

Unlocking New Therapeutic Potentials: An MIS-Driven Framework for Repurposing FDA-Approved Drugs

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ABSTRACT

As pharmaceutical Research and Development (R&D) faces the mounting pressures of Eroom's Law, characterized by a doubling of drug development costs every nine years, traditional de novo drug discovery has become an increasingly unsustainable model. In 2026, the average cost to bring a New Molecular Entity (NME) to market stands at \$2.6 billion, with timelines exceeding 12 years and clinical success rates hovering near 10%. This paper proposes a transformative Management Information System (MIS)-driven framework for drug repurposing to mitigate these inefficiencies.

The framework utilizes a multi-layered digital architecture to identify new therapeutic indications for FDA-approved and failed-but-safe drug candidates. The Data Integration Layer aggregates heterogeneous datasets from DrugBank, PubChem, and ClinicalTrials.gov, creating a centralized knowledge base. The Analytical Layer employs Artificial Intelligence (AI) for Transcriptomic Signature Matching—identifying drugs that inversely mirror disease gene expressions—and in-silico Molecular Docking to simulate physical binding affinities. A Decision Support System (DSS) then filters these results using weighted scoring algorithms, safety hazard filters, and economic "Phase Leap" estimations. By enabling researchers to resume trials at advanced stages (Phase II/III), this model offers a strategic pathway to reduce R&D expenditures from billions to millions and accelerate market entry by 5–7 years. The integration of a continuous feedback loop ensures that validation results refine the AI models, establishing a self-evolving intelligence system for modern pharmacology.

Keywords: Drug Repurposing, Management Information System (MIS), Artificial Intelligence (AI), Molecular Docking, Transcriptomic Signature Matching, Phase Leap Strategy, Eroom's Law, In-silico Screening.

INTRODUCTION

Developing new drugs from scratch is an extremely long and expensive process. Today, the global demand for new medicines is increasing rapidly. However, the pharmaceutical industry is facing a major challenge known as "Eroom's Law." This law suggests that Research and Development (R&D) efficiency is decreasing, halving approximately every nine years [1]. Despite great technological progress, drug discovery is becoming slower and more costly. Currently, bringing a single New Molecular Entity (NME) to the market costs about \$2.6 billion and takes over a decade [2-3]. Even with such massive investment, only about 12% of drugs succeed in

clinical trials [4]. In this situation, Drug Repurposing (also called repositioning) is a highly effective alternative strategy.

Drug Repurposing is the process of finding new medical uses for medicines that are already approved by regulatory bodies like the FDA. It is not a new concept. Historically, many discoveries happened by "serendipity" or accidental luck. For example, Aspirin was launched in 1899 for pain and fever, but decades later, it was repurposed to prevent heart attacks [5-6]. Similarly, Sildenafil (Viagra) was originally designed for chest pain and high blood pressure, but it became famous for treating erectile dysfunction after unexpected results in clinical trials [7-8].

Other notable examples include Thalidomide, which moved from being a banned drug for birth defects to a treatment for leprosy and blood cancer [9-10]. Minoxidil, originally a blood pressure medicine, is now widely used for hair growth [11]. Most recently, during the COVID-19 pandemic, Remdesivir—which had failed as an Ebola treatment—was identified as a potential solution through data analysis [12].

Every year, thousands of drug candidates fail in clinical trials. Most of these drugs are rejected not because they are toxic, but because they do not work for the specific disease they were first tested for. However, these "failed" drugs have already passed many safety tests, and their biological data is stored in massive databases. This paper argues that these drugs are not useless. By using a Management Information System (MIS), we can analyze vast amounts of research data from failed trials. By connecting this data with new medical needs through logic and technology, we can find hidden therapeutic benefits. Our goal is to use the power of MIS to give these forgotten drugs a second chance to save lives.

CONCEPTUAL FRAMEWORK: THE MIS-DRIVEN APPROACH IN DRUG REPURPOSING

The proposed model (Figure 1) outlines a systematic, MIS-driven approach to drug repurposing research. This framework is designed to empower both professional and non-professional researchers by providing a step-by-step pathway that integrates seamlessly with mainstream pharmaceutical development. Central to this approach is the creation of a specialized Management Information System (MIS) that will act as a digital bridge between vast pharmacological datasets and emerging medical needs.

