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Fuzzy linguistic model for bioelectrical impedance vector analysis☆

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SUMMARY

Backgrounds & aims: The boundaries between the categories of body composition provided by vectorial analysis of bioimpedance are not well defined. In this paper, fuzzy sets theory was used for modeling such uncertainty.
Methods: An Italian database with 179 cases 18–70 years was divided randomly into developing ($n = 20$) and testing samples ($n = 159$). From the 159 registries of the testing sample, 99 contributed with unequivocal diagnosis. Resistance/height and reactance/height were the input variables in the model. Output variables were the seven categories of body composition of vectorial analysis. For each case the linguistic model estimated the membership degree of each impedance category. To compare such results to the previously established diagnoses Kappa statistics was used. This demanded singling out one among the output set of seven categories of membership degrees. This procedure (defuzzification rule) established that the category with the highest membership degree should be the most likely category for the case.
Results: The fuzzy model showed a good fit to the development sample. Excellent agreement was achieved between the defuzzified impedance diagnoses and the clinical diagnoses in the testing sample (Kappa = 0.85, $p < 0.001$).
Conclusions: fuzzy linguistic model was found in good agreement with clinical diagnoses. If the whole model output is considered, information on to which extent each BIVA category is present does better advise clinical practice with an enlarged nosological framework and diverse therapeutic strategies.

1. Introduction

Bioelectrical impedance (BIA) is a method to assess body composition based on electrical conduction of tissues. Whole body impedance is represented by Z vector, whose elements are resistance R (the opposition to flow of an alternating electric current through intra and extracellular ionic solutions) and reactance X_c (opposition to flow of the electric current caused by the capacitance produced by tissue interfaces and cell membranes) across tissues. The impedance vector can be expressed with a magnitude $|Z| = \sqrt{R^2 + X_C^2}$ and a phase angle = arctang (X_c/R).[1–3]

Body compartment volumes such as body water, fat-free mass, and fat mass, have been estimated using impedance values in empiric equations. [4–6] This conventional approach requires assumptions on body components. In illness, the violation of assumptions such as fixed hydration of fat-free mass may cause errors in body predictions.[7,8] An alternative approach proposed by Piccoli et al.[9] is the use of bioelectric impedance vector analysis (BIVA). BIVA has been shown to be a successful approach due to its potential as a stand-alone procedure that overcomes the need for assumptions on body components or models.[1,7,10]

According to BIVA, resistance (R) and reactance (X_c), measured at a frequency of 50 kHz, are normalised by height (h) and plotted in $R–X_c$ plane. Assuming a normal bivariate distribution of R/h and X_c/h, tolerance intervals for departures from the mean impedance vector from a reference population can be calculated to define a statistical range of normal values. The bivariate limits of such intervals form ellipses around the mean according to definitions of normal as those 50%, or 75%, or 95% values more close to the mean. The shortening or lengthening of the vector indicates changes in tissue hydration and migration sideways (phase angle variation) indicates changes in body cell mass. A patient vector lying within the mean's tolerance interval is suggestive of normal nutritional status. A vector lying outside the limits is suggestive of a tendency toward one of six nutritional categories other than normal (Fig. 1A).[9] Individual vectors can also be transformed into bivariate height standardized Z-scores (with respect to their reference

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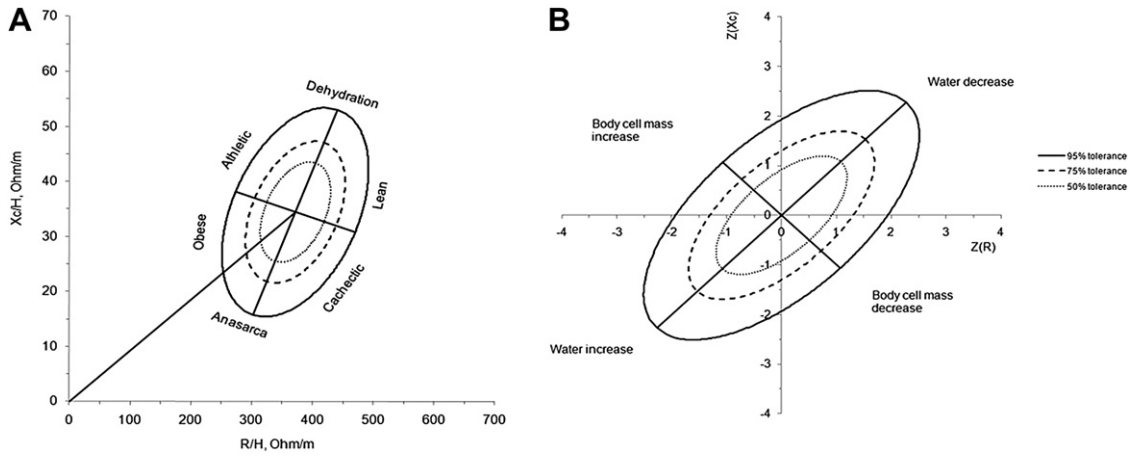

