Appendix 1: Analyses with median number of insertions

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1 Workspace

Load packages.

```
library(lme4)
library(ggplot2)
library(tidyr)
library(dplyr)
library(optimx)
library(multcomp)
library(stargazer)
library(lsr)
library(lmtest)
```

Load data.

```
setwd("/Users/hyesunghwang/Desktop/crows")

byIO <- read.csv("InsetionOrder_water_vs_sand.csv")
byTrial <- read.csv("Trial_water_vs_sand.csv")
Transfer <- read.csv("TransferLong3.csv")
IO.float <- read.csv("Transfer_heavy_light.csv")
IO.hollow <- read.csv("Transfer_solid_hollow.csv")
Transfer2 <- read.csv("TransferLong_onlylearning.csv")
```

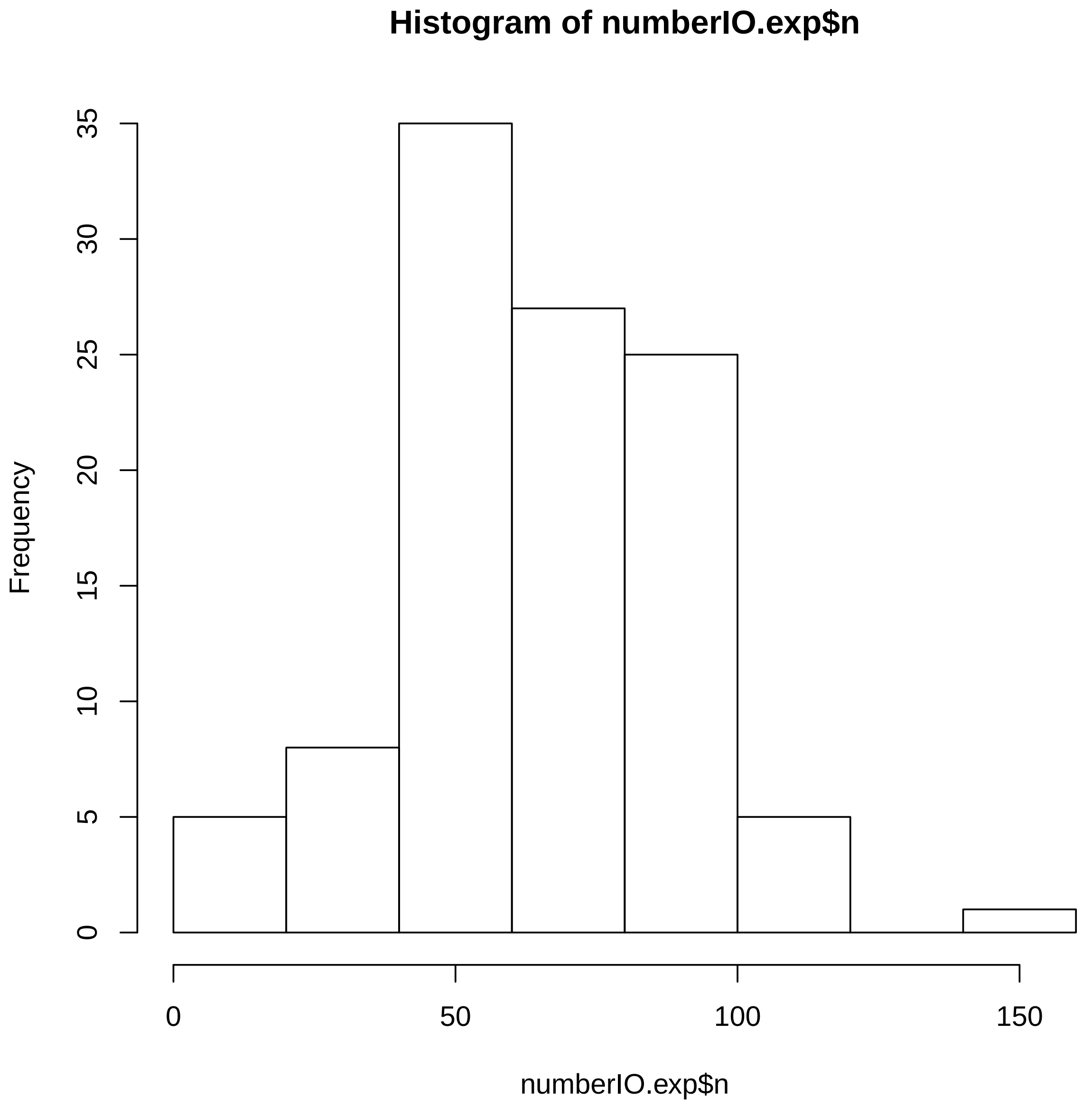
2 Establish cut off points

```
# create histogram of the number of insertions to find median number of insertions
numberIO.exp <- Transfer %>%
  group_by(Bird, Experiment) %>%
  summarise(n = n())
table(numberIO.exp$n)

##
##   1   3   9  19  23  26  28  29  38  42  43  44  47  49  50  51  52  53
##   1   1   1   2   2   1   1   2   2   3   2   2   1   1   1   5   3   2
##  54  55  56  58  59  60  62  63  65  66  68  69  71  72  73  74  75  76
##   3   2   3   1   5   1   1   4   5   1   1   1   2   1   2   2   1   2
```

```
##  77  78  82  83  84  85  86  89  91  94  95  96  98 101 102 103 107 111
##   1   3   3   4   1   5   1   1   4   1   1   2   2   1   1   1   1   1
## 155
##   1
```

```
hist(numberIO.exp$n)
```



The median number of insertions per bird per experiment is 64.

```
IO.cutoff <- median(numberIO.exp$n)
```

