

# Stockport simulations

```
library(calmr)
library(tidyverse)

theme_set(theme_minimal(base_size = 14))
```

## Mackintosh 1975 simulations

### Continuous and partial reinforcement

#### Design

Group	Phase 1	Phase 2
Continuous	20x A-O1	20x A-O3
Partial	10x A-O1 ; 10x A-O2	20x A-O3

```
simple_design <- data.frame(
  Group = c("continuous", "partial"),
  Phase1 = c("20A(01)", "10A(01)/10A(02)"),
  R1 = c(TRUE, TRUE),
  Phase2 = c("20A(03)", "20A(03)"),
  R2 = c(TRUE, TRUE)
)
# parsing the design and showing the original and what was detected
parsed <- parse_design(simple_design)

pars_MAC1975 <- get_parameters(simple_design, model = "MAC1975")

# set to original model with no WCA
```

```

pars_MAC1975$gammas[c("A","B")] <- 0
pars_MAC1975$gammas[c("01","02","03")] <- 1

```

## Run simulation

```

simple_design_results <- run_experiment(
  simple_design, # note we do not need to pass the parsed design
  model = "MAC1975",
  parameters = pars_MAC1975,
  iterations = 10
)

# supported_plots("MAC1975")
# plot(simple_design_results)
# plot(simple_design_results, type = "as")

#slotNames(simple_design_results)

```

## Plot the results

```

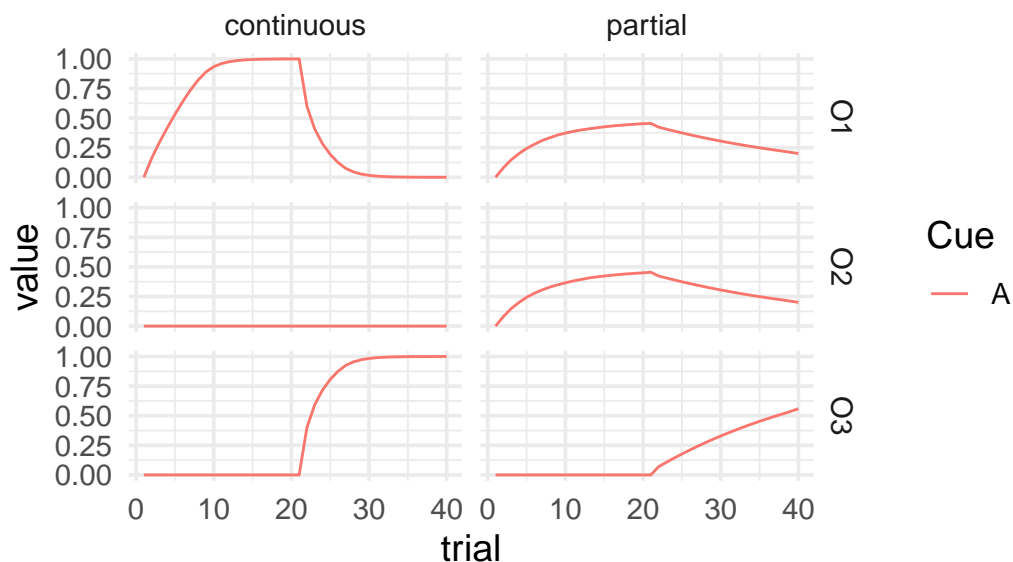
# calculate and plot Vs

vs_res <-
  results(simple_design_results)[["vs"]] %>%
    filter(s1 %in% c("A"),
           s2 %in% c("01", "02", "03")) %>%
    group_by(trial, s1, s2, group) %>%
    summarise(value = mean(value))

vs_res %>%
  ggplot(aes(x = trial, y = value, colour = s1)) +
  geom_line() +
  facet_grid(cols = vars(group), rows = vars(s2)) +
  labs(title = "Associative Strengths",
       colour = "Cue")

