

Package: EDNE.EQ (via r-universe)

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Type Package

Title Implements the EDNE-Test for Equivalence

Version 1.0

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Description Package implements the EDNE-test for equivalence according to Hoffelder et al. (2015) <[DOI:10.1080/10543406.2014.920344](https://doi.org/10.1080/10543406.2014.920344)>.

``EDNE" abbreviates ``Euclidean Distance between the Non-standardized Expected values". The EDNE-test for equivalence is a multivariate two-sample equivalence test. Distance measure of the test is the Euclidean distance. The test is an asymptotically valid test for the family of distributions fulfilling the assumptions of the multivariate central limit theorem (see Hoffelder et al.,2015). The function EDNE.EQ() implements the EDNE-test for equivalence according to Hoffelder et al. (2015). The function EDNE.EQ.dissolution.profiles() implements a variant of the EDNE-test for equivalence analyses of dissolution profiles (see Suarez-Sharp et al.,2020 <[DOI:10.1208/s12248-020-00458-9](https://doi.org/10.1208/s12248-020-00458-9)>). EDNE.EQ.dissolution.profiles() checks whether the quadratic mean of the differences of the expected values of both dissolution profile populations is statistically significantly smaller than 10 [% of label claim]. The current regulatory standard approach for equivalence analyses of dissolution profiles is the similarity factor f_2 . The statistical hypotheses underlying EDNE.EQ.dissolution.profiles() coincide with the hypotheses for f_2 (see Hoffelder et al.,2015, Suarez-Sharp et al., 2020).

Imports MASS

License GPL-3

NeedsCompilation no

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Description

Package implements the EDNE-test for equivalence according to Hoffelder et al. (2015) <DOI:10.1080/10543406.2014.920343>. "EDNE" abbreviates "Euclidean Distance between the Non-standardized Expected values". The EDNE-test for equivalence is a multivariate two-sample equivalence test. Distance measure of the test is the Euclidean distance. The test is an asymptotically valid test for the family of distributions fulfilling the assumptions of the multivariate central limit theorem (see Hoffelder et al.,2015). The function EDNE.EQ() implements the EDNE-test for equivalence according to Hoffelder et al. (2015). The function EDNE.EQ.dissolution.profiles() implements a variant of the EDNE-test for equivalence analyses of dissolution profiles (see Suarez-Sharp et al.,2020 <DOI:10.1208/s12248-020-00458-9>). EDNE.EQ.dissolution.profiles() checks whether the quadratic mean of the differences of the expected values of both dissolution profile populations is statistically significantly smaller than 10 [% of label claim]. The current regulatory standard approach for equivalence analyses of dissolution profiles is the similarity factor f2. The statistical hypotheses underlying EDNE.EQ.dissolution.profiles() coincide with the hypotheses for f2 (see Hoffelder et al.,2015, Suarez-Sharp et al., 2020).

Details

The DESCRIPTION file:

```

Package:      EDNE.EQ
Type:         Package
Title:        Implements the EDNE-Test for Equivalence
Version:      1.0
Date:         2020-09-24
Author:       Thomas Hoffelder
Maintainer:   Thomas Hoffelder <thomas.hoffelder@boehringer-ingelheim.com>
Description:  Package implements the EDNE-test for equivalence according to Hoffelder et al. (2015) <DOI:10.1080/10543406.2014.920343>
Imports:      MASS
License:      GPL-3

```

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Author(s)

Thomas Hoffelder

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References

EMA (2010). Guidance on the Investigation of Bioequivalence. European Medicines Agency, CHMP, London. Doc. Ref.: CPMP/EWP/QWP/1401/98 Rev. 1/ Corr **. URL: https://www.ema.europa.eu/en/documents/scientific-guideline/guideline-investigation-bioequivalence-rev1_en.pdf

FDA (1997). Guidance for Industry: Dissolution Testing of Immediate Release Solid Oral Dosage Forms. Food and Drug Administration FDA, CDER, Rockville. URL: <https://www.fda.gov/media/70936/download>

