Data Article

High-resolution dataset of manual claustrum segmentation

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A B S T R A C T

The claustrum has a unique thin sheet-like structure that makes it hard to identify in typical anatomical MRI scans. Attempts have been made to identify the claustrum in anatomical images with either automatic segmentation techniques or using atlas-based approaches. However, the resulting labels fail to include the ventral claustrum portion, which consists of fragmented grey matter referred to as "puddles". The current dataset is a high-resolution label of the whole claustrum manually defined using an ultra-high resolution postmortem MRI image of one individual. Manual labelling was performed by four independent research trainees. Two trainees labelled the left claustrum and another two trainees labelled the right claustrum. For every hemisphere we created a union of the two labels and assessed the label correspondence using dice coefficients. We provide size measurements of the labels in MNI space by calculating the oriented bounding box size. These data are the first manual claustrum segmentation labels that include both the dorsal and ventral claustrum regions at such a high resolution in standard space. The label can be used to approximate the claustrum location in typical in vivo MRI scans of healthy individuals.

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Specifications Table

Subject	Neuroscience (General)
Specific subject area	Region-of-interest definition for functional MRI experiments; structural segmentation
Data format	Analysed data
Type of data	Data are provided for both left and right claustrum labels as a compressed NIFTI (.nii.gz).
	Oriented bounding box measurements are provided in the form of .json, .mrk.json and .fcsv files, which can be directly imported into 3D slicer software.
Data collection	Claustrum labelling was performed using FreeSurfer version 7.2.0 Freeview program by marking voxels belonging to the claustrum on an ultra-high resolution structural brain scan [1]. We generated 2 labels for the left claustrum and 2 labels for the right claustrum.
	After the labelling, we preprocessed them by first applying spatial smoothing. This was done to remove single voxels that were erroneously mislabeled. We then combined the labels of each hemisphere by performing the union of the two labels.
Data source location	Institution: University of Graz, Department of Psychology
	City/Town/Region: Graz
	Country: Austria
Data accessibility	Repository name: Open Science Framework (OSF)
	Direct URL to data: https://doi.org/10.17605/OSF.IO/TBJV4

1. Value of the Data

- The human claustrum is difficult to identify in standard structural MRI scans due to its thin and fragmented shape. Furthermore, most existing definition approaches do not include the ventral extent of the claustrum. The current dataset represents a high-resolution and high accuracy claustrum label that includes claustrum parts typically omitted by other approaches.
- The data is beneficial to anyone who may be investigating the functional role of the claustrum in the normal adult population using MRI.
- Since the claustrum label is defined in standard MNI space, it can be applied to data of any subject with an anatomical MRI scan by first creating an individual mapping to the MNI space and then applying an inverse transformation to the label.
- The labels can be subsequently used to extract functional, diffusion or any other MRI parameters specific to the claustrum region. and as a seed for functional and structural connectivity studies of the claustrum.

2. Background

The human claustrum is a sheet-like bilateral subcortical brain structure, whose functional role is poorly understood. Due to its thin shape, the claustrum is challenging to study in vivo using conventional MRI. Recent advancements in MRI technology have made it possible to image the brain at higher resolutions, facilitating claustrum investigations. However, there is a lack of tools for identifying the claustrum in typical anatomical images. Standard atlases and automatic segmentation routines often either do not label the claustrum at all (e.g., [2,3]) or label only the dorsal claustrum (e.g., [4,5]), leaving out the large ventral claustrum portion. The only way to acquire an accurate and complete claustrum label is therefore a high-resolution MRI scan of each individual combined with time-consuming manual labelling of the claustrum in each scan [6]. For this dataset, we manually labelled the left and the right claustrum volume in an ultra-high resolution (0.1 mm^3 voxel size) post-mortem MRI scan in standard MNI space [1]. We demonstrate how the label can be used to approximate claustrum location in any standard structural MRI scan automatically within several minutes.

