Expand the Vision: Nanopore Genome Sequencing

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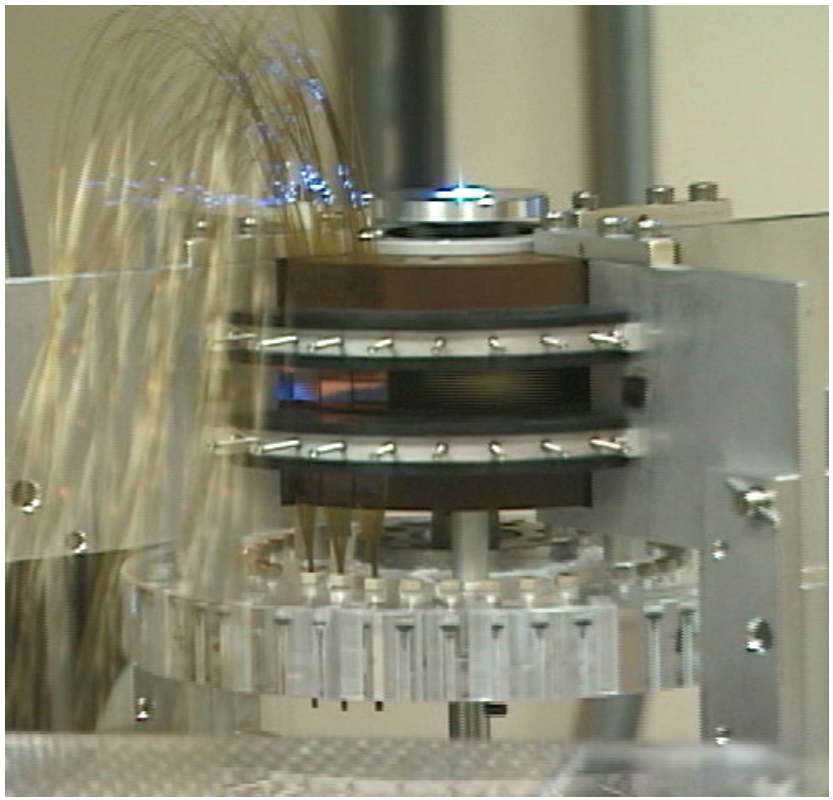
Introduction

- Full genome sequencing (FGS), also known as whole genome sequencing or complete genome sequencing, is a laboratory process that determines the complete DNA sequence of an organism's genome at a single time.

- Sequencing of nearly an entire human genome was first accomplished in 2000 but sequencing of smaller genomes has been done since 1979.

- Capillary sequencing was used to process the first human genome, however it is expensive and still takes too long (~twice as fast as electrophoresis).

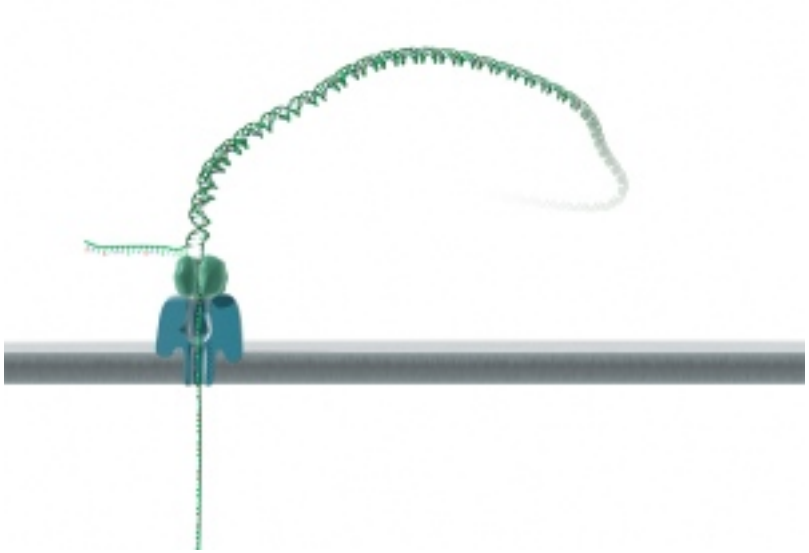


- With the improved technology of nanopore sequencing we can theoretically sequence an entire human genome in as little as 15 minutes.

