Supplementary Information:

Leistungsnachweis: fortgeschrittene Datenanalyse mit R

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Setup:

Always run this Chunk first.

```
#create Operating System Path prefix
if (Sys.info()['sysname'] == "Darwin" ) {
  SysDir="/Volumes/SNFAue/"} else {
    SysDir = "N:/"}
# load necessary library files
if (!require("pacman")) install.packages("pacman")

## Loading required package: pacman

library(pacman)
p_load(readr)
p_load(lme4)
p_load(tableone)
p_load(tidyverse)
p_load(ggplot2)
p_load(merTools)
p_load(brms)
p_load(shinystan)
p_load(ggeffects)
p_load(ggeffects)
```

Einlesen der physiologischen Daten:

```
options(max.print = 99999999)
PhysioData_org<-read_rds(paste0(SysDir,"SoOp/deprecated/Soccer deprecated/ori
ginal/analysis/ECG/AggregatedData/PhysioData_org_noArt_3sdMarked_.rds"))

#exclude Bsp trails
PhysioData<-PhysioData_org  %>% filter(!grepl("Bsp",Spielfeld))
#create condition
PhysioData$Factor1<-if_else(
  grepl(paste(c("Selbst","Ingroup1","Ingroup2"),collapse="|"),PhysioData$Grup
pe),
  "Us","Them")
PhysioData$Factor2<-if_else(grepl(paste(c("Selbst","Konkurrent"),
                                        collapse="|"),PhysioData$Gruppe),"Sin
gle",
                            if_else(grepl(paste(c("Ingroup1","Outgroup1"),
                                                collapse="|"),PhysioData$Grup
pe),
                                    "Team_1","Team_2"))

#make Participant ID unique by adding the between group to the name
PhysioData$BiopacSubject<-paste0(
```

```
  if_else(PhysioData$betweenCond=="soccerPlayer","sp","nsp"),
  "_",PhysioData$BiopacSubject) %>% as.character()


PhysioData<-PhysioData %>% filter(BiopacSubject!="sp_9")
PhysioData<-PhysioData %>% filter(BiopacSubject!="sp_10")

#aggregate spielfeld
PhysioData$Spielfeld<-as.numeric(
  as.character(
    unlist(PhysioData$Spielfeld)))%%16+1

#drop biopactrail (only from merging)

col <- c("Target","Measurement", "BiopacSubject","BiopacTrail",
         "Time","Gruppe","betweenCond","Spielfeld",
         "Factor1","Factor2")
PhysioData["Time"]<-as.numeric(as.character(
  unlist((PhysioData["Time"]))))
PhysioData[col]<-lapply(PhysioData[col],factor)
sapply(PhysioData, class)

##        Target          Time       Measure BiopacSubject   BiopacTrail
##      "factor"      "factor"   "character"      "factor"      "factor"
##   Measurement   betweenCond        Gruppe     Spielfeld  VasSlide.VAS
##      "factor"      "factor"      "factor"      "factor"     "numeric"
##   VasSlide.RT       Factor1       Factor2         Value
##     "numeric"      "factor"      "factor"     "numeric"

if(F){
tbo<-CreateTableOne(data = PhysioData )
summary(tbo)
}
rm(col,PhysioData_org)
```

Plots Measurement by Subject und Ausschluss von VPn

```
plotMeasurementBySubject<- function(measurement,string){
    measurement<-measurement %>% filter(Measurement==string)
    ggplot(data = drop_na(measurement),mapping = aes(x = BiopacSubject,
                          y = Value,
                          fill = Measurement)) +
                      geom_violin() +
                      geom_jitter(width = 0.2, alpha = 0.6) +
                      theme_classic()
}
#Phight:
PhysioData %>% filter(BiopacSubject!="nsp_14")  %>%
  plotMeasurementBySubject("Phight")
#PRQ
PhysioData  %>% filter(BiopacSubject!="nsp_14") %>%
  plotMeasurementBySubject("STev")
```

```r
#QT
PhysioData %>% filter(BiopacSubject!="nsp_14") %>%
  plotMeasurementBySubject("QT")
#QTwidth
PhysioData %>% filter(BiopacSubject!="nsp_14") %>%
  plotMeasurementBySubject("QTwidth")
#RRi
PhysioData %>% filter(BiopacSubject!="nsp_14") %>%
  plotMeasurementBySubject("RRi")
#Rhight
PhysioData %>% filter(BiopacSubject!="nsp_14") %>%
  plotMeasurementBySubject("Rhight")
#ST
PhysioData %>% filter(BiopacSubject!="nsp_14") %>%
  filter(Value<=3) %>%  plotMeasurementBySubject("ST")
#STev
PhysioData  %>% filter(BiopacSubject!="nsp_14") %>%
  plotMeasurementBySubject("STev")

#exclude:

PhysioData_1 <- PhysioData %>%
  filter(BiopacSubject!="nsp_14") %>%
  filter(BiopacSubject!="nsp_3") %>%
  filter(BiopacSubject!="nsp_7") %>%
  filter(Measurement == "RRi")
# Set 0 Values to NA ->
# these trails were either not anwsered or the trail timedout ->
#may lead to skrewed distribution!

PhysioData_1$VasSlide.RT<-if_else(
  PhysioData_1$VasSlide.RT!=0,PhysioData_1$VasSlide.RT,NULL)

saveRDS(PhysioData_1,"physio.RT")
```

Phight: - nsp_14: grosse varianz nach oben - exclude - nsp_17/20 bottem effekt - 0 - nsp_7: alles null