2.1 Predicting probabilty of efficient choice by stone insertion order

We used a multilevel logistic model, modeled with the lme4 package with insertion order nested within bird, and bird nested within study. This allowed us to account for dependency between trials performed by the same bird and dependencies between birds within the same study. We also include species as a predictor of performance, measured at the crow level (Level 2). In the cases where we measured hollow vs. solid, all birds were of the same species (New Caledonian), so this variable was not included in the models. Because the choice was binary (either water (efficient choice) was chosen [1] or it was not [0]), we used a logistic model. The outout of the model is given in logit units (e.g., a one unit increase in insertion order leads to a predicted b_i logit increase in selecting water or the efficient choice). To interpret these effects, we convert the logits to odds ratios with the equation $OR = e^{b_i}$. Intercept results are shown in Table 1. Slope results are shown in Table 2. Tables are created with the stargazer package. Results are also dipicted graphically in Figure 1.
Optional control arguments.

```
# estimation parameters
nlopt <- function(par, fn, lower, upper, control) {
  .nloptr <<- res <- nloptr(par, fn, lb = lower, ub = upper,
                            opts = list
                            (algorithm = "NLOPT_LN_BOBYQA",
                                        print_level = 1,
                                        maxeval = 1000, xtol_abs = 1e-6,
                                        ftol_abs = 1e-6))
  list(par = res$solution,
       fval = res$objective,
       conv = if (res$status > 0) 0 else res$status,
       message = res$message
  )
}
```

```
IO.model.max <- glmer(water ~ Insertion + Species + (1 + Insertion | Article)
                      + (1 + Insertion | Article:Bird) ,
                      data=subset(byIO, Insertion <= IO.cutoff), family="binomial",
                      control=glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))
IO.model.v2 <- glmer(water ~ Insertion + Species + (1 + Insertion | Article) + (1 | Article:Bird),
                     data=subset(byIO, Insertion <= IO.cutoff), family="binomial",
                     control=glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.model.max, IO.model.v2)

## Likelihood ratio test
##
## Model 1: water ~ Insertion + Species + (1 + Insertion | Article) + (1 +
##     Insertion | Article:Bird)
## Model 2: water ~ Insertion + Species + (1 + Insertion | Article) + (1 |
##     Article:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1  10 -662.16
## 2   8 -673.47 -2 22.61  1.231e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#need to allow slope to vary across birds

IO.model.v3 <- glmer(water ~ Insertion + Species + (1 | Article) + (1 + Insertion | Article:Bird),
                     data=subset(byIO, Insertion <= IO.cutoff), family="binomial",
                     control=glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))
lrtest(IO.model.max, IO.model.v3)

## Likelihood ratio test
##
## Model 1: water ~ Insertion + Species + (1 + Insertion | Article) + (1 +
##     Insertion | Article:Bird)
## Model 2: water ~ Insertion + Species + (1 | Article) + (1 + Insertion |
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  10 -662.16
## 2   8 -664.12 -2 3.9129     0.1414

# don't need slope to vary across article

IO.model.v4 <- glmer(water ~ Insertion + Species + (1 | Article) + (1 + Insertion || Article:Bird),
                     data=subset(byIO, Insertion <= IO.cutoff), family="binomial",
                     control=glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))
lrtest(IO.model.v3, IO.model.v4)

## Likelihood ratio test
##
## Model 1: water ~ Insertion + Species + (1 | Article) + (1 + Insertion |
##     Article:Bird)
## Model 2: water ~ Insertion + Species + (1 | Article) + (1 + Insertion ||
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -664.12
## 2   7 -665.61 -1 2.9765    0.08448 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# don't need correlation between intercept and slope at bird level

IO.model <- IO.model.v4
```

```
IO.model2.max <- glmer(heavy ~ Insertion + Species + (1 + Insertion | Article)
                       + (1 + Insertion | Article:Bird),
                       data=subset(IO.float, Insertion <= IO.cutoff),
                       family="binomial",
                       control=glmerControl(optimizer = "nloptwrap",
                                            calc.derivs = FALSE))

IO.model2.v2 <- glmer(heavy ~ Insertion + Species + (1 | Article) + (1 + Insertion | Article:Bird),
                      data=subset(IO.float, Insertion <= IO.cutoff),
                      family="binomial",
                      control=glmerControl(optimizer = "nloptwrap",
```

```
                                           calc.derivs = FALSE))

lrtest(IO.model2.max, IO.model2.v2)

## Likelihood ratio test
##
## Model 1: heavy ~ Insertion + Species + (1 + Insertion | Article) + (1 +
##     Insertion | Article:Bird)
## Model 2: heavy ~ Insertion + Species + (1 | Article) + (1 + Insertion |
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -473.76
## 2   7 -475.57 -2 3.6281      0.163

# don't need slopes to vary across article

IO.model2.v3 <- glmer(heavy ~ Insertion + Species + (1 | Article) + (1 | Article:Bird),
                      data=subset(IO.float, Insertion <= IO.cutoff),
                      family="binomial",
                      control=glmerControl(optimizer = "nloptwrap",
                                      calc.derivs = FALSE))

lrtest(IO.model2.v2, IO.model2.v3)

## Likelihood ratio test
##
## Model 1: heavy ~ Insertion + Species + (1 | Article) + (1 + Insertion |
##     Article:Bird)
## Model 2: heavy ~ Insertion + Species + (1 | Article) + (1 | Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   7 -475.57
## 2   5 -481.07 -2 10.992   0.004104 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need slopes to vary across bird

IO.model2.v4 <- glmer(heavy ~ Insertion + Species + (1 | Article) + (1 + Insertion || Article:Bird),
                      data=subset(IO.float, Insertion <= IO.cutoff),
                      family="binomial",
                      control=glmerControl(optimizer = "nloptwrap",
                                      calc.derivs = FALSE))

lrtest(IO.model2.v2, IO.model2.v4)

## Likelihood ratio test
##
## Model 1: heavy ~ Insertion + Species + (1 | Article) + (1 + Insertion |
##     Article:Bird)
## Model 2: heavy ~ Insertion + Species + (1 | Article) + (1 + Insertion ||
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
```

```
## 1   7 -475.57
## 2   6 -476.27 -1 1.4079     0.2354

# don't need correlation between slope and intercept at bird level

IO.model2 <- IO.model2.v4
```

```
#hollow trials only have one species, so species is not used as a predictor in these models
IO.model3.max <- glmer(Solid ~ Insertion + (1 + Insertion | Article)
                       + (1 + Insertion | Article:Bird),
                       data=subset(IO.hollow, Insertion <= IO.cutoff),
                       family="binomial",
                       control = glmerControl(optimizer = "nloptwrap",
                                        calc.derivs = FALSE))

IO.model3.v2 <- glmer(Solid ~ Insertion + (1 | Article) + (1 + Insertion | Article:Bird),
                      data=subset(IO.hollow, Insertion <= IO.cutoff),
                      family="binomial",
                      control = glmerControl(optimizer = "nloptwrap",
                                        calc.derivs = FALSE))

lrtest(IO.model3.max, IO.model3.v2)

## Likelihood ratio test
##
## Model 1: Solid ~ Insertion + (1 + Insertion | Article) + (1 + Insertion |
##     Article:Bird)
## Model 2: Solid ~ Insertion + (1 | Article) + (1 + Insertion | Article:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   8 -119.28
## 2   6 -119.96 -2 1.358     0.5071

# don't need slope at article level

IO.model3.v3 <- glmer(Solid ~ Insertion + (1 | Article) + (1 | Article:Bird),
                      data=subset(IO.hollow, Insertion <= IO.cutoff),
                      family="binomial",
                      control = glmerControl(optimizer = "nloptwrap",
                                        calc.derivs = FALSE))

lrtest(IO.model3.v2, IO.model3.v3)

## Likelihood ratio test
##
## Model 1: Solid ~ Insertion + (1 | Article) + (1 + Insertion | Article:Bird)
## Model 2: Solid ~ Insertion + (1 | Article) + (1 | Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   6 -119.96
## 2   4 -120.89 -2 1.8573     0.3951

# don't need slope at bird level

IO.model3 <- IO.model3.v3
```

