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Background and aim

Computational models can be used in dialysis divisions to predict the patient's response to the treatment in terms of main electrolytes', breakdown products', and body fluids volumes' intradialytic trends. The potential of a model based on a patient's characteristics in terms of treatment customization is shown here, particularly for elderly ESRD patients characterized by multiple comorbidities [1]. A patient-specific model has been optimized over the course of InterACTIVE-HD 2.0 project involving several patients in treatment in Italian and Swiss centers [2].

Methods

InterACTIVE-HD 2.0 data were acquired in accordance with the guidelines of ethics committees, for 3 consecutive phases in Lugano and Como centers, and for 2 phases for Chur, Sondrio, and Varese, enrolling a total of 145 patients. The acquisition included **clinical records, BIA, machine and laboratory data** (for the latter, see the table below).

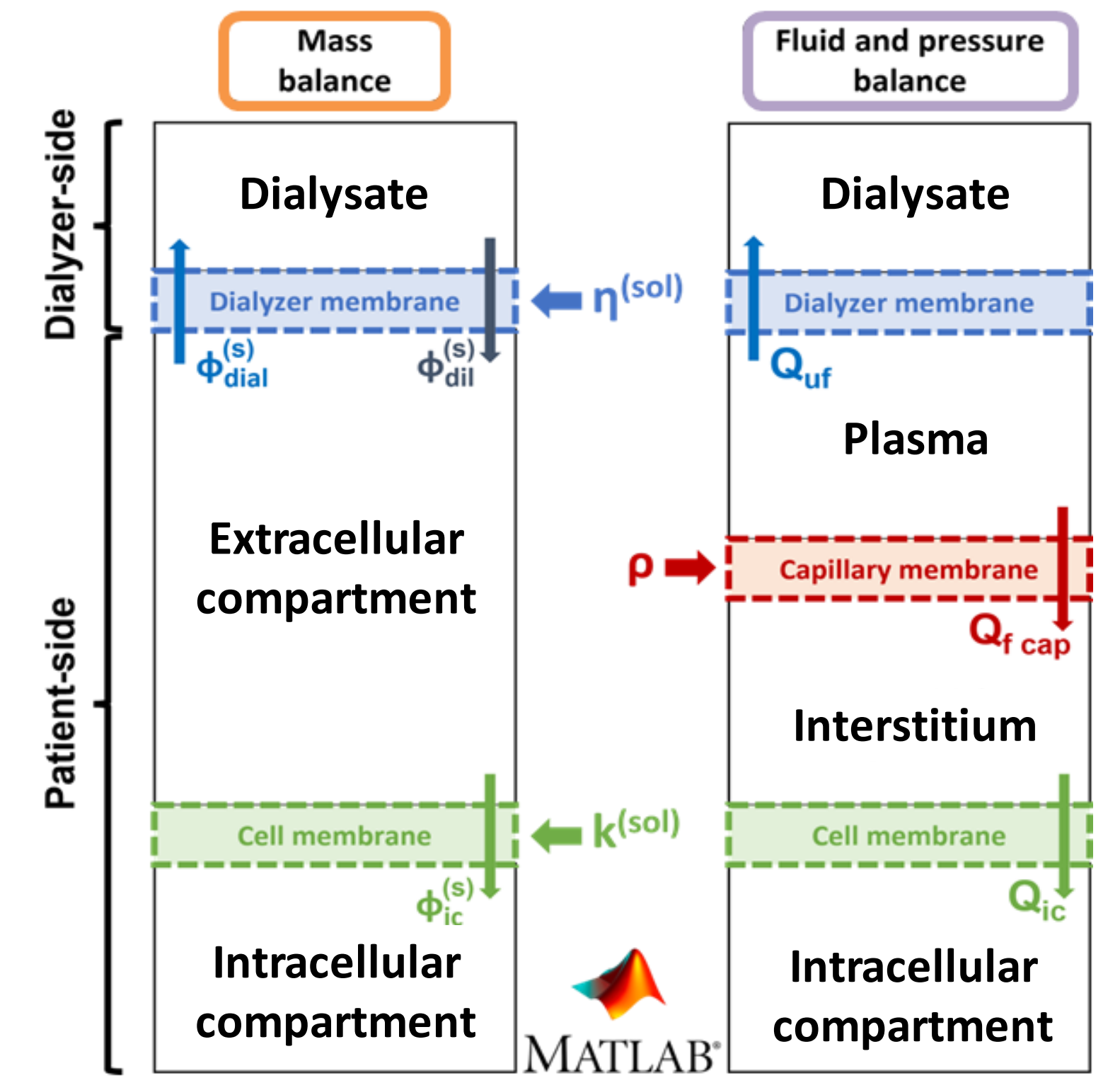
Parameter	InterACTIVE-HD 2.0
pH and pCO ₂	∇hour
Ht and Hb	
Na ⁺ , K ⁺ , Cl ⁻ , Ca ²⁺ , HCO ₃ ⁻ , Mg ²⁺ , and phosphates	
Glycemia and albumine	
Urea and creatinine	
Calcemia _{TOT}	∇(start + end)
PTH	(start + end) ^{1st}
B2M	
BNP dosage	∇minute-by-minute
Machine data	

