

ABIDEI thickness Dx effects

OK let's do the funner thing...let's try to calculate some effect sizes for diagnosis effects

```
library(dplyr)
library(tidyr)
library(broom)
library(ggplot2)
library(knitr)
library(forcats)
```

read in the data

```
fs5.1 = read.csv('../data/cortical_fs5.1_measuresenigma_thickavg.csv', header = T)
#names(fs5.1) <- paste0(names(fs5.1), '_fs5.1')
fs5.3 = read.csv('../data/ABIDE_fs5.3_thickness.csv', header = T)
#names(fs5.3) <- paste0(names(fs5.3), '_fs5.3')
ants = read.csv('../data/ABIDE_ants_thickness_data_r.csv', header = T)
#names(ants) <- paste0(names(ants), '_ants')
pheno = read.csv('../data/ABIDE_Phenotype.csv', header = T)
pheno$DX_GROUP <- factor(pheno$DX_GROUP, levels = c(1,2), labels = c("ASD","TD"))
```

wrangle and merge all three dataframes together

```
## Merge it all into one mega- data - frame
fs5.3_thick <- fs5.3 %>%
  gather(Region, thickness, ends_with("thickavg")) %>%
  mutate(CommonRegion = gsub('_thickavg','',Region)) %>%
  select(SubjID, CommonRegion, thickness)
fs5.3_thick$toolkit <- "freesurfer_5.3"

fs5.1_thick <- fs5.1 %>%
  gather(Region, thickness, ends_with("thickavg")) %>%
  mutate(CommonRegion = gsub('_thickavg','',Region)) %>%
  select(SubjID, CommonRegion, thickness)
fs5.1_thick$toolkit <- "freesurfer_5.1"

ants_thick <- ants %>%
  gather(Region, thickness, starts_with("right"), starts_with("left")) %>%
  mutate(CommonRegion = gsub('\\.','', gsub('right','R_', gsub('left','L_',Region)))) %>%
  filter(CommonRegion %in% unique(fs5.3_thick$CommonRegion)) %>%
  select(Code, CommonRegion, thickness)
ants_thick$toolkit <- "ANTS"
names(ants_thick) <- c("SubjID", "CommonRegion", "thickness", "toolkit")

allthickness <- rbind(fs5.3_thick, fs5.1_thick, ants_thick)

df <- merge(allthickness, pheno, by.x = "SubjID", by.y = "Subject_ID")
```

