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[Physics] NTHU Professors Apply Big Bang Theory to 3D Atomic Tomography [Physics] NTHU Professors Apply Big Bang Theory to 3D Atomic Tomography (Chinese Version)

Taipei Times (2012/07/12) Inspired by the Big Bang Theory, a pair of professors from National Tsing Hua University (NTHU) and the University of Antwerp have developed a new route to atomic-resolution electron tomography.

Fu-rong CHEN (陳福榮) of NTHU's department of engineering and system science and Dirk VAN DYCK were seeking to understand and control the features and functions of protein and other materials.

To this end it is crucial to analyze their 3D atomic structure, CHEN said, adding that although it was possible to analyze atomic structure using classical electron tomographic methods, the resultant images are 2D and the actual 3D structure of the atoms within a material cannot be interpreted directly.

"To use the 2D images taken by classical electron tomographic methods to produce a 3D image, you need to take many shots from more than a hundred angles, but you still cannot achieve the level of atomic resolution," CHEN said.

It takes the selection of about 37,000 proteins from 3,000 images and the use of 7,000 PC clusters for 200 days to calculate the 3D structure of a virus using the classical method of cryoelectron tomography, he added.

However, inspired by Big Bang Theory and the Hubble expansion — which says the universe expanded from a single point of origin, meaning that the distance between galaxies and the origin are linearly proportional to the speed at which they move away from the origin — CHEN and VAN DYCK developed a similar calculation to image the structural arrangement of atoms.

By sending out electron waves from only one viewing direction and calculating the different angles and phases of waves when they reach the image platform after hitting the atoms, the new method is able to calculate the precise location of the atom in its 3D structure faster and easier than classical methods, he said.

The method is likely to have a revolutionary effect on analyzing atomic structures in material and protein in the future, CHEN said, adding that it would greatly reduce the time needed to reconstruct the atomic structure of proteins.

Their breakthrough was published in last month's issue of Nature.

Reference: <u>Taipei Times 2012/07/12</u>

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