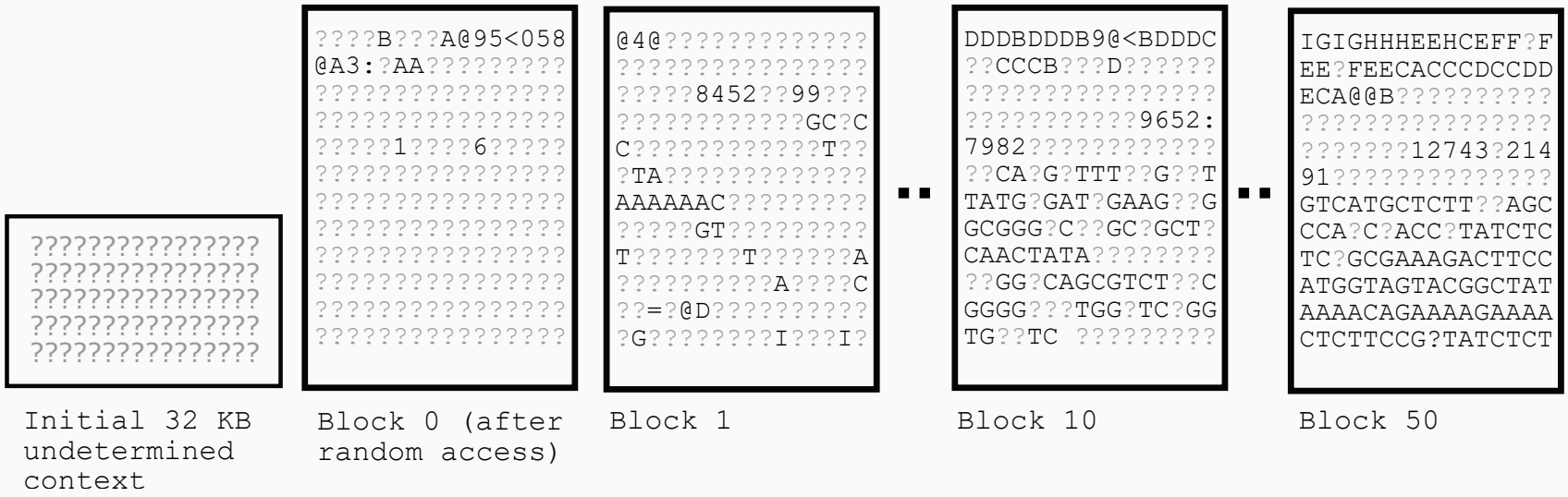
Suppose you start decompressing at the middle of a LZ77 stream.

- Some characters **can be decoded** (those encoded as-is by LZ77).
- But back-references to positions before the start **remain unknown**.



Random access in compressed FASTQs

Decompression of FASTQ starting at the beginning of a block, without context.



