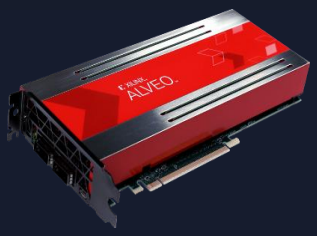
GTX.FPGA - Bioinformatics Acceleration

High Performance Genomic Computing

SOLUTION BRIEF

XILINX ALVEO™



INTRODUCTION

With the development of genome sequencing technology and the reduction of costs, the research on sequencing of large sample sizes of population queues, plants and animals is more and more extensive, resulting in a huge amount of data. By 2025, the size of the sequencing data is expected to reach 2000-40000 PB per year. But the sequencing data analysis is far from fast enough compare to data produce, which severely restricts the wide application of data. In order to maximize the value of sequencing data and promote the development of human health, accelerate bio-informatics analysis is imperative.

KEY BENEFITS

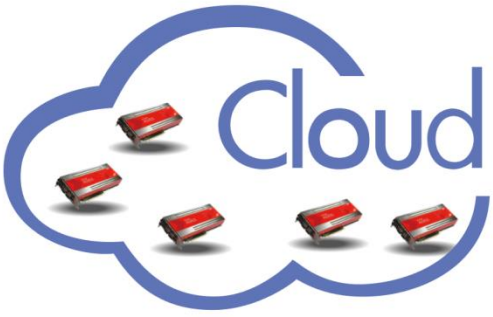
- Saving computing time
- Reducing the cost
- High quality

- High speed
- Low power consumption
- Costs saving

SOLUTION OVERVIEW

The high performance genomic computing solution - GTX.FPGA is a bioinformatics analysis acceleration system. The implementation of bioinformatics algorithms is engineered by CPU and FPGA heterogeneous acceleration. The bioinformatics analysis acceleration system keeps both speed and accuracy balanced, and can be deployed both in local and cloud platform.

Local deployment



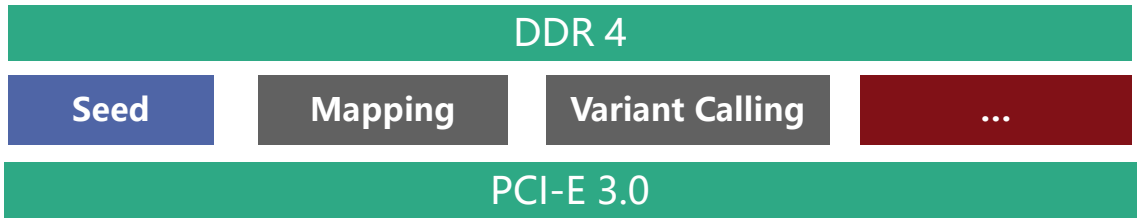
Cloud deployment

GTX.FPGA - Bioinformatics Acceleration

High Performance Genomic Computing

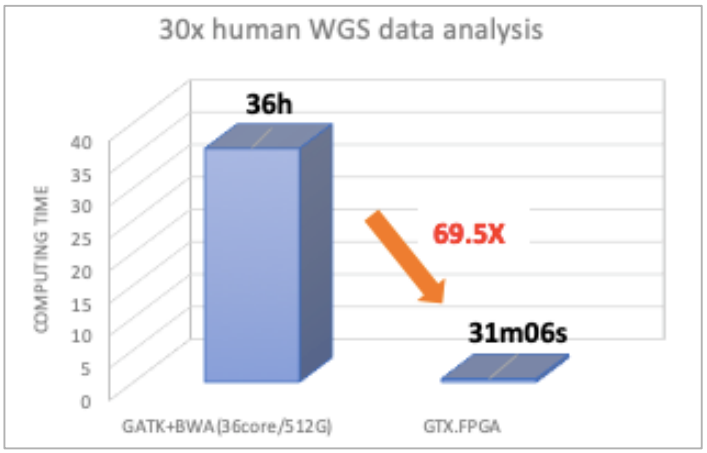
SOLUTION DETAILS

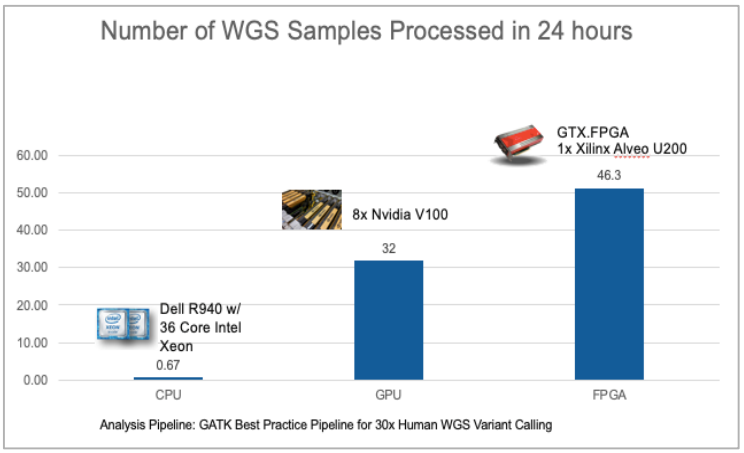
The high performance genomic computing solution - GTX.FPGA integrates mapping, sorting, mark duplicates, and variants calling which are commonly used in whole genome sequencing (WGS) and whole exome sequencing (WES). The core algorithm of GATK (variants calling tool) and BWA (mapping tool) has been accelerated by FPGA logic. Other processes run in CPU-optimized multithreaded software for maximum flexibility. The co-concurrency of different computing cores makes the computing function of the whole system get the best presentation.



RESULTS

A 30x human WGS data analysis (from fastq to vcf) only takes about 30 minutes. Normally, it takes 30-40 hours (see below figures). The acceleration rate of this system is close to 70x. A 100x human whole exome sequencing data analysis takes only five minutes.





TAKE THE NEXT STEP

Learn more about Xilinx Alveo accelerator cards
Learn more about Genetalks (www.genetalks.com)
Reach out to contact@genetalks.com