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Publicado por: Imprensa da Universidade de Coimbra

URL persistente: URI:<http://hdl.handle.net/10316.2/44164>

DOI: DOI:https://doi.org/10.14195/2182-7087_ex2018_101

Accessed : 26-Apr-2023 00:50:52

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EXPLORING POTENTIAL IMMUNE SYSTEM MARKERS FOR PREDICTING FRAILTY SYNDROME IN OLDER ADULTS: DIFFERENT STATISTICAL APPROACHES

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KEYWORDS: Frail older adults, Immune system, Classification algorithms, geriatric assessment.

BACKGROUND

The early identification of older populations with an increased risk for frailty syndrome (FS) is one of the most important goals for geriatricians⁽¹⁾. **Goals:** We aim to assess how different machine learning procedures may be applied to accurately predict FS by testing different immune system markers (ISM) as putative predictors.

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METHODS

A group of 110 institutionalized-dwelling participants (94 females and 16 males; mean age = 82.0±7.8 years old) were assessed for frailty using the Fried's FS protocol⁽²⁾ with 48 being found to be frail and 62 to be non-frail or pre-frail. Twelve blood and salivary ISM were determined by ELISA. Both univariate (receiver operating characteristics, ROC) and multivariate (machine learning) analyses were performed to assess the contribution of the different predictors.

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Results: Only three variables were seen to have statistically significant diagnostic values in the ROC analysis: testosterone, with area under the curve (AUC), sensitivity and specificity equal to 0.63, 66.7% and 59.7%, respectively; α -amylase (0.64, 64.6% and 64.5%) and IL-6 (0.63, 87.5% and 41.9%). Gini coefficients were computed to sort out the relative importance of the number of predictors (m) and allow for a variable reduction strategy. By decreasing order of importance, the latter were: Testosterone, α -amylase, IL-6, Cortisol, IgA, DHEA, CRP, TNF- α , Lysozyme, IL1-b, IL-10, IFN-g. The m most relevant predictors (m ranging from 1 to 8) were taken to build up classification models with Logistic Regression (LR), Support Vector Machines (SVM) and Random Forests (RF) models, which were implemented in R 3.3.2. The models were assessed using Monte Carlo cross-validation with 500 random splits of the data into training and test sets⁽³⁾. For each split, 70% of the data was assigned to the training set. In terms of AUC attained, once again determined by using ROC analyses, the best models were obtained with RF using 8 predictors: Testosterone, α -amylase, IL-6, Cortisol, IgA, DHEA, CRP, TNF- α . The corresponding 95% confidence intervals for the AUC, sensitivity and specificity were (0.71; 0.76), (0.70; 0.77) and (0.70; 0.77), respectively.

CONCLUSION

Models with solely 8 ISM predictors display a promising diagnostic value for a standard immunological screening tool for FS.

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