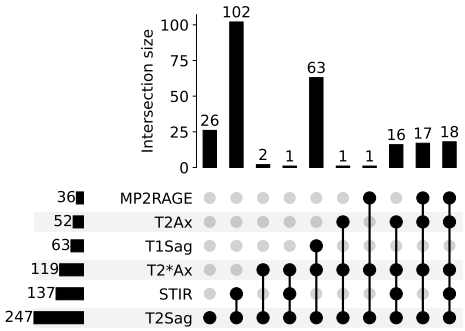

Fig. 1. Left: The total number of subjects with images from each of the six sequences. Top: The number of subjects with specific combinations of sequences, e.g., 102 subjects have T2Sag and STIR and no other sequences. The variability in sequences stems from acquisition protocols across different studies; therefore, we extract test sets from each study cohort, i.e., 20 subjects with T2Sag & STIR ($\mathcal{D}_B$), 20 subjects with T2Sag, T2*Ax & T1Sag ($\mathcal{D}_C$), and all 18 subjects with five sequences ($\mathcal{D}_A$). The median (Q1–Q3) number of lesions was 2 (2–5) for the training & validation subjects, and 9 (7–9.75), 4 (2–7.25), and 2.5 (1.75–5) for $\mathcal{D}_A$, $\mathcal{D}_B$, and $\mathcal{D}_C$, respectively.

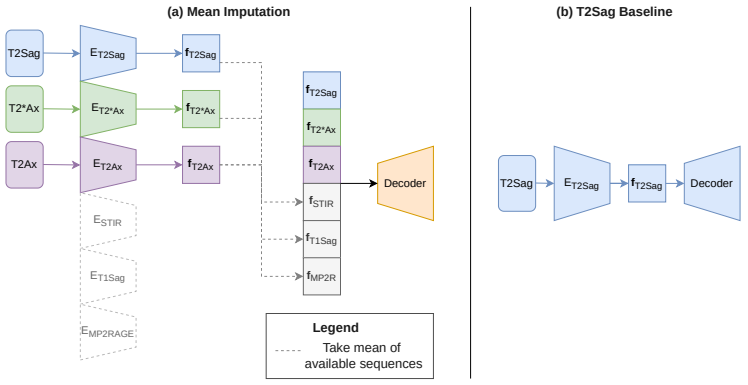

Fig. 2. Main architectures. In (a), an encoder is initialised for each of the six sequences. Where sequences are not available for a subject during training or inference, the mean of the features of the available sequences replaces the missing features. For example, in the scenario above, the features for each of the latter three sequences are imputed by the mean of the features of the first sequences. The T2Sag Baseline (b) is a similar base architecture, but reduced to a single sequence.

Table 1. Distribution of spacing for MRI acquisitions with different sequences (in RPI orientation). The mean and std. deviation are calculated for each axis independently.

Sequence	Mean Spacing (mm)	Std. Deviation (mm)
T2Sag	(3.03, 0.61, 0.61)	(0.43, 0.146, 0.23)
STIR	(3.34, 0.62, 0.62)	(0.34, 0.27, 0.27)
T2*Ax	(0.38, 0.38, 3.30)	(0.10, 0.10, 0.00)
T2Ax	(0.23, 0.23, 3.01)	(0.00, 0.00, 0.18)
T1w	(1.00, 0.98, 0.98)	(0, 0, 0)
MP2RAGE	(1.00, 0.94, 0.94)	(0.00, 0.02, 0.02)

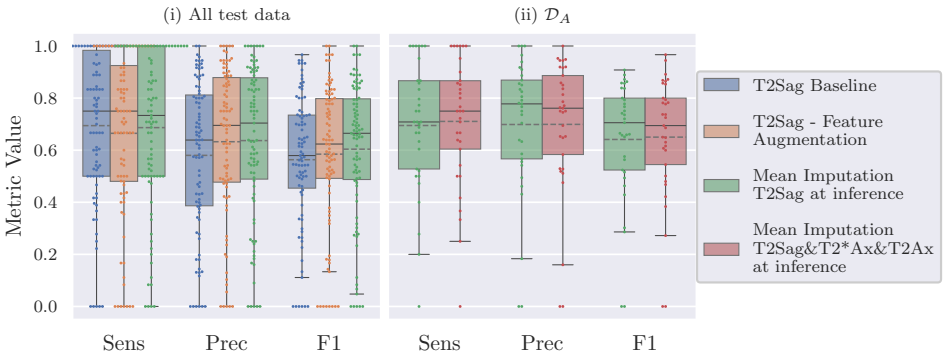

Fig. 3. Distribution of **lesion-wise metrics** calculated for each image in i) all test data and ii) $\mathcal{D}_A$, i.e., subjects with T2Sag, T2*Ax and T2Ax. Each point represents a single image. Median and mean are represented as solid and dashed lines, respectively.

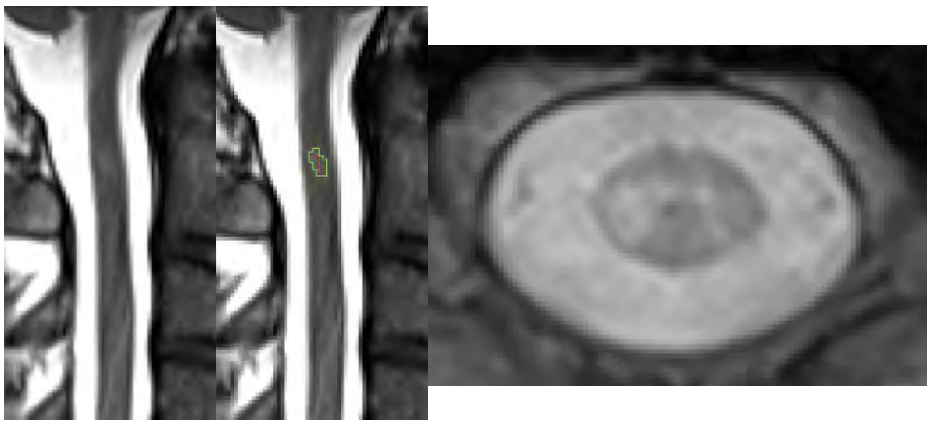

Fig. 4. Example lesion and segmentation. **A)** Subsection of sagittal T2w volume, with lesion at C2 level indicated by arrow. **B)** Ground-truth outline (green) and prediction (red) by Mean Imputation model with T2Sag, T2*Ax and T1Sag as inputs. This lesion was not detected by the other models nor by Mean Imputation with only T2Sag as input. **C)** The lesion is more conspicuous on the T2*Ax acquisition.