Application of IT in Biomedical Field: Present Status and Future Prospects

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Abstract— In the knowledge economy, information has become the most important resource allowing both firms and nations to grow. For every drug that reaches the market, there are more than 10,000 compounds synthesized, characterized, and tested for biological effects if we go by conventional laboratory procedure. This process takes place in about 12 years. But this task of drug discovery and evaluation is going to carry out at much faster rate and at significantly lower cost with the use of computer based program's. called software. Not only pharmaceutical, biotechnological and biomedical research required software but production, automation of process and its control, clinical diagnosis of disease and clinical trials of anti-AIDS and cancer drug all required some sophisticated software. Overall without use of software there is no simple task is possible in biomedical research. Today, computers are so important in biomedical research and development that it may be hard to imagine a time when there were no computers to assist the researchers. In this article we summarized the use of software in different aspects of biomedical research.

Index Terms— Biomedical, IT, Application, Pharmaceutical, Research, Software

1 INTRODUCTION

The development cost of a new drug may be about $250 million (Rs. 900 Crores) and takes about 12 years to launch in the market [1]. For every drug that reaches the market, there are more than 10,000 compounds synthesized, characterized, and tested for biological effects if we go by conventional laboratory procedure [2]. But this task of drug discovery and evaluation is going to carry out at much faster rate and at significantly lower cost with the use of computer based program's. This is not the only application of computer software in pharmaceutical and medicinal field but now a days every aspects of biomedical research is depend on one or more use of software for simple task like drawing to chemical structure, statistical treatment of data to complex task like metabolic kinetic of drug, prediction of pharmacodynamic and pharmacokinetic properties of investigated drug molecules [3]. Overall without use of computers based program that called 'software' there is no simple task is possible in biomedical research. Today, computers are so important in biomedical research and development that it may be hard to imagine a time when there were no computers to assist the biomedical researchers. In this article we summarized the use of software in different aspects of biomedical research with emphasis on pharmaceutical research.

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2 PARADIGM SHIFT IN BIOMEDICAL AND PHARMACEUTICAL RESEARCH

Today, the extent of informatics has enriched other allied subjects, be it biology, chemistry or any life science stream. Numerous biochemical and structural studies have shown the conformations of various receptors that could be influenced by ligand binding. While we have various web based Cheminformatics and molecular property prediction tools that supporting drug design and development, these tools offer many advantages for processing chemical information with a vivid use [4, 5]. This has provided the way for pharmaceutical companies to use such sophisticated web technologies for delivering molecular processing tools directly to the wet-lab chemists and assist in the process of designing and development of new drugs. The technologies include all wet-lab enabled *in silico* calculations of molecular properties, property-based virtual screening, and visualization of molecules, bio isosteric design, diversity analysis, and support of combinatorial chemistry [6].

2.1 Use of Web Based Information in Compounding Chemistry (Chemoinformatics)

Cheminformatics is an inter-disciplinary subject of storage, processing and retrieval of chemical information *in silico* [7]. It has been the descendant of bioinformatics and has value-guided objectives like extracting, envisaging and elucidating the chemical data. Chemical Information is information relating to chemical structures or their properties. On the other hand, this subject has given enough impetus in the hands of the stream basic life sciences. It is more or synonymously used with

computational chemistry that is the application of mathematical and computational methods to chemistry. The whole of cheminformatics is a fusion of many facets of science including math, molecular biology, statistics, and biochemistry in addition to chemistry. However, this field would be inquisitive without molecular modeling where in 3D graphics and optimization techniques are preferentially used to help scientists understand how drugs bind to proteins in the body.

The discipline of using computers for the discovery and design of drugs is named as Computer-Aided Drug Design. All the above techniques are used in this so-called field that uses techniques from the fields of chemoinformatics, computational chemistry and molecular modeling. Cheminformatics, by and large has become a decision making tool in drug discovery.

