

# Package ‘sjSDM’

August 19, 2024

**Type** Package

**Title** Scalable Joint Species Distribution Modeling

**Version** 1.0.6

## Description

A scalable and fast method for estimating joint Species Distribution Models (jSDMs) for big community data, including eDNA data. The package estimates a full (i.e. non-latent) jSDM with different response distributions (including the traditional multivariate probit model). The package allows to perform variation partitioning (VP) / ANOVA on the fitted models to separate the contribution of environmental, spatial, and biotic associations. In addition, the total R-squared can be further partitioned per species and site to reveal the internal metacommunity structure, see Leibold et al., <[doi:10.1111/oik.08618](https://doi.org/10.1111/oik.08618)>. The internal structure can then be regressed against environmental and spatial distinctiveness, richness, and traits to analyze meta-community assembly processes. The package includes support for accounting for spatial autocorrelation and the option to fit responses using deep neural networks instead of a standard linear predictor. As described in Pichler & Hartig (2021) <[doi:10.1111/2041-210X.13687](https://doi.org/10.1111/2041-210X.13687)>, scalability is achieved by using a Monte Carlo approximation of the joint likelihood implemented via 'PyTorch' and 'reticulate', which can be run on CPUs or GPUs.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.0)

**Imports** reticulate, stats, mvtnorm, utils, rstudioapi, abind,  
graphics, grDevices, Metrics, parallel, mgecv, cli, crayon,  
ggplot2, checkmate, mathjaxr, ggtern, beeswarm, qgam, scales

**Suggests** testthat, knitr, rmarkdown, iml, fields

**RoxygenNote** 7.3.2

**URL** <https://github.com/TheoreticalEcology/s-jSDM/>

**BugReports** <https://github.com/TheoreticalEcology/s-jSDM/issues>

**VignetteBuilder** knitr

**RdMacros** mathjaxr

**NeedsCompilation** no

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**Repository** CRAN

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## Contents

AccSGD . . . . .	3
AdaBound . . . . .	4
Adamax . . . . .	5
anova.sjSDM . . . . .	5
bioticStruct . . . . .	7
butterflies . . . . .	11
checkModel . . . . .	13
check_module . . . . .	13
coef.sjSDM . . . . .	13
DiffGrad . . . . .	14
DNN . . . . .	14
eucalypts . . . . .	19
generateSpatialEV . . . . .	20
getCor . . . . .	20
getCov . . . . .	21
getImportance . . . . .	21
getSe . . . . .	22
getWeights . . . . .	23
importance . . . . .	23
installation_help . . . . .	25
install_diagnostic . . . . .	28
install_sjSDM . . . . .	28
internalStructure . . . . .	29
is_torch_available . . . . .	30
linear . . . . .	31
logLik.sjSDM . . . . .	35
madgrad . . . . .	35
new_image . . . . .	36
plot.sjSDM . . . . .	37
plot.sjSDM.DNN . . . . .	38
plot.sjSDManova . . . . .	39
plot.sjSDMimportance . . . . .	40
plot.sjSDMinternalStructure . . . . .	40
plot.sjSDM_cv . . . . .	42
plotAssemblyEffects . . . . .	43
plotsjSDMcoef . . . . .	45
predict.sjSDM . . . . .	46
print.bioticStruct . . . . .	47

print.DNN . . . . .	48
print.linear . . . . .	48
print.sjSDM . . . . .	49
print.sjSDManova . . . . .	49
print.sjSDMimportance . . . . .	50
print.sjSDMinternalStructure . . . . .	51
print.sjSDM_cv . . . . .	52
residuals.sjSDM . . . . .	52
RMSprop . . . . .	53
Rsquared . . . . .	53
setWeights . . . . .	54
SGD . . . . .	55
simulate.sjSDM . . . . .	55
simulate_SDM . . . . .	56
sjSDM . . . . .	57
sjSDMControl . . . . .	64
sjSDM_cv . . . . .	65
summary.sjSDM . . . . .	67
summary.sjSDManova . . . . .	68
summary.sjSDM_cv . . . . .	70
update.sjSDM . . . . .	70
<b>Index</b>	<b>72</b>

---

 AccSGD

*AccSGD*


---

## Description

accelerated stochastic gradient, see Kidambi et al., 2018 for details

## Usage

```
AccSGD(kappa = 1000, xi = 10, small_const = 0.7, weight_decay = 0)
```

## Arguments

kappa	long step
xi	advantage parameter
small_const	small constant
weight_decay	l2 penalty on weights

## Value

Anonymous function that returns optimizer when called.

## References

Kidambi, R., Netrapalli, P., Jain, P., & Kakade, S. (2018, February). On the insufficiency of existing momentum schemes for stochastic optimization. In 2018 Information Theory and Applications Workshop (ITA) (pp. 1-9). IEEE.

---

AdaBound

*AdaBound*

---

## Description

adaptive gradient methods with dynamic bound of learning rate, see Luo et al., 2019 for details

## Usage

```
AdaBound(
  betas = c(0.9, 0.999),
  final_lr = 0.1,
  gamma = 0.001,
  eps = 1e-08,
  weight_decay = 0,
  amsbound = TRUE
)
```

## Arguments

betas	betas
final_lr	eps
gamma	small_const
eps	eps
weight_decay	weight_decay
amsbound	amsbound

## Value

Anonymous function that returns optimizer when called.

## References

Luo, L., Xiong, Y., Liu, Y., & Sun, X. (2019). Adaptive gradient methods with dynamic bound of learning rate. arXiv preprint arXiv:1902.09843.

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Adamax	<i>Adamax</i>
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---

**Description**

Adamax optimizer, see Kingma and Ba, 2014

**Usage**

```
Adamax(betas = c(0.9, 0.999), eps = 1e-08, weight_decay = 0.002)
```

**Arguments**

betas	exponential decay rates
eps	fuzz factor
weight_decay	l2 penalty on weights

**Value**

Anonymous function that returns optimizer when called.

**References**

Kingma, D. P., & Ba, J. (2014). Adam: A method for stochastic optimization. arXiv preprint arXiv:1412.6980.

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anova.sjSDM	<i>Anova / Variation partitioning</i>
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---

**Description**

Compute variance explained by the three fractions env, space, associations

**Usage**

```
## S3 method for class 'sjSDM'
anova(object, samples = 5000L, verbose = TRUE, ...)
```

**Arguments**

object	model of object <a href="#">sjSDM</a>
samples	Number of Monte Carlo samples
verbose	TRUE or FALSE, indicating whether progress should be printed or not
...	optional arguments which are passed to the calculation of the logLikelihood

## Details

The ANOVA function removes each of the three fractions (Environment, Space, Associations) and measures the drop in variance explained, and thus the importance of the three fractions.

Variance explained is measured by Deviance as well as the pseudo-R2 metrics of Nagelkerke and McFadden

In downstream functions such as `plot.sjSDManova` or `plot.sjSDManova` with `add_shared=TRUE`. The anova can get unstable for many species and few occurrences/observations. We recommend using large numbers for 'samples'.

## Value

An S3 class of type 'sjSDManova' including the following components:

results	Data frame of results.
to_print	Data frame, summarized results for type I anova.
N	Number of observations (sites).
spatial	Logical, spatial model or not.
species	individual species R2s.
sites	individual site R2s.
lls	individual site by species negative-log-likelihood values.
model	model

Implemented S3 methods are `print.sjSDManova` and `plot.sjSDManova`

## See Also

`plot.sjSDManova`, `print.sjSDManova`, `summary.sjSDManova`, `plot.sjSDMinternalStructure`

## Examples

```
## Not run:
library(sjSDM)
# simulate community:
community = simulate_SDM(env = 3L, species = 10L, sites = 100L)

Occ <- community$response
Env <- community$env_weights
SP <- data.frame(matrix(rnorm(200, 0, 0.3), 100, 2)) # spatial coordinates

# fit model:
model <- sjSDM(Y = Occ,
  env = linear(data = Env, formula = ~X1+X2+X3),
  spatial = linear(data = SP, formula = ~0+X1*X2),
  family=binomial("probit"),
  verbose = FALSE,
  iter = 20) # increase iter for real analysis
```

```

# Calculate ANOVA for env, space, associations, for details see ?anova.sjSDM
an = anova(model, samples = 10, verbose = FALSE) # increase iter for real analysis

# Show anova fractions
plot(an)

# ANOVA tables with different way to handle fractions
summary(an)
summary(an, fractions = "discard")
summary(an, fractions = "proportional")
summary(an, fractions = "equal")

# Internal structure
int = internalStructure(an, fractions = "proportional")

print(int)

plot(int) # default is negative values will be set to 0
plot(int, negatives = "scale") # global rescaling of all values to range 0-1
plot(int, negatives = "raw") # negative values will be discarded

plotAssemblyEffects(int)
plotAssemblyEffects(int, negatives = "floor")
plotAssemblyEffects(int, response = "sites", pred = as.factor(c(rep(1, 50), rep(2, 50))))
plotAssemblyEffects(int, response = "species", pred = runif(10))
plotAssemblyEffects(int, response = "species", pred = as.factor(c(rep(1, 5), rep(2, 5))))

## End(Not run)

```

---

bioticStruct

*biotic structure*


---

## Description

define biotic (species-species) association (interaction) structure

## Usage

```

bioticStruct(
  df = NULL,
  lambda = 0,
  alpha = 0.5,
  on_diag = FALSE,
  reg_on_Cov = TRUE,
  inverse = FALSE,
  diag = FALSE
)

```

**Arguments**

df	degree of freedom for covariance parametrization, if NULL df is set to $\text{ncol}(Y)/2$
lambda	lambda penalty, strength of regularization: $\lambda * (\text{lasso} + \text{ridge})$
alpha	weighting between lasso and ridge: $(1 - \alpha) *  \text{covariances}  + \alpha * \ \text{covariances}\ ^2$
on_diag	regularization on diagonals
reg_on_Cov	regularization on covariance matrix
inverse	regularization on the inverse covariance matrix
diag	use diagonal matrix with zeros (internal usage)

**Value**

An S3 class of type 'bioticStruct' including the following components:

l1_cov	L1 regularization strength.
l2_cov	L2 regularization strength.
inverse	Logical, use inverse covariance matrix or not.
diag	Logical, use diagonal matrix or not.
reg_on_Cov	Logical, regularize covariance matrix or not.
on_diag	Logical, regularize diagonals or not.

