coAuthor-ENA

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Load packages	
rm(list=ls()) #clear environment	
library(rENA) #library(ona) #library(tma) library(tidyverse) #for wrangling library(lmerTest) #for hlms library(ICC) #for testing clustering of observations library(emmeans) #for comparing subpopulations	
library(performance) #for regression diagnostics	

Prep data

Read data

Add metadata

```
#data1 = left_join(data1,meta_coauthor,by = c("worker_id","session_id"))
```

Prep for ENA model

```
# units = data1[,c("session id",
#
                   "worker id")]
#
#
# conversation = data1[,c("session_id",
                           "worker_id",
                           "sentSeq")]
#
#
# codeCols = c(
  'compose',
#
  #'delete',
#
   'relocate',
#
  'reflect',
  'seekSugg',
#
  'acceptSugg',
#
#
    'dismissSugg',
#
  'lowModification',
    'highModification',
#
#
    'reviseSugg',
    'reviseUser'
#
# )
# codes = data1[,codeCols]
#
# #mask =
#
# meta = data1[,c("genre",
                  "highTemp",
```

```
# "ownershipMetadata",
# "prompt_code"
# )]
```

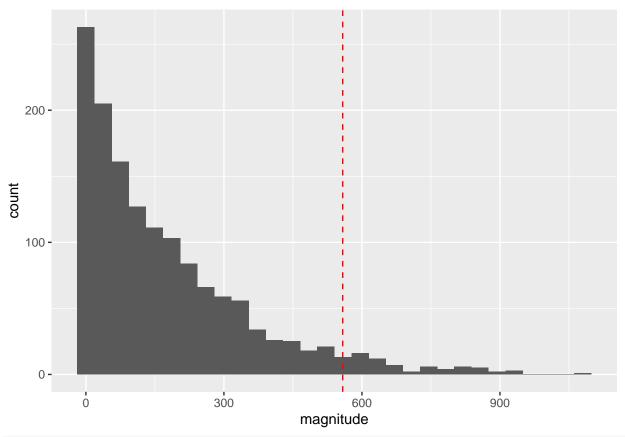
Run ENA accumulation

```
# accum =
# ena.accumulate.data(
# units = units,
# conversation = conversation,
# codes = codes,
# metadata = meta,
# #mask = mask,
# window.size.back = "inf" # each line in the conversation can connect back to the first line--allows
# )
set = ena.make.set(accum)
```

checking networks

```
sparse.nets = accum$connection.counts %>% rowwise(ENA_UNIT) %>% mutate(magnitude = norm(c_across(contain
x = quantile(sparse.nets$magnitude,0.95)

ggplot(sparse.nets, aes(x = magnitude)) + geom_histogram() + geom_vline(xintercept = x, linetype = "das"
#> `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
zeros = which(sparse.nets$magnitude == 0)
length(zeros)
#> [1] 24
```

 $\# Run\ ENA\ dimensional\ reduction$

```
set = ena.make.set(enadata = accum)
```

View space

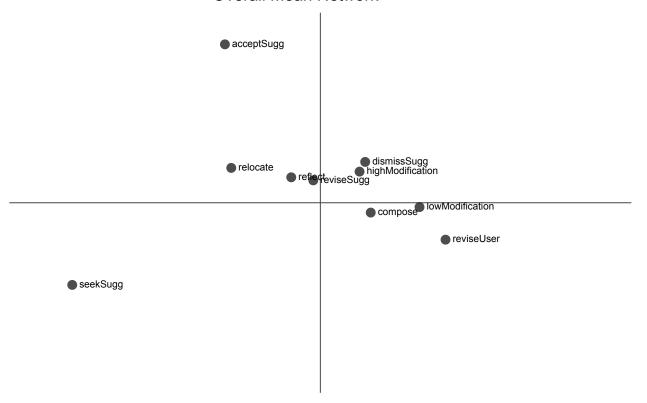
```
network = as.matrix(set$line.weights)
mean_network = colMeans(network)

network_mult = 0

p = ena.plot(set,title = "Overall Mean Network") %>%
    ena.plot.network(mean_network * network_mult,colors = "black")

p$plot
```





