Appendix: Power Analysis

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Design

For this power analysis we will simulate 40 labs contributing 32 infants (1280 participants) from 3 to 15 months of age. (MB5 estimates there will be a minimum of 1200 participants in the final sample.)

Notes: MB1 overall effect size was 0.29 for the single-screen central fixation (CF) method, with additional effect of 0.21 for HPP, and eye-tracking (ET) yielding a slight (non-significant) decrease in effect of -0.06. We expect to have X labs running infant-controlled familiarization duration, and the other 20-X labs running a fixed familiarization procedure.

Factors:

- *stimulus_type*: indicates the type (complexity/difficulty) of the stimuli that infants are familiarized with during training (high/low stimulus type; within-infant, 12 per type)
- *familiarization_time*: indicates how long each stimulus is exposed during familiarization (5, 10, or 15 seconds; within-infant; scaled to [-1,1])
- *trial_num*: indicates the sequential order in which test trials were presented. Trial number thus ranges from 1 to 24.
- *age_mos*: the infants' age in months (3.0-15.0), scaled and centered in *age* column.
- *procedure*: indicates the experimental method that was used to record infants' looking to the stimuli: infant-controlled exposure (IC; total familiarization time is achieved over uncontrolled period of time) vs. fixed-duration exposure (FD; controlled period of exposure, unknown period of infant fixation)

To do our power analysis, we will generate 1,000 datasets of this structure with a given effect size (e.g., .3), run the mixed-effects regression for each simulated dataset, and count the number of times that the effect is significant. Note that we generate normally-distributed looking times, assuming that they have already been log-transformed.

