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Library Support for Biomedical Research in the Omics Era: 2014- 2015 Report

Rolando Garcia-Milian, *Yale University*



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LIBRARY SUPPORT FOR BIOMEDICAL RESEARCH IN THE OMICS ERA

2014-2015 REPORT

Rolando Garcia-Milian
Biomedical Sciences Research Support
Curriculum & Research Support Dpt.
Cushing/Whitney Medical Library

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“The ability to access and analyze molecular data should not be restricted to bioinformaticians or those with exceptional computer skills.”

Introduction

The decreased cost of high-throughput technologies has enabled its use as the main method to assess the implications of genetic variation, gene expression, promoter activity, DNA structure, epigenetic changes to nucleic acids, and mass spectrometry-based proteomics in biological processes and disorders. (Mason, Porter, & Smith, 2014). The massive amount of data generated by these technologies has contributed to the exponential growth of biomedical databases including biomedical literature. In order to understand the relevance of the data generated by these methods, the researcher needs to effectively identify functions, phenotypes, expression, evolutionary conservation, disease association, protein structure, etc. (Hutchins, 2014). This is only possible by mining and integrating the enormous amount of biomedical information and knowledge contained in the text of the scientific literature and biomedical databases. In response to this, the field of bioinformatics has been developing at an accelerated pace and is playing a key role in biomedical research. Accordingly, the ability to access and examine molecular data should not be restricted to bioinformaticians or those with exceptional computer skills. In this regard, a number of end-user bioinformatics programs and software packages are being developed and are becoming an essential component of many labs and classrooms due to their appealing design and user friendliness (Smith, 2014).

In May 2014, the Cushing/Whitney Medical Library hired a librarian to provide information/data support to the biomedical researchers of the Yale School of Medicine (YSM). This report summarizes the results of the first year (from June 2014 to June 2015) of development of an end-user bioinformatics program that provides support on three main fronts: trainings, resources and consultations.

“Overall, 1182 Yale affiliates registered, 664 actually attended, and 140 were waitlisted for these training sessions.”

Trainings Sessions

As bioinformatics becomes essential to biomedical research, there is a growing need to train end-users/ non-bioinformaticians. The concepts of “training” and “end-user” are used here as previously defined by Schneider (2010). Training refers to a short session aimed to deliver skills that allow the audience to optimally use bioinformatics tools and databases. End user refers to a user who needs to access bioinformatics resources and/or tools for research. This access is mediated by a Graphical User Interface (either the web or software). The concept of end user is different from the bioinformatician or computational scientist who develops databases and software tools (Schneider et al., 2010).

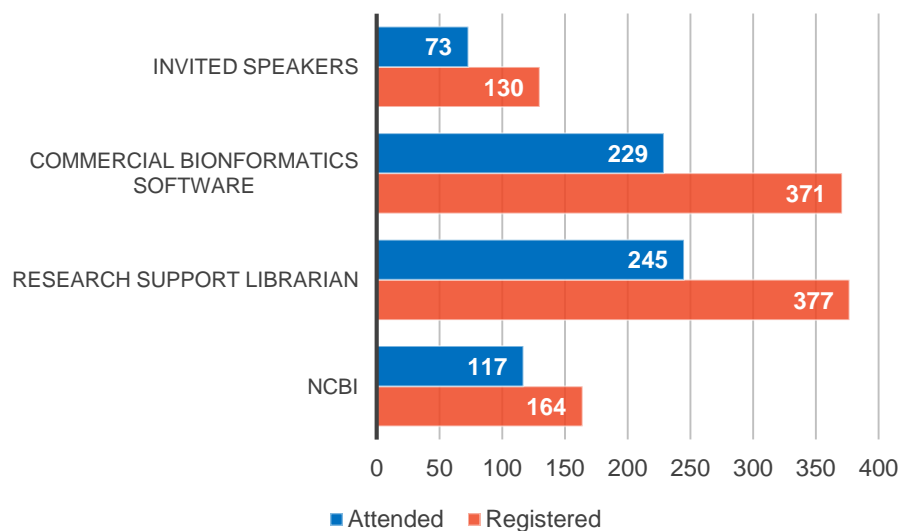


Ingenuity Pathway Analysis training session at the Hope Auditorium, May 2015

Training sessions

From June 2014 to June 2015, the research support librarian organized a total of 32 training sessions. These sessions included a combination of librarian standalone sessions, invited speaker presentations, National Center for Biotechnology Information webinars, and vendor trainings on commercial bioinformatics tools licensed by the Medical Library. A detailed list of these sessions including registration and attendance can be seen in Appendix 1 at the end of this document. Overall, 1182 Yale affiliates registered, 664 actually attended, and 140 were waitlisted for these training sessions (Figure 1).

Figure 1. Total registration versus attendance by type of training sessions from June 2014 to June 2015



TOTAL REGISTERED: 1182

TOTAL ATTENDED: 664

TOTAL WAITLIST: 140

The research support librarian taught a total of 17 standalone training sessions from June 2014 to June 2015 (Table 2 of Appendix). Each semester, a reiteration of these five sessions were available:

- Introduction to genome browsers;
- BioMart: a research data management tool for the biomedical sciences;
- Tools for gene enrichment analysis;
- Novel online tools for mining the biomedical literature;
- My Bibliography and SciENcv: grant reporting, compliance and biosketch through MyNCBI.

