

Inhomogeneity Correction

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1/20/2017

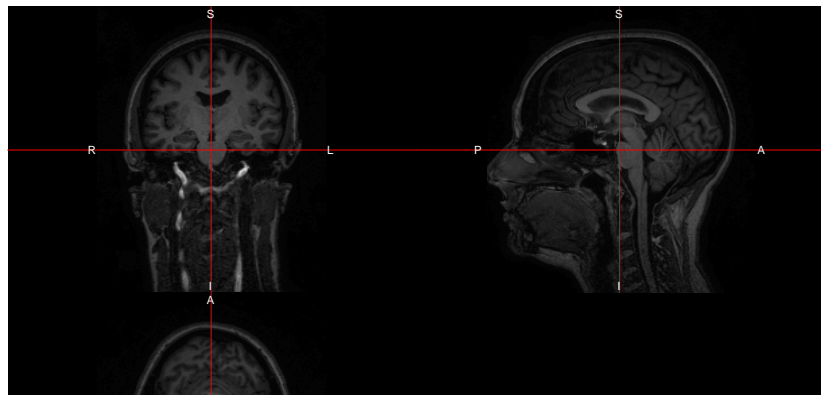
Inhomogeneity correction

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

Kirby21 Data

Let's read in the T1 image from a kirby21 data set for visit 1:

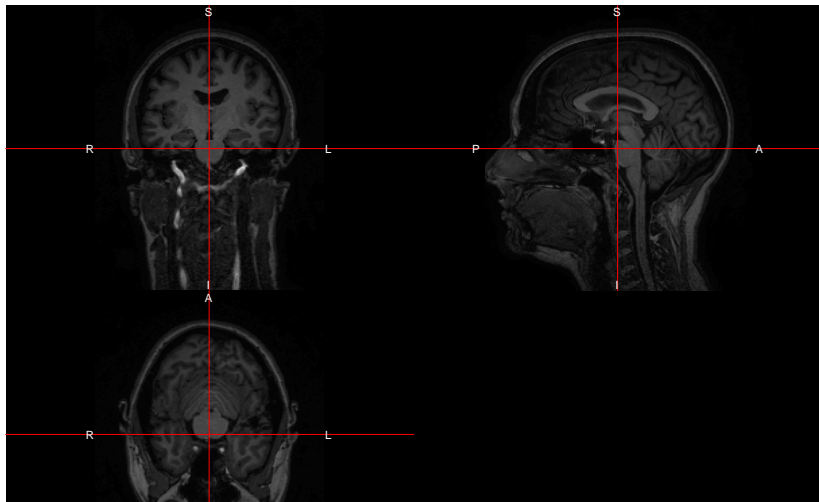
```
library(kirby21.t1)
library(neurobase)
t1_fname = get_t1_filenames(visit = 1, id = 505)
t1 = readnii(t1_fname)
ortho2(t1)
```



Kirby21 Data

We see the head and the neck are images in this T1 (also the orientation is not RPI):

```
ortho2(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")
```

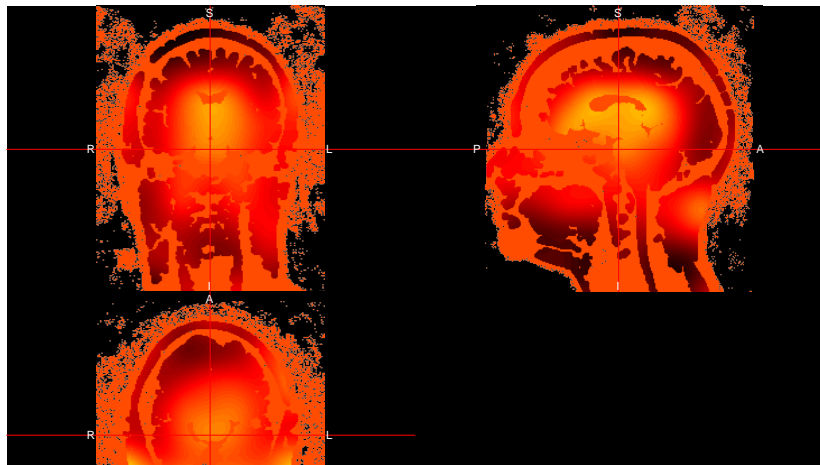
or the filename:

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

Visualizing Bias Field Correction

We can try visualize the bias field. 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

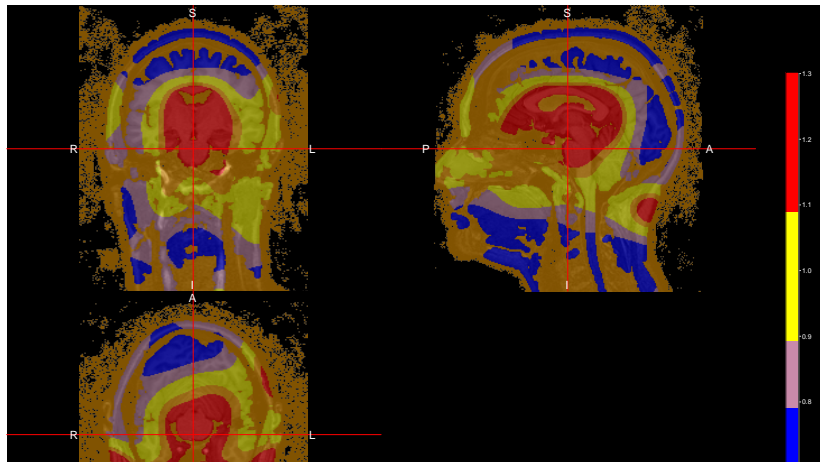
Here we would like to change the colors to something more descriptive. Here we will use a diverging palette and map colors to the quantiles of the ratio image:

```
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 = "yellow")
```

