

Bioinformatics Needs Assessment and Support for Clinical and Translational Science Research

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INTRODUCTION

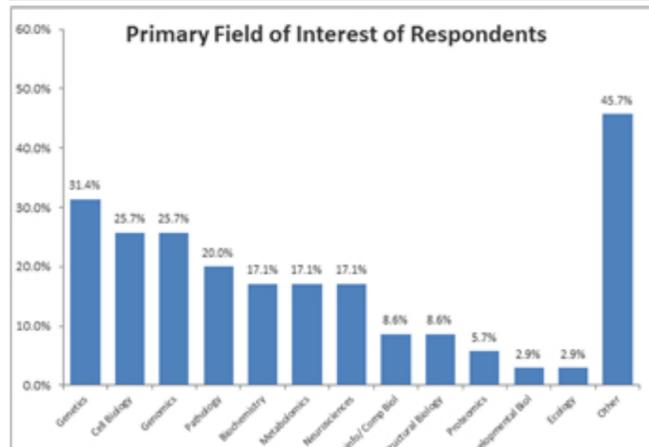
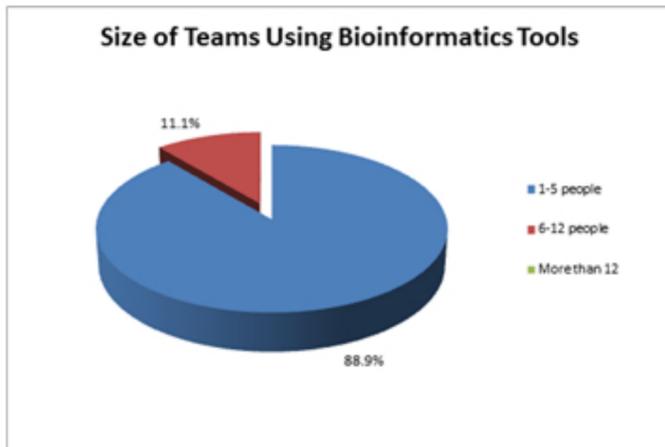
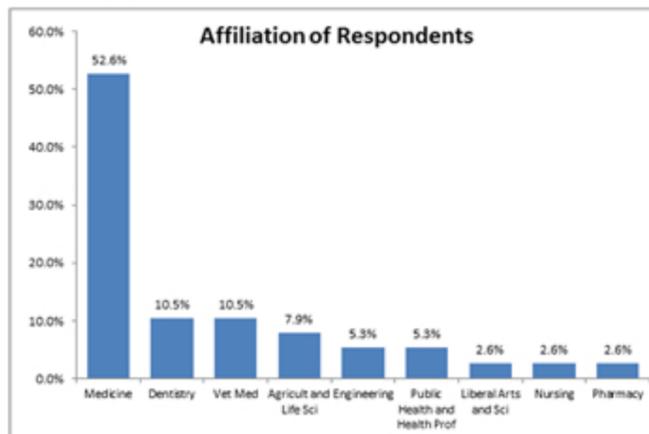
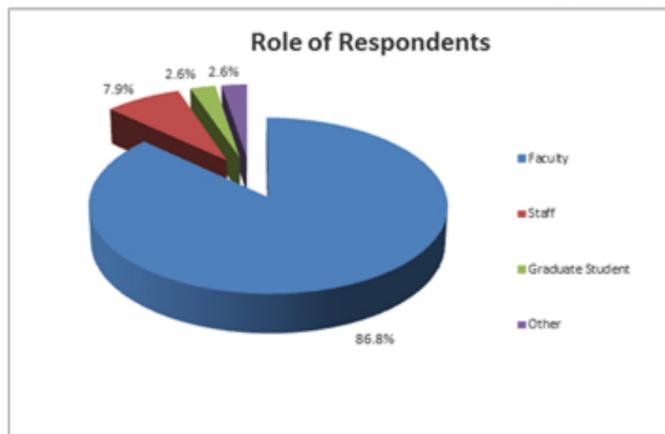
Translational bioinformatics is rapidly developing with the enhancement and specialization of existing and new bioinformatics tools and techniques. The use of these resources allows more efficient mining and analysis of the diverse raw biological data stored in databases and repositories, thus accelerating the translation of bench science results into interventions at the bedside. In order to determine the bioinformatics support needs, in terms of resources/tools, and training, of researchers affiliated with the University of Florida Clinical and Translational Science Institute (UF-CTSI), librarians at the Health Science Center Library (HSCL) developed a multimodal needs assessment.

