

SOFTWARE USED IN DRUG DISCOVERY AND DEVELOPMENT

Abstract

There is a lot of work involved in drug discovery, which includes the design and development of drugs, but only a small number of them make it to market. Over the past three decades, software-based drug discovery and improvement methods have played a major role in the development of bioactive compounds. To study the pharmacokinetic and pharmacodynamics properties of drugs and the structural interest dating between ligand and its target, new software programme based techniques such as molecular modelling, structure-based drug design, structure-based digital screening, lig and interaction, and molecular dynamics are considered effective. As a result of the use of computational methods and docking techniques, hit identification and lead optimization can be achieved. Methods such as this one are more efficient, accurate, and provide valuable information about experimental findings and mechanisms of motion in less time. If these techniques are properly implemented, they could also lead to lower drug design and improvement costs. Nowadays, in biomedical science, these tools play an important role in specific stages of drug discovery. For drug design and development, the most commonly used software is discussed in the study.

Keywords: Pharmacokinetics, Pharmacodynamics, Ligand, docking, drug discovery.

Authors

Syed Ahad Hussain

Department of Pharmacology
JNUTH, Telangana, India

Shariqha Saboor

Department of Pharmaceutics
Kakatiya University, Telangana, India

Zareen Fatima

Department of Pharmaceutical Analysis
JNTUH, Telangana, India

Namreen Fathima

Department of Pharmaceutics
Kakatiya University, Telangana, India

Mohd Salman Ahmed Khan

Department of Pharmaceutics
Anwar ul uloom College of Pharmacy
Telangana, India

I. INTRODUCTION

Discovery and improvement of new drugs with bioactive properties across a wide range of therapeutic areas have been aided in large part by investigation into software programmes and version-based hardware. Drug discovery has been sped up thanks to the widespread adoption of computer-based methods and the elimination of numerous bottlenecks that once hampered the process. Medicinal chemistry methods like molecular modelling and virtual screening, ligand-based modelling, and molecular dynamics are used to understand the pharmacokinetic and pharmacodynamics properties of drugs and the structural interest relationship of ligands with their target, respectively. Ligand-based computer-aided drug designing (CADD) and simulations provide a powerful paradigm for modernizing medical observe design and analysis. To reduce the number of animals needed in preclinical and clinical drug discovery studies, as well as to make it easier to deal with large datasets, these techniques should be implemented.

New drug launch costs about \$1 billion and takes nearly 12 years for a successful drug discovery, development, and launch. Developing a new drug presents a number of significant challenges, including high costs, lengthy development times, high levels of risk, and uncertainty about the results. To address these issues, new and more powerful drug discovery and design strategies, such as computer-aided drug design and molecular docking, must be employed. The most recent review highlights commonly used software for new drug development alongside their potential uses.

II. DRUG DEVELOPMENT, DESIGN, AND DISCOVERY SOFTWARE

As well as categorising software based on its functionality, pharmacokinetic parameters, ligand interactions, molecular dynamics, molecular modelling, structural activity relationship, image analysis and visualisation, information analysis, and conduct evaluation are all subcategories within the broader category of software.

1. Pharmacokinetic parameters pharmaceutical dissolution software

DDD plus: When it comes to in vitro dissolving active pharmaceutical ingredients (API), and formula excipient ingredients, DDD Plus (Dose Disintegration and Dissolution Plus), is a sophisticated generation computer programme that can model and simulate the in vitro dissolving of active pharmaceutical substances (API) and formula excipients under various experimental conditions. The dissolution charge of pharmaceutical dosage forms is critical because the API must be dissolved before it can be absorbed. It is critical to conduct in vitro dissolution testing to screen formulations during development and to ensure batch-to-batch excellent control during manufacturing. Research on biopharmaceutical houses of medicine has been ongoing for more than forty years. Dissolution testing is outlined in all pharmacopoeias, as well as in several tips that have been shared on the internet. Dissolution testing in vitro during drug development is a critical tool for evaluating candidate formulations and for determining potential risks related to specific gastrointestinal factors, capacity for dose dumping, food outcomes on bioavailability, and interplay with excipients. With today's most common equipment, dissolution studies are a vital part of both the formulation development process and the subsequent use of the product.

