

A multistate habitat-driven Langevin diffusion for inferring behaviour-specific utilization distributions

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Langevin diffusion

$$d\boldsymbol{\mu}_t = \frac{\sigma^2}{2} \nabla \log \pi(\boldsymbol{\mu}_t | \boldsymbol{\beta}) dt + \sigma d\mathbf{B}_t$$

$$\pi(\boldsymbol{\mu} | \boldsymbol{\beta}) = \frac{\exp\left(\sum_{k=1}^K x_k(\boldsymbol{\mu}) \beta_k\right)}{\int_{\mathcal{M}} \exp\left(\sum_{k=1}^K x_k(\mathbf{z}) \beta_k\right) d\mathbf{z}}$$



Michelot et al. (2019). The Langevin diffusion as a continuous-time model of animal movement and habitat selection, *Methods Ecol Evol.*

Langevin diffusion (discrete approximation of)

$$\boldsymbol{\mu}_{t+1} = \boldsymbol{\mu}_t + \frac{\sigma^2 \Delta_t}{2} \nabla \log \pi(\boldsymbol{\mu}_t | \boldsymbol{\beta}) + \boldsymbol{\epsilon}_{t+1}$$

$$\nabla \log \pi(\boldsymbol{\mu} | \boldsymbol{\beta}) = \sum_{k=1}^K \beta_k \nabla x_k(\boldsymbol{\mu})$$

$\boldsymbol{\mu}_t$ = location at time t

σ^2 = speed parameter

$\boldsymbol{\epsilon}_{t+1} \sim \mathcal{N}(\mathbf{0}, \sigma^2 \Delta_t \mathbf{I})$

β_k = habitat selection coefficient for covariate k

$x_k(\boldsymbol{\mu})$ = covariate k evaluated at $\boldsymbol{\mu}$

Δ_t = interval duration between times t and $t + 1$

Multistate Langevin diffusion

$$[\boldsymbol{\mu}_{t+1} \mid \boldsymbol{\mu}_t, \boldsymbol{\sigma}, \boldsymbol{\beta}, s_t] \equiv \mathcal{N} \left(\boldsymbol{\mu}_t + \frac{\sigma_{s_t}^2 \Delta_t}{2} \nabla \log \pi_{s_t}(\boldsymbol{\mu}_t \mid \boldsymbol{\beta}_{s_t}), \sigma_{s_t}^2 \Delta_t \mathbf{I} \right)$$

→ This can be the observation distribution (\mathbf{P}_t) of a (continuous-time) hidden Markov model!

Continuous-time HMM

$$\mathcal{L}(\theta | \mu) = \delta \mathbf{P}_1 \left[\prod_{t=2}^T \Gamma_t \mathbf{P}_t \right] \mathbf{1}$$

$$\mathbf{P}_t = \begin{bmatrix} [\mu_{t+1} | \mu_t, \theta, s_t = 1] & 0 & \dots & 0 \\ 0 & [\mu_{t+1} | \mu_t, \theta, s_t = 2] & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & [\mu_{t+1} | \mu_t, \theta, s_t = S] \end{bmatrix}$$

$$\Gamma_t = \exp(\mathbf{Q} \Delta_t)$$

$$\mathbf{Q} = \begin{bmatrix} s_{t+1} = 1 & s_{t+1} = 2 & \dots & s_{t+1} = S \\ -q_{1,1} & q_{1,2} & \dots & q_{1,S} \\ q_{2,1} & -q_{2,2} & \dots & q_{2,S} \\ \vdots & \vdots & \ddots & \vdots \\ q_{S,1} & q_{S,2} & \dots & -q_{S,S} \end{bmatrix} \quad \begin{array}{l} s_t = 1 \\ s_t = 2 \\ \vdots \\ s_t = S \end{array}$$

Fitting multistate Langevin models in momentuHMM

```
library(remote)
install_github("bmcclintock/momentuHMM@develop")
```

- ▶ Relies on the pseudo-design matrix (`DM`) argument and `langevin()` special function
- ▶ Pseudo-design matrix is analogous to \mathbf{X} in GLMs:

$$g(\boldsymbol{\theta}) = \mathbf{X}\boldsymbol{\beta},$$

where $g()$ is a link function (e.g. log, logit)