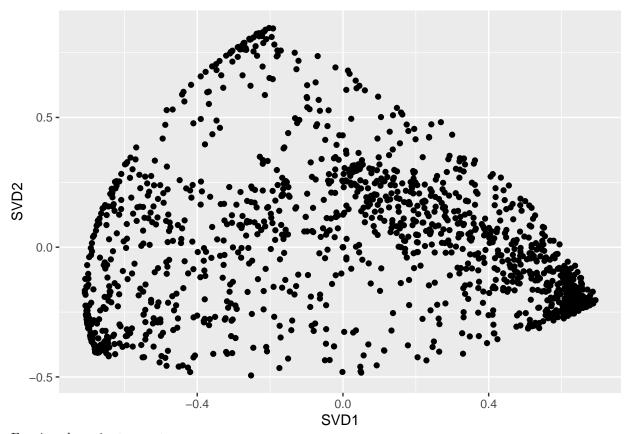
Statistical tests

Set up data and check data

```
#names(set$points)
reg_data = set$points[,c(1:9)]
#glimpse(reg_data)
#table(reg_data$genre)
#t(table(reg_data$genre,reg_data$worker_id))
#summary(reg_data)
```

Checking points

```
ggplot(reg_data,aes(x = SVD1, y = SVD2)) + geom_point()
```

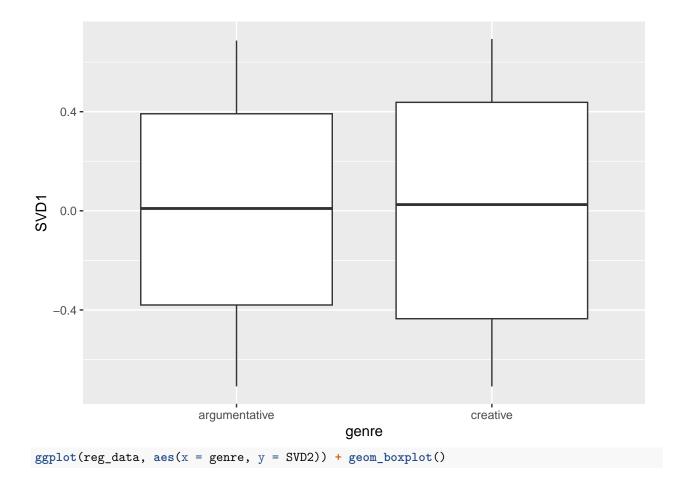


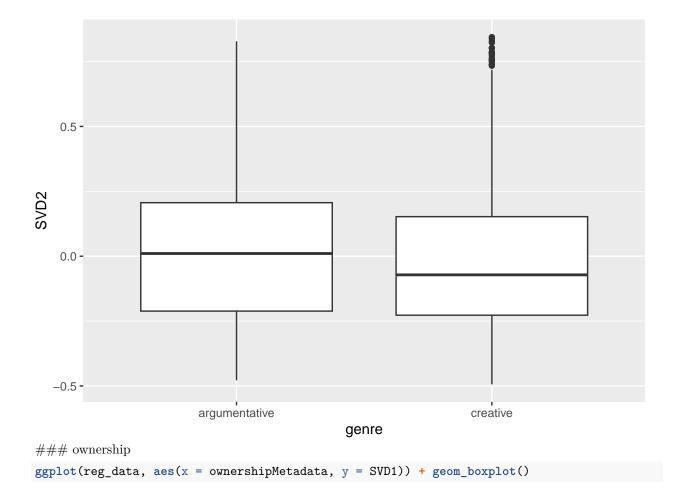
