

## Inhomogeneity Correction

# 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

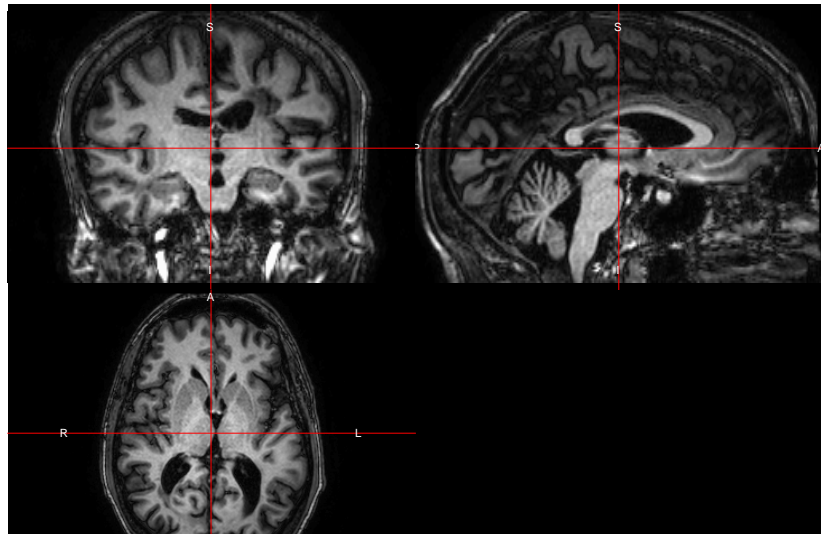
Let's read in the T1 image from a MS lesion data set:

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

## Image Data

It's hard to see bias fields, but sometimes they can be seen visually.

```
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")
```

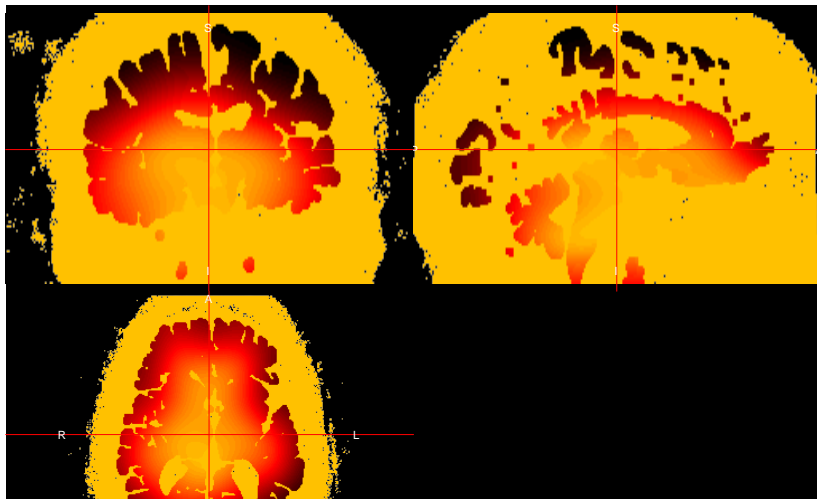
or the filename:

```
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

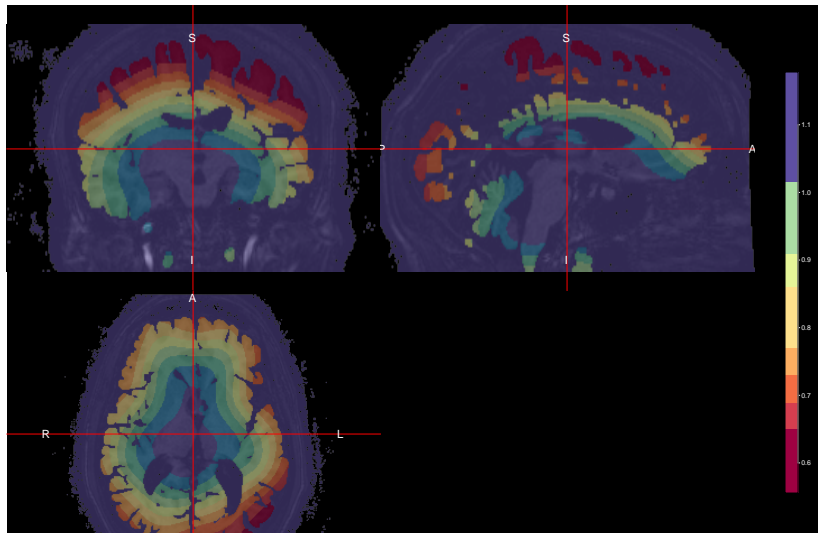
Here we would like to change the colors to something more descriptive. Here we will use a diverging palette and map colors to the quantiles of the ratio image:

