

Intensity Normalization

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Intensity normalization

- ▶ Conventional MRI intensities (T1-w, T2-w, PD, FLAIR) are acquired in arbitrary units, making the images not comparable across scanners and visits.
- ▶ Intensity normalization brings the intensities to a common scale.

Goals of this tutorial

- ▶ Visualize the intensities using boxplots and densities
- ▶ Apply the WhiteStripe intensity normalization

Reading in the images

For the moment, we will work with the T1-w images from the training data.

```
library(ms.lesion)
library(neurobase)
library(WhiteStripe)
fnames = get_image_filenames_list_by_subject(
  group = "training",
  type = "coregistered")
t1s = lapply(fnames, function(x) readnii(x["MPRAGE"]))
tissues = lapply(fnames, function(x) readnii(x["Tissue_Class"]))
masks = lapply(fnames, function(x) readnii(x["Brain_Mask"]))

vals = mapply(function(t1, mask){
  mask_vals(t1, mask)
}, t1s, masks, SIMPLIFY = FALSE)
```

Code for plotting the data

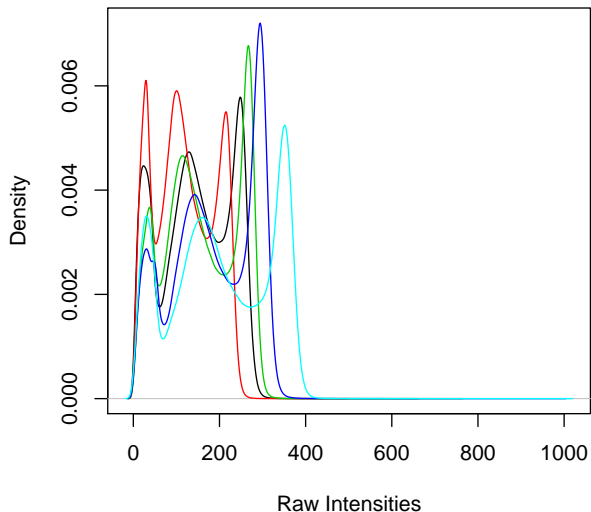
```
plot_densities = function(dens, xlab = "Raw Intensities",
                           main = "Whole Brain") {
  range_x = sapply(dens, function(d) range(d$x))
  range_x = range(range_x)
  range_y = sapply(dens, function(d) range(d$y))
  range_y = range(range_y)
  plot(dens[[1]], xlim = range_x, ylim = range_y,
        xlab = xlab, main = main)
  for (idens in 2:length(dens)) {
    lines(dens[[idens]], col = idens)
  }
}

plot_boxplots = function(vals,
                          main = "Whole Brain") {
  boxplots <- lapply(vals, boxplot, outline = FALSE, plot = FALSE)
  boxplots = lapply(boxplots, function(x) x$stats)
  boxplots <- do.call(cbind, boxplots)
  boxplot(boxplots, main = main)
```

Visualizing the intensities

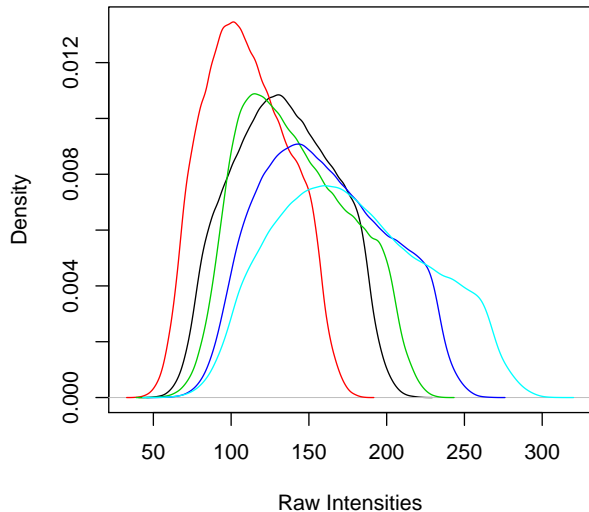
```
dens = lapply(vals, density); plot_densities(dens)
```

