Foraging: introducing our gaze-contingent eye-tracking paradigm for studying foraging

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Chapter 1

First things first

Things about the series of two experiments before we consider experiment one and experiment two separately.

Part I

Experiment One

Chapter 2

Introduction

In experiment 1, the computerized gaze contingent task consisted of 20 individual trials. In each trial participants were presented with a display containing 30 trees, 15 of which contained a hidden fruit item which was the target (the target was an apple, represented by a filled red circle). On each trial, the participant's task was to forage for and retrieve 10 of the 15 fruit items.

We manipulated one factor within-subjects (Resource Distribution) with 2 levels: 'clumped' and 'random'.

We created ten random stimuli in which the 15 target fruit items were uniformly distributed about the 30 trees (random condition) and ten stimuli in which all 15 target fruit items were arranged in one large patch (clumped condition) that covered either the left or the right side of the layout.

This line runs the code that gets the individual participant results files in.

```
# source("e1_process_individual_results_files.R", local = knitr::knit_global())
```

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Number of Trees

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Chapter 4

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Chapter 5

Revisits Per Trial

Experiment 1

5.1 Raw data

This line reads in the dataset that results from collating the results files for each participant.

```r
e1 <- readRDS("fgms_e1_allsubs.rds")
```

This renames the raw data but doesn't do any operations on it.

```r
# this tibble is one row for each tree visited saying whether it was a revisit or not
e1_revisits <-
  e1 %>%
  transmute(
    pp           = pid,
    condition    = R,
    stage        = as_factor(ifelse(trial<=5, "early", "late")),
    progress     = as_factor(trial),
    index        = index,
    tree         = tile,
    is_a_revisit = revisit
  )
```

5.2   Aggregation 1: Trial counts

```
# First level of aggregation collapses over index and yields
# a count for each trial:
# each row is how many revisits they made on that trial
# THESE ARE TRIAL SUMS
TRIAL_SUMS <-
  e1_revisits %>%
  group_by(pp, condition, stage, progress) %>%
  summarise(nrevisits = sum(is_a_revisit), .groups = "drop_last")
```

5.3   Aggregation 2: Participant means

```
# Second level of aggregation collapses over trials
# each row is the average number of revisits that participant
# made in that combination of random/clumped and early/late
# THESE ARE PARTICIPANT MEANS
PARTICIPANT_MEANS <-
  TRIAL_SUMS %>%
  group_by(pp, condition, stage) %>%
  summarise(meanrevisits=mean(nrevisits), .groups="drop_last")
```

5.4   Descriptives

Condition descriptives

```
# To generate mean and sd properly for each level of condition
# (clumped/random), we first need data with one clumped score
# for each participant and one random score for each
# participant, averaging over early and late stages.
tempCond <- PARTICIPANT_MEANS %>%
  group_by(pp,condition) %>% summarise(cmeans=mean(meanrevisits))
# Now we can ask for means and sd for clumped and random
# that each pp contributed one value to
CONDITION_DESCRIPTIVES <- tempCond %>%
  group_by(condition) %>%
  summarise(mean=mean(cmeans), sd=sd(cmeans))
# issue the table
CONDITION_DESCRIPTIVES %>%
```

```r
  gt() %>%
  tab_header("Revisits per trial descriptives") %>%
  fmt_number(columns = c("mean","sd"), decimals=2) %>%
  gtsave("e1_tables/condition_means.png")
```

Revisits per trial descriptives		
condition	mean	sd
clumped	0.81	0.83
random	1.10	0.96

Stage descriptives

```r
# To generate mean and sd properly for each level of stage,
# we first need to collapse over condition (clumped/random)
# to get one score for each participant per level of stage
# (early/late)
tempStage <- PARTICIPANT_MEANS %>%
  group_by(pp,stage) %>%
  summarise(smeans=mean(meanrevisits))
# Now we can ask for means and sd per level of stage
STAGE_DESCRIPTIVES <- tempStage  %>%
  group_by(stage) %>%
  summarise(mean=mean(smeans),sd=sd(smeans))
# issue the table
STAGE_DESCRIPTIVES %>%
  gt() %>%
  tab_header("Revisits per trial descriptives") %>%
  fmt_number(columns = c("mean","sd"), decimals=2) %>%
  gtsave("e1_tables/stage_means.png")
```

| Revisits per trial descriptives		
stage	mean	sd
early	1.12	0.85
late	0.79	0.75

SxC Descriptives

```r
# To get the 2 x 2 interaction means, yielding a 2x2 table with mean and sd
SxC_DESCRIPTIVES <- PARTICIPANT_MEANS %>% group_by(condition,stage) %>% summarise(mean=mean(meanr
SxC_DESCRIPTIVES %>%
  gt(rowname_col = "stage", groupname_col = "condition") %>%
  tab_stubhead(label = "condition") %>%
```

```
fmt_number(columns = c("mean","sd"), decimals=2) %>%
tab_header("Revisits per trial descriptives") %>%
gtsave("e1_tables/SxC_means.png")
```