Simulate Datasets

```
set.seed(123) # reproducible sampling

generate_dataset <- function(n_labs=40, n_per_lab=32,
                             effect_sizes=list(type = .3, familiarization = .1,
                                               age = .1, "age*type"=.1,
                                               "age*familiarization"=0, "type*familiarization"=0,
                                               "type*age*familiarization"=.1)) {
  # critical test is the 3-way interaction?

  # rewrite to use expand.grid ?
```

```
labID = rep(as.character(1:n_labs), each=n_per_lab)
subjID = 1:(n_labs*n_per_lab)

familiarization_times = c(5,10,15) # or maybe we expect linear effect on log(fam_time)?
fam_times_sc = c(-1,0,1) # scaled
#fam_times_sc = log(familiarization_times) # tried this: yields much lower power for main effects, on
stimulus_types = c(rep("high",4), rep("low",4)) # stimulus complexity
# trials each subject gets (but randomly ordered)
fam_by_stim = expand.grid(fam_time = fam_times_sc, stimulus_type = stimulus_types)

# assume each lab uses one procedure
lab_procedure = sample(c("IC","FD"), n_labs, replace=T, prob=c(.5,.5)) # 50/50 IC / FD procedures?
procedure = rep(lab_procedure, each=n_per_lab)

test_order = rep(1:4, n_per_lab/4*n_labs)

# per-subject data
simd <- tibble(subjID, labID, procedure, test_order) %>%
  mutate(subjInt = rnorm(length(subjID), mean=0, sd=1))

# add lab random intercept
simd$labInt = 0.0
for(lab in unique(labID)) {
  labInd = which(simd$labID==lab)
  simd[labInd,]$labInt = rnorm(1, mean=0, sd=1) # could increase per-lab variability ..
}

# uniform random vars
simd$age_mos = runif(nrow(simd), min=3.0, max=15.0)
simd$age = scale(simd$age_mos, center=T, scale=T)[,1]

# generate per-subject data, put in long (row per-trial) df

siml <- tibble()
for(i in 1:nrow(simd)) {
  # randomized trial order (but maybe should be done according to preset pseudorandom orders?)
  tmp_sdat <- fam_by_stim[sample(1:nrow(fam_by_stim), size=nrow(fam_by_stim), replace=F),]
  # let's assume prop_novel is normally-distributed
  stimulus_type = with(tmp_sdat, ifelse(stimulus_type=="high", .5, -.5))
  error_term = rnorm(nrow(tmp_sdat), 0, sd=1) + simd[i,]$labInt + simd[i,]$subjInt # add random slope
  # rescale error to be >0
  # ToDo: scale familiarization time ?
  age_effect_subj = effect_sizes$age * rep(simd[i,]$age, nrow(tmp_sdat))

  # can we assume these are z-scored proportions of novel looking? maybe truncate them?
  # ToDo: check if problems when effect sizes are 0?
  tmp_sdat$dv_zscore = effect_sizes$type * stimulus_type + # main
    age_effect_subj +  # main
    effect_sizes$familiarization * tmp_sdat$fam_time +  # main
    effect_sizes$`age*type` * stimulus_type * effect_sizes$type * age_effect_subj +
    effect_sizes$`age*familiarization` * age_effect_subj * tmp_sdat$fam_time * effect_sizes$familiari
    effect_sizes$`type*familiarization` * tmp_sdat$fam_time * stimulus_type * effect_sizes$type +
    effect_sizes$`type*age*familiarization` * stimulus_type * effect_sizes$type * age_effect_subj * t
```

```
      error_term

    # since DV has SD~.2, and must be in the range [0,1], let's make floor=-2.5 and ceiling=2.5
    min_ind = which(tmp_sdat$dv_zscore< -2.5)
    max_ind = which(tmp_sdat$dv_zscore > 2.5)
    if(length(min_ind)>0) tmp_sdat[min_ind,]$dv_zscore = -2.5
    if(length(max_ind)>0) tmp_sdat[max_ind,]$dv_zscore = 2.5

    siml <- siml %>%
      bind_rows(tmp_sdat %>% mutate(subjID = simd[i,]$subjID,
                                    labID = simd[i,]$labID,
                                    age = simd[i,]$age,
                                    age_mos = simd[i,]$age_mos,
                                    subjInt = simd[i,]$subjInt,
                                    labInt = simd[i,]$labInt,
                                    trial_num = 1:nrow(tmp_sdat)))
          #novel_looking_time = rnorm(n = nrow(tmp_sdat), mean=0, sd=1), # = .05
          #familiar_looking_time = rnorm(n = nrow(tmp_sdat), mean=0, sd=1), # = .05
          #prop_novel = novel_looking_time / (novel_looking_time + familiar_looking_time), # use beta d
          #prop_novel = rbeta(n=nrow(tmp_sdat), shape1=??, shape2=??)
          # mean_beta = .5 + familiarization_time*age*type
               # how to choose beta parameters: more non-central = more of a novelty/familiarity effect
  }

  siml$trial_num_sc = scale(siml$trial_num, center=T, scale=T)

  siml$subjID = as.factor(siml$subjID)
  # switch from dummy-code to effects code
  siml$stimulus_type = as.factor(siml$stimulus_type)
  contrasts(siml$stimulus_type) = contr.sum(2)
  return(siml)
}
```