Fanning shape is strange to me

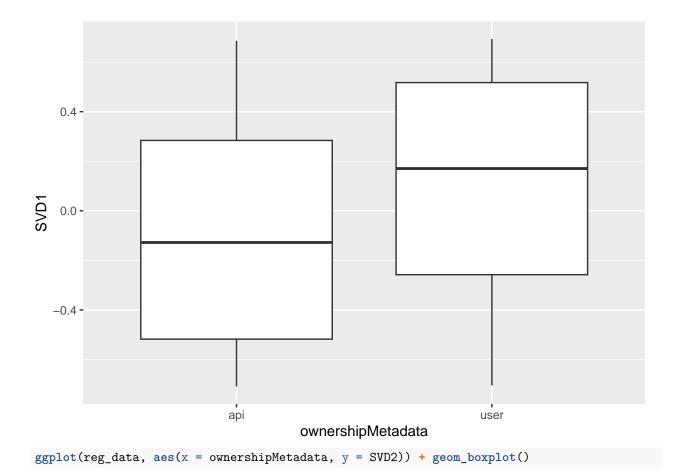
Checking other groups

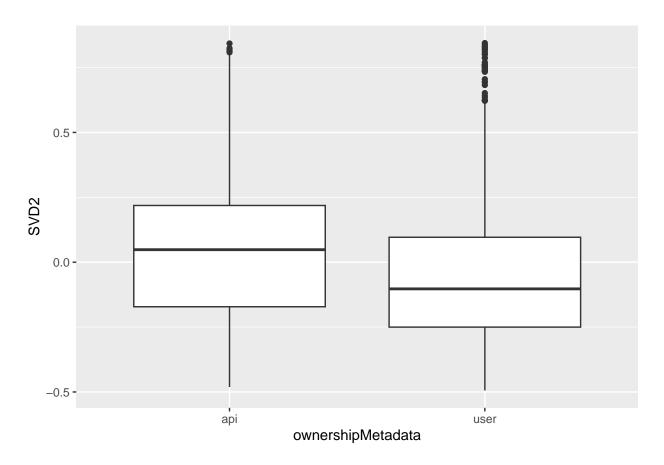
genre

```
ggplot(reg_data, aes(x = genre, y = SVD1)) + geom_boxplot()
```



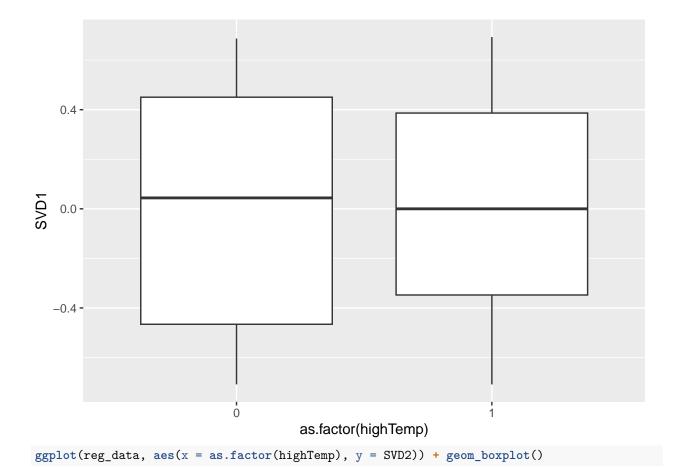


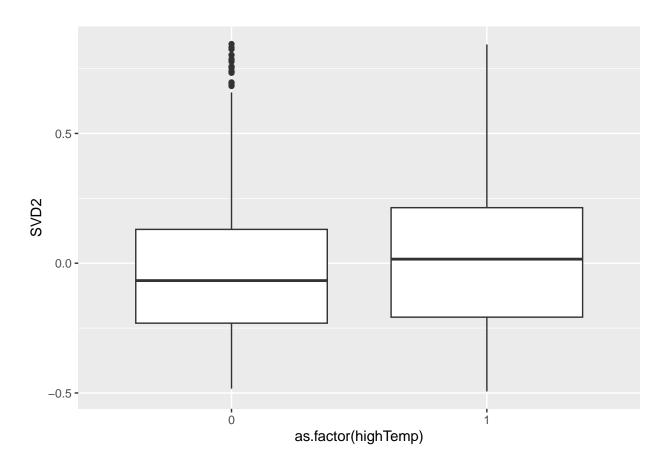




temperature

```
ggplot(reg_data, aes(x = as.factor(highTemp), y = SVD1)) + geom_boxplot()
```





