HELMHOLTZ-ZENTRUM DRESDEN-ROSSENDORF

CENTER FOR ADVANCED SYSTEMS UNDERSTANDING

AniMove 2024, June 17th to 28th

Home range meta-analyses

Using the 'ctmm' R package

Inês Silva, Chris Fleming

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TECHNISCHE UNIVERSITÄT DRESDEN

CBG Max Planck Institute of Molecular Cell Biology and Genetics

UFZ HELMHOLTZ Centre for Environmental Research

Uniwersytet Wrocławski

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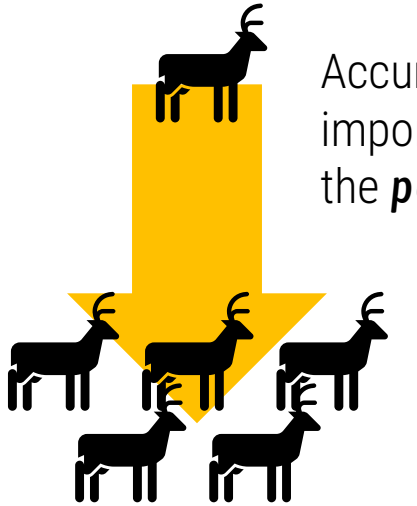
Analyses of ecological data should always account for the ***uncertainty*** in the process(es) that generated the data.



Accurately estimating area requirements is of utmost importance for conservation, from the ***individual*** to the ***population level***.

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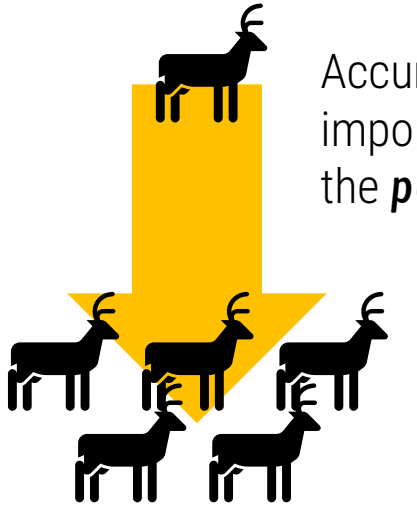

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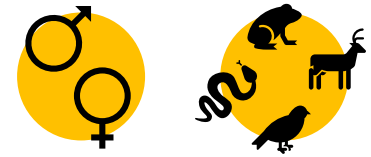

We want to quantify the effect of covariates, such as ***species or taxa***, ***sex***, ***body size***, ***age***, ***movement characteristics***, ***conspecific density***, ***habitat***, ***anthropogenic impact***, *etc.*...

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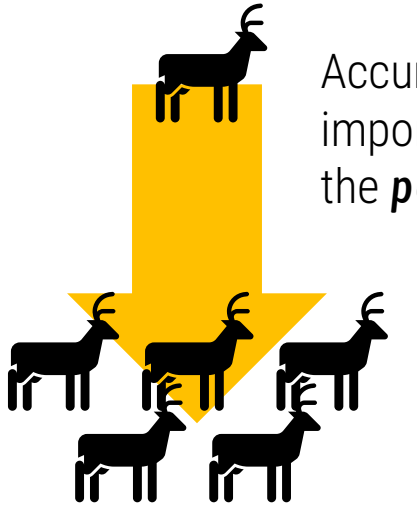

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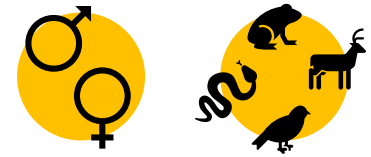

We want to quantify the effect of covariates, such as ***species or taxa***, ***sex***, ***body size***, ***age***, ***movement characteristics***, ***conspecific density***, ***habitat***, ***anthropogenic impact***, *etc.…*

… even if we are comparing different populations with ***different movement behaviors*** or ***sampling schedules***.

