

Abstract

With the number of tools and technologies being used to store, retrieve, and analyze proteomic, genomic, and metabolomic data, there is an increasing need for additional support to the biomedical community, which can be provided by librarians, specifically Bioinformaticists. This poster covers several ways in which librarians can support biomedical research and the bioinformatics community. They can provide instruction in a variety of ways, including hands-on sessions, webinars, and user manuals. The University of Michigan Bioinformaticist has learned to use several bioinformatics resources, such as Cytoscape, ConceptGen, and LRpath. Although the Bioinformaticist started by offering hands-on Cytoscape training sessions, webinars are also offered to reach an expanded audience. The Bioinformaticist updates user manuals for new versions of tools, making it easier for users to teach themselves. In the spring of 2011, the Bioinformaticist jointly conducted a usability study on three network visualization software tools: Cytoscape, VisANT, and ConceptGen. Through these methods and others, the Bioinformaticist has played an important role in helping researchers learn how to use bioinformatics tools for their work and is continuously brainstorming on new tools to teach, new methods for teaching these tools, and new means for providing instruction to further support the biomedical community.

Introduction

With the dramatic increase in the number of databases, data sets, tools, and software being used to store, retrieve, and analyze proteomic, genomic, and metabolomic data, there is an increasing need for someone to make sense of it all. This is an area where librarians, especially Bioinformaticists, can help the biomedical informatics community by learning about such resources and providing instruction on their use. Bioinformaticists are "information specialists who have received graduate training and practical experience that provides them with disciplinary background both in biomedical, behavioral or biological sciences and information sciences/informatics" as defined by the National Library of Medicine (NLM).¹

In addition to the important role of providing instruction, librarians can also help inform development decisions by interacting with users. Usability studies are a recognized method for collecting data and information to improve user interfaces. If a tool has a poor user interface, users will find it frustrating and search for a simpler tool.

This University of Michigan Bioinformaticist has offered training classes on bioinformatics resources such as Cytoscape, ConceptGen, and LRpath. She has helped bioinformatics tool developers test and revise user manuals for new versions of tools. In addition, she has conducted usability studies comparing three network visualization tools: Cytoscape, VisANT, and ConceptGen.

Instruction Classes

Cytoscape

Cytoscape (<http://cytoscape.org>) is a free, open source software tool used to visualize and analyze biological networks and pathways. At the University of Michigan, the Bioinformaticist offers training classes on Cytoscape. These training classes are 2-hour, hands-on sessions. The workshop includes a brief biological background for the genes used throughout much of the session, CLU, CR1, and PICALM, based on two articles in the October 2009 Nature Genetics issue.^{2,3} Core Cytoscape features, in addition to 7 plugins (MiMI, MetScape, MCODE, BINGO, Shortest Path, Enhanced Search, and Agilent Literature Search) are covered. In addition to following the provided workshop, attendees are given practice time during which they can explore various features of the software. These training sessions have been popular, having a total attendance of 32 people over 3 course offerings.

Based on the success of these local trainings, the Bioinformaticist decided to use a different teaching media and expand the audience. In March 2011, the Bioinformaticist held the first Cytoscape webinar, using Adobe Connect streaming software. A second webinar was given in September 2011. Attendees were able to ask questions via a chat window, controlled by a second librarian with Cytoscape familiarity. These sessions were open to anyone, not just those affiliated with the University of Michigan. Across two sessions, sixty-two people viewed the workshop individually or at one of two registered sites. Webinar attendees included various universities and organizations within the continental United States, Puerto Rico, and Europe.



Bioinformatics Instruction via Webinar and In-Person Reaches Widespread Biomedical Informatics Community.

ConceptGen/LRpath

ConceptGen (<http://conceptgen.ncibi.org>) is a free, web-based gene set enrichment and concept mapping tool.

LRpath (<http://lrpath.ncibi.org/main.jsp>) is a free, web-based tool that performs gene set enrichment testing. In October 2011, the Bioinformaticist offered the first training session on these two tools. This was a 1-hour, hands-on session (Table 1). Various features of ConceptGen were covered, in addition to the process and methods for using LRpath. 8 people attended this first session.



ConceptGen Screenshot.

Table 1: Instruction Sessions

Tool	Description	Instructional Session
Cytoscape	Free, open source software tool used to visualize and analyze biological networks and pathways	<ul style="list-style-type: none"> Two hour, hands-on sessions or One hour webinar
ConceptGen	Free, web-based gene set enrichment and concept mapping tool	One hour, hands-on session combined with LR Path
LR Path	Free, web-based tool that performs gene set enrichment testing	One hour, hands-on session combined with ConceptGen

Instruction Documents

MetScape Manual

In addition to providing instructional classes, the Bioinformaticist revised the user manual for new versions of the MetScape plugin for Cytoscape. The MetScape plugin is used to visualize and interpret metabolomics and gene expression data in the context of human metabolic networks. As developers release new versions of a tool, such as the MetScape plugin, it is important to keep the user manuals current for the latest version. Although some new versions only have minor changes, others have substantial changes. The Bioinformaticist helped by updating the manual content before each new release. This involved updating screenshots, text, and often adding entirely new sections to the manual. The Bioinformaticist first did the manual revision for MetScape 2.0 and has continued to do revisions, with the latest revision being for the version 2.3.1.



Usability Studies

As a joint effort between the University of Michigan Taubman Health Sciences Library, the University of Michigan School of Education, and the National Center for Integrative Biomedical Informatics, a usability study was conducted in the spring of 2011. The focus of this study was a user comparison of three free network visualization software products: Cytoscape (<http://cytoscape.org>), VisANT (<http://visant.bu.edu/>), and ConceptGen (<http://conceptgen.ncibi.org>).

The Bioinformaticist helped develop the biologically-relevant test scenarios for each tool. Six University of Michigan researchers were tested for this study. Each session lasted approximately 1.5 hours with the researcher going through all three tool scenarios. The librarian plus one other observer were present at all sessions. In addition, screen capture and audio were recorded using Camtasia software.

Although the data is still being analyzed from this study, the results should provide useful information that will inform future development decisions.

Conclusion

There are many opportunities for librarian involvement regarding training in the biomedical informatics community. Bioinformaticists play an important role in helping researchers learn how to use bioinformatics tools for their work. Librarians also should not limit their roles to post-production, for there are many ways in which they can provide valuable input before then. Usability studies are one method for getting feedback to developers to improve user interfaces. Librarians' knowledge is valuable and should be leveraged beyond the traditional library setting. Biomedical Informatics is a burgeoning field with lots of opportunities for librarians, so they need to be continually brainstorming on new tools to teach, new methods for teaching these tools, and new means for providing instruction.

References:

- NLM Individual Fellowship for Informationist Training (F37) (PAR 06-509). <http://grants.nih.gov/grants/guide/pa-files/PAR-06-509.html>
- Lambert JC, et al. 2009. Genome-wide association study identifies variants at CLU and CR1 associated with Alzheimer's disease. *Nature Genetics* 41(10): 1094-1099.
- Harold D, et al. 2009. Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. *Nature Genetics* 41(10): 1088-1093.