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| Title: | Multifractal analysis of HIV-1 genomes |
| Authors: | Sinha, Somdatta (/jspui/browse?type=author&value=Sinha%2C+Somdatta) |
| Keywords: | Archaeal genome Archaeobacterium |
| Issue Date: | 2012 |
| Publisher: | Elsevier B.V. |
| Citation: | Molecular Phylogenetics and Evolution, 62 (2), pp. 756-763. |
| Abstract: | <p>Pathogens like HIV-1, which evolve into many closely related variants displaying differential infectivity and evolutionary dynamics in a short time scale, require fast and accurate classification. Conventional whole genome sequence alignment-based methods are computationally expensive and involve complex analysis. Alignment-free methodologies are increasingly being used to effectively differentiate genomic variations between viral species. Multifractal analysis, which explores the self-similar nature of genomes, is an alignment-free methodology that has been applied to study such variations. However, whether multifractal analysis can quantify variations between closely related genomes, such as the HIV-1 subtypes, is an open question. Here we address the above by implementing the multifractal analysis on four retroviral genomes (HIV-1, HIV-2, SIVcpz, and HTLV-1), and demonstrate that individual multifractal properties can differentiate between different retrovirus types easily. However, the individual multifractal measures do not resolve within-group variations for different known subtypes of HIV-1 M group. We show here that these known subtypes can instead be classified correctly using a2 combination of the crucial multifractal measures. This method is simple and computationally fast in comparison to the conventional alignment-based methods for whole genome phylogenetic analysis.</p> |
| Description: | Only IISERM authors are available in the record. |
| URI: | http://www.sciencedirect.com/science/article/pii/S105579031100488X (http://www.sciencedirect.com/science/article/pii/S105579031100488X) http://dx.doi.org/10.1016/j.ympev.2011.11.017 (http://dx.doi.org/10.1016/j.ympev.2011.11.017) |
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