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Title:	High Throughput Reproducible Literate Phylogenetic Analysis
Authors:	S., Ruhila (/jspui/browse?type=author&value=S.%2C+Ruhila)
Keywords:	High Throughput Reproducible Literate Phylogenetic Analysis
Issue Date:	2022
Publisher:	IEEE
Citation:	PDGC 2022 - 2022 7th International Conference on Parallel Distributed and Grid Computing, 337-340.
Abstract:	We present a holistic approach from a literate programming perspective to frame and solve systems biology problems. In particular, given the large data-sets required for answering questions relating to evolutionary histories we focus on the generalization and workflow required on a typical SLURM or PBS TORQUE queue driven high performance computing cluster. We demonstrate how to leverage multiple CLI tools compiled for efficient use in a portable manner on heterogeneous computational resources and further demonstrating the use of R to generate literate data-driven plots and analysis. High Performance Computing cluster (HPC) bottlenecks and installation barriers are also discussed and mitigation strategies are developed. As a concrete example we demonstrate the estimation of a phylogenetic tree, used to pose and answer questions on evolutionary lineages. In this manner, a generalized approach which can be used for systems biology is elucidated for manipulating phylogenetic data, including its validation, multiple sequence alignment, tree estimation through different models and reproduction.
Description:	Only IISERM authors are available in the record.
URI:	https://doi.org/10.1109/PDGC56933.2022.10053210 (https://doi.org/10.1109/PDGC56933.2022.10053210) http://hdl.handle.net/123456789/4745 (http://hdl.handle.net/123456789/4745)
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