

Duration reproduction under memory pressure

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1 Load packages and functions and data

1.1 mean reproduction biases and working memory performance

Calculate mean reproduction biases and working memory performance for each experiment.

```
# mean reproduction biases
mRep = ExpData %>% group_by(ExpName, NSub, WMSize, Load, gap, curDur) %>%
  summarise(m_bias = mean(bias), se_bias = sd(bias)/sqrt(n()), n = n())

# general bias
mBias = mRep %>% group_by(ExpName, Load, gap, NSub) %>%
  summarise(ms_bias = mean(m_bias)*1000, se_bias = sd(m_bias)/sqrt(n())*1000)

# mean working memory performance
mWM = ExpData %>% group_by(ExpName, NSub, WMSize, gap, Load) %>%
  summarise(m_WMCrr = mean(WMCrr), se_WMCrr = sd(WMCrr)/sqrt(n()), n = n())
```

1.2 Central tendency effect

Next, we estimate the central tendency effect by using linear regression. First, we prepare several useful functions

```
# a simple linear model function
lm_model <- function(df) {
  lm(m_bias ~ curDur, data = df)
}

# obtain the estimates of the linear model
lm_estimate <- function(df) {
  df %>% group_by(ExpName, NSub, gap, Load) %>% nest() %>%
  mutate(lm = map(data, lm_model)) %>% # linear regression
  mutate(slope = map(lm, broom::tidy)) %>% # get estimates
  unnest(slope) %>% # remove raw data
  dplyr::select(-std.error, -statistic, -p.value) %>% # remove unnecessary columns
  spread(term, estimate) %>% # spread estimates
  dplyr::rename(Intercept = `(Intercept)`, slope = curDur) %>% # rename columns
  mutate(cti = -slope) # central tendency index
}
```

```
# now estimate the central tendency effect
mRep_cti = mRep %>% lm_estimate()
```

1.3 Plotting functions

```
#plot reproduction bias by duration and memory load (central tendency effect) based on mRep
plot_cti <- function(data){
  # from subject-level to group-level
  data %>% group_by(Load, curDur) %>% summarise(mm_bias = mean(m_bias), se_bias = sd(m_bias)/sqrt(n()))
  ggplot(aes(curDur, mm_bias, color = Load, shape = Load)) +
    geom_point(size = 2, stat = 'identity') + geom_line() +
    geom_errorbar(aes(ymin = mm_bias - se_bias, ymax = mm_bias + se_bias), width = 0.05) +
    coord_cartesian(ylim = c(-0.5, 0.5)) +
    scale_x_continuous(breaks=c(0.5, 0.8, 1.1, 1.4, 1.7)) +
    labs(x="Durations (s)", y="Reproduction bias (s)",
         shape = "Memory Load", color = "Memory Load") +
    theme_new + greySet3 + theme(legend.position = c(.7,.8),
                                  legend.text = element_text(size = 10),
                                  legend.title = element_text(size = 10, face = "bold"),
                                  plot.title = element_text(hjust = 0.5))
}

# plot mean biases by memory load based on mBias
plot_bias_Load <- function(data){
  data %>% group_by(Load) %>% summarise(bias = mean(ms_bias), se_bias = sd(ms_bias)/sqrt(n())) %>%
  ggplot(aes(Load, bias, fill = Load)) +
    geom_bar(stat = 'identity', width = 0.75) +
    geom_errorbar(aes(ymin = bias - se_bias, ymax = bias + se_bias, color = Load), width = 0.3) +
    scale_y_reverse() +
    labs(x="Memory Load", y="Mean Underestimate (ms)", fill = "Memory Load", color = 'Memory Load') +
    theme_new + fillGreySet3 + greySet3 + theme(legend.position = "none",
                                                  plot.title = element_text(hjust = 0.5))
}

# plot mean cti by memory load
plot_cti_Load <-function(data){
  data %>% group_by(Load) %>% summarise(m_cti = mean(cti), se_cti = sd(cti)/sqrt(n())) %>%
  ggplot(aes(Load, m_cti, fill = Load)) +
    geom_bar(stat = 'identity', width = 0.75) +
    geom_errorbar(aes(ymin = m_cti - se_cti, ymax = m_cti + se_cti, color = Load), width = 0.3) +
    labs(x="Memory Load", y="Central Tendency Index", fill = "Memory Load", color = "Memory Load") +
    theme_new + fillGreySet3 + greySet3 + theme(legend.position = "none",
                                                  plot.title = element_text(hjust = 0.5))
}

# output three figures together
plot_fig <- function(Name, subfig = FALSE) {
  fig_a = mRep %>% filter(ExpName == Name) %>% plot_cti()
  fig_b = mRep_cti %>% filter(ExpName == Name) %>% plot_cti_Load()
  fig_c = mBias %>% filter(ExpName == Name) %>% plot_bias_Load()
  if(subfig) {
    return(list(fig_a=fig_a, fig_b=fig_b, fig_c=fig_c))
  }
}
```

```

} else {
  plot_grid(fig_a, fig_b, fig_c, labels = c('a', 'b', 'c'), nrow = 1)
}
}

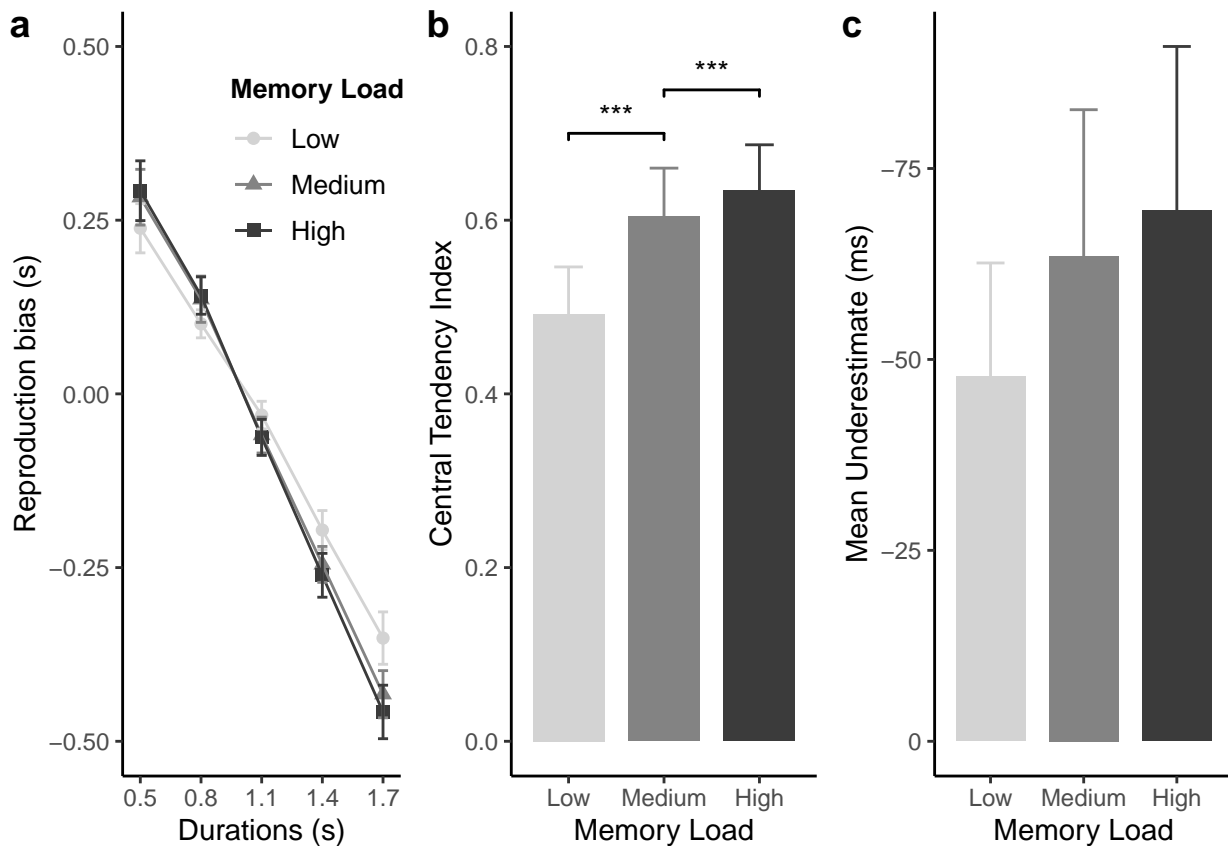
```

