

The Pediatric Template of Brain Perfusion: Quick introduction with *ANTsR*

Brian B. Avants et al.

PICSL

2016-08-08

AdvancedNormalizationTools

HIGH PERFORMANCE METHODS FOR NORMALIZATION, SEGMENTATION AND IMAGE STATISTICS



1 Overview and resources

2 Quick Look

3 Review multiple modality images

4 Templates and joint label fusion

Overview

This is a compilable document with source code located here:

<https://github.com/stnava/ANTsTutorial>

To get this source, do:

```
git clone http://github.com/stnava/ANTsTutorial.git
```

It is expected that you will compile and run this from within the cloned ANTsTutorial directory. The document needs the [ants tutorial data](#) discussed below. It depends on *R*, *rmarkdown* and *ANTsR* primarily.

Herein, [links are in this color](#).

Overview

The Pediatric Template of Brain Perfusion (PTBP) [at figshare](#).

- Free multiple modality MRI data with demographics and psychometrics

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- Each subject contains a slab version of T1, FA, B0, CBF, Thickness, Segmentation and AAL in subject space

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- Each subject contains a slab version of T1, FA, B0, CBF, Thickness, Segmentation and AAL in subject space
- There is also a template contained in the download.

Download the ANTs tutorial data

■ Download

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■ https://www.dropbox.com/s/5p0vlx8en9uzbge/ants_tutorial_data.zip?dl=1

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- Unzip the file in the ANTsTutorial directory.

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- This data has been affinely registered to the template and subsetted with a slab ROI.
- Allows us to speed up examples but still show high-res results.
- Each modality for each subject is in his/her T1 anatomical space.
- An additional deformable mapping is needed to transform this subject space to template space or vice-versa.

A complete reference for PTBP processing

```
git clone http://github.com/jeffduda/NeuroBattery.git
```

This will give you both raw and processed output for a single multiple modality subject.

We test (occasionally) against this reference output to monitor stability of our processing.

If you have not already, download *ANTsR*

- Get *R* from [OSX R](#) or [Linux R](#), optionally [RStudio](#)

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```
pkgmin=c("magrittr","Rcpp") # core dependencies
pkgxtra=c("igraph","randomForest","misc3d","rgl",
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  "pixmap","png","signal","visreg")
install.packages( c( pkgmin, pkgxtra ) )
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```
library(ANTsR)
```

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- Download the *ANTsR* tar.gz to filename.tar.gz
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R CMD INSTALL filename.tar.gz

- Test via (in R) calling:

```
library(ANTsR)
```

- Done!

Get the demographics file

```
library(ANTsR)
csvlink="https://ndownloader.figshare.com/files/1699436"
tfn=tempfile(fileext='.csv')
if ( ! exists("demog") )
{
  demog=download.file(csvlink,tfn)
  if ( demog == 0 ) demog=read.csv( tfn )
}
```

Investigate the demographics

```
str(demog[,1:10])
```

```
## 'data.frame': 183 obs. of 10 variables:  
## $ SubID : Factor w/ 120 levels "PEDSO...  
## $ ScanDate : int 20100709 20100801 2011...  
## $ AgeAtScan : num 9.25 9.25 10.5 11.5 10...  
## $ Sex : Factor w/ 2 levels "F","M"...  
## $ Handedness : Factor w/ 3 levels "Left",  
## $ FullScaleIQ : int 99 99 100 101 119 NA 9...  
## $ Verbal.IQ : int 96 96 106 111 111 NA 9...  
## $ Performance.IQ : int 100 100 95 90 124 NA 8...  
## $ Teen.Ladder.SES.score : int 5 5 3 2 6 NA 5 4 NA 8...  
## $ Teen.Ladder.Community.Score: int 1 1 2 2 1 NA 4 2 NA 2...
```

Investigate the demographics

```
str(demog[,11:20])
```

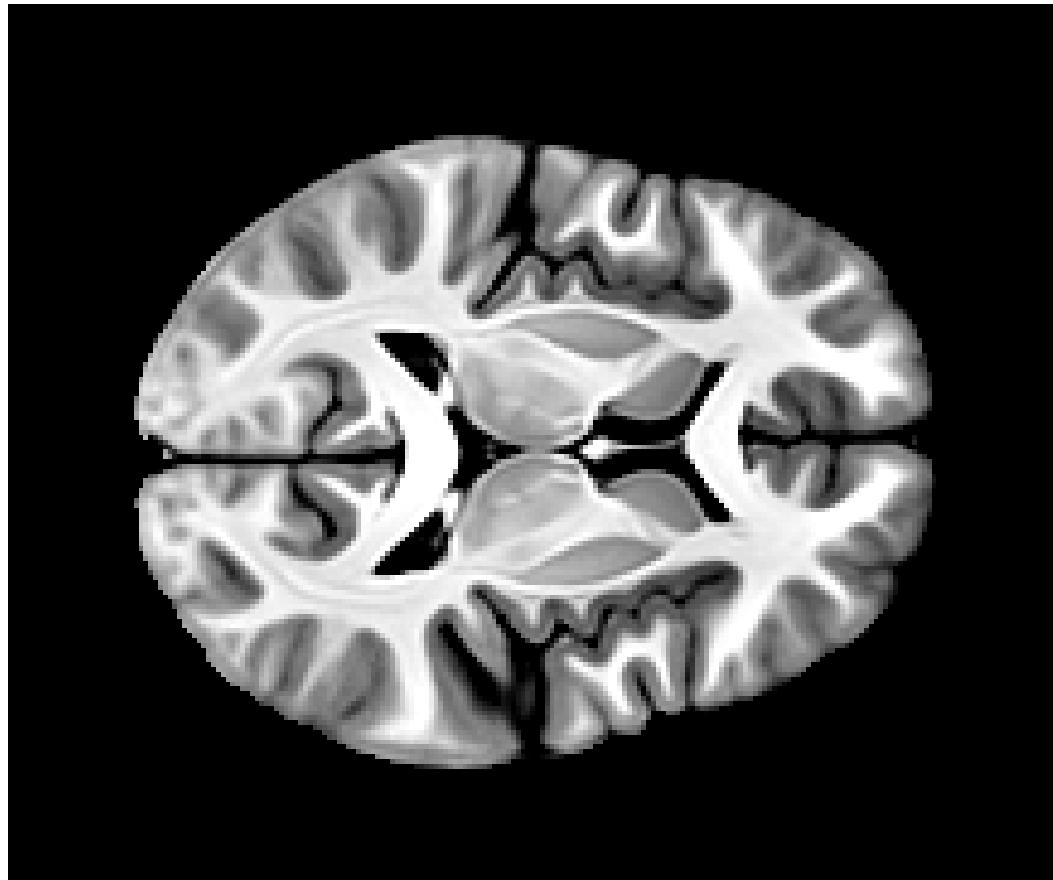
```
## 'data.frame': 183 obs. of 10 variables:  
## $ Income : int 210 210 210 210 NA NA 70 NA ...  
## $ Father.Education : int 20 20 20 20 16 NA 16 20 NA ...  
## $ BV : num 2632317 2614991 2620778 2644 ...  
## $ CSF : num 402388 387787 395315 412062 ...  
## $ Cortex : num 1115803 1109720 1106519 1100 ...  
## $ WM : num 725281 732096 732143 734156 ...  
## $ DGM : num 79423 80384 80793 86355 6799 ...  
## $ BStem : num 33413 32478 33758 35530 2886 ...  
## $ Cerebellum : num 276009 272526 272251 276678 ...  
## $ ThickMeanPrecentral_L: num 2.49 2.5 2.57 2.58 2.85 ...
```

Read the structural PTBP template image