Clinical data acquisition frequency

∇ stands for every session.
1st stands for the only session of each acquisition phase.

For the training of the model (ID), 3 consecutive sessions were chosen, to avoid overburdening the clinical staff and drawing further blood from patients which would expose them to possible hypotensive episodes: by giving as input the acquired data, for each session, a set of patient-specific parameters modulating mass and fluid balance across dialyzer, capillary, and cell membranes (η - ρ - κ) is obtained.

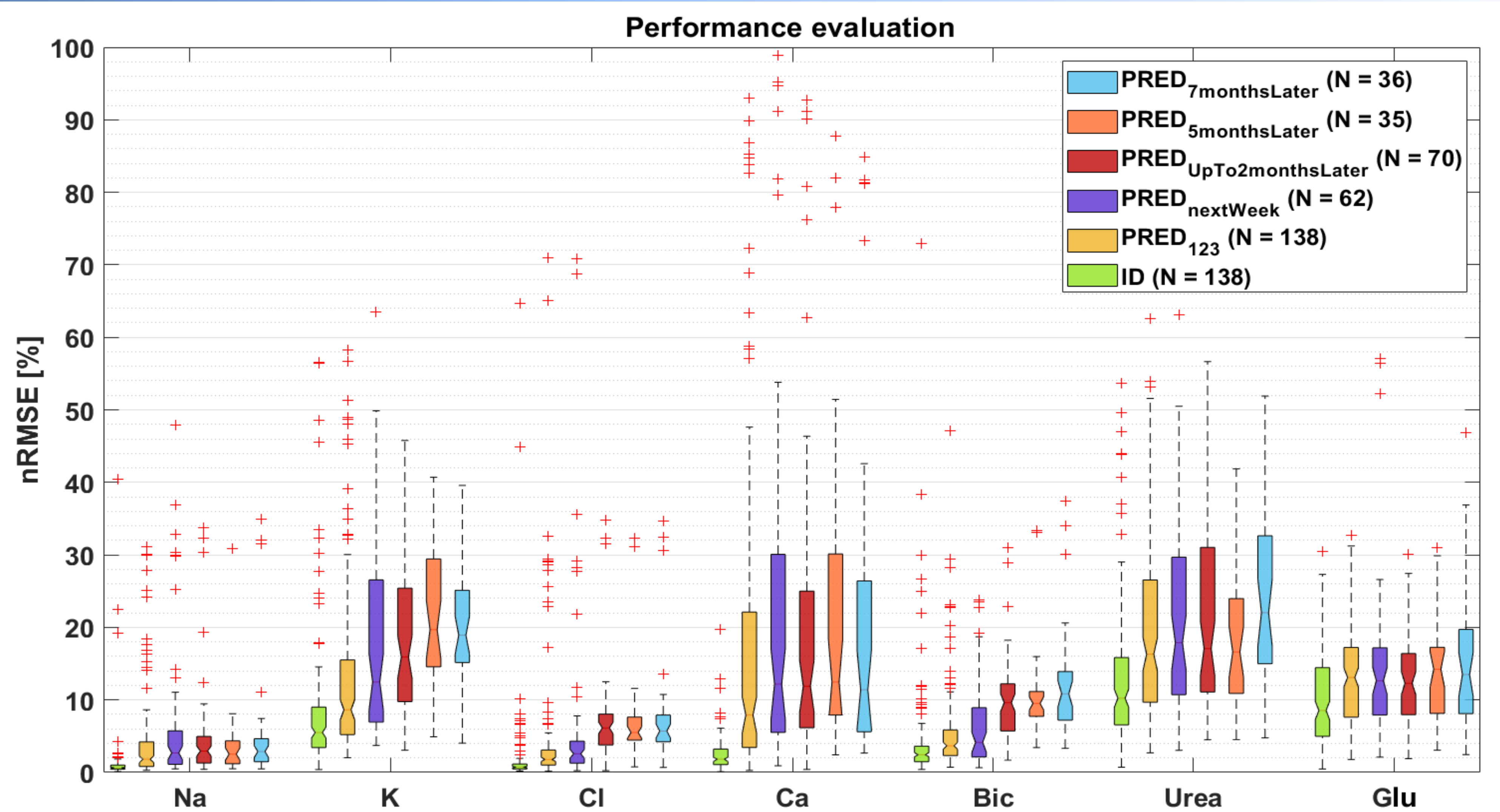
Once the training is completed and the average of the 3 sets of patient-specific parameters is obtained, the model can be run in predictive mode (PRED), using as input only the patient's conditions at the beginning of the session to be simulated: as a result, the prediction of the patient's response to the entire dialytic session is given. Predictive accuracy was evaluated as nRMSE by using available data from Lugano, Como and Varese, both for the training sessions and the following ones.



