# Numerical Models in Hemodialysis

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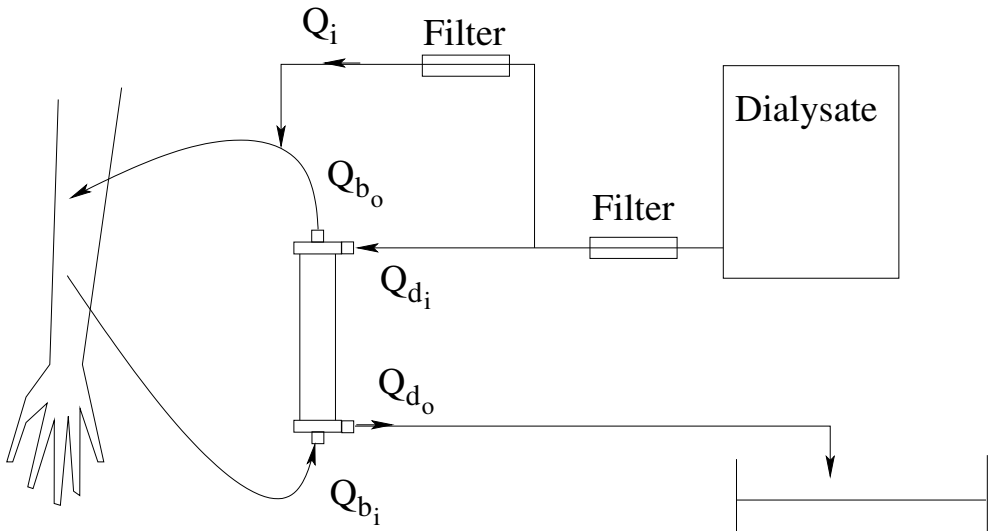
# Overview

# Introduction

Dialysis types and prescription:

- There are many dialysis types, hemodialysis (HD), hemofiltration (HF), hemodiafiltration (HDF)
- Prescription based on the frequency, the length of each treatment, the flow rates ($Q_b$, $Q_w$, $Q_d$) and sometimes the dialysis solutions is changed.




$$Q_{d_o} = Q_{d_i} + Q_i + Q_w$$
$$Q_{b_i} = Q_{b_o} + Q_w$$

# Objectives

- Experiment: Obtain the parameters of an hemodialysis model, fitting the model to real data and obtaining conclusions.
- Which is the objective of an HD model?: obtaining a method for an objective hemodialysis prescription.

# One pool model

Fick's Law:

$$\frac{d(C_e V_e)}{dt} = -K_d C_e, \tag{1}$$

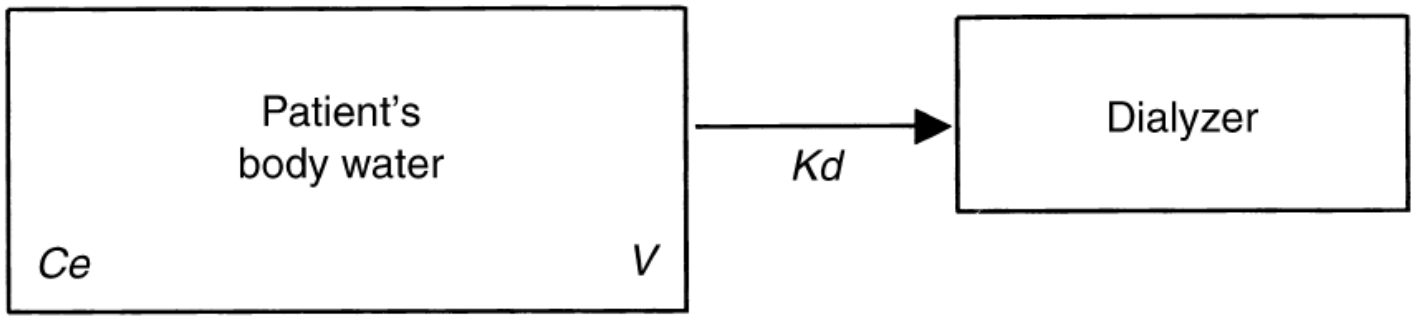



Figure: Scheme of one pool model from M. Ziólko and J. A. Pietrzyk and J. Grabska-Chrzastowska. *Accuracy of hemodialysis modeling*

