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Scalable Genomics Inc.

Creating the future of bioinformatics data analysis platforms.

Scalable Genomics Inc. provides bioinformatics software for plug-n-play analysis of Big Data from genomic sequencing of clinical, environmental, genomic, and forensic samples. In recent years, availability of affordable DNA sequencing technology such as MiSeq from Illumina Inc. or Oxford mini-ION, has enabled researchers in academic laboratories, medical centers and government agencies to adopt genomic sequencing for a range of applications. Given the scale of genomic datasets, scientific value cannot be obtained from an investment in a sequencer, unless it is matched by an equal investment in bioinformatics infrastructure. Analysis of genomic data requires access to a range of technical capabilities including expertise in information technology and software engineering, as well as access to large-scale computational and storage capabilities. This can become a significant impediment, as researchers need to come up with the funds for building an informatics infrastructure with capacity to handle large-scale sequence data, and the funds for hiring trained professionals competent to install, configure and run the bioinformatics software, which in the end sums up to a higher expense than acquiring the sequencer.

Our solution utilizes cloud computing and virtualization technologies, providing broad access to large-scale computational and data storage capacity for sequencing bioinformatics. We have implemented Virtual Machines (VMs) that are pre-configured computer servers with the operating system and software pre-installed and ready to use. The VMs run through a virtualization layer independently of the underlying hardware architecture, and will be available on commercial cloud computing vendors (pay-on-demand), or licensed for local computer clusters and desktop computers. With this plug-and-play solution delivered through virtualization and the cloud we eliminate the need for technical skills required to set-up bioinformatics software, and with availability and also the upfront capital expenses for building IT infrastructure. Furthermore, the VMs require minimal or zero installation effort, are portable across computing platforms from desktop computers to compute clusters, and provide a mechanism for sharing research data, independently of the differences in computing infrastructures used by researchers.

With 42% of the $3 billion sequencing market being analytics and software growing yearly at 17%, Scalable Genomics provides a unique platform and potential to capture a large segment of the market by providing seamless access to complex bioinformatics analytics algorithms. Our founders have 10-year experience in genomic sequencing and cloud computing. While our competitors focus on mainstream data analysis and large research consortia we target the long-tail of researchers, clinical labs, diagnostic providers and pharmas interested in bioinformatics analytics found as *ad hoc*, non-standardized implementations in the literature. Our goal is to change the current paradigm of $1000 genome and $100,000 "interpret-ome", by multi-fold reduction of the costs of sequencing data interpretation .