Appendix: Pilot Experiment

2021-06-10

A pilot study was conducted by one laboratory in March, 2021 to verify the feasibility of the experiment's design, and to test the planned procedures. Given the small size of the pilot, we do not expect to find significant effects, but we nonetheless also carried out the full planned analysis.

Participants

Participants were 19 children 8-12 months of age recruited from... (7 8-month-olds, 2 9-month-olds, 2 10-month-olds, 4 11-month-olds, and 4 12-month-olds). [An addition X participants were excluded due to failure to complete...]

Materials and Design

[include anything here?]

Procedure

[include anything here?]

Results

We carried out the preregistered regression, but without per-lab random effects and procedure fixed effects since these variables have no variation in our sample. Thus, the mixed-effects linear regression predicted infants' log(looking time) the following fixed effects: familiarized rule (ABB vs. ABA), test trial type (same or different as familiarized rule), age (in months) and trial number (1-12), as well as 2-way interactions of trial type and each of 1) familiarized rule, 2) age, and 3) trial number. The model's random effects structure included per-subject intercepts with slopes by test trial number and type. The R syntax for the complete model was thus: log(looking time) ~ 1 + familiarization order * trial_type + age * trial_type + trial_num * trial_type + (trial_num*trial_type | subject)). However, this model's fit was singular, indicating that the random effects structure is too complex for the dataset. Thus, we pruned the random effects structure following standard procedures: removing either random slopes by trial number or by trial type allowed the model to converge. [which do we want to drop?] Table 1 shows the effects from the model with

Table 1:

	Estimate	Std. Error	t value
(Intercept)	8.298	0.582	14.250
fam_conditionABB	0.333	0.187	1.781
trial_typesame	-0.373	0.520	-0.718
age_months	0.003	0.058	0.050
trial	-0.041	0.015	-2.774
fam_conditionABB:trial_typesame	-0.107	0.163	-0.656
trial_typesame:age_months	0.031	0.051	0.607
trial_typesame:trial	0.036	0.021	1.741
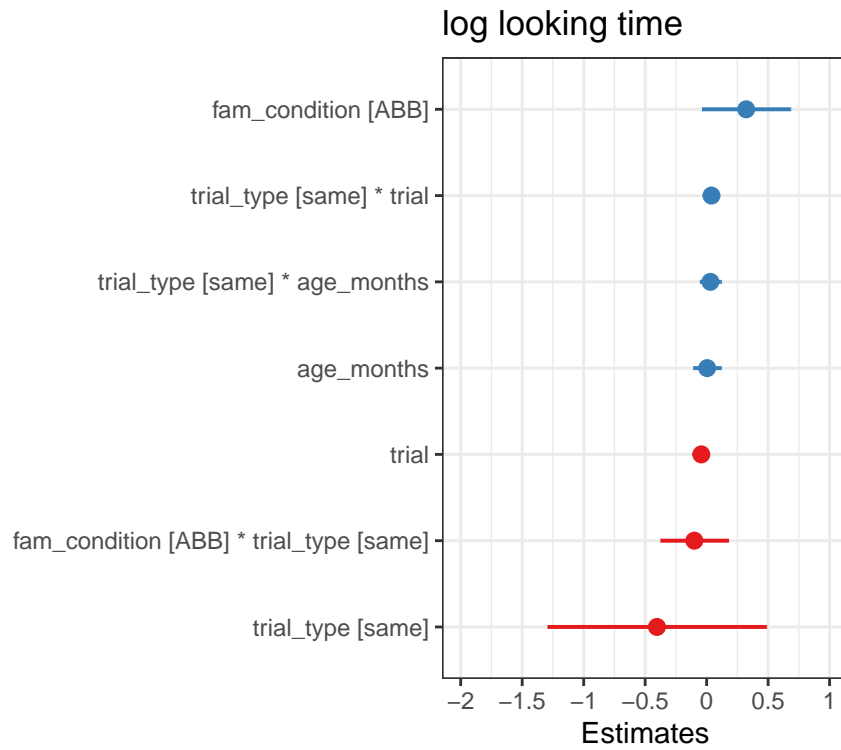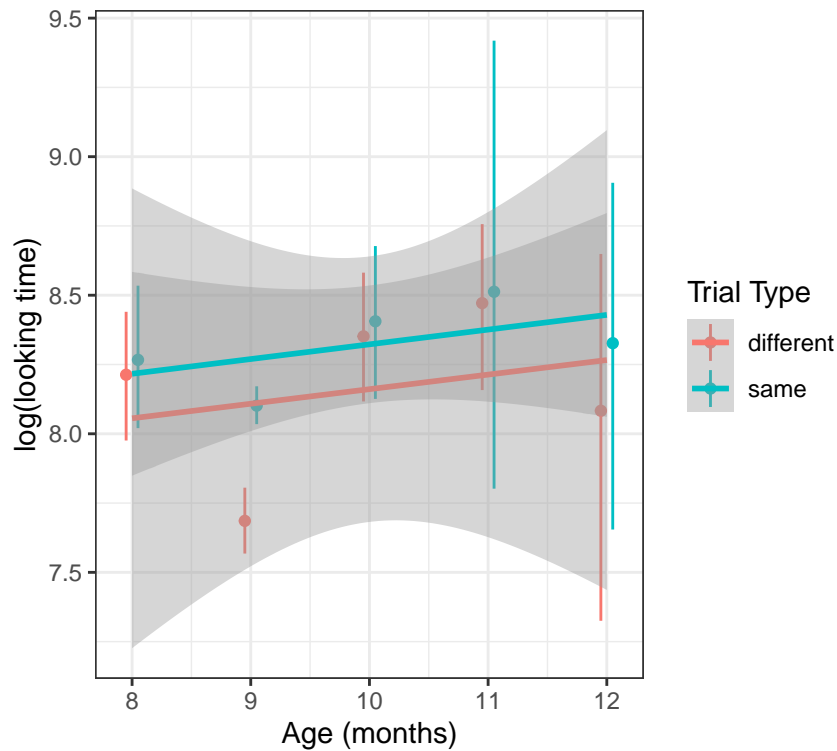
log looking time

