Books 2024-25

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4.	**Book:** Marine Greens **Chapter:** challenges of soil microbioms and food safety **ISBN. : 978- 3-031-71844-1**	Manjunatha B	2024	Chapter in Book	Springer Publishers	25

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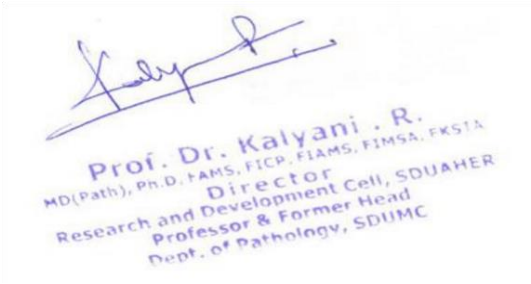

ARTS AND SCIENCE OF SURGICAL GROSSING TECHNIQUES

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Different Tools for Modern Drug Discovery Research

Srinivasan Kameswaran, B. Swapna, Mandala Ramakrishna, Bellamkonda Ramesh, and Manjunatha Bangeppagari

Contents

Abstract The least amount of pharmaceuticals that complete clinical studies makes it to market. Drug discovery, which includes drug creation and development, is a complex and expensive endeavor. Over the past three decades, technologies for finding and developing drugs using software played a significant role in the production of biologically active molecules. The pharmacokinetic and pharmacodynamic properties of drugs, as well as the structural interaction between the ligand and its target that determines how well they work together, can all be examined with the

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help of cutting-edge software-based techniques such as molecular modeling, "structure-based" online testing, a molecule interaction, "structure-based" drug design, and molecular simulation. Through the interactions of tiny compounds with structural macromolecules, computational techniques like docking enable hit detection and lead improvement. These techniques are quicker and more precise, and they offer insightful information on the results and workings of experiments. Additionally, the effective application of these strategies can lower the price of medication developing and development. These software are currently playing a crucial part in the various stages of drug development in the biomedical sciences. The most popular software for medication development and design is discussed in this chapter along with its successful uses.

Keywords Drug discovery · Pharmacokinetic · Docking · Drug designing · Pharmacodynamic · Bioactive compounds

1 Introduction

To find and develop new bioactive pharmaceuticals for a variety of therapeutic indications, the pharmaceutical industry now heavily relies on the use of software and model-based techniques. The process of finding new drugs has sped up, and various obstacles have been lessened with the proper usage of software and computer-based current technologies (Fig. 1). Modern medicinal chemistry techniques, like "molecular modeling," "structure-based drug design," virtual screening using structure, "ligand-based" modeling, and "molecular dynamics," offer helpful "tools" for understanding the pharmacokinetic and pharmacodynamic properties, as well as the structural activity relationship between ligands and their targets (Ferreira et al. 2015; Sliwoski et al. 2014). The use of simulations and modeling, like "ligand-based computer-assisted drug designing" ("CADD"), offers an effective model for modern therapeutic research conception and evaluation (Kimko and Pinheiro 2015; Gill et al. 2016). By using these methods, fewer animals will be required for research and preclinical drug discovery phases, handling large amounts of data will be easier, and study results will be more accurate (Hodos et al. 2016; Liu et al. 2016).

A single new drug's successful discovery, development, and introduction onto the market costs over $1 billion and takes almost 12 years to complete. The main challenges in developing new medications include prohibitively expensive, time-consuming, and inadequate risk, results-ambiguous, and using incredibly complicated processes. To address these challenges, novel and more cost-effective approaches to drug design and discovery—such as "molecular docking," software, and machine-learning drug design—must be used (Hodos et al. 2016; Wasko et al. 2015). This evaluation focuses on frequently used software and its possible applications in the field of novel medication development (Fig. 2).

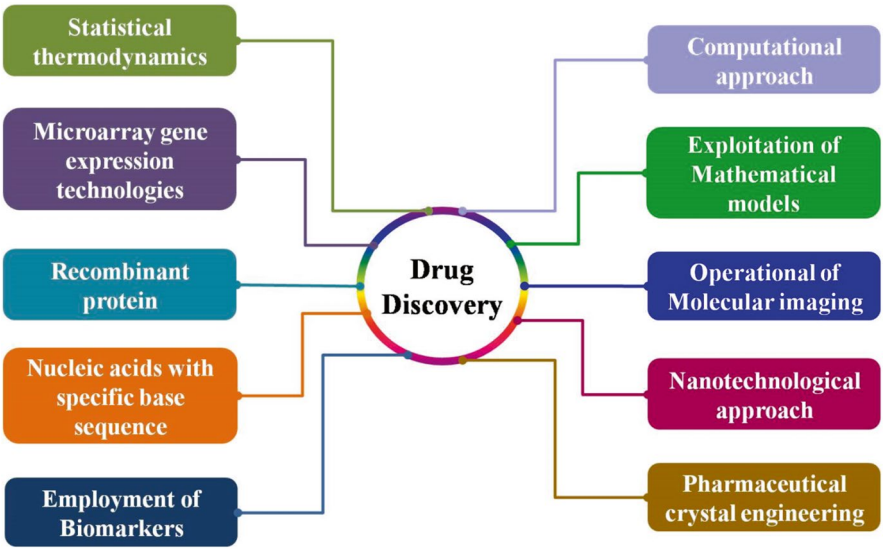

Fig. 1 Modern methods for finding new drugs

Fig. 2 Novel methods and approaches for drug discovery

2 Software for Creating, Finding, and Developing Drugs

Based on the tasks that the software performs and how they work, other categories include software for evaluating "pharmacological parameters," drug connections and "molecular dynamics," "molecular modeling" and "structural activity relationship," visualizations and "visualizers," "data" analyzers, and behavior "analysis software."

2.1 Pharmacokinetic Parameters

2.1.1 "Software for Dose Dissolution and Disintegration," or "DDD Plus"

DDDPlus ("Dosage Disintegration and Dissolution" Plus) is used to study the disintegrating and dissolving pattern of dosage forms and active compounds. Using a complex computer program, formulation specialists simulate the dissolution and disintegration of additives and "API," or "active pharmaceutical ingredients," in vitro under a range of experimental conditions. A single calibration experiment is often needed when formulating a new API. The rate of dissolution is then predicted by DDDPlus based on changes to the formulation or the testing setup. With this program, you may precisely determine the rate of dissolution and disintegration, eliminating the need for conventional "cut" and "try" methods to finish the composition model (Almukainzi et al. 2015; Uebbing et al. 2017; Kollipara et al. 2023).

With DDDPlus, you may choose from five different dosage forms and five different mathematical models that show how a chemical dissolves. The computational approaches used in the in vitro dissolving modeling describe the impact of the following parameters on dissolution:

- Physical and chemical characteristics of the formulation components being examined, including density, solubility, diffusion coefficient, and pKa values
- Producing qualities for dosage formulations with instantaneous release
- The distribution of particle sizes for every ingredient in the mixture
- Various fluid velocities and flow patterns for every experimental equipment
- The interaction between a mixture of ingredients and the drug's active component
- The reliance of the solubility, collapse, and "precipitation" on the pH of the microenvironment

The dissolution of micelles is aided by the addition of surfactants to the media.

2.1.1.1 Applications

- Uses the instrument speed and kind of apparatus to autonomously determine the liquid movement.
- DDDPlus features an optimization module that uses a single experimental data set to calibrate the dissolution rate of a medication.

2.1.2 Drug Development and Discovery Simulation Program, or GastroPlus

GastroPlus is software designed to simulate many absorption routes, including "intramuscular," "oral," "oral cavity," ocular, "intranasal," and "pulmonary," as well as "pharmacokinetic" and "pharmacodynamic" effects in animals and people. Its foundation is mechanistic theory.

It is possible to fit the model parameters to the data for one record at a time or for several records at once. Every time a record is entered, the program does a single simulation and modifies one or more model parameter values. Typically, for every hundred iterations, N simulations will be executed, where N is the total amount of data whose outcomes are compared to the measured results. The most popular weighting strategies are included in user-defined objective function weighting (Honório et al. 2013).

2.1.2.1 Applications

- Interactions between drugs based on transporters.
- Induction of metabolism and/or transporters.
- Associated with the "1-ranked dissolution/absorption (ACAT) model" in the industry.
- When appropriate, use physiological-based pharmacology or "compartmental pharmacokinetics."
- Employ competitively along with dependent on-time inhibitory kinetics for the "parent and/or metabolite."
- Either "simulate DDIs" for humans, beagles, rats, mice, rhesus monkeys, cynomolgus monkeys, rabbits, cats, or any other species.
- Take into account variations in the levels of enzyme expression in different populations.
- An integrated tool for quickly calculating the portion of in vitro experiments that are metabolized.

2.1.3 MapCheck

The results of the ion chamber are compared with the absolute dosage measurements of both systems using MapCheck. It contrasts the Portal Dosimetry from Varian and the MapCheck IMRT QA procedure from Sunnuclear.

The MapCheck system calibrates the diode array, generates an approval strategy for every area, and exports the estimated dose "map" ("Frontal") for every area before collecting data. Plan complexity raises the standard deviation. The average measured dose is not affected by the complexity of the strategy. It is an easy-to-use data analysis program that facilitates the commissioning process and produces thorough reports (Jursinic et al. 2010).

2.1.3.1 Applications

- MapCheck is utilized for verifying IMRT.
- MLC is detected by tiny sensors.
- The use of MapCheck for dose-based EPID IMRT quality assurance.

2.2 Interactions Between Ligands and Molecular Dynamics

2.2.1 AutoDock

An automated tool called AutoDock is used to forecast interactions between ligands and proteins, or biomacromolecular targets. Bimolecular X-ray crystallography is constantly developing, which aids in the provision of structural data for complex biomolecules including proteins along with genetic materials. In addition to being utilized as goals for innovative medications to treat ailments in people, animals, and plants, such frameworks may also be employed to understand fundamental biological principles.

There are several steps involved in AutoDock calculations:

- Using AutoDock tools to prepare coordinate files
- Atomic affinities are precalculated with AutoGrid
- Using AutoDock for ligand docking
- Utilizing AutoDock Tools for outcome analysis

2.2.1.1 Organize the Preparation of the File

AutoDock4.2 has optimized the protein and ligand model to include polarized "hydrogen atoms" rather than "hydrogen atoms" bonded to "carbon atoms." An enhanced "PDB format" called "PDBQT" is used to store collaborative data, including atom charge partials and atomic types. Currently, the "AutoDock force field" for

the most common atoms uses multiple atomic kinds: various varieties of "aliphatic" and "aromatic carbon atoms," and a variety of "polar atoms" that form bonds with hydrogen as well as the ones that do not. The "PDBQT files" additionally contain the "torsional degrees of freedom." When some side chains in the peptide are thought to be flexible, a separate "PDBQT file" is additionally created for those chain locations. With "AutoDock Tools," the visual user experience for "AutoDock," and "PDBQT" files can be generated from standard PDB files.

2.2.1.2 AutoGrid Calculation

Precalculated "atomic affinity" possibilities are used to forecast fast energy evaluation for each type of atom throughout the ligands component getting coupled. Within this three-dimensional protein-embedded grid, an inspection atom appears at every "grid point." An AutoGrid affinity grid has been constructed for each kind of element inside the molecule; these networks primarily comprise electromagnetic and dissolution possibilities as well as carbon, oxygen, nitrogen, and hydrogen. The AutoDock computation uses the grid values to evaluate the kinetics of a particular "ligand" combination.

2.2.1.3 "Using AutoDock for Docking"

For docking, there are numerous techniques. One of the most effective techniques among them is the Lamarckian genetic algorithm (LGA). Genetic algorithms and simulated annealing traditionally accomplish docking. The optimal solution is found by combining the study of the anticipated energy and consistency of data obtained from running AutoDock multiple times, which produces multiple docked conformations for typical systems.