```
t1fn = paste(bd,  
"data/antsExamples/ANTsTutorial/data/template/PTBP_T1_BrainC  
sep='')  
t1tem = antsImageRead( t1fn )
```

Review multiple modality images

Plot the structural PTBP template image



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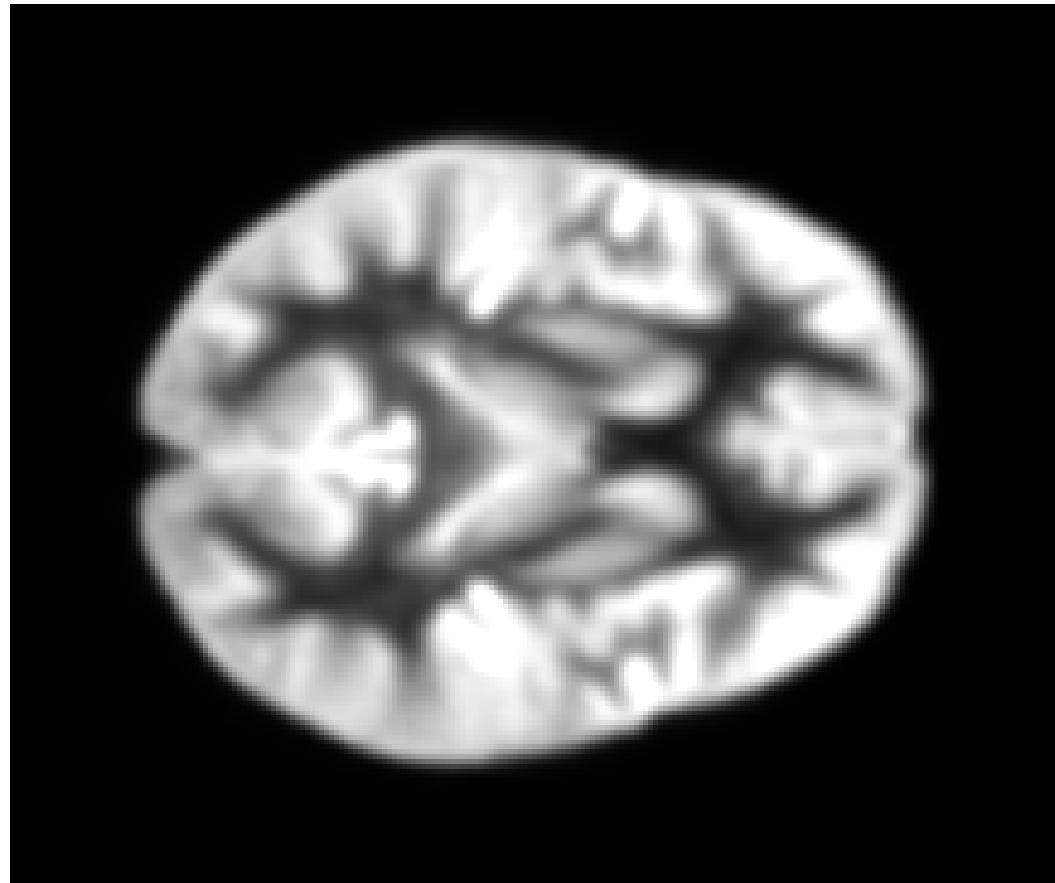
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Review multiple modality images

Plot the CBF PTBP template image



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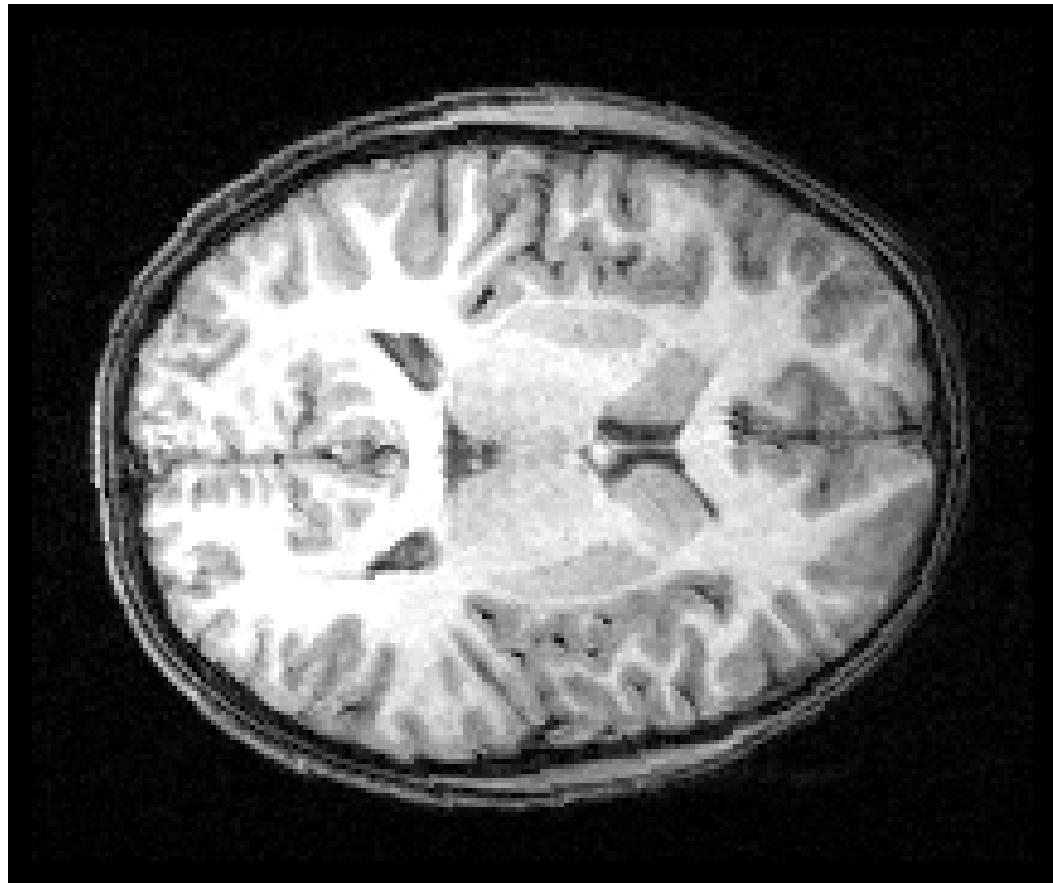
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Find subject image

