



Prediction of the antimicrobial activity of walnut (*Juglans regia* L.) kernel aqueous extracts using artificial neural network and multiple linear regression

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ABSTRACT

The mathematical model was established to determine the diameter of inhibition zone of the walnut extract on the twelve bacterial species. Type of extraction, concentration, and pathogens were taken as input variables. Two models were used with the aim of designing this system. One of them was developed with artificial neural networks (ANN), and the other was formed with multiple linear regression (MLR). Four common training algorithms were used. Levenberg–Marquardt (LM), Bayesian regulation (BR), scaled conjugate gradient (SCG) and resilient back propagation (RP) were investigated, and the algorithms were compared. Root mean squared error and correlation coefficient were evaluated as performance criteria. When these criteria were analyzed, ANN showed high prediction performance, while MLR showed low prediction performance. As a result, it is seen that when the different input values are provided to the system developed with ANN, the most accurate inhibition zone (IZ) estimates were obtained. The results of this study could offer new perspectives, particularly in the field of microbiology, because these could be applied to other type of extraction, concentrations, and pathogens, without resorting to experiments.

1. Introduction

Walnut (*Juglans regia* L.), which is a globally accessible and primarily consumed crop, has attracted a great deal of attention because of its nutritional, healthy, economical and sensory attributes (Fernández-Agulló et al., 2013; Fukuda et al., 2003; Martínez et al., 2013). Therefore, the walnut is classified as a strategic species for human nutrition, and it is included in the FAO list of priority plants (Abbasi et al., 2010). The beneficial effects of walnuts on health which include protection from cardiovascular disease and diabetes can be said to be related to their chemical composition (Pereira et al., 2008). Walnuts are rich sources of phenolic compounds, polyunsaturated fatty acids which are essential dietary fatty acids, essential amino acids, minerals, etc. (Amaral et al., 2003; Blomhoff et al., 2007).

The crushing process of walnut kernel revealed some results that the break cell walls and expose the matrix to enzymes, oxygen, and mild heat. Consequently, many chemical and enzymatic processes take place (Artajo et al., 2006). For example, In intact plant cells, plastid-localized

polyphenol oxidase (PPO) is physically separated from its phenolic substrates, which reside primarily in the vacuole (Escobar et al., 2008). As a result of crushing, PPO activity could change some phenolics.

Walnuts have been studied with regard to the determination of *Salmonella* (CDPH, 2010; FDA, 2010a, 2010b), *E. coli* O157:H7, and *Listeria monocytogenes* (FDA, 2009) because of an *Escherichia coli* O157:H7 outbreak associated with the consumption of walnuts in 2011 (Frelka and Harris, 2015). In this study, based both on this situation and the importance of plant-derived antimicrobial agents which could serve against food spoilage and pathogens, the antimicrobial properties of the walnut kernel were investigated.

During the last years, artificial neural network (ANN) offer real advantages over conventional modeling. ANN solve problems in which the analytical methods are difficult to apply, and their results have to be in a specific interval (Funes et al., 2017). ANN is made of nodes or artificial neuron's which are disposed of in a parallel structure. For each independent variable, the ANN has one input layer containing one node, one or more hidden layers, where the data are processed, and one

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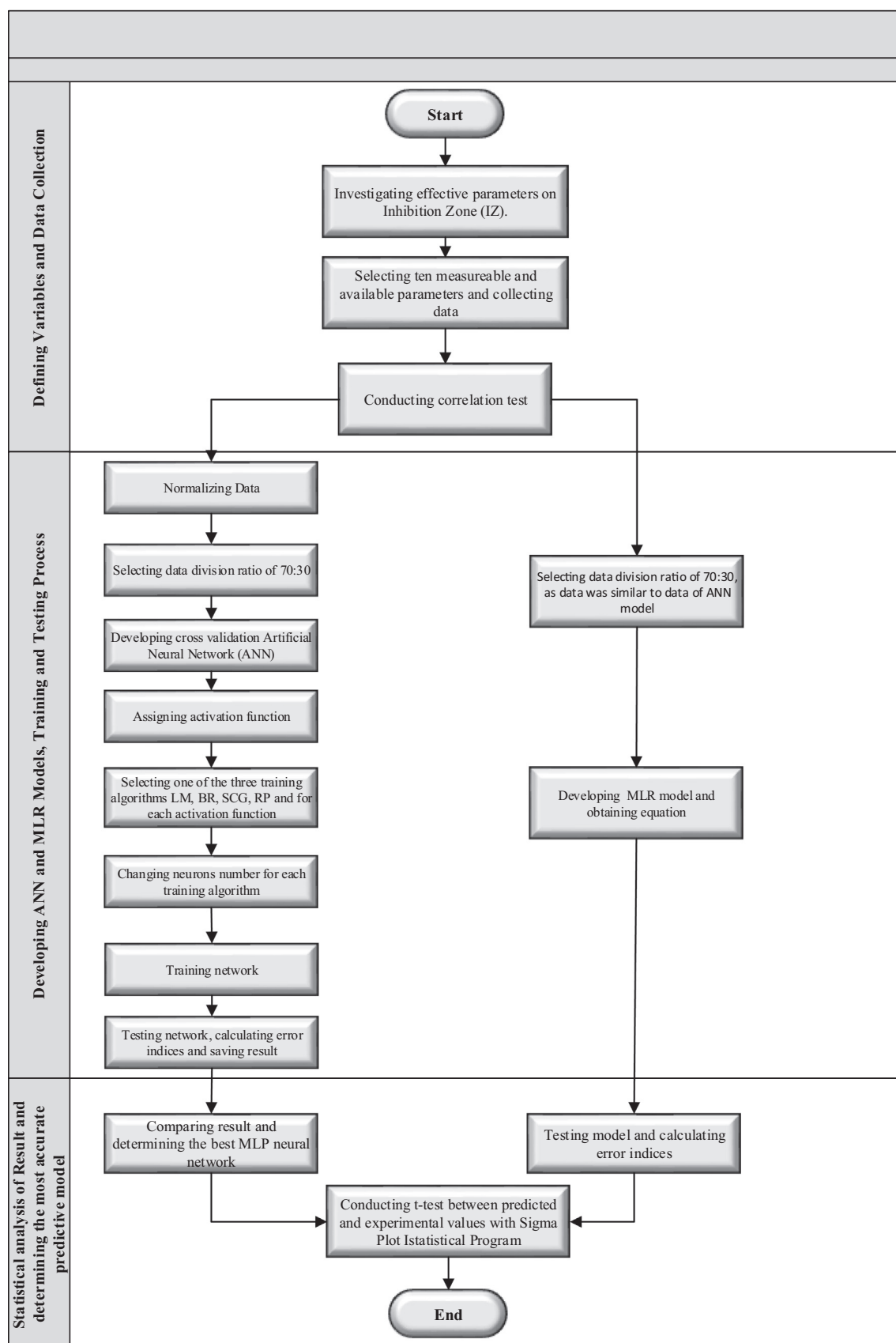


Fig. 1. Flowchart of proposed methodology for determining the best model to predict the antimicrobial effect.

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