Implemented S3 methods include [print.bioticStruct](#)

**See Also**

[sjSDM](#)

**Examples**

```
## Not run:

# Basic workflow:
## simulate community:
com = simulate_SDM(env = 3L, species = 7L, sites = 100L)

## fit model:
model = sjSDM(Y = com$response, env = com$env_weights, iter = 50L,
              verbose = FALSE)
# increase iter for your own data

# Default distribution is binomial("probit"). Alternatively, you can use
# binomial("logit"), poisson("log"), "nbinom" (with log, still somewhat
# experimental) and gaussian("identity")

coef(model)
summary(model)
getCov(model)
```



```

## plot results
species=c("sp1","sp2","sp3","sp4","sp5","sp6","sp7")
group=c("mammal","bird","fish","fish","mammal","amphibian","amphibian")
group = data.frame(species=species,group=group)
plot(model,group=group)

## calculate post-hoc p-values:
p = getSe(model)
summary(p)

## or turn on the option in the sjSDM function:
model = sjSDM(Y = com$response, env = com$env_weights, se = TRUE,
              family = binomial("probit"),
              iter = 2L,
              verbose = FALSE)
summary(model)

## fit model with interactions:
model = sjSDM(Y = com$response,
              env = linear(data = com$env_weights, formula = ~X1:X2 + X3),
              se = TRUE,
              iter = 2L,
              verbose = FALSE) # increase iter for your own data
summary(model)

## without intercept:
model = update(model, env_formula = ~0+X1:X2 + X3,
              verbose = FALSE)

summary(model)

## predict with model:
preds = predict(model, newdata = com$env_weights)

## calculate R-squared:
R2 = Rsquared(model)
print(R2)

# With spatial terms:
## linear spatial model
XY = matrix(rnorm(200), 100, 2)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(XY, ~0+X1:X2),
              iter = 50L,
              verbose = FALSE) # increase iter for your own data
summary(model)
predict(model, newdata = com$env_weights, SP = XY)
R2 = Rsquared(model)
print(R2)

## Using spatial eigenvectors as predictors to account
## for spatial autocorrelation is a common approach:
SPV = generateSpatialEV(XY)

```

```

model = sjSDM(Y = com$response, env = linear(com$env_weights),
             spatial = linear(SPV, ~0+., lambda = 0.1),
             iter = 50L,
             verbose = FALSE) # increase iter for your own data
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

## Visualize internal meta-community structure
an = anova(model,
           verbose = FALSE)

internal = internalStructure(an)
plot(internal)

## Visualize community assembly effects

plotAssemblyEffects(internal)

### see ?anova.sjSDM for more details

## non-linear(deep neural network) model
model = sjSDM(Y = com$response, env = linear(com$env_weights),
             spatial = DNN(SPV,hidden = c(5L, 5L), ~0+.),
             iter = 2L,# increase iter for your own data
             verbose = FALSE)
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

# Regularization
## lambda is the regularization strength
## alpha weights the lasso or ridge penalty:
## - alpha = 0 --> pure lasso
## - alpha = 1.0 --> pure ridge
model = sjSDM(Y = com$response,
             # mix of lasso and ridge
             env = linear(com$env_weights, lambda = 0.01, alpha = 0.5),
             # we can do the same for the species-species associations
             biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
             iter = 2L,# increase iter for your own data
             verbose = FALSE)
summary(model)
coef(model)
getCov(model)

# Anova
com = simulate_SDM(env = 3L, species = 15L, sites = 200L, correlation = TRUE)

XY = matrix(rnorm(400), 200, 2)
SPV = generateSpatialEV(XY)

```

```

model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(SPV, ~0+.),
              verbose = FALSE,
              iter = 50L) # increase iter for your own data
result = anova(model, verbose = FALSE)
print(result)
plot(result)

## visualize internal meta-community structure
internal = internalStructure(an)
plot(internal)

# Deep neural networks
## we can fit also a deep neural network instead of a linear model:
model = sjSDM(Y = com$response,
              env = DNN(com$env_weights, hidden = c(10L, 10L, 10L)),
              verbose = FALSE,
              iter = 2L) # increase iter for your own data
summary(model)
getCov(model)
pred = predict(model, newdata = com$env_weights)

## extract weights
weights = getWeights(model)

## we can also assign weights:
setWeights(model, weights)

## with regularization:
model = sjSDM(Y = com$response,
              # mix of lasso and ridge
              env = DNN(com$env_weights, lambda = 0.01, alpha = 0.5),
              # we can do the same for the species-species associations
              biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
              verbose = FALSE,
              iter = 2L) # increase iter for your own data
getCov(model)
getWeights(model)

## End(Not run)

```

---

butterflies

*butterflies*


---

## Description

This dataset is from [doi:10.1111/2041210X.13106](https://doi.org/10.1111/2041210X.13106).

**Usage**

`butterflies`

**Format**

A 'list': List of 3.

**env** data.frame with 4 environmental covariates

**PA** Presence-absence data for 55 butterfly species

**lat\_lon** Coordinates for the sites

**Details**

This is a dataset about butterfly communities. It consists of 2609 sites and 55 species.

**Author(s)**

Maximilian Pichler

**Source**

[doi:10.1111/2041210X.13106](https://doi.org/10.1111/2041210X.13106)

**Examples**

```
## Not run:
PA = butterflies$PA
E = butterflies$env
LatLon = butterflies$lat_lon

m = sjSDM(PA,
          scale(E),
          spatial = DNN(scale(LatLon), formula = ~0+.),
          se = TRUE,
          iter = 20L, # increase to 100
          step_size = 200L,
          verbose = FALSE)

summary(m)
plot(m)

## End(Not run)
```

---

checkModel	<i>check model check model and rebuild if necessary</i>
------------	---

---

**Description**

check model check model and rebuild if necessary

**Usage**

```
checkModel(object)
```

**Arguments**

object            of class sjSDM

---

check_module	<i>check module</i>
--------------	---------------------

---

**Description**

check if module is loaded

**Usage**

```
check_module()
```

---

coef.sjSDM	<i>Return coefficients from a fitted sjSDM model</i>
------------	--

---

**Description**

Return coefficients from a fitted sjSDM model

**Usage**

```
## S3 method for class 'sjSDM'
coef(object, ...)
```

**Arguments**

object            a model fitted by [sjSDM](#)  
 ...               optional arguments for compatibility with the generic function, no function implemented

**Value**

Matrix of environmental coefficients or list of environmental and spatial coefficients for spatial models.

---

DiffGrad	<i>DiffGrad</i>
----------	-----------------

---

**Description**

DiffGrad

**Usage**

```
DiffGrad(betas = c(0.9, 0.999), eps = 1e-08, weight_decay = 0)
```

**Arguments**

betas	betas
eps	eps
weight_decay	weight_decay

**Value**

Anonymous function that returns optimizer when called.

---

DNN	<i>Non-linear model (deep neural network) of environmental responses</i>
-----	--

---

**Description**

specify the model to be fitted

**Usage**

```
DNN(
  data = NULL,
  formula = NULL,
  hidden = c(10L, 10L, 10L),
  activation = "selu",
  bias = TRUE,
  lambda = 0,
  alpha = 0.5,
  dropout = 0
)
```

**Arguments**

data	matrix of environmental predictors
formula	formula object for predictors
hidden	hidden units in layers, length of hidden corresponds to number of layers
activation	activation functions, can be of length one, or a vector of activation functions for each layer. Currently supported: tanh, relu, leakyrelu, selu, or sigmoid
bias	whether use biases in the layers, can be of length one, or a vector (number of hidden layers including (last layer) but not first layer (intercept in first layer is specified by formula)) of logicals for each layer.
lambda	lambda penalty, strength of regularization: $\lambda * (lasso + ridge)$
alpha	weighting between lasso and ridge: $(1 - \alpha) *  weights  + \alpha   weights  ^2$
dropout	probability of dropout rate

**Value**

An S3 class of type 'DNN' including the following components:

formula	Model matrix formula
X	Model matrix of covariates
data	Raw data
l1_coef	L1 regularization strength, can be -99 if lambda = 0.0
l2_coef	L2 regularization strength, can be -99 if lambda = 0.0
hidden	Integer vector of hidden neurons in the deep neural network. Length of vector corresponds to the number of hidden layers.
activation	Character vector of activation functions.
bias	Logical vector whether to use bias or not in each hidden layer.

Implemented S3 methods include [print.DNN](#)

**See Also**

[linear](#), [sjSDM](#)

**Examples**

```
## Not run:

# Basic workflow:
## simulate community:
com = simulate_SDM(env = 3L, species = 7L, sites = 100L)

## fit model:
model = sjSDM(Y = com$response, env = com$env_weights, iter = 50L,
              verbose = FALSE)
# increase iter for your own data
```

```

# Default distribution is binomial("probit"). Alternatively, you can use
# binomial(logit), poisson("log"), "nbinom" (with log, still somewhat
# experimental) and gaussian("identity")

coef(model)
summary(model)
getCov(model)

## plot results
species=c("sp1","sp2","sp3","sp4","sp5","sp6","sp7")
group=c("mammal","bird","fish","fish","mammal","amphibian","amphibian")
group = data.frame(species=species,group=group)
plot(model,group=group)

## calculate post-hoc p-values:
p = getSe(model)
summary(p)

## or turn on the option in the sjSDM function:
model = sjSDM(Y = com$response, env = com$env_weights, se = TRUE,
              family = binomial("probit"),
              iter = 2L,
              verbose = FALSE)
summary(model)

## fit model with interactions:
model = sjSDM(Y = com$response,
              env = linear(data = com$env_weights, formula = ~X1:X2 + X3),
              se = TRUE,
              iter = 2L,
              verbose = FALSE) # increase iter for your own data
summary(model)

## without intercept:
model = update(model, env_formula = ~0+X1:X2 + X3,
              verbose = FALSE)

summary(model)

## predict with model:
preds = predict(model, newdata = com$env_weights)

## calculate R-squared:
R2 = Rsquared(model)
print(R2)

# With spatial terms:
## linear spatial model
XY = matrix(rnorm(200), 100, 2)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(XY, ~0+X1:X2),
              iter = 50L,
              verbose = FALSE) # increase iter for your own data

```



```

summary(model)
predict(model, newdata = com$env_weights, SP = XY)
R2 = Rsquared(model)
print(R2)

## Using spatial eigenvectors as predictors to account
## for spatial autocorrelation is a common approach:
SPV = generateSpatialEV(XY)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
             spatial = linear(SPV, ~0+., lambda = 0.1),
             iter = 50L,
             verbose = FALSE) # increase iter for your own data
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

## Visualize internal meta-community structure
an = anova(model,
           verbose = FALSE)

internal = internalStructure(an)
plot(internal)

## Visualize community assembly effects
plotAssemblyEffects(internal)

### see ?anova.sjSDM for more details

## non-linear(deep neural network) model
model = sjSDM(Y = com$response, env = linear(com$env_weights),
             spatial = DNN(SPV,hidden = c(5L, 5L), ~0+.),
             iter = 2L,# increase iter for your own data
             verbose = FALSE)
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

# Regularization
## lambda is the regularization strength
## alpha weights the lasso or ridge penalty:
## - alpha = 0 --> pure lasso
## - alpha = 1.0 --> pure ridge
model = sjSDM(Y = com$response,
             # mix of lasso and ridge
             env = linear(com$env_weights, lambda = 0.01, alpha = 0.5),
             # we can do the same for the species-species associations
             biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
             iter = 2L,# increase iter for your own data
             verbose = FALSE)
summary(model)
coef(model)
getCov(model)

```

```

# Anova
com = simulate_SDM(env = 3L, species = 15L, sites = 200L, correlation = TRUE)

XY = matrix(rnorm(400), 200, 2)
SPV = generateSpatialEV(XY)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(SPV, ~0+.),
              verbose = FALSE,
              iter = 50L) # increase iter for your own data
result = anova(model, verbose = FALSE)
print(result)
plot(result)

## visualize internal meta-community structure
internal = internalStructure(an)
plot(internal)

# Deep neural networks
## we can fit also a deep neural network instead of a linear model:
model = sjSDM(Y = com$response,
              env = DNN(com$env_weights, hidden = c(10L, 10L, 10L)),
              verbose = FALSE,
              iter = 2L) # increase iter for your own data
summary(model)
getCov(model)
pred = predict(model, newdata = com$env_weights)

## extract weights
weights = getWeights(model)

## we can also assign weights:
setWeights(model, weights)

## with regularization:
model = sjSDM(Y = com$response,
              # mix of lasso and ridge
              env = DNN(com$env_weights, lambda = 0.01, alpha = 0.5),
              # we can do the same for the species-species associations
              biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
              verbose = FALSE,
              iter = 2L) # increase iter for your own data
getCov(model)
getWeights(model)

## End(Not run)

```

---

eucalypts

*eucalypts*

---

### Description

This dataset is from [doi:10.1111/2041210x.12180](https://doi.org/10.1111/2041210x.12180).