http://med.stanford.edu/sgtc/images/mc3.jpg

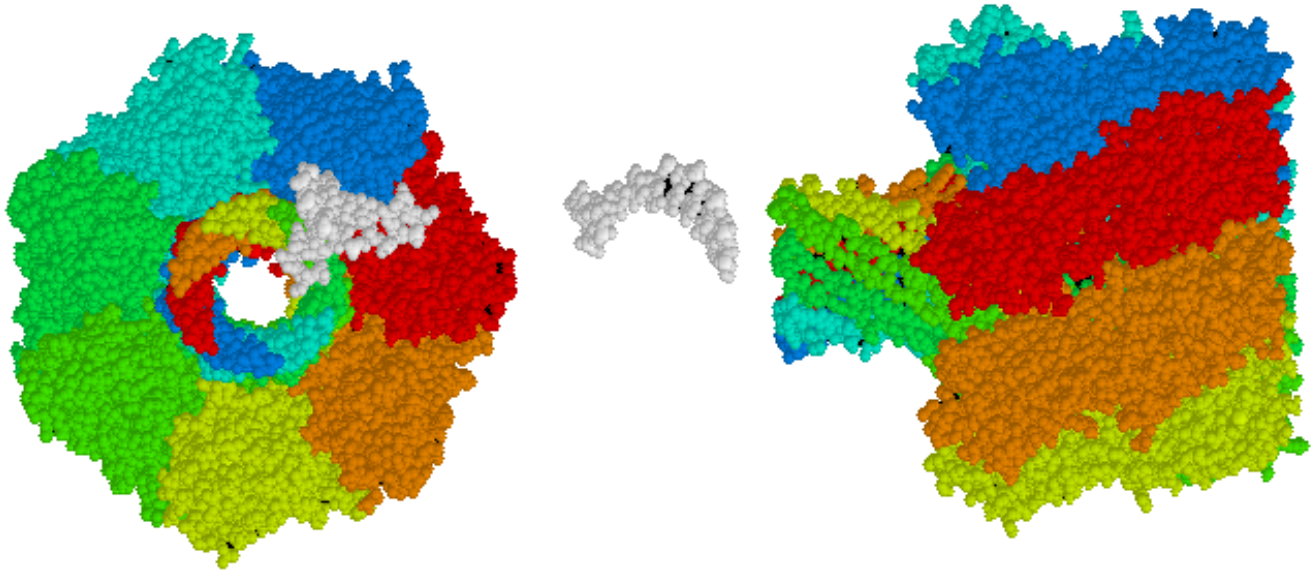
How It Works

- Nanopore sequencing rapidly reads DNA sequences by feeding a strand of DNA through a biological pore.



http://www.nature.com/news/nanopore-genome-sequencer-makes-its-debut-1.10051

- The various bases are identified by measuring the difference in their electrical conductivity as they pass through the pore.



- Some of the advantages of the system are that it could deliver real-time sequencing of single molecules at low cost, and that it does not damages DNA, so the data could be later reanalyzed.

http://en.wikipedia.org/wiki/Nanopore_sequencing

- Another important advantage is that this newly developed technology is relatively simple to use and extremely portable.

