Inhomogeneity Correction

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Inhomogeneity correction

- Scans can have nonuniform intensities throughout the brain
- Usually low frequency - smooth over the brain (assumed)
- Referred to as bias, bias field, or inhomogeneity

MS Lesion

Let's read in the T1 image from a MS lesion data set:

```
library(ms.lesion)
library(neurobase)
files = get_image_filenames_list_by_subject()$training01
t1_fname = files["MPRAGE"]
t1 = readnii(t1_fname)
```

Bright Data

We see areas of brightness, but we also see that an artifact

```
ortho2(t1)
```

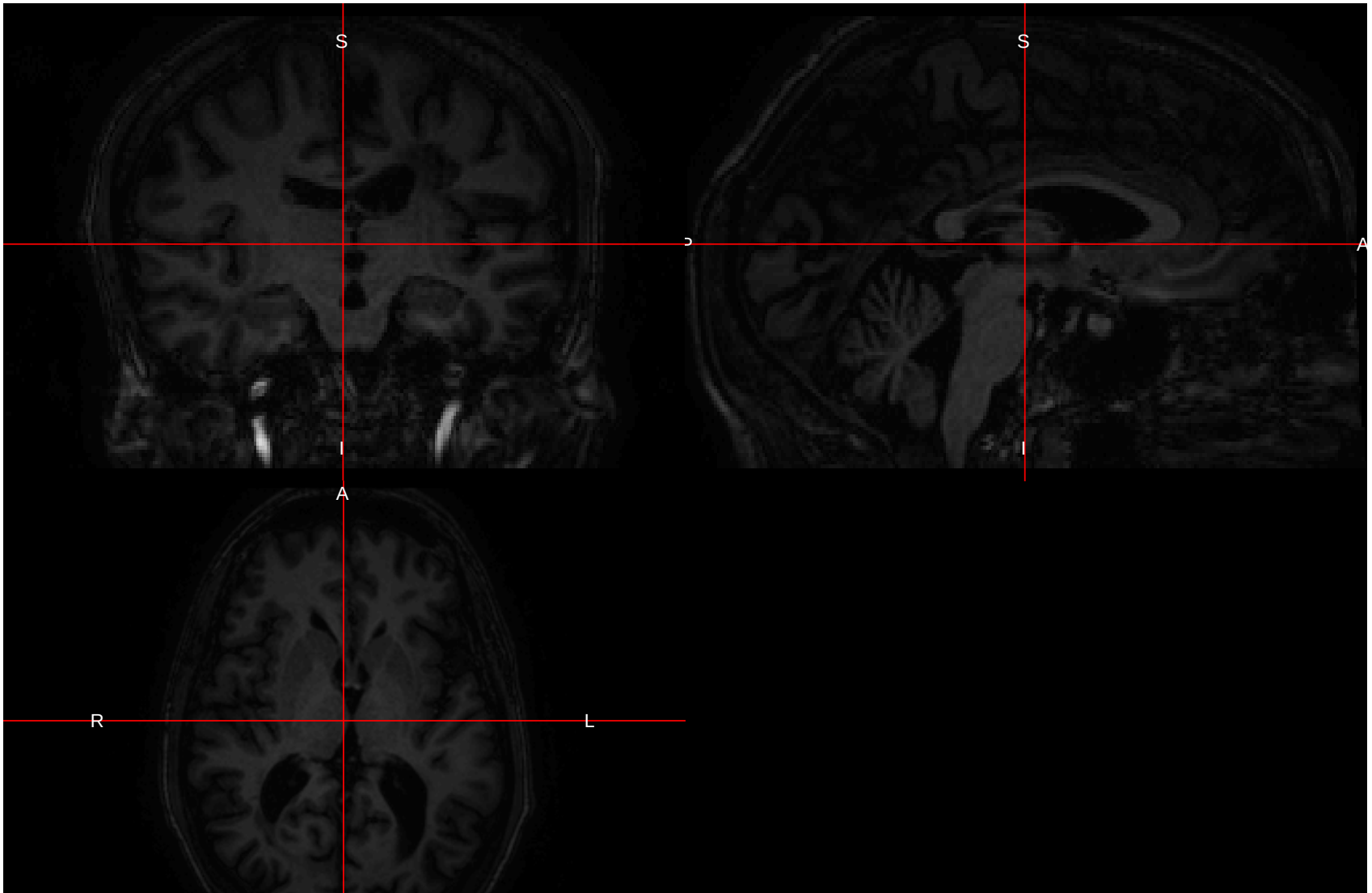
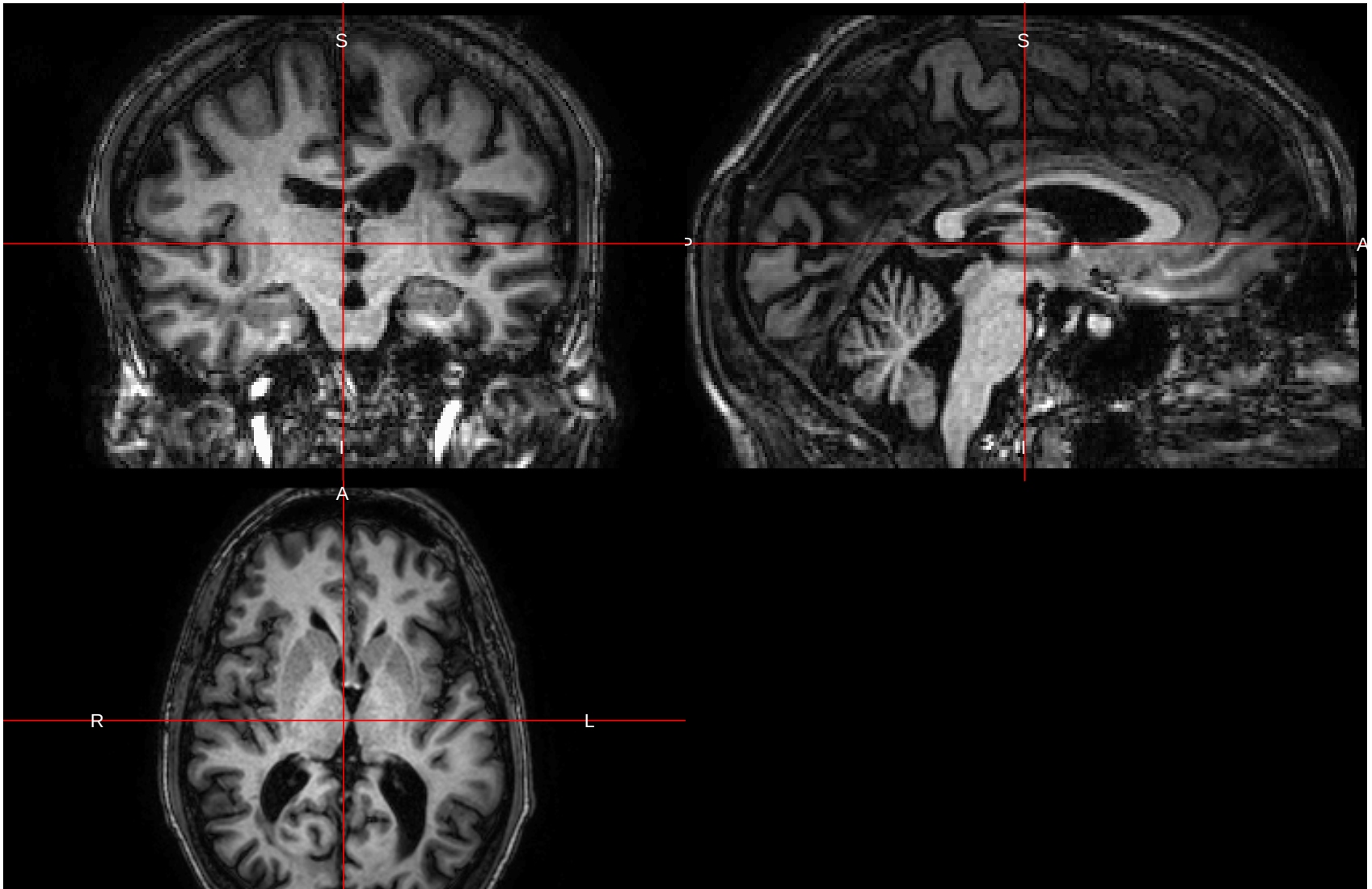


