Movement Ecology

Introduction to analysing animal movement data in R

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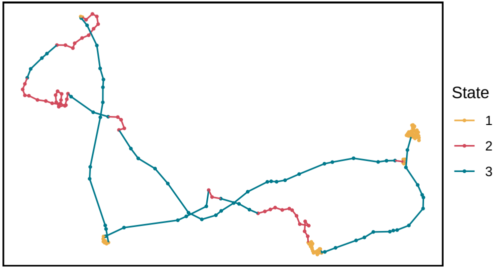

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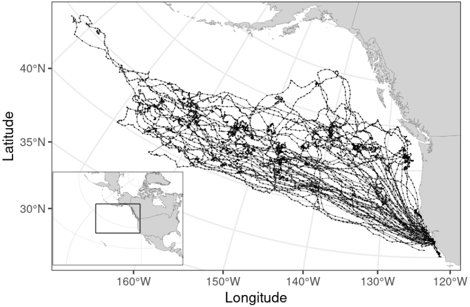


What ecological inferences can we get from statistical models of animal movement?

Movement modelling – myopic overview

Home range estimation

- adehabitatHR
- ctmm (AKDE)

Behaviour segmentation

- moveHMM
- momentuHMM

Path reconstruction (Filtering)

- crawl
- foieGras

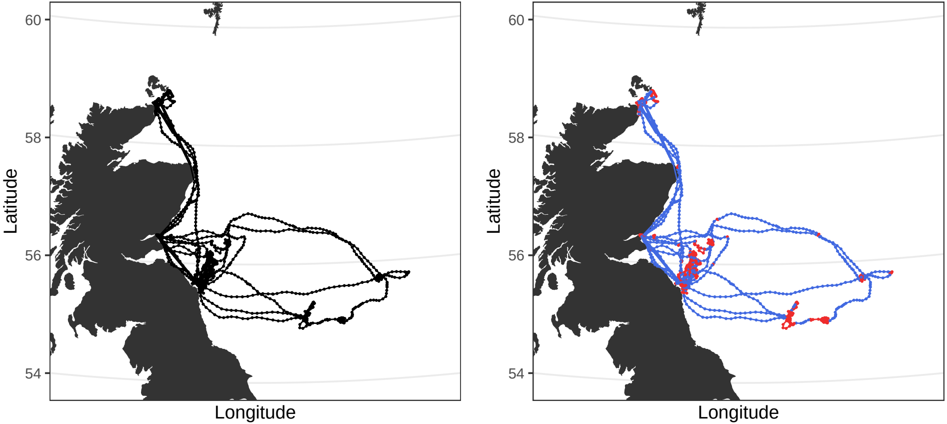
many packages, with different levels of emphasis

Movement parameter estimation (or relationship with habitat)

Step selection analysis

- amt

Hidden Markov models – motivation



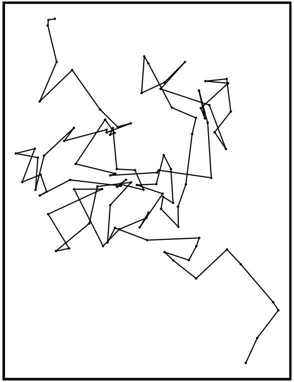
Data from: *Russell et al. (2015), "Intrinsic and extrinsic drivers of activity budgets in sympatric grey and harbour seals", Oikos.*

Correlated random walk

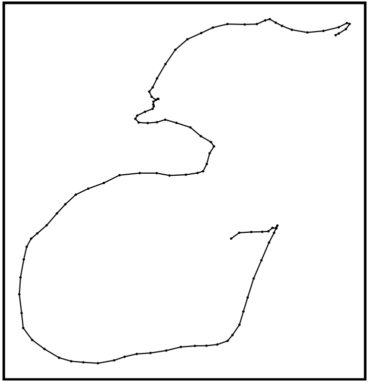
A correlated random walk includes **persistence in direction**.