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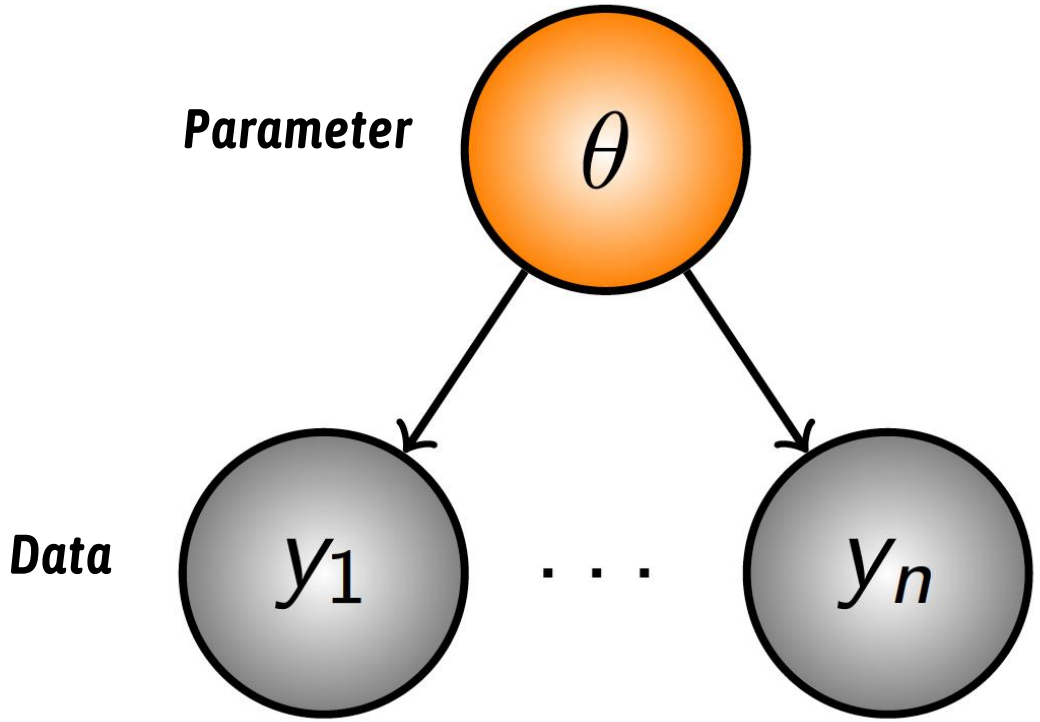
NON-HIERARCHICAL MODELS

How does data inform parameters?



Adapted from Midway (2008)

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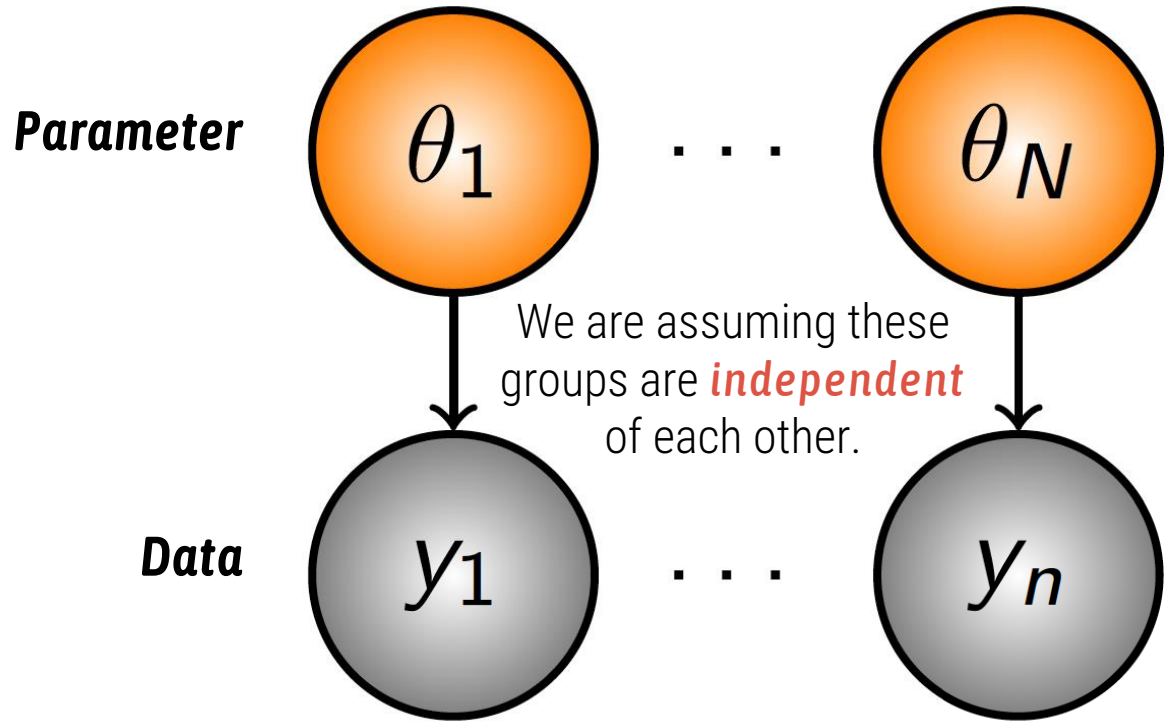