1.4 1. Working memory impacts on the encoding phase

```

# encoding manipulation
fig_encoding = plot_fig('Encoding', subfig = TRUE)
fig_encoding$fig_b = fig_encoding$fig_b +
  geom_signif(y_position = c(0.7, 0.75), xmin = c(1,2), xmax = c(2, 3), annotation = c("***", "***")) +
fig_en = plot_grid(fig_encoding$fig_a, fig_encoding$fig_b, fig_encoding$fig_c, labels = c('a', 'b', 'c'))
# save figures
ggsave("./figures/fig_encoding.png", fig_en, width = 7, height = 3)
fig_en

```



Now rmANOVA on reproduction biases, CTI and general biases

```

# rmANOVA on reproduction biases
av1 = mRep %>% filter(ExpName == 'Encoding') %>%
  ezANOVA(dv = m_bias, wid = NSub, within = .(curDur, Load), detailed = TRUE)
print(av1$ANOVA)

```

##	Effect	DFn	DFd	SSn	SSd	F	p	p < .05
## 1	curDur	1	15	14.37532810	1.7788315	121.219980	1.389187e-08	*
## 2	Load	2	30	0.02019136	0.2019869	1.499456	2.395105e-01	
## 3	curDur:Load	2	30	0.16147340	0.1187061	20.404175	2.544203e-06	*

```
##          ges
## 1 0.872561859
## 2 0.009525504
## 3 0.071416868
```

```
#rmANOVA on cti
```

```
av2 = mRep_cti %>% filter(ExpName == 'Encoding') %>%
  ezANOVA(dv = cti, wid = NSub, within = Load, detailed = TRUE)
print(av2$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  15 15.9725868 1.9764795 121.21998 1.389187e-08      *
## 2          Load    2  30  0.1794149 0.1318957  20.40417 2.544203e-06      *
##          ges
## 1 0.88339253
## 2 0.07842279
```

```
#rmANOVA on general bias
```

```
av3 = mBias %>% filter(ExpName == 'Encoding') %>%
  ezANOVA(dv = ms_bias, wid = NSub, within = Load, detailed = TRUE)
print(av3$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  15 174392.655 211232.03 12.383964 0.003099731      *
## 2          Load    2  30  4038.273  40397.39  1.499456 0.239510546
##          ges
## 1 0.40935122
## 2 0.01579501
```

```
mWM %>% filter(ExpName == 'Encoding') %>% group_by(Load) %>% summarise(mean(m_WMCrr), sd(m_WMCrr)/sqrt(n()))
```

```
## # A tibble: 3 x 3
##   Load   `mean(m_WMCrr)` `sd(m_WMCrr)/sqrt(n())`
##   <fct>         <dbl>         <dbl>
## 1 Low              0.899              0.0100
## 2 Medium           0.724              0.0228
## 3 High             0.664              0.0206
```

```
mWM %>% filter(ExpName == 'Encoding') %>%
  ezANOVA(dv = m_WMCrr, wid = NSub, within = Load, detailed = TRUE)
```

```
## Warning: Converting "NSub" to factor for ANOVA.
```

```
## $ANOVA
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  15 27.90426 0.17549221 2385.08547 5.982001e-18      *
## 2          Load    2  30  0.47617 0.07477734  95.51757 9.770098e-14      *
##          ges
## 1 0.9911109
## 2 0.6554847
```

```
## $`Mauchly's Test for Sphericity`
```

```
##          Effect          W          p p<.05
## 2    Load 0.9782117 0.8570968
##
```

