A new tripartite landmark in human posterior cingulate cortex

# Analysis Notebook

This notebook contains analysis pipeline and figures for the manuscript: Willbrand et al. (2021): *A new tripartite landmark in human posterior cingulate cortex.* All data is available in the repository (INSERT GITHUB LINK). If you have any questions about data cleaning process, storage, or would like access to raw data please contact: Ethan Willbrand ([ewillbrand@berkeley.edu](mailto:ewillbrand@berkeley.edu)) and/or Benjamin Parker ([benparker@berkeley.edu](mailto:benparker@berkeley.edu)).

## Software Requirements

* software: Please consult README.txt

## Data

* All data necessary for the analyses and figures is included in this repository
* Morphological data was extracted with FreeSurfer (see manuscript methods). A sample function to extract the sulcal metrics of interest from cortical surface reconstructions is included here. Testing this requires access to a FreeSurfer directory. Please contact Ethan Willbrand ([ewillbrand@berkeley.edu](mailto:ewillbrand@berkeley.edu)) and/or Benjamin Parker ([benparker@berkeley.edu](mailto:benparker@berkeley.edu)).

## Setup

### Relevant Libraries

## ── Attaching packages ─────────────────────────────────────── tidyverse 1.3.0 ──

## ✓ tibble 3.0.6 ✓ dplyr 1.0.3  
## ✓ tidyr 1.1.2 ✓ stringr 1.4.0  
## ✓ readr 1.3.1 ✓ forcats 0.5.0  
## ✓ purrr 0.3.4

## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

##   
## Attaching package: 'psych'

## The following objects are masked from 'package:ggplot2':  
##   
## %+%, alpha

## \*\*\* Package RVAideMemoire v 0.9-78 \*\*\*

## Loading required package: carData

##   
## Attaching package: 'car'

## The following object is masked from 'package:psych':  
##   
## logit

## The following object is masked from 'package:dplyr':  
##   
## recode

## The following object is masked from 'package:purrr':  
##   
## some

## Registered S3 methods overwritten by 'lme4':  
## method from  
## cooks.distance.influence.merMod car   
## influence.merMod car   
## dfbeta.influence.merMod car   
## dfbetas.influence.merMod car

##   
## Attaching package: 'sjstats'

## The following objects are masked from 'package:RVAideMemoire':  
##   
## bootstrap, cramer, cv, se

## The following object is masked from 'package:psych':  
##   
## phi

##   
## Attaching package: 'rstatix'

## The following object is masked from 'package:stats':  
##   
## filter

# Morphological Analyses

### Q1: Does the *ifrms* appear more consistently than other tertiary sulci in posterior cingulate cortex?

* Chi squared tests to compare the incidence rates of the three tertiary sulci

#### Discovery sample

# Discovery dataset  
chi\_discovery <- read.csv("~/Desktop/RMD\_csvs/PCC\_chisqrd\_discovery.csv")  
chi\_discovery\_tertiary <- chi\_discovery %>% subset(sulcus %in% c("ifrms", "sspls", "icgs.p"))  
chi\_discovery\_tertiary.ct <- xtabs(hemi~presence+sulcus, data = chi\_discovery\_tertiary)  
  
## Run chi squared test  
chi\_discovery\_tertiary.ct

## sulcus  
## presence icgs.p ifrms sspls  
## with 42 72 41  
## without 30 0 31

chisq.test(chi\_discovery\_tertiary.ct) %>% broom::tidy(chisq.test(chi\_discovery\_tertiary.ct))

## # A tibble: 1 x 4  
## statistic p.value parameter method   
## <dbl> <dbl> <int> <chr>   
## 1 42.5 5.80e-10 2 Pearson's Chi-squared test

### post hoc pairwise comparisons  
chisq.multcomp(chi\_discovery\_tertiary.ct) %>% broom::tidy(chisq.multcomp(chi\_discovery\_tertiary.ct))

## # A tibble: 15 x 3  
## group1 group2 p.value  
## <chr> <chr> <dbl>  
## 1 30 0 1.30e- 7  
## 2 31 0 9.68e- 8  
## 3 41 0 7.61e-10  
## 4 42 0 6.85e-10  
## 5 72 0 3.23e-16  
## 6 31 30 9.13e- 1  
## 7 41 30 2.47e- 1  
## 8 42 30 2.36e- 1  
## 9 72 30 8.00e- 5  
## 10 41 31 2.75e- 1  
## 11 42 31 2.47e- 1  
## 12 72 31 1.15e- 4  
## 13 42 41 9.13e- 1  
## 14 72 41 6.64e- 3  
## 15 72 42 8.26e- 3

On the discovery sample the results of this chi squared indicate that the *ifrms* appears at a significantly higher rate than other tertiary sulci in posterior cingulate cortex. See Figure 2b.

#### Replication Sample

# Replication dataset  
chi\_replication <- read.csv("~/Desktop/RMD\_csvs/PCC\_chisqrd\_replication.csv")  
chi\_replication\_tertiary <- chi\_replication %>% subset(sulcus %in% c("ifrms", "sspls", "icgs.p"))  
chi\_replication\_tertiary.ct <- xtabs(hemi~presence+sulcus, data = chi\_replication\_tertiary)  
  
# Chi squared test  
chi\_replication\_tertiary.ct

## sulcus  
## presence icgs.p ifrms sspls  
## with 47 72 37  
## without 25 0 35

chisq.test(chi\_replication\_tertiary.ct) %>% broom::tidy(chisq.test(chi\_replication\_tertiary.ct))

## # A tibble: 1 x 4  
## statistic p.value parameter method   
## <dbl> <dbl> <int> <chr>   
## 1 45 1.69e-10 2 Pearson's Chi-squared test

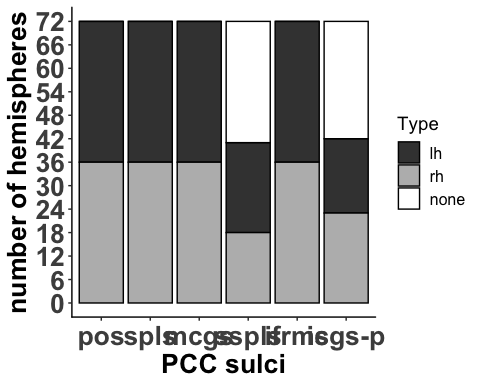
# Post hoc pairwise comparisons  
chisq.multcomp(chi\_replication\_tertiary.ct) %>% broom::tidy(chisq.multcomp(chi\_replication\_tertiary.ct))

## # A tibble: 15 x 3  
## group1 group2 p.value  
## <chr> <chr> <dbl>  
## 1 25 0 1.72e- 6  
## 2 35 0 1.24e- 8  
## 3 37 0 5.91e- 9  
## 4 47 0 5.32e-11  
## 5 72 0 3.23e-16  
## 6 35 25 2.27e- 1  
## 7 37 25 1.74e- 1  
## 8 47 25 1.59e- 2  
## 9 72 25 4.56e- 6  
## 10 37 35 8.14e- 1  
## 11 47 35 2.27e- 1  
## 12 72 35 7.45e- 4  
## 13 47 37 2.95e- 1  
## 14 72 37 1.50e- 3  
## 15 72 47 3.29e- 2

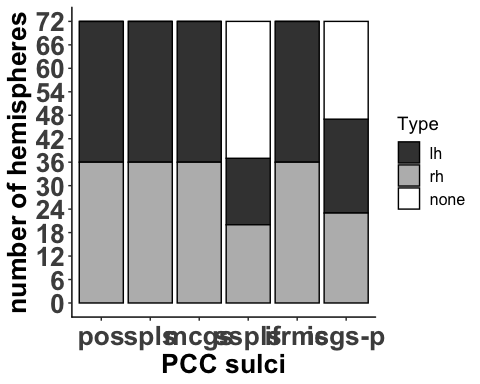
On the replication sample the results of this chi squared indicate that once more the *ifrms* appears at a significantly higher rate than other tertiary sulci in posterior cingulate cortex. See Figure 2d.

### Figure 2b and 2d: Number of hemispheres with each PCC sulcus

# Dataset - all  
HCP\_count\_all <- read.csv("~/Desktop/RMD\_csvs/HCP\_count\_all.csv")  
  
# Discovery dataset   
HCP\_count\_disc <- HCP\_count\_all %>% subset(dataset == "discovery")  
HCP\_count\_disc$Type <- factor(HCP\_count\_disc$Type, levels = c("none", "lh", "rh"))  
  
# Plot  
HCP\_count\_disc.plot <- ggplot(HCP\_count\_disc, aes(x = Sulcus)) +  
 geom\_col(data = HCP\_count\_disc,   
 aes(y = Amount, fill = Type),  
 color = 'black',) +   
 xlim("pos", "spls", "mcgs", "sspls", "ifrms", "icgs-p") +  
 scale\_y\_continuous(name = "number of hemispheres", seq(0,72,6), limits = c(0,72)) +  
 labs(x = "PCC sulci",   
 y = "# of hemispheres") +   
 scale\_fill\_manual(breaks = c("lh", "rh", "none"),  
 values = c("#404040", "#bababa", "#ffffff")  
 ) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 20, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +   
 guides()   
HCP\_count\_disc.plot



# ggplot2::ggsave(filename = "sulc\_count\_disc.png",  
# plot = HCP\_count\_disc.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")  
  
  
# Replication dataset  
HCP\_count\_rep <- HCP\_count\_all %>% subset(dataset == "replication")  
HCP\_count\_rep$Type <- factor(HCP\_count\_rep$Type, levels = c("none", "lh", "rh"))  
  
# Plot  
HCP\_count\_rep.plot <- ggplot(HCP\_count\_rep, aes(x = Sulcus)) +  
 geom\_col(data = HCP\_count\_rep,   
 aes(y = Amount, fill = Type),  
 color = 'black') +   
 xlim("pos", "spls", "mcgs", "sspls", "ifrms", "icgs-p") +  
 scale\_y\_continuous(name = "number of hemispheres", seq(0,72,6), limits = c(0,72)) +  
 labs(x = "PCC sulci",   
 y = "# of hemispheres") +   
 scale\_fill\_manual(breaks = c("lh", "rh", "none"),  
 values = c("#404040", "#bababa", "#ffffff")  
 ) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 20, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +   
 guides()   
HCP\_count\_rep.plot



# ggplot2::ggsave(filename = "sulc\_count\_rep.png",  
# plot = HCP\_count\_rep.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

### Q2a: Is the *ifrms* able to be predicted with cortex based alignment and/or convolutional neural network approaches?

### Q2b: Do these methodologies differ in their accuracy?

* Paired t-test comparing the accuracies (DICE coefficient; IV; see Methods) of these two methods (IV)
* method: cortex based alignment (CBA), convolutional neural networks (CNN)
* metric: DICE coefficient

# CNN Dataset - all  
pmc\_nn\_predicts <- read.csv("~/Desktop/RMD\_csvs/pmc\_cnn\_predicts.csv")  
  
# CNN Dataset - ifrms only  
pmc\_nn\_predicts.ifrms <- pmc\_nn\_predicts %>% subset(sulci == "ifrms") %>% select(-c("X", "type"))  
  
# CBA Dataset   
ifrms\_cba\_predicts.ifrms <- read.csv("~/Desktop/RMD\_csvs/HCP\_dice\_coefficients\_all\_72\_predicts.csv")  
  
# Average across hemispheres (since cnn only analyzed in left hemisphere)  
ifrms\_cba\_predicts.ifrms.avg <- ifrms\_cba\_predicts.ifrms %>%  
 group\_by(sub, sulci, method) %>%  
 summarise(dice = mean(dice))

## `summarise()` has grouped output by 'sub', 'sulci'. You can override using the `.groups` argument.

# Combine for analysis  
ifrms\_predicts.both <- rbind(pmc\_nn\_predicts.ifrms, ifrms\_cba\_predicts.ifrms.avg)  
  
# T-test comparing CNN to CBA (mean of lh and rh for each participant)  
t.test(ifrms\_predicts.both$dice ~ ifrms\_predicts.both$method, paired= T)

##   
## Paired t-test  
##   
## data: ifrms\_predicts.both$dice by ifrms\_predicts.both$method  
## t = -3.6872, df = 71, p-value = 0.0004402  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.17609525 -0.05248568  
## sample estimates:  
## mean of the differences   
## -0.1142905

cohens\_d(data = ifrms\_predicts.both,  
 formula = dice ~ method,   
 paired= T)

## # A tibble: 1 x 7  
## .y. group1 group2 effsize n1 n2 magnitude  
## \* <chr> <chr> <chr> <dbl> <int> <int> <ord>   
## 1 dice CBA CNN -0.435 72 72 small

The t-test shows that the *ifrms* is better predicted by the CNN approach than the CBA.

### Figure X: Evaluation of predictive labeling methodologies

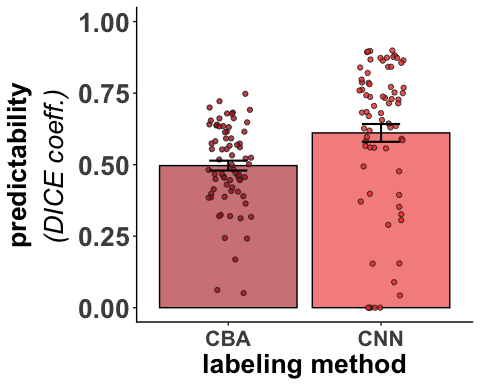
# Bar plot   
  
# Means for plot  
ifrms\_predicts\_mean <- ifrms\_predicts.both %>%   
 group\_by(sulci, method) %>%   
 summarise(dice = mean(dice))

## `summarise()` has grouped output by 'sulci'. You can override using the `.groups` argument.

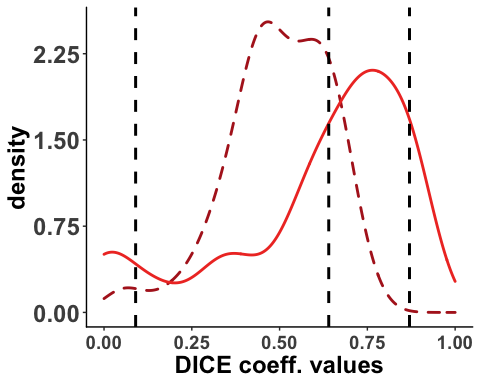
ifrms\_predicts\_sd <- ifrms\_predicts.both %>%   
 group\_by(sulci, method) %>%   
 summarise(n=n(), sd=sd(dice), se=sd/sqrt(n))

## `summarise()` has grouped output by 'sulci'. You can override using the `.groups` argument.

ifrms\_pred\_stats <- merge(ifrms\_predicts\_mean, ifrms\_predicts\_sd, by = c("sulci", "method"))  
  
# Plot  
dice\_y\_2 <- expression(atop(bold("predictability"), paste(italic("(DICE coeff.)"))))  
  
prediction\_comp.plot <- ggplot() +  
 geom\_col(data = ifrms\_pred\_stats, aes(x = method, y = dice, fill = method),   
 color = 'black', alpha = .6, position = dodge) +  
 geom\_jitter(data = ifrms\_predicts.both,   
 aes(x = method, y = dice, fill = method, color = method),   
 alpha = .8, shape = 21,  
 position=  
 position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_errorbar(data = ifrms\_pred\_stats,   
 aes(method, ymin=dice-se, ymax=dice+se),  
 width = .25, size = .75) +  
 xlim("CBA", "CNN") +  
 guides(fill = FALSE, color = FALSE) +  
 scale\_color\_manual(breaks =   
 c("CBA", "CNN"),  
 values = c( "#252525","#252525")) +   
 scale\_fill\_manual(breaks = c("CBA", "CNN"),  
 values = c("firebrick", "#ef3b2c")) +   
 labs(x = "labeling method",  
 y = dice\_y\_2) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 scale\_y\_continuous(breaks=seq(0,1,.25), limits=c(0,1))  
prediction\_comp.plot



# ggplot2::ggsave(filename = "prediction\_comp\_plot.png",  
# plot = prediction\_comp.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")  
  
  
# Distribution plot  
  
prediction\_dist.plot <- ggplot(ifrms\_predicts.both, aes(x = dice, color= method, linetype = method)) +  
 geom\_density(size = 1, alpha = .5) +  
 scale\_color\_manual(breaks = c("CBA", "CNN"),  
 values = c("firebrick", "#ef3b2c")) +   
 labs(x = "DICE coeff. values") +  
 scale\_linetype\_manual(breaks = c("CBA", "CNN"),  
 values = c("dashed", "solid")) +   
 labs(x = "DICE coeff. values") +   
 geom\_vline(aes(xintercept=0.87),  
 linetype="dashed", size = 1.05, color = 'black') +  
 geom\_vline(aes(xintercept=0.64),  
 linetype="dashed", size = 1.05, color = 'black') +  
 geom\_vline(aes(xintercept=0.09),  
 linetype="dashed", size = 1.05, color = 'black') +  
 xlim(0,1) +  
 scale\_y\_continuous(breaks=seq(0,2.5, .75)) +  
  
 guides(color = F, fill = F, linetype = F) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=18, face = "bold", vjust = .9),  
 axis.title.y = element\_text(size=18, face = "bold", vjust = .9),  
 axis.title.y.right = element\_text(size=20, face = "bold", vjust = 1),  
 axis.text.x = element\_text(size = 14, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 18, face = "bold"),  
 legend.title = element\_text(size=12),   
 legend.text = element\_text(size=10),  
 strip.text.x = element\_text(size = 16, face = "bold"),  
 strip.background = element\_blank(),  
 strip.placement = "outside",  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"))   
prediction\_dist.plot



# ggplot2::ggsave(filename = "prediction\_dist\_plot.png",  
# plot = prediction\_dist.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

### Q2: Do the depths of the posterior cingulate cortex sulci differ from one another?

* 2-way (sulcal label x hemi) ANOVA to test for differences in depth
* sulcal label: six PCC sulci (see Methods for description)
* hemi: lh, rh

#### Discovery Sample

# Dataset - all  
HCP\_tot\_depth <- read.csv("~/Desktop/RMD\_csvs/HCP\_PCC\_tot\_depth.csv")   
  
# Discovery dataset  
HCP\_disc\_depth\_PCC <- subset(HCP\_tot\_depth, subset = HCP\_tot\_depth$dataset == "HCP\_discovery")  
  
# ANOVA  
discovery\_depth2.aov <- aov(sulcal\_depth\_mm ~ hemi\*label, data = HCP\_disc\_depth\_PCC)  
summary(discovery\_depth2.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 24 24 8.721 0.00335 \*\*   
## label 5 18280 3656 1323.076 < 2e-16 \*\*\*  
## hemi:label 5 36 7 2.619 0.02421 \*   
## Residuals 359 992 3   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(discovery\_depth2.aov)

## term etasq  
## 1 hemi 0.001  
## 2 label 0.946  
## 3 hemi:label 0.002

# Post hoc tests   
disc\_depth.m1 <- emmeans::emmeans(discovery\_depth2.aov,'label')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_depth.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## (icgs-p) - ifrms 0.242 0.324 359 0.747 0.9759   
## (icgs-p) - mcgs -12.241 0.324 359 -37.819 <.0001   
## (icgs-p) - pos -17.426 0.324 359 -53.836 <.0001   
## (icgs-p) - spls -9.353 0.324 359 -28.895 <.0001   
## (icgs-p) - sspls 0.565 0.367 359 1.538 0.6399   
## ifrms - mcgs -12.483 0.277 359 -45.057 <.0001   
## ifrms - pos -17.668 0.277 359 -63.771 <.0001   
## ifrms - spls -9.595 0.277 359 -34.632 <.0001   
## ifrms - sspls 0.323 0.327 359 0.988 0.9215   
## mcgs - pos -5.185 0.277 359 -18.714 <.0001   
## mcgs - spls 2.888 0.277 359 10.425 <.0001   
## mcgs - sspls 12.806 0.327 359 39.187 <.0001   
## pos - spls 8.073 0.277 359 29.139 <.0001   
## pos - sspls 17.991 0.327 359 55.053 <.0001   
## spls - sspls 9.918 0.327 359 30.349 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 6 estimates

disc\_depth.m2 <- emmeans::emmeans(discovery\_depth2.aov, 'hemi')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_depth.m2, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## lh - rh 0.579 0.179 359 3.236 0.0013   
##   
## Results are averaged over the levels of: label

disc\_depth.i1 <- emmeans::emmeans(discovery\_depth2.aov, ~ hemi | label)  
emmeans::contrast(disc\_depth.i1, method='pairwise')

## label = icgs-p:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.341 0.515 359 0.662 0.5081   
##   
## label = ifrms:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.362 0.392 359 0.925 0.3555   
##   
## label = mcgs:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.879 0.392 359 2.243 0.0255   
##   
## label = pos:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.471 0.392 359 -1.201 0.2305   
##   
## label = spls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.386 0.392 359 3.537 0.0005   
##   
## label = sspls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.978 0.523 359 1.869 0.0625

There is a main effect of sulcal label and hemi on depth, as well as an interaction between sulcal label and hemi. Conducting post hoc analyses supported original conclusion that all tertiary sulci were significantly shallower than the surrounding primary/secondary sulci. See Figure 2c in the main text or the plot below.

#### Replication Sample

# Replication dataset  
HCP\_rep\_depth\_PCC <- subset(HCP\_tot\_depth, subset = HCP\_tot\_depth$dataset == "HCP\_replication")  
  
# ANOVA  
depth\_replication2.aov <- aov(sulcal\_depth\_mm ~ hemi\*label, data = HCP\_rep\_depth\_PCC)  
summary(depth\_replication2.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 41 41 11.203 0.000903 \*\*\*  
## label 5 17116 3423 936.437 < 2e-16 \*\*\*  
## hemi:label 5 72 14 3.943 0.001708 \*\*   
## Residuals 360 1316 4   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(depth\_replication2.aov)

## term etasq  
## 1 hemi 0.002  
## 2 label 0.923  
## 3 hemi:label 0.004

# Post hoc tests   
rep\_depth.m1 <- emmeans::emmeans(depth\_replication2.aov,'hemi')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_depth.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## lh - rh 0.633 0.206 360 3.080 0.0022   
##   
## Results are averaged over the levels of: label

rep\_depth.m2 <- emmeans::emmeans(depth\_replication2.aov,'label')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_depth.m2, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## (icgs-p) - ifrms -0.1461 0.359 360 -0.408 0.9986   
## (icgs-p) - mcgs -11.9168 0.359 360 -33.233 <.0001   
## (icgs-p) - pos -17.0978 0.359 360 -47.681 <.0001   
## (icgs-p) - spls -9.8627 0.359 360 -27.504 <.0001   
## (icgs-p) - sspls 0.0816 0.421 360 0.194 1.0000   
## ifrms - mcgs -11.7707 0.319 360 -36.938 <.0001   
## ifrms - pos -16.9517 0.319 360 -53.197 <.0001   
## ifrms - spls -9.7165 0.319 360 -30.492 <.0001   
## ifrms - sspls 0.2277 0.388 360 0.587 0.9918   
## mcgs - pos -5.1810 0.319 360 -16.259 <.0001   
## mcgs - spls 2.0542 0.319 360 6.446 <.0001   
## mcgs - sspls 11.9984 0.388 360 30.956 <.0001   
## pos - spls 7.2351 0.319 360 22.705 <.0001   
## pos - sspls 17.1793 0.388 360 44.324 <.0001   
## spls - sspls 9.9442 0.388 360 25.657 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 6 estimates

rep\_depth.i1 <- emmeans::emmeans(depth\_replication2.aov,'hemi','label')  
emmeans::contrast(rep\_depth.i1, method='pairwise')

## label = icgs-p:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.595 0.558 360 1.067 0.2869   
##   
## label = ifrms:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.529 0.451 360 1.174 0.2410   
##   
## label = mcgs:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.498 0.451 360 3.325 0.0010   
##   
## label = pos:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -1.076 0.451 360 -2.388 0.0175   
##   
## label = spls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.040 0.451 360 2.307 0.0216   
##   
## label = sspls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.213 0.631 360 1.923 0.0553

The replication sample replicated the results above. In the replication sample there is also a main effect of sulcal label and hemi on depth, as well as an interaction between sulcal label and hemi. Conducting post hoc analyses supported original conclusion that all tertiary sulci were significantly shallower than the surrounding primary/secondary sulci. See Figure 2e in the main text or the plot below.

### Figure 2c & 2e: Depth of PCC Sulci

# Discovery (Figure 2c)  
  
# Plot features - mean & other aspects  
HCP\_tot\_depth\_tert\_disc <- HCP\_disc\_depth\_PCC %>% subset(label %in% c("sspls", "ifrms", "icgs-p"))  
  
HCP\_tert\_depth\_means\_disc <- HCP\_tot\_depth\_tert\_disc %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_tert\_depth\_sd\_disc <- HCP\_tot\_depth\_tert\_disc %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

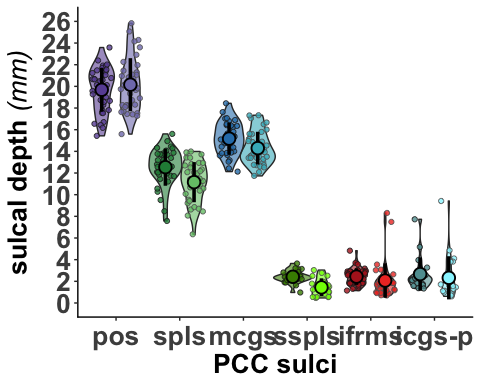
HCP\_tert\_stats\_disc <- merge(HCP\_tert\_depth\_means\_disc, HCP\_tert\_depth\_sd\_disc, by = c("label", "label2"))  
  
HCP\_tot\_depth\_ntert\_disc <- HCP\_disc\_depth\_PCC %>% subset(label %in% c("pos", "spls", "mcgs"))  
  
HCP\_n\_depth\_means\_disc <- HCP\_tot\_depth\_ntert\_disc %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_n\_depth\_sd\_disc <- HCP\_tot\_depth\_ntert\_disc %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_n\_stats\_disc <- merge(HCP\_n\_depth\_means\_disc, HCP\_n\_depth\_sd\_disc, by = c("label", "label2"))  
  
# Plot  
depth\_y <- expression(paste(bold("sulcal depth "), italic("(mm)")))  
  
PCC\_depth\_disc.plot <- ggplot() +  
 geom\_violin(data = HCP\_tot\_depth\_tert\_disc,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1.2) +   
 geom\_jitter(data = HCP\_tot\_depth\_tert\_disc,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = HCP\_tert\_stats\_disc,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
   
 geom\_violin(data = HCP\_tot\_depth\_ntert\_disc,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1.1) +   
 geom\_jitter(data = HCP\_tot\_depth\_ntert\_disc,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3,   
 dodge.width = .9,   
 jitter.height = 0)) +  
 geom\_pointrange(data = HCP\_n\_stats\_disc,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 xlim("pos","spls", "mcgs", "sspls", "ifrms", "icgs-p") +  
 guides(fill = FALSE, color = FALSE) +  
 scale\_color\_manual(breaks =   
 c("POS LH", "POS RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c( "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363")) +   
 scale\_fill\_manual(breaks = c("POS LH", "POS RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c("#6a51a3", "#807dba", #POS  
 "#238b45", "#74c476", #spls  
 "#2c7fb8", "#41b6c4", #mcgs  
 "chartreuse4", "chartreuse", #sspls  
 "firebrick", "#ef3b2c", #ifrms  
 "cadetblue", "cadetblue1")) + #icgs-p  
 labs(x = "PCC sulci",  
 y = depth\_y) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 20, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 scale\_y\_continuous(breaks=seq(0,26,2), limits = c(0,26))  
PCC\_depth\_disc.plot



# ggplot2::ggsave(filename = "PCC\_depth\_disc\_plot.png",  
# plot = PCC\_depth\_disc.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")  
  
  
# Replication (Figure 2e)  
  
# Plot features - mean & other aspects  
HCP\_tot\_depth\_tert\_rep <- HCP\_rep\_depth\_PCC %>% subset(label %in% c("sspls", "ifrms", "icgs-p"))  
  
HCP\_tert\_depth\_means\_rep <- HCP\_tot\_depth\_tert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_tert\_depth\_sd\_rep <- HCP\_tot\_depth\_tert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

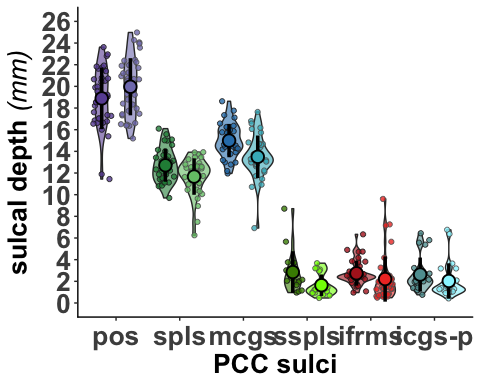
HCP\_tert\_stats\_rep <- merge(HCP\_tert\_depth\_means\_rep, HCP\_tert\_depth\_sd\_rep, by = c("label", "label2"))  
  
HCP\_tot\_depth\_ntert\_rep <- HCP\_rep\_depth\_PCC %>% subset(label %in% c("pos", "spls", "mcgs"))  
  
HCP\_n\_depth\_means\_rep <- HCP\_tot\_depth\_ntert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_n\_depth\_sd\_rep <- HCP\_tot\_depth\_ntert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_n\_stats\_rep <- merge(HCP\_n\_depth\_means\_rep, HCP\_n\_depth\_sd\_rep, by = c("label", "label2"))  
  
# Plot  
depth\_y <- expression(paste(bold("sulcal depth "), italic("(mm)")))  
  
PCC\_depth\_rep.plot <- ggplot() +  
 geom\_violin(data = HCP\_tot\_depth\_tert\_rep,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1.2) +   
 geom\_jitter(data = HCP\_tot\_depth\_tert\_rep,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = HCP\_tert\_stats\_rep,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
   
 geom\_violin(data = HCP\_tot\_depth\_ntert\_rep,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1) +   
 geom\_jitter(data = HCP\_tot\_depth\_ntert\_rep,   
 aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3,   
 dodge.width = .9,   
 jitter.height = 0)) +  
 geom\_pointrange(data = HCP\_n\_stats\_rep,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 xlim("pos","spls", "mcgs", "sspls", "ifrms", "icgs-p") +  
 guides(fill = FALSE, color = FALSE) +  
 scale\_color\_manual(breaks =   
 c("POS LH", "POS RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c( "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363")) +   
 scale\_fill\_manual(breaks = c("POS LH", "POS RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c("#6a51a3", "#807dba", #POS  
 "#238b45", "#74c476", #spls  
 "#2c7fb8", "#41b6c4", #mcgs  
 "chartreuse4", "chartreuse", #sspls  
 "firebrick", "#ef3b2c", #ifrms  
 "cadetblue", "cadetblue1")) + #icgs-p  
 labs(x = "PCC sulci",  
 y = depth\_y) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 20, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 scale\_y\_continuous(breaks=seq(0,26,2), limits = c(0,26))  
PCC\_depth\_rep.plot



# ggplot2::ggsave(filename = "PCC\_depth\_disc\_plot.png",  
# plot = PCC\_depth\_disc.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

### Q3: Does the ratio between cortical thickness and myelination differ between the *ifrms* and other tertiary or primary sulci?

* 3-way (sulc\_type x ant\_post x hemi) ANOVA
* sulc\_type: primary (mcgs/spls), tertiary (ifrms/sspls)
* ant\_post: anterior (mcgs/ifrms), posterior (spls/sspls) - note: identifies whether sulcus is in anterior PCC or posterior PCC
* hemi: lh, rh

#### Discovery Sample

# Dataset - all  
HCP\_tot\_analysis <- read.csv("~/Desktop/RMD\_csvs/HCP\_PCC\_ctmy\_analysis.csv")  
  
# Discovery dataset  
discovery\_PCC\_analysis <- HCP\_tot\_analysis %>% subset(dataset=="HCP\_discovery")  
  
# ANOVA  
discovery\_ratio\_loc.aov <- aov(ratio ~ sulc\_type \* ant\_post \* hemi, data = discovery\_PCC\_analysis)  
summary(discovery\_ratio\_loc.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## sulc\_type 1 22.367 22.367 526.395 <2e-16 \*\*\*  
## ant\_post 1 0.040 0.040 0.938 0.334   
## hemi 1 0.061 0.061 1.428 0.233   
## sulc\_type:ant\_post 1 6.040 6.040 142.143 <2e-16 \*\*\*  
## sulc\_type:hemi 1 0.043 0.043 1.021 0.313   
## ant\_post:hemi 1 0.004 0.004 0.101 0.751   
## sulc\_type:ant\_post:hemi 1 0.067 0.067 1.580 0.210   
## Residuals 249 10.580 0.042   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(discovery\_ratio\_loc.aov) #Eta-squared

## term etasq  
## 1 sulc\_type 0.571  
## 2 ant\_post 0.001  
## 3 hemi 0.002  
## 4 sulc\_type:ant\_post 0.154  
## 5 sulc\_type:hemi 0.001  
## 6 ant\_post:hemi 0.000  
## 7 sulc\_type:ant\_post:hemi 0.002

# Post hoc tests  
disc\_ratio.m1 <- emmeans::emmeans(discovery\_ratio\_loc.aov, ~ sulc\_type)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_ratio.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## primary - tertiary -0.548 0.0266 249 -20.625 <.0001   
##   
## Results are averaged over the levels of: ant\_post, hemi

disc\_ratio.i1 <- emmeans::emmeans(discovery\_ratio\_loc.aov, ~ sulc\_type | ant\_post)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_ratio.i1, method='pairwise')

## ant\_post = anterior:  
## contrast estimate SE df t.ratio p.value  
## primary - tertiary -0.864 0.0344 249 -25.152 <.0001   
##   
## ant\_post = posterior:  
## contrast estimate SE df t.ratio p.value  
## primary - tertiary -0.232 0.0405 249 -5.715 <.0001   
##   
## Results are averaged over the levels of: hemi

The results of the test showed a main effect of sulcal type indicated that there is a difference in cortical thickness/myelination ratio (C/M ratio) between primary and tertiary sulci. There was likewise a significant interaction effect between sulcal type and anterior/posterior sulcal location. The interaction indicated that the difference in the C/M ratio between primary and tertiary sulci was larger in the anterior PCC than in posterior PCC. See Figure 3b and c in the main text or the plot below..

#### Replication Sample

# Replication dataset  
replication\_PCC\_analysis <- HCP\_tot\_analysis %>% subset(dataset=="HCP\_replication")  
  
# ANOVA  
replication\_ratio\_loc.aov <- aov(ratio ~ sulc\_type \* ant\_post \* hemi, data = replication\_PCC\_analysis)  
summary(replication\_ratio\_loc.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## sulc\_type 1 25.053 25.053 682.917 <2e-16 \*\*\*  
## ant\_post 1 0.026 0.026 0.707 0.401   
## hemi 1 0.001 0.001 0.014 0.905   
## sulc\_type:ant\_post 1 6.846 6.846 186.604 <2e-16 \*\*\*  
## sulc\_type:hemi 1 0.005 0.005 0.149 0.700   
## ant\_post:hemi 1 0.000 0.000 0.005 0.945   
## sulc\_type:ant\_post:hemi 1 0.094 0.094 2.556 0.111   
## Residuals 245 8.988 0.037   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(replication\_ratio\_loc.aov) #Eta-squared

## term etasq  
## 1 sulc\_type 0.611  
## 2 ant\_post 0.001  
## 3 hemi 0.000  
## 4 sulc\_type:ant\_post 0.167  
## 5 sulc\_type:hemi 0.000  
## 6 ant\_post:hemi 0.000  
## 7 sulc\_type:ant\_post:hemi 0.002

# Post hoc tests  
rep\_ratio.m1 <- emmeans::emmeans(replication\_ratio\_loc.aov, ~ sulc\_type)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_ratio.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## primary - tertiary -0.574 0.0251 245 -22.842 <.0001   
##   
## Results are averaged over the levels of: ant\_post, hemi

rep\_ratio.i1 <- emmeans::emmeans(replication\_ratio\_loc.aov, ~ sulc\_type | ant\_post)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_ratio.i1, method='pairwise')

## ant\_post = anterior:  
## contrast estimate SE df t.ratio p.value  
## primary - tertiary -0.916 0.0319 245 -28.694 <.0001   
##   
## ant\_post = posterior:  
## contrast estimate SE df t.ratio p.value  
## primary - tertiary -0.232 0.0388 245 -5.979 <.0001   
##   
## Results are averaged over the levels of: hemi

The replication reported identical findings. Specifically, the results of the test showed a main effect of sulcal type indicated that there is a difference in cortical thickness/myelination ratio (C/M ratio) between primary and tertiary sulci. There was likewise a significant interaction effect between sulcal type and anterior/posterior sulcal location. The interaction indicated that the difference in the C/M ratio between primary and tertiary sulci was larger in the anterior PCC than in posterior PCC. See Figure 3b and c in the main text or the plot below.

