

# Package ‘minter’

October 6, 2025

**Title** Effect Sizes for Meta-Analysis of Interactions from Factorial Experiments

**Version** 0.1.0

**Description** Compute effect sizes and their sampling variances from factorial experimental designs. The package supports calculation of simple effects, overall effects, and interaction effects for use in factorial meta-analyses. See Gurevitch et al. (2000) <[doi:10.1086/303337](https://doi.org/10.1086/303337)>, Morris et al. (2007) <[doi:10.1890/06-0442](https://doi.org/10.1890/06-0442)>, Lajeunesse (2011) <[doi:10.1890/11-0423.1](https://doi.org/10.1890/11-0423.1)> and Macartney et al. (2022) <[doi:10.1016/j.neubiorev.2022.104554](https://doi.org/10.1016/j.neubiorev.2022.104554)>.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**URL** <https://fdecunta.github.io/minter/>

**BugReports** <https://github.com/fdecunta/minter/issues>

**Imports** checkmate

**Depends** R (>= 3.5)

**LazyData** true

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**NeedsCompilation** no

**Author** Facundo Decunta [aut, cre] (ORCID: <<https://orcid.org/0009-0004-5774-1085>>), Shinichi Nakagawa [ctb], Daniel Noble [ctb]

**Maintainer** Facundo Decunta <[fdecunta@agro.uba.ar](mailto:fdecunta@agro.uba.ar)>

**Repository** CRAN

**Date/Publication** 2025-10-06 06:00:02 UTC

## Contents

lnCVR_ind . . . . .	2
lnCVR_inter . . . . .	4
lnCVR_main . . . . .	6
lnRR_ind . . . . .	7
lnRR_inter . . . . .	9
lnRR_main . . . . .	11
lnVR_ind . . . . .	13
lnVR_inter . . . . .	15
lnVR_main . . . . .	16
SMD_ind . . . . .	18
SMD_inter . . . . .	20
SMD_main . . . . .	22
time_lnCVR . . . . .	24
time_lnRR . . . . .	26
time_lnVR . . . . .	28
time_SMD . . . . .	29
<b>Index</b>	<b>32</b>

---

lnCVR_ind	<i>Individual Effect: Log Coefficient Of Variation Ratio</i>
-----------	--

---

### Description

Computes the Log of the Coefficient of Variation Ratio between Factor A and the Control treatment.

### Usage

```
lnCVR_ind(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
  A_sd,
  A_n
)
```

### Arguments

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE

Ctrl_mean	Mean outcome from the Control treatment
Ctrl_sd	Standard deviation from the control treatment
Ctrl_n	Sample size from the control treatment
A_mean	Mean outcome from the treatment
A_sd	Standard deviation from the treatment
A_n	Sample size from the treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named  $y_i$  (effect size) and  $v_i$  (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

### References

Nakagawa, S., Poulin, R., Mengersen, K., Reinhold, K., Engqvist, L., Lagisz, M., & Senior, A. M. (2015). Meta-analysis of variation: ecological and evolutionary applications and beyond. *Methods in Ecology and Evolution*, 6(2), 143-152.

### Examples

```
data <- data.frame(
  study_id = 1:3,
  control_mean = c(8.5, 12.3, 6.8),
  control_sd = c(1.8, 2.9, 1.4),
  control_n = c(18, 24, 16),
  nutrient_mean = c(11.2, 16.7, 9.3),
  nutrient_sd = c(3.1, 4.8, 2.7),
  nutrient_n = c(19, 22, 17)
)

result <- InCVR_ind(
  data = data,
  Ctrl_mean = "control_mean", Ctrl_sd = "control_sd", Ctrl_n = "control_n",
  A_mean = "nutrient_mean", A_sd = "nutrient_sd", A_n = "nutrient_n"
)
```

InCVR\_inter

*Interaction Effect: Log Coefficient of Variation Ratio***Description**

Computes the interaction effect between Factors A and B in factorial experiments on the coefficient of variation ratio.

**Usage**

```
InCVR_inter(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
  A_sd,
  A_n,
  B_mean,
  B_sd,
  B_n,
  AB_mean,
  AB_sd,
  AB_n
)
```

**Arguments**

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
Ctrl_mean	Mean outcome from the Control treatment
Ctrl_sd	Standard deviation from the control treatment
Ctrl_n	Sample size from the control treatment
A_mean	Mean outcome from the treatment
A_sd	Standard deviation from the treatment
A_n	Sample size from the treatment
B_mean	Mean outcome from the B treatment
B_sd	Standard deviation from the B treatment
B_n	Sample size from the B treatment

AB_mean	Mean outcome from the interaction AxB treatment
AB_sd	Standard deviation from the interaction AxB treatment
AB_n	Sample size from the interaction AxB treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named  $y_i$  (effect size) and  $v_i$  (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

### Examples

```
# Interaction effect logCVR (Light x Nutrients)
data <- data.frame(
  study_id = 1:2,
  control_mean = c(7.3, 8.9),
  control_sd = c(1.4, 1.7),
  control_n = c(20, 18),
  light_mean = c(12.8, 14.2),
  light_sd = c(3.1, 3.5),
  light_n = c(19, 20),
  nutrients_mean = c(9.6, 11.1),
  nutrients_sd = c(1.9, 2.2),
  nutrients_n = c(21, 17),
  light_nutrients_mean = c(18.4, 20.7),
  light_nutrients_sd = c(4.8, 5.3),
  light_nutrients_n = c(18, 19)
)

result <- InCVR_inter(
  data = data,
  Ctrl_mean = "control_mean",
  Ctrl_sd = "control_sd",
  Ctrl_n = "control_n",
  A_mean = "light_mean",
  A_sd = "light_sd",
  A_n = "light_n",
  B_mean = "nutrients_mean",
  B_sd = "nutrients_sd",
  B_n = "nutrients_n",
  AB_mean = "light_nutrients_mean",
  AB_sd = "light_nutrients_sd",
  AB_n = "light_nutrients_n"
```

)

InCVR\_main

*Main Effect: Log Coefficient Of Variation Ration***Description**

Computes the main effect of Factor A across levels of Factor B in factorial experiments on the coefficient of variation.

