Reanalysis of 26-Keane

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Contents

Reference

Keane, B. P., Paterno, D., Kastner, S., Krekelberg, B., & Silverstein, S. M. (2019). Intact illusory contour formation but equivalently impaired visual shape completion in first- and later-episode schizophrenia. Journal of Abnormal Psychology, 128(1), 57–68. https://doi.org/10.1037/abn0000384

Notes from reading methods section

This study tested three groups, healthy controls, first-espisode psychotic patients and chronic schizophrenia patients using a visual shape completition task. * Dependant variable: threshold values (log deg of rotation) *

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Independent variables: * relatability (illusory, fragmented) * contour type (traditional, wire) * patient group (control (n = 48), first episode (n = 23), chronic (n = 49)) * Covariate: * Chlorpromazine equivalent does (CPZ) * Design: 2 (w) x 2 (w) x 3 (b) mixed ANCOVA (w within; b between)

Reading data

Data is loaded, reshaped into long form, and factors are specified.

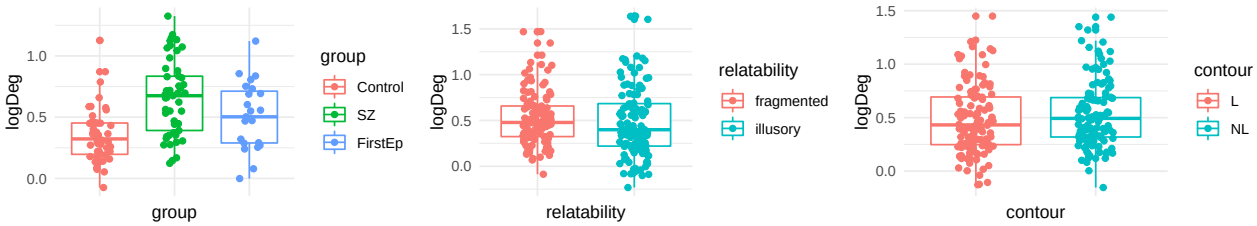
```
##        id           age            logDeg            relatability contour
##  SF001F :  4   Min.   :18.00   Min.   :-0.4250   fragmented:240   L :240
##  SF001S :  4   1st Qu.:24.75   1st Qu.: 0.2578   illusory  :240   NL:240
##  SF002C :  4   Median :33.50   Median : 0.4436
##  SF002F :  4   Mean   :37.13   Mean   : 0.5075
##  SF002S :  4   3rd Qu.:50.00   3rd Qu.: 0.6815
##  SF003C :  4   Max.   :64.00   Max.   : 1.6448
##  (Other):456
##      group          CPZ
##  Control:192   Min.   :   0.0
##  SZ     :196   1st Qu.: 227.3
##  FirstEp: 92   Median : 400.0
##                Mean   : 440.0
##                3rd Qu.: 564.0
##                Max.   :1358.7
##                NA's   :220
```

Descriptives

Dependant variable

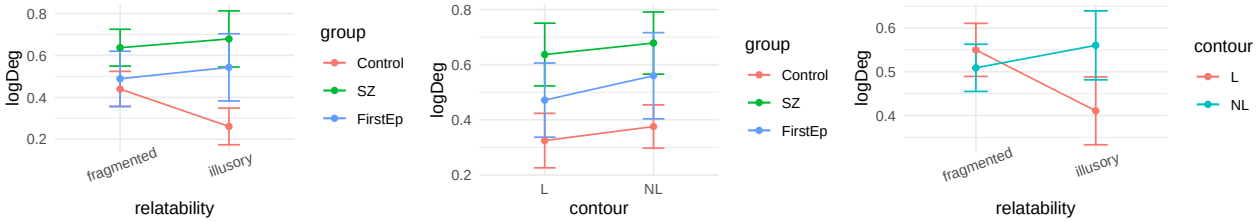
Number of samples and mean (SD) in levels of the independent variables. We reproduce Table 3 and Figure 2A of the study.

```
d.1 = aggregate(. ~ id*group, data = data, FUN = mean, na.rm=TRUE, na.action = "na.pass")
d.2 = aggregate(. ~ id*relatability, data = data, FUN = mean, na.rm=TRUE, na.action = "na.pass")
d.3 = aggregate(. ~ id*contour, data = data, FUN = mean, na.rm=TRUE, na.action = "na.pass")

p1 = ggplot(d.1, aes(y=logDeg, x=group, color=group)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = 0.15, height = 0)) +
  theme_minimal() + theme(axis.text.x = element_blank())

p2 = ggplot(d.2, aes(y=logDeg, x=relatability, color=relatability)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = 0.15, height = 0)) +
  theme_minimal() + theme(axis.text.x = element_blank())

p3 = ggplot(d.3, aes(y=logDeg, x=contour, color=contour)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = 0.15, height = 0)) +
 theme_minimal() + theme(axis.text.x = element_blank())

plot_grid(p1, p2, p3, nrow = 1, ncol = 3)
```



