coAuthor-ENA

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<pre>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</pre>	

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',
  "cursorFwd",
  "cursorBwd",
  "cursorSelect",
  #"reopenSugg",
  "hoverSugg"
```

Run ENA accumulation

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

Run ENA dimensional reduction

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

View space

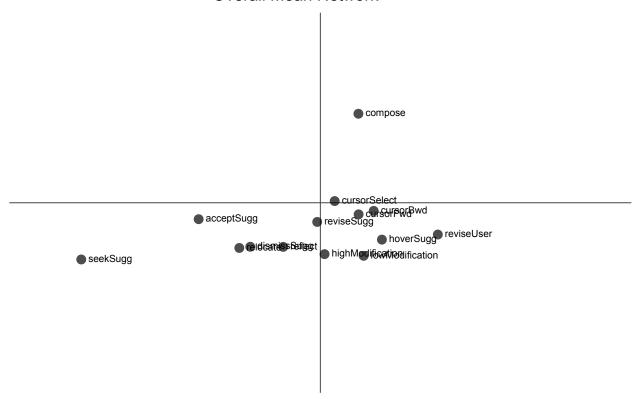
```
network = as.matrix(set$line.weights)
mean_network = colMeans(network)

network_mult = 0

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

p$plot
```





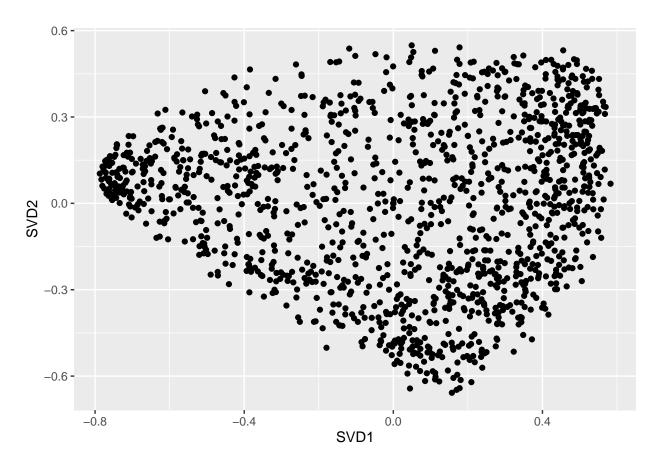
Statistical tests

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

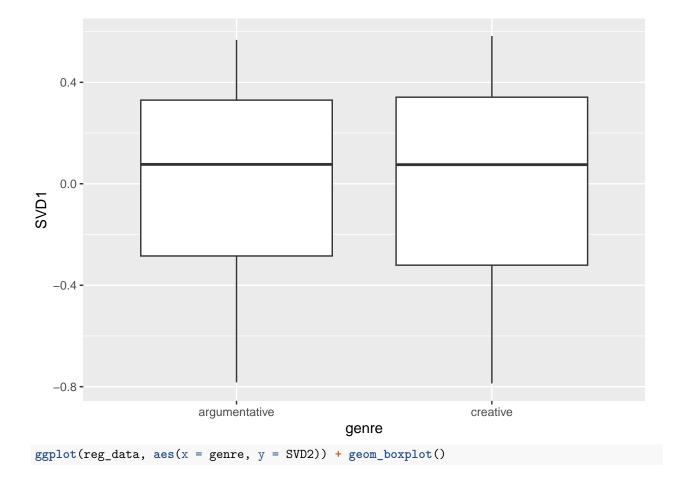
```
ggplot(reg_data,aes(x = SVD1, y = SVD2)) + geom_point()
```

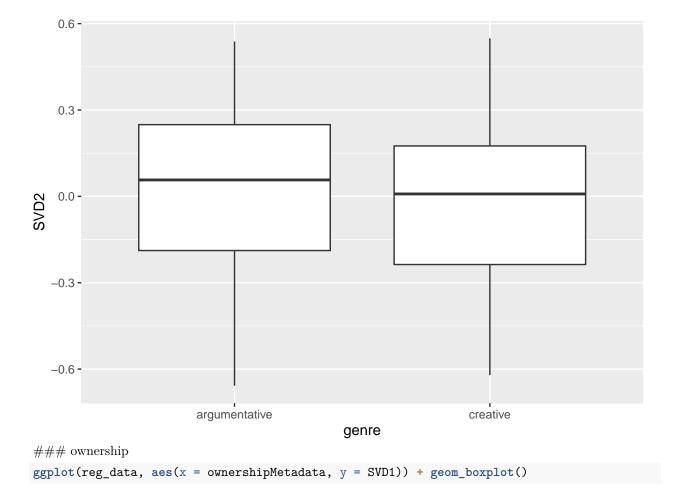


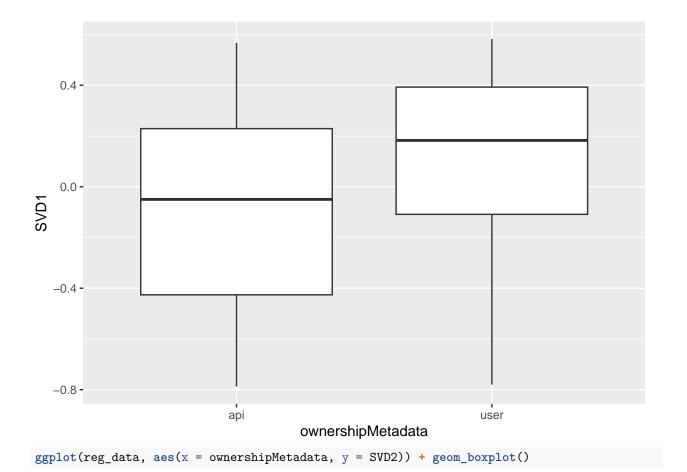
Checking other groups

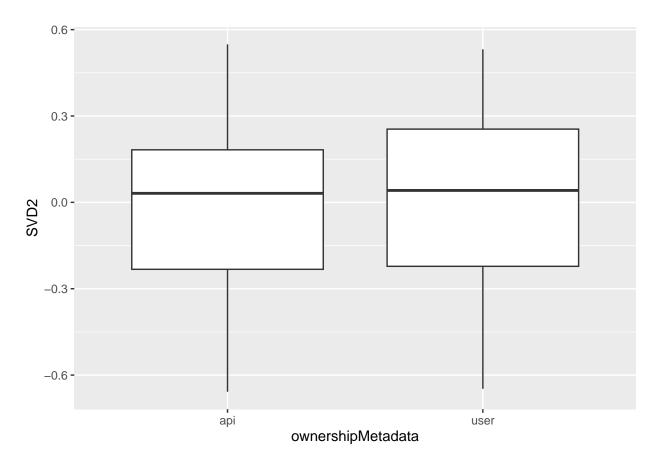
genre

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



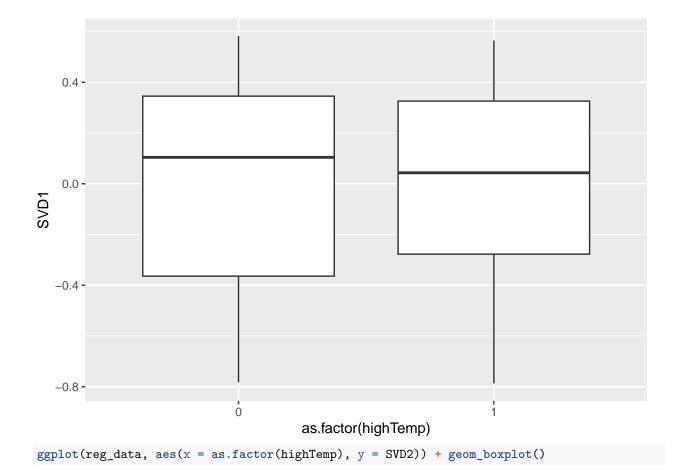


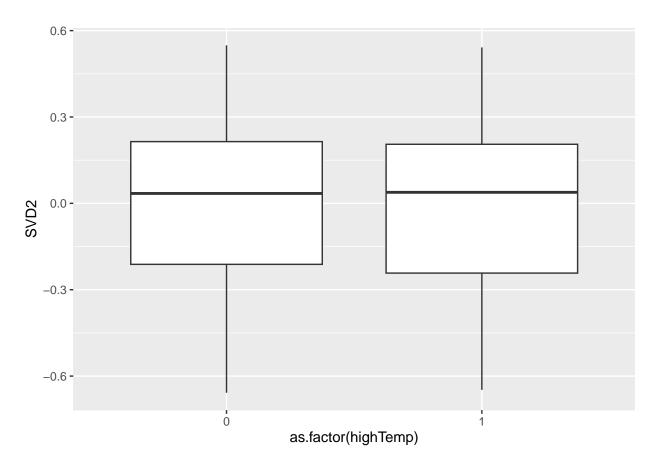




temperature