The framework operates through three primary layers, culminating in a critical validation stage.

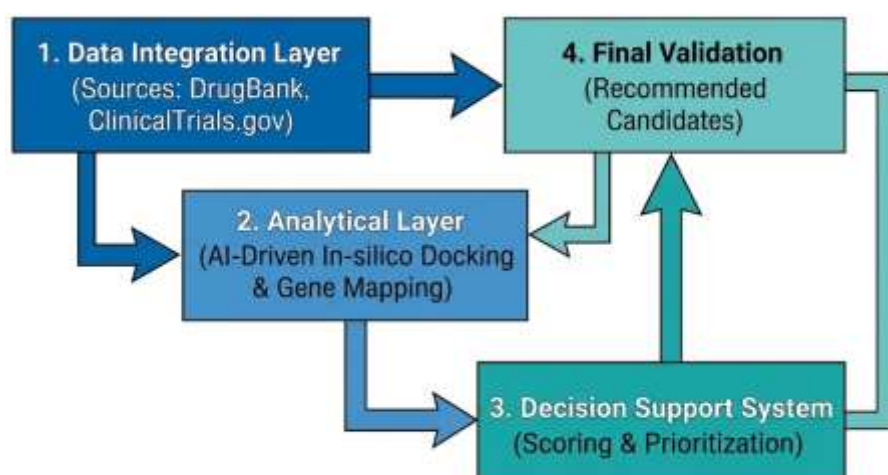


Figure 1: Proposed Model for conducting MIS driven drug repurposing research.

Data Integration Layer (Data Acquisition)

This is the starting point of the framework. In this stage researcher have to set their objective by defining the "Target Disease" and based on the disease profile select the "Candidate Drugs" (FDA-approved or failed drugs). The primary function of the dedicated MIS is to aggregate vast amounts of information from global

databases. The system must be programmed to consolidate data scattered across various platforms, including drug properties, protein interactions, and clinical trial outcomes. Existing AI systems can be integrated into a unified network to perform the following specialized tasks:

- **Molecular and Chemical Data:** The specially designed MIS must have the capability to extract **molecular properties** and **chemical structures** from authoritative databases such as **DrugBank** and **PubChem** [13-14].
- **Clinical Data:** The system should be capable of gathering **safety profiles** and **metabolic data** of failed or existing drugs from **ClinicalTrials.gov** and other similar global data repositories [15].
- **Biological Targets:** To develop a centralized data repository, the MIS must be able to retrieve **disease-related genetic information** from sources like **UniProt** and **GenBank** [16].

The significant tasks within the primary objectives of this level will be:

- **Centralization:** Transforming fragmented data into a unified and integrated knowledge base.
- **Interoperability:** Ensuring that different AI models can communicate seamlessly and exchange datasets without friction.
- **Comprehensive Analysis:** Providing a robust foundation for identifying why certain drugs failed and determining how they can be repurposed for new therapeutic uses.

Analytical Layer (Analytical Activities)

Once the data is collected, the analytical engine of the MIS uses **Artificial Intelligence (AI)** and **Machine Learning (ML)** to process the information.

- **Signature Matching:** The system analyzes "gene expression signatures." It checks if the changes a drug causes in the body are the opposite of the changes caused by a specific disease. If they match inversely, the drug may be a potential cure [17].
- **In-silico Docking:** Through computer simulations, the MIS tests how strongly an old drug molecule can bind to a new disease's protein receptor [18-20]. This predicts effectiveness before any expensive lab work begins.

Table 1: Strategic Phases, Objectives, and Technical Activities of the MIS-Driven Framework

Research Phase	Objective	Key Technical Activities	Outcome
Phase 1: Data Integration	To aggregate fragmented datasets and establish a centralized knowledge base.	Automated retrieval via APIs (DrugBank, PubChem, UniProt); Data cleaning (Salt removal, Standardization).	Integrated Knowledge Base: A structured and unified drug-disease database.
Phase 2: Analytical Layer	To predict drug efficacy using Artificial Intelligence (AI) and Machine Learning (ML).	Transcriptomic Signature Matching (Gene-level inversion); In-silico Molecular Docking (Molecular bond simulation).	Potential Hits: Quantified binding affinity scores and genetic matching profiles.
Phase 3: Decision Support (DSS)	To filter and prioritize the best drug candidates through multi-criteria analysis.	MCDM Algorithms (Weighted scoring); Hazard Filtering (Safety checks); Demographic Alignment (Patient-specific viability).	Ranked Shortlist: A manageable list of the top 5–10 high-probability drug candidates.
Phase 4: Validation & Leap	To biologically confirm digital results and accelerate clinical trial timelines.	In-vitro Cell-based Assays and In-vivo Animal Models; Phase Leap Calculation (Determining Phase II/III restart points).	Validated Candidates: Clinically ready drugs with a strategic R&D cost-reduction report