KT/V prescription method:

$$T = \frac{V_e}{K_d} \ln(C(0)/C(t)) \tag{2}$$

# Two pools model

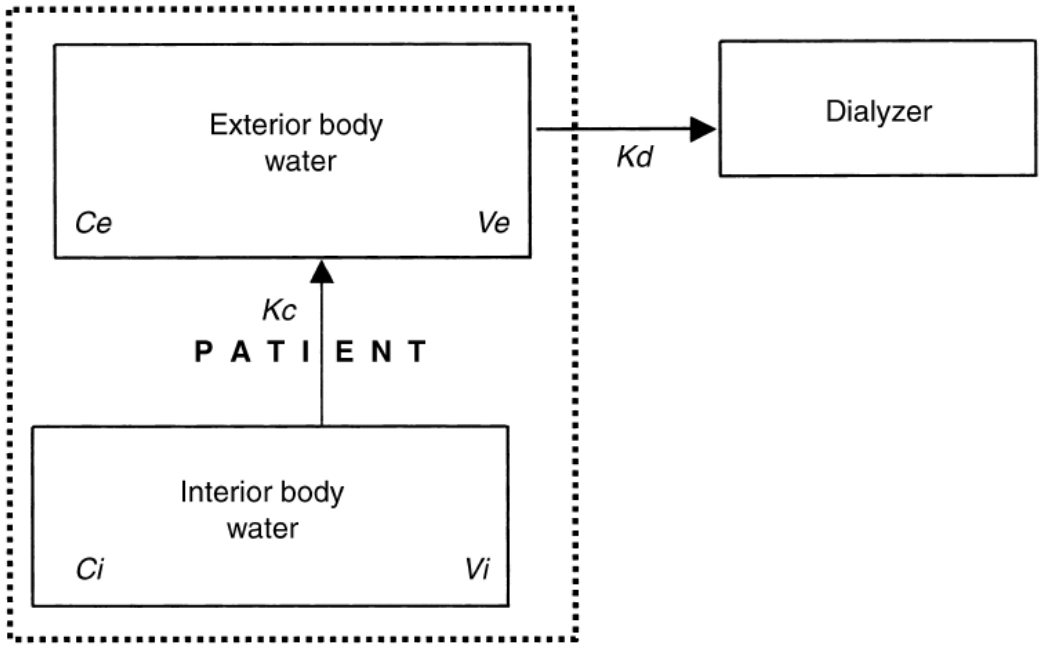



Figure: Scheme of two pools model from M. Ziólko and J. A. Pietrzyk and J. Grabska-Chrzastowska. *Accuracy of hemodialysis modeling*

$$\frac{dC_e}{dt} = -\frac{K_c(C_e - C_i)}{V_e} - \delta\frac{K_d}{V_e}C_e, \tag{3}$$

$$\frac{dC_i}{dt} = \frac{K_c(C_e - C_i)}{V_i} \tag{4}$$

# Extended model

$$\frac{d}{dt}(V_e C_e) = -K_c(C_e - C_i) - \delta K_d C_e + G_e, \tag{5}$$

$$\frac{d}{dt}(V_i C_i) = \quad K_c(C_e - C_i) + G_i \tag{6}$$

New phenomena are included:

- Generation term added.
- Total water volume variation.