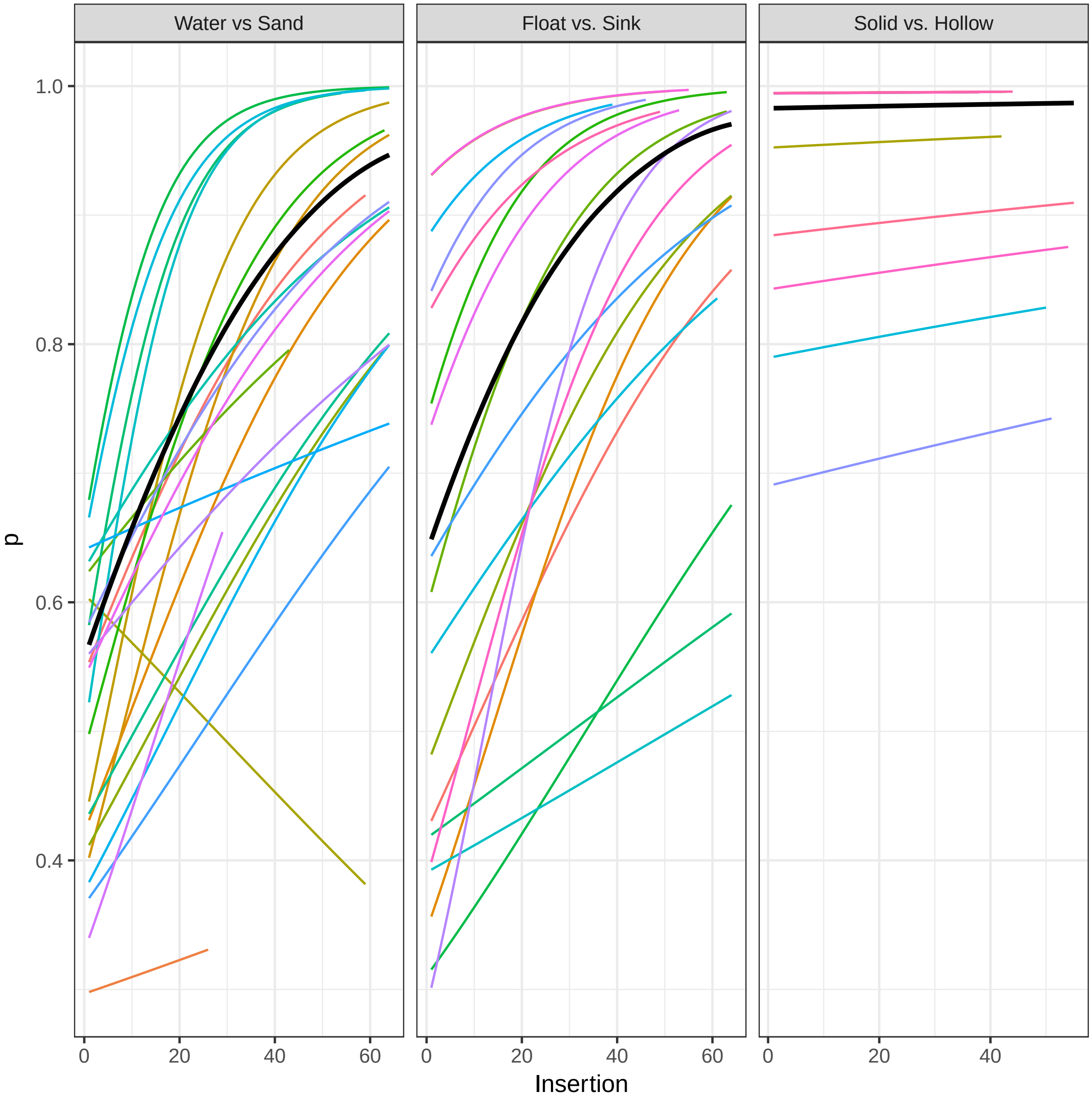
Table 1: Intercept results of multilevel binary logistic regressions predicting probability of efficient choice by insertion order across tasks

	Tasks	N_birds	Intercept	OR	CI	p
1	Water vs. Sand	22	-0.63	0.53	[0.27 , 1.07]	0.08
2	Float vs. Sink	18	0.21	1.23	[0.17 , 9.18]	0.84
3	Solid vs. Hollow	11	4.04	57.02	[10.18 , 319.33]	0.0000

Table 2: Slope Results of multilevel binary logistic regressions predicting probability of efficient choice by insertion order across tasks

	Tasks	N_birds	Slope	OR	CI	p
1	Water vs. Sand	22	0.04	1.04	[1.02 , 1.06]	0.0000
2	Float vs. Sink	18	0.05	1.05	[1.03 , 1.07]	0.0000
3	Solid vs. Hollow	11	0.01	1.01	[0.98 , 1.03]	0.67

```
## ‘geom_smooth()‘ using method = ’loess’
```



```
## Saving 7 x 7 in image
## `geom_smooth()` using method = 'loess'
```

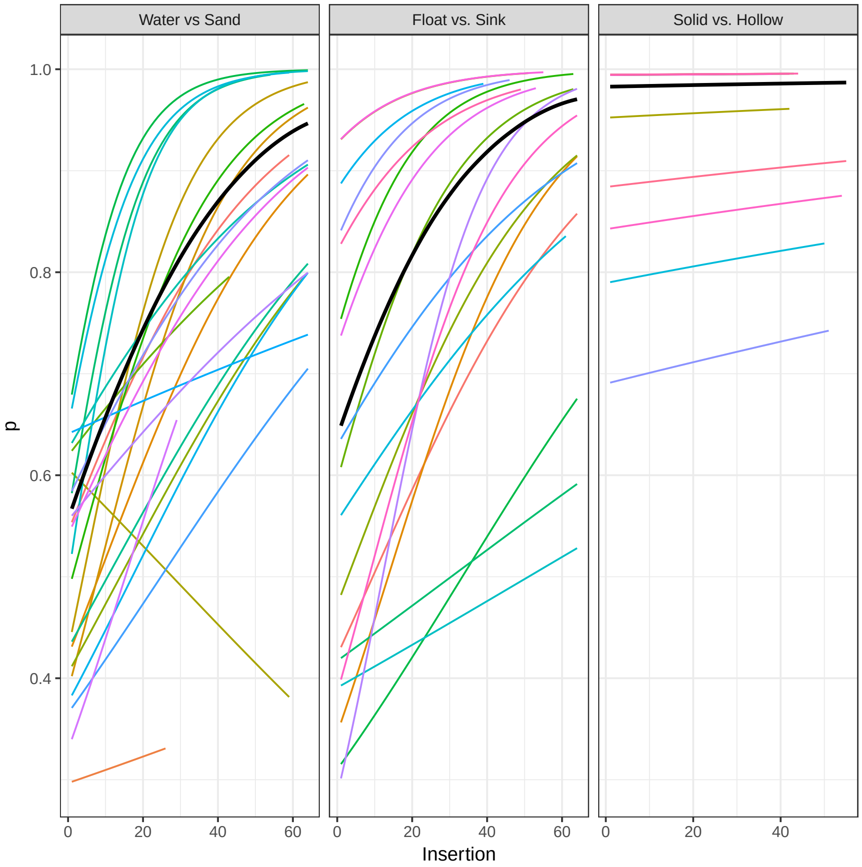


Figure 1: *Probability of picking the most efficient choice (water, sink, and solid, respectively) by insertion order. Colored lines represent different birds, and the black lines represent the overall effect.*