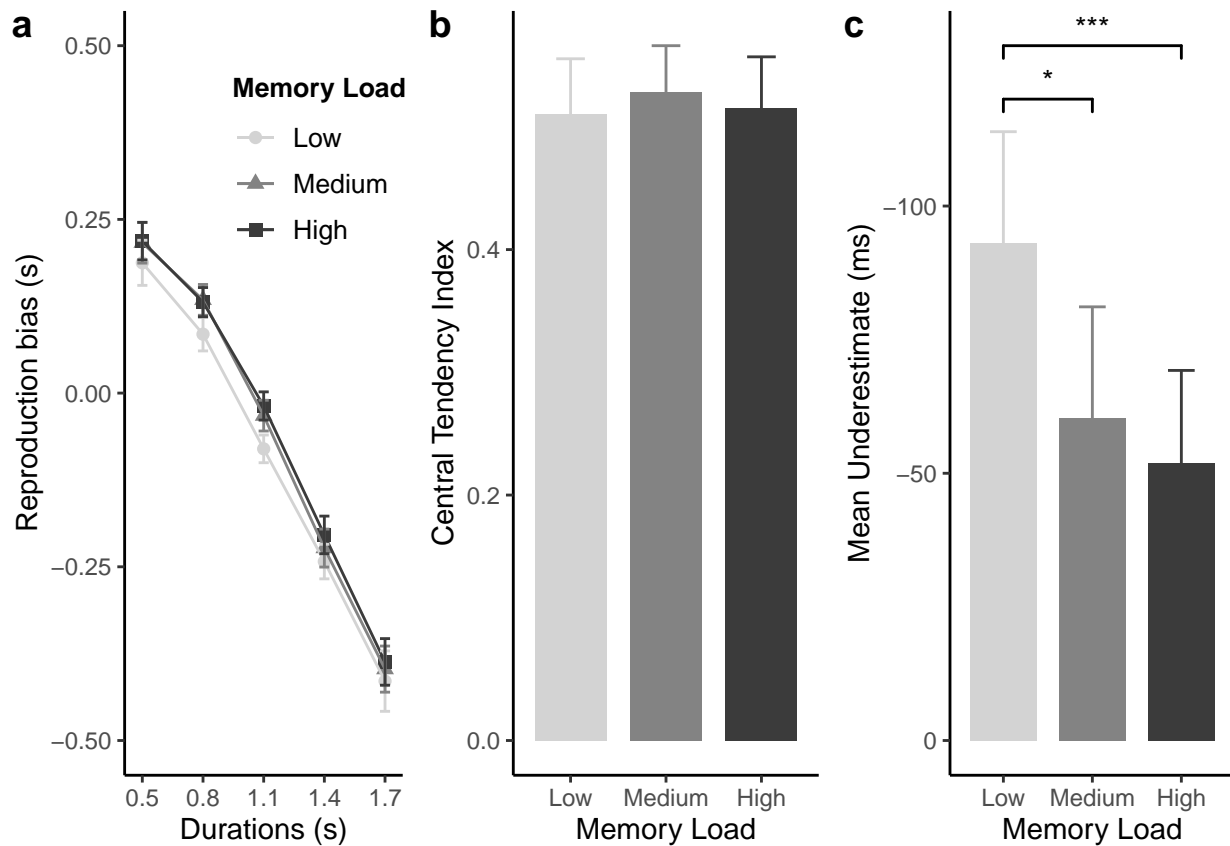
```
## $`Sphericity Corrections`
```

```
##          Effect          GGe          p[GG] p[GG]<.05          HFe          p[HF] p[HF]<.05
## 2    Load 0.9786763 1.729369e-13      * 1.123914 9.770098e-14      *
```

1.5 2. Working memory impacts on the reproduction phase

```
# reproduction manipulation
fig_reproduction = plot_fig('Reproduction', subfig = TRUE)
fig_reproduction$fig_c = fig_reproduction$fig_c +
  geom_signif(y_position = c(120, 130), xmin = c(1,1), xmax = c(2, 3), annotation = c("*", "***")) + ylab('')

fig_rp = plot_grid(fig_reproduction$fig_a, fig_reproduction$fig_b, fig_reproduction$fig_c, labels = c('a', 'b', 'c'))
# save figures
ggsave("./figures/fig_reproduction.png", fig_rp, width = 7, height = 3)
fig_rp
```



Now rmANOVA on reproduction biases, CTI and general biases

```
# rmANOVA on reproduction biases
av1 = mRep %>% filter(ExpName == 'Reproduction') %>%
  ezANOVA(dv = m_bias, wid = NSub, within = .(curDur, Load), detailed = TRUE)
print(av1$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	curDur	1	15	11.591282622	1.05861571	164.2420734	1.750724e-09	*
## 2	Load	2	30	0.075134954	0.08926041	12.6262500	1.050848e-04	*
## 3	curDur:Load	2	30	0.002401303	0.06627483	0.5434874	5.863297e-01	
##	ges							
## 1	0.905184705							
## 2	0.058276409							
## 3	0.001973859							

```

#rmANOVA on cti
av2 = mRep_cti %>% filter(ExpName == 'Reproduction') %>%
  ezANOVA(dv = cti, wid = NSub, within = Load, detailed = TRUE)
print(av2$ANOVA)

##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  15 12.879202913 1.1762397 164.2420734 1.750724e-09      *
## 2          Load    2  30  0.002668114 0.0736387   0.5434874 5.863297e-01
##          ges
## 1 0.911538595
## 2 0.002130152

#rmANOVA on general bias
av3 = mBias %>% filter(ExpName == 'Reproduction') %>%
  ezANOVA(dv = ms_bias, wid = NSub, within = Load, detailed = TRUE)
print(av3$ANOVA)

##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  15 224994.05 261627.36 12.89969 0.0026712111      *
## 2          Load    2  30 15026.99 17852.08 12.62625 0.0001050848      *
##          ges
## 1 0.44599777
## 2 0.05102432

# given the significant of memory load on general bias, we further conduct post hoc pairwise t-test
mBias %>% filter(ExpName == 'Reproduction') -> mBias_rp
pairwise.t.test(x = mBias_rp$ms_bias, g = mBias_rp$Load, paired = TRUE, p.adjust.method = 'holm')

##
## Pairwise comparisons using paired t tests
##
## data:  mBias_rp$ms_bias and mBias_rp$Load
##
##          Low      Medium
## Medium 0.0124 -
## High   0.0006 0.2376
##
## P value adjustment method: holm