METHODS

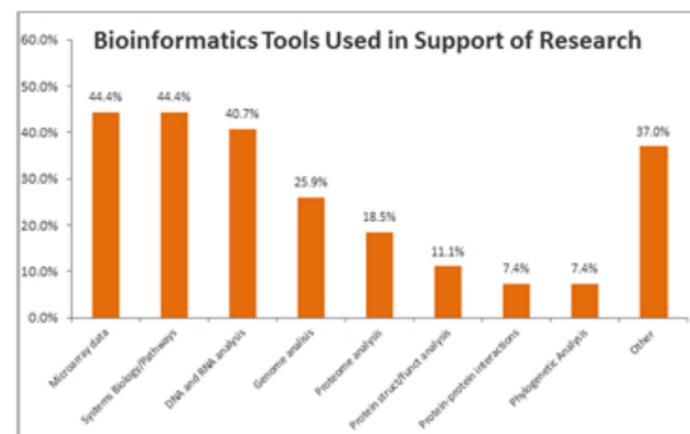
- Online Assessment of 14 questions.
- Developed in collaboration with Dr. David L. Osterbur, Countway Library of Medicine, Harvard Medical School, and Dr. William G. Farmerie, Assistant Director of Interdisciplinary Center for Biotechnology Research, University of Florida.
- Sent to over 800 investigators affiliated with UF's Clinical and Translational Science Institute (CTSI).

RESULTS

DEMOGRAPHICS



Others included: Nutrition Medicine, Clinical Epidemiology and Health Services Research, Physiology, Social Sciences, Pain Research, Pathophysiology, Health Outcomes Research, Immunology, Protocol Development, Evolutionary Biology, Phenotyping, Epidemiology, Population Health, and Health Equity.



Others included: Metabolomics data mining, Targit, MapIT, database searching; population statistics, individual patient level data, SAS, ESRI, ARC, and GIS.

Use of Commercial Software/packages

Most of the UF-CTSI researchers who responded were not familiar with either commercial software packages (e.g. BIOBASE, CLC Genomics, Genego, etc) or the open access platform Galaxy.

Commercial software/tools that researchers would like to have available for use include:

- CLC Genomics Workbench
- CLC Main Workbench
- Galaxy
- Ingenuity Pathway Analysis
- Pathway Studio from Ariadne

TRAINING

Training Interests of Respondents	Number of responses (n= 32)
Statistical software (e.g. SAS, SPSS, R/Bioconductor)	12
Genes and Expression (e.g. GEO)	6
Next Gen Sequence Analysis (e.g. Galaxy)	6
Curated gene-centered resources for human and model organisms (e.g. Entrez gene, RefSeq, etc.)	4
Genome sequence analysis using genome browsers (e.g. UCSC, Ensembl)	4
Structure analysis (e.g. how to visualize and annotate 3D protein structures, identify conserved domain, etc.)	4
Genetics & Medicine (e.g. OMIM, GeneTests, ClinVar, etc)	3
Controlled vocabularies (e.g. Gene Ontology, UMLS)	2
Other (please specify)	2
Sequence similarity analysis using BLAST	1

Others included: NMR 'omics, ARC, and GIS

How would you like to receive instruction/consultation services on bioinformatics?	Number responses (n=18)
Online tutorials	15
In person classroom instruction	13
Individual house call	5
Other (please describe)	2

Others included: someone to call when stuck, and in classroom at the College of Veterinary Medicine

SUMMARY OF CONCLUSIONS

This study not only identifies UF-CTSI researchers' needs in terms of bioinformatics support (e.g. commercial software licensing) but also provides the basis for rational design of learning strategies. Next steps include: performing interviews and focused discussions with researchers regarding bioinformatics information needs, followed by the utilization of those results to develop more effective training courses. A Faculty Enhancement Opportunity project has been funded, facilitating advanced training in the use of bioinformatics tools beyond NCBI (e.g. IPA, GeneGo, Partek Genomics Suite, CLC Main Workbench) for the HSCL librarians.

ACKNOWLEDGEMENT

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