

Genomics Tools Online

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Laurie and Malcolm continue to add to the list of online genomics resources <http://gcat.davidson.edu/Online_Genomics/Online.html>. One new page is the hemoglobin mutagenesis page <<http://gcat.davidson.edu/bioinformatics/hemomut.html>>. This will be used to replace a web site produced by someone else but was no longer available. This page will be used by the ~200 annual introductory biology students at Davidson College. The mutagenesis page is used by intro bio students to see the effects of any mutated DNA. This has proven helpful for students to see the consequences of any type of mutation they want to explore. The value of this page has been established for many years, based on the old page. We assume our page will be at least this successful, if not more so.

We have made substantial progress on MAGIC Tool. We have created a number of new pedagogical resources, all of which are posted on the MAGIC Tool web site <www.bio.davidson.edu/MAGIC>. Furthermore, Laurie and Malcolm have presented MAGIC Tool at many workshops during the summer of 2004. Malcolm led a workshop at the ACS Technology Center in TX.

MAGIC Tool is open source and public domain software for analyzing microarray data. The tutorial and other resources we have created walk users through the many steps for exploring or clustering microarray data. In addition, we created a tutorial for using the DeRisi data, either the raw tiff files or the expression ratios. Furthermore, Laurie created an excel file that illustrates how correlation coefficients are subject to substantial changes when only one or two data points are altered. This is a very helpful tutorial.

We have documented formal assessment on MAGIC Tool. The ACS workshop collected one set of data, but the other workshops also measured faculty attitudes. It is clear that MAGIC Tool is a big hit. Not only is the price free, but students have complete control over data collection and analysis which is ideal for pedagogical purposes. Laurie and Malcolm plan on submitting two publications on MAGIC Tool – one for scientific journal and one for an educational journal. Links to these publications will be created when the time comes.

We are continuing to work on the Phylip web site <<http://gcat.davidson.edu/bioinformatics/phylip/aphylipindex.html>>. Students made substantial progress creating the web forms and writing perl scripts to execute many of the steps and connecting the many programs together.

However, this aspect of our project is still a work in progress. We hope to finish this project during the 2004-2005 academic year.

Once Phylip is operational, we will use it for both research and teaching purposes. Phylip is a collection of software programs that allows the user to measure phylogenetic distances between a set of sequences and then draws a dendrogram to illustrate the evolutionary relationships. When this site is ready, we will have students use and ask questions based on their output. Assessment will come in the form of tests for classes as well as the number of hits this page receives. The number of hits will help us measure its success as an online resource.

Finally, the online clustering tutorial is functional since the PC server was updated. The Gnu plot works and users can access this resource. Tutorials and assessment are complete for this tool and can be found on the web page <www.bio.davidson.edu/courses/compbio/jas/home.htm>.