```

## Associative Strengths

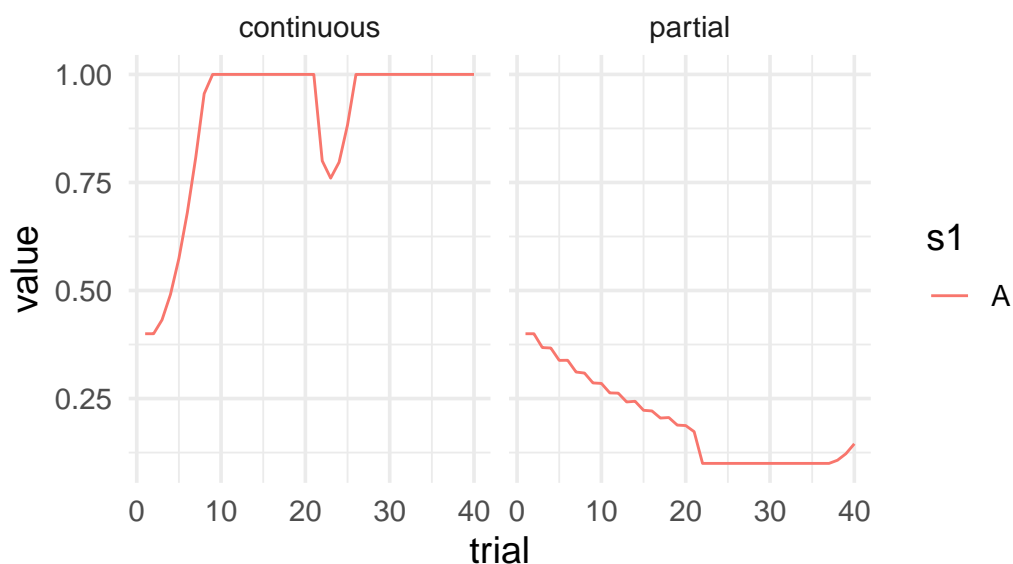


```
# calculate and plot Alphas

alphas_res <-
  results(simple_design_results)[["as"]] %>%
    filter(s1 %in% c("A")) %>%
    group_by(trial, s1, group) %>%
    summarise(value = mean(value))

alphas_res %>%
  ggplot(aes(x = trial, y = value, colour = s1)) +
  geom_line() +
  facet_grid(cols = vars(group)) +
  labs(title = "Alphas")
```

## Alphas



## Le Pelley, Beesley, & Griffiths (2011)

### Design

Phase 1	Phase 2
(10 each)	(10 each)
AV-O1 ; AW-O1	AX-O3
BV-O2 ; BW-O2	BY-O4
CX-O2 ; CY-O2	CV-O3
DX-O1 ; DY-O1	DW-O4

```

LBG_2011 <- data.frame(
  Group = c("LBG_2011"),
  Phase1 = c("10AV(01)/10AW(01)/10BV(02)/10BW(02)/10CX(02)/10CY(02)/10DX(01)/10DY(01)"),
  R1 = c(TRUE),
  Phase2 = c("10AX(03)/10BY(04)/10CV(03)/10DW(04)"),
  R2 = c(TRUE),
  Test = c("1#A/1#B/1#C/1#D/1#V/1#W/1#X/1#Y"),
  R3 = c(TRUE)
)

```

```
# parsing the design and showing the original and what was detected
parsed <- parse_design(LBG_2011)

pars_MAC1975 <- get_parameters(LBG_2011, model = "MAC1975")

# set to original model with no WCA
pars_MAC1975$gammas[c("A","B","C","D","V","W","X","Y")] <- 0
pars_MAC1975$gammas[c("01","02","03","04")] <- 1
```

