

Binary Choice Analysis

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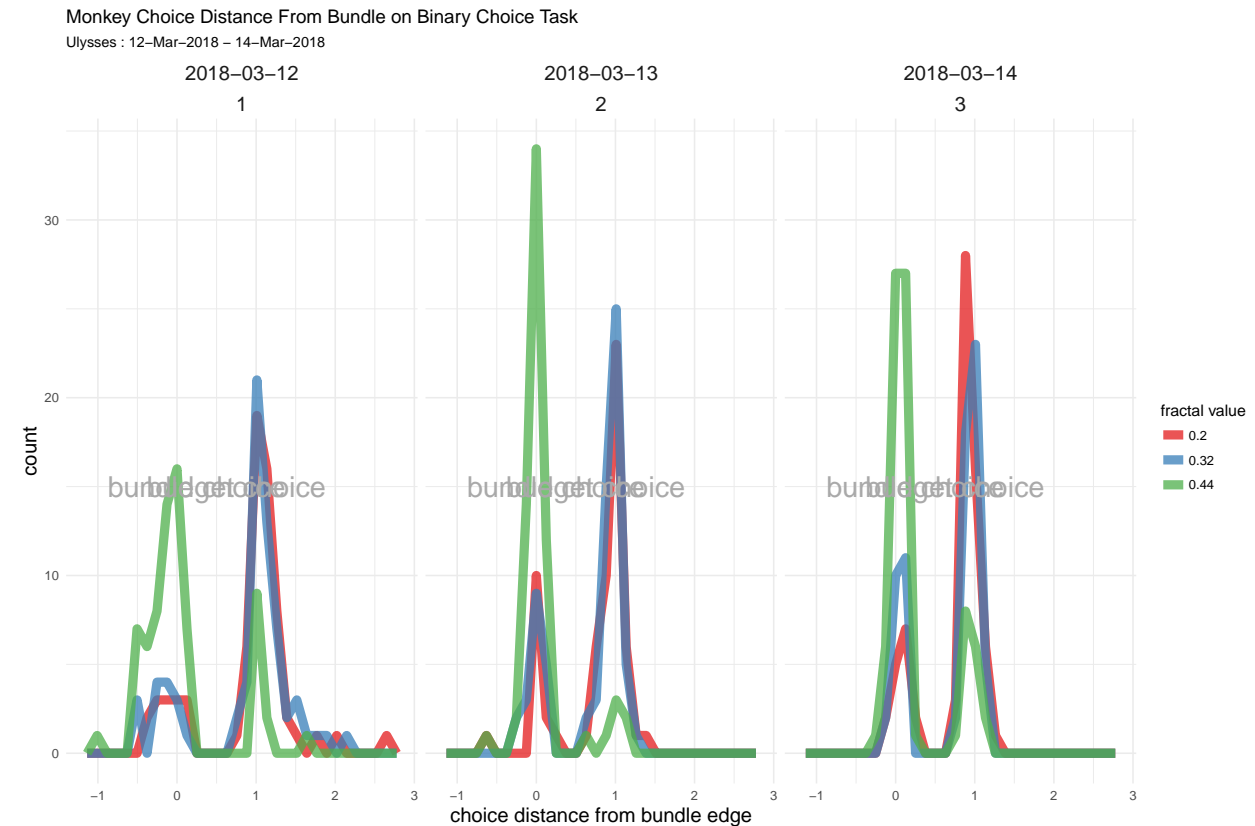
22 February 2018

```
monkey <- "Ulysses"  
today <- "14-Mar-2018"  
look_back <- "12-Mar-2018"
```

```
start_trial <- 0  
stop_trial <- "all"
```

```
merge_days <- TRUE
```

