

Intensity Normalization

Kristin Linn

2017-03-30

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 (Shinohara et al. 2014)

Reading in the images

- ▶ For the moment, we will work with the T1-w images from the training data.
- ▶ `vals` below is restricting to T1-w voxels that are within the brain mask.

```
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_Classification"]))
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)
  }
}

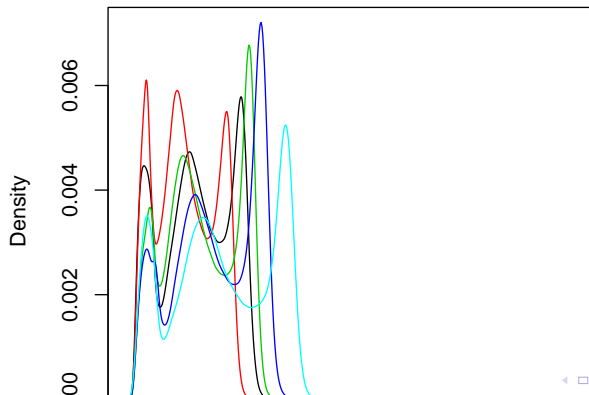
plot_boxplots = function(vals,
                          main = "Whole Brain") {
  boxplots <- lapply(vals, boxplot, outline = FALSE, plot = FALSE)
  boxplots = lapply(boxplots, function(x) x$stats)
  boxplots <- do.call(cbind, boxplots)
  boxplot(boxplots, main = main)
```

Visualizing the intensities

- We see that whole brain densities are mixture distributions of the three tissue classes.

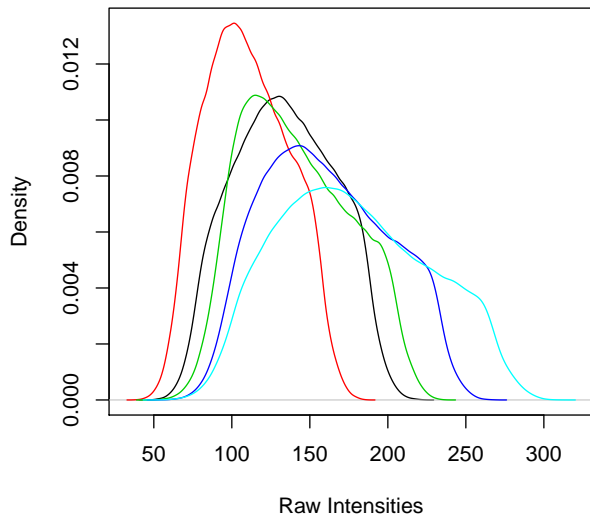
```
dens = lapply(vals, density)  
plot_densities(dens)
```

Whole Brain



Visualizing the intensities by tissue class

Gray Matter

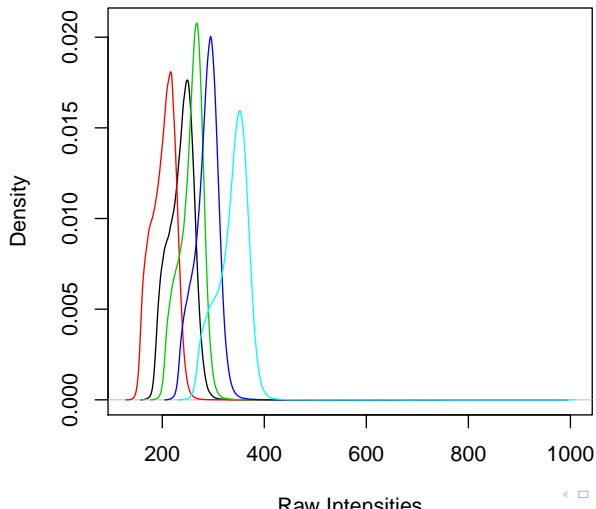


Gray Matter

Visualizing the intensities by tissue class

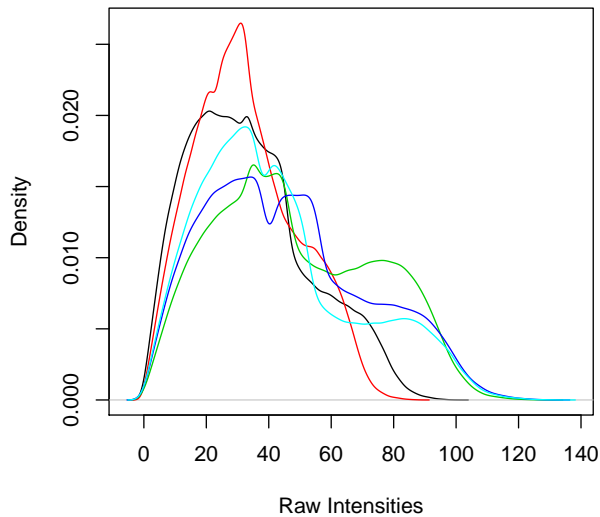
- Notice again the complete non-overlap between some subjects' white matter.

