

# Package ‘dynamo’

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**Type** Package

**Title** Fit a Stochastic Dynamical Array Model to Array Data

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**Description** An implementation of the method proposed in Lund and Hansen (2018) for fitting 3-dimensional dynamical array models. The implementation is based on the glamlasso package, see Lund et al. (2017) <doi:10.1080/10618600.2017.1279548>, for efficient design matrix free lasso regularized estimation in a generalized linear array model. The implementation uses a block relaxation scheme to fit each individual component in the model using functions from the glamlasso package.

**License** GPL (>= 2)

**Depends** glamlasso (>= 3.0), abind, MortalitySmooth

**Imports** Rcpp (>= 0.12.12)

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 6.0.1

**NeedsCompilation** yes

**Repository** CRAN

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## Description

An implementation of the method proposed in *Lund and Hansen, 2018* for fitting 3-dimensional dynamical array models. The implementation is based on the *glamlasso* package, see *Lund et. al, 2017*, for efficient design matrix free lasso regularized estimation in a generalized linear array model. The implementation uses a block relaxation scheme to fit each individual component in the model using functions from the *glamlasso* package.

## Usage

```
fitmodel(V,
         phix, phiy, phil, phit,
         penaltyfactor,
         nlambda = 15,
         lambdaminratio = 0.0001,
         retolinner = 10^-4,
         rextola = 10^-4,
         maxalt = 10)
```

## Arguments

|                |   |
|----------------|---|
| V              | is the $N_x \times N_y \times N_t \times G$ array containing the data   |
| phix           | is a $N_x \times px$ matrix containing spatial basis functions  |
| phiy           | is a $N_y \times py$ matrix containing spatial basis functions  |
| phil           | is a $Lp1 \times pl$ matrix containing temporal basis functions   |
| phit           | is a $Nt \times pt$ matrix containing temporal basis functions  |
| penaltyfactor  | An array of size $p_1 \times \dots \times p_d$ . Is multiplied with each element in lambda to allow differential shrinkage on the coefficients. |
| nlambda        | the number of lambda values to fit  |
| lambdaminratio | the smallest value for lambda, given as a fraction of   |
| retolinner     | the convergence tolerance used with <i>glamlasso</i>  |
| rextola        | the convergence tolerance used for the alternation loop   |
| maxalt         | maximum number of alternations  |

## Details

This package contains an implementation of the method proposed in *Lund and Hansen, 2018* for fitting a (partial) 3-dimensional 3-component dynamical array model to a  $N_x \times N_y \times N_t \times G$  data array  $V$ , where  $N_x, N_y, N_t, G \in \{1, 2, \dots\}$ . Note that  $N_x, N_y, N_t$  gives the number of observations in the two spatial dimensions and the temporal dimension respectively and  $G$  gives the number of

trials. Let  $L$  be positive integer giving the length of the modelled delay,  $M := N_t - L - 1$  and  $\phi^i$  be a  $N_i \times p_i$  matrix for  $i \in \{x, y, l\}$ . Then define a  $M \times p_x p_y p_l$  matrix

$$\Phi_g^{xyt} = \begin{pmatrix} \text{vec}(\Phi_{1,g}^{xyt}) \\ \vdots \\ \text{vec}(\Phi_{M,g}^{xyt}) \end{pmatrix},$$

for each  $g \in \{1, \dots, G\}$ . Here using the so called rotated  $H$ -transform  $\rho$  from *Currie et al., 2006*,  $\Phi_{k,g}^{xyt}$  is a  $p_x \times p_y \times p_l$  array that, for each  $k \in \{1, \dots, M\}$ , can be computed as

$$\Phi_{k,g}^{xyt} := \rho((\phi^l)^\top, \rho((\phi^y)^\top, \rho((\phi^x)^\top, V_{\cdot, (k-L):(k-1), g})))$$

