

CAN COMBINED ASSESSMENT OF SMALL MOLECULE UREMIC MARKERS IMPROVE PREDICTION OF DIALYSIS PATIENTS' SURVIVAL?

J. Holmar¹, I. Fridolin¹, F. Uhlin², M. Luman¹, A. Fernström²

¹Department of Biomedical Engineering, Tallinn University of Technology, Tallinn, ESTONIA

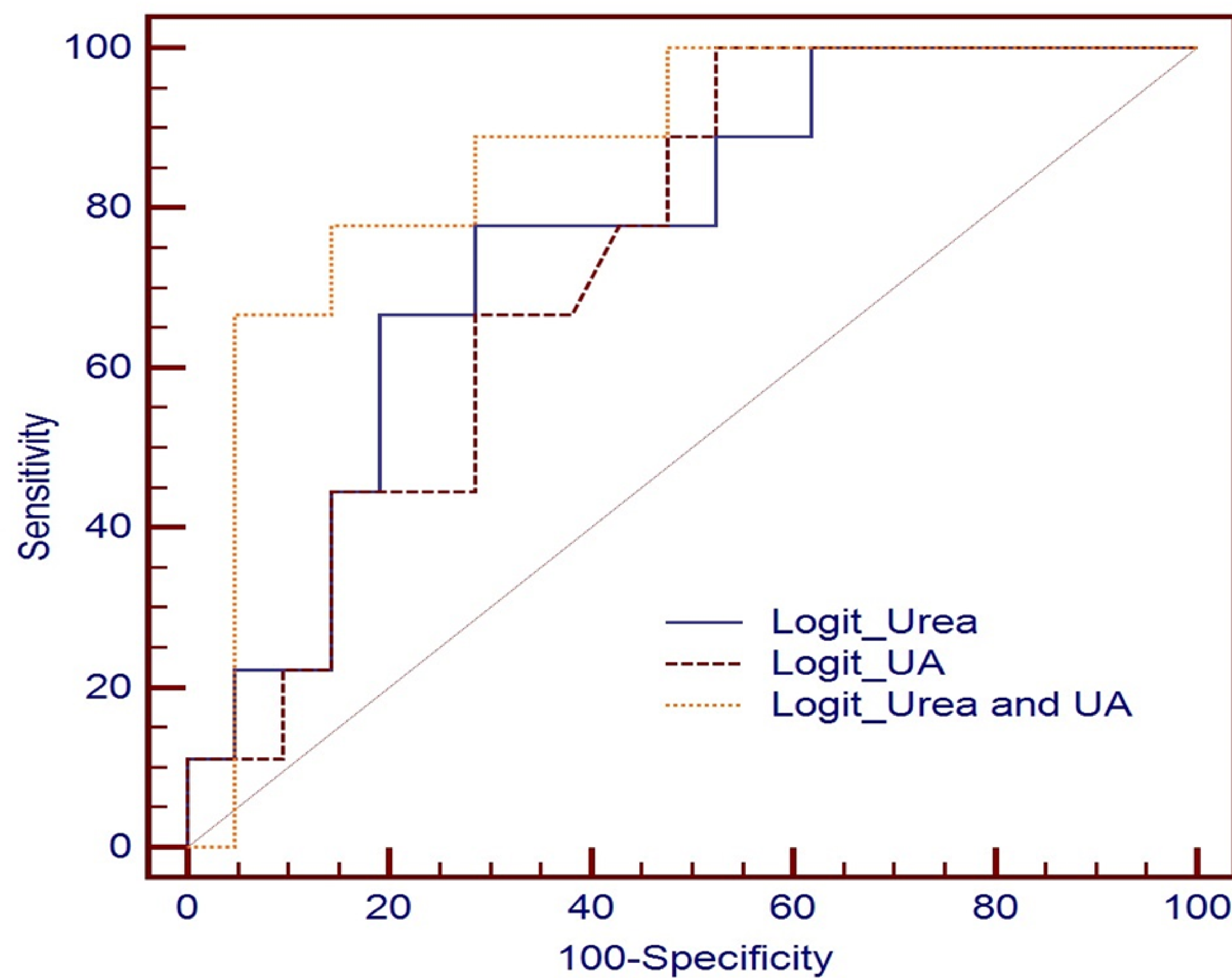
²Department of Medical and Health Sciences, Department of Nephrology, Linköping University, Linköping, SWEDEN



OBJECTIVES

- Mean life expectancy of hemodialysis patient is less than 3 years [1].
- Markers and methods for patient outcome estimation are highly longed for.
- Widely used small molecular weight markers for estimating kidney function and dialysis adequacy are creatinine and urea [2].
- High level of uric acid (UA) may play an important role in the development of hypertension, renal disease and cardiovascular events [3-8].
- In some regions, UA is considered as an essential molecule to monitor in dialysis patients [9].

The purpose of this study was to examine if simultaneous monitoring of two small molecule uremic markers, urea and UA, could be related to 3-year survival of dialysis patients.



	AUC	SE ^a	95% CI ^b
Logit_Urea	0.738	0.092	0.546 to 0.881
Logit_UA	0.762	0.0929	0.572 to 0.897
Logit_Urea and UA	0.868	0.0712	0.694 to 0.963

AUC - area under ROC curve

SE - standard error

CI - confidence interval

^a DeLong et al., 1988 ^b Binomial exact

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METHODS

Subjects:

30 dialysis patients (26 male and 4 female, mean age 73±11 years) from Linköping, Sweden.

Methods:

Baseline serum urea and UA levels were measured in clinical chemistry laboratory. Logistic (logit) regression analysis was used for creating models for 3 years survival probability estimation.

Three models were created: two single molecules based and one combined model.

RESULTS

During the follow-up 21 patients died and 9 survived. Figure 1 shows that using combined logistic regression models could lead to more accurate results, compared to a single molecule model. It suggests that survival probability may be determined by a set of causal factors.

Figure 1. ROC curves of the created models for estimating dialysis patient's 3 year survival. Models used baseline urea, UA or combination of both for prediction.

CONCLUSIONS

Combining two molecules in a model seems to increase the accuracy of predicting survival compared to single-molecule models.

By our knowledge this kind of parameter combining approach is unique and has a potential to improve the quality of dialysis, and hopefully also life expectancy of dialysis patients.

The main limitation of this study was a small study group.

The future goal is to test created models in a larger independent validation cohort and make adjustments if needed.

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