

# Package ‘multid’

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**Title** Multivariate Difference Between Two Groups

**Version** 0.5.0

**Description** Estimation of multivariate differences between two groups (e.g., multivariate sex differences) with regularized regression methods and predictive approach. See Lönnqvist & Ilmarinen (2021) <[doi:10.1007/s11109-021-09681-2](https://doi.org/10.1007/s11109-021-09681-2)> and Ilmarinen et al. (2022) <[doi:10.1177/08902070221088155](https://doi.org/10.1177/08902070221088155)>.

**License** GPL-3

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colwise_pool	<i>Column-wise pooling of standard deviations</i>
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### Description

Column-wise pooling of standard deviations

### Usage

```
colwise_pool(data, n1, n2, m1, m2, sd1, sd2)
```

### Arguments

data	Data frame of d_pooled_sd output for multiple samples.
n1	Sample sizes of group1.
n2	Sample sizes of group2.
m1	Means of group1.
m2	Means of group2.
sd1	Standard deviations of group1.
sd2	Standard deviations of group2.

### Value

pooled SDs for groups and across groups

---

cvv	<i>Coefficient of variance variation</i>
-----	--

---

### Description

Calculates three different indices for variation between two or more variance estimates. VR = Variance ratio between the largest and the smallest variance. CVV = Coefficient of variance variation (Box, 1954). SVH = Standardized variance heterogeneity (Ruscio & Roche, 2012).

### Usage

```
cvv(data)
```

**Arguments**

`data` Data frame of two or more columns or list of two or more variables.

**Value**

A vector including VR, CVV, and SVH.

**References**

Box, G. E. P. (1954). Some Theorems on Quadratic Forms Applied in the Study of Analysis of Variance Problems, I. Effect of Inequality of Variance in the One-Way Classification. *The Annals of Mathematical Statistics*, 25(2), 290–302.

Ruscio, J., & Roche, B. (2012). Variance Heterogeneity in Published Psychological Research: A Review and a New Index. *Methodology*, 8(1), 1–11. <https://doi.org/10.1027/1614-2241/a000034>

**Examples**

```
d <- list(
  X1 = rnorm(10, sd = 10),
  X2 = rnorm(100, sd = 7.34),
  X3 = rnorm(1000, sd = 6.02),
  X4 = rnorm(100, sd = 5.17),
  X5 = rnorm(10, sd = 4.56)
)
cvv(d)
```

---

cvv_manual	<i>Coefficient of variance variation from manual input sample sizes and variance estimates</i>
------------	--

---

**Description**

Calculates three different indices for variation between two or more variance estimates. VR = Variance ratio between the largest and the smallest variance. CVV = Coefficient of variance variation (Box, 1954). SVH = Standardized variance heterogeneity (Ruscio & Roche, 2012).

**Usage**

```
cvv_manual(sample_sizes, variances)
```

**Arguments**

`sample_sizes` Numeric vector of length > 1. Sample sizes used for each variance estimate.

`variances` Numeric vector of length > 1. Variance estimates.

**Value**

A vector including VR, CVV, and SVH.

## References

Box, G. E. P. (1954). Some Theorems on Quadratic Forms Applied in the Study of Analysis of Variance Problems, I. Effect of Inequality of Variance in the One-Way Classification. *The Annals of Mathematical Statistics*, 25(2), 290–302.

Ruscio, J., & Roche, B. (2012). Variance Heterogeneity in Published Psychological Research: A Review and a New Index. *Methodology*, 8(1), 1–11. <https://doi.org/10.1027/1614-2241/a000034>

## Examples

```
cvv_manual(sample_sizes=c(10,100,1000,75,3),
            variances=c(1.5,2,2.5,3,3.5))
```

---

d_pooled_sd	<i>Standardized mean difference with pooled standard deviation</i>
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---

## Description

Standardized mean difference with pooled standard deviation

## Usage

```
d_pooled_sd(
  data,
  var,
  group.var,
  group.values,
  rename.output = TRUE,
  infer = FALSE
)
```

## Arguments

data	A data frame.
var	A continuous variable for which difference is estimated.
group.var	The name of the group variable.
group.values	Vector of length 2, group values (e.g. c("male", "female") or c(0,1)).
rename.output	Logical. Should the output values be renamed according to the group.values? Default TRUE.
infer	Logical. Statistical inference with Welch test? (default FALSE)