### Usage

```
eucalypts
```

### Format

A 'list': List of 3.

**env** data.frame with 7 environmental covariates

**PA** Presence-absence data for 12 eucalypts species

**lat\_lon** Coordinates for the sites

### Details

This is a dataset about butterfly communities. It consists of 458 sites and 12 species.

### Author(s)

Maximilian Pichler

### Source

[doi:10.1111/2041210x.12180](https://doi.org/10.1111/2041210x.12180)

### Examples

```
## Not run:
PA = eucalypts$PA
E = eucalypts$env
LatLon = eucalypts$lat_lon

m = sjSDM(PA,
          scale(E),
          spatial = DNN(scale(LatLon), formula = ~0+.),
          se = TRUE,
          verbose = FALSE)

summary(m)
plot(m)

## End(Not run)
```

---

generateSpatialEV	<i>Generate spatial eigenvectors</i>
-------------------	--------------------------------------

---

**Description**

Generates a Moran's eigenvector map of the distance matrix. See Dray, Legendre, and Peres-Neto, 2006 for more information.

**Usage**

```
generateSpatialEV(coords = NULL, threshold = 0)
```

**Arguments**

coords	matrix or data.frame of coordinates
threshold	ignore distances greater than threshold

**Value**

Matrix of spatial eigenvectors.

**References**

Dray, S., Legendre, P., & Peres-Neto, P. R. (2006). Spatial modelling: a comprehensive framework for principal coordinate analysis of neighbour matrices (PCNM). *Ecological modelling*, 196(3-4), 483-493.

---

getCor	<i>getCor</i>
--------	---------------

---

**Description**

get species-species association correlation matrix

**Usage**

```
getCor(object)

## S3 method for class 'sjSDM'
getCor(object)
```

**Arguments**

object	a model fitted by <code>sjSDM</code> , or <code>sjSDM</code> with <code>DNN</code> object
--------	---

**Value**

Matrix of dimensions species by species corresponding to the covariance (occurrence) matrix.

**See Also**

[sjSDM,DNN](#)

---

getCov	<i>getCov</i>
--------	---------------

---

**Description**

get species-species association (covariance) matrix

**Usage**

```
getCov(object)

## S3 method for class 'sjSDM'
getCov(object)
```

**Arguments**

object            a model fitted by [sjSDM](#), or [sjSDM](#) with [DNN](#) object

**Value**

Matrix of dimensions species by species corresponding to the covariance (occurrence) matrix.

**See Also**

[sjSDM,DNN](#)

---

getImportance	<i>getImportance</i>
---------------	----------------------

---

**Description**

variation partitioning with coefficients

**Usage**

```
getImportance(beta, sp = NULL, association, covX, covSP = NULL)
```

**Arguments**

beta	abiotic weights
sp	spatial weights
association	species associations
covX	environmental covariance matrix
covSP	spatial covariance matrix

**Author(s)**

Maximilian Pichler

---

getSe *Post hoc calculation of standard errors*

---

**Description**

Post hoc calculation of standard errors

**Usage**

```
getSe(object, step_size = NULL, parallel = 0L)
```

**Arguments**

object	a model fitted by <a href="#">sjSDM</a>
step_size	batch size for stochastic gradient descent
parallel	number of cpu cores for the data loader, only necessary for large datasets

**Value**

The object passed to this function but the `object$se` field contains the standard errors now

---

getWeights	<i>Get weights</i>
------------	--------------------

---

**Description**

return weights of each layer

**Usage**

```
getWeights(object)

## S3 method for class 'sjSDM'
getWeights(object)
```

**Arguments**

object            object of class [sjSDM](#) with [DNN](#)

**Value**

- layers - list of layer weights
- sigma - weight to construct covariance matrix

---

importance	<i>Importance of environmental, spatial and association components</i>
------------	--

---

**Description**

Computes standardized variance components with respect to abiotic, biotic, and spatial effect groups.

**Usage**

```
importance(x, save_memory = TRUE, ...)
```

**Arguments**

x	object fitted by <a href="#">sjSDM</a> or a list with beta, the association matrix, and the correlation matrix of the predictors, see details below
save_memory	use torch backend to calculate importance with single precision floats
...	additional arguments

## Details

This approach is based on Ovaskainen et al., 2017, and also used in Leibold et al., 2021. Unlike the `anova.sjSDM` function in the `sjSDM` package, `importance` is not calculated by explicitly switching a particular model component of and refitting the model, but essentially by setting it ineffective.

Although we have no hard reasons to discourage the use of this function, we have decided in `sjSDM` to measure importance mainly based on a traditional ANOVA approach. We therefore recommend users to use the `anova.sjSDM`.

This function is maintained hidden for comparison / benchmarking purpose, and in case there is a need to use it in the future. If you want to access it, use `sjSDM:::importance`.

## Value

An S3 class of type 'sjSDMimportance' including the following components:

<code>names</code>	Character vector, species names.
<code>res</code>	Data frame of results.
<code>spatial</code>	Logical, spatial model or not.

Implemented S3 methods include `print.sjSDMimportance` and `plot.sjSDMimportance`

## Author(s)

Maximilian Pichler

## References

Ovaskainen, O., Tikhonov, G., Norberg, A., Guillaume Blanchet, F., Duan, L., Dunson, D., ... & Abrego, N. (2017). How to make more out of community data? A conceptual framework and its implementation as models and software. *Ecology letters*, 20(5), 561-576.

Leibold, M. A., Rudolph, F. J., Blanchet, F. G., De Meester, L., Gravel, D., Hartig, F., ... & Chase, J. M. (2021). The internal structure of metacommunities. *Oikos*.

## See Also

`print.sjSDMimportance`, `plot.sjSDMimportance`

## Examples

```
## Not run:
library(sjSDM)
com = simulate_SDM(sites = 300L, species = 12L,
                  link = "identical", response = "identical")
Raw = com$response
SP = matrix(rnorm(300*2), 300, 2)
SPweights = matrix(rnorm(12L), 1L)
SPweights[1,1:6] = 0
Y = Raw + (SP[,1,drop=FALSE]*SP[,2,drop=FALSE]) %%% SPweights
Y = ifelse(Y > 0, 1, 0)
```



```

model = sjSDM(Y = Y,env = linear(com$env_weights, lambda = 0.001),
             spatial = linear(SP,formula = ~0+X1:X2, lambda = 0.001),
             biotic = bioticStruct(lambda = 0.001),iter = 40L, verbose = FALSE)
imp = importance(model)
plot(imp)

## End(Not run)

```

---

installation\_help      *Installation help*

---

## Description

Trouble shooting guide for the installation of the sjSDM package

We provide a function `install_sjSDM` to install automatically all necessary python dependencies but it can fail sometimes because of individual system settings or if other python/conda installations get into the way.

## 'PyTorch' Installation - Before you start

A few notes before you start with the installation (skip this point if you do not know 'conda'):

- existing 'conda' installations: make sure you have the latest conda3/miniconda3 version and remove unnecessary 'conda' installations.
- existing 'conda'/'virtualenv' environments (skip this point if you do not know 'conda'): we currently enforce the usage of a specific environment called 'r-sjsdm', so if you want use a custom environment it should be named 'r-sjsdm'

## Windows - automatic installation

Sometimes the automatic 'miniconda' installation (via `install_sjSDM`) doesn't work because of white spaces in the user's name. But you can easily download and install 'conda' on your own:

Download and install the latest **'conda' version**

Afterwards run:

```
install_sjSDM(version = c("gpu")) # or "cpu" if you do not have a proper gpu device
```

Reload the package and run the example , if this doesn't work:

- Restart RStudio
- Install manually 'pytorch', see the following section

## Windows - manual installation

Download and install the latest 'conda' version:

- Install the latest **'conda' version**
- Open the command window (cmd.exe - hit windows key + r and write cmd)

Run in cmd.exe:

```
$ conda create --name r-sjsdm python=3.7
$ conda activate r-sjsdm
$ conda install pytorch torchvision cpuonly -c pytorch # cpu
$ conda install pytorch torchvision cudatoolkit=11.3 -c pytorch #gpu
$ python -m pip install pyro-ppl torch_optimizer madgrad
```

Restart R, try to run the example, and if this doesn't work:

- Restart RStudio
- See the 'Help and bugs' section

### Linux - automatic installation

Run in R:

```
install_sjSDM(version = c("gpu")) # or "cpu" if you do not have a proper 'gpu' device
```

Restart R try to run the example, if this doesn't work:

- Restart RStudio
- Install manually 'PyTorch', see the following section

### Linux - manual installation

We strongly advise to use a 'conda' environment but a virtual env should also work. The only requirement is that it is named 'r-sjsdm'

Download and install the latest 'conda' version:

- Install the latest '[conda](#)' version
- Open your terminal

Run in your terminal:

```
$ conda create --name r-sjsdm python=3.7
$ conda activate r-sjsdm
$ conda install pytorch torchvision cpuonly -c pytorch # cpu
$ conda install pytorch torchvision cudatoolkit=11.3 -c pytorch #gpu
$ python -m pip install pyro-ppl torch_optimizer madgrad
```

Restart R try to run the example, if this doesn't work:

- Restart RStudio
- See the 'Help and bugs' section

### MacOS - automatic installation

Run in R:

```
install_sjSDM(version = c("cpu"))
```

Restart R try to run the example, if this doesn't work:

- Restart RStudio
- Install manually 'PyTorch', see the following section

### MacOS - manual installation

Download and install the latest 'conda' version:

- Install the latest '[conda](#)' version
- Open your terminal

Run in your terminal:

```
$ conda create --name r-sjsdm python=3.7
$ conda activate r-sjsdm
$ python -m pip install torch torchvision torchaudio
$ python -m pip install pyro-ppl torch_optimizer madgrad
```

Restart R try to run the example from, if this doesn't work:

- Restart RStudio
- See the 'Help and bugs' section

### Help and bugs

To report bugs or ask for help, post a [reproducible example](#) via the [sjSDM issue tracker](#) with a copy of the [install\\_diagnostic](#) output as a quote.

### Author(s)

**Maintainer:** Maximilian Pichler <maximilian.pichler@biologie.uni-regensburg.de> ([ORCID](#))

Authors:

- Florian Hartig <florian.hartig@biologie.uni-regensburg.de> ([ORCID](#))

Other contributors:

- Wang Cai <caiwang0503@163.com> [contributor]

### See Also

Useful links:

- <https://github.com/TheoreticalEcology/s-jSDM/>
- Report bugs at <https://github.com/TheoreticalEcology/s-jSDM/issues>

---

install_diagnostic	<i>install diagnostic</i>
--------------------	---------------------------

---

**Description**

Print information about available conda environments, python configs, and pytorch versions.

**Usage**

```
install_diagnostic()
```

**Details**

If the trouble shooting guide [installation\\_help](#) did not help with the installation, please create an issue on [issue tracker](#) with the output of this function as a quote.

**Value**

No return value, called to extract dependency information.

**See Also**

[installation\\_help](#), [install\\_sjSDM](#)

---

install_sjSDM	<i>Install sjSDM and its dependencies</i>
---------------	---

---

**Description**

Install sjSDM and its dependencies

**Usage**

```
install_sjSDM(
  conda = "auto",
  version = c("cpu", "gpu"),
  restart_session = TRUE,
  ...
)
```

**Arguments**

conda	path to conda
version	version = "cpu" for CPU version, or "gpu" for GPU version. (note MacOS users have to install 'cuda' binaries by themselves)
restart_session	Restart R session after installing (note this will only occur within RStudio).
...	not supported

**Value**

No return value, called for side effects (installation of 'python' dependencies).