```
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] 0.4986186
#>
#> $LowerCI
#> [1] 0.4102973
#> $UpperCI
#> [1] 0.6015717
#>
#> $N
#> [1] 60
#>
#> $k
#> [1] 23.39389
#>
#> $varw
#> [1] 0.0774089
#>
#> $vara
#> [1] 0.07698236
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] 0.2856144
#>
#> $LowerCI
#> [1] 0.2140536
#> $UpperCI
#> [1] 0.3825997
#>
#> $N
#> [1] 60
#>
#> $k
#> [1] 23.39389
#>
#> $varw
#> [1] 0.05525751
#> $vara
#> [1] 0.02209219
#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] -0.004754699
#> $LowerCI
#> [1] -0.008726362
#> $UpperCI
#> [1] 0.005742934
#>
#> $N
#> [1] 20
#>
#> $k
#> [1] 71.65773
#>
#> $varw
#> [1] 0.152189
#>
#> $vara
#> [1] -0.0007201885
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] 0.007706712
#>
#> $LowerCI
```

```
#> [1] -0.001464712
#>
#> $UpperCI
#> [1] 0.03149145
#>
#> $N
#> [1] 20
#>
#> $k
#> [1] 71.65773
#>
#> $varw
#> [1] 0.07596133
#>
#> $vara
#> [1] 0.0005899588
```

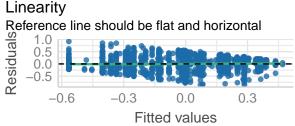
Regression analysis

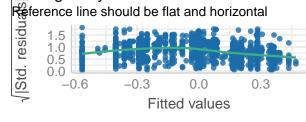
SVD1

```
\#mod.x.1 = lmerTest::lmer(SVD1 \sim genre*ownershipMetadata*highTemp + (1/worker_id), data = reg_data)
\#confint(mod.x.1)
\#mod.x.2 = lmerTest::lmer(SVD1 \sim genre + ownershipMetadata + highTemp + (1/worker_id), data = reg_data)
\#confint (mod.x.2)
#suggests only ownership is signficant
mod.x.3 = lmerTest::lmer(SVD1 ~ ownershipMetadata + (1|worker_id),data = reg_data)
summary(mod.x.3)
#> 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: 547.7
#> Scaled residuals:
#> Min 1Q Median
                           3Q
#>
#> Random effects:
#> Groups Name
                        Variance Std.Dev.
#> worker_id (Intercept) 0.07246 0.2692
                      0.07685 0.2772
#> Number of obs: 1435, groups: worker_id, 60
#> Fixed effects:
                                             df t value Pr(>|t|)
                         Estimate Std. Error
```

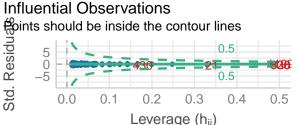
check.x = check_model(mod.x.3, check = c("qq","normality","linearity", "homogeneity", "outliers","reqq"
#> Not enough model terms in the conditional part of the model to check for
#> multicollinearity.

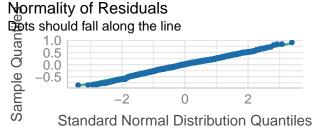
check.x





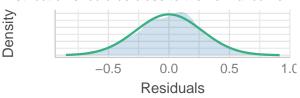
Homogeneity of Variance

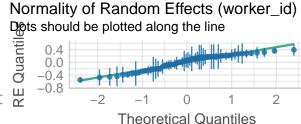




Normality of Residuals

Distribution should be close to the normal curve





Check model

```
check_outliers(mod.x.3,"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)
```