Then we can write the model equation as for each trial  $g$  as

$$V_{\cdot, (L+1):N_t, g} = \text{vec}(\rho(\phi^t, \rho(\phi^y, \rho(\phi^x, A))) + \rho(\Phi^{xyt}, \rho(\phi^y, \rho(\phi^x, B))) + V_{\cdot, -1:(M-1), g} \odot C + E$$

where  $A$  and  $B$  are resp.  $p_x \times p_y \times p_t$  and  $p_x \times p_y \times p_x p_y p_l$  coefficient arrays that are estimated and  $C$  is a  $N_x \times N_y \times M$  array containing  $M$  copies of the  $N_x \times N_y$  matrix  $\rho(\phi^y, \rho(\phi^x, \Gamma))$ , where  $\Gamma$  is a  $p_x \times p_y$  coefficient matrix that is estimated. Finally  $E$  is a  $N_x \times N_y \times M$  array with Gaussian noise. See *Lund and Hansen, 2018* for more details.

## Value

An object with S3 Class "dynamo".

|             |  |
|-------------|--|
| Out         | A list where the first $G$ items are the individual fits to the trials containing:   |
| Out\$V      | The $N_x \times N_y \times N_t$ data array for trial $g$ .   |
| Out\$Phixyl | a $M \times p_x p_y p_l$ matrix, the convolution tensor.   |
| Out\$BetaS  | $p_x p_y p_t \times n\lambda$ matrix containing the estimated parameters for the stimulus component for each $\lambda$ value         |
| Out\$BetaF  | $p_x p_y p_x p_y p_l \times n\lambda$ matrix containing the estimated parameters for the filter component for each $\lambda$ value   |
| Out\$BetaH  | $p_x p_y \times n\lambda$ matrix containing the estimated parameters for the instantaneous memory component for each $\lambda$ value |
| Out\$lambda | vector of length $n\lambda$ containing the penalty parameters.   |
| Out\$Obj    | $\text{maxalt} \times n\lambda$ matrix containing the objective values for each alternation and each $\lambda$                       |
| phix        | is a $N_x \times p_x$ matrix containing the basis functions over the spatial $x$ domain.   |
| phiy        | is a $N_y \times p_y$ matrix containing the basis functions over the spatial $y$ domain.   |
| phil        | is a $L + 1 \times p_l$ matrix containing the basis functions over the temporal domain for the delay.                                |
| phit        | is a $M \times p_t$ matrix containing the basis functions over the temporal domain for the stimulus.                                 |

## Author(s)

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## References

Lund, A. and N. R. Hansen (2018). Sparse Network Estimation for Dynamical Spatio-temporal Array Models. *In preparation*, url = <https://>.

Lund, A., M. Vincent, and N. R. Hansen (2017). Penalized estimation in large-scale generalized linear array models. *Journal of Computational and Graphical Statistics*, 26, 3, 709-724. url = <https://doi.org/10.1080/10618600.2017.1279548>.

Currie, I. D., M. Durban, and P. H. C. Eilers (2006). Generalized linear array models with applications to multidimensional smoothing. *Journal of the Royal Statistical Society. Series B.* 68, 259-280. url = <http://dx.doi.org/10.1111/j.1467-9868.2006.00543.x>.