Averaging subjects across along the third factor to see the two-way interactions. Plots show means (95%-CI as error bar)

```
d.A = aggregate(logDeg ~ group*relatability, data = data, FUN = mean)
d.B = aggregate(logDeg ~ group*contour, data = data, FUN = mean)
d.C = aggregate(logDeg ~ relatability*contour, data = data, FUN = mean)

# get SD
d.A$sd = aggregate(logDeg ~ group*relatability, data = data, FUN = sd)[,3]
d.A$se = d.A$sd/sqrt(rep(c(48, 49, 23), 2))

d.B$sd = aggregate(logDeg ~ group*contour, data = data, FUN = sd)[,3]
d.B$se = d.B$sd/sqrt(rep(c(48, 49, 23), 2))

d.C$sd = aggregate(logDeg ~ relatability*contour, data = data, FUN = sd)[,3]
d.C$se = d.C$sd/sqrt(rep(N, 4))

pA = ggplot(d.A, aes(y=logDeg, x=relatability, group=group, color=group)) +
  geom_errorbar(aes(ymin=logDeg-1.96*se, ymax=logDeg+1.96*se), width=.2) +
  geom_line() + geom_point() +
  theme_minimal() + theme(axis.text.x = element_text(angle = 20) )

pB = ggplot(d.B, aes(y=logDeg, x=contour, group=group, color=group)) +
  geom_errorbar(aes(ymin=logDeg-1.96*se, ymax=logDeg+1.96*se), width=.2) +
  geom_line() + geom_point() +
  theme_minimal()

pC = ggplot(d.C, aes(y=logDeg, x=relatability, group=contour, color=contour)) +
  geom_errorbar(aes(ymin=logDeg-1.96*se, ymax=logDeg+1.96*se), width=.2) +
  geom_line() + geom_point() +
  theme_minimal() + theme(axis.text.x = element_text(angle = 20))

plot_grid(pA, pB, pC, nrow = 1, ncol = 3)
```



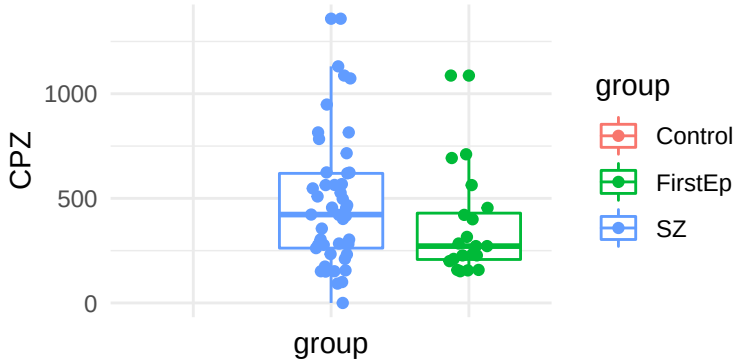
Covariate(s)

The two covariates are DASS_tot scores and log of time.

```
ggplot(d.1, aes(y=CPZ, x=group, color=group)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = 0.15, height = 0)) +
  theme_minimal() + theme(axis.text.x = element_blank())
```

```
## Warning: Removed 55 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 55 rows containing missing values (geom_point).
```



Main analysis ANCOVA

Independent variable: TAS_group (Between Group)

```
# Orthogonal contrasts
contrasts(data$group) = contr.helmert(3)
contrasts(data$relatability) = contr.helmert(2)
contrasts(data$contour) = contr.helmert(2)
```

