

# Package ‘acro’

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**Title** A Tool for Semi-Automating the Statistical Disclosure Control of Research Outputs

**Version** 0.1.5

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**Description** A Tool for Semi-Automating the Statistical Disclosure Control of Research Outputs.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxxygenNote** 7.3.2

**SystemRequirements** Python (>= 3.9)

**Imports** reticulate, admiraldev, png

**Depends** R (>= 2.10)

**LazyData** true

**Suggests** spelling, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Language** en-US

**URL** <https://github.com/AI-SDC/ACRO-R>

**BugReports** <https://github.com/AI-SDC/ACRO-R/issues>

**NeedsCompilation** no

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<b>acro_add_comments</b>	<i>Add comments to outputs</i>
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### Description

Add comments to outputs

### Usage

```
acro_add_comments(name, comment)
```

### Arguments

name	The name of the output.
comment	The comment.

### Value

No return value, called for side effects

---

acro\_add\_exception     *Adds an exception request to an output.*

---

### Description

Adds an exception request to an output.

### Usage

```
acro_add_exception(name, reason)
```

### Arguments

name	The name of the output.
reason	The comment.

### Value

No return value, called for side effects

---

acro\_crosstab     *Compute a simple cross tabulation of two (or more) factors.*

---

### Description

Compute a simple cross tabulation of two (or more) factors.

### Usage

```
acro_crosstab(index, columns, values = NULL, aggfunc = NULL)
```

### Arguments

index	Values to group by in the rows.
columns	Values to group by in the columns.
values	Array of values to aggregate according to the factors. Requires aggfunc be specified.
aggfunc	If specified, requires values be specified as well.

### Value

Cross tabulation of the data

---

**acro\_custom\_output**      *Adds an unsupported output to the results dictionary*

---

### Description

Adds an unsupported output to the results dictionary

### Usage

```
acro_custom_output(filename, comment = NULL)
```

### Arguments

<code>filename</code>	The name of the file that will be added to the list of the outputs.
<code>comment</code>	An optional comment.

### Value

No return value, called for side effects

---

**acro\_finalise**      *Creates a results file for checking.*

---

### Description

Creates a results file for checking.

### Usage

```
acro_finalise(path, ext)
```

### Arguments

<code>path</code>	Name of a folder to save outputs.
<code>ext</code>	Extension of the results file. Valid extensions are json or xlsx.

### Value

No return value, called for side effects

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acro_glm	<i>Fits Logit or Probit model.</i>
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## Description

Fits Logit or Probit model.

## Usage

```
acro_glm(formula, data, family)
```

## Arguments

formula	The formula specifying the model.
data	The data for the model.
family	Decide whether to fit a logit or probit model.

## Value

Regression Results Wrapper

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acro_hist	<i>Histogram</i>
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## Description

Histogram

## Usage

```
acro_hist(  
  data,  
  column,  
  breaks = 10,  
  freq = TRUE,  
  col = NULL,  
  filename = "histogram.png"  
)
```

**Arguments**

<code>data</code>	The object holding the data.
<code>column</code>	The column that will be used to plot the histogram.
<code>breaks</code>	Number of histogram bins to be used.
<code>freq</code>	If False, the result will contain the number of samples in each bin. If True, the result is the value of the probability density function at the bin.
<code>col</code>	The color of the plot.
<code>filename</code>	The name of the file where the plot will be saved.

**Value**

The histogram.

<code>acro_init</code>	<i>Initialise an ACRO object</i>
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**Description**

Initialise an ACRO object

**Usage**

```
acro_init(suppress = FALSE)
```

**Arguments**

<code>suppress</code>	Whether to automatically apply suppression.
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**Value**

No return value, called for side effects

<code>acro_lm</code>	<i>Fits Ordinary Least Squares Regression</i>
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**Description**

Fits Ordinary Least Squares Regression

**Usage**

```
acro_lm(formula, data)
```

**Arguments**

- |         |                                   |
|---------|-----------------------------------|
| formula | The formula specifying the model. |
| data    | The data for the model.           |

**Value**

Regression Results Wrapper.