**Usage**

```
InCVR_main(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
  A_sd,
  A_n,
  B_mean,
  B_sd,
  B_n,
  AB_mean,
  AB_sd,
  AB_n
)
```

**Arguments**

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
Ctrl_mean	Mean outcome from the Control treatment
Ctrl_sd	Standard deviation from the control treatment
Ctrl_n	Sample size from the control treatment
A_mean	Mean outcome from the treatment
A_sd	Standard deviation from the treatment
A_n	Sample size from the treatment
B_mean	Mean outcome from the B treatment

B_sd	Standard deviation from the B treatment
B_n	Sample size from the B treatment
AB_mean	Mean outcome from the interaction AxB treatment
AB_sd	Standard deviation from the interaction AxB treatment
AB_n	Sample size from the interaction AxB treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named  $y_i$  (effect size) and  $v_i$  (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

### Examples

```
data <- data.frame(
  study_id = 1:2,
  control_mean = c(14.2, 16.8), control_sd = c(2.8, 3.1), control_n = c(16, 14),
  irrigation_mean = c(19.5, 22.1), irrigation_sd = c(5.2, 5.8), irrigation_n = c(15, 16),
  co2_mean = c(16.8, 19.4), co2_sd = c(3.1, 3.6), co2_n = c(17, 13),
  irrigation_co2_mean = c(24.3, 27.9), irrigation_co2_sd = c(6.8, 7.4), irrigation_co2_n = c(14, 15)
)

result <- lnCVR_main(
  data = data,
  Ctrl_mean = "control_mean", Ctrl_sd = "control_sd", Ctrl_n = "control_n",
  A_mean = "irrigation_mean", A_sd = "irrigation_sd", A_n = "irrigation_n",
  B_mean = "co2_mean", B_sd = "co2_sd", B_n = "co2_n",
  AB_mean = "irrigation_co2_mean", AB_sd = "irrigation_co2_sd", AB_n = "irrigation_co2_n"
)
```

---

InRR\_ind

*Simple effect: Log Response Ratio*

---

### Description

Computes the individual or simple effect of Factor A over the Control.

**Usage**

```
InRR_ind(  
  data,  
  col_names = c("yi", "vi"),  
  append = TRUE,  
  Ctrl_mean,  
  Ctrl_sd,  
  Ctrl_n,  
  A_mean,  
  A_sd,  
  A_n  
)
```

**Arguments**

<code>data</code>	Data frame containing the variables used.
<code>col_names</code>	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
<code>append</code>	Logical. Append the results to data. Default is TRUE
<code>Ctrl_mean</code>	Mean outcome from the Control treatment
<code>Ctrl_sd</code>	Standard deviation from the control treatment
<code>Ctrl_n</code>	Sample size from the control treatment
<code>A_mean</code>	Mean outcome from the experimental treatment
<code>A_sd</code>	Standard deviation from the experimental treatment
<code>A_n</code>	Sample size from the experimental treatment

**Details**

It is the classic Log Response Ratio (InRR), which can also be computed with `metafor`'s `escalc()` function using `measure = "ROM"`.

See the package vignette for a detailed description of the formula.

**Value**

A data frame containing the effect sizes and their sampling variance. By default, the columns are named `yi` (effect size) and `vi` (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

**Author(s)**

Facundo Decunta - [fdecunta@agro.uba.ar](mailto:fdecunta@agro.uba.ar)



## References

Morris, W. F., Hufbauer, R. A., Agrawal, A. A., Bever, J. D., Borowicz, V. A., Gilbert, G. S., ... & Vázquez, D. P. (2007). Direct and interactive effects of enemies and mutualists on plant performance: a meta-analysis. *Ecology*, 88(4), 1021-1029. <https://doi.org/10.1890/06-0442>

Lajeunesse, M. J. (2011). On the meta-analysis of response ratios for studies with correlated and multi-group designs. *Ecology*, 92(11), 2049-2055. <https://doi.org/10.1890/11-0423.1>

## Examples

```
data <- data.frame(
  study_id = 1:3,
  control_mean = c(10, 15, 12),
  control_sd = c(2.1, 3.2, 2.8),
  control_n = c(20, 25, 18),
  drought_mean = c(12, 18, 14),
  drought_sd = c(2.3, 3.5, 3.1),
  drought_n = c(22, 24, 20)
)

# Compute individual effect of drought vs control
result <- lnRR_ind(
  data = data,
  Ctrl_mean = "control_mean",
  Ctrl_sd = "control_sd",
  Ctrl_n = "control_n",
  A_mean = "drought_mean",
  A_sd = "drought_sd",
  A_n = "drought_n"
)
```

---

 lnRR\_inter

*Interaction effect: Log Response Ratio*


---

## Description

Computes the interaction effect between factors A and B in factorial data.