ANOVA was reported completely, but ANCOVA with a covariate only incompletely.

```
fit.ancova = ezANOVA(dv = .(logDeg), wid = .(id), between = .(group), within = .(relatability, contour)
                     type=3, detailed=TRUE,  data = data)
```

```
## Warning: Data is unbalanced (unequal N per group). Make sure you specified a
## well-considered value for the type argument to ezANOVA().
```

```
print(fit.ancova)
```

```
## $ANOVA
##                         Effect DFn DFd          SSn       SSd           F
## 1                  (Intercept)   1 117 109.62916777 33.889952 378.4783326
## 2                        group   2 117   9.17508513 33.889952  15.8378057
## 3                 relatability   1 117   0.08015607 13.970034   0.6713126
## 5                      contour   1 117   0.38669038  4.793175   9.4389997
## 4           group:relatability   2 117   1.45289310 13.970034   6.0840402
## 6                group:contour   2 117   0.03486400  4.793175   0.4255100
## 7         relatability:contour   1 117   0.73937624  6.546627  13.2139838
## 8 group:relatability:contour   2 117   0.13766369  6.546627   1.2301489
##                p p<.05          ges
## 1 1.795642e-38     * 0.6493505081
## 2 8.181794e-07     * 0.1341879670
## 3 4.142602e-01       0.0013521617
## 5 2.642646e-03     * 0.0064895660
```

```
## 4 3.064033e-03     * 0.0239543098
## 6 6.544435e-01       0.0005885744
## 7 4.142721e-04     * 0.0123354447
## 8 2.960007e-01       0.0023200135
```

Checking interactions of the covariate CPZ with other variables using a linear mixed model as CPZ has inclompelte data.

```
mod1 = lme(logDeg ~ CPZ + group*relatability*contour, data=data, na.action = na.exclude, random = ~1|id,
```

```
## Warning: contrasts dropped from factor group due to missing levels
```

```
result.lme = anova(mod1, type="marginal")
print(result.lme)
```

```
##                              numDF denDF  F-value p-value
## (Intercept)                      1   126 88.48919  <.0001
## CPZ                              1    62  0.33847  0.5628
## group                            1    62  6.05944  0.0166
## relatability                     1    63  1.63038  0.2063
## contour                          1   126  1.63225  0.2037
## group:relatability               1    63  0.02899  0.8653
## group:contour                    1   126  0.06417  0.8004
## relatability:contour             1   126  8.21206  0.0049
## group:relatability:contour       1   126  2.02018  0.1577
```

Comparing ANCOVA in original study with reanalysis

Independant variable

Main effect group

```
tab.IV = rbind(stats.orig.IV.group, stats.rep.IV.group)
rownames(tab.IV) = c("original Study", "reanalysis type III SS")
print(t(tab.IV))
```

```
##        original Study reanalysis type III SS
## Fvalue "15.8"         "15.84"
## df1    "2"            "2"
## df2    "117"          "117"
## pvalue "p < 0.001"    "< 0.0001"
```

Main effect contour

```
tab.IV = rbind(stats.orig.IV.cont, stats.rep.IV.cont)
rownames(tab.IV) = c("original Study", "reanalysis type III SS")
print(t(tab.IV))
```

```
##        original Study reanalysis type III SS
## Fvalue "9.4"          "9.44"
## df1    "1"            "1"
## df2    "117"          "117"
## pvalue "0.003"        "0.003"
```

Interaction group X relatability

```
tab.IV = rbind(stats.orig.IV.groupXrelat, stats.rep.IV.groupXrelat)
rownames(tab.IV) = c("original Study", "reanalysis type III SS")
print(t(tab.IV))
```

```
##        original Study reanalysis type III SS
## Fvalue "6.1"          "6.08"
## df1    "2"            "2"
## df2    "117"          "117"
## pvalue "0.003"        "0.003"
```

Interaction contour X relatability

```
tab.IV = rbind(stats.orig.IV.relatXcont, stats.rep.IV.relatXcont)
rownames(tab.IV) = c("original Study", "reanalysis type III SS")
print(t(tab.IV))
```

```
##        original Study reanalysis type III SS
## Fvalue "13.2"         "13.21"
## df1    "1"            "1"
## df2    "117"          "117"
## pvalue "p < 0.001"    "0.0004"
```