Visualizing Bias Field Correction

Now we put those breaks into ortho2 to plot it:

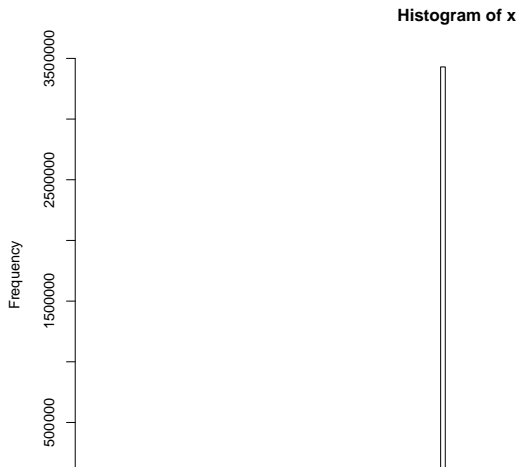
```
ortho2(t1, ratio,  
       col.y = scales::alpha(fcol(seq(0,1, length = length  
ybreaks = q, ycolorbar = TRUE)
```



Histogram of Ratio Values

The majority of voxels have a ratio of 1 because `n4BiasFieldCorrection` does some implicit masking using `ANTsR::getMask`.

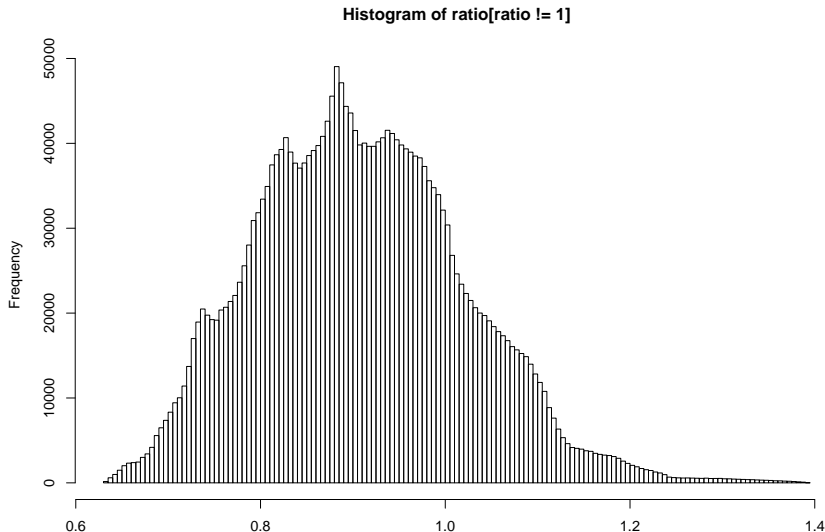
```
hist(ratio, breaks = 200)
```



Visualizing Bias Field Correction

Removing these, we can see what the distribution of ratios look like:

```
hist(ratio[ratio != 1], breaks = 200)
```



Visualizing Bias Field Correction

Let's look at this distribution by areas of the brain. Here we make a data.frame of the indices with the values and cut the z-dimension into the bottom, middle and top:

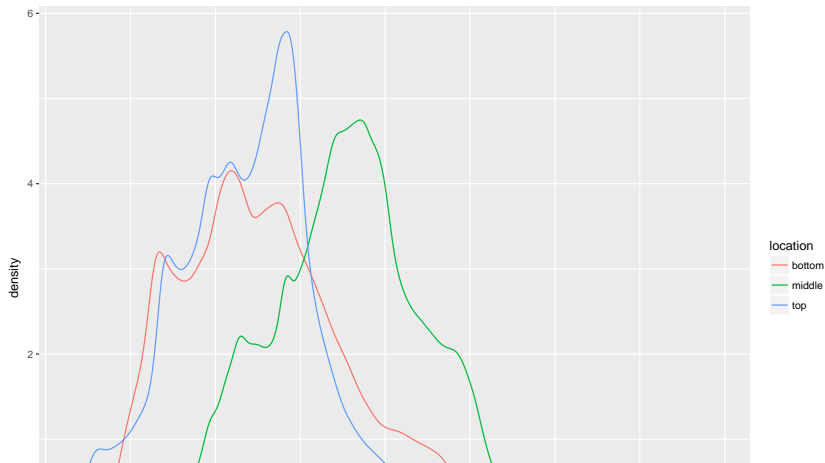
```
df = which(ratio != 1, arr.ind = TRUE)
df = cbind(df, value = ratio[df])
df = data.frame(df, stringsAsFactors = FALSE)
df$location = cut(df$dim3, breaks = c(0, 86, 172, 256),
                  labels = c("bottom", "middle", "top"))
```

##	dim1	dim2	dim3	value	location
## 1	81	96	1	0.7327191	bottom
## 2	82	96	1	0.7335099	bottom
## 3	83	96	1	0.7342617	bottom
## 4	84	96	1	0.7349642	bottom
## 5	85	96	1	0.7356078	bottom
## 6	86	96	1	0.7361845	bottom

Visualizing Bias Field Correction

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

```
library(ggplot2)
g = ggplot(df, aes(x = value, colour = location)) + geom_line()
print(g)
```



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.