

A brief guide to the files contained in the LUMIERE dataset

Imaging data

The following table gives an overview of the imaging and segmentation data. If you are interested in the MRI sequences (T1-weighted pre- and post-contrast (T1, CT1), T2-weighted and Fluid-Attenuated Inversion Recovery (FLAIR)), you find these inside the folder for each patient and study date. These images have been skull-stripped using the tool HD-BET (see the manuscript for references and details). Furthermore, the study folders include subfolders containing the output of DeepBraTumIA and HD-GLIO-AUTO segmentations. For both methods, we include the segmentation label maps in the native/original image space and a version with co-registered data. For DeepBraTumIA, the co-registered data was aligned to an atlas (MNI), for HD-GLIO-AUTO, the tool decided on a reference image for each case, and registered/resampled accordingly. Please be aware that the images/segmentations back-transformed to the native/original image space is not an output of HD-GLIO-AUTO. We modified the docker of such that the registration matrix was retained and used it alongside the inverse of the orientation alignment inside HD-GLIO-AUTO to make this available.

The registration matrices are included to allow further alignments during downstream tasks. Please refer to our GitHub repository for the scripts used to orient, register, and segment the data.

Patient-XXX	week-00N	CT1.nii.gz				Post-contrast T1-weighted MRI image converted from DICOM and skull-stripped using HD-BET. Not registered and not resampled.
		T1.nii.gz				T1-weighted MRI image converted from DICOM and skull-stripped using HD-BET. Not registered and not resampled.
		T2.nii.gz				T2-weighted MRI image converted from DICOM and skull-stripped using HD-BET. Not registered and not resampled.
		FLAIR.nii.gz				Fluid-attenuated inversion recovery MRI image converted from DICOM and skull-stripped using HD-BET. Not registered and not resampled.
		DeepBraTumIA-segmentation	atlas	segmentation	measured_volumes_in_mm3.json	Volumes of the segmented tumor regions by DeepBraTumIA
					seg_mask.nii.gz	Segmentation label map by DeepBraTumIA
				skull_strip	brain_mask.nii.gz	Brain mask used for skull-stripping
					ct1_skull_strip.nii.gz	Skull-stripped post-contrast T1 image in atlas space (MNI)
					t1_skull_strip.nii.gz	Skull-stripped T1 image in atlas space
					t2_skull_strip.nii.gz	Skull-stripped T2 image in atlas space
					flair_skull_strip.nii.gz	Skull-stripped FLAIR image in atlas space
			native	segmentation	ct1_seg_mask.nii.gz	Segmentation output by DeepBraTumIA back-transformed to the native CT1 image space.
					t1_seg_mask.nii.gz	Segmentation output by DeepBraTumIA back-transformed to the native T1 image space.
					t2_seg_mask.nii.gz	Segmentation output by DeepBraTumIA back-transformed to the native T2 image space.
					flair_seg_mask.nii.gz	Segmentation output by DeepBraTumIA back-transformed to the native FLAIR image space.
				skull_strip	ct1_brain_mask.nii.gz	brain mask in native CT1 space used for skull-stripping
					t1_brain_mask.nii.gz	brain mask in native T1 space used for skull-stripping
					t2_brain_mask.nii.gz	brain mask in native T2 space used for skull-stripping
					flair_brain_mask.nii.gz	brain mask in native FLAIR space used for skull-stripping
				transformation	ct1.tfm	transformation mapping the native CT1 space to the atlas space
					t1.tfm	transformation mapping the native T1 space to the atlas space