```
subnum=11
id=demog$SubID[subnum]
dt=demog$ScanDate[subnum]
exts=c( "mprage_t1.nii.gz" ,
       "fa_anatomical.nii.gz",
       "MeanCBFWarpedToT1.nii.gz",
       "CorticalThickness.nii.gz",
       "BrainSegmentation.nii.gz",
       "AAL.nii.gz" )
pre=paste( bd,"data/antsExamples/ANTsTutorial/data/Subjects/",
fns=Sys.glob( paste( pre, exts , sep='')) )
```

Review multiple modality images

Review each modality



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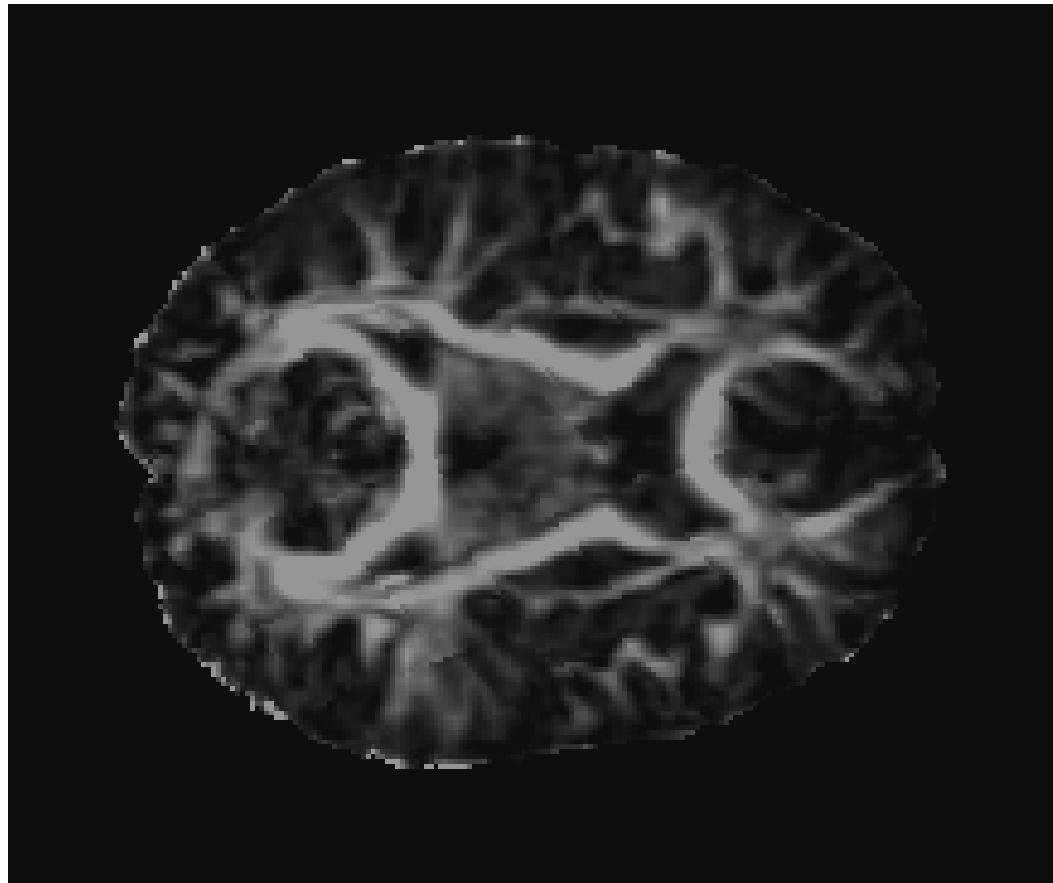


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Review multiple modality images

Review each modality



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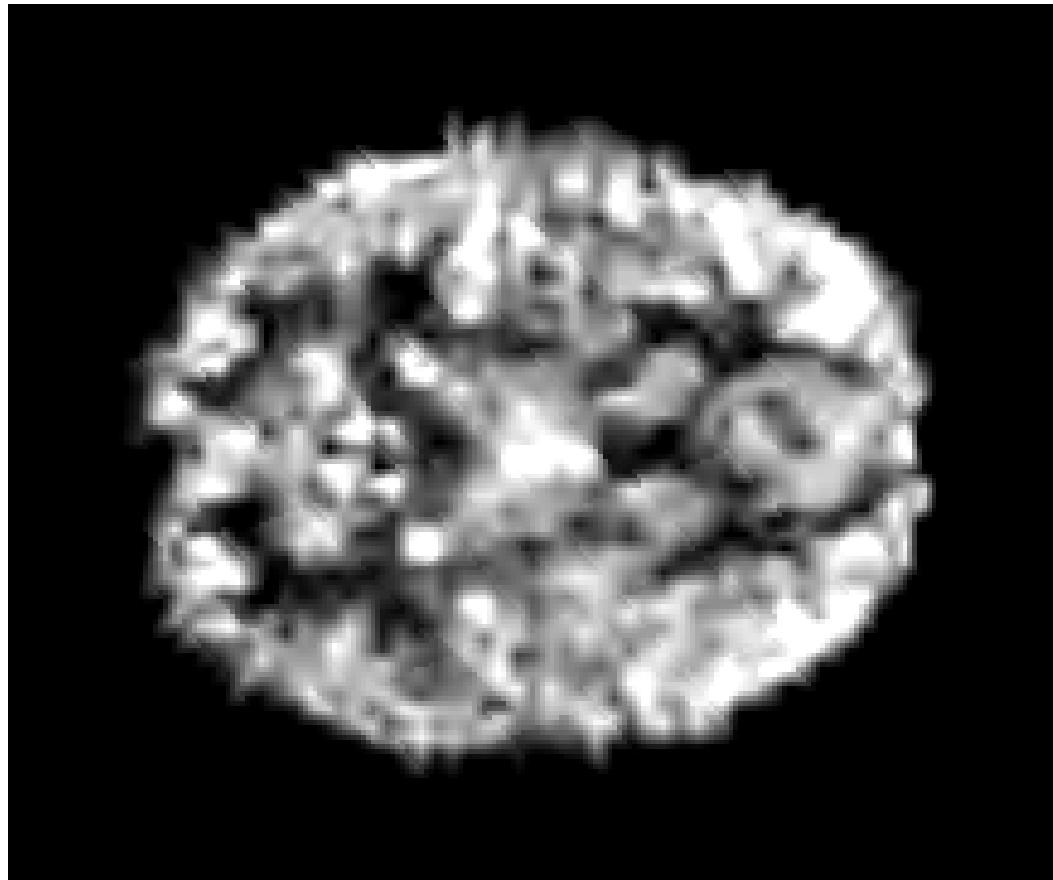


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Review multiple modality images