```
library(scales)
q = quantile(ratio[ (ratio < 0.999 | ratio > 1.0001) & ratio != 1], 10)
q = unique(q)
# get a diverging gradient palette
# fcol = scales::div_gradient_pal(low = "blue", mid = "orange", high = "red")
fcol = scales::brewer_pal(type = "div", palette = "Spectral", n = 11)
colors = scales::alpha(gradient_n_pal(fcol)(seq(0,1, length.out = 11))
```

# Visualizing Bias Field Correction

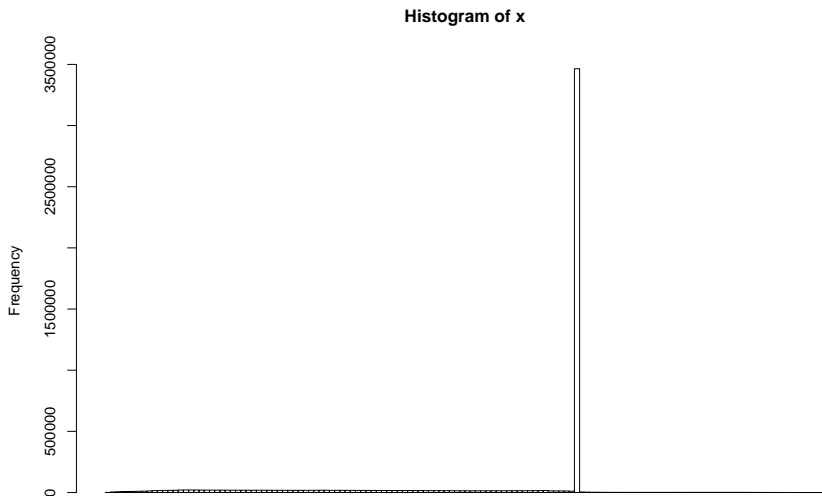
Now we put those breaks into ortho2 to plot it:

```
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 (background excluded).

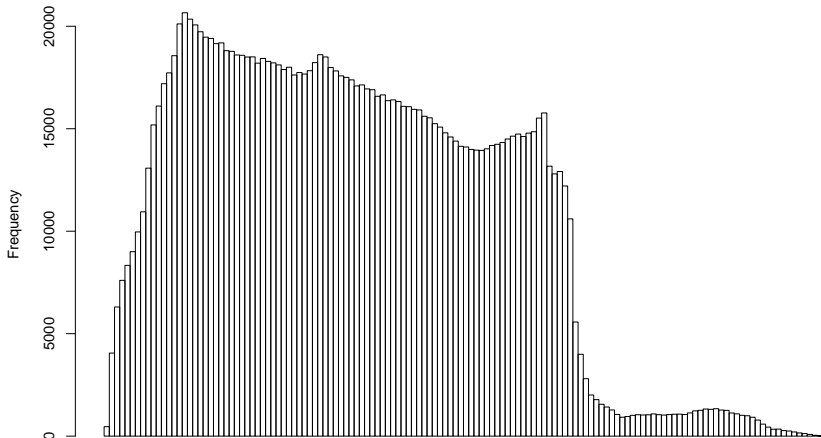


# Visualizing Bias Field Correction

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)
```

Histogram of ratio[ratio < 0.999 | ratio > 1.0001]



## 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:

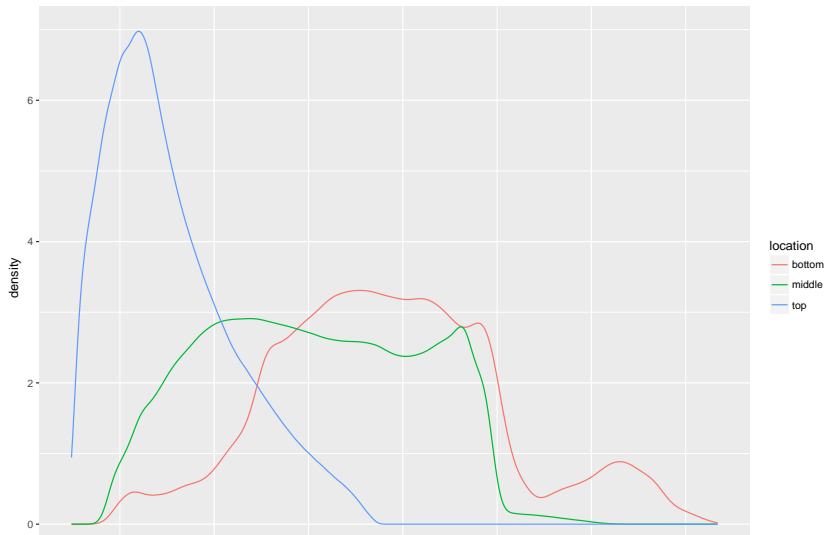
```
df = which(ratio < 0.999 | ratio > 1.0001, arr.ind = TRUE)
df = cbind(df, value = ratio[df])
df = data.frame(df, stringsAsFactors = FALSE)
df$location = cut(df$dim3, breaks = c(0, 38, 76, 115),
                  labels = c("bottom", "middle", "top"))
```

	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.