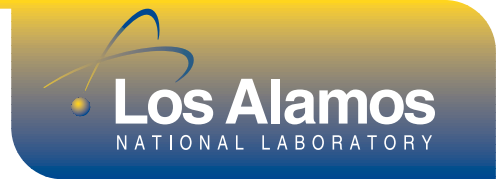


Bioinformatics and the HIV Database



Los Alamos pioneered bioinformatics, a convergence of computer science and biomedicine that permits researchers to organize, interpret and disseminate the huge amounts of biological information generated by the Human Genome Project and other research. Simply put, man's ability to produce huge amounts of biological information about genes, protein structures and clinical trials has outrun capabilities to handle it usefully.

In 1982, Los Alamos created GenBank, a database now maintained by the National Institutes of Health as a national repository of genetic sequencing information.

Since then, Los Alamos has built a database of the human immunodeficiency virus and related viruses. The database incorporates discoveries of the genetic structure and the various subtypes of the virus that causes AIDS, the historic origins of the virus in man and key characteristics required for possible vaccines. Other biological databases from Los Alamos used by researchers around the world include

influenza, sexually transmitted diseases, tuberculosis, anthrax, plague, smallpox, and other pathogens or diseases.

This work led to unique analytical capabilities that permit rapid identification of anthrax strains that then can be compared to the database in actual disease cases, a tool valuable to public health officials as well as forensic scientists. These specialized databases house sequencing and related molecular data for first-level analyses that help researchers understand how bacteria function, discover similarities between pathogens and find the best ways to target drugs. They also are valuable in tracking evolutionary patterns of pathogens.

The Laboratory has developed, and continues to develop, innovative software that enables flexible, sophisticated searches of the databases. Bioinformatics in the future will help scientists track molecular epidemics and bioterrorism, understand cellular responses to infections, develop bacteria sequencing and interpret data from clinical trials.

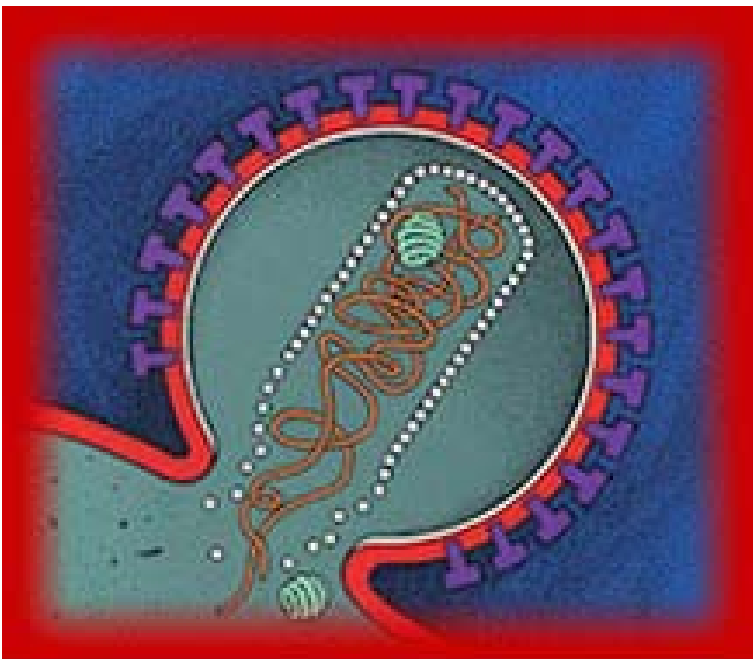
Los Alamos researchers recommended strategies for a vaccine based on a consensus or genetic ancestor HIV, rather than basing vaccines on geographically specific strains, which often are extremely variable genetically. Beginning with a National Institutes of Health request in the mid-1990s to review strategies for HIV vaccine development, Los Alamos researchers recommended considering alternative strategies of selecting vaccine strains that are central to circulating forms of the HIV-1 virus.

The Los Alamos team recently found that people with less common types of proteins on their white blood cells seem to mount a better immune response against the HIV and tend to fight progression of the disease better than people with common white blood cell proteins. The research eventually might help researchers better understand and exploit potential weaknesses in HIV.

The same team in 2000 received international publicity when they published estimates that the most recent common ancestor of the HIV-1 strains responsible for the AIDS pandemic occurred about 1930, nearly 30 years earlier than the oldest known HIV-1 positive blood sample. Using the Laboratory's supercomputers, they analyzed the extensive HIV-1 sequence data compiled at the Los Alamos AIDS and Human Retroviruses Database and estimate the timing of HIV's origins.

By establishing the timing of early events in the AIDS epidemic, health researchers can examine hypotheses about how the virus was introduced, how it spread in humans and how quickly the virus accumulates mutations. This helps them understand what it will take to design successful vaccines. Los Alamos' database is supported by National Institutes of Health.

Probably the best-known element of the Laboratory's extensive bioinformatics program is the effort to use its worldwide database of HIV virus information to better understand HIV-1, the strain that has resulted in the AIDS pandemic and infection of 50 million people.



HIV schematic, courtesy of the National Institutes of Health.



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