

Are there qualitative individual differences in the SNARC effect?

Julia Haaf

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- sanity check with 1+2 and 8+9
- Common-effect model include CHECK
- change to -1, 1 CHECK
- CIs for lm output CHECK

I first looked at one data set with average proportions of negative, positive and null effects according to the preprint (Cipora et al, 2019). The data I picked are from Cipora (2014).

```
# Loading the data
raw_data <- read.table("Cipora_2014_raw_data.txt"
                      , sep="\t", dec=".", header = TRUE)

# Changing part.code variable to be a factor.
raw_data$part.code <- as.factor(raw_data$part.code)

## Julia data inspection
## I want data with accuracy and >200ms filter
# but not the 3SD filter they used.

dat <- subset(raw_data
              , correct.experimental == 1 & filter.correct.exp.antic == 1)
# around 30 trials per person and condition
mean(with(dat, tapply(rt, list(number, resp.side, part.code), length)))

## [1] 28.70455

#Needed later
prep <- prep.models(dat$part.code
                   , side = dat$resp.side
                   , number = dat$number)
```

The Model

The model I used is a hierarchical model on the trial-level. Let Y_{ijkl} be the response time for the i th person, the j th response side, the k th number, and the ℓ th trial. Then

$$Y_{ijkl} \sim \text{Normal}(\mu + \alpha_i + x_j \nu_i + u_k \delta_i + v_{jk} \theta_i, \sigma^2),$$

where μ is the grand mean, α_i is the i th person's baseline effect, ν_i is the i th person's response side effect, δ_i is the i th person's number effect, and θ_i is the i th person's SNARC effect, the congruency effect between side and number. The variable $x_j = \begin{cases} 1, & \text{if } j = 1 \\ 0, & \text{if } j = 2 \end{cases}$, the variable $u_k = k$, and the variable v_{jk} is the product of x_j and u_k .

Observed SNARC

I use a similar linear model on each participant's data to get observed SNARC effects per person.

```
# reorder participants
dat$sub <- prep$sub
dat <- dat[order(dat$sub), ]

# Averaging reaction times for each [participant x number x response side]
# configuration and forming the data frame in convenient manner, calculating dRTs
aggregated_data <- aggregate(rt ~ resp.side + number + part.code, dat, mean)
aggregated_data_dRT <- dcast(aggregated_data, part.code + number ~ resp.side)

## Using rt as value column: use value.var to override.

aggregated_data_dRT$dRT <- aggregated_data_dRT$right - aggregated_data_dRT$left

# Calculating unstandardized slopes with main effect of side and number
testSNARC <- ddply(aggregated_data, "part.code", function(x){
  regression <- lm(x$rt ~ x$number * x$resp.side, data = aggregated_data)
  ind.slope <- regression$coefficients[[4]]
  side.slope <- regression$coefficients[[2]]
  number.slope <- regression$coefficients[[3]]
  p.intercept <- regression$coefficients[[1]]
  coef <- summary(regression)$coefficients[4,1]
  err <- summary(regression)$coefficients[4,2]
```

```

ci <- coef + c(-1,1) * err * qt(0.975, 12)
data.frame(unstdSNARC.slope=ind.slope, side.slope, number.slope, p.intercept, lower =
})
kable(head(testSNARC))