Five mathematical models and five dosage bureaucracies can be used to explain a single factor dissolving in DDDPlus. The in vitro dissolution simulation is accounted for by the mathematical models used in the simulation Aspects of system components' physics include:

- pKa values, solubility, diffusion coefficient, and density.
- production properties for fast-release medication documentation.
- Each formulation ingredient's particle length distribution.
- For each piece of equipment, there are distinct drift patterns and fluid velocities.
- interactions between the active ingredient and the excipients in the formulation
- Solubility and dissolution/precipitation are pH-dependent in a microclimatic setting.
- Surfactant in the media facilitate micelle-facilitated dissolution.

As a result of its complexity, DDDPlus can be studied and used by people who have a background in system and chemistry. DDDPlus has an intuitive and cutting-edge graphical user interface that allows for a fast and easy transition from inputs to results evaluations. The outputs of single simulations are displayed as real-time on-screen text and images; the outputs of multiple simulations can be stored in Microsoft Excel compatible tab-delimited ASCII text documents. An in-depth look at formulation behaviour under various conditions can be gained through Parameter Sensitivity Analyses and digital Trials, which can help direct experimental efforts toward identifying the most valuable assets for which they will be the most precise.

Advantages

- When building your own system-precise models, you can take advantage of the Optimization Module in DDDPlus to quickly construct models based on your own data.
- In terms of evaluating formulas and devising a dissolution strategy, It is possible to run studies that give the researcher an insight into the possible dissolution behaviours as a result of a diffusion of excipient content material and formulation modifications (e.g., particle size distributions, API amount, quantity of excipients, and pill compression pressure) under an expanse of parameters that can be manipulated
- Projected dissolution's sensitivity to key input factors may be assessed using DDDPlus' Parameter Sensitivity Analysis feature.

2. Gastro Plus is a computer software application

What is GastroPlus software?

Mechanistically-based simulation software GastroPlus simulates intravenous, oral, oral hollow space, ocular, inhalation and dermal absorption in humans and animals as well as biopharmaceutics and pharmacokinetics.

Version parameters can be applied to a single record or multiple records at once. Every time a document is run through this system, a simulation is run and one or more

model parameters are modified. Typically, many iterations can be performed, each with N simulations, where N is the range of information that is used to evaluate expected and found values. The most common weighting schemes make up goal function weighting, which is defined by the end user.

Advantages

- A deeper understanding of a compound's mechanisms can be gained by studying its pharmacokinetic (PK) parameters, plasma and tissue exposure time profiles, and other variables.
- Improved human pharmacokinetics prediction accuracy.
- Because of improvements in the in vitro and in silico data on liver metabolism, tissue distribution, and absorption, the PBPK model has seen an increase in its use.
- GastroPlus calculates local solubility based on the fraction of drug ionised at every compartmental pH in accordance with the Henderson-Hasselbalch relation given a known solubility at any single pH and drug Pka price(s).
- In vivo drug solubility and dissolution are now taken into account in newer versions of the software. (GastroPlus 2012)

Disadvantages

- One of the fundamental obstacles for the broader utility of this model has been the full-size range of input information required.
- Many parameters are needed to accurately model drug biopharmaceutical residence time in the GastroPlus™ ACAT model.
- Parameters such as transit time, pH, extent, duration, and the radii of the corresponding GI vicinity are all examples of "population suggest" values based on published data.
- Additionally, the other input parameters include drug solubility, permeability (logP, pKa, diffusion coefficient), clearance (CL), the quantity of distribution (Yc), the percentage of drug extracted in the oral cavity, intestine, and liver, and so on.

3. Ligand interactions and dynamic molecular processes

Molecular docking: In order to predict the affinity and activity of small molecule healing compounds, docking is widely used to predict the alignment of small molecules with their protein targets.

Docking is a critical part of rational drug design. Many efforts have been made to improve docking prediction algorithms due to the importance of docking research in the organic and pharmacological fields. When two or more molecules are linked together, docking is a mathematical technique that predicts the best possible orientation of one molecule in relation to the other when they are linked together.