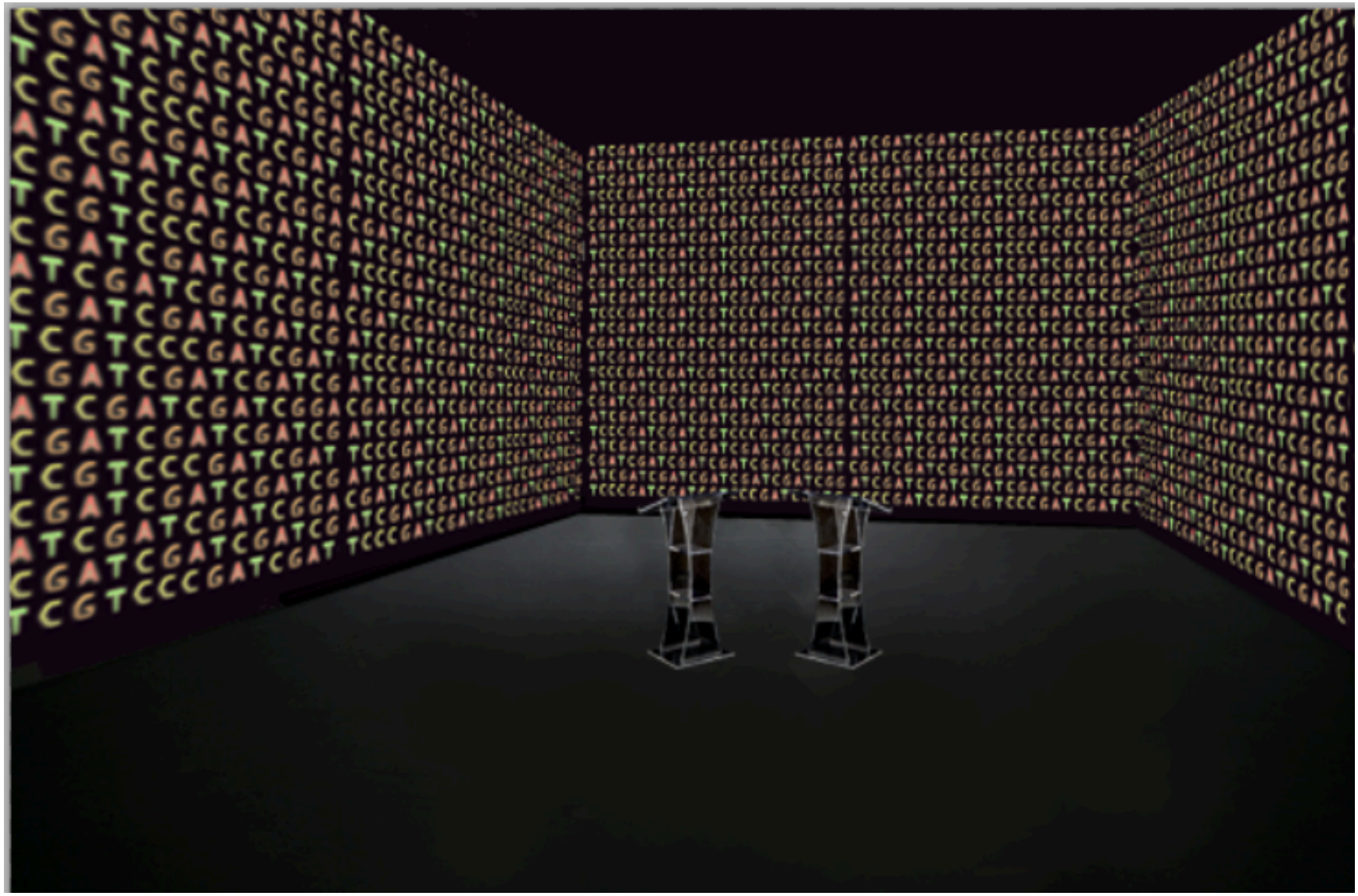
http://www.zmescience.com/wp-content/uploads/2012/02/minION.jpg

Gallery Presentation

- This project will be presented in a dimly lit gallery.
- In the center of the room there will be two computers:
  - The first will be used to take and sequence DNA from participants as well as general information (age, sex, ethnicity, etc)
  - The second computer will be used by viewers to manipulate the data collected from the various genomes

- The genome sequences will be stored in a database and connected to software and projectors that will constantly be scrolling through genetic codes on three of the gallery walls.

- The fourth wall will display information from the second computer which will allow viewers to choose various ways to organize the genetic codes such as: most common sequence, a particular sequence, specific characteristics (ethnicity, age, sex, etc).



Why is this important?

- 96% of subjects included in genome-wide association studies are of European descent.
- Genome-wide association studies give us a better understanding of diseases that are linked to certain populations.
- There needs to be more sampling of racial and ethnic minorities.

- Global genomics needs the financial support of governments and non-profits. ‘Gallery exhibitions showing how simple and relatively cheaply nanopore sequencing can be achieved could bring greater attention to the need for researchers to branch out their studies.

Sources

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