```

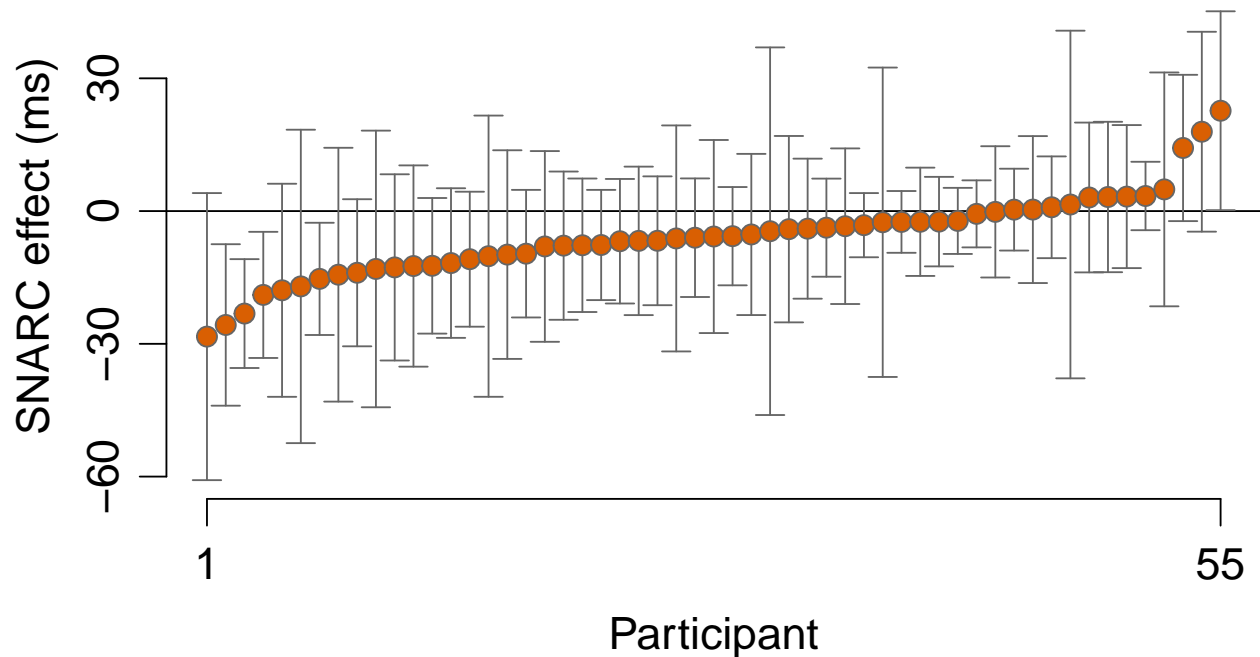
part.code	unstdSNARC.slope	side.slope	number.slope	p.intercept	lower	upper
cipora2014_001	3.2727644	-3.594861	-35.84258	521.9908	-12.8882287	19.433757
cipora2014_002	22.6780546	-8.846886	-152.71972	671.5979	0.2085119	45.147597
cipora2014_003	-9.6235159	5.133972	18.57257	600.3815	-24.0391341	4.792102
cipora2014_004	14.2659935	-8.345508	-69.23341	620.4075	-2.2642890	30.796276
cipora2014_005	-0.6271922	-2.014712	-24.03768	529.7102	-8.2014692	6.947085
cipora2014_006	-2.5249521	3.633429	-33.13579	846.1289	-37.4837674	32.433863

```

cis <- testSNARC[, 6:7]
par(cex = 1.5, mgp = c(2, .7, 0))

plot(sort(testSNARC$unstdSNARC.slope), pch = "+", ylim = range(cis)
      , ylab = "SNARC effect (ms)"
      , xlab = "Participant"
      , col = 0
      , frame.plot = F
      , axes = F)
axis(1, c(1, prep$I))
axis(2, seq(-60, 30, 30))
abline(h = 0)
ind <- order(testSNARC$unstdSNARC.slope)
plotCI(x = 1: nrow(testSNARC)
       , y = testSNARC$unstdSNARC.slope[ind]
       , ui= cis[ind, 2]
       , li= cis[ind, 1]
       , add = TRUE
       , col = "gray40"
       , pch = 21
       , pt.bg= myCols[2]
       )

```



Estimated SNARC

```
out <- quid(id = dat$part.code
  , side = dat$resp.side
  , number = dat$number
  , prior = c(meanScale, effectScale)
  , rt = dat$rt, iter = 15000)
```