3. Data Description

The labels are located in the Open Science Framework (OSF) repository (https://doi.org/10.17605/OSF.IO/TBJV4) and are provided in compressed NIFTI format (.nii.gz) to make it accessible for MRI researchers. The compressed files represent the left or the right claustrum (Fig. 1). They are located in the folders "Left Claustrum" and "Right Claustrum" and are named accordingly
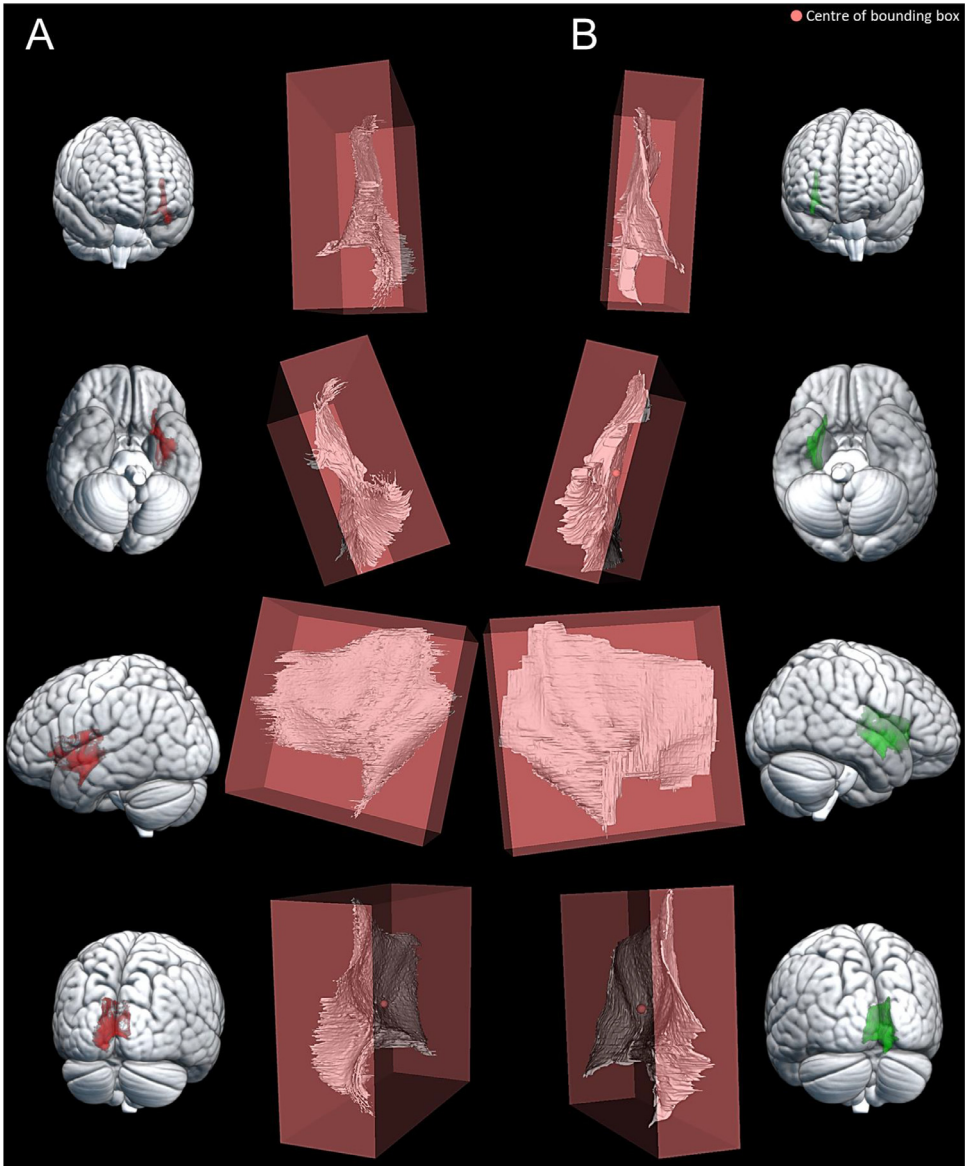

Fig. 1. Claustrum labels with their respective bounding boxes. A) Left claustrum in 3D showing the oriented bounding box in anterior, inferior, left and posterior 3D views. B) Right claustrum in 3D showing the oriented bounding box in anterior, inferior, right and posterior views. 3D brains in A and B represent the viewing angle for the label with the respective bounding box.

Table 1
Label sizes.

Variable	Left claustrum	Right claustrum
Voxel sizes (mm³)	0.1	0.1
Number of Voxels	17,36,236	20,74,404
Volume (mm³)	1736.24	2074.41
Surface area (mm²)	5489.34	4089.92
Oriented bounding box dimensions (x, y, z) (mm)	23.98, 54.88, 56.93	17.21, 52.56, 49.85
Oriented bounding box center coordinates in MNI space (x, y, z) (mm)	−9.21, 21.00, 26.81	28.44, −28.63, 17.28

("claustrum_label_left.nii.gz", "claustrum_label_right.nii.gz"). The labels were generated using a high-resolution anatomical brain scan [1] at 0.1 mm³ resolution. Therefore, the NIFTI files are in the same space as anatomical reference used to generate them (dimensions of the NIFTI files are as follows; $x = 1971$ mm, $y = 2331$ mm, $z = 1891$ mm). Since the claustrum was labelled twice in each hemisphere, we combined two final labels by creating a union of the 2 left- and 2 right-hemisphere labels (the script "label_preprocess.sh" in the repository represents the preprocessing steps for the union of the labels). The dice similarity coefficient between the two labels for the left claustrum was DSC = 0.76 and for the right claustrum DSC = 0.83.

