Assessment of Liver Function Using Hybrid Neuro-Fuzzy Model of Blood Albumin

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ABSTRACT

This paper presents an assessment of liver function using novel neuro-fuzzy model of blood albumin level (BA). The developed model that is used to predict the BA consists of four inputs: Asparate Aminotransferase (AST), Alkaline Phosphate (ALP), Total Bilirubin (T. Bil.) and Total Protein (T. Prot.), which are measured in any routine liver function test. The proposed BA model was trained using 211 measured data and a root-mean square error (RMSE) of 0.29 for 100 epochs was achieved. The performance of the developed BA model was validated using 57 testing data sets and RMSE of 0.34 for 100 epochs was achieved. The correlation coefficient (CC) between the predicted and measured values of blood albumin is statistically significant (CC=0.83), which ensures the efficiency and accuracy of developed fuzzy model for predicting BA. The main clinical benefit of this model is that it improves the assessment capabilities of liver diseases and can be used as an integral part of any medical expert system denoted for assessment and diagnosis of liver disorders.

Keywords: Blood Albumin (BA), BA Model, Liver Functions and Disorders, Medical Expert Systems, Neurofuzzy Inference System

1. INTRODUCTION

Liver is a complex biological organ that has great biochemical functions. These include removing of toxins and drugs from blood stream, regulation of glucose level, fats, hormones and amino acids, and also storing vitamins and iron (Sullivan, 2001; Rodoman, Shaeva, Dobretsov, & Korotaev, 2006; Kratz et al., 2004). Clinically, the assessment of these functions is carried out by making use of different tests (Cales & Oberti, 2002; Blum, 1998) performed on patient’s blood. One of these tests is the albumin test because the albumin is the main protein in blood synthesized by the liver. It provides indication of the ability of the liver to synthesize proteins and it is used to assess the degree of liver damage. Therefore, with normal liver function, the concentration of blood albumin is also normal. Thus, an abnormally elevated level of BA is an efficient measure of impaired liver function and damage of liver tissues. Furthermore, the blood albumin functions as a transport protein and also maintains the osmotic pressure between blood and biological tissues. Thus, accurate measurement or prediction (indirect measurement) of BA has great clinical importance for evaluation of liver function and tissues damage.

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The concentration of blood albumin is measured by making use of immunological (IM), dye-binding (DB), and electrophoretic (EL) and fluorescence immunoassay (FI) methods. Clinically, the dye-binding methods, bromocresol green (BCG) and bromocresol purple (BCP) are routine methods for BA measurements because they have good sensitivity (Evans & Parsons, 1988; Gustafsson, 1976). However, the use of either BCG or BCP can yield false elevated values of BA because they tend to overestimate the blood albumin especially when the BA is low (Hall, 1992; Bush & Reeds, 1987). Further, it consumes large time to conduct the BA measurement and requires well qualified operator to handle the measurement. The IM methods have high specificity but unfortunately they have many limitations (Marre, Clandel, Ciret, Luis, Snarez, & Passa, 1987). First, they need a centrifugation of blood sample in order to carry out the albumin measurement. Second, they require long analysis time to measure the BA. Finally, the IM methods are more expensive than the dye-binding methods. The EL methods have good sensitivity and require short analysis time but again they need more improvements in terms of preparation of blood sample and measuring procedure (Miki, Kaneta, & Imasaka, 2001). Although, the FI methods do not require a centrifugation of blood sample, they still inconvenient because they are time consuming (Brooks, Devine, Harris, Harris, Miller, & Olal, 1999).

Recently, there is a growing demand in a mathematical modelling of blood albumin in order to aid physicians in understanding the albumin metabolism and to develop computer-based systems for assessment of liver functions and treatment of liver disorders (Nikolaev et al., 2005; Svacina, Hovovka, & Skrha, 1990; Chernuckh, Balanter, Mminster, Karpen, & Mikhailova, 1983; Lazzara & Deen, 2007; Calvetti, Kuceyeski, & Somersalo, 2008; Je, Waters, Shakesheff, & Byrne, 2008). However, the main shortcoming of these models is that they were developed using regression methods that are unsuitable for modelling of nonlinear and complex processes such as albumin metabolism. Thus, a more advance technique such as adaptive neuro-fuzzy inference system (ANFIS) suitable for modelling of complex and nonlinear biological processes should be used. To the author’s knowledge, there is no unique model for assessing liver function using neuro-fuzzy technique as a predictor of blood albumin. The ANFIS facilitates the development of expert systems for diagnosis of different metabolic diseases even in case of uncertain or imprecise data (Jang, Sun, & Mitzutani, 1997; Juang & Lin, 1998; Jang & Sun, 1993). The main attractive feature of the adaptive neurofuzzy inference system is that it can automatically divide the input-output data space, select the shape of fuzzy membership functions, extract fuzzy rules and optimize the parameters of membership functions (Jang & Sun, 1993). The use of ANFIS instead of fuzzy inference system eliminates the unnecessary fuzzy rules and reduces the calculation cost and analysis time. In general, the ANFIS is to be the superior in complex and nonlinear biological systems with multi-objective decisions. Furthermore, the neuro-fuzzy inference system is capable of deriving nonlinear models directly from input/output data set without detailed knowledge about the system structure as required by conventional regression-based models. Finally, in comparison with a purely fuzzy logic approach or neural network approach, the ANFIS removes the requirement for manual development of fuzzy rules and manual optimization of fuzzy system parameters and also automatically tunes the system parameters to achieve negligible prediction errors.

The main objective of this paper is to develop an ANFIS model for prediction of blood albumin that enhances the shortcomings of the conventional albumin measuring methods and regression-based albumin mathematical models. The motivation was that the use of ANFIS could result in a fast and convenient measurement of BA. The proposed model represents the brain of any computerized decision support system for diagnosis and assessment of liver disorders especially in case of liver tissues damage. Furthermore, it is a crucial for development
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