#### Discovery - separate statistical analysis of the cortical thickness and myelination of PCC sulci

# Discovery dataset  
  
# compare cortical thickness and myelination of sulci separate (not as ratio)  
  
# ANOVA - cortical thickness  
discovery\_ct\_alone.aov <- aov(cortical\_thickness\_mean ~ hemi\*label, data = discovery\_PCC\_analysis)  
summary(discovery\_ct\_alone.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.00 0.005 0.072 0.788   
## label 3 55.03 18.344 275.943 <2e-16 \*\*\*  
## hemi:label 3 0.07 0.024 0.368 0.776   
## Residuals 249 16.55 0.066   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(discovery\_ct\_alone.aov) #Eta-squared

## term etasq  
## 1 hemi 0.000  
## 2 label 0.768  
## 3 hemi:label 0.001

# Post hoc test  
disc\_ct.m1 <- emmeans::emmeans(discovery\_ct\_alone.aov, ~ label)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_ct.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## ifrms - mcgs 1.161 0.0430 249 27.016 <.0001   
## ifrms - spls 0.733 0.0430 249 17.069 <.0001   
## ifrms - sspls 0.237 0.0507 249 4.667 <.0001   
## mcgs - spls -0.427 0.0430 249 -9.947 <.0001   
## mcgs - sspls -0.924 0.0507 249 -18.237 <.0001   
## spls - sspls -0.497 0.0507 249 -9.804 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 4 estimates

# ANOVA - myelination  
discovery\_my\_alone.aov <- aov(myelin ~ hemi\*label, data = discovery\_PCC\_analysis)  
summary(discovery\_my\_alone.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.0013 0.00125 0.682 0.41   
## label 3 0.3627 0.12090 65.916 < 2e-16 \*\*\*  
## hemi:label 3 0.0430 0.01433 7.816 5.25e-05 \*\*\*  
## Residuals 249 0.4567 0.00183   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(discovery\_my\_alone.aov) #Eta-squared

## term etasq  
## 1 hemi 0.001  
## 2 label 0.420  
## 3 hemi:label 0.050

# Post hoc tests  
disc\_my.m1 <- emmeans::emmeans(discovery\_my\_alone.aov, ~ label)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_my.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## ifrms - mcgs 0.0105 0.00714 249 1.477 0.4528   
## ifrms - spls -0.0109 0.00714 249 -1.529 0.4215   
## ifrms - sspls -0.1001 0.00842 249 -11.886 <.0001   
## mcgs - spls -0.0215 0.00714 249 -3.007 0.0153   
## mcgs - sspls -0.1106 0.00842 249 -13.138 <.0001   
## spls - sspls -0.0892 0.00842 249 -10.589 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 4 estimates

disc\_my.i1 <- emmeans::emmeans(discovery\_my\_alone.aov, ~ hemi | label)  
emmeans::contrast(disc\_my.i1, method='pairwise')

## label = ifrms:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.03919 0.0101 249 3.882 0.0001   
##   
## label = mcgs:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.02504 0.0101 249 -2.481 0.0138   
##   
## label = spls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.01419 0.0101 249 -1.406 0.1611   
##   
## label = sspls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.00726 0.0135 249 0.539 0.5905

Running separate ANOVAs for cortical thickness and myelination confirmed the C/M ratio findings - the *ifrms* is the thickest and one of the lesser myelinated sulci in PCC.

#### Replication - separate statistical analysis of cortical thickness and myelination of PCC sulci

# Replication dataset  
  
# compare cortical thickness and myelination of sulci separate (not as ratio)  
  
# ANOVA - cortical thickness  
replication\_ct\_alone.aov <- aov(cortical\_thickness\_mean ~ hemi\*label, data = replication\_PCC\_analysis)  
summary(replication\_ct\_alone.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.06 0.057 0.930 0.336   
## label 3 59.96 19.986 324.368 <2e-16 \*\*\*  
## hemi:label 3 0.03 0.010 0.167 0.918   
## Residuals 245 15.10 0.062   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(replication\_ct\_alone.aov) #Eta-squared

## term etasq  
## 1 hemi 0.001  
## 2 label 0.798  
## 3 hemi:label 0.000

# Post hoc test  
rep\_ct.m1 <- emmeans::emmeans(replication\_ct\_alone.aov, ~ label)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_ct.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## ifrms - mcgs 1.223 0.0414 245 29.567 <.0001   
## ifrms - spls 0.781 0.0414 245 18.876 <.0001   
## ifrms - sspls 0.281 0.0503 245 5.579 <.0001   
## mcgs - spls -0.442 0.0414 245 -10.691 <.0001   
## mcgs - sspls -0.942 0.0503 245 -18.730 <.0001   
## spls - sspls -0.500 0.0503 245 -9.940 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 4 estimates

# ANOVA - myelination  
replication\_my\_alone.aov <- aov(myelin ~ hemi\*label, data = replication\_PCC\_analysis)  
summary(replication\_my\_alone.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.0060 0.00602 4.514 0.034620 \*   
## label 3 0.3506 0.11688 87.647 < 2e-16 \*\*\*  
## hemi:label 3 0.0263 0.00877 6.574 0.000273 \*\*\*  
## Residuals 245 0.3267 0.00133   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(replication\_my\_alone.aov) #Eta-squared

## term etasq  
## 1 hemi 0.008  
## 2 label 0.494  
## 3 hemi:label 0.037

# Post hoc tests  
rep\_my.m1 <- emmeans::emmeans(replication\_my\_alone.aov, ~ label)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_my.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## ifrms - mcgs 0.00752 0.00609 245 1.236 0.6047   
## ifrms - spls -0.01727 0.00609 245 -2.837 0.0253   
## ifrms - sspls -0.10407 0.00740 245 -14.058 <.0001   
## mcgs - spls -0.02479 0.00609 245 -4.073 0.0004   
## mcgs - sspls -0.11159 0.00740 245 -15.074 <.0001   
## spls - sspls -0.08680 0.00740 245 -11.725 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 4 estimates

rep\_my.i1 <- emmeans::emmeans(replication\_my\_alone.aov, ~ hemi | label)  
emmeans::contrast(rep\_my.i1, method='pairwise')

## label = ifrms:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.0202 0.00861 245 2.350 0.0196   
##   
## label = mcgs:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.0262 0.00861 245 -3.041 0.0026   
##   
## label = spls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.0042 0.00861 245 -0.488 0.6258   
##   
## label = sspls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.0330 0.01205 245 -2.742 0.0066

The replication sample confirmed the findings observed previously in the discovery sample.

#### Figure 3b and 3c: C/M ratio of PCC sulci

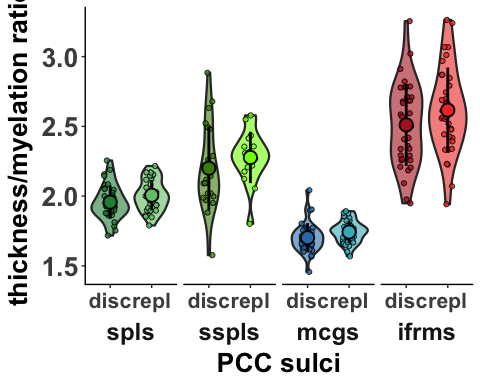
# Feature for plot  
HCP\_tot\_analysis <- HCP\_tot\_analysis %>% mutate(label\_dataset =   
 case\_when(label == "pos" & dataset == "HCP\_discovery" ~ "POS d",   
 label == "pos" & dataset == "HCP\_replication" ~ "POS r",  
 label == "spls" & dataset == "HCP\_discovery" ~ "spls d",   
 label == "spls" & dataset == "HCP\_replication" ~ "spls r",  
 label == "mcgs" & dataset == "HCP\_discovery" ~ "MCGS d",   
 label == "mcgs" & dataset == "HCP\_replication" ~ "MCGS r",  
 label == "sspls" & dataset == "HCP\_discovery" ~ "sspls d",   
 label == "sspls" & dataset == "HCP\_replication" ~ "sspls r",  
 label == "ifrms" & dataset == "HCP\_discovery" ~ "ifrms d",   
 label == "ifrms" & dataset == "HCP\_replication" ~ "ifrms r",   
 label == "icgs-p" & dataset == "HCP\_discovery" ~ "icgs-p d",  
 label == "icgs-p" & dataset == "HCP\_replication" ~ "icgs-p r"))  
  
# Left hemisphere C/M plot  
  
# Means for plot  
HCP\_tot\_analysis\_lh <- HCP\_tot\_analysis %>% subset(hemi == "lh")  
HCP\_tot\_analysis\_rh <- HCP\_tot\_analysis %>% subset(hemi == "rh")  
  
HCP\_tot\_analysis\_lh\_mean <- HCP\_tot\_analysis\_lh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(ratio = mean(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_tot\_analysis\_lh\_sd <- HCP\_tot\_analysis\_lh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(sd = sd(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_tot\_analysis\_lh\_stats <- merge(HCP\_tot\_analysis\_lh\_mean, HCP\_tot\_analysis\_lh\_sd, by = c("label", "label\_dataset"))  
  
# Features for plot  
HCP\_tot\_analysis\_lh\_stats$label <- factor(HCP\_tot\_analysis\_lh\_stats$label, levels = c("spls", "sspls", "mcgs", "ifrms"))  
  
HCP\_tot\_analysis\_lh\_stats$label\_dataset <- factor(HCP\_tot\_analysis\_lh\_stats$label\_dataset, levels = c("sspls d", "sspls r", "MCGS d", "MCGS r", "spls d", "spls r", "ifrms d", "ifrms r"))  
  
HCP\_tot\_analysis\_lh$label <- factor(HCP\_tot\_analysis\_lh$label, levels = c("spls", "sspls", "mcgs", "ifrms"))  
  
HCP\_tot\_analysis\_lh$label\_dataset <- factor(HCP\_tot\_analysis\_lh$label\_dataset, levels = c("sspls d", "sspls r", "MCGS d", "MCGS r", "spls d", "spls r", "ifrms d", "ifrms r"))  
  
# Plot  
ratio\_axis <- expression(paste(bold("thickness/myelation ratio")))  
  
ctmy\_lh.plot <- ggplot(HCP\_tot\_analysis\_lh, aes(x = label\_dataset, fill = label\_dataset)) +   
 geom\_violin(aes(y = ratio), size = .8, alpha = 0.6) +   
 geom\_jitter(aes(y = ratio),   
 shape = 21, color = 'black', alpha = .8,  
 position=position\_jitterdodge(jitter.width = 1.5,   
 dodge.width = .5, jitter.height = 0)) +   
 geom\_pointrange(data = HCP\_tot\_analysis\_lh\_stats,   
 aes(label\_dataset, ratio, ymin=ratio-sd, ymax=ratio+sd,   
 fill = label\_dataset),   
 shape = 21, size = 1, fatten = 4) +  
 scale\_x\_discrete(breaks = c("spls d", "spls r",   
 "sspls d", "sspls r",   
 "MCGS d", "MCGS r",   
 "ifrms d", "ifrms r"),   
 labels = c(  
 "disc", "repl",  
 "disc", "repl",   
 "disc", "repl",  
 "disc", "repl")) +  
 scale\_fill\_manual(breaks = c("spls d", "spls r",   
 "sspls d", "sspls r",   
 "MCGS d", "MCGS r",   
 "ifrms d", "ifrms r"),  
 values = c( "#238b45", "#74c476",   
 "chartreuse4", "chartreuse",   
 "#2c7fb8", "#41b6c4",  
 "firebrick", "#ef3b2c")) +  
 scale\_color\_manual(breaks = c("spls d", "spls r",   
 "sspls d", "sspls r",   
 "MCGS d", "MCGS r",   
 "ifrms d", "ifrms r"),  
 values = c("#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363")) +  
 labs(x = "PCC sulci",  
 y = ratio\_axis) +   
 guides(fill = F, color = F, alpha = F) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y.right = element\_text(size=20, face = "bold", vjust = 1),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 18, face = "bold"),  
 strip.background = element\_blank(),  
 strip.placement = "outside",  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 facet\_wrap( ~ label, strip.position = "bottom", scales = "free\_x", ncol = 4)  
ctmy\_lh.plot



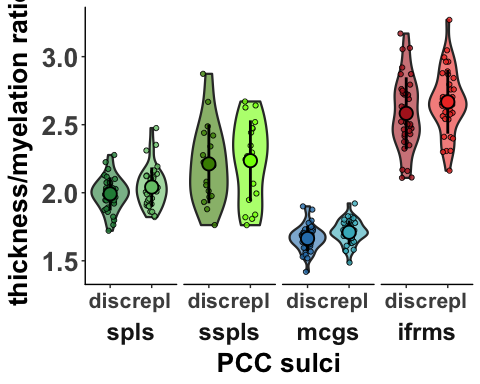
#dev.off()  
# ggplot2::ggsave(filename = "ctmy\_lh\_plot.png",  
# plot = ctmy\_lh,  
# device = "png",  
# width = 12,  
# height = 5,   
# units = "in",  
# dpi = "retina")  
  
  
# Left hemisphere C/M plot  
  
# Means for plot  
HCP\_tot\_analysis\_rh\_mean <- HCP\_tot\_analysis\_rh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(ratio = mean(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_tot\_analysis\_rh\_sd <- HCP\_tot\_analysis\_rh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(sd = sd(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_tot\_analysis\_rh\_stats <- merge(HCP\_tot\_analysis\_rh\_mean, HCP\_tot\_analysis\_rh\_sd, by = c("label", "label\_dataset"))  
  
# Features for plot  
HCP\_tot\_analysis\_rh\_stats$label <- factor(HCP\_tot\_analysis\_rh\_stats$label, levels = c("spls", "sspls", "mcgs", "ifrms"))  
  
HCP\_tot\_analysis\_rh\_stats$label\_dataset <- factor(HCP\_tot\_analysis\_rh\_stats$label\_dataset, levels = c("sspls d", "sspls r", "MCGS d", "MCGS r", "spls d", "spls r", "ifrms d", "ifrms r"))  
  
HCP\_tot\_analysis\_rh$label <- factor(HCP\_tot\_analysis\_rh$label, levels = c("spls", "sspls", "mcgs", "ifrms"))  
  
HCP\_tot\_analysis\_rh$label\_dataset <- factor(HCP\_tot\_analysis\_rh$label\_dataset, levels = c("sspls d", "sspls r", "MCGS d", "MCGS r", "spls d", "spls r", "ifrms d", "ifrms r"))  
  
# Plot  
ctmy\_rh.plot <- ggplot(HCP\_tot\_analysis\_rh, aes(x = label\_dataset, fill = label\_dataset)) +   
 geom\_violin(aes(y = ratio), size = .8, alpha = 0.6) +   
 geom\_jitter(aes(y = ratio),   
 shape = 21, color = 'black', alpha = .8,  
 position=position\_jitterdodge(jitter.width = 1.5,   
 dodge.width = .5, jitter.height = 0)) +   
 geom\_pointrange(data = HCP\_tot\_analysis\_rh\_stats,   
 aes(label\_dataset, ratio, ymin=ratio-sd, ymax=ratio+sd,   
 fill = label\_dataset),   
 shape = 21, size = 1, fatten = 4) +  
 scale\_x\_discrete(breaks = c("spls d", "spls r",   
 "sspls d", "sspls r",   
 "MCGS d", "MCGS r",   
 "ifrms d", "ifrms r"),   
 labels = c(  
 "disc", "repl",  
 "disc", "repl",   
 "disc", "repl",  
 "disc", "repl")) +  
 scale\_fill\_manual(breaks = c("spls d", "spls r",   
 "sspls d", "sspls r",   
 "MCGS d", "MCGS r",   
 "ifrms d", "ifrms r"),  
 values = c( "#238b45", "#74c476",   
 "chartreuse4", "chartreuse",   
 "#2c7fb8", "#41b6c4",  
 "firebrick", "#ef3b2c")) +  
 scale\_color\_manual(breaks = c("spls d", "spls r",   
 "sspls d", "sspls r",   
 "MCGS d", "MCGS r",   
 "ifrms d", "ifrms r"),  
 values = c("#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363")) +  
 labs(x = "PCC sulci",  
 y = ratio\_axis) +   
 guides(fill = F, color = F, alpha = F) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y.right = element\_text(size=20, face = "bold", vjust = 1),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 18, face = "bold"),  
 strip.background = element\_blank(),  
 strip.placement = "outside",  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 facet\_wrap( ~ label, strip.position = "bottom", scales = "free\_x", ncol = 4)  
ctmy\_rh.plot



#ggplot2::ggsave(filename = "ctmy\_rh\_plot.png",  
# plot = ctmy\_rh,  
# device = "png",  
# width = 12,  
# height = 5,   
# units = "in",  
# dpi = "retina")

# Functional Analyses

### Q1: Does the overlap between PCC cognitive networks differ between the *ifrms* and the *spls*?

* 3-way (network x sulcal label x hemi) ANOVA
* network: cognitive control (A,B,C), default mode (A,B,C)
* sulcal label: ifrms, spls
* hemi: lh, rh

#### Discovery Sample

# Dataset - all  
networks\_dice\_ifrms\_spls <- read.csv("~/Desktop/RMD\_csvs/networks\_dice\_ifrms\_spls.csv")  
  
# Discovery dataset  
networks\_ifrms\_spls\_discovery <- networks\_dice\_ifrms\_spls %>% subset(dataset == "HCP\_discovery")  
  
# Subset networks since only looking at these six networks  
six\_networks\_ifrms\_spls\_discovery <- networks\_ifrms\_spls\_discovery %>%   
 subset(network\_name %in% c('ControlA', 'ControlB','ControlC', 'DefaultA','DefaultB', 'DefaultC'))   
  
# ANOVA  
network2.aov <- aov(dice\_coeff ~ hemi\*label\_name\*network\_name, data = six\_networks\_ifrms\_spls\_discovery)  
summary(network2.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.00 0.002 0.059 0.80875   
## label\_name 1 0.01 0.015 0.354 0.55204   
## network\_name 5 23.61 4.723 113.630 < 2e-16 \*\*\*  
## hemi:label\_name 1 0.00 0.001 0.033 0.85613   
## hemi:network\_name 5 0.81 0.162 3.909 0.00165 \*\*   
## label\_name:network\_name 5 24.59 4.917 118.309 < 2e-16 \*\*\*  
## hemi:label\_name:network\_name 5 0.71 0.143 3.430 0.00449 \*\*   
## Residuals 840 34.91 0.042   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(network2.aov) #Eta-squared

## term etasq  
## 1 hemi 0.000  
## 2 label\_name 0.000  
## 3 network\_name 0.279  
## 4 hemi:label\_name 0.000  
## 5 hemi:network\_name 0.010  
## 6 label\_name:network\_name 0.290  
## 7 hemi:label\_name:network\_name 0.008

# Post hoc tests  
network\_aov.i1 <- emmeans::emmeans(network2.aov, ~ label\_name | network\_name)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(network\_aov.i1, method='pairwise')

## network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls 0.0299 0.034 840 0.880 0.3791   
##   
## network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls 0.4226 0.034 840 12.437 <.0001   
##   
## network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls 0.3415 0.034 840 10.050 <.0001   
##   
## network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls -0.5673 0.034 840 -16.695 <.0001   
##   
## network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls -0.2550 0.034 840 -7.505 <.0001   
##   
## network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls -0.0212 0.034 840 -0.623 0.5332   
##   
## Results are averaged over the levels of: hemi

network\_aov.i2 <- emmeans::emmeans(network2.aov, ~ hemi | label\_name | network\_name)  
emmeans::contrast(network\_aov.i2, method='pairwise')

## label\_name = ifrms, network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.024398 0.0481 840 -0.508 0.6118   
##   
## label\_name = spls, network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.008817 0.0481 840 -0.183 0.8545   
##   
## label\_name = ifrms, network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.046293 0.0481 840 -0.963 0.3356   
##   
## label\_name = spls, network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.138786 0.0481 840 -2.888 0.0040   
##   
## label\_name = ifrms, network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.002447 0.0481 840 0.051 0.9594   
##   
## label\_name = spls, network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.037167 0.0481 840 -0.773 0.4395   
##   
## label\_name = ifrms, network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.138286 0.0481 840 2.878 0.0041   
##   
## label\_name = spls, network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.013377 0.0481 840 -0.278 0.7808   
##   
## label\_name = ifrms, network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.009410 0.0481 840 -0.196 0.8448   
##   
## label\_name = spls, network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.203558 0.0481 840 4.236 <.0001   
##   
## label\_name = ifrms, network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.025387 0.0481 840 -0.528 0.5974   
##   
## label\_name = spls, network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.000353 0.0481 840 -0.007 0.9941

There is an interaction effect between sulcal label and network. Post hoc analyses reveal that this effect is driven by differences in dice overlap in cognitive control B and C and default A and B with the *ifrms* and *spls*. Specifically, the *ifrms* overlapped more with the control networks while the *spls* overlapped more with the default networks.

Additionally, there is a 3-way interaction between sulcal label, network, and hemi. Here, the *ifrms* overlapped more with default A in the left hemisphere than it did in the right hemisphere, the *spls* overlapped more with control B in left hemisphere than it did in the right hemisphere, and the *spls* overlapped more with default B in the left hemisphere than it did in the right. See Figure 4b in the main text or the plot below.

#### Replication Sample

# Replication dataset  
networks\_ifrms\_spls\_replication <- networks\_dice\_ifrms\_spls %>% subset(dataset == "HCP\_replication")  
  
# Filter for networks  
six\_networks\_ifrms\_spls\_replication <- networks\_ifrms\_spls\_replication %>% subset(network\_name %in%   
 c('ControlA', 'ControlB','ControlC',  
 'DefaultA','DefaultB', 'DefaultC'))  
  
# ANOVA  
network2\_rep.aov <- aov(dice\_coeff ~ hemi\*label\_name\*network\_name, data = six\_networks\_ifrms\_spls\_replication)  
summary(network2\_rep.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.01 0.006 0.132 0.716   
## label\_name 1 0.01 0.008 0.195 0.659   
## network\_name 5 27.86 5.572 131.194 < 2e-16 \*\*\*  
## hemi:label\_name 1 0.00 0.000 0.005 0.944   
## hemi:network\_name 5 1.47 0.294 6.913 2.50e-06 \*\*\*  
## label\_name:network\_name 5 15.11 3.021 71.129 < 2e-16 \*\*\*  
## hemi:label\_name:network\_name 5 1.53 0.306 7.207 1.31e-06 \*\*\*  
## Residuals 792 33.64 0.042   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(network2\_rep.aov) #Eta-squared

## term etasq  
## 1 hemi 0.000  
## 2 label\_name 0.000  
## 3 network\_name 0.350  
## 4 hemi:label\_name 0.000  
## 5 hemi:network\_name 0.018  
## 6 label\_name:network\_name 0.190  
## 7 hemi:label\_name:network\_name 0.019

# Post hoc tests  
network\_aov\_rep.i1 <- emmeans::emmeans(network2\_rep.aov, ~ label\_name | network\_name)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(network\_aov\_rep.i1, method='pairwise')

## network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls 0.00204 0.0353 792 0.058 0.9540   
##   
## network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls 0.32754 0.0353 792 9.267 <.0001   
##   
## network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls 0.29568 0.0353 792 8.366 <.0001   
##   
## network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls -0.46856 0.0353 792 -13.257 <.0001   
##   
## network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls -0.17252 0.0353 792 -4.881 <.0001   
##   
## network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## ifrms - spls -0.02243 0.0353 792 -0.635 0.5259   
##   
## Results are averaged over the levels of: hemi

network\_aov\_rep.i2 <- emmeans::emmeans(network2\_rep.aov, ~ hemi | label\_name | network\_name)  
emmeans::contrast(network\_aov\_rep.i2, method='pairwise')

## label\_name = ifrms, network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.01425 0.05 792 -0.285 0.7756   
##   
## label\_name = spls, network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.00664 0.05 792 -0.133 0.8944   
##   
## label\_name = ifrms, network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.00984 0.05 792 0.197 0.8440   
##   
## label\_name = spls, network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.20986 0.05 792 -4.198 <.0001   
##   
## label\_name = ifrms, network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.16175 0.05 792 -3.236 0.0013   
##   
## label\_name = spls, network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.04839 0.05 792 -0.968 0.3333   
##   
## label\_name = ifrms, network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.18032 0.05 792 3.607 0.0003   
##   
## label\_name = spls, network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.02955 0.05 792 0.591 0.5545   
##   
## label\_name = ifrms, network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.04853 0.05 792 -0.971 0.3319   
##   
## label\_name = spls, network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.25457 0.05 792 5.093 <.0001   
##   
## label\_name = ifrms, network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.00895 0.05 792 0.179 0.8580   
##   
## label\_name = spls, network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -0.05679 0.05 792 -1.136 0.2562

The same interaction effects are present in the replication sample. On the interaction effect between sulcal label and network, the same relationships between the networks and sulci found in the discovery sample are present in the replication. On the 3-way interaction between sulcal label, network, and hemi, the findings replicated, with the exception that the *ifrms* also overlapped more with control C in the right hemisphere than it did in the left - a hemispheric bias that was not seen in the discovery sample. See Supplementary Figure 4 in the supplementary material or the plot below.

#### Figure 4b: Mean *ifrms* and *spls* connectivity fingerprints - discovery

# Necessary function to make radar plot  
coord\_radar <- function (theta = "x", start = 0, direction = 1)   
{  
 theta <- match.arg(theta, c("x", "y"))  
 r <- if (theta == "x")   
 "y"  
 else "x"  
 ggproto("CordRadar", CoordPolar, theta = theta, r = r, start = start,   
 direction = sign(direction),  
 is\_linear = function(coord) TRUE)  
}  
  
# ifrms  
df.dice <- six\_networks\_ifrms\_spls\_discovery %>% subset(label\_name == "ifrms")  
  
df.dice$network\_name <- gsub("ControlA", "Control A", df.dice$network\_name)  
df.dice$network\_name <- gsub("ControlB", "Control B", df.dice$network\_name)  
df.dice$network\_name <- gsub("ControlC", "Control C", df.dice$network\_name)  
df.dice$network\_name <- gsub("DefaultA", "Default A", df.dice$network\_name)  
df.dice$network\_name <- gsub("DefaultB", "Default B", df.dice$network\_name)  
df.dice$network\_name <- gsub("DefaultC", "Default C", df.dice$network\_name)  
  
df.dice.lh <- df.dice %>% subset(hemi == 'lh')  
df.dice.rh <- df.dice %>% subset(hemi == 'rh')  
  
# Get mean values for network-sulcus overlap   
df.dice.avg <- df.dice %>%   
 group\_by(network\_name, hemi, label\_name) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name', 'hemi'. You can override using the `.groups` argument.

# Rename dfs and add "ifrms.?h" column for color coding  
df.dice.avg.lh <- df.dice.avg %>% subset(hemi == 'lh')  
df.dice.avg.lh ['label\_hemi']='ifrms.lh'  
  
df.dice.avg.rh <- df.dice.avg %>% subset(hemi == 'rh')  
df.dice.avg.rh ['label\_hemi']='ifrms.rh'  
  
# Std error calculation for plot  
ifrms.dice.se <- df.dice %>%   
 group\_by(network\_name, hemi) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'network\_name'. You can override using the `.groups` argument.

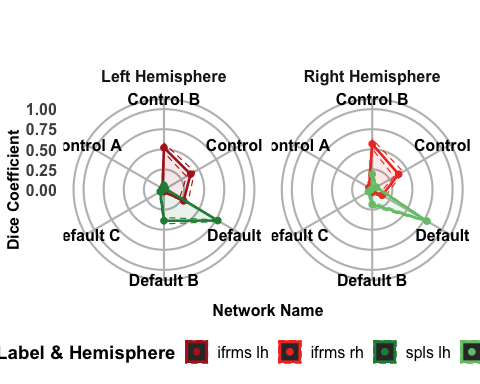
ifrms.dice.se.lh <- ifrms.dice.se %>% subset(hemi %in% c('lh'))   
ifrms.dice.se.rh <- ifrms.dice.se %>% subset(hemi %in% c('rh'))   
names(ifrms.dice.se.lh)[names(ifrms.dice.se.lh) == 'dice\_coeff'] <- "se"  
names(ifrms.dice.se.rh)[names(ifrms.dice.se.rh) == 'dice\_coeff'] <- "se"  
  
ifrms.dice.se.lh = ifrms.dice.se.lh %>% subset(select = -c(hemi))  
ifrms.dice.se.rh = ifrms.dice.se.rh %>% subset(select = -c(hemi))  
  
# Merge together + get upper and lower bounds  
ifrms.dice.se.lh <- merge(ifrms.dice.se.lh, df.dice.avg.lh,  
 by=c("network\_name"))  
ifrms.dice.se.rh <- merge(ifrms.dice.se.rh, df.dice.avg.rh,  
 by=c("network\_name"))  
  
ifrms.dice.se.lh <- ifrms.dice.se.lh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
ifrms.dice.se.rh <- ifrms.dice.se.rh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
ifrms.dice.se.lh.u <- ifrms.dice.se.lh %>% subset(select = -c(lower, dice\_coefficient))  
names(ifrms.dice.se.lh.u)[names(ifrms.dice.se.lh.u) == 'upper'] <- "dice\_coefficient"  
ifrms.dice.se.lh.l <- ifrms.dice.se.lh %>% subset(select = -c(upper, dice\_coefficient))  
names(ifrms.dice.se.lh.l)[names(ifrms.dice.se.lh.l) == 'lower'] <- "dice\_coefficient"  
  
ifrms.dice.se.rh.u <- ifrms.dice.se.rh %>% subset(select = -c(lower, dice\_coefficient))  
names(ifrms.dice.se.rh.u)[names(ifrms.dice.se.rh.u) == 'upper'] <- "dice\_coefficient"  
ifrms.dice.se.rh.l <- ifrms.dice.se.rh %>% subset(select = -c(upper, dice\_coefficient ))  
names(ifrms.dice.se.rh.l)[names(ifrms.dice.se.rh.l) == 'lower'] <- "dice\_coefficient"  
  
# More renaming for plot aesthetics   
df.dice.avg.lh$hemi <- gsub("lh", "Left Hemisphere", df.dice.avg.lh$hemi)  
df.dice.avg.rh$hemi <- gsub("rh", "Right Hemisphere", df.dice.avg.rh$hemi)  
ifrms.dice.se.lh.l$hemi <- gsub("lh", "Left Hemisphere", ifrms.dice.se.lh.l$hemi)  
ifrms.dice.se.lh.u$hemi <- gsub("lh", "Left Hemisphere", ifrms.dice.se.lh.u$hemi)  
ifrms.dice.se.rh.l$hemi <- gsub("rh", "Right Hemisphere", ifrms.dice.se.rh.l$hemi)  
ifrms.dice.se.rh.u$hemi <- gsub("rh", "Right Hemisphere", ifrms.dice.se.rh.u$hemi)  
  
# spls  
spls.dice <- six\_networks\_ifrms\_spls\_discovery %>% subset(label\_name == "spls")  
  
spls.dice$network\_name <- gsub("ControlA", "Control A", spls.dice$network\_name)  
spls.dice$network\_name <- gsub("ControlB", "Control B", spls.dice$network\_name)  
spls.dice$network\_name <- gsub("ControlC", "Control C", spls.dice$network\_name)  
spls.dice$network\_name <- gsub("DefaultA", "Default A", spls.dice$network\_name)  
spls.dice$network\_name <- gsub("DefaultB", "Default B", spls.dice$network\_name)  
spls.dice$network\_name <- gsub("DefaultC", "Default C", spls.dice$network\_name)  
  
spls.dice.lh <- spls.dice %>% subset(hemi == 'lh')  
spls.dice.rh <- spls.dice %>% subset(hemi == 'rh')  
  
# Get mean values for network-sulcus overlap   
spls.dice.avg <- spls.dice %>%   
 group\_by(network\_name, hemi, label\_name) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name', 'hemi'. You can override using the `.groups` argument.

# Rename dfs and add "ifrms.?h" column for color coding  
spls.dice.avg.lh <- spls.dice.avg %>% subset(hemi == 'lh')  
spls.dice.avg.lh['label\_hemi']='spls.lh'  
  
spls.dice.avg.rh <- spls.dice.avg %>% subset(hemi == 'rh')  
spls.dice.avg.rh['label\_hemi']='spls.rh'  
  
# Std error calculation for plot  
spls.dice.se <- spls.dice %>%   
 group\_by(hemi, label\_name, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi', 'label\_name'. You can override using the `.groups` argument.

spls.dice.se.lh <- spls.dice.se %>% subset(hemi %in% c('lh'))   
spls.dice.se.rh <- spls.dice.se %>% subset(hemi %in% c('rh'))   
  
names(spls.dice.se.lh)[names(spls.dice.se.lh) == 'dice\_coeff'] <- "se"  
names(spls.dice.se.rh)[names(spls.dice.se.rh) == 'dice\_coeff'] <- "se"  
  
spls.dice.se.lh = spls.dice.se.lh %>% subset(select = -c(hemi, label\_name))  
spls.dice.se.rh = spls.dice.se.rh %>% subset(select = -c(hemi, label\_name))  
  
# Merge together + get upper and lower bounds  
spls.dice.se.lh <- merge(spls.dice.se.lh, spls.dice.avg.lh,  
 by=c("network\_name"))  
spls.dice.se.rh <- merge(spls.dice.se.rh, spls.dice.avg.rh,  
 by=c("network\_name"))  
  
spls.dice.se.lh <- spls.dice.se.lh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
spls.dice.se.rh <- spls.dice.se.rh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
spls.dice.se.lh.u <- spls.dice.se.lh %>% subset(select = -c(lower, dice\_coefficient))  
names(spls.dice.se.lh.u)[names(spls.dice.se.lh.u) == 'upper'] <- "dice\_coefficient"  
spls.dice.se.lh.l <- spls.dice.se.lh %>% subset(select = -c(upper, dice\_coefficient))  
names(spls.dice.se.lh.l)[names(spls.dice.se.lh.l) == 'lower'] <- "dice\_coefficient"  
  
spls.dice.se.rh.u <- spls.dice.se.rh %>% subset(select = -c(lower, dice\_coefficient))  
names(spls.dice.se.rh.u)[names(spls.dice.se.rh.u) == 'upper'] <- "dice\_coefficient"  
spls.dice.se.rh.l <- spls.dice.se.rh %>% subset(select = -c(upper, dice\_coefficient ))  
names(spls.dice.se.rh.l)[names(spls.dice.se.rh.l) == 'lower'] <- "dice\_coefficient"  
  
# More renaming for plot aesthetics   
spls.dice.avg.lh$hemi <- gsub("lh", "Left Hemisphere", spls.dice.avg.lh$hemi)  
spls.dice.avg.rh$hemi <- gsub("rh", "Right Hemisphere", spls.dice.avg.rh$hemi)  
spls.dice.se.lh.l$hemi <- gsub("lh", "Left Hemisphere", spls.dice.se.lh.l$hemi)  
spls.dice.se.lh.u$hemi <- gsub("lh", "Left Hemisphere", spls.dice.se.lh.u$hemi)  
spls.dice.se.rh.l$hemi <- gsub("rh", "Right Hemisphere", spls.dice.se.rh.l$hemi)  
spls.dice.se.rh.u$hemi <- gsub("rh", "Right Hemisphere", spls.dice.se.rh.u$hemi)  
  
# Plot  
network\_dice\_discovery.plot <- ggplot() +   
 geom\_polygon(data = ifrms.dice.se.lh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = ifrms.dice.se.lh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(data = df.dice.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient,   
 fill = label\_hemi, group = label\_hemi, color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = df.dice.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +   
   
   
 geom\_polygon(data = ifrms.dice.se.rh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = ifrms.dice.se.rh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = df.dice.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient,   
 fill = label\_hemi, group = label\_hemi, color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = df.dice.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +  
   
   
 geom\_polygon(data = spls.dice.se.lh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls.dice.se.lh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls.dice.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient,   
 fill = label\_hemi, group = label\_hemi, color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = spls.dice.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +   
   
   
 geom\_polygon(data = spls.dice.se.rh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls.dice.se.rh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls.dice.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient,   
 fill = label\_hemi, group = label\_hemi, color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = spls.dice.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +  
   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#74c476")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#74c476")) +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position="bottom",   
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1) +   
 facet\_grid(. ~ hemi)  
network\_dice\_discovery.plot



# ggplot2::ggsave(filename = "network\_dice\_discovery\_plot.png",  
# plot = network\_dice\_discovery.plot,  
# device = "png",  
# width = 8,  
# height = 6,   
# units = "in",  
# dpi = "retina")

#### Supplementary Figure 4: Mean *ifrms* and *spls* connectivity fingerprints - replication

# ifrms  
ifrms\_networks\_rep <- six\_networks\_ifrms\_spls\_replication %>% subset(label\_name == "ifrms")  
  
ifrms\_networks\_rep$network\_name <- gsub("ControlA", "Control A", ifrms\_networks\_rep$network\_name)  
ifrms\_networks\_rep$network\_name <- gsub("ControlB", "Control B", ifrms\_networks\_rep$network\_name)  
ifrms\_networks\_rep$network\_name <- gsub("ControlC", "Control C", ifrms\_networks\_rep$network\_name)  
ifrms\_networks\_rep$network\_name <- gsub("DefaultA", "Default A", ifrms\_networks\_rep$network\_name)  
ifrms\_networks\_rep$network\_name <- gsub("DefaultB", "Default B", ifrms\_networks\_rep$network\_name)  
ifrms\_networks\_rep$network\_name <- gsub("DefaultC", "Default C", ifrms\_networks\_rep$network\_name)  
  
ifrms\_networks\_rep\_lh <- ifrms\_networks\_rep %>% subset(hemi == 'lh')  
ifrms\_networks\_rep\_rh <- ifrms\_networks\_rep %>% subset(hemi == 'rh')  
  
# Get mean values for network-sulcus overlap   
ifrms\_networks\_rep.avg <- ifrms\_networks\_rep %>%   
 group\_by(network\_name, hemi, label\_name) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name', 'hemi'. You can override using the `.groups` argument.