---

internalStructure      *Plot internal metacommunity structure*

---

**Description**

Plot internal metacommunity structure

**Usage**

```
internalStructure(
  object,
  Rsquared = c("McFadden", "Nagelkerke"),
  fractions = c("discard", "proportional", "equal"),
  negatives = c("floor", "scale", "raw"),
  plot = FALSE
)
```

**Arguments**

object	anova object from <a href="#">anova.sjSDM</a>
Rsquared	which R squared should be used, McFadden or Nagelkerke (McFadden is default)
fractions	how to handle shared fractions
negatives	how to handle negative R squareds
plot	should the plots be suppressed or not.

Plots and returns the internal metacommunity structure of species and sites (see Leibold et al., 2022). Plots were heavily inspired by Leibold et al., 2022

**Value**

An object of class sjSDMinternalStructure consisting of a list of data.frames with the internal structure.

**References**

Leibold, M. A., Rudolph, F. J., Blanchet, F. G., De Meester, L., Gravel, D., Hartig, F., ... & Chase, J. M. (2022). The internal structure of metacommunities. *Oikos*, 2022(1).

**See Also**

[plot.sjSDMinternalStructure](#), [print.sjSDMinternalStructure](#)

**Examples**

```

## Not run:
library(sjSDM)
# simulate community:
community = simulate_SDM(env = 3L, species = 10L, sites = 100L)

Occ <- community$response
Env <- community$env_weights
SP <- data.frame(matrix(rnorm(200, 0, 0.3), 100, 2)) # spatial coordinates

# fit model:
model <- sjSDM(Y = Occ,
               env = linear(data = Env, formula = ~X1+X2+X3),
               spatial = linear(data = SP, formula = ~0+X1*X2),
               family=binomial("probit"),
               verbose = FALSE,
               iter = 20) # increase iter for real analysis

# Calculate ANOVA for env, space, associations, for details see ?anova.sjSDM
an = anova(model, samples = 10, verbose = FALSE) # increase iter for real analysis

# Show anova fractions
plot(an)

# ANOVA tables with different way to handle fractions
summary(an)
summary(an, fractions = "discard")
summary(an, fractions = "proportional")
summary(an, fractions = "equal")

# Internal structure
int = internalStructure(an, fractions = "proportional")

print(int)

plot(int) # default is negative values will be set to 0
plot(int, negatives = "scale") # global rescaling of all values to range 0-1
plot(int, negatives = "raw") # negative values will be discarded

plotAssemblyEffects(int)
plotAssemblyEffects(int, negatives = "floor")
plotAssemblyEffects(int, response = "sites", pred = as.factor(c(rep(1, 50), rep(2, 50))))
plotAssemblyEffects(int, response = "species", pred = runif(10))
plotAssemblyEffects(int, response = "species", pred = as.factor(c(rep(1, 5), rep(2, 5))))

## End(Not run)

```

**Description**

is\_torch\_available

**Usage**

```
is_torch_available()
```

**Details**

check whether torch is available

**Value**

Logical, is torch module available or not.

linear

*Linear model of environmental response*

**Description**

specify the model to be fitted

**Usage**

```
linear(data = NULL, formula = NULL, lambda = 0, alpha = 0.5)
```

**Arguments**

data	matrix of environmental predictors
formula	formula object for predictors
lambda	lambda penalty, strength of regularization: $\lambda * (lasso + ridge)$
alpha	weighting between lasso and ridge: $(1-\alpha)* coefficients  + \alpha  coefficients  ^2$

**Value**

An S3 class of type 'linear' including the following components:

formula	Model matrix formula
X	Model matrix of covariates
data	Raw data
l1_coef	L1 regularization strength, can be -99 if lambda = 0.0
l2_coef	L2 regularization strength, can be -99 if lambda = 0.0

Implemented S3 methods include [print.linear](#)

**See Also**

[DNN](#), [sjSDM](#)

**Examples**

```
## Not run:

# Basic workflow:
## simulate community:
com = simulate_SDM(env = 3L, species = 7L, sites = 100L)

## fit model:
model = sjSDM(Y = com$response, env = com$env_weights, iter = 50L,
              verbose = FALSE)
# increase iter for your own data

# Default distribution is binomial("probit"). Alternatively, you can use
# binomial(logit), poisson("log"), "nbinom" (with log, still somewhat
# experimental) and gaussian("identity")

coef(model)
summary(model)
getCov(model)

## plot results
species=c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6", "sp7")
group=c("mammal", "bird", "fish", "fish", "mammal", "amphibian", "amphibian")
group = data.frame(species=species, group=group)
plot(model, group=group)

## calculate post-hoc p-values:
p = getSe(model)
summary(p)

## or turn on the option in the sjSDM function:
model = sjSDM(Y = com$response, env = com$env_weights, se = TRUE,
              family = binomial("probit"),
              iter = 2L,
              verbose = FALSE)
summary(model)

## fit model with interactions:
model = sjSDM(Y = com$response,
              env = linear(data = com$env_weights, formula = ~X1:X2 + X3),
              se = TRUE,
              iter = 2L,
              verbose = FALSE) # increase iter for your own data
summary(model)

## without intercept:
model = update(model, env_formula = ~0+X1:X2 + X3,
              verbose = FALSE)
```



```

summary(model)

## predict with model:
preds = predict(model, newdata = com$env_weights)

## calculate R-squared:
R2 = Rsquared(model)
print(R2)

# With spatial terms:
## linear spatial model
XY = matrix(rnorm(200), 100, 2)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
             spatial = linear(XY, ~0+X1:X2),
             iter = 50L,
             verbose = FALSE) # increase iter for your own data
summary(model)
predict(model, newdata = com$env_weights, SP = XY)
R2 = Rsquared(model)
print(R2)

## Using spatial eigenvectors as predictors to account
## for spatial autocorrelation is a common approach:
SPV = generateSpatialEV(XY)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
             spatial = linear(SPV, ~0+., lambda = 0.1),
             iter = 50L,
             verbose = FALSE) # increase iter for your own data
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

## Visualize internal meta-community structure
an = anova(model,
           verbose = FALSE)

internal = internalStructure(an)
plot(internal)

## Visualize community assembly effects

plotAssemblyEffects(internal)

### see ?anova.sjSDM for more details

## non-linear(deep neural network) model
model = sjSDM(Y = com$response, env = linear(com$env_weights),
             spatial = DNN(SPV,hidden = c(5L, 5L), ~0+.),
             iter = 2L,# increase iter for your own data
             verbose = FALSE)
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

```

```

# Regularization
## lambda is the regularization strength
## alpha weights the lasso or ridge penalty:
## - alpha = 0 --> pure lasso
## - alpha = 1.0 --> pure ridge
model = sjSDM(Y = com$response,
              # mix of lasso and ridge
              env = linear(com$env_weights, lambda = 0.01, alpha = 0.5),
              # we can do the same for the species-species associations
              biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
              iter = 2L, # increase iter for your own data
              verbose = FALSE)
summary(model)
coef(model)
getCov(model)

# Anova
com = simulate_SDM(env = 3L, species = 15L, sites = 200L, correlation = TRUE)

XY = matrix(rnorm(400), 200, 2)
SPV = generateSpatialEV(XY)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(SPV, ~0+.),
              verbose = FALSE,
              iter = 50L) # increase iter for your own data
result = anova(model, verbose = FALSE)
print(result)
plot(result)

## visualize internal meta-community structure
internal = internalStructure(an)
plot(internal)

# Deep neural networks
## we can fit also a deep neural network instead of a linear model:
model = sjSDM(Y = com$response,
              env = DNN(com$env_weights, hidden = c(10L, 10L, 10L)),
              verbose = FALSE,
              iter = 2L) # increase iter for your own data
summary(model)
getCov(model)
pred = predict(model, newdata = com$env_weights)

## extract weights
weights = getWeights(model)

## we can also assign weights:

```

```

setWeights(model, weights)

## with regularization:
model = sjSDM(Y = com$response,
              # mix of lasso and ridge
              env = DNN(com$env_weights, lambda = 0.01, alpha = 0.5),
              # we can do the same for the species-species associations
              biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
              verbose = FALSE,
              iter = 2L) # increase iter for your own data
getCov(model)
getWeights(model)

## End(Not run)

```

---

logLik.sjSDM	<i>Extract negative-log-Likelihood from a fitted sjSDM model</i>
--------------	--

---

### Description

Extract negative-log-Likelihood from a fitted sjSDM model

### Usage

```

## S3 method for class 'sjSDM'
logLik(object, individual = FALSE, ...)

```

### Arguments

object	a model fitted by <a href="#">sjSDM</a>
individual	returns internal ll structure, mostly for internal useage
...	optional arguments passed to internal logLik function (only used if individual=TRUE)

### Value

Numeric value or numeric matrix if individual is true.

---

madgrad	<i>madgrad</i>
---------	----------------

---

### Description

stochastic gradient descent optimizer

### Usage

```

madgrad(momentum = 0.9, weight_decay = 0, eps = 1e-06)

```

**Arguments**

momentum	strength of momentum
weight_decay	l2 penalty on weights
eps	epsilon

**Value**

Anonymous function that returns optimizer when called.

**References**

Defazio, A., & Jelassi, S. (2021). Adaptivity without Compromise: A Momentumized, Adaptive, Dual Averaged Gradient Method for Stochastic Optimization. arXiv preprint arXiv:2101.11075.

---

new_image	<i>new_image function</i>
-----------	---------------------------

---

**Description**

new\_image function

**Usage**

```
new_image(  
  z,  
  cols = (grDevices::colorRampPalette(c("white", "#24526E"), bias = 1.5))(10),  
  range = c(0.5, 1)  
)
```

**Arguments**

z	z matrix
cols	cols for gradient
range	rescale to range

---

`plot.sjSDM`*Coefficients plot*

---

**Description**

Plotting coefficients returned by sjSDM model. This function only for model fitted by linear, fitted by DNN is not yet supported.

**Usage**

```
## S3 method for class 'sjSDM'  
plot(x, ...)
```

**Arguments**

```
x          a model fitted by sjSDM  
...       Additional arguments to pass to plotsjSDMcoef.
```

**Value**

ggplot2 object for linear sjSDM model and nothing for DNN sjSDM model.

**Author(s)**

CAI Wang

**See Also**

[plotsjSDMcoef](#)

**Examples**

```
## Not run:  
library(sjSDM)  
# simulate community:  
com = simulate_SDM(env = 6L, species = 7L, sites = 100L)  
  
# fit model:  
model = sjSDM(Y = com$response, env = com$env_weights, iter = 2L, se = TRUE,  
              verbose = FALSE)  
  
# normal plot  
plot(model)  
  
# colored by groups  
species=c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6", "sp7")  
group=c("mammal", "bird", "fish", "fish", "mammal", "amphibian", "amphibian")  
group = data.frame(species=species, group=group)
```

```
plot(model,group=group)

## End(Not run)
```

---

```
plot.sjSDM.DNN      Training history
```

---

## Description

Plot training loss history

## Usage

```
## S3 method for class 'sjSDM.DNN'
plot(x, ...)
```

## Arguments

```
x          a model fitted by sjSDM with DNN object
...        passed to plot
```

## Value

No return value, called for side effects.

