

# New cost-effective means to reconstruct virus populations

**Researchers from the United States and Switzerland have developed mathematical and statistical tools for reconstructing viral populations using pyrosequencing, a novel and effective technique for sequencing DNA. They describe their findings in an article published May 9th in the open-access journal *PLoS Computational Biology*.**

The scientists knew that pyrosequencing reads are short and error-prone, and thus set out to improve upon this process. The new computational method they developed reduces the error rate and yields information faster and more efficiently. The method has been applied to four independent, diverse HIV-1 populations from drug-resistant patients and compared to 165 sequences obtained directly from clonal sequencing of the same samples.

“These new techniques produce results quite close to accepted techniques at a lower cost and potentially higher resolution,” says Niko Beerenwinkel from ETH Zurich, one of the researchers.

Knowledge of the genetic structure of virus populations is critical for furthering biomedical research on disease progression, vaccine design, and drug resistance. The ability to better estimate the structure of virus populations holds great promise for new insights into viral evolution and disease control strategies.

Citation: Eriksson N, Pachter L, Mitsuya Y, Rhee S-Y, Wang C, et al. (2008) Viral Population Estimation Using Pyrosequencing. *PLoS Comput Biol* 4(4): e1000074. doi:10.1371/journal.pcbi.1000074

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