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MODELLING AND SIMULATION 2024

THE EUROPEAN SIMULATION AND MODELLING CONFERENCE 2024

ESM®'2024

**EDITED BY
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and
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OCTOBER 23-25, 2024

**SAN SEBASTIAN
SPAIN**

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DATA-DRIVEN MODEL FOR CHRONIC KIDNEY DISEASE PROGRESSION: A WORK IN PROGRESS

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KEYWORDS

Data-driven model, simulation, chronic kidney disease.

ABSTRACT

In medicine, data-driven models can be used to simulate disease progression and generate clinical decision support systems (CDSS). While artificial intelligence (AI) and machine learning (ML) models are common, their lack of traceability poses challenges in medical contexts, where transparency is crucial. This study aims to create a traceable data-driven model for Chronic Kidney Disease (CKD) progression without using AI or ML. The study will develop and validate a simulator based on this model with real-world data. This paper describes the development of the model, the processing of CKD patient data, the implementation of the simulator, and the validation of results.

INTRODUCTION

In medicine, data-driven models can simulate disease progression, supporting the development of clinical decision support systems (CDSS). These models, when developed using artificial intelligence (AI) or machine learning (ML) techniques Solomatine et al. (2008), often lack traceability, making it challenging to understand their internal processes and decision-making. This is problematic, as the ability to interpret and justify model outputs is crucial for clinical decision-making and gaining the trust of healthcare professionals.

Numerous studies in medicine use data-driven models, such as Frisch et al. (2021). However, there is a notable gap in research on modelling Chronic Kidney Disease (CKD), a growing public health issue defined by kidney damage lasting three or more months. CKD is assessed using glomerular filtration rate (GFR) and albuminuria and is classified into six stages based on GFR ranges (measured in mL/min/1.73 m²): G1 (> 90), G2 (60-89), G3a (45-59), G3b (30-44), G4 (15-29), and G5 (<15). The GFR value is typically estimated using equations; hence, it is referred to as the estimated GFR (eGFR). These equations are defined separately for men and women, and they use the individual's age in years and cre-

atinine level in mg/dL KDIGO (2012).

The main aim of this study is to design a data-driven model for CKD progression with full traceability, avoiding AI or ML techniques. This article details the definition of the model using statistical and data analysis methods, the adaptation of a dataset for predictions, the development of a simulator based on this model using real-world data, and the validation of results with an independent data subset. Finally, the results obtained will be discussed.

Data-driven model for CKD progression

The proposed data-driven model predicts CKD progression in new patients using historical data. It includes variables such as eGFR, CKD stage (G1-G5), age, sex, and laboratory parameters from blood tests, including creatinine, albumin, sodium, potassium, glucose, urea nitrogen, platelet count, and alkaline phosphatase. To reflect the progression of the disease, the model considers that patients may have multiple records at each stage corresponding to different blood tests, and also in different stages. This initial model definition does not incorporate the time variable. This is because the primary objective is to determine the values of the variables at each stage of the disease, temporarily setting aside the rate at which it progresses. Future expansions of the model will include additional information such as progression rate and medications.

The primary feature of the model lies in its application of data analysis and statistics to the dataset for predicting the progression of CKD in a new patient. This approach ensures that the obtained results are traceable and explainable. The procedure involves determining the patient's stage and subsequently predicting their progression through subsequent stages. This second part is conducted following a series of tasks. In this explanation, a patient P in stage G2 is considered as the input, and its progression to G5 is regarded as output. Figure 1 shows the process for predicting the progression from G2 to G3a. The words in blue indicate the parameters that can be modified by the user, and they are: *similarity criteria* (Euclidean or Cosine), *similarity value* (value $\in R$), *similarity variables* (list of

variables), *age window filter* (value $\in R$), *new age option* (CDF filtered or Similar) and *new age filter* (value $\in R$). The words in purple are the new variable values for the patient in G3a.

The first task obtains records of G2 patients similar to P using the *similarity criteria* (cosine similarity or Euclidean distance) and the *similarity value* (percentage or distance) applied to the variables specified by *similarity variables*. The internal process of this task compares P with a subset of real G2 records that have been previously filtered by P 's sex and its age plus the *age window filter* parameter. For cosine similarity, a record is included if its comparison value meets or exceeds the specified percentage. For Euclidean distance, a record is included if the comparison value is less than or equal to the specified distance. If this set, known as the P window in G2, is empty, progression cannot be estimated.