					t2.tfm	transformation mapping the native T2 space to the atlas space
					flair.tfm	transformation mapping the native FLAIR space to the atlas space
		HD-GLIO-AUTO-segmentation	native		segmentation_CT1_origspace.nii.gz	Segmentation label map produced by HD-GLIO-AUTO transformed to the native CT1 space
					segmentation_T1_origspace.nii.gz	Segmentation label map produced by HD-GLIO-AUTO transformed to the native T1 space
					segmentation_T2_origspace.nii.gz	Segmentation label map produced by HD-GLIO-AUTO transformed to the native T2 space
					segmentation_FLAIR_origspace.nii.gz	Segmentation label map produced by HD-GLIO-AUTO transformed to the native FLAIR space
			registered		CT1_r2s_bet.nii.gz	Skull-stripped CT1 image, with orientation matching the atlas (MNI)
					T1_r2s_bet.nii.gz	Skull-stripped T1 image, with orientation matching the atlas (MNI)
					T2_r2s_bet.nii.gz	Skull-stripped T2 image, with orientation matching the atlas (MNI)
					FLAIR_r2s_bet.nii.gz	Skull-stripped FLAIR image, with orientation matching the atlas (MNI)
					CT1_r2s_bet_reg.nii.gz	Skull-stripped CT1 image, registered to the reference image (ref. image differs by case), with orientation matching the atlas (MNI)
					T1_r2s_bet_reg.nii.gz	Skull-stripped T1 image, registered to the reference image (ref. image differs by case), with orientation matching the atlas (MNI)
					T2_r2s_bet_reg.nii.gz	Skull-stripped T2 image, registered to the reference image (ref. image differs by case), with orientation matching the atlas (MNI)
					FLAIR_r2s_bet_reg.nii.gz	Skull-stripped FLAIR image, registered to the reference image (ref. image differs by case), with orientation matching the atlas (MNI)
					CT1_r2s_bet_reg.mat	Transformation to align CT1_r2s_bet.nii.gz to the atlas
					T1_r2s_bet_reg.mat	Transformation to align T1_r2s_bet.nii.gz to the atlas
					T2_r2s_bet_reg.mat	Transformation to align T2_r2s_bet.nii.gz to the atlas
					FLAIR_r2s_bet_reg.mat	Transformation to align FLAIRs_r2s_bet.nii.gz to the atlas
					segmentation.nii.gz	Segmentation label map by HD-GLIO-AUTO, aligned with all sequences with the postfix “_reg”

CoLIAGe features

The CoLIAGe features are provided in the same basic folder structure as outlined above. The features were extracted for both segmentation methods and all MRI sequences, for all study dates where all four MRI sequences were available. Please note that the features were extracted based on the co-registered versions (atlas for DeepBraTumIA, reference image for HD-GLIO-AUTO). For HD-GLIO-AUTO, a lower-resolution image was often chosen to segment, leading to fewer studies where the requirements regarding the minimum number of slices were met. To have a more complete feature set, we extracted the features for HD-GLIO-AUTO on resampled iso-voxel (1mm) images, making it more similar to the version for DeepBraTumIA. Please refer to our GitHub repository to see how this was done. Please note, that no features can be provided for cases where the automated segmentation did not detect any tumor labels.

Expert RANO rating

The reading by an experienced neuroradiologist is included in the file LUMIERE-ExpertRating.csv. A selection according to the RANO guidelines was done to choose which time points to assess. Please note that in some cases the automated segmentation is not available for rated studies since the evaluation could also be done if only a subset of the four

MRI sequences were available. The rationale for the rating includes comments on the spacing of longitudinal time points, the presence of non-measurable, measurable, target, and non-target lesions. For measurable lesions, the bi-dimensional (Macdonald) measurement is included.

MRI acquisition information

The information listed in the CSV file LUMIERE-MRInfo.csv is based on the information in the DICOM header of the MRI images. Please note that the number of slices can deviate from the slice count of the corresponding NIfTI file, since some DICOMs were interleaved (e.g., T2-weighted and PD), or we had to crop some images to eliminate burned-in orientation markers leading to issues with skull-stripping.

Pathology and demographic information

The CSV file includes information on the MGMT methylation promoter status, IDH1, sex, age at diagnosis, and overall survival time.

Please do not hesitate to contact us in case you need further information, assistance to using the dataset, or in case you spot something we should fix.

Also, we are happy to know of publications and projects using this dataset to list it on our GitHub repository.

This dataset is provided for non-commercial use.