$\longrightarrow$ correlation between successive directions

Simple random walk



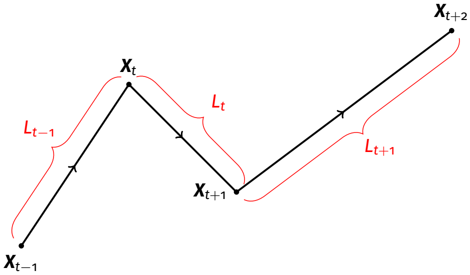
Correlated random walk

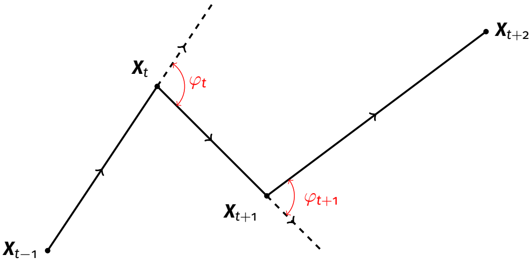


Movement metrics

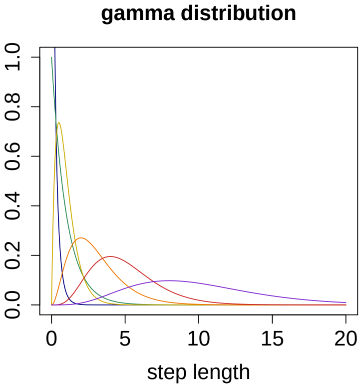
In a correlated random walk, we can model:

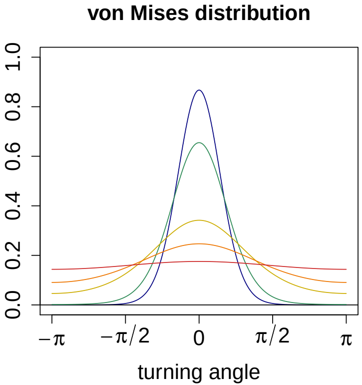
- step lengths (L_t)
- turning angles (φ_t)





Modelling the steps and angles





Parameters often of interest:

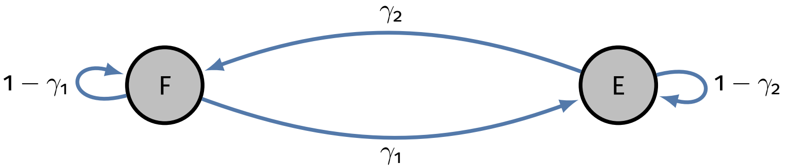
- mean of step length distribution (= measure of speed)
- concentration of turning angle distribution (= measure of directional persistence)

Multistate random walk

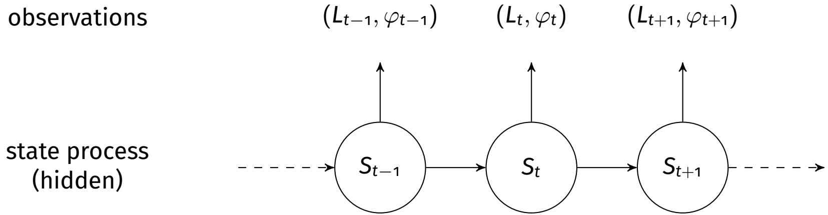
Different behaviours lead to different movement patterns.

