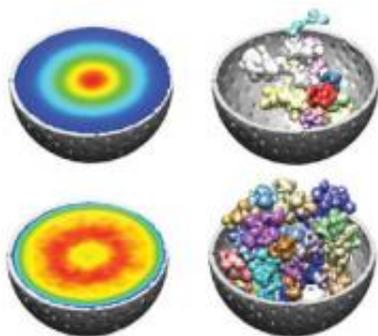


Scientists create first 3-D map of human genome

January 4 2012, By Robert Perkins



Understanding the structure of the human genome is critical to understanding its function as a whole, according to USC Dornsife's Lin Chen.

(PhysOrg.com) -- For the first time, scientists have developed a method for generating accurate three-dimensional models of the entire DNA strand of a cell, known as a genome.

The [genome](#) plays a central role in the functions of almost all [human cells](#), and flaws in its structure are thought to cause various disorders, including [cancer](#).

Understanding the structure of the genome is crucial to understanding its function as a whole, said Lin Chen, professor of [molecular biology](#) in USC Dornsife.

“Everything biological works in the three dimensions,” Chen said. “Therefore, to understand it completely, you have to understand it three-dimensionally.”

The genome inside a cell can be thought of as a bowl of angel hair pasta. Different [cells](#) are like different bowls of pasta in which the noodles are organized differently overall, but they share certain features.

The technique adds a crucial piece of the puzzle for scientists trying to understand the genome — the cornerstone of life — in normal and diseased cells. One of the most likely applications of this research will be to identify potentially cancerous cells based on structural defects in the cell’s genome, Chen said.

“Hopefully in the future, these studies allow scientists to better understand how the genome is involved in disease and how its function can be regulated in those circumstances,” Chen said.

Because of its tiny size and monstrously long length, creating a three-dimensional image of a genome is not as simple as taking a photograph. The genomic [DNA strand](#) is so long that if a nucleus was the size of a soccer ball, the strand of DNA inside it could be unraveled to stretch more than 30 miles long. Nothing biologists normally use for studying the structure of biomolecules works well for the human genome.

Scrunched up inside the nucleus, the DNA forms hundreds of millions of contacts with itself. Using a new technique, USC researchers plotted out the location of each of those DNA-on-DNA contacts and used sophisticated computer algorithms to model the results in 3-D.

“It provides you with a completely new prospective in the genome,” Chen said. The study appeared on the *Nature Biotechnology* Web site on Dec. 25, ahead of its publication in the print edition.

By analyzing the differences and similarities in genome structure between various cells, scientists are able to discern what basic principles of 3-D organization are. In addition, the structure allows scientists to see where each gene is located relative to any other gene and how this arrangement is important to cellular functions.

The method used by the USC team takes into account the fact that each cell is slightly different — the DNA does not always scrunch in the exact same way.

“There is not a single structure of a genome,” said Frank Alber, assistant professor of computational biology in USC Dornsife. Chen and Alber led a team of USC researchers, including Reza Kalhor, Harianto Tjong and Nimanthi Jayathilaka, that solved the problem.

By doing a statistical analysis of many genomes, the team was able to determine “preferred positions” for the DNA strand, providing an idea of how it most likely is to appear.

Provided by USC College

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