Decision Support System (DSS)

The dedicated MIS must possess decision-making capabilities that operate through specific algorithms, assigning scores based on various critical points. It will rank potential drugs according to their probability of success, safety history, and cost-effectiveness.

By utilizing this system, researchers will no longer need to manually analyze thousands of chemical compounds. Instead, they can focus on a "shortlist" of the top 5–10 candidate drugs with the highest likelihood of success as identified by the system.

For example, this stage will filter out drugs whose side effects might be hazardous for a new patient demographic; specifically, if the target condition is heart disease, any drug with even minor side effects affecting heart rate could be eliminated. This will allow researchers to concentrate their efforts exclusively on the most promising shortlisted candidates rather than thousands of possibilities. This stage estimates the time and cost savings of repurposing the drug compared to developing a new one, helping companies make faster investment decisions [1-2; 21].

Final Validation

In this final stage, the framework produces Recommended Candidates—drugs that have cleared all digital screenings and are ready for in-vitro or in-vivo testing.

A unique advantage of this framework is the ability to leverage historical data. Since these drugs previously progressed through various clinical trial phases, researchers can often resume investigations from advanced stages rather than starting over. The specific point of restart directly influences the final cost and time-to-market. Finally, a feedback loop ensures that all validation results are re-integrated into the system, continuously refining the analytical models for future accuracy.

METHODOLOGY

Data Integration Protocols

Methodology for Molecular and Chemical Data Extraction

The extraction of molecular and chemical data is the most critical technical step in the Data Integration Layer. This process transforms raw chemical information into a machine-readable format that the Analytical Layer can process for *in-silico* simulations.

(i). Automated Data Retrieval via APIs

The specialized MIS is programmed to communicate directly with authoritative databases using **Application Programming Interfaces (APIs)** and automated query scripts.

- **DrugBank Integration:** The system targets the **DrugBank Online Vocabulary and Structure** datasets[13]. It extracts comprehensive records including drug synonyms, molecular formulas, and known pharmacological actions.
- **PubChem Querying:** The MIS utilizes the **PubChem PUG-REST** service to retrieve detailed chemical metadata. By using the drug's name or CAS registry number, the system pulls standardized information essential for structural analysis [14].

(ii). Extraction of Structural Identifiers

For the MIS to "understand" a drug's shape and behavior, it must extract specific digital identifiers:

- **SMILES Strings:** The system retrieves the **Simplified Molecular Input Line Entry System (SMILES)** string. This is a linear notation that represents the entire chemical structure, allowing the AI to calculate molecular similarity [22].
- **SDF and PDB Files:** The MIS downloads **Structure-Data Files (SDF)** and **Protein Data Bank (PDB)** formats. These files provide the 3D spatial coordinates of the atoms, which are a prerequisite for **Molecular Docking** in the Analytical Layer [23-24].

(iii). Data Normalization and Cleaning

Since data is collected from multiple sources, the MIS performs a **Standardization Protocol**:

- **Salt Removal:** The system uses "Wash" algorithms to remove salt fragments from the chemical structures (e.g., converting "Metformin Hydrochloride" to "Metformin") to ensure the analysis focuses on the active therapeutic moiety [25].
- **Duplicate Resolution:** Using **InChIKeys** (International Chemical Identifiers), the system identifies and merges duplicate entries from different databases to maintain a clean, unique dataset [26].

(iv). Physicochemical Property Profiling

Before moving to the next layer, the MIS calculates and stores key properties for each candidate:

- **Lipinski's Parameters:** The system automatically calculates molecular weight, Hydrogen bond donors/acceptors, and the Octanol-water partition coefficient (LogP) [27].
- **ADME Profile:** Initial estimates of **Absorption, Distribution, Metabolism, and Excretion** are recorded to ensure the drug has a high probability of reaching the target organ in the human body [28].