## Run simulation

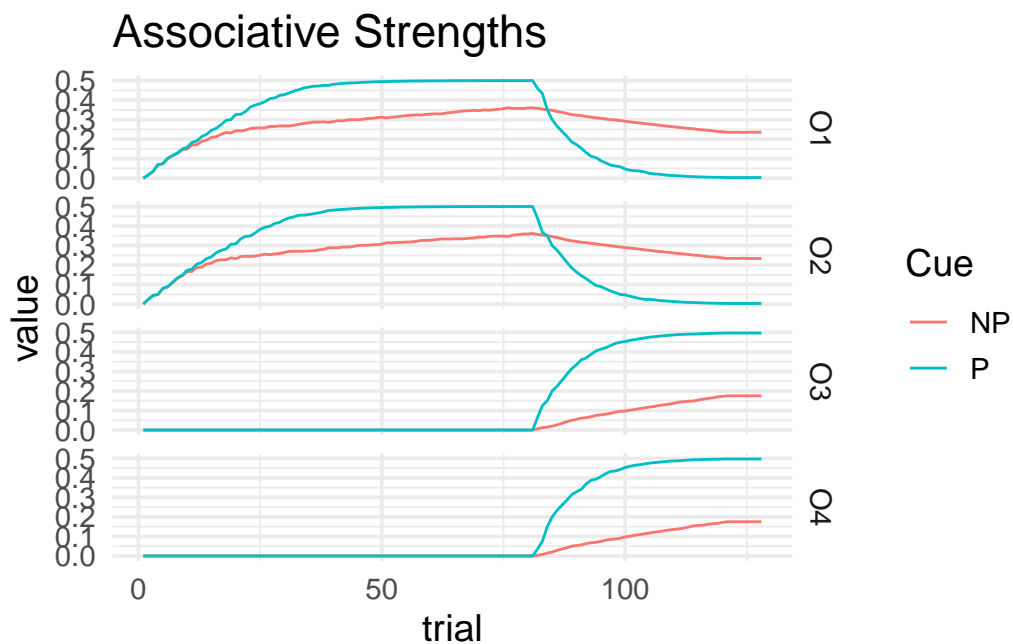
```
LBG_2011_results <- run_experiment(
  LBG_2011, # note we do not need to pass the parsed design
  model = "MAC1975",
  parameters = pars_MAC1975,
  iterations = 10
)
```

## Plot the results

```
# calculate and plot Vs

vs_res <-
  results(LBG_2011_results)[["vs"]] %>%
  mutate(cue_type = case_when(s1 %in% c("A", "B", "C", "D") ~ "P",
                              s1 %in% c("V", "W", "X", "Y") ~ "NP")) %>%
  drop_na() %>%
  filter(s2 %in% c("01", "02", "03", "04")) %>%
  group_by(trial, cue_type, s2) %>%
  summarise(value = mean(value))

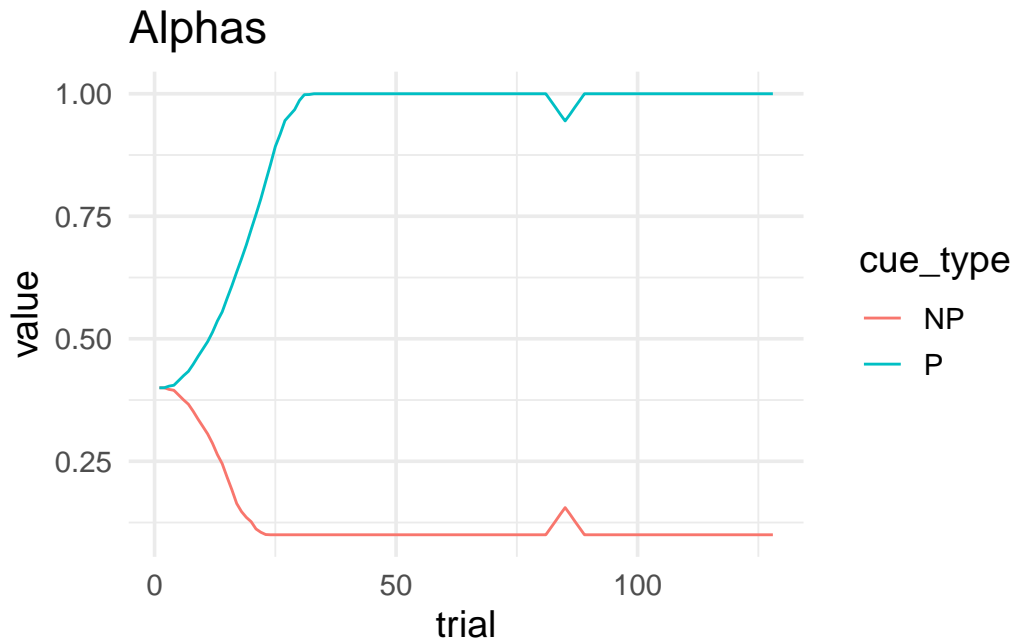
vs_res %>%
  ggplot(aes(x = trial, y = value, colour = cue_type)) +
  geom_line() +
  facet_grid(rows = vars(s2)) +
  labs(title = "Associative Strengths",
       colour = "Cue")
```



```
# calculate and plot Alphas

alphas_res <-
  results(LBG_2011_results)[["as"]] %>%
  mutate(cue_type = case_when(s1 %in% c("A", "B", "C", "D") ~ "P",
                              s1 %in% c("V", "W", "X", "Y") ~ "NP")) %>%
  drop_na() %>%
  group_by(trial, cue_type) %>%
  summarise(value = mean(value))

alphas_res %>%
  ggplot(aes(x = trial, y = value, colour = cue_type)) +
  geom_line() +
  labs(title = "Alphas")
```