Image Data

Let's dampen this artifact and replot the data:

```
ortho2(robust_window(t1))
```



N4 Inhomogeneity Correction

We will use N4: Improved N3 Bias Correction (Tustison et al. 2010).

The model assumed in the N4 is:

$$v(x) = u(x)f(x) + n(x)$$

where v is the given image, u is the uncorrupted image, f is the bias field, and n is the noise (assumed to be independent and Gaussian) and x is a location in the image.

N4 Inhomogeneity Correction

The data is log-transformed and assuming a noise-free scenario, we have:

$$log(v(x)) = log(u(x)) + log(f(x))$$

- N4 uses a B-spline approximation of the bias field
- It iterates until a convergence criteria is met
  - when the updated bias field is the same as the last iteration
- It outputs the data back in the original units (not log-transformed)

Bias Field Correction

Here we will use the `bias_correct` function in `extrantsr`, which calls `n4BiasFieldCorrection` from `ANTsR`.

You can pass in the image:

```
library(extrantsr)
bc_t1 = bias_correct(file = t1, correction = "N4")
```

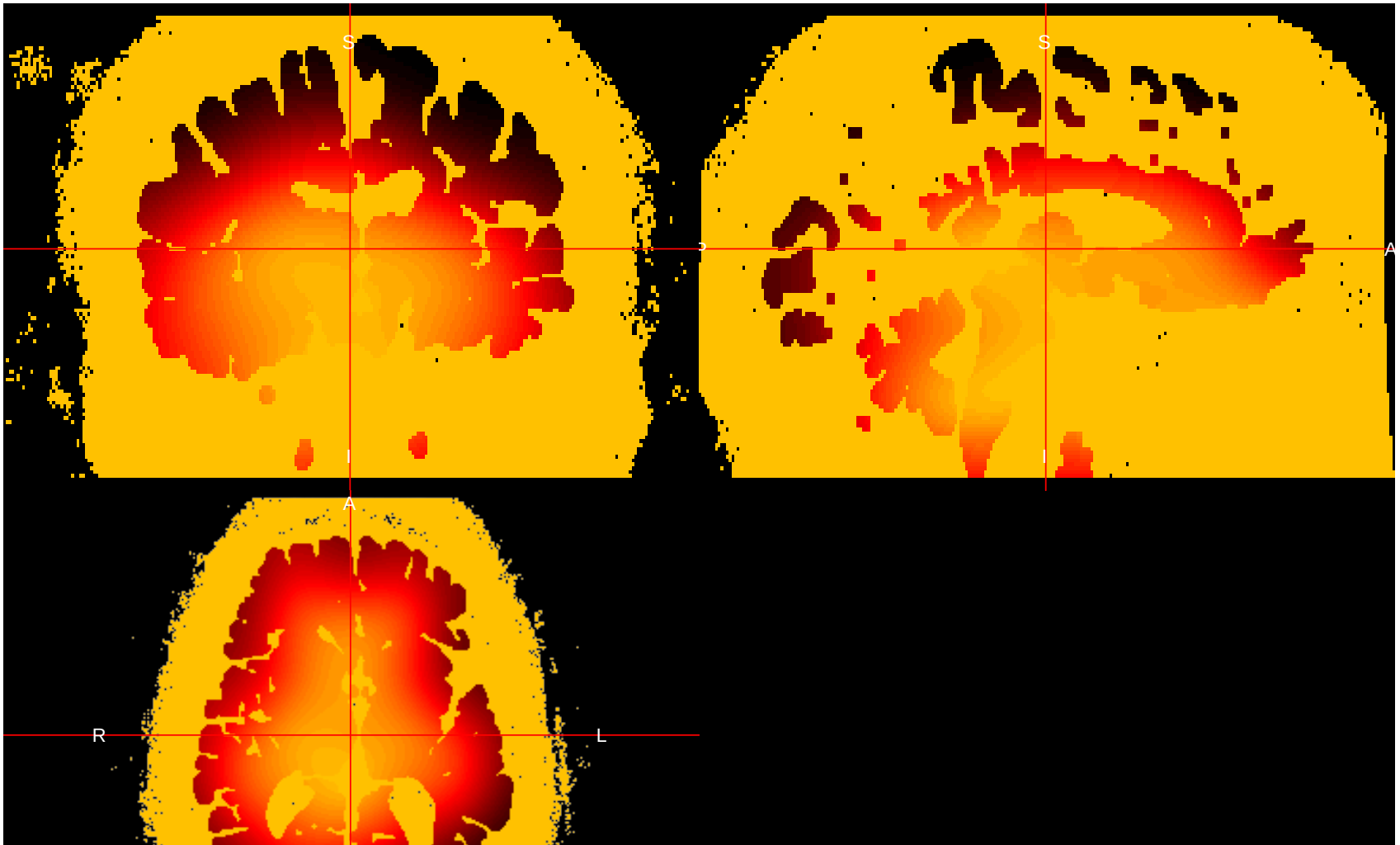
or the filename:

```
bc_t1 = bias_correct(file = t1_fname, correction = "N4")
```