## Usage

```
lnRR_inter(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
```

```

    A_sd,
    A_n,
    B_mean,
    B_sd,
    B_n,
    AB_mean,
    AB_sd,
    AB_n
  )

```

### Arguments

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
Ctrl_mean	Mean outcome from the Control treatment
Ctrl_sd	Standard deviation from the control treatment
Ctrl_n	Sample size from the control treatment
A_mean	Mean outcome from the treatment
A_sd	Standard deviation from the treatment
A_n	Sample size from the treatment
B_mean	Mean outcome from the B treatment
B_sd	Standard deviation from the B treatment
B_n	Sample size from the B treatment
AB_mean	Mean outcome from the interaction AxB treatment
AB_sd	Standard deviation from the interaction AxB treatment
AB_n	Sample size from the interaction AxB treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named yi (effect size) and vi (sampling variance). If append = TRUE, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

## References

Morris, W. F., Hufbauer, R. A., Agrawal, A. A., Bever, J. D., Borowicz, V. A., Gilbert, G. S., ... & Vázquez, D. P. (2007). Direct and interactive effects of enemies and mutualists on plant performance: a meta-analysis. *Ecology*, 88(4), 1021-1029. <https://doi.org/10.1890/06-0442>

## Examples

```
data <- data.frame(
  study_id = 1:2,
  control_mean = c(25, 28), control_sd = c(3.2, 3.8), control_n = c(15, 17),
  predation_mean = c(18, 20), predation_sd = c(2.9, 3.1), predation_n = c(16, 18),
  competition_mean = c(22, 24), competition_sd = c(3.0, 3.5), competition_n = c(14, 16),
  pred_comp_mean = c(12, 15), pred_comp_sd = c(2.1, 2.6), pred_comp_n = c(15, 17)
)

# Compute interaction effect between predation and competition
result <- InRR_inter(
  data = data,
  Ctrl_mean = "control_mean", Ctrl_sd = "control_sd", Ctrl_n = "control_n",
  A_mean = "predation_mean", A_sd = "predation_sd", A_n = "predation_n",
  B_mean = "competition_mean", B_sd = "competition_sd", B_n = "competition_n",
  AB_mean = "pred_comp_mean", AB_sd = "pred_comp_sd", AB_n = "pred_comp_n"
)
```

---

InRR\_main

*Main effect: Log Response Ratio*

---

## Description

Computes the main effect of Factor A across levels of Factor B, analogous to the main effect in a factorial ANOVA.

## Usage

```
InRR_main(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  method = "nakagawa",
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
  A_sd,
  A_n,
  B_mean,
  B_sd,
```

```

    B_n,
    AB_mean,
    AB_sd,
    AB_n
  )

```

### Arguments

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
method	Method to compute InRR. Can be either "nakagawa" or "morris". Default is "nakagawa".
Ctrl_mean	Mean outcome from the Control treatment
Ctrl_sd	Standard deviation from the control treatment
Ctrl_n	Sample size from the control treatment
A_mean	Mean outcome from the A treatment
A_sd	Standard deviation from the A treatment
A_n	Sample size from the A treatment
B_mean	Mean outcome from the B treatment
B_sd	Standard deviation from the B treatment
B_n	Sample size from the B treatment
AB_mean	Mean outcome from the interaction AxB treatment
AB_sd	Standard deviation from the interaction AxB treatment
AB_n	Sample size from the interaction AxB treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named yi (effect size) and vi (sampling variance). If append = TRUE, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

## References

- Morris, W. F., Hufbauer, R. A., Agrawal, A. A., Bever, J. D., Borowicz, V. A., Gilbert, G. S., ... & Vázquez, D. P. (2007). Direct and interactive effects of enemies and mutualists on plant performance: a meta-analysis. *Ecology*, 88(4), 1021-1029. <https://doi.org/10.1890/06-0442>
- Lajeunesse, M. J. (2011). On the meta-analysis of response ratios for studies with correlated and multi-group designs. *Ecology*, 92(11), 2049-2055. <https://doi.org/10.1890/11-0423.1>
- Macartney, E. L., Lagisz, M., & Nakagawa, S. (2022). The relative benefits of environmental enrichment on learning and memory are greater when stressed: A meta-analysis of interactions in rodents. *Neuroscience & Biobehavioral Reviews*, 135, 104554. <https://doi.org/10.1016/j.neubiorev.2022.104554>

## Examples

```
# Example data for 2x2 factorial design (Fertilization x Warming)
data <- data.frame(
  study_id = 1:2,
  control_mean = c(10, 12), control_sd = c(2.0, 2.5), control_n = c(20, 18),
  fertilization_mean = c(15, 16), fertilization_sd = c(2.2, 2.8), fertilization_n = c(20, 19),
  warming_mean = c(11, 13), warming_sd = c(2.1, 2.6), warming_n = c(21, 17),
  fert_warm_mean = c(17, 19), fert_warm_sd = c(2.4, 3.0), fert_warm_n = c(19, 20)
)

# Compute main effect of fertilization
result <- lnRR_main(
  data = data,
  Ctrl_mean = "control_mean", Ctrl_sd = "control_sd", Ctrl_n = "control_n",
  A_mean = "fertilization_mean", A_sd = "fertilization_sd", A_n = "fertilization_n",
  B_mean = "warming_mean", B_sd = "warming_sd", B_n = "warming_n",
  AB_mean = "fert_warm_mean", AB_sd = "fert_warm_sd", AB_n = "fert_warm_n"
)
```

---

InVR\_ind

*Individual effect: Log of Variability Ratio*


---

## Description

Computes the Log of the Variability Ratio between a Factor A and the Control treatment in factorial experiments.

