Project1

1/15/2017

```r
setwd("~/Documents/Biostatistics/Collaboration II")
#setwd("~/Documents/BIOS7352/Project1")

totalData <- readRDS("dataForABP_CBF_2017-01-11.rds")
library(Hmisc)
library(knitr)

crvdata <- totalData[totalData$asl.reac.usable == 1 & totalData$enrolled.dx.factor != "Dementia",
                     c(1:18, 61, grep("asl.reac", names(totalData)),
                       grep("ma.", names(totalData)))]
names(crvdata) <- sub("asl.reac.", "", names(crvdata), fixed = TRUE)
names(crvdata) <- sub(".hct", "", names(crvdata), fixed = TRUE)

exclude <- totalData[totalData$asl.reac.usable == 0 | totalData$enrolled.dx.factor == "Dementia",
                     c(1:18, 61, grep("asl.reac", names(totalData)),
                       grep("ma.", names(totalData)))]
names(exclude) <- sub("asl.reac.", "", names(exclude), fixed = TRUE)
names(exclude) <- sub(".hct", "", names(exclude), fixed = TRUE)


#describe(crvdata)

#totalData$asl.reac.usable == 1,


cats <- names(crvdata)[2:19]
comparison <- c(c(), c(), c(),c())
is <- length(crvdata$map.id)
xs <- length(exclude$map.id)
for (cat in cats){
  if (is.factor(crvdata[,cat])){
    chiData <- rbind(cbind(crvdata[,cat],rep("is", length(crvdata[,cat]))),
                     cbind(exclude[,cat],rep("xs", length(exclude[,cat]))))
    pp <- chisq.test(table(chiData[,1], chiData[,2]))$p.value
    comparison <- rbind(comparison, c(label(crvdata[,cat]),'','', round(pp,4)))
    for (lev in levels(crvdata[,cat])){
      comparison <- rbind(comparison, c(paste("--",lev ),
                    paste(s <- sum(crvdata[,cat]==lev, na.rm=T), " (", round(s*100/is),
                          "%)", sep=""),
                    paste(s <- sum(exclude[,cat]==lev, na.rm=T), " (", round(s*100/xs),
                          "%)", sep=""),""))
    }
    next
  }
  anovaData <- as.data.frame(rbind(cbind(crvdata[,cat],rep("is", length(crvdata[,cat]))),
                  cbind(exclude[,cat],rep("xs", length(exclude[,cat])))))
  anovaData[,1] <- as.numeric(as.character(anovaData[,1]))
  pp <- kruskal.test(anovaData[,1] ~ anovaData[,2])$p.value
  comparison <- rbind(c(label(crvdata[,cat]),
```

```
            paste(round(mean(crvdata[,cat], na.rm=T),1)," (",
                  round(sd(crvdata[,cat],na.rm=T),1), ")",sep=""),
            paste(round(mean(exclude[,cat], na.rm=T),1)," (",
                  round(sd(exclude[,cat],na.rm=T),1), ")",sep=""),
            round(pp,4)), comparison)
}
comparison <- as.data.frame(comparison[,c(1,3,2,4)])
colnames(comparison) <- c("Variable","Excluded", "Analyzed Data", "P-Value")
kable(comparison, width=3,
      caption=paste("Comparison of Demographics for Excluded & Included Data, w/ N=",
                    length(exclude$map.id), " and N=",length(crvdata$map.id),
                                " respectively", sep=""))
```

Table 1: Comparison of Demographics for Excluded & Included Data, w/ N=113 and N=223 respectively