## Value

Descriptive statistics and mean differences

**Examples**

```
d_pooled_sd(iris[iris$Species == "setosa" | iris$Species == "versicolor", ],
  var = "Petal.Length", group.var = "Species",
  group.values = c("setosa", "versicolor"), infer = TRUE
)
```

---

D_regularized	<i>Multivariate group difference estimation with regularized binomial regression</i>
---------------	--

---

**Description**

Multivariate group difference estimation with regularized binomial regression

**Usage**

```
D_regularized(
  data,
  mv.vars,
  group.var,
  group.values,
  alpha = 0.5,
  nfolds = 10,
  s = "lambda.min",
  type.measure = "deviance",
  rename.output = TRUE,
  out = FALSE,
  size = NULL,
  fold = FALSE,
  fold.var = NULL,
  pcc = FALSE,
  auc = FALSE,
  pred.prob = FALSE,
  prob.cutoffs = seq(0, 1, 0.2)
)
```

**Arguments**

data	A data frame.
mv.vars	Character vector. Variable names in the multivariate variable set.
group.var	The name of the group variable.
group.values	Vector of length 2, group values (e.g. c("male", "female") or c(0,1)).
alpha	Alpha-value for penalizing function ranging from 0 to 1: 0 = ridge regression, 1 = lasso, 0.5 = elastic net (default).
nfolds	Number of folds used for obtaining lambda (range from 3 to n-1, default 10).

<code>s</code>	Which lambda value is used for predicted values? Either "lambda.min" (default) or "lambda.1se".
<code>type.measure</code>	Which measure is used during cross-validation. Default "deviance".
<code>rename.output</code>	Logical. Should the output values be renamed according to the group.values? Default TRUE.
<code>out</code>	Logical. Should results and predictions be calculated on out-of-bad data set? (Default FALSE)
<code>size</code>	Integer. Number of cases in regularization data per each group. Default 1/4 of cases.
<code>fold</code>	Logical. Is regularization applied across sample folds with separate predictions for each fold? (Default FALSE)
<code>fold.var</code>	Character string. Name of the fold variable. (default NULL)
<code>pcc</code>	Logical. Include probabilities of correct classification? Default FALSE.
<code>auc</code>	Logical. Include area under the receiver operating characteristics? Default FALSE.
<code>pred.prob</code>	Logical. Include table of predicted probabilities? Default FALSE.
<code>prob.cutoffs</code>	Vector. Cutoffs for table of predicted probabilities. Default seq(0,1,0.20).

**Value**

<code>D</code>	Multivariate descriptive statistics and differences.
<code>pred.dat</code>	A data.frame with predicted values.
<code>cv.mod</code>	Regularized regression model from cv.glmnet.
<code>P.table</code>	Table of predicted probabilities by cutoffs.

**References**

Lönnqvist, J. E., & Ilmarinen, V. J. (2021). Using a continuous measure of genderedness to assess sex differences in the attitudes of the political elite. *Political Behavior*, 43, 1779–1800. <https://doi.org/10.1007/s11109-021-09681-2>

Ilmarinen, V. J., Vainikainen, M. P., & Lönnqvist, J. E. (2022). Is there a g-factor of genderedness? Using a continuous measure of genderedness to assess sex differences in personality, values, cognitive ability, school grades, and educational track. *European Journal of Personality*. <https://doi.org/10.1177/089020702210881>

**See Also**

[cv.glmnet](#)

