

# Package: dmlrs (via r-universe)

November 1, 2026

**Type** Package

**Title** Fast Double / Debiased Machine Learning Implemented in Rust

**Version** 0.1.0

**Description** Double / debiased machine learning (Chernozhukov et al., 2018, <[doi:10.1111/ectj.12097](https://doi.org/10.1111/ectj.12097)>) for causal inference: partially linear, interactive, instrumental variable and difference-in-differences models with cross-fitted nuisance functions, multiplier bootstrap and sensitivity analysis for omitted confounding. Estimation, including the nuisance learners (lasso, logistic regression, random forests, gradient boosting), runs in Rust through the 'dml-core' crate, in parallel. Results match the Python package 'dml-rs', which is validated against 'DoubleML'.

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**URL** <https://asadgudzevic94.github.io/dml-rs/>,  
<https://github.com/AsadGudzevic94/dml-rs>

**BugReports** <https://github.com/AsadGudzevic94/dml-rs/issues>

**Encoding** UTF-8

**Depends** R (>= 4.2)

**Imports** stats

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**SystemRequirements** Cargo (Rust's package manager), rustc >= 1.80

**Roxygen** list(markdown = TRUE)

**Config/roxygen2/version** 8.1.1

**Config/pak/sysreqs** libclang-dev

**Repository** <https://asadgudzevic94.r-universe.dev>

**Date/Publication** 2026-11-01 05:02:56 UTC

**RemoteUrl** <https://github.com/AsadGudzevic94/dml-rs>

**RemoteRef** HEAD  
**RemoteSha** f96392695708d7bfe63d4666825598409ff8573f  
**RemoteSubdir** r/dmlrs

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|                   |                                               |
|-------------------|-----------------------------------------------|
| confint.dmlrs_fit | <i>Confidence intervals for DML estimates</i> |
|-------------------|-----------------------------------------------|

---

**Description**

Pointwise intervals, or simultaneous intervals for all treatments from the multiplier bootstrap (joint = TRUE), as DoubleML's confint().

**Usage**

```
## S3 method for class 'dmlrs_fit'
confint(
  object,
  parm,
  level = 0.95,
  joint = FALSE,
  method = c("normal", "Bayes", "wild"),
  n_boot = 500,
  seed = 0,
  ...
)
```

**Arguments**

- |        |                                                       |
|--------|-------------------------------------------------------|
| object | A fitted model.                                       |
| parm   | Treatments (names or indices); all by default.        |
| level  | Confidence level.                                     |
| joint  | Simultaneous intervals from the multiplier bootstrap. |

|        |                                                 |
|--------|-------------------------------------------------|
| method | Bootstrap weights: "normal", "Bayes" or "wild". |
| n_boot | Number of bootstrap draws.                      |
| seed   | Seed of the bootstrap.                          |
| ...    | Not used.                                       |

**Value**

A matrix with one row per treatment.

**Examples**

```
set.seed(3)
n <- 400
x <- matrix(rnorm(n * 3), n)
d <- cbind(d1 = x[, 1] + rnorm(n), d2 = x[, 2] + rnorm(n))
y <- 0.5 * d[, 1] - 0.2 * d[, 2] + x[, 3] + rnorm(n)
fit <- dml_plr(y, d, x, ml_l = lrn_ols())
confint(fit, joint = TRUE, n_boot = 1000)
```

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|         |                                  |
|---------|----------------------------------|
| dml_did | <i>Difference in differences</i> |
|---------|----------------------------------|

---

**Description**

The average treatment effect on the treated with two periods (Sant'Anna and Zhao, 2020), as DoubleMLDID and DoubleMLDIDCS. With panel data,  $y$  is the change of the outcome between the periods; with repeated cross-sections,  $y$  is the outcome and  $t$  the period (0/1).

**Usage**

```
dml_did(
  y,
  d,
  x,
  t = NULL,
  ml_g = lrn_lasso_cv(),
  ml_m = lrn_logistic_cv(),
  score = c("observational", "experimental"),
  in_sample_normalization = TRUE,
  n_folds = 5,
  n_rep = 1,
  seed = 0
)
```

**Arguments**

|                         |                                                                                                      |
|-------------------------|------------------------------------------------------------------------------------------------------|
| y                       | Outcome change (panel) or outcome (repeated cross-sections).                                         |
| d                       | Binary treatment group indicator (0/1).                                                              |
| x                       | Covariates: a numeric matrix or data frame.                                                          |
| t                       | NULL for panel data, or the period indicator (0/1) of repeated cross-sections.                       |
| ml_g                    | Learner for the outcome regressions.                                                                 |
| ml_m                    | Classifier for the propensity score (not used by the "experimental" score).                          |
| score                   | "observational" or "experimental".                                                                   |
| in_sample_normalization | Normalise the weights in sample, as DoubleML.                                                        |
| n_folds                 | Number of cross-fitting folds.                                                                       |
| n_rep                   | Number of repetitions of the sample split; estimates are aggregated with the median, as in DoubleML. |
| seed                    | Seed of the sample splits.                                                                           |

**Value**

A `dmlrs_fit` object; see `stats::coef()`, `confint.dmlrs_fit()`, `base::summary()` and `sensitivity_analysis()`.