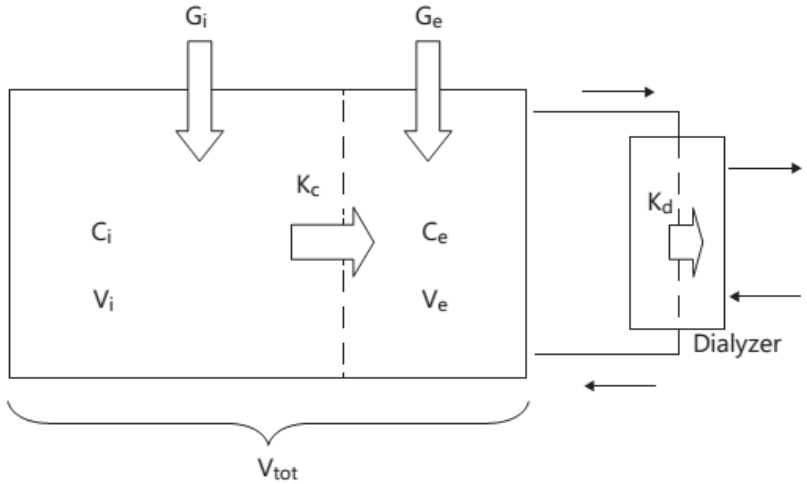



Figure: F.Maduell et al: Blood Purif 2015;39:288296 DOI: 10.1159/000375287

# Generation and volume considerations

Generation expression:

$$G_i = f_G \frac{C_e(0) - C_e(t_r)}{t_f - t_r}.$$

Total water volume:

$$V = 0.57DW$$

Fraction of external and internal compartment:

$$V_e = \alpha V \quad \& \quad V_i = (1 - \alpha)V$$

Volume rate change during and after HD:

$$\beta_d = (1 - V_{t_d}/V_{t_0})/t_d, \quad \& \quad \beta_p = \beta_d t_d/(t_f - t_d)$$

# Others considerations

Assuming that $C_e(0) = C_i(0)$, then:

$$\overline{C}_e = C_e / C_e(0)$$

$$\overline{C}_i = C_i / C_e(0)$$

Clearances:

$$\overline{K}_d = K_d / V_{t_0}$$

$$\overline{K}_c = K_c / V_{t_0}$$

# Solved system

Then the resultant system is:

$$\alpha \overline{V}_t \frac{d\overline{C}_e}{dt} = -\overline{K}_c(\overline{C}_e - \overline{C}_i) - \delta \overline{K}_d \overline{C}_e + \overline{G}_e - \alpha \frac{d\overline{V}_t}{dt}\overline{C}_e \tag{7}$$

$$(1-\alpha)\overline{V}_t \frac{d\overline{C}_i}{dt} = \overline{K}_c(\overline{C}_e - \overline{C}_i) + \overline{G}_i - (1-\alpha)\frac{d\overline{V}_t}{dt}\overline{C}_i, \tag{8}$$

# Fitting

The parameters to fit are:

$$\overline{K}_d,\ \overline{K}_c \text{ and } \alpha$$

Error function to minimize:

$$f(\overline{K}_d, \overline{K}_c, \alpha) = \sum_{j=1}^{m} (\overline{C}_j - C_j^e)^2 \tag{9}$$

# Data available from Hospital Clínic

The data available were the weight (pre and post-HD) and the concentrations for:

- urea (60Da),
- creatinine (96Da),
- phophate (113Da),
- $\beta_2$-microglobulin (11818Da),
- myoglobin (17200Da)
- and prolactin (23000Da)

measured each hour during the dialysis and 3 measures more (post-dialysis). Also the HD time of 4 or 8 h and the infusion rate ($Q_i$) of 50 or 100ml/min.