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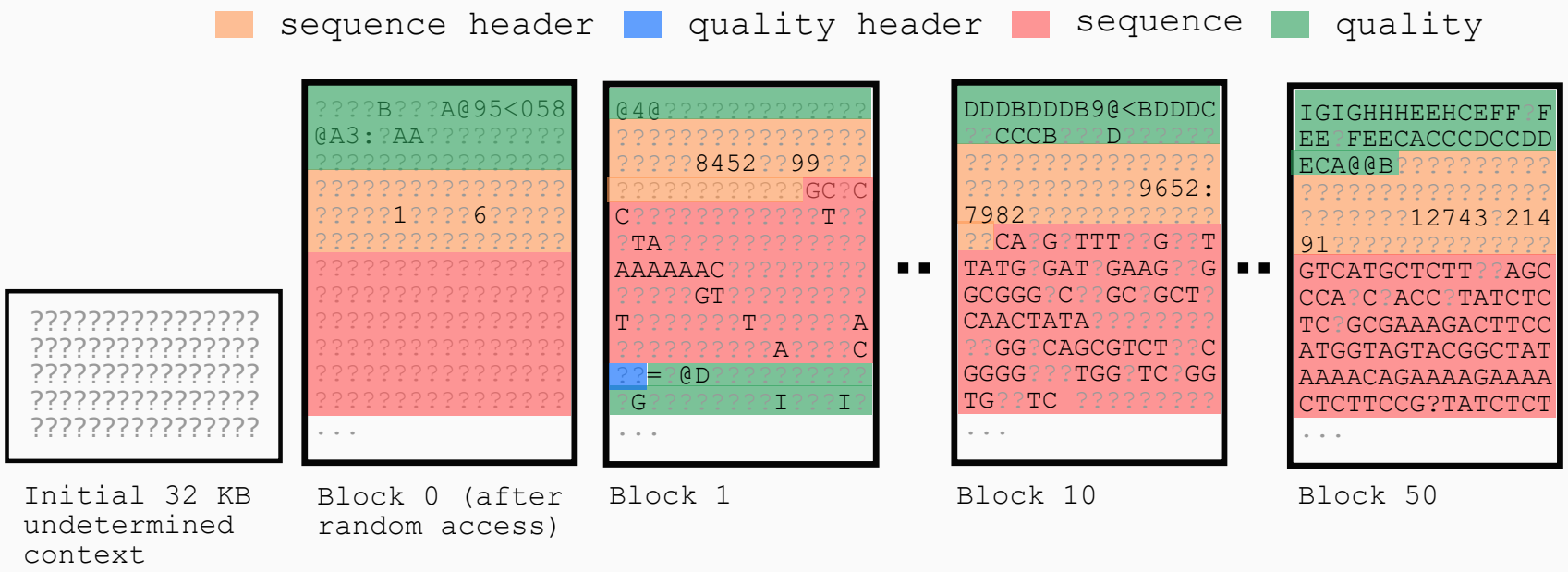
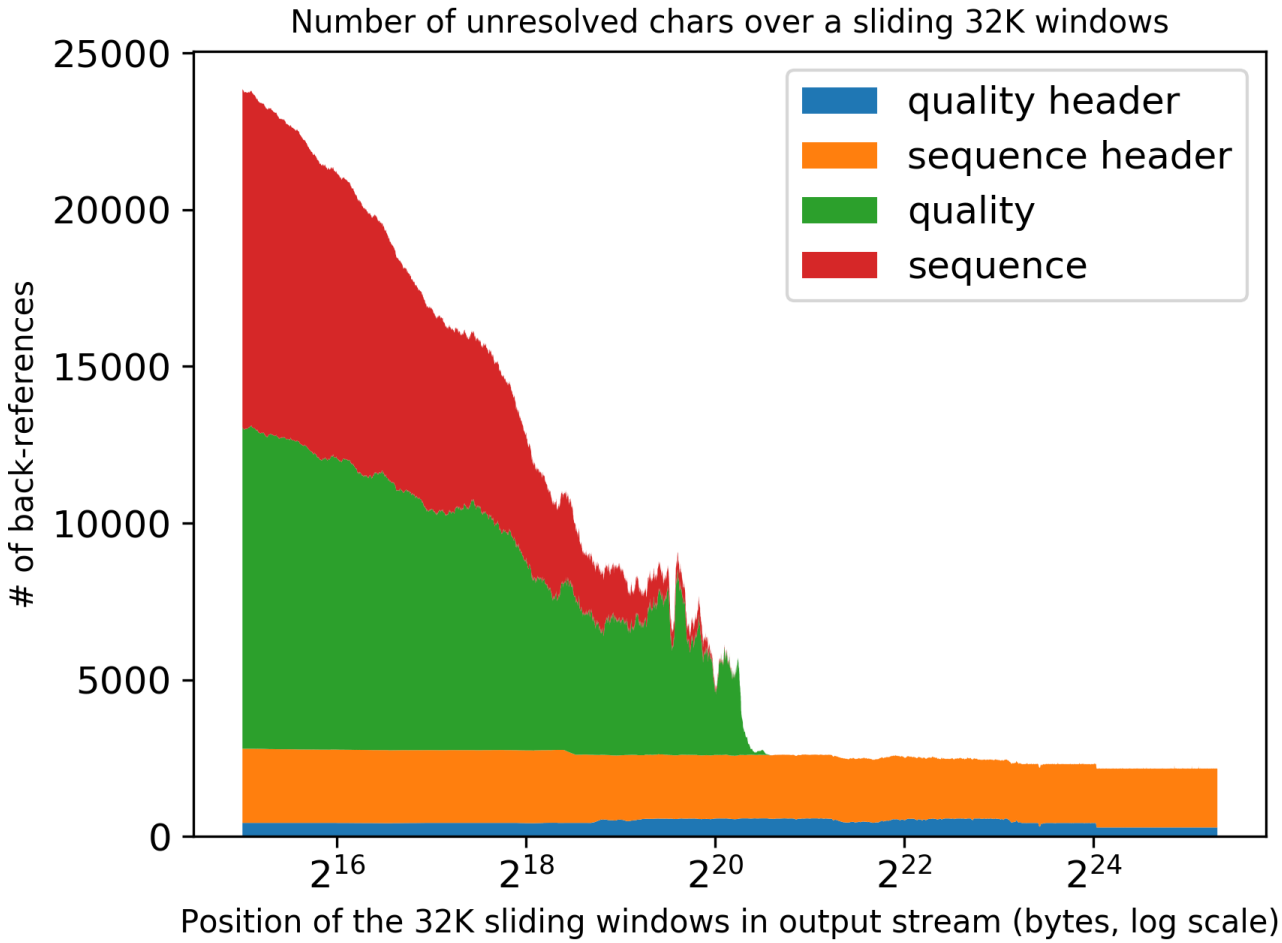