Visualizing Bias Field Correction

Here we take the ratio of the images and overlay it on the original image:

```
ratio = t1 / bc_t1; ortho2(t1, ratio)
```



Visualizing Bias Field Correction

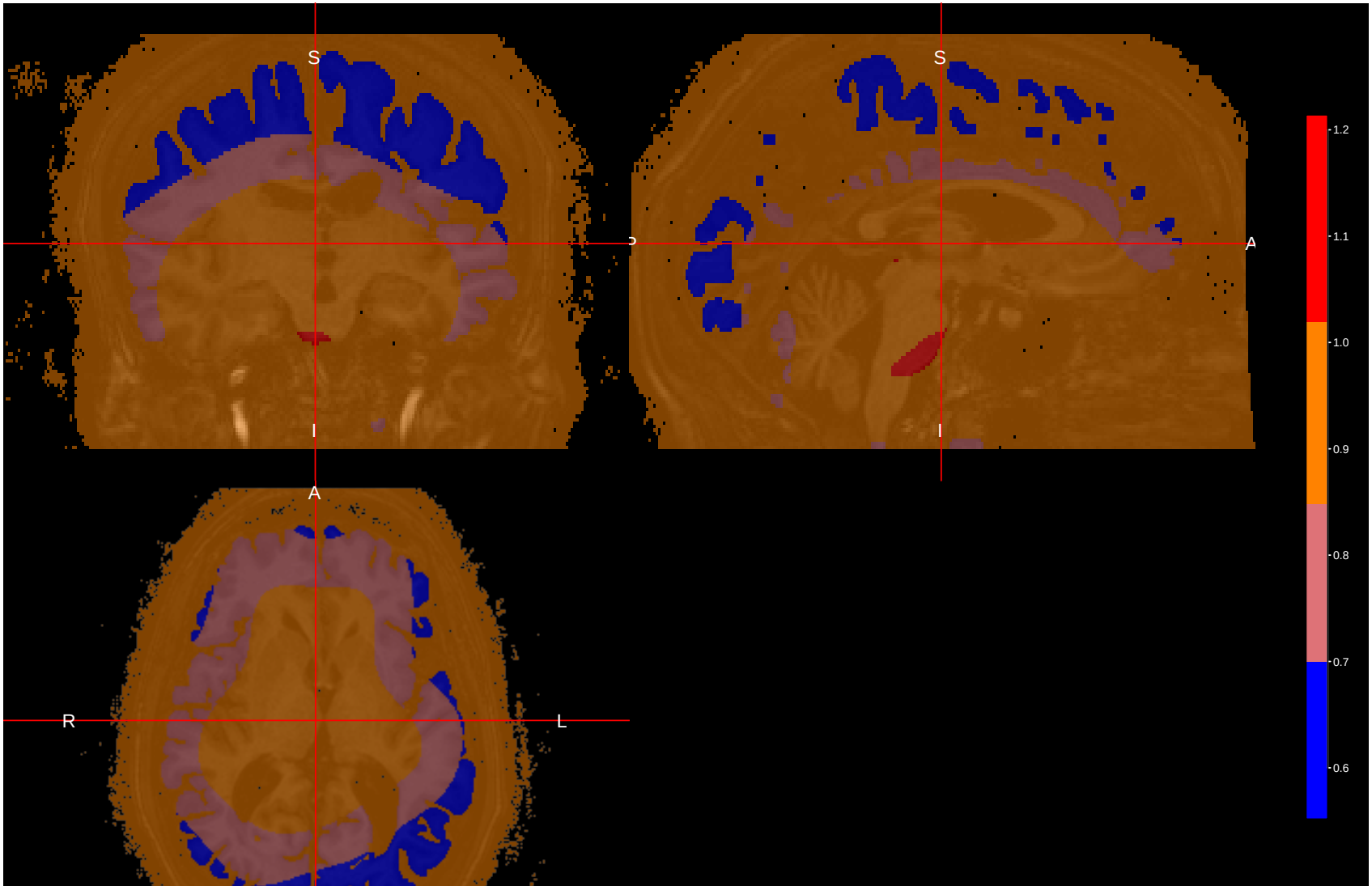
Here we would like to change the colors to something more descriptive. Here we will use a diverging palette and map colors to the quantiles of the ratio image:

```
library(scales)
q = quantile(ratio[ ratio != 0], probs = seq(0, 1, by = 0.1
q = unique(q)
# get a diverging gradient palette
fcol = scales::div_gradient_pal(low = "blue", mid = "orange
colors =  scales::alpha(fcol(seq(0,1, length = length(q) -
```