2.2 Probability of choosing efficient choice (e.g., water) by whether efficient (water) or inefficient (sand) was chosen in previous trial

Before we can conduct these analyses, we must create a new variable which holds the choice of the previous trial.

```
IO.previous <- byIO
colnames(IO.previous) <- gsub("water", "water.previous",colnames(IO.previous))
IO.previous$Insertion <- IO.previous$Insertion + 1
byIO <- merge(byIO, IO.previous, all.x=T)

IO.float.previous <- IO.float
colnames(IO.float.previous) <- gsub("heavy", "heavy.previous",colnames(IO.float.previous))
IO.float.previous <- subset(IO.float.previous, select = -c(light))
IO.float.previous$Insertion <- IO.float.previous$Insertion + 1
IO.float <- merge(IO.float, IO.float.previous, all.x=T)

IO.hollow.previous <- IO.hollow
colnames(IO.hollow.previous) <- gsub("Solid", "Solid.previous",colnames(IO.hollow.previous))
IO.hollow.previous <- subset(IO.hollow.previous, select = -c(Hollow))
IO.hollow.previous$Insertion <- IO.hollow.previous$Insertion + 1
IO.hollow <- merge(IO.hollow, IO.hollow.previous, all.x=T)
```

Again, we use multilevel modeling to determine the probability of selecting water if sand was chosen in the previous trial and if water was chosen in the previous trial. Again, we nest trial within bird and bird with in study to account for potential dependence between the data points.

```
IO.prev.model.max <- glmer(water ~ water.previous + Species +
                             (1 + water.previous | Article) + (1 + water.previous | Article:Bird),
                           data=subset(byIO, Insertion <= IO.cutoff),
                           family="binomial",
                           control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

IO.prev.model.v2 <- glmer(water ~ water.previous + Species +
                            (1 | Article) + (1 + water.previous | Article:Bird),
                          data=subset(byIO, Insertion <= IO.cutoff),
                          family="binomial",
                          control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.prev.model.max, IO.prev.model.v2)

## Likelihood ratio test
##
## Model 1: water ~ water.previous + Species + (1 + water.previous | Article) +
##     (1 + water.previous | Article:Bird)
## Model 2: water ~ water.previous + Species + (1 | Article) + (1 + water.previous |
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  10 -638.22
## 2   8 -640.62 -2 4.8032    0.09057 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# don't need slope at article level

IO.prev.model.v3 <- glmer(water ~ water.previous + Species +
                            (1 | Article) + (1 | Article:Bird),
                          data=subset(byIO, Insertion <= IO.cutoff),
                          family="binomial",
                          control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.prev.model.v2, IO.prev.model.v3)

## Likelihood ratio test
## 
## Model 1: water ~ water.previous + Species + (1 | Article) + (1 + water.previous | 
##     Article:Bird)
## Model 2: water ~ water.previous + Species + (1 | Article) + (1 | Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)    
## 1   8 -640.62                         
## 2   6 -664.83 -2 48.422  3.057e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need slope at bird level

IO.prev.model.v4 <- glmer(water ~ water.previous + Species +
                            (1 | Article) + (1 + water.previous || Article:Bird),
                          data=subset(byIO, Insertion <= IO.cutoff),
                          family="binomial",
                          control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.prev.model.v2, IO.prev.model.v4)

## Likelihood ratio test
## 
## Model 1: water ~ water.previous + Species + (1 | Article) + (1 + water.previous | 
##     Article:Bird)
## Model 2: water ~ water.previous + Species + (1 | Article) + (1 + water.previous || 
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)   
## 1   8 -640.62                        
## 2   7 -644.16 -1 7.0788     0.0078 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need correlation between slope at intercept at bird level

IO.prev.model <- IO.prev.model.v2
```

```r
IO.prev.model2.max <- glmer(heavy ~ heavy.previous + Species +
                              (1 + heavy.previous | Article) + (1 + heavy.previous | Article:Bird) ,
                            data=subset(IO.float, Insertion <= IO.cutoff),
                            family="binomial",
```

```
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

IO.prev.model2.v2 <- glmer(heavy ~ heavy.previous + Species +
                             (1 | Article) + (1 + heavy.previous | Article:Bird),
                           data=subset(IO.float, Insertion <= IO.cutoff),
                           family="binomial",
                           control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.prev.model2.max, IO.prev.model2.v2)

## Likelihood ratio test
##
## Model 1: heavy ~ heavy.previous + Species + (1 + heavy.previous | Article) +
##     (1 + heavy.previous | Article:Bird)
## Model 2: heavy ~ heavy.previous + Species + (1 | Article) + (1 + heavy.previous |
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -405.12
## 2   7 -405.44 -2 0.6495     0.7227

#don't need slope at article level

IO.prev.model2.v3 <- glmer(heavy ~ heavy.previous + Species +
                             (1 | Article) + (1 | Article:Bird) ,
                           data=subset(IO.float, Insertion <= IO.cutoff),
                           family="binomial",
                           control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.prev.model2.v2, IO.prev.model2.v3)

## Likelihood ratio test
##
## Model 1: heavy ~ heavy.previous + Species + (1 | Article) + (1 + heavy.previous |
##     Article:Bird)
## Model 2: heavy ~ heavy.previous + Species + (1 | Article) + (1 | Article:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   7 -405.44
## 2   5 -411.24 -2  11.6   0.003027 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need slope at bird level

IO.prev.model2.v4 <- glmer(heavy ~ heavy.previous + Species +
                             (1 | Article) + (1 + heavy.previous || Article:Bird) ,
                           data=subset(IO.float, Insertion <= IO.cutoff),
                           family="binomial",
                           control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.prev.model2.v2, IO.prev.model2.v4)

## Likelihood ratio test
```

```
##
## Model 1: heavy ~ heavy.previous + Species + (1 | Article) + (1 + heavy.previous |
##     Article:Bird)
## Model 2: heavy ~ heavy.previous + Species + (1 | Article) + (1 + heavy.previous ||
##     Article:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   7 -405.44
## 2   6 -405.48 -1 0.0842     0.7717

# don't need correlation between intercept and slope at bird level

IO.prev.model2 <- IO.prev.model2.v4
```

```
IO.prev.model3.max <- glmer(Solid ~ Solid.previous +
                              (1 + Solid.previous | Article) + (1 + Solid.previous | Article:Bird),
                            data=subset(IO.hollow, Insertion <= IO.cutoff),
                            family="binomial",
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

IO.prev.model3.v2 <- glmer(Solid ~ Solid.previous +
                             (1 | Article) + (1 + Solid.previous | Article:Bird),
                           data=subset(IO.hollow, Insertion <= IO.cutoff),
                           family="binomial",
                           control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(IO.prev.model3.max, IO.prev.model3.v2)

## Likelihood ratio test
##
## Model 1: Solid ~ Solid.previous + (1 + Solid.previous | Article) + (1 +
##     Solid.previous | Article:Bird)
## Model 2: Solid ~ Solid.previous + (1 | Article) + (1 + Solid.previous |
##     Article:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   8 -88.238
## 2   6 -88.238 -2 1e-04     0.9999

# don't need slope at article level

IO.prev.model3.v3 <- glmer(Solid ~ Solid.previous +
                             (1 | Article) + (1 | Article:Bird),
                           data=subset(IO.hollow, Insertion <= IO.cutoff),
                           family="binomial",
                           control = glmerControl(optimizer = "nloptwrap",
                                                  calc.derivs = FALSE))

lrtest(IO.prev.model3.v2, IO.prev.model3.v3)

## Likelihood ratio test
##
## Model 1: Solid ~ Solid.previous + (1 | Article) + (1 + Solid.previous |
```

```
##     Article:Bird)
## Model 2: Solid ~ Solid.previous + (1 | Article) + (1 | Article:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   6 -88.238
## 2   4 -89.484 -2 2.492     0.2877

# don't need slope at bird level

IO.prev.model3 <- IO.prev.model3.v3
```