## Usage

```
lnVR_ind(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  Ctrl_sd,
  Ctrl_n,
```

```

    A_sd,
    A_n
  )

```

### Arguments

<code>data</code>	Data frame containing the variables used.
<code>col_names</code>	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
<code>append</code>	Logical. Append the results to <code>data</code> . Default is TRUE
<code>Ctrl_sd</code>	Standard deviation from the control treatment
<code>Ctrl_n</code>	Sample size from the control treatment
<code>A_sd</code>	Standard deviation from the treatment
<code>A_n</code>	Sample size from the treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named `yi` (effect size) and `vi` (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

### References

Nakagawa, S., Poulin, R., Mengersen, K., Reinhold, K., Engqvist, L., Lagisz, M., & Senior, A. M. (2015). Meta-analysis of variation: ecological and evolutionary applications and beyond. *Methods in Ecology and Evolution*, 6(2), 143-152.

### Examples

```

# Example focusing on variability differences (Herbivory effect)
data <- data.frame(
  study_id = 1:3,
  control_sd = c(2.1, 1.8, 2.5),
  control_n = c(20, 22, 18),
  herbivory_sd = c(3.2, 2.9, 3.8),
  herbivory_n = c(21, 20, 19)
)

result <- InVR_ind(
  data = data,
  Ctrl_sd = "control_sd",

```

```

  Ctrl_n = "control_n",
  A_sd = "herbivory_sd",
  A_n = "herbivory_n"
)

```

---

InVR\_inter

*Interaction effect: Log Variability Ratio*


---

### Description

Computes the interaction of Factors A and B measured as the log of the variability ratio.

### Usage

```

InVR_inter(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  Ctrl_sd,
  Ctrl_n,
  A_sd,
  A_n,
  B_sd,
  B_n,
  AB_sd,
  AB_n
)

```

### Arguments

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
Ctrl_sd	Standard deviation from the control treatment
Ctrl_n	Sample size from the control treatment
A_sd	Standard deviation from the A treatment
A_n	Sample size from the A treatment
B_sd	Standard deviation from the B treatment
B_n	Sample size from the B treatment
AB_sd	Standard deviation from the interaction AxB treatment
AB_n	Sample size from the interaction AxB treatment

**Details**

See the package vignette for a detailed description of the formula.

**Value**

A data frame containing the effect sizes and their sampling variance. By default, the columns are named yi (effect size) and vi (sampling variance). If append = TRUE, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

**Author(s)**

Facundo Decunta - fdecunta@agro.uba.ar

**Examples**

```
# Example for interaction effect in 2x2 factorial focusing on variability (Drought x Temperature)
data <- data.frame(
  study_id = 1:2,
  control_sd = c(1.8, 2.1), control_n = c(22, 19),
  drought_sd = c(2.6, 2.9), drought_n = c(20, 21),
  temperature_sd = c(2.0, 2.3), temperature_n = c(21, 18),
  drought_temp_sd = c(3.2, 3.6), drought_temp_n = c(19, 20)
)

result <- lnVR_inter(
  data = data,
  Ctrl_sd = "control_sd", Ctrl_n = "control_n",
  A_sd = "drought_sd", A_n = "drought_n",
  B_sd = "temperature_sd", B_n = "temperature_n",
  AB_sd = "drought_temp_sd", AB_n = "drought_temp_n"
)
```

---

lnVR\_main

---

*Main Effect: Log of the Variability Ratio*


---

**Description**

Computes the overall log of the variability ratio for Factor A across levels of Factor B.

**Usage**

```
lnVR_main(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  Ctrl_sd,
  Ctrl_n,
```



```

    A_sd,
    A_n,
    B_sd,
    B_n,
    AB_sd,
    AB_n
  )

```

### Arguments

<code>data</code>	Data frame containing the variables used.
<code>col_names</code>	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
<code>append</code>	Logical. Append the results to data. Default is TRUE
<code>Ctrl_sd</code>	Standard deviation from the control treatment
<code>Ctrl_n</code>	Sample size from the control treatment
<code>A_sd</code>	Standard deviation from the A treatment
<code>A_n</code>	Sample size from the A treatment
<code>B_sd</code>	Standard deviation from the B treatment
<code>B_n</code>	Sample size from the B treatment
<code>AB_sd</code>	Standard deviation from the interaction AxB treatment
<code>AB_n</code>	Sample size from the interaction AxB treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named yi (effect size) and vi (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

### Examples

```

# Example for main effect in 2x2 factorial focusing on variability (Fire x Grazing)
data <- data.frame(
  study_id = 1:2,
  control_sd = c(2.0, 2.3), control_n = c(20, 18),
  fire_sd = c(2.8, 3.1), fire_n = c(19, 20),
  grazing_sd = c(2.2, 2.5), grazing_n = c(21, 17),
  fire_grazing_sd = c(3.5, 3.8), fire_grazing_n = c(18, 19)
)

```

```

result <- lnVR_main(
  data = data,
  Ctrl_sd = "control_sd", Ctrl_n = "control_n",
  A_sd = "fire_sd", A_n = "fire_n",
  B_sd = "grazing_sd", B_n = "grazing_n",
  AB_sd = "fire_grazing_sd", AB_n = "fire_grazing_n"
)

```

---

SMD\_ind

*Simple effect: Standardized Mean Difference*


---

### Description

Computes the individual or simple effect of Factor A over the Control.