- ▶ Rows of \mathbf{X} correspond to (real-scale) data stream distribution parameters ($\boldsymbol{\theta}$)
- ▶ Columns of \mathbf{X} correspond to (working-scale) data stream distribution parameters ($\boldsymbol{\beta}$)

The pseudo-design matrix

```
# m is a momentuHMM object (as returned by fitHMM), automatically loaded with the package
m <- example$m

# default identity matrix for step ~ gamma(mean, sd) with no covariates
X <- m$conditions$fullDM$step
X

##      mean_1:(Intercept) mean_2:(Intercept) sd_1:(Intercept) sd_2:(Intercept)
## mean_1                  1                 0                 0                 0
## mean_2                  0                 1                 0                 0
## sd_1                   0                 0                 1                 0
## sd_2                   0                 0                 0                 1

# working-scale parameters (on log scale)
beta <- m$CIbeta$step$est
beta

##      mean_1:(Intercept) mean_2:(Intercept) sd_1:(Intercept) sd_2:(Intercept)
## [1,]        2.680676       5.014916       2.149273       3.034212
```

The pseudo-design matrix

```
# mean and sd use log link function
exp(X %*% t(beta))

## [1,]
## mean_1 14.594959
## mean_2 150.643519
## sd_1    8.578616
## sd_2    20.784598

# compare to real-scale parameter estimates
m$CIreal$step$est

## state 1 state 2
## mean 14.594959 150.6435
## sd    8.578616 20.7846
```

Fitting multistate Langevin models in momentuHMM

prepData can calculate habitat covariate gradients

```
# prepare data and calculate gradients
tracks <- prepData(data, altCoordNames = "mu",
                     spatialCovs = covlist,
                     gradient = TRUE)
head(tracks)

##      ID      step     angle      mu.x      mu.y   forest   forest.x
## 1  1 21.519155       NA 0.000000 0.000000 0.2891083 -0.0001140799
## 2  1 10.041690 0.7570564 3.622225 -21.21211 0.2891083 -0.0001138960
## 3  1 14.921862 1.2452493 11.648896 -27.24602 0.2891083 -0.0001138436
## 4  1  9.860922 -0.5809053 23.959044 -18.81262 0.2891083 -0.0001139168
## 5  1 131.575511 -0.9607220 33.818046 -18.61803 0.2891083 -0.0001139185
## 6  1 166.594165 -0.3801213 111.314764 -124.94946 0.2891083 -0.0001129963
##           forest.y
## 1  2.585472e-05
## 2  4.644763e-06
## 3  4.575148e-06
## 4  4.468384e-06
## 5  4.382878e-06
## 6  3.710758e-06
```

Fitting multistate Langevin models in `momentuHMM`

`langevin()` special function in DM argument of `fitCTHMM`

```
# define observation distribution
dist <- list(mu="rw_mvnorm2") # bivariate normal random walk
```

```
# define single-state pseudo-design matrix
DM1 <- list(mu=matrix(c("mu.x_tm1","langevin(cov1.x)","langevin(cov2.x)",0,0,
                      "mu.y_tm1","langevin(cov1.y)","langevin(cov2.y)",0,0,
                      0,0,0,1,0,
                      0,0,0,0,1,
                      0,0,0,1,0),5,5,byrow=TRUE,
dimnames=list(c("mean.x","mean.y","sigma.x","sigma.xy","sigma.y"),
              c("mean","cov1","cov2","sigma","sigma.xy"))))
```

DM1

```
## $mu
##      mean      cov1      cov2      sigma sigma.xy
## mean.x "mu.x_tm1" "langevin(cov1.x)" "langevin(cov2.x)" "0"    "0"
## mean.y "mu.y_tm1" "langevin(cov1.y)" "langevin(cov2.y)" "0"    "0"
## sigma.x "0"        "0"          "0"          "1"    "0"
## sigma.xy "0"        "0"          "0"          "0"    "1"
## sigma.y "0"        "0"          "0"          "1"    "0"
```

fit model

```
fitLangevin <- fitCTHMM(tracks, nbStates=1, dist=dist, DM=DM1, Par0=Par0)
```

