Validation of a new multi-compartment model to personalize dialysis therapy

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OBJECTIVES

Health conditions and quality of life of uremic patients treated with hemodialysis could be improved by tailoring the treatment on each patient, whereas dialysis is usually based on standard not patient-specific parameters. [1-2]
This work aims at validating a mathematical model, describing fluid and solutes kinetics, in order to simulate the single patient reaction to the therapy and allow the clinician an offline evaluation of the settings and prescriptions to improve the treatment outcomes. [3]
This work was part of the Project DialysIS, founded by a Cross-border Cooperation Programme (INTERREG IT/CH 2007-2013) and concerning the optimization of the therapy through the development of optimized clinical protocols and the therapy personalization. [4]

METHODS

The validation of the kinetic multi-compartment model (3 pools for the fluid balance and 2 pools for the mass balance) was performed using clinical data (blood parameters, therapy prescription and machine settings) recorded from 50 patients treated at A. Manzoni Hospital, Lecco. The acquired data were used to estimate each patient's membrane parameters, needed to tune the model. These parameters are related to the mass exchange across the patient-specific cellular (corresponding to "k", in fig.1) and capillary membranes (ρ in fig.1) and to the dialyzer membrane efficiency (η in fig.1). A sensitivity analysis was performed on the parameters, in order to evaluate the influence of each parameter on each output. Main plasmatic electrolytes and catabolites trends have been simultaneously evaluated.
Patient's membrane parameters were computed using a constrained non-linear optimization algorithm (CNLO).
Results have been compared with those previously obtained on data acquired at the Regional Hospital of Lugano.