Hoffelder, T., Goessl, R., Wellek, S. (2015). Multivariate Equivalence Tests for Use in Pharmaceutical Development. *Journal of Biopharmaceutical Statistics*, 25:3, 417-437. URL: <http://dx.doi.org/10.1080/10543406.2014.920344>

Suarez-Sharp, S., Abend, A., Hoffelder, T., Leblond, D., Delvadia, P., Kovacs, E., Diaz, D.A. (2020). In Vitro Dissolution Profiles Similarity Assessment in Support of Drug Product Quality: What, How, When - Workshop Summary Report. *The AAPS Journal*, 22:74. URL: <http://dx.doi.org/10.1208/s12248-020-00458-9>

Examples

A recalculation of the three-dimensional EDNE example evaluation
in Hoffelder et al. (2015) can be done with the following code:

```
data(ex_data_JoBS)
REF_JoBS <- cbind(ex_data_JoBS[ which(ex_data_JoBS$Group=='REF'), ]
                 [c("Diss_15_min", "Diss_20_min", "Diss_25_min")])
TEST_JoBS <- cbind(ex_data_JoBS[ which(ex_data_JoBS$Group=='TEST'), ]
                  [c("Diss_15_min", "Diss_20_min", "Diss_25_min")])
equivalence_margin_EDNE_JoBS <- 297
test_EDNE_JoBS <- EDNE.EQ(X=REF_JoBS
                          , Y=TEST_JoBS
                          , eq_margin=equivalence_margin_EDNE_JoBS
                          , print.results = TRUE)
```

```

# Apart from simulation errors, a recalculation of the EDNE results
# of some parts (normal distribution only) of the simulation study in
# Hoffelder et al. (2015) can be done with the following code. Please note that
# the simulation takes approximately 7 minutes for 50.000 simulation
# runs (number_of_simu_runs <- 50000). To shorten calculation time for
# test users, number_of_simu_runs is set to 100 here and can/should be adapted.

```

```

library(MASS)
number_of_simu_runs <- 100
set.seed(2020)

mu1 <- c(41,76,97)
mu2 <- mu1 - c(10,10,10)
SIGMA_1 <- matrix(data = c(537.4 , 323.8 , 91.8 ,
                          323.8 , 207.5 , 61.7 ,
                          91.8 , 61.7 , 26.1) ,ncol = 3)
SIGMA_2 <- matrix(data = c(324.1 , 233.6 , 24.5 ,
                          233.6 , 263.5 , 61.4 ,
                          24.5 , 61.4 , 32.5) ,ncol = 3)
SIGMA   <- matrix(data = c(430.7 , 278.7 , 58.1 ,
                          278.7 , 235.5 , 61.6 ,
                          58.1 , 61.6 , 29.3) ,ncol = 3)

SIMULATION_SIZE_EDNE <- function(disttype , Hom , Var , mu_1 , mu_2
                                , n_per_group , n_simus ) {

  n_success_EDNE <- 0
  if ( Hom == "Yes" ) {
    COVMAT_1 <- SIGMA
    COVMAT_2 <- SIGMA
  }
  else {
    COVMAT_1 <- SIGMA_1
    COVMAT_2 <- SIGMA_2
  }
  if ( Var == "Low" ) {
    COVMAT_1 <- COVMAT_1 / 4
    COVMAT_2 <- COVMAT_2 / 4
  }

  d <- ncol(COVMAT_1)
  Mean_diff <- mu_1 - mu_2          # Difference of both exp. values
  dist_edne <- crossprod(Mean_diff) # true EDNE distance and equivalence margin

  if ( n_per_group == 10 ) {
    cat("Expected value sample 1:",mu_1,"\n",
        "Expected value sample 2:",mu_2,"\n",
        "Covariance matrix sample 1:",COVMAT_1,"\n",
        "Covariance matrix sample 2:",COVMAT_2,"\n",
        "EM_EDNE:",dist_edne,"\n")
  }
}