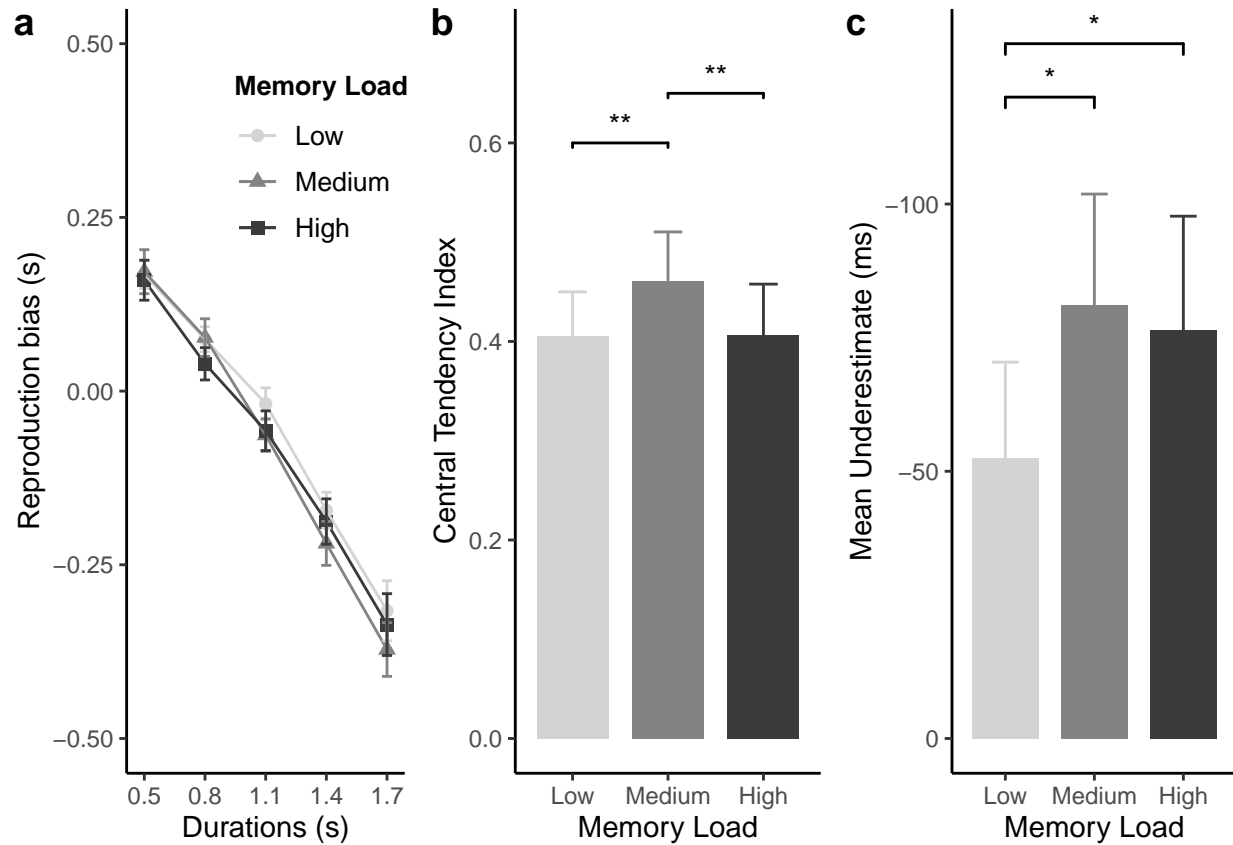
```

1.6 3. Working memory on both encoding and reproduction phases

```

# both manipulation
fig_both = plot_fig('Both', subfig = TRUE)
fig_both$fig_b = fig_both$fig_b +
  geom_signif(y_position = c(0.6, 0.65), xmin = c(1,2), xmax = c(2, 3), annotation = c("***", "**")) + y
fig_both$fig_c = fig_both$fig_c +
  geom_signif(y_position = c(120, 130), xmin = c(1,1), xmax = c(2, 3), annotation = c("*", "**")) + ylim
fig_bt = plot_grid(fig_both$fig_a, fig_both$fig_b, fig_both$fig_c, labels = c('a', 'b', 'c'), nrow = 1)
# save figures
ggsave("./figures/fig_both.png", fig_bt, width = 7, height = 3)
fig_bt

```



ANOVAs on reproduction biases, CTI and general biases

```
# rmANOVA on reproduction biases
av1 = mRep %>% filter(ExpName == 'Both') %>%
  ezANOVA(dv = m_bias, wid = NSub, within = .(curDur, Load), detailed = TRUE)
print(av1$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	curDur	1	15	7.77070236	1.47269604	79.147721	2.273681e-07	*
## 2	Load	2	30	0.03746856	0.07528366	7.465477	2.336867e-03	*
## 3	curDur:Load	2	30	0.02979912	0.06209241	7.198734	2.795412e-03	*
##	ges							
## 1				0.82836469				
## 2				0.02274212				
## 3				0.01817162				

```
# rmANOVA on cti
av2 = mRep_cti %>% filter(ExpName == 'Both') %>%
  ezANOVA(dv = cti, wid = NSub, within = Load, detailed = TRUE)
print(av2$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	(Intercept)	1	15	8.63411374	1.63632894	79.147721	2.273681e-07	*
## 2	Load	2	30	0.03311013	0.06899157	7.198734	2.795412e-03	*
##	ges							
## 1				0.83506636				
## 2				0.01904599				

```
#rmANOVA on general bias
```

```
av3 = mBias %>% filter(ExpName == 'Both') %>%
  ezANOVA(dv = ms_bias, wid = NSub, within = Load, detailed = TRUE)
print(av3$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  15 235369.803 273998.56 12.885276 0.002682227      *
## 2          Load    2  30   7493.713  15056.73   7.465477 0.002336867      *
##          ges
## 1 0.44881491
## 2 0.02526973
```

Post hoc pairwise t-test on general bias

```
mBias %>% filter(ExpName == 'Both') -> mBias_bt
pairwise.t.test(x = mBias_bt$ms_bias, g = mBias_bt$Load, paired = TRUE, p.adjust.method = 'holm')
```

```
##
## Pairwise comparisons using paired t tests
##
## data: mBias_bt$ms_bias and mBias_bt$Load
##
##          Low    Medium
## Medium 0.013 -
## High   0.039 0.428
##
## P value adjustment method: holm
```

Post hoc pairwise t-test on cti

```
mRep_cti %>% filter(ExpName == 'Both') -> mRep_cti_bt
pairwise.t.test(x = mRep_cti_bt$cti, g = mRep_cti_bt$Load, paired = TRUE, p.adjust.method = 'holm')
```