Table 1 describes the label's characteristics. We measured the size of the label using the oriented bounding box function in 3D slicer [7,8]. JSON files within the repository represent the oriented bounding box markups produced in 3D slicer and can be imported in 3D slicer. The files are named according to the label.

We further include an example usage of our label for approximating claustrum location in a typical T1-weighted MRI scan. The main steps of the procedure include mapping of an individual scan (Fig. 2A) to MNI space and applying the resulting inverse transform to the label in MNI space (Fig. 2B), which results in labels in individual subject's space (Fig. 2C). An example script for generating a native-space label is located in the folder "example scripts" and is named "examplePipeline_to_nativeSpace.sh". The script makes use of SPM12 [9] (version 7771, 13 Jan 2020) to obtain the inverse deformation field from the MNI space to individual subject space and applies this to the labels. Additionally, FreeSurfer commands "mri_vol2vol" and "mri_binarize" are used to resample the labels into the same space as the subject and "mri_convert" to convert volumes to compressed NIFTI format and uncompressed NIFTI format for use in SPM.
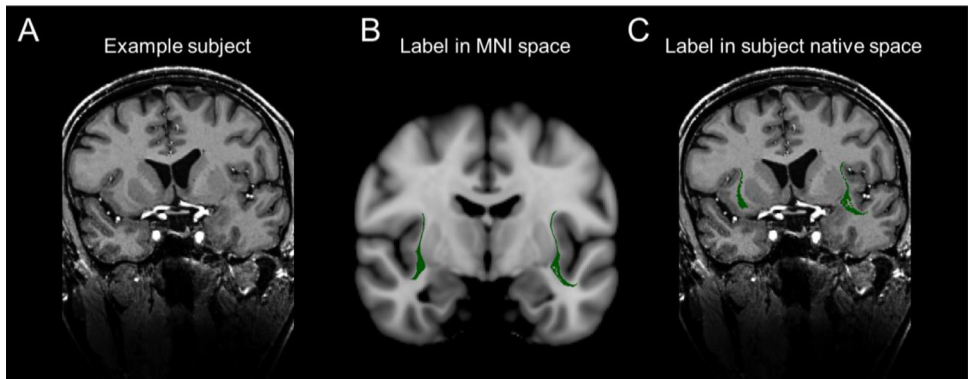

Fig. 2. Screenshots illustrating the claustrum labels mapped to subject's native space. A) Example MRI scan of a subject. B) MNI template with the labels overlaid. C) The respective labels mapped to the subject's native space overlaid with the MRI scan in A).

4. Experimental Design, Materials and Methods

The anatomical location of the claustrum was identified in an ultra-high resolution (0.1 mm^3 voxel size) anatomical postmortem MRI image of an individual 58-year-old female, who died as a result of hypoxic respiratory failure due to pneumonia but had no history of neurological disease [1]. The labelling of each claustrum was performed by a total of four research trainees, each of whom labeled one claustrum in either the left or the right hemisphere. Labelling was performed in Freeview, which is part of FreeSurfer software package (version 7.2.0) [10], running on a Linux Ubuntu (20.04.6 LTS Focal Fossa) computing server and accessed via X2Go client. A standard computer mouse was used to mark individual voxels belonging to the claustrum using the ultra-high resolution anatomical scan as background. In order to get an overall idea of the claustrum structure and shape, trainees used fiber-stained myelin images from Atlas of the Human Brain [11] as well as the Nissl-stained cross-sections of the claustrum from www. BrainMaps.org [12,13]. These histological sections accurately visualize the entire claustrum, including the ventral "puddles", which are not visible in conventional in vivo anatomical MRI scans [14].

Labelling of one claustrum consisted of several steps described below. First, the high-resolution brain was loaded into Freeview. After this, an overlay was created by selecting the option "New ROI…" in Freeview. This creates a binary label map overlayed with the high-resolution brain acting as a template. Initially, the map consists of zero values only. Voxels marked on this map are assigned a value of 1 and the resulting saved file is an ASCII text file containing the x, y and z coordinates of each of the marked voxels.

Since the dorsal claustrum is most visible in the axial plane, each research trainee began with labelling the claustrum in the axial slices on a slice-per-slice basis (left number of slices for the 1st label = 518 and for the 2nd label = 473, right number of slices for the 1st label = 504 and for the 2nd label = 468). Freeview drawing tools allowed the trainee to label either 1 voxel at a time or to draw an outline and then fill in the respective outlined shape. Trainees were instructed to only use the fill tool when a larger volume had to be labelled. The voxel drawing tool allows to increase the brush size, thus covering more than one voxel at a time. This was often used when labelling the ventral "puddles" of the claustrum. The thinnest parts of the dorsal claustrum were labelled on a voxel-per-voxel basis by decreasing the brush stroke to match 0.1 mm^3 voxel size.