# Rename dfs and add "ifrms.?h" column for color coding  
ifrms\_networks\_rep.avg.lh <- subset(x = ifrms\_networks\_rep.avg, subset = ifrms\_networks\_rep.avg$hemi == 'lh')  
ifrms\_networks\_rep.avg.lh['label\_hemi']='ifrms.lh'  
  
ifrms\_networks\_rep.avg.rh<- subset(x = ifrms\_networks\_rep.avg, subset = ifrms\_networks\_rep.avg$hemi == 'rh')  
ifrms\_networks\_rep.avg.rh['label\_hemi']='ifrms.rh'  
  
# Std error calculation for plot  
ifrms\_networks\_rep.se <- ifrms\_networks\_rep %>%   
 group\_by(hemi, label\_name, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi', 'label\_name'. You can override using the `.groups` argument.

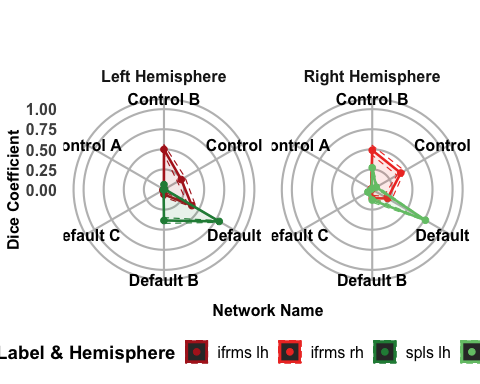
ifrms\_networks\_rep.se.lh <- ifrms\_networks\_rep.se %>% subset(hemi %in% c('lh'))   
ifrms\_networks\_rep.se.rh <- ifrms\_networks\_rep.se %>% subset(hemi %in% c('rh'))   
names(ifrms\_networks\_rep.se.lh)[names(ifrms\_networks\_rep.se.lh) == 'dice\_coeff'] <- "se"  
names(ifrms\_networks\_rep.se.rh)[names(ifrms\_networks\_rep.se.rh) == 'dice\_coeff'] <- "se"  
  
ifrms\_networks\_rep.se.lh = ifrms\_networks\_rep.se.lh %>% subset(select = -c(hemi, label\_name))  
ifrms\_networks\_rep.se.rh = ifrms\_networks\_rep.se.rh %>% subset(select = -c(hemi, label\_name))  
  
# merge together + get upper and lower bounds  
ifrms\_networks\_rep.se.lh <- merge(ifrms\_networks\_rep.se.lh, ifrms\_networks\_rep.avg.lh,  
 by=c("network\_name"))  
ifrms\_networks\_rep.se.rh <- merge(ifrms\_networks\_rep.se.rh, ifrms\_networks\_rep.avg.rh,  
 by=c("network\_name"))  
  
ifrms\_networks\_rep.se.lh <- ifrms\_networks\_rep.se.lh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
ifrms\_networks\_rep.se.rh <- ifrms\_networks\_rep.se.rh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
ifrms\_networks\_rep.se.lh.u <- ifrms\_networks\_rep.se.lh %>% subset(select = -c(lower, dice\_coefficient))  
names(ifrms\_networks\_rep.se.lh.u)[names(ifrms\_networks\_rep.se.lh.u) == 'upper'] <- "dice\_coefficient"  
ifrms\_networks\_rep.se.lh.l <- ifrms\_networks\_rep.se.lh %>% subset(select = -c(upper, dice\_coefficient))  
names(ifrms\_networks\_rep.se.lh.l)[names(ifrms\_networks\_rep.se.lh.l) == 'lower'] <- "dice\_coefficient"  
  
ifrms\_networks\_rep.se.rh.u <- ifrms\_networks\_rep.se.rh %>% subset(select = -c(lower, dice\_coefficient))  
names(ifrms\_networks\_rep.se.rh.u)[names(ifrms\_networks\_rep.se.rh.u) == 'upper'] <- "dice\_coefficient"  
ifrms\_networks\_rep.se.rh.l <- ifrms\_networks\_rep.se.rh %>% subset(select = -c(upper, dice\_coefficient ))  
names(ifrms\_networks\_rep.se.rh.l)[names(ifrms\_networks\_rep.se.rh.l) == 'lower'] <- "dice\_coefficient"  
  
# more renaming to make plot better   
ifrms\_networks\_rep.avg.lh$hemi <- gsub("lh", "Left Hemisphere", ifrms\_networks\_rep.avg.lh$hemi)  
ifrms\_networks\_rep.avg.rh$hemi <- gsub("rh", "Right Hemisphere", ifrms\_networks\_rep.avg.rh$hemi)  
ifrms\_networks\_rep.se.lh.l$hemi <- gsub("lh", "Left Hemisphere", ifrms\_networks\_rep.se.lh.l$hemi)  
ifrms\_networks\_rep.se.lh.u$hemi <- gsub("lh", "Left Hemisphere", ifrms\_networks\_rep.se.lh.u$hemi)  
ifrms\_networks\_rep.se.rh.l$hemi <- gsub("rh", "Right Hemisphere", ifrms\_networks\_rep.se.rh.l$hemi)  
ifrms\_networks\_rep.se.rh.u$hemi <- gsub("rh", "Right Hemisphere", ifrms\_networks\_rep.se.rh.u$hemi)  
  
# spls  
spls\_networks\_rep <- six\_networks\_ifrms\_spls\_replication %>% subset(label\_name == "spls")  
  
spls\_networks\_rep$network\_name <- gsub("ControlA", "Control A", spls\_networks\_rep$network\_name)  
spls\_networks\_rep$network\_name <- gsub("ControlB", "Control B", spls\_networks\_rep$network\_name)  
spls\_networks\_rep$network\_name <- gsub("ControlC", "Control C", spls\_networks\_rep$network\_name)  
spls\_networks\_rep$network\_name <- gsub("DefaultA", "Default A", spls\_networks\_rep$network\_name)  
spls\_networks\_rep$network\_name <- gsub("DefaultB", "Default B", spls\_networks\_rep$network\_name)  
spls\_networks\_rep$network\_name <- gsub("DefaultC", "Default C", spls\_networks\_rep$network\_name)  
  
spls\_networks\_rep.lh <- spls\_networks\_rep %>% subset(hemi == 'lh')  
spls\_networks\_rep.rh <- spls\_networks\_rep %>% subset(hemi == 'rh')  
  
# get mean values for network-sulcus overlap   
spls\_networks\_rep.avg <- spls\_networks\_rep %>%   
 group\_by(network\_name, hemi, label\_name) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name', 'hemi'. You can override using the `.groups` argument.

# Rename dfs and add "ifrms.?h" column for color coding  
spls\_networks\_rep.avg.lh <- spls\_networks\_rep.avg %>% subset(hemi == 'lh')  
spls\_networks\_rep.avg.lh['label\_hemi']='spls.lh'  
  
spls\_networks\_rep.avg.rh <- spls\_networks\_rep.avg %>% subset(hemi == 'rh')  
spls\_networks\_rep.avg.rh['label\_hemi']='spls.rh'  
  
# Std error calculation for plot  
spls\_networks\_rep.se <- spls\_networks\_rep %>%   
 group\_by(hemi, label\_name, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi', 'label\_name'. You can override using the `.groups` argument.

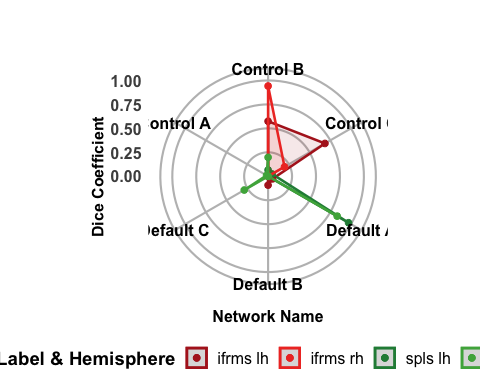
spls\_networks\_rep.se.lh <- spls\_networks\_rep.se %>% subset(hemi %in% c('lh'))   
spls\_networks\_rep.se.rh <- spls\_networks\_rep.se %>% subset(hemi %in% c('rh'))   
  
names(spls\_networks\_rep.se.lh)[names(spls\_networks\_rep.se.lh) == 'dice\_coeff'] <- "se"  
names(spls\_networks\_rep.se.rh)[names(spls\_networks\_rep.se.rh) == 'dice\_coeff'] <- "se"  
  
spls\_networks\_rep.se.lh = spls\_networks\_rep.se.lh %>% subset(select = -c(hemi, label\_name))  
spls\_networks\_rep.se.rh = spls\_networks\_rep.se.rh %>% subset(select = -c(hemi, label\_name))  
  
# Merge together + get upper and lower bounds  
spls\_networks\_rep.se.lh <- merge(spls\_networks\_rep.se.lh, spls\_networks\_rep.avg.lh,  
 by=c("network\_name"))  
spls\_networks\_rep.se.rh <- merge(spls\_networks\_rep.se.rh, spls\_networks\_rep.avg.rh,  
 by=c("network\_name"))  
  
spls\_networks\_rep.se.lh <- spls\_networks\_rep.se.lh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
spls\_networks\_rep.se.rh <- spls\_networks\_rep.se.rh %>%   
 group\_by(network\_name) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
spls\_networks\_rep.se.lh.u <- spls\_networks\_rep.se.lh %>% subset(select = -c(lower, dice\_coefficient))  
names(spls\_networks\_rep.se.lh.u)[names(spls\_networks\_rep.se.lh.u) == 'upper'] <- "dice\_coefficient"  
spls\_networks\_rep.se.lh.l <- spls\_networks\_rep.se.lh %>% subset(select = -c(upper, dice\_coefficient))  
names(spls\_networks\_rep.se.lh.l)[names(spls\_networks\_rep.se.lh.l) == 'lower'] <- "dice\_coefficient"  
  
spls\_networks\_rep.se.rh.u <- spls\_networks\_rep.se.rh %>% subset(select = -c(lower, dice\_coefficient))  
names(spls\_networks\_rep.se.rh.u)[names(spls\_networks\_rep.se.rh.u) == 'upper'] <- "dice\_coefficient"  
spls\_networks\_rep.se.rh.l <- spls\_networks\_rep.se.rh %>% subset(select = -c(upper, dice\_coefficient ))  
names(spls\_networks\_rep.se.rh.l)[names(spls\_networks\_rep.se.rh.l) == 'lower'] <- "dice\_coefficient"  
  
# more renaming to make plot better   
spls\_networks\_rep.avg.lh$hemi <- gsub("lh", "Left Hemisphere", spls\_networks\_rep.avg.lh$hemi)  
spls\_networks\_rep.avg.rh$hemi <- gsub("rh", "Right Hemisphere", spls\_networks\_rep.avg.rh$hemi)  
spls\_networks\_rep.se.lh.l$hemi <- gsub("lh", "Left Hemisphere", spls\_networks\_rep.se.lh.l$hemi)  
spls\_networks\_rep.se.lh.u$hemi <- gsub("lh", "Left Hemisphere", spls\_networks\_rep.se.lh.u$hemi)  
spls\_networks\_rep.se.rh.l$hemi <- gsub("rh", "Right Hemisphere", spls\_networks\_rep.se.rh.l$hemi)  
spls\_networks\_rep.se.rh.u$hemi <- gsub("rh", "Right Hemisphere", spls\_networks\_rep.se.rh.u$hemi)  
  
network\_dice\_replication.plot <- ggplot() +   
 geom\_polygon(data = ifrms\_networks\_rep.se.lh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = ifrms\_networks\_rep.se.lh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(data = ifrms\_networks\_rep.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient, fill = label\_hemi, group = label\_hemi,   
 color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = ifrms\_networks\_rep.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +   
   
   
 geom\_polygon(data = ifrms\_networks\_rep.se.rh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = ifrms\_networks\_rep.se.rh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = ifrms\_networks\_rep.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient, fill = label\_hemi, group = label\_hemi,   
 color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = ifrms\_networks\_rep.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +  
   
   
 geom\_polygon(data = spls\_networks\_rep.se.lh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls\_networks\_rep.se.lh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls\_networks\_rep.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient, fill = label\_hemi, group = label\_hemi,   
 color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = spls\_networks\_rep.avg.lh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +   
   
   
 geom\_polygon(data = spls\_networks\_rep.se.rh.l,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls\_networks\_rep.se.rh.u,   
 aes(x = network\_name, y = dice\_coefficient, fill = NA, group = label\_hemi, color = label\_hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(data = spls\_networks\_rep.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient, fill = label\_hemi, group = label\_hemi,   
 color = label\_hemi),   
 size = .9, alpha = .1) +  
 geom\_point(data = spls\_networks\_rep.avg.rh,   
 aes(x = network\_name, y = dice\_coefficient, color = label\_hemi),   
 size = 2) +  
   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#74c476")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#74c476")) +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1) +   
 facet\_grid(. ~ hemi)  
network\_dice\_replication.plot



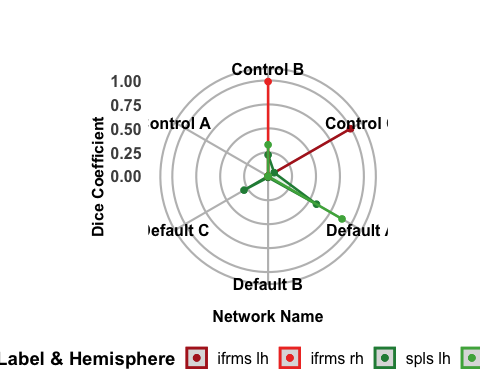
# ggplot2::ggsave(filename = "network\_dice\_replication\_plot.png",  
# plot = network\_dice\_replication.plot,  
# device = "png",  
# width = 8,  
# height = 6,   
# units = "in",  
# dpi = "retina")

#### Figure 4c: Four individual subjects’ radar plots

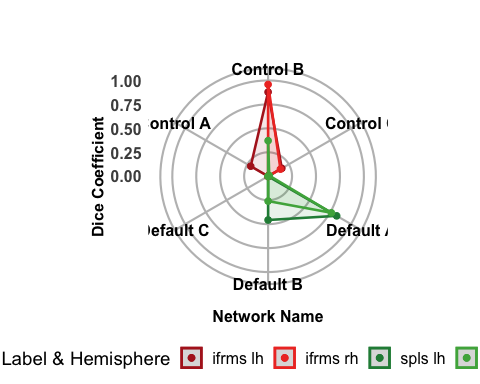
# Four individual radar plots - from the discovery sample  
six\_networks\_ifrms\_spls\_discovery$label\_hemi[six\_networks\_ifrms\_spls\_discovery$label\_name == "ifrms" & six\_networks\_ifrms\_spls\_discovery$hemi == "lh"] <- "ifrms.lh"  
  
six\_networks\_ifrms\_spls\_discovery$label\_hemi[six\_networks\_ifrms\_spls\_discovery$label\_name == "ifrms" & six\_networks\_ifrms\_spls\_discovery$hemi == "rh"] <- "ifrms.rh"  
  
six\_networks\_ifrms\_spls\_discovery$label\_hemi[six\_networks\_ifrms\_spls\_discovery$label\_name == "spls" & six\_networks\_ifrms\_spls\_discovery$hemi == "lh"] <- "spls.lh"  
  
six\_networks\_ifrms\_spls\_discovery$label\_hemi[six\_networks\_ifrms\_spls\_discovery$label\_name == "spls" & six\_networks\_ifrms\_spls\_discovery$hemi == "rh"] <- "spls.rh"  
  
six\_networks\_ifrms\_spls\_discovery$network\_name <- gsub("ControlA", "Control A", six\_networks\_ifrms\_spls\_discovery$network\_name)  
  
six\_networks\_ifrms\_spls\_discovery$network\_name <- gsub("ControlB", "Control B", six\_networks\_ifrms\_spls\_discovery$network\_name)  
  
six\_networks\_ifrms\_spls\_discovery$network\_name <- gsub("ControlC", "Control C", six\_networks\_ifrms\_spls\_discovery$network\_name)  
  
six\_networks\_ifrms\_spls\_discovery$network\_name <- gsub("DefaultA", "Default A", six\_networks\_ifrms\_spls\_discovery$network\_name)  
  
six\_networks\_ifrms\_spls\_discovery$network\_name <- gsub("DefaultB", "Default B", six\_networks\_ifrms\_spls\_discovery$network\_name)  
  
six\_networks\_ifrms\_spls\_discovery$network\_name <- gsub("DefaultC", "Default C", six\_networks\_ifrms\_spls\_discovery$network\_name)  
  
dice.100206 <- six\_networks\_ifrms\_spls\_discovery %>% subset(TRG\_sub == "100206")  
dice.100206.lh <- dice.100206 %>% subset(hemi == "lh")  
dice.100206.rh <- dice.100206 %>% subset(hemi == "rh")  
  
dice.101107 <- six\_networks\_ifrms\_spls\_discovery %>% subset(TRG\_sub == "101107")  
dice.101107.lh <- dice.101107 %>% subset(hemi == "lh")  
dice.101107.rh <- dice.101107 %>% subset(hemi == "rh")  
  
dice.109830 <- six\_networks\_ifrms\_spls\_discovery %>% subset(TRG\_sub == "109830")  
dice.109830.lh <- dice.109830 %>% subset(hemi == "lh")  
dice.109830.rh <- dice.109830 %>% subset(hemi == "rh")  
  
dice.214019 <- six\_networks\_ifrms\_spls\_discovery %>% subset(TRG\_sub == "214019")  
dice.214019.lh <- dice.214019 %>% subset(hemi == "lh")  
dice.214019.rh <- dice.214019 %>% subset(hemi == "rh")  
  
overlap\_100206.plot <- ggplot() +   
 geom\_polygon(data = dice.100206.lh , aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group =  
 label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.100206.lh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi), size = 2) +   
   
 geom\_polygon(data = dice.100206.rh , aes(x = network\_name, y = dice\_coeff, fill = label\_hemi,  
 group = label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.100206.rh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi),   
 size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +  
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1)   
overlap\_100206.plot



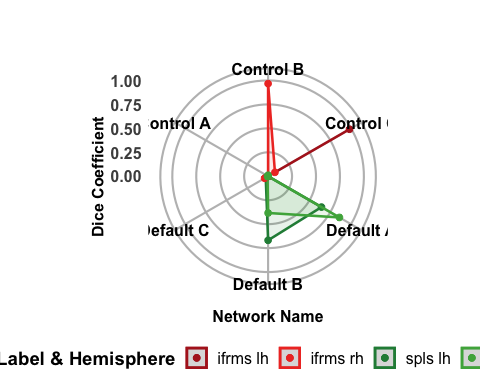
# ggplot2::ggsave(filename = "overlap\_100206\_plot.png",  
# plot = overlap\_100206.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "retina")  
  
  
overlap\_101107.plot <- ggplot() +   
 geom\_polygon(data = dice.101107.lh, aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group =  
 label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.101107.lh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi), size = 2) +   
 geom\_polygon(data = dice.101107.rh, aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group =  
 label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.101107.rh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi), size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1)   
overlap\_101107.plot



# ggplot2::ggsave(filename = "overlap\_101107\_plot.png",  
# plot = overlap\_101107.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "retina")  
  
  
overlap\_109830.plot <- ggplot() +   
 geom\_polygon(data = dice.109830.lh, aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group =  
 label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.109830.lh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi), size = 2) +   
 geom\_polygon(data = dice.109830.rh, aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group =  
 label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.109830.rh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi), size = 2) +   
   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1)   
overlap\_109830.plot



# ggplot2::ggsave(filename = "overlap\_109830\_plot.png",  
# plot = overlap\_109830.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "retina")  
  
  
overlap\_214019.plot <- ggplot() +   
 geom\_polygon(data = dice.214019.lh, aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group =  
 label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.214019.lh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi), size = 2) +   
   
 geom\_polygon(data = dice.214019.rh, aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group =  
 label\_hemi, color = label\_hemi), size = .9, alpha = .1) +  
 geom\_point(data = dice.214019.rh, aes(x = network\_name, y = dice\_coeff, color = label\_hemi), size = 2) +   
   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1)   
overlap\_214019.plot



# ggplot2::ggsave(filename = "overlap\_214019\_plot.png",  
# plot = overlap\_214019.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "retina")

### Q2: Is the location of the ifrms predictive of the location of control network B and/or control network C?

Linear regressions run with the right, anterior, and superior (RAS) coordinates of the ifrms predicting the RAS coordinates of Control B and Control C \* Predictor variable: RAS coordinates of the ifrms (see Methods for data acquisition procedure) \* Outcome variable: RAS coordinates of either control network B or control network C (see Methods for data acquisition procedure) \* Separate analyses were run for each coordinate (RAS), sample (discovery, replication), and hemisphere (lh, rh) \* FDR adjustment used to correct for multiple comparisons

#### Discovery Sample

# Dataset - all  
RAS\_analysis\_all <- read.csv("~/Desktop/RMD\_csvs/RAS\_analysis\_all.csv")  
  
# Discovery dataset  
RAS\_analysis\_all\_disc <- RAS\_analysis\_all %>% subset(dataset == "HCP\_discovery")  
  
# Separate by hemisphere to analyze separately   
RAS\_analysis\_all\_disc\_lh <- RAS\_analysis\_all\_disc %>% subset(hemi == "lh")  
RAS\_analysis\_all\_disc\_rh <- RAS\_analysis\_all\_disc %>% subset(hemi == "rh")  
  
# Linear models  
  
## Control B  
  
### Right coordinate   
right\_cb\_disc\_lh.lm <- lm(ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_lh)  
right\_cb\_disc\_rh.lm <- lm(ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_rh)  
summary(right\_cb\_disc\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -2.6806 -0.2364 0.2851 0.4861 1.2807   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.2060 0.6896 -1.749 0.089620 .   
## R\_coord 0.6056 0.1605 3.773 0.000638 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.8724 on 33 degrees of freedom  
## (1 observation deleted due to missingness)  
## Multiple R-squared: 0.3013, Adjusted R-squared: 0.2802   
## F-statistic: 14.23 on 1 and 33 DF, p-value: 0.0006382

summary(right\_cb\_disc\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -3.0121 -1.0740 -0.3667 0.7622 3.5160   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 3.6312 1.1446 3.172 0.00320 \*\*  
## R\_coord 0.5012 0.1747 2.869 0.00703 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 1.589 on 34 degrees of freedom  
## Multiple R-squared: 0.1949, Adjusted R-squared: 0.1712   
## F-statistic: 8.231 on 1 and 34 DF, p-value: 0.007029

## Anterior coordinate  
ant\_cb\_disc\_lh.lm <- lm(ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_lh)  
ant\_cb\_disc\_rh.lm <- lm(ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_rh)  
summary(ant\_cb\_disc\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -6.9931 -2.6859 0.2947 1.6442 7.5293   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -7.0614 1.3582 -5.199 1.03e-05 \*\*\*  
## A\_coord 0.5735 0.1068 5.370 6.18e-06 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.471 on 33 degrees of freedom  
## (1 observation deleted due to missingness)  
## Multiple R-squared: 0.4664, Adjusted R-squared: 0.4502   
## F-statistic: 28.84 on 1 and 33 DF, p-value: 6.184e-06

summary(ant\_cb\_disc\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -8.4393 -2.3966 -0.0727 2.2634 7.9277   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -11.05185 1.22734 -9.005 1.59e-10 \*\*\*  
## A\_coord 0.43818 0.09821 4.462 8.47e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.458 on 34 degrees of freedom  
## Multiple R-squared: 0.3693, Adjusted R-squared: 0.3507   
## F-statistic: 19.91 on 1 and 34 DF, p-value: 8.468e-05

## Superior coordinate  
sup\_cb\_disc\_lh.lm <- lm(ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_lh)  
sup\_cb\_disc\_rh.lm <- lm(ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_rh)  
summary(sup\_cb\_disc\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -4.6260 -0.8942 -0.1322 1.0136 4.1179   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.2607 1.2626 0.206 0.838   
## S\_coord 0.9838 0.1016 9.680 3.63e-11 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.044 on 33 degrees of freedom  
## (1 observation deleted due to missingness)  
## Multiple R-squared: 0.7396, Adjusted R-squared: 0.7317   
## F-statistic: 93.71 on 1 and 33 DF, p-value: 3.629e-11

summary(sup\_cb\_disc\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -6.7585 -0.7475 0.0789 0.9169 3.8613   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 3.17153 0.99337 3.193 0.00303 \*\*   
## S\_coord 0.73553 0.07626 9.646 2.91e-11 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 1.892 on 34 degrees of freedom  
## Multiple R-squared: 0.7324, Adjusted R-squared: 0.7245   
## F-statistic: 93.04 on 1 and 34 DF, p-value: 2.915e-11

## Control C   
  
### Right coordinate  
right\_cc\_discovery\_lh.mod <- lm(ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_lh)  
right\_cc\_discovery\_rh.mod <- lm(ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_rh)  
summary(right\_cc\_discovery\_lh.mod) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -2.49713 -0.45216 -0.04953 0.69340 1.70128   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.0277 0.6770 -1.518 0.138   
## R\_coord 0.8037 0.1584 5.074 1.38e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.8693 on 34 degrees of freedom  
## Multiple R-squared: 0.4309, Adjusted R-squared: 0.4142   
## F-statistic: 25.75 on 1 and 34 DF, p-value: 1.377e-05

summary(right\_cc\_discovery\_rh.mod) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_disc\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -1.5192 -0.5441 -0.1240 0.4349 2.5125   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 4.42152 0.60965 7.253 2.14e-08 \*\*\*  
## R\_coord 0.31878 0.09304 3.426 0.00162 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.8464 on 34 degrees of freedom  
## Multiple R-squared: 0.2566, Adjusted R-squared: 0.2348   
## F-statistic: 11.74 on 1 and 34 DF, p-value: 0.001617

### Anterior coordinate  
ant\_cc\_disc\_lh.lm <- lm(ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_lh)  
ant\_cc\_disc\_rh.lm <- lm(ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_rh)  
summary(ant\_cc\_disc\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -8.9490 -2.1374 -0.3974 1.5112 9.5681   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -4.4218 1.3940 -3.172 0.003203 \*\*   
## A\_coord 0.4286 0.1109 3.866 0.000475 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.669 on 34 degrees of freedom  
## Multiple R-squared: 0.3053, Adjusted R-squared: 0.2849   
## F-statistic: 14.94 on 1 and 34 DF, p-value: 0.0004753

summary(ant\_cc\_disc\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_disc\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -5.9184 -2.4971 0.2423 1.9158 6.9614   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -5.31652 1.12331 -4.733 3.8e-05 \*\*\*  
## A\_coord 0.30389 0.08989 3.381 0.00183 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.165 on 34 degrees of freedom  
## Multiple R-squared: 0.2516, Adjusted R-squared: 0.2296   
## F-statistic: 11.43 on 1 and 34 DF, p-value: 0.001829

### Superior coordinate  
sup\_cc\_disc\_lh.lm <- lm(ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_lh)  
sup\_cc\_disc\_rh.lm <- lm(ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_rh)  
summary(sup\_cc\_disc\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -4.4938 -1.1500 -0.1699 1.1412 5.4389   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.9108 1.2828 -0.710 0.483   
## S\_coord 0.8997 0.1036 8.687 3.76e-10 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.085 on 34 degrees of freedom  
## Multiple R-squared: 0.6894, Adjusted R-squared: 0.6803   
## F-statistic: 75.47 on 1 and 34 DF, p-value: 3.764e-10

summary(sup\_cc\_disc\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_disc\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -4.1983 -1.1016 -0.0555 0.8971 5.2618   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 2.16690 0.99724 2.173 0.0369 \*   
## S\_coord 0.71248 0.07655 9.307 7.1e-11 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 1.899 on 34 degrees of freedom  
## Multiple R-squared: 0.7181, Adjusted R-squared: 0.7098   
## F-statistic: 86.62 on 1 and 34 DF, p-value: 7.1e-11

The linear regression results shows that the mean RAS coordinate of the *ifrms* is predictive of the respective RAS coordinate of both control network B and control network C in both hemispheres. See Figure 5b and 5c, as well as Tables 4 and 5, for further reference.

#### Replication Sample

# Replication dataset  
RAS\_analysis\_all\_repl <- RAS\_analysis\_all %>% subset(dataset == "HCP\_replication")  
  
# Separate by hemisphere to analyze separately   
RAS\_analysis\_all\_repl\_lh <- RAS\_analysis\_all\_repl %>% subset(hemi == "lh")  
RAS\_analysis\_all\_repl\_rh <- RAS\_analysis\_all\_repl %>% subset(hemi == "rh")  
  
# Linear models  
  
## Control B  
  
### Right coordinate   
right\_cb\_repl\_lh.lm <- lm(ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_lh)  
right\_cb\_repl\_rh.lm <- lm(ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_rh)  
summary(right\_cb\_repl\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -2.7702 -0.4132 0.2088 0.5948 1.6288   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.2632 0.7177 -0.367 0.716   
## R\_coord 0.7701 0.1552 4.961 2.4e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.9662 on 31 degrees of freedom  
## (1 observation deleted due to missingness)  
## Multiple R-squared: 0.4426, Adjusted R-squared: 0.4246   
## F-statistic: 24.61 on 1 and 31 DF, p-value: 2.401e-05

summary(right\_cb\_repl\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -3.6410 -1.2371 -0.4367 0.9792 4.9813   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.2654 2.5337 -0.105 0.91724   
## R\_coord 1.1359 0.3911 2.905 0.00662 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 1.981 on 32 degrees of freedom  
## Multiple R-squared: 0.2086, Adjusted R-squared: 0.1839   
## F-statistic: 8.437 on 1 and 32 DF, p-value: 0.006616

### Anterior coordinate  
ant\_cb\_repl\_lh.lm <- lm(ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_lh)  
ant\_cb\_repl\_rh.lm <- lm(ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_rh)  
summary(ant\_cb\_repl\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -6.7008 -2.0271 -0.0607 1.6723 11.2621   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -9.1901 1.3937 -6.594 2.29e-07 \*\*\*  
## A\_coord 0.3995 0.1077 3.710 0.000811 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.397 on 31 degrees of freedom  
## (1 observation deleted due to missingness)  
## Multiple R-squared: 0.3075, Adjusted R-squared: 0.2852   
## F-statistic: 13.77 on 1 and 31 DF, p-value: 0.0008115

summary(ant\_cb\_repl\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -14.8537 -1.9577 0.4304 2.7138 8.3254   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -12.2074 1.6837 -7.251 3.08e-08 \*\*\*  
## A\_coord 0.4686 0.1585 2.956 0.00582 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 4.694 on 32 degrees of freedom  
## Multiple R-squared: 0.2144, Adjusted R-squared: 0.1899   
## F-statistic: 8.735 on 1 and 32 DF, p-value: 0.005817

### Superior coordinate  
sup\_cb\_repl\_lh.lm <- lm(ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_lh)  
sup\_cb\_repl\_rh.lm <- lm(ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_rh)  
summary(sup\_cb\_repl\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -5.2307 -1.0291 0.1068 1.5484 4.8598   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 2.17086 1.29623 1.675 0.104   
## S\_coord 0.81998 0.09886 8.294 2.28e-09 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.291 on 31 degrees of freedom  
## (1 observation deleted due to missingness)  
## Multiple R-squared: 0.6894, Adjusted R-squared: 0.6793   
## F-statistic: 68.8 on 1 and 31 DF, p-value: 2.278e-09

summary(sup\_cb\_repl\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlB\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -3.5382 -1.5820 0.2669 1.5485 3.7146   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.51467 1.26031 0.408 0.686   
## S\_coord 0.92013 0.09493 9.693 4.84e-11 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 1.967 on 32 degrees of freedom  
## Multiple R-squared: 0.7459, Adjusted R-squared: 0.738   
## F-statistic: 93.95 on 1 and 32 DF, p-value: 4.838e-11

## Control C  
  
### Right coordinate   
right\_cc\_repl\_lh.lm <- lm(ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_lh)  
right\_cc\_repl\_rh.lm <- lm(ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_rh)  
summary(right\_cc\_repl\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -1.1870 -0.4433 0.1003 0.3585 1.2504   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.77413 0.43205 -4.106 0.00026 \*\*\*  
## R\_coord 0.56339 0.09363 6.017 1.03e-06 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.583 on 32 degrees of freedom  
## Multiple R-squared: 0.5309, Adjusted R-squared: 0.5162   
## F-statistic: 36.21 on 1 and 32 DF, p-value: 1.032e-06

summary(right\_cc\_repl\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_R\_coord ~ R\_coord, data = RAS\_analysis\_all\_repl\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -1.3520 -0.5688 0.1311 0.4442 2.2981   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 2.8681 0.9346 3.069 0.004355 \*\*   
## R\_coord 0.5516 0.1443 3.824 0.000573 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.7307 on 32 degrees of freedom  
## Multiple R-squared: 0.3136, Adjusted R-squared: 0.2922   
## F-statistic: 14.62 on 1 and 32 DF, p-value: 0.0005731

### Anterior coordinate  
ant\_cc\_repl\_lh.lm <- lm(ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_lh)  
ant\_cc\_repl\_rh.lm <- lm(ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_rh)  
summary(ant\_cc\_repl\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -8.9930 -1.7137 -0.0951 1.5330 8.4347   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -5.5889 1.3089 -4.27 0.000163 \*\*\*  
## A\_coord 0.3176 0.1021 3.11 0.003919 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.254 on 32 degrees of freedom  
## Multiple R-squared: 0.232, Adjusted R-squared: 0.208   
## F-statistic: 9.669 on 1 and 32 DF, p-value: 0.003919

summary(ant\_cc\_repl\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_A\_coord ~ A\_coord, data = RAS\_analysis\_all\_repl\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -3.7381 -2.7608 -0.5497 1.1598 6.4819   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -3.8242 1.0936 -3.497 0.001404 \*\*   
## A\_coord 0.4143 0.1030 4.023 0.000328 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.049 on 32 degrees of freedom  
## Multiple R-squared: 0.3359, Adjusted R-squared: 0.3152   
## F-statistic: 16.19 on 1 and 32 DF, p-value: 0.0003281

### Superior coordinate  
sup\_cc\_repl\_lh.lm <- lm(ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_lh)  
sup\_cc\_repl\_rh.lm <- lm(ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_rh)  
summary(sup\_cc\_repl\_lh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_lh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -4.2500 -1.1076 0.3013 1.3649 3.4623   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.16081 1.17565 -0.137 0.892   
## S\_coord 0.80866 0.09025 8.961 3.09e-10 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.105 on 32 degrees of freedom  
## Multiple R-squared: 0.715, Adjusted R-squared: 0.7061   
## F-statistic: 80.29 on 1 and 32 DF, p-value: 3.095e-10

summary(sup\_cc\_repl\_rh.lm) # significant relationship, p<0.001

##   
## Call:  
## lm(formula = ControlC\_S\_coord ~ S\_coord, data = RAS\_analysis\_all\_repl\_rh)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -3.8738 -1.3162 0.4313 1.3505 2.7459   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.12539 1.11549 -1.009 0.321   
## S\_coord 0.86057 0.08402 10.242 1.26e-11 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 1.741 on 32 degrees of freedom  
## Multiple R-squared: 0.7663, Adjusted R-squared: 0.759   
## F-statistic: 104.9 on 1 and 32 DF, p-value: 1.258e-11

The linear regression results in the replication sample confirm those in the discovery sample. Once more, the mean RAS coordinate of the *ifrms* is predictive of the respective RAS coordinate of both control network B and control network C in both hemispheres. See Figure 5d and 5e, as well as Tables 4 and 5, for reference.