PRQ: nicht interpretierbare Verteilungen

QT: - nsp_14 riesige varianz exclude - nsp_7 alles null

QTwidth: sehr komische Verteilungen, viele nullen, bei 100 beschränkt ?? komisch

Rhight: - nsp_3 viele 0 - nsp_7 alles 0 - nsp_14 riesige varianz exclude - nsp_4 grosse varianz

RRi: - nsp_3 lot of values at 0 –> exclude - nsp_14 grosse varianz

ST: - nsp_7 alles 0 - ausreisser bei nsp_16, nsp_4 und sp_14 (Werte zwischen 10 und 70) -> filtern - nsp4,5,6 grosse varianz

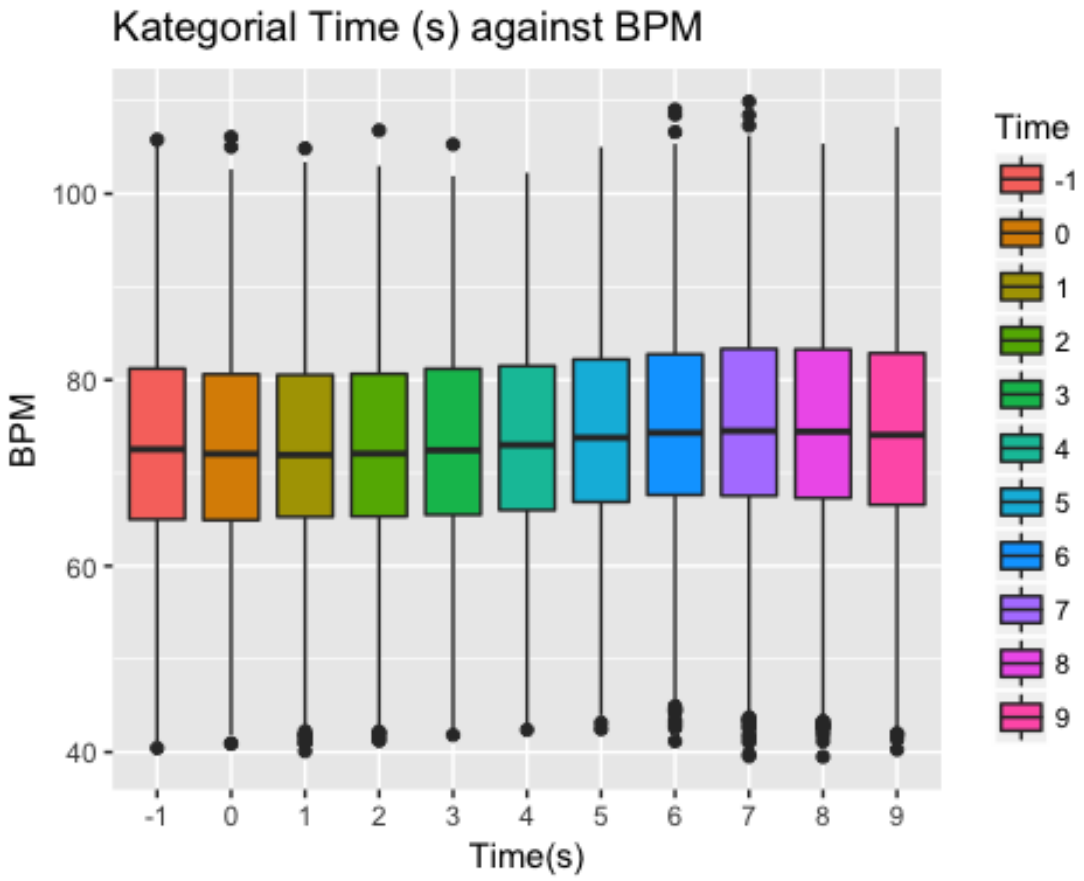
STev: - prakisch alle nsp haben bottem effekt - nsp_4 grosse varianz - nsp_14 riesen varianz exclude

–> nur analyse von RRi, da nur für dieses Mass eine Hypothese besteht. Aussschluss von VP: nsp_14,nsp_3,nsp_7

TimePlot RRi

```
PhysioData_1<-read_rds("physio.RT")
 physio_RRi<-na.omit(filter(PhysioData_1,
                            (Measurement=="RRi")&(grepl("Stimulus",Target))
                            &(Time!=-2)))


qplot(Time, Value, data=physio_RRi, geom=c("boxplot"),
   fill=Time, main="Kategorial Time (s) against BPM",
   xlab="Time(s)", ylab="BPM")
```




```
if (F){
  mg <- ggplot(physio_RRi, aes(x = VasSlide.RT, y =VasSlide.VAS ,
                               colour = factor(BiopacSubject)))
  + geom_point()
  mg + facet_grid(Factor1 + Factor2 ~ betweenCond)
}
```