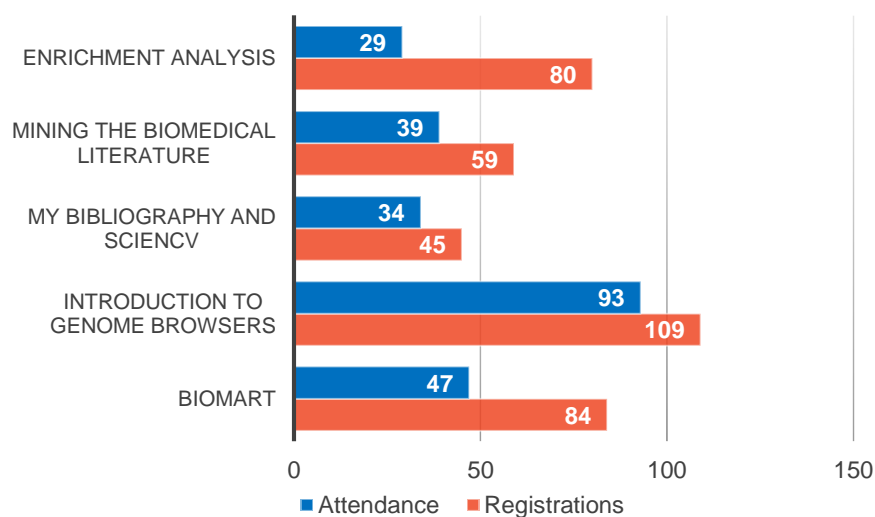
A description of each can be found in Appendix 2. Three hundred seventy-seven Yale affiliates registered, 245 attended and 126 were waitlisted for these sessions. Figure 2 (A) and (B)

Figure 2. Librarian-taught training sessions. (A) Number of sessions (B) Registration versus attendance. June 2014 - June 2015.

(A)

Title	No. sessions offered
ENRICHMENT ANALYSIS	3
MINING THE BIOMEDICAL LITERATURE	3
MY BIBLIOGRAPHY AND SCIENC V	3
INTRODUCTION TO GENOME BROWSERS	4
BIOMART TABLE BROWSER	4

(B)



TOTAL REGISTERED: 377

TOTAL ATTENDED: 245

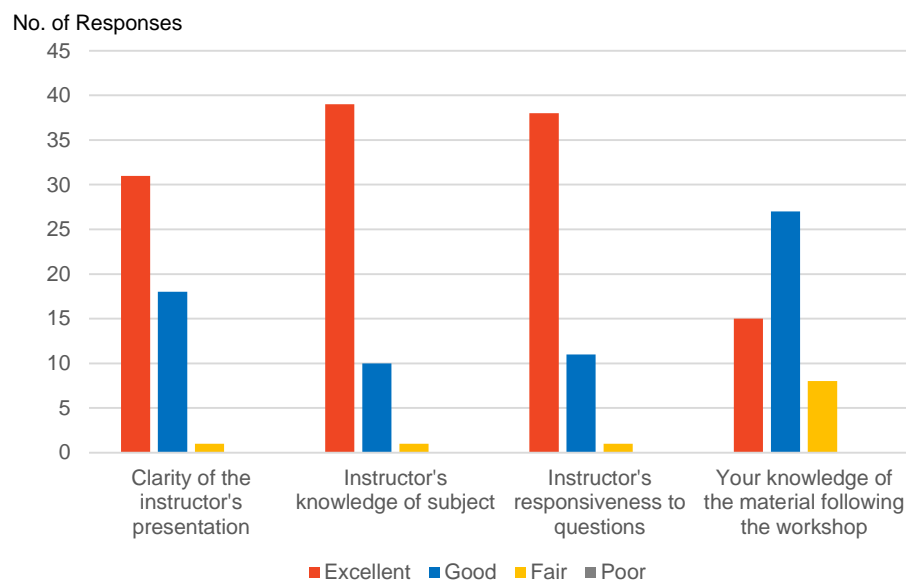
TOTAL WAITLIST: 126

Feedback on the librarian-taught training sessions

After each training session, attendees were invited to provide anonymous feedback through a Qualtrics survey form.

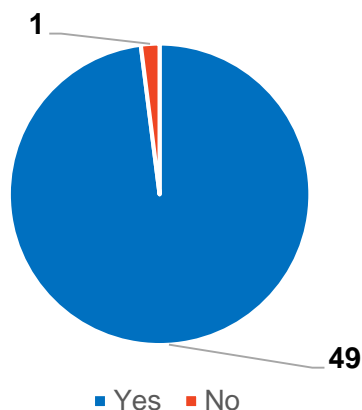
(https://yalesurvey.qualtrics.com/SE/?SID=SV_5vR1IGZ7sj1LNbf). A total of 50 attendees responded to the assessment. When asked to rate the instructor based on clarity, knowledge, and responsiveness to questions, most of the responses ranged between excellent and good (Figure 3). The majority of the respondents considered that their knowledge of the material improved following the sessions (42 excellent/good responses out of 50). Accordingly, 49 out of 50 said they would recommend the training sessions to a colleague or a student (see Figure 4)

Figure 3. Question: Please rate the instructor/ session.



