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HOW TO BUILD A BIOINFORMATICS SERVICE IN A YEAR

Natalie Clairoux, M. Sc., M.I.S.
Biomedical librarian

CHLA/ABSC 2011
May 29th, Session E

Université de Montréal

THINK ABOUT IT
Determine scope of project for your context

GET APPROVAL FROM STAKEHOLDERS
Find your niche

START YOUR SERVICE
Workshop, specialised reference and online guide

EVALUATE SUCCESS
Pie charts galore!

Bioinformatics in libraries

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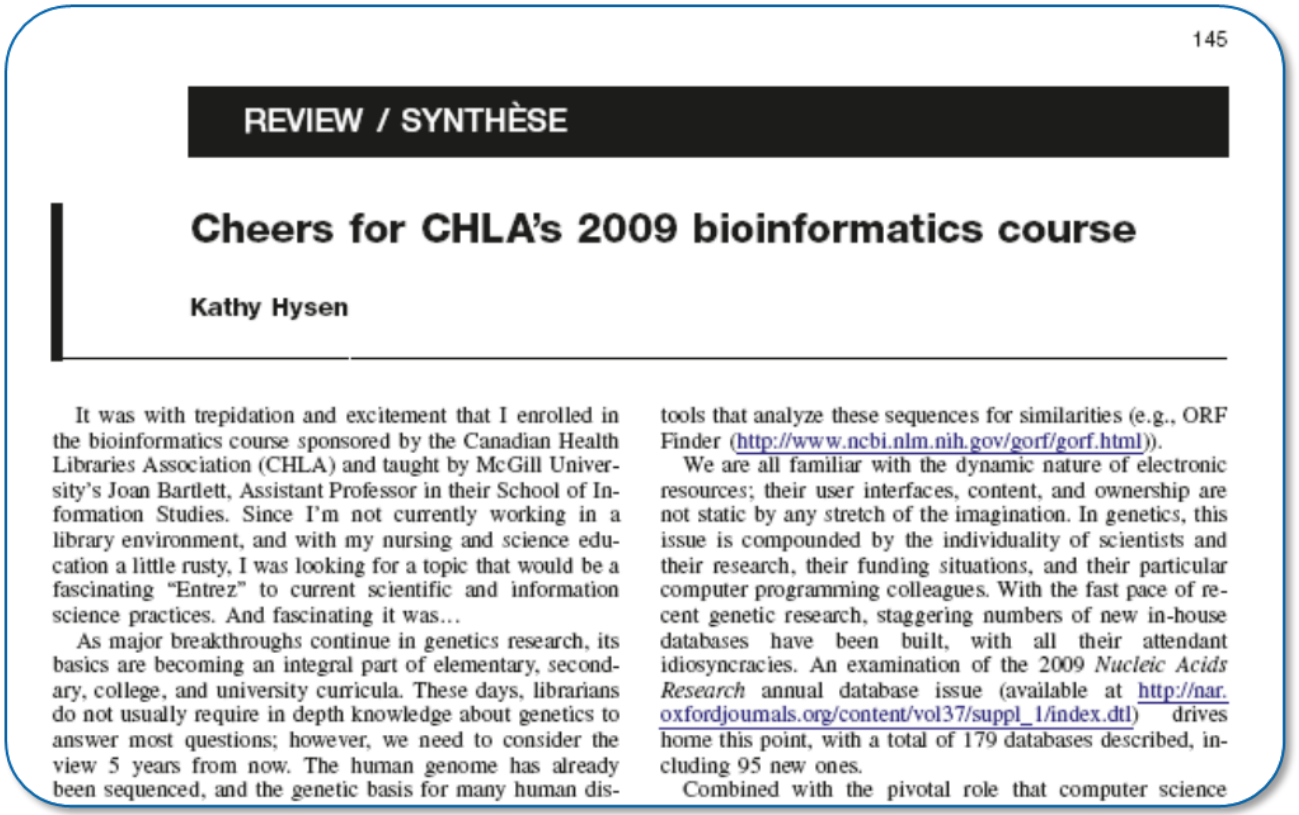
Tipping point: an inspiring CE course



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REVIEW / SYNTHÈSE

Cheers for CHLA's 2009 bioinformatics course

Kathy Hysen

It was with trepidation and excitement that I enrolled in the bioinformatics course sponsored by the Canadian Health Libraries Association (CHLA) and taught by McGill University's Joan Bartlett, Assistant Professor in their School of Information Studies. Since I'm not currently working in a library environment, and with my nursing and science education a little rusty, I was looking for a topic that would be a fascinating "Entrez" to current scientific and information science practices. And fascinating it was…

