



D1.1 – Ultra-high resolution mapping of the anatomical structure of the retinofugal visual system in in congenitally blind subjects using 7T and 9.4 MRI.

Version	Edited by	Changes
01	Maastricht University	

**TABLE OF CONTENTS**

**INTRODUCTION ..... 3**

**1. SCANNING PARAMETERS ..... 4**

**2. DATA ANALYSES ..... 4**

**3. PROGRESS ..... 7**

## Introduction

We investigated the brain anatomical structures of both congenitally blind participants and normal sighted controls, by acquiring anatomical images in the ultra-high field scanner (7-Tesla).

## 1. Scanning parameters

The anatomical data were acquired in Maastricht brain imaging center, Maastricht University (Netherlands), with a 7T Magnetom scanner (Siemens, Erlangen, Germany), with a whole-brain coil (1Tx/32Rx, Nova Medical Inc., USA).

For each participant, we acquired anatomical images in 3 contrasts, including T1-weighted, proton density, T2\*-weighted. For aiding segmentation of subcortical areas, a turbo spin echo sequence was used to cover subcortical structures for 5 congenitally blind participants and 4 sighted controls; for the rest of the participants a short inversion time T1 sequence was used.

- T1-weighted sequence:  
MPRAGE, TR = 3100 ms, TE = 2.52 ms, TI = 1500 ms, flip angle = 5°, FOV read = 230 mm, matrix size = 384×384×256, 0.6 mm isotropic resolution.
- Proton density sequence:  
MPRAGE, TR = 1440 ms, TE = 2.52 ms, flip angle = 5°, FOV read = 230 mm, matrix size = 384×384×256, 0.6 mm isotropic resolution.
- T2\*-weighted sequence:  
TurboFLASH, TR = 4910 ms, TE = 16 ms, flip angle = 5°, FOV read = 230 mm, matrix size = 384×384×256, 0.6 mm isotropic resolution.
- Turbo spin echo sequence:  
TurboFLASH, TR = 14300 ms, TE = 73 ms, flip angle = 180°, FOV read = 192 mm, matrix size = 384×336×20, 0.6×0.6×2 mm<sup>3</sup> resolution.
- Short inversion time T1 sequence:  
MPRAGE, TR = 4500 ms, TE = 3.46 ms, TI = 670 ms, flip angle = 4°, FOV read = 230 mm, matrix size = 384×384×256, 0.6 mm isotropic resolution.

## 2. Data analyses

The data was processed in BrainVoyager QX 2.8 (Brain Innovation, Maastricht, the Netherlands). The anatomical images of T1 and T2\* contrasts were aligned to the proton density (PD) image. The magnetic field inhomogeneity was corrected by dividing the T1 image by the PD image, where the resulting image served as the anatomical basis for subsequent analyses. The myelin content information was obtained by dividing the T1 image by the T2\* image. The T1/PD image was then brought into AC-PC space, and finally transformed into Talairach space.

Both the analysis of cortical thickness and myelin content depend on the correct segmentation of the white-gray matter boundary. The segmentation was done in AC-PC space for each participant. For segmentation, the skull and non-brain tissues were peeled from the brain (Fig. 1), and the advanced segmentation tool in BrainVoyager was used to create an initial segmentation. Manual correction was performed by overlying the initial segmentation onto the anatomical file (see Fig. 2), and the white-gray matter border was manually corrected in sagittal, transverse, coronal views subsequently, using a tablet pen. This resulted in correction of ~600 slices per hemisphere. The boundary of brain to the cerebral-spinal fluid (CSF) was also manually corrected in the same manner.

Cortical thickness was then calculated in BrainVoyager, by taking in the information of both the white-gray matter boundary, and the brain-CSF boundary, resulting in a whole-brain measurement of gray matter thickness (See Fig. 3).

The myelin content analysis will be performed by including only the gray matter regions of the T1/T2\* data, and subsequently projected onto a surface of white-gray matter boundary.