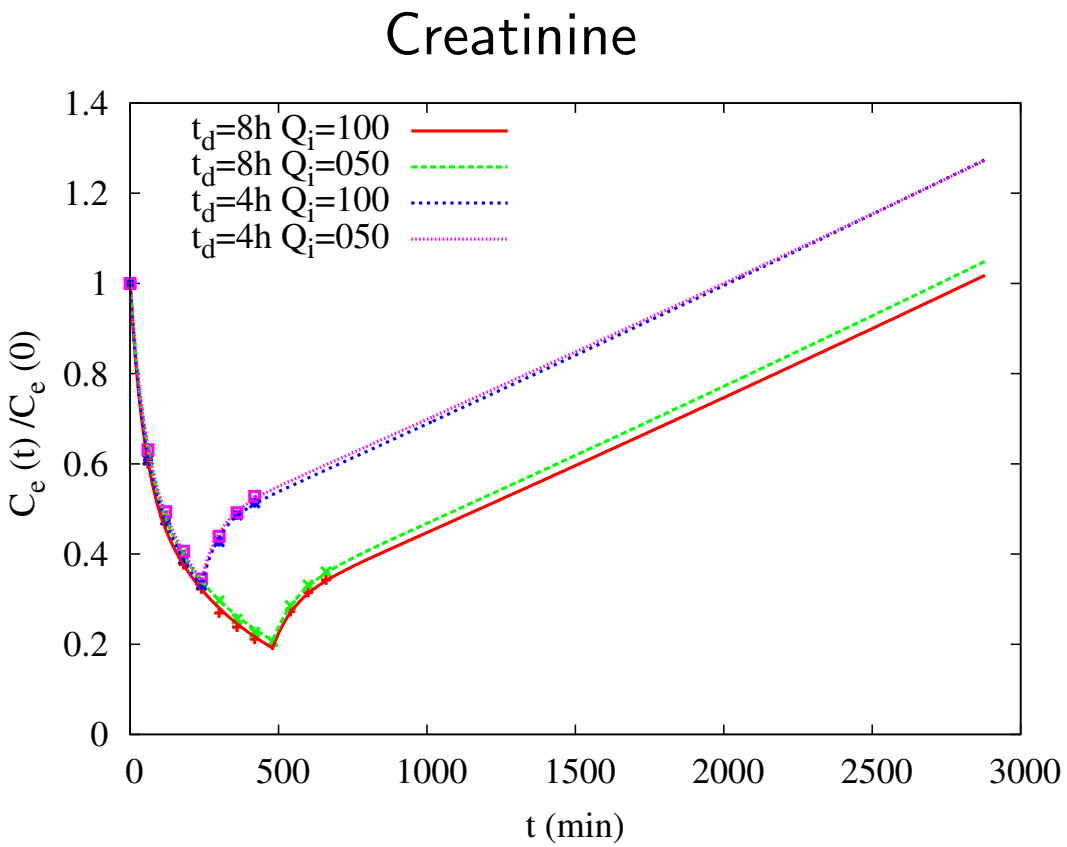
# Three models compared

- **M. 1**: Two compartmental model with $\alpha$ free parameter.
- **M. 2**: Two compartmental model with $\alpha$ free parameter, Bergtröm and Wehle correction and no change in the Volume.

$$f_{B\&W} = \frac{1}{1 + \Delta DW(t)/0.2DW}$$

- **M. 3**: Two compartmental model with $\alpha$ fixed at 0.4.