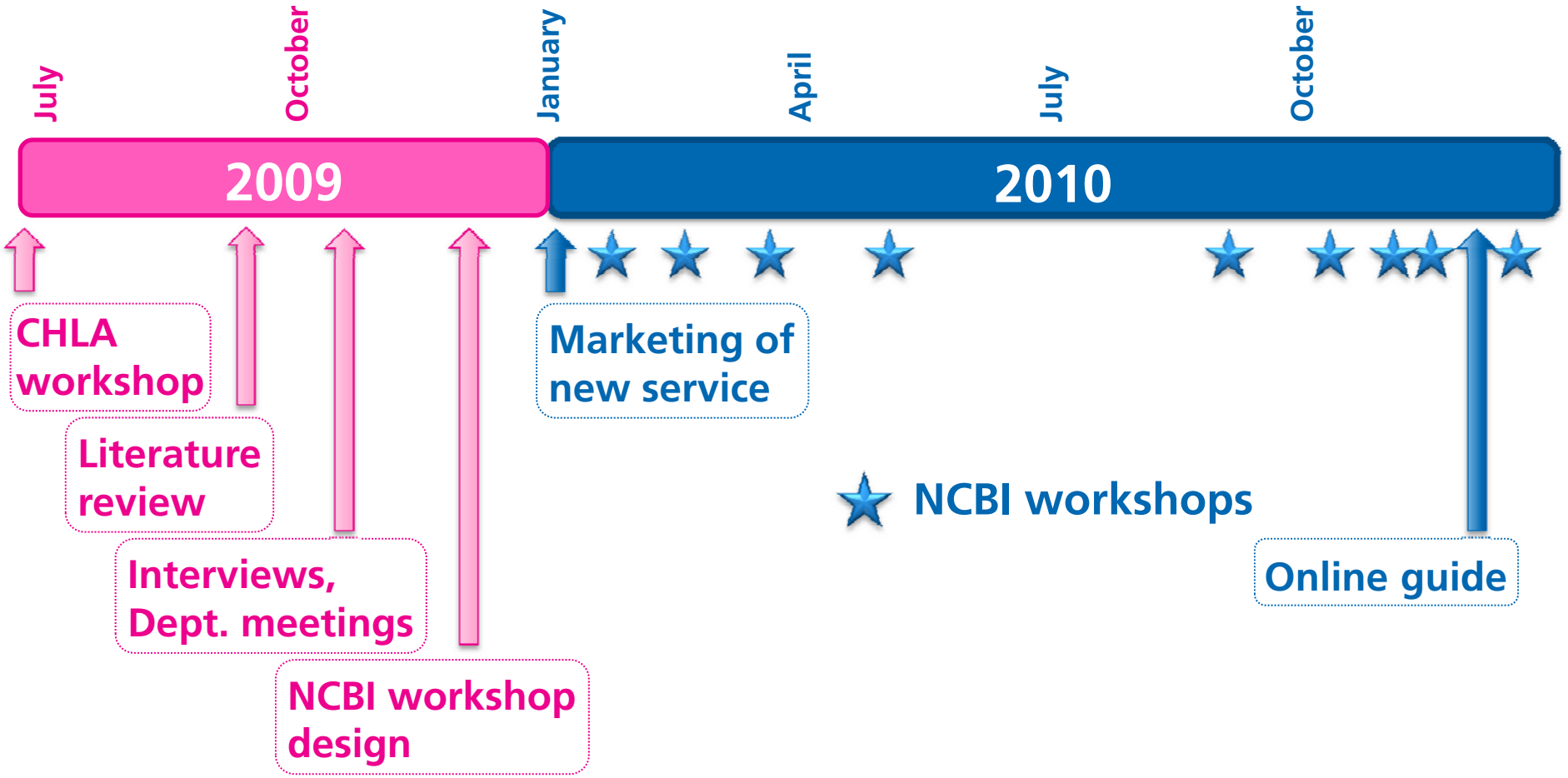
As major breakthroughs continue in genetics research, its basics are becoming an integral part of elementary, secondary, college, and university curricula. These days, librarians do not usually require in depth knowledge about genetics to answer most questions; however, we need to consider the view 5 years from now. The human genome has already been sequenced, and the genetic basis for many human disease tools that analyze these sequences for similarities (e.g., ORF Finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html)).