$\longrightarrow$ behavioural process = unobserved Markov chain (S_t)

Example: foraging ("F") and exploring ("E")



Hidden Markov model for animal movement



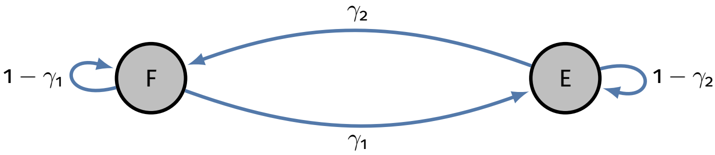
The steps and angles are modelled by state-dependent distributions. For example:

$$L_t | \{S_t = j\} \sim \text{gamma}(\alpha_j, \beta_j)$$
$$\varphi_t | \{S_t = j\} \sim \text{von Mises}(\theta_j, \kappa_j)$$

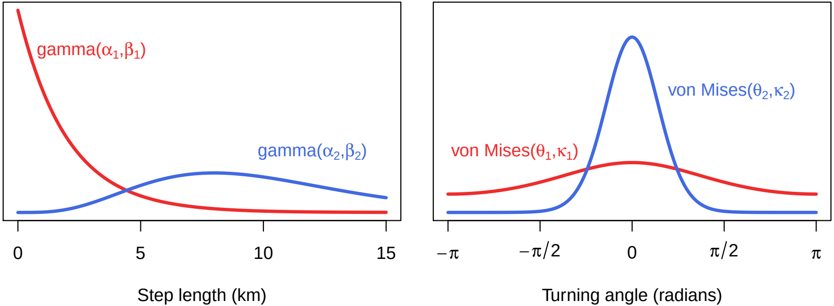
HMM parameters

There are two sets of parameters:

- The transition probabilities $\Pr(S_t = j | S_{t-1} = i)$, e.g.



- The state-dependent movement parameters, e.g.



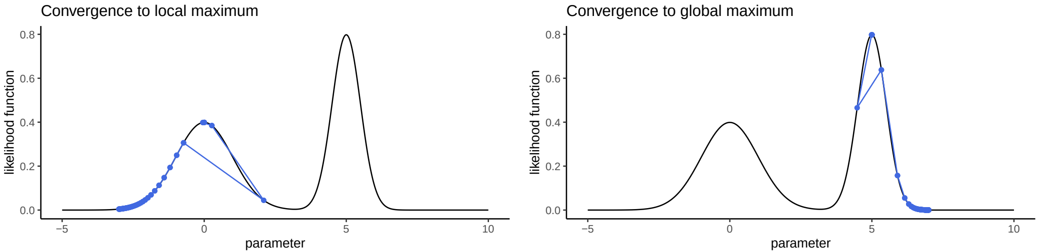
HMM inference

1. Derive step lengths and turning angles from location data.
2. Estimate transition probabilities and movement parameters in each state, possibly as functions of covariates (usually using numerical methods).
3. Compute “most likely state sequence” to segment tracks into behavioural phases.

Common challenge 1: choice of starting parameters

HMMs are fitted by numerical optim. (to find parameters that maximise the likelihood)

- user needs to set a starting point for optimisation
- convergence to "global" maximum (i.e., best model) requires good starting point



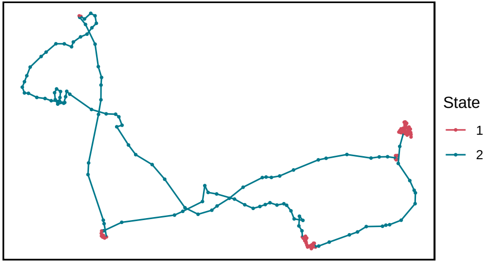
Partial solutions: try many starting values; look at data to pick plausible values.

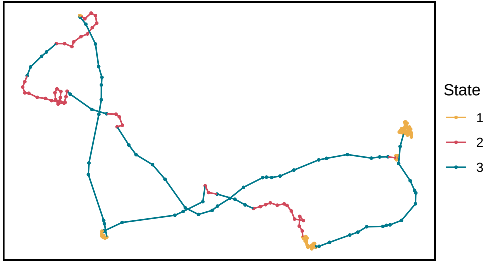
- vignette: "*A short guide to choosing initial parameter values for the estimation in moveHMM*"