TOTAL RESPONSES: 50

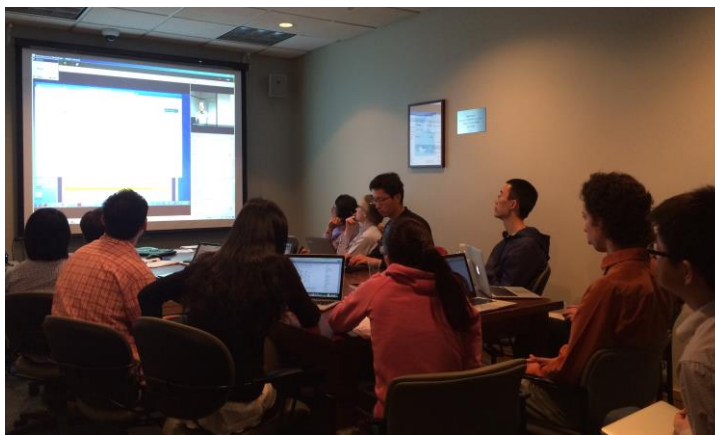
Figure 4. Question: Would you recommend this workshop to a colleague/ student?



TOTAL RESPONSES: 50

When asked what did you like most about the training session, respondents commented on the content of the session, length, format, instructor style, etc. These comments can be read in the Appendix 3 at the end of this document.

When asked to suggest improvements to the workshop, respondents provided useful comments that included the room size, more hands on exercises, sending the handouts in advance, case studies, having more advance workshops that build upon the intro ones, etc. These comments can be read in the Appendix section at the end of this document.



“Human Genes, Variation, and Medical Genetics Resource“, National Center for Biotechnology Information webinar hosted at the Medical Library. May 2015

"Thank you again for your continued work to get the IPA licenses for Yale researchers; this is of tremendous support for the work that we do here at our MS and Proteomics resource for Yale investigators."

*TuKiet T. Lam, PhD,
Director, FT-ICR MS
Resource, MS &
Proteomics
Resource, Molecular
Biophysics &
Biochemistry*

I used IPA before. It is very helpful. Because it is expensive, I have stopped using it for a while. If it is available, I would be happy to use it again. Appreciate!"

Yale user of IPA

Resources

The ability to access, analyze and make sense of molecular data should not be restricted to bioinformaticians or those with exceptional computer skills. In this regard, a number of end user bioinformatics programs and software packages are being developed and are becoming an essential part in the research life cycle due to their appealing design and user friendliness (Smith, 2014). This cutting-edge bioinformatics software provides an excellent intuitive, Graphical User Interface (GUI), to access and analyze omics data. Although commercial bioinformatics software are essential for data analysis, they often come with an excessive price tag, meaning that most researchers, teachers and students cannot afford to buy them. As one of the Yale researchers commented on the Ingenuity Pathway Analysis registration form:

(https://yalesurvey.qualtrics.com/jfe/form/SV_3t2b8Fcl0mRuXxX) "I used IPA before. It is very helpful. Because it is expensive, I have stopped using it for a while. If it is available, I would be happy to use it again. Appreciate!"

Commercial bioinformatics software

Between November 2014 and March 2015, the research support librarian met with a number of researchers and faculty at Yale School of Medicine (YSM) to determine their need of commercial end user bioinformatics software for the analysis of omics data. As a result of these meetings, in May 2015, the Cushing/Whitney Medical Library began to provide access to two powerful knowledge bases for the analysis of omics data: Ingenuity Pathway Analysis (QUIAGEN) and MetaCore (Thomson Reuters). This is part of a pilot project to evaluate the usage of these tools at YSM. The Medical Library already licenses and has access for several years to BIOBASE (Proteome and TRANSFAC) for transcription factor analysis.

In less than one month, 73 researchers requested an Ingenuity Pathway Analysis (IPA) account and 83 requested a MetaCore one (Figure 5). Genetics, Pathology, Internal Medicine, and the Department of Immunobiology— in this order— are the departments with the higher number of users (Figure 6). As shown in Figure 7, the majority of researchers will be using IPA for gene expression analysis followed by metabolomics.

Figure 5. Usage of IPA vs MetaCore by user position. Data collected one month after licensing.

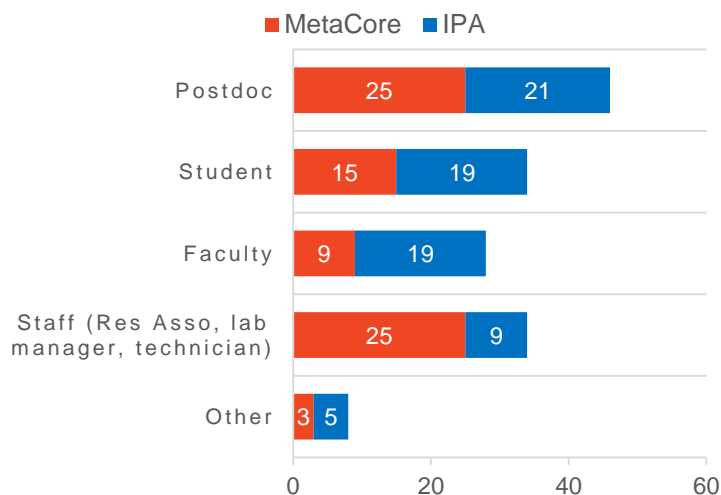


Figure 6. Usage of IPA vs MetaCore by department. Data collected one month after licensing.