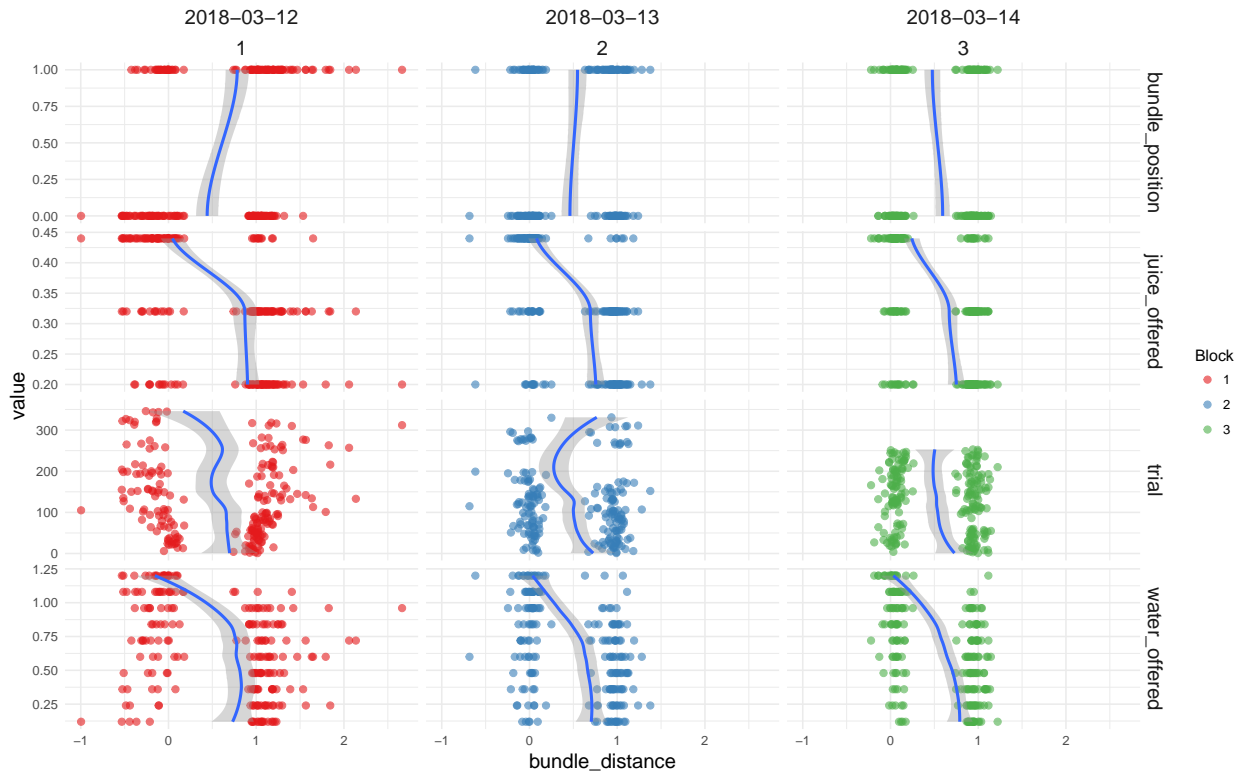
p1



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Monkey Choice Distance From Bundle on Binary Choice Task

Ulysses : 12-Mar-2018 - 14-Mar-2018



*#generate a model of likelihood to choice for the fractal dependent on it's position,
#value and associated water*

```
model <- glm(data = task_data,
             fractal_choice ~ bundle_position + water_offered + juice_offered + trial + date,
             family = "binomial")
```

#summarise the parameters

```
summary(model)
```

```
##
## Call:
## glm(formula = fractal_choice ~ bundle_position + water_offered +
##     juice_offered + trial + date, family = "binomial", data = task_data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.19521  -0.50639  -0.09836   0.48047   2.47106
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.399e+03  2.530e+03  -0.948   0.343
## bundle_position -3.087e-01  2.393e-01  -1.290   0.197
## water_offered  5.542e+00  4.961e-01  11.171 < 2e-16 ***
## juice_offered  2.096e+01  1.774e+00  11.815 < 2e-16 ***
## trial         7.366e-03  1.465e-03   5.029 4.93e-07 ***
## date          1.356e-01  1.437e-01   0.943   0.346
## ---
```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 872.44  on 633  degrees of freedom
## Residual deviance: 450.08  on 628  degrees of freedom
##    (362 observations deleted due to missingness)
## AIC: 462.08
##
## Number of Fisher Scoring iterations: 6
#test for side bias with an exact binomial test
binom.test(c(nrow(task_data %>%
              .[c(bundle_position != fractal_choice)]),
            nrow(task_data %>%
              .[c(bundle_position == fractal_choice)])))

##
## Exact binomial test
##
## data:  c(nrow(task_data %>% .[c(bundle_position != fractal_choice)]),      nrow(task_data %>% .[c(bun
## number of successes = 326, number of trials = 634, p-value =
## 0.4996
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.4745139 0.5537445
## sample estimates:
## probability of success
##          0.5141956
#generate a model of likelihood to choice for the fractal dependent on it's position,
#value and associated water
model <- glm(data = dplyr::filter(task_data, block_no == max(block_no)),
             fractal_choice ~ bundle_position + water_offered + as.factor(juice_offered) + trial + date,
             family = "binomial")