Variable	Excluded	Analyzed Data	P-Value
Diff. in mean SBP, wake - sleep, self-reported periods	14.5 (10.5)	13.4 (9.4)	0.6075
systolic.post.wake.mean minus systolic.pre.wake.mean	11.1 (12.3)	12.3 (12.2)	0.4331
systolic.post.wake.1 minus systolic.pre.wake.1	8.6 (14.2)	8.4 (13.6)	0.8162
ICV (calculated)	1431.2 (146.7)	1360.3 (134.6)	1e-04
Education (years)	16.5 (2.5)	15.5 (2.7)	9e-04
Age at medhx.date, recalculated	73.1 (7.1)	72.8 (7.4)	0.5341
Consensus Decision for Diagnosis			0.3736
– Normal	55 (49%)	121 (54%)	
– MCI	46 (41%)	86 (39%)	
– Dementia	1 (1%)	0 (0%)	
– Ambiguous At Risk	11 (10%)	16 (7%)	
Sex			0
– Male	90 (80%)	109 (49%)	
– Female	23 (20%)	114 (51%)	
Two-level race/ethnicity			0.9012
– Non-Hispanic White	97 (86%)	194 (87%)	
– Other	16 (14%)	29 (13%)	
ApoE4+ (at least one E4 allele)			0.7178
– Yes	41 (36%)	75 (34%)	
– No	72 (64%)	148 (66%)	
Consensus Decision for Diagnosis			0.3736
– Normal	55 (49%)	121 (54%)	
– MCI	46 (41%)	86 (39%)	
– Dementia	1 (1%)	0 (0%)	
– Ambiguous At Risk	11 (10%)	16 (7%)	
Taking at least 1 anti-hypertensive med			0.9461
– Yes	62 (55%)	120 (54%)	
– No	51 (45%)	103 (46%)	
Diabetic, determined by a1c, glucose, and/or rx			0.4304
– Yes	24 (21%)	38 (17%)	
– No	89 (79%)	185 (83%)	
Current smoker (or quit in this or last calendar yr)			0.3542
– Yes	4 (4%)	3 (1%)	
– No	109 (96%)	220 (99%)	
CVD, determined from variables in med hx			0.897
– Yes	3 (3%)	8 (4%)	

Variable	Excluded	Analyzed Data	P-Value
– No	110 (97%)	215 (96%)	
A-fib, determined by med hx and/or echo and/or cmr rhythm			1
– Yes	6 (5%)	13 (6%)	
– No	106 (94%)	209 (94%)	
LV hypertrophy, determined by sex and scaled LV mass			1
– Yes	5 (4%)	11 (5%)	
– No	108 (96%)	211 (95%)	
At least 39 readings AND max gap btw readings is <3h			0.0525
– No	6 (5%)	30 (13%)	
– Yes	91 (81%)	174 (78%)	

Missingness

```
nrow(totalData)
```

```
## [1] 336
```

```
#Start with 336
nrow(crvdata)
```

```
## [1] 223
```

```
#223 left after exclusions

missing <- c(c(), c())
#comparison[,c("Variable", "Analyzed Data")]
for (cat in cats){
    missing <- rbind(missing, c(label(crvdata[,cat]), paste(s <- sum(is.na(crvdata[,cat])), " (", round
 }

missing <- as.data.frame(missing)
colnames(missing) <- c("Variable", "Missingness")

kable(missing, width=3,
      caption=paste("Missingness (N=", nrow(crvdata), ")", sep=""))
```

Table 2: Missingness (N=223)

| Variable	Missingness
Consensus Decision for Diagnosis	0 (0%)
Sex	0 (0%)
Two-level race/ethnicity	0 (0%)
ApoE4+ (at least one E4 allele)	0 (0%)
Consensus Decision for Diagnosis	0 (0%)
Taking at least 1 anti-hypertensive med	0 (0%)
Diabetic, determined by a1c, glucose, and/or rx	0 (0%)
Current smoker (or quit in this or last calendar yr)	0 (0%)
CVD, determined from variables in med hx	0 (0%)
A-fib, determined by med hx and/or echo and/or cmr rhythm	1 (0.45%)