Behavior

```
p_load(readxl)
sp<-read_excel(paste0(SysDir,
                      "SoOp/deprecated/Soccer deprecated/original/rawDaten/so
ccerPlayer/E-Prime Daten/Merge_VP01_VP30.xlsx"))
sp$betweenCond<-"soccerPlayer"
nsp<-read_excel(paste0(SysDir,
                       "SoOp/deprecated/Soccer deprecated/original/rawDaten/n
onSoccerPlayer/E-Prime Daten/Merge_VP01_VP30.xlsx"))
nsp$betweenCond<-"nonSoccerPlayer"
behaviorData<-rbind(sp,nsp) %>%
  select(c(Name,Gruppe,betweenCond,
           Spielfeld,VasSlide.RT,VasSlide.VAS))
behaviorData<-behaviorData %>%
  filter(!grepl("Bsp",Spielfeld))
#create condition
behaviorData$Factor1<-if_else(
  grepl(paste(c("Selbst","Ingroup1","Ingroup2"),
              collapse="|"),behaviorData$Gruppe),"Us","Them")
behaviorData$Factor2<-if_else(
  grepl(paste(c("Selbst","Konkurrent"),collapse="|"),
        behaviorData$Gruppe),"Single",
  if_else(grepl(paste(c("Ingroup1","Outgroup1"),
                      collapse="|"),behaviorData$Gruppe),
          "Team_1","Team_2"))
#aggregate spielfeld
behaviorData$Spielfeld<-as.numeric(
  as.character(unlist(behaviorData$Spielfeld)))%%16+1
behaviorData$VasSlide.RT<-if_else(
  behaviorData$VasSlide.RT!=0,behaviorData$VasSlide.RT,NULL)
#Modeling
saveRDS(behaviorData,"behavior.rds")
```

Baysian Modelling

Modelle müssen zuerst berechnet werden. Dazu bitte die entsprechenden R Scripte ausführen.

Modeling Function (getBRMModel.R)

```
getBRMModel <- function(dataframe=NULL,form=NULL,measurement=NULL,data=NULL,name=NULL,path="",family = student() ,control=NULL, prior=NULL,autocor=NULL) {
  options (mc.cores=parallel::detectCores ()) # Run on multiple cores
  # load necessary library files
  if (!require("pacman")) install.packages("pacman")
  library(pacman)
  p_load(readr)
  p_load(dplyr)
  p_load(brms)

  if (!is.null( dataframe)){
    form=as.formula(eval(parse(text =dataframe$formulas)))
    name=as.character(dataframe$names)
    measurement=dataframe$measurement
  }

  assertthat::not_empty(form)
  assertthat::not_empty(data)
  assertthat::not_empty(name)
  assertthat::not_empty(measurement)

  dir.create(file.path( path), showWarnings = F)

  tryCatch(
    {
      data<- filter(data,Measurement==measurement)
    },
    error=function(cond) {
      message(cond)
    }
  )

  out <- tryCatch(
    {
      read_rds(paste0(path,measurement,"_",name,".rds"))
    },
    error=function(cond) {
      message(cond)
      cat(paste("\n\nFile does not exist: ", paste0(path, name), "\nnew Model will be calculated and saved with the specified name. \nGo grab a cup of coffee  and do 10 Push-ups:)\n\n"))

      model<-brm(form,data = data,prior=prior,family = family,control=control, autocor=autocor)
```

```
      saveRDS(model,paste0(path,measurement,"_",name,".rds"))
      return(model)
    }
  )
  return(out)
}
```

Behavior (brms_b.R)

```
#!/usr/bin/env Rscript
args = commandArgs(trailingOnly=TRUE)

if (length(args)!=0){
  print(class(args))

}

# load necessary library files
if (!require("pacman")) install.packages("pacman")
library(pacman)
p_load(dplyr)
p_load(readr)
source("getBRMModel.R")

behaviorData<-read_rds("behavior.rds")

names<-list("m0","m1a","m1b",
            "m2","m2a","m2b","m2c",
            "m3a", "m3b"
)
formulas<-list("VasSlide.VAS~1",

               "VasSlide.VAS~1+(1|Name)",
               "VasSlide.VAS~1+(1|Spielfeld)",

               "VasSlide.VAS~1+Factor1+Factor2 + (1|Name)+ (1|Spielfeld)",
               "VasSlide.VAS~1+Factor1*Factor2 + (1|Name)+ (1|Spielfeld)",

               "VasSlide.VAS~1+Factor1*Factor2 + betweenCond + (1|Name)+ (1|Sp
ielfeld)",
               "VasSlide.VAS~1+Factor1*Factor2 * betweenCond + (1|Name)+ (1|Sp
ielfeld)",

                     "VasSlide.VAS~1+Factor1+Factor2 + betweenCond + (1|Name)+
(1|Spielfeld)",
                     "VasSlide.VAS~1+Factor1+Factor2 * betweenCond + (1|Name)+
(1|Spielfeld)"
)

models<-data_frame(formulas,names)
models$measurement<-"VAS"
```

```
models <- split(models, seq(nrow(models)))

est_model<-lapply(models[args],function(x,y){getBRMModel(dataframe = x,data =
y,path = "models/",family=student())},y=behaviorData)
```

Reaktion Times (brms_RT.R)

```
#!/usr/bin/env Rscript
args = commandArgs(trailingOnly=TRUE)

if (length(args)!=0){
  print(class(args))

}

# load necessary library files
if (!require("pacman")) install.packages("pacman")
library(pacman)
p_load(dplyr)
p_load(readr)
source("getBRMModel.R")

behaviorData<-read_rds("behavior.rds")


names<-list("m0","m1a","m1b",
            "m2","m2a", "m2b","m2c",
            "m3a","m3b"
)
formulas<-list(   "VasSlide.RT~1",

                  "VasSlide.RT~1+(1|Name)",
                  "VasSlide.RT~1+(1|Spielfeld)",

                  "VasSlide.RT~1+Factor1+Factor2 + (1|Name)",
                  "VasSlide.RT~1+Factor1*Factor2 + (1|Name)",

                      "VasSlide.RT~1+Factor1*Factor2 + betweenCond+(1|Name)",
                  "VasSlide.RT~1+Factor1*Factor2 * betweenCond + (1|Name)",

                      "VasSlide.RT~1+Factor1+Factor2 + betweenCond+(1|Name)",
                  "VasSlide.RT~1+Factor1+Factor2 * betweenCond + (1|Name)"
)
models<-data_frame(formulas,names)
models$measurement<-"RT"
models <- split(models, seq(nrow(models)))

est_model<-lapply(models[args],function(x,y){getBRMModel(dataframe = x,data =
y,control = list(adapt_delta = 0.95),family = weibull(),path = "models/")},y=
behaviorData)
```