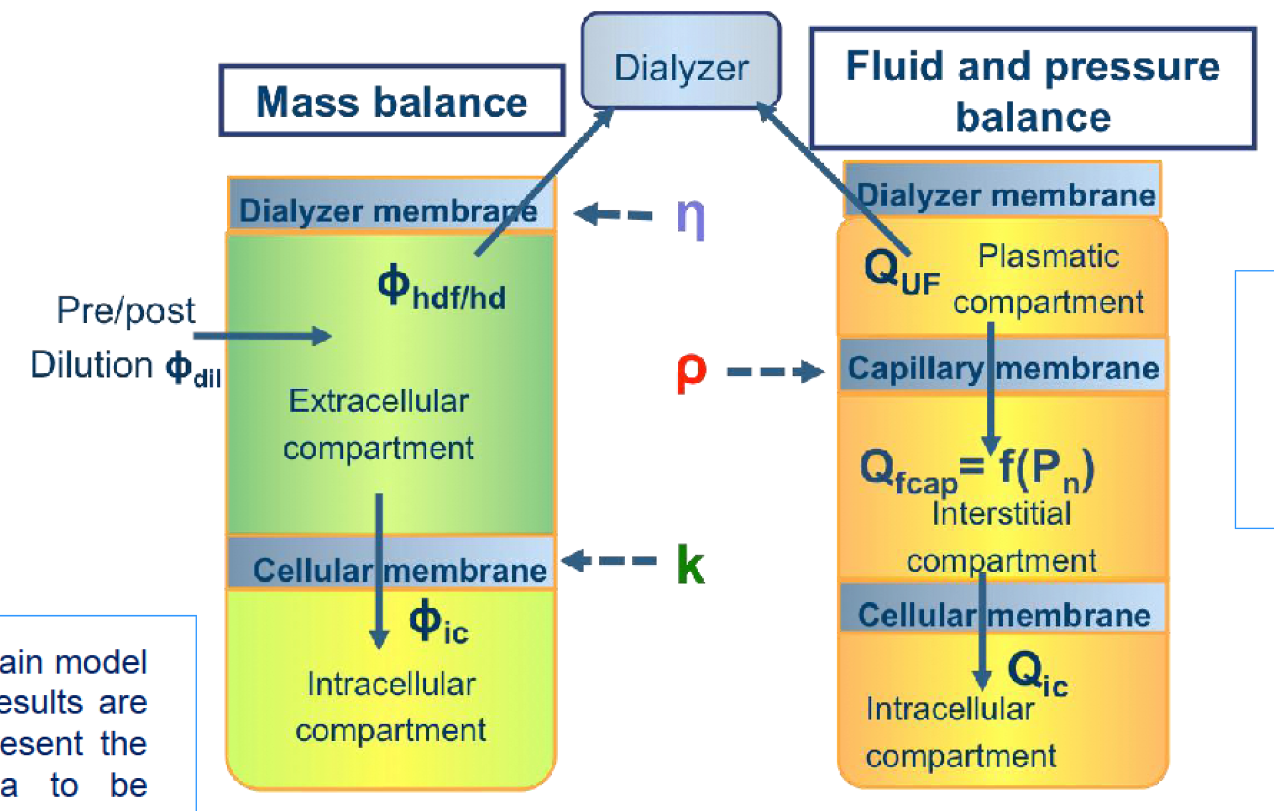


Figure 1 - Scheme of the body compartments as considered in the model. Fluid and mass exchanges across the relevant biological and artificial membranes are represented.

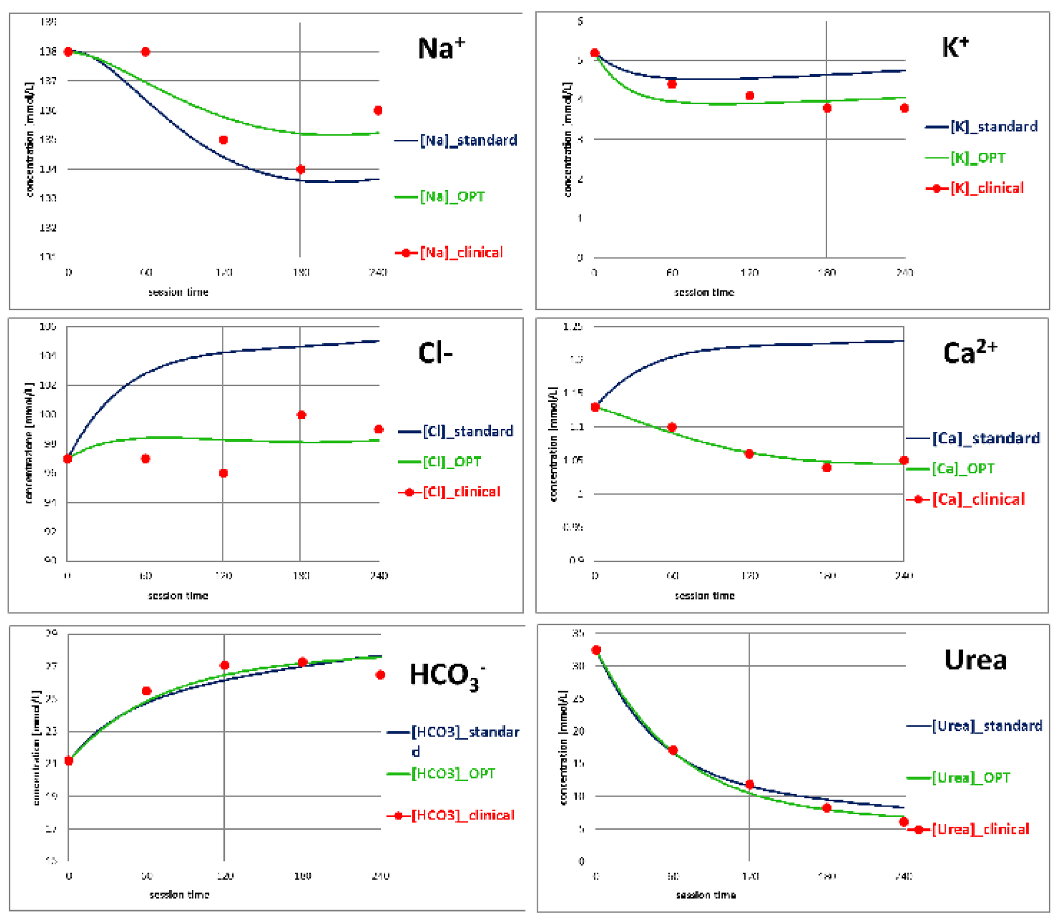
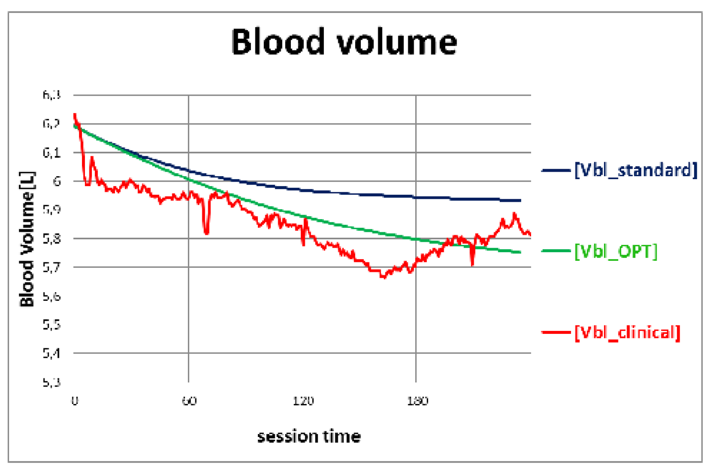