Random access in compressed FASTQs

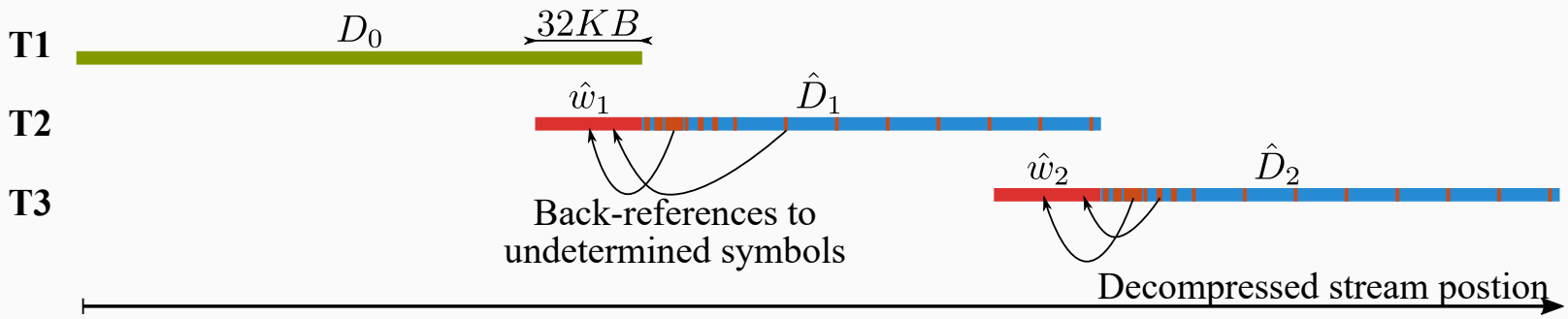
At normal compression level, after a random access, sequences can be fully determined after a while (2^{20} bytes), but not headers.



Parallel decompression

We designed 2-step parallel decompression algorithm.

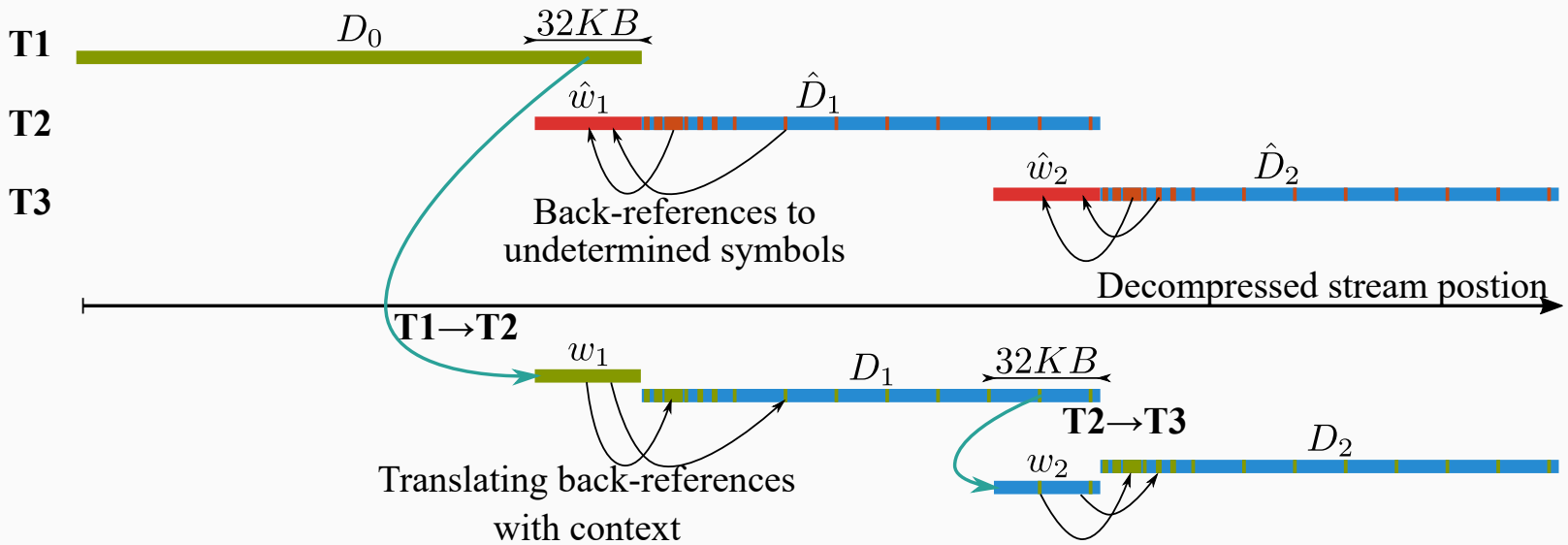
1. Partition file, decompress chunks independently, record unresolved back-references