Methodology for Clinical Data Mining and Safety Profiling

The extraction of clinical data involves moving beyond chemical structures to understand how a drug behaves in the human body. The MIS is designed to retrieve, categorize, and analyze historical trial data to determine a drug's suitability for a new indication.

(i). Interface with Clinical Repositories

The MIS utilizes automated protocols to access and scrape data from primary clinical registries:

- **ClinicalTrials.gov (NLM):** The system connects via the **ClinicalTrials.gov API** to download XML or JSON formatted data regarding study designs, eligibility criteria, and adverse events [15].
- **EU Clinical Trials Register:** The system retrieves supplementary data on trials conducted within the European Union to ensure a globally representative safety profile [29].
- **FDA Post-Market Reports:** For existing drugs, the MIS gathers data from the **FAERS (FDA Adverse Event Reporting System)** to identify long-term safety trends [30].

(ii). Extraction of Safety and Toxicity Profiles

The MIS specifically targets data from **Phase I and Phase II clinical trials**. Even if a drug failed Phase III due to lack of efficacy, the system extracts:

- **Maximum Tolerated Dose (MTD):** Data on the highest dose that does not cause unacceptable side effects.

- **Adverse Events (AEs):** Categorization of reported side effects. The MIS uses **MedDRA (Medical Dictionary for Regulatory Activities)** coding to standardize these reports, allowing for a structured comparison between different drugs [31].
- **Inclusion/Exclusion Criteria:** The system analyzes previous trial demographics to determine if the drug's safety is proven for specific age groups, genders, or ethnicities.

(iii). Retrieval of Metabolic and Pharmacokinetic (PK) Data

Understanding the drug's "journey" through the body is essential for determining if it can reach the site of a new disease. The MIS extracts:

- **ADME Parameters:** Data on Absorption, Distribution, Metabolism, and Excretion.
- **Half-life ($t_{1/2}$):** How long the drug remains active in the bloodstream.
- **Metabolic Pathways:** Identification of specific liver enzymes (e.g., CYP450) involved in breaking down the drug. This helps the Decision Support System (Stage 3) predict potential drug-drug interactions.

(iv). Data Categorization for Decision Support

Finally, the MIS organizes the clinical data into a "**Safety Score**":

- **Approved Drugs:** High-priority candidates with the most complete clinical data.
- **Failed Candidates:** Drugs that failed for **efficacy** (but remained safe) are marked as high-potential for repurposing, while those that failed for **toxicity** are flagged for caution or eliminated [16].
- **Data Integrity Check:** The system verifies the "Status" of trials (e.g., Completed, Terminated, or Suspended) to ensure the framework is not using unreliable or incomplete evidence.

Methodology for Biological Target Identification and Genetic Mapping

This phase focuses on the "Target Disease" side of the framework. The MIS identifies the specific proteins, enzymes, or genes responsible for a disease, which then serves as the foundation for the Analytical Layer (Stage 2).

(i). Automated Retrieval of Protein Sequences (UniProt)

The MIS connects to the **UniProt Knowledgebase (UniProtKB)** to gather detailed information on human proteins.

- **Protein Identification:** For a defined target disease (e.g., Alzheimer's), the system identifies associated proteins (like Amyloid-beta or Tau) [32].
- **Sequence Extraction:** The system retrieves the **Amino Acid Sequences** in FASTA format. This sequence is essential for the AI to understand the 3D shape of the protein [32].
- **Functional Annotation:** The MIS extracts "Active Site" information—the specific part of the protein where a drug needs to attach to have a therapeutic effect.

(ii). Genetic Data Acquisition (GenBank & NCBI)

The system mines **GenBank** and the **NCBI Gene database** to understand the genetic drivers of the disease.

- **Gene-Disease Association:** The MIS identifies which genes are "up-regulated" (overactive) or "down-regulated" (underactive) in a patient with the target disease [33].
- **Nucleotide Sequences:** It retrieves the DNA and RNA sequences related to the disease, providing a "genetic footprint" that the framework will later use for **Transcriptomic Mapping** [33].