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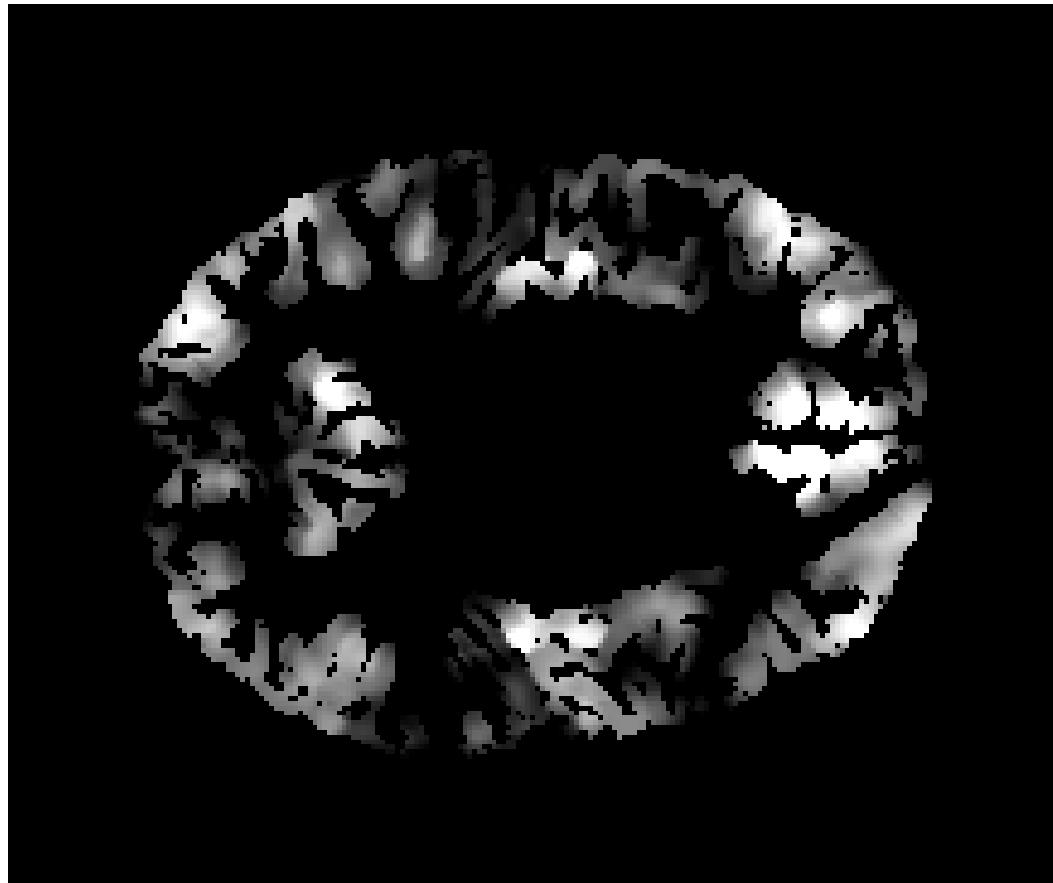


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Review multiple modality images

Review each modality



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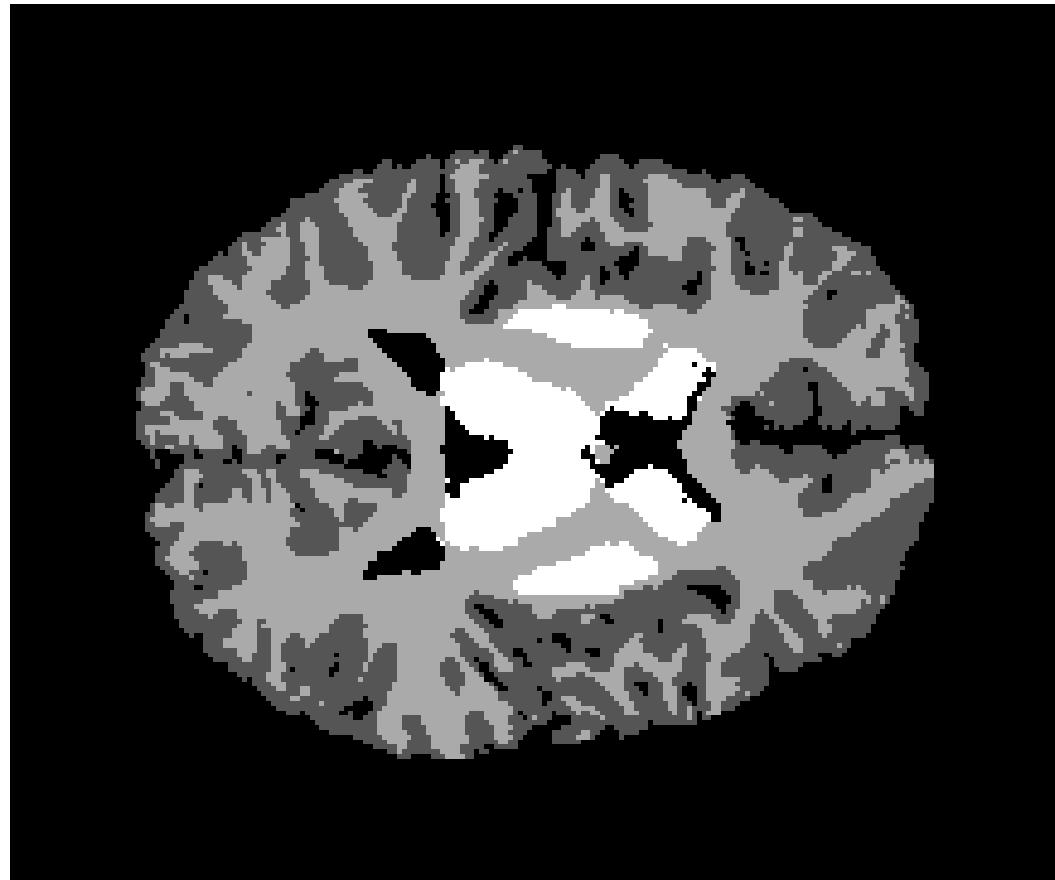


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Review multiple modality images

Review each modality



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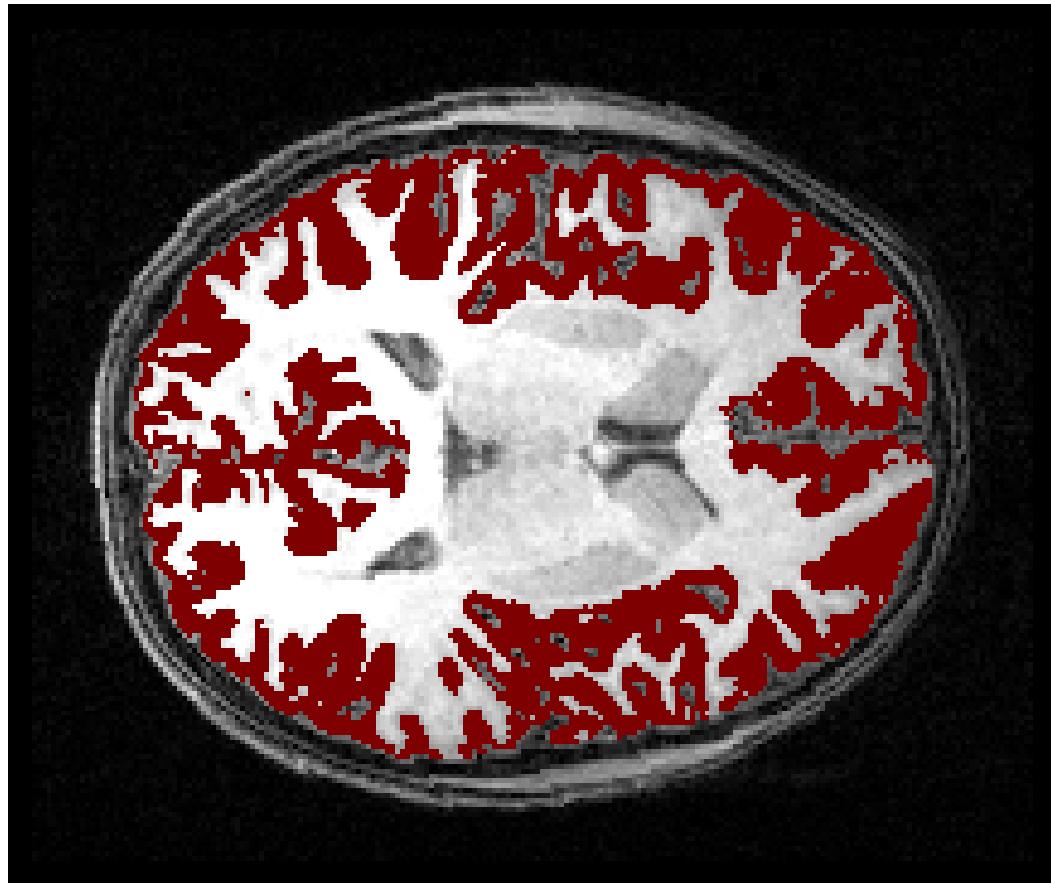


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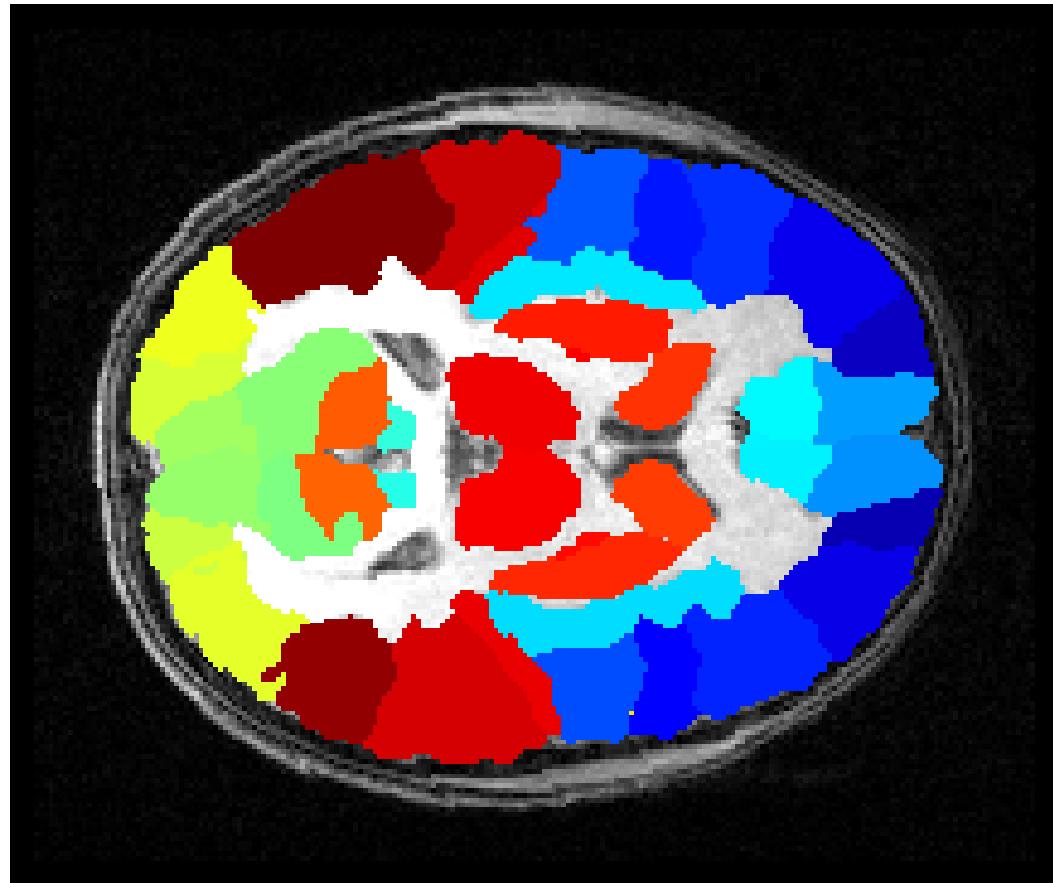


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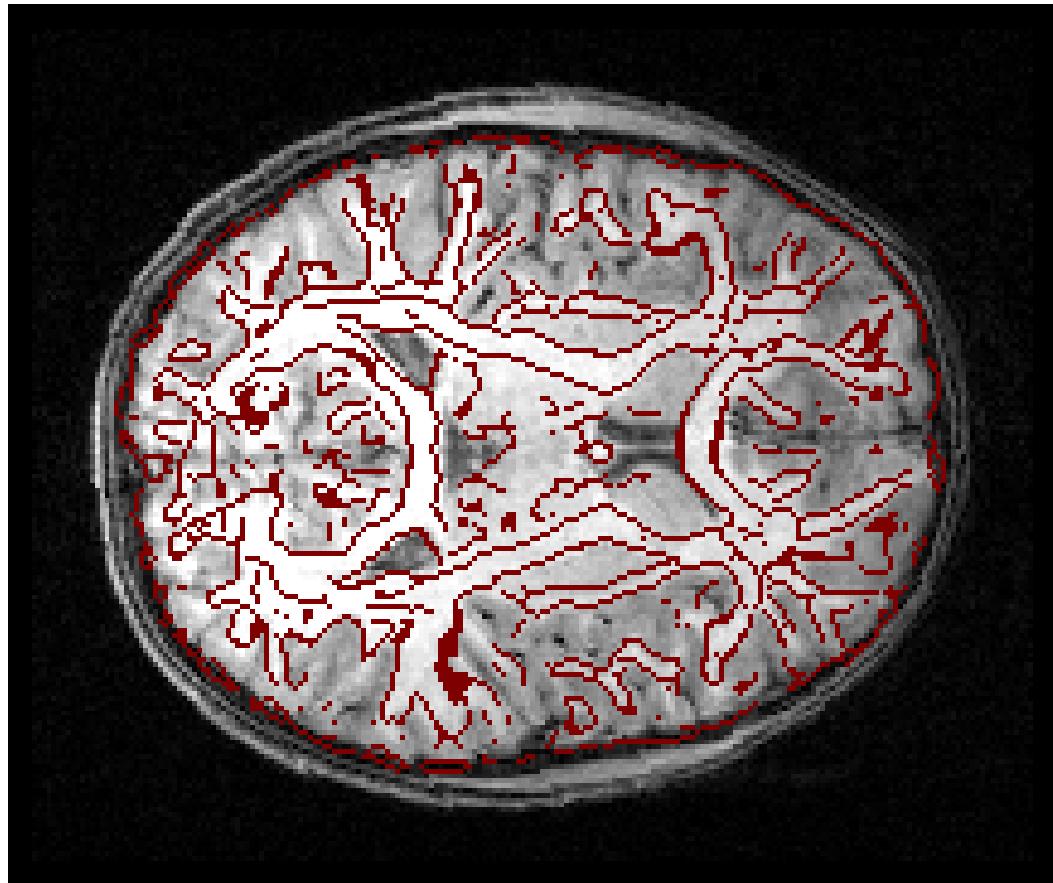


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Count complete subject images