Table 3: Odds of making inefficient choice based on previous choice

	Tasks	Slope	OddInefficient	CI	p
1	Water vs. Sand	-0.40	0.67	[0.43 , 1.05]	0.08
2	Float vs. Sink	0.45	1.57	[0.55 , 4.44]	0.40
3	Solid vs. Hollow	3.37	28.94	[5.34 , 156.86]	0.0001

Table 4: Odds of making efficient choice based on previous choice

	Tasks	Slope	OddEfficient	CI	p
water.previous	Water vs. Sand	1.61	5.00	[2.66 , 9.38]	0.0000
heavy.previous	Float vs. Sink	0.89	2.43	[1.23 , 4.8]	0.01
Solid.previous	Solid vs. Hollow	0.17	1.18	[0.47 , 3.01]	0.72

Table 5: Differences in odds of making efficient choice based on previous choice

	Task	Odds if Inefficient	Odds if Efficient	Test of difference
water.previous	Water	0.67	5.00	0.0000
heavy.previous	Sink	1.57	2.43	0.01
Solid.previous	Solid	28.94	1.18	0.72

2.3 Transfer effects - including all water displacement tasks

Within these studies, crows participated in multiple experiments. It is quite possible that learning the most efficient choice in one experiment transfered to the next, so that crows learned faster – and perhaps began more likely to choose the most efficient option – in each subsequent experiment.

```
Transfer$Experiment <- Transfer$Experiment - 1
```

2.3.1 Order effect

The next analyses test whether the order of the particular experiment was a significant predictor of learning. Efficient is a binary varible assesing whether the crow made the more efficient choice. Experiment is an integer variable indicating the order in which the experiments occurred.

```
order.mod1.max <- glmer(Efficient ~ Insertion + Experiment + Species
                        + (1 + Insertion + Experiment | Study)
                        + (1 + Insertion + Experiment | Study:Bird),
                        family="binomial", data=Transfer,
                        control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

order.mod1.v2 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion | Study)
                       + (1 + Insertion + Experiment | Study:Bird),
                       family="binomial", data=Transfer,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod1.max, order.mod1.v2)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion |
##     Study) + (1 + Insertion + Experiment | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  17 -3770.5
## 2  14 -3765.1 -3 10.766    0.01306 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need experiment slope at study level

order.mod1.v3 <- glmer(Efficient ~ Insertion + Experiment + Species
                        + (1 + Experiment | Study)
                        + (1 + Insertion + Experiment | Study:Bird),
                        family="binomial", data=Transfer,
                        control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod1.max, order.mod1.v3)

## Likelihood ratio test
##
```

```
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Experiment |
##     Study) + (1 + Insertion + Experiment | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  17 -3770.5
## 2  14 -3760.1 -3 20.757  0.0001183 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# need insertion slope at study level

order.mod1.v4 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion + Experiment || Study)
                       + (1 + Insertion + Experiment | Study:Bird),
                       family="binomial", data=Transfer,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod1.max, order.mod1.v4)
```

```
## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + (1 + Insertion + Experiment | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  17 -3770.5
## 2  14 -3761.7 -3 17.538  0.0005477 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# need correlation between intercept and insertion slope at study level

order.mod1.v5 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion + Experiment | Study)
                       + (1 + Insertion | Study:Bird),
                       family="binomial", data=Transfer,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod1.max, order.mod1.v5)
```

```
## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  17 -3770.5
## 2  14 -3775.9 -3 10.728    0.01329 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# don't need experiment slope at bird level

order.mod1.v6 <- glmer(Efficient ~ Insertion + Experiment + Species
                        + (1 + Insertion + Experiment | Study)
                        + (1  | Study:Bird),
                        family="binomial", data=Transfer,
                        control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod1.v5, order.mod1.v6)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  14 -3775.9
## 2  12 -3789.9 -2 28.062  8.061e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need insertion slope at bird level

order.mod1.v7 <- glmer(Efficient ~ Insertion + Experiment + Species
                        + (1 + Insertion + Experiment | Study)
                        + (1 + Insertion || Study:Bird),
                        family="binomial", data=Transfer,
                        control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod1.v5, order.mod1.v7)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion || Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  14 -3775.9
## 2  13 -3773.8 -1 4.1389    0.04191 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# don't need correlations between random effects at bird level

order.mod1 <- order.mod1.v7
```

```
ord.coef1 <- summary(order.mod1)$coefficients
lb1 <- ord.coef1[,"Estimate"] - 1.96*ord.coef1[,"Std. Error"]
lb1 <- exp(lb1)
```

```
ub1 <- ord.coef1[,"Estimate"] + 1.96*ord.coef1[,"Std. Error"]
ub1 <- exp(ub1)

ord.f1 <- data.frame(Coefficient = c("Intercept","Insertion Order", "Experiment Order",
                                     "Species (New Caledonian)", "Species (Rook)"),
                     OR = round(exp(ord.coef1[,"Estimate"]),2),
                     CI = paste("[",round(lb1,2),",",round(ub1,2),"]",sep=""),
                     z = round(ord.coef1[,"z value"],2),
                     p =round(ord.coef1[,4],2))
```

