A Data-Driven Simulation of Aspirin's Pharmacokinetics and Pharmacodynamics Using Open-Source Tools

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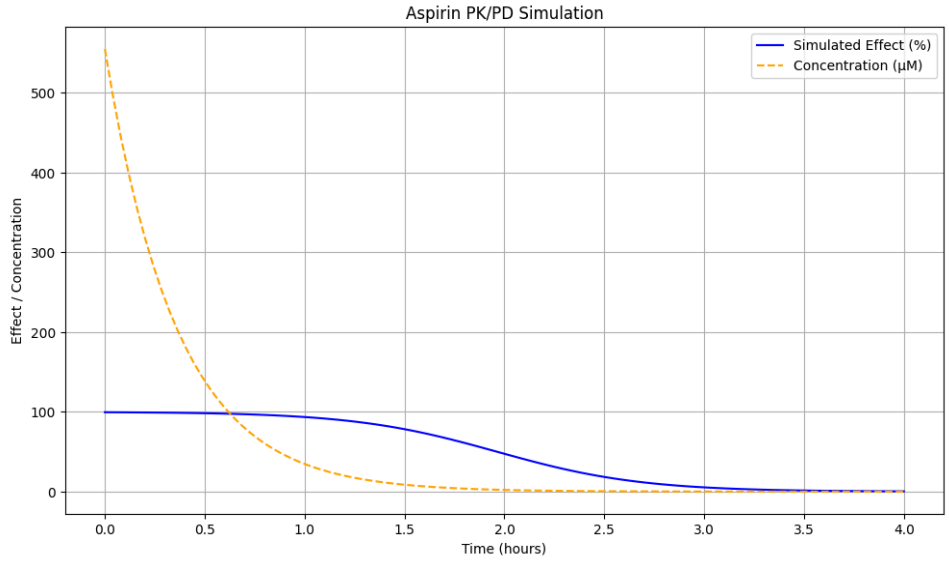

Abstract

This study presents an open-source simulation of aspirin's pharmacokinetic and pharmacodynamic (PK/PD) behavior using publicly available biochemical data and Python-based tools. A structured SQLite database was developed to store molecular, target, and physiological parameters sourced from DrugBank, PubChem, UniProt, and the Protein Data Bank (PDB). The simulation models aspirin's plasma concentration decay over time and computes its pharmacodynamic response using a sigmoid inhibitory model. This prototype demonstrates the feasibility of building scalable and transparent in silico pharmacological tools using only free software and open-access data.

Introduction

The development of reliable PK/PD models is critical in modern drug development. However, many computational tools are proprietary and inaccessible to underfunded researchers. This project investigates the potential of open-source alternatives by building a data-driven simulator for aspirin, a well-characterized non-steroidal anti-inflammatory drug (NSAID) with an established mechanism of action via inhibition of cyclooxygenase enzymes COX-1 and COX-2.

Methods

The following values were extracted from primary sources:

Parameter	Value	Source
Molecular Weight	180.16 g/mol	PubChem (CID: 2244)
SMILES	CC(=O)OC1=CC=CC=C1C(=O)O	PubChem
InChIKey	BSYNRYMUTXBXSQ-UHFFFAOYSA-N	PubChem
Primary Targets	COX-1 (P23219), COX-2 (P35354)	PubChem
Binding Sites	Ser530, Tyr385, Arg120	PDB ID: 3N8Z (COX-1)
Half-life	0.25 hours	DrugBank (DB00945)
Bioavailability	~68%	DrugBank
Onset of Action	~15 minutes	DrugBank
IC50 (COX-1)	2.4 μM	ChEMBL (CHEMBL25)
Binding Affinity (COX-1)	-7.3 kcal/mol	PDB/ChEMBL

Simulation Model

A single-compartment model was used to estimate plasma concentration (C) over time (t) based on first-order kinetics:

$$C(t) = C_0 \cdot e^{-kt} \quad \text{where} \quad k = \frac{\ln(2)}{\text{half-life}}$$

Pharmacodynamic effect (E) was modeled via a Hill-type sigmoid inhibition curve:

$$E(t) = \frac{E_{\max} \cdot C(t)^h}{IC_{50}^h + C(t)^h}$$

where h=1, E_{max}=100%, and IC50 = 2.4 μM.

Results

The simulation showed an initial peak plasma concentration (~500 mg dose / 5L blood volume ≈ 100 mg/L ≈ 555 μM), followed by rapid decay over 4 hours. The pharmacodynamic effect remained near maximal (≥90%) for approximately the first 1.5 hours of the simulation. A rapid decline in effect was observed thereafter, corresponding to the time at which plasma concentrations fell below the IC_{50} threshold of 2.4 μM. This behavior reflects the nonlinear, buffered nature of sigmoid inhibition kinetics.

A dual-axis plot was generated using Matplotlib to visualize the concentration vs. effect over time, illustrating the temporal relationship between pharmacokinetics and pharmacodynamics.

Conclusion

This simulation validates the feasibility of building scientific-grade models using only open-source software and public biomedical datasets. The codebase and database schema are modular and extensible, designed to support further drug simulations, dose optimization studies, and educational visualization tools. Future extensions will include support for multiple drug compounds, machine learning integration, and web-based accessibility.

Acknowledgments

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developed entirely on a Linux system using open-source libraries, including SQLite, NumPy, SciPy, and Matplotlib.

References

1. Aspirin: Uses, interactions, mechanism of action | drugbank online. (n.d.). https://go.drugbank.com/drugs/DB00945

2. Bank, R. P. D. (n.d.). *3N8Z: Crystal structure of cyclooxygenase-1 in complex with Flurbiprofen*. RCSB PDB. https://www.rcsb.org/structure/3N8Z

3. Compound: Aspirin (chembl25) - chembl. (n.d.). https://www.ebi.ac.uk/chembl/explore/compound/CHEMBL25

4. U.S. National Library of Medicine. (n.d.). *Aspirin*. National Center for Biotechnology Information. PubChem Compound Database. https://pubchem.ncbi.nlm.nih.gov/compound/aspirin

5. Uzzaman, M., & Mahmud, T. (2020, March 4). *Structural modification of aspirin to design a new potential cyclooxygenase (COX-2) inhibitors*. In silico pharmacology. https://pmc.ncbi.nlm.nih.gov/articles/PMC7056757/