(iii). Network Construction and Disease Pathways

Instead of looking at a single gene, the MIS uses systems biology to map how proteins interact.

- **Pathway Mapping:** The system retrieves data from **KEGG (Kyoto Encyclopedia of Genes and Genomes)** to visualize the biological pathways. For example, if a drug blocks one protein, the MIS predicts how that will affect the rest of the cellular 'circuit' [34].
- **Target Prioritization:** Not all proteins are good targets. The MIS ranks biological targets based on "druggability"—how easy it is for a chemical molecule to bind to and change the behavior of that specific protein [35].

(iv). Centralized Knowledge Integration

The final step is the creation of a **Relational Target-Drug Map**.

- **Cross-Referencing:** The MIS links the genetic data from GenBank with the protein data from UniProt [36].
- **Knowledge Graph Construction:** This data is stored as a "Knowledge Graph," allowing the **Analytical Layer** to run complex queries such as: *"Which FDA-approved drugs have a structure that matches the binding pocket of Protein X in Disease Y?"*

Methodology for Analytical Layer (AI-Driven Activities)

Once the raw data is centralized in the Integration Layer, the **Analytical Engine** of the MIS takes over. This stage represents the "Intelligent Insights" phase, where the system applies advanced **Artificial Intelligence (AI)** and **Machine Learning (ML)** algorithms to simulate biological interactions.

The methodology for this layer is divided into two primary computational activities:

Transcriptomic Signature Matching

This activity focuses on the genetic harmony between a drug and a disease. The goal is to find drugs that can "reverse" the disease state at a cellular level.

- **Step 1: Disease Signature Extraction:** The MIS identifies the "Disease Signature"—the specific pattern of genes that are turned on or off when a person has the target disease.
- **Step 2: Drug Signature Comparison:** The system then scans its database for "Drug Signatures" (the genetic changes a drug causes in healthy cells).
- **Step 3: Inverse Pattern Matching:** Using ML algorithms, the system looks for an **inverse relationship**. For example, if Disease X causes Gene A to be overactive, the MIS searches for a drug that causes Gene A to be underactive.
- **Outcome:** If the drug's genetic footprint is the "mirror image" of the disease's footprint, the MIS flags it as a potential cure with a high probability of reversing the disease pathology [17].

In-silico Molecular Docking

While signature matching looks at genes, **In-silico Docking** looks at the physical "lock and key" fit between a drug molecule and a disease protein.

- **Step 1: 3D Protein Preparation:** The MIS retrieves the 3D structure of the target protein (from Stage 1.3) and "cleans" it by removing water molecules and adding missing hydrogen atoms to prepare it for simulation [19; 37].
- **Step 2: Active Site Identification:** The AI identifies the "binding pocket"—the specific area on the protein where a drug must attach to stop the disease [38-39].
- **Step 3: High-Throughput Simulation:** The system performs thousands of simulations, rotating and moving the drug molecule in 3D space to see how it fits into the protein's pocket [18; 40].
- **Step 4: Scoring Binding Affinity:** The MIS calculates a "**Binding Energy Score or ΔG (Gibbs free energy).**" A lower energy score indicates a stronger, more stable bond [41; 42].
- **Outcome:** This digital prediction identifies which "old" drugs have the physical strength to block "new" disease proteins, allowing researchers to skip thousands of unsuccessful manual lab tests [17; 43].

Methodology: Decision Support System (DSS)

The **Decision Support System (DSS)** serves as the "intelligent filter" of the framework. While the Analytical Layer (Stage 2) provides raw predictions, the DSS translates those insights into a prioritized, actionable strategy. It operates through multi-criteria decision-making (MCDM) algorithms to evaluate drugs across biological, safety, and economic dimensions [44; 45].