## Examples

```
## Not run:
library(sjSDM)
# simulate community:
com = simulate_SDM(env = 6L, species = 7L, sites = 100L)

# fit model:
model = sjSDM(Y = com$response,env = com$env_weights, iter = 2L, se = TRUE,
              verbose = FALSE)

# normal plot
plot(model)

# colored by groups
species=c("sp1","sp2","sp3","sp4","sp5","sp6","sp7")
group=c("mammal","bird","fish","fish","mammal","amphibian","amphibian")
group = data.frame(species=species,group=group)

plot(model,group=group)

## End(Not run)
```

---

plot.sjSDManova	<i>Plot anova results</i>
-----------------	---------------------------

---

**Description**

Plot anova results

**Usage**

```
## S3 method for class 'sjSDManova'
plot(
  x,
  y,
  type = c("McFadden", "Deviance", "Nagelkerke"),
  fractions = c("discard", "proportional", "equal"),
  cols = c("#7FC97F", "#BEAED4", "#FDC086"),
  alpha = 0.15,
  env_deviance = NULL,
  ...
)
```

**Arguments**

x	anova object from <a href="#">anova.sjSDM</a>
y	unused argument
type	deviance, Nagelkerke or McFadden R-squared
fractions	how to handle shared fractions
cols	colors for the groups
alpha	alpha for colors
env_deviance	environmental deviance
...	Additional arguments to pass to plot()

**Value**

List with the following components:

VENN	Matrix of shown results.
------	--------------------------

**References**

Leibold, M. A., Rudolph, F. J., Blanchet, F. G., De Meester, L., Gravel, D., Hartig, F., ... & Chase, J. M. (2022). The internal structure of metacommunities. *Oikos*, 2022(1).

---

plot.sjSDMimportance *Plot importance*

---

### Description

Plot importance

### Usage

```
## S3 method for class 'sjSDMimportance'
plot(x, y, col.points = "#24526e", cex.points = 1.2, ...)
```

### Arguments

x	a model fitted by <a href="#">importance</a>
y	unused argument
col.points	point color
cex.points	point size
...	Additional arguments to pass to plot()

### Value

The visualized matrix is silently returned.

---

plot.sjSDMinternalStructure  
*Plot internal structure*

---

### Description

Creates a ternary diagram of an object of class

### Usage

```
## S3 method for class 'sjSDMinternalStructure'
plot(
  x,
  alpha = 0.15,
  env_deviance = NULL,
  negatives = c("floor", "scale", "raw"),
  ...
)
```



**Arguments**

x	and object of class sjSDMinternalStructure create by anova object from <a href="#">internalStructure</a>
alpha	alpha of points
env_deviance	environmental deviance/gradient (points will be colored)
negatives	how to handle negative R squareds
...	no function

**Examples**

```
## Not run:
library(sjSDM)
# simulate community:
community = simulate_SDM(env = 3L, species = 10L, sites = 100L)

Occ <- community$response
Env <- community$env_weights
SP <- data.frame(matrix(rnorm(200, 0, 0.3), 100, 2)) # spatial coordinates

# fit model:
model <- sjSDM(Y = Occ,
               env = linear(data = Env, formula = ~X1+X2+X3),
               spatial = linear(data = SP, formula = ~0+X1*X2),
               family=binomial("probit"),
               verbose = FALSE,
               iter = 20) # increase iter for real analysis

# Calculate ANOVA for env, space, associations, for details see ?anova.sjSDM
an = anova(model, samples = 10, verbose = FALSE) # increase iter for real analysis

# Show anova fractions
plot(an)

# ANOVA tables with different way to handle fractions
summary(an)
summary(an, fractions = "discard")
summary(an, fractions = "proportional")
summary(an, fractions = "equal")

# Internal structure
int = internalStructure(an, fractions = "proportional")

print(int)

plot(int) # default is negative values will be set to 0
plot(int, negatives = "scale") # global rescaling of all values to range 0-1
plot(int, negatives = "raw") # negative values will be discarded

plotAssemblyEffects(int)
plotAssemblyEffects(int, negatives = "floor")
```

```

plotAssemblyEffects(int, response = "sites", pred = as.factor(c(rep(1, 50), rep(2, 50))))
plotAssemblyEffects(int, response = "species", pred = runif(10))
plotAssemblyEffects(int, response = "species", pred = as.factor(c(rep(1, 5), rep(2, 5))))

## End(Not run)

```

---

plot.sjSDM\_cv

*Plot elastic net tuning*


---

## Description

Plot elastic net tuning

## Usage

```

## S3 method for class 'sjSDM_cv'
plot(x, y, perf = c("logLik", "AUC", "AUC_macro"), resolution = 6, k = 3, ...)

```

## Arguments

x	a model fitted by <a href="#">sjSDM_cv</a>
y	unused argument
perf	performance measurement to plot
resolution	resolution of grid
k	number of knots for the gm
...	Additional arguments to pass to <code>plot()</code>

## Value

Named vector of optimized regularization parameters.

Without space:

lambda_cov	Regularization strength in the <a href="#">bioticStruct</a> object.
alpha_cov	Weigthing between L1 and L2 in the <a href="#">bioticStruct</a> object.
lambda_coef	Regularization strength in the <a href="#">linear</a> or <a href="#">DNN</a> object.
alpha_coef	Weigthing between L1 and L2 in the <a href="#">linear</a> or <a href="#">DNN</a> object.

With space:

lambda_cov	Regularization strength in the <a href="#">bioticStruct</a> object.
alpha_cov	Weigthing between L1 and L2 in the <a href="#">bioticStruct</a> object.
lambda_coef	Regularization strength in the <a href="#">linear</a> or <a href="#">DNN</a> object.
alpha_coef	Weigthing between L1 and L2 in the <a href="#">linear</a> or <a href="#">DNN</a> object.
lambda_spatial	Regularization strength in the <a href="#">linear</a> or <a href="#">DNN</a> object for the spatial component.
alpha_spatial	Weigthing between L1 and L2 in the <a href="#">linear</a> or <a href="#">DNN</a> object for the spatial component.

---

plotAssemblyEffects *Plot predictors of assembly processes*

---

### Description

The function plots correlations between assembly processes and predictors or traits

### Usage

```
plotAssemblyEffects(
  object,
  response = c("sites", "species"),
  pred = NULL,
  cols = c("#A38310", "#B42398", "#20A382"),
  negatives = c("raw", "scale", "floor")
)
```

### Arguments

object	An sjSDManova object from the <a href="#">anova.sjSDM</a> function.
response	whether to use sites or species. Default is sites
pred	predictor variable. If NULL, environment uniqueness, spatial uniqueness, and richness is calculated from the fitted object and used as predictor.
cols	Colors for the three assembly processes.
negatives	how to handle negative R squareds

### Details

Correlation and plots of the three assembly processes (environment, space, and codist) against environmental and spatial uniqueness and richness. The importance of the three assembly processes is measured by the partial R-squared (shown in the internal structure plots).

Importances are available for species and sites. Custom environmental predictors or traits can be specified. Environmental predictors are plotted against site R-squared and traits are plotted against species R-squared. Regression lines are estimated by 50\

### Value

A list with the following components:

env	A list of summary tables for env, space, and codist R-squared.
space	A list of summary tables for env, space, and codist R-squared.
codist	A list of summary tables for env, space, and codist R-squared.

### Note

Defaults for negative values are different than for [plot.sjSDMinternalStructure](#)

## References

Leibold, M. A., Rudolph, F. J., Blanchet, F. G., De Meester, L., Gravel, D., Hartig, F., ... & Chase, J. M. (2022). The internal structure of metacommunities. *Oikos*, 2022(1).

## Examples

```
## Not run:
library(sjSDM)
# simulate community:
community = simulate_SDM(env = 3L, species = 10L, sites = 100L)

Occ <- community$response
Env <- community$env_weights
SP <- data.frame(matrix(rnorm(200, 0, 0.3), 100, 2)) # spatial coordinates

# fit model:
model <- sjSDM(Y = Occ,
               env = linear(data = Env, formula = ~X1+X2+X3),
               spatial = linear(data = SP, formula = ~0+X1*X2),
               family=binomial("probit"),
               verbose = FALSE,
               iter = 20) # increase iter for real analysis

# Calculate ANOVA for env, space, associations, for details see ?anova.sjSDM
an = anova(model, samples = 10, verbose = FALSE) # increase iter for real analysis

# Show anova fractions
plot(an)

# ANOVA tables with different way to handle fractions
summary(an)
summary(an, fractions = "discard")
summary(an, fractions = "proportional")
summary(an, fractions = "equal")

# Internal structure
int = internalStructure(an, fractions = "proportional")

print(int)

plot(int) # default is negative values will be set to 0
plot(int, negatives = "scale") # global rescaling of all values to range 0-1
plot(int, negatives = "raw") # negative values will be discarded

plotAssemblyEffects(int)
plotAssemblyEffects(int, negatives = "floor")
plotAssemblyEffects(int, response = "sites", pred = as.factor(c(rep(1, 50), rep(2, 50))))
plotAssemblyEffects(int, response = "species", pred = runif(10))
plotAssemblyEffects(int, response = "species", pred = as.factor(c(rep(1, 5), rep(2, 5))))

## End(Not run)
```

---

plotsjSDMcoef                      *Internal coefficients plot*

---

### Description

Plotting coefficients returned by sjSDM model. This function only for model fitted by linear, fitted by DNN is not yet supported.

### Usage

```
plotsjSDMcoef(object, wrap_col = NULL, group = NULL, col = NULL, slist = NULL)
```

### Arguments

object	a model fitted by <a href="#">sjSDM</a>
wrap_col	Scales argument passed to wrap_col
group	Define the taxonomic characteristics of a species, you need to provide a dataframe with column1 named "species" and column2 named "group", default is NULL. For example, group[1,1]== "sp1", group[1,2]== "Mammal".
col	Define colors for groups, default is NULL.
slist	Select the species you want to plot, default is all, parameter is not supported yet.

### Value

ggplot2 object

### Author(s)

CAI Wang

### Examples

```
## Not run:
library(sjSDM)
# simulate community:
com = simulate_SDM(env = 6L, species = 7L, sites = 100L)

# fit model:
model = sjSDM(Y = com$response, env = com$env_weights, iter = 2L, se = TRUE,
              verbose = FALSE)

# normal plot
plot(model)

# colored by groups
species=c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6", "sp7")
group=c("mammal", "bird", "fish", "fish", "mammal", "amphibian", "amphibian")
group = data.frame(species=species, group=group)
```

```
plot(model,group=group)

## End(Not run)
```

---

predict.sjSDM                      *Predict from a fitted sjSDM model*

---

### Description

Predict from a fitted sjSDM model

### Usage

```
## S3 method for class 'sjSDM'
predict(
  object,
  newdata = NULL,
  SP = NULL,
  Y = NULL,
  type = c("link", "raw"),
  dropout = FALSE,
  ...
)
```

### Arguments

object	a model fitted by <a href="#">sjSDM</a>
newdata	newdata for predictions
SP	spatial predictors (e.g. X and Y coordinates)
Y	Known occurrences of species, must be a matrix of the original size, species to be predicted must consist of NAs
type	raw or link
dropout	use dropout for predictions or not, only supported for DNNs
...	optional arguments for compatibility with the generic function, no function implemented

### Value

Matrix of predictions (sites by species)

**Examples**

```
## Not run:

## Conditional predictions based on focal species
com = simulate_SDM(sites = 200L)
## first 100 observations are the training data
model = sjSDM(com$response[1:100, ], com$env_weights[1:100,])
## Assume that for the other 100 observations, only the first species is missing
## and we want to use the other 4 species to improve the predictions:
Y_focal = com$response[101:200, ]
Y_focal[,1] = NA # set to NA because occurrences are unknown

pred_conditional = predict(model, newdata = com$env_weights[101:200,], Y = Y_focal)
pred_unconditional = predict(model, newdata = com$env_weights[101:200,])[,1]

## Compare performance:
Metrics::auc(com$response[101:200, 1], pred_conditional)
Metrics::auc(com$response[101:200, 1], pred_unconditional)

## Conditional predictions are better, however, it only works if occurrences of
## other species for new sites are known!

## End(Not run)
```

