

# Package ‘sinar’

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**Title** Conditional Least Squared (CLS) Method for the Model SINAR(1,1)

**Version** 0.1.0

**Description** Implementation of the Conditional Least Square (CLS) estimates and its covariance matrix for the first-order spatial integer-valued autoregressive model (SINAR(1,1)) proposed by Ghodsi (2012) <[doi:10.1080/03610926.2011.560739](https://doi.org/10.1080/03610926.2011.560739)>.

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**Imports** MASS, stats, numDeriv

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**BugReports** <https://github.com/gilberto-sassi/sinar/issues>

**NeedsCompilation** no

**Author** Gilberto P. Sassi [aut, cre],  
Carolina C. M. Parafba [aut]

**Maintainer** Gilberto P. Sassi <[sassi.pereira.gilberto@gmail.com](mailto:sassi.pereira.gilberto@gmail.com)>

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carabidae	<i>Counts of arthropods in a grid-sampled wheat field</i>
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**Description**

A matrix with the counts of arthropods (carabidae) in a grid-sampled wheat field

**Usage**

```
data("carabidae")
```

**Format**

A matrix where each row and column is a count of carabidae species at the first cell.

**Source**

Kevin Wright (2020). agridat: Agricultural Datasets. R package version 1.17. <https://CRAN.R-project.org/package=agridat>

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cls	<i>Conditional least square estimates for a SINAR(1,1) process.</i>
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**Description**

cls computes the conditional least square for a process described by

$$X_{i,j} = a_{10}X_{i-1,j} + a_{01}X_{i,j-1} + a_{11}X_{i-1,j-1} + \epsilon_{i,j}$$

where  $\epsilon_{i,j}$  is an iid process with poisson distribution. Note the  $a_{10}, a_{01}, a_{11}$  must belong to the interval  $[0, 1]$ . We obtain estimates for  $a_{10}, a_{01}, a_{11}$  and  $\mu_\epsilon$ . We do not make any assumption about the distribution of the innovation in the process.

**Usage**

```
cls(X)
```

**Arguments**

X                    A integer matrix where each cell is the observed value in the regular lattice.

**Value**

a vector with the estimates of  $a_{10}, a_{01}, a_{11}, \mu$ .

**Examples**

```
data("nematodes")
cls(nematodes)
```

---

emp\_cov

*Empirical estimate for the Covariance matrix in the Klimko-Nelson.*


---

**Description**

$\Sigma$  is the covariance matrix in the Klimko-Nelson seminal paper. Basically, we know

$$\sqrt{n}(\hat{a}_{10} - a_{10}, \hat{a}_{01} - a_{01}, \hat{a}_{11} - a_{11}, \hat{\mu}_\epsilon - \mu_\epsilon)^\top \sim MNV(0, \Sigma)$$

where

$$\Sigma = V^{-1}WV^{-1}.$$

For more details, check Klimko and Nelson (1978).

**Usage**

```
emp_cov(X)
```

**Arguments**

X                    A integer matrix where each cell is the observed value in the regular lattice.

**Value**

The covariance matrix estimated empirically.

**Examples**

```
data("nematodes")
emp_cov(nematodes)
```

---

 emp\_V

*Empirical estimate for the matrix V in the Klimko-Nelson.*


---

**Description**

emp\_V is the matrix in the Klimko-Nelson seminal paper. Basically, we know

$$\sqrt{n}(\hat{a}_{10} - a_{10}, \hat{a}_{01} - a_{01}, \hat{a}_{11} - a_{11}, \hat{\mu}_\epsilon - \mu_\epsilon)^\top \sim MNV(0, \Sigma)$$

where

$$\Sigma = V^{-1}WV^{-1}.$$

For more details, check Klimko and Nelson (1978).

**Usage**

emp\_V(X)

**Arguments**

X                    A integer matrix where each cell is the observed value in the regular lattice.

**Value**

The matrix V estimated empirically.

**Examples**

```
data("nematodes")
emp_V(nematodes)
```

---

 emp\_W

*Empirical estimate for the matrix W in the Klimko-Nelson.*


---

**Description**

emp\_W is the matrix in the Klimko-Nelson seminal paper. Basically, we know

$$\sqrt{n}(\hat{a}_{10} - a_{10}, \hat{a}_{01} - a_{01}, \hat{a}_{11} - a_{11}, \hat{\mu}_\epsilon - \mu_\epsilon)^\top \sim MNV(0, \Sigma)$$

where

$$\Sigma = V^{-1}WV^{-1}.$$

For more details, check Klimko and Nelson (1978).

**Usage**

emp\_W(X)

**Arguments**

X                    A integer matrix where each cell is the observed value in the regular lattice.

