# Classification of Multiple Sclerosis Patients from the Geometry 

 and Texture of White Matter LesionsBernd Taschler ${ }^{1}$, Kerstin Bendfeldt ${ }^{2}$, Nicole Müller-Lenke ${ }^{2}$ Ernst-Wilhelm Radiit and Thomas E. Nichols ${ }^{3}$

${ }^{1}$ Centre for Complexity Science, University of Warwick, Coventry, UK, ${ }^{2}$ Medical Image Analysis Center, University Hospital Basel, Basel, Switzerland, WARWICK HIDR MIAC.ch ${ }^{3}$ Department of Statistics, University of Warwick, Coventry, UK

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## Introduction

Multiple Sclerosis (MS) is a chronic inflammatorydemyelinating disease of the central nervous system. MS is divided into five distinct clinical categories and disease progression differs significantly between these subtypes [3] Among the five groups, relapsing-remitting (RLRM) is the most common type of MS. The others are primary progressive (PRP), secondary progressive (SCP), progressive relapsing (PRL) and clinically isolated syndrome (CIS). Currently, in the assessment of MS, MRI data is to a large extent only used in a qualitative way to assess the dissemination of lesions in space and time $[5,6]$. Other studies have shown that conventional MRI measures have rather low predictive value and are therefore poor indicators for determining clinical outcomes in MS [4]

We propose an objective classification of MS disease subtype using support vector machine (SVM). Unlike previous work, we use a large number of quantitative features derived from three MRI sequences. In addition to traditional demographic and clinical measures, our features include aspects of lesion geometry, measured by Minkowski functionals, and statistics of the image intensities within the lesions

## Methods

Minkowski functionals [1] are used to characterize the connectivity and shape of lesions. In 3D space there are four functionals, corresponding to volume, surface area, mean breadth and Euler-Poincaré characteristic, which provide pose-independent summaries of lesion geometry. Furthermore, the original images (T1w, T1w-Gd \& T2w, normalized to whole-brain median of 100) are used to compute various 'texture' statistics (see Tab.1).
These features, computed for every lesion, are combined into summary measures over the whole brain. To preserve information about the location of lesions the summary measures are also computed separately for each of 13 ROI's according to segmentation into white matter track regions. In addition to demographic information and clinical scores (EDSS, PASAT), the fraction of gray matter volume to whole brain volume is also included in the feature list.

SVM is a binary classification scheme based on finding a separating hyperplane that splits the data set into two groups. As a non-linear kernel, radial basis functions are employed: $K\left(\mathbf{x}_{i}, \mathbf{x}_{\mathbf{j}}\right)=\exp \left[-\left\|\mathbf{x}_{i}-\mathbf{x}_{j}\right\|^{2} / 2 \sigma^{2}\right]$. Since this is a multi-class problem, we adopt an one-vs-one approach based on a total set of ten pairwise classifiers for all combinations of the five MS subtypes and combine this with a majority voting scheme [1] to make predictions.
To estimate prediction accuracies, stratified k-fold crossvalidation is carried out, where k is given by the number of elements in the smallest class (here $\mathrm{k}=10$ ). Additionally, nested cross-validation is used to optimize the model parameters and ensure unbiased estimates of out-of-sample accuracy.

Data. The data set used for our analysis consists of 250 subjects scanned at the University Hospital Basel, on a 1.5T scanner, collecting $\mathrm{T} 1 \mathrm{w}, \mathrm{T} 2 \mathrm{w}$ \& T 1 w -Gd-enhanced images. White matter lesion masks were created by a semiautomatic procedure and each scan was affine registered to MNI space using trilinear interpolation [2]. The number of subjects per subtype are: 11 CIS, 173 RLRM, 13 PRP, 43 SCP, 10 PRL.


## Results

An exhaustive combinatorial search across all features is computationally infeasible. Instead we consider a subset of possible feature combinations which are guided by the magnitude of weights of the support vectors. Tab. 2 shows the confusion matrix for the feature set with the highest average prediction accuracy of $47.8 \%$ (overall $56.0 \%$ ). In comparison, using only demographic and clinical covariates yields considerably lower accuracies ( $42.0 \%$ overall and $39.8 \%$ average accuracy respectively).
An example of normalized support vector weights for the classifier involving the two MS subtypes RLRM and PRL is given in Fig.2. The relevance of different geometry and intensity based features varies depending on which groups are involved in the classification. For instance, median T2w lesion volume is important in RLRM vs. PRL, but less so in other classifiers; and among the seven EDSS subscores, PYRSC and MNSC seem to be most significant.
The quadratic means of SVM-weights (Fig.1) give a comparison between different sorts of features and their variability. Demographic attributes and clinical scores carry a considerable amount of information about the disease.

In general, with regard to lesion geometry, a comparison across different classifiers indicates that the median is in many cases a better measure than the mean, that the maximum lesion volume, area or mean breadth for a single lesions is more meaningful than the respective minimum, and that the Euler-Poincaré characteristic is more significant than a simple lesion count.

## Conclusions

Our work shows that geometry and intra-lesion intensity of T1w hypo-intense and T 2 w hyper-intense lesions improve objective classification of MS subtype, over and above that obtained by simple demographic, lesion volume and count measures.

## References:

[1] Arns CH, et al. (2001), Phys Rev E 63(3), 031112
[2] Bendfeldt K, et al. (2009), NeuroImage 45: 60-67
[3] Cohen JA, et al. (2010), Springer, London.
[4] Lövblad KO, et al. (2010), AJNR 31: 983-989.
[5] MacKay-Altman R, et al. (2011), Stat Med 31: 449-469 [6] Morgan C, et al. (2010), Mult Scl 16: 926-934.

