

# Supplementary file 2

Code ▾

## Sympathetic nervous system functioning during the Face-to-face Still-face paradigm in the first year of life

### prepare contrasts

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```
nlme_cont <- matrix(c(-.5,.5), ncol=1)
contrasts(nlme_prep$device) <- nlme_cont
```

### fit models

the following models apply `lmeControl(opt="optim")` optimiser based on Nelder-Mead algorithm; `method = "ML"` selected for comparison of models with different fixed effects specification

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```
summary(without_adjustment)
```

Linear mixed-effects model fit by maximum likelihood  
Data: nlme\_prep

	AIC <dbl>	BIC <dbl>	logLik <dbl>
	7816502	7816634	-3908240

1 row

#### Random effects:

Formula: ~phase | participant  
Structure: General positive-definite, Log-Cholesky parametrization  
StdDev Corr  
(Intercept) 11.519924 (Intr) phsrnn  
phasereunion 7.643464 -0.338  
phasesf 6.570379 -0.219 0.680  
Residual 7.143237

Fixed effects: conduc ~ 0 + phase + device

	Value <chr>	Std.Error <chr>	DF <chr>	t-value <chr>	p-value <chr>
phaseplay	19.205207	0.7236766	1153480	26.53838	0
phasereunion	24.927411	0.7226463	1153480	34.49463	0
phasesf	24.506073	0.7501269	1153480	32.66924	0
device1	-1.007595	0.0133562	1153480	-75.44037	0

4 rows

#### Correlation:

phsply phsrnn phassf  
phasereunion 0.772  
phasesf 0.840 0.872  
device1 0.000 0.000 0.000

#### Standardized Within-Group Residuals:

Min Q1 Med Q3 Max  
-6.07129945 -0.44755475 -0.01080869 0.45903568 16.33293663

Number of Observations: 1153738  
Number of Groups: 255

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```
summary(with_adjustment)
```

Linear mixed-effects model fit by maximum likelihood  
Data: nlme\_prep

	AIC <dbl>	BIC <dbl>	logLik <dbl>
	7609542	7609889	-3804742

1 row

#### Random effects:

Formula: ~phase\_t \* phase | participant  
Structure: General positive-definite, Log-Cholesky parametrization  
StdDev Corr  
(Intercept) 13.20895975 (Intr) phas\_t phsrnn phassf phs\_t:  
phase\_t 0.03831527 0.516  
phasereunion 10.25317576 -0.405 -0.404  
phasesf 11.02018590 -0.475 -0.467 0.545  
phase\_t:phasereunion 0.09379166 -0.145 -0.340 0.666 -0.049  
phase\_t:phasesf 0.10796576 -0.520 -0.584 0.475 0.859 0.033  
Residual 6.51886854

Fixed effects: conduc ~ 0 + phase\_t \* phase + device

	Value <chr>	Std.Error <chr>	DF <chr>	t-value <chr>	p-value <chr>
phase_t	0.004544	0.0024260	1153477	1.87291	0.0611
phaseplay	19.758245	0.8294197	1153477	23.82177	0.0000
phasereunion	23.128190	0.8247686	1153477	28.04203	0.0000
phasesf	26.735478	0.7889789	1153477	33.88618	0.0000
device1	-1.028377	0.0122131	1153477	-84.20292	0.0000
phase_t:phasereunion	-0.036337	0.0060273	1153477	-6.02877	0.0000
phase_t:phasesf	0.036357	0.0068441	1153477	5.31214	0.0000

7 rows

#### Correlation:

phas\_t phsply phsrnn phassf devic1 phs\_t:phsr  
phaseplay 0.515  
phasereunion 0.201 0.686  
phasesf 0.131 0.631 0.675  
device1 0.001 0.000 0.000 0.000  
phase\_t:phasereunion -0.336 -0.143 0.389 -0.190 0.000  
phase\_t:phasesf -0.579 -0.516 -0.150 0.212 0.000 0.035

#### Standardized Within-Group Residuals:

Min Q1 Med Q3 Max  
-9.058820947 -0.398857449 -0.004808991 0.407582593 17.734416636

Number of Observations: 1153738  
Number of Groups: 255

comparing the 'Value' column between the model with and without adjustment variable indicates that predicted differences between still-face phase and reunion play phase not observed

### compare models

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```
anova.lme(without_adjustment,with_adjustment)
```

	Model <int>	df <dbl>	AIC <chr>	BIC <chr>	logLik <chr>	Test <fctr>	L.Ratio <chr>	p-value <chr>
without_adjustment	1	11	7816502	7816634	-3908240			
with_adjustment	2	29	7609542	7609889	-3804742	1 vs 2	206995.9	<.0001

2 rows

significant difference found between the two models, note that lower IC values indicate better fit, indicating again superiority of the model with adjustment variable included

### print session info

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```
sessionInfo()
```

```
R version 4.0.2 (2020-06-22)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Catalina 10.15.6