Clustering of observations

```
ICCest(worker_id,SVD1,reg_data) #CI does not contain zero; significant
\#> Warning in ICCest(worker_id, SVD1, reg_data): 'x' has been coerced to a factor
#> $ICC
#> [1] 0.4679765
#>
#> $LowerCI
#> [1] 0.3809611
#> $UpperCI
#> [1] 0.5714229
#>
#> $N
#> [1] 61
#>
#> $k
#> [1] 23.02129
#>
#> $varw
#> [1] 0.1109908
#>
#> $vara
#> [1] 0.09762927
ICCest(worker_id,SVD2,reg_data) #CI does not contain zero; significant
\#> Warning in ICCest(worker_id, SVD2, reg_data): 'x' has been coerced to a factor
```

```
#> $ICC
#> [1] 0.1101448
#>
#> $LowerCI
#> [1] 0.07055893
#> $UpperCI
#> [1] 0.1707893
#>
#> $N
#> [1] 61
#>
#> $k
#> [1] 23.02129
#>
#> $varw
#> [1] 0.07647555
#> $vara
#> [1] 0.009466017
#suggests multilevel models are appropriate for these data
ICCest(prompt_code,SVD1,reg_data) #CI does contains zero; not significant
#> Warning in ICCest(prompt_code, SVD1, reg_data): 'x' has been coerced to a
#> factor
#> $ICC
#> [1] -0.006923188
#> $LowerCI
#> [1] -0.009977924
#> $UpperCI
#> [1] 0.001177918
#>
#> $N
#> [1] 20
#>
#> $k
#> [1] 71.70869
#>
#> $varw
#> [1] 0.2063118
#>
#> $vara
#> [1] -0.001418515
ICCest(prompt_code,SVD2,reg_data) #CI contains zero; not significant
#> Warning in ICCest(prompt_code, SVD2, reg_data): 'x' has been coerced to a
#> factor
#> $ICC
#> [1] 0.007406709
#>
#> $LowerCI
```

```
#> [1] -0.001636156
#>
#> $UpperCI
#> [1] 0.03086913
#>
#> $N
#> [1] 20
#>
#> $k
#> [1] 71.70869
#>
#> $varw
#> [1] 0.08498509
#>
#> $vara
#> [1] 0.0006341568
```

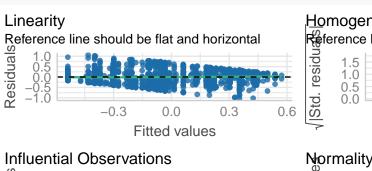
Regression analysis

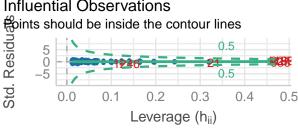
SVD1

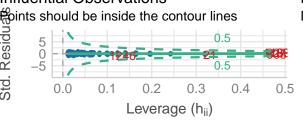
```
\# mod.x.1 = lmerTest::lmer(SVD1 \sim genre*ownershipMetadata*highTemp + (1/worker_id), data = reg_data)
\# mod.x.2 = lmerTest::lmer(SVD1 ~ genre*ownershipMetadata + genre*highTemp + ownershipMetadata*highTemp
#
#
\# anova(mod.x.1, mod.x.2)
# mod.x.3 = lmerTest::lmer(SVD1 ~ qenre + ownershipMetadata + highTemp + (1|worker_id),data = req_data)
\# anova(mod.x.2, mod.x.3)
mod.x.4 = lmerTest::lmer(SVD1 ~ ownershipMetadata + (1|worker_id),data = reg_data)
\#anova(mod.x.3, mod.x.4)
summary(mod.x.4)
#> Linear mixed model fit by REML. t-tests use Satterthwaite's method [
#> lmerModLmerTest]
#> Formula: SVD1 ~ ownershipMetadata + (1 | worker id)
#> Data: reg_data
#>
#> REML criterion at convergence: 1061.9
#>
#> Scaled residuals:
     Min 1Q Median
                            3Q
#> Random effects:
           Name
#> Groups
                        Variance Std.Dev.
#> worker_id (Intercept) 0.09539 0.3089
#> Residual
                       0.11026 0.3321
#> Number of obs: 1436, groups: worker_id, 61
```

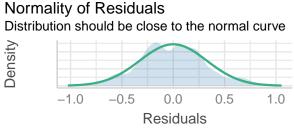
```
#> Fixed effects:
                                                      df t value Pr(>/t/)
                          Estimate Std. Error
#>
                         3.360e-03 4.593e-02 6.577e+01
                                                           0.073 0.941916
#> (Intercept)
#> ownershipMetadatauser 9.557e-02 2.450e-02 1.434e+03
                                                           3.900 0.000101 ***
#> Signif. codes:
                   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Correlation of Fixed Effects:
#>
               (Intr)
#> ownrshpMtdt -0.317
```