```
havecompletesubject=rep(FALSE,nrow(demog))
for ( x in 1:nrow(demog) )
{
  id = demog$SubID[x]
  dt = demog$ScanDate[x]
  pre = paste( bd,"data/antsExamples/ANTsTutorial/data/Subject"
  fns = Sys.glob( paste( pre, exts , sep='')) )
  if ( length( fns ) == 6 ) havecompletesubject [x]=TRUE
}
nsub=sum( havecompletesubject )
```

PTBP in our tutorial

We have 1 multiple modality subjects to process and to analyze.

We will use them to:

- Build a template

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- relating imaging modalities to each other.
- Finally, put all this together to create a reproducible analysis document for the PTBP.

We built a template, now what?

- Suppose a dataset that already contains segmentations.

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- Suppose a dataset that already contains segmentations.
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We built a template, now what?

- Suppose a dataset that already contains segmentations.
- Transform these segmentations to the template.
- Perform a weighted voting to customize the segmentations for the template.

Template priors with SyN-Quick

```
# t1tem read before
ilist=list()
seglist=list()
for ( x in which( havecompletesubject ) )
{
  id = demog$SubID[x]
  dt = demog$ScanDate[x]
  pre = paste( bd, "data/antsExamples/ANTsTutorial/data/Subject"
  fns = Sys.glob( paste( pre, exts , sep='.' ) )
  t1 = antsImageRead( fns[1] )
  mytx = antsRegistration( t1tem, t1, "SyN" )
  seg = antsImageRead( fns[5] )
  segw = antsApplyTransforms( t1tem, seg, mytx$fwd, interpolation="nearest-neighbor" )
  ilist = lappend( ilist, mytx$warpedmovout )
  seglist = lappend( seglist, segw )
}
```

Template, intensity images, segmentations → JLF

- Joint label fusion is a multi-atlas segmentation method.

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- It performed well in several recent competitions ([SATA 2012](#), [SATA 2013](#))

Template, intensity images, segmentations → JLF

- Joint label fusion is a multi-atlas segmentation method.
- It performed well in several recent competitions (**SATA 2012, SATA 2013**)
- We use it regularly in our studies to build template priors and to label cortical or deep structures in the brain.

JLF theory: “Multi-Atlas Segmentation with Joint Label Fusion”

A matrix M_x is defined by the number of atlas segmentations one has. $M_x(i, j)$ measures joint atlas errors wrt a target segmentation at a voxel. Entries in M_x relate to the likelihood two atlases make the same error.

The key difference between joint label fusion and other label fusion methods is that it explicitly considers correlations among atlases, i.e., the dependence matrix, into voting weight assignment to reduce bias in the atlas set.

JLF theory: “Multi-Atlas Segmentation with Joint Label Fusion”

The expected label difference between the consensus solution obtained from weighted voting and the target segmentation is: $w_x^T M_x w_x$.

Find atlas weights, w_x , for each of A^i atlases, st

$$w_x^T (M_x + \alpha \mathbf{Id}) w_x$$

is minimized subject to $\sum_{i=1}^n w_x(i) = 1$.

JLF theory: “Multi-Atlas Segmentation with Joint Label Fusion”

Define

$$K_m = \langle | A_N^{i,m} - T_N^m |, | A_N^{j,m} - T_N^m | \rangle$$

then

$$M_x(i, j) = (\sum_m K_m)^\beta$$

with N representing a neighborhood calculation, $A^{i,m}$ representing the i^{th} atlas and the m^{th} modality. Lagrange multipliers yield:

$$w_x = \frac{M_x^{-1} 1_n}{1_n^t M_x^{-1} 1_n}$$

Finally, local patch search is used to improve the neighborhoods that correspond.

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JLF Example

Suppose that a pair of atlases A_1 and A_2 produce statistically independent label errors for a given target image. If A_1 produces a wrong label 50% of the time and A_2 produces a wrong label 20% of the time, we have

$$M_x = \begin{bmatrix} 0.5 & 0.1 \\ 0.1 & 0.2 \end{bmatrix}$$

The optimal voting weights are then $w_x = [0.2, 0.8]^t$.

Template Joint Label/Intensity Fusion

