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# A machine learning algorithm based on a 15-autoantibody profile by a novel fully automated multiplexed microarray immunoassay for the diagnosis of autoimmune connective tissue diseases (CTD)

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# **Background-aim**

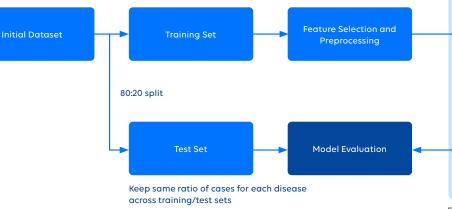
Detection of relevant autoantibodies is key in the identification of autoimmune CTD. The evaluation of multiple autoantibodies for extended serological profiling may improve the diagnosis of these conditions. We evaluated the diagnostic utility, in patients with CTD and controls, of machine learning classifiers based on the 15-autoantibody profile performed by a novel, single-use, multiplexed microarray immunoassay (MosaiQ AiPlex® CTDplus microarray, AliveDx, Switzerland) (*Figure 1*), used with its fully automated high-throughput proprietary system (*Figure 2*) for the detection of IgG autoantibodies directed to dsDNA, SS-A 60, TRIM21 (SS-A 52), SS-B, Sm, Sm/RNP, U1RNP, Jo-1, Scl-70, Centromere B, Chromatin, Ribosomal P, DFS70, RNAP III and CCP2.

## **Methods**

Banked, de-identified sera from 475 patients diagnosed with CTD in accordance with current guidelines [127 patients with systemic lupus erythematosus (SLE), 74 with systemic sclerosis, 76 with Sjögren's syndrome (SjS), 71 with idiopathic inflammatory myopathies, 54 with mixed CTD, 73 with rheumatoid arthritis] and 652 disease controls were tested with MosaQ AiPlex CTDplus. Classification models were developed using all 15 autoantibodies or a selected subset, employing Random Forest, Logistic Regression with Regularization and XGBoost algorithms (see *Figure 3* for model pipeline). Each model type was trained using all fifteen autoantibodies and autoantibodies currently considered for each disease: (9-plex for SLE, 3-plex for SjS). Diagnostic performance was evaluated by receiver operating characteristic (ROC) curve analysis.

### Figure 3. Model pipeline

~30 cases and 270 controls per disease in each of the folds + test set



#### ~90 cases and 810 controls per disease in each of cross validation iterations

Model Training and Hyperparameter Selection 4-fold cross validation

Fold 1

Fold 2

Fold 3

Fold 4

Keep same number of cases for each disease in each fold

Training

Set

Each model is a binary classification (One-vs-All) Case: sample positive for the disease Control: All other samples

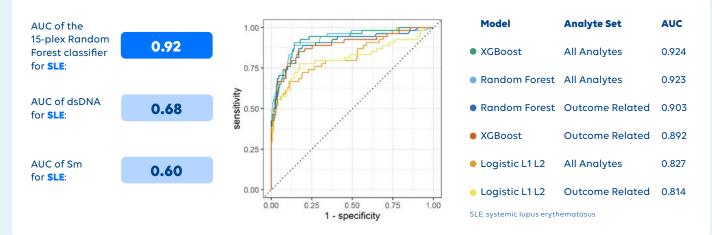
## Summary results

A Random Forest classifier with all 15 autoantibodies outperformed individual markers or groups of markers in predicting autoimmune CTD.

# **Detailed results**

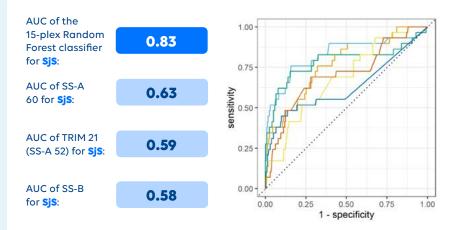
A Random Forest classifier with all 15 autoantibodies showed robust performance in predicting SLE, achieving an area under the curve (AUC) of 0.92 (*Figure 4*), versus individual SLE-specific markers dsDNA (0.68) and Sm (0.60). For SjS, the 15-plex Random Forest classifier achieved an AUC of 0.83 (*Figure 5*), outperforming a 3-plex Random Forest classifier based on SS-A 60, TRIM21 and SS-B autoantibodies (0.62). For other CTD, 15-plex classifiers consistently outperformed the individual disease-specific markers (data not shown).





\*Antibodies directed to dsDNA, Sm, Chromatin, Ribosomal P, Sm/RNP, U1RNP, SS-A 60, TRIM21, SS-B. ROC: receiver operating characteristic. AUC: area under the curve

### Figure 5. ROC Curves and AUCs - SjS. All 15 analytes vs. 3 Outcome-related analytes



Model	Analyte Set	AUC
Random Forest	All Analytes	0.827
XGBoost	All Analytes	0.785
• Logistic L1 L2	All Analytes	0.769
XGBoost	Outcome Related	0.704
Logistic L1 L2	Outcome Related	0.68
Random Forest	Outcome Related	0.629
SjS: Sjögren's syndrome		

\*Antibodies directed to SS-A 60, TRIM21 and SS-B. ROC: receiver operating characteristic. AUC: area under the curve.

### Conclusions

Multiplex autoantibody testing combined with machine learning algorithms has the potential to improve the diagnosis of autoimmune CTD.

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instrument