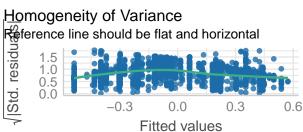
check.x = check_model(mod.x.4, check = c("qq","normality","linearity", "homogeneity", "outliers", "reqq" #> Not enough model terms in the conditional part of the model to check for multicollinearity. check.x

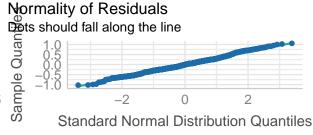


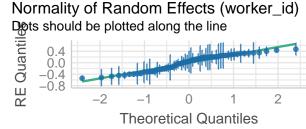












Check model

```
check_outliers(mod.x.4, "mahalanobis")
#> Converting missing values (`NA`) into regular values currently not
     possible for variables of class `NULL`.
#> OK: No outliers detected.
#> - Based on the following method and threshold: mahalanobis (10.828).
#> - For variable: (Whole model)
```

```
cohensd = function(diff_,g1,g2){
   diff_/(sqrt((sd(g1)^2 + sd(g2)^2)/2))
}

diff_ = coefficients(mod.x.4)$worker_id$ownershipMetadatauser[1]
g1 = as.matrix(set$points$ownershipMetadata$user)[,"SVD1"]
g2 = as.matrix(set$points$ownershipMetadata$api)[,"SVD1"]

cohensd(diff_ = diff_,g1 = g1, g2 = g2)
#> [1] 0.2157699
```

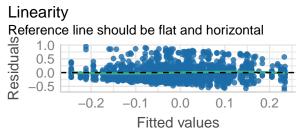
Effect size

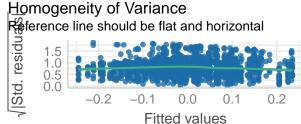
SVD2

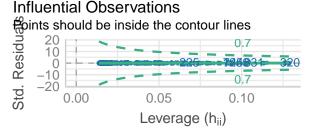
```
\#mod.y.1 = lmerTest::lmer(SVD2 \sim genre*ownershipMetadata*highTemp + (1/worker_id), data = reg_data)
mod.y.2 = lmerTest::lmer(SVD2 ~ genre*ownershipMetadata + genre*highTemp + ownershipMetadata*highTemp +
#anova(mod.y.1, mod.y.2)
\#mod.y.3 = lmerTest::lmer(SVD2 \sim genre*highTemp + (1|worker_id), data = reg_data)
#anova(mod.y.2,mod.y.3) #prefer mod.y.2
summary(mod.y.2)
#> Linear mixed model fit by REML. t-tests use Satterthwaite's method [
#> lmerModLmerTest]
#> Formula:
\#> SVD2 ~ genre * ownershipMetadata + genre * highTemp + ownershipMetadata *
#>
     highTemp + (1 | worker id)
#>
    Data: reg\_data
#>
#> REML criterion at convergence: 435.2
#> Scaled residuals:
#> Min 1Q Median
                            3Q \qquad Max
#> -2.2982 -0.6969 -0.1193 0.4837 3.4913
#> Random effects:
#> Groups Name
                       Variance Std.Dev.
#> worker_id (Intercept) 0.01008 0.1004
#> Residual
                       0.07392 0.2719
#> Number of obs: 1436, groups: worker_id, 61
#>
#> Fixed effects:
                                      Estimate Std. Error df t value
#>
#> (Intercept)
                                       0.01230 0.02997 232.67943 0.411
                                       -0.02239 0.02725 1419.38959 -0.822
#> genrecreative
#> ownershipMetadatauser
                                      -0.10556 0.03052 1339.07994 -3.459
#> highTemp
                                       0.11331 0.02715 1400.36167 4.173
```