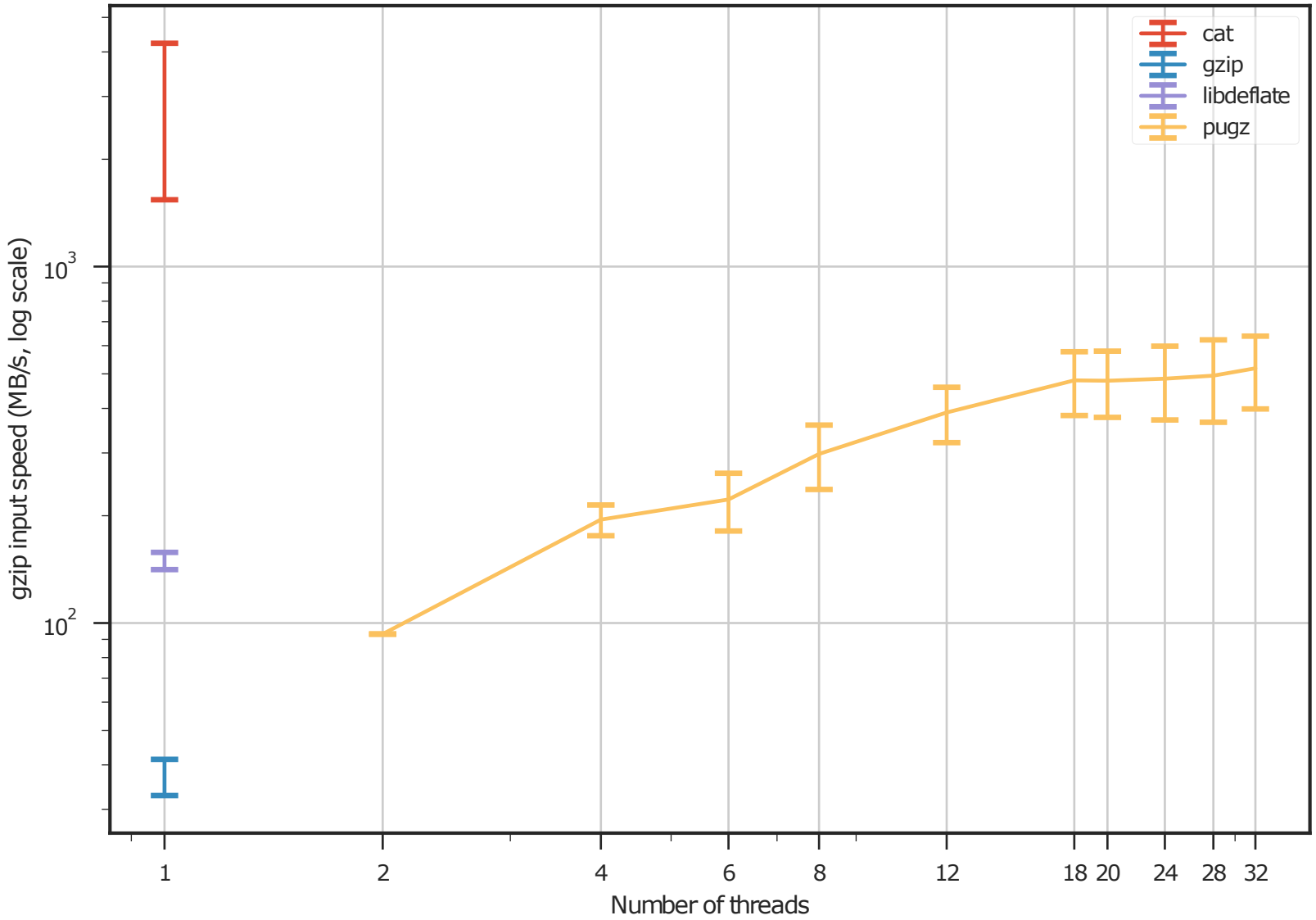
Parallel decompression

We designed 2-step parallel decompression algorithm.

1. Partition file, decompress chunks independently, record unresolved back-references
2. Propagate context across chunks, resolve back-references



Performance



Time for a demo?

Summary

In the paper (on Github):

- We study random access to **.fastq.gz** files
- Probabilistic model of compression
- Description of a **general parallel decompression** algorithm
- Implementation for ASCII files
- up to 700 MB/sec decompression (20x speedup over `gzip`)

Open questions:

- In FASTQs, one could possibly guess LZ-contexts (hard)
- Whether a `.gz.index` file would be useful in bioinfo (like `.bai` files in BAMs)

github.com/Piezoid/pugz