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DRUG DESIGN AND DEVELOPMENT INVOLVING NOVEL SOFTWARE IN PHARMACEUTICALS

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ABSTRACT

The designing and development of a new pharmaceutical drug molecule or products is generally known as complex process which takes a lot of time and resources for developing. The drug molecules are the primary components in the drug formulation, which combined with the numbers of compounds. Recent days computer aided drug design (CADD) approaches are used very widely to increase the efficiency of the drug designing and development for drug. Computational are useful tools to interpret and guide experiments to expedite the antibiotic drug design process initially. Simultaneously structure based drug design (SBDD) and ligand-based drug design (LBDD) are the two category of computer-aided drug design (CADD) approaches in existence. The drug discovery is mainly based on the different types of parameters follow such as pharmacokinetic, ligand-based and structure-based designing and other basis for the drug designing and development. Novel software-based methods such as molecular modelling, structure-based drug design, structure-based virtual screening, ligand interaction, and molecular dynamics are regarded as powerful tools for studying drug pharmacokinetic and pharmacodynamic properties. Mostly drug designing and discovery solutions for screening, predictive analytics, modeling, simulation, and computational capabilities. Software-based drug discovery and development methods have important role in the development of drug molecules. Drug designing software has key role to design novel proteins or drugs in pharmaceutical field. The review article initially broadly focused in drug designing and development, different types of novel software used in the drug discovery and as well as the formulation designing process of the any pharmaceutical products or dosage form. The various numbers of novel software used in the drug design and development within the combination as well as the individual in the form of images and table data form.

KEYWORDS

Computer-aided drug design (CADD), Novel software, Drug designing and Development.

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INTRODUCTION

Generally, in order to interact with and bind to biomolecular targets that are complementary to one another in shape and charge, small molecules must be created as part of the drug design process. The process of combining various chemical compounds

or structure, including the API, to create a finished pharmaceutical medicinal product or medicine is known as product formulation in pharmaceutics. In today's time, computers are so essential in pharmaceutical research and development that it can be difficult to remember a time before they might help a medicinal chemist or a biological researcher of the products. All the criteria depend on the initially the designing or development of drug molecules is necessary. Example including numbers class of drugs Anti-hemorrhoid drugs, topical antibiotics, cough suppressants, non-steroidal anti-inflammatory drugs (NSAIDs), antibiotics and many more including these[1].

The major use of computer-aided drug design (CADD) approaches to find out, create, and optimize new, powerful, and secure medications for patients while lowering patient compliance is crucial. Finding a chemical substance that is both geometrically and chemically suited to a specific cavity on a protein target while taking into account the physiology of the patient is the goal of medication design. Recent technological developments in biochemistry, biomedical science and nanotechnology have made computer-aided drug design and delivery systems possible on a molecular basis. Therefore, several factors for the main purpose to discover the new drug product reason including, High cost, insufficient and lengthy time duration, high level of risk, uncertainty in the results, and highly complex procedures are the main challenges in the development of new drug. To overcome these development problems, it is needed to employ new and more cost-effective drug discovery and designing methods such as software and computer aided drug design and molecular docking[2]. Another term "structure-based drug design" refers to drug development that is predicated on knowledge of the three-dimensional (3D) structure of the biomolecular target of the drug medicament. The drug designing is the broader area for the discovery and development. Therapeutic designing and development, which involves several stages in the creation of drug molecules, is generally the process for starting research, their clinical and preclinical studies, and FDA approval authority. Post-approval marketing is the final step in the process[3]. Drug development idea is originated from the basics of drug molecules properties for the particular disease treatment. These are visualized in the given images of the drug designing and development with the DOE (Design of Experiment). Showing in (Figure No.1) complete processing of experiment.

Basically, mainly of their five phases which included in the designing of drug which discussed in below description with all phases with the selection of drug molecules parameters[4].

Drug molecule selection for the designing and development

The drug selection is the most important or key factor for the drug designing and discovery in initial stage with the help of software, all points discussed in the below section for the drug molecule selection.

Drugs must be polar which should be soluble in aqueous conditions which are interact with molecular targets.

Drugs must be 'fatty' - to cross cell membranes and also to avoid rapid excretion

Drugs must have both hydrophilic and lipophilic characteristics in its structure.

Many drugs are weak bases with pKa is 6-8.

Drug components or molecules are important to select the drug for the designing and their development[5]. Commonly, allpoints describe as followed for the selection correspond discussed in above points.

PRINCIPLES OF DRUG DESIGN AND DEVELOPMENT

The first important software for drug designing and development is "The Lipinski's Rule of five" which is the important of principle key for the development or discovery for the drug molecules. For the primary step drug designing and discovery will perform with the use of novel software, then the first step is knowing the pharmacokinetics and preformulation study is more important. So, this needs for the study of drug likeness or pharmacological or pharmacokinetic activity of the drug molecules[6].

Lipinski's rule offives

Lipinski's rule of five also known as the *Pfizer's rule of five* or simply *the Rule offive (RO5)* is use to evaluate drug likeness or determine if a chemical compound with a certain pharmacological or biological activity has properties that would make it a likely orally active drug in humans' beings. The rule outlines molecular characteristics crucial to a drug's pharmacokinetics which are absorption, distribution, metabolism, and excretionin the human body ("ADME").The rule is important to remember during drug discovery when a pharmacologically active lead structure is optimised step by step to increase activity and selectivity while also ensuring drug-like physicochemical properties are maintained, as described by Lipinski's rule[7].

Components of the rule

Lipinski's rule states that, in general, an orally active drug has no more than one violation of the following criteria:

Not more than 5 hydrogen bond donors (nitrogen or oxygenatoms with one or more hydrogenatoms)

Not more than 10 hydrogen bond acceptors (nitrogen or oxygenatoms)

A molecular weight less than 500 Dalton.