RRi (brms_RRi.R)

```
#!/usr/bin/env Rscript
args = commandArgs(trailingOnly=TRUE)

if (length(args)!=0){
  print(class(args))
}

# load necessary library files
if (!require("pacman")) install.packages("pacman")
library(pacman)
p_load(readr)
p_load(dplyr)
source("getBRMModel.R")

physio<-read_rds("physio.rds")

names<-c(1:12)
formulas<-list("Value~1",

               "Value~1+(1|Spielfeld)",
               "Value~1+(1|BiopacSubject)",


               "Value~1+Factor1 + (1|BiopacSubject)",
               "Value~1+Factor2 + (1|BiopacSubject)",

               "Value~1+Factor2+ betweenCond + (1|BiopacSubject)",
               "Value~1+Factor2 * betweenCond + (1|BiopacSubject)",

               "Value~1+Factor2 * betweenCond+ Time  + (1|BiopacSubject)",
               "Value~1+Factor2 * betweenCond* Time  + (1|BiopacSubject)",

               "Value~1+Factor1+Factor2 * betweenCond + Time + (1|BiopacSubje
ct)",
               "Value~1+Factor1*Factor2 + betweenCond + Time + (1|BiopacSubje
ct)",
               "Value~1+Factor1*Factor2 * betweenCond + Time + (1|BiopacSubje
ct)"
)
measurement<-list("RRi")

models<-lapply(measurement,function(x,y){within(y,measurement<-x)},y= data_fr
ame(formulas,names)) %>% bind_rows()
models <- split(models, seq(nrow(models)))

est_model<-lapply(models[args],function(x,y){getBRMModel(dataframe = x,data=y
,path = "models/")},y=physio)
```

Behavior

```
# EXECUTE brms_b.R to generate Models!

models<-data_frame(list("m0",
              "m1a",
              "m1b",

              "m2",
              "m2a",
              "m2b",
              "m2c"
              ))
colnames(models)[1]<-"names"
models$measurement<-"VAS"
models <- split(models, seq(nrow(models)))
M<- lapply(models,
           function(x){read_rds(
             paste0("models/",x$measurement,
                    "_",x$names,".rds"))})

if (F){
  loo_behavior<- loo(M$`1`,M$`2`,M$`3`,M$`4`,M$`5`,M$`6`,M$`7`,
                     pointwise = F,
                     cores = parallel::detectCores ())
  saveRDS(loo_behavior,"models/loo_behavior.rds")
} else{
  loo_behavior<-read_rds("models/loo_behavior.rds")
}
lapply(M,function(x){x$formula})

## $`1`
## VasSlide.VAS ~ 1
##
## $`2`
## VasSlide.VAS ~ 1 + (1 | Name)
##
## $`3`
## VasSlide.VAS ~ 1 + (1 | Spielfeld)
##
## $`4`
## VasSlide.VAS ~ 1 + Factor1 + Factor2 + (1 | Name) + (1 | Spielfeld)
##
## $`5`
## VasSlide.VAS ~ 1 + Factor1 * Factor2 + (1 | Name) + (1 | Spielfeld)
##
## $`6`
## VasSlide.VAS ~ 1 + Factor1 * Factor2 + betweenCond + (1 | Name) + (1 | Spi
elfeld)
##
## $`7`
```

```
## VasSlide.VAS ~ 1 + Factor1 * Factor2 * betweenCond + (1 | Name) + (1 | Spi
elfeld)
```