We are all familiar with the dynamic nature of electronic resources; their user interfaces, content, and ownership are not static by any stretch of the imagination. In genetics, this issue is compounded by the individuality of scientists and their research, their funding situations, and their particular computer programming colleagues. With the fast pace of recent genetic research, staggering numbers of new in-house databases have been built, with all their attendant idiosyncracies. An examination of the 2009 *Nucleic Acids Research* annual database issue (available at http://nar.oxfordjournals.org/content/vol37/suppl_1/index.dtl) drives home this point, with a total of 179 databases described, including 95 new ones.

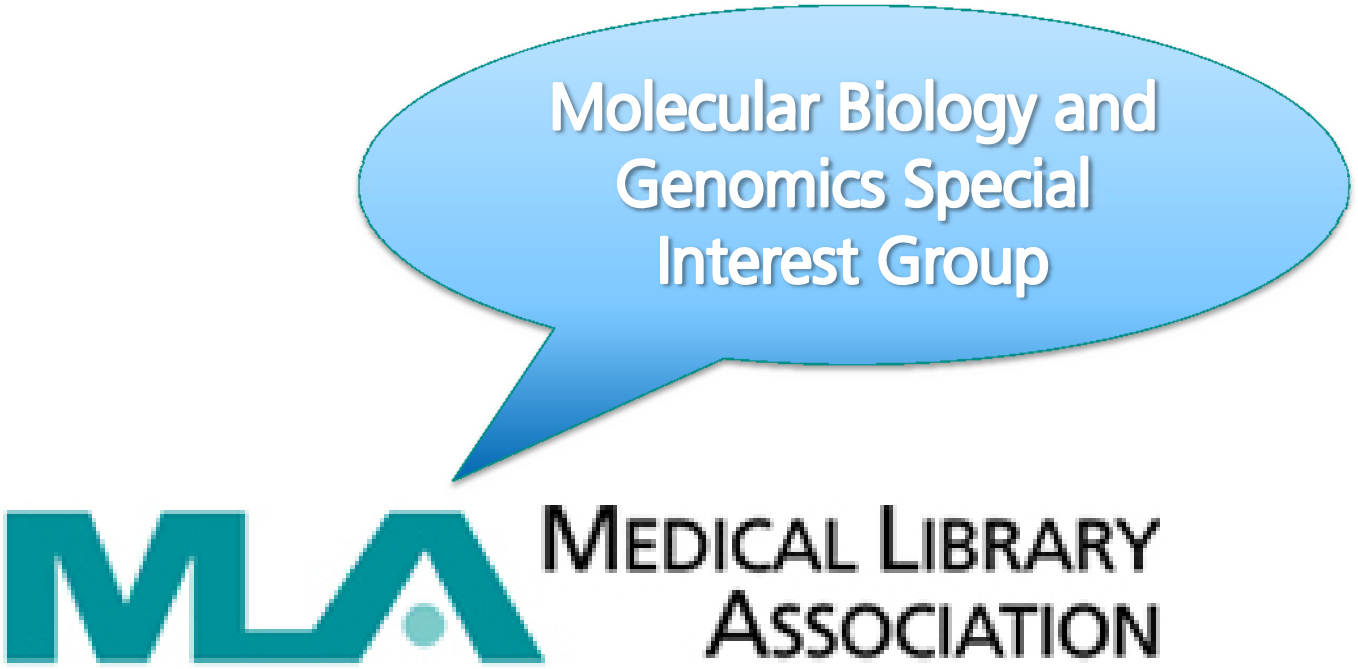
Combined with the pivotal role that computer science

Hysen K. Cheers for CHLA's 2009 Bioinformatics Course. Journal of the Canadian Health Libraries Association (JCHLA). 2009;30(4):145-6.

Project timeline



Get a little help from your friends



Contact other bioinformationists for inspiration (*and* justification for your project!)

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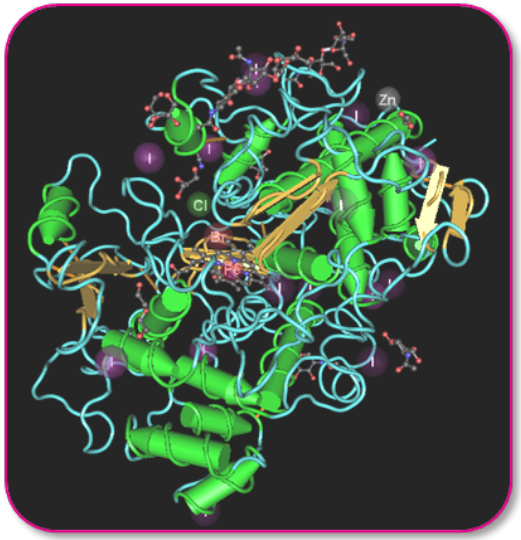
DESCRIPTION DU NOUVEAU SERVICE
Activité de formation, référence spécialisée et guide en ligne

AUTRES POSSIBILITÉS DE COLLABORATION
Veille informationnelle, EndNote, etc.