Illustration: Steller sea lions

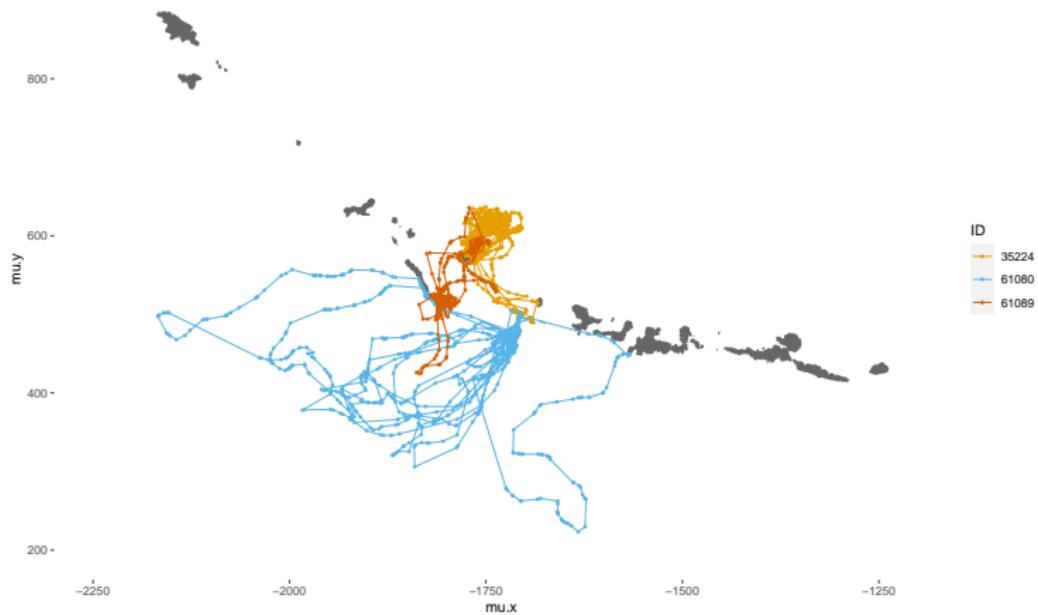
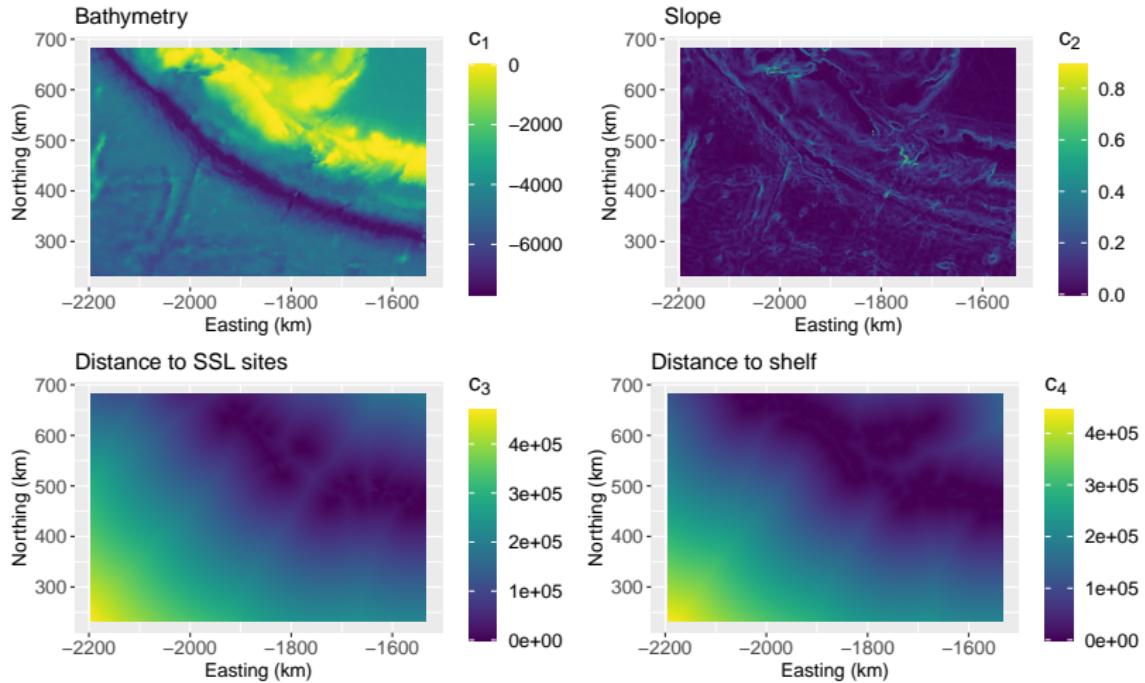
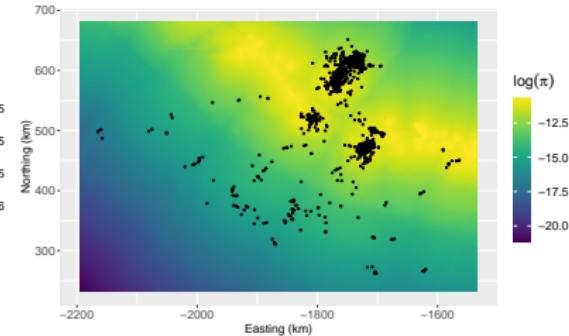
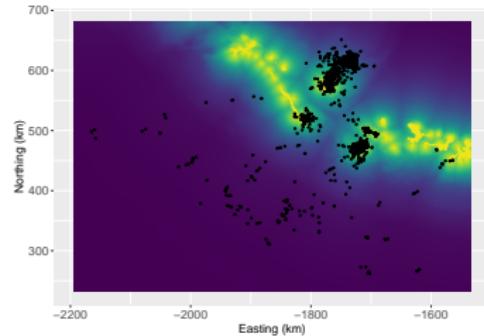


