

# Tissue-Class Segmentation

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# Image segmentation

- ▶ We are often interested in subdividing or segmenting the brain into meaningful biological regions of interest (ROIs) for an analysis.
- ▶ Examples: tissue segmentation, segmentation of gray matter structures, segmentation of pathology (MS lesions, tumors, ...)

# Goals of this tutorial

- ▶ Perform tissue segmentation in R using FSL and ANTs.
- ▶ Discuss multi-atlas label fusion techniques for segmentation.
- ▶ Perform automatic MS lesion segmentation using OASIS.

## Loading Data

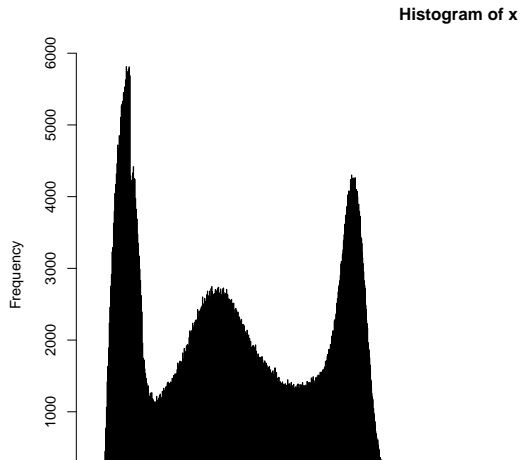
- ▶ Let's read in the training T1s and brain mask for subject 05.

```
library(ms.lesion)
library(neurobase)
library(fslr)
library(scales)
library(extrantsr)
all_files = get_image_filenames_list_by_subject(
  group = "training",
  type = "coregistered")
files = all_files$training05
t1 = readnii(files["MPRAGE"])
mask = readnii(files["Brain_Mask"])
# t1s = lapply(files, function(x) readnii(x["MPRAGE"]))
# t1 = t1s[[5]]
# masks = lapply(files, function(x) readnii(x["Brain_Mask"]))
# mask = masks[[5]]
```

# Tissue Segmentation: Large Outliers

- ▶ Many tissue class segmentations are based on k-means clustering.
- ▶ These methods can be skewed by large outliers.

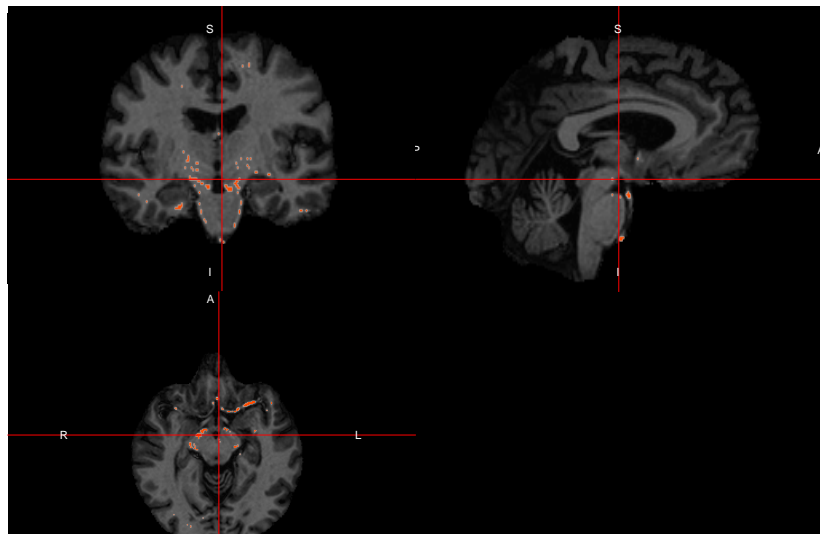
```
hist(t1, mask = mask, breaks = 2000)
```



## Where are the outliers

We see some values that may have been improperly segmented:

```
ortho2(t1, t1 > 400, xyz = xyz(t1 > 400))
```



# Tissue Segmentation using FSL FAST

The `fs1r` function `fast` calls `fast` from FSL (Zhang, Brady, and Smith 2001). The `--nobias` option tells FSL to not perform inhomogeneity correction.

```
t1file = files["MPRAGE"]
t1fast = fast(t1,
              outfile = paste0(nii.stub(t1file), "_FAST"),
              opts = "--nobias")
```