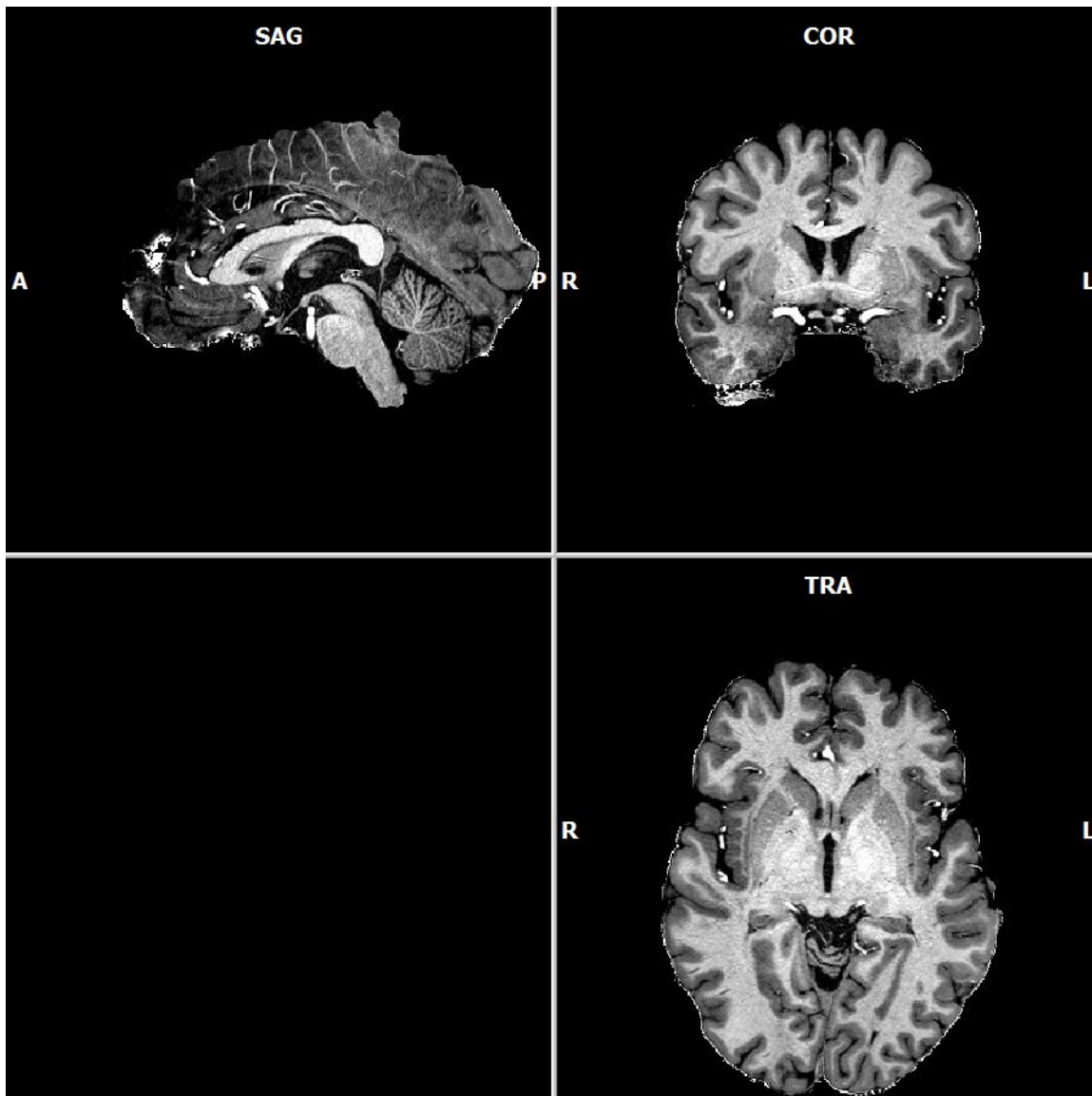


Figure 1. An example of T1/PD anatomical image in AC-PC space, from one sighted control participant.