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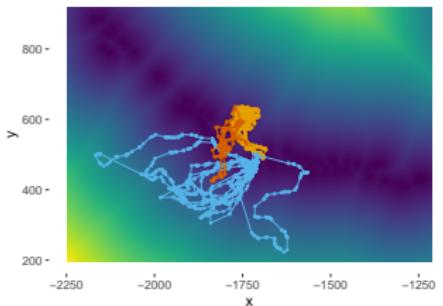
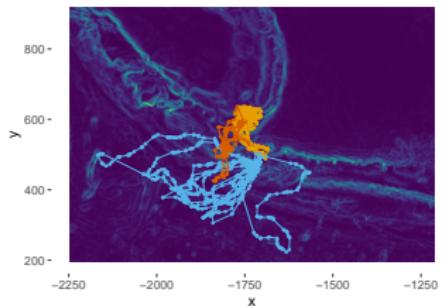
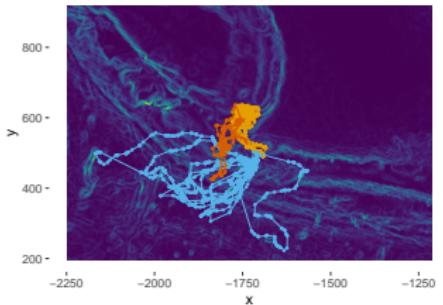
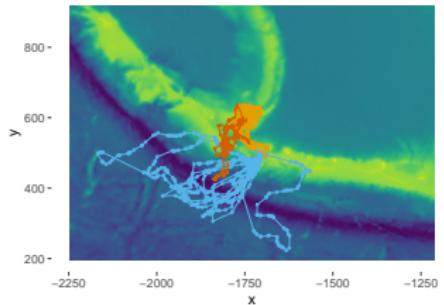


Illustration: Steller sea lions

$$[\mu_{n,t+1} \mid \mu_{n,t}, \theta, s_{n,t}] \equiv \\ \begin{cases} \mathcal{N}\left(\mu_{n,t} + \frac{\sigma_{n,AS}^2 \Delta_t}{2} \nabla \log \pi_{s_{n,t}}(\mu_{n,t} \mid \beta_{s_{n,t}}), \sigma_{n,AS}^2 \Delta_t \mathbf{I}\right) & \text{if } s_{n,t} \in \{1, 2, 3\} \\ \mathcal{N}(\mu_{n,t}, \sigma_{HO}^2 \Delta_t \mathbf{I}) & \text{if } s_{n,t} = 4 \end{cases}$$

$$[\mu_{n,t+1} \mid \mu_{n,t}, \theta, s_{n,t}] \equiv \\ \begin{cases} \mathcal{N}\left(\mu_{n,t} + \frac{\sigma_{n,AS}^2 \Delta_{n,t}}{2} \nabla \log \pi_{s_{n,t}}(\mu_{n,t} \mid \beta_{s_{n,t}}), \sigma_{n,AS}^2 \Delta_{n,t} \mathbf{I}\right) & \text{if } s_{n,t} \in \{1, 3, 4\} \\ \mathcal{N}\left(\mu_{n,t} + \frac{\sigma_{n,2}^2 \Delta_{n,t}}{2} \nabla \log \pi_2(\mu_{n,t} \mid \beta_2), \sigma_{n,2}^2 \Delta_{n,t} \mathbf{I}\right) & \text{if } s_{n,t} = 2 \\ \mathcal{N}(\mu_{n,t}, \sigma_{HO}^2 \Delta_{n,t} \mathbf{I}) & \text{if } s_{n,t} = 5 \end{cases}$$

$$\beta_s = (\beta_{depth,s}, \beta_{slope,s}, \beta_{depth:slope,s}, \beta_{d2site,s}, \beta_{d2site^2,s})$$