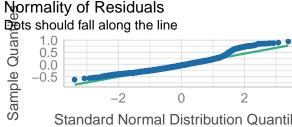
```
#> genrecreative:ownershipMetadatauser
                                          0.05532
                                                     0.03049 1421.28379
                                                                          1.815
#> genrecreative:highTemp
                                         -0.06380
                                                     0.02977 1396.09968
                                                                         -2.143
#> ownershipMetadatauser:highTemp
                                         -0.03290
                                                     0.02946 1399.14816
                                                                         -1.117
#>
                                       Pr(>|t|)
#> (Intercept)
                                       0.681817
#> genrecreative
                                       0.411405
#> ownershipMetadatauser
                                       0.000559 ***
#> highTemp
                                       3.18e-05 ***
#> genrecreative:ownershipMetadatauser 0.069809 .
#> genrecreative:highTemp
                                       0.032306 *
#> ownershipMetadatauser:highTemp
                                       0.264368
#> Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Correlation of Fixed Effects:
#>
               (Intr) qnrcrt ownrsM hqhTmp qnrc:M qnrc:T
#> genrecreatv -0.618
#> ownrshpMtdt -0.661 0.472
#> highTemp
              -0.587 0.466 0.459
#> gnrcrtv:wnM 0.385 -0.644 -0.607 -0.157
#> gnrcrtv:hgT 0.379 -0.620 -0.177 -0.653 0.156
#> ownrshpMt:T 0.303 -0.059 -0.483 -0.537 0.000 0.013
```

check.y = check_model(mod.y.2, check = c("qq", "normality", "linearity", "homogeneity", "outliers", "reqq" check.y





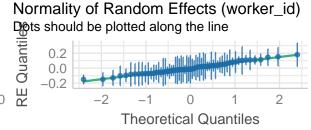




Standard Normal Distribution Quantiles

Distribution should be close to the normal curve Density -0.50.0 0.5 1.0 Residuals

Normality of Residuals



check model

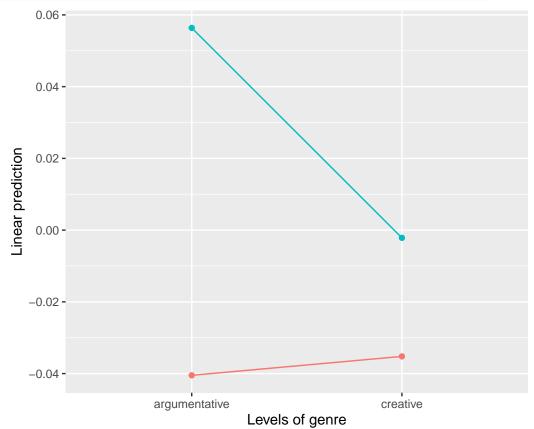
```
check_outliers(mod.y.2,"mahalanobis")
#> Converting missing values (`NA`) into regular values currently not
#> possible for variables of class `NULL`.
#> OK: No outliers detected.
#> - Based on the following method and threshold: mahalanobis (13.816).
#> - For variable: (Whole model)

emm.y.1 = emmeans(mod.y.2, specs = pairwise ~ ownershipMetadata, weights = "proportional")
#> NOTE: Results may be misleading due to involvement in interactions
emm.y.2 = emmeans(mod.y.2, specs = pairwise ~ highTemp, weights = "proportional")
```

Estimate marginal means

```
emmip(mod.y.2, highTemp ~ genre)
```

#> NOTE: Results may be misleading due to involvement in interactions



Viewing interactions

```
#x = ref_grid(mod.y.2)
#broom::tidy(x)

diff_ = 0.0899
g1 = as.matrix(set$points$ownershipMetadata$user)[,"SVD2"]
g2 = as.matrix(set$points$ownershipMetadata$api)[,"SVD2"]
```

```
cohensd(diff_ = diff_,g1 = g1, g2 = g2)
#> [1] 0.3113426
```

Effect sizes (ownership)

