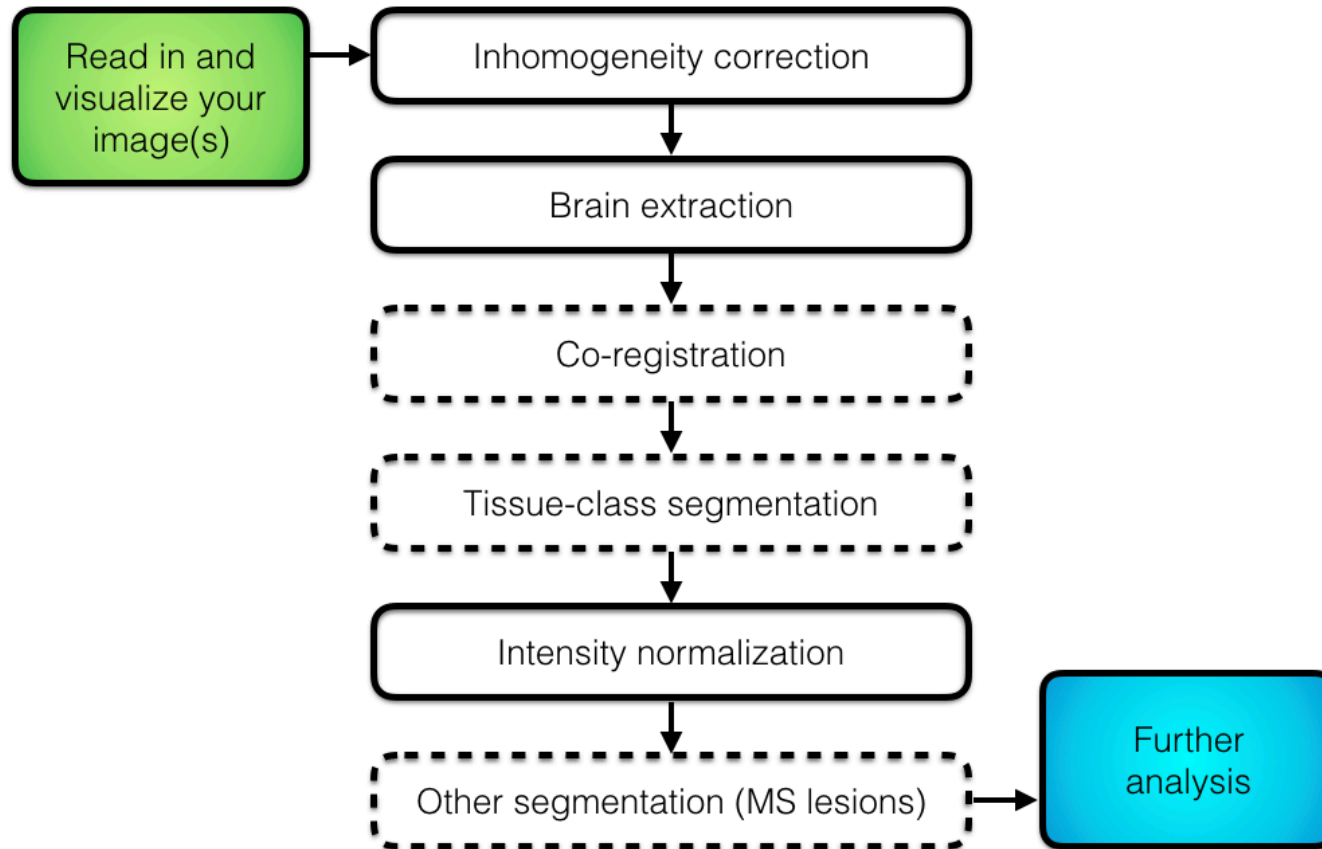


Intensity Normalization

Overall Pipeline

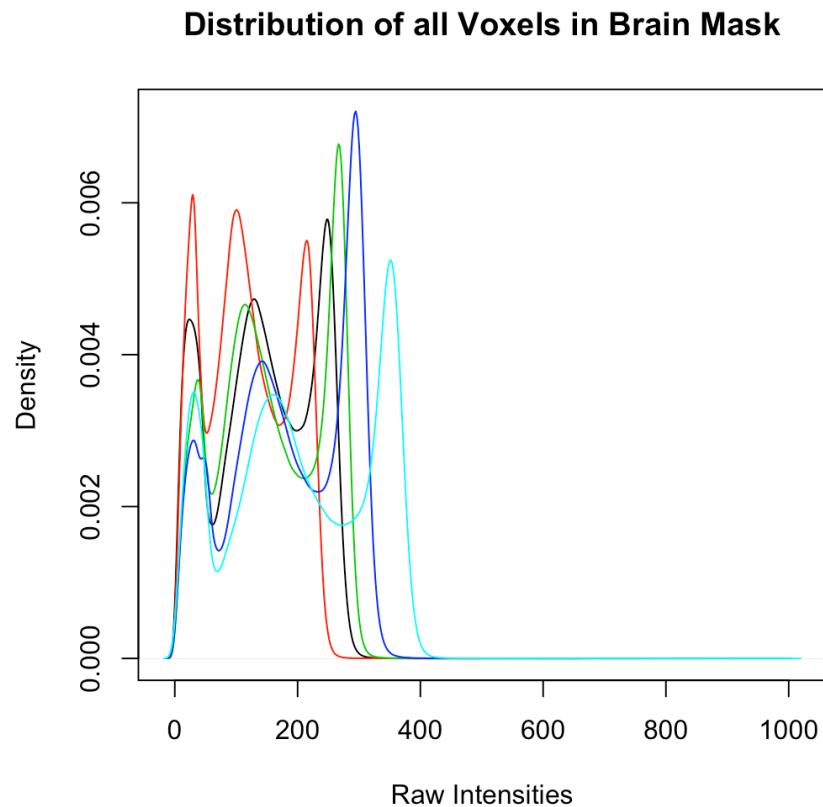


Intensity normalization

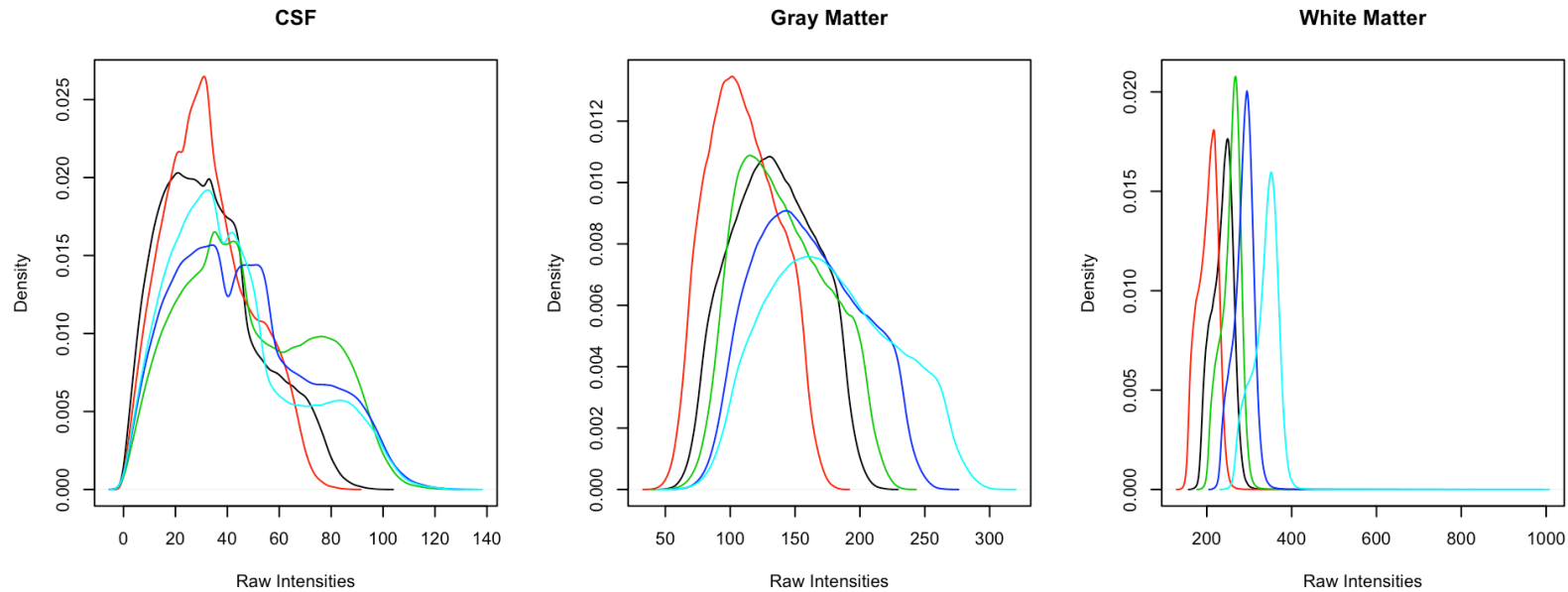
- Conventional MRI intensities (T1-w, T2-w, PD, FLAIR) are acquired in arbitrary units
- Images are not comparable across scanners, subjects, and visits, even when the same protocol is used.
 - This affects algorithm performance, prediction, inference.
 - Even simple things like thresholding an image
- Intensity normalization brings the intensities to a common scale across people.
- In this tutorial we will normalize intensities within subject using two methods:
 - Whole-brain normalization
 - White Stripe normalization (Shinohara et al. 2014).

