

# Package: ecostatscale (via r-universe)

September 16, 2024

**Title** Statistical Scaling Functions for Ecological Systems

**Version** 1.1

**Description** Implementation of the scaling functions presented in  
"General statistical scaling laws for stability in ecological  
systems" by Clark et al in Ecology Letters  
<[DOI:10.1111/ele.13760](https://doi.org/10.1111/ele.13760)>. Includes functions for extrapolating  
variability, resistance, and resilience across spatial and  
ecological scales, as well as a basic simulation function for  
producing time series, and a regression routine for generating  
unbiased parameter estimates. See the main text of the paper  
for more details.

**Imports** mvtnorm, stats, graphics, deSolve

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

**RemoteUrl** <https://github.com/adamtclark/ecostatscale>

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df0	<i>Simulate deterministic dynamics of a N competing species</i>
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### Description

Helper function for symdynN, used to simulate dynamics between disturbance events.

### Usage

```
df0(time, state, pars)
```

### Arguments

time	time step - ignored, but required for consistency with ode function
state	vector of current states
pars	parameter list, including matrix A with full interaction matrix (and growth rates along the diagonal)

### Value

rate of change for each species

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df_col	<i>Simulate deterministic dynamics of N patches with dispersal</i>
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### Description

Helper function for symdynN, used to simulate dynamics between disturbance events. Note that K is set to 1 for all species.

### Usage

```
df_col(time, state, pars)
```

**Arguments**

time	time step - ignored, but required for consistency with ode function
state	vector of current states
pars	parameter list, including matrix A with full interaction matrix (and growth rates along the diagonal), and a value Ifrac, which is the dispersal rate (D in the main text), and Ksim, which is the carrying capacity

**Value**

rate of change for each species

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df_col_loss	<i>Simulate deterministic dynamics of N patches with dispersal and loss</i>
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**Description**

Helper function for symdynN, used to simulate dynamics between disturbance events. Note that K is set to 1 for all species.

**Usage**

```
df_col_loss(time, state, pars)
```

**Arguments**

time	time step - ignored, but required for consistency with ode function
state	vector of current states
pars	parameter list, including matrix A with full interaction matrix (and growth rates along the diagonal), and a value Ifrac, which is the dispersal rate (D in the main text), and Ksim, which is the carrying capacity, and Iloss which is the loss rate.

**Value**

rate of change for each species

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res\_scale                      *Resilience scaling function*

---

### Description

Extrapolate resilience observed at the scale of a single spatial or ecological scale  $b$  (e.g. a patch or species) to a larger scale,  $B$  (e.g. functional group or landscape).

### Usage

```
res_scale(
  mvar_b,
  murho_b_abundance,
  mucov_b_abundance = NULL,
  msd_b,
  murho_b_disturbance,
  mucov_b_disturbance = NULL,
  b = 1,
  B,
  lambda
)
```

### Arguments

mvar_b	Mean abundance variance observed at scale $b$
murho_b_abundance	Mean Pearson correlation coefficient of abundance values observed at scale $b$
mucov_b_abundance	Mean covariance of abundance values observed at scale $b$ . Ignored unless murho_b_abundance is NULL Defaults to NULL.
msd_b	Mean disturbance standard deviation observed at scale $b$
murho_b_disturbance	Mean Pearson correlation coefficient of disturbances observed at scale $b$
mucov_b_disturbance	Mean covariance of disturbances observed at scale $b$ . Ignored unless murho_b_abundance is NULL Defaults to NULL.
b	Size of observed scale. Defaults to 1.
B	Larger scale being extrapolated to (e.g. total number of species, or size of patch $B$ relative to $b$ )
lambda	Mean disturbance frequency.

### Value

Extrapolated median resilience at scale of  $M$  species.

**Examples**

```
# extrapolate from scale of 1 species to 10 species
res_scale(mvar_b = 0.25, murho_b_abundance = -0.034, msd_b = sqrt(0.1),
          murho_b_disturbance = 0, B = 30, lambda=1)

# plot relationship for groups of 1 to 30 species
plot(1:30, res_scale(mvar_b = 0.25, murho_b_abundance = -0.034, msd_b = sqrt(0.1),
                    murho_b_disturbance = 0, B = 1:30, lambda=1),
     xlab="ecological scale", ylab="resilience, r", type="b")
```

sd\_scale

*Sigma scaling function***Description**

Extrapolate disturbance standard deviation observed at spatial or ecological scale  $b$  to a different scale,  $B$  (inversely related to resistance). Equivalent to Eq.7b in the main text.

**Usage**

```
sd_scale(msd_b, murho_b, mucov_b = NULL, b = 1, B)
```

**Arguments**

msd_b	Mean disturbance standard deviation observed at scale $b$ .
murho_b	Mean Pearson correlation coefficient of disturbances observed at scale $b$ , calculated as $\text{mucov}_b/\text{mvar}_b$ . If NULL, $\text{mucov}_b$ is used instead.
mucov_b	Mean covariane of disturbances observed at scale $b$ . Ignored if $\text{mrho}_b$ is not NULL. Defaults to NULL.
b	Size of observed scale. Defaults to 1.
B	Size of desired scale for extrapolation.