2.2.1.4 AutoDock Tools Are Used for Analysis

Tools for "visualizing confirmations," "ligand-protein interactions," "affinity potentials" produced by "AutoGrid," and grouping results based on conformational similarity are all included in the AutoDock Tools suite of methods for evaluating the outcomes of docking simulations (Rizvi et al. 2013).

2.2.1.5 Applications

- Aromatic ring identification.
- This applies to the investigation of a flexible ligand's conformational states; the ligand-protein interaction is assessed at every stage of the docking simulation using the maps produced by AutoGrid.

2.2.2 Schrodinger

Most of the problems these biomolecules will present can be resolved by using the extensive variety of applications available in Schrodinger software. It focuses on specific developments in biologics, ligand-receptor docking, molecular dynamics, and molecular modeling that were made to address these issues. The "hydrophobicity" and change in conformation of structure can be analyzed with this software, along with other structure-based properties of molecules.

Macrocysteine confirmation for biomolecular systems is carried out using an advanced virtual reality system which includes rapidity and precision. This program provides information about the atomic movements of macrocycles, which is utilized to gain a deeper understanding of energies, form, and durability. For setting up systems, executing simulations, and examining trajectories, Schrodinger offers robust and user-friendly graphical interfaces.

Molecular dynamics simulation software is used to study an array of stabilized folded "α-helical peptides" at various temperatures. The circular dichroism melting curves seen experimentally and the expected α-helical propensities generated from the simulations agreed well. Different stapled peptide binding affinities to MDM2 may be associated with the local flexibility of critical residues. These simulations investigate novel methods for creating "α-helical folded peptides" and creating strong inhibitors of α-helical protein-protein interactions (Kumar et al. 2010).

2.2.2.1 Applications

- Studies using molecular dynamics simulations
- Quantum mechanics
- Estimating binding affinity

2.2.3 Genomics-Oriented "Ligand Docking" or "GOLD"

"GOLD" ("Genetic Optimisation for Ligand Docking") is a genetic approach that makes it easier to dock adaptable ligands with a substance that possesses dynamic "hydroxyl groups." The Cambridge Structural Database's favorable conformations and empirical findings about weak chemical interactions serve as the foundation for the score function used by this software. The balance between GOLD's speed and the accuracy of its forecasts are managed by varying the genetic algorithm's parameter settings. It provides accurate atom typing for both ligands and proteins with dependable findings.

Gold is a component of the GOLD Suite program, which also consists of Hermes and GoldMine. GOLD offers all the capability needed to dock ligands into protein binding sites from prepared input files. The docking results are visualized,

descriptors are calculated, and input files are prepared for docking with GOLD using the Hermes visualization. Protein residues' tautomeric states and appropriate ionization can be defined by adding hydrogen atoms, which can be retrieved from Hermes along with other input data. Additionally, the binding site and constraint settings are defined using the Hermes visualizer in the interactive docking setup. An analytical and post-processing tool for docking findings is called Gold Mine. The creation and editing of initial models will probably be done using GOLD in tandem with a modeling program (Yurieva et al. 2011).

2.2.3.1 Applications

- The genetic algorithm is employed for protein-ligand docking.
- Predicting binding modes.

2.2.4 BioSuite

Algorithms, chemoinformatics, macromolecular sequence analysis, and structural analysis are all used by BioSuite to support drug discovery. Across a large range of "bioinformatics" usage, it provides most of the few all-inclusive packages available. There are 79 distinct programs inside each of the four major sections that comprise it. "Molecular Dynamics Simulations," "Drug Design," "3D Modelling Structural Analysis," and "Genome and Proteome Sequence Analysis" are four of the core parts. Each has an intuitive graphics-user interface, ample documentation, and tutorials.

The BioSuite "Genome and Proteome Sequence Analysis module" handles applications for analyzing protein and nucleic acid sequences, including those of entire genomes and proteomes as well as single molecules. This module would make it possible to annotate genomes, forecast the secondary structures of proteins, determine the evolutionary relationships between animals, and compare two genomes to look for gene or protein similarities.

Building, analyzing, and forecasting the "3D structures of macromolecules" and "macromolecular complexes" are all possible with the 3D modeling and analysis module. The "Simulations" package successfully simulates a molecule's behavior in terms of its 3D form (NMITLI-BioSuite Team 2007; Bhattacharya et al. 2023). The following structural functionalities are available through the drug design module:

(a) To forecast the biological functioning of unidentified compounds, use QSAR.
(b) Discovery of pharmacophores with physiologically interacting compounds.
(c) Molecular set superimposition in three dimensions using alignment.
(d) Docking is used to identify the ligand's posture in three dimensions when it binds to a target.

2.2.4.1 Applications

- Studying sequences and genomes.
- Comparative genomics, 3D modeling, simulation, structural alterations, drug design, route modeling, and SNP analysis.

2.3 Structure-Activity Connection and Molecular Modeling

2.3.1 Maestro

A fully functional molecular visualization program is available for free called Maestro. For managing, sharing, and analyzing the outcomes of computer experiments, Maestro is an effective tool. Creating, displaying, and exchanging three-dimensional chemical models are made easier with its aid.

The foundation of Schrodinger's computational technology is Maestro. It is an effective and adaptable tool for computational chemistry molecular modeling. It oversees the gathering, organizing, and analysis of data. Calculations are simple and easy to set up because of Maestro's user-friendly interface. Projects requiring additional research automatically receive the computed results back. Gaining knowledge of detailed intermolecular interactions and molecular characteristics is made feasible by Maestro's extensive visualization options (Sabitha and Habeeb 2011; Hussain et al. 2023).

2.3.1.1 Applications

- Analysis of structures quantitatively.
- Molecular properties, electron density, and vibrational modes can all be visualized.

2.3.2 ArgusLab

The genetic modeling, imagery, and formulation program "ArgusLab" are available for Windows operating systems. Using an MS window-operated system PC, a kinematic study, like a geometrical optimization study, was performed using ArgusLab.

This program helps with the calculation of possible energy sources, molecular shapes, geometrical improvement, "atom coordinate vibration frequencies," "bond length," "bond angle," and "reaction pathways." It is based on the ideas of quantum mechanics. ArgusLab uses the geometry convergence function to get the least potential energy (Naz et al. 2009; Mathew et al. 2012).

2.3.2.1 Applications

- Calculations for molecular docking.
- It is utilized in the building of compounds.
- Molecules are constructed utilizing a model design.
- For the package of molecular modeling.

2.3.3 "Global Range Molecular Matching" or "GRAMM"

Proteins docking are performed using GRAMM software. By utilizing the two molecules' atomic coordinates, it makes structural predictions. It generates a list of high-score (low-energy) ligand locations that can be used directly or subsequently processed using different methods. Instead of using statistical sampling, this software conducts a thorough search to find any complex configuration that has a high-score steric fit.

Through the molecules' relative translations and rotations, this software does a thorough six-dimensional search. The molecular pairings could consist of two transmembrane helices, two proteins, or a protein plus a smaller molecule. When there are significant conformational changes, it is employed to obtain high-resolution molecules for erroneous structures.

The intermolecular energy function is empirically smoothed using this method by varying an array of "atom-to-atom" abilities. The method determines the region with the world's lowest level of "intermolecular energy" for structures with different levels of precision. Prediction accuracy determines prediction quality. "High-resolution" models with few structural modifications can be docked to generate accurate predictions, as "ultralow-resolution" models will only generate the overall properties of the complex (Kundrotas and Vakser 2010; Devi and Mikilli 2013).

2.3.3.1 Applications

- It is employed in protein-ligand and protein-protein docking.

2.3.4 "SYBYL-X Suite"

"SYBYL-X" offers knowledge to help comprehend and assess different SARs to every one of the requirements that a suitable medicine candidate must meet. Using the analytical powers of the novel "Molecular Data Explorer" ("MDE") in "SYBYL-X," it quickly gains insights into data by examining and visualizing connections between various properties. The unmatched is extended while offering fresh perspectives on life science molecular discovery efforts.

SYBYL-X explores multiple aspects of the drug interaction mechanism with its receptor, hoping to uncover novel interaction mechanisms that could result in step

leaps in potency or ways to enhance ADME or physical qualities without disrupting critical receptor connections (Dubey and Kalra 2013; Xu et al. 2014, 2023).

SYBYL-X enables anyone to:

- Create a three-dimensional homologous or skeletal model of the intended receptor.
- Define the features of the target protein's cavities and the surface where the protein interacts with the ligand.
- Use the docking software Surflex-Dock to anticipate and rationalize possible drug interactions with its receptor.
- Build libraries of snippets so that you may virtually filter them to locate useful bits. After such pieces are identified, either construct forms out of them or build a database of forms that can be inserted into an immune system aperture.
- To identify possible lead candidates, use "Surflex Dock" to virtually scan data that comprise proprietary or widely accessible compounds.

2.3.4.1 Applications

- Lead optimization to molecular modeling from the sequence.
- Design based on ligands.
- Design based on structure.
- A protein model can also be constructed using the SYBYL-X Suite.

2.3.5 "Sanjeevini"

The goal of this computer programming project is to provide an automated computing path for result designing. It makes use of a candidate medication and a bimolecular (protein) target. Potential active sites are located, docked, and scored, and four alternative medicine structures attached to peptide targets in addition to attaching liberated energies are returned using the software.

This software is used to upload the target protein and pharmaceutical molecule. The software opens a window with the results of several crucial pretests that were conducted based on the specifications required for the medication and protein files to be in an acceptable format when the file is uploaded. The software includes modules for "protein-ligand" complex synthesis, drug formulation, docks and assessing, and other functions (Jayaram et al. 2012; Singh et al. 2021; Alavi and Sharma 2023).

2.3.5.1 Applications

- It serves as a tool for creating drugs.
- It forecasts the affinity for binding.
- Estimating the affinity of protein-ligand binding.

2.3.6 Prediction of a Substance's Activity Spectrum, or PSAS

By comparing a database of existing structures, this software forecasts the potential biological activities of a novel pharmacological compound including a lead molecule. Averaging almost 95% of its predictions, PSAS predicts 4366 distinct kinds of biological activity. The biological activity prediction in PSAS is described in a qualitative "yes or no" or "active or inactive" manner. To find possible biological activities, a novel compound's structure is converted into two-dimensional structural equations. The molecular structure in PSAS is represented by the set of unique "MNA descriptors." Compounds with an identical array of "MNA descriptors" are considered similar in PSAS. Bayesian estimations of the likelihood of molecules falling into the groups of active and inert substances, respectively, form the basis of the biological activity spectrum prediction system known as PSAS. A "molecule's structural formula" can be found in a MOL file, which is used to do PSAS predictions (Pramely and Raj 2012; Azhaguraj et al. 2012; Islam et al. 2022; Talebi et al. 2023).

2.3.6.1 Applications

- Disclose novel effects and modes of action for compounds that are well-known in business and private databases.
- Find fresh leads based on particular biologically active features among the compounds in commercial and internal databases.
- Select the compounds with the most potential for a rapid screening process from the given samples.

2.4 Visualizers and Image Analysis

2.4.1 "A Medical Image Data Examiner" or "AMIDE"

The goal of AMIDE's development was to offer multimodality volumetric medical picture analysis. To allow a limitless amount of such components to be exhibited, changed, and evaluated at the same time, regions of interest (ROIs) and data sets (such as PET, CT, and MRI) are logically placed inside the framework of trees.

A tree abstraction made up of a series of items, including data sets and ROIs, serves as the foundation for AMIDE's data structure. This native data structure is located about the world data structure, and every item in "AMIDE" has an "Euclidean space" given to it (Loening and Gambhir 2012; You et al. 2022). The aforementioned types of objects are executed in AMIDE.

- Analyze the "AMIDE" root object, which functions to monitor variables that affect the entire study and arranges a set of related ROIs and medical images within an organized body.

- This data collection, which is used to encapsulate volumetric medical images, contains the raw picture data as well as the information needed to analyze it.
- A portion of a region designated for statistical computations is known as a "region of interest object" (ROI). Currently, ellipsoids, boxes, cylinders, and contours (two or three dimensions) are employed as ROIs.
- Fiducial reference markers: These are employed for rigid body registration of data sets, and they only encode a place in space.