Table 6: Fixed effects of logistic model predicting odds of making the efficient choice by insertion order and experimental order

Coefficient	OR	CI	z	p
Intercept	1.530	[0.85,2.76]	1.410	0.160
Insertion Order	1.020	[1.01,1.04]	4.200	0
Experiment Order	0.810	[0.57,1.14]	-1.230	0.220
Species (New Caledonian)	2.030	[1.21,3.38]	2.700	0.010
Species (Rook)	0.610	[0.28,1.36]	-1.210	0.230

Table 6 shows the fixed effects of the model predicting the effects of insertion order and experimental position in the study. Experimental order is not significant ($b = -0.214, p > .05$), indicating that the order of the experiment in the study had no effect on probability of corvids choosing the more efficient choice. The two species coefficients were included in the model to control for species level effects and relfect the comparison of New Caledonians and Rooks to the Eurasian Jays. Species (New Caledonian) coefficient was significant, suggesting New Caledonians were more likely to choose the efficient choices than Eurasian Jays.

```
var.est <- c(attr(VarCorr(order.mod1)$'Study.Bird.1',"stddev")^2, attr(VarCorr(order.mod1)$'Study.Bird'
slopes <- coef(order.mod1)$'Study:Bird'

chi.1 <- sum((slopes[,1]-ord.coef1[1,"Estimate"])^2)/var.est[1]
chi.2 <- sum((slopes[,2]-ord.coef1[2,"Estimate"])^2)/var.est[2]
#chi.3 <- sum((slopes[,3]-ord.coef1[3,"Estimate"])^2)/var.est[3]
df <- nrow(slopes)

p.1 <- pchisq(chi.1, df, lower.tail=F)
p.2 <- pchisq(chi.2, df, lower.tail=F)
#p.3 <- pchisq(chi.3, df, lower.tail=F)

IO.r1 <- data.frame(Coefficient = c("Intercept","Insertion Order"),
                    Variance = var.est,'Chi Sq' = c(chi.1, chi.2), df = rep(df,2),
                    p = c(p.1, p.2))
```

Table 7 shows the variability of the coefficients across birds for the model. None of the variances are significant, indicating that the birds did not differ significantly in their rates of learning or in how the experiment position affected them. [1]

---

[1] These analyses were also tested with experimental order as a binary variable, with 0 = first experiment and 1 = not the first experiment. Again, the order of experiment did not significantly predict the intercept (likelihood of choosing the efficient choice at the start of the experiment) or slope (rate of learning across the experiment).

Table 7: Random effects across birds predicting odds of making the efficient choice predicted by insertion order and experimental order

Coefficient	Variance	Chi.Sq	df	p
Intercept	0.21	22.45	34	0.94
Insertion Order	0.0002	15.76	34	1.00

2.3.2 Check nonlinearity in experiment order

```
# add a nonlinear term
Transfer$Experiment2 <- Transfer$Experiment^2
```

Centered the Experiment term to get rid of convergence issues

```
# Center experiment number
Transfer$Experiment.c <- (Transfer$Experiment - mean(Transfer$Experiment))
Transfer$Experiment.c2 <- Transfer$Experiment.c^2

order.mod_non.c.max <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                             + (1 + Insertion + Experiment.c+ Experiment.c2 | Study)
                             + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                             family="binomial", data=Transfer,
                             control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

order.mod_non.c.v2 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Insertion + Experiment.c | Study)
                            + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod_non.c.max, order.mod_non.c.v2)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Insertion + Experiment.c + Experiment.c2 | Study) +
##     (1 + Insertion + Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Insertion + Experiment.c | Study) + (1 + Insertion +
##     Experiment.c + Experiment.c2 | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  26 -3717.3
## 2  22 -3718.9 -4 3.3185      0.506

#don't need squared term at study level

order.mod_non.c.v3 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Insertion | Study)
                            + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
```

```
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod_non.c.v2, order.mod_non.c.v3)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Insertion + Experiment.c | Study) + (1 + Insertion +
##     Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Insertion | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1  22 -3718.9
## 2  19 -3724.7 -3 11.55   0.009094 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need experiment term at study level

order.mod_non.c.v4 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Experiment.c | Study)
                            + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod_non.c.v2, order.mod_non.c.v4)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Insertion + Experiment.c | Study) + (1 + Insertion +
##     Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  22 -3718.9
## 2  19 -3719.8 -3 1.6833     0.6407

# don't need insertion term at study level

order.mod_non.c.v5 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Experiment.c || Study)
                            + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod_non.c.v4, order.mod_non.c.v5)

## Likelihood ratio test
```

```
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c || Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  19 -3719.8
## 2  18 -3724.4 -1 9.2745   0.002324 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# need correlation between intercept and experiment slope at study level

order.mod_non.c.v6 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Experiment.c | Study)
                            + (1 + Insertion + Experiment.c| Study:Bird),
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod_non.c.v4, order.mod_non.c.v6)
```

```
## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c |
##     Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  19 -3719.8
## 2  15 -3754.2 -4 68.912  3.851e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# need squared term at bird level

order.mod_non.c.v7 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Experiment.c | Study)
                            + (1 + Insertion +  Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod_non.c.v4, order.mod_non.c.v7)
```

```
## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
```

```
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c2 |
##     Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  19 -3719.8
## 2  15 -3735.6 -4 31.657  2.248e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need experiment term at bird level

order.mod_non.c.v8 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Experiment.c | Study)
                            + (1 + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))
lrtest(order.mod_non.c.v4, order.mod_non.c.v8)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Experiment.c + Experiment.c2 |
##     Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  19 -3719.8
## 2  15 -3753.9 -4 68.319  5.137e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need insertion term at bird level

order.mod_non.c.v9 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species
                            + (1 + Experiment.c | Study)
                            + (1 + Insertion + Experiment.c+ Experiment.c2 || Study:Bird),
                            family="binomial", data=Transfer,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order.mod_non.c.v4, order.mod_non.c.v9)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 || Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  19 -3719.8
```

```
## 2  13 -3727.6 -6 15.577    0.01621 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need covariance among random effects

order.mod_non.c <- order.mod_non.c.v4
```

```
# Center experiment number
summary (order.mod_non.c)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: Efficient ~ Insertion + Experiment.c + Experiment.c2 + Species +
##     (1 + Experiment.c | Study) + (1 + Insertion + Experiment.c +
##     Experiment.c2 | Study:Bird)
##    Data: Transfer
## Control: glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE)
##
##      AIC      BIC   logLik deviance df.resid
##   7477.5   7607.4  -3719.8   7439.5     6852
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.0527 -0.8393  0.3930  0.6206  1.7702
##
## Random effects:
##  Groups     Name          Variance  Std.Dev. Corr
##  Study:Bird (Intercept)   0.2790235 0.5282
##             Insertion     0.0002529 0.0159    0.55
##             Experiment.c  0.1919426 0.4381   -0.18  0.39
##             Experiment.c2 0.0990761 0.3148   -0.64 -0.45  0.49
##  Study      (Intercept)   0.4132135 0.6428
##             Experiment.c  0.2724923 0.5220   1.00
## Number of obs: 6871, groups:  Study:Bird, 34; Study, 5
##
## Fixed effects:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -0.009158   0.409928  -0.022  0.98218
## Insertion                0.023979   0.003674   6.526 6.73e-11 ***
## Experiment.c            -0.376607   0.263070  -1.432  0.15226
## Experiment.c2           -0.109168   0.064726  -1.687  0.09168 .
## SpeciesNew_Caledonian  0.813769   0.312531   2.604  0.00922 **
## SpeciesRook             -0.319023   0.458348  -0.696  0.48641
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Insrtn Exprm. Expr.2 SpcN_C
## Insertion    0.092
```

```
## Experimnt.c  0.644  0.119
## Expermnt.c2 -0.171 -0.375  0.215
## SpcsNw_Cldn -0.611 -0.023  0.019  0.035
## SpeciesRook -0.389 -0.036  0.084  0.098  0.554
```

