



A Clustering Analysis of MS Lesions with T1-&T2-weighted, Diffusion, QSM, and MTR Imaging Sarah Scott ^{1,3}, M. Ethan MacDonald ¹⁻³, Deepthi Rajashekar ¹, Wei-Quan Liu ^{1,3}, Hongfu Sun ⁴, G. Bruce Pike ¹⁻³, Yunyan Zhang ¹, Luanne Metz ⁵ . Radiology & Clinical Neurosciences, University of Calgary, Calgary, AB, Canada 2. Seaman Family MR Research Centre, Foothills Medical Centre, Calgary AB, Canada 3. Healthy Brain Aging Lab, University of Calgary, Calgary, AB, Canada 4. School of Information Technology and Electrical Engineering, University of Queensland, Brisbane, Australia 5. Division of Neurology, University of Calgary, Calgary, AB, Canada

INTRODUCTION

- Multiple Sclerosis (MS) is an autoimmune degenerative disorder affecting the central nervous system, often characterized by the presence of lesions in the white matter apparent on T2- and T1-weighted MR images
- MS lesions are also characterized by
 - reductions:
 - fractional anisotropy (FA) (Roosendaal et al., 2009)
 - magnetic transfer ratio (MTR),
- increases in:



- mean diffusivity (MD)
- magnetic susceptibility (QSM) (Chen et al., 2014),
- Changes in quantitative MRI parameters listed above are caused by demyelination, cell-loss, and hemosiderin deposits (Haacke & Makki, et al., 2009)
- The possibility of characterizing these lesions according to their features across many contrasts requires further exploration
- We aim to extend current knowledge through quantitative MR measures as well as lesion volume on T1-and-T2 images
- We use a dimension-reduction technique, known as t-Distributed Stochastic Neighbor Embedding (t-SNE), followed by a clustering algorithm to assign lesions to fixed numbers of independent classes, which can then be analyzed for feature differences

METHODS

- 207 relapsing remitting MS (RRMS) patients (155-F, mean age 44, ranging from 23 to 60) undergoing an approved disease modifying therapy were scanned on a 3T MR scanner (GE Discovery 750)
- T1w, FLAIR, QSM, DTI, and MTR images were acquired 3D T1w and FLAIR images were acquired with isotropic 1 mm resolution
- An 8-echo monopolar GRE was collected and used to calculate QSM (Sun et al., 2018)

Figure 1: Examples of MS lesions in each of the contrast types



- DTI data was acquired with a 45-direction b=1000 protocol
- MT contrast was generated using an RF pulse 1600 Hz off-resonance
- All images were registered to the T1w for each subject using ANTs (Advanced Normalization Tools v2.1. 2018)
- WM lesions were segmented using FreeSurfer (FreeSurfer v6.0.0. 2018) and a lesion predication algorithm in the LST toolbox of SPM (Schmidt et al., 2012) for T1 and FLAIR images, respectively.
- MD, FA, susceptibility (QSM), MTR, and volumes were calculated for every lesion
- This parameter space was reduced to two dimensions using the TSNE algorithm, which uses a non-linear projection to define relationships between high-dimensional points in a low-dimensional space
- This was followed by a density-based spatial clustering of applications with noise (DBSCAN) algorithm to separate the TSNE processed data into differentiable clusters.

RESULTS

- Figure 1 Shows examples of the lesion metrics
- Figure 2 Shows examples of clustering in in the TSNE space

CONCLUSIONS

• Our analysis suggests the existence of distinct MS lesion categories based on a collective evaluation of diffusion metrics, QSM, MTR, and volume

Figure 2: TSNE and DBSCAN indicate the 4 distinct lesion classes shown above. Each point represents an individual lesion. Axes are arbitrary



- The use of TSNE to preprocess the parameter space reduced the dimensionality of lesion variables into a 2D space, improving the application of the DBSCAN clustering algorithm and demonstrating the presence of 4 unique clusters, or lesion 'types'
- We aim to test alternate metrics to determine if these lesion classes are replicated

values.

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