---

```
print.bioticStruct      Print a bioticStruct object
```

---

**Description**

Print a bioticStruct object

**Usage**

```
## S3 method for class 'bioticStruct'
print(x, ...)
```

**Arguments**

x	object created by <code>bioticStruct</code>
...	optional arguments for compatibility with the generic function, no function implemented

---

`print.DNN`                    *Print a DNN object*

---

**Description**

Print a DNN object

**Usage**

```
## S3 method for class 'DNN'  
print(x, ...)
```

**Arguments**

<code>x</code>	object created by <a href="#">DNN</a>
<code>...</code>	optional arguments for compatibility with the generic function, no function implemented

---

`print.linear`                    *Print a linear object*

---

**Description**

Print a linear object

**Usage**

```
## S3 method for class 'linear'  
print(x, ...)
```

**Arguments**

<code>x</code>	object created by <a href="#">linear</a>
<code>...</code>	optional arguments for compatibility with the generic function, no function implemented

**Value**

Invisible formula object



---

print.sjSDM	<i>Print a fitted sjSDM model</i>
-------------	-----------------------------------

---

**Description**

Print a fitted sjSDM model

**Usage**

```
## S3 method for class 'sjSDM'
print(x, ...)
```

**Arguments**

x	a model fitted by <a href="#">sjSDM</a>
...	optional arguments for compatibility with the generic function, no function implemented

**Value**

No return value

---

print.sjSDManova	<i>Print sjSDM anova object</i>
------------------	---------------------------------

---

**Description**

This is a wrapper for [summary.sjSDManova](#), maintained for backwards compatibility - prefer to use `summary()` instead

**Usage**

```
## S3 method for class 'sjSDManova'
print(x, ...)
```

**Arguments**

x	an object of type sjSDManova created by <a href="#">anova.sjSDM</a>
...	additional arguments to <a href="#">summary.sjSDManova</a>

**Examples**

```

## Not run:
library(sjSDM)
# simulate community:
community = simulate_SDM(env = 3L, species = 10L, sites = 100L)

Occ <- community$response
Env <- community$env_weights
SP <- data.frame(matrix(rnorm(200, 0, 0.3), 100, 2)) # spatial coordinates

# fit model:
model <- sjSDM(Y = Occ,
               env = linear(data = Env, formula = ~X1+X2+X3),
               spatial = linear(data = SP, formula = ~0+X1*X2),
               family=binomial("probit"),
               verbose = FALSE,
               iter = 20) # increase iter for real analysis

# Calculate ANOVA for env, space, associations, for details see ?anova.sjSDM
an = anova(model, samples = 10, verbose = FALSE) # increase iter for real analysis

# Show anova fractions
plot(an)

# ANOVA tables with different way to handle fractions
summary(an)
summary(an, fractions = "discard")
summary(an, fractions = "proportional")
summary(an, fractions = "equal")

# Internal structure
int = internalStructure(an, fractions = "proportional")

print(int)

plot(int) # default is negative values will be set to 0
plot(int, negatives = "scale") # global rescaling of all values to range 0-1
plot(int, negatives = "raw") # negative values will be discarded

plotAssemblyEffects(int)
plotAssemblyEffects(int, negatives = "floor")
plotAssemblyEffects(int, response = "sites", pred = as.factor(c(rep(1, 50), rep(2, 50))))
plotAssemblyEffects(int, response = "species", pred = runif(10))
plotAssemblyEffects(int, response = "species", pred = as.factor(c(rep(1, 5), rep(2, 5))))

## End(Not run)

```

**Description**

Print importance

**Usage**

```
## S3 method for class 'sjSDMimportance'  
print(x, ...)
```

**Arguments**

x	an object of <a href="#">importance</a>
...	optional arguments for compatibility with the generic function, no function implemented

**Value**

The matrix above is silently returned

---

`print.sjSDMinternalStructure`  
*Print internal structure object*

---

**Description**

Print internal structure object

**Usage**

```
## S3 method for class 'sjSDMinternalStructure'  
print(x, ...)
```

**Arguments**

x	object of class <code>sjSDMinternalStructure</code>
...	no function

---

```
print.sjSDM_cv          Print a fitted sjSDM_cv model
```

---

**Description**

Print a fitted sjSDM\_cv model

**Usage**

```
## S3 method for class 'sjSDM_cv'
print(x, ...)
```

**Arguments**

x	a model fitted by <a href="#">sjSDM_cv</a>
...	optional arguments for compatibility with the generic function, no function implemented

**Value**

Above data frame is silently returned.

---

```
residuals.sjSDM        Residuals for a sjSDM model
```

---

**Description**

Returns residuals for a fitted sjSDM model

**Usage**

```
## S3 method for class 'sjSDM'
residuals(object, type = "raw", ...)
```

**Arguments**

object	a model fitted by <a href="#">sjSDM</a>
type	residual type. Currently only supports raw
...	further arguments, not supported yet.

**Value**

residuals in the format of the provided community matrix

---

RMSprop	<i>RMSprop</i>
---------	----------------

---

**Description**

RMSprop optimizer

**Usage**

```
RMSprop(
  alpha = 0.99,
  eps = 1e-08,
  weight_decay = 1e-04,
  momentum = 0.1,
  centered = FALSE
)
```

**Arguments**

alpha	decay factor
eps	fuzz factor
weight_decay	l2 penalty on weights
momentum	momentum
centered	centered or not

**Value**

Anonymous function that returns optimizer when called.

---

Rsqared	<i>R-squared</i>
---------	------------------

---

**Description**

calculate R-squared following McFadden or Nagelkerke

**Usage**

```
Rsqared(model, method = c("McFadden", "Nagelkerke"), verbose = TRUE)
```

**Arguments**

model	model
method	McFadden or Nagelkerke
verbose	TRUE or FALSE, indicating whether progress should be printed or not

**Details**

Calculate R-squared following Nagelkerke or McFadden:

- Nagelkerke:  $R^2 = 1 - \exp(2/N \cdot (\log\mathcal{L}_0 - \log\mathcal{L}_1))$
- McFadden:  $R^2 = 1 - \log\mathcal{L}_1/\log\mathcal{L}_0$

**Value**

R-squared as numeric value

**Author(s)**

Maximilian Pichler

---

setWeights	<i>Set weights</i>
------------	--------------------

---

**Description**

set layer weights and sigma in [sjSDM](#) with [DNN](#) object

**Usage**

```
setWeights(object, weights)

## S3 method for class 'sjSDM'
setWeights(object, weights = NULL)
```

**Arguments**

object	object of class <a href="#">sjSDM</a> with <a href="#">DNN</a> object
weights	list of layer weights: <code>list(env=list(matrix(...)), spatial=list(matrix(...)), sigma=matrix(...))</code> , see <a href="#">getWeights</a>

**Value**

No return value, weights are changed in place.

---

 SGD

*SGD*


---

**Description**

stochastic gradient descent optimizer

**Usage**

```
SGD(momentum = 0.5, dampening = 0, weight_decay = 0, nesterov = TRUE)
```

**Arguments**

momentum	strength of momentum
dampening	decay
weight_decay	l2 penalty on weights
nesterov	Nesterov momentum or not

**Value**

Anonymous function that returns optimizer when called.

---

 simulate.sjSDM

*Generates simulations from sjSDM model*


---

**Description**

Simulate `nsim` responses from the fitted model following a multivariate probit model. So currently only supported for `family = stats::binomial("probit")`

**Usage**

```
## S3 method for class 'sjSDM'
simulate(object, nsim = 1, seed = NULL, ...)
```

**Arguments**

object	a model fitted by <a href="#">sjSDM</a>
nsim	number of simulations
seed	seed for random number generator
...	optional arguments for compatibility with the generic function, no functionality implemented

**Value**

Array of simulated species occurrences of dimension order (`nsim`, `sites`, `species`)

---

 simulate\_SDM

 Simulate joint Species Distribution Models
 

---

### Description

Simulate species distributions

### Usage

```
simulate_SDM(
  env = 5L,
  sites = 100L,
  species = 5L,
  correlation = TRUE,
  weight_range = c(-1, 1),
  link = "probit",
  response = "pa",
  sparse = NULL,
  tolerance = 0.05,
  iter = 20L,
  seed = NULL
)
```

### Arguments

env	number of environment variables
sites	number of sites
species	number of species
correlation	correlated species TRUE or FALSE, can be also a function or a matrix
weight_range	sample true weights from uniform range, default -1,1
link	probit, logit or identical
response	pa (presence-absence) or count
sparse	sparse rate
tolerance	tolerance for sparsity check
iter	tries until sparse rate is achieved
seed	random seed. Default = 42

### Details

Probit is not possible for abundance response (response = 'count')



**Value**

List of simulation results:

env	Number of environmental covariates
species	Number of species
sites	Number of sites
link	Which link
response_type	Which response type
response	Species occurrence matrix
correlation	Species covariance matrix
species_weights	Species-environment coefficients
env_weights	Environmental covariates
corr_acc	Method to calculate sign accuracy

**Author(s)**

Maximilian Pichler

---

 sjSDM

*Fitting scalable joint Species Distribution Models (sjSDM)*

---

**Description**

sjSDM is used to fit joint Species Distribution models (jSDMs) using the central processing unit (CPU) or the graphical processing unit (GPU). The default is a multivariate probit model based on a Monte-Carlo approximation of the joint likelihood. sjSDM can be used to fit linear but also deep neural networks and supports the well known formula syntax.

**Usage**

```
sjSDM(
  Y = NULL,
  env = NULL,
  biotic = bioticStruct(),
  spatial = NULL,
  family = stats::binomial("probit"),
  iter = 100L,
  step_size = NULL,
  learning_rate = 0.01,
  se = FALSE,
  sampling = 100L,
  parallel = 0L,
  control = sjSDMControl(),
```

```

device = "cpu",
dtype = "float32",
seed = 758341678,
verbose = TRUE
)

sjSDM.tune(object)

```

### Arguments

Y	matrix of species occurrences/responses in range
env	matrix of environmental predictors, object of type <a href="#">linear</a> or <a href="#">DNN</a>
biotic	defines biotic (species-species associations) structure, object of type <a href="#">bioticStruct</a>
spatial	defines spatial structure, object of type <a href="#">linear</a> or <a href="#">DNN</a>
family	error distribution with link function, see details for supported distributions
iter	number of fitting iterations
step_size	batch size for stochastic gradient descent, if NULL then step_size is set to: $\text{step\_size} = 0.1 * \text{nrow}(X)$
learning_rate	learning rate for Adamax optimizer
se	calculate standard errors for environmental coefficients
sampling	number of sampling steps for Monte Carlo integration
parallel	number of cpu cores for the data loader, only necessary for large datasets
control	control parameters for optimizer, see <a href="#">sjSDMControl</a>
device	which device to be used, "cpu" or "gpu"
dtype	which data type, most GPUs support only 32 bit floats.
seed	seed for random operations
verbose	TRUE or FALSE, indicating whether progress should be printed or not
object	object of type <a href="#">sjSDM_cv</a>

### Details

The function fits per default a multivariate probit model via Monte-Carlo integration (see Chen et al., 2018) of the joint likelihood for all species.