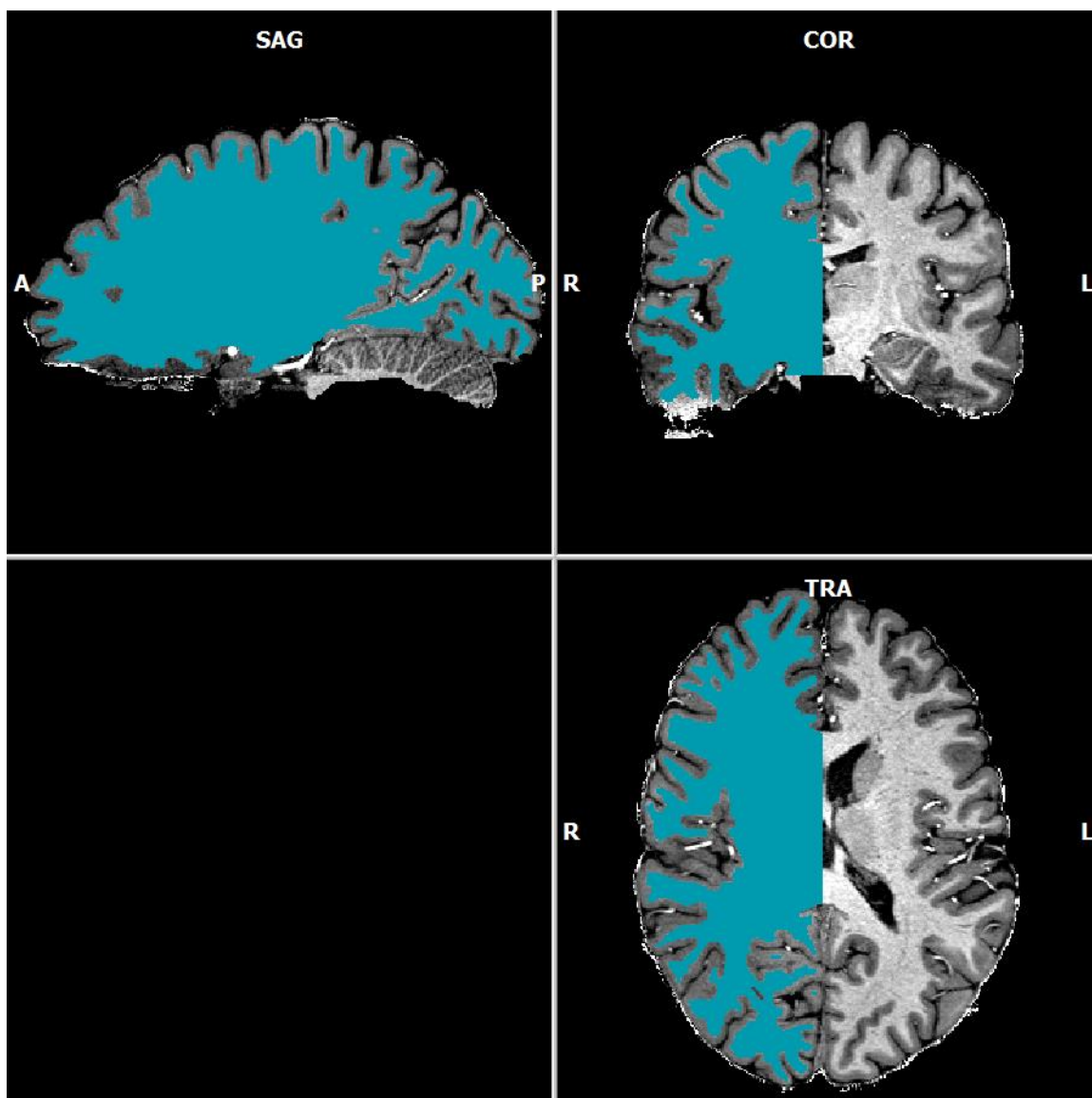


Figure 2. Manually corrected segmentation of the white-gray matter boundary (with the colored region covering the white matter), right hemisphere of the same participant.