#summarise the parameters
summary(model)

##
## Call:
## glm(formula = fractal_choice ~ bundle_position + water_offered +
##      as.factor(juice_offered) + trial + date, family = "binomial",
##      data = dplyr::filter(task_data, block_no == max(block_no)))
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.12661  -0.41591  -0.02862   0.27799   2.40763
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -11.657850   1.763320  -6.611 3.81e-11 ***
## bundle_position    2.317640   0.577181   4.015 5.93e-05 ***
## water_offered     8.568024   1.315536   6.513 7.37e-11 ***
## as.factor(juice_offered)0.32  1.131911   0.572396   1.977  0.048 *

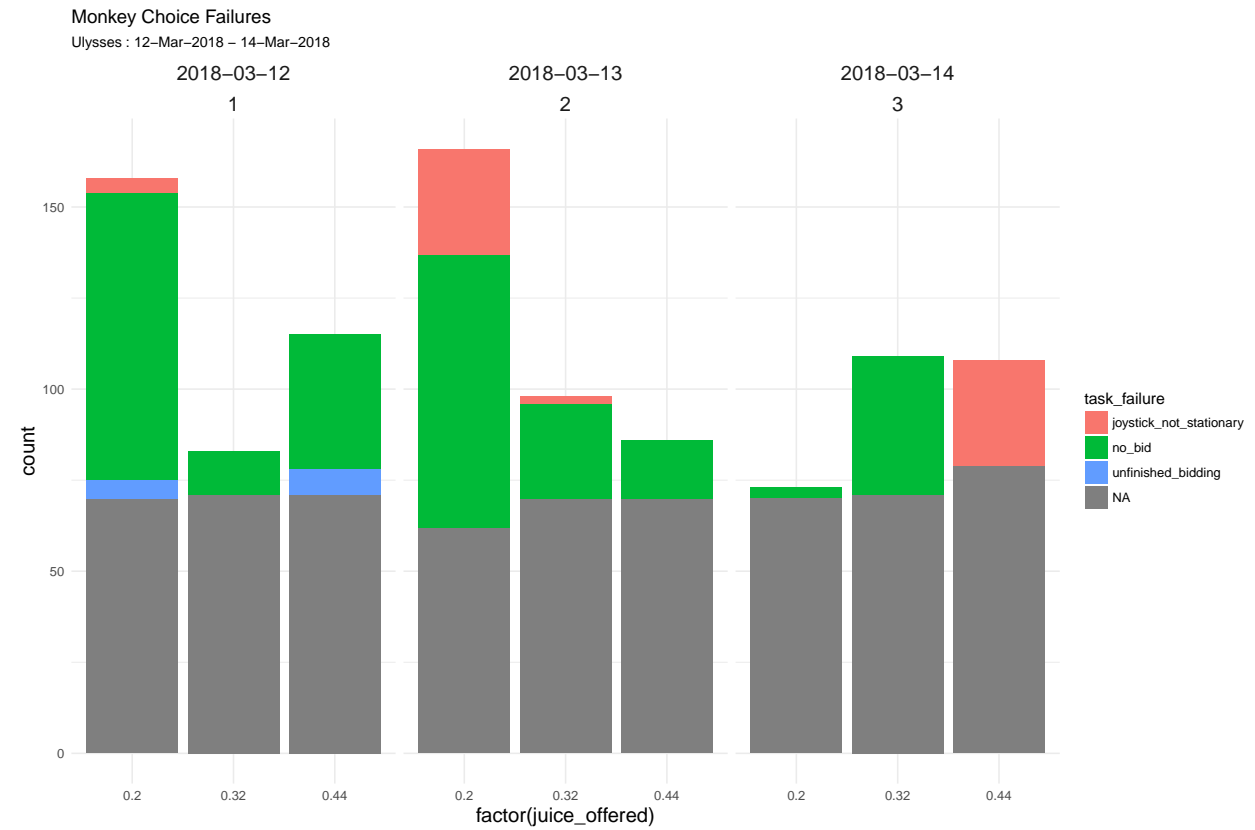
```

```

## as.factor(juice_offered)0.44    6.369143    1.017742    6.258 3.90e-10 ***
## trial                          0.014788    0.003632    4.071 4.68e-05 ***
## date                           NA          NA          NA      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 303.51  on 219  degrees of freedom
## Residual deviance: 122.50  on 214  degrees of freedom
##    (70 observations deleted due to missingness)
## AIC: 134.5
##
## Number of Fisher Scoring iterations: 7
#test for side bias with an exact binomial test
binom.test(c(nrow(task_data %>%
              .[c(bundle_position != fractal_choice & block_no == max(block_no))]),
            nrow(task_data %>%
              .[c(bundle_position == fractal_choice & block_no == max(block_no))])))