Visualizing whole-brain intensities (each line is a person)

- We will work with the T1-w images from the training data.
- Full brain densities are mixtures of the three tissue class distributions.



Visualizing the intensities by tissue class



And these are all the same scanner/protocol!

Whole-brain normalization

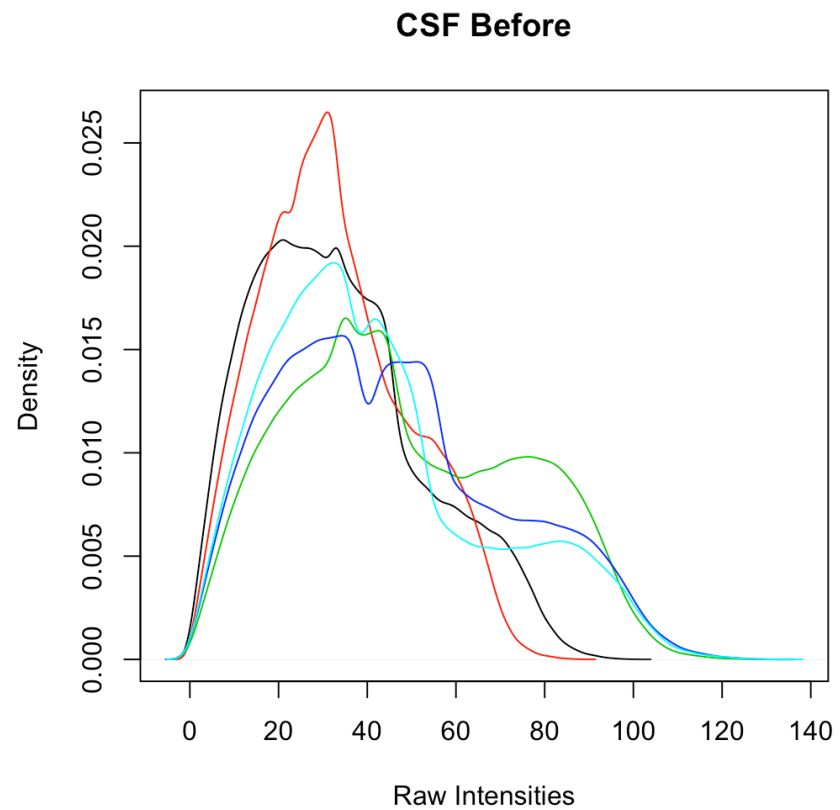
- Let's Z-score each voxel using mean μ_{WB} and standard deviation σ_{WB} computed from all voxels in the brain mask.

$$T1_{WB} = \frac{T1 - \mu_{WB}}{\sigma_{WB}}$$

- `zscore_img` is a function in `neurobase` that does this.
- It takes an image and a binary mask. The default is to use all voxels in the brain mask.