Once the records within the window have been computed, their real progression towards G3a is obtained. If no records show progression to G3a, the procedure cannot continue. In such cases, an attempt should be made to estimate progression to another stage like G3b or G4 from the same window of P in G2. If records are available, the age for P in G3a is determined according to the *new age option* parameter. If 'Similar' is selected, the age for P in G3a matches the age of the most similar patient in the window who progressed to G3a. If 'CDF filtered' is chosen, the cumulative distribution function (CDF) table t is calculated for the age values in the progression records of real patients in G3a. Next, a uniformly distributed random decimal r between 0 and 1 is generated. Then the variable value v from table t whose CDF value is the closest to r is used as the value of AGE_YEARS.

Subsequently, data from the G3a subset is filtered using the age calculated plus the *new age filter* parameter. Laboratory variables are then calculated from this filtered data, using the same procedure of CDF table and random value. Finally, the eGFR value is obtained and checked to ensure it falls within the defined range for G3a. If affirmative, the progression of P from G2 to G3a is finished. If negative, no progression to G3a is achieved. This scenario may occur if there are limited progression records, resulting in age and creatinine values that, when applied to eGFR equations with patient sex, yield out-of-range results. At this point, the process of generating new variables could be repeated, but we have chosen not to do so.

Following this, the entire procedure is repeated based on the data calculated for P in G3a: calculating its window of similar real patients in G3a, obtaining the evolution of these records towards G3b, and calculating the values of the new variables for P in G3b using the evolution data. By repeating this sequence, the progression of P towards G4 and subsequently towards G5 can be estimated.

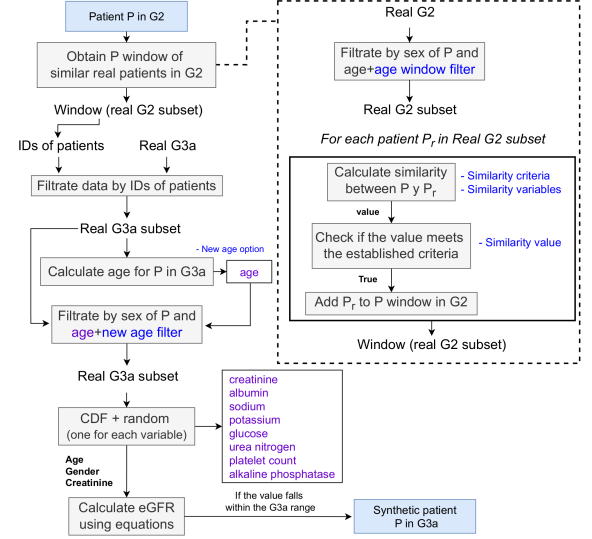


Figure 1: Process for predicting CKD progression.

Data preprocessing

This study uses the MIMIC-III 1.4 dataset Johnson et al. (2016), which comprises clinical data for over forty thousand patients admitted to critical care units at Beth Israel Deaconess Medical Center (Boston, USA) from 2001 to 2012. Specifically, the selected data includes general patient information, details of admissions and results of laboratory tests conducted during each stay. Before using this information in the simulation process, it was necessary to perform several tasks in the dataset: conditioning, filtering and reduction.

The **conditioning** process aimed to reorganise the tables into a comprehensive format, with each row containing complete information about the patient, the admission, and one laboratory result. Thus, for each patient admission, there will be as many rows as laboratory tests conducted. In order to do this, the tables for patients, admissions, diagnoses, and laboratory results were processed and merged. Finally, two new columns were added: one for eGFR, calculated using the equations mentioned previously, and another for the CKD stage. The **filtering** task involved selecting rows relevant to CKD patients by using 28 diagnostic codes for CKD and related conditions, along with 69 laboratory item codes from blood and urine, corresponding to the analytical variables defined in the model. The conditioned data were filtered by these codes, resulting in a table of CKD patients and their relevant laboratory parameters. Lastly, during the **reduction** task, the 69 columns of laboratory items were reduced: for each analytical variable defined in the model, the column with the greatest amount of data was selected.