III. GOLD

The genetic algorithms GOLD can be used to dock flexible ligands into protein binding sites (Genetic Optimisation for Ligand Docking). GOLD's posture prediction and virtual screening capabilities have been proven after extensive testing. Besides Hermes, GOLD is part of the CSD-Discovery package. Hermes is used to provide GOLD with a user-friendly graphical interface. It is designed to assist in the training of GOLD docking data, visualising docking results, and calculating descriptors.

When the ligands' protonation states are properly set up, GOLD will produce accurate results. Using the information provided, Hermes is able to identify the SYBYL atom types (see Atom and Bond kinds). SYBYL atom types can be configured well enough in modern molecular modelling software to create protein and ligand systems. Prior to docking, the CSD Conformer Generator significantly reduces the amount of ligand entering structures.

There are a plethora of customization options available with GOLD to ensure that it is uniquely tailored to your business and that it makes the most of your data. These options (including scoring criteria, limitations, adaptability and speed) will be explained in detail in this paper.

IV. AUTO DOCK

Ligand interactions with biomacromolecular targets can be predicted using an automated method called "AutoDock" An attempt at computer-aided drug design was sparked by issues with bioactive chemical design in particular. Advances in biomolecular x-ray crystallography continue to uncover important protein and nucleic acid structures. These systems may also serve as bioactive agent targets for the prevention and treatment of ailments in plants and animals, or they may clearly be essential for understanding the fundamental principles of life. How precisely those marketers or candidate compounds interact with their targets is critical to this technique of improvement.

One must choose between two competing demands when designing a docking strategy: the need for a robust and accurate process and the desire to keep computational costs low. For a system to find the lowest possible level of interplay energy, it must explore all available degrees of freedom (DOF) for the machine. A crystallographic refinement is an example of another type of computation that a structural researcher might use, so it must also run on a laboratory computer within the same timeframe. To meet these needs, docking strategies that simplify the docking system have been developed. Fast grid-based energy evaluation and the green search for torsional freedom are the two strategies AutoDock uses to achieve these goals,

Calculations for AutoDock are broken down into multiple steps:

1. Coordinate file preparation using AutoDockTools,
2. Atom affinity precomputation using AutoGrid,
3. Ligands docking using AutoDock and
4. Results analysis using AutoDockTools

- 1. Coordinate file preparation using AutoDock tools:** AutoDock4.2 has been optimised to work with proteins and ligands that contain polar hydrogen atoms, but not hydrogen atoms bound to carbon atoms. For coordinate documents, an extended PDB layout known as PDBQT is used, which includes atomic partial costs and atom sorts. The current AutoDock force field employs a variety of atom types for the most common atoms, including aliphatic and fragrant carbon atoms, and polar atoms that form hydrogen bonds and those that don't. Additionally, PDBQT documents include torsional data statistics. A separate PDBQT document is also created for the coordinates of the protein's unique bendy side chains. It is possible to create PDBQT files from conventional PDB files using the AutoDock gear graphical user interface.
- 2. Atom affinity precomputation using AutoGrid:** Precalculated atomic affinity potentials for every atom type in the ligand molecule being docked are used to predict the docking's power. On this protein, a three-dimensional grid is embedded, and at each grid point, a probe atom is placed. The AutoGrid affinity grids for every atom in the ligand, including carbon, oxygen, nitrogen, and hydrogen, as well as grids of electrostatic and desolvation potentials, are calculated using AutoGrid software. The energetics of a particular ligand configuration is evaluated using grid values in AutoDock calculations.
- 3. Ligands docking using AutoDock:** When it comes to docking, there are a plethora of options. In terms of environmental impact, the Lamarckian genetic algorithm (LGA) is one of the most environmentally friendly options available. Genetic algorithms and simulated annealing are two of the most commonly used methods for docking. Many docked conformations are generated by running several iterations of AutoDock on a common system, and then the expected energy and consistency of results are compared to find the best solution.
- 4. Results analysis using AutoDock tools:** It includes gear for clustering results by conformational similarity, visualising confirmation and ligand protein interactions, as well as AutoGrid-generated affinity potentials and AutoDock equipment for reading the results of docking simulations.