# Results

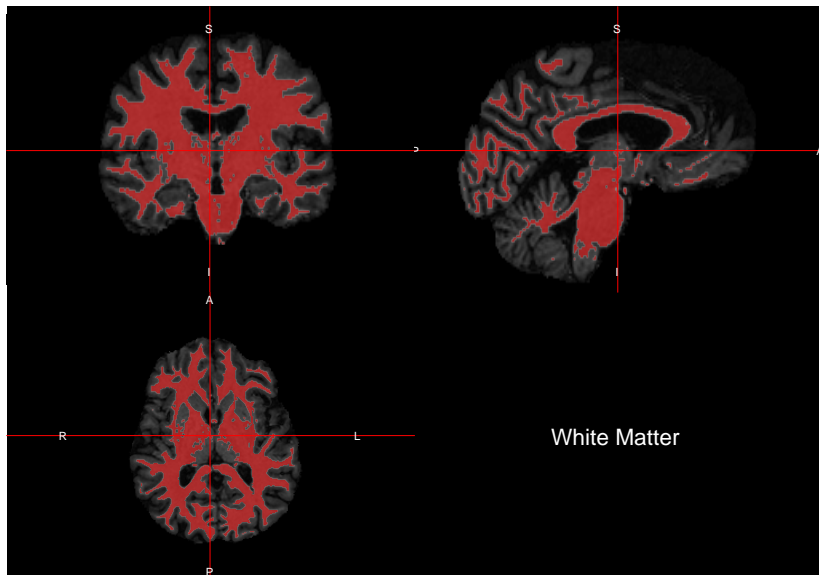
FAST assumes three tissue classes and produces an image with the three labels, ordered by increasing within-class mean intensities. In a T1 image, this results in:

- ▶ Level 1: CSF
- ▶ Level 2: Gray Matter
- ▶ Level 3: White Matter



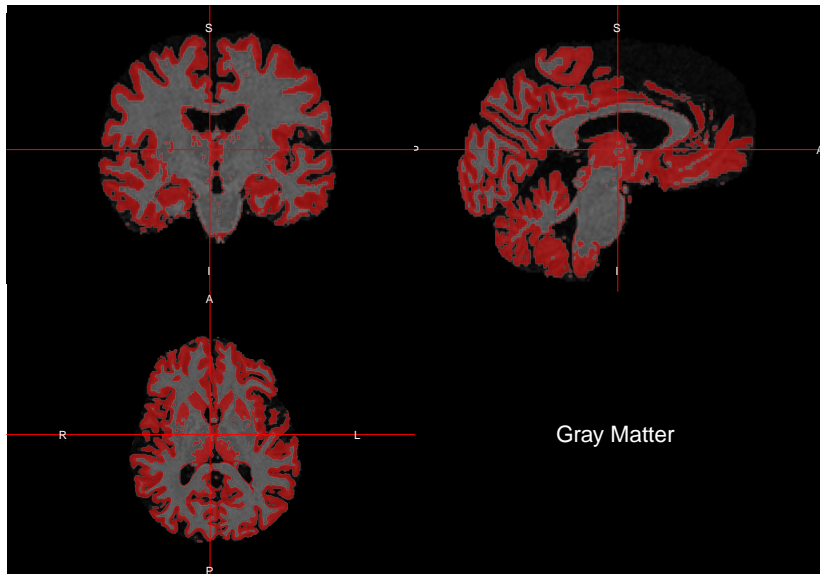
# White Matter

```
ortho2(t1, t1fast == 3, col.y = alpha("red", 0.5), text = "
```



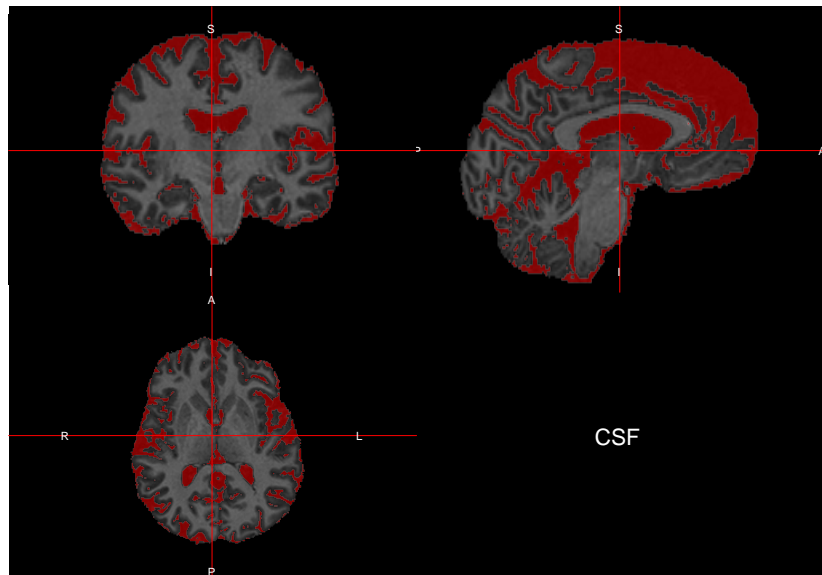
# Gray Matter

```
ortho2(t1, t1fast == 2, col.y = alpha("red", 0.5), text = "
```