---

acro\_pivot\_table      *Pivot table*

---

**Description**

Pivot table

**Usage**

```
acro_pivot_table(  
  data,  
  values = NULL,  
  index = NULL,  
  columns = NULL,  
  aggfunc = "mean"  
)
```

**Arguments**

- |         |  |
|---------|--|
| data    | The data to operate on.  |
| values  | Column to aggregate, optional.   |
| index   | If an array is passed, it must be the same length as the data. The list can contain any of the other types (except list). Keys to group by on the pivot table index. If an array is passed, it is being used as the same manner as column values.  |
| columns | If an array is passed, it must be the same length as the data. The list can contain any of the other types (except list). Keys to group by on the pivot table column. If an array is passed, it is being used as the same manner as column values. |
| aggfunc | If list of strings passed, the resulting pivot table will have hierarchical columns whose top level are the function names   |

**Value**

Cross tabulation of the data.

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`acro_print_outputs`     *Prints the current results dictionary.*

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### Description

Prints the current results dictionary.

### Usage

```
acro_print_outputs()
```

### Value

No return value, called for side effects

---

`acro_remove_output`     *Remove outputs*

---

### Description

Remove outputs

### Usage

```
acro_remove_output(name)
```

### Arguments

`name`     Key specifying which output to remove, e.g., 'output\_0'.

### Value

No return value, called for side effects

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acro_rename_output	<i>Rename outputs</i>
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---

**Description**

Rename outputs

**Usage**

```
acro_rename_output(old, new)
```

**Arguments**

old	The old name of the output.
new	The new name of the output.

**Value**

No return value, called for side effects

---

acro_surv_func	<i>Survival analysis</i>
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**Description**

Survival analysis

**Usage**

```
acro_surv_func(time, status, output, filename = "kaplan-meier.png")
```

**Arguments**

time	An array of times (censoring times or event times).
status	Status at the event time.
output	A string determine the type of output. Available options are table or plot.
filename	The name of the file where the plot will be saved.

**Value**

The survival table or plot.

**acro\_table***Compute a simple cross tabulation of two (or more) factors.***Description**

Compute a simple cross tabulation of two (or more) factors.

**Usage**

```
acro_table(index, columns, dnn = NULL, deparse.level = 0, ...)
```

**Arguments**

<code>index</code>	Values to group by in the rows.
<code>columns</code>	Values to group by in the columns.
<code>dnn</code>	The names to be given to the dimensions in the result
<code>deparse.level</code>	Controls how the default <code>dnn</code> is constructed.
<code>...</code>	Any other parameters.

**Value**

Cross tabulation of the data

**create\_virtualenv***Create a python virtual environment***Description**

Create a python virtual environment

**Usage**

```
create_virtualenv(...)
```

**Arguments**

<code>...</code>	Any other parameters.
------------------	-----------------------

**Value**

No return value, called for side effects

---

**install\_acro***Install acro*

---

**Description**

Install acro

**Usage**

```
install_acro(envname = "r-acro", ...)
```

**Arguments**

envname	the name of the Python virtual environment
...	Any other parameters.

**Value**

No return value, called for side effects

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**lung***Lung Cancer Survival Data*

---

**Description**

The lung dataset contains information about lung cancer survival.

**Usage**

```
lung
```

**Format**

A data frame with columns:

**inst** institutional identification  
**time** Survival time in months.  
**status** Survival status (1 = death, 0 = censored).  
**age** Age of the patient at the start of the study.  
**sex** Gender of the patient.  
**ph.ecog** Performance status (Eastern Cooperative Oncology Group).  
**ph.karno** 'Karnofsky' performance status.  
**pat.karno** 'Karnofsky' performance status as assessed by the patient.  
**meal.cal** Daily caloric intake at the start of the study.  
**wt.loss** Weight loss in the last six months.

**Examples**

```
data(lung)
```

---

nursery\_data

*Nursery Database*

---

**Description**

This dataset is originated from a hierarchical decision model created to evaluate applications for nursery schools.

**Usage**

```
nursery_data
```

**Format**

A data frame with columns: A data frame with 12960 rows and 9 columns:

**parents** Parents' occupation

**has\_nurs** Child's nursery

**form** Form of the family

**children** Number of children

**housing** Housing conditions

**finance** Financial standing of the family

**social** Social conditions

**health** Health conditions

**recommend** The ranking of applications for nursery schools

**Source**

<https://www.openml.org/search?type=data&status=active&id=26&sort=runs>

**Examples**

```
data(nursery_data)
```

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