Target clientele

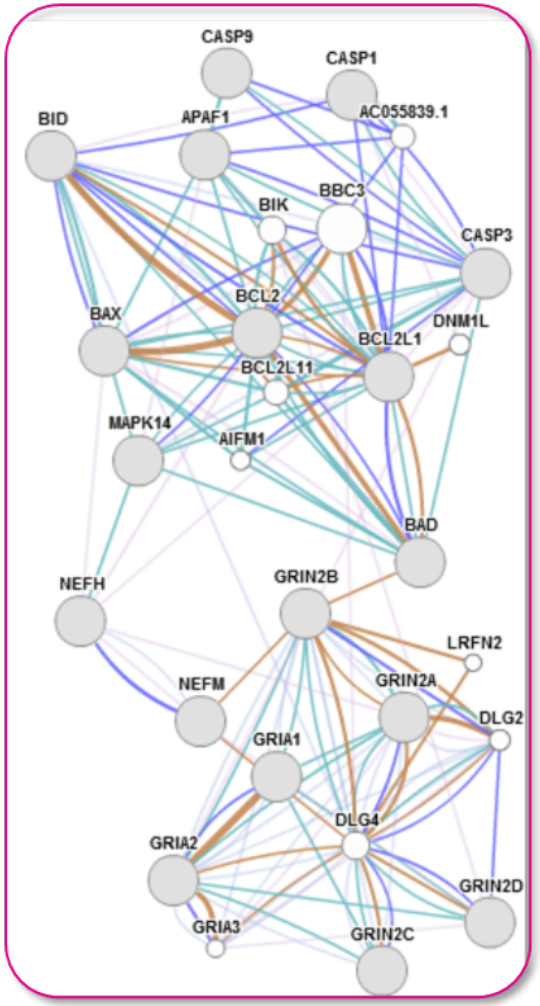
- **Molecular biology** researchers:
  - Graduates (M.Sc., Ph.D.) and post-docs
  - Professors
  - Laboratory personnel
- **Targeted** departments, Faculty of Medicine:
  - Biochemistry and Molecular Medicine
  - Physiology
  - Pathology and Cell Biology
  - Microbiology and Immunology



3D view of a calcium channel

Consult with stakeholders

- Meeting with the **Computer Lab Manager** from the Biochemistry department – review of available bioinformatics tools
- **Phone calls/interviews** with heads of M.Sc. and Ph.D. graduate programs from targeted departments
- **Departmental meetings**: Biochemistry, Microbiology and Immunology
- Emails to targeted **student associations**



Part of the amyotrophic lateral sclerosis gene network

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«NCBI Databases» Workshop - Objectives

- Explore **most useful resources at NCBI**, including Gene, OMIM, CDD and BioSystems.
- Present differences between primary data sources and **value-added databases**.
- Emphasis on **practical exercises** to favor **discovery**.

Multiple protein sequence alignment

Specialised Reference

- Help **find the appropriate database(s)** for the **information** seeked.
- Optimize a **gene search** in PubMed.
- Some examples of questions asked:
  - "I want to use an siRNA cited in an article, but I don't know where it is in the GenBank record given! "(Physiology M.Sc. student)
  - "I'm looking for articles on the M28668 gene but can't find anything in PubMed!" (3rd-year Biochemistry student)
  - "Where can I find expression data for the NPM1 gene?" (Biochemistry Ph.D. student)

Online Bioinformatics Guide

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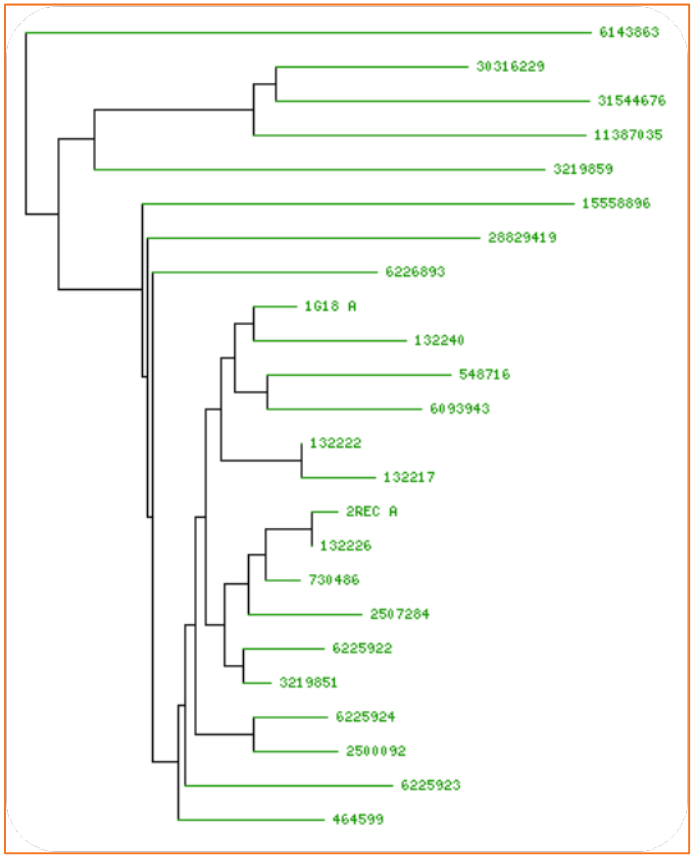
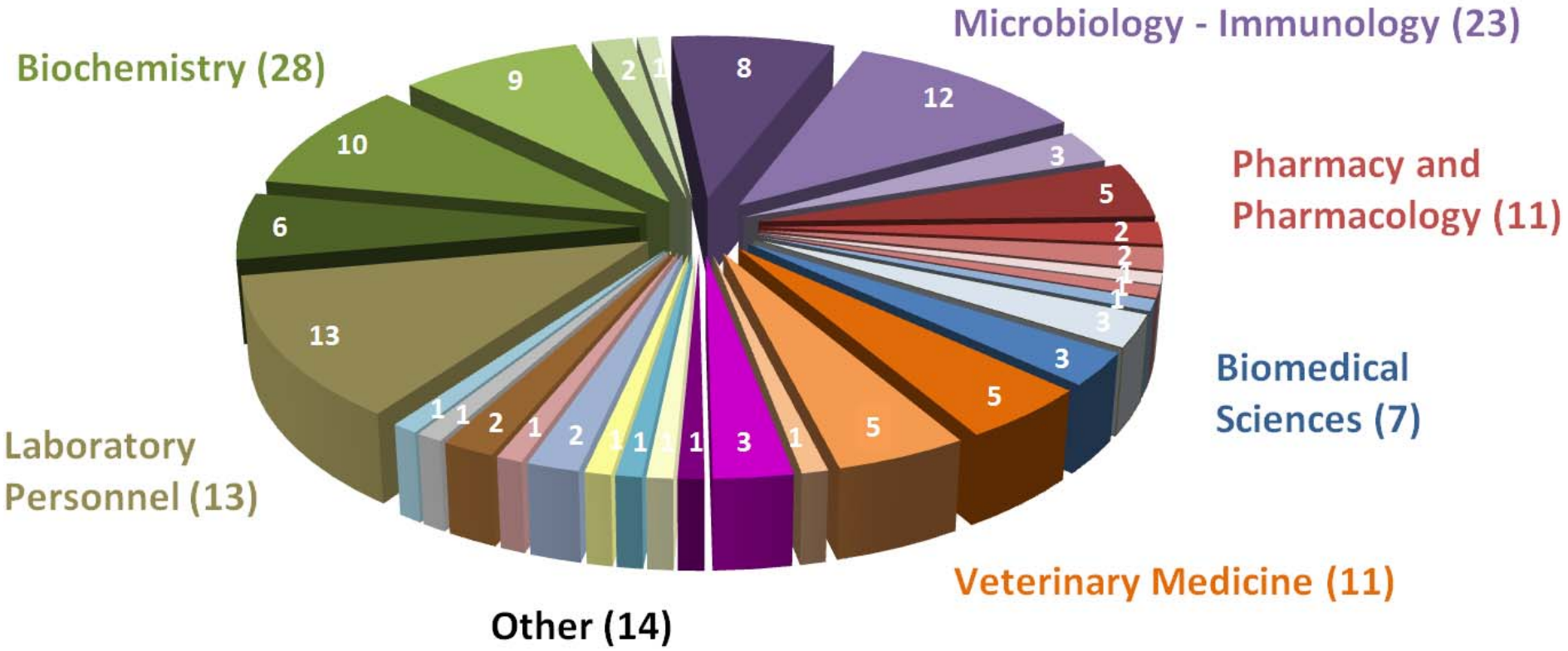
One-on-one reference: 2010 statistics

- Two appointments with graduate students.
- Half a dozen bioinformatics-related questions at the reference desk.
- Mostly: patrons who attended the NCBI databases workshop.