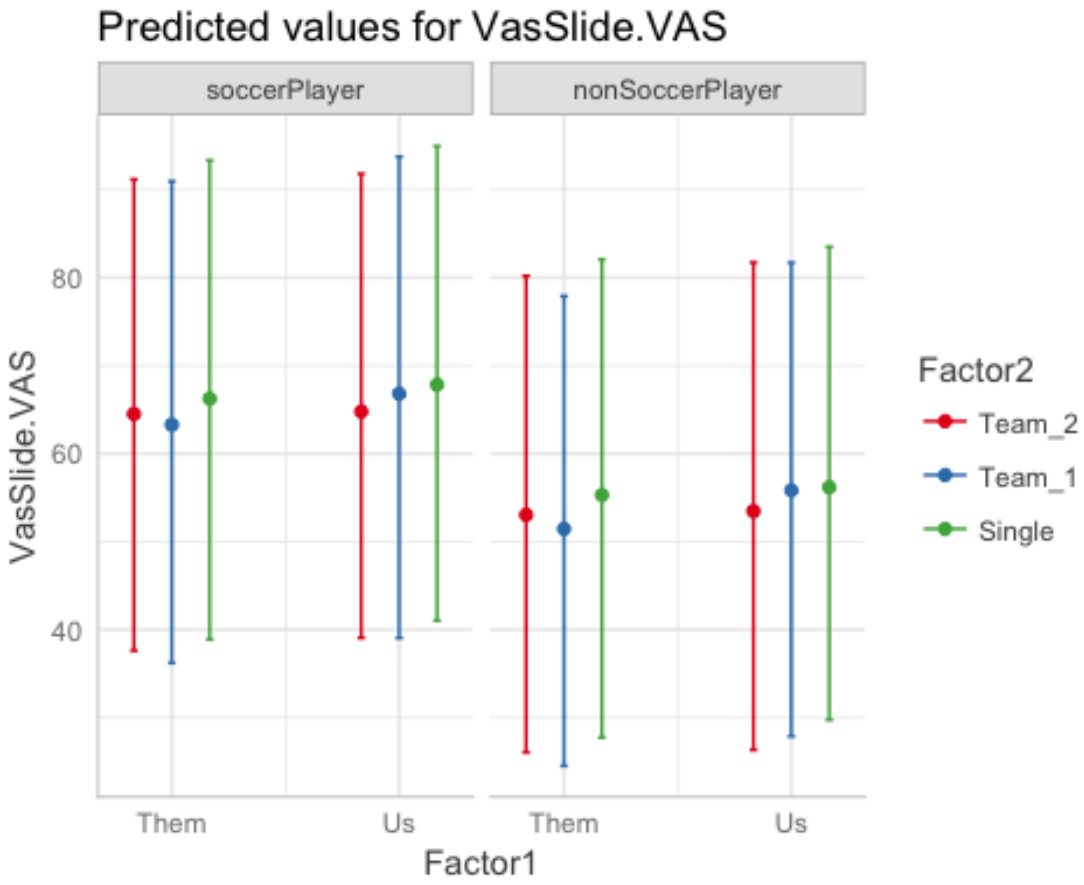
```
loo_behavior
```

```
##                   LOOIC     SE
## M$`1`          52188.44  88.73
## M$`2`          50988.69 103.42
## M$`3`          50009.53 105.09
## M$`4`          48024.60 117.65
## M$`5`          48017.50 117.68
## M$`6`          47979.33 117.38
## M$`7`          47980.64 117.37
## M$`1` - M$`2`  1199.75  69.59
## M$`1` - M$`3`  2178.91  89.09
## M$`1` - M$`4`  4163.84 111.85
## M$`1` - M$`5`  4170.94 111.87
## M$`1` - M$`6`  4209.11 111.37
## M$`1` - M$`7`  4207.80 111.33
## M$`2` - M$`3`   979.16 123.28
## M$`2` - M$`4`  2964.09  97.56
## M$`2` - M$`5`  2971.20  97.64
## M$`2` - M$`6`  3009.37  97.86
## M$`2` - M$`7`  3008.06  97.84
## M$`3` - M$`4`  1984.93  92.08
## M$`3` - M$`5`  1992.03  92.19
## M$`3` - M$`6`  2030.20  91.92
## M$`3` - M$`7`  2028.89  92.05
## M$`4` - M$`5`     7.11   6.62
## M$`4` - M$`6`    45.28  14.05
## M$`4` - M$`7`    43.97  14.99
## M$`5` - M$`6`    38.17  12.28
## M$`5` - M$`7`    36.86  13.19
## M$`6` - M$`7`    -1.31   5.11
```

```r
summary(M$`6`)
```

```
##  Family: student
##   Links: mu = identity; sigma = identity; nu = identity
## Formula: VasSlide.VAS ~ 1 + Factor1 * Factor2 + betweenCond + (1 | Name) +
(1 | Spielfeld)
##    Data: data (Number of observations: 5716)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##     ICs: LOO = NA; WAIC = NA; R2 = NA
##
## Group-Level Effects:
## ~Name (Number of levels: 58)
##               Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)    10.97      1.12     8.98    13.44        476 1.01
##
## ~Spielfeld (Number of levels: 16)
##               Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)    14.56      2.95    10.02    21.52        631 1.00
##
## Population-Level Effects:
##                          Estimate Est.Error l-95% CI u-95% CI Eff.Sample
## Intercept                   54.79      4.05    46.67    62.62        258
## Factor1Us                    1.81      0.72     0.39     3.22       1657
## Factor2Team_1               -2.94      0.90    -4.71    -1.18       1897
## Factor2Team_2               -1.31      0.66    -2.62    -0.02       1996
## betweenCondsoccerPlayer     11.62      1.87     8.15    15.48        501
## Factor1Us:Factor2Team_1      1.57      1.15    -0.62     3.85       1677
## Factor1Us:Factor2Team_2     -1.68      0.98    -3.60     0.25       1796
##                          Rhat
## Intercept                1.02
## Factor1Us                1.00
## Factor2Team_1            1.00
## Factor2Team_2            1.00
## betweenCondsoccerPlayer 1.01
## Factor1Us:Factor2Team_1 1.00
## Factor1Us:Factor2Team_2 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma    14.96      0.25    14.48    15.45       2139 1.00
## nu       16.29      3.89    10.95    25.89       1827 1.00
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```r
dat <- ggpredict(M$`6`,
                 terms = c("Factor1", "Factor2","betweenCond"),ppd=T)
plot(dat,alpha = 0.05, dodge = 0.5)
```


Predicted values for VasSlide.VAS
soccerPlayer
nonSoccerPlayer
VasSlide.VAS
80
60
40
Them
Us
Them
Us
Factor1
Factor2
Team_2
Team_1
Single