##
## Exact binomial test
##
## data:  c(nrow(task_data %>% .[c(bundle_position != fractal_choice &      block_no == max(block_no))])
## number of successes = 93, number of trials = 220, p-value =
## 0.02587
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.3566164 0.4909493
## sample estimates:
## probability of success
##      0.4227273
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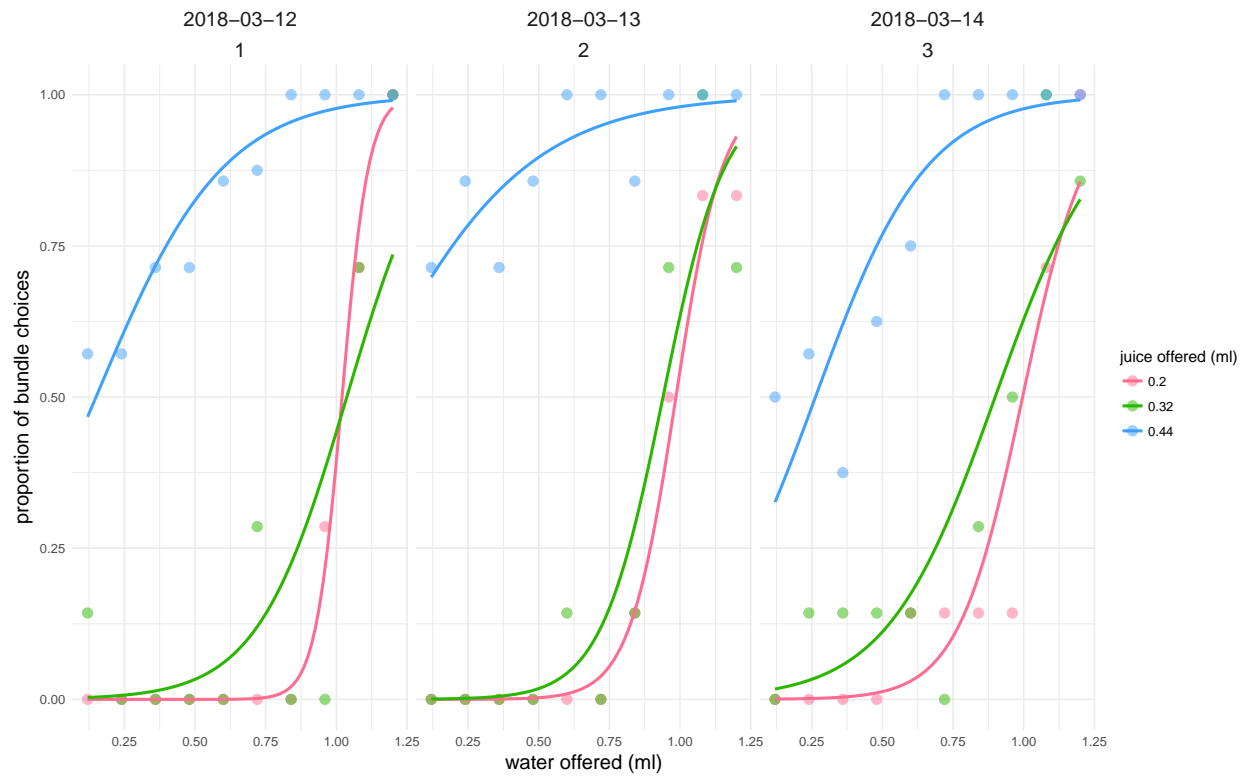