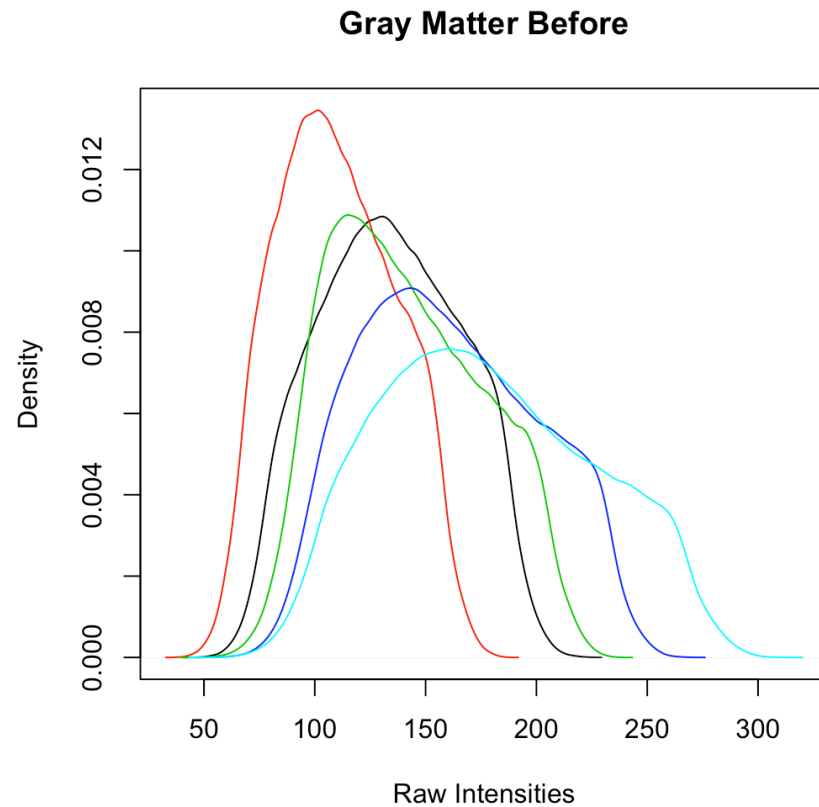
```
zscore_img(img = img, mask = mask)
```

Whole-brain normalized intensities



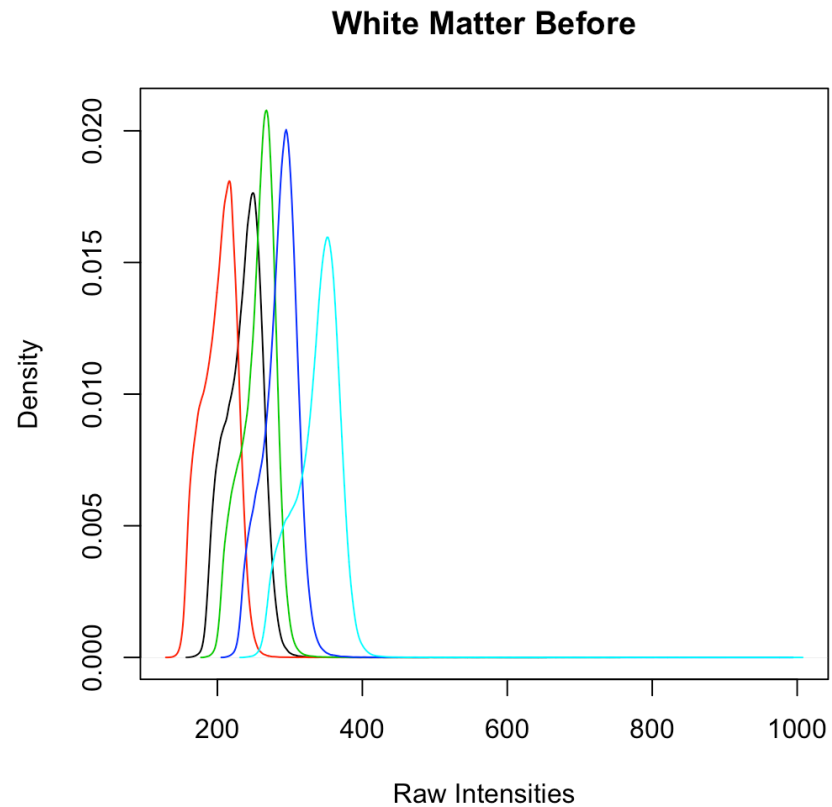
Whole-brain normalized intensities

- Gray matter distributions are more comparable.



Whole-brain normalized intensities

- White matter distributions are more comparable.