Results

Below, baseline characteristics of the population enrolled for InterACTIVE-HD 2.0 project, i.e., gender, age (years), dialysis vintage (months), type of HD therapy, initial solutes' plasmatic concentrations (mmol/L), and presence of comorbidities, are reported.

Parameter	InterACTIVE-HD 2.0
Gender	27 M – 18 F
Age	76 (68, 83)
Dialysis age	61 (37, 113)
Therapy	226 HDF – 115 SHD
[Na ⁺] _{in}	138.00 (136.00, 140.25)
[K ⁺] _{in}	4.80 (4.40, 5.20)
[Cl ⁻] _{in}	103.00 (99.00, 105.00)
[Ca ²⁺] _{in}	1.11 (1.06, 1.17)
[HCO ₃ ⁻] _{in}	21.90 (19.90, 23.60)
[Mg ²⁺] _{in}	1.07 (0.97, 1.60)
[Urea] _{in}	17.90 (13.61, 22.30)
[Glucose] _{in}	7.00 (5.60, 9.03)
[Creatinine] _{in}	0.64 (0.52, 0.78)
Cardiopathy	73.33%
Diabetes	42.22%
Hypertension	86.67%



All the solutes showed difference between ID and PRED mode ($p \leq 0.001$) on the training sessions: ID median nRMSE% of 3.97% vs PRED₁₂₃ one of 7.60%. However, for Na⁺, Ca²⁺, urea, and glucose, no statistical difference was highlighted up to 7 months, while for K⁺, Cl⁻, and HCO₃⁻ a difference was highlighted after 2 months from the training ($p \leq 0.05$).

Discussion and conclusions

InterACTIVE-HD 2.0 ID nRMSEs' dispersion can be attributed to a high dialysis vintage subset of patients, itself characterized by greater variability; for urea specifically, a larger error is expected given that it undergoes sudden intradialytic variation: however, at 5 months from training, PRED nRMSE% equal to 16.61% is lower to what stated in literature [3]. In conclusion, the model shows good performances. A reevaluation of the patients every 2 or 5 months could help increasing medium to long-term predictive accuracy. A further predictive optimization can be done training the model by using also a second session after the weekend.

References

- [1] Neal, 2009, *Brief Bioinform*
- [2] Balsamello, 2023, *Artif. Org.*
- [3] Pietribiasi, 2018, *PLoS ONE*

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