Plot Example Dataset

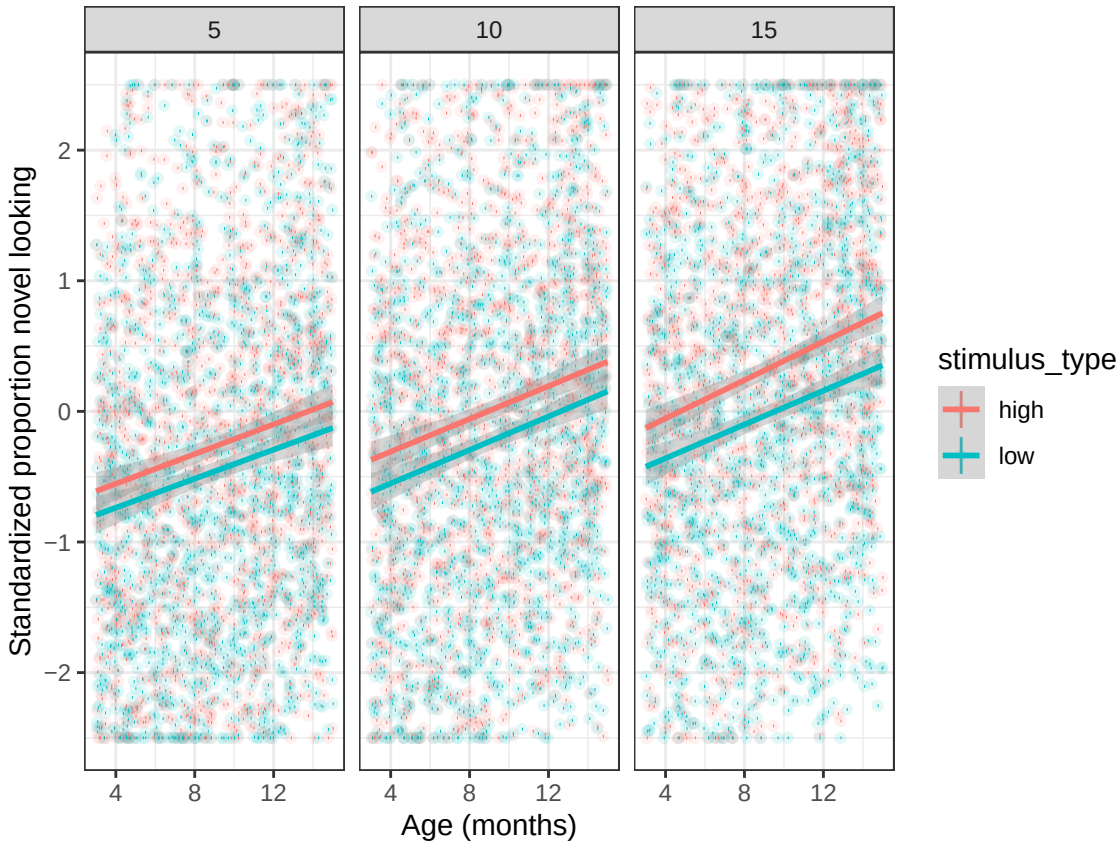
We generate and plot an example dataset with all effect sizes = .3 (main, 2-way, and 3-way).

```
## `summarise()` has grouped output by 'subjID', 'stimulus_type', 'fam_time'. You
## can override using the `.groups` argument.
## `summarise()` has grouped output by 'subjID', 'stimulus_type', 'fam_time'. You
## can override using the `.groups` argument.

## Warning: `as_data_frame()` was deprecated in tibble 2.0.0.
## Please use `as_tibble()` instead.
## The signature and semantics have changed, see `?as_tibble`.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was generated.

## Warning: `cols` is now required when using unnest().
## Please use `cols = c(strap)`

## `geom_smooth()` using formula 'y ~ x'
```



Model Structure

Infants' proportion of looking at novel object (DV) ~ 1 + familiarization time (5, 10, 15) * stimulus type (high/low complexity) * age + (fam_time*stim_type | subject) + (fam_time*stim_type*age | lab)

```
# power for either just main effects, or just the 3-way
effects <- c("stimulus_type1","age_mos","fam_time",
             "stimulus_type1:fam_time", "stimulus_type1:age_mos", "fam_time:age_mos",
             "stimulus_type1:fam_time:age_mos")

# power for just the 3-way
fit_simple_model <- function(siml) {
  m1 <- lmer(dv_zscore ~ 1 + stimulus_type * fam_time * age_mos + (1 | subjID) + (1 | labID),
             data=siml)
  return(summary(m1)$coefficients[effects,"Pr(>|t|)"])
}

#fit_simple_model(siml)

fit_model <- function(siml) {
  m1 <- lmer(dv_zscore ~ 1 + stimulus_type * fam_time * age_mos +
             (fam_time*stimulus_type | subjID) + (fam_time*stimulus_type | labID), data=siml)
  sig = summary(m1)$coefficients[effects,"Pr(>|t|)"]
  return(sig)
}
```

```
#fit_model(siml) # boundary (singular) fit -- and is quite slow
```

Power Analysis

We use this simplified model for the power analysis: y ~ 1 + * stimulus_type * age * fam_time + (1 | subjID) + (1 | labID)

