Task 1 - SMLP 2022: Analysis MS 2

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Cardiac synchrony and its role in language development

This is part of my PhD project which examines the role of mother-infant interpersonal synchrony on language development. Specifically, in this script, I test the following RQ. Does mother-infant cardiac synchrony predict infants' word segmentation ability? We include data of 29 dyads who performed two different tasks:

- word-segmentation task: infants underwent an eye-tracking task. During the familiarization phase they were listening to a story containing target words (i.e., familiar words). Then, they were tested with familiar (6 trials) and novel (6 trials) words. We measured their looking time (LT) in msec while listening to novel vs. familiar words. LT was our dependent variable.
- 5-minutes free play interaction: mothers were asked to play with the baby as they would do at home. During this time we recorded dual ECG. We then followed the following processing steps:
- 1. we extracted offline Interbeat-intervals (IBIs)
- 2. we calculated Respiratory Sinus Arrhythmia (RSA)
- 3. to collect a more continuous measure of RSA, a sliding window of 15 s was used to extract a continuous estimate of cardiac vagal tone for both participants
- 4. to identify coupling/synchrony between mothers' and infants' RSA time-series we used cross-recurrence quantification analysis (CRQA)
- 5. CRQA gave us a bunch of metrics: RR, det, NRLINE, maxline, entropy, lam, TT
- 6. we ran principal component analysis and we decide to include the first two components (pc1 and pc2), which had eigenvalues higher than 1 (Kaiser Rule).