2.4.1.1 Applications

- Offers the community studying molecular imaging research multimodality medical picture analysis
- Creates complex medical imaging techniques (such as factor analysis and heart polar maps) with interactive "wizard" interfaces

2.4.2 Visualizer for Discovery Studio

With "Discovery Studio Visualizer" ("DS Visualizer"), one may view, exchange, and analyze data related to proteins and small molecules. It is available for free and can be applied to both small and macromolecule applications.

It makes data analysis and transfer possible in a variety of formats, including images, 3D structures, SMILES, and sequences. You can get the necessary sequence and structures from PDB or NCBI. Through structure modification and computational work, molecular characteristics can be investigated (Rizvi et al. 2013; Sharma et al. 2022; Baroroh et al. 2023).

2.4.2.1 Applicability: Visual Aid

- Sophisticated visuals of molecules
- Graphics of publication quality

Macromolecule design:

- Editing protein sequences with many domains, such as antibodies.
- Secondary structure prediction.
- Modify and overlay protein structures.

Ligand-oriented architecture:

- Tools for sketching and assembling pieces
- Pharmacophore creation
- Adaptable cover ligands

Design based on structure:

- Identify, highlight, and modify ligand-binding sites.
- Draw 2D interaction graphs between ligands and receptors.
- Keep an eye on interactions that do not include bonds, such as satisfied, unsatisfied, and favorable encounters.

Exhibit several different molecular surface characteristics, such as:

- Charge, solvent accessibility, lipophilicity, ionizability, aromaticity, and H-bonds.
- Use ActiveX Control to see 3D molecules on websites and in Microsoft Office©.
- Record and distribute scenes using "Storyboard."
- Get access to heat maps, 2D and 3D charts, and more.

2.4.3 SCGE-Pro Imaging Software

Comet test and single-cell gel electrophoresis are two common uses for SCGE-Pro. We are working with the Computer Division to develop "imaging software" for "cytogenetic" and DNA repair analysis. The gene toxicity of factors from the environment such as chemicals, medicines, elevated and decreased "LET" radiation, and carcinogens is investigated using the comet assay. One imaging method that quantifies "loss of heterozygosity" ("LOH") for a "single gene" or "gene-specific repair" concerning "total DNA" is "fluorescence in situ hybridization" ("FISH"). These experiments investigate the process of "eukaryotic cell" healing as well as "intracellular DNA damage" with different types of cells. The influence of "3.3 MeV proton beams" on "DNA damage" in rat "leukocytes from the peripheral blood" is one study that uses the neutral comet test (Chaubey et al. 2001; Qian et al. 2021).

2.4.3.1 Applications

- Clinical applications include genetic instability, diabetes, cancer susceptibility, prenatal diagnostics, and DNA repair deficiency syndrome.
- Human biomonitoring: nutrition and aging.
- Aquatic or terrestrial environmental biomonitoring settings.
- Assessing the genotoxicity of chemicals and radiation using animal and human models.
- Agricultural sciences, radiation biology, clinical, and molecular epidemiology.

2.4.4 Software for Xenogen Living Images

"Wave Metrics IGOR Pro1," an efficient statistical analysis and computer device, is used by "Xenogen Living Image Software." The program creates a unique environment that is used for data collection and analysis. The software functions on both

Macintosh® and Windows®. Among the software's functional elements are a lab book window, a visual projection and interpretation window, an entire system condition and communication window, and an image acquisition control panel. The "Living Image" and IGOR Pro software tools are situated in the upper section of the "menu bar." To prevent interface clutter and confusion, the remaining menu items supporting Living Image software stay dormant while Igor Pro software operates.

A distinct image window display is displayed by software when opening or acquiring a Living Image data collection. The operable portion of the window overlays a luminous or fluorescent pseudo-color image on top of a photographic image. Unless otherwise noted, the software operates similarly for fluorescent and luminous images. The analysis tool that controls how the image is shown and measured is located at the top of the image. The image's right side features a color bar that illustrates the correlation between the image's pseudo-colors and its numerical data values. At the bottom of the window display, labeling information produced by the imaging system and the user together describes how to utilize each of the various controls in the image window (Xie et al. 2007).

2.4.4.1 Applications

- Applications for in vivo imaging
- Imaging at low light levels, including binning and sensitivity, calibrations and measurements, light sources in the background, and "dark charge management"

2.5 "Data Analysis"

2.5.1 GeneSpring

GeneSpring offers an overview of the info and analytical models that are accessible in the program, as well as definitions of terms related to important organizational features in the user interface.

Utilizing arrays to test hypotheses related to a certain scientific subject, this software represents a set of samples. Out of a chosen project, a fresh experiment is made in this. In a new experiment, specimens of a specific method are loaded and put through several common preliminary processing steps, including normalization, summarization, and baseline transformation, to retrieve the raw data in a format that is ready for analysis. The experiment that gave rise to it contained several samples, multiple interpretations that categorized the samples according to user-specified experimental criteria, and all additional objects that were produced as a consequence of different analysis stages in the experiment (Dey et al. 2023).

The three components of the software are the file system, database, and user interface layer. All objects are physically stored in the file system. These are kept in the installation folder's app/data subdirectory. All annotations (searchable attributes such as names, notes, and other details) connected to different file system objects

are stored in an SQL database, which facilitates quick searches. Ultimately, pertinent objects are arranged into projects, experiments, analyses, etc. via the UI layer (Trivedi et al. 2023).

2.5.1.1 Applications

- Correction for batch effects
- Segmenting binary circles
- Filters for region of allelic imbalance and copy-neutral LOH events identification
- Find recurring patterns in a collection of samples

2.5.2 "QSARPro"

Using reliable statistical modeling, this program determines the relationship between a molecular activity or property and architectural factors, examines the association, and generates predictions quickly. Approximately 1000 molecular descriptors are evaluated with it, including physicochemical, electro-topological, topological, information theory-based, electrostatic, quantum, hydrophobic properties, MMFF atom types, etc.

Common tasks related to QSAR modeling include characteristic collection and estimation, empirical assessment for the calculated descriptions, assigning test and training groups, regression analysis, and outcomes analysis. To find the solution most suited for a given project, it evaluates several alternatives for test set, regression approach, linear or nonlinear regression, and classes of descriptors (Hung et al. 2014).

2.5.2.1 Applications

- Learn about and practice a range of variable selection and regression technique combinations.
- Creating a base for the ligand's position by lining up a specific group of atoms in the peptide that are active in the "co-crystal" molecule.
- Protein-protein interaction studies.

2.5.3 REST 2009 Software

REST 2009 Software is one program that can be used to analyze data on gene expression using qRT polymerase chain reaction investigations. Gene expression of reference genes is employed in compared gene activity analysis or quantification to standardize the activity levels of "genes of interest" (GOI) across different samples. This technique makes it possible to modify quantitative PCR data, for instance, to account for changes brought on by variations in sample loading.

The PCR efficiency of the reference genes and the gene of interest vary, and this software accounts for this variation using a mathematical model. When one reference gene is compared to several reference genes for normalization, the reliability of the results is increased (Ismail et al. 2011).

2.5.3.1 Applications

- Analyze whether there is a discernible difference between the samples and the controls.

2.6 Behavioral Study

2.6.1 Ethowatcher

Changes in behavior are thought to be a key indicator for diagnosing a variety of diseases. An experimental animal's complex behaviors are linked to changes in its morphology and physiology. These changes are commonly seen in the lab or "free-ranging animals" for a variety of biochemical or biological research-related causes, such as "ecology," "physiology," "neurosciences," "psychology," "genetics," "pharmacology," and disease. Advanced automated techniques capture specific behaviors indirectly by detecting their impacts through the use of "pressure" or "infrared" sensor activation or "image processing" techniques like those employed in the "video-tracking analysis." It is easy to collect a variety of data using video-tracking analysis, including variations in mobility action, including the duration and frequency of walking, movement velocity, and horizontal position.

C++ is the foundation of Ethowatcher, which runs in environments with C++ Builder 5.0. With the help of this integrated application, users can create and save behavioral changes for "offline" behavioral recordings (from digital video files) or "real-time" behavioral scoring (from analog video files or events occurring in the environment). The obtained digital video file can be processed using digital image processing techniques to automatically extract parameters (the length traveled, direction, speed, estimate target region, monitor plot), along with enabling subject (biological) monitoring. The software provides reports that are time-segmented and synchronized with identical timing sources. The reports cover the activity-related indices, sequence, length, rate, and length among the measured behaviors (Junior et al. 2012).

2.6.1.1 Applications

- Approval of an instrument for analyzing behavior in experimental animals.
- Analysis of laboratory animal video-tracking.

2.6.2 "Multimodal Animal Rotation System" or "MARS"

The entire 360° range of motion of an experiment animal is recorded via the Multimodal Animal Rotation System or MARS. Because of the software's clever design, tracking all the pertinent chemical and anatomical data of the experimental animal involves simply rotating a mouse to the appropriate locations or angles. Optical signals produced by the experimental orientation are also captured.

With this program, multimodal and multispectral data sets may be automatically co-registered and captured from all angles of acquisition. The program measures the ideal image or exports the whole rotation movements or video, increasing the resulting signal sensitivity. A co-registration program, multimodal visualization, and animal rotation device are all included in this software (Buehlmann et al. 2020).

2.6.2.1 Applications

- Cell monitoring
- Activities of enzymes
- Illness of the bones
- Infectious illness
- Monitoring and delivery of nanoparticles

3 Conclusion

The numerous software-based approaches that are currently being widely used in drug design and discovery have been addressed in this chapter. Without favoring known hits or leads, the effective application of software-based approaches made it possible to identify biologically active compounds in vitro. The various mechanisms underlying the complex target-ligand interaction are also being unlocked with the aid of novel techniques like docking. Drug discovery has benefited from the significant advancements and ongoing use of new software in the fields of pharmacokinetics and pharmacodynamics. The many biochemical industries' financial problems and drug discovery are improved by this intern. The most compelling proof that programmable and computer-aided methods will be employed to assist the costly, intricate, and very challenging process of designing and discovering new drugs will come from several previous drug examples, including the HIV viral enzyme inhibitor indinavir, which was discovered through software-based drug discovery.

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PPKPCON04

SERUM BIOMARKERS FOR PAIN IN KNEE OSTEOARTHRITIS: A REVIEW OF CURRENT EVIDENCE AND FUTURE DIRECTIONS

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oduction: Osteoarthritis of Knee (OA) is one of the major causes of chronic and impairment. While radiographic severity often correlates poorly with perception, serum biomarkers have emerged as potential objective cators of pain in knee OA. Understanding these biomarkers may improve assessment, early diagnosis, and guide targeted therapies.

Methods: A comprehensive review of peer-reviewed studies from major databases (PubMed, Scopus, and Web of Science) were conducted, focusing on biomarkers linked to pain in knee OA. The search included studies investigating inflammatory markers and cartilage degradation products.

Results: Several biomarkers have shown associations with pain severity in knee OA. Pro-inflammatory cytokines like interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF-α), and C-reactive protein (CRP) have been linked to pain sensitization and inflammation. Cartilage degeneration markers such as cartilage oligomeric matrix protein (COMP) and C-terminal telopeptide of type II collagen (CTX-II) correlate with pain progression.

Conclusion Serum biomarkers offer promising insights into the pathophysiology of pain in knee OA. Although they provide a more objective assessment of pain, further research is needed to validate their clinical utility, establish standardized thresholds, integrate them into personalized pain management strategies. Exploring multi-biomarker panels is also essential.

Clinical Relevance: Serum biomarkers are emerging as quantifiable outcome measure that can provide insight into pathological conditions and help plan effective therapeutic intervention and prognosis.