```



p4

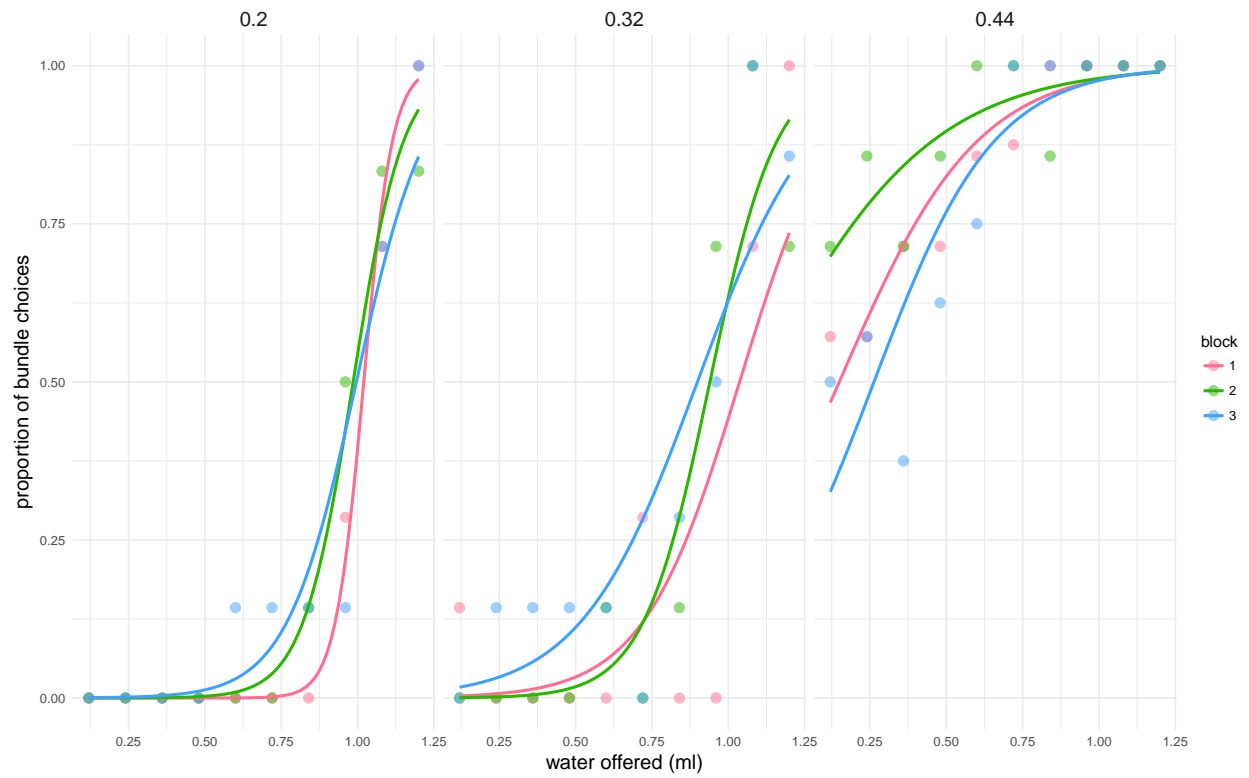
Monkey Bundle Choice Binoimial Curves

Ulysses : 12-Mar-2018 – 14-Mar-2018



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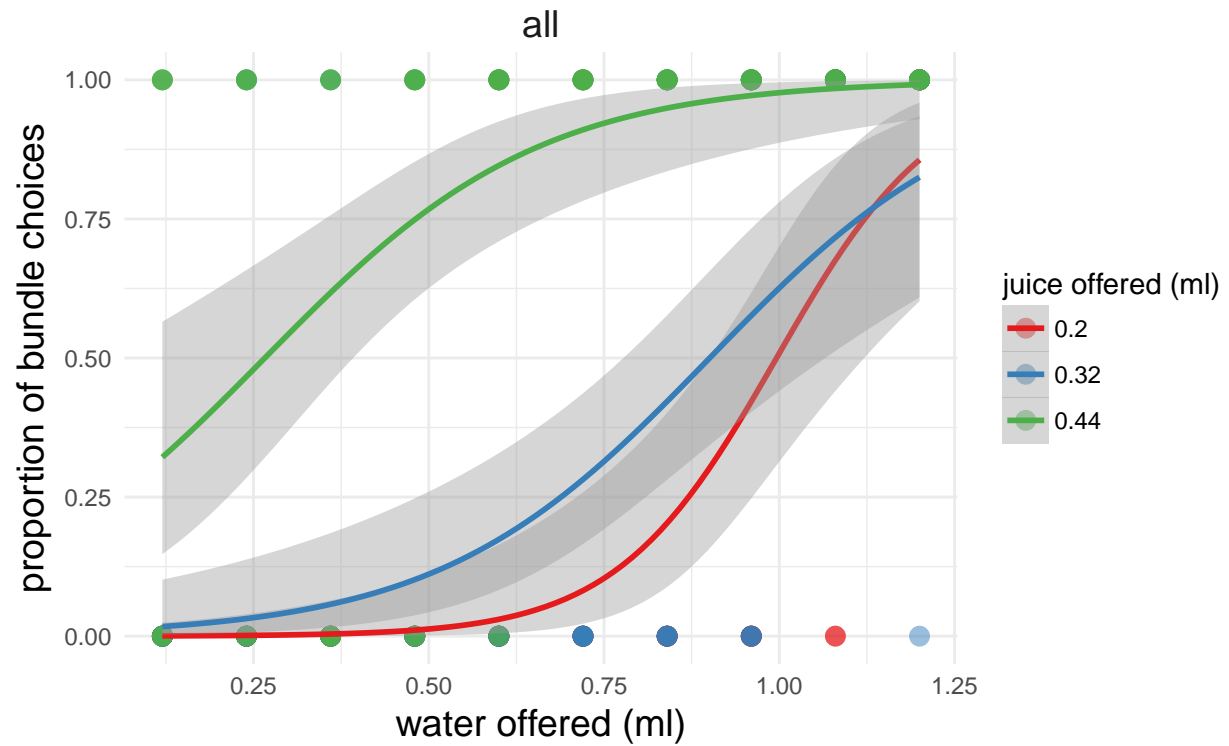
Monkey Bundle Choice Binoimial Curves
 Ulysses : 12-Mar-2018 – 14-Mar-2018