```
##
## Pairwise comparisons using paired t tests
##
## data: mRep_cti_bt$cti and mRep_cti_bt$Load
##
##          Low    Medium
## Medium 0.0097 -
## High   0.9564 0.0097
##
## P value adjustment method: holm
```

1.7 4. Working memory on both encoding and reproduction phases with gap

```
# both manipulation with gap
```

```
fig_a = mRep %>% filter(ExpName == 'Both_gap', gap == 1) %>% plot_cti() + #add text 'Short Gap' on the
  geom_text(aes(x = 0.8, y = 0.5, label = 'Short Gap'), size = 3, color = 'black') +
  theme(axis.title.x=element_blank(), axis.text.x=element_blank(), axis.ticks.x=element_blank(), legend
fig_b = mRep_cti %>% filter(ExpName == 'Both_gap', gap == 1) %>% plot_cti_Load() +
  theme(axis.title.x=element_blank(), axis.text.x=element_blank(), axis.ticks.x=element_blank())
fig_c = mBias %>% filter(ExpName == 'Both_gap', gap == 1) %>% plot_bias_Load()
```

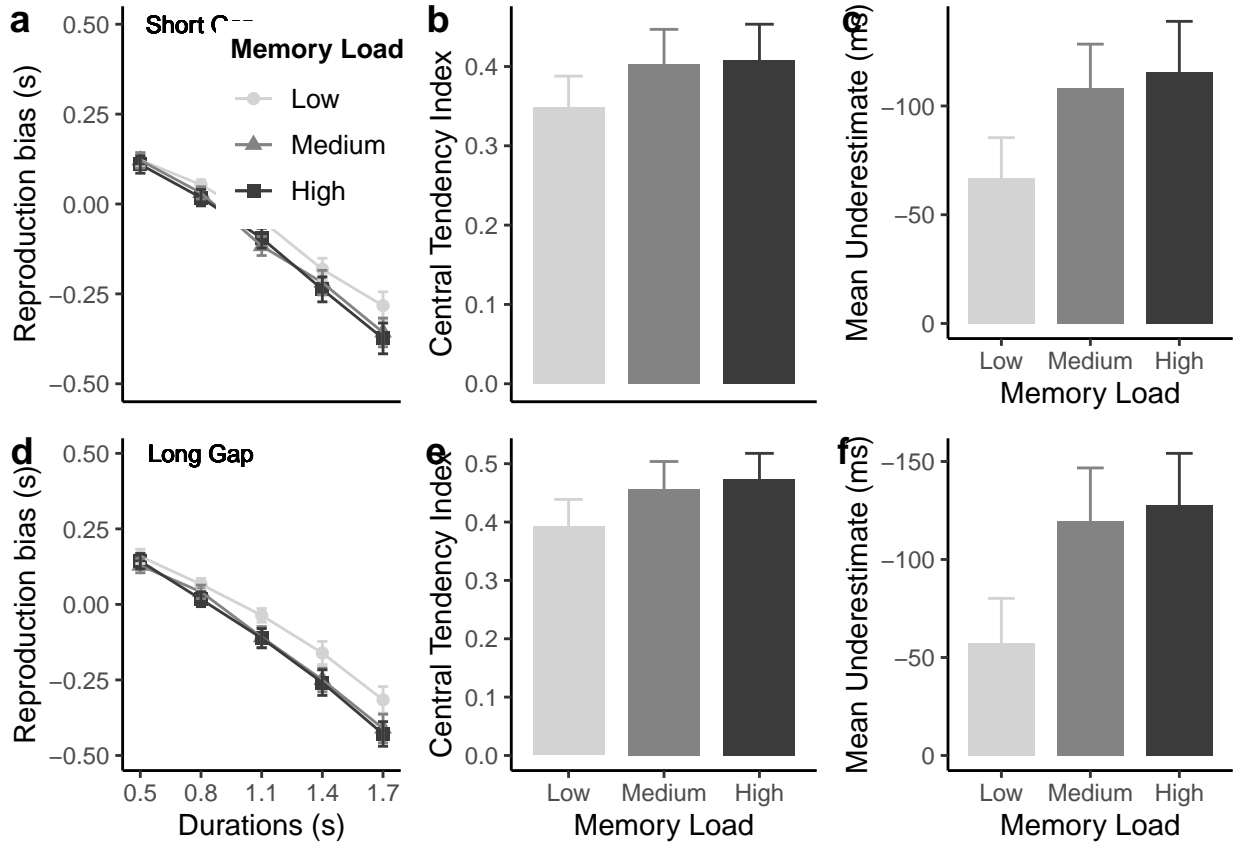


```

fig_a2 = mRep %>% filter(ExpName == 'Both_gap', gap == 2) %>% plot_cti() + # remove legend
  geom_text(aes(x = 0.8, y = 0.5, label = 'Long Gap'), size = 3, color = 'black') +
  theme(legend.position = "none")
fig_b2 = mRep_cti %>% filter(ExpName == 'Both_gap', gap == 2) %>% plot_cti_Load()
fig_c2 = mBias %>% filter(ExpName == 'Both_gap', gap == 2) %>% plot_bias_Load()

# combine figures
fig_gap = plot_grid(fig_a, fig_b, fig_c, fig_a2, fig_b2, fig_c2, labels = c('a', 'b', 'c', 'd', 'e', 'f'))
# save figure
ggsave("./figures/fig_gap.png", fig_gap, width = 7, height = 6)
fig_gap

```



ANOVAs on reproduction biases, CTI and general biases

```

# rmANOVA on reproduction biases
av1 = mRep %>% filter(ExpName == 'Both_gap') %>% mutate(gap = as.factor(gap)) %>%
  ezANOVA(dv = m_bias, wid = NSub, within = .(curDur, Load, gap), detailed = TRUE)
print(av1$ANOVA)

```

##	Effect	DFn	DFd	SSn	SSd	F	p	p < .05
## 1	curDur	1	15	14.769798631	2.33210332	94.9987841	6.995472e-08	*
## 2	Load	2	30	0.335512188	0.50079354	10.0494165	4.564620e-04	*
## 3	gap	1	15	0.002752928	0.10622926	0.3887246	5.423358e-01	
## 4	curDur:Load	2	30	0.081758356	0.13899499	8.8231620	9.691206e-04	*
## 5	curDur:gap	1	15	0.064638396	0.07475635	12.9698135	2.618334e-03	*
## 6	Load:gap	2	30	0.011958925	0.05465190	3.2822990	5.139333e-02	
## 7	curDur:Load:gap	2	30	0.001681400	0.04016814	0.6278857	5.405869e-01	
##	ges							