Reaction Times

```
# EXECUTE brms_RT.R to generate Models!
models<-data_frame(list("m0",
             "m1a",
             "m1b",

             "m2",
             "m2a",
             "m2b",
             "m2c"
             ))
colnames(models)[1]<-"names"
models$measurement<-"RT"
models <- split(models, seq(nrow(models)))
M_RT<- lapply(models,
              function(x){read_rds(
                paste0("models/",
                       x$measurement,"_",x$names,".rds"))})

if (F){
  loo_RT<- loo(M_RT$`1`,M_RT$`2`,M_RT$`3`,M_RT$`4`,
               M_RT$`5`,M_RT$`6`,M_RT$`7`,
               pointwise = F,
               cores = parallel::detectCores ())
  saveRDS(loo_RT,"models/loo_RT.rds")
} else{
  loo_RT<-read_rds("models/loo_RT.rds")
}
lapply(M_RT,function(x){x$formula})
```

```
## $`1`
## VasSlide.RT ~ 1
##
## $`2`
## VasSlide.RT ~ 1 + (1 | Name)
##
## $`3`
## VasSlide.RT ~ 1 + (1 | Spielfeld)
##
## $`4`
## VasSlide.RT ~ 1 + Factor1 + Factor2 + (1 | Name)
##
## $`5`
## VasSlide.RT ~ 1 + Factor1 * Factor2 + (1 | Name)
##
## $`6`
## VasSlide.RT ~ 1 + Factor1 * Factor2 + betweenCond + (1 | Name)
##
## $`7`
## VasSlide.RT ~ 1 + Factor1 * Factor2 * betweenCond + (1 | Name)
```

```
loo_RT
```

```
##                         LOOIC    SE
## M_RT$`1`             79481.93 75.68
## M_RT$`2`             78469.09 92.81
## M_RT$`3`             79467.19 76.15
## M_RT$`4`             78468.99 92.87
## M_RT$`5`             78471.98 92.95
## M_RT$`6`             78472.26 92.94
## M_RT$`7`             78459.05 93.41
## M_RT$`1` - M_RT$`2`  1012.84 66.27
## M_RT$`1` - M_RT$`3`    14.73  8.52
## M_RT$`1` - M_RT$`4`  1012.93 66.31
## M_RT$`1` - M_RT$`5`  1009.95 66.44
## M_RT$`1` - M_RT$`6`  1009.66 66.45
## M_RT$`1` - M_RT$`7`  1022.88 67.22
## M_RT$`2` - M_RT$`3`  -998.10 67.21
## M_RT$`2` - M_RT$`4`     0.10  5.77
## M_RT$`2` - M_RT$`5`    -2.89  6.00
## M_RT$`2` - M_RT$`6`    -3.17  6.01
## M_RT$`2` - M_RT$`7`    10.04 12.07
## M_RT$`3` - M_RT$`4`   998.20 67.24
## M_RT$`3` - M_RT$`5`   995.21 67.37
## M_RT$`3` - M_RT$`6`   994.93 67.38
## M_RT$`3` - M_RT$`7`  1008.14 68.11
## M_RT$`4` - M_RT$`5`    -2.99  2.17
## M_RT$`4` - M_RT$`6`    -3.27  2.28
## M_RT$`4` - M_RT$`7`     9.94 11.05
## M_RT$`5` - M_RT$`6`    -0.28  0.79
## M_RT$`5` - M_RT$`7`    12.93 10.82
## M_RT$`6` - M_RT$`7`    13.21 10.77
```

```
summary(M_RT$`2`)
```

```
##  Family: weibull
##   Links: mu = log; shape = identity
## Formula: VasSlide.RT ~ 1 + (1 | Name)
##    Data: data (Number of observations: 4457)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##     ICs: LOO = NA; WAIC = NA; R2 = NA
##
## Group-Level Effects:
## ~Name (Number of levels: 52)
##               Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)     0.56      0.06     0.46     0.69        304 1.01
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## Intercept    32.72      0.39    31.97    33.50       1424 1.00
##
## Family Specific Parameters:
```

```
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## shape     3.74      0.04     3.66     3.83       1967 1.00
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Herzfrequenz (RRi)

```
# EXECUTE brms_RRi.R to generate Models!
models<-data_frame(c(1:12))
colnames(models)[1]<-"names"
models$measurement<-"RRi"
models <- split(models, seq(nrow(models)))
M_RRi<- lapply(models,
               function(x){read_rds(
                 paste0("models/",
                        x$measurement,"_",
                        x$names,".rds"))})

if (F){
  loo_RRi<- loo(M_RRi$`1`,M_RRi$`2`,M_RRi$`3`,M_RRi$`4`,
                M_RRi$`5`,M_RRi$`6`,M_RRi$`7`,M_RRi$`8`,
                M_RRi$`9`,M_RRi$`10`,M_RRi$`11`,M_RRi$`12`,
                pointwise = F,cores = parallel::detectCores ())
  saveRDS(loo_RRi,"models/loo_RRi.rds")
} else {
  loo_RRi<-read_rds("models/loo_RRi.rds")
}
lapply(M_RRi,function(x){x$formula})