An octanol-water partition coefficient log *P* not greater than 5

It should be noted in previously that every number is a multiple of five, which is how the rule got its name denied.As with many other rules of thumb, there are many exceptions to Lipinski's Rule[8].

PHASES INVOLVING IN DRUG DESIGNING AND DEVELOPMENT

Phases are the steps involving in the drug designing, mainly of five general steps or phases included in the drug designing and development discussed in the below section with their complete necessary applications

Step No.1: Drug Designing and Development.

Step No.2: Preclinical Research.

Step No.3: Clinical Research.

Step No.4: FDA Drug Review.

Step No.5: mFDA Post-Marketing Drug Safety Monitoring[9].

The basic function or role in the new drug designing and the development are commonly discussed in the below (Table No.1).

After the all steps the new drug molecule will designed as per all criteria follow, generally purpose for the patient's compliance. Drug discovery is a series of processes which when followed identify the drug compounds for the effective treatment or control of disease targets[4,5]. There are five critical steps in the U.S. FDA drug development process in the (Table No.1). This article discussed idea of drug development to develop an in-depth understanding of the entire process. The phases of drug designing and development-

These all the primary phases for the drug designing till the post marketing of that particular drug molecules for the disease treatment with the complete help of software (Figure No.2). Drug discovery process starts with understanding the disease for which the drug to be designed[8,9]. The different types of drugs designing and development of the basis of molecules attachment discussed below description.

TYPES OF DRUG DESIGNING AND DEVELOPMENT

There are mainly of four different methodologies which are commonly used in the basic or scientific drug designing and drug discovery. Majorly four types of basics to design and discovered the drug molecule are discussed below section-

Ligand- based drug design or indirect drug design (LBDD).

Structure-Based drug design or direct drug design (SBDD).

Rational drug design.

Computer-Assisted Drug Design (CADD).

Ligand-Based Drug Design OR Indirect Drug Design (LBDD)

In the absence of receptor 2D information, ligand-based drug design relies on knowledge of molecules that bind to the biological target of interest for the disease treatment[10]. The most important and widely used tools in ligand-based drug design are 3D quantitative structure activity relationship (3D QSAR) and pharmacophore modelling.

They can provide predictive models that can be used to identify and optimised leads. More information on these methods and their applications to 5-LOX inhibitor design and development can be found in the reviews mentioned above[9].

Structure-Based Drug Design OR direct Drug design (SBDD)

One of the first techniques used in drug design, structure-based drug design, aided in the discovery of new drugs. Calculation during the design process yields information about the structure, structural dynamics, and electronic properties of ligands. Structure-based drug design (also known as direct drug design) is based on knowledge of the three-dimensional structure of the biological target obtained through methods such as x-ray crystallography or NMR spectroscopy[11]. Structure-based drug design can be divided roughly into two categories.

Ligand based drug design or Database searching

Receptor based drug design

The design and optimization of a chemical structure with the goal of identifying a compound suitable for clinical testing a drug molecule is known as structure-based drug design. Firstly, finding the ligands for a given receptor, which is usually referred as database searching. This method usually referred as ligand-based drug design.

Rational drug design

The development of medications or drug product based on the study of the structures and functions of target molecules is referred to as rational drug design. The primary role of rational drug design is to take a methodical approach to developing a new drug rather than hoping for a lucky break or randomly testing hundreds of drug molecules in the hope that one of them binds to a receptor and exerts a therapeutic effect. During rational drug design, researchers take three general steps to create a new drug:

Step No.1: Firstly, identify a receptor or enzyme that is relevant to a particular disease, they are going to design or development of drug molecules or product.

Step No.2: Secondly, find out more about the structure and function of this receptor or enzyme for the product design.

Step No.3: Lastly, use the information from step two in order to design a drug molecule that interacts with the receptor or enzyme in a therapeutically beneficial way[8,9].

Computer-Assisted Drug-Design (CADD)

To design novel pharmaceutical medications and determine whether they will be successful in treating a certain condition, drug discovery software is utilized. Computational chemistry is used in computer-aided drug design to find new ways to improve existing medications and related biologically active compounds. Computer- assist drug design (CADD), also called Computer assist molecular design (CAMD) and represent more recent applications of computer as tools in the drug design process and many new software used in modern days and in the fields of biochemistry, molecular biology, and cell biology, facilitated by development in genomics and proteomics[8-10]. The CADD has several advantages, including the ability to reduce synthetic and biological testing efforts while identifying the most promising drug candidates by removing compounds with undesirable properties.

NOVEL SOFTWARE FOR THE DRUG DESIGNING AND DEVELOPMENT

The drug designing and development process is primarily carried out with the following parameters for the new drug molecules, as well as accurate testing, particularly for the patients' cure. The software is further categorized on the basis of task performing by the software and their working principle like software assessing pharmacokinetics parameters, ligand interaction and molecular dynamic, molecular modelling and structural activity relationship, image analysis, visualizers, data analyzer and behavior analysis software for designing and development of new molecules of the drug[10]. All the parameter with the some of the name of software mentioned in the (Table No.2) below-

This all software used majorly of the drug molecules deigning and development which

discussed in the above (Table No.2). Novel software discussed in the below data completely, with proper uses of the particular software with following important parameter.

PHARMACOKINETICS PARAMETERS

When a human being consumes a pharmaceutical drug, the chemical makeup of the drug and the body's natural processes combine to generate a complex biochemical drug molecule. These complicated interactions are measured and described using *pharmacokinetic* and *pharmacodynamic* parameters. Pharmacokinetics (PK) describes the absorption, distribution, metabolism, and excretion also known as ADME of drugs molecule in the body. PK parameters are used in drug development to understand the complex interplay between drugs and the body in order to design, refine, and create safe and effective therapeutics[10]. Generally, pharmacokinetics (PK) performed with the different type of software using such as DDDPlus, GastroPlus and MapCheck and many more software used. All software discussed in the below section broadly mentioned-

DDDPlus (Dose Dissolution and Disintegration Software)

A scientist to simulate *in vitro* disintegration and dissolution of DDDPlus (Dose Disintegration and Dissolution Plus) is used to study active pharmaceutical ingredients (API) and additive in the formulation.