#### FDR adjustment for LMs

# Adjust p-values for multiple comparisons  
  
lg\_p\_values <- c(0.000638, 0.0006382, # right, lh CCNb  
 0.00703, 0.007029, # right, rh CCNb  
 0.00000618, 0.000006184, # anterior, lh CCNb  
 0.000084683827, 0.00008468, # anterior, rh CCNb  
 0.0000000000363, 0.00000000003629, # superior, lh CCNb  
 0.0000000000291, 0.00000000002915, # superior, rh CCNb  
   
 0.0000138, 0.00001377, # right, lh CCNc  
 0.00162, 0.001617, # right, rh CCNc  
 0.000475, 0.0004753, # anterior, lh CCNc  
 0.00183, 0.001829, # anterior, rh CCNc  
 0.000000000376, 0.0000000003764, # superior, lh CCNc  
 0.000000000071, 0.000000000071, # superior, rh CCNc  
   
   
 0.000024, 0.00002401, # right, lh CCNb  
 0.00662, 0.006616, # right, rh CCNb  
 0.000811, 0.0008115, # anterior, lh CCNb  
 0.00582, 0.005817, # anterior, rh CCNb  
 0.00000000228, 0.000000002278, # superior, lh CCNb  
 0.0000000000484, 0.00000000004838, # superior, rh CCNb  
   
 0.00000103, 0.000001032, # right, lh CCNc  
 0.000573, 0.0005731, # right, rh CCNc  
 0.003919, 0.003919, # right, lh CCNc  
 0.000328, 0.0003281, # right, rh CCNc  
 0.000000000309, 0.0000000003095, # superior, lh CCNb  
 0.0000000000126, 0.00000000001258 # superior, rh CCNb  
)  
  
p.adjust(p = lg\_p\_values,  
 method = "fdr")

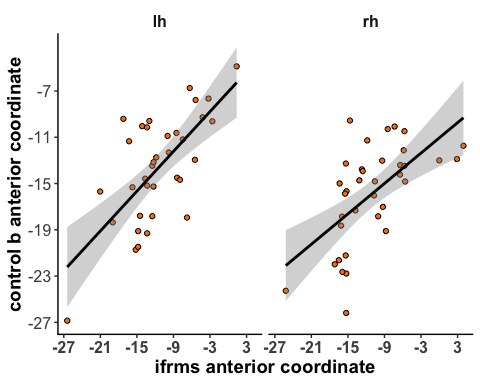
## [1] 9.009882e-04 9.009882e-04 7.030000e-03 7.030000e-03 1.484160e-05  
## [6] 1.484160e-05 1.563394e-04 1.563394e-04 2.904000e-10 2.904000e-10  
## [11] 2.904000e-10 2.904000e-10 3.010909e-05 3.010909e-05 2.046316e-03  
## [16] 2.046316e-03 7.604800e-04 7.604800e-04 2.196000e-03 2.196000e-03  
## [21] 1.290514e-09 1.290514e-09 3.408000e-10 3.408000e-10 4.802000e-05  
## [26] 4.802000e-05 6.907826e-03 6.907826e-03 1.082000e-03 1.082000e-03  
## [31] 6.349091e-03 6.349091e-03 6.840000e-09 6.840000e-09 2.904000e-10  
## [36] 2.904000e-10 2.752000e-06 2.752000e-06 8.596500e-04 8.596500e-04  
## [41] 4.478857e-03 4.478857e-03 5.624571e-04 5.624571e-04 1.238000e-09  
## [46] 1.238000e-09 2.904000e-10 2.904000e-10

All linear model results remain significant after FDR correction.

#### Figure 5b and 5d: Locational coupling between the *ifrms* and control b network

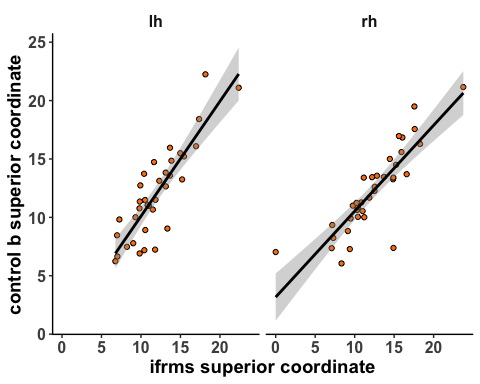
# Discovery Sample  
  
## Figure 5b (left): in left and right hemisphere   
  
### Plot   
#### ControlB\_A\_coord ~ A\_coord   
Ant\_CB\_disc.plot <- ggplot(RAS\_analysis\_all\_disc, aes(x = A\_coord, y = ControlB\_A\_coord)) +  
 geom\_jitter(shape = 21, fill = '#ff7f00') +   
 geom\_smooth(method = "lm", color = "black") + facet\_grid(~ hemi) +  
 labs(x = "ifrms anterior coordinate",  
 y = "control b anterior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 guides(fill = F, color = F) +   
 scale\_x\_continuous(breaks = seq(-27, 4, 6)) +   
 scale\_y\_continuous(breaks = seq(-27, -5, 4))  
Ant\_CB\_disc.plot

## `geom\_smooth()` using formula 'y ~ x'



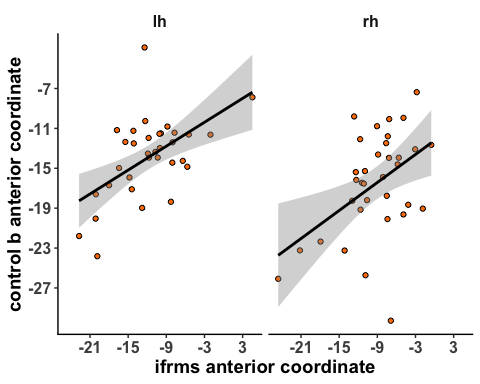
# ggplot2::ggsave(filename = "Ant\_CB\_disc\_plot.png",  
# plot = Ant\_CB\_disc.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")  
  
  
## Figure 5b (right): left and right hemisphere   
  
### Plot   
#### ControlB\_S\_coord ~ S\_coord  
Sup\_CB\_disc.plot <- ggplot(RAS\_analysis\_all\_disc, aes(x = S\_coord, y = ControlB\_S\_coord)) +   
 geom\_jitter(fill = '#ff7f00', shape = 21) +   
 geom\_smooth(method = "lm", color = "black") +   
 guides(fill = F, color = F) +   
 facet\_grid(~ hemi) +  
 scale\_color\_manual(limit = c("with\_3", "without\_3"),   
 values = c("#377eb8", "#e41a1c")) +  
 labs(x = "ifrms superior coordinate",  
 y = "control b superior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"))   
Sup\_CB\_disc.plot

## `geom\_smooth()` using formula 'y ~ x'



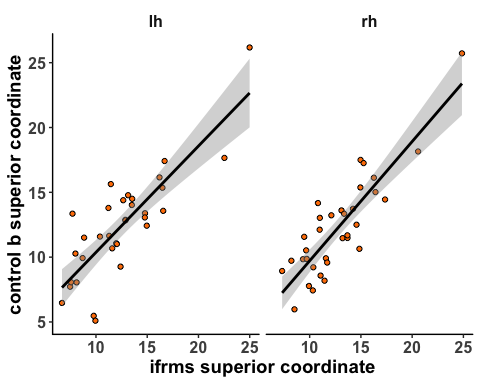
# ggplot2::ggsave(filename = "Sup\_CB\_disc\_plot.png",  
# plot = Sup\_CB\_disc.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")  
  
  
# Replication sample  
  
## Figure 5c (left): left and right hemisphere  
  
### Plot   
#### ControlB\_A\_coord ~ A\_coord  
Ant\_CB\_repl.plot <- ggplot(RAS\_analysis\_all\_repl,  
 aes(x = A\_coord, y = ControlB\_A\_coord)) +   
 geom\_jitter(shape = 21, fill = '#ff7f00') +   
 geom\_smooth(method = "lm", color = "black") +   
 facet\_grid(~ hemi) +  
 labs(x = "ifrms anterior coordinate",  
 y = "control b anterior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 guides(fill = F, color = F) +   
 scale\_x\_continuous(breaks = seq(-27, 4, 6)) +   
 scale\_y\_continuous(breaks = seq(-27, -5, 4))  
Ant\_CB\_repl.plot

## `geom\_smooth()` using formula 'y ~ x'



# ggplot2::ggsave(filename = "Ant\_CB\_repl\_plot.png",  
# plot = Ant\_CB\_repl.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")   
  
  
## Figure 5d (right): left and right hemisphere   
  
### Plot   
#### ControlB\_S\_coord ~ S\_coord  
Sup\_CB\_repl.plot <- ggplot(RAS\_analysis\_all\_repl,  
 aes(x = S\_coord, y = ControlB\_S\_coord)) +   
 geom\_jitter(fill = '#ff7f00', shape = 21) +   
 geom\_smooth(method = "lm", color = "black") +   
 guides(fill = F, color = F) +   
 facet\_grid(~ hemi) +  
 scale\_color\_manual(limit = c("with\_3", "without\_3"),   
 values = c("#377eb8", "#e41a1c")) +  
 labs(x = "ifrms superior coordinate",  
 y = "control b superior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"))   
Sup\_CB\_repl.plot

## `geom\_smooth()` using formula 'y ~ x'

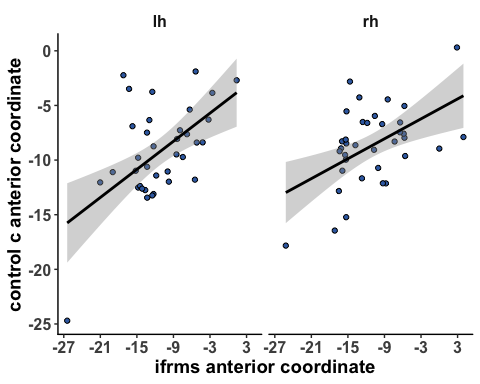


# ggplot2::ggsave(filename = "Sup\_CB\_repl\_plot.png",  
# plot = Sup\_CB\_repl.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")

#### Figure 5c and 5e: Locational coupling between the *ifrms* and control c network

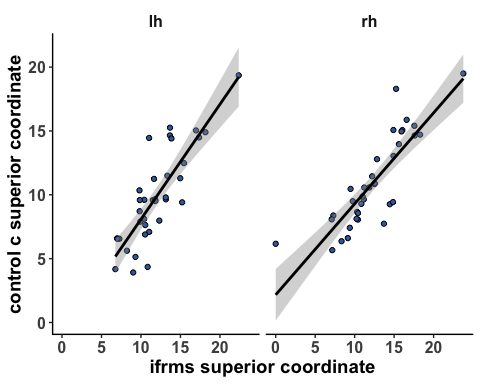
# Discovery Sample  
  
## Figure 5c (left): left and right hemisphere  
  
### Plot   
#### ControlC\_A\_coord ~ A\_coord  
Ant\_CC\_disc.plot <- ggplot(RAS\_analysis\_all\_disc, aes(x = A\_coord, y = ControlC\_A\_coord)) +   
 geom\_jitter(fill = '#386cb0', shape = 21) +   
 geom\_smooth(method = "lm", color = "black") + facet\_grid(~ hemi) +  
scale\_color\_manual(limit = c("with\_3", "without\_3"),   
 values = c("#377eb8", "#e41a1c")) +  
 labs(x = "ifrms anterior coordinate",  
 y = "control c anterior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 guides(fill = F, color = F) +   
 scale\_x\_continuous(breaks = seq(-27, 4, 6)) +   
 scale\_y\_continuous(breaks = seq(-30, 30, 5))  
Ant\_CC\_disc.plot

## `geom\_smooth()` using formula 'y ~ x'



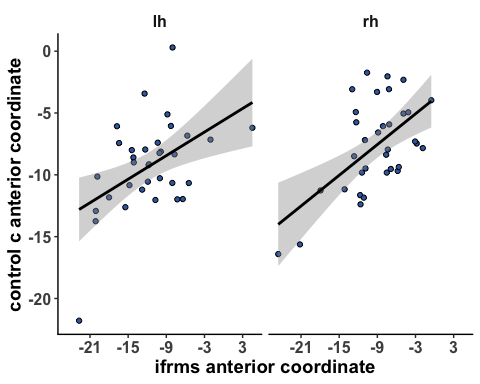
# ggplot2::ggsave(filename = "Ant\_CC\_disc\_plot.png",  
# plot = Ant\_CC\_disc.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")   
  
  
## Figure 5c (right): left and right hemisphere   
  
### Plot   
#### ControlC\_S\_coord ~ S\_coord  
Sup\_CC\_disc.plot <- ggplot(RAS\_analysis\_all\_disc, aes(x = S\_coord, y = ControlC\_S\_coord)) +   
 geom\_jitter(fill = '#386cb0', shape = 21) +   
 geom\_smooth(method = "lm", color = "black") +   
 guides(fill = F, color = F) +   
 facet\_grid(~ hemi) +  
 scale\_color\_manual(limit = c("with\_3", "without\_3"),   
 values = c("#377eb8", "#e41a1c")) +  
 labs(x = "ifrms superior coordinate",  
 y = "control c superior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"))   
Sup\_CC\_disc.plot

## `geom\_smooth()` using formula 'y ~ x'



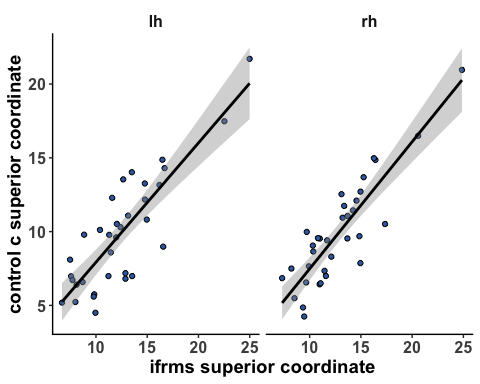
# ggplot2::ggsave(filename = "Sup\_CC\_disc\_plot.png",  
# plot = Sup\_CC\_disc.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")   
  
  
# Replication Sample   
  
## Figure 5e (left): left and right hemisphere   
  
### Plot   
#### ControlC\_A\_coord ~ A\_coord  
Ant\_CC\_repl.plot <- ggplot(RAS\_analysis\_all\_repl, aes(x = A\_coord, y = ControlC\_A\_coord)) +   
 geom\_jitter(fill = '#386cb0', shape = 21) +   
 geom\_smooth(method = "lm", color = "black") +   
 facet\_grid(~ hemi) +  
scale\_color\_manual(limit = c("with\_3", "without\_3"),   
 values = c("#377eb8", "#e41a1c")) +  
 labs(x = "ifrms anterior coordinate",  
 y = "control c anterior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 guides(fill = F, color = F) +   
 scale\_x\_continuous(breaks = seq(-27, 4, 6)) +   
 scale\_y\_continuous(breaks = seq(-30, 30, 5))  
Ant\_CC\_repl.plot

## `geom\_smooth()` using formula 'y ~ x'



# ggplot2::ggsave(filename = "Ant\_CC\_repl\_plot.png",  
# plot = Ant\_CC\_repl.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")   
  
  
## Figure 5e (right): left and right hemisphere  
  
### Plot   
#### ControlC\_S\_coord ~ S\_coord  
Sup\_CC\_repl.plot <- ggplot(RAS\_analysis\_all\_repl, aes(x = S\_coord, y = ControlC\_S\_coord)) +  
 geom\_jitter(fill = '#386cb0', shape = 21) +   
 geom\_smooth(method = "lm", color = "black") +   
 guides(fill = F, color = F) +   
 facet\_grid(~ hemi) +  
 scale\_color\_manual(limit = c("with\_3", "without\_3"),   
 values = c("#377eb8", "#e41a1c")) +  
 labs(x = "ifrms superior coordinate",  
 y = "control c superior coordinate") +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=14, face = "bold"),  
 axis.title.y = element\_text(size=14, face = "bold"),  
 axis.text.x = element\_text(size = 12, face = "bold"),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 strip.background = element\_blank(),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"))   
Sup\_CC\_repl.plot

## `geom\_smooth()` using formula 'y ~ x'



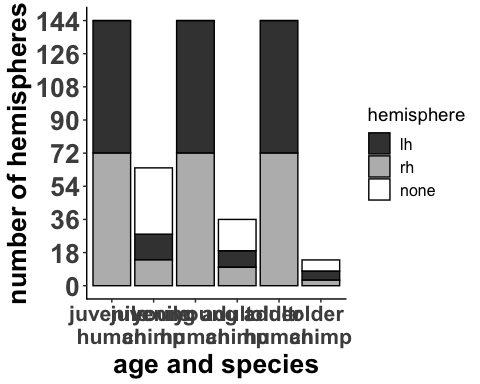
# ggplot2::ggsave(filename = "Sup\_CC\_repl\_plot.png",  
# plot = Sup\_CC\_repl.plot,  
# device = "png",  
# width = 8,  
# height = 4,   
# units = "in",  
# dpi = "retina")

# Comparative and Developmental Analyses

### Q1: Can the ifrms be identified across the lifespan in both humans and chimpanzees?

#### Figure 6b: Presence comparison

# Dataset  
perc2 <- read.csv("~/Desktop/RMD\_csvs/percent\_present\_age.csv")  
  
# Features for the plot  
perc2$age\_species <- factor(perc2$age\_species,   
 levels = c("young\_human", "young\_chimp",   
 "young\_adult\_human", "young\_adult\_chimp",   
 "older\_adult\_human", "older\_adult\_chimp"))   
  
per2\_total <- perc2 %>% subset(hemisphere == "total")  
perc2\_other <- perc2 %>% subset(hemisphere %in% c("lh", "rh", "none"))  
perc2\_other$hemisphere <- factor(perc2\_other$hemisphere, levels = c("none", "lh", "rh"))  
  
xticks\_label <- c("juvenile \nhuman", "juvenile \nchimp",   
 "young adult \nhuman", "young adult \nchimp",   
 "older \nhuman", "older \nchimp")  
  
# Plot  
compdev\_count.plot <- ggplot(perc2\_other, aes(x = age\_species)) +  
 geom\_col(data = perc2\_other, aes(y = Amount, fill = hemisphere),  
 color = 'black') +   
 scale\_y\_continuous(name = "number of hemispheres", seq(0,144,18), limits = c(0,144)) +  
 labs(x = "age and species") +   
 scale\_fill\_manual(breaks = c("lh", "rh", "none"),  
 values = c("#404040", "#bababa", "#ffffff")  
 ) +   
 scale\_x\_discrete(breaks=c("young\_human", "young\_chimp",   
 "young\_adult\_human", "young\_adult\_chimp",   
 "older\_adult\_human", "older\_adult\_chimp"),  
 labels=xticks\_label) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 16, face = "bold"),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +   
 guides()   
compdev\_count.plot



# ggplot2::ggsave(filename = "compdev\_count\_plot.png",  
# plot = compdev\_count.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

In addition to being present every hemisphere in the young adult human sample, the *ifrms* is present in every hemisphere in our juvenile and healthy older adult human samples. However, the *ifrms* is less consistent in chimpanzees, being present in about half of the hemispheres included in our sample.

### Q2: Is the depth (normalized) of the ifrms different across the lifepsan and between species?

* 3-way (group, species, hemi) ANOVA
* group: juvenile, young adult, older adult
* species: human, chimpanzee
* hemi: lh, rh

#### Statistical analyses

# Dataset - used for all comp/dev morphological analyses  
ifrms\_compdev\_morphology <- read.csv("~/Desktop/RMD\_csvs/ifrms\_compdev\_morphology.csv")  
  
# ANOVA  
comp\_norm\_depth.aov <- aov(depth\_pct\_max ~ hemi \* group \* species, data = ifrms\_compdev\_morphology)  
summary(comp\_norm\_depth.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.0740 0.07398 15.430 9.83e-05 \*\*\*  
## group 2 0.1024 0.05118 10.675 2.92e-05 \*\*\*  
## species 1 0.0329 0.03286 6.854 0.00912 \*\*   
## hemi:group 2 0.0067 0.00334 0.697 0.49839   
## hemi:species 1 0.0006 0.00064 0.134 0.71444   
## group:species 2 0.0088 0.00439 0.915 0.40110   
## hemi:group:species 2 0.0006 0.00028 0.058 0.94352   
## Residuals 475 2.2772 0.00479   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(comp\_norm\_depth.aov)

## term etasq  
## 1 hemi 0.030  
## 2 group 0.041  
## 3 species 0.013  
## 4 hemi:group 0.003  
## 5 hemi:species 0.000  
## 6 group:species 0.004  
## 7 hemi:group:species 0.000

# Main effect of hemisphere  
ifrms\_compdev\_morphology %>% group\_by(hemi) %>% summarise(mean = mean(depth\_pct\_max))

## # A tibble: 2 x 2  
## hemi mean  
## \* <chr> <dbl>  
## 1 lh 0.116   
## 2 rh 0.0911

# Main effect of group  
ifrms\_compdev\_morphology %>% group\_by(group) %>% summarise(mean = mean(depth\_pct\_max))

## # A tibble: 3 x 2  
## group mean  
## \* <chr> <dbl>  
## 1 juvenile 0.105   
## 2 older-adult 0.122   
## 3 young-adult 0.0854

# Main effect of group  
ifrms\_compdev\_morphology %>% group\_by(species) %>% summarise(mean = mean(depth\_pct\_max))

## # A tibble: 2 x 2  
## species mean  
## \* <chr> <dbl>  
## 1 chimpanzee 0.0779  
## 2 human 0.107

There are three main effects - for each independent variable. First, on hemisphere, the *ifrms* is generally deeper in the left hemisphere. Second, on age group, the *ifrms* is generally deepest in juveniles, slightly shallower in older adults, and shallowest in young adults. Third, the *ifrms* is deeper in humans than chimpanzees. No interaction effects are present.

#### Figure 6d: Normalized depth comparison

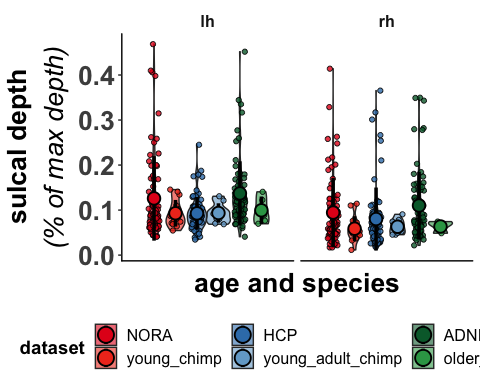
# Organize factors in order  
ifrms\_compdev\_morphology$dataset <- factor(ifrms\_compdev\_morphology$dataset,   
 levels = c("NORA", "young\_chimp",   
 "HCP", "young\_adult\_chimp",   
 "ADNI", "older\_adult\_chimp"))  
  
# Means for plot  
comp\_depth\_avg <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(depth\_pct\_max = mean(depth\_pct\_max))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

comp\_depth\_sd <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(sd = sd(depth\_pct\_max))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

comp\_depth\_stats <- merge(comp\_depth\_avg, comp\_depth\_sd, by = c("label", "dataset", "hemi"))  
  
# Features for plot  
comp\_depth\_title <- expression(atop(bold("sulcal depth"), paste(italic("(% of max depth)"))))  
comp\_norm\_x <- expression(paste(bold("age and species")))  
  
# Plot  
comp\_depth.plot <- ggplot(data = ifrms\_compdev\_morphology, aes(x = label, y = depth\_pct\_max)) +  
 geom\_violin(aes(x = label, y = depth\_pct\_max, fill = dataset), alpha = .6, position = dodge, width = 1) +   
 geom\_jitter(aes(x = label, y = depth\_pct\_max, fill = dataset), alpha = .8, shape = 21, color = 'black',  
 position=position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = comp\_depth\_stats,   
 aes(label, depth\_pct\_max, ymin=depth\_pct\_max-sd, ymax=depth\_pct\_max+sd, fill = dataset),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 labs(x = comp\_norm\_x,  
 y = comp\_depth\_title) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 0, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",   
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 axis.ticks.x = element\_blank(),   
 strip.background = element\_blank()) +   
 scale\_color\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#41b6c4", "#006837", "#2ca25f")) +   
 scale\_fill\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#74a9cf", "#006837", "#31a354")) +  
   
 guides(alpha = F) +   
 facet\_wrap(~hemi)  
comp\_depth.plot



# ggplot2::ggsave(filename = "comp\_depth\_plot.png",  
# plot = comp\_depth.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

### Q3: Does the cortical thickness (normalized) of the ifrms differ across the lifespan and between species?

* 3-way (group, species, hemi) ANOVA
* group: juvenile, young adult, older adult
* species: human, chimpanzee
* hemi: lh, rh

#### Statistical analyses

# ANOVA  
comp\_norm\_thick.aov<- aov(label\_mean\_thickness\_pct\_max ~ hemi \* group \* species,   
 data = ifrms\_compdev\_morphology)  
summary(comp\_norm\_thick.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.0055 0.0055 0.860 0.35420   
## group 2 1.7324 0.8662 135.373 < 2e-16 \*\*\*  
## species 1 0.4069 0.4069 63.586 1.15e-14 \*\*\*  
## hemi:group 2 0.0072 0.0036 0.565 0.56900   
## hemi:species 1 0.0447 0.0447 6.981 0.00851 \*\*   
## group:species 2 0.0244 0.0122 1.910 0.14925   
## hemi:group:species 2 0.0128 0.0064 1.004 0.36726   
## Residuals 475 3.0393 0.0064   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(comp\_norm\_thick.aov)

## term etasq  
## 1 hemi 0.001  
## 2 group 0.329  
## 3 species 0.077  
## 4 hemi:group 0.001  
## 5 hemi:species 0.008  
## 6 group:species 0.005  
## 7 hemi:group:species 0.002

# Main effect of group  
ifrms\_compdev\_morphology %>% group\_by(group) %>% summarise(mean = mean(label\_mean\_thickness\_pct\_max))

## # A tibble: 3 x 2  
## group mean  
## \* <chr> <dbl>  
## 1 juvenile 0.734  
## 2 older-adult 0.588  
## 3 young-adult 0.677

# Main effect of species  
ifrms\_compdev\_morphology %>% group\_by(species) %>% summarise(mean = mean(label\_mean\_thickness\_pct\_max))

## # A tibble: 2 x 2  
## species mean  
## \* <chr> <dbl>  
## 1 chimpanzee 0.613  
## 2 human 0.677

# Interaction effect between hemi and species  
ifrms\_compdev\_morphology %>% group\_by(hemi, species) %>% summarise(mean = mean(label\_mean\_thickness\_pct\_max))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

## # A tibble: 4 x 3  
## # Groups: hemi [2]  
## hemi species mean  
## <chr> <chr> <dbl>  
## 1 lh chimpanzee 0.582  
## 2 lh human 0.677  
## 3 rh chimpanzee 0.645  
## 4 rh human 0.676

There is first a main effect of group, where the *ifrms* is thins from the juvenile to healthy older adult age group. Second, there is a main effect of species. The *ifrms* is thicker in humans than chimpanzees. Finally, there is an interaction between hemi and species such that, in chimpanzees, the *ifrms* is thicker in the right hemisphere; however, there is no hemispheric difference present in humans.

#### Figure 6c: Normalized thickness comparison

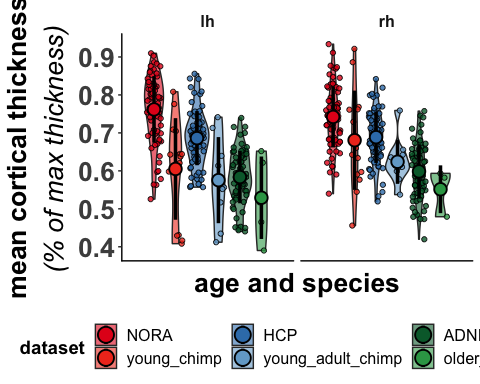
# Means for plot  
norm\_ct\_avg <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(label\_mean\_thickness\_pct\_max = mean(label\_mean\_thickness\_pct\_max))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

norm\_ct\_sd <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(sd = sd(label\_mean\_thickness\_pct\_max))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

norm\_ct\_stats <- merge(norm\_ct\_avg, norm\_ct\_sd, by = c("label", "dataset", "hemi"))  
  
# Features for plot  
comp\_norm\_x <- expression(paste(bold("age and species")))  
comp\_norm\_title <- expression(atop(bold("mean cortical thickness"), paste(italic("(% of max thickness)"))))  
  
# Plot  
comp\_ct.plot <- ggplot(data = ifrms\_compdev\_morphology, aes(x = label, y = label\_mean\_thickness\_pct\_max)) +  
 geom\_violin(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = label\_mean\_thickness\_pct\_max, fill = dataset),   
 alpha = .6, position = dodge, width = 1) +   
 geom\_jitter(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = label\_mean\_thickness\_pct\_max, fill = dataset),   
 color = 'black', alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .4, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = norm\_ct\_stats,   
 aes(label, label\_mean\_thickness\_pct\_max,   
 ymin=label\_mean\_thickness\_pct\_max-sd,   
 ymax=label\_mean\_thickness\_pct\_max+sd, fill = dataset),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 labs(x = comp\_norm\_x,  
 y = comp\_norm\_title) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 0, face = "bold"),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 axis.ticks.x = element\_blank(),   
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.position = "bottom",  
 strip.background = element\_blank()) +   
 scale\_color\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#41b6c4", "#006837", "#2ca25f")) +   
 scale\_fill\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#74a9cf", "#006837", "#31a354")) +  
 guides(color = F, alpha = F) +   
 scale\_y\_continuous(breaks=seq(0,1,.1)) +  
 facet\_wrap(~hemi)  
comp\_ct.plot

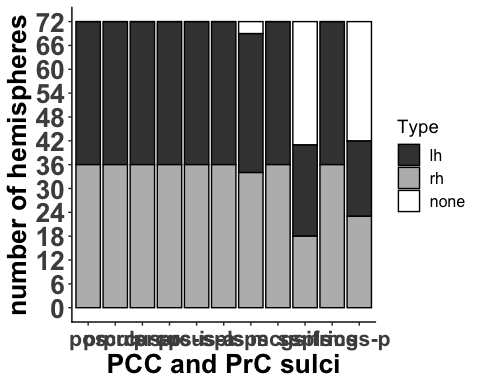


# ggplot2::ggsave(filename = "comp\_ct\_plot.png",  
# plot = comp\_ct.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

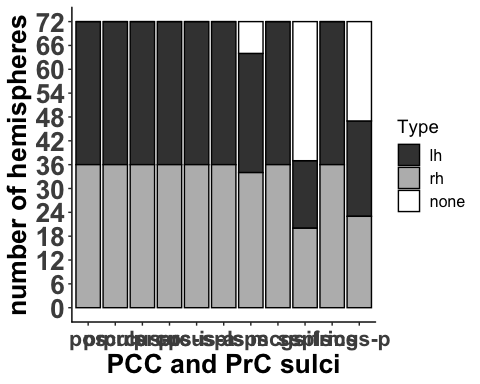
# Supplementary Analyses and Figures

## Supplementary Figure 1a, 1c: Incidence rates of all 11 sulci

# Discovery dataset plot   
HCP\_count\_disc\_11.plot <- ggplot(HCP\_count\_disc, aes(x = Sulcus)) +  
 geom\_col(data = HCP\_count\_disc, aes(y = Amount, fill = Type), color = 'black') +   
 xlim("pos", "prculs", "prcus-p", "prcus-i", "prcus-a", "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p") +  
 scale\_y\_continuous(name = "number of hemispheres", seq(0,72,6), limits = c(0,72)) +  
 labs(x = "PCC and PrC sulci",   
 y = "# of hemispheres") +   
 scale\_fill\_manual(breaks = c("lh", "rh", "none"),  
 values = c("#404040", "#bababa", "#ffffff")  
 ) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size = 20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size = 20, face = "bold"),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +   
 guides()   
HCP\_count\_disc\_11.plot



# ggplot2::ggsave(filename = "sulc\_count\_disc\_11.png",  
# plot = HCP\_count\_disc\_11.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")  
  
  
# Replication dataset plot  
HCP\_count\_rep\_11.plot <- ggplot(HCP\_count\_rep, aes(x = Sulcus)) +  
 geom\_col(data = HCP\_count\_rep, aes(y = Amount, fill = Type), color = 'black') +   
 xlim("pos", "prculs", "prcus-p", "prcus-i", "prcus-a", "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p") +  
 scale\_y\_continuous(name = "number of hemispheres", seq(0,72,6), limits = c(0,72)) +  
 labs(x = "PCC and PrC sulci",   
 y = "# of hemispheres") +   
 scale\_fill\_manual(breaks = c("lh", "rh", "none"),  
 values = c("#404040", "#bababa", "#ffffff")  
 ) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +   
 guides()   
HCP\_count\_rep\_11.plot



# ggplot2::ggsave(filename = "sulc\_count\_rep\_11.png",  
# plot = HCP\_count\_rep\_11.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

## Supplemental Figure X: evaluation of the spherical deep convolutional neural network & training of the PMC sulci’s location

# Features for plot  
pmc\_nn\_predicts$sulci <- factor(pmc\_nn\_predicts$sulci, levels = c("pos", "prculs", "spls", "mcgs", "prcus-p", "prcus-i", "prcus-a", "ifrms"))  
pmc\_nn\_predicts$type <- factor(pmc\_nn\_predicts$type, levels = c("prominent sulci", "less prominent sulci"))  
  
# Means for plot  
pmc\_pred\_avg <- pmc\_nn\_predicts %>%   
 group\_by(sulci, type) %>%   
 summarise(dice = mean(dice))

## `summarise()` has grouped output by 'sulci'. You can override using the `.groups` argument.

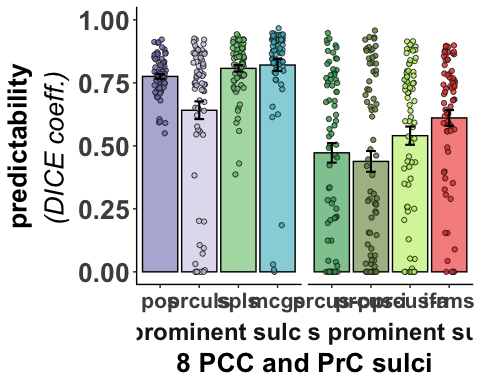
pmc\_pred\_sd <- pmc\_nn\_predicts %>%   
 group\_by(sulci, type) %>%   
 summarise(n=n(), sd=sd(dice), se=sd/sqrt(n))

## `summarise()` has grouped output by 'sulci'. You can override using the `.groups` argument.

pmc\_pred\_stats <- merge(pmc\_pred\_avg, pmc\_pred\_sd, by = c("sulci", "type"))  
  
# Plot  
dice\_y <- expression(atop(bold("predictability"), paste(italic("(DICE coeff.)"))))  
  
cnn\_all.plot <- ggplot() +  
 geom\_col(data = pmc\_pred\_stats, aes(x = sulci, y = dice, fill = sulci), color = 'black',  
 alpha = .6, position = dodge) +  
 geom\_jitter(data = pmc\_nn\_predicts,   
 aes(x = sulci, y = dice, fill = sulci, color = sulci),   
 alpha = .8, shape = 21,  
 position=  
 position\_jitterdodge(jitter.width = 1.5, dodge.width = .9, jitter.height = 0)) +  
 geom\_errorbar(data = pmc\_pred\_stats, aes(sulci, ymin=dice-se, ymax=dice+se),  
 width = .25, size = .75) +  
 scale\_x\_discrete(breaks = c("pos", "prculs", "spls", "mcgs", "prcus-p", "prcus-i", "prcus-a", "ifrms"),   
 labels = c("pos", "prculs", "spls", "mcgs", "prcus-p", "prcus-i", "prcus-a",  
 "ifrms")) +  
scale\_y\_continuous(breaks=seq(0,1,.2)) + ylim(0,1) +  
scale\_color\_manual(breaks =   
 c("pos", "prculs", "prcus-p", "prcus-i",   
 "prcus-a", "spls", "mcgs", "ifrms"),  
 values = c( "#252525","#252525", "#252525","#252525",  
 "#252525","#252525","#252525", "#252525")) +   
 scale\_fill\_manual(breaks = c("pos", "prculs", "prcus-p", "prcus-i",   
 "prcus-a", "spls", "mcgs", "ifrms"),  
 values = c("#807dba",   
 "#cbc9e2",   
 "#31a354",   
 "darkolivegreen4",   
 "darkolivegreen2",   
 "#74c476",   
 "#41b6c4",   
 "#ef3b2c")) +   
 labs(x = "8 PCC and PrC sulci",  
 y = dice\_y) +  
 guides(fill = F, color = F, alpha = F) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y.right = element\_text(size=20, face = "bold", vjust = 1),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 18, face = "bold"),  
 strip.background = element\_blank(),  
 strip.placement = "outside",  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 facet\_grid(. ~ type,   
 scales = "free\_x", space='free', switch="both")

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

cnn\_all.plot



# ggplot2::ggsave(filename = "cnn\_all\_plot.png",  
# plot = cnn\_all.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

## Supplementary Figure 1b, 1d: Depth of PCC and PrC sulci

### Statistics

* Focusing on the three *prcus* (since this is the first study to consistently identify three in-vivo).