Automated Scoring and Ranking Algorithm

The Decision Support System (DSS) applies a weighted scoring system to every drug candidate that clears the initial digital screening. To mathematically integrate the heterogeneous biological predictions, the total prioritized score (S_{Total}) for each drug candidate is calculated using a normalized multi-criteria decision-making (MCDM) weighted linear combination model:

$$S_{\text{Total}} = (w_1 \cdot \bar{S}_{\text{BA}}) + (w_2 \cdot \bar{S}_{\text{TM}})$$

Where:

$\bar{S}_{\text{BA}}$ is the Min-Max normalized Binding Affinity Score, derived from the raw molecular docking Gibbs free Energy (ΔG). Higher binding strength yields a higher score [20; 41]. Because a lower (more negative) ΔG signifies stronger, more stable thermodynamic physical binding, the raw docking outputs are normalized to ensure higher binding strength yields a higher relative score :

$$\bar{S}_{\text{BA}} = \frac{\Delta G_{\text{max}} - \Delta G}{\Delta G_{\text{max}} - \Delta G_{\text{min}}}$$

- $\bar{S}_{\text{TM}}$ is the normalized Transcriptomic Matching Score, reflecting the computed degree of inverse correlation in gene expression signatures between the drug footprint and the disease pathology [46; 47].
- **w1 and w2** are the relative scaling weights dynamically assigned to structural binding and genetic harmony respectively, subject to the strict programmatic constraint:

$$w_1 + w_2 = 1.0$$

Through this weighted aggregation framework, the MIS resolves the disparate scales of genomic correlation matrices and thermodynamic binding affinities into a single, unified metric. This computational filter allows the system to efficiently screen thousands of compounds and produce a highly prioritized, manageable shortlist of the top 5–10 high-probability drug candidates for subsequent laboratory validation [44, 48-49].

Safety and Demographic Filtering

Unlike traditional screening, the DSS incorporates a "**Hazard Filter**" to ensure the repurposed drug is clinically appropriate for the new target population [50; 51].

- **Context-Specific Filtering:** The system identifies potential contraindications. For instance, if the target condition is a cardiovascular disorder, the algorithm scans the clinical data (from Stage 1.2) and automatically eliminates any drug known to cause tachycardia or arrhythmias, even if its docking score is high [52-54].
- **Demographic Alignment:** The system assesses the safety of the drug for specific groups (e.g., pediatric, geriatric, or pregnant patients) to ensure the proposed repurposed use is viable for the actual patient demographic [55-57].

Economic and Time-to-Market Estimation

The DSS provides a high-level strategic analysis to assist pharmaceutical companies and researchers in investment decisions.

- **Phase Leap Calculation:** The system determines the earliest clinical trial stage the drug can restart. Since the drug has already passed various safety phases, the DSS calculates the years saved (typically 5–7 years) compared to *de novo* drug development [21; 58-59].
- **Cost-Benefit Analysis:** By utilizing current market data, the system estimates the reduction in R&D expenditure—often moving from billions of dollars down to millions. This report helps stakeholders visualize the financial viability of the project [1-2; 21].

Interactive Dashboard for Researchers

The final output of the DSS is an interactive interface that provides:

- **Visual Evidence:** 3D visualizations of the docking site and gene expression heatmaps.
- **Justification Reports:** A detailed summary explaining *why* a specific drug has shortlisted, including its historical successes and failures.
- **Risk Profiles:** A transparency report on potential side effects that must be monitored during the subsequent validation stages.

Methodology: Final Validation and Feedback Integration

The **Final Validation** stage represents the transition from digital prediction to biological confirmation. At this level, the MIS framework outputs a definitive list of **Recommended Candidates**, providing a strategic roadmap for physical laboratory testing and clinical re-entry.

Transition to Biological Validation (In-vitro & In-vivo)

Once the Decision Support System (Stage 3) identifies the highest-scoring candidates, the methodology moves into the physical laboratory environment:

- **In-vitro Testing:** Researchers perform cell-based assays to observe if the drug produces the predicted biochemical effect. For example, if the MIS predicted a drug would block a specific cancer enzyme, in-vitro tests confirm this interaction in a controlled cellular environment [43; 60].
- **In-vivo Testing:** High-potential drugs then move to animal models to observe systemic behavior, ensuring the drug reaches the target organ and performs effectively within a living biological system [61-62].

Strategic Clinical Trial Resumption

A defining feature of this MIS framework is the **"Phase Leap"** strategy [17; 21]. Because the candidates are existing FDA-approved or previously tested drugs, the validation process is significantly accelerated:

- **Historical Data Leveraging:** The MIS provides a comprehensive package of the drug's previous Phase I (Safety) and Phase II (Dose-finding) data [17; 63].
- **Determining the Restart Point:** Based on the drug's history, researchers can often skip early safety trials and resume at **Phase II** or **Phase III** for the new therapeutic indication [17; 59; 64].
- **Impact on R&D:** By skipping the first 5–7 years of traditional drug development, this stage directly minimizes the time-to-market and reduces the financial burden from billions to millions of dollars.