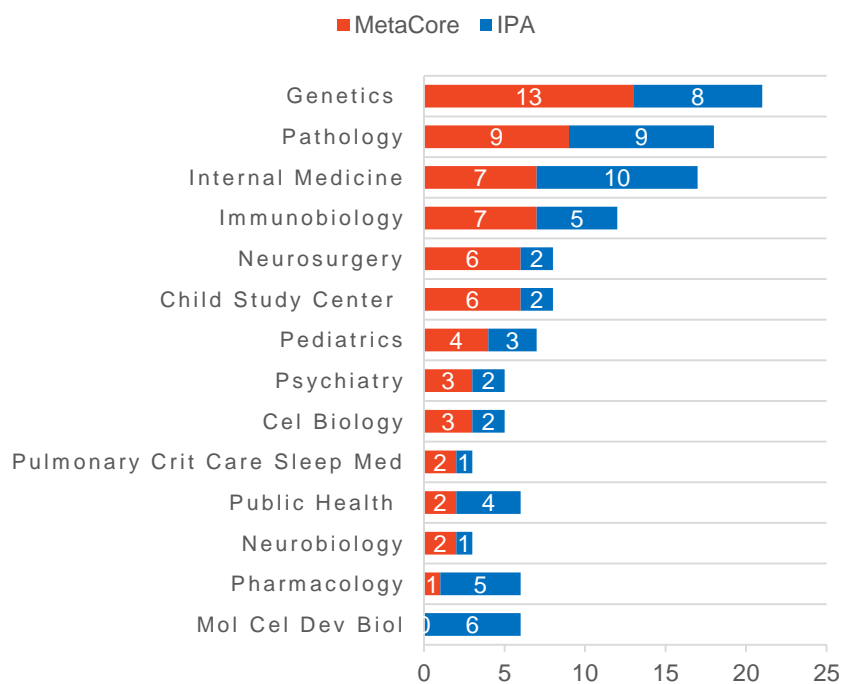
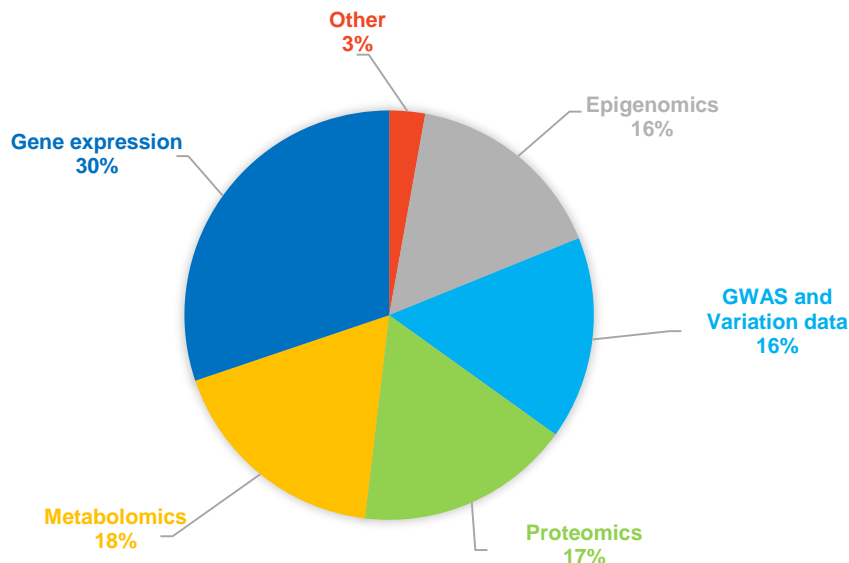


Figure 7. Usage of Ingenuity Pathway Analysis by type of data

Blog and Library Guides to Support the Basic Biomedical Sciences.

The “Bioinformatics at the Medical Library” blog

(<http://library.medicine.yale.edu/blog/bioinformatics>) began on October 2014. This blog has been posting announcements on bioinformatics news, trainings, resources, new NIH policies, library services, etc. As of June 4, 2015 it had 1085 page views, 836 of those unique page views.

Two Medical Library resource guides provide information support to the biomedical researchers at YSM: Basic Science Resources and Collections

(http://guides.library.yale.edu/basic_science) and Bioinformatics Tools for Research and Discovery at Yale University (<http://guides.library.yale.edu/bioinformatics>). These guides summarize resources and services available at the medical library for the biomedical researchers. The bioinformatics guide was created in collaboration with the Life Sciences librarian and the Computational Biology and Bioinformatics Department.

Access to the blog and the biomedical sciences library guides.