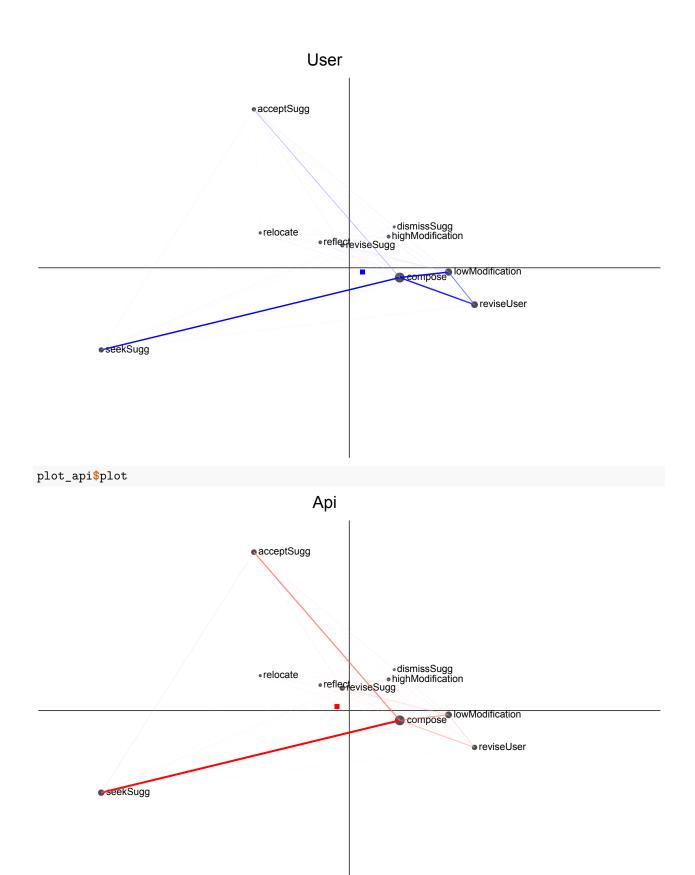
```
diff_ = -0.067
g1 = as.matrix(set$points$highTemp$'1')[,"SVD2"]
g2 = as.matrix(set$points$highTemp$'0')[,"SVD2"]

cohensd(diff_ = diff_,g1 = g1, g2 = g2)
#> [1] -0.2303132
```

Effect sizes (temp)

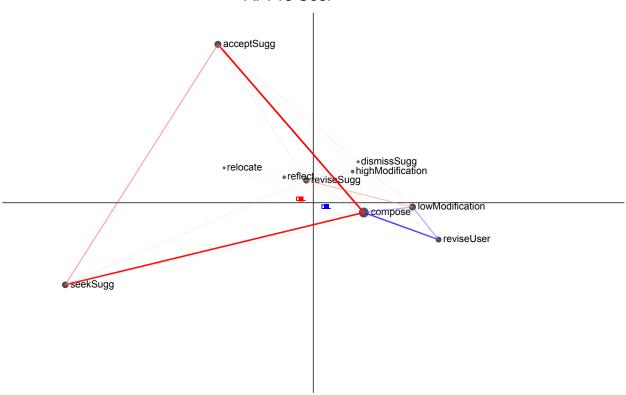
ENA plots

Mean networks (ownership)

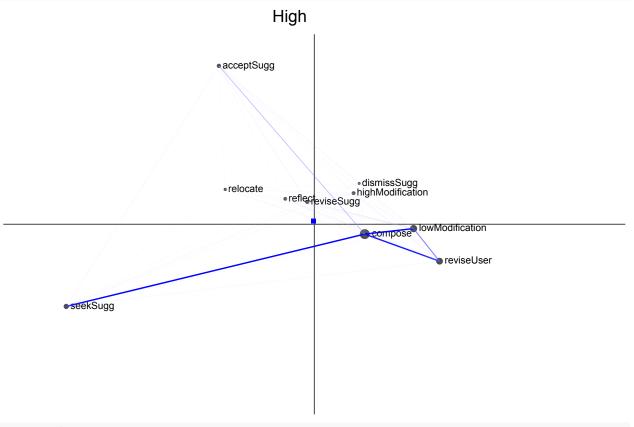


Network subtraction (ownership)

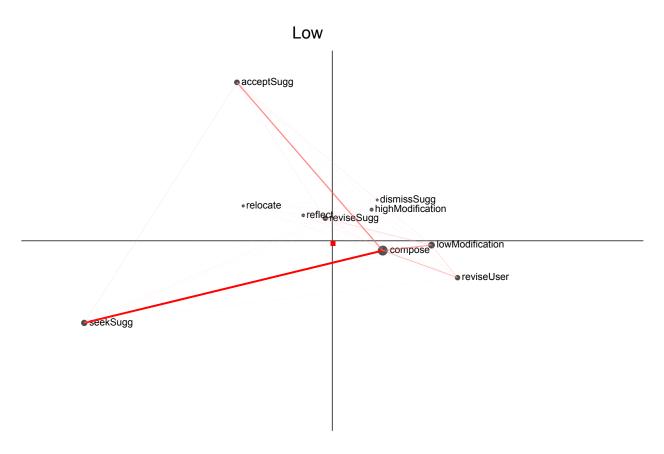
API vs User



Mean networks (temp)



plot_low\$plot



Network subtraction (temp)