## Examples

```
## Not run:
# Example showcasing the application from Lund and Hansen (2018).
##### data
data(V)
##### constants
Nx <- dim(V)[1]
Ny <- dim(V)[2]
Nt <- dim(V)[3]
L <- 50          #lag length in steps
Lp1 <- L + 1     #number of lag time points (= initial points)
t0 <- 0
M <- Nt - Lp1    #number of modelled time points
sl <- floor(200 / 0.6136) - 0 + 1 #stim start counted from -tau
sr <- sl + floor(250 / 0.6136) #stim end counted from -tau
##no. of basis func.
px <- 8
py <- 8
pl <- max(ceiling(Lp1 / 5), 4)
pt <- max(ceiling((Nt - sl) / 25), 4)
degx <- 2
degy <- 2
degl <- 3
degt <- 3
##### basis functions
library(MortalitySmooth)
phix <- round(MortSmooth_bbase(x = 1:Nx, x1 = 1, xr = Nx, ndx = px - degx, deg = degx), 10)
phiy <- round(MortSmooth_bbase(x = 1:Ny, x1 = 1, xr = Ny, ndx = py - degy, deg = degy), 10)
phil <- round(MortSmooth_bbase(x = -tau:(t0 - 1), x1 = -tau, xr = (t0 - 1),
ndx = pl - degl, deg = degl), 10)
phit <- round(MortSmooth_bbase(x = sl:Nt, x1 = sl, xr = Nt, ndx = pt - degt, deg = degt), 10)
phit <- rbind(matrix(0, (sl - 1) - Lp1, dim(phit)[2]), phit)
##### penalty weights
wt <- c(1, 1, 2, 2, 3, 3, 3, 3, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 3, 3, 3, 3, 2, 1, 1)
penSlist <- list(matrix(1, px, py), matrix(1 / wt, dim(phit)[2], 1))
penF <- array(1, c(px, py, px * py * pl))
penH <- matrix(1, px, py)
penaltyfactor <- list(penSlist, penF, penH)
##### run algorithm
system.time({Fit <- fitmodel(V,
```

```

                                phix, phiy, phil, phit,
                                penaltyfactor,
                                nlambda = 10,
                                lambdaminratio = 10^-1,
                                reltolinner = 10^-4,
                                reltola = 10^-4,
                                maxalt = 10))

##### get one fit
modelno <- 6
fit <- Fit[[1]]
A <- array(fit$BetaS[, modelno], c(px, py, pt))
B <- array(fit$BetaF[, modelno], c(px, py, px * py * pl))
C <- array(fit$BetaH[, modelno], c(px, py))
shat <- RH(phit, RH(phiy, RH(phix, A)))
beta <- array(B, c(px, py, px, py, pl))
what <- RH(phil, RH(phiy, RH(phix, RH(phiy, RH(phix, beta)))))
##### compute summary network quantities
wbar <- apply(abs(what), c(1, 2, 3, 4), sum)
win <- apply(wbar, c(1, 2), sum)
wout <- apply(wbar, c(3, 4), sum)
indeg <- apply((what != 0), c(1, 2), sum)
outdeg <- apply((what != 0), c(3, 4), sum)
winnorm <- ifelse(indeg > 0, win / indeg, win)
woutnorm <- ifelse(outdeg > 0, wout / outdeg, wout)
##### plot summary network quantities
par(mfrow = c(2, 2), oma = c(0, 0, 1, 0), mar = c(0, 0, 1, 0))
image(winnorm, main = paste("Time aggregated in effects"), axes = FALSE)
image(woutnorm, main = paste("Time aggregated out effects"), axes = FALSE)
timepoint <- which(shat[9, 9, ] == min(shat[9, 9, ]))
image(shat[, , timepoint], axes = FALSE, main = "Stimulus function")
plot(shat[1, 1, ], ylim = range(shat), type="l", main = "Stimulus function")
for(i in 1:Nx){for(j in 1:Ny){lines(shat[i, j, ])}
abline(v = sl - Lp1, lty = 2)
abline(v = sr - Lp1, lty = 2)

## End(Not run)

```

## Description

This data set contains one trial of processed voltage sensitive dye recordings from animal 308. The original raw data set contains integer values indicating the fluorescence. See *Roland et. al, 2006*

## Format

A three dimensional  $25 \times 25 \times 977$  array.

**References**

Per E. Roland, Akitoshi Hanazawa, Calle Undeman, David Eriksson, Tamas Tompa, Hiroyuki Nakamura, Sonata Valentiniene and Bashir Ahmed (2006). Cortical feedback depolarization waves: A mechanism of top-down influence on early visual areas. *PNAS*, 103, 33, 12586-12591. url = <https://doi.org/10.1073/pnas.0604925103>.

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