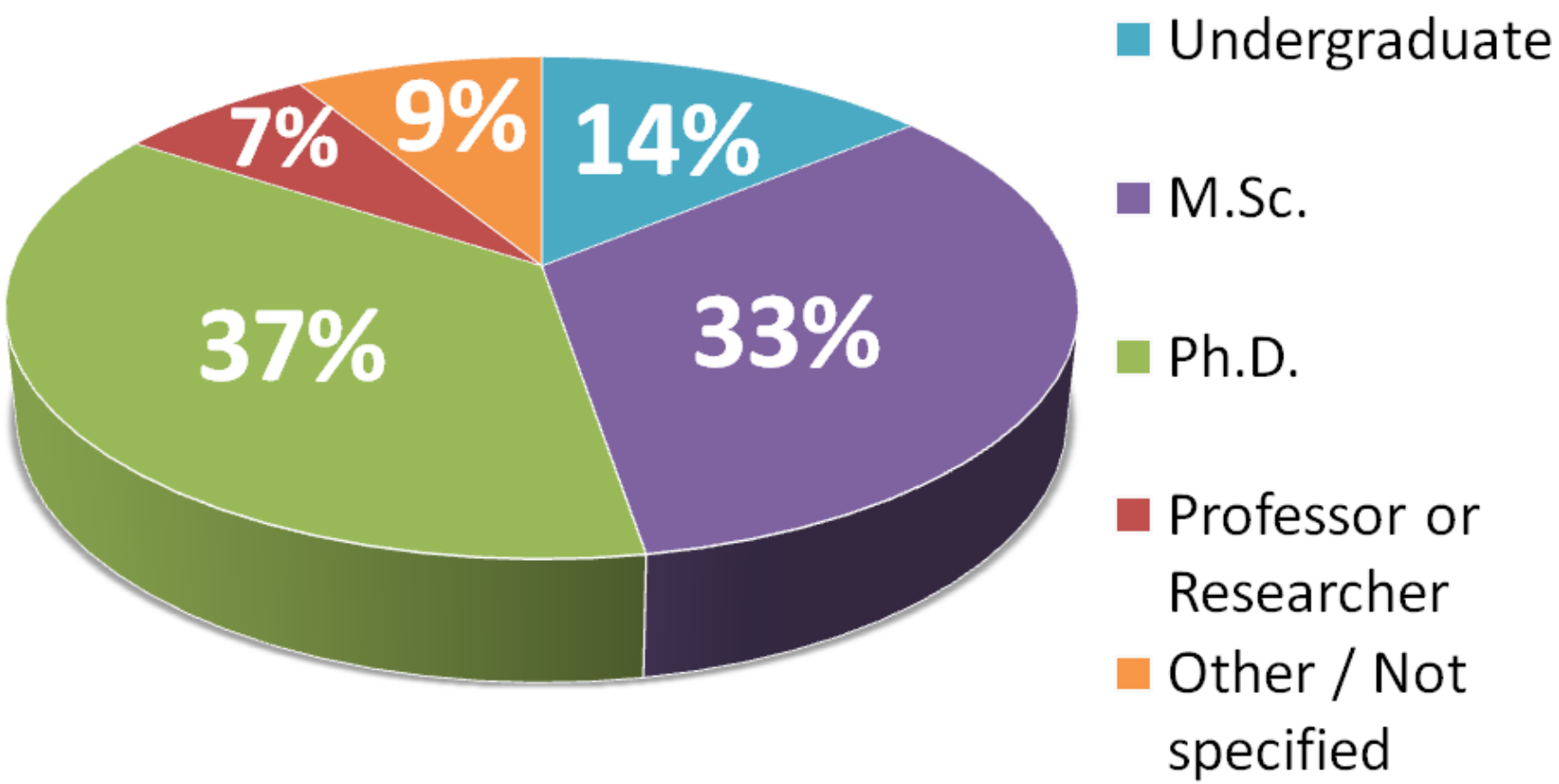


Phylogenetic tree of RecA protein sequence alignment

Workshops attendees by field (n=107)