Figure 2 - Plots of the main model outputs, on which the results are focused. Red dots represent the clinically acquired data to be compared with solutes concentrations trends in the optimized model (green line) and in the model set with standard values for the patient-dependent parameters (blue line).



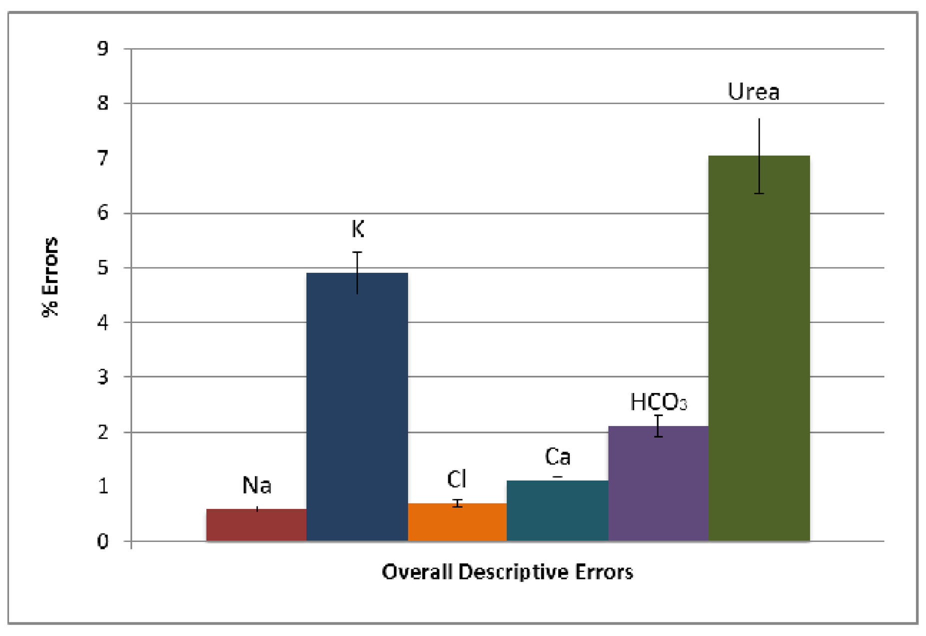


Figure 3 - Overall averaged descriptive errors evaluated for each solute, comparing the optimized model results with the clinical data.

RESULTS

Solutes concentrations and volume profiles simulated in about 125 dialysis sessions by the kinetic model optimized through the CNLO method, show to better fit clinical data than using the non-optimized model, as already noticed on the Lugano data (fig. 2). The effects of different parameter settings are highlighted in terms of different molecules removal efficiency.
The overall descriptive error of the model (fig.3), evaluated as percent difference between simulation outputs and clinical measurements, is always below 10% for the solute concentrations and 7% for the blood volume trend. These results were consistent with those obtained on the previous set of data and demonstrate the reliability of the model and the applicability to different clinical protocols.

CONCLUSIONS

The kinetic model, coupled with a robust method to identify patient-specific parameters, allows an accurate and reliable prediction of electrolytes and fluid transfer during dialysis. Therefore, the model can be used by the clinician as a decision support system to improve dialysis therapy planning, evaluating the effects of different therapy settings or prescription in an integrated and efficient way.

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