Web based services like CORINA (http://www2.chemie.uni-erlangen.de/software/corina), OSIRIS (http://www2.organic-chemistry.org.prog/peo), PETRA (http://www2.chemie.uni-erlangen.de/service/petra) and Pre-ADME (http://preadme.bmdrc.org/preadme) is widely useful for solving the so many problem of synthetic c+ solubility, toxicity and drug likeness, determination of physico-chemical properties of the compounds, molecular descriptions and various ADME-Tox properties [8, 9]. Example of some web based services is summarized in **Table 1**

Table 1
Software and Web Based Service Used in Chemoinformatics

Software name	Application	Source
Libghemical-2	Used in quantum mechanics Molecular Mechanics Used in geometry optimization	http://www.uku.fi/~thassine/ projects/ghemical/
Jchem	Database used for search of mixed structural and nonstructural data	http://www.chemaxon.com/jc hem/intro/index.html
VEGA [Vega]	To convert, manage and visualize of 3D structure for several platforms	http://www.ddl.unimi.it/
VCCLAB	Molecular descriptors, physico-chemical properties and data analysis	http://www.vcclab.org
ALOGPS2.1	Used to predict lipophilicity, partition coefficient, dissociation constant and aqueous solubility of molecules	http://vcclab.org/lab/alogps/ Tetko and Tanchuk, 2002
ASNN	Highly predictive non-linear neurall network model	http://vcclab.org/lab/asnn/
PNN	Produces clearly interpretable analytical non-linear models	http://vcclab.org/lab/pnn/
PCLIENT	Generates more than 3000 descriptors	http://vcclab.org/lab/pclient/
E-DRAGON 1.0	Calculates DRAGON molecular descriptors	http://vcclab.org/lab/edragon/
HelixTree	Genetic analysis software	www.goldenhelix.com

2.2 Computer Aided Drug Design (CADD)

Drug discovery and development are extremely time-consuming and costly processes. For every drug that reaches the market, there are more than 10,000 compounds synthesized, characterized, and tested for biological effects. Hundreds of millions of dollars are invested in the basic research and clinical studies which lead to its FDA approval and subsequent marketing. It was observed that there is a direct relationship between molecular structure and biological activity. The combined application of molecular graphics, computational chemistry, as well as chemical and biological information is commonly called computer-assisted drug design (CADD). These computer-based approaches promise to fulfill a long-coveted goal of medicinal chemists: the prediction of biological activity prior to extensive laboratory synthesis and biological testing. One day it may not be unreasonable to expect medicinal chemists to design active molecular structures in a fashion analogous to the way engineers plan buildings, although the problems associated with biological problems are much more complex and frankly less understood. In present scenario number of new drug molecules that is in the market like Indinavir the anti-HIV protease inhibitor and haloperidol have been synthesized and evaluated in one or more steps in their drug discovery with the help of CADD. The different software that used and useful in the molecular modeling is summarized in **Table 2.**