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dml\_iivm

---

Interactive IV model

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**Description**

Local average treatment effect of a binary treatment with a binary instrument, as DoubleMLIIVM.

**Usage**

```
dml_iivm(
  y,
  d,
  z,
  x,
  ml_g = lrn_lasso_cv(),
  ml_m = lrn_logistic_cv(),
  ml_r = ml_m,
  subgroups = c(always_takers = TRUE, never_takers = TRUE),
  n_folds = 5,
  n_rep = 1,
  seed = 0
)
```

**Arguments**

|           |                                                                                                      |
|-----------|------------------------------------------------------------------------------------------------------|
| y         | Outcome (numeric vector).                                                                            |
| d         | Binary treatment (0/1).                                                                              |
| z         | Binary instrument (0/1).                                                                             |
| x         | Covariates: a numeric matrix or data frame.                                                          |
| ml_g      | Learner for $E[Y \mid Z, X]$ .                                                                       |
| ml_m      | Classifier for $P(Z = 1 \mid X)$ .                                                                   |
| ml_r      | Classifier for $P(D = 1 \mid Z, X)$ .                                                                |
| subgroups | Named logical vector: whether there can be always_takers and never_takers (as DoubleML's subgroups). |
| n_folds   | Number of cross-fitting folds.                                                                       |
| n_rep     | Number of repetitions of the sample split; estimates are aggregated with the median, as in DoubleML. |
| seed      | Seed of the sample splits.                                                                           |

**Value**

A dmlrs\_fit object; see [stats::coef\(\)](#), [confint.dmlrs\\_fit\(\)](#), [base::summary\(\)](#) and [sensitivity\\_analysis\(\)](#).

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|         |                                     |
|---------|-------------------------------------|
| dml_irm | <i>Interactive regression model</i> |
|---------|-------------------------------------|

---

**Description**

Average treatment effect ("ATE") or average treatment effect on the treated ("ATTE") of a binary treatment, as DoubleMLIRM.

**Usage**

```
dml_irm(
  y,
  d,
  x,
  ml_g = lrn_lasso_cv(),
  ml_m = lrn_logistic_cv(),
  score = c("ATE", "ATTE"),
  clipping_threshold = 0.01,
  normalize_ipw = FALSE,
  n_folds = 5,
  n_rep = 1,
  seed = 0
)
```

**Arguments**

|                                 |                                                                                                      |
|---------------------------------|------------------------------------------------------------------------------------------------------|
| <code>y</code>                  | Outcome (numeric vector).                                                                            |
| <code>d</code>                  | Binary treatment (0/1).                                                                              |
| <code>x</code>                  | Covariates: a numeric matrix or data frame.                                                          |
| <code>ml_g</code>               | Learner for $E[Y \mid D, X]$ (fitted on each treatment arm).                                         |
| <code>ml_m</code>               | Classifier for the propensity score $P(D = 1 \mid X)$ .                                              |
| <code>score</code>              | "ATE" or "ATTE".                                                                                     |
| <code>clipping_threshold</code> | Propensity scores are clipped to $[c, 1 - c]$ .                                                      |
| <code>normalize_ipw</code>      | Normalise the inverse-probability weights.                                                           |
| <code>n_folds</code>            | Number of cross-fitting folds.                                                                       |
| <code>n_rep</code>              | Number of repetitions of the sample split; estimates are aggregated with the median, as in DoubleML. |
| <code>seed</code>               | Seed of the sample splits.                                                                           |

**Value**

A `dmlrs_fit` object; see `stats::coef()`, `confint.dmlrs_fit()`, `base::summary()` and `sensitivity_analysis()`.

**Examples**

```
set.seed(2)
n <- 1000
x <- matrix(rnorm(n * 4), n)
d <- rbinom(n, 1, plogis(x[, 1]))
y <- d + x[, 1] + rnorm(n)
dml_irm(y, d, x, ml_g = lrn_ols(), ml_m = lrn_logistic())
```

---

dml\_pliv

*Partially linear IV regression*


---

**Description**

The partially linear model with an endogenous treatment and one instrument  $Z$ , as DoubleMLPLIV ("partialling out" score).