The simulation results (Vs) show the Learned Predictiveness effect, with stronger learning about P cues compared to NP cues in Stage 2. The alpha results show a maintenance of the high associability for P cues in Stage 2. The initial blip in Stage 2 is probably due to all cues having  $V = 0$  with respect to new outcomes. So NP cues are initially an equally valid predictor and gain some associability...I'm not sure why associability declines for P cues, but their high associability means learning is more rapid and they quickly become the best available predictor.

### Does uncertainty increase associability for NP cues? (Stockport)

Design:

Phase 1	Phase 2
(10 each)	
AV-O1	5x AV-O1 ; 5 x AV(O2)
AW-O1	10x AW(O1)
BV-O2	5x BV-O2 ; 5 x BV(O1)
BW-O2	10x BW(O2)

```

STK <- data.frame(
  Group = c("LBG_2011"),
  Phase1 = c("10AV(01)/10AW(01)/10BV(02)/10BW(02)"),
  R1 = c(TRUE),
  Phase2 = c("5AV(01)/5AV(02)/10AW(01)/5BV(02)/5BV(01)/10BW(02)"),
  R2 = c(TRUE),
  Test = c("1#A/1#B/1#V/1#W"),
  R3 = c(TRUE)
)
# parsing the design and showing the original and what was detected
parsed <- parse_design(STK)

pars_MAC1975 <- get_parameters(STK, model = "MAC1975")

# set to original model with no WCA
pars_MAC1975$gammas[c("A", "B", "V", "W")] <- 0
pars_MAC1975$gammas[c("01", "02")] <- 1

```

## Run simulation

```

STK <- run_experiment(
  STK, # note we do not need to pass the parsed design
  model = "MAC1975",
  parameters = pars_MAC1975,
  iterations = 50
)

```

## Plot the results

```

# calculate and plot Vs

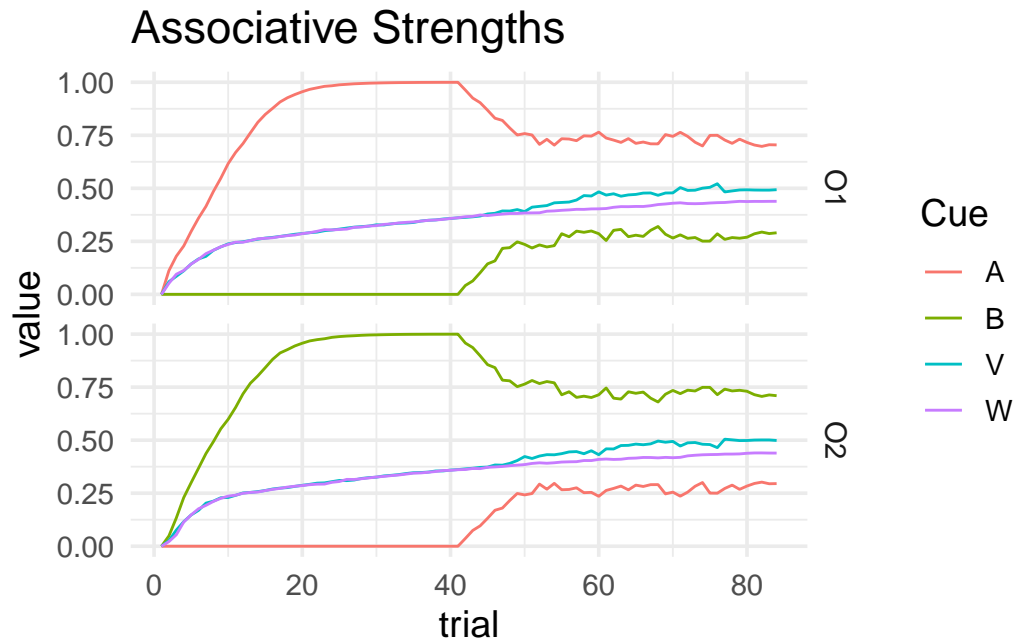
vs_res <-
  results(STK)[["vs"]] %>%
  filter(s1 %in% c("A", "B", "V", "W"),
         s2 %in% c("01", "02")) %>%
  group_by(trial, s1, s2) %>%
  summarise(value = mean(value))

vs_res %>%