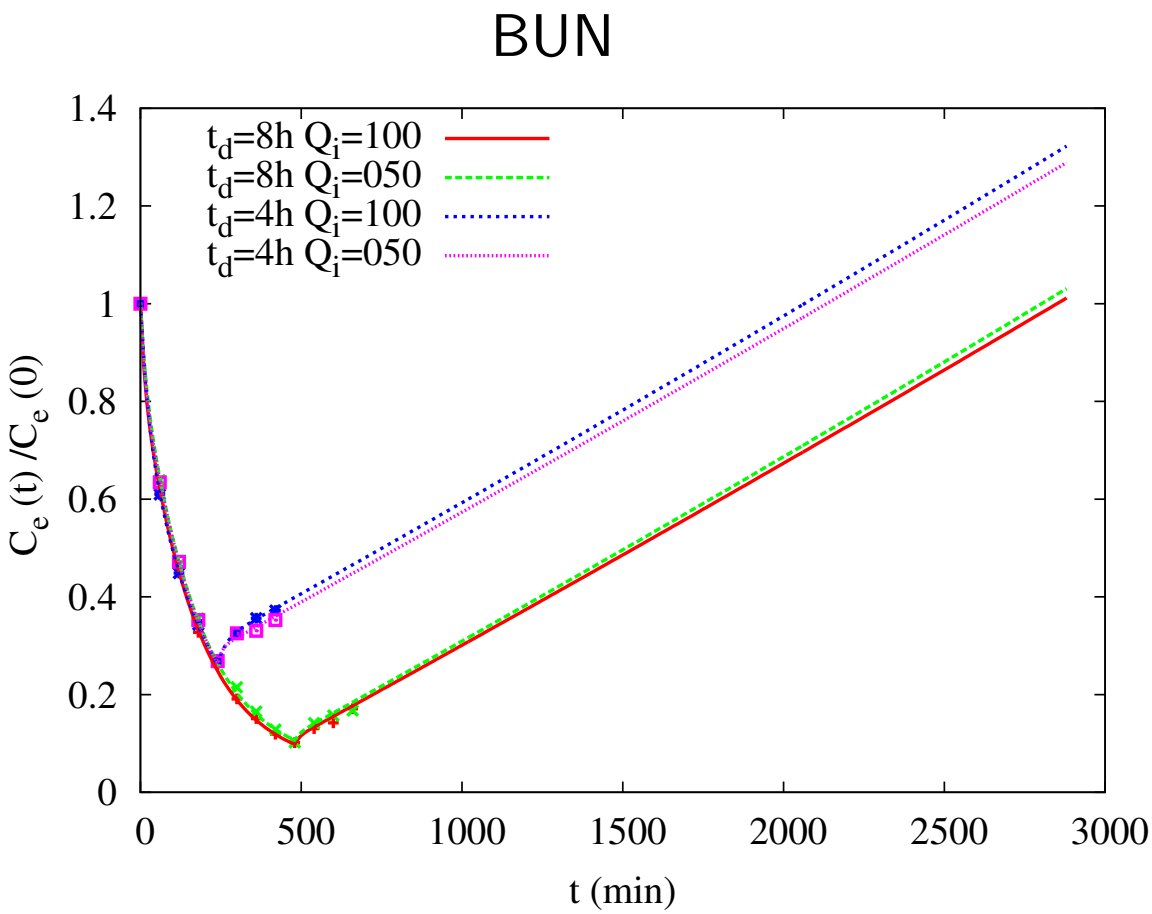
# HD, post HD and generation




Exponential extraction, rebound phenomena and generation. No great differences between models.

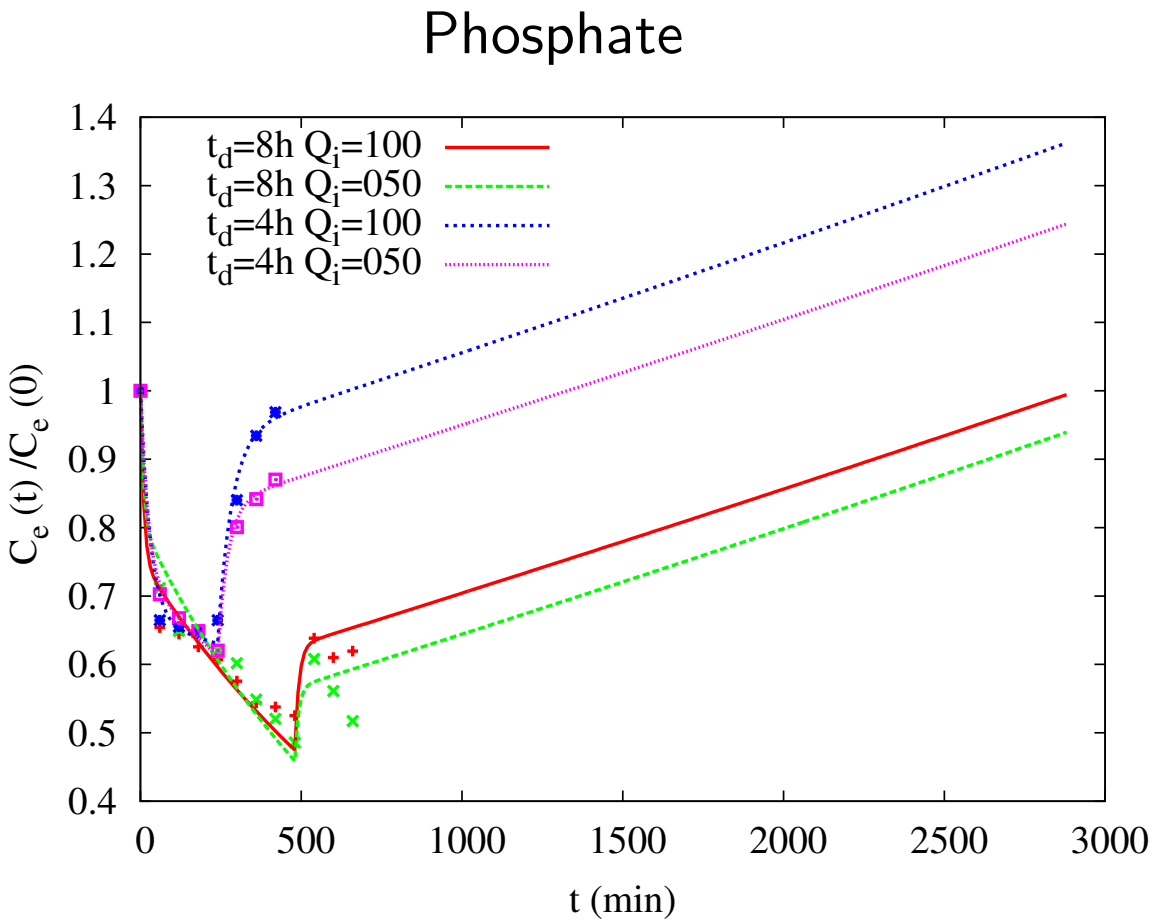
Overlapping of all HD types, filtration not affected by the value of $Q_i$.