DDDPlus forecasts the effects of changes to the formulation or experimental parameters on the dissolution rate after only one calibration trial in the formulation of new API. This software initially provides the dissolution and disintegration rate information, eliminating the need for traditional 'cut and try' methods to finalise a formulation design. DDDPlus allows to choose from one of five mathematical models or drug product and five dosage forms to demonstrate the dissolution of a single ingredient using. It is the mathematical models which is used for the *in vitro* dissolution simulation describes the effect of following parameters on dissolution:

To determine the physicochemical properties of the formulation ingredients under study such as pKa, solubility, diffusion coefficient, and density.

Each particle size distribution for all ingredients used in the formulation.

Simultaneously, Interactions between the active ingredient i.e., API and other formulation excipients involving.

Application

Automatically calculates fluid velocity based on instrument speed and apparatus type using. It is an optimizing module which uses a single experimental data set to calibrate a drug's dissolution rate[12].

GASTROPLUS (SIMULATION SOFTWARE FOR DRUG DISCOVERY AND DEVELOPMENT)

GastroPlus is a mechanistically based simulation software package that simulates intravenous (IV), oral, oral cavity, ocular, intranasal and pulmonary absorption, pharmacokinetics (pK), and pharmacodynamics in human and animals. Model parameters can be simultaneously fitted to data from several records or data from a single record. The number of records whose observations are being utilized to compare anticipated and observed values is N. Typically, hundreds of iterations will be carried out, each having N simulations. Objective function weighting is user-defined, and includes the most common weighting schemes.

Application

It determined, transporter-based drug-drug interactions (DDI), metabolic and/or transporter induction use for drug design.

Use compartmental or physiologically based pharmacokinetics to simulate DDIs for any species (human, beagle, rat, mouse, rhesus monkey, cynomolgus monkey, rabbit, or cat) (PBPKPlus)[13].

MapCheck

The MapCheck compare absolute dose measurements of both systems with ion chamber results. The MapCheck system creates a verification plan for every field before data collection, exports a calculated dosage map (Frontal) for every field, and calibrates the diode array. As the plan gets more

intricate, the standard deviation increases. It is user friendly software for data analysis, easier commissioning process and generates comprehensive report.

Application

The MapCheck used for IMRT (Intensity-modulated radiation therapy) verification and small detectors identify MLC.

Dose based EPID IMRT QA generally, done by using of MapCheck[14].

LIGAND INTERACTIONS AND MOLECULAR DYNAMIC

AutoDock

AutoDock is a programme or software which predicts ligand-protein (bio-macromolecular target) interactions. The structures obtained from the Autodock, could be employed as targets for new drug molecules designing especially in controlling human, animal and plant diseases and disorders, and understanding of fundamental aspects of biology. Multiple steps are employed for AutoDock calculations:

Preparation of coordinate files using AutoDock tools and Pre-calculation of atomic affinities using AutoGrid.

Docking of ligands using AutoDock and Analysis of results using AutoDock Tools.

Application

The identification of aromatic rings or compounds which used to explore the conformational states of a flexible ligand, using the maps generated by AutoGrid to evaluate the ligand-protein interaction at each point in the docking simulation[15].

Schrodinger

Schrodinger software has wide range of applications which solved most of the challenges these bio-molecules will bring during the designing. It focuses on specific advances in molecular modelling, molecular dynamics, ligand-receptor docking, and biologics that were developed to address these challenges. Structure-based character of the drug molecule such as understanding of conformational changes and hydrophobicity of structures can be analyzed with the help of this software. Many examples are studied using molecular dynamics simulation software such as Schrodinger, such as a series of stabilised stapled-helical peptides at various temperatures. The majority of pharmaceutical industries, biotechnology industry, government companies, university, and lots of computing centers use this Schrodinger software. The various products of Schrodinger such as:

Glide

Prime

Jaguar

Macro Model

Glide

Glide provides the full range of speed and accuracy which is from high-throughput virtual screening of millions of compounds or API to extremely accurate binding mode predictions, ensuring consistent high enrichment at all levels. Commonly, GLIDE is most accurate binding mode prediction for the drug designing. Glide offers the complete solution for ligand-receptor docking with speed and accuracy. It can also exhibit excellent range of docking accuracy across diverse range of receptors.

Prime

Prime is a package used for protein structure predictions in drug medicament designing and it is user friendly for the study. Prime provides users the complete control over calculational settings which increase the accuracy of the obtained result. It provides the accurate receptor models for structure-based drug design and development.

Jaguar

Jaguar known as the high-performance for both gas and solution phase recreation or reagents, with particular strength in the treating metal containing systems. Jaguar proceeds faster than the other traditional methods and it makes more possible to carry out more calculations at a single time. Jaguar computes a comprehensive array of molecular properties such as NMR, IR, pKa, partial charges analysis.

Macro model

Macro Model is a complete molecular modeling packaging software which is suitable for using leading force fields which provides accurate results in the designing. It performs molecular dynamics at constant temperatures using mixed Monte Carlo

algorithm and stochastic dynamics. There are different types of force fields such as MM2, MM3, AMBER 94, AMBER, are supported by Macro Model to do a wide range of research applications or drug product designing.

Application

Macro Model used for molecular dynamics simulation studies, Quantum mechanics and Prediction of binding affinity[16].

Gold (genetic optimization for ligand docking)

GOLD (Genetic Optimization for Ligand Docking) is a genetic algorithm which provide docking of flexible ligand and a protein with flexible hydroxyl groups and other functional groups. The function of this software is based on favourable conformations found in the *Cambridge Structural Database* as well as resulting on weak chemical interactions. It gives different values of the genetic algorithm parameters are used to control the balance between the speed of GOLD and the reliability of its predictions. It gives reliable results and correct atom typing for both protein and ligand. GOLD is a part of GOLD Suite software. GOLD includes all of the functionality needed to dock ligands into protein binding sites from prepared input files in the software. To create and edit starting models, GOLD will most likely be used in conjunction with a modelling programme.