Matrix products: default
BLAS: /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framework/Versions/A/libBLA
S.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib

locale:
[1] en_AU.UTF-8/en_AU.UTF-8/en_AU.UTF-8/C/en_AU.UTF-8/en_AU.UTF-8

attached base packages:
[1] stats graphics grDevices utils datasets methods base

other attached packages:
 [1] permute_0.9-5          rstatix_0.6.0          ggpubr_0.4.0           broomExtra_4.2.1       broom_0.7.8
 [6] kableExtra_1.3.4      magrittr_2.0.1         lubridate_1.7.10       tsibble_1.0.1          knitr_1.33
[11] easypackages_0.1.0    forcats_2.0.5          stringr_1.4.0          dplyr_1.0.7            purrr_0.3.4
[16] readr_2.0.0           tidyr_1.1.3           tibble_3.1.2          ggplot2_3.3.5         tidyverse_1.3.1.9000
[21] nlme_3.1-152

loaded via a namespace (and not attached):
 [1] utf8_1.2.1            tidyselct_1.1.1       lme4_1.1-26           htmlwidgets_1.5.3
 [5] grid_4.0.2           devtools_2.4.0       lmselect_1.0.5.0      effects_size_0.4.4-1
 [9] statmod_1.4.35       withr_2.4.2          colorspace_2.0-2     rstudioapi_0.13
[13] EMATools_0.1.3      DescTools_0.99.41    ggsignif_0.6.1       labeling_0.4.2
[17] emmeans_1.6.0       bit64_4.0.5          farver_2.1.0         rprojroot_2.0.2
[21] coda_0.19-4         vctrs_0.3.8          generics_0.1.0       xfun_0.24
[25] R6_2.5.0            arm_1.11-2           cachem_1.0.4         assertthat_0.2.1
[29] showtext_0.9-2     scales_1.1.1         vroom_1.5.3          nnet_7.3-15
[33] rootSolve_1.8.2.1   gtable_0.3.0         ResourceSelection_0.3-5 processx_3.5.2
[37] lmom_2.8            rlang_0.4.11         systemfonts_1.0.1    splines_4.0.2
[41] TMB_1.7.20         rapportools_1.0       checkmate_2.0.0      yaml_2.2.1
[45] reshape2_1.4.4      abind_1.4-5          modelr_0.1.8         backports_1.2.1
[49] rsmconnect_0.8.17  Hmisc_4.5-0         tools_4.0.2         rmarkdown_2.11
[53] ellipsis_0.3.2     jquerylib_0.1.4     RColorBrewer_1.1-2  proxy_0.4-25
[57] sessioninfo_1.1.1  Rcpp_1.0.7          plyr_1.8.6           base64enc_0.1-3
[61] ps_1.6.0           prettyunits_1.1.1   rpart_4.1-15        broman_1.4.1
[65] cowplot_1.1.1     haven_2.4.1         cluster_2.1.2       fs_1.5.0
[69] data.table_1.14.0  openxlsx_4.2.3       lmerTest_3.1-3      reprex_2.0.0
[73] mvtnorm_1.1-1      sjmisc_2.8.6        pkgload_1.2.1       hms_1.1.0
[77] patchwork_1.1.1    evaluate_0.14        xtable_1.8-4        rno_0.5.26
[81] sjstats_0.18.1     jpeg_0.1-8.1        broom.mixed_0.2.6    readxl_1.3.1
[85] kableExtra_2.3     testthat_3.0.2      compiler_4.0.2      crayon_1.4.1
[89] minqa_1.2.4        htmltools_0.5.1.1   tzdb_0.1.2          DataCombine_0.2.21
[93] Formula_1.2-4      expm_0.999-6         Exact2_1             DBI_1.1.1
[97] sjlabelled_1.1.7   dbplyr_2.1.1        MASS_7.3-53.1       boot_1.3-27
[101] Matrix_1.3-2       car_3.0-10          cli_3.0.1            parallel_4.0.2
[105] insight_0.13.2     pkeconfig_2.0.3     numDeriv_2016.8-1.1 foreign_0.8-81
[109] xml2_1.3.2         svglite_2.0.0       rslib_0.2.4         webshot_0.5.2
[113] estimability_1.3   anytime_0.3.9       rvest_1.0.0         callr_3.7.0
[117] digest_0.6.27      parameters_0.13.0   showtextdb_3.0      rmarkdown_2.9
[121] cellranger_1.1.0  htmlTable_2.1.0     gld_2.6.2           curl_4.3.2
[125] nloptr_1.2.2-2     lifecycle_1.0.0     jsonlite_1.7.2      carData_3.0-4
[129] desc_1.3.0         viridisLite_0.4.0   fansi_0.5.0         pillar_1.6.1
[133] lattice_0.20-44    fastmap_1.1.0       httr_1.4.2          pkgbuild_1.2.0
[137] survival_3.2-11    glue_1.4.2          remotes_2.3.0       bayestestR_0.9.0
[141] zip_2.1.1          png_0.1-7           pandoc_0.6.3        bit_4.0.4
[145] class_7.3-18       stringr_1.7.3       sass_0.3.1          performance_0.7.1
[149] latticeExtra_0.6-29 memoise_2.0.0       e1071_1.7-6         sysfonts_0.8.3
```