Variable	Missingness
LV hypertrophy, determined by sex and scaled LV mass	1 (0.45%)
Age at medhx.date, recalculated	0 (0%)
Education (years)	0 (0%)
ICV (calculated)	0 (0%)
systolic.post.wake.1 minus systolic.pre.wake.1	72 (32.29%)
systolic.post.wake.mean minus systolic.pre.wake.mean	76 (34.08%)
Diff. in mean SBP, wake - sleep, self-reported periods	64 (28.7%)
At least 39 readings AND max gap btw readings is <3h	19 (8.52%)

```r
require(GGally)

predictors <- crvdata[,16:18]
outcomes <- crvdata[, 20:33]

outlong <- c()
for (out in names(outcomes)){
  lab <- rep(out, length(outcomes[,out]))
  temp <- cbind(outcomes[, out], lab, predictors)
  outlong <- rbind(outlong, temp)
}
names(outlong)[1] <- "outcome"
levels(outlong$lab) <- c("Left Hemisphere", "Right Hemisphere", "Left Frontal Lobe",
                         "Right Frontal Lobe", "Full Frontal Lobe", "Left Occipital Lobe",
                         "Right Occipital Lobe", "Full Occipital Lobe", "Left Temporal Lobe",
                         "Right Temporal Lobe", "Full Temporal Lobe", "Left Parietal Lobe",
                         "Right Parietal Lobe", "Full Parietal Lobe")

ggplot(outlong, aes(systolic.rising.surge, outcome, group=1)) +
  geom_point() + geom_smooth() + facet_wrap(~lab, ncol=3) +
