

The Human Genome Project(HGP) is an international scientific research project with a primary goal of determining the sequence of chemical base pairs which make up DNA, and of identifying and mapping the approximately 20,000–25,000 genes of the human genome from both a physical and functional standpoint. It remains one of the largest single investigative projects in modern science. The process of identifying the boundaries between genes and other features in a raw DNA sequence is called genome annotation and is the domain of bioinformatics. While expert biologists make the best annotators, their work proceeds slowly, and computer programs are increasingly used to meet the high-throughput demands of genome sequencing projects. Personalized genomics can establish the relationship between DNA sequence variations among individuals and their health conditions and responses to drugs and treatments. To make genome sequencing a routine procedure, however, the time must be reduced to less than a day, and the cost to less than \$1,000 — a feat not possible with current knowledge and technologies.

In 2008, a research team led by Aleksei Aksimentiev, assistant professor in the physics department at the University of Illinois-Urbana-Champaign, began a project to create machines for personal genome sequencing that will be more accessible to hospitals. Using Oak Ridge National Laboratory's Jaguar, one of the world's fastest supercomputers, Aksimentiev and his team is developing a nanopore approach, which promises a drastic reduction in time and costs for DNA sequencing. The research received 10 million processor hours on Jaguar through the Innovative and Novel Computational Impact on Theory and Experiment, or INCITE, program, which awards considerable allocations on some of the world's most powerful supercomputers to projects addressing grand challenges in science and engineering. "We have carried out a pilot study and observed considerable reduction of the DNA strand speed," Aksimentiev said. "These very preliminary results suggest that achieving a 100-fold reduction of DNA velocity, which should be sufficient to read out the DNA sequence with single-nucleotide resolution, is within reach. Future studies will be directed toward this goal." The team hopes to achieve this project's objective by 2013 and plans to pursue a number of exciting spin-off projects. The ability to make genome sequencing affordable will enable such programs as the Cancer Genome Project, which characterizes DNA mutations in cancer cells in various tissues throughout all stages of cancer development.

Jaguar is the most powerful descendant of the Red Storm2 computer system developed by Sandia National Laboratories with Cray and first installed at Sandia in 2004. Jaguar is a massively parallel, distributed memory system . Jaguar has a peak performance of just over 1,750 teraflops (1.75 petaflops). It has 224,256 x86-based AMD Opteron processor cores, and operates with a version of Linux called the Cray Linux Environment. Jaguar ranked 1st in the list of top 500 super computers in November 2009, and was continuously in top 5 from 2008 – 2011. In the latest rankings on November 2012 Jaguar, transformed Titan by adding GPU's, once again emerged as the fastest.

References:

<http://www.scientificcomputing.com/news-HPC-Jaguar-Supercomputer-Helps-Develop-Affordable-Personal-Genome-Sequencing-022811.aspx>

[http://en.wikipedia.org/wiki/Jaguar_\(computer\)](http://en.wikipedia.org/wiki/Jaguar_(computer))

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