Whole Brain



Visualizing the intensities by tissue class

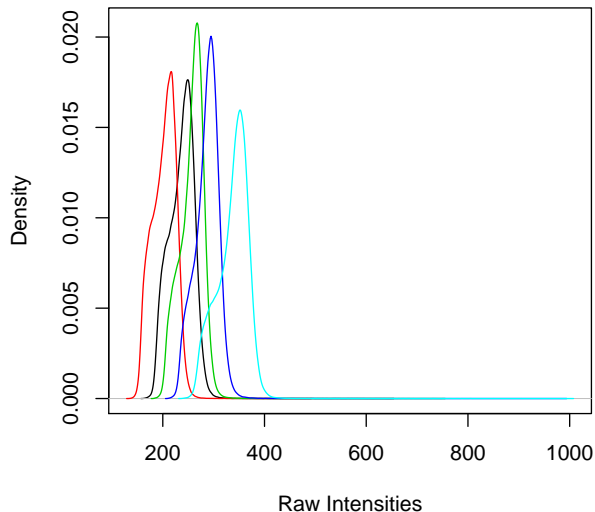
Gray Matter



Gray Matter

Visualizing the intensities by tissue class

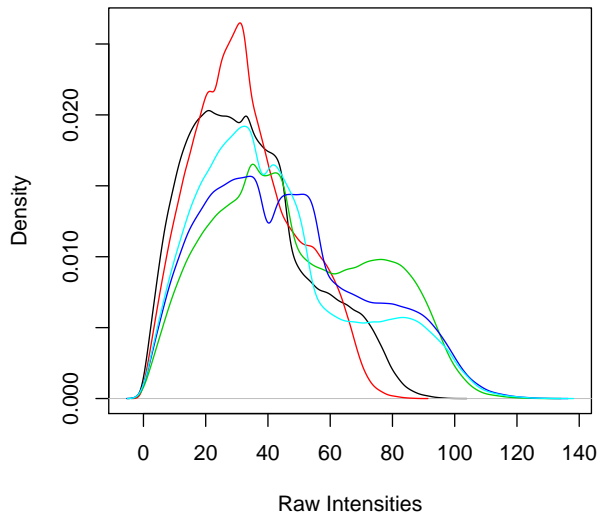
White Matter



White Matter

Visualizing the intensities by tissue class

CSF



CSF

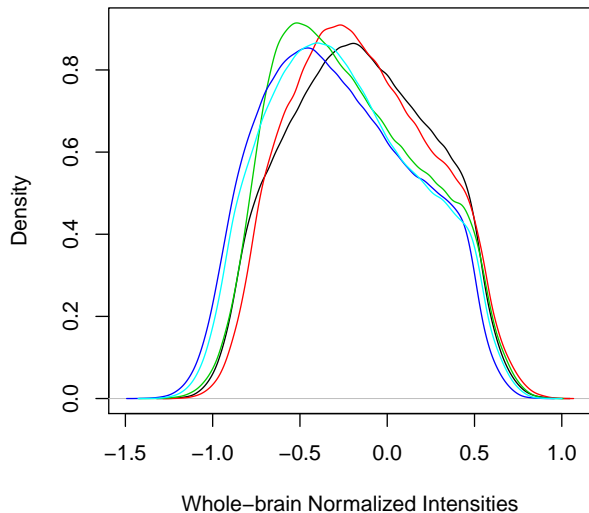
Whole-brain normalization

- Z-score each voxel using mean and standard deviation computed from all voxels in the brain mask.

```
t1_norm = mapply(function(img, mask){  
  zscore_img(img = img, mask = mask, margin = NULL)  
}, t1s, masks, SIMPLIFY = FALSE)
```