Keywords: Knee osteoarthritis, pain biomarkers, serum biomarkers, inflammation, cartilage degradation

PKPCON11

EXERCISE FOR POSTPARTUM PELVIC GIRDLE PAIN: SCOPING REVIEW

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Introduction: Pelvic girdle pain (PGP) defined as "pain experienced between the posterior iliac crest and the gluteal fold, particularly in the vicinity of the sacroiliac joint (SIJ)". The pain radiates to the posterior thigh and can occur with pain in the symphysis. Exercise intervention can be implemented to address the joint laxity and pelvic instability by building support to pelvic.

Aim: This study aims to summarize the effect of exercise on postpartum pelvic girdle pain.

Methodology: The electronic database used in this review were PubMed and google scholar. The search was carried out using the terms Postpartum, postnatal, pelvic girdle pain, postpartum pelvic girdle pain, exercises, exercise

Result: Total of 13 articles were yielded and screened in the following order i.e., title, abstract and full article screening. Screening was done based on inclusion and exclusion criteria. Inclusion criteria: articles addressing exercise for postpartum pelvic girdle pain, type of studies: RCT and systematic review, studies published in English language. Exclusion criteria: studies done on antenatal mothers, animal study. Six articles met the inclusion criteria were included in the study

Conclusion: There is significant improvement after exercise in postpartum pelvic girdle pain, quality of life. However, the gaps in the research remain in terms of standardized protocol, using appropriate assessment tool and improving accessibility for physiotherapy services among postpartum mothers.

Clinical implication: Exercise therapy should be implemented in day-to-day practice in clinical set up to address postpartum pelvic girdle pain.

Keyword: postnatal mothers, postpartum pelvic girdle pain, exercises

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PPKPCON08

EFFECT OF MCKENZIE EXERCISES ON H REFLEX IN LUMBAR RADICULOPATHY

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Introduction: Pain which originates from the lumbar spine and radiates down to either one or both legs can be described as lumbar radiculopathy. McKenzie exercises are among the commonly used treatments for lumbar radiculopathy by physiotherapists. Recently, to assess the neurophysiological changes in compromised nerve root and to judge the efficacy of lumbar radiculopathy management techniquesneurophy siological testing, especially H-reflex, has been used. Investigation of patients with unilateral lumbar radiculopathy has found asymmetry in H reflex amplitude, increased threshold, increased latency and a decrease in the slope of the H-reflex when compared to the unaffected side.

Aim and Objectives: To understand if Mckenzie exercises can normalize H reflex parameters in lumbar radiculopathy.

and used McKenzie exercise as intervention. Exclusion criteria- Studied that added any other special intervention along with McKenzie exercise and animal studies. Original search revealed 12 Studies, after screening 5 studies were included into the literature review. Findings of the studies were synthesized and analysis of results was done.

Results: Among the studies included, 2 studied were of level 2 evidence and 3 were level 3 evidence. All the studies noted an abnormal H reflex findings on the affected side among the patients. 3 studies showed a statically significant reduction in H reflex latency and threshold reduction, and concluded that Mckenzie exercise can significantly normalize the H reflex parameters. 2 studies indicated that there was no significant change in the H reflex findings with McKenzie exercises.

Conclusion: The effect of McKenzie exercise on H reflex is conflicting, more long-term follow-up studies are required to prove if Mckenzie exercise can alter of H reflex parameters.

Clinical Relevance: There is inadequate evidence suggesting McKenzie exercise can alter neurophysiology in nerve root compression in patients with lumbar radiculopathy.

Keywords: Lumbar radiculopathy, H reflex, McKenzie exercise, spine extension exercise.

OPKPCON06

INTERPROFESSIONAL SKILLS IN TELEHEALTH SIMULATION AMONG HEALTH SCIENCE INTERNS: AN OBSERVATIONAL STUDY

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Introduction: Telehealth (TH) has transformed healthcare by integrating professionals and services to enhance access and care quality. Evidence suggests that interprofessional (IP) simulation-based training fosters collaboration, improves communication, and enhances patient safety. Despite theoretical support for IP telehealth simulation, empirical studies on its effectiveness in education are scarce. Research varies in methodology and outcomes, limiting comparisons. This study addresses the gap by examining three healthcare

disciplines—Medicine, Physiotherapy, and Audiology & Speech-Language Pathology—to provide insights into IP dynamics in rehabilitation-focused TH education.

Objective: To evaluate IP collaboration among healthcare students during telehealth simulation training, focusing on role clarity, communication, teamwork, problem-solving, and conflict management. To assess the effect of didactic education on TH knowledge.

Methods: Following ethical clearance (SDUAHER/KLR/CEC/Collaborative project/06/2024-25), 50 participants consented and enrolled for the activity, who were divided into 10 groups. Each group consisted of 5 interns from all the 3 disciplines. The training was conducted in two phases. Phase one: Participants engaged in flipped classroom sessions that included a video lecture. Phase Two: Participants, comprising interns from Medicine (MBBS), Physiotherapy (BPT), and Audiology & Speech-Language Pathology (ASLP), were grouped and given a simulation scenario to interview a standardized patient. Objectives and guides were provided to ensure structured engagement. Phase 1 & 2 was spread out for duration of 3 weeks. The sessions were recorded, and outcomes were assessed using the Modified Interprofessional Collaborator Assessment Rubric (Mod. ICAR).

Results: Paired t-test showed $p > 0.001$, indicating no significant changes in knowledge. MICAR scores did not meet expected IP skill levels ($p > 0.001$). Discipline wise MICAR Mean scores (±SD): MBBS: 4.70 ± 0.44; BPT: 3.81 ± 0.75; B. ASLP: 3.89 ± 0.90.

Conclusion: This study showed no significant changes in TH knowledge levels of the health care interns through a didactic recorded flipped classroom. Participants showed acceptable levels of knowledge in general TH concepts and poor levels in specific TH concepts. Healthcare interns across the 3 disciplines showed below expected levels of IP skills. The participants did not show expected levels of IP through collaboration, role clarity, communication, patient centred care, team work, conflict management during TH simulation activity.

Clinical Relevance: These findings support the integration of structured interprofessional skill

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Revolutionising Health Professional Education: The Power of Interactive Tools

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ABSTRACT

Background: Interactive tools have gained popularity in health professional education due to their potential to enhance active learning, engagement, and learning outcomes. Effective use of these tools can lead to improved patient care and healthcare quality. However, existing literature lacks comprehensive insights into their optimal implementation across different healthcare settings and disciplines, as well as strategies to ensure accessibility and inclusivity for diverse learners.

Objective: This narrative review aims to address these gaps by exploring the impact of interactive tools on learning outcomes and knowledge retention, evaluating their effectiveness across various healthcare disciplines, comparing different tools for specific educational purposes, and identifying best practices for curriculum integration while ensuring accessibility and inclusivity.

Methods: A comprehensive search of electronic databases (MEDLINE, Embase, ERIC) was conducted to identify studies published in English from 2010 to 2021. The selection process included systematic reviews, randomised controlled trials, qualitative studies, cohort studies, and cross-sectional studies, while excluding studies in other languages and case reports. The inclusion and exclusion criteria were applied systematically to ensure methodological rigour. Data from selected studies were synthesised narratively.

Results: Interactive tools have demonstrated significant benefits in promoting active learning and student engagement, leading to improved knowledge retention. Specific tools, such as simulation-based learning, virtual patient cases, and gamification strategies, have shown varying levels of effectiveness depending on the educational context. Their successful implementation requires clear learning objectives, structured integration into curricula, and appropriate

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INTRODUCTION

Transverse myelitis is a rare neurological condition affecting the spinal cord (1). The term "Myelitis" simply refers to the inflammation of the spinal cord and the term "Transverse" describes the position of the inflammation, that is, across the width of the spinal cord (2). It is a rapidly progressive autoimmune disease that results in demyelination of the spinal cord, with symptoms that develop within hours to days and progressively worsen over a period that can last up to several weeks (3,4). In most instance, the exact trigger for the inflammation remains unknown (5). But there are several potential causes for transverse myelitis and the causes can be broadly divided into idiopathic which is the most common cause, post infectious like West Nile virus, herpes viruses and HIV, systemic inflammation that have an association with lupus erythematosus and rheumatoid arthritis, or multifocal central nervous system diseases that includes multiple sclerosis and neuromyelitis optica spectrum disorders (6,7). Neurological symptoms are prominent and include motor, sensory and autonomic dysfunction. Depending on the level of the spinal cord involved, motor symptoms such as paraparesis, which mostly affect the lower limb, can also affect the upper limb (8). Sensory symptoms include pain, dysesthesia and paresthesia. Autonomic features include bladder and bowel incontinence and sexual dysfunction (6,9). The incidence of Transverse Myelitis is 1-8 per million people with peak rates from 10-19 years and 30-39 years without specific etiology (6,10). The incidence of Acute Transverse Myelitis has been estimated to be between 1.7 and 2 per million children per year. Within the pediatric population, idiopathic myelitis has been more frequently reported in children under 5 years and over 10 years of age (7,11). The recommended investigations for transverse myelitis include a MRI of the spine and brain, both with and without gadolinium contrast, to help distinguish between compressive and non-compressive lesions and evaluate for brain lesions. Lumbar puncture for CSF analysis (cell count, protein, glucose, VDRL, oligoclonal bands, IgG index, cytology).Blood tests: anti-AQP4-IgG, anti-MOG, B12, methylmalonic acid, ANA, Ro/SSA, La/SSB, syphilis serologies, HIV antibodies, TSH, and viral tests as needed (6,12) However, the recovery ranges from patient to patient, with approximately one third experience complete recovery, another one third have mild residual deficits and the remaining third remain severely disabled. Consequently, rehabilitation plays a crucial role in the management of transverse myelitis, particularly in severe cases requiring a multidisciplinary approach headed by physiatrists, physical therapists, and occupational therapists. Enhancing endurance, balance, coordination, joint range of motion, reconditioning, mobility, and independence in everyday activities are the main goals of physical therapy rehabilitation. The ultimate goal is to achieve the highest level of independence (12,13).

CASE PRESENTATION

This case study focused on a 14-year-old female adolescent, who was admitted to R.L. Jalappaon 14March,2024 and presented with notable weakness of bilateral lower limbs for a day.After waking up she noticed weakness in the feet and ankles, which was sudden in onset, initially and progressed to knees. She also had difficulty of gripping chappals. However, she was able to appreciate the sensation of chappals; the patient developed buckling of knees on standing and had to support the bed and furniture to balance posture, an hour following that she noticed that she was unable to get up from sitting position, unable to lift lower legs below knee joints.10 hours after admission, the adolescent had truncal weakness and was catheterized as she lost bladder control. Based on the findings of MRI and Lumbar puncture the diagnosis of Transverse myelitis was made After the vitals were stabilized, the adolescent was referred to the physiotherapy department at R.L.Jalappa Hospital for rehabilitation to address her lower limb weakness and improve overall functional recovery. She was accompanied by her mother for the treatment. Written informed consent was taken from patient 's mother and information sheet were also given and a comprehensive assessment was taken and appropriate treatment protocol was derived, also the procedure was clearly explained to the patient before starting the treatment protocol. The goal of the physiotherapy interventions was to improve strength, balance, gait and make her functional independent.