#### Discovery

# Dataset - all  
HCP\_all\_sulci\_depth <- read.csv("~/Desktop/RMD\_csvs/HCP\_all\_sulci\_depth.csv")  
  
# Discovery dataset  
all\_depth\_2\_disc <- HCP\_all\_sulci\_depth %>% subset(dataset == "HCP\_discovery")  
  
# ANOVA  
all\_depth\_disc.aov <- aov(sulcal\_depth\_mm ~ hemi \* label, all\_depth\_2\_disc)  
summary(all\_depth\_disc.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 27 27.0 3.674 0.0557 .   
## label 10 19750 1975.0 268.579 <2e-16 \*\*\*  
## hemi:label 10 66 6.6 0.896 0.5363   
## Residuals 706 5192 7.4   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(all\_depth\_disc.aov)

## term etasq  
## 1 hemi 0.001  
## 2 label 0.789  
## 3 hemi:label 0.003

# Post hoc tests  
disc\_all\_depth.m1 <- emmeans::emmeans(all\_depth\_disc.aov,'label')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_all\_depth.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## (icgs-p) - ifrms 0.2417 0.528 706 0.458 1.0000   
## (icgs-p) - mcgs -12.2413 0.528 706 -23.183 <.0001   
## (icgs-p) - pos -17.4260 0.528 706 -33.002 <.0001   
## (icgs-p) - prculs -11.1362 0.528 706 -21.090 <.0001   
## (icgs-p) - (prcus-a) -7.1443 0.528 706 -13.530 <.0001   
## (icgs-p) - (prcus-i) -7.0558 0.528 706 -13.362 <.0001   
## (icgs-p) - (prcus-p) -4.9040 0.528 706 -9.287 <.0001   
## (icgs-p) - spls -9.3530 0.528 706 -17.713 <.0001   
## (icgs-p) - sps -7.9232 0.532 706 -14.886 <.0001   
## (icgs-p) - sspls 0.5647 0.599 706 0.943 0.9974   
## ifrms - mcgs -12.4830 0.452 706 -27.620 <.0001   
## ifrms - pos -17.6677 0.452 706 -39.091 <.0001   
## ifrms - prculs -11.3779 0.452 706 -25.175 <.0001   
## ifrms - (prcus-a) -7.3860 0.452 706 -16.342 <.0001   
## ifrms - (prcus-i) -7.2975 0.452 706 -16.146 <.0001   
## ifrms - (prcus-p) -5.1457 0.452 706 -11.385 <.0001   
## ifrms - spls -9.5947 0.452 706 -21.229 <.0001   
## ifrms - sps -8.1649 0.457 706 -17.871 <.0001   
## ifrms - sspls 0.3230 0.533 706 0.606 0.9999   
## mcgs - pos -5.1847 0.452 706 -11.472 <.0001   
## mcgs - prculs 1.1052 0.452 706 2.445 0.3393   
## mcgs - (prcus-a) 5.0970 0.452 706 11.278 <.0001   
## mcgs - (prcus-i) 5.1855 0.452 706 11.473 <.0001   
## mcgs - (prcus-p) 7.3373 0.452 706 16.234 <.0001   
## mcgs - spls 2.8883 0.452 706 6.391 <.0001   
## mcgs - sps 4.3181 0.457 706 9.452 <.0001   
## mcgs - sspls 12.8060 0.533 706 24.022 <.0001   
## pos - prculs 6.2899 0.452 706 13.917 <.0001   
## pos - (prcus-a) 10.2817 0.452 706 22.749 <.0001   
## pos - (prcus-i) 10.3702 0.452 706 22.945 <.0001   
## pos - (prcus-p) 12.5220 0.452 706 27.706 <.0001   
## pos - spls 8.0730 0.452 706 17.862 <.0001   
## pos - sps 9.5028 0.457 706 20.800 <.0001   
## pos - sspls 17.9907 0.533 706 33.747 <.0001   
## prculs - (prcus-a) 3.9918 0.452 706 8.832 <.0001   
## prculs - (prcus-i) 4.0803 0.452 706 9.028 <.0001   
## prculs - (prcus-p) 6.2322 0.452 706 13.789 <.0001   
## prculs - spls 1.7831 0.452 706 3.945 0.0042   
## prculs - sps 3.2130 0.457 706 7.033 <.0001   
## prculs - sspls 11.7009 0.533 706 21.949 <.0001   
## (prcus-a) - (prcus-i) 0.0885 0.452 706 0.196 1.0000   
## (prcus-a) - (prcus-p) 2.2403 0.452 706 4.957 <.0001   
## (prcus-a) - spls -2.2087 0.452 706 -4.887 0.0001   
## (prcus-a) - sps -0.7789 0.457 706 -1.705 0.8330   
## (prcus-a) - sspls 7.7090 0.533 706 14.461 <.0001   
## (prcus-i) - (prcus-p) 2.1518 0.452 706 4.761 0.0001   
## (prcus-i) - spls -2.2972 0.452 706 -5.083 <.0001   
## (prcus-i) - sps -0.8674 0.457 706 -1.898 0.7183   
## (prcus-i) - sspls 7.6205 0.533 706 14.295 <.0001   
## (prcus-p) - spls -4.4490 0.452 706 -9.844 <.0001   
## (prcus-p) - sps -3.0192 0.457 706 -6.608 <.0001   
## (prcus-p) - sspls 5.4687 0.533 706 10.258 <.0001   
## spls - sps 1.4298 0.457 706 3.130 0.0670   
## spls - sspls 9.9177 0.533 706 18.604 <.0001   
## sps - sspls 8.4879 0.537 706 15.798 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 11 estimates

disc\_all\_depth.m2 <- emmeans::emmeans(all\_depth\_disc.aov, 'hemi')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(disc\_all\_depth.m2, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## lh - rh 0.433 0.206 706 2.101 0.0360   
##   
## Results are averaged over the levels of: label

#### Replication

# Replication sample   
all\_depth\_2\_rep <- HCP\_all\_sulci\_depth %>% subset(dataset == "HCP\_replication")  
  
# ANOVA  
all\_depth\_rep.aov <- aov(sulcal\_depth\_mm ~ hemi \* label, all\_depth\_2\_rep)  
summary(all\_depth\_rep.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 127 126.5 19.828 9.86e-06 \*\*\*  
## label 10 19329 1932.9 302.944 < 2e-16 \*\*\*  
## hemi:label 10 139 13.9 2.172 0.0178 \*   
## Residuals 702 4479 6.4   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(all\_depth\_rep.aov)

## term etasq  
## 1 hemi 0.005  
## 2 label 0.803  
## 3 hemi:label 0.006

# Post hoc tests  
rep\_all\_depth.m1 <- emmeans::emmeans(all\_depth\_rep.aov,'label')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_all\_depth.m1, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## (icgs-p) - ifrms -0.1461 0.474 702 -0.308 1.0000   
## (icgs-p) - mcgs -11.9168 0.474 702 -25.154 <.0001   
## (icgs-p) - pos -17.0978 0.474 702 -36.091 <.0001   
## (icgs-p) - prculs -11.8305 0.474 702 -24.972 <.0001   
## (icgs-p) - (prcus-a) -7.1417 0.474 702 -15.075 <.0001   
## (icgs-p) - (prcus-i) -6.9679 0.474 702 -14.708 <.0001   
## (icgs-p) - (prcus-p) -4.4119 0.474 702 -9.313 <.0001   
## (icgs-p) - spls -9.8627 0.474 702 -20.818 <.0001   
## (icgs-p) - sps -9.1701 0.486 702 -18.880 <.0001   
## (icgs-p) - sspls 0.0816 0.556 702 0.147 1.0000   
## ifrms - mcgs -11.7707 0.421 702 -27.959 <.0001   
## ifrms - pos -16.9517 0.421 702 -40.266 <.0001   
## ifrms - prculs -11.6843 0.421 702 -27.754 <.0001   
## ifrms - (prcus-a) -6.9956 0.421 702 -16.617 <.0001   
## ifrms - (prcus-i) -6.8218 0.421 702 -16.204 <.0001   
## ifrms - (prcus-p) -4.2657 0.421 702 -10.133 <.0001   
## ifrms - spls -9.7165 0.421 702 -23.080 <.0001   
## ifrms - sps -9.0239 0.434 702 -20.773 <.0001   
## ifrms - sspls 0.2277 0.512 702 0.445 1.0000   
## mcgs - pos -5.1810 0.421 702 -12.307 <.0001   
## mcgs - prculs 0.0863 0.421 702 0.205 1.0000   
## mcgs - (prcus-a) 4.7751 0.421 702 11.342 <.0001   
## mcgs - (prcus-i) 4.9489 0.421 702 11.755 <.0001   
## mcgs - (prcus-p) 7.5050 0.421 702 17.827 <.0001   
## mcgs - spls 2.0542 0.421 702 4.879 0.0001   
## mcgs - sps 2.7468 0.434 702 6.323 <.0001   
## mcgs - sspls 11.9984 0.512 702 23.432 <.0001   
## pos - prculs 5.2673 0.421 702 12.512 <.0001   
## pos - (prcus-a) 9.9561 0.421 702 23.649 <.0001   
## pos - (prcus-i) 10.1299 0.421 702 24.062 <.0001   
## pos - (prcus-p) 12.6859 0.421 702 30.133 <.0001   
## pos - spls 7.2351 0.421 702 17.186 <.0001   
## pos - sps 7.9277 0.434 702 18.250 <.0001   
## pos - sspls 17.1793 0.512 702 33.550 <.0001   
## prculs - (prcus-a) 4.6887 0.421 702 11.137 <.0001   
## prculs - (prcus-i) 4.8626 0.421 702 11.550 <.0001   
## prculs - (prcus-p) 7.4186 0.421 702 17.622 <.0001   
## prculs - spls 1.9678 0.421 702 4.674 0.0002   
## prculs - sps 2.6604 0.434 702 6.124 <.0001   
## prculs - sspls 11.9120 0.512 702 23.263 <.0001   
## (prcus-a) - (prcus-i) 0.1738 0.421 702 0.413 1.0000   
## (prcus-a) - (prcus-p) 2.7299 0.421 702 6.484 <.0001   
## (prcus-a) - spls -2.7209 0.421 702 -6.463 <.0001   
## (prcus-a) - sps -2.0283 0.434 702 -4.669 0.0002   
## (prcus-a) - sspls 7.2233 0.512 702 14.106 <.0001   
## (prcus-i) - (prcus-p) 2.5560 0.421 702 6.071 <.0001   
## (prcus-i) - spls -2.8947 0.421 702 -6.876 <.0001   
## (prcus-i) - sps -2.2022 0.434 702 -5.069 <.0001   
## (prcus-i) - sspls 7.0495 0.512 702 13.767 <.0001   
## (prcus-p) - spls -5.4508 0.421 702 -12.947 <.0001   
## (prcus-p) - sps -4.7582 0.434 702 -10.953 <.0001   
## (prcus-p) - sspls 4.4934 0.512 702 8.775 <.0001   
## spls - sps 0.6926 0.434 702 1.594 0.8846   
## spls - sspls 9.9442 0.512 702 19.420 <.0001   
## sps - sspls 9.2516 0.523 702 17.685 <.0001   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 11 estimates

rep\_all\_depth.m2 <- emmeans::emmeans(all\_depth\_rep.aov, 'hemi')

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(rep\_all\_depth.m2, method='pairwise')

## contrast estimate SE df t.ratio p.value  
## lh - rh 0.819 0.192 702 4.258 <.0001   
##   
## Results are averaged over the levels of: label

rep\_all\_depth.i1 <- emmeans::emmeans(all\_depth\_rep.aov,'hemi','label')  
emmeans::contrast(rep\_all\_depth.i1, method='pairwise')

## label = icgs-p:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.5951 0.737 702 0.807 0.4198   
##   
## label = ifrms:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.5292 0.595 702 0.889 0.3743   
##   
## label = mcgs:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.4982 0.595 702 2.516 0.0121   
##   
## label = pos:  
## contrast estimate SE df t.ratio p.value  
## lh - rh -1.0761 0.595 702 -1.807 0.0711   
##   
## label = prculs:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.9563 0.595 702 1.606 0.1087   
##   
## label = prcus-a:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 2.4574 0.595 702 4.127 <.0001   
##   
## label = prcus-i:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.0388 0.595 702 0.065 0.9481   
##   
## label = prcus-p:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.0876 0.595 702 1.827 0.0682   
##   
## label = spls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.0397 0.595 702 1.746 0.0812   
##   
## label = sps:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 0.6663 0.633 702 1.053 0.2927   
##   
## label = sspls:  
## contrast estimate SE df t.ratio p.value  
## lh - rh 1.2128 0.833 702 1.455 0.1460

Across both samples, while the *prcus* are deeper than the poster cingulate tertiary sulci, they are the shallowest sulci in precuneus cortex. Among the three *prcus*, *prcus-p* is the shallowest while *prcus-i* and *prcus-a* have comparable depths. In the replication sample there is an interaction effect between label and hemi driven by the *mcgs* and *prcus-a* being significantly deeper in the left hemisphere. See Supplementary Figure 1 and supplementary results.

### Plots

# Discovery dataset   
  
## Means for plot  
all\_depth\_2\_disc\_tert <- all\_depth\_2\_disc %>% subset(label %in% c("sspls", "ifrms", "icgs-p"))  
all\_depth\_tert\_means\_disc <- all\_depth\_2\_disc\_tert %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

all\_depth\_2\_tert\_sd\_disc <- all\_depth\_2\_disc\_tert %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

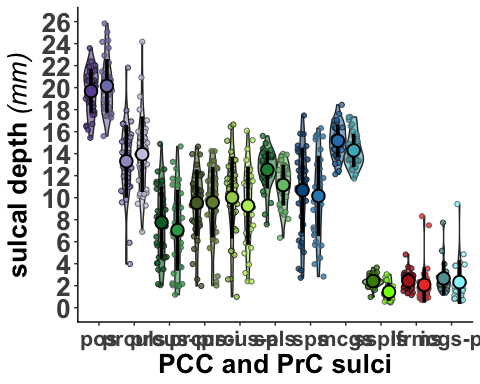
all\_depth\_tert\_stats\_disc <- merge(all\_depth\_tert\_means\_disc, all\_depth\_2\_tert\_sd\_disc,   
 by = c("label", "label2"))  
  
all\_depth\_ntert\_disc <- all\_depth\_2\_disc %>% subset(label %in% c("pos", "prculs",   
 "prcus-p", "prcus-i", "prcus-a",  
 "sps", "spls", "mcgs"))  
all\_depth\_n\_means\_disc <- all\_depth\_ntert\_disc %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

all\_depth\_n\_sd\_disc <- all\_depth\_ntert\_disc %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

all\_depth\_n\_stats\_disc <- merge(all\_depth\_n\_means\_disc, all\_depth\_n\_sd\_disc, by = c("label", "label2"))  
  
  
# Plot  
depth\_y <- expression(paste(bold("sulcal depth "), italic("(mm)")))  
  
all\_sulc\_depth\_disc.plot <- ggplot() +  
 geom\_violin(data = all\_depth\_2\_disc\_tert, aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1.2) +   
 geom\_jitter(data = all\_depth\_2\_disc\_tert, aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = all\_depth\_tert\_stats\_disc,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
   
 geom\_violin(data = all\_depth\_ntert\_disc, aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1.1) +   
 geom\_jitter(data = all\_depth\_ntert\_disc, aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3,   
 dodge.width = .9,   
 jitter.height = 0)) +  
 geom\_pointrange(data = all\_depth\_n\_stats\_disc,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 xlim("pos", "prculs", "prcus-p", "prcus-i", "prcus-a", "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p") +  
 guides(fill = FALSE, color = FALSE) +  
 scale\_color\_manual(breaks =   
 c("POS LH", "POS RH",  
 "prculs LH", "prculs RH",  
 "prcus-p LH", "prcus-p RH",  
 "prcus-i LH", "prcus-i RH",  
 "prcus-a LH", "prcus-a RH",  
 "sps LH", "sps RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c( "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363")) +   
 scale\_fill\_manual(breaks = c("POS LH", "POS RH",  
 "prculs LH", "prculs RH",  
 "prcus-p LH", "prcus-p RH",  
 "prcus-i LH", "prcus-i RH",  
 "prcus-a LH", "prcus-a RH",  
 "sps LH", "sps RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c("#6a51a3", "#807dba", #POS  
 "#9e9ac8", "#cbc9e2", #prculs  
 "#006d2c","#31a354", #prcus-p  
 "darkolivegreen","darkolivegreen4", #prcus-i  
 "darkolivegreen3","darkolivegreen2", #prcus-a  
 "#045a8d", "#2b8cbe", #sps  
 "#238b45", "#74c476", #spls"  
 "#2c7fb8", "#41b6c4", #mcgs  
 "chartreuse4", "chartreuse", #sspls  
 "firebrick", "#ef3b2c", #ifrms  
 "cadetblue", "cadetblue1")) + #icgs-p  
 labs(x = "PCC and PrC sulci",  
 y = depth\_y) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 scale\_y\_continuous(breaks=seq(0,26,2), limits = c(0,26))  
all\_sulc\_depth\_disc.plot



# ggplot2::ggsave(filename = "all\_sulc\_depth\_disc\_plot.png",  
# plot = all\_sulc\_depth\_disc.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")  
  
  
# Replication dataset   
  
## Means for plot  
all\_depth\_tert\_rep <- all\_depth\_2\_rep %>% subset(label %in% c("sspls", "ifrms", "icgs-p"))  
all\_tert\_depth\_means\_rep <- all\_depth\_tert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

all\_tert\_depth\_sd\_rep <- all\_depth\_tert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

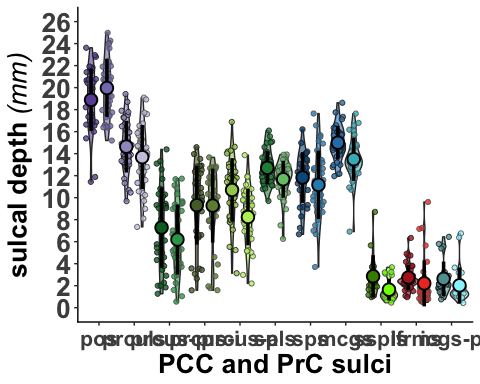
all\_tert\_stats\_rep <- merge(all\_tert\_depth\_means\_rep, all\_tert\_depth\_sd\_rep, by = c("label", "label2"))  
  
all\_depth\_ntert\_rep <- all\_depth\_2\_rep %>% subset(label %in% c("pos", "prculs","prcus-p", "prcus-i",   
 "prcus-a", "sps",   
 "spls", "mcgs"))  
all\_n\_depth\_means\_rep <- all\_depth\_ntert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

all\_n\_depth\_sd\_rep <- all\_depth\_ntert\_rep %>%   
 group\_by(label, label2) %>%   
 summarise(sd = sd(sulcal\_depth\_mm),  
 n = n(),  
 se = sd/sqrt(n))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

all\_n\_stats\_rep <- merge(all\_n\_depth\_means\_rep, all\_n\_depth\_sd\_rep, by = c("label", "label2"))  
  
  
# Plot  
depth\_y <- expression(paste(bold("sulcal depth "), italic("(mm)")))  
  
all\_sulc\_depth\_repl.plot <- ggplot() +  
 geom\_violin(data = all\_depth\_tert\_rep, aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1.2) +   
 geom\_jitter(data = all\_depth\_tert\_rep, aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = all\_tert\_stats\_rep,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
   
 geom\_violin(data = all\_depth\_ntert\_rep, aes(x = label, y = sulcal\_depth\_mm, fill = label2),   
 alpha = .6, position = dodge, width = 1) +   
 geom\_jitter(data = all\_depth\_ntert\_rep, aes(x = label, y = sulcal\_depth\_mm, fill = label2, color = label2),   
 alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3,   
 dodge.width = .9,   
 jitter.height = 0)) +  
 geom\_pointrange(data = all\_n\_stats\_rep,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd, ymax=sulcal\_depth\_mm+sd, fill = label2),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 xlim("pos", "prculs", "prcus-p", "prcus-i", "prcus-a", "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p") +  
 guides(fill = FALSE, color = FALSE) +  
 scale\_color\_manual(breaks =   
 c("POS LH", "POS RH",  
 "prculs LH", "prculs RH",  
 "prcus-p LH", "prcus-p RH",  
 "prcus-i LH", "prcus-i RH",  
 "prcus-a LH", "prcus-a RH",  
 "sps LH", "sps RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c( "#252525", "#636363",  
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 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363")) +   
 scale\_fill\_manual(breaks = c("POS LH", "POS RH",  
 "prculs LH", "prculs RH",  
 "prcus-p LH", "prcus-p RH",  
 "prcus-i LH", "prcus-i RH",  
 "prcus-a LH", "prcus-a RH",  
 "sps LH", "sps RH",  
 "spls LH", "spls RH",  
 "MCGS LH", "MCGS RH",  
 "sspls LH", "sspls RH",  
 "ifrms LH", "ifrms RH",  
 "icgs-p LH", "icgs-p RH"),  
 values = c("#6a51a3", "#807dba", #POS  
 "#9e9ac8", "#cbc9e2", #prculs  
 "#006d2c","#31a354", #prcus-p  
 "darkolivegreen","darkolivegreen4", #prcus-i  
 "darkolivegreen3","darkolivegreen2", #prcus-a  
 "#045a8d", "#2b8cbe", #sps  
 "#238b45", "#74c476", #spls"  
 "#2c7fb8", "#41b6c4", #mcgs  
 "chartreuse4", "chartreuse", #sspls  
 "firebrick", "#ef3b2c", #ifrms  
 "cadetblue", "cadetblue1")) + #icgs-p  
 labs(x = "PCC and PrC sulci",  
 y = depth\_y) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 16, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 10),  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 scale\_y\_continuous(breaks=seq(0,26,2), limits = c(0,26))  
all\_sulc\_depth\_repl.plot



# ggplot2::ggsave(filename = "all\_sulc\_depth\_repl\_plot.png",  
# plot = all\_sulc\_depth\_repl.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "retina")

## Supplementary Figure 3: C/M with all 11 sulci

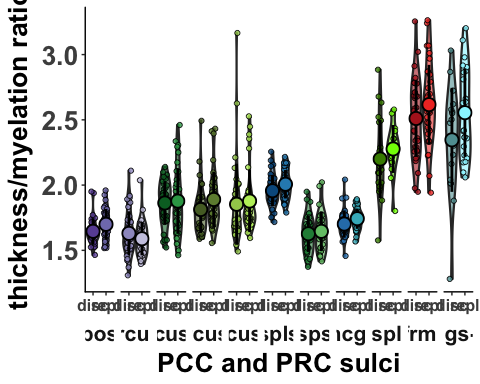
# Dataset  
HCP\_figure3\_supplement <- read.csv("~/Desktop/RMD\_csvs/HCP\_figure3\_supplement.csv")  
  
## LH plot  
HCP\_figure3\_supplement\_lh <- subset(HCP\_figure3\_supplement,   
 subset = HCP\_figure3\_supplement$hemi == "lh")  
  
### Means for plot  
HCP\_figure3\_supplement\_lh\_mean <- HCP\_figure3\_supplement\_lh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(ratio = mean(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_figure3\_supplement\_lh\_sd <- HCP\_figure3\_supplement\_lh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(sd = sd(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_figure3\_supplement\_lh\_stats <- merge(HCP\_figure3\_supplement\_lh\_mean,   
 HCP\_figure3\_supplement\_lh\_sd,   
 by = c("label", "label\_dataset"))  
  
### Plot  
ratio\_axis <- expression(paste(bold("thickness/myelation ratio")))  
  
HCP\_figure3\_supplement\_lh\_stats$label <- factor(HCP\_figure3\_supplement\_lh\_stats$label,   
 levels =   
 c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs",   
 "sspls", "ifrms", "icgs-p"))  
  
HCP\_figure3\_supplement\_lh\_stats$label\_dataset <- factor(HCP\_figure3\_supplement\_lh\_stats$label\_dataset,   
 levels = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"))  
  
HCP\_figure3\_supplement\_lh$label <- factor(HCP\_figure3\_supplement\_lh$label, levels =   
 c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs",   
 "sspls", "ifrms", "icgs-p"))  
  
HCP\_figure3\_supplement\_lh$label\_dataset <- factor(HCP\_figure3\_supplement\_lh$label\_dataset,   
 levels = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"))  
  
ctmy\_11.plot <- ggplot(HCP\_figure3\_supplement\_lh, aes(x = label\_dataset, fill = label\_dataset)) +   
 geom\_violin(aes(y = ratio), size = .8, alpha = 0.6) +   
 geom\_jitter(aes(y = ratio),   
 shape = 21, color = 'black', alpha = .8,  
 position=position\_jitterdodge(jitter.width = 4,   
 dodge.width = .5, jitter.height = 0)) +   
 geom\_pointrange(data = HCP\_figure3\_supplement\_lh\_stats,   
 aes(label\_dataset, ratio, ymin=ratio-sd, ymax=ratio+sd,   
 fill = label\_dataset),   
 shape = 21, size = 1, fatten = 4) +  
 scale\_x\_discrete(breaks = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"),  
 labels = c("disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl")) +  
 scale\_fill\_manual(breaks = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"),  
 values = c("#6a51a3", "#807dba", #POS  
 "#9e9ac8", "#cbc9e2", #prculs  
 "#006d2c","#31a354", #prcus-p  
 "darkolivegreen","darkolivegreen4", #prcus-i  
 "darkolivegreen3","darkolivegreen2", #prcus-a  
 "#045a8d", "#2b8cbe", #sps  
 "#238b45", "#74c476", #spls"  
 "#2c7fb8", "#41b6c4", #mcgs  
 "chartreuse4", "chartreuse", #sspls  
 "firebrick", "#ef3b2c", #ifrms  
 "cadetblue", "cadetblue1")) + #icgs-p +  
 scale\_color\_manual(breaks = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"),  
 values = c(  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363"  
 )) +  
 labs(x = "PCC and PRC sulci",  
 y = ratio\_axis) +   
 guides(fill = F, color = F, alpha = F) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y.right = element\_text(size=20, face = "bold", vjust = 1),  
 axis.text.x = element\_text(size = 12, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 16, face = "bold"),  
 strip.background = element\_blank(),  
 strip.placement = "outside",  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 facet\_wrap( ~ label, strip.position = "bottom", scales = "free\_x", nrow = 1)  
ctmy\_11.plot



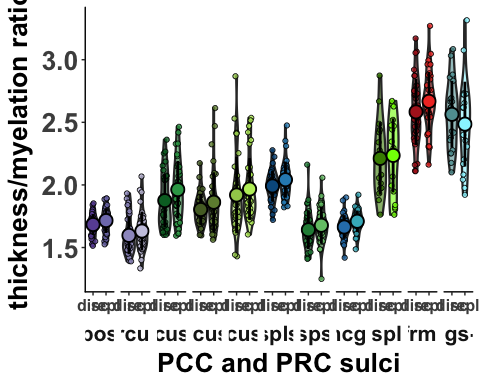
# ggplot2::ggsave(filename = "ctmy\_11\_lh\_plot.png",  
# plot = ctmy\_11.plot,  
# device = "png",  
# width = 12,  
# height = 5,   
# units = "in",  
# dpi = "print")  
  
  
## RH plot  
HCP\_figure3\_supplement\_rh <- subset(HCP\_figure3\_supplement,   
 subset = HCP\_figure3\_supplement$hemi == "rh")  
  
## Means for plot   
HCP\_figure3\_supplement\_rh\_mean <- HCP\_figure3\_supplement\_rh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(ratio = mean(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

HCP\_figure3\_supplement\_rh\_sd <- HCP\_figure3\_supplement\_rh %>%   
 group\_by(label, label\_dataset) %>%   
 summarise(sd = sd(ratio))

## `summarise()` has grouped output by 'label'. You can override using the `.groups` argument.

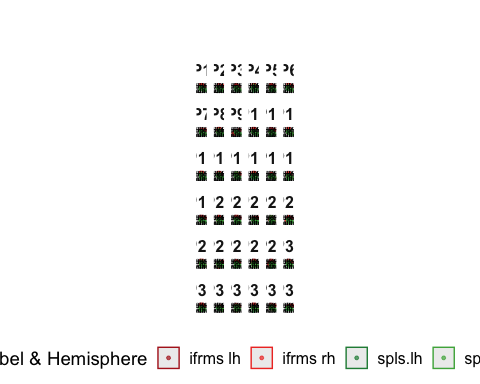
HCP\_figure3\_supplement\_rh\_stats <- merge(HCP\_figure3\_supplement\_rh\_mean,   
 HCP\_figure3\_supplement\_rh\_sd,   
 by = c("label", "label\_dataset"))  
  
HCP\_figure3\_supplement\_rh\_stats$label <- factor(HCP\_figure3\_supplement\_rh\_stats$label,   
 levels =   
 c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs",   
 "sspls", "ifrms", "icgs-p"))  
  
HCP\_figure3\_supplement\_rh\_stats$label\_dataset <- factor(HCP\_figure3\_supplement\_rh\_stats$label\_dataset,   
 levels = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"))  
  
HCP\_figure3\_supplement\_rh$label <- factor(HCP\_figure3\_supplement\_rh$label, levels =   
 c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs",   
 "sspls", "ifrms", "icgs-p"))  
  
HCP\_figure3\_supplement\_rh$label\_dataset <- factor(HCP\_figure3\_supplement\_rh$label\_dataset,   
 levels = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"))  
  
### Plot  
ctmy\_11\_rh.plot <- ggplot(HCP\_figure3\_supplement\_rh,   
 aes(x = label\_dataset,   
 fill = label\_dataset)) +   
 geom\_violin(aes(y = ratio), size = .8, alpha = 0.6) +   
 geom\_jitter(aes(y = ratio),   
 shape = 21, color = 'black', alpha = .8,  
 position=position\_jitterdodge(jitter.width = 4,   
 dodge.width = .5, jitter.height = 0)) +   
 geom\_pointrange(data = HCP\_figure3\_supplement\_rh\_stats,   
 aes(label\_dataset, ratio,   
 ymin=ratio-sd, ymax=ratio+sd,   
 fill = label\_dataset),   
 shape = 21, size = 1, fatten = 4) +  
 scale\_x\_discrete(breaks = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"),  
 labels = c("disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl",  
 "disc", "repl")) +  
 scale\_fill\_manual(breaks = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"),  
 values = c("#6a51a3", "#807dba", #POS  
 "#9e9ac8", "#cbc9e2", #prculs  
 "#006d2c","#31a354", #prcus-p  
 "darkolivegreen","darkolivegreen4", #prcus-i  
 "darkolivegreen3","darkolivegreen2", #prcus-a  
 "#045a8d", "#2b8cbe", #sps  
 "#238b45", "#74c476", #spls"  
 "#2c7fb8", "#41b6c4", #mcgs  
 "chartreuse4", "chartreuse", #sspls  
 "firebrick", "#ef3b2c", #ifrms  
 "cadetblue", "cadetblue1")) + #icgs-p +  
 scale\_color\_manual(breaks = c("POS d", "POS r",  
 "prculs d", "prculs r",  
 "prcus-p d", "prcus-p r",  
 "prcus-i d", "prcus-i r",  
 "prcus-a d", "prcus-a r",  
 "spls d", "spls r",  
 "sps d", "sps r",  
 "MCGS d", "MCGS r",   
 "sspls d", "sspls r",  
 "ifrms d", "ifrms r",  
 "icgs-p d", "icgs-p r"),  
 values = c(  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363",  
 "#252525", "#636363"  
 )) +  
 labs(x = "PCC and PRC sulci",  
 y = ratio\_axis) +   
 guides(fill = F, color = F, alpha = F) +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y = element\_text(size=20, face = "bold", vjust = .9),  
 axis.title.y.right = element\_text(size=20, face = "bold", vjust = 1),  
 axis.text.x = element\_text(size = 12, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 strip.text.x = element\_text(size = 16, face = "bold"),  
 strip.background = element\_blank(),  
 strip.placement = "outside",  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round")) +  
 facet\_wrap( ~ label, strip.position = "bottom", scales = "free\_x", nrow = 1)  
ctmy\_11\_rh.plot



# ggplot2::ggsave(filename = "ctmy\_11\_rh\_plot.png",  
# plot = ctmy\_11\_rh.plot,  
# device = "png",  
# width = 12,  
# height = 5,   
# units = "in",  
# dpi = "print")