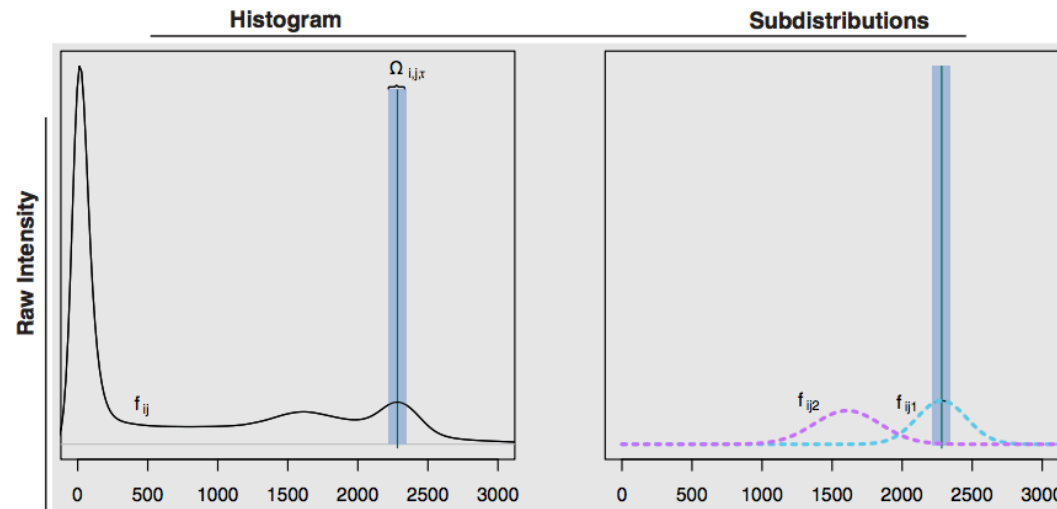
Other Normalizations: White Stripe

- Whole-brain normalization may be sensitive to outliers.
- Lesions in MS can have very high intensities, which lead to bad estimates of mean/variance
 - Other more robust transformations may be used, such as using the median to center, IQR to scale, etc.
- White Stripe (Shinohara et al. 2014) is based on parameters obtained from a sample of normal appearing white matter (NAWM), which is robust to outliers.
 - The idea is to make normal appearing white matter comparable across subjects and visits.

White Stripe normalization

Procedure:

1. Find white matter area on histogram



White Stripe normalization

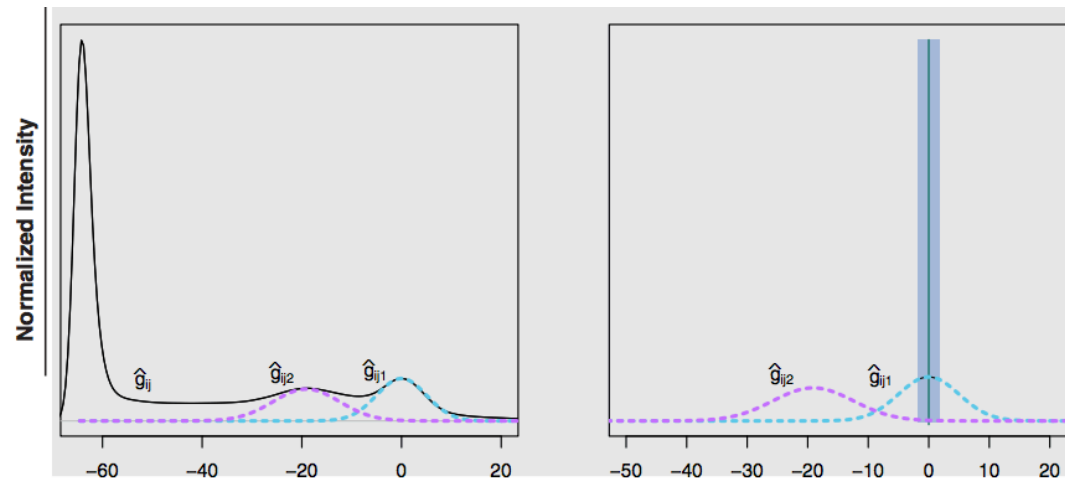
Procedure:

1. Find white matter area on histogram
2. Estimate mean μ_{WS} and variance σ_{WS} of voxel intensities in that area
3. Normalize with those means/variances:

$$T1_{WS} = \frac{T1 - \mu_{WS}}{\sigma_{WS}}$$

White Stripe normalization

- After normalization, NAWM will have a standard normal distribution and units will be in standard deviations of NAWM.
- Gray matter and CSF distributions may not be comparable after White Stripe.