Online resource	Page Views	Unique Views	Users
Bioinformatics at the Medical Library	1085	836	N/A
*Bioinformatics Tools for Research and Discovery at Yale University	430	380	368
*Basic Science Resources and Collections	811	627	593

* Data available from Feb 2015- June 2015.

Harvey Cushing/John Hay Whitney
Medical Library

Bioinformatics Tools for Research and Discovery at Yale University Tags: bioinformatics, dna, gene enrichment analysis, gene expression, gene expression analysis, gene prediction, gene regulation, genomics, mma, pathway analysis, protein, snps, variation, workshops Admin Sign In

This guide contains a curated set of resources and tools that will help you with your research data analysis. It also includes those medical library workshops available at Yale University on many of these bioinformatics tools.

Text Mining | Gene Prediction/ Annotation | Expression Analysis | Gene Regulation | Variation | Pharmacogenomics
Integrative Analysis Tools | Animal Resources | Plant Resources | Key Journals | Microbiology Resources

Expression Analysis Comments(0) Print Page Search: Google Search of Guides Search

NCBI Resources

Gene Expression Databases

Biomedical Sciences Research Support

NCBI
GEO DataSets **Gene Expression Omnibus DataSets** is an NCBI repository that contains curated gene expression DataSets, as well as original Series and Platform records in the Gene Expression Omnibus (GEO) repository.

NCBI
GEO Profiles **Gene Expression Omnibus Profiles** is an NCBI repository that contains individual gene expression profiles from curated DataSets.

ALLEN BRAIN ATLAS
DATA PORTAL **Allen Brain Atlas** Gene expression and neuroanatomical data

The Cancer Genome Atlas Data Portal **The Cancer Genome Atlas (TCGA) Data Portal** provides a platform for researchers to search, download, and analyze data sets generated by TCGA. It contains clinical information, genomic characterization data, and high level sequence analysis of the tumor genomes.

The International Cancer Genome Consortium (ICGC) Data Portal provides tools for visualizing, querying and downloading the data released quarterly by the consortium's member projects. It contains copy number, rearrangement, expression, and mutation data.

Rolando Garcia-Milian
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Screenshot of the library guide on bioinformatics tools for research and discovery
<http://guides.library.yale.edu/bioinformatics>

"The list of SNP's that you identified allowed us to check association of these SNP's within the GWAS study that we completed."

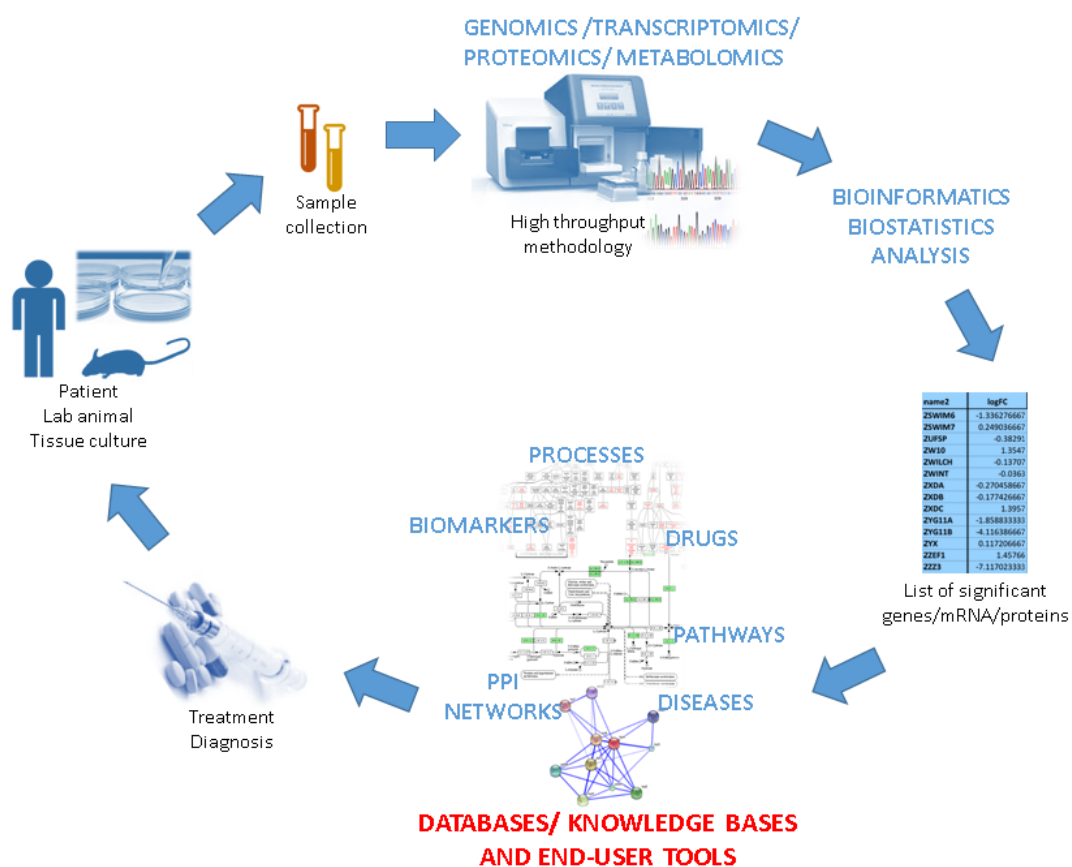
*Dr. Chirag R Parikh,
Associate Professor of
Medicine (Nephrology)
and of Investigative
Medicine; Director,
Program of Applied
Translational Research*