## Supplementary Figure 4.1: Individual subject fingerprints - discovery dataset

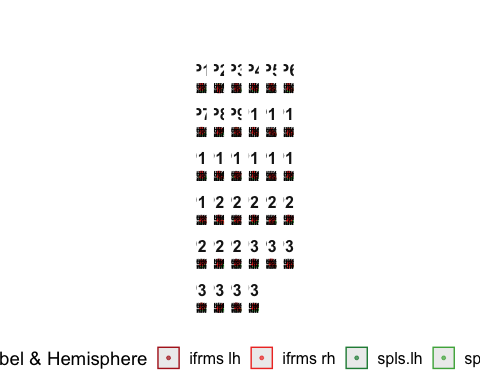
# Dataset  
networks\_ifrms\_spls\_discovery.2 <- six\_networks\_ifrms\_spls\_discovery  
  
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("100206", "P1", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("100307", "P2", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("100408", "P3", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("100610", "P4", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("101006", "P5", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("101107", "P6", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("107725", "P7", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("109830", "P8", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("112920", "P9", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("114924", "P10", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("128127", "P11", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("133928", "P12", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("144125", "P13", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("146937", "P14", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("151425", "P15", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("151829", "P16", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("164939", "P17", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("176744", "P18", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("180937", "P19", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("185947", "P20", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("214019", "P21", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("268749", "P22", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("365343", "P23", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("380036", "P24", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("517239", "P25", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("522434", "P26", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("531536", "P27", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("566454", "P28", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("585256", "P29", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("622236", "P30", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("644044", "P31", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("679770", "P32", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("687163", "P33", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("867468", "P34", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("910241", "P35", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- gsub("959574", "P36", networks\_ifrms\_spls\_discovery.2$TRG\_sub)   
  
# Features for plot  
networks\_ifrms\_spls\_discovery.2$TRG\_sub <- factor(networks\_ifrms\_spls\_discovery.2$TRG\_sub,   
 levels = c("P1", "P2", "P3", "P4", "P5", "P6", "P7", "P8", "P9", "P10",  
 "P11", "P12", "P13", "P14", "P15", "P16", "P17", "P18", "P19",  
 "P20", "P21", "P22", "P23", "P24", "P25", "P26", "P27", "P28",  
 "P29", "P30", "P31", "P32", "P33", "P34", "P35", "P36"))   
  
  
networks\_ifrms\_spls\_discovery.2$label\_hemi[networks\_ifrms\_spls\_discovery.2$label\_name == "ifrms"   
 & networks\_ifrms\_spls\_discovery.2$hemi == "lh"] <- "ifrms.lh"  
  
networks\_ifrms\_spls\_discovery.2$label\_hemi[networks\_ifrms\_spls\_discovery.2$label\_name == "ifrms"   
 & networks\_ifrms\_spls\_discovery.2$hemi == "rh"] <- "ifrms.rh"  
  
networks\_ifrms\_spls\_discovery.2$label\_hemi[networks\_ifrms\_spls\_discovery.2$label\_name == "spls"   
 & networks\_ifrms\_spls\_discovery.2$hemi == "lh"] <- "spls.lh"  
  
networks\_ifrms\_spls\_discovery.2$label\_hemi[networks\_ifrms\_spls\_discovery.2$label\_name == "spls"   
 & networks\_ifrms\_spls\_discovery.2$hemi == "rh"] <- "spls.rh"  
  
# Plot  
all\_conn\_fp\_disc.plot <- ggplot() +   
 geom\_polygon(data = networks\_ifrms\_spls\_discovery.2,   
 aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group = label\_hemi, color = label\_hemi),  
 size = .5,  
 alpha = .1) +  
 geom\_point(data = networks\_ifrms\_spls\_discovery.2, aes(x = network\_name, y = dice\_coeff, color = label\_hemi),  
 size = 1, alpha = .70) +   
   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls.lh", "spls.rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 0),  
 axis.title.y = element\_text(size = 0),  
 axis.text.x = element\_text(size = 5, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 0, face = "bold"),  
 strip.text.y = element\_text(size = 0),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(color = "gray"),   
 panel.grid.major = element\_line(color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1) +   
 facet\_wrap(~TRG\_sub)  
all\_conn\_fp\_disc.plot



# ggplot2::ggsave(filename = "all\_conn\_fp\_disc\_plot.png",  
# plot = all\_conn\_fp\_disc.plot,  
# device = "png",  
# width = 8.5,  
# height = 11,   
# units = "in",  
# dpi = "print")

## Supplementary Figure 4.3: individual subject fingerprints, replication dataset

# Dataset  
## Two marked out participants did not have network data available   
six\_networks\_ifrms\_spls\_replication2 <- six\_networks\_ifrms\_spls\_replication  
  
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("101309", "P1",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("101410", "P2",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("101915", "P3",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("102008", "P4",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)  
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("102311", "P5",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("102513", "P6",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("102816", "P7",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("103111", "P8",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("103414", "P9",   
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("103515", "P10",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("103818", "P11",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("104416", "P12",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("104820", "P13",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("105014", "P14",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("105115", "P15",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("105216", "P16",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("105620", "P17",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("106016", "P18",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("106319", "P19",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("106521", "P20",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("107018", "P21",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
#six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("107220", "P22",  
# six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("107321", "P23",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("107422", "P24",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
#six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("108121", "P25",  
# six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("108222", "P26",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("108323", "P27",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("108525", "P28",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("108828", "P29",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("109123", "P30",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("109325", "P31",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("110007", "P32",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("110411", "P33",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("110613", "P34",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("120111", "P35",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- gsub("168240", "P36",  
 six\_networks\_ifrms\_spls\_replication2$TRG\_sub)   
  
# Features for plot  
six\_networks\_ifrms\_spls\_replication2$TRG\_sub <- factor(six\_networks\_ifrms\_spls\_replication2$TRG\_sub,   
 levels = c("P1", "P2", "P3", "P4", "P5", "P6", "P7", "P8", "P9", "P10",  
 "P11", "P12", "P13", "P14", "P15", "P16", "P17", "P18", "P19",  
 "P20", "P21", "P22", "P23", "P24", "P25", "P26", "P27", "P28",  
 "P29", "P30", "P31", "P32", "P33", "P34", "P35", "P36"))   
  
  
six\_networks\_ifrms\_spls\_replication2$label\_hemi[six\_networks\_ifrms\_spls\_replication2$label\_name == "ifrms" &  
 six\_networks\_ifrms\_spls\_replication2$hemi == "lh"] <- "ifrms.lh"  
  
six\_networks\_ifrms\_spls\_replication2$label\_hemi[six\_networks\_ifrms\_spls\_replication2$label\_name == "ifrms" &  
 six\_networks\_ifrms\_spls\_replication2$hemi == "rh"] <- "ifrms.rh"  
  
six\_networks\_ifrms\_spls\_replication2$label\_hemi[six\_networks\_ifrms\_spls\_replication2$label\_name == "spls" &  
 six\_networks\_ifrms\_spls\_replication2$hemi == "lh"] <- "spls.lh"  
  
six\_networks\_ifrms\_spls\_replication2$label\_hemi[six\_networks\_ifrms\_spls\_replication2$label\_name == "spls" &  
 six\_networks\_ifrms\_spls\_replication2$hemi == "rh"] <- "spls.rh"  
  
# Plot  
all\_conn\_fp\_repl.plot <- ggplot() +   
 geom\_polygon(data = six\_networks\_ifrms\_spls\_replication2,   
 aes(x = network\_name, y = dice\_coeff, fill = label\_hemi, group = label\_hemi, color = label\_hemi),   
 size = .5, alpha = .1) +  
 geom\_point(data = six\_networks\_ifrms\_spls\_replication2,   
 aes(x = network\_name, y = dice\_coeff, color = label\_hemi),   
 size = 1, alpha = .70) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 title = "",  
 subtitle = "",  
 color = "Label & Hemisphere",  
 fill = "Label & Hemisphere") +   
 scale\_fill\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls lh", "spls rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +  
 scale\_color\_manual(limit = c("ifrms.lh", "ifrms.rh", "spls.lh", "spls.rh"),   
 labels = c("ifrms lh", "ifrms rh", "spls.lh", "spls.rh"),  
 values = c("firebrick", "#ef3b2c", "#238b45", "#4daf4a")) +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 0),  
 axis.title.y = element\_text(size = 0),  
 axis.text.x = element\_text(size = 5, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 0, face = "bold"),  
 strip.text.y = element\_text(size = 0),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(color = "gray"),   
 panel.grid.major = element\_line(color = "gray")) +   
 guides(fill = F) +   
 ylim(0,1) +   
 facet\_wrap(~TRG\_sub)  
all\_conn\_fp\_repl.plot



# ggplot2::ggsave(filename = "all\_conn\_fp\_repl\_plot.png",  
# plot = all\_conn\_fp\_repl.plot,  
# device = "png",  
# width = 8.5,  
# height = 11,   
# units = "in",  
# dpi = "print")

## Supplementary Figure 4.4: *prcus* connectivity fingerprints

### Discovery

#### Statistics

# Dataset - all   
prcus\_dice\_all <- read.csv("~/Desktop/RMD\_csvs/prcus\_dice\_all.csv")  
  
# Discovery dataset  
prcus\_dice\_disc <- prcus\_dice\_all %>% subset(dataset == "HCP\_discovery")  
  
# ANOVA  
prcus\_network.aov <- aov(dice\_coeff ~ hemi\*label\_name\*network\_name, data = prcus\_dice\_disc)  
summary(prcus\_network.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.29 0.289 8.741 0.00313 \*\*   
## label\_name 2 0.12 0.060 1.820 0.16219   
## network\_name 16 52.43 3.277 99.137 < 2e-16 \*\*\*  
## hemi:label\_name 2 0.00 0.001 0.023 0.97692   
## hemi:network\_name 16 4.39 0.274 8.294 < 2e-16 \*\*\*  
## label\_name:network\_name 32 17.11 0.535 16.179 < 2e-16 \*\*\*  
## hemi:label\_name:network\_name 32 1.21 0.038 1.146 0.26275   
## Residuals 3570 118.00 0.033   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(prcus\_network.aov) #Eta-squared

## term etasq  
## 1 hemi 0.001  
## 2 label\_name 0.001  
## 3 network\_name 0.271  
## 4 hemi:label\_name 0.000  
## 5 hemi:network\_name 0.023  
## 6 label\_name:network\_name 0.088  
## 7 hemi:label\_name:network\_name 0.006

# Post hoc test  
network\_aov.i1 <- emmeans::emmeans(prcus\_network.aov, ~ label\_name | network\_name)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(network\_aov.i1, method='pairwise')

## network\_name = Auditory:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.005287 0.0303 3570 0.174 0.9834   
## (prcus-a) - (prcus-p) 0.012187 0.0303 3570 0.402 0.9147   
## (prcus-i) - (prcus-p) 0.006900 0.0303 3570 0.228 0.9718   
##   
## network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.040272 0.0303 3570 -1.329 0.3791   
## (prcus-a) - (prcus-p) -0.028445 0.0303 3570 -0.939 0.6158   
## (prcus-i) - (prcus-p) 0.011828 0.0303 3570 0.390 0.9195   
##   
## network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.037173 0.0303 3570 -1.227 0.4374   
## (prcus-a) - (prcus-p) -0.157521 0.0303 3570 -5.198 <.0001   
## (prcus-i) - (prcus-p) -0.120348 0.0303 3570 -3.972 0.0002   
##   
## network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.010653 0.0303 3570 0.352 0.9341   
## (prcus-a) - (prcus-p) -0.007907 0.0303 3570 -0.261 0.9632   
## (prcus-i) - (prcus-p) -0.018560 0.0303 3570 -0.613 0.8133   
##   
## network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.185094 0.0303 3570 -6.108 <.0001   
## (prcus-a) - (prcus-p) -0.505906 0.0303 3570 -16.696 <.0001   
## (prcus-i) - (prcus-p) -0.320811 0.0303 3570 -10.587 <.0001   
##   
## network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.011128 0.0303 3570 0.367 0.9284   
## (prcus-a) - (prcus-p) 0.051971 0.0303 3570 1.715 0.1996   
## (prcus-i) - (prcus-p) 0.040843 0.0303 3570 1.348 0.3688   
##   
## network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.083442 0.0303 3570 -2.754 0.0163   
## (prcus-a) - (prcus-p) 0.231715 0.0303 3570 7.647 <.0001   
## (prcus-i) - (prcus-p) 0.315157 0.0303 3570 10.401 <.0001   
##   
## network\_name = DorsalAttentionB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.018051 0.0303 3570 0.596 0.8224   
## (prcus-a) - (prcus-p) 0.020694 0.0303 3570 0.683 0.7735   
## (prcus-i) - (prcus-p) 0.002643 0.0303 3570 0.087 0.9958   
##   
## network\_name = DorsAttnA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.026421 0.0303 3570 -0.872 0.6581   
## (prcus-a) - (prcus-p) 0.119972 0.0303 3570 3.959 0.0002   
## (prcus-i) - (prcus-p) 0.146393 0.0303 3570 4.831 <.0001   
##   
## network\_name = SomatomotorB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.000684 0.0303 3570 0.023 0.9997   
## (prcus-a) - (prcus-p) 0.000684 0.0303 3570 0.023 0.9997   
## (prcus-i) - (prcus-p) 0.000000 0.0303 3570 0.000 1.0000   
##   
## network\_name = SomMotorA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.080202 0.0303 3570 2.647 0.0222   
## (prcus-a) - (prcus-p) 0.085960 0.0303 3570 2.837 0.0127   
## (prcus-i) - (prcus-p) 0.005757 0.0303 3570 0.190 0.9803   
##   
## network\_name = TemporalParietal:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.020720 0.0303 3570 0.684 0.7730   
## (prcus-a) - (prcus-p) 0.022779 0.0303 3570 0.752 0.7326   
## (prcus-i) - (prcus-p) 0.002058 0.0303 3570 0.068 0.9975   
##   
## network\_name = VenAttnA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.055201 0.0303 3570 1.822 0.1626   
## (prcus-a) - (prcus-p) 0.091282 0.0303 3570 3.012 0.0074   
## (prcus-i) - (prcus-p) 0.036081 0.0303 3570 1.191 0.4588   
##   
## network\_name = VenAttnB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.113409 0.0303 3570 3.743 0.0005   
## (prcus-a) - (prcus-p) 0.165314 0.0303 3570 5.456 <.0001   
## (prcus-i) - (prcus-p) 0.051905 0.0303 3570 1.713 0.2004   
##   
## network\_name = VisualA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.014814 0.0303 3570 0.489 0.8766   
## (prcus-a) - (prcus-p) 0.037475 0.0303 3570 1.237 0.4315   
## (prcus-i) - (prcus-p) 0.022661 0.0303 3570 0.748 0.7349   
##   
## network\_name = VisualB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.041803 0.0303 3570 1.380 0.3517   
## (prcus-a) - (prcus-p) 0.065944 0.0303 3570 2.176 0.0754   
## (prcus-i) - (prcus-p) 0.024141 0.0303 3570 0.797 0.7051   
##   
## network\_name = VisualC:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.000000 0.0303 3570 0.000 1.0000   
## (prcus-a) - (prcus-p) 0.000000 0.0303 3570 0.000 1.0000   
## (prcus-i) - (prcus-p) 0.000000 0.0303 3570 0.000 1.0000   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 3 estimates

The *prcus* show a posterior to anterior decrease in the amount of overlap with default A and a posterior to anterior increase in overlap with default C. *Prcus-p* overlaps with control B. *Prcus-i* and *prcus-a* both overlap more with dorsal attention A than *prcus-p*. *Prcus-a* overlaps more with somatomotor A and ventral attention B than the other two *prcus*, as well as overlaps more with ventral attention A and visual B than *prcus-p*, but about the same as *prcus-i* did with both networks. See Supplementary Figure 4.4 and supplementary results.

#### Plots

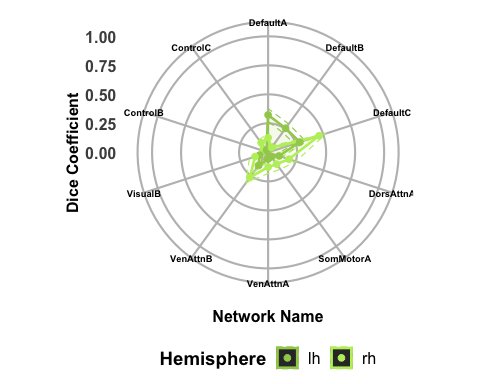
# Prcus-a  
  
# Dataset  
prcusa\_dice <- prcus\_dice\_disc %>% subset(label\_name == "prcus-a")  
  
# Subset to networks that it overlapped most with in order to clear up plot  
prcusa\_dice.2 <- prcusa\_dice %>% subset(network\_name %in% c('ControlB', 'ControlC', 'DefaultA', 'DefaultB', 'DefaultC', 'DorsAttnA', 'SomMotorA', 'VenAttnA', 'VenAttnB', 'VisualB'))  
  
# Get mean for each network dice value   
prcusa\_dice\_avg <- prcusa\_dice.2 %>%   
 group\_by(network\_name, hemi) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name'. You can override using the `.groups` argument.

# Get se value for each network by hemi   
prcusa\_dice\_se <- prcusa\_dice.2 %>%   
 group\_by(hemi, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

# Merge & add and subtract se from mean to get upper and lower   
prcusa\_dice\_all <- merge(prcusa\_dice\_avg, prcusa\_dice\_se,  
 by=c("network\_name", "hemi"))  
prcusa\_dice\_all <- prcusa\_dice\_all %>%   
 group\_by(network\_name, hemi) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
  
## Plot  
prcusa\_conn\_fp\_disc.plot <- ggplot(data = prcusa\_dice\_all) +   
 geom\_polygon(aes(x = network\_name, y = upper, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(aes(x = network\_name, y = lower, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(aes(x = network\_name, y = dice\_coefficient, fill = hemi, group = hemi, color = hemi),   
 size = .9, alpha = .1) +  
 geom\_point(aes(x = network\_name, y = dice\_coefficient, color = hemi), size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",  
 color = "Hemisphere",  
 fill = "Hemisphere") +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 7, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.position = "bottom",  
 legend.text = element\_text(size=12),  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +  
 scale\_fill\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen3","darkolivegreen2")) +  
 scale\_color\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen3", "darkolivegreen2")) +   
 guides(fill = F) +  
 ylim(0,1)  
prcusa\_conn\_fp\_disc.plot



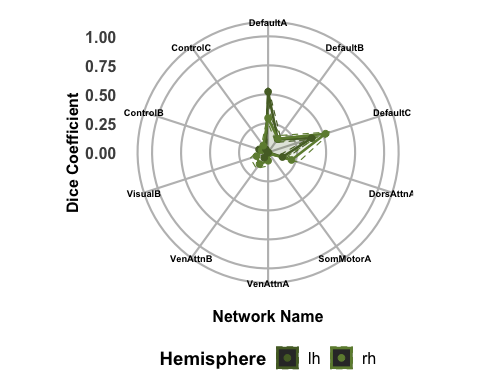
# ggplot2::ggsave(filename = "prcusa\_conn\_fp\_disc\_plot.png",  
# plot = prcusa\_conn\_fp\_disc.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "print")  
  
  
# Prcus-i   
  
# Dataset  
prcusi\_dice <- prcus\_dice\_disc %>% subset(label\_name == "prcus-i")  
  
# Subset to networks that it overlapped most with in order to clear up plot  
prcusi\_dice.2 <- prcusi\_dice %>% subset(network\_name %in% c('ControlB', 'ControlC', 'DefaultA',  
 'DefaultB', 'DefaultC', 'DorsAttnA', 'SomMotorA',  
 'VenAttnA', 'VenAttnB', 'VisualB'))  
# Get mean for each network dice value   
prcusi\_dice\_avg <- prcusi\_dice.2 %>%   
 group\_by(network\_name, hemi) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name'. You can override using the `.groups` argument.

# Get se value for each network by hemi   
prcusi\_dice\_se <- prcusi\_dice.2 %>%   
 group\_by(hemi, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

# Merge & add and subtract se from mean to get upper and lower   
prcusi\_dice\_all <- merge(prcusi\_dice\_avg, prcusi\_dice\_se,  
 by=c("network\_name", "hemi"))  
  
prcusi\_dice\_all <- prcusi\_dice\_all %>%   
 group\_by(network\_name, hemi) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
## Plot  
prcusi\_conn\_fp\_disc.plot <- ggplot(data = prcusi\_dice\_all) +   
 geom\_polygon(aes(x = network\_name, y = upper, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(aes(x = network\_name, y = lower, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(aes(x = network\_name, y = dice\_coefficient, fill = hemi, group = hemi, color = hemi),   
 size = .9, alpha = .1) +  
 geom\_point(aes(x = network\_name, y = dice\_coefficient, color = hemi), size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 color = "Hemisphere",  
 fill = "Hemisphere") +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold",),  
 axis.title.y = element\_text(size = 12, face = "bold",),  
 axis.text.x = element\_text(size = 7, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold",),  
 strip.text.x = element\_text(size = 12, face = "bold",),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +  
 scale\_fill\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen","darkolivegreen4")) +  
 scale\_color\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen","darkolivegreen4")) +   
 guides(fill = F) +  
 ylim(0,1)   
prcusi\_conn\_fp\_disc.plot



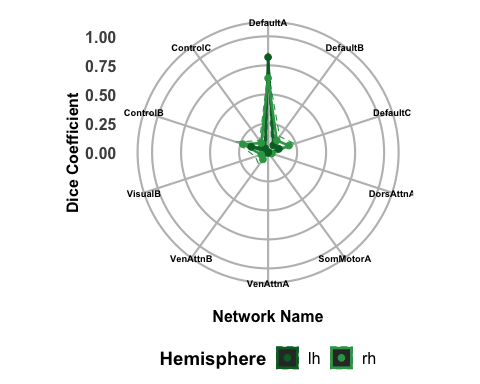
# ggplot2::ggsave(filename = "prcusi\_conn\_fp\_disc\_plot.png",  
# plot = prcusi\_conn\_fp\_disc.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "print")  
  
  
# Prcus-p  
  
# Dataset  
prcusp\_dice <- prcus\_dice\_disc %>% subset(label\_name == "prcus-p")  
  
# Subset to networks that it overlapped most with in order to clear up plot  
prcusp\_dice.2 <- prcusp\_dice %>% subset(network\_name %in% c('ControlB', 'ControlC', 'DefaultA',  
 'DefaultB', 'DefaultC', 'DorsAttnA', 'SomMotorA',  
 'VenAttnA', 'VenAttnB', 'VisualB'))  
# Get mean for each network dice value   
prcusp\_dice\_avg <- prcusp\_dice.2 %>%   
 group\_by(network\_name, hemi) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name'. You can override using the `.groups` argument.

# Get se value for each network by hemi   
  
prcusp\_dice\_se <- prcusp\_dice.2 %>%   
 group\_by(hemi, network\_name) %>%  
 summarize(n=n(), sd=sd(dice\_coeff), se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

# Merge & add and subtract se from mean to get upper and lower   
prcusp\_dice\_all <- merge(prcusp\_dice\_avg, prcusp\_dice\_se,  
 by=c("network\_name", "hemi"))  
prcusp\_dice\_all <- prcusp\_dice\_all %>%   
 group\_by(network\_name, hemi) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
## Plot   
prcusp\_conn\_fp\_disc.plot <- ggplot(data = prcusp\_dice\_all) +   
 geom\_polygon(aes(x = network\_name, y = upper, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(aes(x = network\_name, y = lower, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(aes(x = network\_name, y = dice\_coefficient, fill = hemi, group = hemi, color = hemi),   
 size = .9, alpha = .1) +  
 geom\_point(aes(x = network\_name, y = dice\_coefficient, color = hemi), size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 color = "Hemisphere",  
 fill = "Hemisphere") +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 7, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray"))+  
 scale\_fill\_manual(breaks = c("lh", "rh"),   
 values = c("#006d2c","#31a354")) +  
 scale\_color\_manual(breaks = c("lh", "rh"),   
 values = c("#006d2c", "#31a354")) +  
 guides(fill = F) +  
 ylim(0,1)   
prcusp\_conn\_fp\_disc.plot



# ggplot2::ggsave(filename = "prcusp\_conn\_fp\_disc\_plot.png",  
# plot = prcusp\_conn\_fp\_disc.plot,  
# device = "png",  
# width = 8.5,  
# height = 11,   
# units = "in",  
# dpi = "print")

### Replication

#### Statistics

# Replication dataset  
prcus\_dice\_repl <- prcus\_dice\_all %>% subset(dataset == "HCP\_replication")  
  
# Anova  
prcus\_network\_rep.aov <- aov(dice\_coeff ~ hemi\*label\_name\*network\_name, data = prcus\_dice\_repl)  
summary(prcus\_network\_rep.aov) #p-values

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.00 0.000 0.021 0.8847   
## label\_name 2 0.15 0.076 3.785 0.0228 \*   
## network\_name 16 53.05 3.316 165.302 < 2e-16 \*\*\*  
## hemi:label\_name 2 0.00 0.001 0.054 0.9474   
## hemi:network\_name 16 1.48 0.092 4.597 3.07e-09 \*\*\*  
## label\_name:network\_name 32 17.17 0.537 26.754 < 2e-16 \*\*\*  
## hemi:label\_name:network\_name 32 0.67 0.021 1.051 0.3896   
## Residuals 3366 67.52 0.020   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(prcus\_network\_rep.aov) #Eta-squared

## term etasq  
## 1 hemi 0.000  
## 2 label\_name 0.001  
## 3 network\_name 0.379  
## 4 hemi:label\_name 0.000  
## 5 hemi:network\_name 0.011  
## 6 label\_name:network\_name 0.123  
## 7 hemi:label\_name:network\_name 0.005

# Post hoc test  
prcus\_network\_rep\_aov.i1 <- emmeans::emmeans(prcus\_network\_rep.aov, ~ label\_name | network\_name)

## NOTE: Results may be misleading due to involvement in interactions

emmeans::contrast(prcus\_network\_rep\_aov.i1, method='pairwise')

## network\_name = Auditory:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.00199 0.0243 3366 -0.082 0.9963   
## (prcus-a) - (prcus-p) 0.00725 0.0243 3366 0.299 0.9521   
## (prcus-i) - (prcus-p) 0.00924 0.0243 3366 0.380 0.9233   
##   
## network\_name = ControlA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.03583 0.0243 3366 -1.475 0.3029   
## (prcus-a) - (prcus-p) -0.03750 0.0243 3366 -1.544 0.2706   
## (prcus-i) - (prcus-p) -0.00166 0.0243 3366 -0.068 0.9974   
##   
## network\_name = ControlB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.05799 0.0243 3366 -2.388 0.0448   
## (prcus-a) - (prcus-p) -0.03774 0.0243 3366 -1.554 0.2662   
## (prcus-i) - (prcus-p) 0.02026 0.0243 3366 0.834 0.6819   
##   
## network\_name = ControlC:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.04435 0.0243 3366 1.826 0.1612   
## (prcus-a) - (prcus-p) 0.02616 0.0243 3366 1.077 0.5284   
## (prcus-i) - (prcus-p) -0.01819 0.0243 3366 -0.749 0.7342   
##   
## network\_name = DefaultA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.22929 0.0243 3366 -9.440 <.0001   
## (prcus-a) - (prcus-p) -0.56103 0.0243 3366 -23.098 <.0001   
## (prcus-i) - (prcus-p) -0.33174 0.0243 3366 -13.658 <.0001   
##   
## network\_name = DefaultB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.01044 0.0243 3366 -0.430 0.9032   
## (prcus-a) - (prcus-p) 0.05235 0.0243 3366 2.155 0.0792   
## (prcus-i) - (prcus-p) 0.06279 0.0243 3366 2.585 0.0264   
##   
## network\_name = DefaultC:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.00355 0.0243 3366 0.146 0.9883   
## (prcus-a) - (prcus-p) 0.31132 0.0243 3366 12.818 <.0001   
## (prcus-i) - (prcus-p) 0.30778 0.0243 3366 12.672 <.0001   
##   
## network\_name = DorsalAttentionA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) -0.01613 0.0243 3366 -0.664 0.7844   
## (prcus-a) - (prcus-p) 0.06714 0.0243 3366 2.764 0.0158   
## (prcus-i) - (prcus-p) 0.08327 0.0243 3366 3.428 0.0018   
##   
## network\_name = DorsalAttentionB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.01400 0.0243 3366 0.577 0.8327   
## (prcus-a) - (prcus-p) 0.01835 0.0243 3366 0.756 0.7303   
## (prcus-i) - (prcus-p) 0.00435 0.0243 3366 0.179 0.9825   
##   
## network\_name = SomatomotorA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.04254 0.0243 3366 1.752 0.1864   
## (prcus-a) - (prcus-p) 0.04254 0.0243 3366 1.752 0.1864   
## (prcus-i) - (prcus-p) 0.00000 0.0243 3366 0.000 1.0000   
##   
## network\_name = SomatomotorB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.00000 0.0243 3366 0.000 1.0000   
## (prcus-a) - (prcus-p) 0.00000 0.0243 3366 0.000 1.0000   
## (prcus-i) - (prcus-p) 0.00000 0.0243 3366 0.000 1.0000   
##   
## network\_name = TemporalParietal:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.01813 0.0243 3366 0.747 0.7357   
## (prcus-a) - (prcus-p) 0.02469 0.0243 3366 1.017 0.5664   
## (prcus-i) - (prcus-p) 0.00656 0.0243 3366 0.270 0.9606   
##   
## network\_name = VentralAttentionA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.08757 0.0243 3366 3.605 0.0009   
## (prcus-a) - (prcus-p) 0.09694 0.0243 3366 3.991 0.0002   
## (prcus-i) - (prcus-p) 0.00937 0.0243 3366 0.386 0.9212   
##   
## network\_name = VentralAttentionB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.08570 0.0243 3366 3.528 0.0012   
## (prcus-a) - (prcus-p) 0.14114 0.0243 3366 5.811 <.0001   
## (prcus-i) - (prcus-p) 0.05544 0.0243 3366 2.283 0.0584   
##   
## network\_name = VisualA:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.02350 0.0243 3366 0.967 0.5975   
## (prcus-a) - (prcus-p) 0.02872 0.0243 3366 1.182 0.4637   
## (prcus-i) - (prcus-p) 0.00522 0.0243 3366 0.215 0.9748   
##   
## network\_name = VisualB:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.07593 0.0243 3366 3.126 0.0051   
## (prcus-a) - (prcus-p) 0.07706 0.0243 3366 3.172 0.0043   
## (prcus-i) - (prcus-p) 0.00112 0.0243 3366 0.046 0.9988   
##   
## network\_name = VisualC:  
## contrast estimate SE df t.ratio p.value  
## (prcus-a) - (prcus-i) 0.00000 0.0243 3366 0.000 1.0000   
## (prcus-a) - (prcus-p) 0.00000 0.0243 3366 0.000 1.0000   
## (prcus-i) - (prcus-p) 0.00000 0.0243 3366 0.000 1.0000   
##   
## Results are averaged over the levels of: hemi   
## P value adjustment: tukey method for comparing a family of 3 estimates

Similar to the discovery sample, these sulci show a posterior to anterior decrease in default A overlap and a posterior to anterior increase in overlap with default C. *Prcus-a* overlaps more with control B than *prcus-i*, but about the same as *prcus-p* in this sample. *Prcus-a* overlaps more with ventral attention A, ventral attention B, and visual B than the other two sulci. Finally, *prcus-i* and *prcus-a* overlap more with dorsal attention A than *prcus-p*. See Supplementary Figure 4.4 and supplementary results.

#### Plots

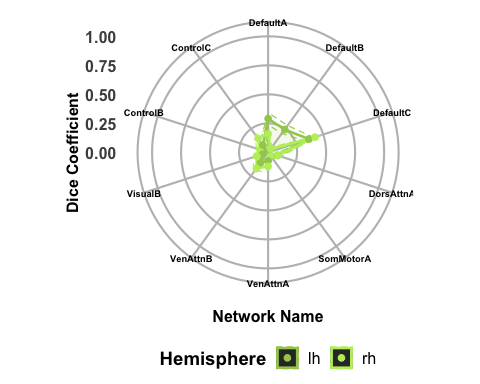
# Prcus-a  
  
# Dataset  
prcusa\_rep\_dice <- prcus\_dice\_repl %>% subset(label\_name == "prcus-a")  
  
# Features for plot  
prcusa\_rep\_dice$network\_name <- gsub("DorsalAttentionA", "DorsAttnA", prcusa\_rep\_dice$network\_name)  
prcusa\_rep\_dice$network\_name <- gsub("SomatomotorA", "SomMotorA", prcusa\_rep\_dice$network\_name)  
prcusa\_rep\_dice$network\_name <- gsub("VentralAttentionA", "VenAttnA", prcusa\_rep\_dice$network\_name)  
prcusa\_rep\_dice$network\_name <- gsub("VentralAttentionB", "VenAttnB", prcusa\_rep\_dice$network\_name)  
  
  
prcusa\_rep\_dice.2 <- prcusa\_rep\_dice %>% subset(network\_name %in% c('ControlB', 'ControlC', 'DefaultA', 'DefaultB', 'DefaultC', 'DorsAttnA', 'SomMotorA', 'VenAttnA', 'VenAttnB', 'VisualB'))   
  
# Get mean for each network dice value   
prcusa\_rep\_dice\_avg <- prcusa\_rep\_dice.2 %>%   
 group\_by(network\_name, hemi) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name'. You can override using the `.groups` argument.

# Get se value for each network by hemi   
prcusa\_rep\_dice\_se <- prcusa\_rep\_dice.2 %>%   
 group\_by(hemi, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

# Merge & add and subtract se from mean to get upper and lower   
prcusa\_rep\_dice\_all <- merge(prcusa\_rep\_dice\_avg, prcusa\_rep\_dice\_se,  
 by=c("network\_name", "hemi"))  
  
prcusa\_rep\_dice\_all <- prcusa\_rep\_dice\_all %>%   
 group\_by(network\_name, hemi) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
## Plot  
prcusa\_conn\_fp\_repl.plot <- ggplot(data = prcusa\_rep\_dice\_all) +   
 geom\_polygon(aes(x = network\_name, y = upper, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(aes(x = network\_name, y = lower, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(aes(x = network\_name, y = dice\_coefficient, fill = hemi, group = hemi, color = hemi),   
 size = .9, alpha = .1) +  
 geom\_point(aes(x = network\_name, y = dice\_coefficient, color = hemi), size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",  
 color = "Hemisphere",  
 fill = "Hemisphere") +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 7, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size = 14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +  
 scale\_fill\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen3","darkolivegreen2")) +  
 scale\_color\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen3", "darkolivegreen2")) +   
 guides(fill = F) +  
 ylim(0,1)  
prcusa\_conn\_fp\_repl.plot



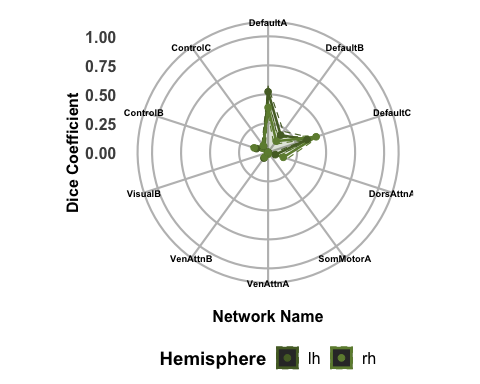
# ggplot2::ggsave(filename = "prcusa\_conn\_fp\_repl\_plot.png",  
# plot = prcusa\_conn\_fp\_repl.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "print")  
  
  
# Prcus-i  
  
# Dataset  
prcusi\_dice\_rep <- prcus\_dice\_repl %>% subset(label\_name == "prcus-i")  
  
# Features for plot  
prcusi\_dice\_rep$network\_name <- gsub("DorsalAttentionA", "DorsAttnA", prcusi\_dice\_rep$network\_name)  
prcusi\_dice\_rep$network\_name <- gsub("SomatomotorA", "SomMotorA", prcusi\_dice\_rep$network\_name)  
prcusi\_dice\_rep$network\_name <- gsub("VentralAttentionA", "VenAttnA", prcusi\_dice\_rep$network\_name)  
prcusi\_dice\_rep$network\_name <- gsub("VentralAttentionB", "VenAttnB", prcusi\_dice\_rep$network\_name)  
  
prcusi\_dice\_rep.2 <- prcusi\_dice\_rep %>% subset(network\_name %in% c('ControlB', 'ControlC', 'DefaultA',  
 'DefaultB', 'DefaultC', 'DorsAttnA', 'SomMotorA',  
 'VenAttnA', 'VenAttnB', 'VisualB'))  
# Get mean for each network dice value   
prcusi\_dice\_rep\_avg <- prcusi\_dice\_rep.2 %>%   
 group\_by(network\_name, hemi) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name'. You can override using the `.groups` argument.

