

Scientists use world's fastest supercomputer to create the largest HIV evolutionary tree

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Supporting Los Alamos National Laboratory's role in the international Center for HIV/AIDS Vaccine Immunology (CHAVI) consortium, researchers are using the Roadrunner supercomputer to analyze vast quantities of genetic sequences from HIV infected people in the hope of zeroing in on possible vaccine target areas.

Physicist Tanmoy Bhattacharya and HIV researcher Bette Korber have used samples taken by CHAVI across the globe - from both chronic and acute <u>HIV</u> patients - and created an evolutionary genetic family tree, known as a phylogenetic tree, to look for similarities in the acute versus chronic sequences that may identify areas where vaccines would be most effective.

In this study the evolutionary history of more than 10,000 sequences from more than 400 HIV-infected individuals was compared.

The idea, according to Korber, is to identify common features of the transmitted virus, and attempt to create a <u>vaccine</u> that enables recognition the original transmitted virus before the body's <u>immune</u> <u>response</u> causes the virus to react and mutate.

"DNA Sequencing technology, however, is currently being revolutionized, and we are at the cusp of being able to obtain more than 100,000 viral sequences from a single person," said Korber. "For this new kind data to be useful, computational advances will have to keep pace with the experimental, and the current study begins to move us into



this new era."

"The petascale supercomputer gives us the capacity to look for similarities across whole populations of acute patients," said Bhattacharya. "At this scale we can begin to figure out the relationships between chronic and acute infections using statistics to determine the interconnecting branches - and it is these interconnections where a specially-designed vaccine might be most effective.

Source: Los Alamos National Laboratory (news : web)

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