```



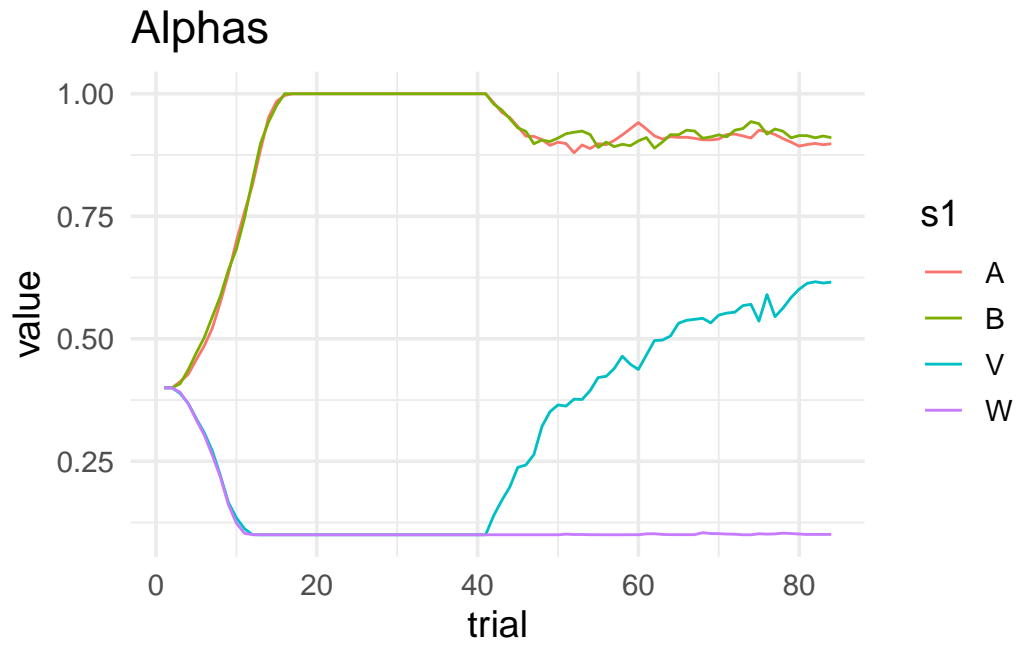
```
ggplot(aes(x = trial, y = value, colour = s1)) +
  geom_line() +
  facet_grid(rows = vars(s2)) +
  labs(title = "Associative Strengths",
        colour = "Cue")
```



```
# calculate and plot Alphas

alphas_res <-
  results(STK)[["as"]] %>%
  filter(s1 %in% c("A", "B", "V", "W")) %>%
  group_by(trial, s1) %>%
  summarise(value = mean(value))

alphas_res %>%
  ggplot(aes(x = trial, y = value, colour = s1)) +
  geom_line() +
  labs(title = "Alphas")
```



Interestingly, the Mackintosh model does predict that associability for the NP cue X will rise over the course of Stage 2. This is because on AX-O2 and BX-O1 trials, X is a better predictor of the alternative outcome than A and B, for which  $V = 0$  (initially).