Physiotherapy intervention

The treatment regimen for this patient, was meticulously crafted to enhance muscle strength and promote greater functional independence. This comprehensive therapeutic protocol not only focused on the strengthening but also

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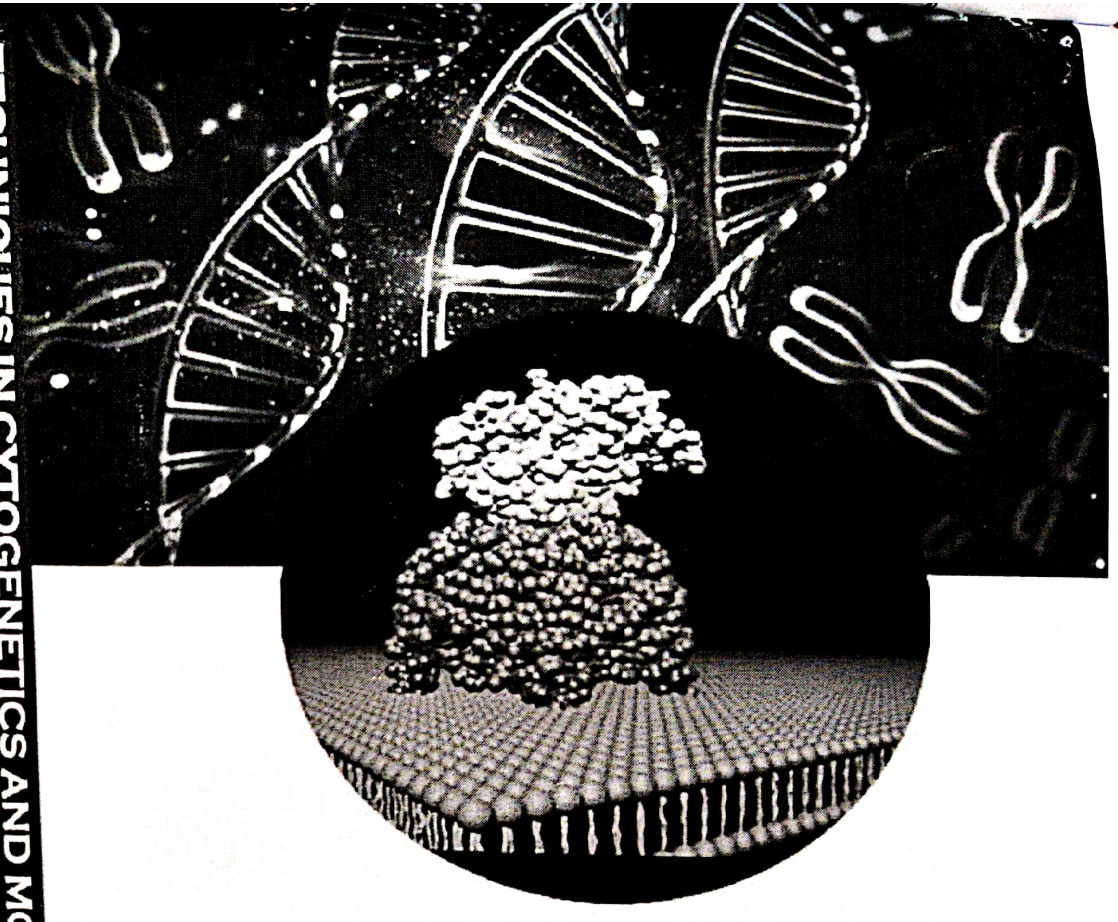

TECHNIQUES IN CYTOGENETICS AND MOLECULAR BIOLOGY

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Dr. Sharath B.
Dr. Venakateswarlu Raavi
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Chapter 13

Flaxseed Bioactives in Oncoprevention: Investigating Omega-3-Enriched Nutraceutical Strategies for Cancer Risk Reduction

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Abstract

Flaxseed (Linum usitatissimum) is a rich source of bioactive compounds, including omega-3 fatty acids (alpha-linolenic acid, ALA), lignans, fiber, and polyphenols, which have demonstrated significant potential in cancer prevention. These bioactives exert antioxidative, anti-inflammatory, and hormone-modulating effects, contributing to reduced cancer risk. Omega-3 fatty acids from flaxseed influence oncogenic signaling pathways such as PI3K/Akt, NF-κB, and Wnt/β-catenin, leading to apoptosis induction and suppression of tumor growth, angiogenesis, and metastasis. Additionally, lignans modulate estrogen metabolism, which is particularly beneficial in hormone-related cancers like breast and prostate cancer. Flaxseed's role as a functional food and nutraceutical makes it a promising candidate in integrative oncology. However, challenges related to bioavailability, dosage standardization, and clinical validation remain. Future research should focus on optimizing flaxseed-derived formulations and exploring its potential in precision oncology. Large-scale clinical trials are essential to establish its efficacy in cancer prevention and therapy.

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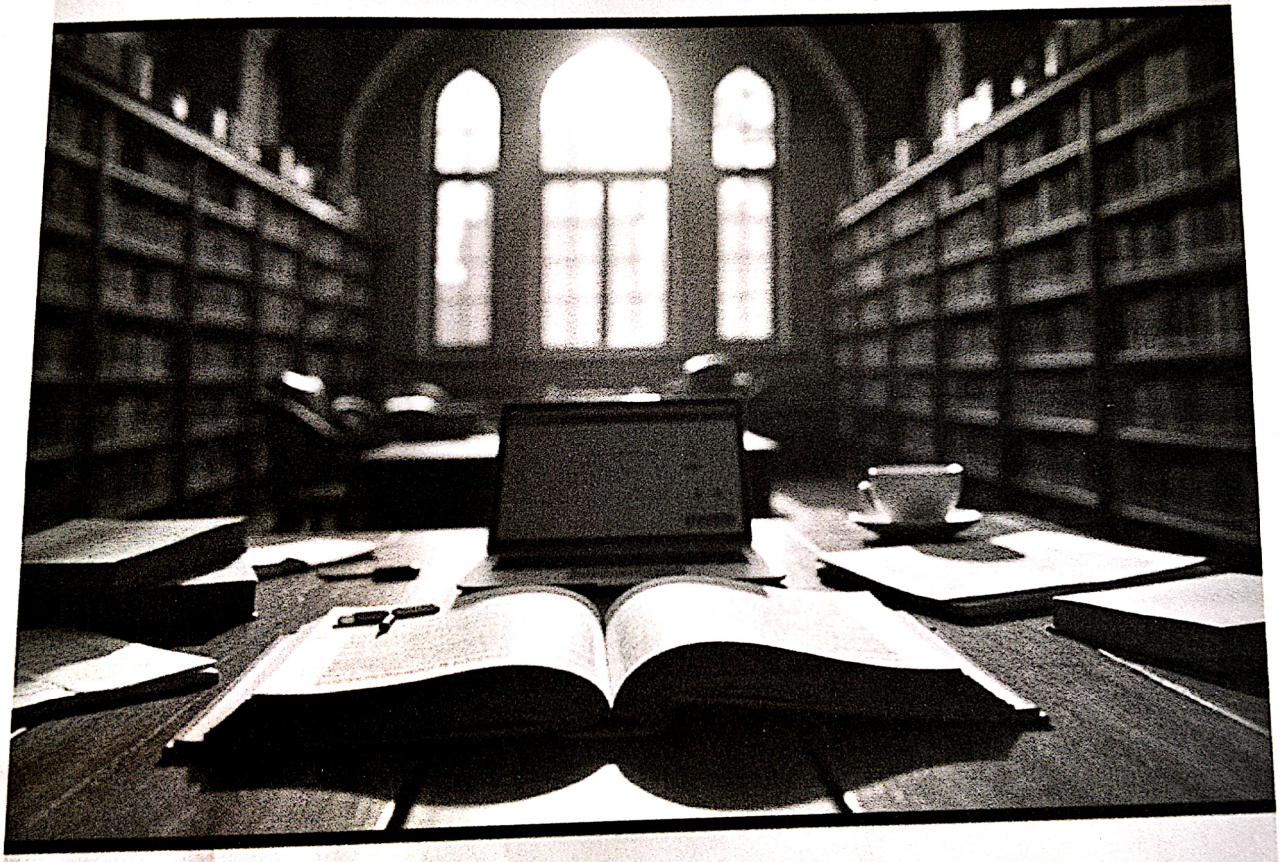

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Chapter 2

Revolutionising Health Professional Education: The Power of Interactive Tools

Naveen Kumar [a++*]

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ABSTRACT

Background: Interactive tools have gained popularity in health professional education due to their potential to enhance active learning, engagement, and learning outcomes. Effective use of these tools can lead to improved patient care and healthcare quality. However, existing literature lacks comprehensive insights into their optimal implementation across different healthcare settings and disciplines, as well as strategies to ensure accessibility and inclusivity for diverse learners.

Objective: This narrative review aims to address these gaps by exploring the impact of interactive tools on learning outcomes and knowledge retention, evaluating their effectiveness across various healthcare disciplines, comparing different tools for specific educational purposes, and identifying best practices for curriculum integration while ensuring accessibility and inclusivity.

Methods: A comprehensive search of electronic databases (MEDLINE, Embase, ERIC) was conducted to identify studies published in English from 2010 to 2021. The selection process included systematic reviews, randomised controlled trials, qualitative studies, cohort studies, and cross-sectional studies, while excluding studies in other languages and case reports. The inclusion and exclusion criteria were applied systematically to ensure methodological rigour. Data from selected studies were synthesised narratively.

Results: Interactive tools have demonstrated significant benefits in promoting active learning and student engagement, leading to improved knowledge retention. Specific tools, such as simulation-based learning, virtual patient cases, and gamification strategies, have shown varying levels of effectiveness depending on the educational context. Their successful implementation requires clear learning objectives, structured integration into curricula, and appropriate

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Chapter 3

Pharmacological Profiling of Ginger-Derived Bioactive Constituents: Anti-Inflammatory and Pro-Apoptotic Interventions in Cancer Pathophysiology

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Abstract

Ginger (*Zingiber officinale*) has garnered significant attention in oncology due to its bioactive constituents, including gingerols, shogaols, paradols, and zingerone, which exhibit potent anti-inflammatory, pro-apoptotic, and anti-proliferative properties. These phytochemicals modulate key molecular pathways such as NF-κB, COX-2, PI3K/AKT, MAPK, and p53, contributing to tumorigenesis inhibition, immune regulation, and oxidative stress reduction. Despite promising preclinical and clinical evidence, challenges related to bioavailability, metabolism, and clinical translation hinder therapeutic application. Advances in nanotechnology, combination therapies, and precision oncology offer potential strategies to enhance the efficacy of ginger-derived compounds. This chapter explores the molecular mechanisms, pharmacokinetics, and therapeutic implications of ginger in cancer prevention and treatment, highlighting future directions for clinical translation.

Keywords

Ginger, Zingiber officinale, cancer prevention, bioactive phytochemicals, anti-inflammatory, pro-apoptotic, tumorigenesis inhibition, immune modulation

Chapter 7
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Awareness of Cancer among Adults in a Rural Health Field Practice Area: A Cross-Sectional Study from a Tertiary Medical College

Sudhakar.S [a++*] and Pradeep.T.S [a#]

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ABSTRACT

Background: India has many factors such as an aging population with poor awareness, increased disparity due to varied economic conditions, and environmental influences leading to higher incidence and mortality rates of cancer. The present study was planned with the objective of assessing the awareness of cancer among villagers and the factors associated with awareness of cancer.

Materials and Methods: The present study was a cross-sectional study carried out for a period of 1 year in 20 villages of Devarayasamudra where cancer awareness was assessed using a pretested questionnaire. The sample size was calculated based on a pilot study. Individuals above 18 years were included in the study and participants who were already diagnosed from cancer or family members suffering from cancer were excluded from the study. Data was entered in an Excel sheet and analysed using SPSS V 22. Descriptive statistics were applied, and to assess differences, t-tests and ANOVA were used. A p-value of less than 0.05 was considered statistically significant.

Results: Out of 425 villagers who took part in the study, 66.4% belonged to the nuclear family and 31.1% belonged to the joint family as per BG Prasad Classification 2024. Comparing the awareness scores among the villagers, those who were aged 61 years and above, those belonging to joint family, Class I Bramha Govind Prasad classification 2024 and graduates had higher awareness scores with statistically significant p-value.

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Chapter 6

Phytopharmacological Insights into Aloe Vera: Bridging Cytoprotective Mechanisms and Therapeutic Applications in Cancer and Tissue Repair

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Abstract

Aloe vera is a well-recognized medicinal plant with extensive applications in cancer therapy and tissue repair. Its diverse bioactive compounds, including polysaccharides, anthraquinones, flavonoids, and vitamins, contribute to its cytoprotective, antioxidant, and immunomodulatory effects. *Aloe vera* exhibits anticancer properties through multiple mechanisms, including apoptosis induction, cell cycle arrest, anti-inflammatory modulation, and inhibition of metastasis and angiogenesis. Additionally, its wound healing potential is attributed to fibroblast stimulation, collagen synthesis, and angiogenic regulation. Despite its therapeutic promise, challenges such as bioavailability, standardization, and clinical translation remain. Advances in nanomedicine, metabolomics, and integrative oncology may further optimize *Aloe vera*'s role in cancer treatment and regenerative medicine.