```

```

for (i in 1:n_simus) {
  if ( disttype == "Normal" ) {
    REF <- mvrnorm(n = n_per_group, mu=mu_1, Sigma=COVMAT_1)
    TEST<- mvrnorm(n = n_per_group, mu=mu_2, Sigma=COVMAT_2)
  }
  n_success_EDNE <- n_success_EDNE + EDNE.EQ.dissolution.profiles(X=REF
    , Y=TEST
    , print.results = FALSE)$testresult.num
}
empirical_succ_prob_EDNE <- n_success_EDNE / n_simus
simuresults <- data.frame(dist = disttype , Hom = Hom , Var = Var
  , dimension = d , em_edne = dist_edne
  , sample.size = n_per_group
  , empirical.size.edne = empirical_succ_prob_EDNE)
}

SIMULATION_LOOP_SAMPLE_SIZE <- function(disttype , Hom , Var , mu_1 , mu_2
  , n_simus ) {

run_10 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
  , mu_1 = mu_1 , mu_2 = mu_2
  , n_per_group = 10 , n_simus = n_simus)
run_30 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
  , mu_1 = mu_1 , mu_2 = mu_2
  , n_per_group = 30 , n_simus = n_simus)
run_50 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
  , mu_1 = mu_1 , mu_2 = mu_2
  , n_per_group = 50 , n_simus = n_simus)
run_100 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
  , mu_1 = mu_1 , mu_2 = mu_2
  , n_per_group = 100 , n_simus = n_simus)
RESULT_MATRIX <- rbind(run_10 , run_30 , run_50 , run_100)
RESULT_MATRIX
}

simu_1 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "Yes"
  , Var = "High"
  , mu_1 = mu1
  , mu_2 = mu2
  , n_simus = number_of_simu_runs)
simu_2 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "Yes"
  , Var = "Low"
  , mu_1 = mu1
  , mu_2 = mu2
  , n_simus = number_of_simu_runs)
simu_3 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "No"
  , Var = "High"
  , mu_1 = mu1
  , mu_2 = mu2
  , n_simus = number_of_simu_runs)
simu_4 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "No"
  , Var = "Low"

```

```

, mu_1 = mu1
, mu_2 = mu2
, n_simus = number_of_simu_runs)

FINAL_RESULT <- rbind(simu_1 , simu_2 , simu_3 , simu_4)

cat("**** Simu results n_simu_runs: ",number_of_simu_runs," **** \n")
FINAL_RESULT

```

EDNE.EQ

The EDNE-test for equivalence

Description

The function `EDNE.EQ()` implements the EDNE-test for equivalence according to Hoffelder et al. (2015). It is a multivariate two-sample equivalence procedure. Distance measure of the test is the Euclidean distance.

Usage

```
EDNE.EQ(X, Y, eq_margin, alpha = 0.05, print.results = TRUE)
```

Arguments

<code>X</code>	numeric data matrix of the first sample (REF). The rows of <code>X</code> contain the individual observations of the REF sample, the columns contain the variables/components of the multivariate sample.
<code>Y</code>	numeric data matrix of the second sample (TEST). The rows of <code>Y</code> contain the individual observations of the TEST sample, the columns contain the variables/components of the multivariate sample.
<code>eq_margin</code>	numeric (>0). The equivalence margin of the test.
<code>alpha</code>	numeric ($0 < \alpha < 1$). The significance level of the EDNE-test for equivalence. Usually set to 0.05 which is the default.
<code>print.results</code>	logical; if TRUE (default) summary statistics and test results are printed in the output. If NO no output is created

Details

This function implements the EDNE-test for equivalence. Distance measure of the test is the Euclidean distance. The test is an asymptotically valid test for the family of distributions fulfilling the assumptions of the multivariate central limit theorem (for further details see Hoffelder et al., 2015).