# CSF

```
ortho2(t1, t1fast == 1, col.y = alpha("red", 0.5), text = "
```



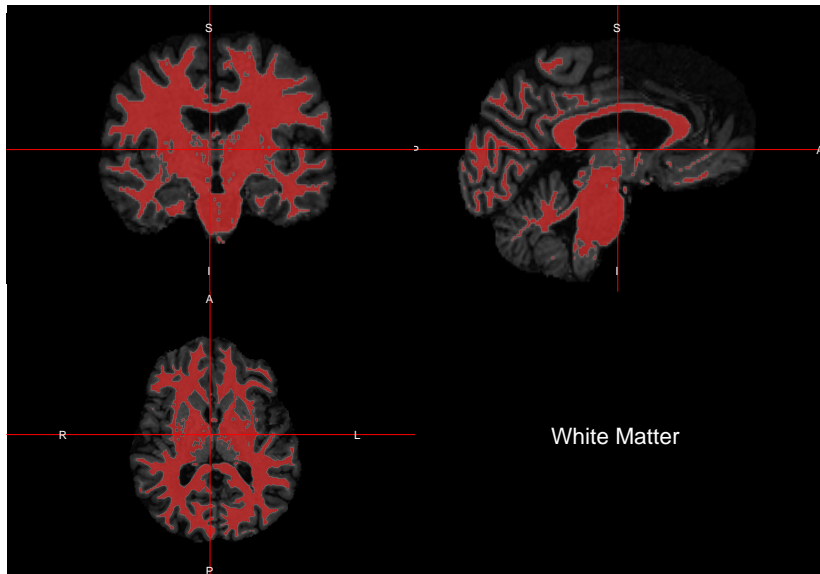
# Windowing

```
rb = robust_window(t1)
robust_fast = fast(t1,
                   outfile = paste0(nii.stub(t1file), "_FAST"),
                   opts = "--nobias")
```

```
separate = separate_img(robust_fast, levels = 1:3)
names(separate) = c("CSF", "GM", "WM")
L = c(MPRAGE = list(t1), separate)
L$MPRAGE = robust_window(L$MPRAGE)
r = range(L$MPRAGE)
L$MPRAGE = (L$MPRAGE - r[1])/(r[2] - r[1])
dd = dropEmptyImageDimensions(t1fast > 0, other.imgs = L)
L = dd$other.imgs
multi_overlay(L, z = 58, text = names(L), text.x = 0.5, text.y = 0.5,
              text.cex = 2.5)
```

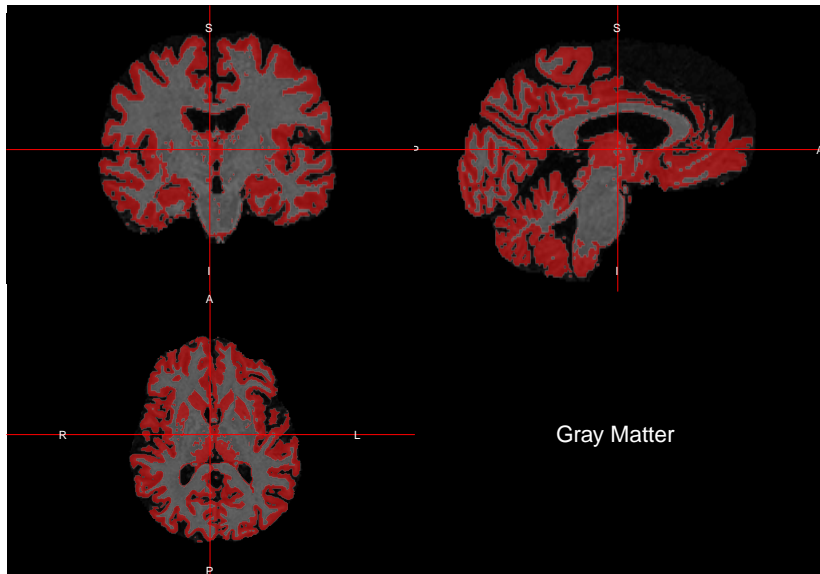
# White Matter

```
ortho2(t1, robust_fast == 3, col.y = alpha("red", 0.5), tex
```



