Title: Support vector machine predicts 2-year MS disease progression using MRI, blood serum biomarkers, and clinical data

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Background
Multiple sclerosis (MS) disease progression is heterogeneous across patients and can be difficult to predict. There is currently no unique imaging or blood serum biomarker to reliably determine if and when the disease will worsen. Combining potential biomarkers and training a machine learning model may provide a more accurate prediction of disease worsening.
Objective
Predict the 2-year risk of MS progression using a support vector machine (SVM) trained on baseline imaging, blood serum biomarkers, and clinical data.
Methods
Clinical data were collected at baseline, year 1 and year 2, and were used to identify patients progressing in their clinical disease based on predefined criteria. Baseline diffusion tensor imaging (DTI) data was used to calculate the fractional anisotropy (FA), which reflects tissue integrity, and myelin water imaging (MWI) was used to extract the mean myelin water fraction (MWF, myelin content), standard deviation (SD, myelin heterogeneity), and myelin heterogeneity index (MHI=SD/MWF, myelin damage composite measure). 71 immune-related proteins were quantified by nELISA in blood serum samples at baseline. An SVM was trained to classify patients as progressor or non-progressor at 2 years. The accuracy, sensitivity, and precision were calculated with 5-fold cross-validation. Bagging and recursive feature elimination with cross-validation (RFECV) were implemented to reduce bias and variance and improve model accuracy.
Results
The cohort of 107 (79 F) participants included 73 with relapsing-remitting MS, 15 primary progressive MS, and 19 radiologically isolated syndrome. The mean age was 42yrs (24-63), disease duration 3yrs (1-13), and median EDSS was 1.5 (0-6). The SVM achieved an AUC of 0.80, accuracy 0.85, sensitivity 0.67, and precision of 0.87. The discriminant features selected by RFECV included mean MWF, SD, and MHI, as well as FA. The highlighted proteins were

Eotaxin, FLT-3L, IP-10, and TRAIL. Several clinical features were also predictors of MS progression; age, disease duration, EDSS, and sex.

Conclusion

An SVM trained on multimodal clinical data, MRI, and blood biomarkers showed promising results in predicting 2-year risk of disease progression, which demonstrates the clinical utility of both MWI and DTI. SVM could become a tool that will aid in personalized treatment recommendations for people with MS.

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