The estimated effects for the SNARC are flipped in sign for some reason. I will see if I can fix that, but for now I flip the observed SNARC effects for comparison.

```
layout(matrix(1:4, ncol = 2, byrow = T))
par(mgp = c(2, .7, 0))
## check

#Individuals' effect of number
i.delta0 <- 1 * prep$I + 2 #index for the common effect
i.delta <- (1 * prep$I + 3):(2 * prep$I + 2) #indices for the individual effects

#add overall effect to individuals' deviations
myDelta <- out$mcmc.unconstrained[, i.delta] +
  out$mcmc.unconstrained[, i.delta0]
```

```

plot(colMeans(myDelta), testSNARC$number.slope)
abline(0, 1)

#Individuals' effect of response side
i.nu0 <- 2 * prep$I + 3 #index for the common effect
i.nu <- (2 * prep$I + 4):(3 * prep$I + 3) #indices for the individual effects

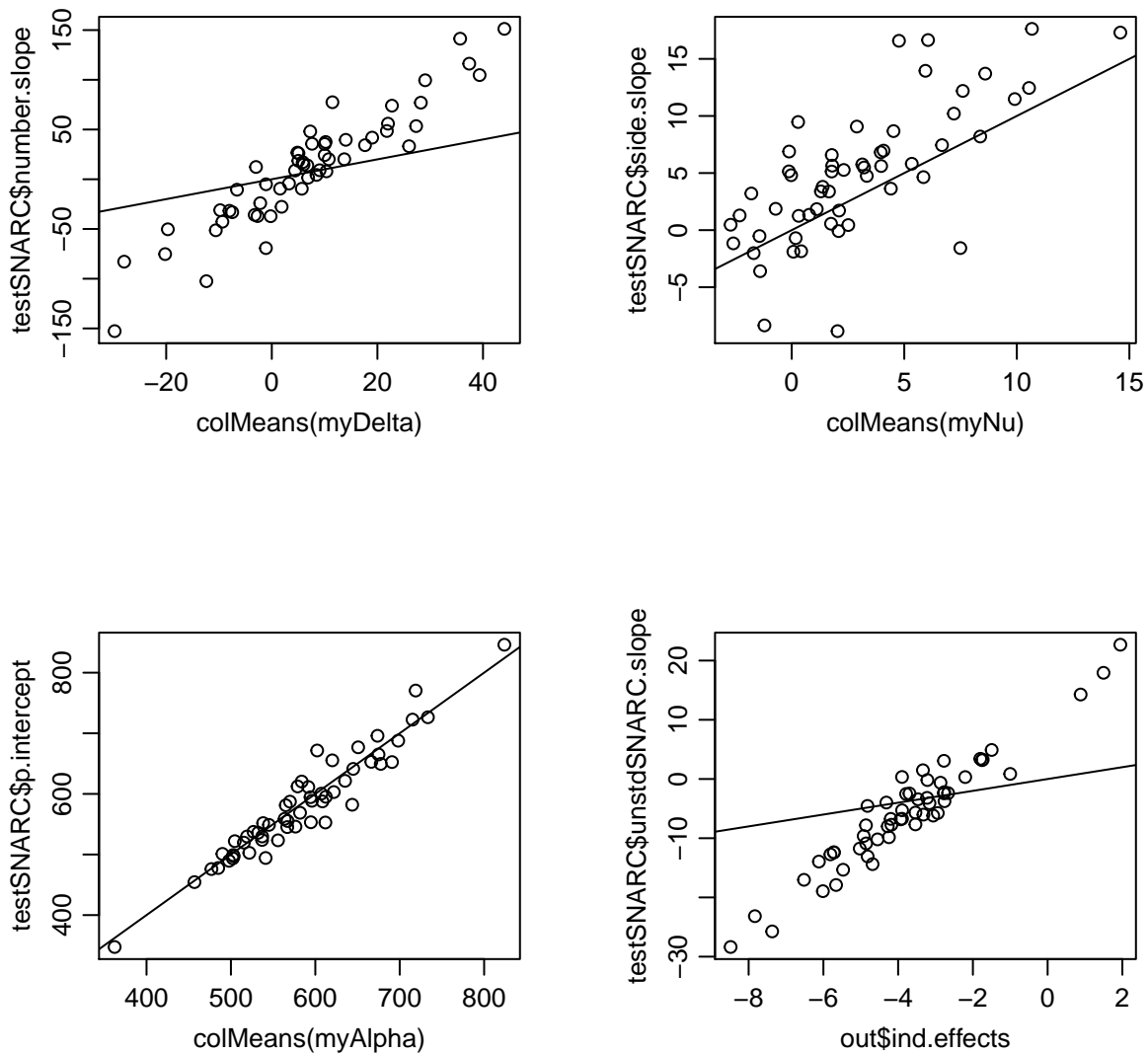
#add overall effect to individuals' deviations
myNu <- out$mcmc.unconstrained[, i.nu] +
  out$mcmc.unconstrained[, i.nu0]
plot(colMeans(myNu), testSNARC$side.slope)
abline(0, 1)

#Individuals' baseline estimate
i.mu <- 1 #index for the common effect
i.alpha <- (2):(prep$I + 1) #indices for the individual effects

#add overall effect to individuals'
myAlpha <- out$mcmc.unconstrained[, i.mu] +
  out$mcmc.unconstrained[, i.alpha]
plot(colMeans(myAlpha), testSNARC$p.intercept)
abline(0, 1)

#Individuals' SNARC effect
plot(out$ind.effects, testSNARC$unstdSNARC.slope)
abline(0, 1)

```



Some hierarchical shrinkage for the effects. I may change the scales for ν and δ .