About The Editor :

Prof. (Dr.) A. K. Singh Is A Distinguished Medical Professional With Impressive Credentials. As A Seasoned Physician, Educator, And Researcher, He Has Held Pivotal Roles, Including HOD Medicine At S.S.P.G. Divisional District Hospital, Varanasi, President Of The Various societies including Indian College Of Haematology And Oncology Society And Geriatric Society of India. His Leadership Extends To Various Prestigious Organizations, Including Geriatric Society Of India, Association Of Physicians Of India, IMA And RSSDI Dr. Singh's Expertise In Geriatric Medicine And Commitment To Medical Education Have Earned Him Numerous Fellowships And Accolades.

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DEMENTIA IN ELDERLY

Dr. B. Vengamma

According to the World Health Organization (WHO), India's population of those aged over 65, which was 40 million in 1997, is to increase to 108 million by 2025 and 240 million by 2050. In India, life expectancy at birth has increased by 30 years since Independence, and it is higher for women than men. These observations indicate that there will be a several-fold increase in age-related problems such as dementia. The WHO, which estimates that two out of every three patients with dementia will soon be in the developing countries, warns of a virtual "dementia epidemic" in India. Thus, there is an urgent need to face this problem.

The central problem of dementia is that it is under-recognized largely because memory loss, the main symptom, is common in old age. There is thus a general perception that dementia is simply because of old age. But this is not true as it is a disease of the brain. A host of diseases, including infections, can cause dementia. But the most common cause (>60%) is Alzheimer's Disease (AD). The other important cause is vascular disease, that is, stroke. Typically, it is not the massive stroke but the small ones, which people may not even be aware of, that cause dementia. The small strokes that normally go unnoticed build up and lead to dementia.

Definition

Dementia is an acquired disorder that is characterized by a decline in cognition involving one or more cognitive domains (learning and memory, language, executive function, complex attention, perceptual-motor, social cognition). While traditional definitions of dementia required a decline in at least two cognitive domains, the definition **of major neurocognitive disorder as outlined in the Diagnostic and Statistical Manual of Mental Disorders (DSM) only requires a substantial decline in a single cognitive area.** The deficits must represent a decline from previous level of function and be **severe enough to interfere with daily function and independence**. The most common form of dementia in older adults is Alzheimer disease (AD), accounting for 60 to 80 percent of cases.

Mild cognitive impairment (MCI) is an intermediate state between normal cognition and dementia in which there are objective cognitive impairments but no decline in overall level of function. While specific subtle changes in cognition can occur in normal aging, **MCI can also be a precursor to dementia.** The definitional boundary between mild cognitive impairment and dementia is based on the preservation or loss of independence in daily life. Given the diversity of life experiences and circumstances, the concept of the distinction between mild cognitive impairment and dementia has more conceptual clarity than operational precision.

Dementia is cognitive impairment that interferes with the ability to function at work or at usual activities; *and*

- It represents a decline from prior levels of functioning and performing; *and*

Tata Memorial Centre Textbook of Oncology

Rajendra A. Badwe • Sudeep Gupta
Shailesh V. Shrikhande • Siddhartha Laskar
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Tata Memorial Centre Textbook of Oncology

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The *TMC Textbook of Oncology* is dedicated to…

…. the countless patients who visit Tata Memorial Centre bestowing their faith upon this institution in their darkest hours. They are our *raison d'être!* We are grateful to them for their inspiration to work harder towards ever higher levels of clinical excellence...

… the trainee doctors, the heartbeat of our hospitals, whose hard work and commitment to service and education make TMC a great institution…

… the nursing staff whose unwavering commitment and profound dedication to patient care embody the heart and soul of our institution…

… to the paramedical staff of TMC, whose skills and dedication are indispensable to the care we provide…

… to colleagues from the departments of general and hospital administration, accounts, purchase, engineering, and all other supportive teams operating seamlessly in the background, who are the pillars that enable the smooth and efficient functioning of our institution…

… medical social workers who provide practical assistance, addressing vital aspects of patient care…

… to the workforce members of TMC, including housekeeping and other staff, whose work is often unseen, yet indispensable, and is the backbone of patient care...

… to the volunteers and Non-Governmental Organizations (NGOs) that collaborate with TMC and offer invaluable support to our patients…

Preface

It is with immense pride and a deep sense of responsibility that we present the *Tata Memorial Centre Textbook of Oncology.* This comprehensive volume, a collaborative effort led by faculty member colleagues of Tata Memorial Centre (TMC), along with contributions from TMC alumni, is more than just a textbook. It is a testament to the spirit of multidisciplinary oncology practice at TMC.

Our journey in creating the *Textbook of Oncology* was inspired by the diverse and complex landscape of cancer care in India. As a nation with vast demographic and geographic diversity, the challenges in cancer care are as unique as they are formidable. Recognizing this, our aim was to provide a resource that is not only academically rigorous but also deeply rooted in the practical realities of local practice. It offers an authentic overview of the TMC approach to multidisciplinary cancer care, with insights that, we hope, will be valuable both within and beyond India.

In presenting the *Textbook of Oncology*, our objective is twofold: to provide a comprehensive resource that contextualizes the practice of oncology in TMC and to offer insights into delivering high-quality cancer care in diverse global settings. Our focus has been on the practical application of oncological principles within Indian and similar healthcare systems. However, oncologists and healthcare professionals from developed countries will also find this resource enlightening, providing a broader perspective on how quality cancer care can be delivered in different parts of the world.

The *Textbook* is designed to cater to a wide array of readers—from undergraduate medical students to postgraduates specializing in general surgery, general medicine, paediatrics, gynaecology, radiation oncology, and other disciplines. A notable feature of the *Textbook* is its utility in preparing students for entrance and exit examinations. However, the content is not just theoretical; it is enriched with practical insights, thus preparing students for the practical aspects of cancer care. To the community of practising oncologists, it will serve as a reliable and up-to-date reference that encapsulates the essence of contemporary oncology practice.

As editors, two of us being surgical oncologists, one a medical oncologist, and another a radiation oncologist, we have witnessed firsthand the evolution of cancer diagnosis and treatment. Our collective experiences have taught us that cancer care is an ever-changing landscape requiring continuous learning and adaptation. The *Textbook*, therefore, not only covers the specifics of various cancers but also delves into broader themes such as cancer epidemiology, genetics, principles of systemic therapy, oncology-related training and education, and others. The chapters are structured to facilitate easy understanding and retention of complex concepts, making it an ideal study aid.

We extend our gratitude to all the authors who have contributed their knowledge and experience. Their dedication and expertise have been instrumental in shaping this work. We also wish to thank our publisher, Springer, for their collaboration and support in bringing this project to fruition. A special acknowledgement goes to the staff, particularly Mr Yogesh Kembhavi, the Editorial Assistant, whose diligent efforts and commitment have been crucial in the successful compilation and publication of the Textbook.

We are mindful of the profound influence that a great textbook can have on its readers. Throughout the history of medical education, certain texts have transcended their basic role as educational resources, becoming lifelong companions. Through this inaugural edition of the *TMC Textbook of Oncology*, we hope to sow the seeds of a work that will make its place as a trusted companion in the minds of its readers, to be consulted and cherished throughout their professional lives.

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Advancement of Analytical Techniques in Some Ethnomedicinal Plants: Current and Future Perspectives

Chapter | First Online: 01 September 2024

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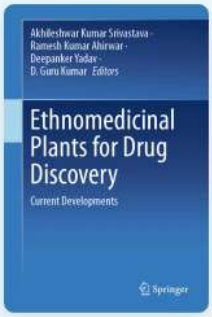


Ethnomedicinal Plants for Drug Discovery

L. Sunil, Sadashivaiah, R. Chandrakanth, Akhileshwar Kumar Srivastava & C. S. Shivakumara

Abstract

Devendra Prasad Kalavagunta J

Shock Indices as Prognostic Indicators

among Sepsis and Septic Shock Patients with and without Comorbidities Presenting to Emergency Department

CHAPTER 105

Metabolic Syndrome: An Overview

Prabhakar K

ABSTRACT

Metabolic syndrome (MetS) is a constellation of metabolic abnormalities, including central obesity, hypertension, atherogenic dyslipidemia, and insulin resistance. With an increasingly sedentary lifestyle and access to calorie-dense food, there has been a global increase in MetS, which leads to an increasing trend of diabetes, coronary artery disease, and stroke. Multicomponent approach is necessary for weight reduction that includes diet, exercise, pharmacological therapy, and surgical intervention.

INTRODUCTION

Metabolic syndrome (MetS) is characterized by a cluster of metabolic abnormalities, including central obesity, hypertension, atherogenic dyslipidemia, and insulin resistance. The condition was first identified by Gerald Reaven, who referred to it as Reaven syndrome or Syndrome X, highlighting its association with cardiovascular risk factors. Over time, it has been referred to by various names, including "the deadly quartet," "the silent killer," and "insulin resistance syndrome."

The prevalence of MetS has risen globally, largely due to increasingly sedentary lifestyles and greater access to calorie-dense foods. This increase is contributing to a rising trend in related conditions, such as diabetes, coronary artery disease, and stroke.

EPIDEMIOLOGY

The burden of noncommunicable diseases has shown an unprecedented rise in recent decades. Globally, estimates for the prevalence vary from 25 to 50%. Variation in the definition and criteria, a lack of awareness among the population and medical personnel has likely led to an underestimation of its true prevalence and may account for the difference in the prevalence in various studies. About 85% of diabetic individuals are estimated to have MetS.

Most studies estimate that India has a prevalence of about 30%. There is considerable regional variation. Additionally, the disease is more prevalent in older individuals, in women more than men, in the obese, and in the urban population. Urban Indians have a higher prevalence compared to the rural population, with some estimates suggesting that the prevalence may be as high as 62% in some areas. Due to less access to healthcare, social attitudes, and poor compliance, the rural population is less likely to have been diagnosed or be on treatment for the various components of MetS, particularly dyslipidemia.

DEFINITION

The definition of MetS has varied greatly over the years and as given by various bodies, including the EHO and IDF. Overall, all the criteria include a cutoff of waist circumference often with ethnicity-specific cutoffs, blood glucose levels, HDL-cholesterol, triglycerides, and blood pressure. The definitions use a single cutoff instead of a range for the diagnosis of MetS for ease. Commonly used definitions are included in **Table 1**.

TABLE 1: Definition of metabolic syndrome.

Adult Treatment Panel III (2005 revision)	International Diabetes Federation
Any three of the five criteria below	Waist circumference ≥94 cm (men) or ≥80 cm (women) and at least two of the following:
• Waist circumference >102 cm (men) or > 88 cm (women)	• Blood glucose >100 mg/dL (5.6 mmol/L) or diagnosed diabetes
• Blood glucose >100 mg/dL (5.6 mmol/L) or diagnosed diabetes	• HDL cholesterol <40 mg/dL (1.0 mmol/L) in men, <50 mg/dL (1.3 mmol/L) in women, or specific drug treatment
• HDL-cholesterol <40 mg/dL (1.0 mmol/L) in men, <50 mg/dL (1.3 mmol/L) in women, or specific drug treatment	• Plasma triglycerides >150 mg/dL (1.7 mmol/L) or specific drug treatment
• Plasma triglycerides >150 mg/dL (1.7 mmol/L) or specific drug treatment	• Blood pressure >130/85 mm Hg or specific drug treatment
• Blood pressure >130/85 mm Hg or specific drug treatment	

ETIOPATHOGENESIS

Metabolic syndrome was first proposed as an umbrella term for risk factors to assess those with an increased risk of cardiovascular disease and type 2 diabetes mellitus using parameters that are more routinely tested in the clinical scenario compared to insulin resistance **(Box 1)**.