Application

GOLD software used to predict binding modes and for protein-ligand docking using the Genetic Algorithm[17].

Biosuite

BioSuite utilizing in the functioning of macromolecular sequence and structural analysis, chemo informatics and algorithms for aiding drug designing and discovery. The four major modules, Genome and Proteome Sequence Analysis, 3D Modeling and Structural Analysis, Molecular Dynamics Simulations, and Drug Design, are accessible via a user-friendly graphics interface, as well as adequate documentation and tutorials. The BioSuite Genome and Proteome Sequence Analysis module is concerned with applications relating to the analysis of nucleic acid and protein sequences, rather than individual molecules. This BIOSUITE module would allow you to annotate genomes, predict protein secondary structures, derive a phylogenetic relationship between organisms, and compare two genomes for gene or protein similarities. The 'Simulations' module essentially simulates the behavior of a molecule, in terms of its three-dimensional structure.

Application

Genome analyzing and sequence analyzing with the use of BIOSUITE.

BIOSUITE used for the create the 3D modelling, simulation, structural changes, drug design, pathway modelling, SNP analysis, and comparative genomics are some of the techniques used.

MOLECULAR MODELING AND STRUCTURAL ACTIVITY RELATIONSHIP

MAESTRO

Maestro is freely available, full-featured molecular visualization software. Maestro is a powerful tool for interpreting, managing, and sharing the results of computational experiments. It is useful for creating, visualizing, and sharing three-dimensional chemical models. The central tenet of Schrodinger's computational technology is Maestro. It's a versatile and powerful tool for molecular modelling in computational chemistry. It is in charge of organising and analysing data. Maestro's user-friendly interface makes it simple to set up calculations. The computed results are returned automatically and incorporated into projects for further investigation. Users can gain insight into molecular properties as well as detailed intermolecular interactions thanks to Maestro's extensive visualisation capabilities.

Application

It performed Quantitative structural analysis.

Display of vibrational modes, molecular orbitals, or electron density, as well as molecular properties.

ArgusLab

ArgusLab is a molecular modeling, graphics, and drug design program for Windows operating systems. ArgusLab was used on a window-based computer to perform conformational analysis such as geometry optimization studies. Using quantum mechanics principles, this software predicts

potential energies, molecular structures, geometry optimization of structure, vibration frequencies of atom coordinates, bond length, bond angle, and reaction pathway. ArgusLab calculate minimum potential energy using geometry convergence function.

Application

Molecular docking calculations are used in the construction of molecules, the construction of molecules using template structures, and molecular modelling.

GRAMM (GLOBAL RANGE MOLECULAR MATCHING)

GRAMM software is used for protein docking. It predicts structure using atomic coordinates of the two molecules. It generates a list of high-scoring (low-energy) ligand positions, which can then be used as is or refined using other techniques. Instead of using statistical sampling, this software performs an exhaustive search to find all complex configurations with a high-score steric fit. This software conducts a thorough 6-dimensional search of the molecules' relative translations and rotations. Molecular pairs include two proteins, a protein and a smaller compound, two transmembrane helices, and so on. It is used for high-resolution molecule structures that have large conformational changes. It is an empirical approach to smoothing the intermolecular energy function by changing the range of the atom-atom potentials.

Application

GRAMM is used for the protein-protein docking and as well as the protein-ligand docking[18-19].

Sybyl–X Suite

SYBYL-X gives information to understand and balance the competing SARs for each of the multiple criteria which successful drug candidate must meet. It visualizes and explores relationships between multiple properties using the analysis tools in SYBYL-new X's Molecular Data Explorer (MDE), and obtains insights into data in the shortest amount of time. It provides new ways to approach life science molecular discovery projects, while extending the unrivaled. SYBYL-X investigates various aspects of the drug-receptor interaction mechanism in order to identify potential new binding interactions that will provide' step jumps' in potency, or to identify options for improving ADME or physical properties without disrupting key receptors.

Application

Molecular modeling from sequence through lead optimization with this software.

Ligand Based Design and Structural Based Design and build a Protein Model in the resulting of SYBYL-X SUITE.

Sanjeevini

This software was designed for a computational pathway for lead design automation. It targets a bimolecular (protein) target along with a candidate drug. Software identifies potential active sites, docking and scores the candidate drug and returns four structures of the candidate drug bound to protein target with binding free energies. In this software the drug molecule is uploaded along with target protein. When the software is uploaded, it displays the results of some critical pre-tests that were carried out based on the parameters required for the acceptable format of the drug and protein files. The software consists of following modules such as Drug Preparation, Protein Preparation, Docking and Scoring, and Protein Ligand Complex.

Application

It is used for drug designing and predicts binding affinity.

Prediction of protein-ligand binding affinity.

PASS (PREDICTION OF ACTIVITY SPECTRA OF SUBSTANCES)

Based on a comparison of already existing structures, this software predicts maximum biological activities of a new pharmaceutical substance of lead molecule. PASS predicts 4366 different types of biological activity with its average accuracy of about 95%.In PASS, the prediction of biological activities is described qualitatively as a 'yes/no' or 'active/inactive' result. The structure of a new chemical compound is converted into 2D structural formulae to learn about its biological activities. The molecular structure is represented in PASS by the set of unique MNA (Master of

Navigation) file. The substances are equivalent in PASS if they have the same set of MNA file. The structural formula of a molecule, for which PASS prediction should be carried out, is presented as a MOL (Mol files) file.

Application

Reveal new effects and mechanisms of action for known substances in corporate and personal databases, used as leads with given biological activity profiles among the compounds from in-house, commercial databases and select the most promising compounds from available samples for high throughput screening[20,21].

