

FPGA-Accelerated genomic data analysis with Hugenomic Nanopolish

INTRODUCTION

Analyze more than 800,000 long reads of genomic data (about 102 GB) in 3 hours thanks to Huxelerate Hugenomic Nanopolish(*).

PRODUCT OVERVIEW

Huxelerate Hugenomic Nanopolish enables **ultra-fast signal-level analysis of large datasets** of Oxford Nanopore Sequencing data.

The software is based on Nanopolish (<https://github.com/jts/nanopolish>) and can calculate an improved consensus sequence for a draft genome assembly, detect base modifications, call SNPs and indels with respect to a reference genome and more.

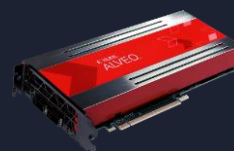
The **accelerated implementation** exploits **FPGAs to accelerate the computation and provide high performance and faster time to result.**

Current implementation allows to accelerate the eventalign tool, **reducing computational time from days to hours when compared to software-only executions.**

The functionalities provided in this release, mirror Nanopolish v0.13.2.

Huxelerate supports academic research. If you are willing to use Hugenomic Nanopolish for your academic research, please contact us at info@huxelerate.it.

(*) Dataset taken from WGS Consortium: <https://github.com/nanopore-wgs-consortium/NA12878/blob/master/Genome.md> flowcell_id: FAB42451



Huxelerate[↗]

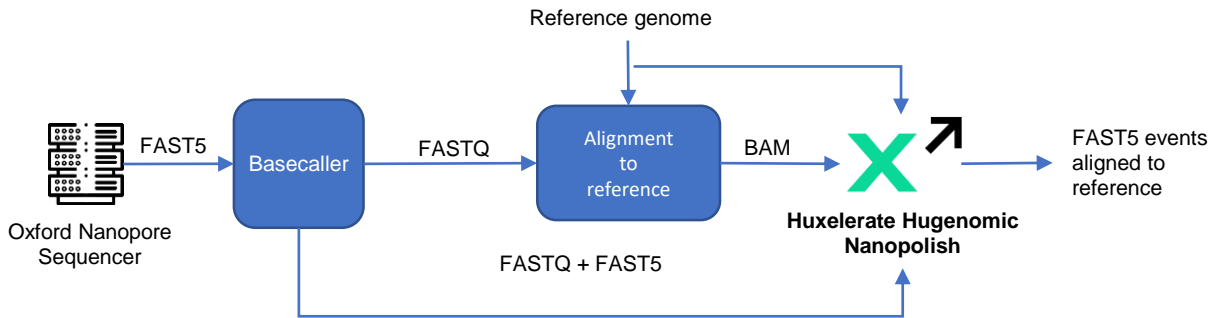
Highlights

- > Ultra-fast genomic analysis
- > Faster time to results
- > 10x performance improvement



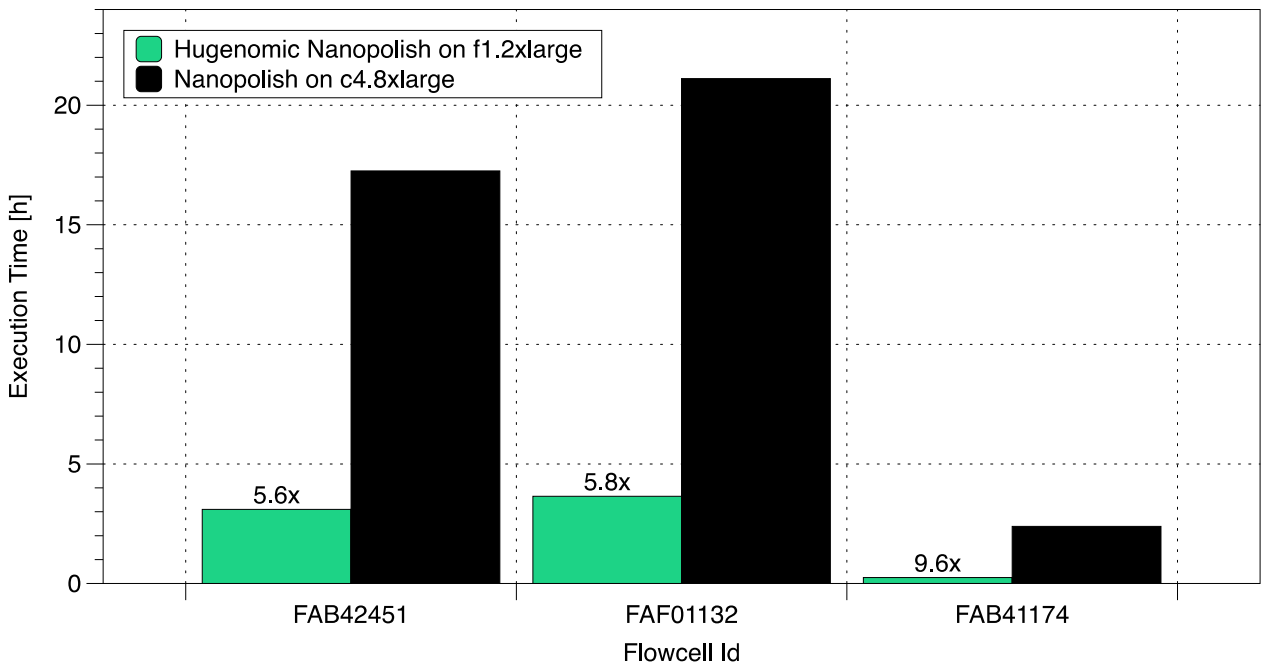
Adaptable. **Intelligent.**

SOLUTION OVERVIEW



SOLUTION BENCHMARKS

Huxelerate Hugenomic Nanopolish Performance vs Original Nanopolish



Dataset WGS Consortium: <https://github.com/nanopore-wgs-consortium/NA12878/blob/master/Genome.md>

Software equivalent tested on c4.8xlarge (2.9 GHz Intel Xeon E5-2666 v3) using 36 cores

TAKE THE NEXT STEP

1. Learn more about [Huxelerate](#)
2. Learn more about [Huxelerate Hugenomic Nanopolish](#)
3. Reach out [Huxelerate Sales](#)