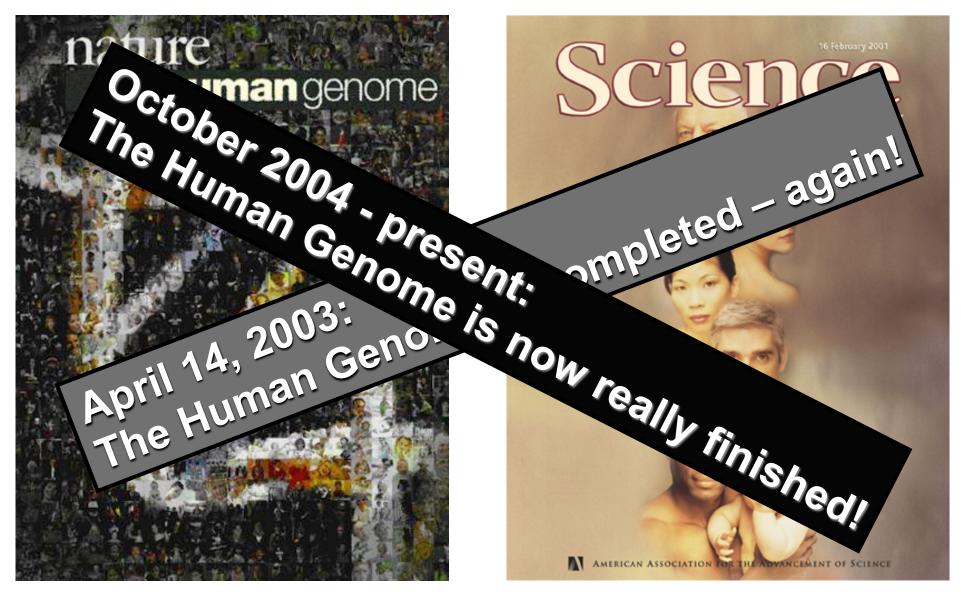


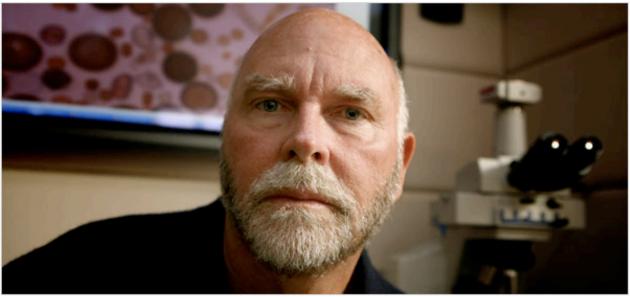
Bioinformatics The Human Genome Project

The Human Genome Project



February 2001: Completion of the Draft Human Genome

In the Genome Race, the Sequel Is Personal



Thor Swift for The New York Times

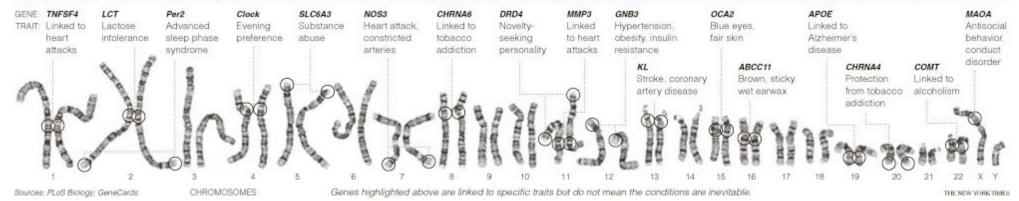
A team led by J. Craig Venter, above, has finished the first mapping of a full, or diploid, genome, made up of DNA inherited from both parents. The genome is Dr. Venter's own.

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The New York Times

September 3, 2007

DECODING HIMSELF A team led by J. Craig Venter, above, has finished the first mapping of a full, or diploid, genome, made up of DNA inherited from both parents. The genome is Dr. Venter's own.



To carry the sequence of my genome in my pocket, I need:

(A) supercomputer

(B) my laptop (brand new)

(C) my home computer (Oops, it's old)

If compressed, the 3GB human genome will also fit on a single CD

(F) floppy disk

DVD

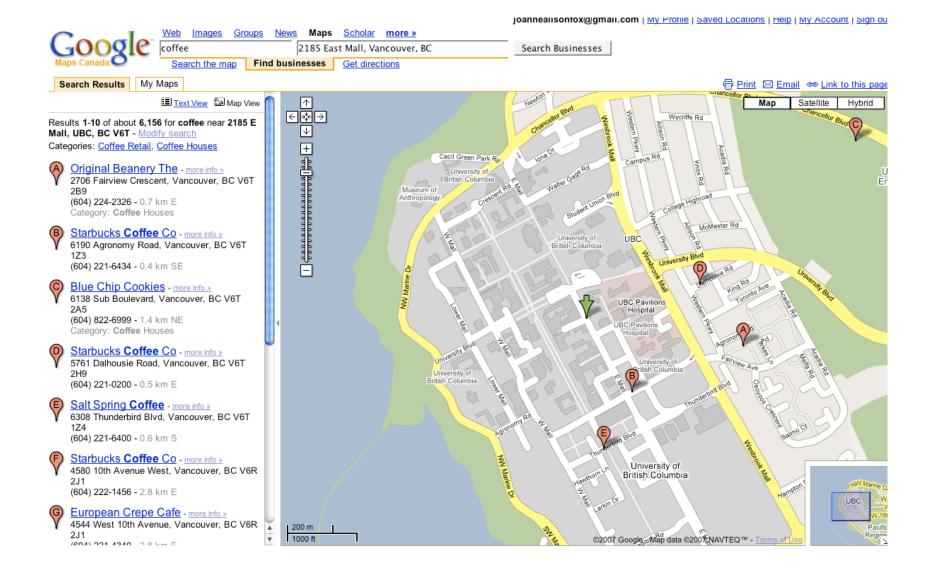
(E)