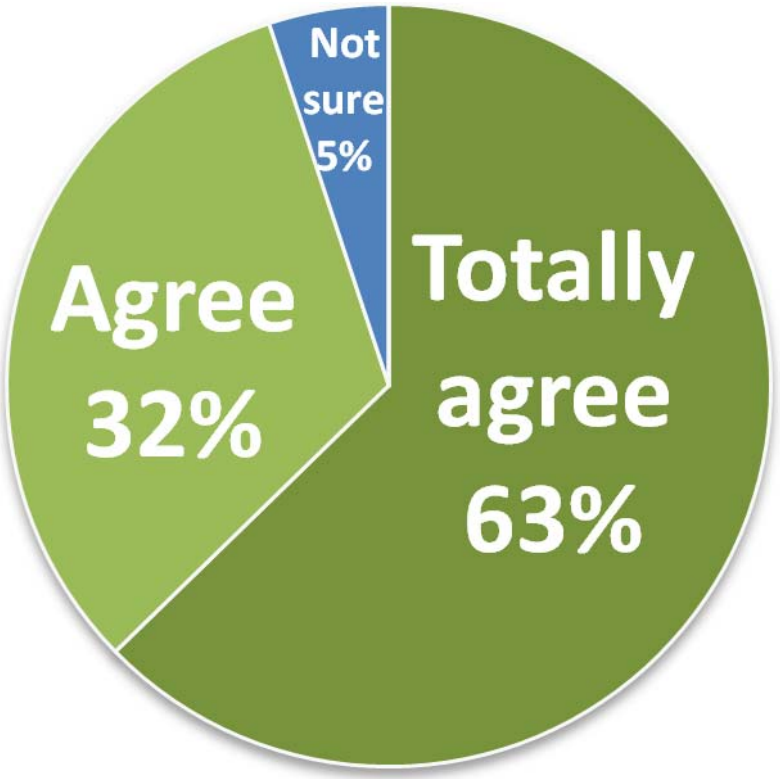


Respondents to online workshop evaluation (n=55)

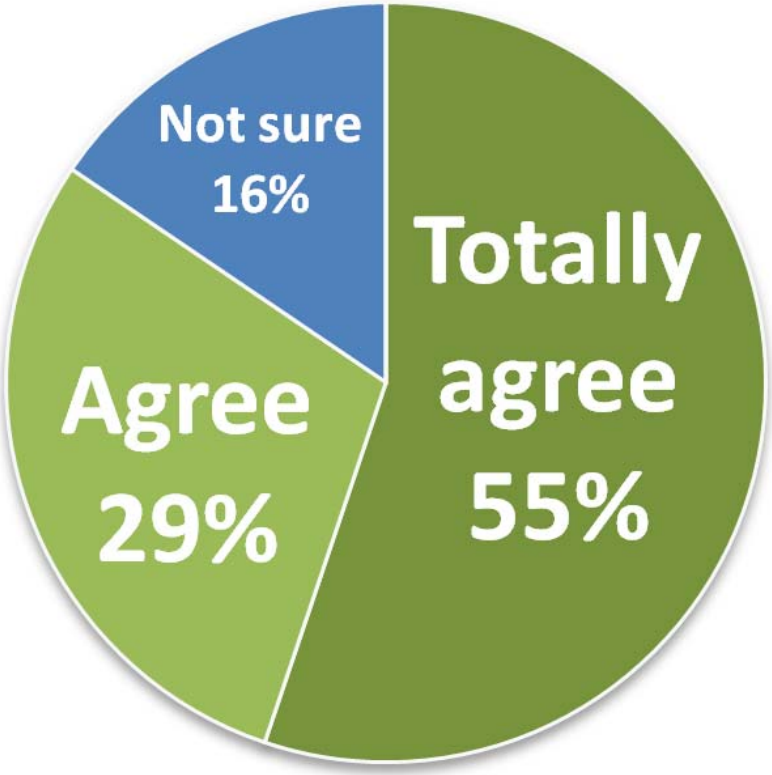


Were the NCBI resources already used by respondents?

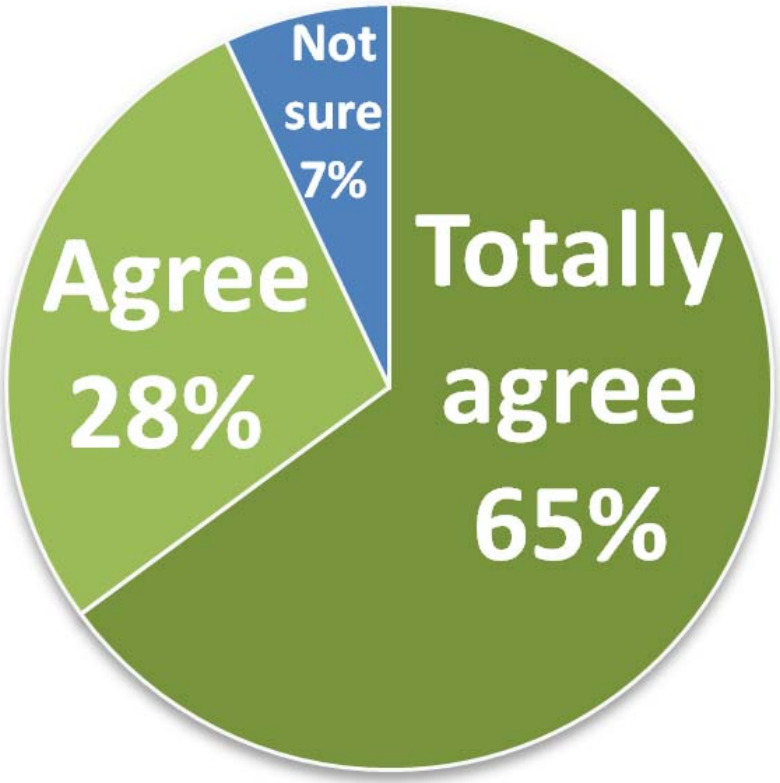
Were the resources presented considered relevant?