```
## 1 0.8197475677
## 2 0.0936345392
## 3 0.0008469375
## 4 0.0245560716
## 5 0.0195144449
## 6 0.0036687686
## 7 0.0005174528

#rmANOVA on cti
av2 = mRep_cti %>% filter(ExpName == 'Both_gap') %>% mutate(gap = as.factor(gap)) %>%
  ezANOVA(dv = cti, wid = NSub, within = .(Load, gap), detailed = TRUE)
print(av2$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	(Intercept)	1	15	16.410887368	2.59122591	94.9987841	6.995472e-08	*
## 2	Load	2	30	0.090842618	0.15443888	8.8231620	9.691206e-04	*
## 3	gap	1	15	0.071820440	0.08306261	12.9698135	2.618334e-03	*
## 4	Load:gap	2	30	0.001868222	0.04463127	0.6278857	5.405869e-01	

ges

## 1	0.8509996882
## 2	0.0306465754
## 3	0.0243857632
## 4	0.0006497652

```
#rmANOVA on general bias
av3 = mBias %>% filter(ExpName == 'Both_gap') %>% mutate(gap = as.factor(gap)) %>%
  ezANOVA(dv = ms_bias, wid = NSub, within = .(Load, gap), detailed = TRUE)
print(av3$ANOVA)
```

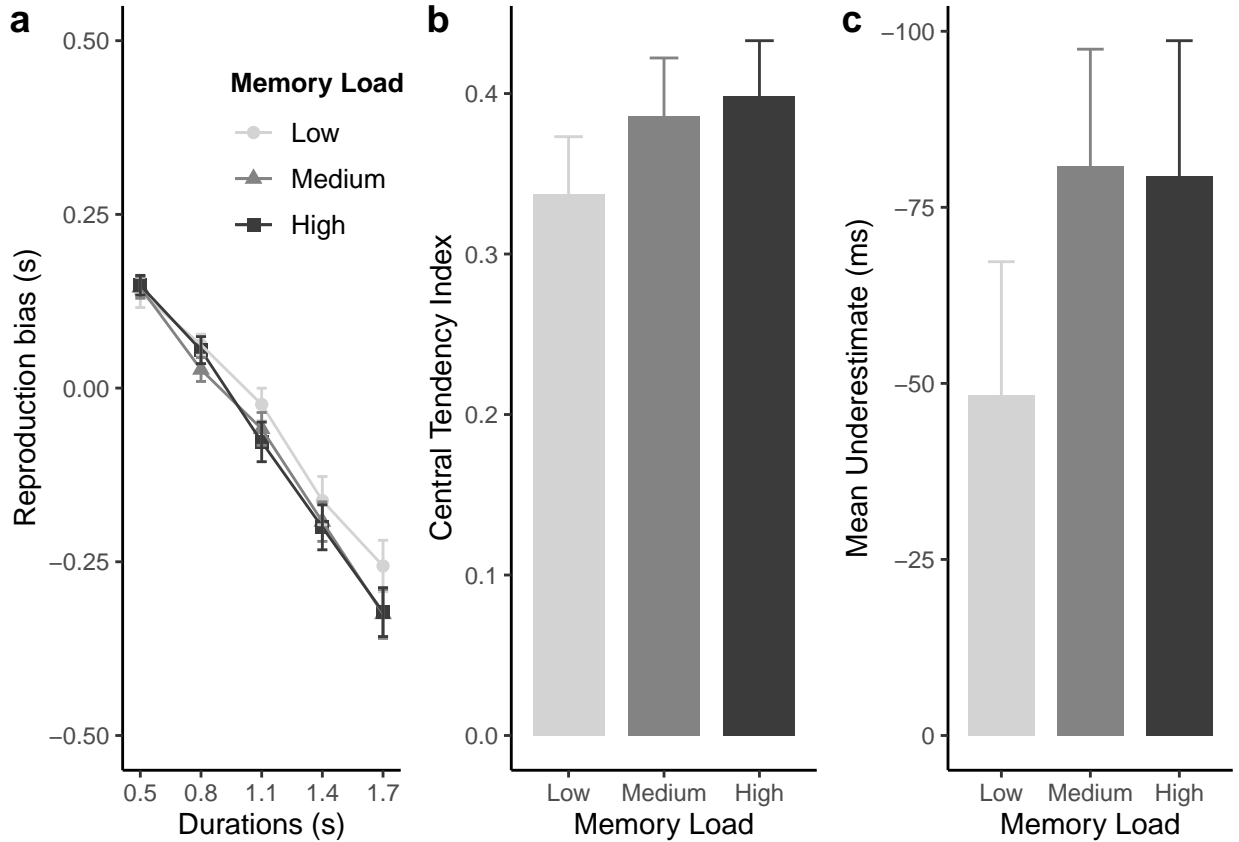
##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	(Intercept)	1	15	946497.0875	642354.82	22.1022024	0.0002839936	*
## 2	Load	2	30	67102.4377	100158.71	10.0494165	0.0004564620	*
## 3	gap	1	15	550.5857	21245.85	0.3887246	0.5423357620	
## 4	Load:gap	2	30	2391.7851	10930.38	3.2822990	0.0513933324	

ges

## 1	0.5499095509
## 2	0.0797137793
## 3	0.0007102129
## 4	0.0030779074

2 5. working memory on encoding 2 (within-subject design)

```
# encoding manipulation
fig_encoding2 = plot_fig('Encoding2')
fig_encoding2
```



Now rmANOVA on reproduction biases, CTI and general biases

```
# rmANOVA on reproduction biases
av1 = mRep %>% filter(ExpName == 'Encoding2') %>%
  ezANOVA(dv = m_bias, wid = NSub, within = .(curDur, Load), detailed = TRUE)
print(av1$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	curDur	1	17	6.79976474	0.97028396	119.136259	4.227922e-09	*
## 2	Load	2	34	0.06111974	0.25564376	4.064389	2.613973e-02	*
## 3	curDur:Load	2	34	0.03415354	0.06270192	9.259845	6.161196e-04	*
##	ges							
## 1				0.84068165				
## 2				0.04528229				
## 3				0.02581945				