Interaction group X relatability X contour

```
tab.IV = rbind(stats.orig.IV.groupXrelatXcont, stats.rep.IV.groupXrelatXcont)
rownames(tab.IV) = c("original Study", "reanalysis type III SS")
print(t(tab.IV))
```

```
##        original Study reanalysis type III SS
## Fvalue "1.2"          "1.23"
## df1    "2"            "2"
## df2    "117"          "117"
## pvalue "0.296"        "0.30"
```

Covariate

```
tab.CV = rbind(stats.orig.CV, stats.rep.CV)
rownames(tab.CV) = c("original Study", "reanalysis type I SS")
print(t(tab.CV))
```

```
##        original Study  reanalysis type I SS
## Fvalue NA              "0.34"
## df1    NA              " 1"
## df2    NA              "62"
## pvalue "all ps > 0.60" "0.56"
```

Assumptions

1. Homogeneity of variance

- ANOVA/ANCOVA is fairly robust in terms of the error rate when sample sizes are equal.
- When groups with larger sample sizes have larger variances than the groups with smaller sample sizes, the resulting F-ratio tends to be conservative. That is, it's more likely to produce a non-significant result when a genuine difference does exist in the population.

- Conversely, when the groups with larger sample sizes have smaller variances than the groups with smaller samples sizes, the resulting F-ratio tends to be liberal and can inflate the false positive rate.

```
tapply(d.1$logDeg, d.1$group, sd)
```

```
##   Control        SZ   FirstEp
## 0.2215591 0.3066081 0.2741038
```

```
leveneTest(logDeg ~ group, data = d.1)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value  Pr(>F)
## group   2  3.4726 0.03427 *
##       117
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2. Independence between covariate and IV.

When the covariate and the experimental effect (independent variable) are not independent the treatment effect is obscured, spurious treatment effects can arise and the interpretation of the ANCOVA is seriously compromised.

We test whether our groups differ on the CV. If the groups do not significantly differ then is appropriate to use the covariate.

```
fit.cv1 = aov(CPZ ~ group, data = d.1)
summary(fit.cv1)
```

```
##             Df  Sum Sq Mean Sq F value Pr(>F)
## group        1  186302  186302   2.235   0.14
## Residuals   63 5251381   83355
## 55 observations deleted due to missingness
```

3. Homogeneity of regression slopes

```
fit.hrs = aov(logDeg ~ CPZ*group, data = d.1)
Anova(fit.hrs, type = "III")
```

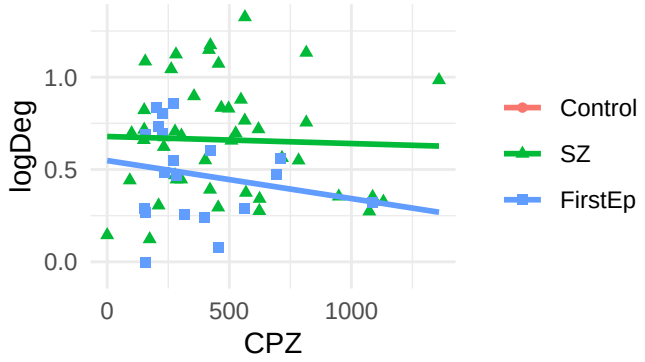
```
## Anova Table (Type III tests)
##
## Response: logDeg
##             Sum Sq Df F value   Pr(>F)
## (Intercept) 5.9951  1 69.9641 1.04e-11 ***
## CPZ         0.0060  1  0.0701   0.7920
## group       0.0697  1  0.8130   0.3708
## CPZ:group   0.0246  1  0.2869   0.5942
## Residuals   5.2270 61
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(d.1, aes(y=logDeg, x=CPZ, color=group, shape=group)) +
  geom_point() +
  geom_smooth(formula = y ~ x,method=lm, se=FALSE, fullrange=TRUE) +
```