Value

a data frame; three columns containing the results of the test

p.value numeric; the p-value of the equivalence test according to Hoffelder et al. (2015)

testresult.num numeric; 0 (null hypothesis of nonequivalence not rejected) or 1 (null hypothesis of nonequivalence rejected, decision in favor of equivalence)

testresult.text

character; test result of the test in text mode

Author(s)

Thomas Hoffelder <thomas.hoffelder at boehringer-ingenelheim.com>

References

Hoffelder, T., Goessl, R., Wellek, S. (2015). Multivariate Equivalence Tests for Use in Pharmaceutical Development. *Journal of Biopharmaceutical Statistics*, 25:3, 417-437. URL: <http://dx.doi.org/10.1080/10543406.2014.920344>

Examples

A recalculation of the three-dimensional EDNE example evaluation
in Hoffelder et al. (2015) can be done with the following code:

```
data(ex_data_JoBS)
REF_JoBS <- cbind(ex_data_JoBS[ which(ex_data_JoBS$Group=='REF'), ],
  [c("Diss_15_min", "Diss_20_min", "Diss_25_min")])
TEST_JoBS <- cbind(ex_data_JoBS[ which(ex_data_JoBS$Group=='TEST'), ],
  [c("Diss_15_min", "Diss_20_min", "Diss_25_min")])
equivalence_margin_JoBS <- 297
test_EDNE_JoBS <- EDNE.EQ(X=REF_JoBS
  , Y=TEST_JoBS
  , eq_margin=equivalence_margin_JoBS
  , print.results = TRUE)
```

EDNE.EQ.dissolution.profiles

The EDNE-test for equivalence for dissolution profile data

Description

The function `EDNE.EQ.dissolution.profiles()` implements a variant of the EDNE-test for equivalence with a concrete equivalence margin for analyses of dissolution profiles. It is a multivariate two-sample equivalence procedure. Distance measure of the test is the Euclidean distance. The equivalence margin is compliant with current regulatory requirements. (see Hoffelder et al.,2015).

Usage

```
EDNE.EQ.dissolution.profiles(X, Y, alpha = 0.05, print.results = TRUE)
```

Arguments

<code>X</code>	numeric data matrix of the first sample (REF). The rows of <code>X</code> contain the individual observations of the REF sample, the columns contain the variables/components of the multivariate sample. More precisely, the variables are the measured dissolution time points and the rows contain the individual dissolution profiles.
<code>Y</code>	numeric data matrix of the second sample (TEST). The rows of <code>Y</code> contain the individual observations of the TEST sample, the columns contain the variables/components of the multivariate sample. More precisely, the variables are the measured dissolution time points and the rows contain the individual dissolution profiles.
<code>alpha</code>	numeric ($0 < \alpha < 1$). The significance level of the test. Usually set to 0.05 which is the default.
<code>print.results</code>	logical; if TRUE (default) summary statistics and test results are printed in the output. If NO no output is created

Details

This function implements a variant of the EDNE-test for equivalence with a concrete equivalence margin for analyses of dissolution profiles. The current regulatory standard approach for comparing dissolution profiles is the similarity factor `f2` (see FDA, 1997, EMA, 2010, among others). Analogous to `f2` the equivalence margin implemented in this function is defined by a shift of 10 [% of label claim] at all dissolution time points. Thus, the statistical hypotheses of `f2` and `EDNE.EQ.dissolution.profiles()` coincide (see Hoffelder et al., 2015, Suarez-Sharp et al., 2020). The test checks whether the quadratic mean of the differences between REF and TEST mean profiles is statistically significantly smaller than 10%.

With `f2`, the current regulatory standard approach for comparing dissolution profiles, the type I error cannot be controlled. According to EMA (2010) "similarity acceptance limits should be pre-defined and justified and not be greater than a 10% difference". The functions

- `EDNE.EQ.dissolution.profiles`
- [T2EQ.dissolution.profiles.hoffelder](#)

and `f2` have in common that they all check whether a kind of average difference between the expected values is smaller than 10 [% of label claim] (see Suarez-Sharp et al., 2020). Thus, the methods

- `EDNE.EQ.dissolution.profiles`
- [T2EQ.dissolution.profiles.hoffelder](#)

are compliant with current regulatory requirements. In contrast to the standard approach `f2` they allow (at least approximate) type I error control.