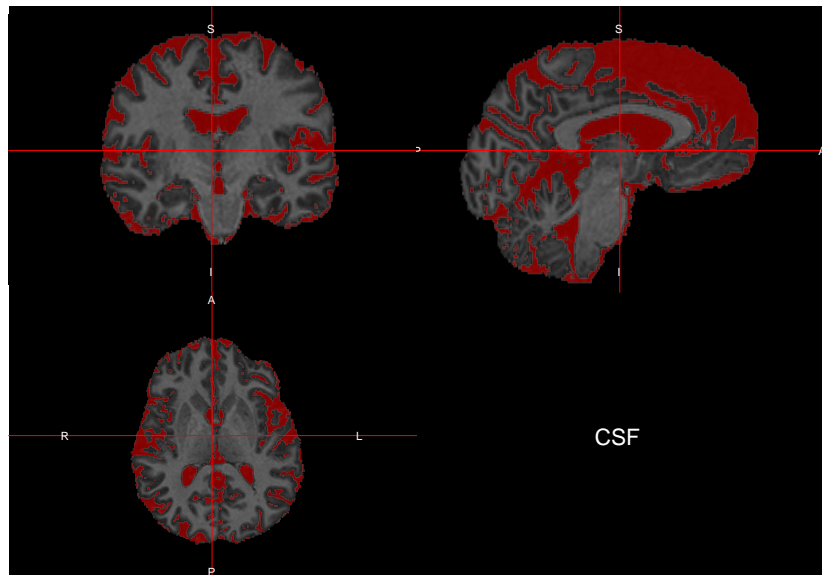
# Gray Matter

```
ortho2(t1, robust_fast == 2, col.y = alpha("red", 0.5), tex
```



# CSF

```
ortho2(t1, robust_fast == 1, col.y = alpha("red", 0.5), tex
```



# Tissue Segmentation using ANTsR, extrantsr

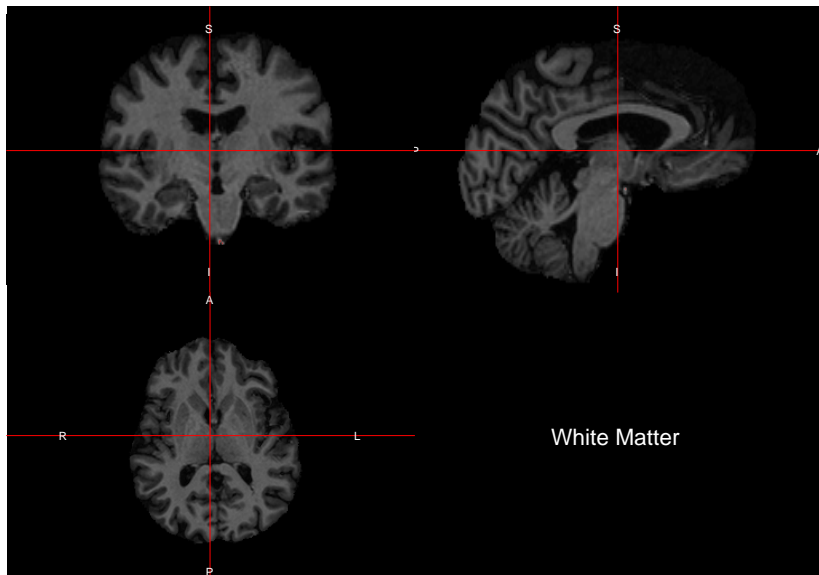
- ▶ Uses Atropos (Avants et al. 2011)

```
t1_otropos = otropos(a = t1, x = mask) # using original data  
t1seg = t1_otropos$segmentation
```