Visualizing Bias Field Correction

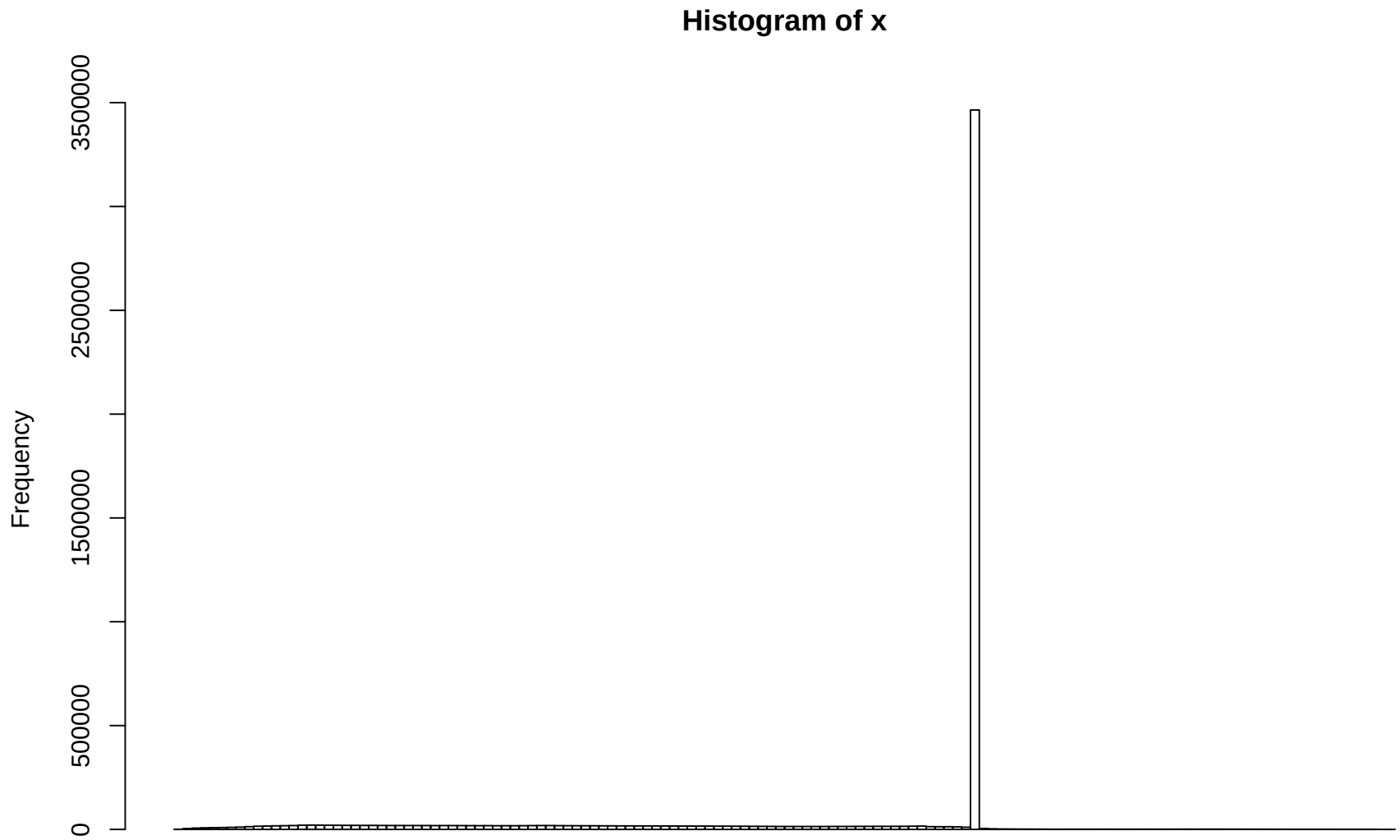
Now we put those breaks into `ortho2` to plot it:

```
ortho2(t1, ratio, col.y = colors, ybreaks = q, ycolorbar =
```