Value

a data frame; three columns containing the results of the test

<code>p.value</code>	numeric; the p-value of the equivalence test according to Hoffelder et al. (2015)
<code>testresult.num</code>	numeric; 0 (null hypothesis of nonequivalence not rejected) or 1 (null hypothesis of nonequivalence rejected, decision in favor of equivalence)
<code>testresult.text</code>	character; test result of the test in text mode

Author(s)

Thomas Hoffelder <thomas.hoffelder at boehringer-ingenheim.com>

References

- EMA (2010). Guidance on the Investigation of Bioequivalence. European Medicines Agency, CHMP, London. Doc. Ref.: CPMP/EWP/QWP/1401/98 Rev. 1/ Corr **. URL: https://www.ema.europa.eu/en/documents/scientific-guideline/guideline-investigation-bioequivalence-rev1_en.pdf
- FDA (1997). Guidance for Industry: Dissolution Testing of Immediate Release Solid Oral Dosage Forms. Food and Drug Administration FDA, CDER, Rockville. URL: <https://www.fda.gov/media/70936/download>
- Hoffelder, T., Goessl, R., Wellek, S. (2015). Multivariate Equivalence Tests for Use in Pharmaceutical Development. *Journal of Biopharmaceutical Statistics*, 25:3, 417-437. URL: <http://dx.doi.org/10.1080/10543406.2014.920344>
- Suarez-Sharp, S., Abend, A., Hoffelder, T., Leblond, D., Delvadia, P., Kovacs, E., Diaz, D.A. (2020). In Vitro Dissolution Profiles Similarity Assessment in Support of Drug Product Quality: What, How, When - Workshop Summary Report. *The AAPS Journal*, 22:74. URL: <http://dx.doi.org/10.1208/s12248-020-00458-9>

Examples

```
# Apart from simulation errors, a recalculation of the EDNE results
# of some parts (normal distribution only) of the simulation study in
# Hoffelder et al. (2015) can be done with the following code. Please note that
# the simulation takes approximately 7 minutes for 50.000 simulation
# runs (number_of_simu_runs <- 50000). To shorten calculation time for
# test users, number_of_simu_runs is set to 100 here and can/should be adapted.
```

```
library(MASS)
number_of_simu_runs <- 100
set.seed(2020)

mu1 <- c(41,76,97)
mu2 <- mu1 - c(10,10,10)
SIGMA_1 <- matrix(data = c(537.4 , 323.8 , 91.8 ,
                          323.8 , 207.5 , 61.7 ,
                          91.8 , 61.7 , 26.1) ,ncol = 3)
SIGMA_2 <- matrix(data = c(324.1 , 233.6 , 24.5 ,
                          233.6 , 263.5 , 61.4 ,
                          24.5 , 61.4 , 32.5) ,ncol = 3)
SIGMA <- matrix(data = c(430.7 , 278.7 , 58.1 ,
                        278.7 , 235.5 , 61.6 ,
                        58.1 , 61.6 , 29.3) ,ncol = 3)

SIMULATION_SIZE_EDNE <- function(disttype , Hom , Var , mu_1 , mu_2
                                , n_per_group , n_simus ) {

  n_success_EDNE <- 0
```

```

if ( Hom == "Yes" ) {
  COVMAT_1 <- SIGMA
  COVMAT_2 <- SIGMA
}
else {
  COVMAT_1 <- SIGMA_1
  COVMAT_2 <- SIGMA_2
}
if ( Var == "Low" ) {
  COVMAT_1 <- COVMAT_1 / 4
  COVMAT_2 <- COVMAT_2 / 4
}

d <- ncol(COVMAT_1)
Mean_diff <- mu_1 - mu_2          # Difference of both exp. values
dist_edne <- crossprod(Mean_diff) # true EDNE distance and equivalence margin

if ( n_per_group == 10 ) {
  cat("Expected value sample 1:",mu_1,"\n",
      "Expected value sample 2:",mu_2,"\n",
      "Covariance matrix sample 1:",COVMAT_1,"\n",
      "Covariance matrix sample 2:",COVMAT_2,"\n",
      "EM_EDNE:",dist_edne,"\n")
}

for (i in 1:n_simus) {
  if ( disttype == "Normal" ) {
    REF <- mvrnorm(n = n_per_group, mu=mu_1, Sigma=COVMAT_1)
    TEST<- mvrnorm(n = n_per_group, mu=mu_2, Sigma=COVMAT_2)
  }
  n_success_EDNE <- n_success_EDNE + EDNE.EQ.dissolution.profiles(X=REF
      , Y=TEST
      , print.results = FALSE)$testresult.num
}
empirical_succ_prob_EDNE <- n_success_EDNE / n_simus
simureults <- data.frame(dist = disttype , Hom = Hom , Var = Var
      , dimension = d , em_edne = dist_edne
      , sample.size = n_per_group
      , empirical.size.edne = empirical_succ_prob_EDNE)
}

SIMULATION_LOOP_SAMPLE_SIZE <- function(disttype , Hom , Var , mu_1 , mu_2
      , n_simus ) {

run_10 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
      , mu_1 = mu_1 , mu_2 = mu_2
      , n_per_group = 10 , n_simus = n_simus)
run_30 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
      , mu_1 = mu_1 , mu_2 = mu_2
      , n_per_group = 30 , n_simus = n_simus)
run_50 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
      , mu_1 = mu_1 , mu_2 = mu_2
      , n_per_group = 50 , n_simus = n_simus)
}

