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GRID COMPUTING

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State-of-Art with PhyloGrid: Grid Computing Phylogenetic Studies on the EELA-2 Project Infrastructure

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Abstract

PhyloGrid is an application developed in the framework of the EELA-2 project devoted to the calculation of Phylogenies by means of the MrBayes software, that is, Bayesian statistics. To the moment, it has been used to perform studies on the Human Immunodeficiency Virus (HIV), the Human Papillomavirus (HPV), and the DENGUE Virus (DENV). PhyloGrid aims to offer an easy interface for the bioinformatics community, which abstracts the final user from the ICT (Information and Communications Technology) underneath, so only the definition of the parameters for doing the Bayesian calculation should be set, including the model of evolution as well as a multiple alignment of the sequences previously to the final result. This chapter provides a description of the application and some new results related to the aforementioned diseases is also shown.

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