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Humane genome: Now online

Silicon Valley / San Jose Business Journal

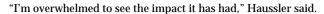
David Haussler and Jim Kent are co-directors of the Genome Browser project at the University of California, Santa Cruz. The browser, located at www.genome.ucsc.edu, provides online interactive exploration of certain genome sequences.

Haussler, a Howard Hughes Medical Institute investigator and director of UC Santa Cruz's Center for Biomolecular Science and Engineering, or CBSE, said the browser essentially offers a Web-based "digital microscope" for exploring the human genome sequence and is used daily by thousands of biomedical researchers throughout the world.

"It is now as indispensable in the lab as the light microscope," Haussler said.

CBSE research scientist Kent, who assembled the first working draft of the human genome, is responsible for creating the Genome Browser. He works on Web tools to help understand the human genome and leads a team of engineers that maintains the browser. The project receives funding from the HHMI, the National Human Genome Research Institute, the National Cancer Institute and the California Institute for Quantitative Biosciences.

The team gave a tutorial on the browser in November at an American Society for Human Genetics meeting, and the auditorium was packed to capacity with more than 1,000 researchers attending.



Q: How did you and your team create the Genome Browser? How long did it take?

A: The project was done very incrementally. The initial version was done by Kent in the fall of 2001. The year before, Kent had done a browser, called the Intronerator, a collection of tools for exploring the molecular biology and the genomics of a species of worm called C. elegans. The human genome browser incorporated a lot of lessons he learned from the Intronerator. In particular, he learned that people would want to continually add more annotation tracks, so he made this easy in the human genome browser. By 2002, other UC Santa Cruz graduate students, Chuck Sugnet and Terry Furey in particular, were also working on the browser. Back then, the code was small enough they would release new, improved versions several times a week. Later that year, they got a National Human Genome Research Institute grant and were able to hire a professional programming and testing staff to work on it. They made the browser able to handle the mouse as well as the human genome. The browser has grown gradually in scale to the point now where it handles more than 50 organisms and hundreds of types of genomic information.

Q: How many people are tapping into it and why?

A: Approximately 10,000 scientists use it every week. The uses range from very simple, such as getting the DNA around a gene in order to design widely used processes known as PCR primers, to the very complicated, such as combining multiple lines of evidence to look for genetic factors behind diseases.

Q: What was the reason behind it? What triggered the project?

A: The need to understand the human genome at a level more useful than just a long list of A,C,G and T's (which refer to the four structural units of DNA).

Q: How are the results beneficial to the people and companies using the site?

A: There's a humorous saying in biomedical research that "three months in the lab can save you an afternoon in the library." With the Genome Browser, bringing all the information available on a particular gene into one place, it's safe to say that an afternoon with the Genome Browser can save three months in the library.

Q: Are other universities doing anything similar?

A: The most similar thing is the Ensembl Project, which is run out of the European Bioinformatics Institute and is not a university. The project produces genome databases for vertebrates and other eukaryotic species, and makes this information freely available online. It is a joint project between EBI, an outstation of the European Molecular Biology Laboratory, and the Wellcome Trust Sanger Institute. Both institutes are located on the Wellcome Trust Genome Campus in Hinxton, south of Cambridge, England.

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