  theme(legend.position="none", strip.text = element_text(size=12),
        axis.text.x = element_text(size=14), axis.text.y  = element_text(size=14),
        panel.grid.major.x=element_line(colour='grey')) +
  ylab("Measured CVR") + xlab("Systolic Rising Surge Blood Pressure")
```
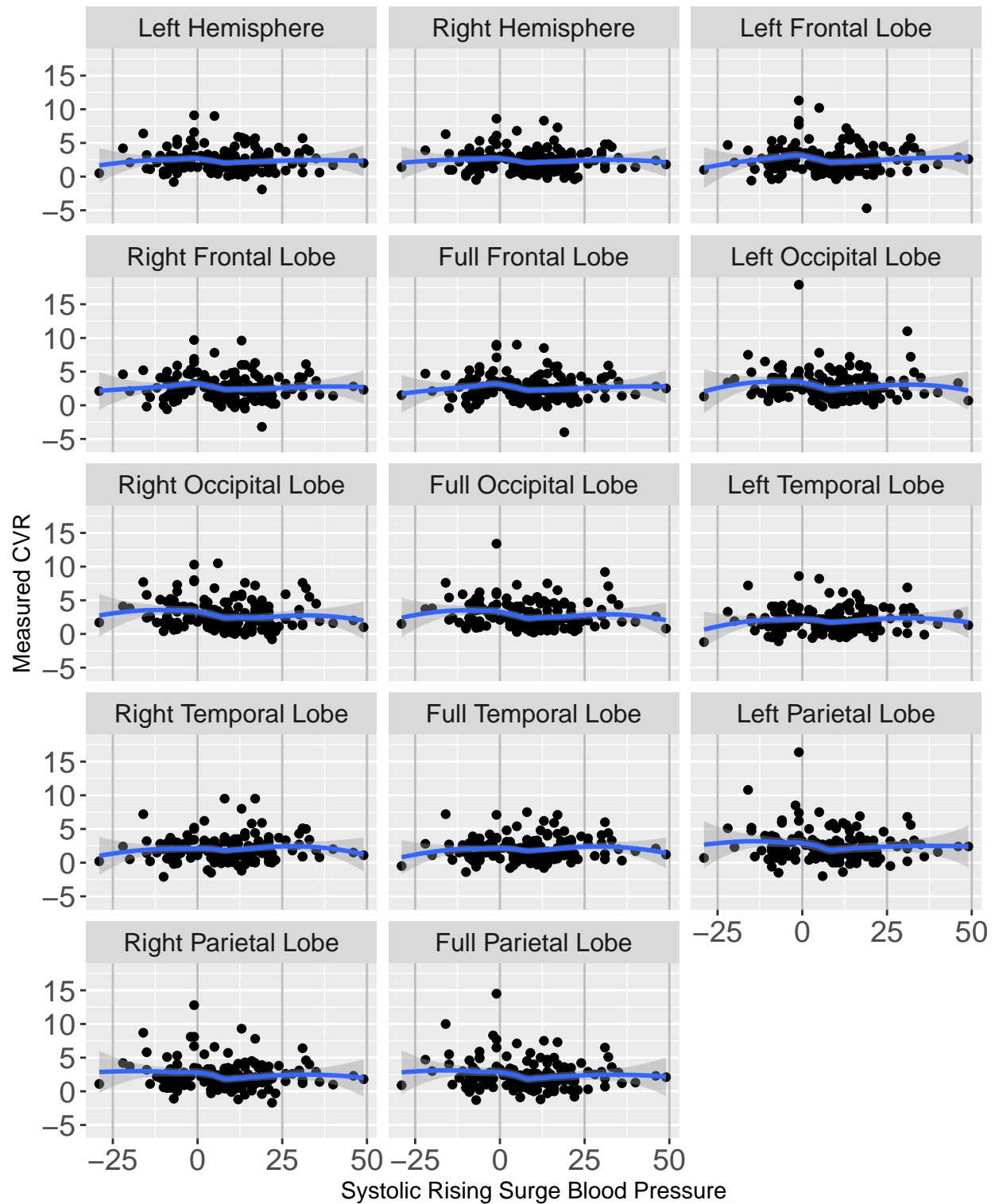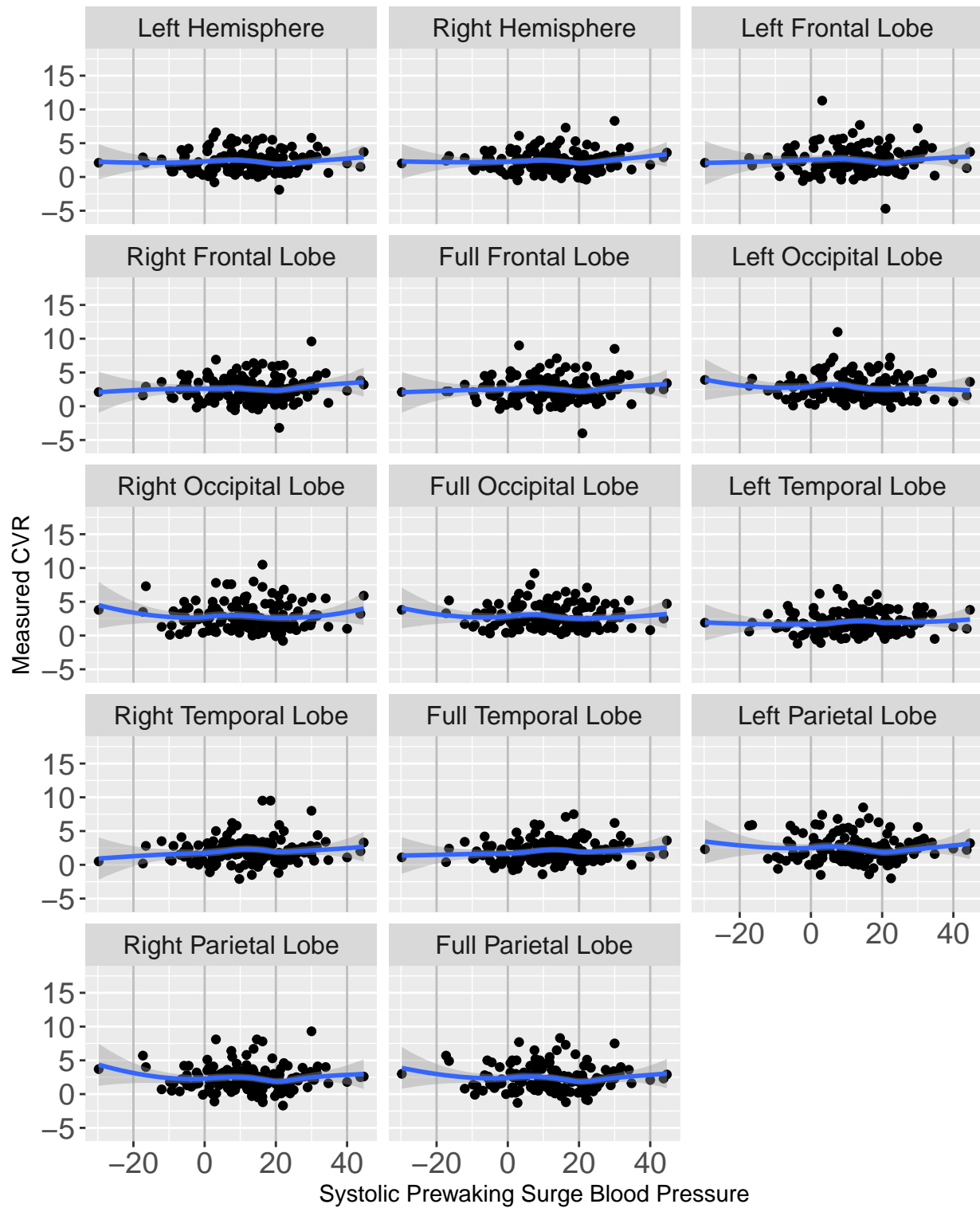
```
ggplot(outlong, aes(systolic.prewaking.surge, outcome, group=1)) +
  geom_point() + geom_smooth() + facet_wrap(~lab, ncol=3) +
  theme(legend.position="none", strip.text = element_text(size=12),
        axis.text.x = element_text(size=14), axis.text.y  = element_text(size=14),
        panel.grid.major.x=element_line(colour='grey')) +
```

```
ylab("Measured CVR") + xlab("Systolic Prewaking Surge Blood Pressure")
```



```
ggplot(outlong, aes(nocturnal.systolic.diff.sleep.self.reported, outcome, group=1)) +
  geom_point() + geom_smooth() + facet_wrap(~lab, ncol=3) +
  theme(legend.position="none", strip.text = element_text(size=12),
```

```
        axis.text.x = element_text(size=14), axis.text.y = element_text(size=14),
        panel.grid.major.x=element_line(colour='grey')) +
ylab("Measured CVR") + xlab("Difference in Awake/Sleeping Systolic Blood Pressure")
```