Fig. 1. BIVA body composition patterns at $R-X_c$ graph (A) and Z-score graph (B). The figure A represents the bivariate normal distribution of Resistance/height and Reactance/height, with 50%, 75% and 95% tolerance intervals from a reference Italian population. Figure B represents the bivariate normal distribution of Z-scores of Resistance/height and Reactance/height from the reference population. The shortening or lengthening (water increase and water decrease, respectively) of the vector indicates changes in tissue hydration and migration sideways (Left: body mass cell increase; Right: body cell mass decrease) indicates changes in body cell mass.

population) and plotted on the RX_c-score graph (Fig. 1B). The $R-X_c$ score graph represents the bivariate distribution of R/h and X_c/h with zero mean and standardized units where 50%, 75% and 95% tolerance ellipses are drawn.[9,11]

Clinical validation studies on BIVA are available from literature.[12–15] BIVA provides means to expand clinical diagnoses beyond the classical categorization of obese, malnourished or hyperhydration. The different regions of the BIVA graph portray different body patterns, as anasarca, dehydration, cachexia, obesity, athletics, and lean.[11]

However, the boundaries between the BIVA body patterns are not well defined in the literature. Only one attempt to draw a boundary between anasarca and obesity was found at Piccoli et al.[16] This boundary was conceived as a clear-cut line constructed with multivariate linear and quadratic discriminant analysis which may be a fair representation of the phenomena we were dealing with. Anyhow, the transition between BIVA body patterns is gradual rather than clear-cut. The closer to the supposed boundary lines the individuals are positioned, the more uncertain becomes their classification. Taking for instance the Fig. 1A one can suppose a line separating obese from anasarca but one can hardly believe that just by crossing it a new definite nutritional category should be assumed. Individuals positioned near the boundary are both obese and anasarcatous to some extent. In such circumstances, one dithers between two categories and would be much better off if allowed to express his doubt with linguistic expressions as "this patient position suggests more the diagnosis of obese than anasarcatous" or "the patient seems more anasarcatous than obese" Hence, there is room for consideration of a different approach, a new strategy robust enough to deal with the uncertainty and gradual transition between BIVA categories.

Fuzzy sets theory provides a mathematical tool for modeling the uncertainty present in the real physical world.[17] This theory was developed by Loft Zadeh[17] and came from classical sets theory. Briefly, a classical or crisp set can be defined within a given universal set U (universe of discourse containing all the possible elements of concern) by its *characteristic function*, that declares which elements x of universe U are members of the set A and which are not:

$$\mu_A \begin{cases} 1 \text{ if } x \in A \\ 0 \text{ if } x \in A \end{cases}$$

where $\mu_A(x)$ represents the membership of element x in set A. The membership is "1" if it belongs to the set or "0" if it is not a member of the set, i.e. the membership in a crisp set is found to be binary.

Zadeh generalized the idea of a crisp set by extending the valuation set {0,1} (definitely in/definitely out) to the interval of real values (degrees of membership) between 0 and 1, [0,1].[18] Values in brackets indicate a continuum space between 0 and 1. A fuzzy set A of U is then characterized by a *membership function* $\mu_A(x)$, which associates each point in X to a real number in the interval [0,1]. The value of $\mu_A(x)$ at x represents the "grade of membership" of x in A.[17] The degree of membership indicates the compatibility degree of the assertion "*x is A*".[19]

Even though fuzzy sets theory has found a large application in control systems of biotechnological devises,[20] its use as a methodological tool in health sciences is meager and as to the study of impedance may be restricted to Wieskotten et al.[21] experience of using a fuzzy linguistic model to ascertain malnutrition.

In the present study a fuzzy linguistic model was developed to deal with human body impedance data. Accounting for the uncertainty of an individual's diagnosis, this should help the interpretation of his clinical status in relation to all BIVA categories of human body composition. A fuzzy linguistic model is a rule-based system based on fuzzy sets theory whose basic structure is formed by fuzzification, base of rules, fuzzy inference and defuzzification. This system links input variables to output variables. In the fuzzification step, quantitative variables are turned into linguistic variables. A linguistic variable is one whose value is a linguistic term. It is characterized by {n, T, X, $m(n)$}, where n is the name of variable, T is the set of linguistic terms of n (very low, low, […], high, very high), X is the domain, the universe of values used for determining the meaning of linguistic term and $m(n)$ is the function mapping the meaning of the elements in each linguistic term, i.e. a fuzzy set. Fuzzy sets characterize each of the linguistic terms. The base of rules is a set of expressions of the form "IF < a given antecedent condition > or/and < another given antecedent condition >, THEN < consequent, one diagnosis >", conceived by expert knowledge. Fuzzy inference refers to how operators or/and are dealt with and how the output of rules are treated and combined. Defuzzification is the process of interpretation of results.

2. Materials and methods

Data were taken from the Italian database provided by the BIVA software developed by Piccoli and Pastori,[11] which processes vector