```
if ( !exists("ilist") )
  ilist=imageFileNames2ImageList(
    Sys.glob( paste(bd,"data/antsExamples/ANTsTutorial/data/JI"))
if ( !exists("seglist") )
  seglist=imageFileNames2ImageList(
    Sys.glob( paste(bd,"data/antsExamples/ANTsTutorial/data/JI"))
mk=getMask(t1item)
jlf=jointIntensityFusion( t1item, mk, ilist,
  labelList=seglist, rad=rep(3,3), rSearch=2,
  computeProbs=TRUE, includezero=TRUE)
# write out results
if ( ! exists("tf") ) tf=tempfile()
antsImageWrite( jlf$segimg, paste(tf,'seg.nii.gz',sep=' ') )
antsImageWrite( jlf$predimg, paste(tf,'pred.nii.gz',sep=' ') )
for ( i in 1:length(jlf$probimgs) )
  antsImageWrite( jlf$probimgs[[i]],
```

Augment CSF probability

- Standard JLF doesnt capture CSF very well.

```
if ( !exists("mk") ) mk=getMask(t1item)
ktem=kmeansSegmentation(t1item,3,mk)
jlcsf=jlif$probimgs[[1]][ mk==1 ]
kmcsf=ktem$probabilityimages[[1]][ mk==1 ]
csfmat=rbind( jlcsf, kmcsf )
newcsfvec = apply( csfmat, MARGIN=2, FUN=max )
newcsf=makeImage( mk, newcsfvec )
```

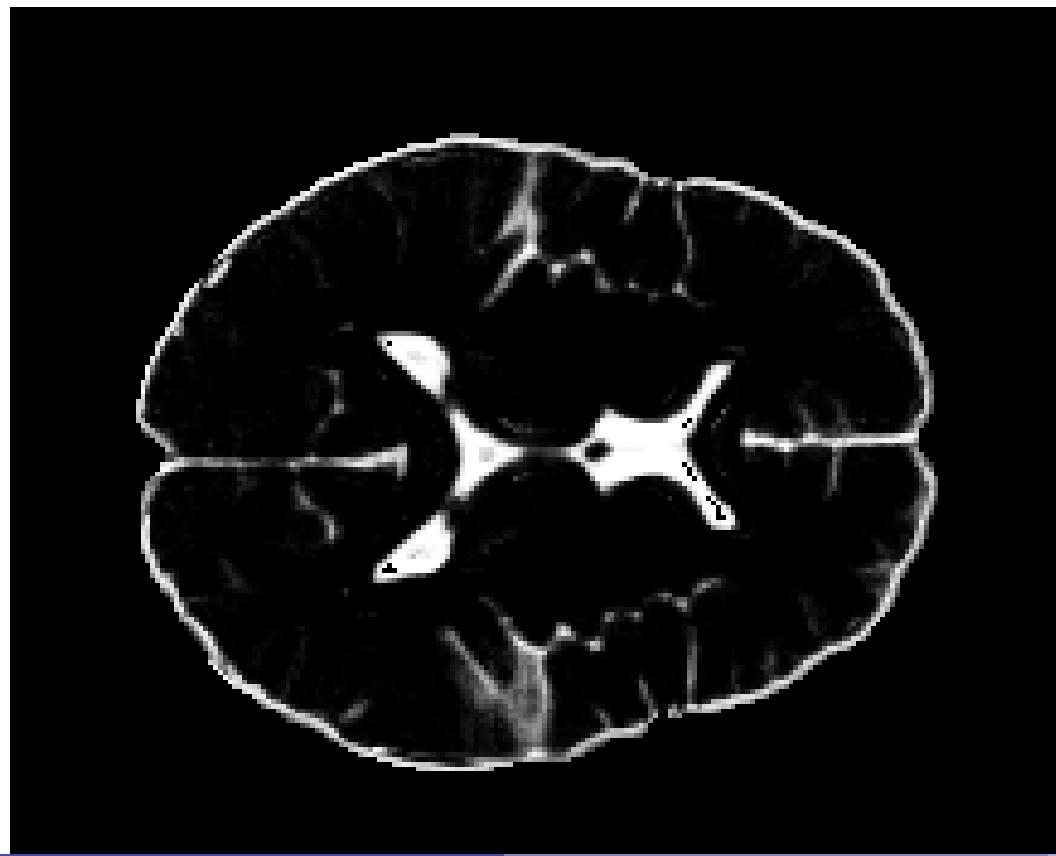
Augment CSF probability

- Standard JLF doesn't capture CSF very well.
- Let's fix that.