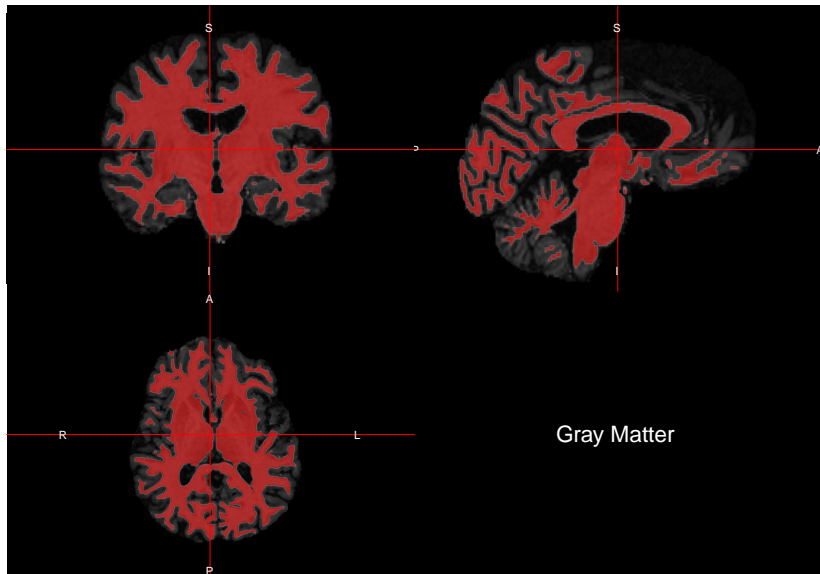
# White Matter

```
ortho2(t1, t1seg == 3, col.y = alpha("red", 0.5), text = "W
```



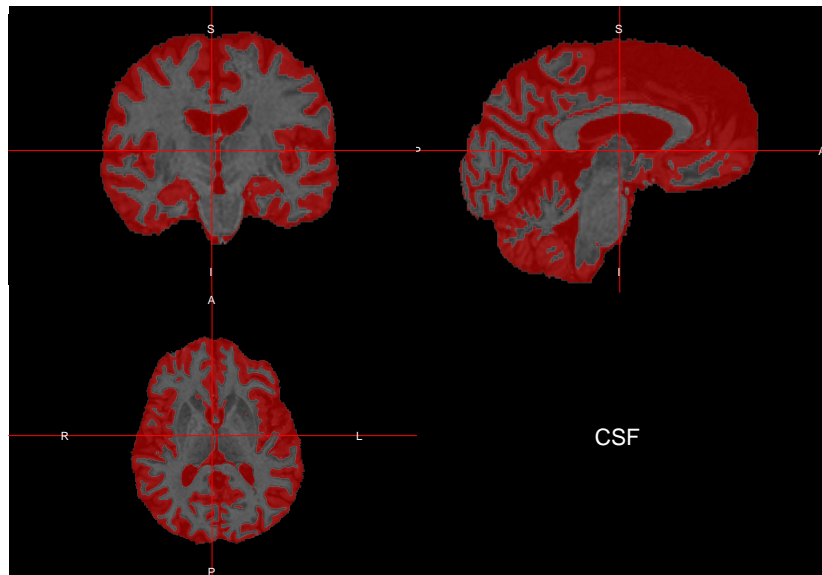
# Gray Matter

```
ortho2(t1, t1seg == 2, col.y = alpha("red", 0.5), text="Gra
```



# CSF

```
ortho2(t1, t1seg == 1, col.y = alpha("red", 0.5), text="CSF")
```

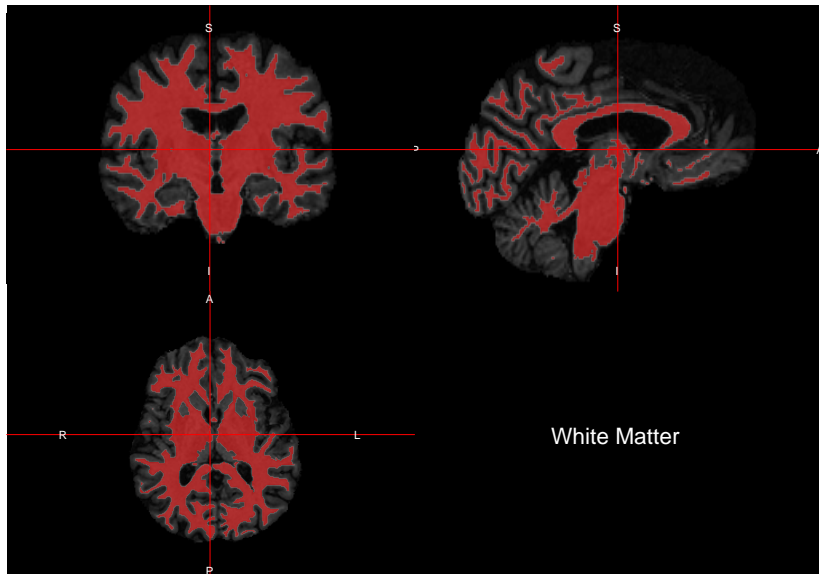


## Tissue Segmentation using ANTsR, extrantsr

```
robust_t1_otropos = otropos(a = rb, x = mask) # using robu  
robust_t1seg = robust_t1_otropos$segmentation
```