White Matter



Visualizing the intensities by tissue class

CSF



CSF

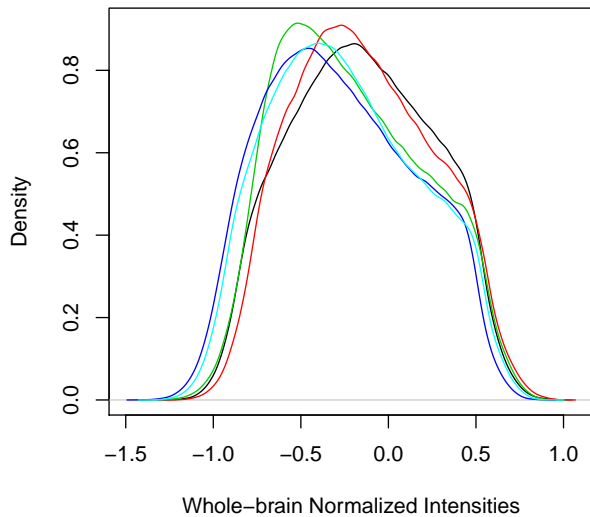
Whole-brain normalization

- ▶ Let's 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

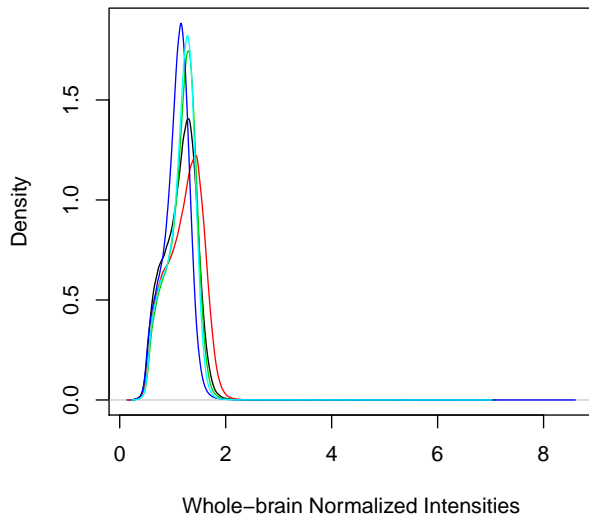
Gray Matter



Gray Matter

Whole-brain normalized intensities

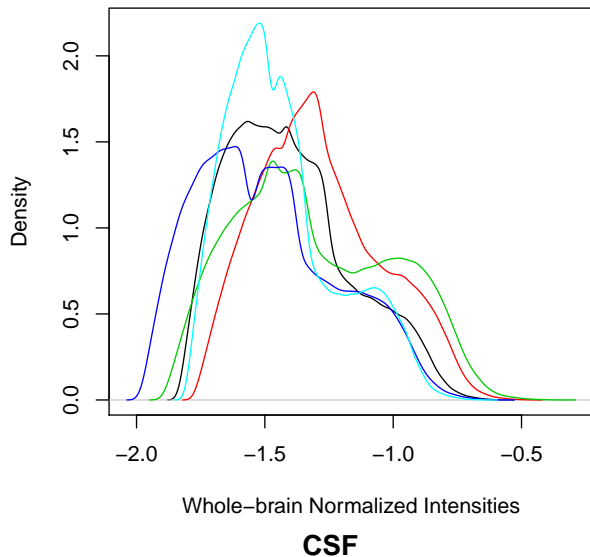
White Matter



White Matter

Whole-brain normalized intensities

CSF



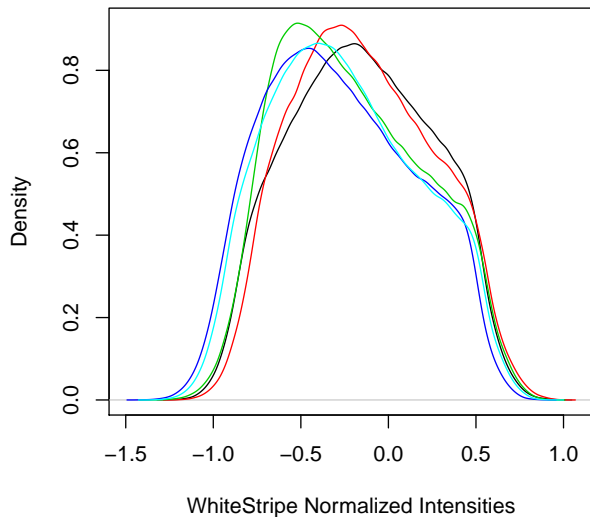
White Stripe normalization

- ▶ 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

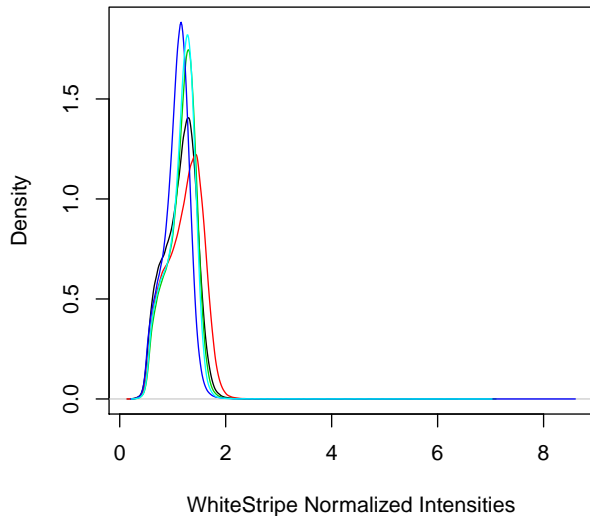
Gray Matter



Gray Matter

WhiteStripe normalized intensities

White Matter



White Matter

WhiteStripe normalized intensities

CSF