In summary, each row in the final table contains the results of one blood test for a CKD patient during a hospital admission: PATIENT.ID, HADM.ID (Admission

identifier), eGFR (Estimated GFR, mL/min), AGE-YEARS, FEMALE (Female (1) or Male (0)), 50912 (Creatinine in mg/dL), 50862 (Albumin in mg/dL), 50863 (Alkaline phosphatase in IU/L), 50931 (Glucose in mg/dL), 51006 (Urea nitrogen in mg/dL), 51265 (Platelets in K/uL), 50983 (Sodium in mEq/L), 50971 (Potassium in mEq/L). The final table contains 6273 rows for 591 patients in G1, 15035 rows for 1702 patients in G2, 17977 rows for 2440 patients in G3a, 27084 rows for 3033 patients in G3b, 35783 rows for 3094 patients in G4 and 36873 rows for 2178 patients in G5.

Validation

The simulator based on the model was implemented in Python. The validation process was configured using two new parameters: *validation stages* and *validation percentage*. The former specifies the stages (e.g., G2 to G5) for patient data used in validation. From the pool of identifiers meeting this criteria, a random sample is selected based on the *validation percentage*. This sample is used for the validation, and the other is used for the data-driven model in the simulator. The parameters for the validation process were the following: Euclidean (similarity criteria), 0.5 (similarity value), [eGFR, Creatinine, Female, Age] (similarity variables), 0.5 (age window filter), CDF filtered (new age option), 0.5 (new age filter), 20% (validation percentage) and G2-G5 (validation stages). Patients in G1 were not considered for validation as they exhibit greater disparities due to the absence of an upper limit for the eGFR value.

Firstly, a simulation was carried out for each patient from G2 to G5. Subsequently, simulations were performed starting from other states of the validation records, in this case G3a, G3b, and G4. These results will enable an analysis of the accuracy of simulations starting from real patient data in more advanced stages, thus requiring fewer simulation steps. With this configuration, 2,975 rows corresponding to 45 different patient identifiers were used as validation data. The validation process resulted in a table with a total of 3,950 rows; this value is greater than the number of validation rows because there are simulations starting from different initial stages for the same patient. In the following subsections, the analysis of the results is explained.

Patient results

An analysis was performed to verify the performance of the model and simulator by visualising the differences between the real and simulated mean eGFR for an individual patient. The results obtained for the combinations of each CKD stage and initial stage were analysed to determine the influence of successive simulation steps. eGFR was chosen for this analysis because it is the principal indicator of CKD progression.

For the initial analysis, the mean eGFR was calculated

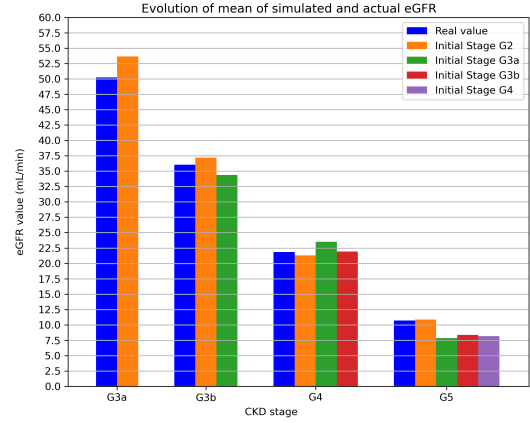


Figure 2: Simulated and real mean of eGFR for one patient.

for the validation data grouped by patient and CKD stage. Subsequently, the mean eGFR was calculated for the simulation results grouped by patient, CKD stage, and initial stage. Figure 2 illustrates these results for a specific patient, where the blue bars depict the real progression, and the other bars show the simulated progression for each initial stage. The graphic begins at G3a because the first simulated result is derived from G2 to G3a. In this case, it is observed that the simulated value in G3a (starting from G2) is 3.4 units higher than the real value. Moving to G3b, there are two simulated values: in orange from the initial stage G2, and in green from the initial stage G3a. Both are close to the real value, with differences of +1.17 and -1.65, respectively. In G4, the simulated values from G2 and G3b show very small differences from the real value (-0.52 and +0.11), while the green value is slightly higher (+1.66). Finally, in G5, the orange value from simulation starting from G2 closely matches the real value (+0.1502), whereas the others differ by approximately -2.5 units.