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Today's Monkey Bundle Choice Binoimial Curves

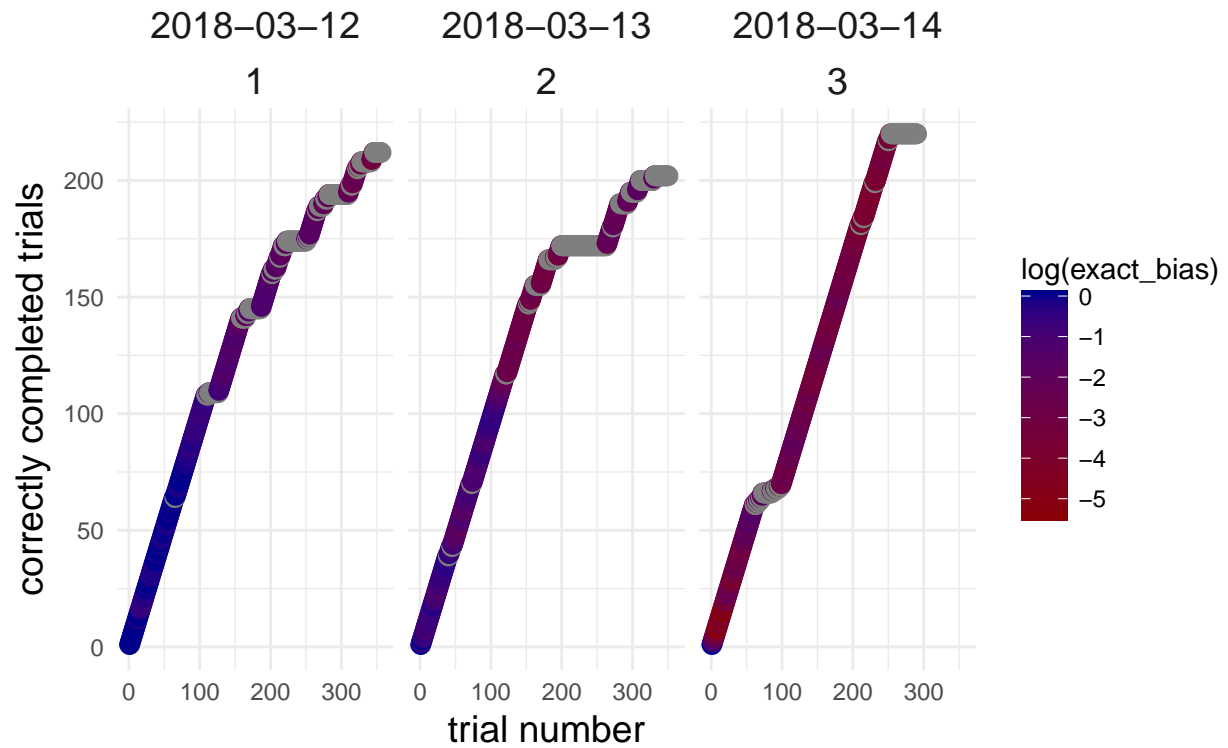
Ulysses : 14-Mar-2018



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Monkey Trial Progression and Bias

Ulysses : 12-Mar-2018 – 14-Mar-2018



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Monkey Trial Progression and Bias

Ulysses : 12-Mar-2018 – 14-Mar-2018