#### Model description:

The most common jSDM structure describes the site ( $i = 1, \dots, I$ ) by species ( $j = 1, \dots, J$ ) matrix  $Y_{ij}$  as a function of environmental covariates  $X_{in}$  ( $n = 1, \dots, N$  covariates), and the species-species covariance matrix  $\Sigma$  accounts for correlations in  $e_{ij}$ :

$$g(Z_{ij}) = \beta_{j0} + \sum_{n=1}^N X_{in} \beta_{nj} + e_{ij}$$

with  $g(\cdot)$  as link function. For the multivariate probit model, the link function is:

$$Y_{ij} = 1(Z_{ij} > 0)$$

The probability to observe the occurrence vector  $\mathbf{Y}_i$  is:

$$Pr(\mathbf{Y}_i | \mathbf{X}_i \beta, \Sigma) = \int_{\mathbf{A}_{iJ}} \dots \int_{\mathbf{A}_{i1}} \phi_J(\mathbf{Y}_i^*; \mathbf{X}_i \beta, \Sigma) d\mathbf{Y}_{i1}^* \dots d\mathbf{Y}_{iJ}^*$$

in the interval  $A_{ij}$  with  $(-\infty, 0]$  if  $Y_{ij} = 0$  and  $[0, +\infty)$  if  $Y_{ij} = 1$ .

and  $\phi$  being the density function of the multivariate normal distribution.

The probability of  $\mathbf{Y}_i$  requires to integrate over  $\mathbf{Y}_i^*$  which has no closed analytical expression for more than two species which makes the evaluation of the likelihood computationally costly and needs a numerical approximation. The previous equation can be expressed more generally as:

$$\mathcal{L}(\beta, \Sigma; \mathbf{Y}_i, \mathbf{X}_i) = \int_{\Omega} \prod_{j=1}^J Pr(\mathbf{Y}_{ij} | \mathbf{X}_i \beta + \zeta) Pr(\zeta | \Sigma) d\zeta$$

sjSDM approximates this integral by  $M$  Monte-Carlo samples from the multivariate normal species-species covariance. After integrating out the covariance term, the remaining part of the likelihood can be calculated as in an univariate case and the average of the  $M$  samples are used to get an approximation of the integral:

$$\mathcal{L}(\beta, \Sigma; \mathbf{Y}_i, \mathbf{X}_i) \approx \frac{1}{M} \sum_{m=1}^M \prod_{j=1}^J Pr(\mathbf{Y}_{ij} | \mathbf{X}_i \beta + \zeta_m)$$

with  $\zeta_m \sim MVN(0, \Sigma)$ .

sjSDM uses 'PyTorch' to run optionally the model on the graphical processing unit (GPU). Python dependencies needs to be installed before being able to use the sjSDM function. We provide a function which installs automatically python and the python dependencies. See [install\\_sjSDM](#), vignette("Dependencies", package = "sjSDM")

See Pichler and Hartig, 2020 for benchmark results.

### Supported distributions:

Currently supported distributions and link functions, which are :

- **binomial**: "probit" or "logit"
- **poisson**: "log"
- "nbinom": "log"
- **gaussian**: "identity"

### Space:

We can extend the model to account for spatial auto-correlation between the sites by:

$$g(Z_{ij}) = \beta_{j0} + \sum_{n=1}^N X_{in} \beta_{nj} + \sum_{m=1}^M S_{im} \alpha_{mj} + e_{ij}$$

There are two ways to generate spatial predictors  $S$ :

- trend surface model - using spatial coordinates in a polynomial:  
linear(data=Coords, ~0+poly(X, Y, degree = 2))

- eigenvector spatial filtering - using spatial eigenvectors. Spatial eigenvectors can be generated by the [generateSpatialEV](#) function:

```
SPV = generateSpatialEV(Coords)
```

Then we use, for example, the first 20 spatial eigenvectors:

```
linear(data=SPV[,1:20], ~0+.)
```

It is important to set the intercept to 0 in the spatial term (e.g. via `~0+.`) because the intercept is already set in the environmental object.

#### Installation:

[install\\_sjSDM](#) should be theoretically able to install conda and 'PyTorch' automatically. If [sjSDM](#) still does not work after reloading RStudio, you can try to solve this on your following our trouble shooting guide [installation\\_help](#). If the problem remains, please create an issue on [issue tracker](#) with a copy of the [install\\_diagnostic](#) output as a quote.

#### Value

An S3 class of type 'sjSDM' including the following components:

<code>cl</code>	Model call
<code>formula</code>	Formula object for environmental covariates.
<code>names</code>	Names of environmental covariates.
<code>species</code>	Names of species (can be NULL if columns of Y are not named).
<code>get_model</code>	Method which builds and returns the underlying 'python' model.
<code>logLik</code>	negative log-Likelihood of the model and the regularization loss.
<code>model</code>	The actual model.
<code>settings</code>	List of model settings, see arguments of <a href="#">sjSDM</a> .
<code>family</code>	Response family.
<code>time</code>	Runtime.
<code>data</code>	List of Y, X (and spatial) model matrices.
<code>sessionInfo</code>	Output of <a href="#">sessionInfo</a> .
<code>weights</code>	List of model coefficients (environmental (and spatial)).
<code>sigma</code>	Lower triangular weight matrix for the covariance matrix.
<code>history</code>	History of iteration losses.
<code>se</code>	Matrix of standard errors, if <code>se = FALSE</code> the field 'se' is NULL.

Implemented S3 methods include [summary.sjSDM](#), [plot.sjSDM](#), [print.sjSDM](#), [predict.sjSDM](#), and [coef.sjSDM](#). For other methods, see section 'See Also'.

[sjSDM.tune](#) returns an S3 object of class 'sjSDM', see above for information about values.

#### Author(s)

Maximilian Pichler

## References

Chen, D., Xue, Y., & Gomes, C. P. (2018). End-to-end learning for the deep multivariate probit model. arXiv preprint arXiv:1803.08591.

Pichler, M., & Hartig, F. (2021). A new joint species distribution model for faster and more accurate inference of species associations from big community data. *Methods in Ecology and Evolution*, 12(11), 2159-2173.

## See Also

[getCor](#), [getCov](#), [update.sjSDM](#), [sjSDM\\_cv](#), [DNN](#), [plot.sjSDM](#), [print.sjSDM](#), [predict.sjSDM](#), [coef.sjSDM](#), [summary.sjSDM](#), [simulate.sjSDM](#), [getSe](#), [anova.sjSDM](#), [importance](#)

## Examples

```
## Not run:

# Basic workflow:
## simulate community:
com = simulate_SDM(env = 3L, species = 7L, sites = 100L)

## fit model:
model = sjSDM(Y = com$response, env = com$env_weights, iter = 50L,
              verbose = FALSE)
# increase iter for your own data

# Default distribution is binomial("probit"). Alternatively, you can use
# binomial(logit), poisson("log"), "nbinom" (with log, still somewhat
# experimental) and gaussian("identity")

coef(model)
summary(model)
getCov(model)

## plot results
species=c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6", "sp7")
group=c("mammal", "bird", "fish", "fish", "mammal", "amphibian", "amphibian")
group = data.frame(species=species, group=group)
plot(model, group=group)

## calculate post-hoc p-values:
p = getSe(model)
summary(p)

## or turn on the option in the sjSDM function:
model = sjSDM(Y = com$response, env = com$env_weights, se = TRUE,
              family = binomial("probit"),
              iter = 2L,
              verbose = FALSE)
summary(model)

## fit model with interactions:
```

```

model = sjSDM(Y = com$response,
              env = linear(data = com$env_weights, formula = ~X1:X2 + X3),
              se = TRUE,
              iter = 2L,
              verbose = FALSE) # increase iter for your own data
summary(model)

## without intercept:
model = update(model, env_formula = ~0+X1:X2 + X3,
              verbose = FALSE)

summary(model)

## predict with model:
preds = predict(model, newdata = com$env_weights)

## calculate R-squared:
R2 = Rsquared(model)
print(R2)

# With spatial terms:
## linear spatial model
XY = matrix(rnorm(200), 100, 2)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(XY, ~0+X1:X2),
              iter = 50L,
              verbose = FALSE) # increase iter for your own data
summary(model)
predict(model, newdata = com$env_weights, SP = XY)
R2 = Rsquared(model)
print(R2)

## Using spatial eigenvectors as predictors to account
## for spatial autocorrelation is a common approach:
SPV = generateSpatialEV(XY)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(SPV, ~0+., lambda = 0.1),
              iter = 50L,
              verbose = FALSE) # increase iter for your own data
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

## Visualize internal meta-community structure
an = anova(model,
           verbose = FALSE)

internal = internalStructure(an)
plot(internal)

## Visualize community assembly effects

plotAssemblyEffects(internal)

```

```

### see ?anova.sjSDM for more details

## non-linear(deep neural network) model
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = DNN(SPV,hidden = c(5L, 5L), ~0+.),
              iter = 2L,# increase iter for your own data
              verbose = FALSE)
summary(model)
predict(model, newdata = com$env_weights, SP = SPV)

# Regularization
## lambda is the regularization strength
## alpha weights the lasso or ridge penalty:
## - alpha = 0 --> pure lasso
## - alpha = 1.0 --> pure ridge
model = sjSDM(Y = com$response,
              # mix of lasso and ridge
              env = linear(com$env_weights, lambda = 0.01, alpha = 0.5),
              # we can do the same for the species-species associations
              biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
              iter = 2L,# increase iter for your own data
              verbose = FALSE)
summary(model)
coef(model)
getCov(model)

# Anova
com = simulate_SDM(env = 3L, species = 15L, sites = 200L, correlation = TRUE)

XY = matrix(rnorm(400), 200, 2)
SPV = generateSpatialEV(XY)
model = sjSDM(Y = com$response, env = linear(com$env_weights),
              spatial = linear(SPV, ~0+.),
              verbose = FALSE,
              iter = 50L) # increase iter for your own data
result = anova(model, verbose = FALSE)
print(result)
plot(result)

## visualize internal meta-community structure
internal = internalStructure(an)
plot(internal)

# Deep neural networks
## we can fit also a deep neural network instead of a linear model:
model = sjSDM(Y = com$response,
              env = DNN(com$env_weights, hidden = c(10L, 10L, 10L)),

```

```

        verbose = FALSE,
        iter = 2L) # increase iter for your own data
summary(model)
getCov(model)
pred = predict(model, newdata = com$env_weights)

## extract weights
weights = getWeights(model)

## we can also assign weights:
setWeights(model, weights)

## with regularization:
model = sjSDM(Y = com$response,
              # mix of lasso and ridge
              env = DNN(com$env_weights, lambda = 0.01, alpha = 0.5),
              # we can do the same for the species-species associations
              biotic = bioticStruct(lambda = 0.01, alpha = 0.5),
              verbose = FALSE,
              iter = 2L) # increase iter for your own data
getCov(model)
getWeights(model)

## End(Not run)

```

---

sjSDMControl

*sjSDM control object*


---

## Description

sjSDM control object

## Usage

```

sjSDMControl(
  optimizer = RMSprop(),
  scheduler = 0,
  lr_reduce_factor = 0.99,
  early_stopping_training = 0,
  mixed = FALSE
)

```

## Arguments

optimizer	object of type <a href="#">RMSprop</a> , <a href="#">Adamax</a> , <a href="#">SGD</a> , <a href="#">AccSGD</a> , <a href="#">madgrad</a> , or <a href="#">AdaBound</a>
scheduler	reduce lr on plateau scheduler or not (0 means no scheduler, > 0 number of epochs before reducing learning rate)
lr_reduce_factor	factor to reduce learning rate in scheduler



early_stopping_training	number of epochs without decrease in training loss before invoking early stopping (0 means no early stopping).
mixed	mixed (half-precision) training or not. Only recommended for GPUs > 2000 series

### Value

List with the following fields:

optimizer	Function which returns an optimizer.
scheduler_boolean	Logical, use scheduler or not.
scheduler_patience	Integer, number of epochs to wait before applying plateau scheduler.
lr_reduce_factor	Numerical, learning rate reduce factor.
mixed	Logical, use mixed training or not.
early_stopping_training	Numerical, early stopping after n epochs.