**Value**

Extrapolated disturbance standard deviation at scale  $B$ .

**Examples**

```
#extrapolate from scale of 1 to 10 - e.g. from a 1m2 patch to a 10m2 patch
sd_scale(msd_b = 1, murho_b = 0.5, b = 1, B = 10)
```

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 symdyn

*Simulate time series for a single species in a single patch*


---

### Description

Function for simulating dynamics from Eq.1 in the main text.

### Usage

```

symdyn(
  r,
  f,
  d,
  d_sd,
  sf,
  tmax,
  stochd = TRUE,
  stocht = TRUE,
  as.matrix = FALSE,
  oscillate_dist = FALSE
)

```

### Arguments

r	per-capita growth rate (r in Eq.1)
f	the waiting time (or average waiting time) between disturbance events (equal to 1/lambda in Eq.1)
d	mean size of disturbance function (mu in Eq.1)
d_sd	standard deviation of disturbance function (sigma in Eq.1)
sf	waiting time between sampling events
tmax	the time series length to be simulated
stochd	a logical variable, indicating whether disturbance size should be stochastic - otherwise, all disturbances are of magnitude d - defaults to TRUE
stocht	a logical variable, indicating whether waiting time between disturbance events should be stochastic - otherwise, waiting time is always f - defaults to TRUE
as.matrix	indicates whether results should be returned as matrix (potentially faster for some applications) - defaults to FALSE
oscillate_dist	a logical variable indicating whether the sign of the disturbance should oscillate between positive and negative - ignored if stochd==TRUE - defaults to FALSE

### Value

a matrix or data.frame with columns for sampling times, abundances, and number of disturbances for each time interval

**Examples**

```
# see xt2fun
```

---

symdynN	<i>Simulate time series for N species or patches</i>
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**Description**

Function for simulating dynamics from Eq.2-3 in the main text.

**Usage**

```
symdynN(
  r,
  amu,
  asd,
  f,
  d,
  d_sd,
  d_cov,
  N,
  sf,
  tmax,
  stochd = TRUE,
  stocht = TRUE,
  as.matrix = FALSE,
  amax = 0,
  amin = -Inf,
  Ifrac = NULL,
  Iloss = NULL,
  dffun = df0,
  fullout = FALSE,
  xstart = NULL,
  Ksim = 1
)
```

**Arguments**

r	per-capita growth rate (r in Eq.2-3)
amu	the mean interaction strength
asd	standard deviation used to generate interaction strengths
f	the waiting time (or average waiting time) between disturbance events (equal to 1/lambda in Eq.2-3)
d	mean size of disturbance function (mu in Eq.2-3)
d_sd	standard deviation of disturbance function (sigma in Eq.5)

d_cov	the covariance for generating disturbances
N	number of species or patches
sf	waiting time between sampling events
tmax	the time series length to be simulated
stochd	a logical variable, indicating whether disturbance size should be stochastic - otherwise, all disturbances are of magnitude d - defaults to TRUE
stocht	a logical variable, indicating whether waiting time between disturbance events should be stochastic - otherwise, waiting time is always f - defaults to TRUE
as.matrix	indicates whether results should be returned as matrix (potentially faster for some applications) - defaults to FALSE
amax	the maximum value allowed for interaction coefficients - defaults to zero
amin	the minimum value allowed for interaction coefficients - defaults to -Inf
Ifrac	dispersal rate (D in Eq. 2) - defaults to NULL (i.e. no dispersal)
Iloss	loss rate from dispersal that falls outside of the patch - defaults to NULL
dffun	the function handed to the ODE solver - should be df_col for spatial simulations, and df0 for multi-species simulations - defaults to df0
fullout	a logical, determining whether the full output or just a summary is returned - defaults to fullout
xstart	optional vector of starting abundances - defaults to NULL (i.e. no values)
Ksim	carrying capacities - defaults to 1

### Value

a matrix or data.frame with columns for sampling times, abundances, and number of disturbances for each time interval

### Examples

```
### Example 1: 10 patches
r<-1 #rate of recovery
d<-(0) #mean size of disturbance (mu in text)
d_sd<-sqrt(0.1) #SD of disturbances (sigma in text)
f<-1 #average time between disturbances (1/lambda in text)
sf<-0.1 #sampling interval
tmax<-120 #maximum time for simulation
d_cov<-d_cov0<-(d_sd)^2/2 #covariance in disturbance size among patches

xtNpatches<-symdynN(r = r, amu=0, asd=0, f=f, d=d,
                    d_sd=d_sd, d_cov=d_cov, N=10,
                    sf=sf, tmax=tmax, Ifrac=0, dffun = df_col)

### Example 2: 30 species
r<-1 #rate of recovery
d<-(0) #mean size of disturbance (mu in text)
d_sd<-sqrt(0.1) #SD of disturbances (sigma in text)
```



```

f<-1 #average time between disturbances (1/lambda in text)
sf<-0.1 #sampling interval
tmax<-120 #maximum time for simulation
d_cov<-0 #covariance in disturbances among species
amu<-(-r/2) #average interaction coefficient
asd<-0.1 #standard deviation of interaction coefficient

xtNsp<-syndynN(r = r, amu=amu, asd=asd, f=f, d=d,
              d_sd=d_sd, d_cov=d_cov, N=30,
              sf=sf, tmax=tmax)

```

---

var\_scale

*Variance scaling function*


---

### Description

Extrapolate variance observed at spatial or ecological scale  $b$  to a different scale,  $B$ . Equivalent to Eq.7a in the main text.