Illustration: Steller sea lions

$$\Gamma_t = \exp(\mathbf{Q}_t \Delta_t)$$

$$\mathbf{Q}_t = \begin{bmatrix} s_{t+1}=1 & s_{t+1}=2 & \dots & s_{t+1}=S \\ -q_{t,1,1} & q_{t,1,2} & \dots & q_{t,1,S} \\ q_{t,2,1} & -q_{t,2,2} & \dots & q_{t,2,S} \\ \vdots & \vdots & \ddots & \vdots \\ q_{t,S,1} & q_{t,S,2} & \dots & -q_{t,S,S} \end{bmatrix} \begin{array}{l} s_t=1 \\ s_t=2 \\ \vdots \\ s_t=S \end{array}$$

$$\log(q_{t,i,j}) = \alpha_{0,i,j} + \alpha_{1,i,j} \text{d2site}(\boldsymbol{\mu}_t) \text{ for } i \neq j$$

Illustration: Steller sea lions

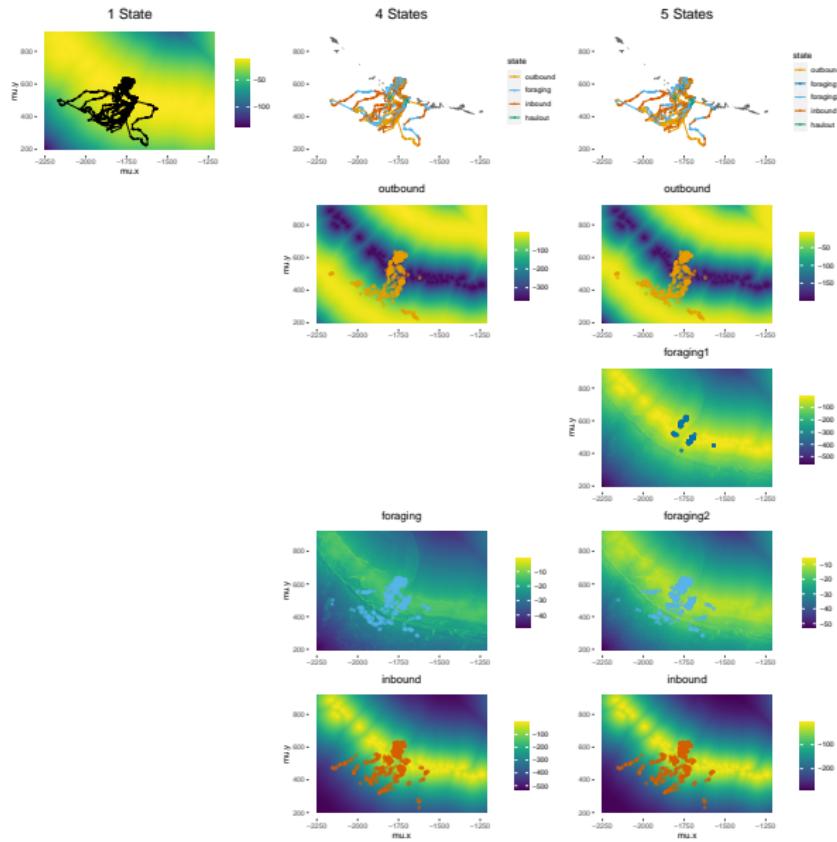
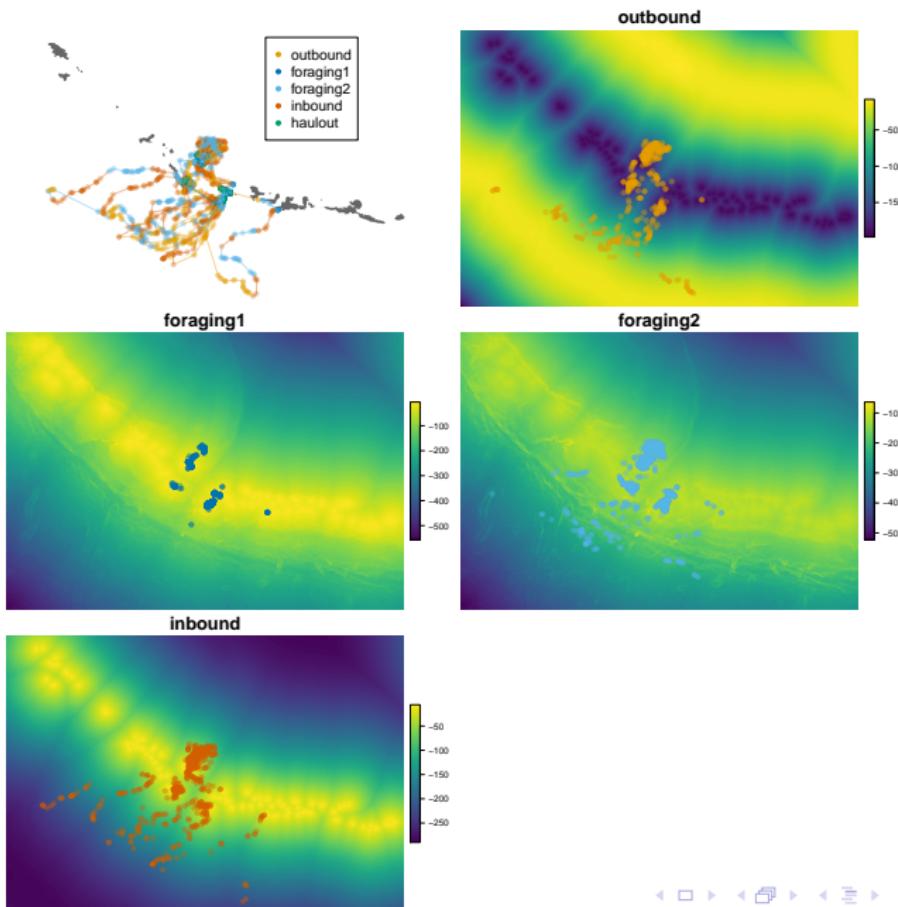
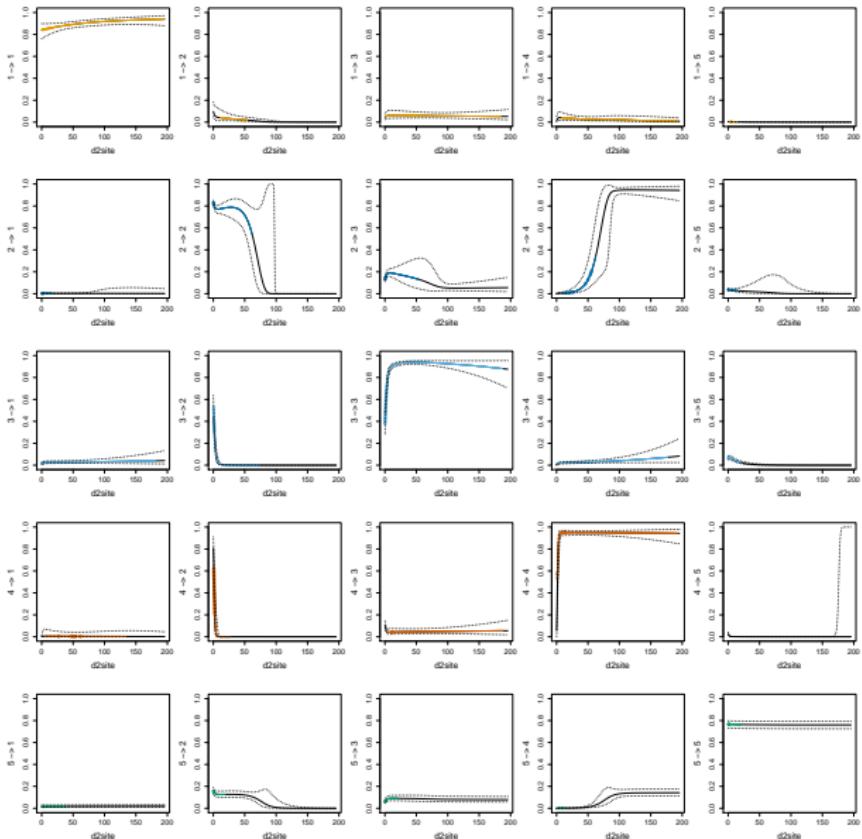


