

An Integrated Genetic Data Environment (GDE)-Based LINUX Interface for Analysis of HIV-1 and Other Microbial Sequences

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Motivation: Sequence databases encode a wealth of information needed to develop improved vaccination and treatment strategies for the control of HIV and other important pathogens. To facilitate effective utilization of these datasets, we developed a user-friendly GDE-based LINUX interface that reduces input/output file formatting.

Design and Results: GDE was adapted to the Linux operating system, bioinformatics tools were integrated with microbe-specific databases, and up-to-date GDE menus were developed for several clinically important viral, bacterial and parasitic genomes. Each microbial interface was designed for local access and contains Genbank, BLAST-formatted and phylogenetic databases.

Conclusion: GDE-LINUX is an efficient, user-friendly interface that facilitates access to a broad spectrum of bioinformatics tools without the complexities of input/output file formatting between modules. The system is easily adapted to the needs of individual researchers, providing them with the expertise they need to analyse and annotate their own sequences.

Availability: GDE-Linux is available for research purposes by direct application to the original author; the application-specific menus and support files can be downloaded from (<http://www.bioafrica.net>).

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