Table 2
Commonly Used Software in Molecular Modeling

Software name	Application	Source
Macromodel	Interactive molecular modeling system	http://convex.hhmi.columbia.edu/comp/macromodel/manuals
q-Screen 3.3	Molecular and statistical physics in molecular modeling	Quantum Pharmaceuticals
q-Tox/q-ADME	Linking biological activity profile to molecular toxicity	Quantum Pharmaceuticals [Compuetrr AIDED Drug Design, drug discovery]
Jsim	Used in physiology and bio-medicine	http://www.j-sim.org/
Simcyp	Determination of enzyme kinetics Simulation drug-drug interactions	http://www.simcyp.com/
WinNonLIn	Pharmacokinetic, pharmacodynamic and noncompartmental analysis	http://www.pharsight.com/products/prod_winnonlin_home.php
Biokinetica 3.1	Training standard software for pharmacokinetic, pharmacodynamic and non compartmental analysis	http://www.pbpk.org/joomla/component/option,com_fireboard/func,view/id,28/catid,16/Itemid,30/]
PharmaDM	Used in data analysis, data mining in QSAR/SAR analysis	www.pharmadm.com
ArgusLab	Used for molecular modeling and drug docking	http://www.arguslab.com
Moloc	A molecular Design software suite	http://www.moloc.ch/
Power MV	A software environment for statistical analysis, molecular viewing, descriptor generation and similar search	http://www.niss.org/PowerMV/
ACD Lab	Wide range of software applicable in Spectroscopy Drawing and Modeling Naming Physico-chemical properties	www.acdlabs.com
Drawing software ChemDraw/ ISIS Draw ACD/ChemSketch Chemistry 4-D Draw 6.0 Pro and 7.6 Life	Used for drawing the chemical structure	MDL Information system Cambridge Soft BioRaD Advanced Chemistry Development ChemInnovation Software Inc
CIARA™	Stores chemical information and assists in planning chemical reaction	Vogel Scientific Software
RasMol	Used to view molecular structure on screen and to manipulate them	www.openrasmol.org
SMILIB v2.0	independend software tool for rapid combinatorial library enumeration in the flexible and portable SMILES notation. SmiLib enumerates combinatorial libraries at rates of approximately 9,000,000 molecules per second on fast computers	Johann Wolfgang Goethe-University, Frankfurt am Main, Germany
ChemSoft	Used for management of large database, spectra and the automated building of virtual combinatorial librariescalculation of ADME-relevant parameters and tools for QSAR studies.	www.chemsoft.com

2.3 Software Used in Prediction of Toxicity

With the advancement in combinatorial chemistry, the numbers of new candidate structures coming out of the discovery cycle has increased significantly. This has created a demand for faster screening of the toxicological properties of these candidates before coming in clinical trial. Testing of toxicity profile of these compounds in laboratory animal and than in human is time consuming. Not surprisingly, computer methods for toxicity prediction offer an attractive solution to this problem because of their ability to screen large numbers of structures even before synthesis has occurred [10].

Toxicity of compounds using computer based approach is calculated by two approaches knowledge-based approaches and statistically based systems. Knowledge- based software systems such as DEREK, OncoLogic and HazardExpert use rules about generalized relationships between structure and biological activity that are derived from human expert opinion and interpretation of toxicological data to predict the potential toxicity of novel chemicals. On the other hand, statistically based software systems such as TOPKAT, and MultiCASE use calculated parameters, structural connectivity and the application of various statistical methods to derive mathematical relationships for a training set of non-congeneric compounds. Different commercial used software used in predicting the toxicity of compounds are summarized in **Table 3**

2.4 Software Used in Automation of Pharmaceutical Technology

The importance of automation in the pharmaceutical, nanotechnology and biotechnology industries have increased dramatically in recent years. Process automation serves to enhance product quality, master the whole range of products, improve process safety and plant availability, efficiently utilize resources and lower the wastage [11]. In the rapidly developing countries, mass production is the main motivation for applying process automation. The greatest demand for process automation in these industries is fulfilled by use of highly sophisticated software program. These softwares control the different process steps [12]. **Table 4** summarized the software used in automation of pharmaceutical technology.

2.5 Use of Different Software in Bioinformatics

Bioinformatics develops computer databases and algorithms for accelerating, simplifying, and thus enhancing, research in bioscience. Within this, however, the nature and variety of different bioinformatics activities are hard to quantify. Bioinformatics is as much a melting pot of interdisciplinary techniques as it is a branch of information science: It operates at the level of protein and nucleic acid sequences, their structures, and their functions, using data from microarray experiments, traditional biochemistry, as well as theoretical biophysics.

A stunning amount of freely available bioinformatics software and services are available on the Internet and widely used by user in comparison to chemoinformatics services. There may not be a single reason, but rather a combination of factors that have led to the wealth of useful open-source bioinformatics software. One distinct difference between cheminformatics and bioinformatics is the availability of data. A vast amount of genomic data are freely available on the Internet. By contrast, public domain chemical, or at least structural, data are scarce. The availability of bioinformatics data could be driving the development of open source tools. Almost all successful open-source software is driven by a clear understanding of the specifications [13].