IMAGE ANALYSIS AND VISUALIZATION

AMIDE (A Medical Image Data Examiner)

AMIDE is developed in such a way that; it should provide multimodality volumetric medical image analysis. Data sets (e.g., PET, CT, and MRI) and regions of interest (ROI's) are logically organized within a tree structure so that an unlimited number of these items can beanalyzed, displayed, and modified simultaneously.

Application

Provides multi-modality medical image analysis to the molecular imaging research community and gives interactive "wizard" interfaces for making advanced medical imaging algorithms (e.g., factor analysis and cardiac polar maps).

Discovery studio® Visualizer

Discovery Studio Visualizer (DS Visualizer) is employed for analyzing, viewing, and sharing protein along with small molecule data. It is a free of cost and employed for either small molecule or macromolecule applications or both. It allows data to beanalyzing and transferred data in various formats like3D structures, SMILES, graphics, and sequences. The required sequence and structures can be downloaded by PDB or NCBI. Molecular properties are explored by editing structures and performing calculations.

Application

Visualization: Ligand-based design and Structure-based design, advanced molecular visualizations and Publication quality graphics, Macromolecule design.

Imaging software SCGE-Pro

SCGE-Pro is mostly employed in Comet assay and single cell gel electrophoresis. It is a collaborative project with Computer Division for the development of imaging software for DNA damage analysis and cytogenetic. Genotoxicity of environmental factors such as high and low LET radiations, chemical mutagens, drugs, and carcinogens is investigated by employing Comet assay. The fluorescence in-situ hybridization (FISH) technique is used in this imaging method to determine gene specific repair in relation to total DNA or loss of heterozygozity (LOH) for a single gene.

Application

Clinical application i.e., prenatal diagnosis, cancer susceptibility, DNA repair deficiency syndrome, diabetes, genomic instability.

Genotoxicity evaluation of chemicals and radiation in human and animal models.

Clinical and molecular epidemiology, radiation biology, agricultural sciences.

Xenogen living image software

Xenogen Living Image Software employes Wave Metrics IGOR Pro1, a powerful programming tool and data analysis. The software gives a customized environment for data analysis and acquisition. Macintosh® and Windows® both helps software functioning. The software works similar for fluorescent images and luminescent image until it's specified. The colour bar is located on the right side of the image and depicts the relationship between the image's pseudo colors and the numerical values of the image data. At the bottom of the window, labelling information generated by both the user as well as by the imaging system explains how to use the individual controls found in the image window.

Application

In vivo imaging application and Low light-level imaging such as sensitivity and binning, background sources of light, measurements and calibrations, and dark charge management[21,22].

DATA ANALYSIS

Genespring

GeneSpring gives terminology information for various organizational elements in the user interface, as well as a high-level overview of the data and analysis paradigms available in the application. This software gives a collection of samples, then software run in order to answer a specific scientific question. A new experiment is created from a selected project by loading samples of a specific technology and performing a set of standard pre-processing steps such as summarization, normalisation, baseline transform, and so on, which convert the raw data to its ready for analysis stage. All data are physically stored in the file system. These are saved in the app/data subfolder of the installed folder. A SQL database stores all annotations associated with various objects in the file system (properties such as names, notes, and so on that can be searched on); a database is used for fast search.

Application

Batch effect correction and circular binary segmentation are two techniques.

Identify common variations across a set of samples with GENESPRING using.

QSAR (Quantitative Structure-Activity Relationships)

A descriptor is a molecular property that can be calculated with the help of QSAR. QSAR gives a range of descriptors that discovers new QSAR relationships. There is a limit for datasets and minute information regarding by training and validation provided by previous researchers. The use of *SMILES* or *.sdf files* by website to promote the calculation of additional parameters along with other drug discovery scientists.

QSARPro

This software recognizes the relationship of a molecular activity and structural parameters analyses (such relationships and makes quick predictions using reliable statistical modelling). It can employ to evaluate more than 1000 molecular descriptors including topological, physicochemical, electro-topological, information theory based, quantum mechanical, electrostatic and hydrophobic. QSAR modelling typically involves activities such as statistical evaluation of the calculated descriptors, descriptor selection and calculation, training and test set assignment, regression analysis, and results analysis.It assesses multiple options for test set, descriptor classes, linear or non-linear regression, and regression technique to determine the best option for a particular project.

Application

QSARPro, explore, exercise of various combinations of variable selection methods and regression methods determine with this use.

Aligningthe set of molecules within protein active site with respect to the co-crystal ligand for the development of a bedrock for the placement of ligand and Protein-protein interaction studies[22,23].

BEHAVIORAL STUDY

ETHOWATCHER

Behavioral change is regarded as a critical parameter in the diagnosis of a variety of disorders. Experiment animal complex behaviours are associated with morphological and physiological changes. All obtaining changes are recorded in laboratory or free-ranging animals for many purposes relevant to biological or biomedical research such as ecology, physiology, neurosciences, psychology, genetics, pharmacology and pathology. Advanced automated methods Indirectly record behaviours by detecting their consequences using pressure or infrared sensors, or image processing techniques derived from video-tracking analysis. This software is integrated tool to build and save behavioral changes, used for 'real-time' behavioral scoring (like directly from the ongoing events in the environment or from analog video files) or 'off-line' behavioral recordings (from digital video files).

Application

Etho watcher is used in the validation of behavior analysis in laboratory animal and human being and Video-tracking analysis in laboratory animals.

MARS (Multimodal Animal Rotation System)

MARS is a Multimodal Animal Rotation System that records an experimental animal's 360° movement. The MARS software is programmed to

automatically rotate a mouse to the required positions or angles in order to track all relevant molecular and anatomical information of the experimental animal. This software allows especially for automatic co-registration and capture of multimodal and multispectral data sets from all acquired angles.

This software includes animal rotation device, controlling software, multimodal visualization and co-registration software.

