



## Storing genotypic resistance data and linking to other clinical information

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**BACKGROUND :** HIV drug resistance is a major threat to the successful disease management of HIV. Since 1995, sequencing has been used to detect HIV resistance associated mutations. Management of HIV nucleotide sequences is not easy as current database systems do not offer tools to handle genetic information.

**METHODS :** To develop: (1) a database enabling HIV sequences submission, analysis and storage; (2) automated tools for : (a) interpretation of large number of sequences, (b) real-time prevalence of main mutations; (c) querying HIV sequences for specific patterns; and (d) a standardized format for exchanging resistance information.

**RESULTS :** We designed an online relational database (HIV LogiCare, [www.ablnetworks.org](http://www.ablnetworks.org)) which is implemented on Linux. ViroScorer technology enables to submit sequences, and uses the detected mutations to predict levels of resistance for each drug based on several algorithms. An in-house extensive ViroScorer release (LargeScale) allows to submit in one time larger datasets: outputs (mutations, interpretations) can be opened using Microsoft Excel. Each submitted sequence is stored in the database. Detected mutations are derived in five tables : one for protease, one for the reverse transcriptase, two for main resistance associated mutations (IAS-USA), and one for interpretations (each drug-algorithm combination: 112 interpretations). These tables can be queried for real-time surveillance of detected mutations (EpiVisor) or for a specific mutations pattern (HIVLib). A file in XML (extensible markup language) format is automatically generated to have the latest sample-related information (laboratory, resistance, quality control) ready for upload and exchange.

**CONCLUSIONS :** A patient care monitoring system coupled with bioinformatics tools makes it easy to link resistance data to other parameters. Stored information (clinics, virology and resistance) can be exported in various formats and queried for surveillance program or research topics.

## Abstracts