```
  theme_minimal() +
  theme(legend.title = element_blank())
```

```
## Warning: Removed 55 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 55 rows containing missing values (geom_point).
```



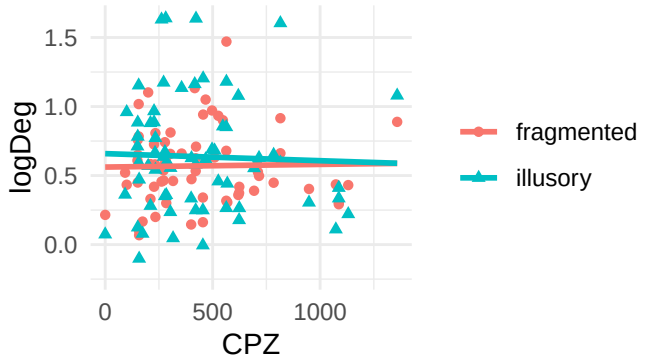

```
mod1 = lme(logDeg ~ CPZ + group*relatability, data=d.2, na.action = na.exclude, random = ~1|id/relatabil
result.lme = anova(mod1, type="marginal")
print(result.lme)
```

```
##                     numDF denDF   F-value p-value
## (Intercept)             1    63 19.081155  <.0001
## CPZ                     1    62  0.337127  0.5636
## group                   1    62  3.916756  0.0523
## relatability            1    63  0.197828  0.6580
## group:relatability      1    63  0.028879  0.8656
```

```
ggplot(d.2, aes(y=logDeg, x=CPZ, color=relatability, shape=relatability)) +
  geom_point() +
  geom_smooth(formula = y ~ x,method=lm, se=FALSE, fullrange=TRUE) +
  theme_minimal() +
  theme(legend.title = element_blank())
```

```
## Warning: Removed 110 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 110 rows containing missing values (geom_point).
```




```
mod1 = lme(logDeg ~ CPZ + group*contour, data=d.3, na.action = na.exclude, random = ~1|id/contour, metho
result.lme = anova(mod1, type="marginal")
print(result.lme)
```

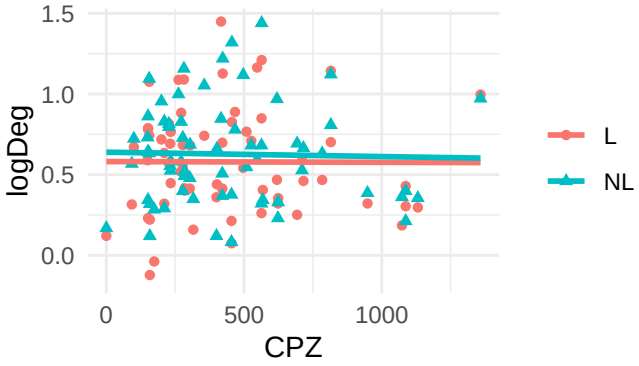
```
##                numDF denDF   F-value p-value
```

```
## (Intercept)       1    63 25.243911  <.0001
## CPZ               1    62  0.337127  0.5636
## group             1    62  5.782202  0.0192
## contour           1    63  0.008563  0.9266
## group:contour     1    63  0.074571  0.7857
```

```
ggplot(d.3, aes(y=logDeg, x=CPZ, color=contour, shape=contour)) +
  geom_point() +
  geom_smooth(formula = y ~ x,method=lm, se=FALSE, fullrange=TRUE) +
  theme_minimal() +
  theme(legend.title = element_blank())
```

```
## Warning: Removed 110 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 110 rows containing missing values (geom_point).
```



Notes

- Five subjects were excluded, but this was reported in the paper.
- Results from ANCOVA were not fully reported but result from ANOVA were reported and reproduced. The authors performed an ANCOVA to find no influence of chlorpromazine and then conducted and reported ANOVAs instead due to missingness on the covariate.
- Multiple follow-up ANOVAs were reported which may not be necessary and required to adjust for multiplicity, but such a correction was not performed.
- Some non-significant effects and interactions were not reported (main effect repeatability and interaction group X contour).
- The result from the ANCOVA was not clearly reported, the covariate CPZ was reported as "medication did not interact with any other variable (all ps>.6). But ANCOVA tests an overall effect of CPZ on the outcome and produces a single p-value.
- Homogeneity of variances was not met for groups.
- Independence between covariate CPZ and the IV group was met, but controls had no CPZ value.
- Homogeneity of regression slopes was met at least for the patient groups as controls had missingness.

Data was analyzed according to recommendations by Field, Miles, & Field (2012).