"You did a fantastic job of helping me identify and tutoring me on software and processes to uncover network relationships of multiple genes generated from RNA-Seq"

*Dr. Kim RM Blenman,
Associate Res. Sci.,
Department of
Dermatology*

Consultations

Regardless which specific high throughput technology used, the result is often a list of multiple genes, transcripts or proteins which is given to the researcher in the form of an identifier (e.g. platform identifiers, accession numbers, protein names, etc.) accompanied by other data related to the experiment such as score, intensity, fold change, etc. The researcher then has to make sense of these unfamiliar lists and try to find the biological processes, pathways, networks, biomarkers, etc., that are relevant to the research question (see diagram below).



During this period, a total of 55 consultations on bioinformatics/ research support were provided to 60 researchers. A typical consultation begins when a researcher send a question on a specific topic (see some examples below). Most of these questions require prior identification of the appropriate tool or set of tools. The average time of in-person consultation was 60.7 minutes. In some cases there is a follow-up. Twelve of these consultations were on making sense of lists resulting from high throughput technology.

Examples of consultation topics

- Tools for mining the biomedical literature (e.g. Semantic MEDLINE, Coremine Medical), Controlled vocabularies (e.g. Gene Ontology, MeSH)
- Networked data visualization on Cytoscape
- Comprehensive search on specific gene and annotation of gene lists-
- Enrichment analysis using different online tools (e.g. WebGestalt, DAVID, Babelonomics FatiGO, Ingenuity Pathway Analysis, MetaCore)
- Polypeptide annotation (e.g. identification of DNA binding motifs)
- Analysis/visualization of methylation data
- Protein-protein interaction analysis
- Annotation of genomic sequences (e.g. phenotypes associated with LOH)
- Annotation of SNPs lists
- Compliance with NIH Public Access, grant reporting, and biosketch through MyNCBI (SciENCv and My Bibliography)

Conclusions

The Cushing Whitney Medical Library has been providing end-user bioinformatics support to the biomedical researchers at the Yale School of Medicine including faculty, associates, and fellows. This support was mainly in the form of training sessions and consultations on end-user bioinformatics resources and tools. In addition, the Medical Library has begun a pilot project aimed at providing long term and sustainable access to the most important commercial bioinformatics tools for the analysis of the omics data. As part of this project, the library is providing two robust knowledge bases: Ingenuity Pathway Analysis (QUIAGEN), and MetaCore (Thomson Reuters).

There is a lot of interest on the training sessions either taught or hosted by the medical library. This is apparent by the high number of attendees (1182) and by the feedbacks requesting more in-depth or advanced training sessions. Likewise, interest is rapidly building for the tools that the Medical Library has licensed to support the analysis of data resulting from high-throughput technology (e.g. IPA, MetaCore, BIOBASE).

The coming period will include not only an assessment of the services and resources that the Medical Library is currently providing but also of the general information/data needs of YSM biomedical researchers.

References

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Appendix 1

Training sessions provided or hosted by the Medical Library.

Training Session	Registered + Waiting list	Attend	Presenter
Introducing 3 NCBI Resources to Navigate Testing for Disease Linked Variants: MedGen, GTR and ClinVar	32	21	NCBI
Novel Online Tools for Mining the Biomedical Literature	86	39	Medical Library
Introduction to Genome Browsers	137	96	Medical Library
BioMart: a research data management tool for the biomedical sciences	93	47	Medical Library
Webinar: Using the New NCBI Variation Viewer to Explore Human Genetic Variation	27	19	NCBI
BIOBASE Proteome/TRANSFAC, ExPlain, and HGMD	150	87	QUIAGEN
A hands-on practical workshop in: Mouse Genome Informatics	63	38	Jackson Lab
Semantic MEDLINE: An Advanced Information Management Application for Biomedicine	67	35	Lister Hill Nat. Cr. for Biomed. Comm
Tools for gene enrichment analysis	79	29	Medical Library
NCBI webinar: The Next Generation of Access to Sequencing Data: Using NCBI's SRA Toolkit to Access Data from dbGaP and SRA	18	8	NCBI
My Bibliography and SciENcv: grant reporting, compliance and biosketch through MyNCBI	45	34	Medical Library
Using the dbGaP Data Browser to browse aligned reads and genotypes from the Database of Genotypes and Phenotypes	6	6	NCBI
Broadcast: Navigating NCBI Molecular Data through the Integrated Entrez System and BLAST	24	20	NCBI
Broadcast: Gene Expression Resources at the NCBI	26	19	NCBI
Broadcast: Human Genes, Variation, and Medical Genetics Resources	25	17	NCBI
Broadcast: NCBI Genomes, Assemblies and Annotation Products: Microbiome to Human	20	7	NCBI
MetaCore WORKSHOP: Enabling Systems Biology Research Through Pathway Analysis	124	74	Thomson Reuters
Introduction to Ingenuity Pathway Analysis	97	68	QUIAGEN
TOTAL	1119	664	

Training sessions taught by the research support librarian.