Model the Diagnosis Effect Without Covariates and plot

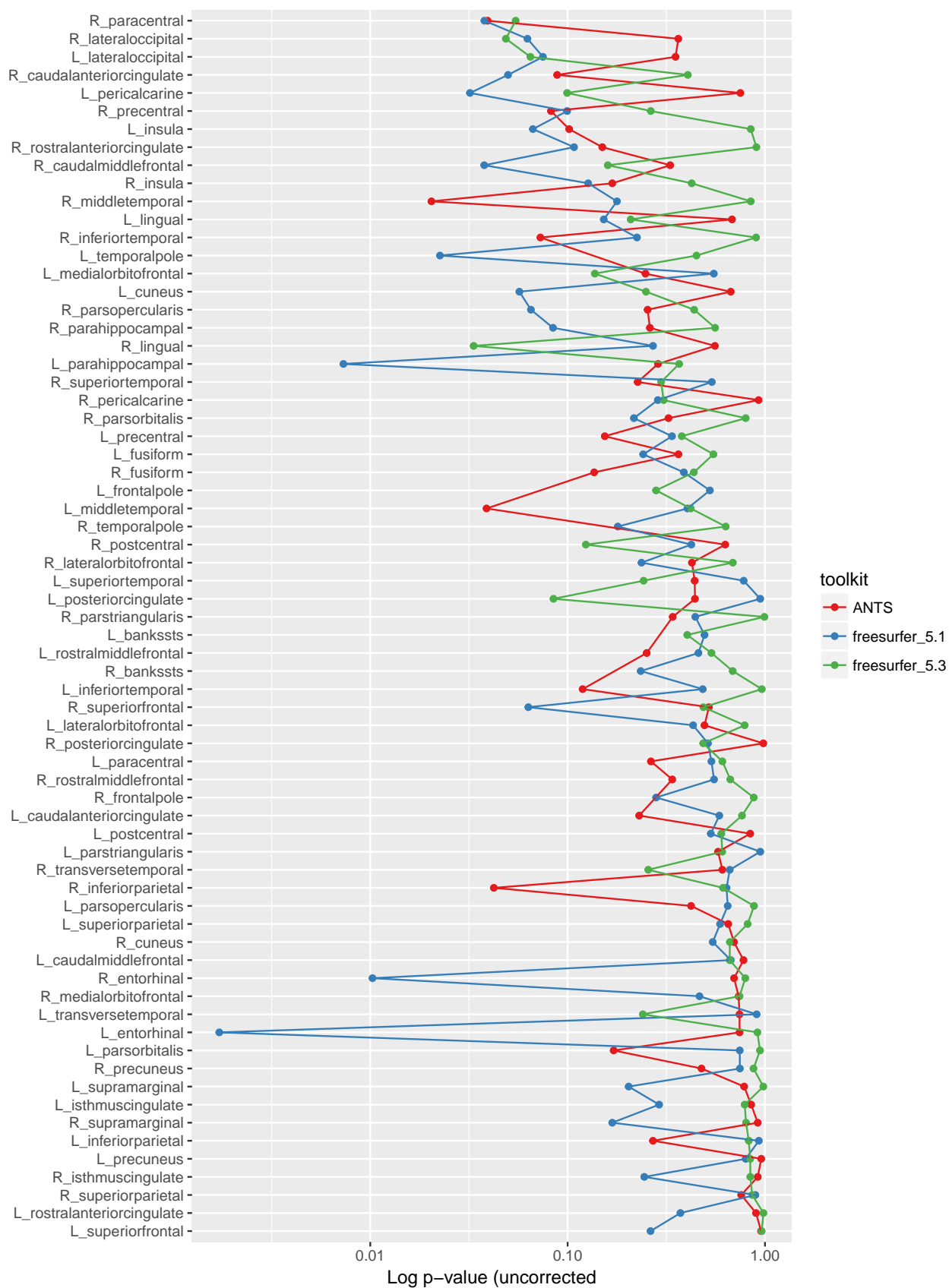
```
dx_raw <- df %>%
  group_by(CommonRegion, toolkit) %>%
  do(glance(lm(thickness ~ DX_GROUP, .)))

ggplot(dx_raw, aes(y=p.value ,
                   x= fct_reorder(CommonRegion, p.value, .desc=TRUE),
                   color = toolkit)) +

  geom_point() +
  geom_line(aes(x = as.numeric(fct_reorder(CommonRegion, p.value, .desc=TRUE)), y = p.value)) +
  scale_color_brewer(palette = "Set1") +
  scale_y_reverse() +
  scale_y_log10() +
  coord_flip() +
  labs(title = "Effect of Diagnosis, no covariates ",
       x = NULL,
       y = "Log p-value (uncorrected)")

## Scale for 'y' is already present. Adding another scale for 'y', which
## will replace the existing scale.
```