Uses

- A variety of docking techniques, such as blind docking, protein-ligand docking, and so on.
- Additionally, Autodock Vina (Autodock tools) makes it easier to edit proteins and ligands, including making changes to their shape.
- It can also be used to display large or small molecule libraries.
- On both Linux and Windows, it can be accessed without any problems at all.
- Visualizing interactions between the receptor and the ligand can be done using Autodock's user interface (GUI).
- It can be used to look into the docking outcomes.
- PDB to PDBQT conversion is quick and painless.
- For both rigid and pliable docking, it's a useful tool.
- simple digital screening results analysis.

- 5. FlexX:** Programs like FlexX are used to analyse protein-ligand interactions. FlexX also provides an estimate of the binding strength for a given protein and ligand combination. FlexX's first model assumes that the protein is rigid. Thus, the protein must be delivered in a similar conformation to the bound country. In FlexX's docking rules work without the assistance of a guide. However, in some cases, additional information about the ligand or the complex is available. FlexX allows you to manually perform individual steps and then incorporate that knowledge into your computations. It is therefore a great tool for both interactive painting of protein-ligand complexes and screening a large number of potential drugs.
- 6. Schrodinger:** Schrodinger software has a wide range of packages that can address all of the problems that biomolecules will inevitably cause. Progress in molecular dynamics, ligand receptor docking, and biologics have all been made specifically to address these problems as a result of the advances described in this paper. This software can be used to examine the structure-based properties of a molecule, such as its conformational modifications and hydrophobicity.

A high-performance molecular dynamics simulation engine for bimolecular systems is used to verify macrocycles, combining speed and accuracy. These macrocycle atomic actions provide information that can be used to identify form, stability, and energy in this intern. For system setup, simulations, and trajectory reading, Schrodinger provides powerful and intuitive graphical tools.

The molecular dynamics simulations software is used to study a series of stabilised peptides at unique temperatures. According to the circular dichroism melting curves, the predicted α -helical propensities derived from the simulations are correct. Stapled peptides' affinity for MDM2 may be related to the flexibility of key residues in the molecule. For example, these simulations reveal new ways to design and improve effective inhibitors of the α -helical protein-protein interface.

Uses

- Simulated Molecular Dynamics (MD)
 - Quantum Mechanics
 - Binding affinity forecasting
- 7. Bio Suite:** Drug discovery is made easier by combining the power of macromolecular series and structural evaluation with chemoinformatics and algorithms. More than 80 bioinformatics packages are included in the suite's four essential modules, making it one of the few complete bioinformatics suites available.
 - Genome and Proteome collection analysis,
 - 3D structural modelling and analysis
 - computational molecular dynamics simulations
 - via a user-friendly snap shots-user interface and good documentation and tutorials, drug design is made available

As a whole, the four modules of Bio Suite cover a wide range of bioinformatics activities, from genome sequences to individual and multiple protein sequences to structural predictions and analysis as well as molecular mechanics calculations, molecular dynamics simulations, cheminformatics analysis of the sequence and structural analyses, and finally integration with rational drug design.

V. DESCRIPTION OF THE INDIVIDUAL MODULES

The programmes contained in the four essential modules are outlined below in a brief description.

- 1. Genome and proteome collection analysis:** BioSuite's Genome And Proteome series Analysis module includes packages for the analysis of nucleic acid and protein sequences, not only of character molecules, but also of the entire genome and proteome sequences. Researchers could use this module in conjunction with a number of other tools to annotate genomes, predict protein secondary systems, derive a phylogenetic relationship between organisms, and evaluate genomes for similarities at the gene or protein level. There are four sub-modules in this module as well: evaluation of sequences, genome analysis, comparative genomics, and utilities.
- 2. 3D structural modelling and analysis:** The macromolecule and macromolecular complex three-dimensional structure modelling and evaluation module is capable of creating, analysing, and predicting three-dimensional structures. The following sub-modules make up this module: (a) Homology Modeling (b) Threading (c) Proteins building, (d) building Nucleic Acids, (e) building Carbohydrates, (f) generation of Symmetry related Molecules, (g) Structural Superposition (h) Surfaces and Volumes Binding site evaluation, Nucleic Acid evaluation, (ok) interactions, (l) quality assessment, and (m) Fold Detection are the steps included in this analysis: I
- 3. Computational molecular dynamics simulations:** Simulating a molecule in terms of its three-dimensional structure is the goal of the 'Simulations' module. Forcefield, energy minimization, Molecular Dynamics, Monte Carlo simulations, and Electrostatics are just some of the unique sub-modules included. The molecular simulation of a device can be conceptually broken down into three additives: (a) producing a computational description of a biological/chemical machine usually in terms of atoms, molecules and associated force area parameters, (b) the numerical answer to the equations that govern their evolution and (c) the software of statistical mechanics to relate the behaviour of some individual atoms/molecules to the collective behaviour of many.
- 4. Drug design:** QSAR, Pharmacophore identification, Alignment, and Docking are some of the functions provided by the Drug Design module. A set of molecules can be transformed into lead-like molecules using the Drug design module's functionalities, and their activities can be predicted using these modifications. As a result, lead optimization can be carried out in stages. If the desired structure is known, lead optimization can be accomplished using a structure-based approach that includes docking.