```
#rmANOVA on cti
av2 = mRep_cti %>% filter(ExpName == 'Encoding2') %>%
  ezANOVA(dv = cti, wid = NSub, within = Load, detailed = TRUE)
print(av2$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	(Intercept)	1	17	7.55529416	1.0780933	119.136259	4.227922e-09	*
## 2	Load	2	34	0.03794837	0.0696688	9.259845	6.161196e-04	*
##	ges							
## 1				0.86811965				
## 2				0.03200475				

```
#rmANOVA on general bias
```

```
av3 = mBias %>% filter(ExpName == 'Encoding2') %>%
  ezANOVA(dv = ms_bias, wid = NSub, within = Load, detailed = TRUE)
print(av3$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1   17 261276.85 255606.60 17.377120 0.000643839      *
## 2          Load    2   34  12223.95   51128.75   4.064389 0.026139730      *
##          ges
## 1 0.45998457
## 2 0.03832448
```

Post hoc pairwise t-test on general bias

```
mBias %>% filter(ExpName == 'Encoding2') -> mBias_rp
pairwise.t.test(x = mBias_rp$ms_bias, g = mBias_rp$Load, paired = TRUE, p.adjust.method = 'holm')
```

```
##
## Pairwise comparisons using paired t tests
##
## data: mBias_rp$ms_bias and mBias_rp$Load
##
##          Low   Medium
## Medium 0.077 -
## High   0.151 0.848
##
## P value adjustment method: holm
```

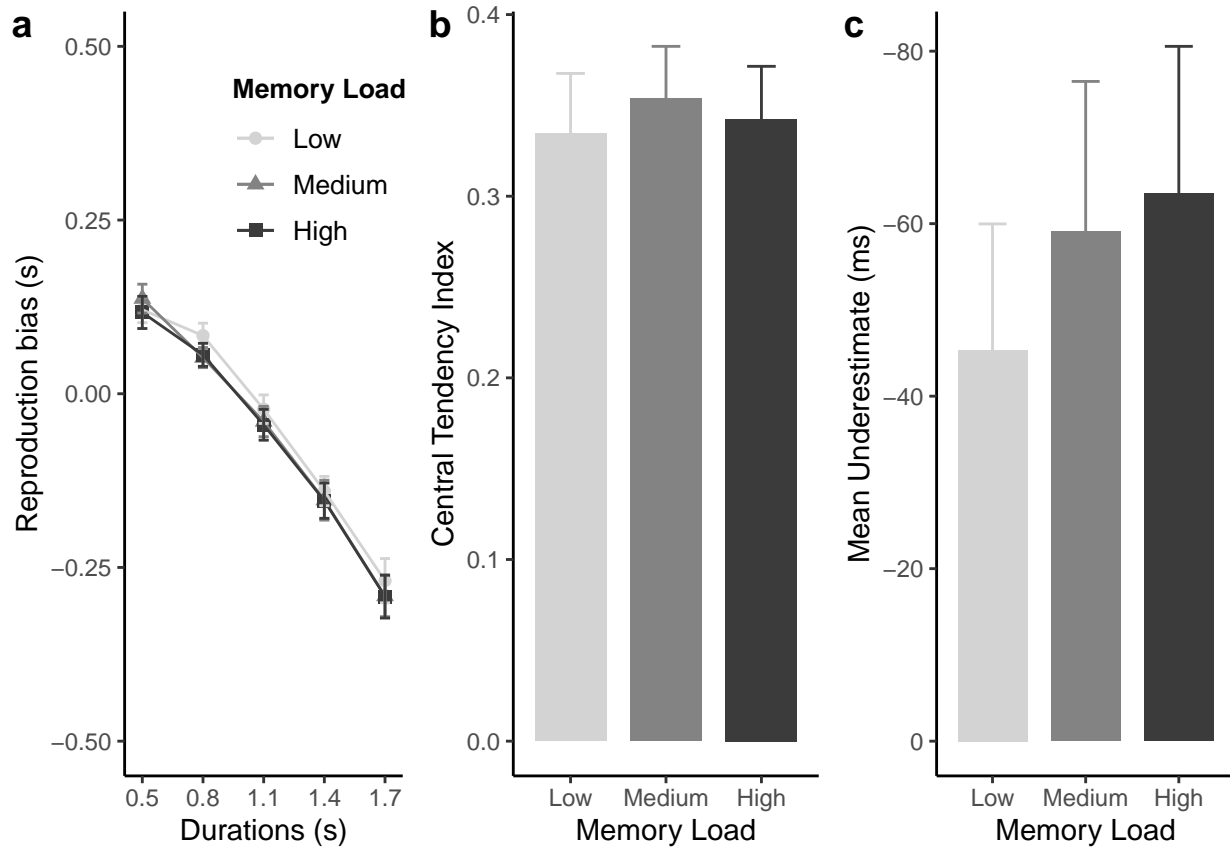
Post hoc pairwise t-test on cti

```
mRep_cti %>% filter(ExpName == 'Encoding2') -> mRep_cti_rp
pairwise.t.test(x = mRep_cti_rp$cti, g = mRep_cti_rp$Load, paired = TRUE, p.adjust.method = 'holm')
```

```
##
## Pairwise comparisons using paired t tests
##
## data: mRep_cti_rp$cti and mRep_cti_rp$Load
##
##          Low   Medium
## Medium 0.0032 -
## High   0.0015 0.4935
##
## P value adjustment method: holm
```

3 6. working memory on reproduction 2 (within-subject design)

```
# reproduction manipulation
fig_reproduction2 = plot_fig('Reproduction2')
fig_reproduction2
```



Now rmANOVA on reproduction biases, CTI and general biases

```
# rmANOVA on reproduction biases
av1 = mRep %>% filter(ExpName == 'Reproduction2') %>%
  ezANOVA(dv = m_bias, wid = NSub, within = .(curDur, Load), detailed = TRUE)
print(av1$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	curDur	1	17	5.738532640	0.66508475	146.6806379	8.737141e-10	*
## 2	Load	2	34	0.016109655	0.08553925	3.2016196	5.321897e-02	
## 3	curDur:Load	2	34	0.003033015	0.09395962	0.5487596	5.826965e-01	
##	ges							
## 1	0.871704587							
## 2	0.018717068							
## 3	0.003578286							

