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FRAMA 1.0: Framework for Moving Average Operators Calculation in Data Analysis

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Abstract. Moving Average (MA) operators are used in Box-Jenkins's ARIMA models in time series analysis (1). We can used MA operators of structural descriptors are useful to quantify multiple conditions or parameters in complex Omics. datasets in Medicinal Chemistry, Nanotechnology, etc. (2-7). Speck-Planche and Cordeiro have also used this kind of models in multiple problems (8-11). In this work, we develop a desktop application that allows applying mathematical and statistical calculations in batches, on input and output variables selected by the user. From the obtained result a percentage sample of data is taken with a random contrast on which Machine Learning algorithms are applied

Introduction

In principle, we can calculate numerical parameters to quantify the structure of chemical compounds, peptides, and/or proteins. We can also use them as input variables for Machine Learning (ML) algorithms in order to predict the biological properties of these drugs, peptides, or proteins (13-29). On the other hand, Perturbation Theory (PT) models allow us to predict the solutions to a query problem (q) based on a previous known solution for a similar problem or problem of reference (r). In a recent works, we outlined a new type of ML method called PTML (PT + ML) based on both kind of models with applications in drug discovery and proteome research (25, 30). The PTML method uses different kind of PT operators to predict the properties of one system based on the properties of a system of reference. For instance, Moving Average (MA) operators used in Box-Jenkins's ARIMA models in time series analysis (31). We have used MA operators of structural descriptors are useful to quantify multiple conditions or parameters in complex datasets in Omics, Medicinal Chemistry,

Nanotechnology, *etc.* (32-37). Speck-Planche and Cordeiro have also used this kind of models in multiple problems (38-41).

Discussion

González-Díaz *et al.* introduced a general-purpose PTML modeling technique useful to quantify the effect of perturbations in complex bio-molecular systems including DPINS and other networks (48, 49). Using PTML the model we can predict the values of the scoring function $f(\epsilon_{ij})_{new}$ for the DPI. The PTML model start using as input with the expected value of biological activity $f(\epsilon_{ij})_{expt}$ for one compound assayed in the conditions c_j and add the values of the PT operators $\Delta D_k(m_i, c_j)$. The expected value $f(\epsilon_{ij})_{expt} = \langle \epsilon_{ij} \rangle$ is the average value of the biological activity parameter ϵ_{ij} for all cases in ChEMBL dataset with the same $c_0 = Activity$ parameter ϵ_{ij} (Units). These PT operators added $\Delta D_k(m_i, c_j) = D_k(m_j) - \langle D_k(c_j) \rangle$ are intended to account for the changes (perturbations) in the system with respect to the expected value $\langle D_k(c_j) \rangle$ for a drug measured under the conditions of the drug $D_k(m_j)$ with respect to the expected value $\langle D_k(c_j) \rangle$ for a drug measured under the conditions of the experiment c_j . These PT operators resemble the Box-Jenkins MA operators (25, 30). We use both Linear Discriminant Analysis (LDA) and Artificial Neural Network (ANN) algorithms to seek alternative linear and non-linear models (50). At follow, we depict the compact and developed forms of a PTML linearmodel:

$$f(\varepsilon_{ij})_{new} = a_0 \cdot f(\varepsilon_{ij})_{expt} + \sum_{k=1}^{kmax} \sum_{j=0}^{jmax} a_{jk} \cdot \Delta D_k (\mathbf{m}_i, \mathbf{c}_j) + \mathbf{e}_0 \quad (1)$$

$$f(\varepsilon_{ij})_{new} = a_0 \cdot f(\varepsilon_{ij})_{expt} + \sum_{k=1}^{kmax} \sum_{j=0}^{jmax} a_{jk} \cdot (\mathbf{D}_k (\mathbf{m}_i)_{new} - \langle \mathbf{D}_k (\mathbf{c}_j) \rangle_{ref}) + \mathbf{e}_0 \quad (2)$$

Results and Discussion

FRAMA, is a desktop application that supports different file formats, allows perform data preprocessing tasks on the selection of input and output variables, and its sub classification as grouping variables and continuous variables, where operations, operators and obtaining parametric values are applied, such as Mergin Data, Shannon Entropy, Z-Score, Moving Average, Euclidian Distance, among others. From the results obtained, a sample is selected for the application of Machine Learning algorithms on a sample of data

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