VI. MODELLING OF MOLECULES AND SAR

1. **Maestro:** Free and feature-rich, Maestro is a powerful tool for visualising molecular structures. As a powerful tool for analysing and sharing the results of computational experiments you can create and share 3-D chemical models using this tool.

It is impossible for Schrodinger's computer technology to function without Maestro. When used for molecular modelling in computational chemistry, it's a much more powerful and versatile tool. It is responsible for organising and analysing the data that has been collected. The user-friendly interface of Maestro makes it simple to enter calculations. It is automated once more, and the results are then used in projects where they can be observed in the same way. Maestro's wide range of visualisation options makes it possible to gain insight into molecular locations and targeted intermolecular interactions.

2. **GRAMM (global range molecular matching):** Protein docking is done using the GRAMM software programme. The two molecules' atomic coordinates are used to predict the structure. It generates a list of high-score (low-power) ligand positions that can be used as-is or improved upon using various methods. Rather than using statistical sampling, this programme conducts an exhaustive search for all possible configurations of the complicated steric suit with a high-rating coefficient of variation.

An exhaustive six-dimensional search of the molecules is carried out by this software programme. It's possible that the paired molecules are proteins, proteins and a smaller compound, trans membrane helices, and so on. It is used to identify erroneous molecular structures in the context of large-scale conformational shifts.

By altering the number of atom-atom potentials, it is an empirical method to smooth out the intermolecular electricity function Using this method, it is possible to find the area of lowest intermolecular electricity for systems of different accuracy. The quality of a prediction is determined by the accuracy of its shape. This means that a more accurate prediction can be made when docking high-decision systems with small conformational changes and a simpler prediction can be made when docking ultralow-resolution structures.

3. **PASS (prediction of activity spectra of substances):** New pharmaceutical substances can be predicted based on a comparison of existing structures using this software programme. PASS is able to accurately predict 4366 different types of biological activity, with an average accuracy of about 95%.

'Yes/no' or 'lively/inactive' are used to describe the prediction of organic activities in PASS. To better grasp the viability of organic sports, the most recent chemical compound's structure is changed into a 2D structural formula. MNA descriptors provide a PASS representation of the molecule's stucture. In PASS, if the materials have the same MNA descriptors, they are considered equal. Based on Bayesian estimates of molecular possibilities, the pass algorithm for organic interest spectrum prediction predicts active and inactive compounds. For skip prediction, the molecule's structural method is provided as a MOL document.

- **Photo analysis and visualisation: Xenogen living image software:** To create the Xenogen-residing picture software, Wave Metrics IGOR Pro1 was utilised. The software bureaucracy custom environment that is used to collect and analyse statistics. The software is supported by both Macintosh® and Windows®. The running of software includes an acquisition control panel, a photo display and analysis window, a system status and communication window, and a lab book window. the top of the menu bar for each IGOR professional and home photograph software programme contains software tools. During Igor's software strolling, the final menu items that assist home photo software remain inactive to avoid interface clutter and confusion are kept inactive.