Revisits per trial descriptives		
condition	mean	sd
clumped		
early	0.99	0.98
late	0.64	0.85
random		
early	1.24	1.00
late	0.95	1.08

5.5   Plots
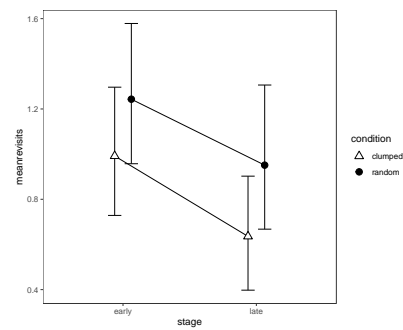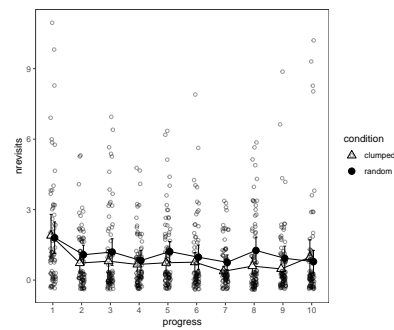
5.6   ANOVA

```
ez1 <- ezANOVA(
  data=PARTICIPANT_MEANS,
  wid=pp,
  within=.c(condition, stage),
  dv=meanrevisits
)
```

Revisits per trial
ANOVA table

Effect	DFn	DFd	F	p	p<.05
condition	1	41	3.76	0.059	
stage	1	41	18.17	0.000	*
condition:stage	1	41	0.12	0.735	

Chapter 6

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Part II

Experiment Two

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In experiment 2, n trials. Task.

We manipulated two factors: one within-subjects (Resource Distribution) with two levels: 'clumped' and 'random'; and one between-subjects (Fading) with two levels 'fade' and 'no-fade'. The fade condition differeed from experiment 1 in that once a tree had been visited, it was thereafter displayed faded out such that it was apparent to the participant which trees had been visited previously and which had not. The no-fade condition was the same as experiment 1. We expected that the fading would function as a memory aid and reduce revisits as well as making the task easier overall on the other metrics.

We created ?? random stimuli in which the ?? target fruit items were uniformly distributed about the ?? trees (random condition) and ?? stimuli in which all ?? target fruit items were arranged in one large area (clumped condition) that covered either the left or the right side of the layout.

This line runs the code that gets the individual participant results files in.

```
source("e2_process_individual_results_files.R", local = knitr::knit_global())
#>
#>   ***********************************************************
#>           Loading standardize package version 0.2.2
#>       Call standardize.news() to see new features/changes
#>   ***********************************************************
#> -- Attaching packages ------------------ tidyverse 1.3.1 --
#> v ggplot2 3.3.6     v purrr   0.3.4
#> v tibble  3.1.7     v dplyr   1.0.9
#> v tidyr   1.2.0     v stringr 1.4.0
#> v readr   2.1.2     v forcats 0.5.1
```

```
#> -- Conflicts --------------------- tidyverse_conflicts() --
#> x dplyr::filter() masks stats::filter()
#> x dplyr::lag()    masks stats::lag()
#> P001 done
#> P002 done
#> P003 done
#> P004 done
#> P005 done
#> P006 done
#> P007 done
#> P008 done
#> P009 done
#> P010 done
#> P011 done
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#> P030 done
#> P031 done
#> P032 done
#> P033 done
#> P034 done
#> P035 done
#> P036 done
#> P037 done
#> P038 done
#> P039 done
#> P040 done
#> P041 done
#> P042 done
```

Chapter 9

Number of trees

Experiment 2

Load the libraries.

This line reads in the dataset that results from collating the results files for each participant.

```
e2 <- readRDS("fgms_e2_allsubs.rds")
```

This renames the raw data but doesn't do any operations on it.

```
# this tibble is one row for each tree visited saying whether it was a revisit or not
e2_revisits <-
  e2 %>%
  transmute(
    pp          = participant,
    trial       = trial_number,
    resources   = factor(R, levels=c(".pat","dis"), labels=c("clumped", "random")),
    stage       = as_factor(ifelse(trial<=10, "early", "late")),
    progress    = factor(trial),
    index       = index,
    tree        = tile,
    is_a_revisit = revisit
  )
```

Here

Chapter 10

Trial Duration

E2

Chapter 11

Revisits Per Trial

Experiment 2

11.1 Raw data

This line reads in the dataset that results from collating the results files for each participant.

```
e2 <- readRDS("fgms_e2_allsubs.rds")
```

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Retrieval Rate

E2

Chapter 13

Inter-tree-distance

E2

Appendix A

Appendix A

Content ...

Appendix B

Appendix B

Content ...