The quadratic term is not significant indicating we do not have any non-linearity problems and therefore the model we have is best fitted by a linear relationship.

2.4 Transfer effects - only including tasks that were claimed to show learning

It is possible that learning the most efficient choice in one experiment transfered to the next, so that crows learned faster – and perhaps began more likely to choose the most efficient option – in each subsequent experiment. We restricted our analyses to the tasks that were claimed to show successful learning.

```
Transfer2$Experiment <- Transfer2$Experiment - 1
```

2.4.1 Order effect

The next analyses test whether the order2 of the particular experiment was a significant predictor of learning. Efficient is a binary varible assesing whether the crow made the more efficient choice. Experiment is an integer variable indicating the order2 in which the experiments occurred.

```
order2.mod1.max <- glmer(Efficient ~ Insertion + Experiment + Species
                        + (1 + Insertion + Experiment | Study)
                        + (1 + Insertion + Experiment | Study:Bird),
                        family="binomial", data=Transfer2,
                        control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

order2.mod1.v2 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion  | Study) + (1 + Insertion + Experiment | Study:Bird),
                       family="binomial", data=Transfer2,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod1.max, order2.mod1.v2)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion |
##     Study) + (1 + Insertion + Experiment | Study:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1  17 -2174.8
## 2  14 -2174.3 -3  1.13     0.7698

# don't need experiment term at study level

order2.mod1.v3 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Experiment | Study) + (1 + Insertion + Experiment | Study:Bird),
                       family="binomial", data=Transfer2,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod1.max, order2.mod1.v3)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Experiment |
##     Study) + (1 + Insertion + Experiment | Study:Bird)
```

```
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  17 -2174.8
## 2  14 -2175.3 -3 1.0163     0.7973

# don't need insertion term at study level

order2.mod1.v4 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion + Experiment || Study) +
                       + (1 + Insertion + Experiment | Study:Bird),
                       family="binomial", data=Transfer2,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod1.max, order2.mod1.v4)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment | Study) + (1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + +(1 + Insertion + Experiment | Study:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1  17 -2174.8
## 2  14 -2175.4 -3 1.038     0.7921

# don't need correlation at study level

order2.mod1.v5 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion + Experiment || Study) +
                       + (1 + Insertion | Study:Bird),
                       family="binomial", data=Transfer2,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod1.v4, order2.mod1.v5)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + +(1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + +(1 + Insertion | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  14 -2175.4
## 2  11 -2225.8 -3 100.83  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need experiment term at bird level

order2.mod1.v6 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion + Experiment || Study) +
                       + (1  + Experiment | Study:Bird),
                       family="binomial", data=Transfer2,
```

```
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod1.v4, order2.mod1.v6)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + +(1 + Insertion + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + +(1 + Experiment | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  14 -2175.4
## 2  11 -2184.7 -3 18.742  0.0003091 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# don't need insertion term at bird level

order2.mod1.v7 <- glmer(Efficient ~ Insertion + Experiment + Species
                       + (1 + Insertion + Experiment || Study) +
                       + (1  + Experiment || Study:Bird),
                       family="binomial", data=Transfer2,
                       control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod1.v6, order2.mod1.v7)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + +(1 + Experiment | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment + Species + (1 + Insertion +
##     Experiment || Study) + +(1 + Experiment || Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  11 -2184.7
## 2  10 -2193.7 -1 17.853  2.387e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need covariance at bird level

order2.mod1 <- order2.mod1.v6
```

```
ord.coef1 <- summary(order2.mod1)$coefficients
lb1 <- ord.coef1[,"Estimate"] - 1.96*ord.coef1[,"Std. Error"]
lb1 <- exp(lb1)
ub1 <- ord.coef1[,"Estimate"] + 1.96*ord.coef1[,"Std. Error"]
ub1 <- exp(ub1)

ord.f1 <- data.frame(Coefficient = c("Intercept","Insertion Order", "Experiment Order",
                                     "Species (New Caledonian)", "Species (Rook)"),
                     OR = round(exp(ord.coef1[,"Estimate"]),2),
```

```
                     CI = paste("[",round(lb1,2),",",round(ub1,2),"]",sep=""),
                     z = round(ord.coef1[,"z value"],2),
                     p =round(ord.coef1[,4],2))
```

Table 8: Fixed effects of logistic model predicting odds of making the efficient choice by insertion order2 and experimental order2

Coefficient	OR	CI	z	p
Intercept	0.780	[0.42,1.44]	-0.800	0.430
Insertion Order	1.030	[1.02,1.04]	6.130	0
Experiment Order	1.430	[0.99,2.08]	1.900	0.060
Species (New Caledonian)	2.760	[1.49,5.11]	3.230	0
Species (Rook)	0.660	[0.29,1.52]	-0.980	0.330

Table 8 shows the fixed effects of the model predicting the effects of insertion order2 and experimental position in the study. Experimental order2 is not significant ($b = 0.361, p > .05$), indicating that the order2 of the experiment in the study had no effect on probability of corvids choosing the more efficient choice. The two species coefficients were included in the model to control for species level effects and relfect the comparison of New Caledonians and Rooks to the Eurasian Jays. Species (New Caledonian) coefficient was significant, indicating New Caledonians were more likely to choose the efficient choices than Eurasian Jays.

```
var.est <- (attr(VarCorr(order2.mod1)$'Study.Bird',"stddev"))^2
slopes <- coef(order2.mod1)$'Study:Bird'

chi.1 <- sum((slopes[,1]-ord.coef1[1,"Estimate"])^2)/var.est[1]
chi.2 <- sum((slopes[,2]-ord.coef1[2,"Estimate"])^2)/var.est[2]
#chi.3 <- sum((slopes[,3]-ord.coef1[3,"Estimate"])^2)/var.est[3]
df <- nrow(slopes)

p.1 <- pchisq(chi.1, df, lower.tail=F)
p.2 <- pchisq(chi.2, df, lower.tail=F)
#p.3 <- pchisq(chi.3, df, lower.tail=F)

IO.r1 <- data.frame(Coefficient = c("Intercept", "Experiment Order"),
                    Variance = var.est,'Chi Sq' = c(chi.1, chi.2), df = rep(df,2),
                    p = c(p.1, p.2))
```