```
demean = function(x){
  return(x - mean(x))
```

```
cohensd = function(diff_,x1,x2){
  num = diff_
  denom = sqrt((sum(demean(x1)^2) + sum(demean(x2)^2))/(length(x1) + length(x2) - 2))
  return(num/denom)
}

diff_ = coefficients(mod.x.3)$worker_id$ownershipMetadatauser[1]
  x1 = as.matrix(set$points$ownershipMetadata$user)[,"SVD1"]
  x2 = as.matrix(set$points$ownershipMetadata$api)[,"SVD1"]

cohensd(diff_ = diff_,x1,x2)
#> [1] 0.2246755
```

Effect size

SVD2

```
\# mod.y.1 = lmerTest::lmer(SVD2 \sim genre*ownershipMetadata*highTemp + (1/worker_id), data = reg_data)
# summary(mod.y.1)
#
# mod.y.2 = lmerTest::lmer(SVD2 ~ genre + ownershipMetadata + highTemp + (1/worker_id),data = reg_data
# summary(mod.y.2)
mod.y.3 = lmerTest::lmer(SVD2 ~ genre + (1|worker_id),data = reg_data)
summary(mod.y.3)
#> Linear mixed model fit by REML. t-tests use Satterthwaite's method [
#> lmerModLmerTest]
#> Formula: SVD2 ~ genre + (1 | worker_id)
#>
    Data: reg_data
#> REML criterion at convergence: 9.3
#> Scaled residuals:
#> Min 1Q Median
                              3Q
#> -2.7701 -0.7390 0.0760 0.6919 3.1611
#> Random effects:
                        Variance Std.Dev.
#> Groups
            Name
#> worker_id (Intercept) 0.01918  0.1385
#> Residual
                         0.05446 0.2334
#> Number of obs: 1435, groups: worker_id, 60
#> Fixed effects:
                  Estimate Std. Error
                                             df t value Pr(>/t/)
#> (Intercept)
                  0.03788 0.02280
                                      70.97054 1.661
                                                           0.101
#> genrecreative (-0.06144 0.01306 1417.27777 -4.704 2.8e-06 ***
```

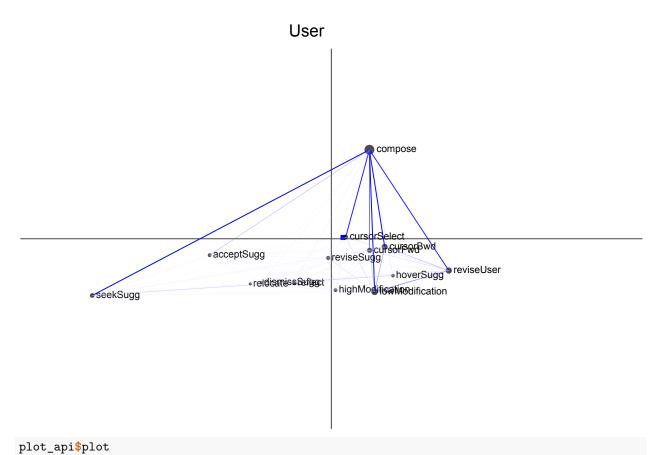
```
#> Signif. codes:
                     0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#> Correlation of Fixed Effects:
#>
                (Intr)
#> genrecreatv -0.372
check.y = check_model(mod.y.3, check = c("qq","normality","linearity", "homogeneity", "outliers", "reqq"
#> Not enough model terms in the conditional part of the model to check for
   multicollinearity.
check.y
                                                               Homogeneity of Variance
               Linearity
               Reference line should be flat and horizontal
                                                               Reference line should be flat and horizontal
                                                               Std. residua
                                                                    1.5
                                                                    1.0
                                                                    0.5
                                                                    0.0
                                                                      -0.4
                                                                                -0.2
                     -0.4