**Examples**

```
D_regularized(
  data = iris[iris$Species == "setosa" | iris$Species == "versicolor", ],
  mv.vars = c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"),
  group.var = "Species", group.values = c("setosa", "versicolor")
)$D
```

```

# out-of-bag predictions
D_regularized(
  data = iris[iris$Species == "setosa" | iris$Species == "versicolor", ],
  mv.vars = c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"),
  group.var = "Species", group.values = c("setosa", "versicolor"),
  out = TRUE, size = 15, pcc = TRUE, auc = TRUE
)$D

# separate sample folds
# generate data for 10 groups
set.seed(34246)
n1 <- 100
n2 <- 10
d <-
  data.frame(
    sex = sample(c("male", "female"), n1 * n2, replace = TRUE),
    fold = sample(x = LETTERS[1:n2], size = n1 * n2, replace = TRUE),
    x1 = rnorm(n1 * n2),
    x2 = rnorm(n1 * n2),
    x3 = rnorm(n1 * n2)
  )

# Fit and predict with same data
D_regularized(
  data = d,
  mv.vars = c("x1", "x2", "x3"),
  group.var = "sex",
  group.values = c("female", "male"),
  fold.var = "fold",
  fold = TRUE,
  rename.output = TRUE
)$D

# Out-of-bag data for each fold
D_regularized(
  data = d,
  mv.vars = c("x1", "x2", "x3"),
  group.var = "sex",
  group.values = c("female", "male"),
  fold.var = "fold",
  size = 17,
  out = TRUE,
  fold = TRUE,
  rename.output = TRUE
)$D

```

---

D\_regularized\_fold

*Use manually defined data folds for regularization and obtain estimates for each separately.*

---

**Description**

Use manually defined data folds for regularization and obtain estimates for each separately.

**Usage**

```
D_regularized_fold(
  data,
  mv.vars,
  group.var,
  group.values,
  alpha = 0.5,
  s = "lambda.min",
  type.measure = "deviance",
  rename.output = TRUE,
  fold.var
)
```

**Arguments**

<code>data</code>	A data frame.
<code>mv.vars</code>	Character vector. Variable names in the multivariate variable set.
<code>group.var</code>	The name of the group variable.
<code>group.values</code>	Vector of length 2, group values (e.g. <code>c("male", "female")</code> or <code>c(0,1)</code> ).
<code>alpha</code>	Alpha-value for penalizing function ranging from 0 to 1: 0 = ridge regression, 1 = lasso, 0.5 = elastic net (default).
<code>s</code>	Which lambda value is used for predicted values? Either "lambda.min" (default) or "lambda.1se".
<code>type.measure</code>	Which measure is used during cross-validation. Default "deviance".
<code>rename.output</code>	Logical. Should the output values be renamed according to the <code>group.values</code> ? Default TRUE.
<code>fold.var</code>	Character string. Name of the fold variable.

**Value**

<code>D</code>	Multivariate descriptive statistics and differences.
<code>pred.dat</code>	A data.frame with predicted values.
<code>cv.mod</code>	Regularized regression model from <code>cv.glmnet</code> .

**See Also**

[cv.glmnet](#)



**Examples**

```

set.seed(34246)
n1 <- 100
n2 <- 10
d <-
  data.frame(
    sex = sample(c("male", "female"), n1 * n2, replace = TRUE),
    fold = sample(x = LETTERS[1:n2], size = n1 * n2, replace = TRUE),
    x1 = rnorm(n1 * n2),
    x2 = rnorm(n1 * n2),
    x3 = rnorm(n1 * n2)
  )

D_regularized_fold(
  data = d,
  mv.vars = c("x1", "x2", "x3"),
  group.var = "sex",
  group.values = c("female", "male"),
  fold.var = "fold"
)$D

```

---

D\_regularized\_fold\_out

*Use separate data partitions for regularization and estimation across defined data folds.*

---

**Description**

Use separate data partitions for regularization and estimation across defined data folds.

**Usage**

```

D_regularized_fold_out(
  data,
  mv.vars,
  group.var,
  group.values,
  alpha = 0.5,
  s = "lambda.min",
  type.measure = "deviance",
  rename.output = TRUE,
  size = NULL,
  fold.var,
  pcc = FALSE,
  auc = FALSE,
  pred.prob = FALSE,
  prob.cutoffs = seq(from = 0, to = 1, by = 0.2)
)