2.6 Use of Software in Clinical Diagnosis of Disease

In present scenario treatment of diseases is based on some clinical diagnosis test like tumor volume and the tumor cross-sectional diameter measured from MR or CT images in clinical trials for cancer drugs [14]; the total number of lesions and lesion volume measured from multi-echo MR images of the brain in multiple sclerosis (MS) [15] (the cartilage thickness and cartilage volume measured from MR images of the knees for osteoarthritis [16-19] and the total brain volume and total hippocampus volume measured from MR images of the brain are used as indicators of Alzheimer's disease progression.

In clinical diagnosis and drug trials, there is a particular need to quantify results from the images. Thus, a variety of segmentation methods are needed to identify structures of interest [20] and to extract information such as volume, surface area and mean pixel intensity. Because clinical trials require statistical information across the studies, the ability to consistently and accurately quantify, correlate, report and store this information is extremely important. Imaging during clinical trials places additional emphasis on the examination of longitudinal data. Thus, the software must enable tracking and registration of longitudinal data, allow the quantification of differences between datasets and allow the analysis of trends across patient groups [21]. The ability to store quantified results in a database and to perform cross-subject queries and to

create quantitative reports is essential for statistical analysis [22].

2.7 Data Mining and its Application in Pharmaceuticals

Generally, data mining (sometimes called data or knowledge discovery) is the process of analyzing data from different perspectives and summarizing it into useful information - information that can be used to increase revenue, cuts costs, or both. Data mining software is one of a number of analytical tools for analyzing data. It allows users to analyze data from many different dimensions or angles, categorize it, and summarize the relationships identified. Technically, data mining is the process of finding correlations or patterns among dozens of fields in large relational databases. Statistics show that pharmacy professionals spend at least 20 minutes to 2 hours of their time everyday manually capturing online information (like sales leads, marketing leads, home business leads etc.) into their database. This is the most unproductive use of your time. Use of data mining software like Web Content Grabbercan save the valuable time of pharmacy professionals **(Table 5).**

Table 3
Summary of Software used for Prediction of Toxicity of Compound

Software name	Advantages	Limitation
DEREK	User friendly Used for testing and validation of large Scale of data due to batch processing	Activation and detoxification effect of metabolite needs to explore
OncoLogic	Used for prediction of carcinogenicity Metabolism of compounds can calculated	Not able to classify compounds chemically Unable to calculate physiological parameters of compound
HazardExpert	Used to estimate bioavailability and bioaccumulation Provides semi quantitative estimate for toxicity	Provides no information about metabolites
Compact	Easy to use	Not giving any toxicity profile
CASE	Used number of physicochemical properties for prediction Used for predicting rodent carcinogenicity of pharmaceuticals	Quality of prediction is poor
TOPKAT	Processing is very fast	Lack of batch processing capability

Table 4
Software Used in Automation of Pharmaceutical Industries.

Name	Use	Suppliers or web side address
ApotheSoft-Rx	Compounding operation	Francom's Software Ltd. France
FormRules	Granulation process	Intelligensys Ltd, Teeside, UK
INFForm	Granulation process	Intelligensys Ltd, Teeside, UK
Biological Safety cabinet	Training related to safe use of biological safety cabinet, Fume hoods	Eagleson Institute, Eagleson
DavaPlus	Automated the activity of Pharmaceuticals retailers	Dava Infotec Pvt. Ltd.
PharmaSoft	Automated the activity of Pharmaceuticals retailers	Essel Software & Service Ltd.

Table 5
Data Mining Software Used in Pharmaceuticals

S.No	Software
1	Pharmamine
2	Weka
3	RapidMiner
4	KNIME

3 CONCLUSION

Future of drug discovery is development of drug based on disease-gene association. This process will lead to relatively many, smaller-use drugs. To capture the promise of this vision, we will also need much less expensive safety and efficacy drug testing. As fewer patients will be exposed to these specialized medicines and they are the ones that will directly benefit or suffer side effects, risk/benefit will be more individually focused. It seems clear that safety testing strategies will have to be modified to move to individualized medicine. In this case systemic approach using software will be helpful that will save the lot of time along with cost.

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