                               -0.2
                                    Fitted values
                                                                                    Fitted values
               Influential Observations
                                                               Normality of Residuals
               hints should be inside the contour lines
                                                               Dets should fall along the line
               Residu
                                                               Sample Quar
                                                 0.5
                     5
                                                                    0.5
                                                                    0.0
                                                 0.5
                                                                   -0.5
                        0.0
                                                0.2
                                                                                                    2
                                   Leverage (hii)
                                                                       Standard Normal Distribution Quantiles
                                                               Normality of Random Effects (worker id)
               Normality of Residuals
                                                               Dets should be plotted along the line
               Distribution should be close to the normal curve
                                                               Quantile
                                                                   0.4
0.2
0.0
-0.2
               Density
                                                                   -0.4
                                                               RE
                             -0.4
                                       0.0
                                                 0.4
                                                           8.0
                                                                                                        2
                                     Residuals
                                                                                Theoretical Quantiles
check model
check_outliers(mod.y.3,"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)
diff_ = coefficients(mod.y.3)$worker_id$genre[1]
x1 = as.matrix(set$points$genre$creative)[,"SVD2"]
x2 = as.matrix(set$points$genre$argumentative)[,"SVD2"]
cohensd(diff ,x1,x2)
```

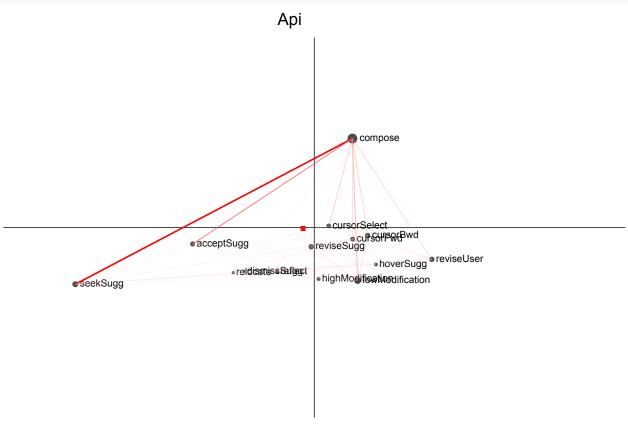
```
#> [1] -0.2227939
```

Effect size (genre)

ENA plots

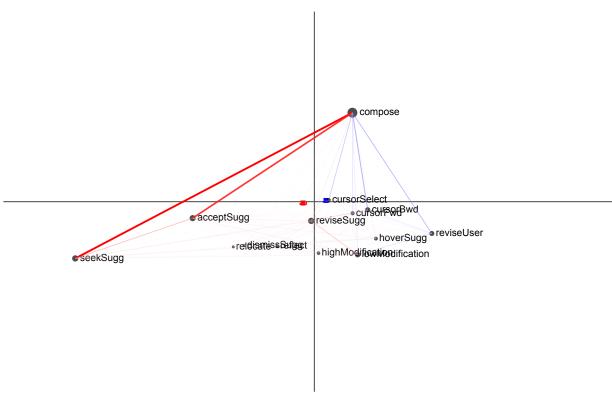
Mean networks (ownership)



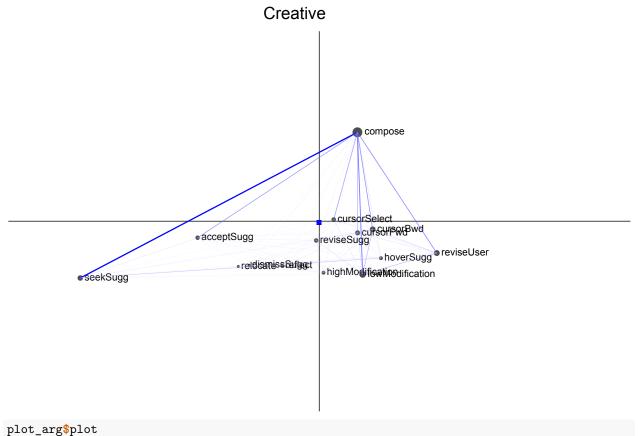


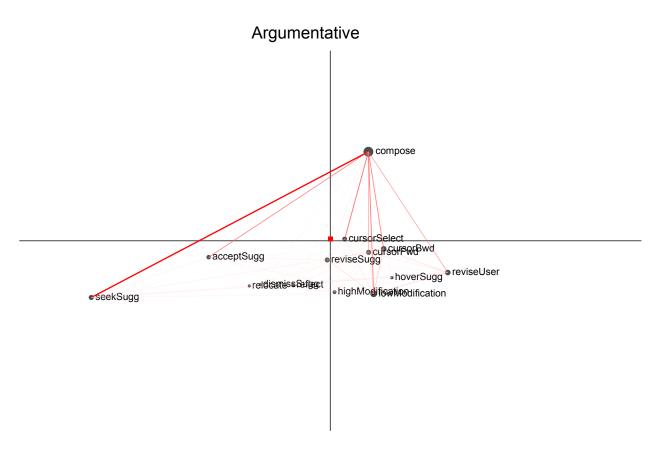
Network subtraction (ownership)

API vs User



Mean networks (genre)





Network subtraction (genre)