### Usage

```
var_scale(mvar_b, murho_b, mucov_b = NULL, b = 1, B)
```

### Arguments

mvar_b	Mean variance of abundance values observed at scale $b$ .
murho_b	Mean Pearson correlation coefficient of abundance values observed at scale $b$ , calculated as $\text{mucov}_b/\text{mvar}_b$ . If NULL, $\text{mucov}_b$ is used instead.
mucov_b	Mean covariance of abundances observed at scale $b$ . Ignored if $\text{murho}_b$ is not NULL. Defaults to NULL.
b	Size of observed scale. Defaults to 1.
B	Size of desired scale for extrapolation.

### Value

Extrapolated variance at scale  $B$ .

### Examples

```

# extrapolate from scale of 1 to 10 - e.g. from a 1m2 patch to a 10m2 patch
var_scale(mvar_b = 1, murho_b = 0.5, b = 1, B = 10)

# example with 100 simulated species
nsp<-100 # number of species
var_b<-1 # species-level abundance variance
cov_b<-(-0.01) # between-specie abundance covariance
# note - if nsp is large, cov_b must be near zero
# this is because, e.g. many variables cannot all be

```

```

# simultaneously negatively correlated

# make a covariance matrix based on var_b and cov_b
sigmamat<-diag(nsp)*var_b+(1-diag(nsp))*cov_b
# simulate 1000 observations of 100 species
sim_x<-mvtnorm::rmvnorm(n=1e3, mean = rep(0,100), sigma = sigmamat)

# calculate mean variance, covariance, and correlation from sim_x
cvmat<-cov(sim_x)
mvar_b<-mean(diag(cvmat))
mucov_b<-mean(cvmat[row(cvmat)!=col(cvmat)])
murho_b<-mucov_b/mvar_b

# test function vs. observation
# note - answers match exactly
var(rowSums(sim_x))
var_scale(mvar_b, murho_b = murho_b, b=1, B=100)

```

---

xt

*Simulate deterministic dynamics of a single species*


---

## Description

Helper function for symdyn, used to simulate dynamics between disturbance events.

## Usage

```
xt(t0, t1, B0, r)
```

## Arguments

t0	initial time step
t1	desired time step
B0	initial abundance
r	relative growth rate

## Value

predicted value of x at time t1

## Examples

```
# see xt2fun
```

---

xt2fun                      *Unbiased stability parameter estimation*

---

### Description

Function for solving for stability parameter values from observed time series. Equivalent to Eq.5 in the main text.

### Usage

```
xt2fun(x0, r, d, d_sd, dt, ndist)
```

### Arguments

x0	value of $x^2$ at time t ( $x(t)$ in Eq.5)
r	per-capita growth rate (r in Eq.5)
d	mean size of disturbance function ( $\mu$ in Eq.5)
d_sd	standard deviation of disturbance function ( $\sigma$ in Eq.5)
dt	time step (i.e. time between $x_0$ and $x_1$ ) - can be a vector of the same length as $x_0$ , or a number if all time steps are of equal length
ndist	number of disturbances in each time step (equivalent to $p(t+\tau)$ in Eq.5) - must be same length as $x_0$

### Value

predicted value of  $x^2$  at time  $t+dt$

### Examples

```
# simulate dynamics, with r=1, d=0, and d_sd=0.1
xtout<-symdyn(r=1, f=1, d=0, d_sd=0.1, sf=0.1, tmax=100)

# abundance in current time step
x0<-xtout$state[1:(nrow(xtout)-1)]
# abundance at t+1
x1<-xtout$state[2:nrow(xtout)]

dt<-diff(xtout$time)
ndist<-xtout$disturbed[-1]

# fit model - note square root transform of response variable,
# and log transform of parameter values

mod<-nls(sqrt(x1^2)~sqrt(xt2fun(x0, r=exp(lr), d=0, d_sd=exp(ld_sd), dt, ndist)),
        start=c(lr=log(1), ld_sd=log(0.1)))
exp(coef(mod)) # model estimates
```

---

`xtN`*Simulate deterministic dynamics*

---

**Description**

Helper function for `symdynN`. Simulate an ODE given parameters, starting value, and times.

**Usage**

```
xtN(t0, t1, B0, odepars, dffun, nsteps = 2)
```

**Arguments**

<code>t0</code>	initial time step
<code>t1</code>	desired time step
<code>B0</code>	initial abundance
<code>odepars</code>	parameter list
<code>dffun</code>	function for calculating derivatives
<code>nsteps</code>	number of time steps to return - defaults to 2

**Value**

a matrix of species abundances

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