For the second analysis, the results were grouped according to patient identifier and CKD stage (G3b, G4 or G5). For each group containing more than one row, the initial state that generated the smallest difference between the mean simulated eGFR and the mean real eGFR was identified and counted. These results are presented in the third column in Table 1. It is noteworthy that in no case did starting from the previous state yield the best results. In the case of simulations in G5, approximately 60% of the best results were obtained from simulations that began in G2 and G3a (involving 4 and 3 simulation steps, respectively).

General results

To assess the quality of predictions overall, metrics based on the eGFR variable were calculated. Simulated eGFR values served as the estimated values, while the mean eGFR of the validation records (computed in the

Table 1: Frequency of the smallest difference between the mean simulated eGFR and the mean real eGFR, grouped by CKD stage and the initial stage.

CKD stage	Initial stage	Frequency
G3b	G2	26 (60.46%)
	G3a	17 (39.54%)
G4	G2	11 (25%)
	G3a	19 (43.18%)
	G3b	14 (31.82%)
G5	G2	12 (27.27%)
	G3a	15 (34.09%)
	G3b	11 (25%)
	G4	6 (13.64%)

Table 2: Metrics for the comparison between real and simulated eGFR.

CKD stage	Initial stage	MSE	RMSE	MAE
G3a	G2	15.93	3.99	3.32
G3b	G2	18.22	4.27	3.61
	G3a	21.49	4.64	3.89
G4	G2	20.24	4.5	3.84
	G3a	18.07	4.25	3.61
	G3b	17.64	4.2	3.53
G5	G2	18.65	4.32	3.51
	G3a	16.75	4.09	3.28
	G3b	15.51	3.94	3.21
	G4	19.2	4.38	3.58

previous analysis) served as the actual values. The comparison was conducted for each initial stage, and the data were grouped by CKD stage. The results obtained are presented in Table 2. The values in columns MSE (mean squared error), RMSE (root mean square error) and MAE (mean absolute error) are expressed in the unit of measure of eGFR (mL/min).

In general terms, the average RMSE is 4.258 and the average MAE is 3.538. This indicates that simulated eGFR values differ from real values by between 3.5 and 4.3 mL/min. In each row, the RMSE and MAE metrics show a slight variation, differing by less than 1 unit. Specifically, MAE consistently yields lower values as it penalises errors less severely. However, given the minimal discrepancy between RMSE and MAE, it can be concluded that there are no significant discrepancies between real and simulated values. Within each CKD stage, we observe slight variations in RMSE and MAE values depending on the initial stage. Similar to patient-level analysis, it is notable that in cases like G5, conducting more simulation steps (from G2, G3a, or G3b) results in smaller errors compared to starting from the previous stage (G4).

CONCLUSION AND FUTURE WORK

After conducting this research, it can be concluded that the proposed objectives have been met. An initial data-

driven model for CKD progression was defined. Then, a dataset of real clinical data was adapted for this work. A simulator based on this model and dataset was developed, and simulations validated the model. Finally, the quality of predictions was assessed against real data. It is crucial to highlight the importance of providing explainable tools in the medical field. Traceability remains a significant advantage of the data-driven model over other ML or AI techniques.

After the validation, it was observed that the best results were not obtained in a single simulation step. This finding is particularly significant, as it might initially be assumed that starting from the previous state would provide the most accurate results, involving a single simulation step based on the real data of the validation patient. Therefore, it is concluded that the methodology presented improves result quality by utilising the patient's evolution history and similar real patients.

Future work will focus on analysing correlations among the variables defining the patient, with the aim of incorporating any detected correlations into the model's predictions. Integrating the time variable into both the model and simulator is also a key objective. Once this is achieved, the accuracy of the new results will be compared to those from a temporal series algorithm, such as LSTM. Long-term goals include validating the model with medical professionals and implementing a Clinical Decision Support System (CDSS) to offer treatment recommendations for new CKD patients.

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