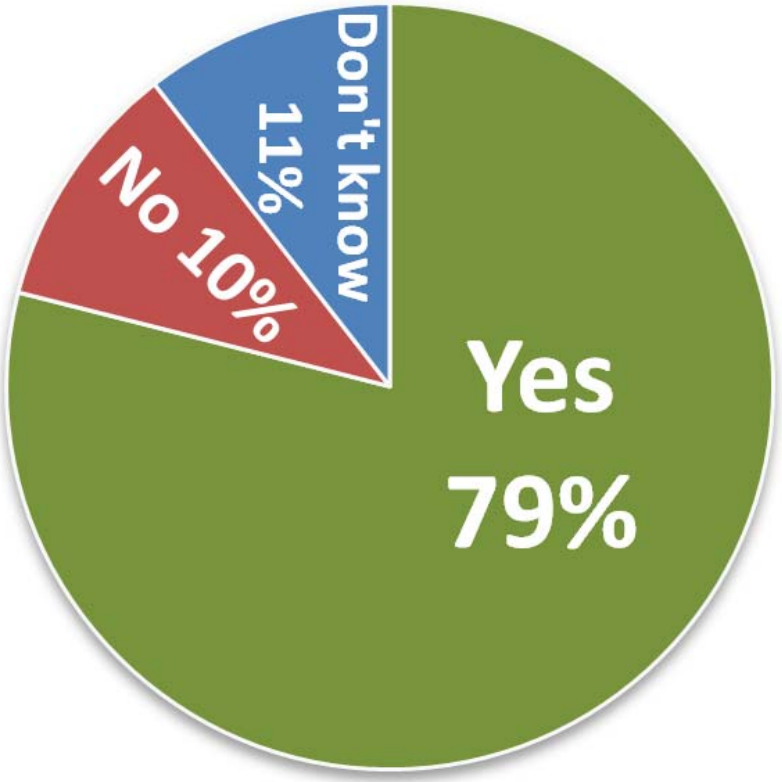
Is the difficulty level of the workshop suitable to respondents?



Will respondents find more easily the information they need?

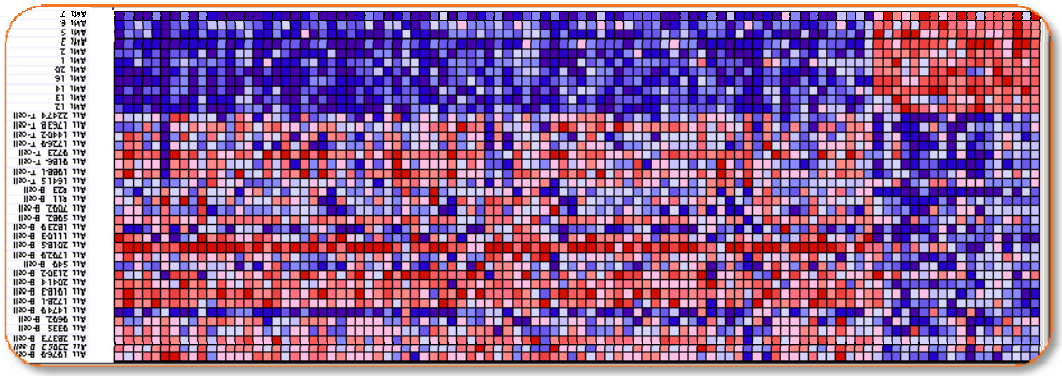


Should the workshop be integrated in a course?



Things to do next

- **Promote bioinformatics service** (student poster competitions, emails, other workshops)
- **Integrate workshop in various programs of study**: currently approaching various departments
- Add **complementary workshops** (BLAST, EBI resources)



Heat map of gene expression

Dreams

NCBI-sponsored workshops

OpenHelix tutorials

GeneGO license

Blog and/or Twitter feed

Ingenuity license

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