Histogram of Ratio Values

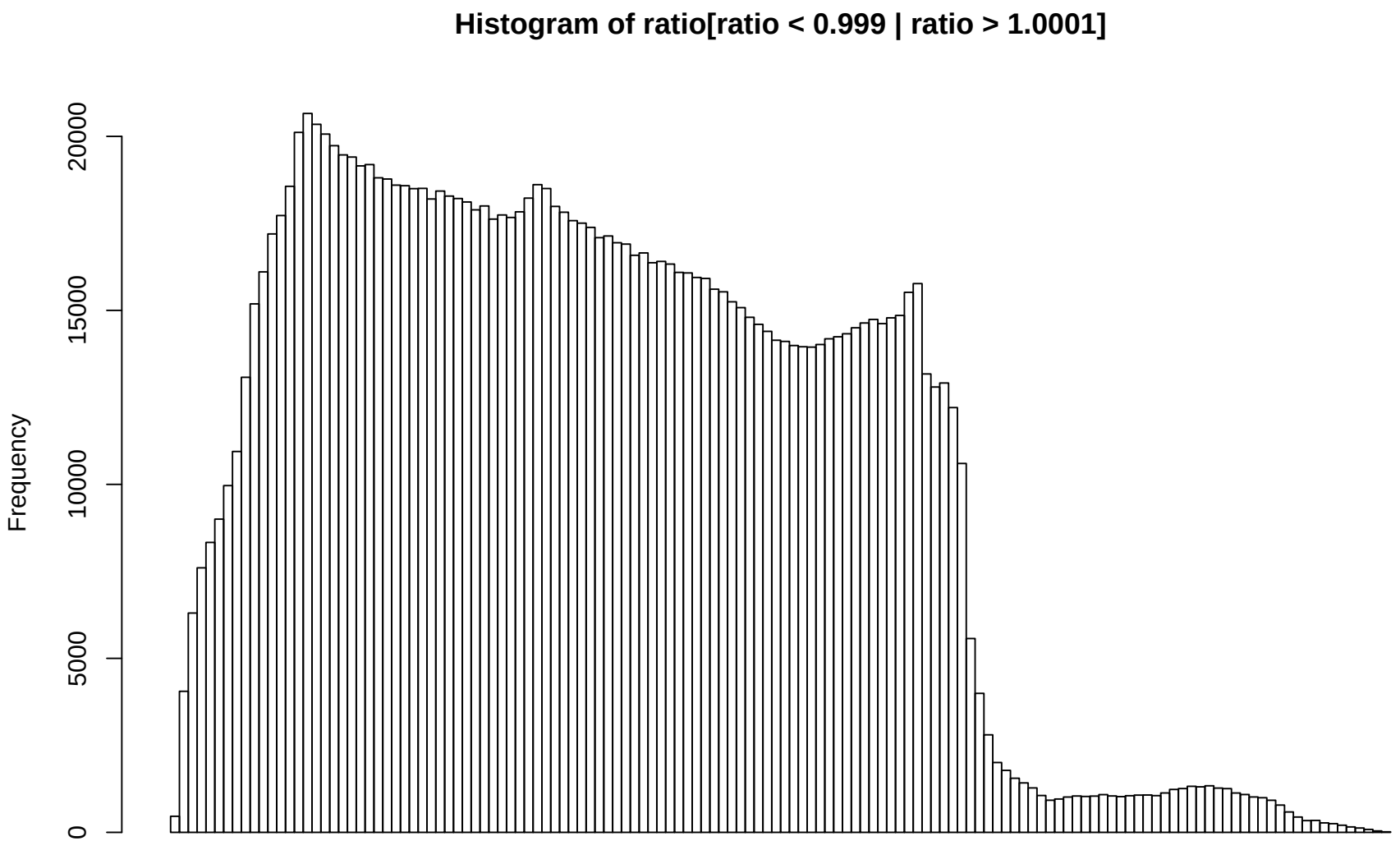
The majority of voxels have a ratio of 1 because `n4BiasFieldCorrection` does some implicit masking using `ANTsR::getMask`, and those values are unchanged (backround excluded).



Visualizing Bias Field Correction

Removing these, we can see what the distribution of ratios look like (most are below 1):

```
hist(ratio[ratio < 0.999 | ratio > 1.0001], breaks = 200)
```



Visualizing Bias Field Correction

We would like to see how the ratio changes in different areas of the brain. Here we make a `data.frame` of voxel location and intensity. We cut the location into the bottom, middle, and top of the brain:

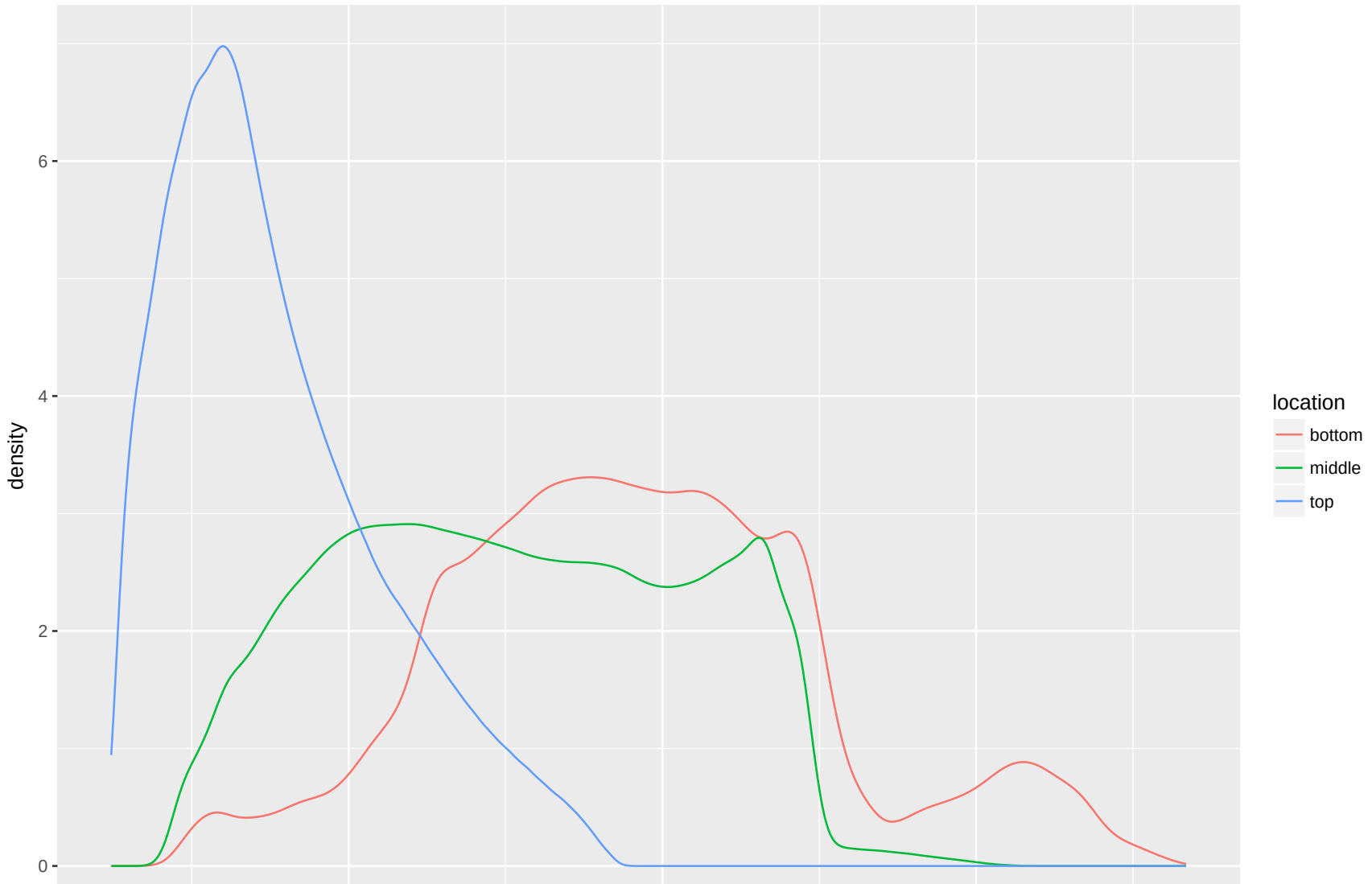
```
df = which(ratio < 0.999 | ratio > 1.0001, arr.ind = TRUE)
df = cbind(df, value = ratio[df])
df = data.frame(df, stringsAsFactors = FALSE)
df$location = cut(df$dim3, breaks = c(0, 38, 76, 115),
                  labels = c("bottom", "middle", "top"))
```

```
##   dim1 dim2 dim3     value location
## 1  131   97    1 0.8248509   bottom
## 2  132   97    1 0.8217719   bottom
## 3  133   97    1 0.8195554   bottom
## 4  134   97    1 0.8176278   bottom
## 5  135   97    1 0.8159310   bottom
## 6  136   97    1 0.8149298   bottom
```

Visualizing Bias Field Correction

Let's plot these with a density plot for each different location:

```
ggplot(df, aes(x = value, colour = location)) + geom_line(s
```



Conclusions

- Inhomogeneity correction is one of the first steps of most structural MRI pipelines
- Inhomogeneity can cause problems for other methods/segmentation
- Corrections try to make tissues of the same class to have similar intensities
- You may also want to run corrections after skull stripping on the brain only
  - we will do this in the brain extraction lecture
  - correction before skull-stripping may be necessary and can improve after correction

References

Tustison, Nicholas J., Brian B. Avants, Philip A. Cook, Yuanjie Zheng, Alexander Egan, Paul A. Yushkevich, and James C. Gee. 2010. "N4ITK: Improved N3 Bias Correction." *IEEE Transactions on Medical Imaging* 29 (6): 1310–20. doi:10.1109/TMI.2010.2046908.