White Stripe normalization

Procedure:

1. Find white matter area on histogram
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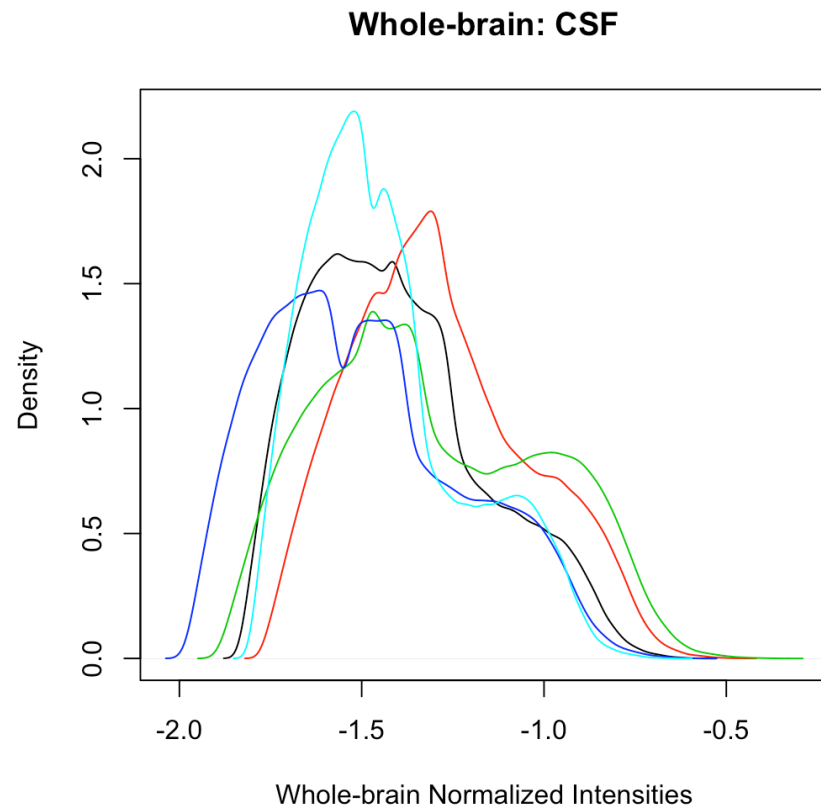
- After normalization, NAWM will have a standard normal distribution and units will be in standard deviations of NAWM.
- Gray matter and CSF distributions may not be comparable after White Stripe.

White Stripe normalization code

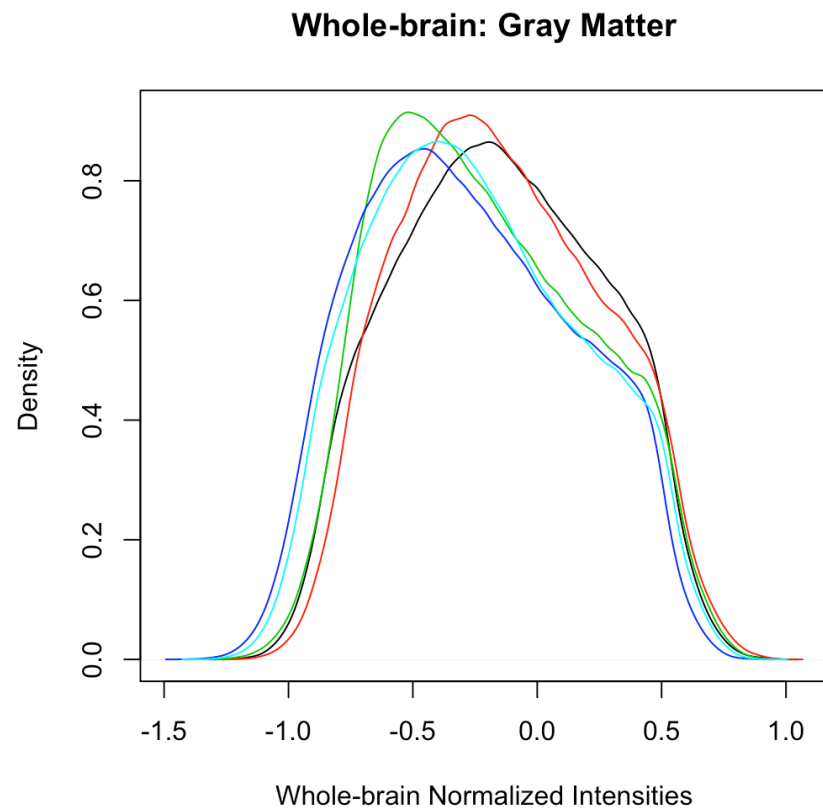
```
library(WhiteStripe)
ind = whitestripe(img = t1, type = "T1", stripped = TRUE)$whitestripe.ind
ws_t1 = whitestripe_norm(t1, indices = ind)
```