The Feedback Loop and Machine Learning Refinement

The methodology concludes with a "Continuous Learning" protocol to ensure the system evolves with every experiment.

- **Result Re-integration:** Whether a lab test succeeds or fails, the data is fed back into the **Data Integration Layer**.
- **Model Optimization:** If a predicted drug fails in the lab, the AI analyzes the discrepancy and adjusts its docking and signature-matching algorithms to avoid similar errors in the future.
- **Data Enrichment:** This loop ensures the MIS becomes more accurate over time, transforming it from a static tool into a dynamic, self-improving intelligence system.

RESULT

The strategic technical alignment across the four operational layers of the proposed framework yields a centralized, automated system. The granular breakdown of the phases, core objectives, matching technical implementations, and quantitative deliverables generated by the system are structured systematically in Table 1.

DISCUSSION

The findings of this study highlight a transformative shift in pharmaceutical research: the transition from "Accidental Discovery" to "Data-Driven Intelligence." Historically, drug repurposing successes such as Sildenafil or Aspirin were products of clinical "luck." However, in the current landscape—where the global drug repurposing market is projected to reach \$36.69 billion by late 2026 and nearly \$50 billion by 2033 [65-66]—reliance on accidental discovery is no longer a viable industrial strategy. The core of this discussion centers on how the proposed MIS framework addresses the structural inefficiencies of traditional drug development through several critical advantages.

(i). Overcoming Eroom's Law with Informatics:

The primary bottleneck in modern pharmacology is the astronomical cost and time required to prove drug

safety. Our framework addresses this by targeting drugs that have already cleared the "Safety Barrier" (Phase I trials). By utilizing an MIS to harvest historical clinical data, we effectively re-monetize the billions of dollars previously "lost" on drugs that failed Phase III trials due to efficacy issues. These drugs are not biological failures; they are simply keys that were tried in the wrong locks. The MIS Analytical Layer acts as a digital locksmith, matching these existing molecules to new disease receptors with high precision.

(ii). Technological Synergy: Signature Matching and Docking

A unique aspect of this framework is the dual-validation at the Analytical Layer. While many systems focus solely on structural binding (Molecular Docking), our inclusion of Transcriptomic Signature Matching provides essential biological context. Traditional discovery often focuses on a single target protein, but our "systems biology" approach analyzes gene expression signatures. If a disease turns specific genes "on," the MIS identifies a drug that turns them "off." By merging these two computational approaches, the MIS significantly reduces the "false-positive" rate that often plagues early-stage AI drug discovery, ensuring that a drug is both structurally and genetically viable before wet-lab resources are spent.

(iii). Logic-Based Filtering and Safety

The Decision Support System (DSS) adds a layer of clinical logic missing in pure computational models. For example, if the target condition is heart disease, the DSS automatically eliminates any drug with historical side effects affecting heart rate, even if its docking score is perfect. This automated, safety-first approach ensures that the "shortlist" of 5–10 candidates is clinically viable for the specific patient demographic. This reduces the cognitive load on researchers and minimizes the risk of late-stage clinical trial failures—the primary drivers of pharmaceutical debt.

(iv). The Economic and Regulatory Imperative

The core strength of the proposed model lies in its ability to circumvent the "valley of death" in drug development. Our "Phase Leap" strategy leverages historical clinical data to bypass redundant safety testing, reducing the development cycle from 12 years to approximately 3–5 years. This aligns with recent FDA 2025/2026 guidelines that increasingly permit AI-derived data and real-world evidence (RWE) in supplemental drug applications [67]. Such efficiency significantly lowers the "entry barrier" for researchers in settings like South Asia, where computational expertise can compensate for scarce laboratory infrastructure.