Title	Registrations	Attendance	Waitlist Count
BioMart: a research data management tool for the biomedical sciences	84	47	34
Introduction to genome browsers	109	93	53
My Bibliography and SciENcv: grant reporting, compliance and biosketch through MyNCBI	45	34	0
Novel online tools for mining the biomedical literature	59	39	27
Tools for gene enrichment analysis	80	29	62
TOTAL	377	242	176

NCBI training sessions hosted by the medical library.

Title	Registrations	Attendance	Waitlist Count
Introducing 3 NCBI Resources to Navigate Testing for Disease Linked Variants: MedGen, GTR and ClinVar	20	21	12
Webinar: Using the New NCBI Variation Viewer to Explore Human Genetic Variation	25	19	2
NCBI webinar: The Next Generation of Access to Sequencing Data: Using NCBI's SRA Toolkit to Access Data from dbGaP and SRA	18	8	0
Using the dbGaP Data Browser to browse aligned reads and genotypes from the Database of Genotypes and Phenotypes	6	6	0
Broadcast: Navigating NCBI Molecular Data through the Integrated Entrez System and BLAST	24	20	0
Broadcast: Gene Expression Resources at the NCBI	26	19	0
Broadcast: Human Genes, Variation, and Medical Genetics Resources	25	17	0
Broadcast: NCBI Genomes, Assemblies and Annotation Products: Microbiome to Human	20	7	0
TOTAL	144	96	14

Appendix 2

Training sessions taught by the research support librarian:

- **“Introduction to genome browsers”**. Description: In this workshop we will learn how to navigate the genome browsers from NCBI's Genome Workbench, UCSC Genome Browser, and Ensembl. These browsers are valuable tools when identifying, localizing genes, and looking at their information in the genomic context. By using concrete examples, it will be shown how to locate a human gene, download a gene sequence and its upstream sequence, locate Single Nucleotide Polymorphisms (SNPs) and conserved regions, and use the browsers to download results in a batch
- **“BioMart: a research data management tool for the biomedical sciences”**. Description: Complex biomedical questions cannot be answered by reading the published literature. These may require aggregation of data from several data sets. In this regard, BioMart (www.biomart.org) is a freely available open source system that allows complex queries across more than 40 different biological data sets through a single web interface. Originally developed for the Ensembl genome browser, BioMart has been integrated into widely used software such as Galaxy, BioConductor, and Cytoscape. The BioMart interface is also used by data portals such as Ensembl, Wormbase, Gramene, and Reactome. In this workshop we will use simple examples to demonstrate how to navigate, build queries, and save and export the results on BioMart such as: retrieving the Ensembl mouse genes and genomic locations in the first 10 Mbp of chromosome 1 region; retrieving 1 kb of upstream sequences from a cluster of human genes identified by an expression profile experiment; obtaining a list of the SNPs that have been associated with RB1. For the SNPs, obtain several attributes such as source, rs ID, chromosome location, and pathogenicity.
- **“Novel online tools for mining the biomedical literature”**. Description: The rapid growth of experimental and computational biomedical data is being accompanied by an increase in the number of biomedical publications discussing these results. This makes retrieving relevant scientific information and identifying connections between findings, a challenging task. New literature-mining tools that make use of Natural Language Processing Algorithms and data visualization (e.g. KNALIJ, Quertle, NextBio, iHOP, SemMed, GoPubMed, etc) may be of help when sorting through this abundance of literature, as discovery and hypothesis generating tools. This workshop provides an introduction on how to use some of these literature-mining tools for answering daily research questions and for generating and narrowing research hypothesis.

- **“Tools for gene enrichment analysis”**. Description: Bioinformatics enrichment tools play an important role in identifying, annotating, and functionally analyzing large list of genes generated by high-throughput technologies (e.g. microarray, RNA-seq, ChIP-chip). This workshop will provide an overview of the principle, type of enrichments, and the infrastructure of enrichment tools. By using concrete examples, it will also introduce some of the most popular tools for gene enrichment analysis such as DAVID, GSEA, and WebGestalt. In addition, it will show how to do enrichment analysis using the commercial licensed software Ingenuity Pathway Analysis (IPA), MetaCore, and BIOBASE.
- **“My Bibliography and SciENcv: grant reporting, compliance and biosketch through MyNCBI”**. Description: Complying with the NIH Public Access policy is becoming key for publicly funded research as four more agencies: the Centers for Disease Control and Prevention (CDC), the Food and Drug Administration (FDA), the Agency for Healthcare Research and Quality (AHRQ), and the Office of the Assistant Secretary for Preparedness and Response (ASPR) have released their plans to enforce this policy. In addition, although not required at this point, the NIH suggest the use of the Science Experts Network Curriculum Vitae (SciENcv), -a MyNCBI online tool- that serves as an interagency system designed to create biosketches for multiple federal agencies. This, along with the use of My Bibliography for grant activity reporting and NIH Public Access Policy compliance, increases the importance using MyNCBI as a tool for managing NIH-sponsored research. This workshop introduce researchers, research assistants and administrators on the effective use of these online tools and will cover the following among other topics: creating a MyNCBI account and how to link it to the eRA Commons account; delegating your account; populating and managing My Bibliography; using My Bibliography for grant reporting/compliance; using SciENcv to create different biosketches (from scratch, from external source, etc); creating and ORCID ID; and linking SciENcv to that ORCID ID.