Application

Use for the cell tracking, Enzyme activity, Bone disease as well as Inflammatory disease.

Nanoparticle tracking and delivery with the help of MARS software.

All the software above mentioned in the (Table No.2) with the proper parameters follows, in the formulating, designing and development of the drug molecules as well as the drug products[23,24]. Here the next below section article define the individual applications with the respective novel software name simultaneously.

The all application with the software name discussed into the below section highlights,

This table explaining the proper application or major uses with proper name of novel software explained in the above (Table No.3), broadly.

Additional novel software as drug designing

The computer needs software for drug designing and development procedure. These extra pieces of software simplify and speed up the drug development process for us. The Software for developing drugs molecules is offered by a number of businesses, including Accelrys, Schrodinger, Auto Dock, and Argus Lab. Accelrys, a software company based in the United States, also has offices in Europe and Japan. It specialises in software for drug discovery and materials science. The different software produced by Accelrys are:

Insight II

Pipeline Pilot

Materials Studio

Insight II

A graphical molecular modeling program. Using this software, we can build and manipulate virtually any class of molecules or molecular systems. Insight II computational engines have the capacity to restart calculations from information in the saved files.

Pipeline pilot

Pipeline Pilot data are based on powerful client server platform that leads to construct graphical workflows for data retrieval, filtering, analysis. This *PIPELINE PLOT Software* is used for sequence analysis, gene expression, in cheminformatics to study the ADME properties of the drug and check the toxic constituents present in the drugs.

Materials studio

Materials studio software is the most advanced technology and is used to solve the problems in R and D process. It is designed for structural and computational researchers in chemicals and materials R and D. They provide various ranges of quantum mechanics-based tools for predicting structures, density functional methods, linear scaling and semi-empirical tools[27].

Chemdraw

ChemDraw is a molecule editor first developed in 1985 by David A. Evans and Stewart Rubenstein (later by the cheminformatics company *Cambridge Soft*). The company was sold to PerkinElmer in the year 2011. ChemDraw, along with Chem3D and ChemFinder, is the part of the ChemOffice suite of programs and is available and is available for Macintosh and Microsoft Windows. These all are the part of Chemdraw office which used to draw the chemical molecule. While hand sketching is most efficiency used during discussions and learning, neat drawing is required for official reports, publications and theses.

Such drawing can be created with several computer programs and one example is ChemDraw[13]. ChemDraw is an easy-to-use application that enables intuitive and effective two-dimensional drawing of simple chemical molecular representations. It is accessible on both the PC and Mac platforms.

Chem 3D

3D compound modelling, structure import from a sizable database, and compatibility with ChemDraw.

ChemFinder

Generally, Transfer files into tables for search, import structure data.

Feature of ChemDraw

ChemDraw is a chemical structure drawing software which helps in many chemical structures drawing. There main properties discussed below-

To draw the Chemical structure to name conversion and Chemical name to structure conversion.

NMR and Mass spectrum simulation and Structure cleanup.

An extensive collection of templates, including style templates for most major chemical journals and export the structure into PDF (Mac version only)[28,29].

SWISSADME

The SwissADME website allows us to computed physiochemical pharmacokinetics (pK) descriptors as well as predict (ADME) parameters in the drug development. To promote drug discovery, one or more small compounds' pharmacokinetic properties, such as drug-like nature and medicinal chemistry friendliness, should be used. SwissADMEa free web tool to evaluate pharmacokinetics (pK). Drug-likeness and medicinal chemistry friendliness of small molecule.

SwissADME drug development involves assessment of Absorption, Distribution, Metabolism And Excretion (ADME) increased in early of the discovery process, at a stage when considered compounds are numerous but access to the physical samples is limited.

A user-friendly interface on the login-free website https://www.swissadme.ch ensures simple and efficient input and interpretation. SwissADME software from the Swiss Institute of Bioinformatics (http://www.sib.swiss) was accessed, and a web server that displays the SwissADME submission page in Google was used to estimate individual ADME behaviours of plant compounds.

The actual input for computation is the structure that was transferred as a list to the submission page's right side.

The list is made to contain one input molecule per line with several inputs, defined by *Simplified Molecular Input Line Entry System* (SMILES) this resulting presented for each molecule in the dosage form (tables/capsules), graphs and also an excel spreadsheet. Lots of additional novel software used in the checking of pharmacokinetics (pK) value of the drug molecules. SwissADME is one of them[30,31].

Including these types of novel designing software used in the drug designing and development of the drug molecules. Software plays as important role for the initially drug design. Drug discovery software is used to develop new pharmaceutical drugs and test whether a newly created drug will be effective in treating a particular disease.

Table No.1: List of steps with the uses in the drug designing

S.No	Steps involving drug designing	Application or role
1	Drug designing and development	Research for a new drug begins in the laboratory.
2	Preclinical research	Drugs undergo laboratory and animal testing to answer basic questions about safety.
3	Clinical research	Drugs are tested on people to make sure they are safe and effective.
4	FDA Drug Review	FDA review teams thoroughly examine all of the submitted data related to the drug or device and make a decision to approve or not to approve it.
5	FDA Post-Marketing Drug Safety Monitoring	FDA monitors all drug and device safety once products are available for use by the public.

