GrAPPA Rebuild Continues Apace

GrAPPA is an acronym for Graph Algorithms Pipeline for Pathway Analysis. It furnishes the bioinformatics user community with a web-based interface constructed on the Galaxy framework, and primarily consists of novel, scalable graph theoretical modules developed by the Langston Lab at the University of Tennessee. With GrAPPA, users can employ powerful combinatorial tools for interpreting high-throughput biological data. Access methods for uploading raw data and visualizing results are also provided.

GrAPPA is now back online after a variety of needed enhancements. Its server has been upgraded for increased storage and performance. All software packages are current. Additional improvements in functionality include a larger repertoire of pre-processing options including Gaussian graphical models, an expanded set of correlation metrics including mutual information, and more powerful post-processing capabilities including software tools for Bayesian analysis.

As GrAPPA’s rebuild nears completion, major remaining tasks include an upgrade to Galaxy’s latest release, migration of GrAPPA’s codebase to a version-controlled environment, and implementation a system for automated software updates. We wish to thank all GrAPPA users for their patience. Suggestions, feedback, and beta testers are welcomed. For more information, please communicate with Levente Dojcsak.