# Low molecular weight



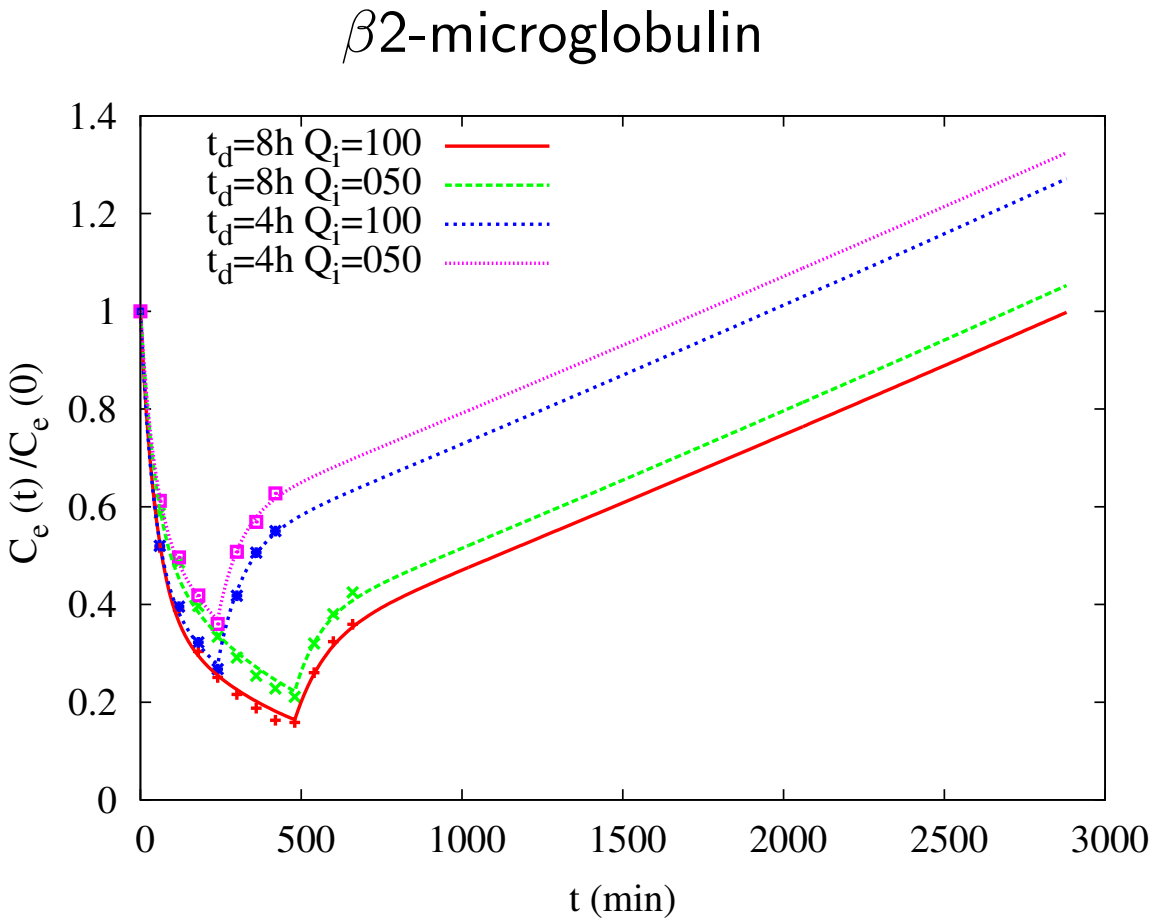

No rebound phenomena in Urea, one compartment is good. Reflected in $K_c$ results.