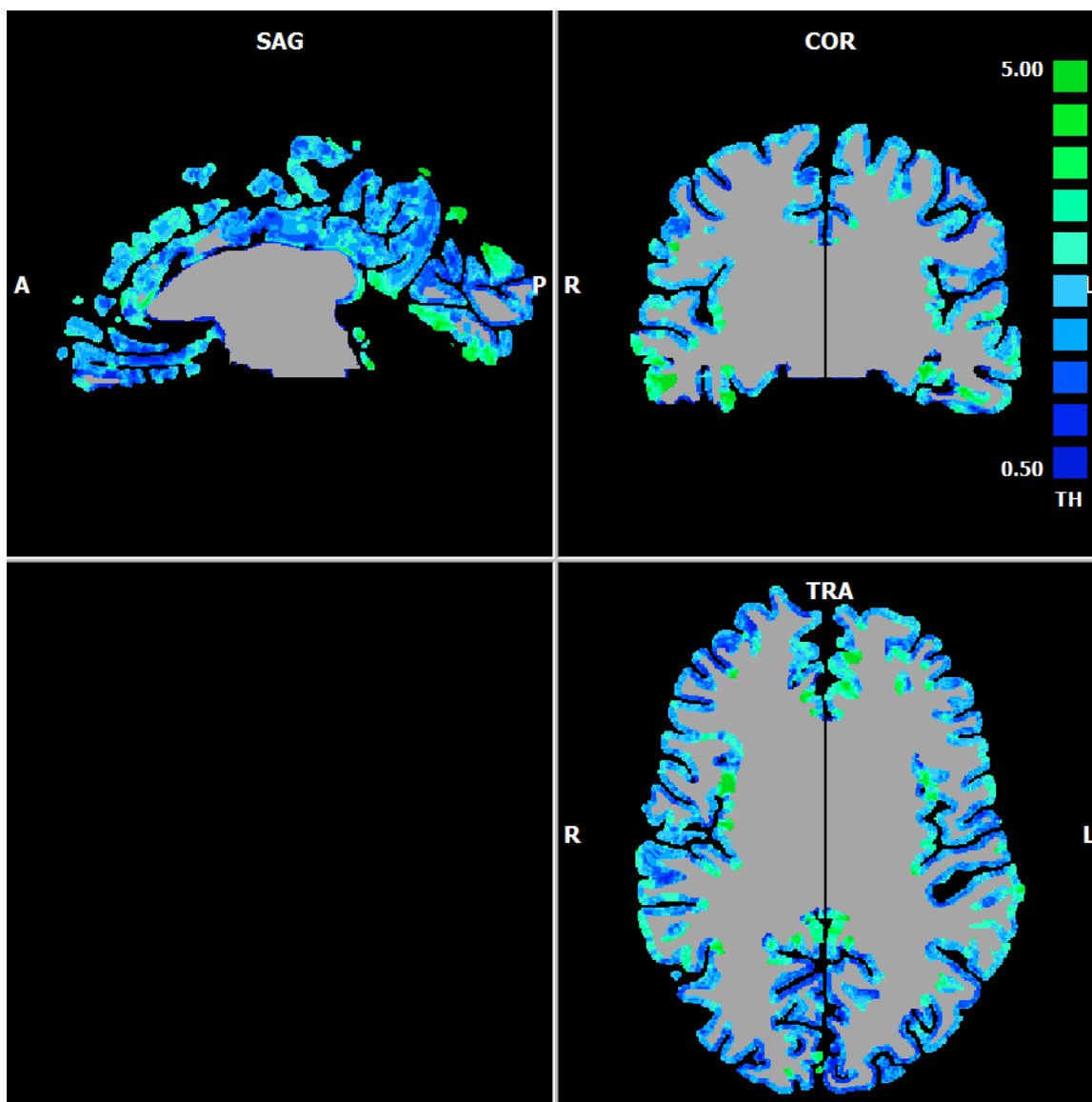


Figure 3. Cortical thickness analysis of the same participant. Color bar denotes the cortical thickness in millimeters.

### 3. Progress

We acquired anatomical images from 14 congenitally blind participants, and 11 sighted control participants. After excluding participants who had big movements in the scanner, it resulted in 13 congenitally blind datasets and 9 sighted control datasets.

The manual segmentation correction of white-gray matter boundary was performed on 9 congenitally blind datasets, and 5 sighted control datasets.

Future steps involve the segmentation (white-gray matter boundary, brain-CSF boundary) for the rest of the datasets. After the segmentation, cortical thickness analysis and myelin content analysis will be performed on the datasets.