```

**Arguments**

<code>data</code>	A data frame.
<code>mv.vars</code>	Character vector. Variable names in the multivariate variable set.
<code>group.var</code>	The name of the group variable.
<code>group.values</code>	Vector of length 2, group values (e.g. <code>c("male", "female")</code> or <code>c(0,1)</code> ).
<code>alpha</code>	Alpha-value for penalizing function ranging from 0 to 1: 0 = ridge regression, 1 = lasso, 0.5 = elastic net (default).
<code>s</code>	Which lambda value is used for predicted values? Either "lambda.min" (default) or "lambda.1se".
<code>type.measure</code>	Which measure is used during cross-validation. Default "deviance".
<code>rename.output</code>	Logical. Should the output values be renamed according to the <code>group.values</code> ? Default TRUE.
<code>size</code>	Integer. Size of regularization data per each group. Default 1/4 of cases.
<code>fold.var</code>	Name of the fold variable.
<code>pcc</code>	Logical. Include probabilities of correct classification? Default FALSE.
<code>auc</code>	Logical. Include area under the receiver operating characteristics? Default FALSE.
<code>pred.prob</code>	Logical. Include table of predicted probabilities? Default FALSE.
<code>prob.cutoffs</code>	Vector. Cutoffs for table of predicted probabilities. Default <code>seq(0,1,0.20)</code> .

**Value**

<code>D</code>	Multivariate descriptive statistics and differences.
<code>pred.dat</code>	A data.frame with predicted values.
<code>cv.mod</code>	Regularized regression model from <code>cv.glmnet</code> .
<code>P.table</code>	Table of predicted probabilities by cutoffs.

**Examples**

```

set.seed(34246)
n1 <- 100
n2 <- 10
d <-
  data.frame(
    sex = sample(c("male", "female"), n1 * n2, replace = TRUE),
    fold = sample(x = LETTERS[1:n2], size = n1 * n2, replace = TRUE),
    x1 = rnorm(n1 * n2),
    x2 = rnorm(n1 * n2),
    x3 = rnorm(n1 * n2)
  )
D_regularized_fold_out(
  data = d,
  mv.vars = c("x1", "x2", "x3"),
  group.var = "sex",
  group.values = c("female", "male"),

```

```

    fold.var = "fold",
    size = 17,
    pcc = TRUE
  )$D

```

---

D\_regularized\_out      *Use separate data partition for regularization and estimation.*

---

## Description

Use separate data partition for regularization and estimation.

## Usage

```

D_regularized_out(
  data,
  mv.vars,
  group.var,
  group.values,
  alpha = 0.5,
  nfolds = 10,
  s = "lambda.min",
  type.measure = "deviance",
  rename.output = TRUE,
  size = NULL,
  pcc = FALSE,
  auc = FALSE,
  pred.prob = FALSE,
  prob.cutoffs = seq(from = 0, to = 1, by = 0.2)
)

```

## Arguments

data	A data frame.
mv.vars	Character vector. Variable names in the multivariate variable set.
group.var	The name of the group variable.
group.values	Vector of length 2, group values (e.g. c("male", "female") or c(0,1)).
alpha	Alpha-value for penalizing function ranging from 0 to 1: 0 = ridge regression, 1 = lasso, 0.5 = elastic net (default).
nfolds	Number of folds used for obtaining lambda (range from 3 to n-1, default 10).
s	Which lambda value is used for predicted values? Either "lambda.min" (default) or "lambda.1se".
type.measure	Which measure is used during cross-validation. Default "deviance".
rename.output	Logical. Should the output values be renamed according to the group.values? Default TRUE.

size	Integer. Size of regularization data per each group. Default 1/4 of cases.
pcc	Logical. Include probabilities of correct classification? Default FALSE.
auc	Logical. Include area under the receiver operating characteristics? Default FALSE.
pred.prob	Logical. Include table of predicted probabilities? Default FALSE.
prob.cutoffs	Vector. Cutoffs for table of predicted probabilities. Default seq(0,1,0.20).

**Value**

D	Multivariate descriptive statistics and differences.
pred.dat	A data.frame with predicted values.
cv.mod	Regularized regression model from cv.glmnet.
P.table	Table of predicted probabilities by cutoffs.

**Examples**

```
D_regularized_out(
  data = iris[iris$Species == "setosa" |
    iris$Species == "versicolor", ],
  mv.vars = c(
    "Sepal.Length", "Sepal.Width",
    "Petal.Length", "Petal.Width"
  ),
  group.var = "Species",
  group.values = c("setosa", "versicolor"),
  size = 40,
  pcc = TRUE
)$D
```

---

D\_regularized\_vanilla *Use same data partition for regularization and estimation.*

---

**Description**

Use same data partition for regularization and estimation.