Part 1: data preparation

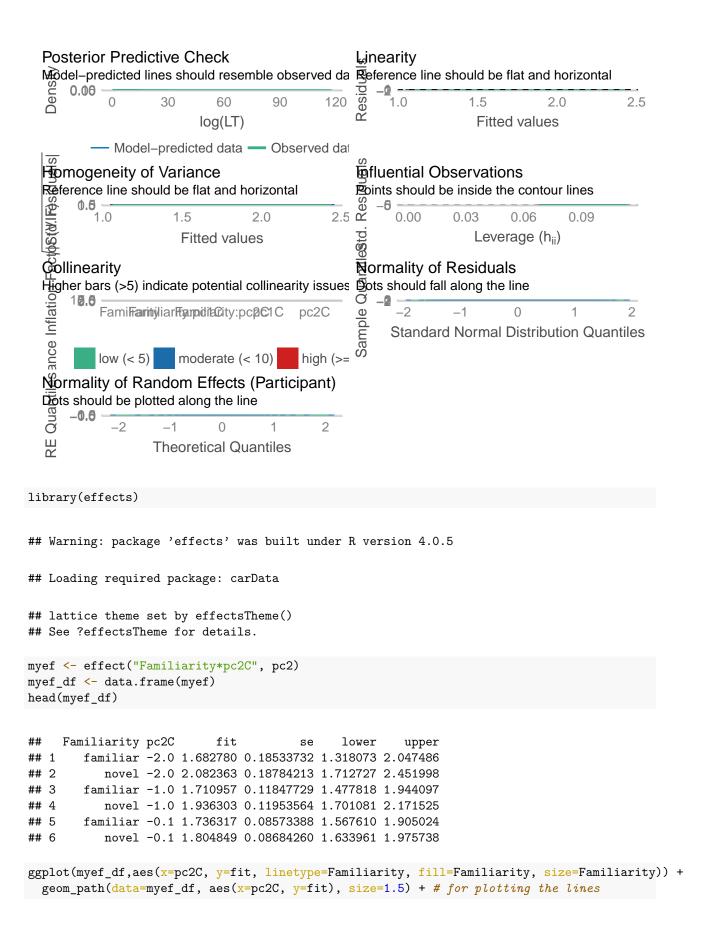
```
library(readxl)
## Warning: package 'readxl' was built under R version 4.0.5
lang_ECG <- read.csv("D:/PhD project/Conferences-SummerSchools/SMLP 2022/lang_ECG.csv", header=TRUE, se</pre>
str(lang_ECG)
## 'data.frame':
                    426 obs. of 7 variables:
   $ Participant: int
                        10 10 10 10 10 10 10 10 10 10 ...
                 : chr
                        "familiarization" "familiarization" "familiarization" "familiarization" ...
   $ Familiarity: chr
                        "famphase" "famphase" "famphase" ...
  $ LT
                        1.17 2.65 15.26 11.68 5.49 ...
                 : num
                        -0.572 -0.572 -0.572 -0.572 -0.572 ...
##
   $ PC1
                 : num
##
   $ PC2
                        -0.092 -0.092 -0.092 -0.092 ...
                 : num
                       -2.25 -2.25 -2.25 -2.25 ...
   $ PC3
                 : num
lang_ECG$Participant <- as.factor(lang_ECG$Participant)</pre>
lang ECG$Phase <- as.factor(lang ECG$Phase)</pre>
lang_ECG$Familiarity <- as.factor(lang_ECG$Familiarity)</pre>
str(lang_ECG)
```

```
## 'data.frame': 426 obs. of 7 variables:
## $ Participant: Factor w/ 29 levels "10","14","17",..: 1 1 1 1 1 1 1 1 1 ...
            : Factor w/ 2 levels "familiarization",..: 1 1 1 1 2 2 2 2 2 2 ...
## $ Familiarity: Factor w/ 3 levels "familiar", "famphase",..: 2 2 2 2 3 1 1 3 1 1 ...
              : num 1.17 2.65 15.26 11.68 5.49 ...
## $ PC1
               : num -0.572 -0.572 -0.572 -0.572 -0.572 ...
                : num -0.092 -0.092 -0.092 -0.092 ...
## $ PC2
## $ PC3
                : num -2.25 -2.25 -2.25 -2.25 ...
#select only the data of the test phase
lang_ECG <- subset(lang_ECG, lang_ECG$Phase !="familiarization")</pre>
summary(lang_ECG)
   Participant
                            Phase
                                       Familiarity
                                                         LT
## 14
         : 12
                familiarization: 0
                                     familiar:160
                                                    Min. : 1.059
## 19
         : 12
                testing :310
                                     famphase: 0
                                                    1st Qu.: 3.378
## 30
         : 12
                                     novel :150
                                                    Median : 5.938
## 32
         : 12
                                                    Mean : 7.893
## 33
         : 12
                                                    3rd Qu.:10.002
         : 12
## 37
                                                    Max. :31.696
## (Other):238
##
        PC1
                         PC2
                                           PC3
## Min.
         :-4.8247
                   Min. :-2.19475 Min.
                                             :-2.25027
## 1st Qu.:-1.0780 1st Qu.:-0.76545 1st Qu.:-0.42031
## Median: -0.2899 Median: 0.05161 Median: 0.20945
## Mean :-0.0308 Mean : 0.01955 Mean : 0.03938
## 3rd Qu.: 1.0833
                    3rd Qu.: 0.78577
                                      3rd Qu.: 0.57058
## Max. : 5.3849 Max. : 2.03139 Max. : 1.40010
##
#set contrasts
library(stats)
levels(droplevels(lang_ECG$Familiarity))
## [1] "familiar" "novel"
contrasts(lang_ECG$Familiarity)
##
           famphase novel
## familiar
                0
## famphase
                       0
                  1
## novel
#center predictors
lang_ECG$pc1C <- lang_ECG$PC1 - mean(lang_ECG$PC1)</pre>
lang_ECG$pc2C <- lang_ECG$PC2 - mean(lang_ECG$PC2)</pre>
```