**Usage**

```
dml_pliv(
  y,
  d,
  z,
  x,
  ml_l = lrn_lasso_cv(),
```

```

    ml_m = ml_l,
    ml_r = ml_l,
    n_folds = 5,
    n_rep = 1,
    seed = 0
  )

```

### Arguments

|         |                                                                                                                   |
|---------|-------------------------------------------------------------------------------------------------------------------|
| y       | Outcome (numeric vector).                                                                                         |
| d       | Treatment: a numeric vector, or a matrix with one column per treatment (column names become the treatment names). |
| z       | Instrument (numeric vector).                                                                                      |
| x       | Covariates: a numeric matrix or data frame.                                                                       |
| ml_l    | Learner for $E[Y \mid X]$ .                                                                                       |
| ml_m    | Learner for $E[Z \mid X]$ .                                                                                       |
| ml_r    | Learner for $E[D \mid X]$ .                                                                                       |
| n_folds | Number of cross-fitting folds.                                                                                    |
| n_rep   | Number of repetitions of the sample split; estimates are aggregated with the median, as in DoubleML.              |
| seed    | Seed of the sample splits.                                                                                        |

### Value

A `dmlrs_fit` object; see [stats::coef\(\)](#), [confint.dmlrs\\_fit\(\)](#), [base::summary\(\)](#) and [sensitivity\\_analysis\(\)](#).

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|         |                                    |
|---------|------------------------------------|
| dml_plr | <i>Partially linear regression</i> |
|---------|------------------------------------|

---

### Description

Double / debiased machine learning for the partially linear model  $Y = D\theta + g(X) + \varepsilon$ , as DoubleMLPLR. The nuisance functions are cross-fitted in Rust.

### Usage

```

dml_plr(
  y,
  d,
  x,
  ml_l = lrn_lasso_cv(),
  ml_m = ml_l,
  ml_g = NULL,
  score = c("partialling out", "IV-type"),
  n_folds = 5,

```

```

    n_rep = 1,
    seed = 0
  )

```

### Arguments

|                      |                                                                                                                   |
|----------------------|-------------------------------------------------------------------------------------------------------------------|
| <code>y</code>       | Outcome (numeric vector).                                                                                         |
| <code>d</code>       | Treatment: a numeric vector, or a matrix with one column per treatment (column names become the treatment names). |
| <code>x</code>       | Covariates: a numeric matrix or data frame.                                                                       |
| <code>ml_l</code>    | Learner for $E[Y \mid X]$ (see <a href="#">learners</a> ).                                                        |
| <code>ml_m</code>    | Learner for $E[D \mid X]$ .                                                                                       |
| <code>ml_g</code>    | Learner for $g(X)$ , used by the "IV-type" score (default: <code>ml_l</code> ).                                   |
| <code>score</code>   | "partialling out" or "IV-type".                                                                                   |
| <code>n_folds</code> | Number of cross-fitting folds.                                                                                    |
| <code>n_rep</code>   | Number of repetitions of the sample split; estimates are aggregated with the median, as in DoubleML.              |
| <code>seed</code>    | Seed of the sample splits.                                                                                        |

### Value

A `dmlrs_fit` object; see [stats::coef\(\)](#), [confint.dmlrs\\_fit\(\)](#), [base::summary\(\)](#) and [sensitivity\\_analysis\(\)](#).

### Examples

```

set.seed(1)
n <- 500
x <- matrix(rnorm(n * 5), n)
d <- x[, 1] + rnorm(n)
y <- 0.5 * d + x[, 2] + rnorm(n)
fit <- dml_plr(y, d, x, ml_l = lrn_lasso_cv())
fit
confint(fit)

```

---

learners

*Built-in nuisance learners*


---

### Description

Learners for the nuisance functions of the DML models, implemented in Rust. Parameters follow scikit-learn, and results match the learners of the Python package `dml-rs`. Regressors learn conditional means; classifiers (`lrn_logistic()`, `lrn_logistic_cv()`, and the tree ensembles) learn probabilities of a binary variable.

**Usage**

```
lrn_ols(ridge = 0)

lrn_lasso(alpha = 1, tol = 1e-04, max_iter = 1e+05)

lrn_lasso_cv(n_alphas = 100, eps = 0.001, cv = 5)

lrn_logistic(C = 1)

lrn_logistic_cv(n_cs = 10, cv = 5)

lrn_random_forest(
  n_estimators = 100,
  max_depth = NULL,
  min_samples_leaf = 1,
  max_features = NULL,
  random_state = 0
)

lrn_gradient_boosting(
  n_estimators = 100,
  learning_rate = 0.1,
  max_depth = 3,
  min_samples_leaf = 1,
  subsample = 1,
  random_state = 0
)

lrn_hist_gradient_boosting(
  max_iter = 100,
  learning_rate = 0.1,
  max_leaf_nodes = 31,
  min_samples_leaf = 20,
  l2_regularization = 0,
  random_state = 0
)

lrn_regression_forest(n_estimators = 2000, min_node_size = 5, random_state = 0)
```