Multiple factors increase the risk of developing MetS.

The exact pathogenesis of MetS is not entirely elucidated, but the most accepted theory includes insulin resistance, chronic inflammation, and neurohormonal activation, which cause progression of MetS and subsequently cause diabetes and CVDs **(Flowchart 1)**.

Insulin Resistance

Insulin, an anabolic hormone, inhibits lipolysis and hepatic gluconeogenesis while increasing glucose uptake in the liver, muscles, and adipose tissue. In individuals with insulin resistance, these actions are impaired. Increased lipolysis in adipose tissue results in increased circulating free fatty acid (FFA), which in turn worsens the insulin resistance by affecting the insulin signaling cascade and creates a vicious cycle. In muscles, these FFA decrease GLUT4 translocation to the surface, reduce glucose uptake, and also cause an increased gluconeogenesis and lipogenesis in the liver.

All of these results in a hyperinsulinemic state in an attempt to maintain normal glucose levels, but this compensation eventually fails, leading to an increase in the insulin levels and hyperglycemia. This is further exacerbated by the toxic effect of FFA on beta cells.

High concentrations of FFA also increase cholesterol esters and triglyceride synthesis, and subsequently increase the production of very-low-density lipoprotein (VLDL) rich in TG. It also increases the clearance of HDL, leading to their decrease. This results in an atherogenic lipidemia, finally predisposing the individual to CVDs.

Insulin resistance contributes to hypertension due to the loss of the vasodilator effect of insulin. The FFA also causes vasoconstriction.

Adipose tissue also releases pro-inflammatory cytokines, contributing to CVD.

Visceral fat, which is metabolically active, plays a more important role in this, as the FFA released from the visceral fat affects the liver more directly via the splanchnic circulation. It releases plasminogen activator inhibitor and heparin-binding epidermal growth factors, which cause a prothrombotic state and vascular remodeling.

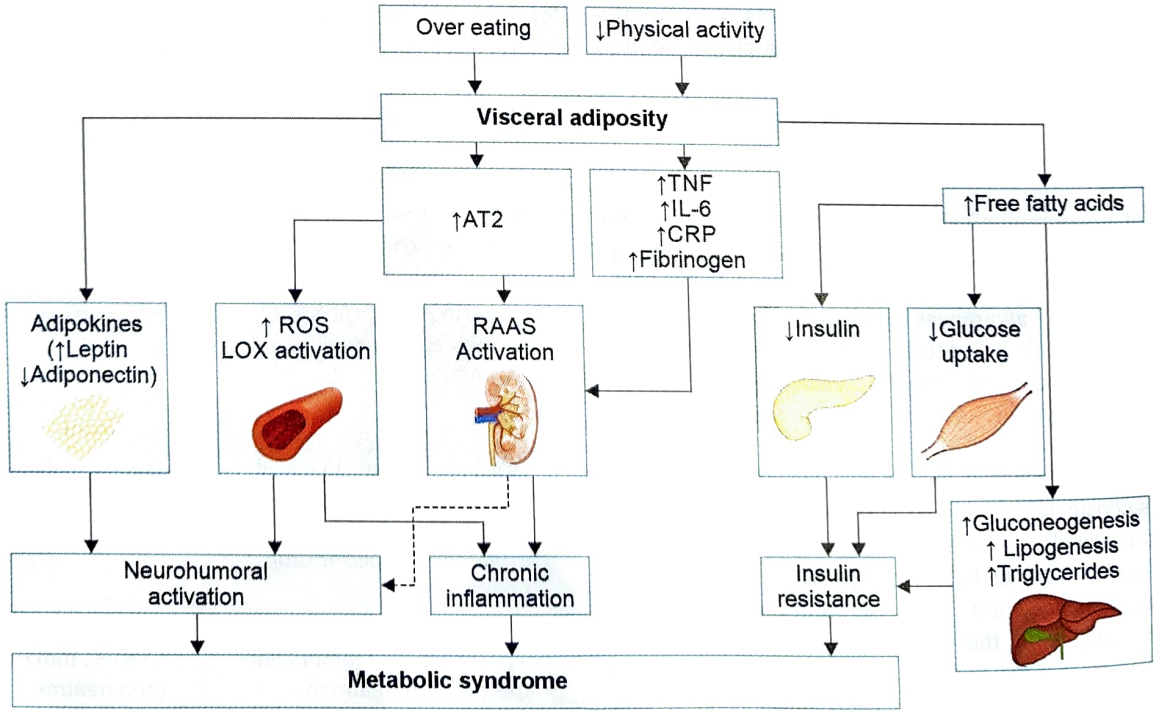
BOX 1: Risk factors for metabolic syndrome.

- Positive family history
- Increasing age
- Ethnicity, genetic factors
- Postmenopausal status
- Physical inactivity
- Low socioeconomic status
- Smoking
- Obesity
- High-calorie, low-fiber diets
- Antipsychotic use

Neurohormonal Activation

Adipocytes not only store fat but also act as an endocrine organ. Adipokines released from visceral fat have been shown to be associated with MetS.

Inflammatory cytokines interleukin-6 (IL-6), interleukin-1, tumor necrosis factor-α (TNF-α), and adipocytokines such as



FLOWCHART 1: Pathophysiology of metabolic syndrome.

Source: Adapted from Rochlani Y, Pothineni NV, Kovelamudi S, et al. Metabolic syndrome: pathophysiology, management, and modulation by natural compounds. Ther Adv Cardiovasc Dis. 2017;11(8):215-25.

IL-6, plasminogen-activator inhibitor-1, C-reactive protein, leptin, ghrelin, resistin, visfatin, and retinol-binding protein-4, as well as nonesterified fatty acids, are produced from visceral fat. These above inflammatory adipokines are key indicators of pathogenesis.

The FFAs also change the profile of hepatic lipid synthesis, making it more atherogenic in terms of having low high-density cholesterol and elevated triglycerides and low-density cholesterol.

In obesity, there is a decrease in adiponectin, which is protective, and an increase in leptin, which leads to an increased risk of CVDs.

As a whole, the metabolic derangements that make up the MetS are mainly focused on increased visceral adipose tissue lipolysis, increased FFAs synthesis and decreased production of apolipoprotein B-100 in the liver, which leads to fatty liver occurred due to insulin resistance, a main pathophysiological derangement.

Obesity and insulin resistance also increase angiotensin II, which not only increases the blood pressure but also results in an increased production of reactive oxygen species. These have multiple effects, including endothelial injury, oxidation of LDL, and platelet aggregation. This contributes to hypertension and CVD.

Inflammation

Obesity and insulin resistance increase the oxidant stress, which activates various proatherogenic pathways and signaling cascades that lead to atherogenesis and tissue fibrosis. Various inflammatory markers have been found to be increased in MetS, but their exact role is still controversial.

Tumor Necrosis Factor-alpha

Tumor necrosis factor-alpha is secreted by macrophages in adipose tissue and increases with obesity. It causes the phosphorylation and inactivation of insulin receptors and induces lipolysis, resulting in increased FFA, and thus contributes to insulin resistance. It also inhibits the release of adiponectin.

Interleukin-6 and C-reactive Protein

Interleukin-6 levels are increased with obesity and insulin resistance. It plays a role in complex regulatory pathways, including an increase in the production of acute-phase reactants in the liver including CRP. IL-6 also increases fibrinogen, resulting in a prothrombotic state, and also leads to endothelial dysfunction.

COMPLICATIONS (FIG. 1)

- *Nervous system*: Alzheimer's disease, cerebrovascular diseases (33.7%)
- *Cardiovascular system*: Myocardial infarction, coronary artery disease (29.4%), hypertension
- *GIT*: MASLD (54.1%), liver cirrhosis, diabetes (61.5%)
- *Kidneys*: CKD (50%)
- *Oncology*: Carcinoma breast, colorectal, prostate, pancreas (4.9%), adrenocortical, endometrial
- Polycystic ovary syndrome (37.25%)

NONPHARMACOLOGICAL MANAGEMENT

Multicomponent approach is necessary for weight reduction, which includes diet, exercise, pharmacological therapy, and surgical intervention.

Lifestyle modifications: Physical activity and weight reduction are the primary goals of therapy for MetS.

DIET AND EXERCISE RECOMMENDATION

The cornerstone of lifestyle modification is weight reduction, which improves insulin sensitivity.

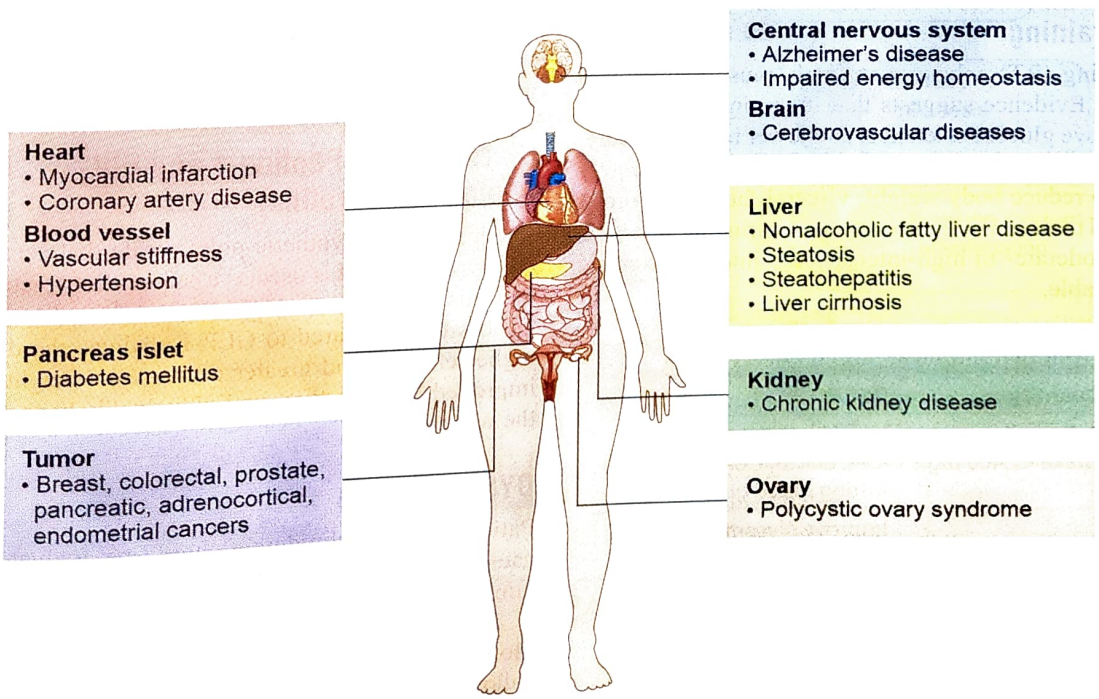


FIG. 1: Complications of metabolic syndrome.
Source: Zhao et al. (2023).

Mediterranean diet is associated with reduction in all components of MetS. It includes plenty of fruits, vegetables, bread and other grains, potatoes, beans, nuts, and seeds. Olive oil as a primary fat source, and dairy products, eggs, fish, and poultry in low to moderate amounts. Other diets are as follows in **Table 2**.

EXERCISE

Insufficient levels of physical activity significantly contribute to the development of insulin resistance by impairing the function of pancreatic β-cells through various mechanisms, including mitochondrial dysfunction, oxidative stress, chronic inflammation, and apoptosis. A decrease in physical activity is associated with an increased risk of obesity. Effective methods for reducing body fat include dietary changes and increasing energy expenditure through exercise. Enhancing energy expenditure while decreasing caloric intake can help mitigate excess body fat and obesity.

There is an inverse relationship between physical activity and metrics such as BMI, waist-to-hip ratio, and waist circumference. Higher lean body mass has a protective effect against excessive fat accumulation, primarily by increasing resting energy expenditure. A reduction in fat mass leads to elevated adiponectin levels and improved cytokine profiles.