(v). Addressing Potential Challenges: Overcoming Intellectual Property and Data Hurdles

Despite the structural efficiency of the proposed MIS framework, two major hurdles remain: Intellectual Property (IP) and Data Interoperability. When an FDA-approved or failed-but-safe drug molecule is off-patent or approaching generic status, novel composition-of-matter protection is no longer legally viable, often causing repurposed drugs to face a "weak patent" status. The DSS directly addresses this commercial bottleneck by automatically generating data-dense "Justification Reports" to assist in filing robust new "method-of-use" (second medical use) patents. Rather than acting as a speculative algorithm, these reports compile precise 3D spatial binding coordinates, Gibbs free energy (ΔG) dynamics, and gene-level inversion data. This structural and mechanistic evidence transforms raw bioinformatics metrics into a defensible technical dossier that satisfies the strict legal thresholds of non-obviousness and clinical plausibility required by global patent offices.

Furthermore, our architectural standardization protocols (e.g., automated SMILES extraction, salt removal via wash algorithms, and InChIKey duplicate resolution) are critical to solving technical database fragmentation and ensuring interoperability across heterogeneous platforms. However, the ultimate success of this model depends on a shifting paradigm toward an "Open Science" approach. We strongly advocate for treating historical failed clinical trial data as a public health asset rather than a corporate secret, allowing the self-evolving MIS framework to leverage complete clinical datasets and reach its full therapeutic potential.

CONCLUSION

This paper has demonstrated that the future of pharmaceutical innovation lies in the intelligent reuse of existing molecular assets. By developing an MIS-driven framework, we have provided a roadmap to move beyond the limitations of "Eroom's Law" and the prohibitive costs of *de novo* drug discovery. The integration of the Data Integration Layer, Analytical AI, and a robust Decision Support System creates a pipeline that is faster, cheaper, and safer than traditional methods.

The historical successes of drug repurposing, once driven by chance, can now be replicated at scale through computational logic. Our framework proves that the thousands of "failed" drugs currently sitting in global databases are a goldmine of therapeutic potential. By utilizing *in-silico* docking and transcriptomic matching, we can identify life-saving treatments for cancers, rare diseases, and emerging viral threats without the need for decade-long research cycles.

Furthermore, this MIS-driven approach democratizes drug research. It allows academic institutions and smaller pharmaceutical entities to contribute to global health solutions by focusing on data analysis and targeted validation. The feedback loop integrated into our model ensures that the system becomes more intelligent and accurate with every trial, creating a self-evolving repository of medical knowledge.

In conclusion, unlocking the therapeutic potential of FDA-approved and failed drugs is a logical necessity in an era of rising healthcare costs and declining R&D productivity. The transition to an MIS-driven repurposing model will not only save billions of dollars but, more importantly, it will accelerate the delivery of life-saving medications to patients who cannot afford to wait. We recommend that regulatory bodies and pharmaceutical

leaders adopt this structured informatics approach to ensure that no viable medicine is left behind simply because its original purpose was not met. The "second life" of a drug may well be the one that changes the world.

Abbreviations

ADME	Absorption, Distribution, Metabolism, and Excretion
AI	Artificial Intelligence
API	Application Programming Interface
CAS	Chemical Abstracts Service
DSS	Decision Support System
FDA	United States Food and Drug Administration
InChIKey	International Chemical Identifier Key
KEGG	Kyoto Encyclopedia of Genes and Genomes
MCDM	Multi-Criteria Decision-Making
MedDRA	Medical Dictionary for Regulatory Activities
MIS	Management Information System
ML	Machine Learning
MTD	Maximum Tolerated Dose
NCBI	National Center for Biotechnology Information
NME	New Molecular Entity
PDB	Protein Data Bank
PK	Pharmacokinetics
R&D	Research and Development
RWE	Real-World Evidence
SDF	Structure-Data File
SMILES	Simplified Molecular Input Line Entry System
UniProtKB	UniProt Knowledgebase

Author Contributions

- **A F M Nazmus Sadat:** Conceptualization, Software, Methodology, Resources, Writing – original draft.
- **Tanjina Piash:** Formal Analysis, Resources, Visualization.
- **Md. Mustafa Al Hussain:** Data curation, Investigation, Validation.
- **Niloy Saha:** Investigation, Data curation, Methodology.
- **Masud Rana:** Validation, Visualization, Writing – review & editing.
- **Zaber Ahmed Mostafa:** Data curation, Methodology, Software.
- **Afroza Sultana:** Project administration, Funding acquisition, Supervision, Writing – review & editing.

Conflicts of Interest

The authors declare no conflicts of interest.

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