Conclusion: We developed a proof-of-concept fully automated QA model for real-world brain MRI of MS patients, requiring minimal data prerequisites. Our method can be extended to other common brain MRI sequences and has the potential to be applied to large-scale real-world data.
Disclosure of interest: Z.S., A.K., and R.C. are employees of Genentech/Roche and are stockholders of Roche.

P1448/1169

FLAWS against flaws: Improving Automated Cortical Lesion Segmentation

Pedro M. Gordaliza[1,2], Jannis Müller[3,4], Charidimos Tsagkas[3,4,5], Reza Rahmanzadeh[3,4], Nataliia Molchanova[1,2], Francesco La Rosa[6], Cristina Granziera[3,4], Meritxell Bach Cuadra[1,2]
[1]CIBM Center for Biomedical Imaging, Lausanne, Switzerland, [2]Radiology Department, Lausanne University Hospital (CHUV) and University of Lausanne (UNIL), Lausanne, Switzerland, [3]Translational Imaging in Neurology (ThINk) Basel, Department of Medicine and Biomedical Engineering, University Hospital Basel and University of Basel, Basel, Switzerland, [4]Neurologic Clinic and Polyclinic, Switzerland, Departments of Medicine, Clinical Research and Biomedical Engineering, University Hospital Basel and University of Basel, Basel, Switzerland, [5]Translational Neuroradiology Section, National Institute of Neurological Disorders and Stroke, National Institutes of Health (NIH), Bethesda, Switzerland, [6]Icahn School of Medicine at Mount Sinai, New York, United States

Introduction: Cortical lesions (CL) are crucial magnetic resonance imaging (MRI) biomarkers for Multiple Sclerosis (MS) diagnosis and prognosis [Filippi et al. 2018]. However, their manual identification poses significant challenges even when specialized T1-weighted sequences are employed such as Magnetization Prepared 2 Rapid Acquisition Gradient Echoes (MP2RAGE) [Marques et al., 2010] and the novel FLuid And White matter Suppression (FLAWS) [Tanner et al. 2012].
Objectives/Aims: To develop and explore a fully automated method to detect and segment CL with FLAWS, building upon our previous manual identification study [Müller et al. 2022]. This represents the first exploration of such a method to our knowledge.
Methods: Our study includes 72 MS patients who underwent MP2RAGE and FLAWS MRI (Magnetom Prisma; Siemens Healthineers) at 3T with an isotropic spatial resolution (1mm³). CL were manually segmented on MP2RAGE and two reconstructed FLAWS contrasts (FLAWS-HCO and FLAWS-MIN) individually by 3 trained experts and refined through consensus. All images were skull stripped using SynthStrip [Hoopes et al. 2022] and MP2RAGE were patient-wise coregistered to the FLAWS space.
To evaluate the sensitivity for automated CL annotation of each sequence individually and their combinations, namely, MP2RAGE, FLAWS-HCO, FLAWS-MIN, the combination of the two FLAWS contrasts (FLAWS-ALL) and MP2RAGE+FLAWS-ALL, we trained 5 nnUNet [Insensee et al. 2021] models with 57 subjects. We chose nnUNet since it has shown superior performance for a big variety of segmentation tasks.
For the test subjects (n=15), we report averaged sensitivity and precision per patient for lesion detection performance metrics (S_L, P_L), and Dice coefficient (DSC) as overlapping metric.
Results: We summarize the results for the top-3 models. The MP2RAGE+FLAWS-ALL model showed the highest performance with DSC=$0.43\pm_{0.21}$, P_L=$0.68\pm_{0.18}$ and S_L=$0.42\pm_{0.15}$, while the automated detection performance for MP2RAGE was DSC=$0.40\pm_{0.20}$, P_L=$0.74\pm_{0.18}$, S_L=$0.37\pm_{0.16}$, and for FLAWS-ALL was DSC=$0.41\pm_{0.22}$, P_L=$0.55\pm_{0.14}$, S_L=$0.41\pm_{0.12}$.
Conclusion: Our findings suggest that incorporating FLAWS information into MP2RAGE enhances the automated detection and segmentation of CL beyond what is achieved by FLAWS and MP2RAGE independently. Each contrast carries unique information about CL, which the model can effectively extract and combine automatically. Future work will explore the performance of this method when FLAWS images are reconstructed from MP2RAGE acquisitions.
Disclosure of interest: PMG: nothing to disclose.
JM: nothing to disclose.
CT: nothing to disclose.
RR: nothing to disclose.
NM: nothing to disclose.
FLR: nothing to disclose.
CG:The University Hospital Basel (USB), as the employer of C.G., has received the following fees which were used exclusively for research support: (i) advisory boards and consultancy fees from Actelion, Novartis, Genzyme-Sanofi, GeNeuro, Hoffmann La Roche and Siemens; (ii) speaker fees from Biogen, Hoffmann La Roche, Teva, Novartis, Merck, Jannsen Pharmaceuticals and Genzyme-Sanofi; (iii) research grants: Biogen, Genzyme Sanofi, Hoffmann La Roche, GeNeuro.
MBC: nothing to disclose.

P1449/304

Digital biomarkers for early detection of disability worsening in MS: the MS-DETECT study design

Patrick Vermersch[1], Massimo Filippi[2], Celia Oreja-Guevara[3], Jiwon Oh[4], Tobias Sejbæk[5], Jennifer Graves[6], Lissandra Klaeylé[7], Séverine Bieuvelet[7], Loïc Carment[7], Léa Diouf[7], Saad Zinaï[7], Pascal Rufi[8], Bruno Padrazzi[9], Tjalf Ziemssen[10]
[1]Univ. Lille, UMR Inserm U1172, CHU Lille, FHU Precise, F-59000, Lille, France, [2]Department of Neurology, IRCCS San Raffaele Scientific Institute, Vita-Salute San Raffaele University, Milan, Italy, [3]Hospital Clinico San Carlos, IdISSC, Madrid, Spain, [4]Division of Neurology, St. Michael's Hospital, University of Toronto, Toronto, Canada, [5]Department of Neurology, Esbjerg Hospital, University Hospital of Southern Denmark, Esbjerg, Denmark, [6]Department of Neurosciences, University of California, San Diego, United States, [7]Ad Scientiam, Paris, France, [8]Sanofi, Chilly-Mazarin, France, [9]Sanofi, Paris, France, [10]Universitätsklinikum Carl Gustav Carus, Dresden, Germany