**Arguments**

|                         |                                                                                                                                                     |
|-------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| ridge, alpha, C         | Penalties (see above).                                                                                                                              |
| tol, max_iter           | Convergence tolerance and maximum iterations (sweeps of coordinate descent, or boosting iterations for <code>lrn_hist_gradient_boosting()</code> ). |
| n_alphas, eps, n_cs, cv | Grid size, smallest-to-largest penalty ratio and number of folds of the cross-validated learners.                                                   |
| n_estimators            | Number of trees.                                                                                                                                    |

|                                |                                                                                                                         |
|--------------------------------|-------------------------------------------------------------------------------------------------------------------------|
| <code>max_depth</code>         | Maximum tree depth (NULL: unlimited).                                                                                   |
| <code>min_samples_leaf</code>  | Minimum observations per leaf.                                                                                          |
| <code>max_features</code>      | Features tried per split: NULL (all for regression, "sqrt" for classification), "sqrt", "log2", a fraction or a number. |
| <code>random_state</code>      | Seed.                                                                                                                   |
| <code>learning_rate</code>     | Shrinkage of each tree.                                                                                                 |
| <code>subsample</code>         | Share of observations used for each tree.                                                                               |
| <code>max_leaf_nodes</code>    | Maximum leaves per tree (NULL: unlimited).                                                                              |
| <code>l2_regularization</code> | L2 penalty on leaf values.                                                                                              |
| <code>min_node_size</code>     | Minimum observations per leaf (grf's <code>min.node.size</code> ).                                                      |

## Details

- `lrn_ols()`: least squares with intercept, optionally ridge-penalised (ridge is scikit-learn's `Ridge(alpha)`).
- `lrn_lasso()`: lasso with penalty `alpha` (scikit-learn's Lasso).
- `lrn_lasso_cv()`: lasso with the penalty chosen by cv-fold cross-validation over `n_alphas` values (scikit-learn's `LassoCV`).
- `lrn_logistic()`: L2-penalised logistic regression with inverse penalty `C`.
- `lrn_logistic_cv()`: logistic regression with `C` chosen by stratified cross-validation (log loss) over `n_cs` values from `1e-4` to `1e4`.
- `lrn_random_forest()`: random forest (regressor or classifier).
- `lrn_gradient_boosting()`: gradient boosting with the trees of scikit-learn's `GradientBoosting*`.
- `lrn_hist_gradient_boosting()`: histogram gradient boosting, identical to scikit-learn's `HistGradientBoosting*`; the learner for large data.
- `lrn_regression_forest()`: honest regression forest (R's `grf::regression_forest`), regression only.

## Value

A learner specification (class `dmlrs_learner`).

## Examples

```
lrn_lasso_cv()
lrn_random_forest(n_estimators = 200, min_samples_leaf = 5)
```

---

sensitivity\_analysis    *Sensitivity analysis for omitted confounding*


---

**Description**

Bounds on the effect and robustness values when the confounding is as strong as `cf_y` (share of the residual outcome variance) and `cf_d` (share of the residual Riesz representer variance), with correlation  $\rho$  (Chernozhukov et al., 2022), as DoubleML's `sensitivity_analysis()`. Available for PLR, IRM and DID fits.

**Usage**

```
sensitivity_analysis(
  object,
  cf_y = 0.03,
  cf_d = 0.03,
  rho = 1,
  level = 0.95,
  null_hypothesis = 0
)
```

**Arguments**

|                                       |                                                              |
|---------------------------------------|--------------------------------------------------------------|
| <code>object</code>                   | A fitted model.                                              |
| <code>cf_y</code> , <code>cf_d</code> | Confounding strengths.                                       |
| <code>rho</code>                      | Correlation of the confounding in the outcome and treatment. |
| <code>level</code>                    | Confidence level of the bounds.                              |
| <code>null_hypothesis</code>          | Value of the effect under the null hypothesis.               |

**Value**

A data frame with one row per treatment: the bounds on the effect (`theta_lower`, `theta_upper`), their confidence bounds (`ci_lower`, `ci_upper`) and the robustness values `rv` and `rva` (in percent).

**Examples**

```
set.seed(4)
n <- 500
x <- matrix(rnorm(n * 3), n)
d <- x[, 1] + rnorm(n)
y <- 0.5 * d + x[, 2] + rnorm(n)
sensitivity_analysis(dml_plr(y, d, x, ml_l = lrn_ols()))
```

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