The Human Genome...By the Numbers

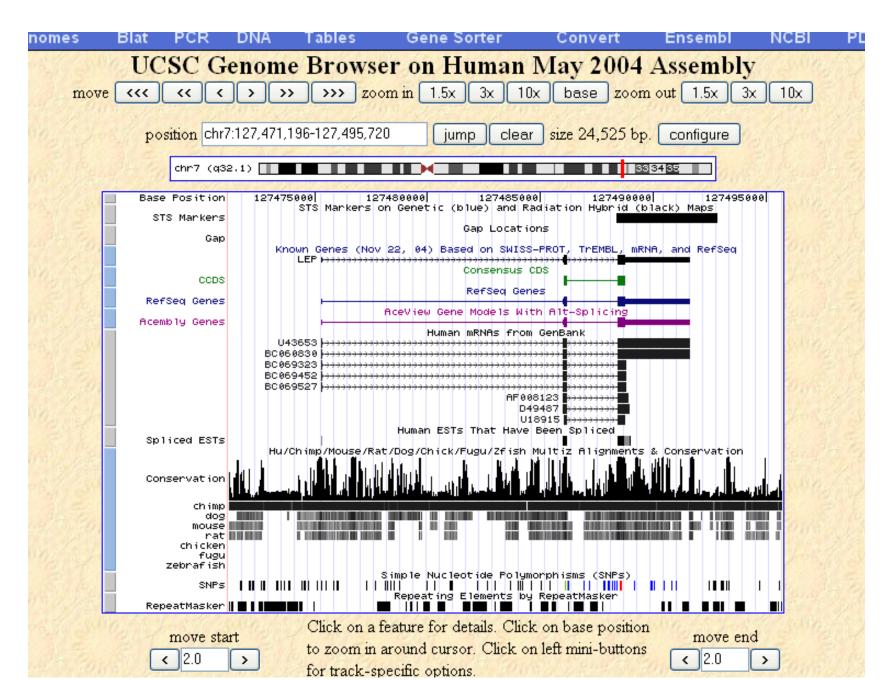
- 75-100 trillion...Cells in the human body
- 3.1 billion...Base pairs in each cell
- 2.4 million...Base pairs in the largest human gene
- **28,000-35,000...**Genes in the human genome
- **46...**Chromosomes in each cell



maps.google.ca



Let's Look at the Human Genome...



Google "Genome Browser"

Doing a Search

Human (Homo sapiens) Genome Browser Gateway		
	The UCSC Genome Browser was created by the <u>Genome Bioinformatics Group of UC Santa Cruz</u> . Software Copyright (c) The Regents of the University of California. All rights reserved.	
clade	genome assembly position or search term image width	
Vertebrate	▼ Human ▼ Mar. 2006 ▼ chrX:151,073,054-151,383,976 620 submit	
	Click here to reset the browser user interface settings to their defaults.	
add custom tracks configure tracks and display clear position enter a gene the submit be search.		
About the Human Mar. 2006 (hg18) assembly (sequences)		

other genomes available

The March 2006 human reference sequence (NCBI Build 36.1) was produced by the Internation: Sequencing Consortium.

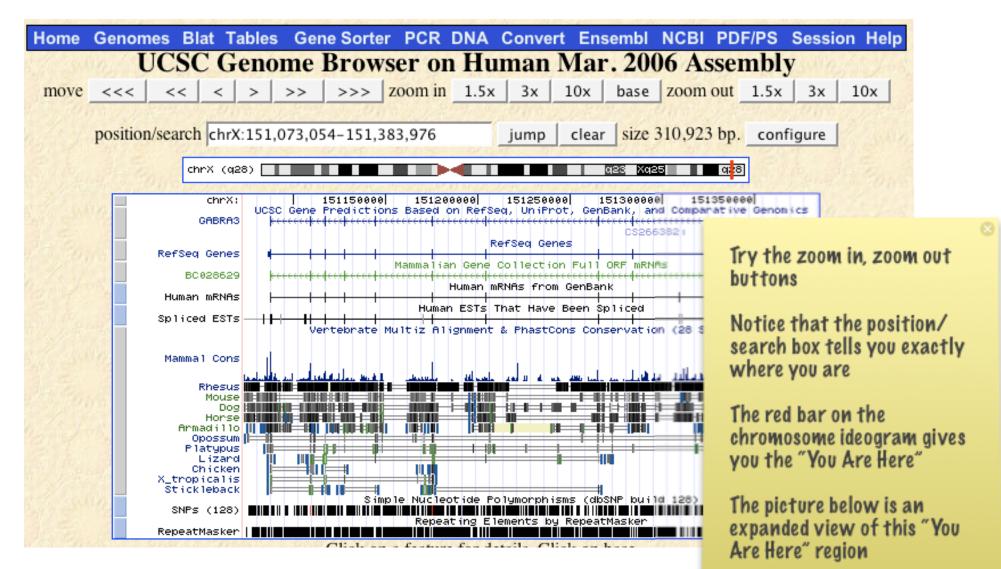
Sample position queries

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, or a cytological band, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the <u>User's Guide</u> for more information.

Request: Genome Browser Response:

chr7	Displays all of chromosome 7
20p13	Displays region for band p13 on chr 20
chr3:1-1000000	Displays first million bases of chr 3, counting from p arm telomere

Moving Around



¹

Websites visited:

- Google <u>www.google.ca</u>
- Google Maps <u>http://maps.google.ca</u>
- UCSC Human Genome Browser Gateway
- http://genome.ucsc.edu/cgi-bin/hgGateway
- (hint: use google to look up "Genome Browser")