- The `whitestripe` function takes an image, image type (in our case T1), and a logical indicating whether the image has been skull stripped.
- The indices of voxels in the NAWM used for estimating the normalization parameters are located in the list element `$whitestripe.ind`.
- The function `whitestripe_norm` takes an image and the indices from a call to `whitestripe` and returns the White Stripe normalized image as a nifti.

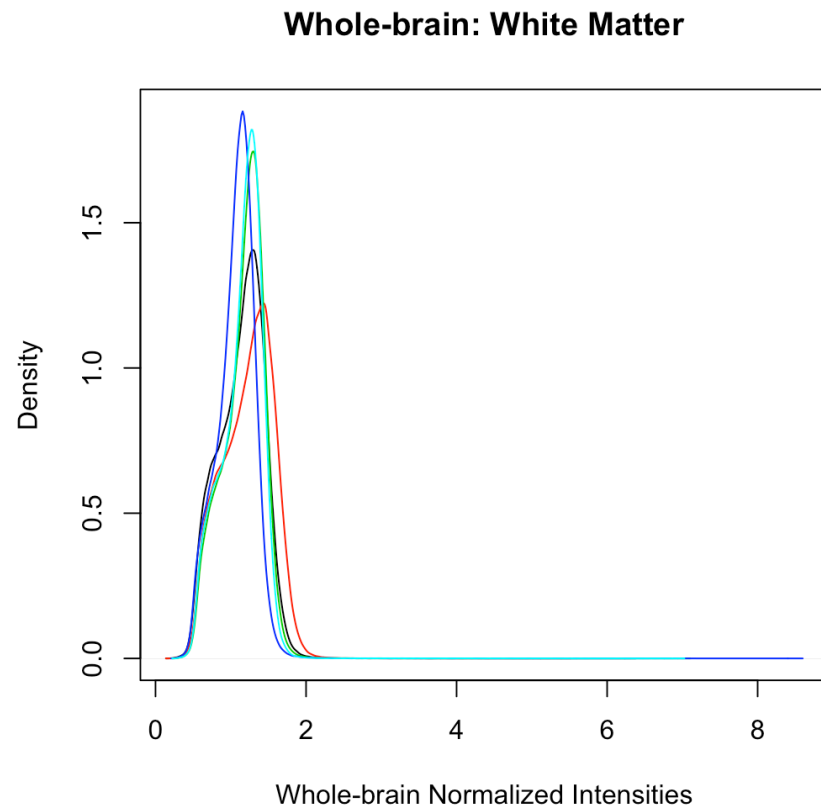
WhiteStripe normalized intensities



WhiteStripe normalized intensities



WhiteStripe normalized intensities



Conclusions

- Intensity normalization is an important step in any image analysis with more than one subject or time point to ensure comparability across images.
- White Stripe normalization may work better and have better interpretation than whole-brain normalization for subsequent lesion segmentation algorithms and analysis.
- Other intensity normalization methods that make intensities comparable across subjects for all tissues exist.
 - RAVEL, which is an extension of WhiteStripe is one example (Fortin et al. 2016).
 - Located at <https://github.com/Jfortin1/RAVEL>
 - This was shown to have better comparability than histogram matching

Website

http://johnmuschelli.com/imaging_in_r

References

Fortin, Jean-Philippe, Elizabeth M Sweeney, John Muschelli, Ciprian M Crainiceanu, Russell T Shinohara, Alzheimer's Disease Neuroimaging Initiative, and others. 2016. "Removing Inter-Subject Technical Variability in Magnetic Resonance Imaging Studies." *NeuroImage* 132. Elsevier: 198–212.

Shinohara, Russell T, Elizabeth M Sweeney, Jeff Goldsmith, Navid Shiee, Farrah J Mateen, Peter A Calabresi, Samson Jarso, et al. 2014. "Statistical Normalization Techniques for Magnetic Resonance Imaging." *NeuroImage: Clinical* 6. Elsevier: 9–19.