## $`1`
## Value ~ 1
##
## $`2`
## Value ~ 1 + (1 | Spielfeld)
##
## $`3`
## Value ~ 1 + (1 | BiopacSubject)
##
## $`4`
## Value ~ 1 + Factor1 + (1 | BiopacSubject)
##
## $`5`
## Value ~ 1 + Factor2 + (1 | BiopacSubject)
##
## $`6`
## Value ~ 1 + Factor2 + betweenCond + (1 | BiopacSubject)
##
## $`7`
## Value ~ 1 + Factor2 * betweenCond + (1 | BiopacSubject)
##
## $`8`
## Value ~ 1 + Factor2 * betweenCond + Time + (1 | BiopacSubject)
##
## $`9`
## Value ~ 1 + Factor2 * betweenCond * Time + (1 | BiopacSubject)
##
## $`10`
```

```
## Value ~ 1 + Factor1 + Factor2 * betweenCond + Time + (1 | BiopacSubject)
##
## $`11`
## Value ~ 1 + Factor1 * Factor2 + betweenCond + Time + (1 | BiopacSubject)
##
## $`12`
## Value ~ 1 + Factor1 * Factor2 * betweenCond + Time + (1 | BiopacSubject)


loo_RRi

##                              LOOIC     SE
## M_RRi$`1`                345560.44 280.17
## M_RRi$`2`                345555.91 280.23
## M_RRi$`3`                281800.12 361.12
## M_RRi$`4`                281799.72 361.11
## M_RRi$`5`                281798.60 360.99
## M_RRi$`6`                281800.26 360.97
## M_RRi$`7`                281763.98 360.64
## M_RRi$`8`                280218.01 362.61
## M_RRi$`9`                279960.31 362.81
## M_RRi$`10`               280219.43 362.60
## M_RRi$`11`               280255.71 363.02
## M_RRi$`12`               280187.45 362.49
## M_RRi$`1` - M_RRi$`2`        4.53   5.14
## M_RRi$`1` - M_RRi$`3`    63760.32 402.18
## M_RRi$`1` - M_RRi$`4`    63760.72 402.17
## M_RRi$`1` - M_RRi$`5`    63761.84 402.09
## M_RRi$`1` - M_RRi$`6`    63760.18 402.07
## M_RRi$`1` - M_RRi$`7`    63796.46 401.84
## M_RRi$`1` - M_RRi$`8`    65342.43 404.92
## M_RRi$`1` - M_RRi$`9`    65600.13 406.07
## M_RRi$`1` - M_RRi$`10`   65341.01 404.91
## M_RRi$`1` - M_RRi$`11`   65304.73 405.17
## M_RRi$`1` - M_RRi$`12`   65372.99 404.64
## M_RRi$`2` - M_RRi$`3`    63755.79 402.38
## M_RRi$`2` - M_RRi$`4`    63756.19 402.37
## M_RRi$`2` - M_RRi$`5`    63757.31 402.29
## M_RRi$`2` - M_RRi$`6`    63755.65 402.27
## M_RRi$`2` - M_RRi$`7`    63791.93 402.04
## M_RRi$`2` - M_RRi$`8`    65337.90 405.13
## M_RRi$`2` - M_RRi$`9`    65595.60 406.28
## M_RRi$`2` - M_RRi$`10`   65336.48 405.12
## M_RRi$`2` - M_RRi$`11`   65300.20 405.37
## M_RRi$`2` - M_RRi$`12`   65368.46 404.84
## M_RRi$`3` - M_RRi$`4`        0.39   2.19
## M_RRi$`3` - M_RRi$`5`        1.52   3.91
## M_RRi$`3` - M_RRi$`6`       -0.14   3.67
## M_RRi$`3` - M_RRi$`7`       36.14  13.03
## M_RRi$`3` - M_RRi$`8`     1582.10  79.71
## M_RRi$`3` - M_RRi$`9`     1839.80  93.12
```

```
## M_RRi$`3` - M_RRi$`10`    1580.69  79.69
## M_RRi$`3` - M_RRi$`11`    1544.41  78.90
## M_RRi$`3` - M_RRi$`12`    1612.67  80.56
## M_RRi$`4` - M_RRi$`5`        1.13   4.40
## M_RRi$`4` - M_RRi$`6`       -0.54   4.20
## M_RRi$`4` - M_RRi$`7`       35.75  12.79
## M_RRi$`4` - M_RRi$`8`     1581.71  79.71
## M_RRi$`4` - M_RRi$`9`     1839.41  93.13
## M_RRi$`4` - M_RRi$`10`    1580.29  79.71
## M_RRi$`4` - M_RRi$`11`    1544.02  78.90
## M_RRi$`4` - M_RRi$`12`    1612.28  80.56
## M_RRi$`5` - M_RRi$`6`       -1.67   0.45
## M_RRi$`5` - M_RRi$`7`       34.62  12.26
## M_RRi$`5` - M_RRi$`8`     1580.58  79.51
## M_RRi$`5` - M_RRi$`9`     1838.28  92.96
## M_RRi$`5` - M_RRi$`10`    1579.16  79.49
## M_RRi$`5` - M_RRi$`11`    1542.89  78.73
## M_RRi$`5` - M_RRi$`12`    1611.15  80.39
## M_RRi$`6` - M_RRi$`7`       36.28  12.25
## M_RRi$`6` - M_RRi$`8`     1582.25  79.52
## M_RRi$`6` - M_RRi$`9`     1839.95  92.96
## M_RRi$`6` - M_RRi$`10`    1580.83  79.50
## M_RRi$`6` - M_RRi$`11`    1544.56  78.74
## M_RRi$`6` - M_RRi$`12`    1612.81  80.39
## M_RRi$`7` - M_RRi$`8`     1545.96  78.68
## M_RRi$`7` - M_RRi$`9`     1803.66  92.32
## M_RRi$`7` - M_RRi$`10`    1544.55  78.65
## M_RRi$`7` - M_RRi$`11`    1508.27  79.60
## M_RRi$`7` - M_RRi$`12`    1576.53  79.55
## M_RRi$`8` - M_RRi$`9`      257.70  37.72
## M_RRi$`8` - M_RRi$`10`      -1.42   0.88
## M_RRi$`8` - M_RRi$`11`     -37.69  12.03
## M_RRi$`8` - M_RRi$`12`      30.57  12.50
## M_RRi$`9` - M_RRi$`10`    -259.12  37.72
## M_RRi$`9` - M_RRi$`11`    -295.39  39.51
## M_RRi$`9` - M_RRi$`12`    -227.13  39.95
## M_RRi$`10` - M_RRi$`11`    -36.27  12.24
## M_RRi$`10` - M_RRi$`12`     31.99  12.52
## M_RRi$`11` - M_RRi$`12`     68.26  17.44
```