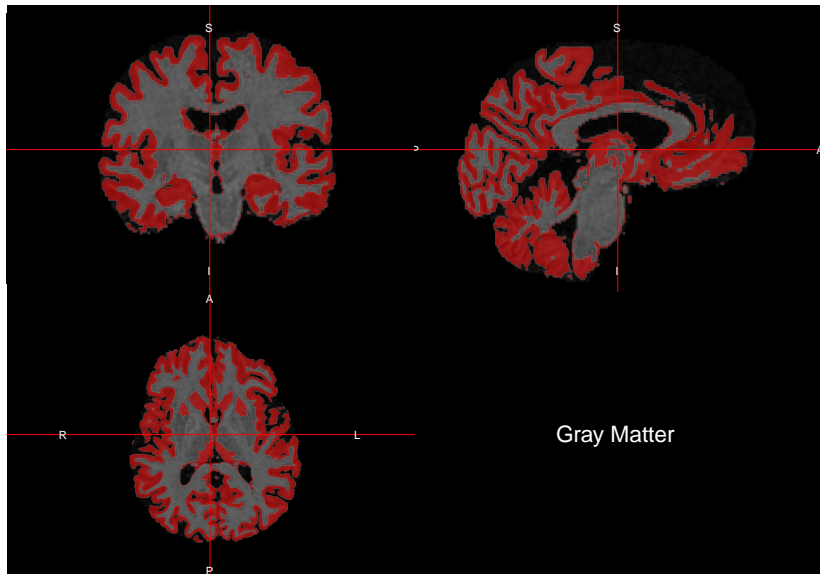
# White Matter

```
ortho2(t1, robust_t1seg == 3, col.y = alpha("red", 0.5), te
```



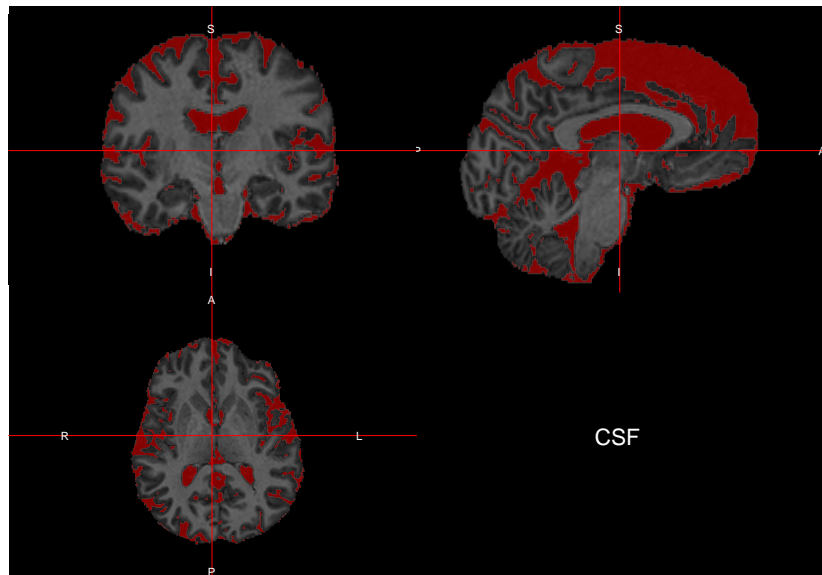
# Gray Matter

```
ortho2(t1, robust_t1seg == 2, col.y = alpha("red", 0.5), te
```



# CSF

```
ortho2(t1, robust_t1seg == 1, col.y = alpha("red", 0.5), te
```



## References

Avants, Brian B, Nicholas J Tustison, Jue Wu, Philip A Cook, and James C Gee. 2011. "An Open Source Multivariate Framework for N-Tissue Segmentation with Evaluation on Public Data." *Neuroinformatics* 9 (4). Springer: 381–400.

Zhang, Yongyue, Michael Brady, and Stephen Smith. 2001. "Segmentation of Brain MR Images Through a Hidden Markov Random Field Model and the Expectation-Maximization Algorithm." *Medical Imaging, IEEE Transactions on* 20 (1): 45–57. [http://ieeexplore.ieee.org/xpls/abs\\_all.jsp?arnumber=906424](http://ieeexplore.ieee.org/xpls/abs_all.jsp?arnumber=906424).