```
#rmANOVA on cti
av2 = mRep_cti %>% filter(ExpName == 'Reproduction2') %>%
  ezANOVA(dv = cti, wid = NSub, within = Load, detailed = TRUE)
print(av2$ANOVA)
```

##	Effect	DFn	DFd	SSn	SSd	F	p	p<.05
## 1	(Intercept)	1	17	6.376147378	0.7389831	146.6806379	8.737141e-10	*
## 2	Load	2	34	0.003370016	0.1043996	0.5487596	5.826965e-01	
##	ges							
## 1	0.88318040							
## 2	0.00397993							

```
#rmANOVA on general bias
```

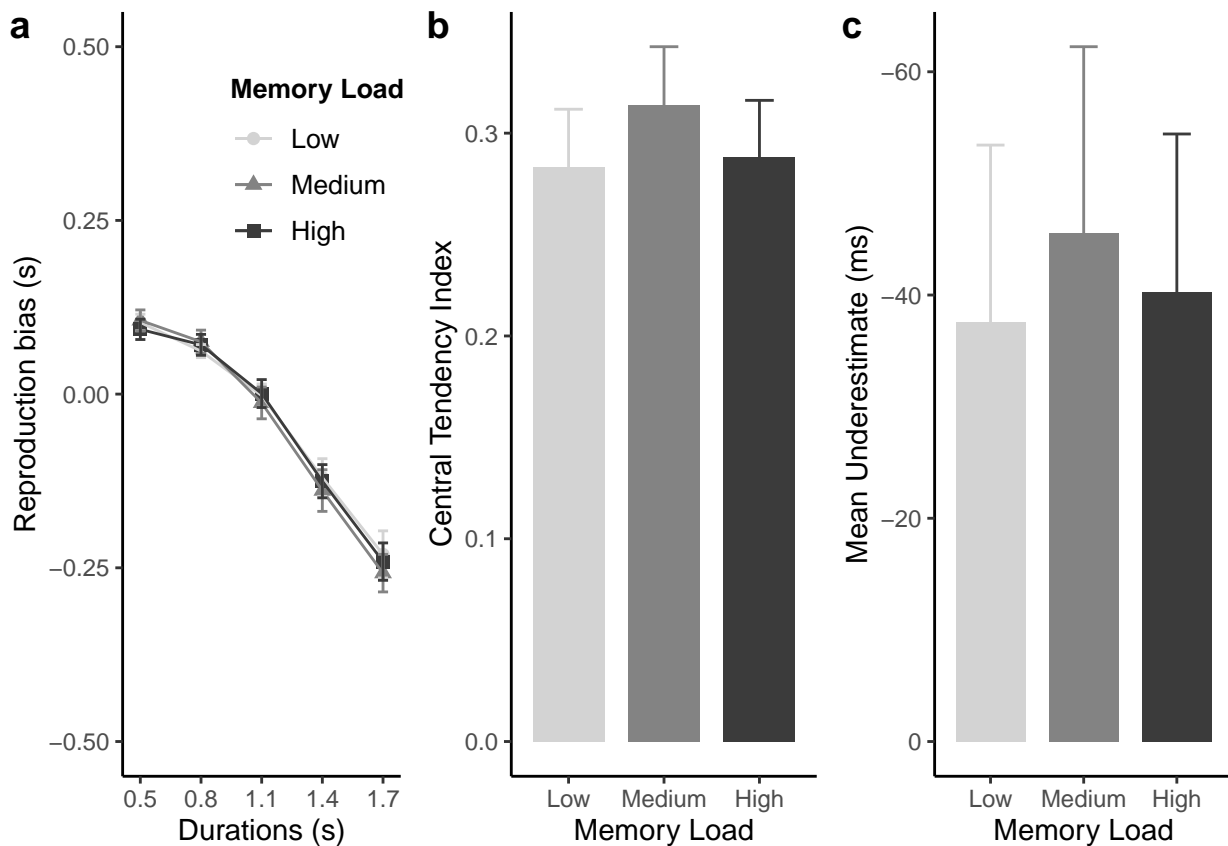
```
av3 = mBias %>% filter(ExpName == 'Reproduction2') %>%
  ezANOVA(dv = ms_bias, wid = NSub, within = Load, detailed = TRUE)
print(av3$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1   17 169106.747 230592.43 12.46708 0.002566336      *
## 2          Load    2   34   3221.931  17107.85   3.20162 0.053218967
##          ges
## 1 0.40571952
## 2 0.01284036
```

Results showed only the main effect of Duration. Memory loads were marginal. . .

4 7. working memory on baseline 2 (within-subject design)

```
# baseline manipulation
fig_baseline2 = plot_fig('baseline2')
fig_baseline2
```



Now rmANOVA on reproduction biases, CTI and general biases

```
# rmANOVA on reproduction biases
```

```
av1 = mRep %>% filter(ExpName == 'baseline2') %>%
  ezANOVA(dv = m_bias, wid = NSub, within = .(curDur, Load), detailed = TRUE)
print(av1$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1      curDur    1  17 4.233692214 0.61651895 116.740560 4.922194e-09      *
## 2          Load    2  34 0.002916080 0.04861866   1.019637 3.714917e-01
## 3 curDur:Load    2  34 0.008762427 0.04946308   3.011564 6.249625e-02
##          ges
## 1 0.855586420
## 2 0.004064129
## 3 0.012113456
```

```
#rmANOVA on cti
av2 = mRep_cti %>% filter(ExpName == 'baseline2') %>%
  ezANOVA(dv = cti, wid = NSub, within = Load, detailed = TRUE)
print(av2$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  17 4.70410246 0.68502106 116.740560 4.922194e-09      *
## 2          Load    2  34 0.00973603 0.05495898   3.011564 6.249625e-02
##          ges
## 1 0.86407626
## 2 0.01298629
```

```
#rmANOVA on general bias
av3 = mBias %>% filter(ExpName == 'baseline2') %>%
  ezANOVA(dv = ms_bias, wid = NSub, within = Load, detailed = TRUE)
print(av3$ANOVA)
```

```
##          Effect DFn DFd          SSn          SSd          F          p p<.05
## 1 (Intercept)    1  17 91376.2002 213761.839 7.266944 0.01531098      *
## 2          Load    2  34  583.2161  9723.731 1.019637 0.37149172
##          ges
## 1 0.290210527
## 2 0.002602844
```

Only the main effect of Duration was significant.