```
print(M_RRi$`12`,digits=2)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: Value ~ 1 + Factor1 * Factor2 * betweenCond + Time + (1 | BiopacS
ubject)
##    Data: data_f (Number of observations: 45626)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##     ICs: LOO = NA; WAIC = NA; R2 = NA
##
## Group-Level Effects:
## ~BiopacSubject (Number of levels: 50)
##               Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)     8.73      0.88     7.21    10.64        986 1.00
##
## Population-Level Effects:
##                                                  Estimate Est.Error
## Intercept                                           76.61      1.74
## Factor1Us                                           -0.13      0.12
## Factor2Team_1                                       -0.49      0.12
## Factor2Team_2                                       -0.21      0.12
## betweenCondsoccerPlayer                             -8.28      2.47
## Time0                                               -0.22      0.12
## Time1                                               -0.32      0.11
## Time2                                               -0.11      0.11
## Time3                                                0.20      0.11
## Time4                                                0.72      0.11
## Time5                                                1.51      0.11
## Time6                                                2.08      0.11
## Time7                                                2.28      0.11
## Time8                                                2.06      0.11
## Time9                                                1.48      0.11
## Factor1Us:Factor2Team_1                              0.28      0.17
## Factor1Us:Factor2Team_2                              0.33      0.17
## Factor1Us:betweenCondsoccerPlayer                    0.38      0.17
## Factor2Team_1:betweenCondsoccerPlayer                2.39      0.34
## Factor2Team_2:betweenCondsoccerPlayer                0.30      0.16
## Factor1Us:Factor2Team_1:betweenCondsoccerPlayer      -2.07      0.39
## Factor1Us:Factor2Team_2:betweenCondsoccerPlayer      -0.89      0.24
##                                                  l-95% CI u-95% CI
## Intercept                                           73.21    80.04
## Factor1Us                                           -0.37     0.11
## Factor2Team_1                                       -0.72    -0.25
## Factor2Team_2                                       -0.45     0.03
## betweenCondsoccerPlayer                            -12.97    -3.35
## Time0                                               -0.44     0.01
## Time1                                               -0.55    -0.10
## Time2                                               -0.34     0.11
## Time3                                               -0.02     0.43
## Time4                                                0.49     0.95
```

```
## Time5                                                 1.29     1.73
## Time6                                                 1.86     2.30
## Time7                                                 2.05     2.49
## Time8                                                 1.85     2.29
## Time9                                                 1.25     1.70
## Factor1Us:Factor2Team_1                              -0.06     0.61
## Factor1Us:Factor2Team_2                              -0.02     0.66
## Factor1Us:betweenCondsoccerPlayer                     0.05     0.71
## Factor2Team_1:betweenCondsoccerPlayer                 1.73     3.08
## Factor2Team_2:betweenCondsoccerPlayer                -0.03     0.62
## Factor1Us:Factor2Team_1:betweenCondsoccerPlayer      -2.83    -1.35
## Factor1Us:Factor2Team_2:betweenCondsoccerPlayer      -1.36    -0.41
##                                                   Eff.Sample Rhat
## Intercept                                                858 1.00
## Factor1Us                                               2536 1.00
## Factor2Team_1                                           2861 1.00
## Factor2Team_2                                           2806 1.00
## betweenCondsoccerPlayer                                  856 1.00
## Time0                                                   2698 1.00
## Time1                                                   2740 1.00
## Time2                                                   3124 1.00
## Time3                                                   2878 1.00
## Time4                                                   2988 1.00
## Time5                                                   2457 1.00
## Time6                                                   2905 1.00
## Time7                                                   2752 1.00
## Time8                                                   2996 1.00
## Time9                                                   2690 1.00
## Factor1Us:Factor2Team_1                                 2734 1.00
## Factor1Us:Factor2Team_2                                 2559 1.00
## Factor1Us:betweenCondsoccerPlayer                       2624 1.00
## Factor2Team_1:betweenCondsoccerPlayer                   3333 1.00
## Factor2Team_2:betweenCondsoccerPlayer                   2898 1.00
## Factor1Us:Factor2Team_1:betweenCondsoccerPlayer         3013 1.00
## Factor1Us:Factor2Team_2:betweenCondsoccerPlayer         2647 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sigma     5.21      0.02     5.18     5.24       4000 1.00
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
p_load(ggeffects)

dat <- ggpredict(M_RRi$`12`,
                 terms = c("Factor1", "Factor2","betweenCond"),ppd=T)
plot(dat,alpha = 0.05, dodge = 0.5 )
```