After labelling the claustrum on the axial slices, labelling continued on the coronal sections of the claustrum (left number of slices for the 1st label = 544 and for the 2nd label = 593, right number of slices for the 1st label = 481 and for the 2nd label = 473) in which the ventral "puddles" are more visible. Only after labelling the slices in the axial and coronal views, the trainees switched to the sagittal view. Since the labelling was done in 3D space, the markings made on both the axial and coronal planes were present in the sagittal plane and thus most of the sagittal view of the claustrum was already labelled. The trainee was instructed to go through the sagittal slices and check for potentially missing parts or segments that are clearly sticking out. We avoided labelling the claustrum in sagittal slices directly given that the claustrum shape is difficult to distinguish from the surrounding white matter in sagittal views. A similar protocol was described previously by others [6]. In total, each label took approximately 120 hours to complete. Due to time constraints, the first label for the right claustrum was not completed entirely by the trainee and so one author (A.C.) later finished the labelling to include the ventral regions of the claustrum. After completion, marked voxels were saved in a FreeSurfer label format (an ASCII file listing the *x, y* and *z* coordinate of every marked voxel).

Label files were converted into a volume format by using the FreeSurfer command "mri_label2vol". This command converts the raw label ASCII file into a volume (NIFTI) that matches the template (MRI volume) dimension and voxel size. After this, we smoothed the label using a full-width-half-maximum (FWHM) of 0.1 mm^3 3D Gaussian kernel using the FreeSurfer "mri_fwhm" command and binarized the label after smoothing to include values 0.9 or greater. This was done to remove noise stemming from accidentally mislabelled individual voxels and to smooth the label edges. We then combined the labels produced by individual trainees by creat-

ing a logical union of the two labels using the FSL (version 6.0.4) "fslmaths" [15] command. The output is a volume containing voxels with a value of 1 for all voxels that are labelled as claustrum by either one of the trainees. In sum, the resulting claustrum label of each hemisphere is a union of two original smoothed labels. The final labels are shown in Fig. 1.

Dice coefficients were calculated in MATLAB (version 9.13, 2022b, MathWorks, Natick, MA) using the custom written script "dice_coeff.m" in the repository. The script uses SPM12 [9] (version 7771, 13 Jan 2020) to read in the labels. The script works with binary volumetric data that have the same dimensions and calculates the number of non-zero elements of label 1 and label 2 divided by the sum of the number of non-zero elements of both labels (written in notation form below).

$$\frac{2 \; nnz(v1 \cap v2)}{nnz(v1) + nnz(v2)}$$

Given that the Dice similarity coefficients were not very high, we visually inspected the overlap between the two labels. The main regions where the labels mismatched were the puddle regions of the ventral claustrum (data not shown).

Limitations

The first limitation concerns labelling consistency. Although we instructed the trainees on the general procedure for labelling, our guidelines were not as precise as a previously published protocol [6]. This may have decreased the consistency between labels. Future studies should therefore adhere to a more detailed labelling protocol.

Additionally, our label does not distinguish between the anatomical subdivisions within the claustrum. Dorsal and ventral claustrum have different connectivity targets and potentially also different functions. Future work should therefore focus on refining the label by distinguishing these individual parts.

A further limitation is that each claustrum was segmented only twice. A higher number of segmentations would help to improve the label accuracy. However, this was not possible due to time constraints of the trainees, who performed the labelling as part of a 120-hour internship, and the constraints of the project timeline.

Finally, we produced the labels from an ultra-high resolution scan of a single subject. Individual differences in claustrum size and shape may result in slight mismatches between inferred and actual claustrum positions in each individual. Additionally, since the claustrum volume decreases with age [16,17] and in neurodevelopmental disorders [18], the label may be most suitable for the neurotypical adults.

Data Availability

High-resolution manual Claustrum segmentation label (Original data) (Open Science Framework).

CRediT Author Statement

Adam Coates: Conceptualization, Methodology, Software, Formal analysis, Visualization, Writing – original draft, Writing – review & editing; **Natalia Zaretskaya:** Conceptualization, Methodology, Funding acquisition, Project administration, Supervision, Resources, Validation, Writing – review & editing.

Ethics Statement

Authors have read and agreed to the ethical requirements for publication in Data in Brief and confirm that the current work and data does not involve human subjects, animal experiments, or any data collected from social media platforms. While the template used was from a deceased human subject the data provided here does not pertain to any information that may result from identifying this individual. Individual MRI scan used as an example in Fig. 2 is a scan of one of the authors and is provided with the author's consent.

Acknowledgments

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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