# Phosphate



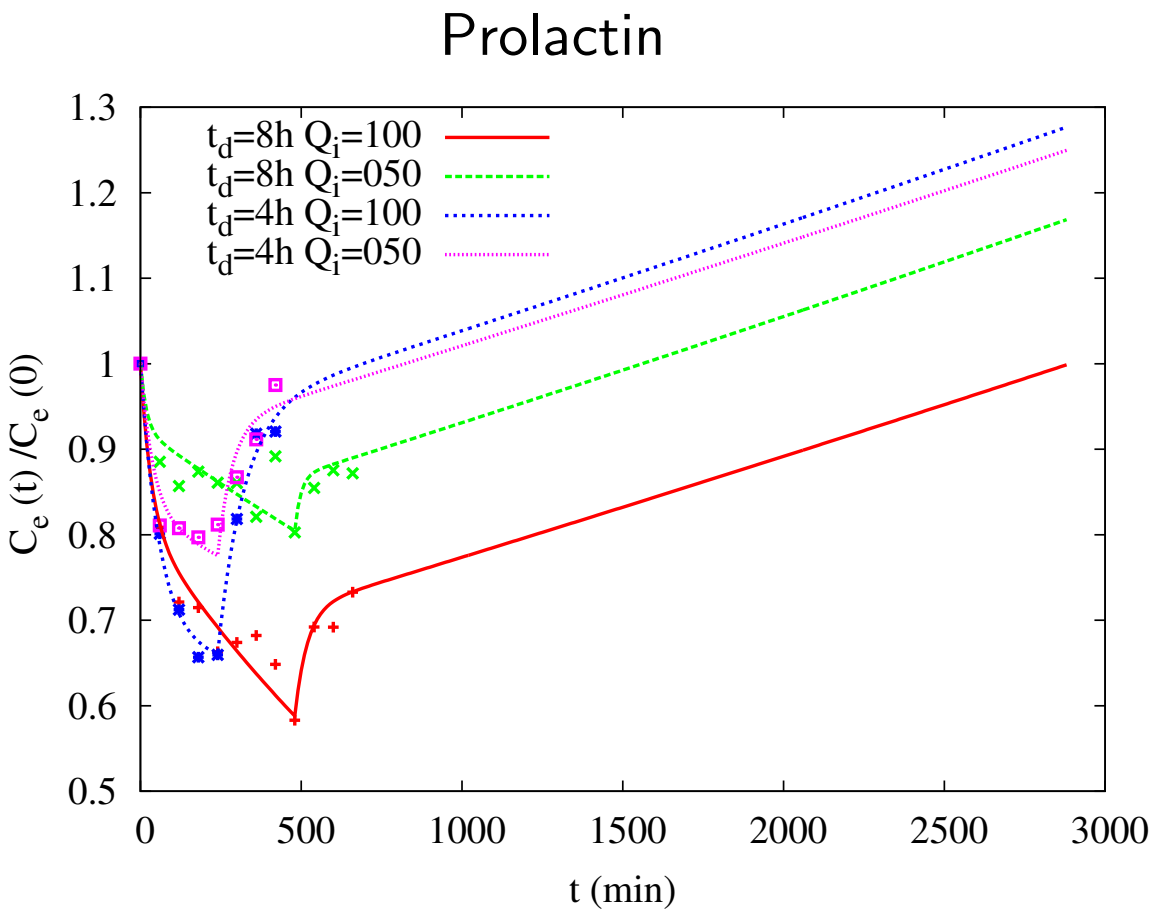

Low fraction parameter ($\alpha < 0.1$), low molecular weight.
Importance of the $\alpha$ Strange behaviour, errors added due to dialyzate.