Whole-brain normalized intensities

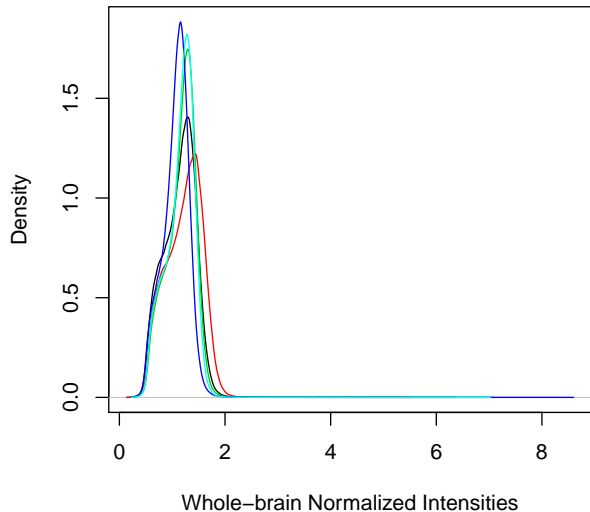
Gray Matter



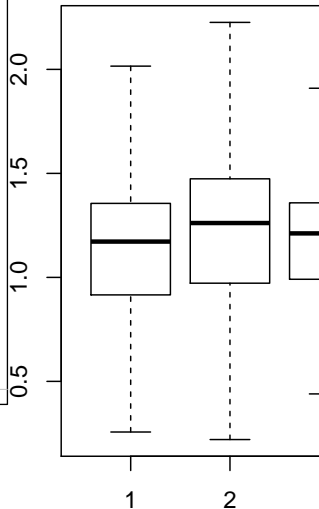
Gray Matter

Whole-brain normalized intensities

White Matter

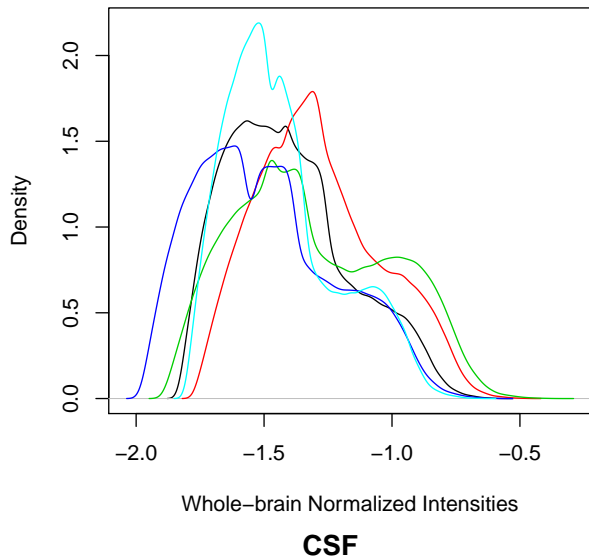


White



Whole-brain normalized intensities

CSF



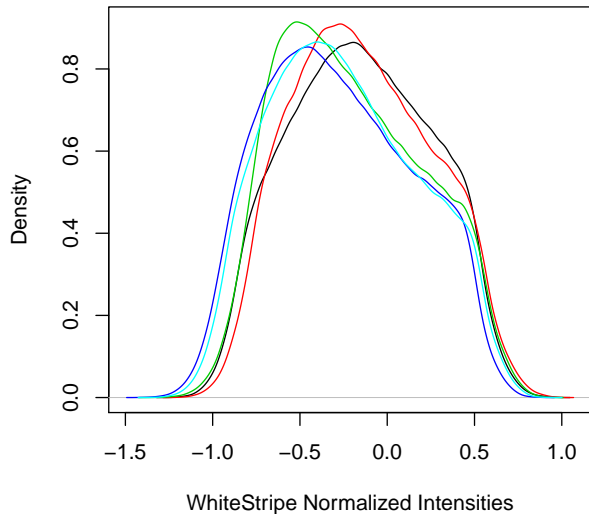
White Stripe normalization

- ▶ Normalize each voxel using mean and standard deviation computed from normal appearing white matter voxels.
- ▶ Normal appearing white matter will have a standard normal distribution.
- ▶ Units will correspond to variability (standard deviation) of normal appearing white matter.

```
ws_norm = function(t1) {  
  ind = whitestripe(img = t1,  
                    type = "T1",  
                    stripped = TRUE)$whitestripe.ind  
  whitestripe_norm(t1, indices = ind)  
}  
t1_ws_norm = lapply(t1s, ws_norm)
```

WhiteStripe normalized intensities

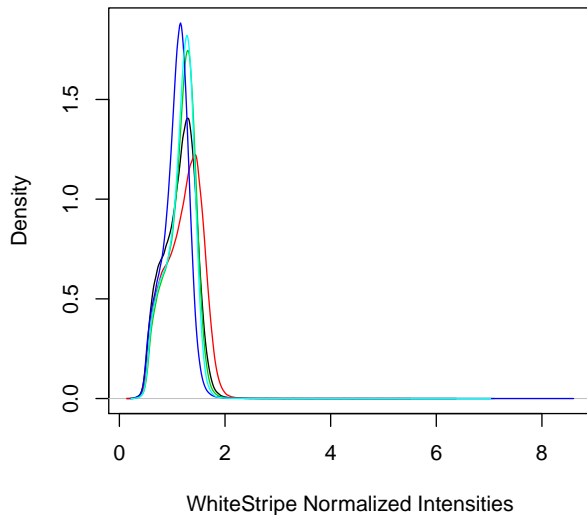
Gray Matter



Gray Matter

WhiteStripe normalized intensities

White Matter



White Matter

WhiteStripe normalized intensities

CSF

