

## Workpackage 1

**Link:** <http://grappa.eecs.utk.edu/welcome.php>

### Introduction

The Graph Algorithms Pipeline for Pathway Analysis (GrAPPA) is a web portal designed to simplify the process of high throughput data analysis. The main focus is on graph theory for computational biology. GrAPPA's core is based on a simple chaining of complementary tools. This provides the functionality of each tool, but with a level of abstraction to make invisible distracting technicalities of operation and implementation. The user can thus upload data and perform various analyses through a seamless graphical user interface, all in a matter of clicks.

### Functionality

GrAPPA currently includes:

- Box plots, histograms and intensity diagrams
- Correlation analysis
- Data normalization
- Graph creation and decomposition
- GPLGeneMap gene annotation
- Huge libraries of clustering algorithms
- Visualization tools for graphs and clusters

We are constantly adding functionality and welcome beta testers.

### Typical Usage

Usage usually begins by uploading raw microarray CEL files. With a Java applet, the user navigates and selects an entire batch of files. These are then normalized with RMA, GCRMA or MAS5. The user may also generate box plots, histograms and log intensity diagrams. Graphs are created using user-selected correlation thresholds or correlation p-values. Thresholds can be restricted to negative or positive correlations if desired. Graphs can be decomposed with a variety of parametric and non-parametric clustering algorithms. GrAPPA harnesses mathematical and computational resources sufficient to make even clique-centric and other state-of-the-art combinatorial algorithms practical. Visualization provides flexibility in the display of graphs and clusters. Output is currently supported in PNG, PDF, PS, PostScript2 and Structured Vector Graphics formats.