Mixed models

```
library(lme4)
## Loading required package: Matrix
library(lmerTest)
## Warning: package 'lmerTest' was built under R version 4.0.5
##
## Attaching package: 'lmerTest'
## The following object is masked from 'package:lme4':
##
##
       lmer
## The following object is masked from 'package:stats':
##
##
       step
options(scipen = 999)
lang_ECG$Familiarity <- relevel(lang_ECG$Familiarity, ref = "familiar")</pre>
#run different models
pc0 =lmer(log(LT)~Familiarity+(1|Participant), data=lang_ECG, REML=FALSE)
pc1=lmer(log(LT)~Familiarity*pc1C+(1|Participant), data=lang_ECG, REML=FALSE)
pc2=lmer(log(LT)~Familiarity*pc1C+Familiarity*pc2C+(1|Participant), data=lang_ECG, REML=FALSE)
#compare models with Anova
anova(pc0,pc1,pc2)
## Data: lang ECG
## Models:
## pc0: log(LT) ~ Familiarity + (1 | Participant)
## pc1: log(LT) ~ Familiarity * pc1C + (1 | Participant)
## pc2: log(LT) ~ Familiarity * pc1C + Familiarity * pc2C + (1 | Participant)
##
      npar
              AIC
                     BIC logLik deviance Chisq Df Pr(>Chisq)
## pc0
         4 689.45 704.39 -340.72
                                    681.45
## pc1
         6 693.34 715.76 -340.67
                                    681.34 0.1029 2
                                                        0.94984
         8 691.46 721.35 -337.73 675.46 5.8801 2
## pc2
                                                        0.05286 .
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
summary(pc2)
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
    method [lmerModLmerTest]
## Formula: log(LT) ~ Familiarity * pc1C + Familiarity * pc2C + (1 | Participant)
##
     Data: lang_ECG
##
##
       AIC
                BIC logLik deviance df.resid
              721.4 -337.7
      691.5
                                675.5
                                            302
##
```

```
##
## Scaled residuals:
               1Q Median
      Min
## -3.02876 -0.61309 -0.07738 0.63312 2.50248
## Random effects:
## Groups
                        Variance Std.Dev.
          Name
## Participant (Intercept) 0.1280
                                0.3578
## Residual
                         0.4546
                                 0.6743
## Number of obs: 310, groups: Participant, 29
## Fixed effects:
                        Estimate Std. Error
                                                 df t value
## (Intercept)
                        ## Familiaritynovel
                        0.011466 0.041902 42.172058
## pc1C
                                                     0.274
## pc2C
                        ## Familiaritynovel:pc1C 0.003251
                                 0.036957 280.777680 0.088
## Familiaritynovel:pc2C -0.174237 0.074902 281.417164 -2.326
                                Pr(>|t|)
                      <0.00000000000000002 ***
## (Intercept)
## Familiaritynovel
                                  0.5071
## pc1C
                                  0.7857
## pc2C
                                  0.7339
## Familiaritynovel:pc1C
                                 0.9300
## Familiaritynovel:pc2C
                                 0.0207 *
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
## Correlation of Fixed Effects:
##
             (Intr) Fmlrty pc1C pc2C
                                      Fml:1C
## Familrtynvl -0.434
## pc1C
             -0.013 0.006
## pc2C
             0.002 0.011 0.000
## Fmlrtynv:1C 0.006 0.000 -0.443 -0.001
## Fmlrtynv:2C 0.011 0.001 -0.001 -0.429 -0.018
#plot results
library(performance)
## Warning: package 'performance' was built under R version 4.0.5
library(ggplot2)
## Warning: package 'ggplot2' was built under R version 4.0.5
check_model(pc2)
```



```
geom_ribbon(data=myef_df, aes(x=pc2C, ymin=lower, ymax=upper, group=Familiarity), alpha=.3) +
geom_point(data=lang_ECG, aes(x=pc2C, y=log(LT), shape=Familiarity, colour=Participant), size=1.5) +
#scale_y_continuous(trans='logit') + # y-scale is now reflecting the logit space
#theme_bw()
#xlab("pc2 centered") + ylab("LT (fit)") +
labs(x = "pc2 (centered)", y = "Log LT for test trials") +
scale_fill_manual(values=c("black", "black"))+
guides(shape = guide_legend(title = "Trial type"), colour=FALSE, fill=FALSE, size=FALSE) +
labs(linetype="Group")+
theme(axis.title = element_text(size = 15), axis.text = element_text(size = 12),
legend.text = element_text(size = 10), legend.title = element_text(size = 10))
```

Warning: 'guides(<scale> = FALSE)' is deprecated. Please use 'guides(<scale> =
"none")' instead.

Warning: Using size for a discrete variable is not advised.