### Usage

```

SMD_ind(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  hedges_correction = TRUE,
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
  A_sd,
  A_n
)

```

### Arguments

<code>data</code>	Data frame containing the variables used.
<code>col_names</code>	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
<code>append</code>	Logical. Append the results to data. Default is TRUE
<code>hedges_correction</code>	Boolean. If TRUE correct for small-sample bias. Default is TRUE.
<code>Ctrl_mean</code>	Mean outcome from the Control treatment
<code>Ctrl_sd</code>	Standard deviation from the control treatment
<code>Ctrl_n</code>	Sample size from the control treatment
<code>A_mean</code>	Mean outcome from the experimental treatment
<code>A_sd</code>	Standard deviation from the experimental treatment
<code>A_n</code>	Sample size from the experimental treatment

## Details

It is the classic Standardized Mean Difference (SMD), which can also be computed with metafor's `escalec()` function using `measure = "SMD"`.

See the package vignette for a detailed description of the formula.

## Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named `yi` (effect size) and `vi` (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

## Author(s)

Facundo Decunta - [fdecunta@agro.uba.ar](mailto:fdecunta@agro.uba.ar)

## References

Gurevitch, J., Morrison, J. A., & Hedges, L. V. (2000). The interaction between competition and predation: a meta-analysis of field experiments. *The American Naturalist*, 155(4), 435-453.

Morris, W. F., Hufbauer, R. A., Agrawal, A. A., Bever, J. D., Borowicz, V. A., Gilbert, G. S., ... & Vázquez, D. P. (2007). Direct and interactive effects of enemies and mutualists on plant performance: a meta-analysis. *Ecology*, 88(4), 1021-1029. <https://doi.org/10.1890/06-0442>

## Examples

```
data <- data.frame(
  study_id = 1:3,
  control_mean = c(45.2, 52.8, 38.9),
  control_sd = c(8.1, 11.2, 7.3),
  control_n = c(18, 23, 16),
  pollinator_exclusion_mean = c(28.7, 35.4, 22.1),
  pollinator_exclusion_sd = c(6.8, 9.1, 5.9),
  pollinator_exclusion_n = c(20, 22, 18)
)

# With Hedges' correction (default)
result <- SMD_ind(
  data = data,
  Ctrl_mean = "control_mean",
  Ctrl_sd = "control_sd",
  Ctrl_n = "control_n",
  A_mean = "pollinator_exclusion_mean",
  A_sd = "pollinator_exclusion_sd",
  A_n = "pollinator_exclusion_n",
  hedges_correction = TRUE
)

# Without Hedges' correction
result_no_hedges <- SMD_ind(
  data = data,
```

```

Ctrl_mean = "control_mean",
Ctrl_sd = "control_sd",
Ctrl_n = "control_n",
A_mean = "pollinator_exclusion_mean",
A_sd = "pollinator_exclusion_sd",
A_n = "pollinator_exclusion_n",
hedges_correction = FALSE
)

```

---

SMD\_inter

*Interaction effect: Standardized mean difference*


---

### Description

Computes the interaction effect between factors A and B in factorial data.

### Usage

```

SMD_inter(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  hedges_correction = TRUE,
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
  A_sd,
  A_n,
  B_mean,
  B_sd,
  B_n,
  AB_mean,
  AB_sd,
  AB_n
)

```

### Arguments

<code>data</code>	Data frame containing the variables used.
<code>col_names</code>	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
<code>append</code>	Logical. Append the results to data. Default is TRUE
<code>hedges_correction</code>	Logical. Apply or not Hedges' correction for small-sample bias. Default is TRUE

Ctrl_mean	Mean outcome from the Control treatment
Ctrl_sd	Standard deviation from the control treatment
Ctrl_n	Sample size from the control treatment
A_mean	Mean outcome from the treatment
A_sd	Standard deviation from the treatment
A_n	Sample size from the treatment
B_mean	Mean outcome from the B treatment
B_sd	Standard deviation from the B treatment
B_n	Sample size from the B treatment
AB_mean	Mean outcome from the interaction AxB treatment
AB_sd	Standard deviation from the interaction AxB treatment
AB_n	Sample size from the interaction AxB treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named  $y_i$  (effect size) and  $v_i$  (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - [fdecunta@agro.uba.ar](mailto:fdecunta@agro.uba.ar)

### References

- Gurevitch, J., Morrison, J. A., & Hedges, L. V. (2000). The interaction between competition and predation: a meta-analysis of field experiments. *The American Naturalist*, 155(4), 435-453.
- Morris, W. F., Hufbauer, R. A., Agrawal, A. A., Bever, J. D., Borowicz, V. A., Gilbert, G. S., ... & Vázquez, D. P. (2007). Direct and interactive effects of enemies and mutualists on plant performance: a meta-analysis. *Ecology*, 88(4), 1021-1029. <https://doi.org/10.1890/06-0442>

### Examples

```
data <- data.frame(
  study_id = 1:2,
  control_mean = c(24.8, 27.2), control_sd = c(4.1, 4.6), control_n = c(18, 16),
  salinity_mean = c(19.3, 21.7), salinity_sd = c(3.8, 4.2), salinity_n = c(17, 18),
  temperature_mean = c(28.9, 31.4), temperature_sd = c(4.7, 5.1), temperature_n = c(19, 15),
  salt_temp_mean = c(15.2, 17.8), salt_temp_sd = c(3.1, 3.5), salt_temp_n = c(16, 17)
)

result <- SMD_inter(
  data = data,
```

```

Ctrl_mean = "control_mean", Ctrl_sd = "control_sd", Ctrl_n = "control_n",
A_mean = "salinity_mean", A_sd = "salinity_sd", A_n = "salinity_n",
B_mean = "temperature_mean", B_sd = "temperature_sd", B_n = "temperature_n",
AB_mean = "salt_temp_mean", AB_sd = "salt_temp_sd", AB_n = "salt_temp_n"
)

```

---

SMD\_main

*Main effect: Standardized Mean Difference*


---

### Description

Computes the main effect of Factor A across levels of Factor B, analogous to the main effect in a factorial ANOVA.

