

Thomas Leitner

Theoretical Biology & Biophysics
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Short Bio:

Thomas Leitner is a staff scientist in the Theoretical Biology & Biophysics group at Los Alamos National Laboratory (LANL). He received his Ph.D. from the Karolinska Institute, Stockholm, Sweden in 1996. He did a postdoc at LANL 1996-1998, with part time at University of California, Irvine, Department of Ecology and Evolutionary Biology. In 1998-2003 he was the head of the HIV & Retrovirus Section at the Swedish Institute for Infectious Disease Control, Sweden, and started a Genomics Core facility at the same institute in 2001. In 2003 he moved back to the Theoretical Biology & Biophysics group at LANL to join the HIV database and to pursue more theoretical aspects of HIV evolution. He now collaborates with experimentalists and other theoreticians in both the USA and Europe. He has published over 100 scientific publications, mostly related to computational analyses of HIV evolution and molecular epidemiology, but also other pathogens and the molecular history of the domestic dog. He enjoys solving problems related to molecular evolutionary processes and their effects on pathogenesis, epidemiology and the pathogens themselves. Outside science, he loves to explore the great outdoors, gardening and woodworking.

Research Interests:

I'm interested in molecular evolution and how phylogenetics can be used to understand how pathogens spread. This is complex as it involves host factors such as the immune response and drug treatment, epidemiological factors such as how a pathogen spreads and, naturally, pathogen factors such as replication errors and population structure. I'm currently involved in several projects studying HIV evolution within patients, in HIV outbreaks among intravenous drug users, and in transmission histories. I'm also involved in analyzing 454 sequence data to understand sequence diversification in early and chronic infections, to study drug resistance, superinfection and population based screening. I'm starting to investigate fitness effects on viral evolution and how that relates to competition and recombination. I'm a co-PI on the HIV database, which serves the international HIV research community, and interested in bioinformatics development and database content. Aside from HIV and the closely related SIVs, I have also been involved in evolutionary research of other viruses such as HCV, norovirus, papilloma virus, and bacteria such as Mycoplasma, Tuberculosis, and Chlamydia, and finally the evolutionary history of the domestic dog.