**Usage**

```
D_regularized_vanilla(
  data,
  mv.vars,
  group.var,
  group.values,
  alpha = 0.5,
  nfolds = 10,
  s = "lambda.min",
  type.measure = "deviance",
  rename.output = TRUE
)
```

**Arguments**

data	A data frame.
mv.vars	Character vector. Variable names in the multivariate variable set.
group.var	The name of the group variable.
group.values	Vector of length 2, group values (e.g. c("male", "female") or c(0,1)).
alpha	Alpha-value for penalizing function ranging from 0 to 1: 0 = ridge regression, 1 = lasso, 0.5 = elastic net (default).
nfolds	Number of folds used for obtaining lambda (range from 3 to n-1, default 10).
s	Which lambda value is used for predicted values? Either "lambda.min" (default) or "lambda.1se".
type.measure	Which measure is used during cross-validation. Default "deviance".
rename.output	Logical. Should the output values be renamed according to the group.values? Default TRUE.

**Value**

D	Multivariate descriptive statistics and differences.
pred.dat	A data.frame with predicted values.
cv.mod	Regularized regression model from cv.glmnet.

**See Also**

[cv.glmnet](#)

**Examples**

```
D_regularized(
  data = iris[iris$Species == "setosa" | iris$Species == "versicolor", ],
  mv.vars = c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"),
  group.var = "Species", group.values = c("setosa", "versicolor")
)$D
```

**Description**

Decomposes difference score predictions to predictions of difference score components by probing simple effects at the levels of the binary moderator.

**Usage**

```
ml_dadas(
  model,
  predictor,
  diff_var,
  diff_var_values,
  scaled_estimates = FALSE,
  re_cov_test = FALSE,
  var_boot_test = FALSE,
  nsim = NULL,
  level = 0.95,
  seed = NULL
)
```

**Arguments**

model	Multilevel model fitted with lmerTest.
predictor	Character string. Variable name of independent variable predicting difference score.
diff_var	Character string. A variable indicative of difference score components (two groups).
diff_var_values	Vector. Values of the component score groups in diff_var.
scaled_estimates	Logical. Are scaled estimates obtained? Does fit a reduced model for correct standard deviations. (Default FALSE)
re_cov_test	Logical. Significance test for random effect covariation? Does fit a reduced model without the correlation. (Default FALSE)
var_boot_test	Logical. Compare variance by lower-level groups at the upper-level in a reduced model with bootstrap? (Default FALSE)
nsim	Numeric. Number of bootstrap simulations.
level	Numeric. The confidence level required for the var_boot_test output (Default .95)
seed	Numeric. Seed number for bootstrap simulations.

**Value**

dadas	A data frame including regression coefficients for component scores and dadas.
scaled_estimates	Scaled regression coefficients for difference score components and difference score.
vpc_at_reduced	Variance partition coefficients in the model without the predictor and interactions.
re_cov_test	Likelihood ratio significance test for random effect covariation.
boot_var_diffs	List of different variance bootstrap tests.

**Examples**

```
## Not run:
set.seed(95332)
n1 <- 10 # groups
n2 <- 10 # observations per group

dat <- data.frame(
  group = rep(c(LETTERS[1:n1]), each = n2),
  x = sample(c(-0.5, 0.5), n1 * n2, replace = TRUE),
  w = rep(sample(1:5, n1, replace = TRUE), each = n2),
  y = sample(1:5, n1 * n2, replace = TRUE)
)
library(lmerTest)
fit <- lmerTest::lmer(y ~ x * w + (x | group),
  data = dat
)

round(ml_dadas(fit,
  predictor = "w",
  diff_var = "x",
  diff_var_values = c(0.5, -0.5)
)$dadas, 3)

## End(Not run)
```

pcc

---

*Returns probabilities of correct classification for both groups in independent data partition.*

---

**Description**

Returns probabilities of correct classification for both groups in independent data partition.

