Original Data

Format: no-header, unsigned short 16 bit (byte order: MSB LSB)
Acquisition information:
SPGR T1 POST GAD
resolution: 256x256x124
pixel size: 0.9375 x 0.9375 mm
slice thickness: 1.5 mm
slice gap: 0.0 mm
acquisition order: LR

Case information:

Case	Tumor	Location	Slice#
1	meningioma	left frontal	44
2	meningioma	left parasellar	58
3	meningioma	right parietal	78
4	low grade glioma	left frontal	35
5	astrocytoma	right frontal	92
6	low grade glioma	right frontal	81
7	astrocytoma	right frontal	92
8	astrocytoma	left temporal	39
9	astrocytoma	left frontotemporal	31
10	low grade glioma	left temporal	35

Automated Segmentation

Format: no-header, unsigned short 16 bit (byte order: MSB LSB)
Location:
Greyscale images
./case[0-10]/spgr/I.[1-124] (124 slices)
Segmented images
./case[0-10]/seg/seg.[1-124] (124 slices)

Segmented Region	Label Values
Brain	5
Tumor	6
Ventricles	7
Necrosis	10

Viewing the data

Each of the ten sub-directories contain two scene files (scene.xml and scene3.mrml).
The scene.xml and scene3.mrml files can be opened with the 3D Slicer2 and Slicer3 respectively.

Data manipulation

The images can be viewed and processed with 3D Slicer (http://www.slicer.org/). A comprehensive set of tutorials on Slicer is available online at:
http://wiki.na-mic.org/Wiki/index.php/Slicer:Workshops:User_Training_101

Manual segmentation

The table below is showing the single slice manual segmentation by four expert segmenters and the automated segmentation: