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Simultaneous Spectrophotometric Determination of Lisinopril and Argenine Based on Charge-Transfer Complex Formation with 1,2-Naphthoquinone-4-sulfunate

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Lisinopril is a member of angiotensin-converting enzyme (ACE) inhibitor's family. ACE inhibitors have been shown to be very effective and universally well-tolerated for the long-term treatment of hypertension and congestive heart failure.

Arginine -the natural precursor of nitric oxide- with lisinopril is combined to complete imperfect effect of lisinopril in kidney disease with balancing endothelin/NO ratio. Accordingly, the simultaneous determination of Lisinopril and Argenine is important. In other words, this work can be a pattern for simultaneous determination of other aminoacids.

1,2-Naphthoquinone-4-sulphonate (NQS), reacts with both primary and secondary amines and amino acids, non-selectively [1]. Hence spectrum of reaction product of lisinopril with NQS is very similar to that of arginine. Linear ranges for lisinopril and arginine are between 10 to 500 µM.

Hence these amino acids cannot be determined in the mixture directly. However, since reaction kinetics of lisinopril and arginine with NQS are different, multivariate calibration methods are suitable and applicable. Due to nonlinear effects in the kinetics of mixtures, artificial neural network (ANN) – a method for non-linear multivariate calibration – was selected [2].

For the application of neural networks, the kinetic curves corresponding to 40 binary mixtures of the considered analytes were obtained. And randomly splitted into three set consisting of training (18 mixture), test (12 mixture) and validation (10 mixture) set.

Principal component analysis (PCA) was applied to the raw of data matrix previous to ANN in order to reduce the volume of data and network running time . The optimum number of scores as inputs and concentration compositions as targets were applied to ANN. The network was trained and its related parameters were optimized with training and test sets. The prediction ability of constructed network then was investigated by validation set.

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[2] I.A. Basheer, M. Hajmeer, Journal of Microbiological Methods, 43 (2000) 3.