Exercise promotes the utilization of fat by skeletal muscle rather than glycogen by enhancing the activity of lipoprotein lipase, an enzyme that hydrolyzes chylomicrons and VLDL, resulting in lower plasma lipid levels. Additionally, exercise helps reduce body fat and subsequently increases insulin sensitivity.

Aerobic Training

Aerobic training (AT) increases energy expenditure, thereby reducing body weight and body fat, including visceral fat. It is also effective in controlling blood pressure in patients with uncontrolled hypertension.

Resistance Training

Resistance training (RT) enhances strength, muscle mass, and lean body mass. Evidence suggests that it can increase insulin sensitivity, improve glucose tolerance, and lower blood pressure.

Moderate-intensity aerobic training is particularly recommended to reduce body weight, visceral fat, and improve blood pressure. To maintain lean body mass during weight loss, incorporating moderate- to high-intensity RT into the exercise program is advisable.

TABLE 2: Diet recommendations for metabolic syndrome.

Diet	Quantity	Result
DASH	Daily sodium intake <2,400 mg	Improvements in triglycerides, diastolic blood pressure, fasting blood glucose
Low glycemic index		Improve glycemia and dyslipidemia
High fiber diet	≥30 g/day	Reduction in blood pressure
Intermittent fasting	8-hour restricted eating	Reduces all components

The American Heart Association (AHA) and the American College of Cardiology (ACC) recommend at least 150 minutes of moderate-intensity or 75 minutes of high-intensity physical activity weekly. Additionally, meditation and yoga are considered cost-effective preventive strategies.

Behavioral Changes

- Self-monitoring (keeping track of daily food intake and activities)
- Controlling stimulus (buying healthy food and avoiding junk food)
- Setting relevant achievable goals
- Improving self-efficacy
- Providing social support
- Preventing relapses

PHARMACOLOGICAL TREATMENT

In patients with MetS, drug therapy is commonly recommended for the treatment of dyslipidemia, hypertension, and insulin resistance or diabetes mellitus. Hypertension is another component of MetS that requires pharmacotherapy.

The drugs recommended for treating insulin resistance include metformin, dipeptidyl peptidase-4 (DPP-4) inhibitors, glucagon-like peptide-1 (GLP-1) agonists, and pioglitazone **(Fig. 2)**.

Glucagon-like Peptide-1 Analogs (Fig. 3)

Glucagon-like peptide-1 receptor agonists (GLP-1 RAs) are suggested to lower inflammation due to direct anti-inflammatory effects on various tissues and immune cells, and partly because of the weight loss.

Semaglutide is a GLP-1 RA that has been approved for the use in diabetes and in the management of obesity and overweight, with at least one weight-related condition. It has shown an improvement in weight, central obesity, diabetes, and reduces MetS severity. The drug has been used in both diabetic and nondiabetic individuals and has shown improvement in both groups.

Glucagon-like Peptide-1 and GIP Analog (Twincretins)

Tirzepatide is a synthetic polypeptide that acts as an analog of GLP-1 and GIP. It is used as a second-line treatment for diabetes mellitus and causes weight loss, and is also approved for use in obesity. Compared to GLP-1 analogs, the drug has shown a higher efficacy and greater decrease in weight. The drugs also improved MetS in these individuals, likely as a consequence of the weight loss.

DYSLIPIDEMIA

Patients with dyslipidemia should be evaluated for reversible causes, and pharmacotherapies must be advised according to the clinical practice guidelines with fibrates and statins.

Management includes dietary and lifestyle interventions, along with drug treatment according to CVD risk. Statins followed by nonstatin drug options such as bempedoic acid and inclisiran for statins intolerant and insufficient response.

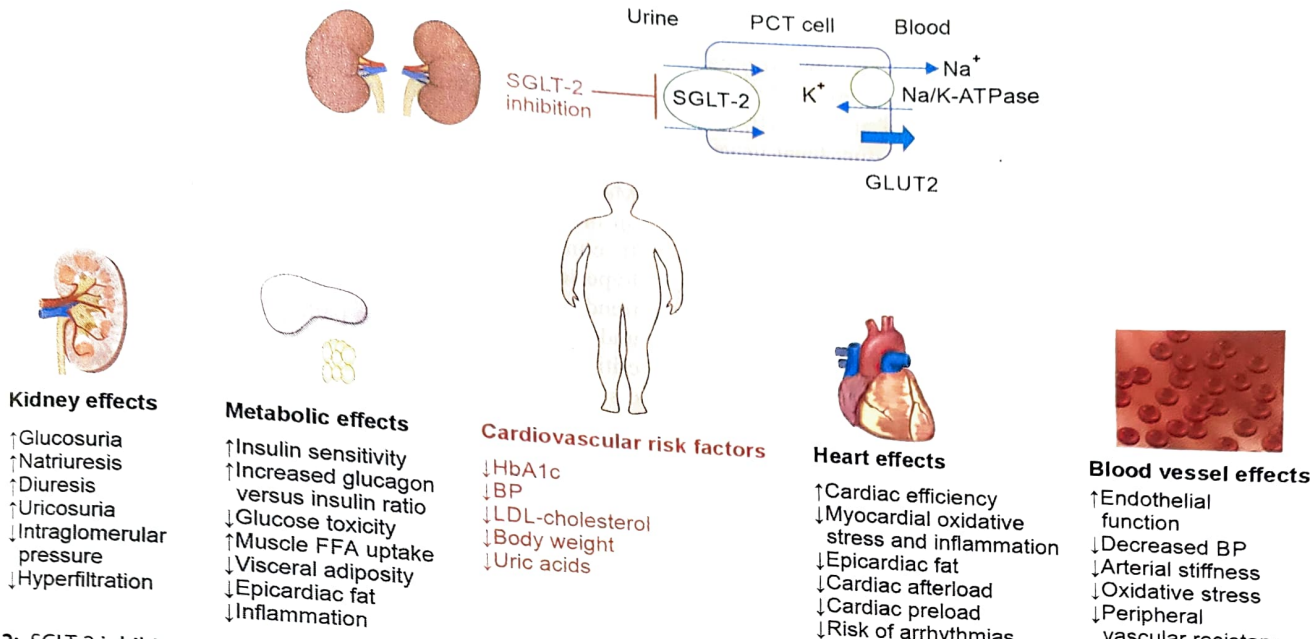


FIG. 2: SGLT-2 inhibitors beyond antidiabetic effect.
Source: Adapted from Stanciu S, Rusu E, Miricescu D, et al. Links between metabolic syndrome and hypertension: the relationship with the current antidiabetic drugs. Metabolites. 2023;13(1):87.

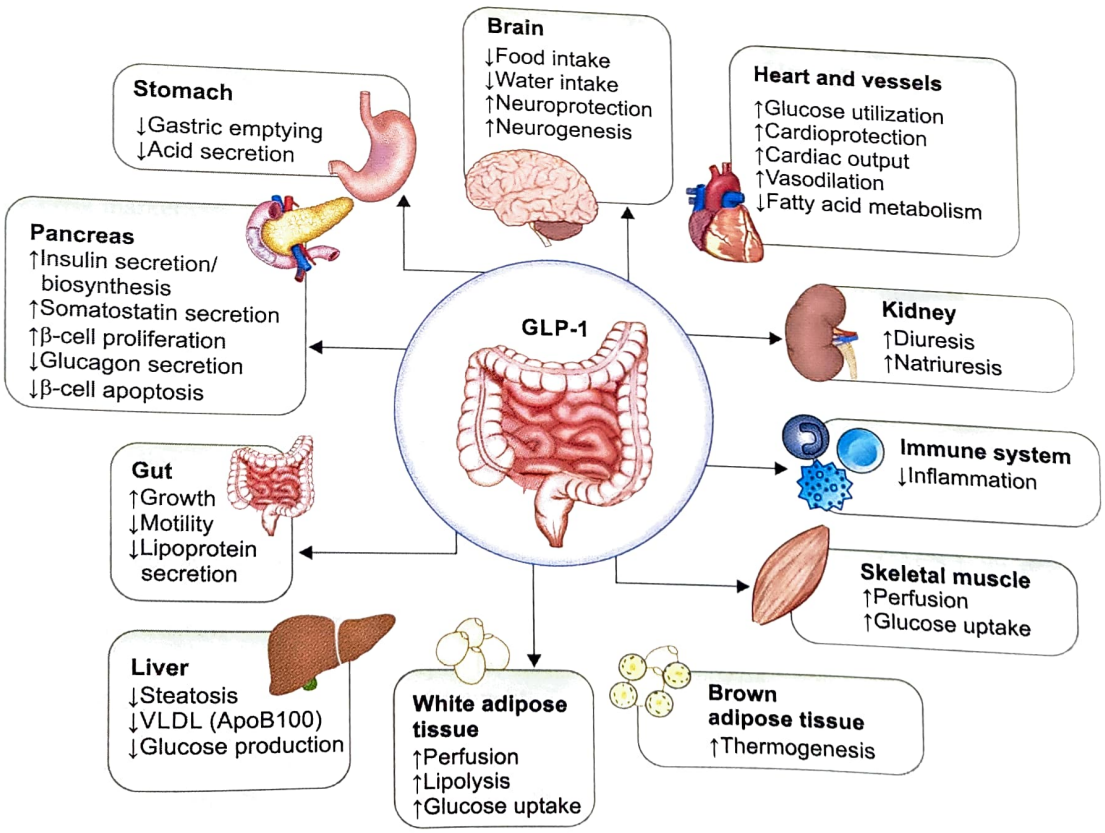


FIG. 3: GLP-1 analogs—mechanism of action.
Source: Adapted from Kalra S, Das AK, Sahay RK, et al. Consensus recommendations on GLP-1 RA use in the management of type 2 diabetes mellitus: South Asian Task Force. Diabetes Ther. 2019;10(5):1645-717.

OBESITY

Orlistat, a lipase inhibitor that acts in the GI tract to prevent the action of lipases and reduces the absorption of about 30% of dietary fat. This leads to a weigh loss of about 9–10% after 1 year. Common adverse effects include flatus, fecal urgency, and increased defecation in about 10% of patients.

Bupropion hydrochloride and naltrexone hydrochloride in a fixed-dose combination medication of a dopamine and norepinephrine reuptake inhibitor and opioid antagonist. They cause a reduction in the food intake by stimulating the production of MSH. Adverse effects include nausea and constipation.

Glucagon-like peptide-1 receptor agonists—liraglutide (target dose of 3 mg), semaglutide (target dose of 2.4 mg) *(see details above)*.

Surgical Management

Bariatric surgery is recommended for patients with a BMI of $\geq$40 kg/m^2 or those with a BMI $\geq$ 35 kg/m^2 and other comorbidities.

Common procedures done are laparoscopic adjustable gastric banding, laparoscopic Roux-en-Y gastric bypass, and laparoscopic sleeve gastrectomy.

HYPERTENSION

Antihypertensives with demonstrated cardiovascular benefit which include ACE inhibitors, ARBs, thiazide-like diuretics, dihydropyridine calcium channel blockers, and the mineralocorticoid receptor antagonists can be used.

EMERGING THERAPIES

- Receptor trap—newer drug-suppresses appetite, body weight, blood glucose levels
- Single cell transcriptomics
- Gut microbiota
- Epigenetics-based therapies
- Cell-based therapies—beta-cell transplant

CONCLUSION

Metabolic syndrome is a cluster of risk factors that predispose an individual to diabetes mellitus and cardiovascular diseases. It consists of atherogenic dyslipidemia, central obesity, hypertension, and hyperglycemia. MetS parallels the rising trend of obesity with an increasing prevalence globally. A good understanding of MetS, its pathophysiology and management is critical to decrease the risk of diabetes mellitus and cardiovascular diseases, which are quickly overtaking infectious disease as a leading cause of death in our country. Regular screening and recognition of MetS in the population, adopting healthier living with regular exercise and better diets with pharmacotherapy for those who need it is the need of the hour to improve outcomes and make a meaningful change.

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