---

sjSDM\_cv

*Cross validation of elastic net tuning*

---

### Description

Cross validation of elastic net tuning

### Usage

```
sjSDM_cv(
  Y,
  env = NULL,
  biotic = bioticStruct(),
  spatial = NULL,
  tune = c("random", "grid"),
  CV = 5L,
  tune_steps = 20L,
  alpha_cov = seq(0, 1, 0.1),
  alpha_coef = seq(0, 1, 0.1),
  alpha_spatial = seq(0, 1, 0.1),
  lambda_cov = 2^seq(-10, -1, length.out = 20),
  lambda_coef = 2^seq(-10, -0.5, length.out = 20),
  lambda_spatial = 2^seq(-10, -0.5, length.out = 20),
  device = "cpu",
  n_cores = NULL,
```

```

    n_gpu = NULL,
    sampling = 5000L,
    blocks = 1L,
    ...
)

```

## Arguments

<code>Y</code>	species occurrence matrix
<code>env</code>	matrix of environmental predictors or object of type <code>linear</code> , or <code>DNN</code>
<code>biotic</code>	defines biotic (species-species associations) structure, object of type <code>bioticStruct</code> . Alpha and lambda have no influence
<code>spatial</code>	defines spatial structure, object of type <code>linear</code> , or <code>DNN</code>
<code>tune</code>	tuning strategy, random or grid search
<code>CV</code>	n-fold cross validation or list of test indices
<code>tune_steps</code>	number of tuning steps
<code>alpha_cov</code>	weighting of l1 and l2 on covariances: $(1 - \alpha) *  cov  + \alpha   cov  ^2$
<code>alpha_coef</code>	weighting of l1 and l2 on coefficients: $(1 - \alpha) *  coef  + \alpha   coef  ^2$
<code>alpha_spatial</code>	weighting of l1 and l2 on spatial coefficients: $(1 - \alpha) *  coef_{sp}  + \alpha   coef_{sp}  ^2$
<code>lambda_cov</code>	overall regularization strength on covariances
<code>lambda_coef</code>	overall regularization strength on coefficients
<code>lambda_spatial</code>	overall regularization strength on spatial coefficients
<code>device</code>	device, default cpu
<code>n_cores</code>	number of cores for parallelization
<code>n_gpu</code>	number of GPUs
<code>sampling</code>	number of sampling steps for Monte Carlo integration
<code>blocks</code>	blocks of parallel tuning steps
<code>...</code>	arguments passed to <code>sjSDM</code> , see <code>sjSDM</code>

## Value

An S3 class of type 'sjSDM\_cv' including the following components:

<code>tune_results</code>	Data frame with tuning results.
<code>short_summary</code>	Data frame with averaged tuning results.
<code>summary</code>	Data frame with summarized averaged results.
<code>settings</code>	List of tuning settings, see the arguments in <code>DNN</code> .
<code>data</code>	List of <code>Y</code> , <code>env</code> (and <code>spatial</code> ) objects.
<code>config</code>	List of <code>sjSDM</code> settings, see arguments of <code>sjSDM</code> .
<code>spatial</code>	Logical, spatial model or not.

Implemented S3 methods include `sjSDM.tune`, `plot.sjSDM_cv`, `print.sjSDM_cv`, and `summary.sjSDM_cv`

**See Also**

[plot.sjSDM\\_cv](#), [print.sjSDM\\_cv](#), [summary.sjSDM\\_cv](#), [sjSDM.tune](#)

**Examples**

```
## Not run:
# simulate sparse community:
com = simulate_SDM(env = 5L, species = 25L, sites = 50L, sparse = 0.5)

# tune regularization:
tune_results = sjSDM_cv(Y = com$response,
                       env = com$env_weights,
                       tune = "random", # random steps in tune-parameter space
                       CV = 2L, # 3-fold cross validation
                       tune_steps = 2L,
                       alpha_cov = seq(0, 1, 0.1),
                       alpha_coef = seq(0, 1, 0.1),
                       lambda_cov = seq(0, 0.1, 0.001),
                       lambda_coef = seq(0, 0.1, 0.001),
                       n_cores = 2L,
                       sampling = 100L,
                       # small models can be also run in parallel on the GPU
                       iter = 2L # we can pass arguments to sjSDM via...
                       )

# print overall results:
tune_results

# summary (mean values over CV for each tuning step)
summary(tune_results)

# visualize tuning and best points:
# best = plot(tune_results, perf = "logLik")

# fit model with best regularization parameter:
model = sjSDM.tune(tune_results)

summary(model)

## End(Not run)
```

---

summary.sjSDM

*Return summary of a fitted sjSDM model*


---

**Description**

Return summary of a fitted sjSDM model

**Usage**

```
## S3 method for class 'sjSDM'
summary(object, ...)
```

**Arguments**

`object` a model fitted by [sjSDM](#)

`...` optional arguments for compatibility with the generic function, no functionality implemented

**Value**

The above matrix is silently returned.

---

summary.sjSDManova	<i>Summary table of sjSDM anova</i>
--------------------	-------------------------------------

---

**Description**

The function prints and returns invisible a summary table of an sjSDM ANOVA, created by [anova.sjSDM](#)

**Usage**

```
## S3 method for class 'sjSDManova'
summary(
  object,
  method = c("ANOVA"),
  fractions = c("all", "discard", "proportional", "equal"),
  ...
)
```

**Arguments**

`object` an object of [anova.sjSDM](#)

`method` method used to calculate the ANOVA

`fractions` how to handle the shared fractions. See details

`...` optional arguments for compatibility with the generic function, no function implemented

**Details**

The function returns a ANOVA table with Deviance as well as the pseudo-R2 metrics of Nagelkerke and McFadden

There are four options to handle shared ANOVA fractions, which is variance that can be explained, typically as a result of collinearity, by several of the fractions:

1. "all" returns the shared fractions explicitly
2. "discard" discards the fractions, as typically in a type II Anova
3. "proportional" distributes shared fractions proportional to the unique fractions
4. "equal" distributions shared fractions equally to the unique fractions

## Value

The matrix that is printed out is silently returned

## Examples

```
## Not run:
library(sjSDM)
# simulate community:
community = simulate_SDM(env = 3L, species = 10L, sites = 100L)

Occ <- community$response
Env <- community$env_weights
SP <- data.frame(matrix(rnorm(200, 0, 0.3), 100, 2)) # spatial coordinates

# fit model:
model <- sjSDM(Y = Occ,
               env = linear(data = Env, formula = ~X1+X2+X3),
               spatial = linear(data = SP, formula = ~0+X1*X2),
               family=binomial("probit"),
               verbose = FALSE,
               iter = 20) # increase iter for real analysis

# Calculate ANOVA for env, space, associations, for details see ?anova.sjSDM
an = anova(model, samples = 10, verbose = FALSE) # increase iter for real analysis

# Show anova fractions
plot(an)

# ANOVA tables with different way to handle fractions
summary(an)
summary(an, fractions = "discard")
summary(an, fractions = "proportional")
summary(an, fractions = "equal")

# Internal structure
int = internalStructure(an, fractions = "proportional")

print(int)

plot(int) # default is negative values will be set to 0
plot(int, negatives = "scale") # global rescaling of all values to range 0-1
plot(int, negatives = "raw") # negative values will be discarded

plotAssemblyEffects(int)
```

```

plotAssemblyEffects(int, negatives = "floor")
plotAssemblyEffects(int, response = "sites", pred = as.factor(c(rep(1, 50), rep(2, 50))))
plotAssemblyEffects(int, response = "species", pred = runif(10))
plotAssemblyEffects(int, response = "species", pred = as.factor(c(rep(1, 5), rep(2, 5))))

## End(Not run)

```

---

summary.sjSDM_cv	<i>Return summary of a fitted sjSDM_cv model</i>
------------------	--

---

### Description

Return summary of a fitted sjSDM\_cv model

### Usage

```

## S3 method for class 'sjSDM_cv'
summary(object, ...)

```

### Arguments

object	a model fitted by <a href="#">sjSDM_cv</a>
...	optional arguments for compatibility with the generic function, no functionality implemented

### Value

Above data frame is silently returned.

---

update.sjSDM	<i>Update and re-fit a model call</i>
--------------	---------------------------------------

---

### Description

Update and re-fit a model call

### Usage

```

## S3 method for class 'sjSDM'
update(object, env_formula = NULL, spatial_formula = NULL, biotic = NULL, ...)

```

**Arguments**

<code>object</code>	of class 'sjSDM'
<code>env_formula</code>	new environmental formula
<code>spatial_formula</code>	new spatial formula
<code>biotic</code>	new biotic config
<code>...</code>	additional arguments

**Value**

An S3 class of type 'sjSDM'. See [sjSDM](#) for more information.

# Index

- \* **datasets**
  - butterflies, 11
  - eucalypts, 19
- AccSGD, 3, 64
- AdaBound, 4, 64
- Adamax, 5, 64
- anova.sjSDM, 5, 24, 29, 39, 43, 49, 61, 68
- binomial, 59
- bioticStruct, 7, 42, 47, 58, 66
- butterflies, 11
- check\_module, 13
- checkModel, 13
- coef.sjSDM, 13, 60, 61
- DiffGrad, 14
- DNN, 14, 20, 21, 23, 32, 38, 42, 48, 54, 58, 61, 66
- eucalypts, 19
- gaussian, 59
- generateSpatialEV, 20, 60
- getCor, 20, 61
- getCov, 21, 61
- getImportance, 21
- getSe, 22, 61
- getWeights, 23, 54
- importance, 23, 40, 51, 61
- install\_diagnostic, 27, 28, 60
- install\_sjSDM, 25, 28, 28, 59, 60
- installation\_help, 25, 28, 60
- internalStructure, 29, 41
- is\_torch\_available, 30
- linear, 15, 31, 42, 48, 58, 66
- logLik.sjSDM, 35
- madgrad, 35, 64
- new\_image, 36
- plot.sjSDM, 37, 60, 61
- plot.sjSDM.DNN, 38
- plot.sjSDM\_cv, 42, 66, 67
- plot.sjSDManova, 6, 39
- plot.sjSDMimportance, 24, 40
- plot.sjSDMinternalStructure, 6, 29, 40, 43
- plotAssemblyEffects, 43
- plotsjSDMcoef, 37, 45
- poisson, 59
- predict.sjSDM, 46, 60, 61
- print.bioticStruct, 8, 47
- print.DNN, 15, 48
- print.linear, 31, 48
- print.sjSDM, 49, 60, 61
- print.sjSDM\_cv, 52, 66, 67
- print.sjSDManova, 6, 49
- print.sjSDMimportance, 24, 50
- print.sjSDMinternalStructure, 29, 51
- residuals.sjSDM, 52
- RMSprop, 53, 64
- Rsquared, 53
- sessionInfo, 60
- setWeights, 54
- SGD, 55, 64
- simulate.sjSDM, 55, 61
- simulate\_SDM, 56
- sjSDM, 5, 8, 13, 15, 20–23, 32, 35, 37, 38, 45, 46, 49, 52, 54, 55, 57, 60, 66, 68, 71
- sjSDM-package (installation\_help), 25
- sjSDM.tune, 60, 66, 67
- sjSDM\_cv, 42, 52, 58, 61, 65, 70
- sjSDMControl, 58, 64
- summary.sjSDM, 60, 61, 67
- summary.sjSDM\_cv, 66, 67, 70
- summary.sjSDManova, 6, 49, 68



update.sjSDM, [61](#), [70](#)