Bayesian Regression

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: log_looking_time ~ 1 + fam_condition * trial_type + age_months * trial_type + trial * trial_
##    Data: test_dat (Number of observations: 228)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Group-Level Effects:
## ~id (Number of levels: 19)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.37      0.09     0.23     0.58 1.00     1268     1880
##
## Population-Level Effects:
##                             Estimate Est.Error l-95% CI u-95% CI Rhat
## Intercept                       8.30      0.62     7.10     9.55 1.00
## fam_conditionABB                0.33      0.20    -0.05     0.74 1.00
## trial_typesame                 -0.39      0.48    -1.34     0.52 1.00
## age_months                      0.00      0.06    -0.13     0.12 1.00
## trial                          -0.04      0.02    -0.07    -0.01 1.00
## fam_conditionABB:trial_typesame -0.11     0.14    -0.39     0.18 1.00
## trial_typesame:age_months       0.03      0.05    -0.06     0.12 1.00
## trial_typesame:trial            0.04      0.02    -0.00     0.08 1.00
##                             Bulk_ESS Tail_ESS
## Intercept                       1209     2027
## fam_conditionABB                1129     1601
## trial_typesame                  1845     2246
## age_months                      1148     2165
```

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```
## trial                                 2472     2906
## fam_conditionABB:trial_typesame       3834     2877
## trial_typesame:age_months             1759     2562
## trial_typesame:trial                  2535     2485
##
## Family Specific Parameters:
##        Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma      0.54      0.03     0.49     0.60 1.00     4248     2664
##
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Generate posterior predictive values.