# The $Q_i$ importance




$Q_i$ has an effect in the efficiency which is shown in the result parameters. $\bar{K}_d \sim 5E-3$ with $Q_i$ =100ml/min and $\bar{K}_d \sim 3E-3$ with $Q_i$ =50ml/min

# Measurement problem

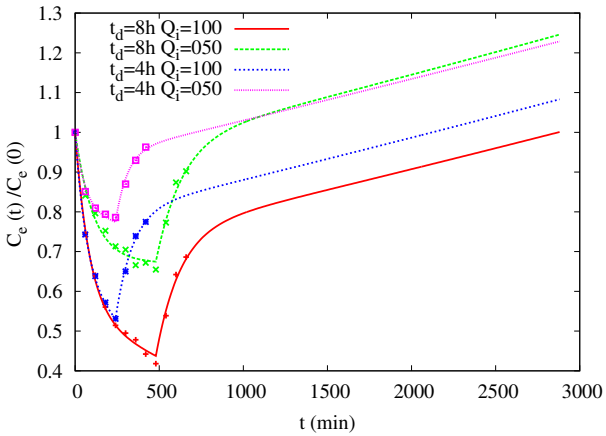



The presence of prolactin in blood is difficult to measure. $Q_i$ has an important effect in the efficiency which is shown in the result parameters.

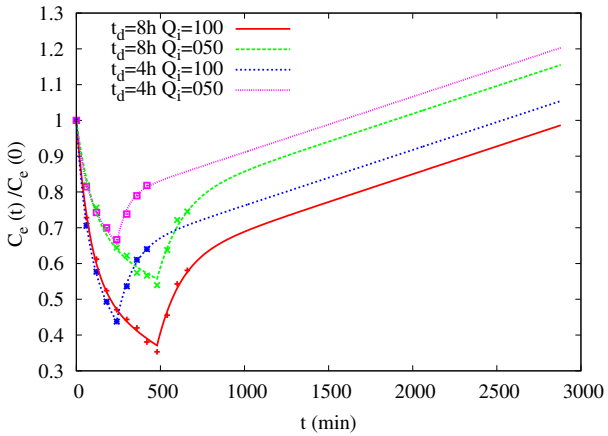
# M.1 Vs M.2 Vs M.3

## Myoglobin

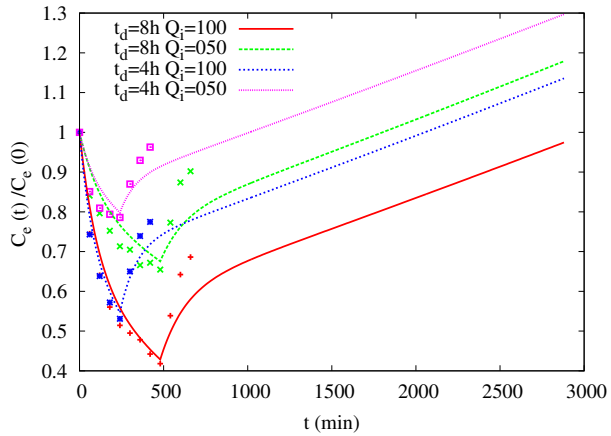
### Model 1




### Model 2




### Model 3




Including the fitting of $\alpha$ allows a better adjusting in $f(\overline{K}_d, \overline{K}_c, \alpha)$.

| | Model 1 | Model 2 | Model 3 |
|---|---|---|---|
| $Q_i$=100, $t_d$=8 | 1.30e-3 | 1.10e-3 | 35.58e-3 |
| $Q_i$=100, $t_d$=4 | 2.43e-3 | 2.0e-3 | 44.81e-3 |
| $Q_i$=50, $t_d$=8 | 0.23e-3 | 0.16e-3 | 10.38e-3 |
| $Q_i$=50, $t_d$=4 | 0.59e-3 | 0.42e-3 | 14.75e-3 |

# Error function

The minimization of the error function gives $f \sim 1E-3$ except:

- Phosphorus $f \sim 1E-0$
- Prolactin $f \sim 5E-3$

# Conclusions

- From the three models, the importance of the third parameter to which the HD has access.
- The impact of $Q_i$ on the efficiency of high molecular weight.
- Relation of the rebound time established from parameters (Intercompartmental clearance and fraction of external volume).
- Possibility to quantify the effects of the HD time, infusion flow $Q_i$ and the total mass of solutes extracted.

# Thank You
# for your attention