```
if ( !exists("mk") ) mk=getMask(t1item)
ktem=kmeansSegmentation(t1item,3,mk)
jlcsf=jlif$probimgs[[1]][ mk==1 ]
kmcsf=ktem$probabilityimages[[1]][ mk==1 ]
csfmat=rbind( jlcsf, kmcsf )
newcsfvec = apply( csfmat, MARGIN=2, FUN=max )
newcsf=makeImage( mk, newcsfvec )
```

Augment CSF probability

```
plot( jlf$probimsgs[[1]], dorot=1, window.img=c(0,4), slices=10 )
```

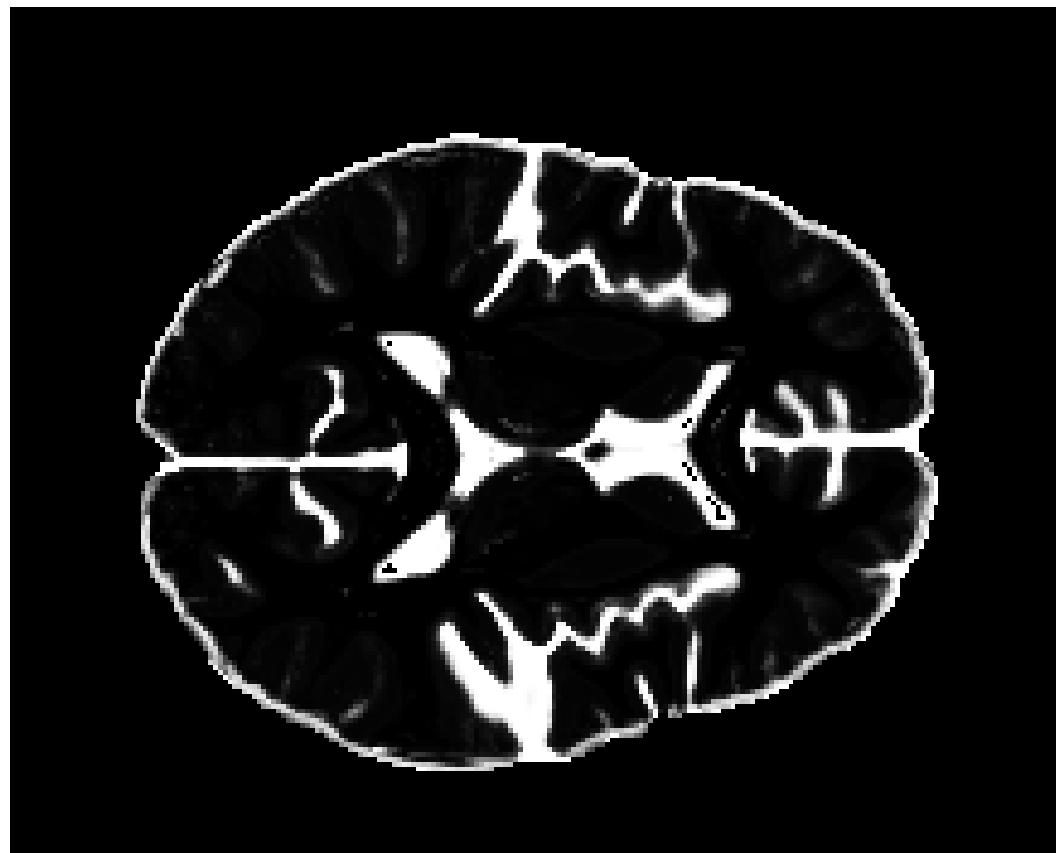


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Augment CSF probability

```
plot( newcsf,dorot=1,window.img=c(0,4), slices=10 )
```



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Renormalize probabilities

```
csfind=1
ncsf=2:length(jlf$probimgs)
jlfmat=imageListToMatrix( jlf$probimgs, mk )
prsums=colSums( jlfmat ) # i=26 for testing
for ( i in 1:ncol(jlfmat) ) {
  colvec=jlfmat[,i]
  ncsfsum=sum( colvec[ncsf] )
  csfval=newcsfvec[i]
  colvec[csfind]=csfval # the fix is in!
  if ( ncsfsum > 0 )
    colvec[ncsf]=colvec[ncsf]/ncsfsum*(1.0-csfval)
  else colvec[csfind]=1
  jlfmat[,i]=colvec
}
newprobimgs=matrixToImages( jlfmat, mk )
```

Renormalize probabilities: ANTsR function

```
jlf$probimgs[[ 1 ]] = newcsf  
newprobimgs2 = renormalizeProbabilityImages(  
  jlf$probimgs, mk, 1 )
```

Segment new images with these modified priors

We can use the template, itself, as an example.

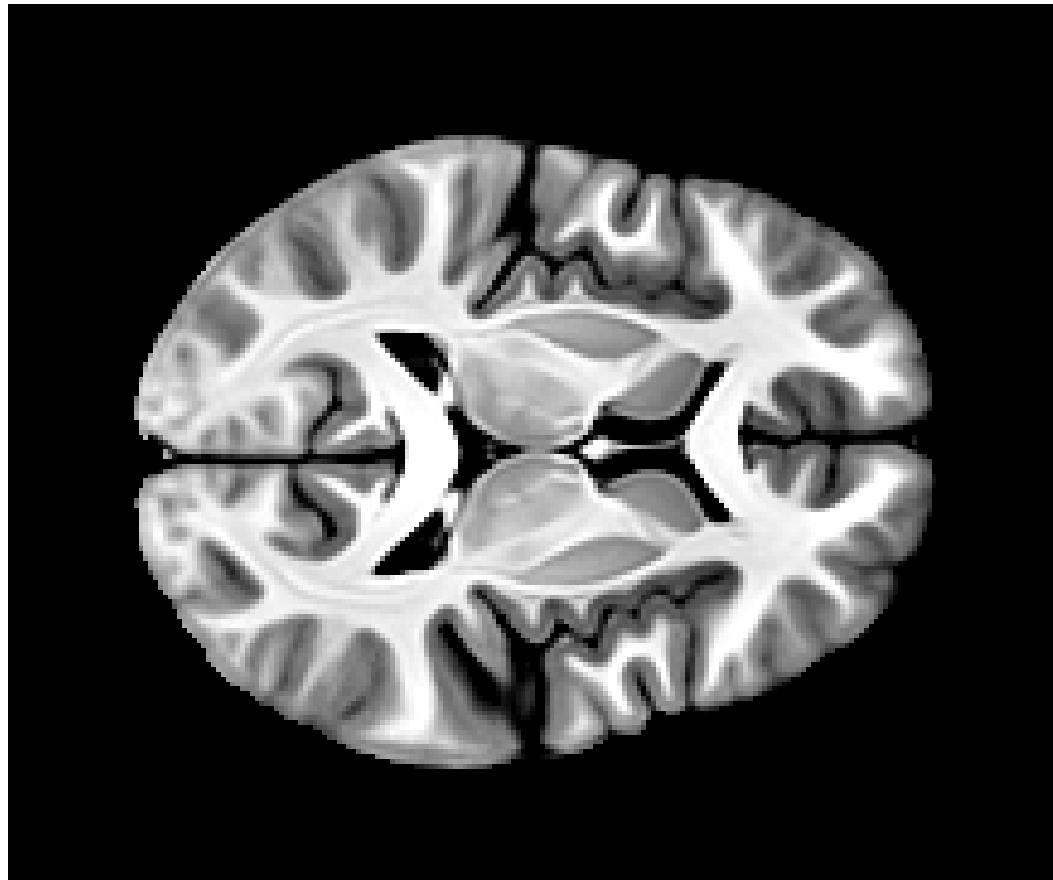
Obviously, we skip the registration step.

