Chapter 57
Biomedical Librarianship in the Post–Genomic Era

Shubhada Prashant Nagarkar
Savitribai Phule Pune University, India

ABSTRACT

Post genomic era is known for the explosive growth in biomedical information. Bibliographic and sequence databases are increasing continuously and have voluminous data sets. Biomedical librarians are facing challenges in retrieval of relevant information from these electronic databases and related sources of information. This chapter discusses the changing role of biomedical librarians in post genomic era. The chapter covers features of the biomedical librarianship including library collection development, users' information needs and strategies adopted to provide services. Moreover, it focuses on the competencies required by librarians to face the challenges of management of information and services needed by biomedical researchers in the post genomic era.

INTRODUCTION

The librarianship is a trinity of acquisition, organization and dissemination of information, in which acquisition relates to the proper selection of library materials, organization to their preparation for efficient/effective use, and dissemination to the processes of making the contents available to the users. To achieve this, librarians should act as a mediator and must know the intellectual contents of information resources, user information needs and the methods to bring both contents and users together (Shera, 1972). Trinity of librarianship has become challenging over the period due to remarkable changes in the containers of information, interdisciplinary approach of researchers and new communication technology for dissemination of information. Containers of information changed over the period i.e. from paper to electronic. Organization of information has become more challenging to meet the interdisciplinary information needs of users.

The present chapter discusses the trinity of librarianship in the field of Bioinformatics and the changing role of librarian in bringing information and user together. This particular subject area is selected due to two reasons. Firstly, the author has worked as a practicing librarian in the field of Bioinformatics

for almost seventeen years and secondly, the librarianship in this field has changed to a great extent especially in the post-genomic era. The chapter has three main sections viz. library collection, user information needs and library services to Bioinformaticians. Each of this section discusses the challenges for librarians and efforts by librarians. The initial part of the chapter talks about the information explosion in the field of biology, interdisciplinary nature of research and features of post genomic librarianship. The chapter has the context of Bioinformatics libraries and services evolved during last 10 years which cater to the needs of Bioinformatics community including students, teachers and researchers.

Bioinformatics in the Post Genomic Era

There is a remarkable difference in Pre and Post genomic era in respect to biological research and information. The research in pre genomic era was non interdisciplinary and individual scientist worked for individual research. In the post genomic era research has become interdisciplinary and there is integration between parallel studies in the allied research fields (Torshin, 2006). The pre genomic era or the beginning of the Bioinformatics era is marked by the contributions during the 1960s by Late Dr. Margaret Dayhoff for the compilation and analysis of large data sets of protein sequences to study the molecular evolution (Dayhoff, 1965). The fusion of biology and computer—Bioinformatics—evolved in the late 20th century. The major event in computing, the introduction to the World Wide Web in 1990 which was coincided with the beginning of the Human Genome Project (HGP) (Bergeron, 2003). WWW and Human Genome Project significantly represents the convergence of computing, communication, and molecular biology (Benoît, 2006; Bergeron, 2003). The HGP is an example where researchers from a variety of disciplines viz. biotechnology and molecular biology, computer science, engineering, physics, chemistry, mathematics, statistics and medicine worked together to reveal all (approximately 21,000 genes) human genes. The collaboration among scientists is required in managing the large quantities of data necessary to reveal biological relationships and in using innovative techniques to locate, aggregate, manipulate, and present such data through user-friendly, cross-platform applications (Goodman, 2003; MacMullen & Denn, 2005). Apart from HGP several other projects including research into specific organism or cell type, gene expression, metabolic pathways, regulatory networks, and protein-protein interaction data, have been responsible for explosive growth in the generation of biological information (Benoît, 2006). This explosive growth leads towards the creation of various databases, databanks, and software tools. The 2015 *Nucleic Acids Research* Database Issue contains 172 papers that include descriptions of 56 new molecular biology databases, and updates on existing 115 databases (Galperin et. al, 2014).

As the discipline evolved and its scope became broader, the demand for trained human resource started growing. This necessitated the establishment of formal training programmes. Very few research institutes started short terms training programmes in Bioinformatics which later grown into diploma, masters, and Ph.D. programmes (Magana et. al., 2014; Kulkarni-Kale, Sawant, & Chavan, 2010).

The tremendous growth in published biological literature is the mark of the post genomic era. In literature database, the term Bioinformatics appeared in the year 1997 with the description "A field of biology concerned with the development of techniques for the collection and manipulation of biological data, and the use of such data to make biological discoveries or predictions. This field encompasses all computational methods and theories for solving biological problems including manipulation of models and datasets" (http://www.ncbi.nlm.nih.gov/mesh/?term=bioinformatics). PubMed search results on "bioinformatics / computational biology" as a major MeSH term shows 63224 (retrieved on 15/2/2016) research publications which are growing geometrically.

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