Table No.2: List of Software name with some parameters for drug design

S.No	Study Parameters	Software Name
1	Pharmacokinetics parameters	DDDPlus GastroPlus Map Check
2	Ligand interaction a molecule dynamic	Auto Dock Schrodinger GOLD BioSuite
3	Molecular modelling and structure relationship	Maestro Argus Lab GRAMM SYBYL-X Suite SANJEEVINI, PASS
4	Image analysis and visualization	AMIDE Discovery Studio Visualizer Imaging Software SCGE-Pro Xenogen Living Image Software
5	Data analysis	Gene Spring QSARPro
6	Behavioral study	Ethowatcher MARS

Table No.3: Applications of novel software dug designing

S.No	Novel Software Name	Major Applications
1	DDDPlus GastroPlus MapCheck	Dissolution and disintegration study *In-vitro* and *in vivo* correlation for various formulations Compare dose or fluency measurement
2	Autodock Schrodinger GOLD BioSuite	Evaluate the ligand-protein interaction Ligand-receptor docking Protein-ligand docking Genome analyzing and sequence analyzing
3	Maestro ArgusLab GRAMM SYBYL-X Suite Sanjeevini PASS	Molecular modeling analysis Molecular docking calculations and molecular modeling package Protein-protein docking and protein-ligand docking Molecular modeling and ligand-based design Predict protein-ligand binding affinity Create and analysis of SAR models
4	AMIDE (A medical image data examiner) Discovery studio Visualizer QSARPro	Medical image analysis in molecular imaging Viewing and analyzing protein data Protein-protein interaction study
5	MARS (Multimodal Animal Rotation System)	Animal activity tracking, enzyme activity, nanoparticle tracking and delivery study[24-26]

Table No.4: List additional novel software in drug designing

S.No	Software	Silent features
1	Design Expert	An effective and compact package for improving pharmaceutical formulation and procedure[32].
2	Minitab	Powerful DOE software for automated data analysis data analysis MS-Excel compatibility.
3	DOE PRO XL	MS-Excel compatible DOE software for automated data analysis.
4	CARD	Powerful DOE software for data analysis includes graphics and help feature.