```

```

run_100 <- SIMULATION_SIZE_EDNE(disttype = disttype , Hom = Hom , Var = Var
                                , mu_1 = mu_1 , mu_2 = mu_2
                                , n_per_group = 100 , n_simus = n_simus)
RESULT_MATRIX <- rbind(run_10 , run_30 , run_50 , run_100)
RESULT_MATRIX
}

simu_1 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "Yes"
                                       , Var = "High"
                                       , mu_1 = mu1
                                       , mu_2 = mu2
                                       , n_simus = number_of_simu_runs)
simu_2 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "Yes"
                                       , Var = "Low"
                                       , mu_1 = mu1
                                       , mu_2 = mu2
                                       , n_simus = number_of_simu_runs)
simu_3 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "No"
                                       , Var = "High"
                                       , mu_1 = mu1
                                       , mu_2 = mu2
                                       , n_simus = number_of_simu_runs)
simu_4 <- SIMULATION_LOOP_SAMPLE_SIZE(disttype = "Normal", Hom = "No"
                                       , Var = "Low"
                                       , mu_1 = mu1
                                       , mu_2 = mu2
                                       , n_simus = number_of_simu_runs)

FINAL_RESULT <- rbind(simu_1 , simu_2 , simu_3 , simu_4)

cat("**** Simu results n_simu_runs: ",number_of_simu_runs," **** \n")
FINAL_RESULT

```

ex_data_JoBS

Example dataset from Hoffelder et al. (2015)

Description

Multivariate example dataset of dissolution profiles. Dataset consists of two three-dimensional samples. The names of the three variables are "Diss_15_min", "Diss_20_min" and "Diss_25_min". Variable "Group" discriminates between first sample (Group == "REF") and second sample (Group == "Test"). Sample size is 12 per group.

Usage

```
data("ex_data_JoBS")
```

Format

A data frame with 24 observations on the following 4 variables.

Group a factor with levels REF TEST

Diss_15_min a numeric vector

Diss_20_min a numeric vector

Diss_25_min a numeric vector

Details

Example dataset from Hoffelder et al. (2015).

Source

Hoffelder, T., Goessl, R., Wellek, S. (2015), "Multivariate Equivalence Tests for Use in Pharmaceutical Development", *Journal of Biopharmaceutical Statistics*, 25:3, 417-437.

References

URL: <http://dx.doi.org/10.1080/10543406.2014.920344>

Examples

```
data(ex_data_JoBS)
```

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