Table 9: Random effects across birds predicting odds of making the efficient choice predicted by insertion order2 and experimental order2

Coefficient	Variance	Chi.Sq	df	p
Intercept	0.58	19.73	27	0.84
Experiment Order	0.78	0	27	1

Table 9 shows the variability of the coefficients across birds for the model. None of the variances are significant, indicating that the birds did not differ significantly in their rates of learning or in how the experiment position affected them. [2]

2.4.2 Check nonlinearity in experiment order2

```
# add a nonlinear term
Transfer2$Experiment2 <- Transfer2$Experiment^2
```

Centered the Experiment term to get rid of convergence issues

```
# Center experiment number
Transfer2$Experiment.c <- (Transfer2$Experiment - mean(Transfer2$Experiment))
Transfer2$Experiment.c2 <- Transfer2$Experiment.c^2

order2.mod_non.c.max <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2
                             + (1 + Insertion + Experiment.c+ Experiment.c2 | Study)
                             + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                             family="binomial", data=Transfer2,
                             control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

order2.mod_non.c.v2 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 +
                              (1 + Insertion + Experiment.c | Study) +
                              (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer2,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod_non.c.max, order2.mod_non.c.v2)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 + Insertion +
##     Experiment.c + Experiment.c2 | Study) + (1 + Insertion +
##     Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 + Insertion +
##     Experiment.c | Study) + (1 + Insertion + Experiment.c + Experiment.c2 |
##     Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  24 -2109.0
## 2  20 -2110.8 -4 3.7644     0.4388

# don't need quadratic term at study level

order2.mod_non.c.v3 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2
                            + (1 + Insertion | Study)
                            + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer2,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod_non.c.v2, order2.mod_non.c.v3)
```

---

[2] These analyses were also tested with experimental order2 as a binary variable, with 0 = first experiment and 1 = not the first experiment. Again, the order2 of experiment did not significantly predict the intercept (likelihood of choosing the efficient choice at the start of the experiment) or slope (rate of learning across the experiment).

```
## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 + Insertion +
##     Experiment.c | Study) + (1 + Insertion + Experiment.c + Experiment.c2 |
##     Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 + Insertion |
##     Study) + (1 + Insertion + Experiment.c + Experiment.c2 |
##     Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  20 -2110.8
## 2  17 -2113.6 -3 5.4236     0.1433
```

```
# don't need experiment term at study level

order2.mod_non.c.v4 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2
                            + (1 | Study) +
                            + (1 + Insertion + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer2,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod_non.c.v3, order2.mod_non.c.v4)
```

```
## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 + Insertion |
##     Study) + (1 + Insertion + Experiment.c + Experiment.c2 |
##     Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Insertion + Experiment.c + Experiment.c2 | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  17 -2113.6
## 2  15 -2115.8 -2 4.5975     0.1004
```

```
# don't need insertion term at study level

order2.mod_non.c.v5 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 +
                              + (1 | Study) +
                              (1 + Insertion + Experiment.c | Study:Bird),
                            family="binomial", data=Transfer2,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod_non.c.v4, order2.mod_non.c.v5)
```

```
## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Insertion + Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + +(1 |
##     Study) + (1 + Insertion + Experiment.c | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  15 -2115.8
## 2  11 -2162.7 -4 93.695  < 2.2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need quadratic term at bird level

order2.mod_non.c.v6 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2
                            + (1 | Study) +
                            + (1 + Insertion + Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer2,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod_non.c.v4, order2.mod_non.c.v6)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Insertion + Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Insertion + Experiment.c2 | Study:Bird)
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1  15 -2115.8
## 2  11 -2219.1 -4 206.5  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need slope term at bird level

order2.mod_non.c.v7 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2
                            + (1 | Study) +
                            + (1  + Experiment.c+ Experiment.c2 | Study:Bird),
                            family="binomial", data=Transfer2,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod_non.c.v4, order2.mod_non.c.v7)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Insertion + Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Experiment.c + Experiment.c2 | Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  15 -2115.8
## 2  11 -2124.4 -4 17.038     0.0019 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need insertion term at bird level

order2.mod_non.c.v8 <- glmer(Efficient ~ Insertion + Experiment.c + Experiment.c2 +
                              (1 | Study) +
                              (1 + Insertion + Experiment.c + Experiment.c2 || Study:Bird),
```

```
                            family="binomial", data=Transfer2,
                            control = glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE))

lrtest(order2.mod_non.c.v4, order2.mod_non.c.v8)

## Likelihood ratio test
##
## Model 1: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Insertion + Experiment.c + Experiment.c2 | Study:Bird)
## Model 2: Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     (1 + Insertion + Experiment.c + Experiment.c2 || Study:Bird)
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  15 -2115.8
## 2   9 -2135.8 -6 39.962  4.635e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# need covariance at bird level

order2.mod_non.c <- order2.mod_non.c.v4

summary (order2.mod_non.c)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## Efficient ~ Insertion + Experiment.c + Experiment.c2 + (1 | Study) +
##     +(1 + Insertion + Experiment.c + Experiment.c2 | Study:Bird)
##    Data: Transfer2
## Control: glmerControl(optimizer = "nloptwrap", calc.derivs = FALSE)
##
##      AIC      BIC   logLik deviance df.resid
##   4261.7   4359.0  -2115.9   4231.7     4834
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -8.4418  0.1339  0.3023  0.5017  1.9186
##
## Random effects:
##  Groups     Name          Variance  Std.Dev. Corr
##  Study:Bird (Intercept)   1.9022930 1.37924
##             Insertion     0.0002156 0.01468  -0.49
##             Experiment.c  0.7427364 0.86182   0.39 -0.02
##             Experiment.c2 0.3983241 0.63113  -0.84  0.41  0.17
##  Study      (Intercept)   0.1747490 0.41803
## Number of obs: 4849, groups:  Study:Bird, 27; Study, 5
##
## Fixed effects:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.360287   0.355694   3.824 0.000131 ***
## Insertion      0.031709   0.003767   8.417  < 2e-16 ***
```

```
## Experiment.c   0.593543   0.191221   3.104 0.001909 **
## Experiment.c2 -0.208655   0.142584  -1.463 0.143364
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Insrtn Exprm.
## Insertion   -0.397
## Experimnt.c  0.313  0.006
## Expermnt.c2 -0.641  0.303  0.241
```

The quadratic term is not significant indicating we do not have any non-linearity problems and therefore the model we have is best fitted by a linear relationship.