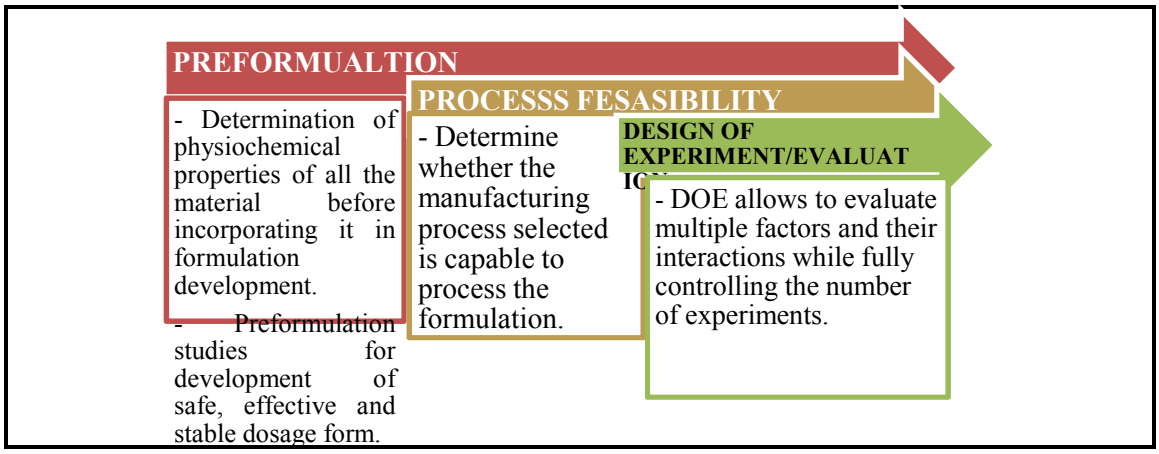

Figure No.1: Design development process and computerized application

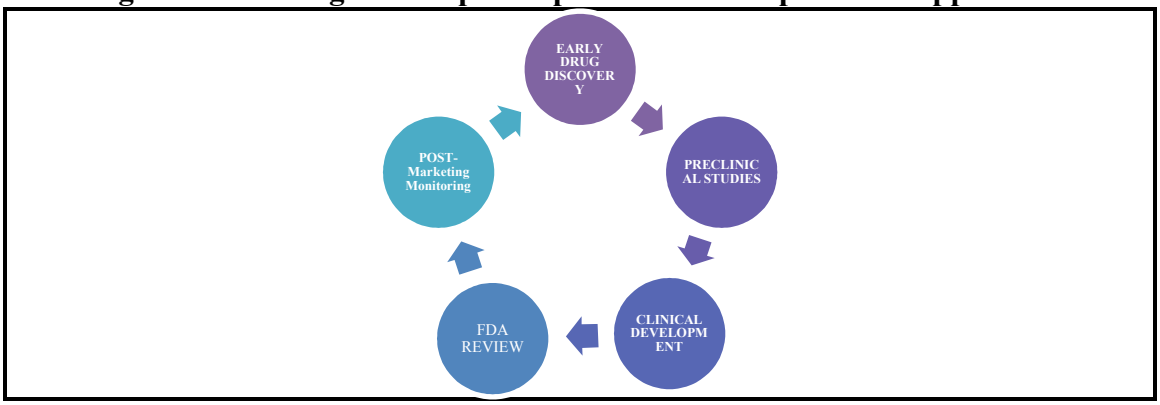

Figure No.2: Phases of drug designing and discovery

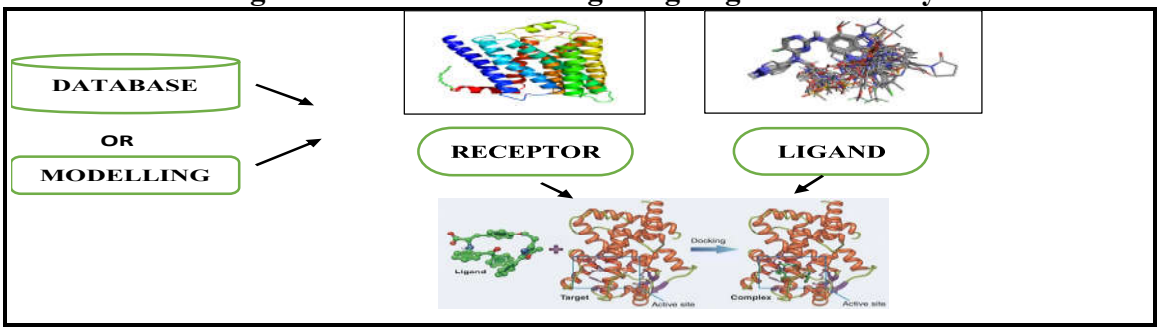

Figure No.3: Ligand-based drug design

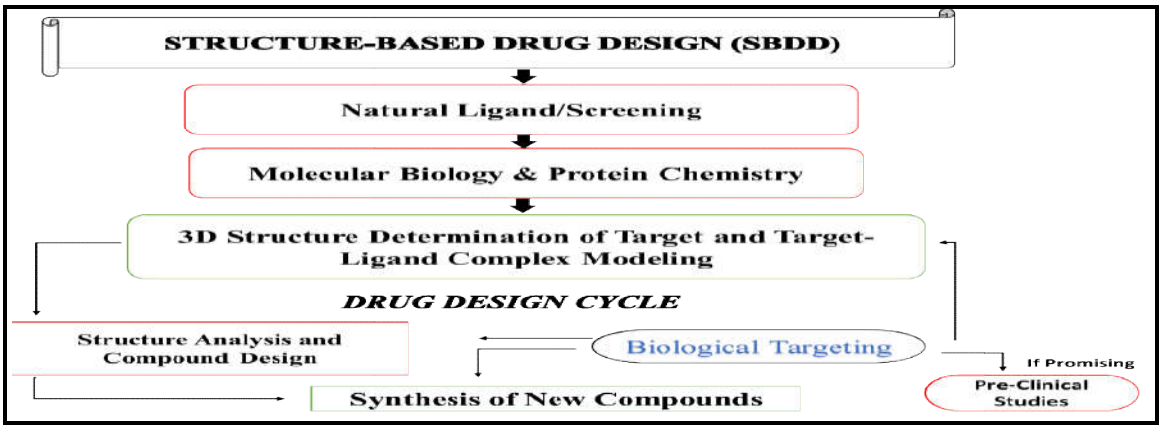

Figure No.4: Structure-Based Drug Design (SBDD)

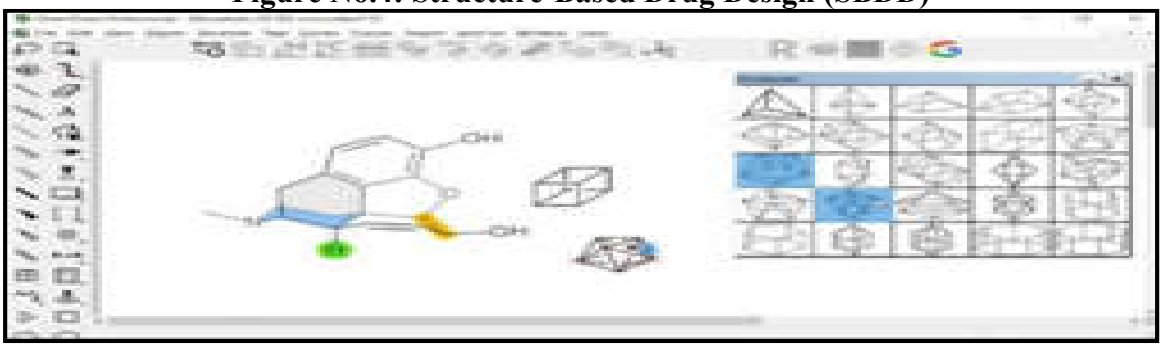

Figure No.5: ChemDraw software view

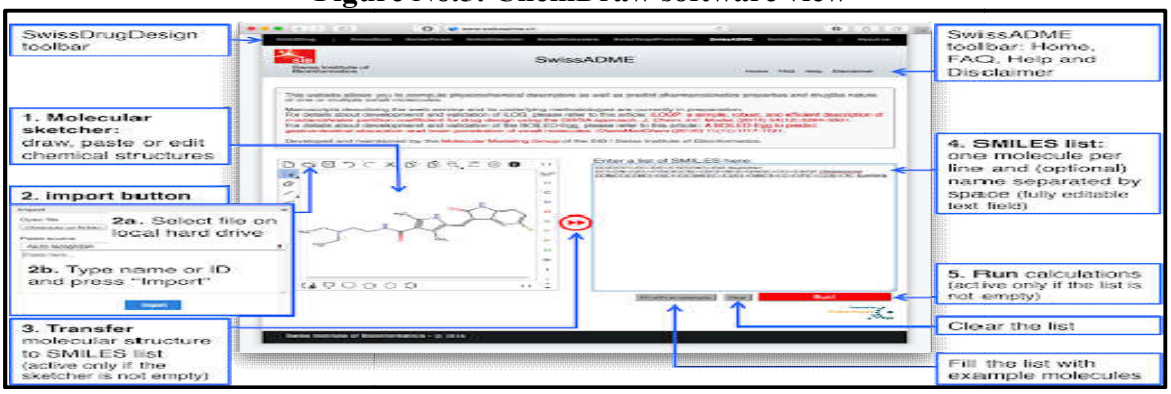

Figure No.6: SwissADME pharmacokinetics

CONCLUSION

In this review, have covered the different software-based approaches that are playing major role in the drug designing and drug discovery now days. The effective use of software-based methodologies gave way to the opportunity to identify physiologically active compounds in vitro utilizing several revolutionary software programmes. Drug design is the process of coming up with new treatments based on an understanding of a biological target. The entire evaluation examined several unique software based on various methodologies that are currently playing a vital role in drug development and drug discovery. In the field of drug research and discovery, computer-aided drug design is a useful tool. A significant part of drug discovery continues to be played by computer-aided drug design due to its numerous successes. In this, a therapeutic candidate against coronavirus disease has been proposed using completely novel software (COVID-19).

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CONFLICT OF INTEREST

We declare that we have no conflict of Interest.

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