



The University of Texas **Health Science Center at Houston** 

#### **School of Biomedical** Informatics

#### Introduction

There are two deep-learning-based vancomycin therapeutic drug monitoring (TDM) models (PK-RNN) where the two-compartment pharmacokinetic (PK) model theoretically outperforms the one-compartment model on prediction tasks. The results from a real-world dataset show that the two-compartment PK-RNN model does not consistently outperform the onecompartment PK-RNN model.

The hypothesis this research design wants to use simulation to test is whether the twocompartment PK-RNN model will definitely give more accurate predictions than the onecompartment PK-RNN model after adding enough measurements.

# Method

The original dataset: EHR data were retrospectively retrieved from Memorial Hermann Hospital (MHH) System to generate the PK-RNN model. All patients who received vancomycin and had any vancomycin levels were eligible. 5,483 patients with 9,504 encounters were included in the dataset.

Simulation: There will be 10 measurements simulated per dose for every patient.

The dataset for the recommended design: the same inclusion and exclusion criteria will be used on the MIMIC IV dataset to select suitable patients for the recommended design followed by the same simulation.

Types of validity	Recommended research design	Alternative resea
Statistical Conclusion	(+) Adding multiple replications will <b>increase</b> statistical conclusion validity because it will improve the confidence and significance of the results.	(+) Adding switcl conclusion validi and significance
Internal	(+) The randomness in the simulation will increase the internal validity.	(+) Switching rep used for every in increase the inte
Construct	(-) The original dataset has more patients with stable PK parameters, which may <b>decrease</b> construct validity.	(-) The lack of te construct validity
External	(+) The external validity will be <b>increased</b> since this design contains tests on different datasets.	(-) The external v design contains

# Comparison of the one- and two-compartment deep-learning-based vancomycin therapeutic drug monitoring models using simulated data

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#### **Figure 1**: PK-RNN model architecture

All data were aggregated at the timestep, and the data were fed into the models RNN updates k (vancomycin elimination rate) and v (volume distribution of vancomycin). Those two parameters and infusion data (dose and timing) were used to generate vancomycin pharmacokinetic (PK) curves with the PK formula

The vancomycin serum concentration is demonstrated in the upper figure. Blue line demonstrates the predicted vancomycin serum concentration in the patient. Blue stars indicate the actual vancomycin levels. In the middle graph, orange dots are vancomycin doses, and the green line in the lower figure is creatinine level.

## Research designs



#### Table 1: Discussion



#### Figure 2: The simple schematic time sequence of an example patient

Statistical analysis for the simulated dataset and model quality test will be provided by training the models 10 times on both datasets after the simulation and then calculating the mean and standard deviation of all the results.

Three model evaluation metrics will be used, which are Root Mean Square Error (RMSE), Mean Absolute Error (MAE), and Mean Absolute Percentage Error (MAPE).

> Figure 3: Workflow of the two research designs

# arch design

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olications make the data after simulation ndividual in the MHH dataset, thus will ernal validity.

ests on other datasets will **decrease** the of this research design.

validity will be **decreased** since this tests only on one dataset.

The two research designs will improve the pretest experiment which is training and evaluating the two models on the MHH dataset. The main difference is that the recommended research design will add multiple replications while the alternative design will add switching replications. The recommended design will test the PK-RNN models on a different dataset which is important for deep learning models when considering the generalizability.

In conclusion, the recommended research design will be more suitable for both interrupted timeseries data and the two types of PK-RNN models.



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### Conclusion

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