To do the power analysis, we simply generate 1000 datasets with main effect sizes of 0.1, 0.2, and 0.3 for trial type, age, and their interaction, run the above linear mixed-effects model, and report how many times 1) the trial type main effect and 2) the trial type * age interaction is significant.

```
# repeatedly generate data and  significance of trial_typesame
get_power <- function(effect_sizes, N=100, alpha=.05) {
  p = tibble()
  # parallelize
  for(i in 1:N) {
    p <- p %>% bind_rows(fit_simple_model(generate_dataset(effect_sizes=effect_sizes)))
  }
  return(p)
}

N = 1000

effect_size_pt1 = list(type = .1, familiarization = .1, age = .1, "age*type"=.1,
                       "age*familiarization"=.1, "type*familiarization"=.1,
                       "type*age*familiarization"=.1)
effect_size_pt2 = list(type = .2, familiarization = .2, age = .2, "age*type"=.2,
                       "age*familiarization"=.2, "type*familiarization"=.2,
                       "type*age*familiarization"=.2)

pvalues_pt1 = get_power(effect_sizes=effect_size_pt1, N=N)
pvalues_pt2 = get_power(effect_sizes=effect_size_pt2, N=N)
pvalues_pt3 = get_power(effect_sizes=effect_size_pt3, N=N)

report_main_effects <- function(pvalues) {
  paste(length(which(pvalues$stimulus_type1<.05)), "of",N, "simulations had p <",.05, "for stimulus typ
        length(which(pvalues$age_mos<.05)), "of",N, "simulations had p <",.05, "for age.",
        length(which(pvalues$fam_time<.05)), "of",N, "simulations had p <",.05, "for familiarization ti
}

report_interactions <- function(pvalues) {
  paste(length(which(pvalues[,"stimulus_type1:fam_time"]<.05)), "of",N, "simulations had p <",.05, "for
        length(which(pvalues[,"stimulus_type1:age_mos"]<.05)), "of",N, "simulations had p <",.05, "stimu
        length(which(pvalues[,"fam_time:age_mos"]<.05)), "of",N, "simulations had p <",.05, "for familia
        length(which(pvalues[,"stimulus_type1:fam_time:age_mos"]<.05)), "of",N, "simulations had p <",.
}
```

Effect sizes = .1

837 of 1000 simulations had $p < 0.05$ for stimulus type. 926 of 1000 simulations had $p < 0.05$ for age. 996 of 1000 simulations had $p < 0.05$ for familiarization time. 48 of 1000 simulations had $p < 0.05$ for stimulus type * familiarization time. 50 of 1000 simulations had $p < 0.05$ stimulus type * age. 59 of 1000 simulations

had $p < 0.05$ for familiarization time * age. 41 of 1000 simulations had $p < 0.05$ for age * stimulus type * familiarization time.

Effect sizes = .2

1000 of 1000 simulations had $p < 0.05$ for stimulus type. 1000 of 1000 simulations had $p < 0.05$ for age. 1000 of 1000 simulations had $p < 0.05$ for familiarization time. 160 of 1000 simulations had $p < 0.05$ for stimulus type * familiarization time. 101 of 1000 simulations had $p < 0.05$ stimulus type * age. 189 of 1000 simulations had $p < 0.05$ for familiarization time * age. 45 of 1000 simulations had $p < 0.05$ for age * stimulus type * familiarization time.

Effect sizes = .3

1000 of 1000 simulations had $p < 0.05$ for stimulus type. 1000 of 1000 simulations had $p < 0.05$ for age. 1000 of 1000 simulations had $p < 0.05$ for familiarization time. 498 of 1000 simulations had $p < 0.05$ for stimulus type * familiarization time. 544 of 1000 simulations had $p < 0.05$ stimulus type * age. 929 of 1000 simulations had $p < 0.05$ for familiarization time * age. 63 of 1000 simulations had $p < 0.05$ for age * stimulus type * familiarization time.

For context, .3 is the average effect size across all published developmental experiments. (Any idea of the average empirical effect size (of age, complexity, or familiarization time) for habituation experiments??)