# Get se value for each network by hemi   
prcusi\_dice\_rep\_se <- prcusi\_dice\_rep.2 %>%   
 group\_by(hemi, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

# Merge & add and subtract se from mean to get upper and lower   
prcusi\_dice\_rep\_all <- merge(prcusi\_dice\_rep\_avg, prcusi\_dice\_rep\_se,  
 by=c("network\_name", "hemi"))  
prcusi\_dice\_rep\_all <- prcusi\_dice\_rep\_all %>%   
 group\_by(network\_name, hemi) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
## Plot  
prcusi\_conn\_fp\_repl.plot <- ggplot(data = prcusi\_dice\_rep\_all) +   
 geom\_polygon(aes(x = network\_name, y = upper, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(aes(x = network\_name, y = lower, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(aes(x = network\_name, y = dice\_coefficient, fill = hemi, group = hemi, color = hemi),   
 size = .9, alpha = .1) +  
 geom\_point(aes(x = network\_name, y = dice\_coefficient, color = hemi), size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 color = "Hemisphere",  
 fill = "Hemisphere") +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 7, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray")) +  
 scale\_fill\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen","darkolivegreen4")) +  
 scale\_color\_manual(breaks = c("lh", "rh"),   
 values = c("darkolivegreen","darkolivegreen4")) +   
 guides(fill = F) +  
 ylim(0,1)   
prcusi\_conn\_fp\_repl.plot



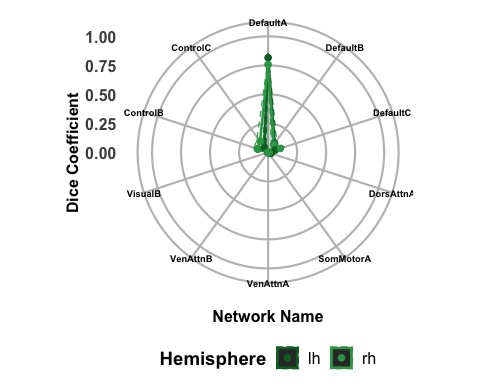
# ggplot2::ggsave(filename = "prcusi\_conn\_fp\_repl\_plot.png",  
# plot = prcusi\_conn\_fp\_repl.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "print")  
  
  
# Prcus-p  
  
# Dataset  
prcusp\_dice\_rep <- prcus\_dice\_repl %>% subset(label\_name == "prcus-p")  
  
# Features for plot  
prcusp\_dice\_rep$network\_name <- gsub("DorsalAttentionA", "DorsAttnA", prcusp\_dice\_rep$network\_name)  
prcusp\_dice\_rep$network\_name <- gsub("SomatomotorA", "SomMotorA", prcusp\_dice\_rep$network\_name)  
prcusp\_dice\_rep$network\_name <- gsub("VentralAttentionA", "VenAttnA", prcusp\_dice\_rep$network\_name)  
prcusp\_dice\_rep$network\_name <- gsub("VentralAttentionB", "VenAttnB", prcusp\_dice\_rep$network\_name)  
  
prcusp\_dice\_rep.2 <- prcusp\_dice\_rep %>% subset(network\_name %in% c('ControlB', 'ControlC', 'DefaultA',  
 'DefaultB', 'DefaultC', 'DorsAttnA', 'SomMotorA',  
 'VenAttnA', 'VenAttnB', 'VisualB'))  
# Get mean for each network dice value   
prcusp\_dice\_rep\_avg <- prcusp\_dice\_rep.2 %>%   
 group\_by(network\_name, hemi) %>%   
 summarise(dice\_coefficient = mean(dice\_coeff))

## `summarise()` has grouped output by 'network\_name'. You can override using the `.groups` argument.

# Get se value for each network by hemi   
  
prcusp\_dice\_rep\_se <- prcusp\_dice\_rep.2 %>%   
 group\_by(hemi, network\_name) %>%  
 summarise(n=n(),   
 sd=sd(dice\_coeff),   
 se=sd/sqrt(n))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

# Merge & add and subtract se from mean to get upper and lower   
prcusp\_dice\_rep\_all <- merge(prcusp\_dice\_rep\_avg, prcusp\_dice\_rep\_se,  
 by=c("network\_name", "hemi"))  
prcusp\_dice\_rep\_all <- prcusp\_dice\_rep\_all %>%   
 group\_by(network\_name, hemi) %>%  
 mutate(upper = dice\_coefficient + se,   
 lower = dice\_coefficient - se)  
  
# Plot  
prcusp\_conn\_fp\_repl.plot <- ggplot(data = prcusp\_dice\_rep\_all) +   
 geom\_polygon(aes(x = network\_name, y = upper, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +   
 geom\_polygon(aes(x = network\_name, y = lower, fill = NA, group = hemi, color = hemi),   
 linetype = 2, size = .4) +  
 geom\_polygon(aes(x = network\_name, y = dice\_coefficient, fill = hemi, group = hemi, color = hemi),   
 size = .9, alpha = .1) +  
 geom\_point(aes(x = network\_name, y = dice\_coefficient, color = hemi), size = 2) +   
 coord\_radar(start = -pi/2) +  
 labs(x = "Network Name",  
 y = "Dice Coefficient",   
 color = "Hemisphere",  
 fill = "Hemisphere") +   
 theme\_minimal() +  
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(hjust = 0, size = 14),  
 plot.caption = element\_text(size = 12),  
 axis.text=element\_text(size=14),  
 axis.title.x = element\_text(size = 12, face = "bold"),  
 axis.title.y = element\_text(size = 12, face = "bold"),  
 axis.text.x = element\_text(size = 7, face = "bold", color = "black", vjust = .50),  
 axis.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.y = element\_text(size = 12, face = "bold"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 legend.title = element\_text(size = 14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black",   
 size = 0, linetype = "solid", lineend = "round"),  
 panel.grid.minor = element\_line(size = 0.5, color = "gray"),   
 panel.grid.major = element\_line(size = .75, color = "gray"))+  
 scale\_fill\_manual(breaks = c("lh", "rh"),   
 values = c("#006d2c","#31a354")) +  
 scale\_color\_manual(breaks = c("lh", "rh"),   
 values = c("#006d2c", "#31a354")) +  
 guides(fill = F) +  
 ylim(0,1)   
prcusp\_conn\_fp\_repl.plot



# ggplot2::ggsave(filename = "prcusp\_conn\_fp\_repl\_plot.png",  
# plot = prcusp\_conn\_fp\_repl.plot,  
# device = "png",  
# width = 4,  
# height = 4,   
# units = "in",  
# dpi = "print")

## Supplementary Figure 6a: Raw sulcal depth (mm)

### Statistics

# ANOVA  
comp\_raw\_depth.aov <- aov(sulcal\_depth\_mm ~ hemi \* group \* species, data = ifrms\_compdev\_morphology)  
summary(comp\_raw\_depth.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 75.4 75.39 21.259 5.16e-06 \*\*\*  
## group 2 68.2 34.09 9.613 8.08e-05 \*\*\*  
## species 1 14.6 14.56 4.106 0.0433 \*   
## hemi:group 2 6.4 3.20 0.901 0.4067   
## hemi:species 1 0.2 0.20 0.055 0.8145   
## group:species 2 6.9 3.44 0.970 0.3800   
## hemi:group:species 2 0.5 0.27 0.075 0.9280   
## Residuals 475 1684.5 3.55   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(comp\_raw\_depth.aov)

## term etasq  
## 1 hemi 0.041  
## 2 group 0.037  
## 3 species 0.008  
## 4 hemi:group 0.003  
## 5 hemi:species 0.000  
## 6 group:species 0.004  
## 7 hemi:group:species 0.000

# Main effect of hemi  
ifrms\_compdev\_morphology %>% group\_by(hemi) %>% summarise(mean = mean(sulcal\_depth\_mm))

## # A tibble: 2 x 2  
## hemi mean  
## \* <chr> <dbl>  
## 1 lh 3.25  
## 2 rh 2.47

# Main effect of group  
ifrms\_compdev\_morphology %>% group\_by(group) %>% summarise(mean = mean(sulcal\_depth\_mm))

## # A tibble: 3 x 2  
## group mean  
## \* <chr> <dbl>  
## 1 juvenile 2.97  
## 2 older-adult 3.27  
## 3 young-adult 2.36

# Main effect of species  
ifrms\_compdev\_morphology %>% group\_by(species) %>% summarise(mean = mean(sulcal\_depth\_mm))

## # A tibble: 2 x 2  
## species mean  
## \* <chr> <dbl>  
## 1 chimpanzee 2.33  
## 2 human 2.93

The observed results hold even with non-normalized depth values.

### Plot

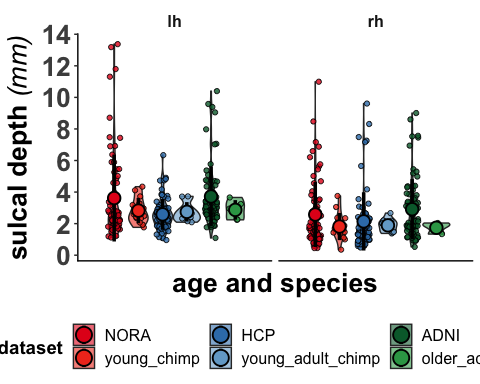
# Means for plot  
comp\_depth\_raw\_avg <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(sulcal\_depth\_mm = mean(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

comp\_depth\_raw\_sd <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(sd = sd(sulcal\_depth\_mm))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

# Plot  
comp\_depth\_raw\_stats <- merge(comp\_depth\_raw\_avg, comp\_depth\_raw\_sd, by = c("label", "dataset", "hemi"))  
  
comp\_depth\_raw.plot <- ggplot(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = sulcal\_depth\_mm)) +  
 geom\_violin(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = sulcal\_depth\_mm, fill = dataset), alpha = .6, position = dodge, width = 1) +   
 geom\_jitter(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = sulcal\_depth\_mm, fill = dataset),   
 alpha = .8, shape = 21, color = 'black',  
 position=position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = comp\_depth\_raw\_stats,   
 aes(label, sulcal\_depth\_mm, ymin=sulcal\_depth\_mm-sd,   
 ymax=sulcal\_depth\_mm+sd,   
 fill = dataset),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 labs(x = comp\_norm\_x,  
 y = depth\_y) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 0, face = "bold", vjust = .70),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"),  
 strip.text.x = element\_text(size = 12, face = "bold"),  
 axis.ticks.x = element\_blank(),   
 strip.background = element\_blank()) +   
 scale\_color\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#41b6c4", "#006837", "#2ca25f")) +   
 scale\_fill\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#74a9cf", "#006837", "#31a354")) +  
   
 guides(alpha = F) +   
 facet\_wrap(~hemi) +   
 scale\_y\_continuous(breaks=seq(0,15,2))  
comp\_depth\_raw.plot



# ggplot2::ggsave(filename = "comp\_depth\_raw\_plot.png",  
# plot = comp\_depth\_raw.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "print")

## Supplemental Figure 6b: Raw cortical thickness

### Statistics

# ANOVA  
comp\_raw\_thick.aov<- aov(cortical\_thickness\_mean ~ hemi \* group \* species,   
 data = ifrms\_compdev\_morphology)  
summary(comp\_raw\_thick.aov)

## Df Sum Sq Mean Sq F value Pr(>F)   
## hemi 1 0.14 0.138 0.860 0.35431   
## group 2 43.32 21.658 135.401 < 2e-16 \*\*\*  
## species 1 10.17 10.172 63.593 1.15e-14 \*\*\*  
## hemi:group 2 0.18 0.090 0.565 0.56866   
## hemi:species 1 1.12 1.116 6.979 0.00852 \*\*   
## group:species 2 0.61 0.306 1.910 0.14916   
## hemi:group:species 2 0.32 0.161 1.005 0.36665   
## Residuals 475 75.98 0.160   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

eta\_sq(comp\_raw\_thick.aov)

## term etasq  
## 1 hemi 0.001  
## 2 group 0.329  
## 3 species 0.077  
## 4 hemi:group 0.001  
## 5 hemi:species 0.008  
## 6 group:species 0.005  
## 7 hemi:group:species 0.002

# Main effect of group  
ifrms\_compdev\_morphology %>% group\_by(group) %>% summarise(mean = mean(cortical\_thickness\_mean))

## # A tibble: 3 x 2  
## group mean  
## \* <chr> <dbl>  
## 1 juvenile 3.67  
## 2 older-adult 2.94  
## 3 young-adult 3.39

# Main effect of species  
ifrms\_compdev\_morphology %>% group\_by(species) %>% summarise(mean = mean(cortical\_thickness\_mean))

## # A tibble: 2 x 2  
## species mean  
## \* <chr> <dbl>  
## 1 chimpanzee 3.07  
## 2 human 3.38

# Interaction effect between hemi and species  
ifrms\_compdev\_morphology %>% group\_by(hemi, species) %>% summarise(mean = mean(cortical\_thickness\_mean))

## `summarise()` has grouped output by 'hemi'. You can override using the `.groups` argument.

## # A tibble: 4 x 3  
## # Groups: hemi [2]  
## hemi species mean  
## <chr> <chr> <dbl>  
## 1 lh chimpanzee 2.91  
## 2 lh human 3.39  
## 3 rh chimpanzee 3.23  
## 4 rh human 3.38

The thickness results hold even with non-normalized thickness values.

### Plot

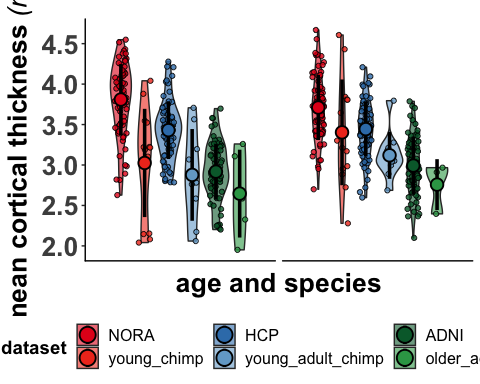
# Means for plot  
comp\_ct\_avg <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(cortical\_thickness\_mean = mean(cortical\_thickness\_mean))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

comp\_ct\_sd <- ifrms\_compdev\_morphology %>%   
 group\_by(label, dataset, hemi) %>%   
 summarise(sd = sd(cortical\_thickness\_mean))

## `summarise()` has grouped output by 'label', 'dataset'. You can override using the `.groups` argument.

# Plot  
comp\_ct\_stats <- merge(comp\_ct\_avg, comp\_ct\_sd, by = c("label", "dataset", "hemi"))  
ct\_y <- expression(paste(bold("mean cortical thickness "), italic("(mm)")))  
  
comp\_ct\_raw.plot <- ggplot(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = cortical\_thickness\_mean)) +  
 geom\_violin(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = cortical\_thickness\_mean, fill = dataset),   
 alpha = .6, position = dodge, width = 1) +   
 geom\_jitter(data = ifrms\_compdev\_morphology,   
 aes(x = label, y = cortical\_thickness\_mean, fill = dataset),   
 color = 'black', alpha = .8, shape = 21,  
 position=position\_jitterdodge(jitter.width = .3, dodge.width = .9, jitter.height = 0)) +  
 geom\_pointrange(data = comp\_ct\_stats,   
 aes(label, cortical\_thickness\_mean,   
 ymin=cortical\_thickness\_mean-sd, ymax=cortical\_thickness\_mean+sd,   
 fill = dataset),   
 shape = 21, position = dodge, size = 1.25, fatten = 3) +  
 labs(x = comp\_norm\_x,  
 y = ct\_y) +   
 theme(plot.title = element\_text(face = "bold", hjust = 0, size = 14),   
 plot.subtitle = element\_text(size = 12),  
 plot.caption = element\_text(size = 12, hjust = 1),  
 axis.title.x = element\_text(size=20, face = "bold", vjust = .70),  
 axis.title.y = element\_text(size=20, face = "bold"),  
 axis.text.x = element\_text(size = 0, face = "bold"),  
 axis.text.y = element\_text(size = 20, face = "bold"),  
 legend.title = element\_text(size=14, face = "bold"),   
 legend.text = element\_text(size=12),  
 legend.position = "bottom",  
 axis.ticks.x = element\_blank(),   
 axis.line = element\_line(colour = "black", linetype = "solid", lineend = "round"),  
 strip.text.x = element\_text(size = 0),  
 strip.background = element\_blank()) +   
 scale\_color\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#41b6c4", "#006837", "#2ca25f")) +   
 scale\_fill\_manual(breaks =   
 c("NORA", "young\_chimp", "HCP", "young\_adult\_chimp", "ADNI", "older\_adult\_chimp"),  
 values = c("#e41a1c", "#f03b20","#377eb8", "#74a9cf", "#006837", "#31a354")) +  
 scale\_y\_continuous(breaks=seq(0,4.5,.5)) +  
 guides(alpha = F) +   
 facet\_wrap(~hemi)  
comp\_ct\_raw.plot



# ggplot2::ggsave(filename = "comp\_ct\_raw\_plot.png",  
# plot = comp\_ct\_raw.plot,  
# device = "png",  
# width = 10,  
# height = 5,   
# units = "in",  
# dpi = "print")

# Main Text Tables

## Table 1: ADNI Table

adni\_scanning <- data.frame("participants" <- c(26, 8, 6, 6,   
 5, 5, 4, 2,  
 2, 1, 1, 1,  
 1, 1, 1, 1,  
 1),  
 "scanner" <- c("Siemens", "Siemens", "Philips", "GE",  
 "Philips", "Siemens", "GE", "Siemens",  
 "GE", "Philips", "Philips", "Philips",  
 "GE", "GE", "GE", "GE",  
 "Siemens"),  
 "magnetic field strength (T)" <- c("3", "3", "3", "1.5",  
 "3", "3", "1.5", "1.5",  
 "1.5", "3", "1.5", "1.5",  
 "1.5", "1.5", "1.5", "3",  
 "1.5"),  
 "TR (ms)" <- c(2300, 2300, 6.5, 8.6,  
 6.8, 2300, 8.9, 2400,  
 9.2, 6.8, 8.6, 8.5,  
 9.2, 9.1, 7.0, 7.0,  
 3000  
 ),  
 "TE (ms)" <- c(3.0, 3.0, 2.9, 3.8,  
 3.2, 3.0, 3.9, 3.5,  
 4.1, 3.1, 4.0, 4.0,  
 4.0, 4.0, 3.9, 3.0,  
 3.6  
 ),  
 "voxel\_size" <- c("1 x 1 x 1", "1.1 x 1.1 x 1.2", "1 x 1 x 1", "0.9 x 0.9 x 1.2",  
 "1 x 1 x 1.2", "1 x 1 x 1.2", "0.9 x 0.9 x 1.2", "1.3 x 1.3 x 1.2",  
 "0.9 x 0.9 x 1.2", "1 x 1 x 1.2", "0.9 x 0.9 x 1.2", "0.9 x 0.9 x 1.2",  
 "0.9 x 0.9 x 1.2", "0.9 x 0.9 x 1.2", "0.9 x 0.9 x 1.2", "1 x 1 x 1.2",  
 "1.3 x 1.3 x 1.2")  
 )  
  
names(adni\_scanning)[1] <- "participants"  
names(adni\_scanning)[2] <- "scanner manufacturer"  
names(adni\_scanning)[3] <- "magnetic field strength (T)"  
names(adni\_scanning)[4] <- "TR (ms)"  
names(adni\_scanning)[5] <- "TE (ms)"  
names(adni\_scanning)[6] <- "voxel\_size"  
adni\_scanning

## participants scanner manufacturer magnetic field strength (T) TR (ms)  
## 1 26 Siemens 3 2300.0  
## 2 8 Siemens 3 2300.0  
## 3 6 Philips 3 6.5  
## 4 6 GE 1.5 8.6  
## 5 5 Philips 3 6.8  
## 6 5 Siemens 3 2300.0  
## 7 4 GE 1.5 8.9  
## 8 2 Siemens 1.5 2400.0  
## 9 2 GE 1.5 9.2  
## 10 1 Philips 3 6.8  
## 11 1 Philips 1.5 8.6  
## 12 1 Philips 1.5 8.5  
## 13 1 GE 1.5 9.2  
## 14 1 GE 1.5 9.1  
## 15 1 GE 1.5 7.0  
## 16 1 GE 3 7.0  
## 17 1 Siemens 1.5 3000.0  
## TE (ms) voxel\_size  
## 1 3.0 1 x 1 x 1  
## 2 3.0 1.1 x 1.1 x 1.2  
## 3 2.9 1 x 1 x 1  
## 4 3.8 0.9 x 0.9 x 1.2  
## 5 3.2 1 x 1 x 1.2  
## 6 3.0 1 x 1 x 1.2  
## 7 3.9 0.9 x 0.9 x 1.2  
## 8 3.5 1.3 x 1.3 x 1.2  
## 9 4.1 0.9 x 0.9 x 1.2  
## 10 3.1 1 x 1 x 1.2  
## 11 4.0 0.9 x 0.9 x 1.2  
## 12 4.0 0.9 x 0.9 x 1.2  
## 13 4.0 0.9 x 0.9 x 1.2  
## 14 4.0 0.9 x 0.9 x 1.2  
## 15 3.9 0.9 x 0.9 x 1.2  
## 16 3.0 1 x 1 x 1.2  
## 17 3.6 1.3 x 1.3 x 1.2

adni\_scanning\_tab <- adni\_scanning %>% gt() %>%  
tab\_header(  
 title = html("<b>Table 1</b>"),  
 subtitle = html("<i>Scanning parameters of the healthy older adult participants<i/>")) %>%  
   
 cols\_label(  
 voxel\_size = html("voxel size (mm<sup>3</sup>)")   
 ) %>%  
tab\_source\_note(html("<i>Note.</i> This table illustrates the different scanning parameters used for each of our randomly-selected, healthy older adult participants from the Alzheimer's Disease Neuroimaging Initiative (ADNI) online database (http://adni.loni.usc.edu). For each different set of parameters, the number of participants, scanner manufacturer, magnetic field strength in Teslas (T), repetition time (TR) in ms, time to echo (TE) in ms, and voxel size in mm<sup>3</sup> are provided.")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:6) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
adni\_scanning\_tab

Table 1

Scanning parameters of the healthy older adult participants

participants

scanner manufacturer

magnetic field strength (T)

TR (ms)

TE (ms)

voxel size (mm3)

26

Siemens

3

2300.0

3.0

1 x 1 x 1

8

Siemens

3

2300.0

3.0

1.1 x 1.1 x 1.2

6

Philips

3

6.5

2.9

1 x 1 x 1

6

GE

1.5

8.6

3.8

0.9 x 0.9 x 1.2

5

Philips

3

6.8

3.2

1 x 1 x 1.2

5

Siemens

3

2300.0

3.0

1 x 1 x 1.2

4

GE

1.5

8.9

3.9

0.9 x 0.9 x 1.2

2

Siemens

1.5

2400.0

3.5

1.3 x 1.3 x 1.2

2

GE

1.5

9.2

4.1

0.9 x 0.9 x 1.2

1

Philips

3

6.8

3.1

1 x 1 x 1.2

1

Philips

1.5

8.6

4.0

0.9 x 0.9 x 1.2

1

Philips

1.5

8.5

4.0

0.9 x 0.9 x 1.2

1

GE

1.5

9.2

4.0

0.9 x 0.9 x 1.2

1

GE

1.5

9.1

4.0

0.9 x 0.9 x 1.2

1

GE

1.5

7.0

3.9

0.9 x 0.9 x 1.2

1

GE

3

7.0

3.0

1 x 1 x 1.2

1

Siemens

1.5

3000.0

3.6

1.3 x 1.3 x 1.2

Note. This table illustrates the different scanning parameters used for each of our randomly-selected, healthy older adult participants from the Alzheimer’s Disease Neuroimaging Initiative (ADNI) online database (<http://adni.loni.usc.edu>). For each different set of parameters, the number of participants, scanner manufacturer, magnetic field strength in Teslas (T), repetition time (TR) in ms, time to echo (TE) in ms, and voxel size in mm3 are provided.

#gtsave(adni\_scanning\_tab, file = "table1\_ADNI.png")

## Table 2: Discovery incidence rates

discovery\_IR <- data.frame("sulcus" <- c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p"   
 ),  
 "LH count" <- c("36/36", "36/36", "36/36", "36/36", "36/36",  
 "36/36", "35/36", "36/36", "23/36", "36/36", "19/36"  
 ),  
 "LH %" <- c(100, 100, 100, 100, 100,  
 100, 97.22, 100, 63.89, 100, 52.78  
 ),  
 "RH count" <- c("36/36", "36/36", "36/36", "36/36", "36/36",  
 "36/36", "34/36", "36/36", "18/36", "36/36", "23/36"  
 ),  
 "RH %" <- c(100, 100, 100, 100, 100,  
 100, 94.44, 100, 50, 100, 63.89  
 )  
 )  
  
names(discovery\_IR)[1] <- "sulci"  
names(discovery\_IR)[2] <- "appearance in LH"  
names(discovery\_IR)[3] <- "LH %"  
names(discovery\_IR)[4] <- "appearance in RH"  
names(discovery\_IR)[5] <- "RH %"  
  
  
discovery\_IR\_tab <- discovery\_IR %>% gt() %>%  
tab\_header(  
 title = md("\*\*Table 2\*\*"),  
 subtitle = md("\*Incidence rates of PCC and PRC sulci in the discovery sample\*")) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(1),  
 rows = 1:11  
 )) %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the \*discovery\* young adult sample (N = 36 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); parieto-occipital sulcus (\*pos\*); posterior intracingulate sulcus (\*icgs-p\*); posterior precuneal sulcus (\*prcus-p\*); precuneal limiting sulcus (\*prculs\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*); superior parietal sulcus (\*sps\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:5) %>%  
 tab\_style(  
style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
discovery\_IR\_tab

Table 2

Incidence rates of PCC and PRC sulci in the discovery sample

sulci

appearance in LH

LH %

appearance in RH

RH %

pos

36/36

100.00

36/36

100.00

prculs

36/36

100.00

36/36

100.00

prcus-p

36/36

100.00

36/36

100.00

prcus-i

36/36

100.00

36/36

100.00

prcus-a

36/36

100.00

36/36

100.00

spls

36/36

100.00

36/36

100.00

sps

35/36

97.22

34/36

94.44

mcgs

36/36

100.00

36/36

100.00

sspls

23/36

63.89

18/36

50.00

ifrms

36/36

100.00

36/36

100.00

icgs-p

19/36

52.78

23/36

63.89

Note. This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the discovery young adult sample (N = 36 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); parieto-occipital sulcus (pos); posterior intracingulate sulcus (icgs-p); posterior precuneal sulcus (prcus-p); precuneal limiting sulcus (prculs); splenial sulcus (spls); subsplenial sulcus (sspls); superior parietal sulcus (sps).

#gtsave(discovery\_IR\_tab, file = "Table\_2\_disc\_IR.png")

## Table 3: Replication incidence rates

replication\_IR <- data.frame("sulcus" <- c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p"   
 ),  
 "LH count" <- c("36/36", "36/36", "36/36", "36/36", "36/36",  
 "36/36", "30/36", "36/36", "17/36", "36/36", "24/36"  
 ),  
 "LH %" <- c(100, 100, 100, 100, 100,  
 100, 83.33, 100, 47.22, 100, 66.67  
 ),  
 "RH count" <- c("36/36", "36/36", "36/36", "36/36", "36/36",  
 "36/36", "34/36", "36/36", "20/36", "36/36", "23/36"  
 ),  
 "RH %" <- c(100, 100, 100, 100, 100,  
 100, 94.44, 100, 55.56, 100, 63.89  
 )  
 )  
  
names(replication\_IR)[1] <- "sulci"  
names(replication\_IR)[2] <- "appearance in LH"  
names(replication\_IR)[3] <- "LH %"  
names(replication\_IR)[4] <- "appearance in RH"  
names(replication\_IR)[5] <- "RH %"  
  
  
replication\_IR\_tab <- replication\_IR %>% gt() %>%  
tab\_header(  
 title = md("\*\*Table 3\*\*"),  
 subtitle = md("\*Incidence rates of PCC and PRC sulci in the replication sample\*")) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(1),  
 rows = 1:11  
 )) %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the \*replication\* young adult sample (N = 36 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); parieto-occipital sulcus (\*pos\*); posterior intracingulate sulcus (\*icgs-p\*); posterior precuneal sulcus (\*prcus-p\*); precuneal limiting sulcus (\*prculs\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*); superior parietal sulcus (\*sps\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:5) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
replication\_IR\_tab

Table 3

Incidence rates of PCC and PRC sulci in the replication sample

sulci

appearance in LH

LH %

appearance in RH

RH %

pos

36/36

100.00

36/36

100.00

prculs

36/36

100.00

36/36

100.00

prcus-p

36/36

100.00

36/36

100.00

prcus-i

36/36

100.00

36/36

100.00

prcus-a

36/36

100.00

36/36

100.00

spls

36/36

100.00

36/36

100.00

sps

30/36

83.33

34/36

94.44

mcgs

36/36

100.00

36/36

100.00

sspls

17/36

47.22

20/36

55.56

ifrms

36/36

100.00

36/36

100.00

icgs-p

24/36

66.67

23/36

63.89

Note. This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the replication young adult sample (N = 36 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); parieto-occipital sulcus (pos); posterior intracingulate sulcus (icgs-p); posterior precuneal sulcus (prcus-p); precuneal limiting sulcus (prculs); splenial sulcus (spls); subsplenial sulcus (sspls); superior parietal sulcus (sps).

#gtsave(replication\_IR\_tab, file = "Table\_3\_repl\_IR.png")

## Table 4 and 5: Locational coupling between the IFRMS and Control B network (tables)

# Control B  
discovery\_replication\_lg <- data.frame(  
 "coordinate" <- c("right (LH)", "right (RH)", "anterior (LH)", "anterior (RH)",   
 "superior (LH)", "superior (RH)",  
   
 "right (LH)", "right (RH)", "anterior (LH)", "anterior (RH)",   
 "superior (LH)", "superior (RH)"  
 ),  
 "df" <- c("1, 33", "1, 34", "1, 33", "1, 34", "1, 33", "1, 34",  
   
 "1, 31", "1, 32", "1, 31", "1,32", "1, 31", "1, 32"  
   
 ),  
 "β" <- c(0.61, 0.5, 0.57, 0.44, 0.98, 0.74,  
   
 0.77, 1.14, 0.4, 0.47, 0.82, 0.92  
 ),  
 "standard error" <- c(0.16, 0.17, 0.11, 0.1, 0.1, 0.08,  
   
 0.16, 0.39, 0.11, 0.16, 0.1, 0.09  
 ),   
 "t" <- c(3.77, 2.87, 5.37, 4.46, 9.68, 9.65,  
   
 4.96, 2.91, 3.71, 2.96, 8.29, 9.69  
 ),  
 "p-value" <- c("<0.001", "0.007", "<0.001", "<0.001", "<0.001", "<0.001",  
   
 "<0.001", "0.007", "0.001", "0.006", "<0.001", "<0.001"  
 ),  
 "adjusted R^2" <- c(0.28, 0.17, 0.45, 0.35, 0.73, 0.72,  
   
 0.42, 0.18, 0.29, 0.19, 0.68, 0.74  
 ),  
 "F" <- c(14.23, 8.23, 28.84, 19.91, 93.71, 93.04,  
   
 24.61, 8.44, 13.77, 8.74, 68.8, 93.95  
 ),  
 "Adjusted p-value" <- c("<0.001", "0.007", "<0.001", "<0.001", "<0.001", "<0.001",  
   
 "<0.001", "0.007", "0.001", "0.006", "<0.001", "<0.001"  
 )  
 )  
  
names(discovery\_replication\_lg)[1] <- "RAS coordinate"  
names(discovery\_replication\_lg)[2] <- "df"  
names(discovery\_replication\_lg)[3] <- "coefficient"  
names(discovery\_replication\_lg)[4] <- "SE"  
names(discovery\_replication\_lg)[5] <- "t value"  
names(discovery\_replication\_lg)[6] <- "p\_value"  
names(discovery\_replication\_lg)[7] <- "adjusted\_R2"  
names(discovery\_replication\_lg)[8] <- "F-statistic"  
names(discovery\_replication\_lg)[9] <- "adjusted\_p\_value"  
  
discovery\_replication\_lg\_tab <- discovery\_replication\_lg %>% gt() %>%  
tab\_header(  
 title = md("<b>Table 4</b>"),  
 subtitle = md("<i>Regression analysis summary for ifrms location predicting CCN-b location<i/>")) %>%  
 cols\_label(  
 coefficient = html("<i>β</i>"),  
 adjusted\_R2 = html("adjusted R<sup>2</sup>"),  
 p\_value = html("<i>p</i>-value"),  
 adjusted\_p\_value = html("adjusted <i>p</i>-value")  
 ) %>%  
 tab\_row\_group(  
 group = "replication",  
 rows = 7:12) %>%  
 tab\_row\_group(  
 group = "discovery",  
 rows = 1:6) %>%  
tab\_source\_note(html("<i>Note.</i> This table provides the output of each linear regression run between each of the RAS (right, anterior, superior) coordinates of the inframarginal sulcus (<i>ifrms</i>; predictor variable) and cognitive control network B (CCN-b; outcome variable). A separate linear regression was run for each coordinate in each hemisphere (left (LH) and right (RH)) and sample (<i>discovery</i> and <i>replication</i>). The <i>p</i>-values presented in this table are FDR corrected for multiple comparisons. Exclusions: The LH of one participant in each sample was not included due to not having a CCN-b node near the <i>ifrms</i> and two participants from the <i>replication</i> sample were not included due to not having resting-state parcellations available. The other abbreviations used are as follows: degrees of freedom (df); regression beta coefficient (<i>β</i>); standard error (SE).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 column\_labels.border.top.color = "black",  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:9) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )   
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
discovery\_replication\_lg\_tab

Table 4

Regression analysis summary for ifrms location predicting CCN-b location

RAS coordinate

df

β

SE

t value

p-value

adjusted R2

F-statistic

adjusted p-value

discovery

right (LH)

1, 33

0.61

0.16

3.77

<0.001

0.28

14.23

<0.001

right (RH)

1, 34

0.50

0.17

2.87

0.007

0.17

8.23

0.007

anterior (LH)

1, 33

0.57

0.11

5.37

<0.001

0.45

28.84

<0.001

anterior (RH)

1, 34

0.44

0.10

4.46

<0.001

0.35

19.91

<0.001

superior (LH)

1, 33

0.98

0.10

9.68

<0.001

0.73

93.71

<0.001

superior (RH)

1, 34

0.74

0.08

9.65

<0.001

0.72

93.04

<0.001

replication

right (LH)

1, 31

0.77

0.16

4.96

<0.001

0.42

24.61

<0.001

right (RH)

1, 32

1.14

0.39

2.91

0.007

0.18

8.44

0.007

anterior (LH)

1, 31

0.40

0.11

3.71

0.001

0.29

13.77

0.001

anterior (RH)

1,32

0.47

0.16

2.96

0.006

0.19

8.74

0.006

superior (LH)

1, 31

0.82

0.10

8.29

<0.001

0.68

68.80

<0.001

superior (RH)

1, 32

0.92

0.09

9.69

<0.001

0.74

93.95

<0.001

Note. This table provides the output of each linear regression run between each of the RAS (right, anterior, superior) coordinates of the inframarginal sulcus (ifrms; predictor variable) and cognitive control network B (CCN-b; outcome variable). A separate linear regression was run for each coordinate in each hemisphere (left (LH) and right (RH)) and sample (discovery and replication). The p-values presented in this table are FDR corrected for multiple comparisons. Exclusions: The LH of one participant in each sample was not included due to not having a CCN-b node near the ifrms and two participants from the replication sample were not included due to not having resting-state parcellations available. The other abbreviations used are as follows: degrees of freedom (df); regression beta coefficient (β); standard error (SE).