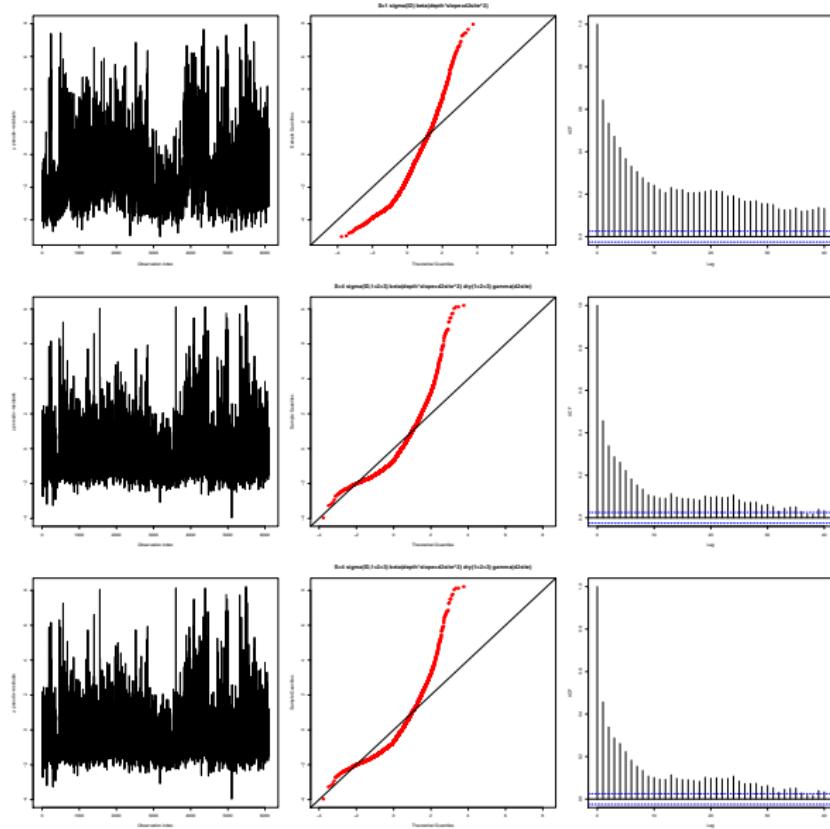
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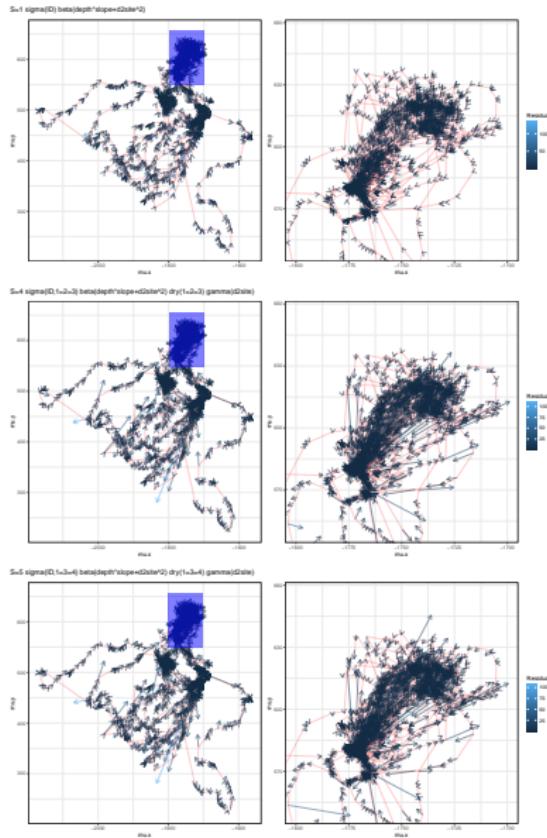
State transition probabilities



Pseudo-residuals



Predicted steps and residuals



Simulation

```
# simulate from fitted model  
simLangevin <- simCTHMM(model=fitLangevin, spatialCovs=covlist)
```