**Value**

The matrix W estimated empirically.

**Examples**

```
data("nematodes")
emp_V(nematodes)
```

---

nematodes	<i>A matrix of counting data with 15 rows and 15 columns.</i>
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---

**Description**

A matrix of counting data with 15 rows and 15 columns.

**Usage**

```
data("nematodes")
```

**Format**

Dataset of  $15 \times 15$  regular grid on counts of cereal cyst-nematode (*Heterodera avenae* collected in soil core).

**Source**

PERRY, J. N. et al. SADIE: software to measure and model spatial pattern. Aspects of applied biology, v. 46, p. 95-102, 1996.

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sinar_pois	<i>Simulating SINAR(1,1) process with innovations from a poison distribution.</i>
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**Description**

sinar\_pois returns a matrix representing a simulated regular lattice from a SINAR(1,1) process with innovations from a poison distribution.

**Usage**

```
sinar_pois(n_row, n_col, a10, a01, a11, l)
```

**Arguments**

n_row	Number of rows in the simulated lattice.
n_col	Number of columns in the simulated lattice.
a10	Coefficient from the element $X_{i-1,j}$ .
a01	Coefficient from the element $X_{i,j-1}$ .
a11	Coefficient from the element $X_{i-1,j-1}$ .
l	Mean of the poison distribution used as innovations.

**Details**

This function simulates a regular lattice from the model

$$X_{i,j} = a_{10}X_{i-1,j} + a_{01}X_{i,j-1} + a_{11}X_{i-1,j-1} + \epsilon_{i,j}$$

where  $\epsilon_{i,j}$  is an iid process with poison distribution. Note the  $a_{10}, a_{01}, a_{11}$  must belong to the interval  $[0, 1]$ .

**Value**

A integer matrix.

**Examples**

```
n_row <- 20
n_col <- 50
a10 <- 0.2
a01 <- 0.2
a11 <- 0.5
l <- 1
sinar_pois(n_row, n_col, a10, a01, a11, l)
```

---

teo\_V

*Compute the value of matrix V using the coefficients.*

---

**Description**

V is the theoretical matrix from Klimko-Nelson for the SINAR(1,1) model. Basically, we know

$$\sqrt{n}(\hat{a}_{10} - a_{10}, \hat{a}_{01} - a_{01}, \hat{a}_{11} - a_{11}, \hat{\mu}_\epsilon - \mu_\epsilon)^\top \sim MNV(0, \Sigma)$$

where

$$\Sigma = V^{-1}WV^{-1}.$$

For more details, check Klimko and Nelson (1978).

**Usage**

```
teo_V(a10, a01, a11, mu_e, s2_e)
```

**Arguments**

a10	is the parameter in the equation $X[i, j]a_{10}X[i-1, j] + a_{01}X[i, j-1] + a_{11}X[i-1, j-1] + \epsilon_{i,j}$
a01	is the parameter in the equation $X[i, j]a_{10}X[i-1, j] + a_{01}X[i, j-1] + a_{11}X[i-1, j-1] + \epsilon_{i,j}$
a11	is the parameter in the equation $X[i, j]a_{10}X[i-1, j] + a_{01}X[i, j-1] + a_{11}X[i-1, j-1] + \epsilon_{i,j}$
mu_e	is the mean of the innovations $\epsilon_{i,j}$
s2_e	is the standar deviation of the innovations $\epsilon_{i,j}$

**Value**

The matrix V estimated empirically.

**Examples**

```
n_row <- 20
n_col <- 50
a10 <- 0.2
a01 <- 0.2
a11 <- 0.5
l <- 1 # mean and variance for poison innovations

teo_V(a10, a01, a11, l, sqrt(1))
```

---

var\_hat\_sigma

*Variance of standard deviation of epsilon.*


---

**Description**

$\hat{\sigma}_\epsilon$  is the standard deviation of *SINAR*(1, 1) model.

**Usage**

```
var_hat_sigma(X)
```

**Arguments**

X A integer matrix where each cell is the observed value in the regular lattice.

**Value**

The variance of standard deviation of the estimate of  $\sigma_\epsilon$ .

**Examples**

```
data("nematodes")
var_hat_sigma(nematodes)
```

---

var\_sinar

*Empirical estimate for the variance of innovations.*

---

**Description**

$\sigma_\epsilon^2$  is the variance the innovations for the *SINAR*(1, 1) model.

**Usage**

```
var_sinar(X)
```

**Arguments**

X                    A integer matrix where each cell is the observed value in the regular lattice.

**Value**

The estimated standard deviation in the *SINAR*(1, 1).

**Examples**

```
data("nematodes")
var_sinar(nematodes)
```



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