#gtsave(discovery\_replication\_lg\_tab, file = "lg\_Table\_4.png")  
  
  
# Control C  
discovery\_replication\_lg\_CCNc <- data.frame(  
 "coordinate" <- c("right (LH)", "right (RH)", "anterior (LH)", "anterior (RH)",   
 "superior (LH)", "superior (RH)",  
   
 "right (LH)", "right (RH)", "anterior (LH)", "anterior (RH)",   
 "superior (LH)", "superior (RH)"  
 ),  
 "df" <- c("1, 34", "1, 34", "1, 34", "1, 34", "1, 34", "1, 34",  
   
 "1, 32", "1, 32", "1, 32", "1,32", "1, 32", "1, 32"  
 ),  
 "coefficient" <- c(0.8, 0.32, 0.43, 0.3, 0.9, 0.71,  
   
 0.56, 0.55, 0.32, 0.41, 0.81, 0.86  
 ),  
 "standard error" <- c(0.16, 0.09, 0.11, 0.09, 0.1, 0.08,  
   
 0.09, 0.14, 0.1, 0.1, 0.09, 0.08  
 ),   
 "t" <- c(5.07, 3.43, 3.87, 3.38, 8.69, 9.31,  
   
 6.02, 3.82, 3.11, 4.02, 8.96, 10.24  
 ),  
 "p-value" <- c("<0.001", "0.002", "<0.001", "0.002", "<0.001","<0.001",  
   
 "<0.001", "<0.001", "0.004", "<0.001", "<0.001", "<0.001"  
 ),  
 "adjusted R^2" <- c(0.41, 0.23, 0.28, 0.23, 0.68, 0.71,  
   
 0.52, 0.29, 0.21, 0.32, 0.71, 0.76  
 ),  
 "F" <- c(25.75, 11.74, 14.94, 11.43, 75.47, 86.62,  
   
 36.21, 14.62, 9.67, 16.19, 80.29, 104.9  
 ),  
 "Adjusted p-value" <- c("<0.001", "0.002", "<0.001", "0.002", "<0.001", "<0.001",  
   
 "<0.001", "<0.001", "0.004", "<0.001", "<0.001", "<0.001"  
 )  
 )  
  
names(discovery\_replication\_lg\_CCNc)[1] <- "RAS coordinate"  
names(discovery\_replication\_lg\_CCNc)[2] <- "df"  
names(discovery\_replication\_lg\_CCNc)[3] <- "coefficient"  
names(discovery\_replication\_lg\_CCNc)[4] <- "SE"  
names(discovery\_replication\_lg\_CCNc)[5] <- "t value"  
names(discovery\_replication\_lg\_CCNc)[6] <- "p\_value"  
names(discovery\_replication\_lg\_CCNc)[7] <- "adjusted\_R2"  
names(discovery\_replication\_lg\_CCNc)[8] <- "F-statistic"  
names(discovery\_replication\_lg\_CCNc)[9] <- "adjusted\_p\_value"  
  
discovery\_replication\_lg\_CCNc\_tab <- discovery\_replication\_lg\_CCNc %>% gt() %>%  
tab\_header(  
 title = md("<b>Table 5</b>"),  
 subtitle = md("<i>Regression analysis summary for ifrms location predicting CCN-c location</i>")) %>%  
 cols\_label(  
 coefficient = html("<i>β</i>"),  
 adjusted\_R2 = html("adjusted R<sup>2</sup>"),  
 p\_value = html("<i>p</i>-value"),  
 adjusted\_p\_value = html("adjusted <i>p</i>-value")  
 ) %>%  
 tab\_row\_group(  
 group = "replication",  
 rows = 7:12) %>%  
 tab\_row\_group(  
 group = "discovery",  
 rows = 1:6) %>%  
tab\_source\_note(html("<i>Note.</i> This table provides the output of each linear regression run between each of the RAS (right, anterior, superior) coordinates of the inframarginal sulcus (<i>ifrms</i>; predictor variable) and cognitive control network C (CCN-c; outcome variable). A separate linear regression was run for each coordinate in each hemisphere (left (LH) and right (RH)) and sample (<i>discovery</i> and <i>replication</i>). The <i>p</i>-values presented in this table are FDR corrected for multiple comparisons. Exclusions: Two participants from the <i>replication</i> sample were not included due to not having resting-state parcellations available. The other abbreviations used are as follows: degrees of freedom (df); regression beta coefficient (<i>β</i>); standard error (SE).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 column\_labels.border.top.color = "black",  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:9) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
discovery\_replication\_lg\_CCNc\_tab

Table 5

Regression analysis summary for ifrms location predicting CCN-c location

RAS coordinate

df

β

SE

t value

p-value

adjusted R2

F-statistic

adjusted p-value

discovery

right (LH)

1, 34

0.80

0.16

5.07

<0.001

0.41

25.75

<0.001

right (RH)

1, 34

0.32

0.09

3.43

0.002

0.23

11.74

0.002

anterior (LH)

1, 34

0.43

0.11

3.87

<0.001

0.28

14.94

<0.001

anterior (RH)

1, 34

0.30

0.09

3.38

0.002

0.23

11.43

0.002

superior (LH)

1, 34

0.90

0.10

8.69

<0.001

0.68

75.47

<0.001

superior (RH)

1, 34

0.71

0.08

9.31

<0.001

0.71

86.62

<0.001

replication

right (LH)

1, 32

0.56

0.09

6.02

<0.001

0.52

36.21

<0.001

right (RH)

1, 32

0.55

0.14

3.82

<0.001

0.29

14.62

<0.001

anterior (LH)

1, 32

0.32

0.10

3.11

0.004

0.21

9.67

0.004

anterior (RH)

1,32

0.41

0.10

4.02

<0.001

0.32

16.19

<0.001

superior (LH)

1, 32

0.81

0.09

8.96

<0.001

0.71

80.29

<0.001

superior (RH)

1, 32

0.86

0.08

10.24

<0.001

0.76

104.90

<0.001

Note. This table provides the output of each linear regression run between each of the RAS (right, anterior, superior) coordinates of the inframarginal sulcus (ifrms; predictor variable) and cognitive control network C (CCN-c; outcome variable). A separate linear regression was run for each coordinate in each hemisphere (left (LH) and right (RH)) and sample (discovery and replication). The p-values presented in this table are FDR corrected for multiple comparisons. Exclusions: Two participants from the replication sample were not included due to not having resting-state parcellations available. The other abbreviations used are as follows: degrees of freedom (df); regression beta coefficient (β); standard error (SE).

#gtsave(discovery\_replication\_lg\_CCNc\_tab, file = "lg\_Table\_5.png")

## Table 6: NORA incidence rates

nora\_IR <- data.frame("sulcus" <- c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p"   
 ),  
 "LH count" <- c("72/72", "72/72", "72/72", "72/72", "72/72",  
 "72/72", "64/72", "72/72", "38/72" , "72/72", "32/72"  
 ),  
 "LH %" <- c(100, 100, 100, 100, 100,  
 100, 88.89, 100, 52.78, 100, 44.44  
 ),  
 "RH count" <- c("72/72", "72/72", "72/72", "72/72", "72/72",  
 "72/72", "67/72", "72/72", "34/72" , "72/72", "36/72"  
 ),  
 "RH %" <- c(100, 100, 100, 100, 100,  
 100, 93.06, 100, 47.22, 100, 50  
 )  
 )  
  
names(nora\_IR)[1] <- "sulci"  
names(nora\_IR)[2] <- "appearance in LH"  
names(nora\_IR)[3] <- "LH %"  
names(nora\_IR)[4] <- "appearance in RH"  
names(nora\_IR)[5] <- "RH %"  
  
  
nora\_IR\_tab <- nora\_IR %>% gt() %>%  
tab\_header(  
 title = md("\*\*Table 6\*\*"),  
 subtitle = md("\*Incidence rates of PCC and PRC sulci in the juvenile sample\*")) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(1),  
 rows = 1:11  
 )) %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the juvenile sample (N = 72 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); parieto-occipital sulcus (\*pos\*); posterior intracingulate sulcus (\*icgs-p\*); posterior precuneal sulcus (\*prcus-p\*); precuneal limiting sulcus (\*prculs\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*); superior parietal sulcus (\*sps\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:5) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
nora\_IR\_tab

Table 6

Incidence rates of PCC and PRC sulci in the juvenile sample

sulci

appearance in LH

LH %

appearance in RH

RH %

pos

72/72

100.00

72/72

100.00

prculs

72/72

100.00

72/72

100.00

prcus-p

72/72

100.00

72/72

100.00

prcus-i

72/72

100.00

72/72

100.00

prcus-a

72/72

100.00

72/72

100.00

spls

72/72

100.00

72/72

100.00

sps

64/72

88.89

67/72

93.06

mcgs

72/72

100.00

72/72

100.00

sspls

38/72

52.78

34/72

47.22

ifrms

72/72

100.00

72/72

100.00

icgs-p

32/72

44.44

36/72

50.00

Note. This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the juvenile sample (N = 72 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); parieto-occipital sulcus (pos); posterior intracingulate sulcus (icgs-p); posterior precuneal sulcus (prcus-p); precuneal limiting sulcus (prculs); splenial sulcus (spls); subsplenial sulcus (sspls); superior parietal sulcus (sps).

#gtsave(nora\_IR\_tab, file = "Table\_6\_nora\_IR.png")

## Table 7: ADNI incidence rates

ADNI\_IR <- data.frame("sulcus" <- c("pos", "prculs", "prcus-p", "prcus-i", "prcus-a",   
 "spls", "sps", "mcgs", "sspls", "ifrms", "icgs-p"   
 ),  
 "LH count" <- c("72/72", "72/72", "72/72", "72/72", "72/72",  
 "72/72", "59/72", "72/72", "33/72" , "72/72", "27/72"  
 ),  
 "LH %" <- c(100, 100, 100, 100, 100,  
 100, 81.94, 100, 45.83, 100, 37.5  
 ),  
 "RH count" <- c("72/72", "72/72", "72/72", "72/72", "72/72",  
 "72/72", "55/72", "72/72", "32/72" , "72/72", "28/72"  
 ),  
 "RH %" <- c(100, 100, 100, 100, 100,  
 100, 76.39, 100, 44.44, 100, 38.89  
 )  
 )  
  
names(ADNI\_IR)[1] <- "sulci"  
names(ADNI\_IR)[2] <- "appearance in LH"  
names(ADNI\_IR)[3] <- "LH %"  
names(ADNI\_IR)[4] <- "appearance in RH"  
names(ADNI\_IR)[5] <- "RH %"  
  
  
ADNI\_IR\_tab <- ADNI\_IR %>% gt() %>%  
tab\_header(  
 title = md("\*\*Table 7\*\*"),  
 subtitle = md("\*Incidence rates of PCC and PRC sulci in the healthy older adult sample\*")) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(1),  
 rows = 1:11  
 )) %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the healhty older adult sample (N = 72 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); parieto-occipital sulcus (\*pos\*); posterior intracingulate sulcus (\*icgs-p\*); posterior precuneal sulcus (\*prcus-p\*); precuneal limiting sulcus (\*prculs\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*); superior parietal sulcus (\*sps\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:5) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
ADNI\_IR\_tab

Table 7

Incidence rates of PCC and PRC sulci in the healthy older adult sample

sulci

appearance in LH

LH %

appearance in RH

RH %

pos

72/72

100.00

72/72

100.00

prculs

72/72

100.00

72/72

100.00

prcus-p

72/72

100.00

72/72

100.00

prcus-i

72/72

100.00

72/72

100.00

prcus-a

72/72

100.00

72/72

100.00

spls

72/72

100.00

72/72

100.00

sps

59/72

81.94

55/72

76.39

mcgs

72/72

100.00

72/72

100.00

sspls

33/72

45.83

32/72

44.44

ifrms

72/72

100.00

72/72

100.00

icgs-p

27/72

37.50

28/72

38.89

Note. This table illustrates the incident rates of the 8-11 definable PCC and PRC sulci in the healhty older adult sample (N = 72 participants). The incidence rate of each sulcus (posterior to anterior) is provided in number and percent for both the left (LH) and right hemispheres (RH). The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); parieto-occipital sulcus (pos); posterior intracingulate sulcus (icgs-p); posterior precuneal sulcus (prcus-p); precuneal limiting sulcus (prculs); splenial sulcus (spls); subsplenial sulcus (sspls); superior parietal sulcus (sps).

#gtsave(ADNI\_IR\_tab, file = "Table\_7\_adni\_IR.png")

# Supplementary Tables: Sulcal Type Tables

## Table 1: Discovery Prcuneal Sulci

disc\_prcus\_types <- data.frame("mcst" <- c("LH (n=36)", "RH (n=36)", "LH (n=36)", "RH (n=36)", "LH (n=36)", "RH (n=36)"),  
 "1" <- c("spls", "spls", "spls", "spls", "spls", "spls"),  
 "percent" <- c(55.6, 41.7, 47.2, 61.1, 77.8, 58.3),  
 "2" <- c("free", "free", "free", "prcus-a", "prcus-i", "mcgs"),  
 "percent" <- c(36.1, 38.9, 38.9, 22.2, 13.9, 27.8),  
 "3" <- c("prcus-i", "prcus-i", "prcus-p", "prcus-p","free", "prcus-i"),  
 "percent" <- c(13.9, 13.9, 13.9, 13.9, 11.1, 22.2))  
  
names(disc\_prcus\_types)[1] <- "Sulci"  
names(disc\_prcus\_types)[2] <- "First"  
names(disc\_prcus\_types)[3] <- "first\_percent"  
names(disc\_prcus\_types)[4] <- "Second"  
names(disc\_prcus\_types)[5] <- "second\_percent"  
names(disc\_prcus\_types)[6] <- "Third"  
names(disc\_prcus\_types)[7] <- "third\_percent"  
  
disc\_prcus\_types\_tab <- disc\_prcus\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 1\*\*"),  
 subtitle = md("\*Most common intersections of the discovery sample's precuneal sulci\*")) %>%  
tab\_row\_group(  
 group = "prcus-p",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "prcus-i",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "prcus-a",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (\*prcus\*) identified in the \*discovery\* young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); posterior precuneal sulcus (\*prcus-p\*); splenial sulcus (\*spls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
disc\_prcus\_types\_tab

Supplementary Table 1

Most common intersections of the discovery sample’s precuneal sulci

Sulci

First

%

Second

%

Third

%

prcus-a

LH (n=36)

spls

77.8

prcus-i

13.9

free

11.1

RH (n=36)

spls

58.3

mcgs

27.8

prcus-i

22.2

prcus-i

LH (n=36)

spls

47.2

free

38.9

prcus-p

13.9

RH (n=36)

spls

61.1

prcus-a

22.2

prcus-p

13.9

prcus-p

LH (n=36)

spls

55.6

free

36.1

prcus-i

13.9

RH (n=36)

spls

41.7

free

38.9

prcus-i

13.9

Note. This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (prcus) identified in the discovery young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); posterior precuneal sulcus (prcus-p); splenial sulcus (spls).

#gtsave(disc\_prcus\_types\_tab, file = "supp\_Table1.png")

## Table 2: Discovery Tertiary Sulci

disc\_tert\_types <- data.frame("mcst" <- c("LH (n=23)", "RH (n=18)", "LH (n=36)", "RH (n=36)", "LH (n=19)", "RH (n=23)"),  
 "1" <- c("free", "free", "free", "free", "free", "free"),  
 "percent" <- c(73.9, 77.8, 83.3, 80.6, 78.9, 95.7),  
 "2" <- c("cas", "cas", "icgs-p", "spls", "ifrms", "mcgs"),  
 "percent" <- c(26.1, 22.2, 8.3, 16.7, 15.8, 4.3),  
 "3" <- c("---", "---", "mcgs", "mcgs", "mcgs", "---"),  
 "percent" <- c(0, 0, 5.6, 2.8, 5.3, 0))  
  
names(disc\_tert\_types)[1] <- "Sulci"  
names(disc\_tert\_types)[2] <- "First"  
names(disc\_tert\_types)[3] <- "first\_percent"  
names(disc\_tert\_types)[4] <- "Second"  
names(disc\_tert\_types)[5] <- "second\_percent"  
names(disc\_tert\_types)[6] <- "Third"  
names(disc\_tert\_types)[7] <- "third\_percent"  
  
disc\_tert\_types\_tab <- disc\_tert\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 2\*\*"),  
 subtitle = md("\*Most common intersections of the discovery sample's PCC tertiary sulci\*")) %>%  
#tab\_stubhead(label = md("Sulci")) %>%  
tab\_row\_group(  
 group = "sspls",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "ifrms",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "icgs-p",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the \*discovery\* young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (\*cas\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); no other option (---); posterior intracingulate sulcus (\*icgs-p\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
disc\_tert\_types\_tab

Supplementary Table 2

Most common intersections of the discovery sample’s PCC tertiary sulci

Sulci

First

%

Second

%

Third

%

icgs-p

LH (n=19)

free

78.9

ifrms

15.8

mcgs

5.3

RH (n=23)

free

95.7

mcgs

4.3

—

0.0

ifrms

LH (n=36)

free

83.3

icgs-p

8.3

mcgs

5.6

RH (n=36)

free

80.6

spls

16.7

mcgs

2.8

sspls

LH (n=23)

free

73.9

cas

26.1

—

0.0

RH (n=18)

free

77.8

cas

22.2

—

0.0

Note. This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the discovery young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (cas); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); no other option (—); posterior intracingulate sulcus (icgs-p); splenial sulcus (spls); subsplenial sulcus (sspls).

#gtsave(disc\_tert\_types\_tab, file = "supp\_Table2.png")

## Table 3: Replication Prcuneal Sulci

rep\_prcus\_types <- data.frame("mcst" <- c("LH (n=36)", "RH (n=36)", "LH (n=36)", "RH (n=36)", "LH (n=36)", "RH (n=36)"),  
 "1" <- c("spls", "spls", "spls", "spls", "spls", "spls"),  
 "percent" <- c(55.6, 55.6, 63.9, 63.9, 83.3, 72.2),  
 "2" <- c("free", "free", "prcus-a", "free", "prcus-i", "prcus-i"),  
 "percent" <- c(33.3, 36.1, 22.2, 25.0, 22.2, 19.4),  
 "3" <- c("prcus-i", "prcus-i", "free", "prcus-a", "mcgs", "mcgs"),  
 "percent" <- c(13.9, 11.1, 22.2, 19.4, 13.9, 16.7))  
  
names(rep\_prcus\_types)[1] <- "Sulci"  
names(rep\_prcus\_types)[2] <- "First"  
names(rep\_prcus\_types)[3] <- "first\_percent"  
names(rep\_prcus\_types)[4] <- "Second"  
names(rep\_prcus\_types)[5] <- "second\_percent"  
names(rep\_prcus\_types)[6] <- "Third"  
names(rep\_prcus\_types)[7] <- "third\_percent"  
  
rep\_prcus\_types\_tab <- rep\_prcus\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 3\*\*"),  
 subtitle = md("\*Most common intersections of the replication sample's precuneal sulci\*")) %>%  
tab\_row\_group(  
 group = "prcus-p",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "prcus-i",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "prcus-a",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (\*prcus\*) identified in the \*replication\* young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); posterior precuneal sulcus (\*prcus-p\*); splenial sulcus (\*spls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
rep\_prcus\_types\_tab

Supplementary Table 3

Most common intersections of the replication sample’s precuneal sulci

Sulci

First

%

Second

%

Third

%

prcus-a

LH (n=36)

spls

83.3

prcus-i

22.2

mcgs

13.9

RH (n=36)

spls

72.2

prcus-i

19.4

mcgs

16.7

prcus-i

LH (n=36)

spls

63.9

prcus-a

22.2

free

22.2

RH (n=36)

spls

63.9

free

25.0

prcus-a

19.4

prcus-p

LH (n=36)

spls

55.6

free

33.3

prcus-i

13.9

RH (n=36)

spls

55.6

free

36.1

prcus-i

11.1

Note. This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (prcus) identified in the replication young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); posterior precuneal sulcus (prcus-p); splenial sulcus (spls).

#gtsave(rep\_prcus\_types\_tab, file = "supp\_Table3.png")

## Table 4: Replication Tertiary Sulci

rep\_tert\_types <- data.frame("mcst" <- c("LH (n=17)", "RH (n=20)", "LH (n=36)", "RH (n=36)", "LH (n=24)", "RH (n=23)"),  
 "$1^st$" <- c("free", "free", "free", "free", "free", "free"),  
 "percent" <- c(76.5, 55.0, 66.7, 61.1, 87.5, 82.6),  
 "$2^nd$" <- c("cas", "cas", "spls", "spls", "ifrms", "ifrms"),  
 "percent" <- c(17.6, 40.0, 16.7, 25.0, 8.3, 8.7),  
 "$3^rd$" <- c("spls", "spls", "mcgs", "mcgs", "mcgs", "cgs"),  
 "percent" <- c(5.9, 5.0, 11.1, 8.3, 4.2, 8.7))  
  
names(rep\_tert\_types)[1] <- "Sulci"  
names(rep\_tert\_types)[2] <- "First"  
names(rep\_tert\_types)[3] <- "first\_percent"  
names(rep\_tert\_types)[4] <- "Second"  
names(rep\_tert\_types)[5] <- "second\_percent"  
names(rep\_tert\_types)[6] <- "Third"  
names(rep\_tert\_types)[7] <- "third\_percent"  
  
rep\_tert\_types\_tab <- rep\_tert\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 4\*\*"),  
 subtitle = md("\*Most common intersections of the replication sample's PCC tertiary sulci\*")) %>%  
#tab\_stubhead(label = md("Sulci")) %>%  
tab\_row\_group(  
 group = "sspls",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "ifrms",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "icgs-p",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the \*replication\* young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (\*cas\*); cingulate sulcus (\*cgs\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); posterior intracingulate sulcus (\*icgs-p\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
rep\_tert\_types\_tab

Supplementary Table 4

Most common intersections of the replication sample’s PCC tertiary sulci

Sulci

First

%

Second

%

Third

%

icgs-p

LH (n=24)

free

87.5

ifrms

8.3

mcgs

4.2

RH (n=23)

free

82.6

ifrms

8.7

cgs

8.7

ifrms

LH (n=36)

free

66.7

spls

16.7

mcgs

11.1

RH (n=36)

free

61.1

spls

25.0

mcgs

8.3

sspls

LH (n=17)

free

76.5

cas

17.6

spls

5.9

RH (n=20)

free

55.0

cas

40.0

spls

5.0

Note. This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the replication young adult sample (N = 36 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (cas); cingulate sulcus (cgs); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); posterior intracingulate sulcus (icgs-p); splenial sulcus (spls); subsplenial sulcus (sspls).

#gtsave(rep\_tert\_types\_tab, file = "supp\_Table4.png")

## Table 5: NORA Prcuneal Sulci

nora\_prcus\_types <- data.frame("mcst" <- c("LH (n=72)", "RH (n=72)", "LH (n=72)", "RH (n=72)", "LH (n=72)", "RH (n=72)"),  
 "1" <- c("spls", "spls", "spls", "spls", "spls", "spls"),  
 "percent" <- c(55.6, 52.8, 68.1, 61.1, 79.2, 68.1),  
 "2" <- c("free", "free", "prcus-a", "free", "prcus-i", "prcus-i"),  
 "percent" <- c(33.3, 37.5, 22.2, 31.9, 19.4, 22.2),  
 "3" <- c("prcus-i", "prcus-i", "free", "prcus-a", "mcgs", "free"),  
 "percent" <- c(15.3, 19.4, 20.8, 22.2, 9.7, 20.8))  
  
names(nora\_prcus\_types)[1] <- "Sulci"  
names(nora\_prcus\_types)[2] <- "First"  
names(nora\_prcus\_types)[3] <- "first\_percent"  
names(nora\_prcus\_types)[4] <- "Second"  
names(nora\_prcus\_types)[5] <- "second\_percent"  
names(nora\_prcus\_types)[6] <- "Third"  
names(nora\_prcus\_types)[7] <- "third\_percent"  
  
nora\_prcus\_types\_tab <- nora\_prcus\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 5\*\*"),  
 subtitle = md("\*Most common intersections of the juvenile sample's precuneal sulci\*")) %>%  
tab\_row\_group(  
 group = "prcus-p",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "prcus-i",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "prcus-a",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (\*prcus\*) identified in the juvenile sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); posterior precuneal sulcus (\*prcus-p\*); splenial sulcus (\*spls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
nora\_prcus\_types\_tab

Supplementary Table 5

Most common intersections of the juvenile sample’s precuneal sulci

Sulci

First

%

Second

%

Third

%

prcus-a

LH (n=72)

spls

79.2

prcus-i

19.4

mcgs

9.7

RH (n=72)

spls

68.1

prcus-i

22.2

free

20.8

prcus-i

LH (n=72)

spls

68.1

prcus-a

22.2

free

20.8

RH (n=72)

spls

61.1

free

31.9

prcus-a

22.2

prcus-p

LH (n=72)

spls

55.6

free

33.3

prcus-i

15.3

RH (n=72)

spls

52.8

free

37.5

prcus-i

19.4

Note. This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (prcus) identified in the juvenile sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); posterior precuneal sulcus (prcus-p); splenial sulcus (spls).

#gtsave(nora\_prcus\_types\_tab, file = "supp\_Table5.png")

## Table 6: NORA Tertiary Sulci

nora\_tert\_types <- data.frame("mcst" <- c("LH (n=38)", "RH (n=34)", "LH (n=72)", "RH (n=72)", "LH (n=32)", "RH (n=36)"),  
 "1" <- c("free", "free", "free", "free", "free", "free"),  
 "percent" <- c(78.9, 85.3, 80.6, 73.6, 75.0, 83.3),  
 "2" <- c("cas", "cas", "mcgs", "spls", "mcgs", "cgs"),  
 "percent" <- c(15.8, 11.8, 11.1, 18.1, 12.5, 11.1),  
 "3" <- c("spls", "spls", "spls", "mcgs", "cgs", "ifrms"),  
 "percent" <- c(5.3, 2.9, 8.3, 5.6, 9.4, 2.8))  
  
names(nora\_tert\_types)[1] <- "Sulci"  
names(nora\_tert\_types)[2] <- "First"  
names(nora\_tert\_types)[3] <- "first\_percent"  
names(nora\_tert\_types)[4] <- "Second"  
names(nora\_tert\_types)[5] <- "second\_percent"  
names(nora\_tert\_types)[6] <- "Third"  
names(nora\_tert\_types)[7] <- "third\_percent"  
  
nora\_tert\_types\_tab <- nora\_tert\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 6\*\*"),  
 subtitle = md("\*Most common intersections of the juvenile sample's PCC tertiary sulci\*")) %>%  
tab\_row\_group(  
 group = "sspls",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "ifrms",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "icgs-p",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the juvenile sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (\*cas\*); cingulate sulcus (\*cgs\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); posterior intracingulate sulcus (\*icgs-p\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
nora\_tert\_types\_tab

Supplementary Table 6

Most common intersections of the juvenile sample’s PCC tertiary sulci

Sulci

First

%

Second

%

Third

%

icgs-p

LH (n=32)

free

75.0

mcgs

12.5

cgs

9.4

RH (n=36)

free

83.3

cgs

11.1

ifrms

2.8

ifrms

LH (n=72)

free

80.6

mcgs

11.1

spls

8.3

RH (n=72)

free

73.6

spls

18.1

mcgs

5.6

sspls

LH (n=38)

free

78.9

cas

15.8

spls

5.3

RH (n=34)

free

85.3

cas

11.8

spls

2.9

Note. This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the juvenile sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (cas); cingulate sulcus (cgs); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); posterior intracingulate sulcus (icgs-p); splenial sulcus (spls); subsplenial sulcus (sspls).

#gtsave(nora\_tert\_types\_tab, file = "supp\_Table6.png")

## Table 7: ADNI Prcuneal Sulci

adni\_prcus\_types <- data.frame("mcst" <- c("LH (n=72)", "RH (n=72)", "LH (n=72)", "RH (n=72)", "LH (n=72)", "RH (n=72)"),  
 "1" <- c("free", "spls", "spls", "spls", "spls", "spls"),  
 "percent" <- c(52.4, 56.9, 54.2, 52.8, 70.8, 75),  
 "2" <- c("spls", "free", "free", "free", "free", "free"),  
 "percent" <- c(44.4, 34.7, 30.6, 38.9, 20.8, 15.3),  
 "3" <- c("prcus-i", "prcus-i", "prcus-a", "prcus-p", "prcus-i", "mcgs"),  
 "percent" <- c(6.9, 13.9, 9.7, 13.9, 9.7, 9.7))  
  
names(adni\_prcus\_types)[1] <- "Sulci"  
names(adni\_prcus\_types)[2] <- "First"  
names(adni\_prcus\_types)[3] <- "first\_percent"  
names(adni\_prcus\_types)[4] <- "Second"  
names(adni\_prcus\_types)[5] <- "second\_percent"  
names(adni\_prcus\_types)[6] <- "Third"  
names(adni\_prcus\_types)[7] <- "third\_percent"  
  
adni\_prcus\_types\_tab <- adni\_prcus\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 7\*\*"),  
 subtitle = md("\*Most common intersections of the healthy older adult sample's precuneal sulci\*")) %>%  
tab\_row\_group(  
 group = "prcus-p",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "prcus-i",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "prcus-a",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (\*prcus\*) identified in the healthy older adult sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (\*prcus-a\*); intermediate precuneal sulcus (\*prcus-i\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); posterior precuneal sulcus (\*prcus-p\*); splenial sulcus (\*spls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
adni\_prcus\_types\_tab

Supplementary Table 7

Most common intersections of the healthy older adult sample’s precuneal sulci

Sulci

First

%

Second

%

Third

%

prcus-a

LH (n=72)

spls

70.8

free

20.8

prcus-i

9.7

RH (n=72)

spls

75.0

free

15.3

mcgs

9.7

prcus-i

LH (n=72)

spls

54.2

free

30.6

prcus-a

9.7

RH (n=72)

spls

52.8

free

38.9

prcus-p

13.9

prcus-p

LH (n=72)

free

52.4

spls

44.4

prcus-i

6.9

RH (n=72)

spls

56.9

free

34.7

prcus-i

13.9

Note. This table illustrates the different sulcal patterns, or types, of the three precuneal sulci (prcus) identified in the healthy older adult sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: anterior precuneal sulcus (prcus-a); intermediate precuneal sulcus (prcus-i); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); posterior precuneal sulcus (prcus-p); splenial sulcus (spls).

#gtsave(adni\_prcus\_types\_tab, file = "supp\_Table7.png")

## Table 8: ADNI Tertiary Sulci

adni\_tert\_types <- data.frame("mcst" <- c("LH (n=33)", "RH (n=32)", "LH (n=72)", "RH (n=72)", "LH (n=27)", "RH (n=28)"),  
 "1" <- c("free", "free", "free", "free", "free", "free"),  
 "percent" <- c(69.7, 87.5, 80.6, 77.8, 88.9, 82.1),  
 "2" <- c("cas", "cas", "mcgs", "spls", "mcgs", "mcgs"),  
 "percent" <- c(21.2, 9.4, 9.7, 13.9, 3.7, 10.7),  
 "3" <- c("spls", "spls", "spls", "mcgs", "cas", "cgs"),  
 "percent" <- c(9.1, 3.1, 6.9, 4.2, 3.7, 7.1))  
  
names(adni\_tert\_types)[1] <- "Sulci"  
names(adni\_tert\_types)[2] <- "First"  
names(adni\_tert\_types)[3] <- "first\_percent"  
names(adni\_tert\_types)[4] <- "Second"  
names(adni\_tert\_types)[5] <- "second\_percent"  
names(adni\_tert\_types)[6] <- "Third"  
names(adni\_tert\_types)[7] <- "third\_percent"  
  
adni\_tert\_types\_tab <- adni\_tert\_types %>% gt() %>%  
tab\_header(  
 title = md("\*\*Supplementary Table 8\*\*"),  
 subtitle = md("\*Most common intersections of the healthy older adult sample's PCC tertiary sulci\*")) %>%  
tab\_row\_group(  
 group = "sspls",  
 rows = 1:2) %>%  
tab\_row\_group(  
 group = "ifrms",  
 rows = 3:4) %>%  
tab\_row\_group(  
 group = "icgs-p",  
 rows = 5:6) %>%  
tab\_style(  
 style = cell\_text(style = "italic"),  
 locations = cells\_body(  
 columns = c(2,4,6),  
 rows = 1:6  
 )) %>%  
cols\_label(  
 first\_percent = "%",  
 second\_percent = "%",  
 third\_percent = "%") %>%  
tab\_source\_note(md("\*Note.\* This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the healthy older adult sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (\*cas\*); cingulate sulcus (\*cgs\*); inframarginal sulcus (\*ifrms\*); marginal ramus of the cingulate sulcus (\*mcgs\*); no intersections (\*free\*); posterior intracingulate sulcus (\*icgs-p\*); splenial sulcus (\*spls\*); subsplenial sulcus (\*sspls\*).")) %>%  
 tab\_options(table.font.size = 20,  
 heading.title.font.size = 20,  
 heading.subtitle.font.size = 20,  
 heading.align = "left",  
 heading.border.bottom.color = 'black',  
 table.border.top.color = "white",  
 #column\_labels.border.top.width = 3,  
 column\_labels.border.top.color = "black",  
 #column\_labels.border.bottom.width = 3,  
 column\_labels.border.bottom.color = "black",  
 column\_labels.vlines.color = "black",  
 row\_group.border.bottom.color = "black",  
 row\_group.border.top.color = "black",  
 row\_group.border.right.color = "black",  
 stub.border.color = "black",  
 table\_body.border.bottom.color = "black",  
 table\_body.hlines.color = "black",  
 table\_body.vlines.color = "black",  
 table.border.bottom.color = "white",  
 table.width = pct(100),  
 table.background.color = "white"  
 ) %>%  
 cols\_align(align="center", columns = 1:7) %>%  
 tab\_style(  
 style = list(  
 cell\_borders(  
 sides = c("top", "bottom"),  
 color = "white",  
 weight = px(1)  
 ),  
 cell\_text(  
 align="center"  
 ),  
 cell\_fill(color = "white", alpha = NULL)  
 ),  
 locations = cells\_body(  
 columns = everything(),  
 rows = everything()  
 )  
 ) %>%  
 opt\_table\_font(font = google\_font(name = "Times"))  
adni\_tert\_types\_tab

Supplementary Table 8

Most common intersections of the healthy older adult sample’s PCC tertiary sulci

Sulci

First

%

Second

%

Third

%

icgs-p

LH (n=27)

free

88.9

mcgs

3.7

cas

3.7

RH (n=28)

free

82.1

mcgs

10.7

cgs

7.1

ifrms

LH (n=72)

free

80.6

mcgs

9.7

spls

6.9

RH (n=72)

free

77.8

spls

13.9

mcgs

4.2

sspls

LH (n=33)

free

69.7

cas

21.2

spls

9.1

RH (n=32)

free

87.5

cas

9.4

spls

3.1

Note. This table illustrates the different sulcal patterns, or types, of the three PCC tertiary sulci identified in the healthy older adult sample (N = 72 participants). For each sulcus, the top three most prevalent sulcal patterns and their percent of occurrence are provided for both the left (LH) and right hemispheres (RH). The incidence of each sulcus in this sample is also provided for each hemisphere for reference. The abbreviations used are as follows: callosal sulcus (cas); cingulate sulcus (cgs); inframarginal sulcus (ifrms); marginal ramus of the cingulate sulcus (mcgs); no intersections (free); posterior intracingulate sulcus (icgs-p); splenial sulcus (spls); subsplenial sulcus (sspls).

#gtsave(adni\_tert\_types\_tab, file = "supp\_Table8.png")