### Usage

```

SMD_main(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  hedges_correction = TRUE,
  Ctrl_mean,
  Ctrl_sd,
  Ctrl_n,
  A_mean,
  A_sd,
  A_n,
  B_mean,
  B_sd,
  B_n,
  AB_mean,
  AB_sd,
  AB_n
)

```

### Arguments

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
hedges_correction	Boolean. If TRUE correct for small-sample bias. Default is TRUE.
Ctrl_mean	Mean outcome from the Control treatment
Ctrl_sd	Standard deviation from the control treatment

Ctrl_n	Sample size from the control treatment
A_mean	Mean outcome from the A treatment
A_sd	Standard deviation from the A treatment
A_n	Sample size from the A treatment
B_mean	Mean outcome from the B treatment
B_sd	Standard deviation from the B treatment
B_n	Sample size from the B treatment
AB_mean	Mean outcome from the interaction AxB treatment
AB_sd	Standard deviation from the interaction AxB treatment
AB_n	Sample size from the interaction AxB treatment

### Details

See the package vignette for a detailed description of the formula.

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named  $y_i$  (effect size) and  $v_i$  (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

### References

Gurevitch, J., Morrison, J. A., & Hedges, L. V. (2000). The interaction between competition and predation: a meta-analysis of field experiments. *The American Naturalist*, 155(4), 435-453.

Morris, W. F., Hufbauer, R. A., Agrawal, A. A., Bever, J. D., Borowicz, V. A., Gilbert, G. S., ... & Vázquez, D. P. (2007). Direct and interactive effects of enemies and mutualists on plant performance: a meta-analysis. *Ecology*, 88(4), 1021-1029. <https://doi.org/10.1890/06-0442>

### Examples

```
# Main effect of Mycorrhiza in 2x2 factorial design (AMF x Phosphorus)
data <- data.frame(
  study_id = 1:2,
  control_mean = c(12.4, 15.1), control_sd = c(2.8, 3.2), control_n = c(16, 14),
  mycorrhizae_mean = c(18.7, 21.3), mycorrhizae_sd = c(3.4, 3.9), mycorrhizae_n = c(15, 16),
  phosphorus_mean = c(14.9, 17.8), phosphorus_sd = c(3.1, 3.6), phosphorus_n = c(17, 13),
  myco_phos_mean = c(22.1, 25.4), myco_phos_sd = c(4.2, 4.8), myco_phos_n = c(14, 15)
)

result <- SMD_main(
  data = data,
  Ctrl_mean = "control_mean", Ctrl_sd = "control_sd", Ctrl_n = "control_n",
  A_mean = "mycorrhizae_mean", A_sd = "mycorrhizae_sd", A_n = "mycorrhizae_n",
```

```

B_mean = "phosphorus_mean", B_sd = "phosphorus_sd", B_n = "phosphorus_n",
AB_mean = "myco_phos_mean", AB_sd = "myco_phos_sd", AB_n = "myco_phos_n"
)

```

---

time\_InCVR

*Log Coefficient of Variation Ratio: Interaction Between Treatment and Time*


---

### Description

Log Coefficient of Variation Ratio: Interaction Between Treatment and Time

### Usage

```

time_InCVR(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  t0_Ctrl_mean,
  t0_Ctrl_sd,
  t1_Ctrl_mean,
  t1_Ctrl_sd,
  Ctrl_n,
  Ctrl_cor,
  t0_Exp_mean,
  t0_Exp_sd,
  t1_Exp_mean,
  t1_Exp_sd,
  Exp_n,
  Exp_cor
)

```

### Arguments

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
t0_Ctrl_mean	Sample mean from the control group at time 0
t0_Ctrl_sd	Standard deviation from the control group at time 0
t1_Ctrl_mean	Sample mean from the control group at time 1
t1_Ctrl_sd	Standard deviation from the control group at time 1
Ctrl_n	Sample size of the control group



Ctrl_cor	Number or numeric vector. Correlation between the means of the control group at t0 and t1
t0_Exp_mean	Sample mean from the experimental group at time 0
t0_Exp_sd	Standard deviation from the experimental group at time 0
t1_Exp_mean	Sample mean from the experimental group at time 1
t1_Exp_sd	Standard deviation from the experimental group at time 1
Exp_n	Sample size of the experimental group
Exp_cor	Number or numeric vector. Correlation between the means of the experimental group at t0 and t1

**Value**

A data frame containing the effect sizes and their sampling variance. By default, the columns are named  $y_i$  (effect size) and  $v_i$  (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

**Author(s)**

Facundo Decunta - fdecunta@agro.uba.ar

**References**

Shinichi Nakagawa and Daniel Noble, personal communication.