Appendix 3

What did you like most about the training session?

"That all of the tools are one I can easily access, and I felt that I got a great introduction to each tool without being overwhelmed by excess detail."

"small friendly group and straight to the point lecture."

"The contents"

"Knowing about different databases that exist now"

"I thought it was an excellent overview with demonstration of how to navigate to find some of the more basic features provided by genome browsers. I found the description of the different types of information files and their contents especially helpful, as was the introduction of many different types of browsers which curate different information and information in different ways."

"It was very basic and clear"

"Very important topic"

"Reactomes"

"Giving us information about the online tools that are available"

"it helped my research"

"Examples of how to use the data mining were very good"

"I learned about a new tool that holds much promise in helping to dig deeper into my data sets."

"I really liked learning about multiple genome browsers. I previously only knew about NCBI. Also, I liked learning that the other genome browsers UCS and Ensembl have more interactive help tools than NCBI."

that it is available, for it is was badly needed....."

"That it was held at all, and that it demystified the information overload of the UCSC browser."

"Small group and almost one on one interaction with the instructor. Instructor sent the specific question that would be addressed which was very easy to follow."

"Atmosphere- love the setting! Slides were clear, good variety of presentation format"

"learning a new way to mine publications"

"The speaker demonstrated the use of Semantic MedLine in addition to the slide presentation"

"Informal. Great setting. Good presenter. Interesting topic."

"easy to follow as a basic introductory class"

"The speaker showed examples of how to use the browsers. The hand-out materials are very helpful."

"Very clear with specific walk-through examples."

"It is a comprehensive look on all the tools that are available for gene enrichment analysis. It gave me an idea of the various tools out there instead of asking me to stick to one or two. In addition, I got the sense for sure that not all databases are updated properly."

"I really like being introduced to this information and availability of the resources with the slides to go back to as needed."

"Pitched just right; showed me useful websites that I didn't know about."

"Seeing different websites that can be used to process a list of genes"

"instructor knew exactly what he was talking about"

"Small audience."

"The screen shots and user tips provided"

"content and length of time"

"The selection of the genome browser"

"Very informative, flexible instructor, happy to help, interested in teaching his class and it shows."

"Good introduction to genome browsers, their basic features and how to navigate them."

"Informal setting, small class size"

"The variety of tools introduced"

"Rolando's excitement and willingness to share his knowledge. I MOST appreciate receiving slides/handouts after. This allows me to listen and absorb the presentation without worrying about taking notes."

"The use of examples to demonstrate how to use each platform"

What improvements would you suggest to the workshop?

"It may be a bigger classroom"

"Although I would be hesitant to sign up for a full-day class on this, I think maybe a two-hour presentation might be a bit better, where there would be some time to delve into the typical things people may want to identify from a genome browser with respect to a given gene: for example, alternative splicing, different protein transcripts, single nucleotide polymorphisms and how they may relate to disease, and promoter analysis. Having the time to provide a basic example of how to do these things (albeit not in great depth) would augment the course substantially, I think. Each of these was touched on, but very, VERY briefly due to the time constraints; that's why I think an extra half-hour or an extra hour would really help."

"Bigger room"

"Take a case example and walk the audience through showing what can you get out of genome browsers"

"none"

"Maybe try a question from the audience? Overall, very good for 1 hour presentation"

"Find a way to get higher resolution on the projection screen"

"perhaps extend it to 1:30 hours to have more hands-on exercises...."

"none"

"a case study with clear aim would be beneficial"

"A bigger room to hold this workshop."

"None; just right in detail and length."

"It would be interesting to give us a dataset (or ask us to bring our own if we have it) and then make us go through one or two tools to teach us how to go about it."

"I suggest creating a question that we will be able to answer during the workshop. The question could be sent out a day ahead and then we could be anticipating what will be happening in class."

"Focus less on what a "gene list" is. Assume those attending already have one, or expect to have one and therefore know what it is. Spend more time processing the list in the different websites. Explaining the necessary and optional decisions for processing the list will automatically explain what a "gene list" is."

"larger room"

"1) Send presentation to registrants via e-mail in advance and/or - ideally - provide link to presentation maintained on Yale (Med Library) website in advance. 2) Promote such classes to business office managers and/or staff!"

"larger space"

"If the instructor can collect some specific questions before the class, he can be more knowledgeable about the clinical need."

"In the future, it would be nice to have more advanced workshops that build upon the topics/features from the intro course."

"I still got into the class on my own but had been wait-listed from another.....can you send an alert to wait-listed people about up-coming new sessions???? Thanks!!"

"More repetition of key points"

Contact Information



John Gallagher
Interim Library Director
203-785-5352
john.gallagher@yale.edu



Janis Glover
Head of Curriculum and Research Support
Department
(203) 737-2962
janis.glover@yale.edu



Rolando Garcia-Milian
Biomedical Sciences Research Support
203-785-6194
rolando.milian@yale.edu



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