When a living photo statistics set is opened or acquired, the software displays a unique picture window show. In the running part of the window, the luminescent or fluorescent photo is overlaid on a photographic image. Unless otherwise stated, luminescent and fluorescent images can be processed using the same software. The analysis tool is a gift at the pinnacle of photo manipulation, allowing you to manipulate the image and its metrics. To show the relationship between the photo's colours and the numerical values of its stats, a colour bar is shown on both sides of the image, on the right side of the image. The bottom of the window shows labelling information generated by both the user and the imaging system that explains how to use the person controls found in the image window.

- **Data analysis: Gene spring:** In the user interface, GeneSpring provides information about terminology used to refer to various organisational factors, as well as a high-level evaluation of the data and evaluation paradigms available in the application.

Samples for which arrays have been run are represented in this software, which is used to answer a specific scientific question new experiment is made up of ventures in this case. a new experiment using data from a particular era and performing common pre-processing steps like normalisation, summarization, and baseline remodel, among others, to prepare the raw data for analysis. this data will then be evaluated. This is a complex experiment that includes a number of samples, a number of interpretations, and a number of other items that were created as a direct result of the numerous evaluation steps that were used in its creation.

A user interface layer, a database, and a document system make up the software. The file gadget is where all of the gadgets are physically kept. In the installation folder, these files can be found in the app/records subdirectory. In order to speed up searches, a database is used to store all annotations associated with the various objects in the file gadget (residences like notes, names, and so on). the relevant items are organised into projects, experiments, and evaluations at the end of the UI layer

Uses

- Batch effect correction.
- Binary Segmentation in a circle.

- Filters to identify LOH events and areas of allelic imbalance that are not related to reproduction.
- Take into account a wide range of standard deviations to arrive at a final conclusion.

4. QSARPro: Useful statistical modelling is used to make fast and accurate predictions about molecular activities and properties that are linked to structural parameters. Over a thousand molecular descriptors, including MMFF atom types, electrostatic and hydrophobic properties, topological and electro-topological properties, facts-based idea evaluation, quantum mechanical, electrostatic and hydrophobic evaluation, are assessed by this company.

As part of QSAR modelling, descriptor selection and calculation, statistical evaluation of the descriptors derived from those calculations, training and evaluation of a set project, regression and effects evaluation are all common activities. It evaluates several options for descriptor classes, sets, linear or nonlinear regression, and regression method to determine which option is best suited to a specific project.

5. Behavioral study

- **Ethowatcher:** It is widely accepted that behavioural exchange is the most important parameter for diagnosing a wide variety of issues. An experimental animal's morphological and physiological adaptations are linked to its complex behavioural patterns. Numerous biological and biomedical disciplines, including ecology, physiology, neurobiology, behavioural genetics, pharmacology, and pathology, routinely monitor these alterations in laboratory and free-ranging animals. Selected behaviours are selectively documented using advanced automated techniques, such as pressure or infrared sensor activation or photograph processing strategies derived from video-tracking analysis. The video-monitoring evaluation of locomotor activity, frequency and time spent ambulating, velocity of motion, and horizontal position can easily gather an array of data.

Ethowatcher is written in C++ and runs on C++ builder 5.0 environments. For 'real-time' behavioural scoring (such as immediately from the ongoing activities within the environment or from analogue video documents) or 'off-line' behavioural recordings, this software is a tool for creating and storing behavioural modifications (from digital video documents). It is possible to extract pastime-related parameters (distance, angle, speed, approximate object location and track graph) using virtual photo processing techniques from the received virtual video document. The software provides time-segmentation reports on the collection of behaviours, duration, frequency, and latency, and also those reports are synchronised through the same clock source.

Uses

- To evaluate the behaviour of laboratory animals is being tested.
- Analysis of video recordings made by lab animals.

VII. CONCLUSION

Software-based methods that are currently playing a significant role in drug design and discovery are included in this review. Methods based on computer software allowed for the identification of biologically active compounds in vitro without favouring known hits or leads. By using new techniques like docking, researchers are uncovering the many mechanisms that underlie complex goal-ligand interactions. It is possible to discover new drugs because of the tremendous advances in pharmacokinetics and pharmacodynamics, as well as the use of cutting-edge technology. As a result, the various biochemical companies' cost problems and difficulties finding new drugs are exacerbated

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