**Usage**

```
pcc(data, pred.var, group.var, group.values)
```

**Arguments**

data	Data frame including predicted values (e.g., pred.dat from D_regularized_out).
pred.var	Character string. Variable name for predicted values.
group.var	The name of the group variable.
group.values	Vector of length 2, group values (e.g. c("male", "female) or c(0,1)).

**Value**

Vector of length 2. Probabilities of correct classification.

**Examples**

```

D_out <- D_regularized_out(
  data = iris[iris$Species == "versicolor" | iris$Species == "virginica", ],
  mv.vars = c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"),
  group.var = "Species", group.values = c("versicolor", "virginica"),
  size = 15
)

pcc(
  data = D_out$pred.dat,
  pred.var = "pred",
  group.var = "group",
  group.values = c("versicolor", "virginica")
)

```

sem\_dadas

*Predicting algebraic difference scores in structural equation model***Description**

Predicting algebraic difference scores in structural equation model

**Usage**

```

sem_dadas(
  data,
  var1,
  var2,
  center = FALSE,
  scale = FALSE,
  predictor,
  covariates = NULL,
  estimator = "MLR",
  level = 0.95,
  sampling.weights = NULL
)

```

**Arguments**

data	A data frame.
var1	Character string. Variable name of first component score of difference score (Y <sub>1</sub> ).
var2	Character string. Variable name of second component score of difference score (Y <sub>2</sub> ).
center	Logical. Are var1 and var2 centered around their grand mean? (Default FALSE)
scale	Logical. Are var1 and var2 scaled with their pooled sd? (Default FALSE)



predictor	Character string. Variable name of independent variable predicting difference score.
covariates	Character string or vector. Variable names of covariates (Default NULL).
estimator	Character string. Estimator used in SEM (Default "MLR").
level	Numeric. The confidence level required for the result output (Default .95)
sampling.weights	Character string. Name of sampling weights variable.

**Value**

descriptives	Means, standard deviations, and intercorrelations.
parameter_estimates	Parameter estimates from the structural equation model.
variance_test	Variances and covariances of component scores.
transformed_data	Data frame with variables used in SEM.
dadas	One sided dadas-test for positivity of $\text{abs}(b_{11}-b_{21})-\text{abs}(b_{11}+b_{21})$ .
results	Summary of key results.

**References**

Edwards, J. R. (1995). Alternatives to Difference Scores as Dependent Variables in the Study of Congruence in Organizational Research. *Organizational Behavior and Human Decision Processes*, 64(3), 307–324.

**Examples**

```
set.seed(342356)
d <- data.frame(
  var1 = rnorm(50),
  var2 = rnorm(50),
  x = rnorm(50)
)
sem_dadas(
  data = d, var1 = "var1", var2 = "var2",
  predictor = "x", center = TRUE, scale = TRUE
)$results
```

vpc\_at

*Variance partition coefficient calculated at different level-1 values***Description**

Calculates variance estimates (level-2 Intercept variance) and variance partition coefficients (i.e., intra-class correlation) at selected values of predictor values in two-level linear models with random effects (intercept, slope, and their covariation).

**Usage**

```
vpc_at(model, lv11.var, lv11.values)
```

**Arguments**

model	Two-level model fitted with lme4. Must include random intercept, slope, and their covariation.
lv11.var	Character string. Level 1 variable name to which random slope is also estimated.
lv11.values	Level 1 variable values.

**Value**

Data frame of level 2 variance and std.dev. estimates at level 1 variable values and respective VPCs.

**References**

Goldstein, H., Browne, W., & Rasbash, J. (2002). Partitioning Variation in Multilevel Models. *Understanding Statistics*, 1(4), 223–231. [https://doi.org/10.1207/S15328031US0104\\_02](https://doi.org/10.1207/S15328031US0104_02)

**Examples**

```
fit <- lme4::lmer(Sepal.Length ~ Petal.Length +
  (Petal.Length | Species),
  data = iris
)

lv11.values <-
  c(
    mean(iris$Petal.Length) - stats::sd(iris$Petal.Length),
    mean(iris$Petal.Length),
    mean(iris$Petal.Length) + stats::sd(iris$Petal.Length)
  )

vpc_at(
  model = fit,
  lv11.var = "Petal.Length",
  lv11.values = lv11.values
)
```

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