**Examples**

```
# Pre-post design for coefficient of variation changes over time (Disturbance experiment)
data <- data.frame(
  study_id = 1:2,
  pre_control_mean = c(12.8, 15.4), pre_control_sd = c(2.6, 3.1),
  post_control_mean = c(13.2, 15.9), post_control_sd = c(2.7, 3.2),
  control_n = c(20, 18),
  pre_disturbed_mean = c(12.9, 15.2), pre_disturbed_sd = c(2.5, 3.0),
  post_disturbed_mean = c(8.7, 10.1), post_disturbed_sd = c(3.8, 4.3),
  disturbed_n = c(19, 21)
)

result <- time_InCVR(
  data = data,
  t0_Ctrl_mean = "pre_control_mean", t0_Ctrl_sd = "pre_control_sd",
  t1_Ctrl_mean = "post_control_mean", t1_Ctrl_sd = "post_control_sd",
  Ctrl_n = "control_n", Ctrl_cor = 0.8,
  t0_Exp_mean = "pre_disturbed_mean", t0_Exp_sd = "pre_disturbed_sd",
  t1_Exp_mean = "post_disturbed_mean", t1_Exp_sd = "post_disturbed_sd",
  Exp_n = "disturbed_n", Exp_cor = 0.5
)
```

time\_InRR

*Log Response Ratio: Interaction Between Treatment and Time***Description**

Log Response Ratio: Interaction Between Treatment and Time

**Usage**

```
time_InRR(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  t0_Ctrl_mean,
  t0_Ctrl_sd,
  t1_Ctrl_mean,
  t1_Ctrl_sd,
  Ctrl_n,
  Ctrl_cor,
  t0_Exp_mean,
  t0_Exp_sd,
  t1_Exp_mean,
  t1_Exp_sd,
  Exp_n,
  Exp_cor
)
```

**Arguments**

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
t0_Ctrl_mean	Sample mean from the control group at time 0
t0_Ctrl_sd	Standard deviation from the control group at time 0
t1_Ctrl_mean	Sample mean from the control group at time 1
t1_Ctrl_sd	Standard deviation from the control group at time 1
Ctrl_n	Sample size of the control group
Ctrl_cor	Number or numeric vector. Correlation between the means of the control group at t0 and t1
t0_Exp_mean	Sample mean from the experimental group at time 0
t0_Exp_sd	Standard deviation from the experimental group at time 0
t1_Exp_mean	Sample mean from the experimental group at time 1

t1_Exp_sd	Standard deviation from the experimental group at time 1
Exp_n	Sample size of the experimental group
Exp_cor	Number or numeric vector. Correlation between the means of the experimental group at t0 and t1

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named  $y_i$  (effect size) and  $v_i$  (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

### Author(s)

Facundo Decunta - fdecunta@agro.uba.ar

### References

Shinichi Nakagawa and Daniel Noble, personal communication.

### Examples

```
data <- data.frame(
  study_id = 1:2,
  pre_control_mean = c(8.4, 10.2),      # Control before restoration
  pre_control_sd = c(1.8, 2.1),
  post_control_mean = c(8.9, 10.7),    # Control after restoration period
  post_control_sd = c(1.9, 2.2),
  control_n = c(22, 18),
  pre_restoration_mean = c(8.6, 10.1), # Restoration sites before
  pre_restoration_sd = c(1.9, 2.0),
  post_restoration_mean = c(15.3, 17.8), # Restoration sites after
  post_restoration_sd = c(3.2, 3.7),
  restoration_n = c(20, 19)
)

result <- time_lnRR(
  data = data,
  t0_Ctrl_mean = "pre_control_mean", t0_Ctrl_sd = "pre_control_sd",
  t1_Ctrl_mean = "post_control_mean", t1_Ctrl_sd = "post_control_sd",
  Ctrl_n = "control_n", Ctrl_cor = 0.7, # Correlation within control sites
  t0_Exp_mean = "pre_restoration_mean", t0_Exp_sd = "pre_restoration_sd",
  t1_Exp_mean = "post_restoration_mean", t1_Exp_sd = "post_restoration_sd",
  Exp_n = "restoration_n", Exp_cor = 0.6 # Correlation within restoration sites
)

# Using different correlations for each study
result2 <- time_lnRR(
  data = data,
  t0_Ctrl_mean = "pre_control_mean", t0_Ctrl_sd = "pre_control_sd",
  t1_Ctrl_mean = "post_control_mean", t1_Ctrl_sd = "post_control_sd",
  Ctrl_n = "control_n", Ctrl_cor = c(0.6, 0.8),
```

```

t0_Exp_mean = "pre_restoration_mean", t0_Exp_sd = "pre_restoration_sd",
t1_Exp_mean = "post_restoration_mean", t1_Exp_sd = "post_restoration_sd",
Exp_n = "restoration_n", Exp_cor = c(0.5, 0.7)
)

```

---

time\_InVR

---

*Log of Variability Ratio: Interaction Between Treatment and Time*


---

### Description

Log of Variability Ratio: Interaction Between Treatment and Time

### Usage

```

time_InVR(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  t0_Ctrl_sd,
  t1_Ctrl_sd,
  Ctrl_n,
  Ctrl_cor,
  t0_Exp_sd,
  t1_Exp_sd,
  Exp_n,
  Exp_cor
)

```

### Arguments

data	Data frame containing the variables used.
col_names	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
append	Logical. Append the results to data. Default is TRUE
t0_Ctrl_sd	Standard deviation from the control group at time 0
t1_Ctrl_sd	Standard deviation from the control group at time 1
Ctrl_n	Sample size of the control group
Ctrl_cor	Number or numeric vector. Correlation between the means of the control group at t0 and t1
t0_Exp_sd	Standard deviation from the experimental group at time 0
t1_Exp_sd	Standard deviation from the experimental group at time 1
Exp_n	Sample size of the experimental group
Exp_cor	Number or numeric vector. Correlation between the means of the experimental group at t0 and t1

**Value**

A data frame containing the effect sizes and their sampling variance. By default, the columns are named *yi* (effect size) and *vi* (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

**Author(s)**

Facundo Decunta - fdecunta@agro.uba.ar

**References**

Shinichi Nakagawa and Daniel Noble, personal communication.