```
segnew <- atropos( d = 3, a = t1tem, m = '[0.05,1x1x1]',  
c = '[2,0]', i = newprobimsgs2, x = mk )
```

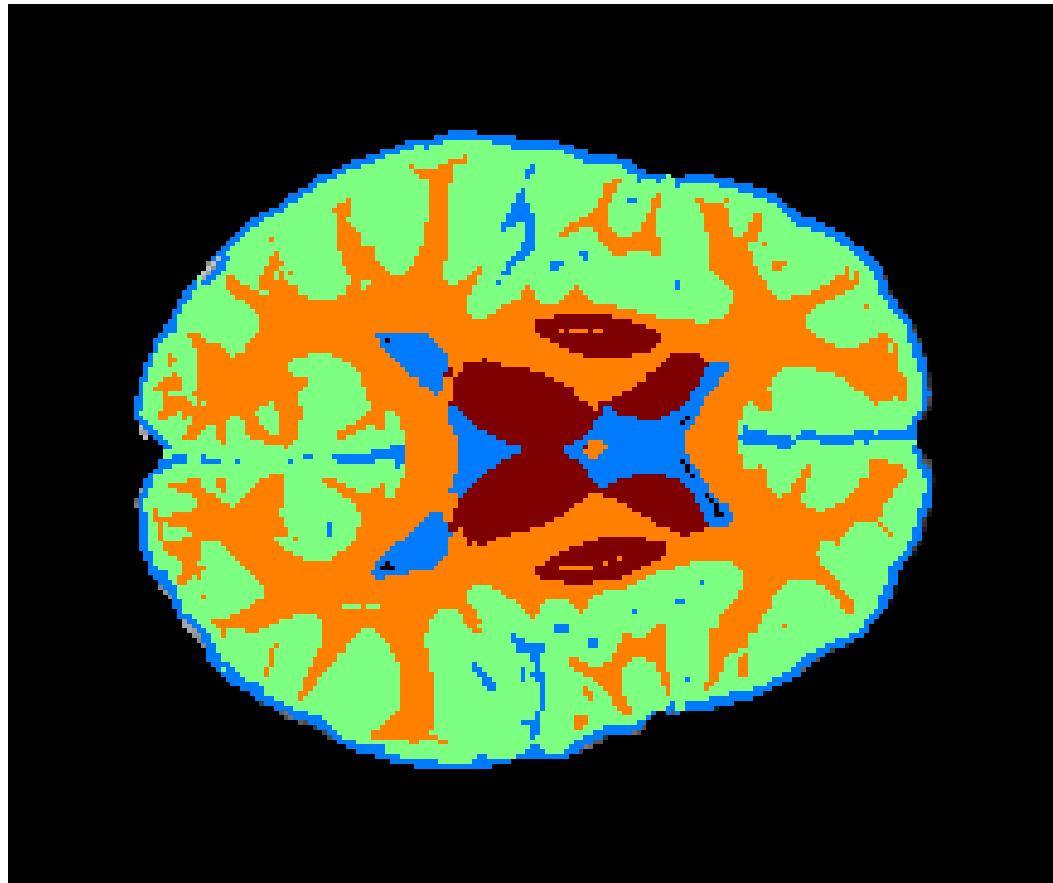
A more complete process is available in `antsAtroposN4.sh` which is what we use for production.

We might go further and force the posteriors to be zero where the priors are zero ...

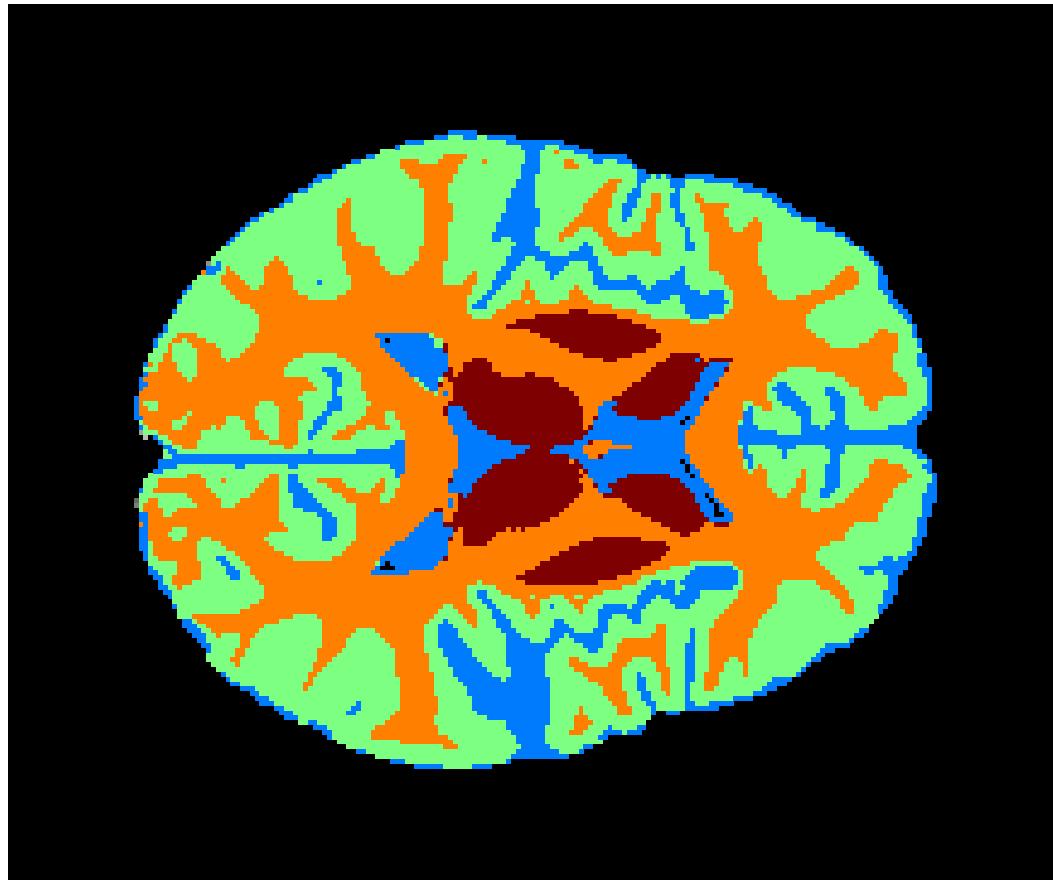
Template and segmentation



Template and *JLF* segmentation



Template and *Atropos* segmentation



Try the same thing on a subject (need registration)

Let's do this as example later ...

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- We showed how to get the template “into shape” such that it can be used for processing new data.
- JLF is key to this process.
- We will discuss modality-specific processing and statistical testing procedures elsewhere.