Effect of Diagnosis, no covariates



Model the Diagnosis Effect With Diagnosis plus Site

```
dx_wcovs<- df %>%
  group_by(CommonRegion, toolkit) %>%
  do(tidy(lm(thickness ~ DX_GROUP + AGE_AT_SCAN + SITE_ID, .)))

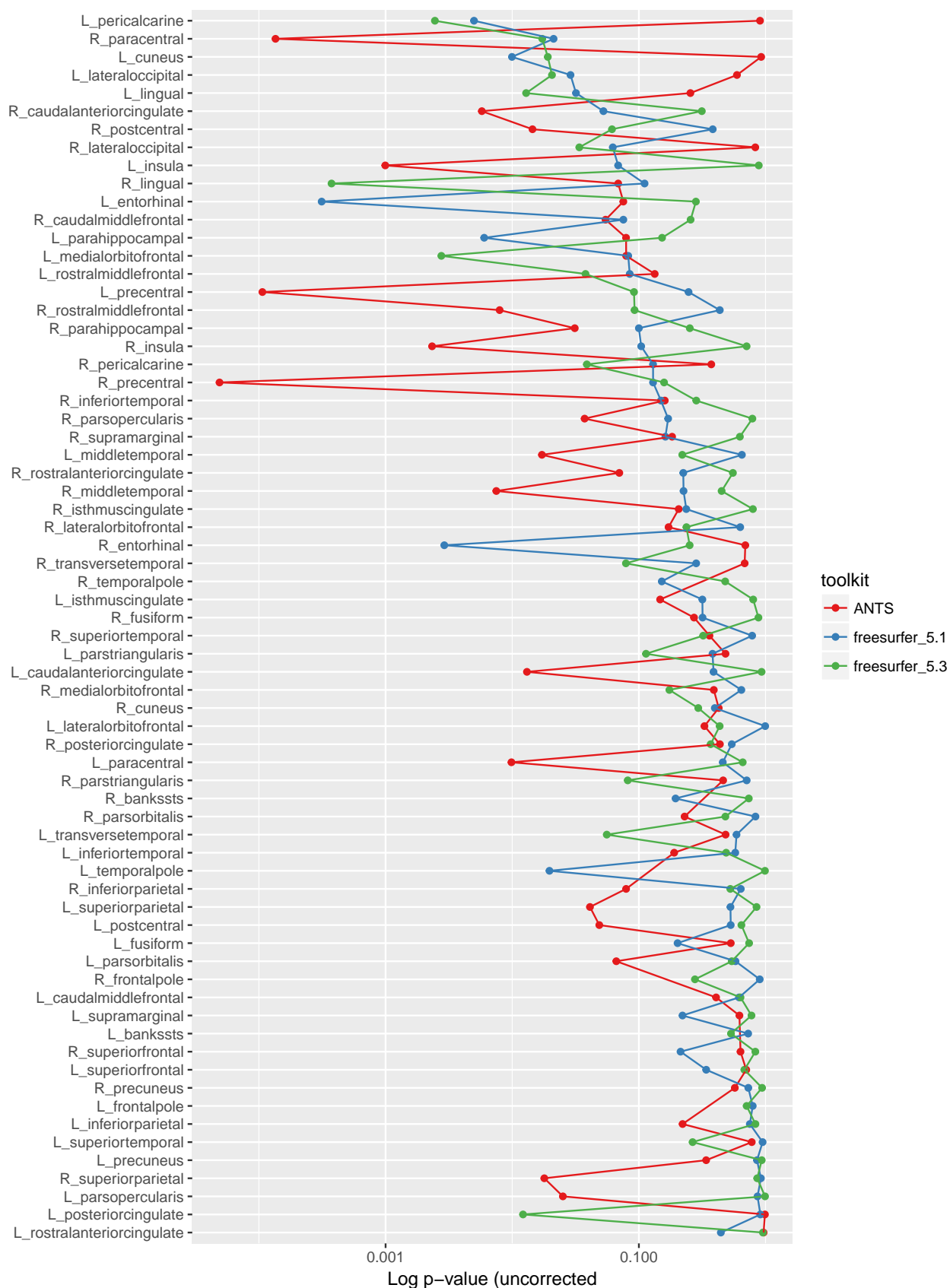
dx_effect_wcov <- filter(dx_wcovs, term == "DX_GROUPTD")
age_effect_wcov <- filter(dx_wcovs, term == "AGE_AT_SCAN")

ggplot(dx_effect_wcov, aes(y=p.value ,
                           x= fct_reorder(CommonRegion, p.value, .desc=TRUE),
                           color = toolkit)) +

  geom_point() +
  geom_line(aes(x = as.numeric(fct_reorder(CommonRegion, p.value, .desc=TRUE)), y = p.value)) +
  scale_color_brewer(palette = "Set1") +
  scale_y_reverse() +
  scale_y_log10() +
  coord_flip() +
  labs(title = "Effect of ASD diagnosis, controlling for Age and Site ",
       x = NULL,
       y = "Log p-value (uncorrected)")

## Scale for 'y' is already present. Adding another scale for 'y', which
## will replace the existing scale.
```

Effect of ASD diagnosis, controlling for Age and Site



Plotting the Age term

```
ggplot(age_effect_wcov, aes(y=p.value ,
                           x= fct_reorder(CommonRegion, p.value, .desc=TRUE),
                           color = toolkit)) +

  geom_point() +
  geom_line(aes(x = as.numeric(fct_reorder(CommonRegion, p.value, .desc=TRUE)), y = p.value)) +
  scale_color_brewer(palette = "Set1") +
  scale_y_reverse() +
  scale_y_log10() +
  coord_flip() +
  labs(title = "Effect of Age, controlling for Diagnosis and Site ",
       x = NULL,
       y = "Log p-value (uncorrected)")
```

```
## Scale for 'y' is already present. Adding another scale for 'y', which
## will replace the existing scale.
```

Effect of Age, controlling for Diagnosis and Site