Common challenge 2: choice of number of states

We need to choose the number of states a priori

- most studies use 2 states (“slow” and “fast”)
- 3-4 can sometimes be interpreted biologically – beyond that it might be hard!
- AIC/BIC often select much more complex models





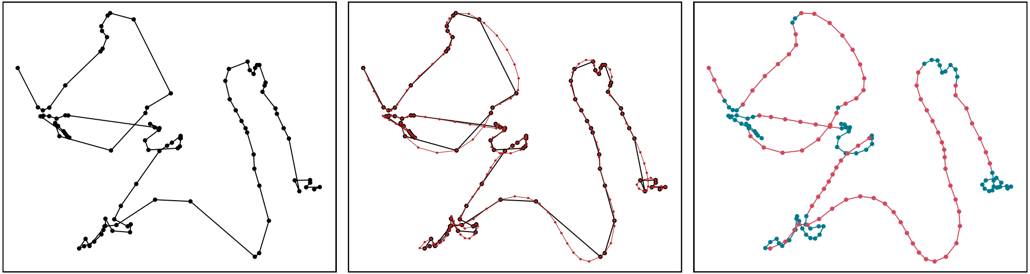
Partial solution: use a combination of model checking and biological knowledge.

- *Pohle et al. (2017). “Selecting the number of states in hidden Markov models: pragmatic solutions illustrated using animal movement”. JABES.*

Common challenge 3: irregular or noisy locations

HMM requirements:

- measurement error should be negligible
- locations should be observed at regular time intervals

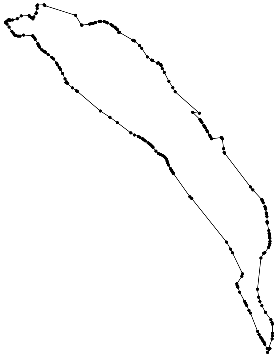


Partial solution: filter noise and regularise tracks with a state-space model first (e.g., packages `crawl` and `foieGras`)

Multiple imputation

Multiple imputation procedure:

1. generate several plausible filtered/regularised tracks from state-space model
2. fit an HMM to each imputed regular track
3. combine HMMs to get parameters with better uncertainty estimates



- *McClintock (2017). "Incorporating telemetry error into hidden Markov models of animal movement using multiple imputation". JABES.*

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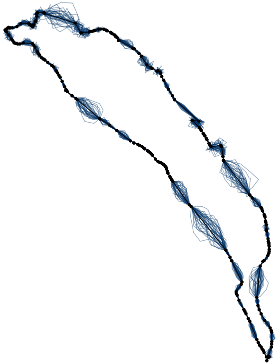

- *McClintock (2017). "Incorporating telemetry error into hidden Markov models of animal movement using multiple imputation". JABES.*

Software

moveHMM:

- fairly specialised package for movement analysis with HMMs
- *Michelot et al. (2016). moveHMM: an R package for the statistical modelling of animal movement data using hidden Markov models. MEE.*

momentuHMM:

- more general package, for more complex HMMs
- *McClintock & Michelot (2018). momentuHMM: R package for generalized hidden Markov models of animal movement. MEE.*

A few references

Hidden Markov models in (movement) ecology:

- Patterson et al. (2009), "*Classifying movement behaviour in relation to environmental conditions using hidden Markov models*", Journal of Animal Ecology, 78(6), 1113-1123.
- Langrock et al. (2012), "*Flexible and practical modeling of animal telemetry data: hidden Markov models and extensions*", Ecology, 93(11), 2336-2342.
- McClintock et al. (2020), "*Uncovering ecological state dynamics with hidden Markov models*", Ecology letters, 23(12), 1878-1903.

Modelling noisy/irregular movement data:

- Johnson et al. (2008), "*Continuous-time correlated random walk model for animal telemetry data*", Ecology, 89(5), 1208-1215.
- Jonsen et al. (2020), "*A continuous-time state-space model for rapid quality control of argos locations from animal-borne tags*", Movement Ecology, 8(1), 1-13.