Does anybody SNARC?

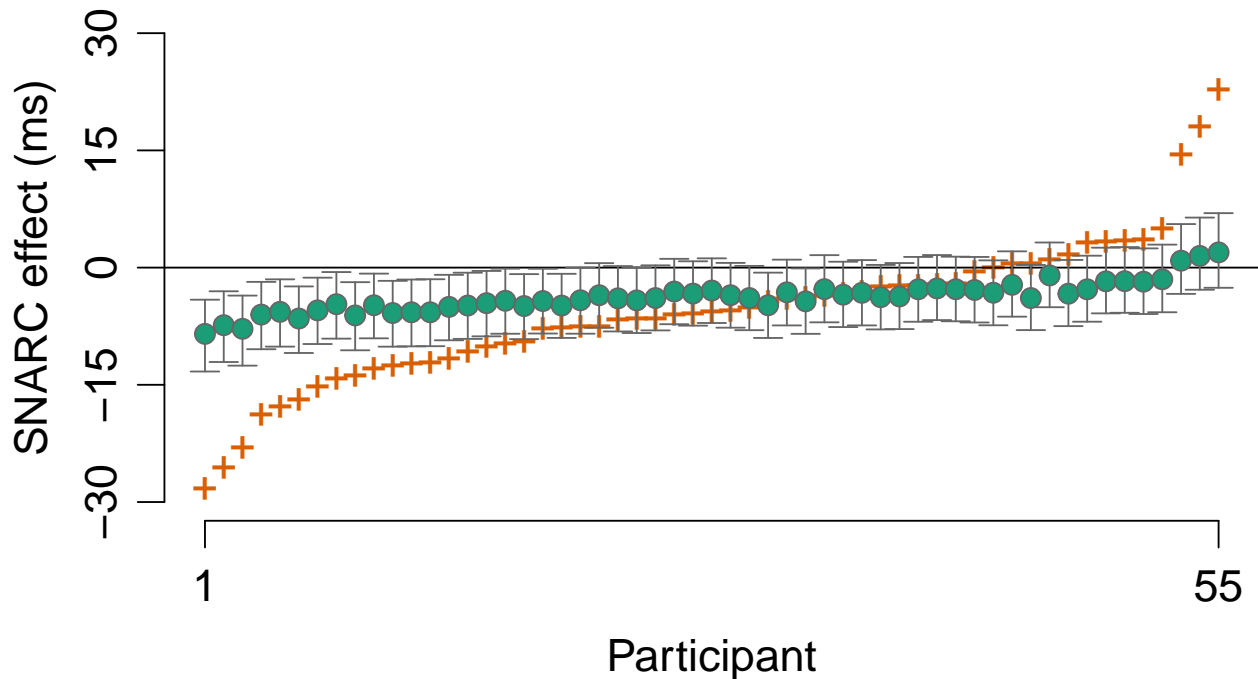
```
cis <- apply(out$theta, 2, quantile, probs = c(.025, .975))
par(cex = 1.5, mgp = c(2, .7, 0))

plot(sort(testSNARC$unstdSNARC.slope), pch = "+", ylim = c(-30, 30)
      , ylab = "SNARC effect (ms)"
      , xlab = "Participant"
      , col = myCols[2]
      , frame.plot = F
      , axes = F)
```

```

axis(1, c(1, prep$I))
axis(2, seq(-30, 30, 15))
abline(h = 0)
ind <- order(testSNARC$unstdSNARC.slope)
plotCI(x = 1: nrow(testSNARC)
      , y = out$ind.effects[ind]
      , ui= cis[2, ind]
      , li= cis[1, ind]
      , add = TRUE
      , col = "gray40"
      , pch = 21
      , pt.bg= myCols[1]
      )

```



Now. The estimates show quite a bit of hierarchical shrinkage. I might change the scales to see what happens. But They reflect the expected size of effect. We would expect effects around 5 ms on average, and the trial by trial variability to be around 150 ms. Likewise, we would expect variability around 5 ms. The scales therefore should be around 5 ms/150 ms, or $1/30$. So, the chosen scales are quite wide.

I first looked at the Bayes factor of no SNARC effect, the null model, and a varying SNARC effect, the unconstrained model. The Bayes factor is 6.9407361×10^7 in favor of the null model.

```
out$bf$
```

```
##          bf.pu          bf.1u          bf.0u  
## 1.397854e-01 6.577654e+19 6.940736e+07
```