**Examples**

```
data <- data.frame(
  study_id = 1:2,
  pre_control_sd = c(2.1, 2.4),
  post_control_sd = c(2.2, 2.5),
  control_n = c(24, 19),
  pre_invaded_sd = c(2.0, 2.3),
  post_invaded_sd = c(4.1, 4.6),
  invaded_n = c(21, 22)
)

result <- time_lnVR(
  data = data,
  t0_Ctrl_sd = "pre_control_sd", t1_Ctrl_sd = "post_control_sd",
  Ctrl_n = "control_n", Ctrl_cor = 0.6,
  t0_Exp_sd = "pre_invaded_sd", t1_Exp_sd = "post_invaded_sd",
  Exp_n = "invaded_n", Exp_cor = 0.4
)
```

---

time\_SMD

*Standardized Mean Difference: Interaction Between Treatment and Time*

---

**Description**

Standardized Mean Difference: Interaction Between Treatment and Time

**Usage**

```
time_SMD(
  data,
  col_names = c("yi", "vi"),
  append = TRUE,
  hedges_correction = TRUE,
```

```

t0_Ctrl_mean,
t0_Ctrl_sd,
t1_Ctrl_mean,
t1_Ctrl_sd,
Ctrl_n,
Ctrl_cor,
t0_Exp_mean,
t0_Exp_sd,
t1_Exp_mean,
t1_Exp_sd,
Exp_n,
Exp_cor
)

```

### Arguments

<code>data</code>	Data frame containing the variables used.
<code>col_names</code>	Vector of two strings to name the output columns for the effect size and its sampling variance. Default is 'yi' and 'vi'.
<code>append</code>	Logical. Append the results to data. Default is TRUE
<code>hedges_correction</code>	Logical. Apply or not Hedges' correction for small-sample bias. Default is TRUE.
<code>t0_Ctrl_mean</code>	Sample mean from the control group at time 0
<code>t0_Ctrl_sd</code>	Standard deviation from the control group at time 0
<code>t1_Ctrl_mean</code>	Sample mean from the control group at time 1
<code>t1_Ctrl_sd</code>	Standard deviation from the control group at time 1
<code>Ctrl_n</code>	Sample size of the control group
<code>Ctrl_cor</code>	Number or numeric vector. Correlation between the means of the control group at t0 and t1
<code>t0_Exp_mean</code>	Sample mean from the experimental group at time 0
<code>t0_Exp_sd</code>	Standard deviation from the experimental group at time 0
<code>t1_Exp_mean</code>	Sample mean from the experimental group at time 1
<code>t1_Exp_sd</code>	Standard deviation from the experimental group at time 1
<code>Exp_n</code>	Sample size of the experimental group
<code>Exp_cor</code>	Number or numeric vector. Correlation between the means of the experimental group at t0 and t1

### Value

A data frame containing the effect sizes and their sampling variance. By default, the columns are named yi (effect size) and vi (sampling variance). If `append = TRUE`, the results are appended to the input data; otherwise, only the computed effect size columns are returned.

**Author(s)**

Facundo Decunta - fdecunta@agro.uba.ar

**References**

Shinichi Nakagawa and Daniel Noble, personal communication.

**Examples**

```
# Pre-post design for standardized mean difference with time interaction (Conservation experiment)
data <- data.frame(
  study_id = 1:2,
  pre_control_mean = c(18.3, 21.7), pre_control_sd = c(4.1, 4.8),
  post_control_mean = c(18.8, 22.1), post_control_sd = c(4.2, 4.9),
  control_n = c(16, 14),
  pre_conservation_mean = c(18.1, 21.4), pre_conservation_sd = c(4.0, 4.7),
  post_conservation_mean = c(26.7, 31.2), post_conservation_sd = c(5.8, 6.4),
  conservation_n = c(15, 16)
)

result <- time_SMD(
  data = data,
  t0_Ctrl_mean = "pre_control_mean", t0_Ctrl_sd = "pre_control_sd",
  t1_Ctrl_mean = "post_control_mean", t1_Ctrl_sd = "post_control_sd",
  Ctrl_n = "control_n", Ctrl_cor = 0.9,
  t0_Exp_mean = "pre_conservation_mean", t0_Exp_sd = "pre_conservation_sd",
  t1_Exp_mean = "post_conservation_mean", t1_Exp_sd = "post_conservation_sd",
  Exp_n = "conservation_n", Exp_cor = 0.7,
  hedges_correction = TRUE
)

# Without Hedges' correction
result_no_hedges <- time_SMD(
  data = data,
  t0_Ctrl_mean = "pre_control_mean", t0_Ctrl_sd = "pre_control_sd",
  t1_Ctrl_mean = "post_control_mean", t1_Ctrl_sd = "post_control_sd",
  Ctrl_n = "control_n", Ctrl_cor = 0.9,
  t0_Exp_mean = "pre_conservation_mean", t0_Exp_sd = "pre_conservation_sd",
  t1_Exp_mean = "post_conservation_mean", t1_Exp_sd = "post_conservation_sd",
  Exp_n = "conservation_n", Exp_cor = 0.7,
  hedges_correction = FALSE
)
```

# Index

InCVR\_ind, 2  
InCVR\_inter, 4  
InCVR\_main, 6  
InRR\_ind, 7  
InRR\_inter, 9  
InRR\_main, 11  
InVR\_ind, 13  
InVR\_inter, 15  
InVR\_main, 16

SMD\_ind, 18  
SMD\_inter, 20  
SMD\_main, 22

time\_InCVR, 24  
time\_InRR, 26  
time\_InVR, 28  
time\_SMD, 29