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HIERARCHICAL MODELS

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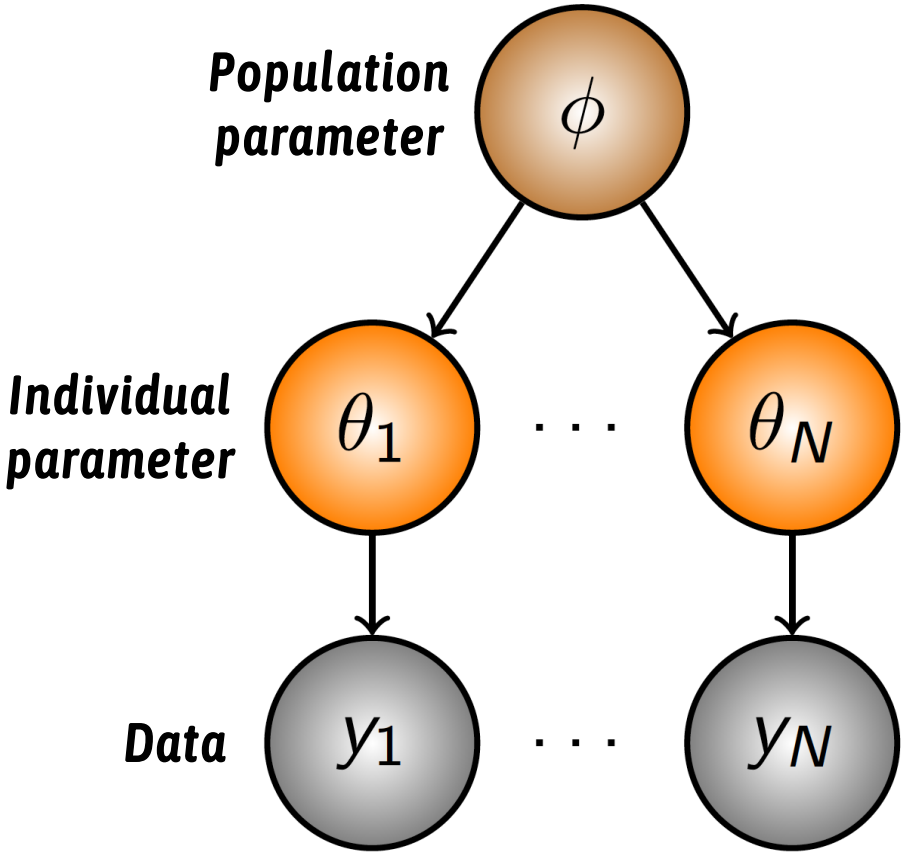

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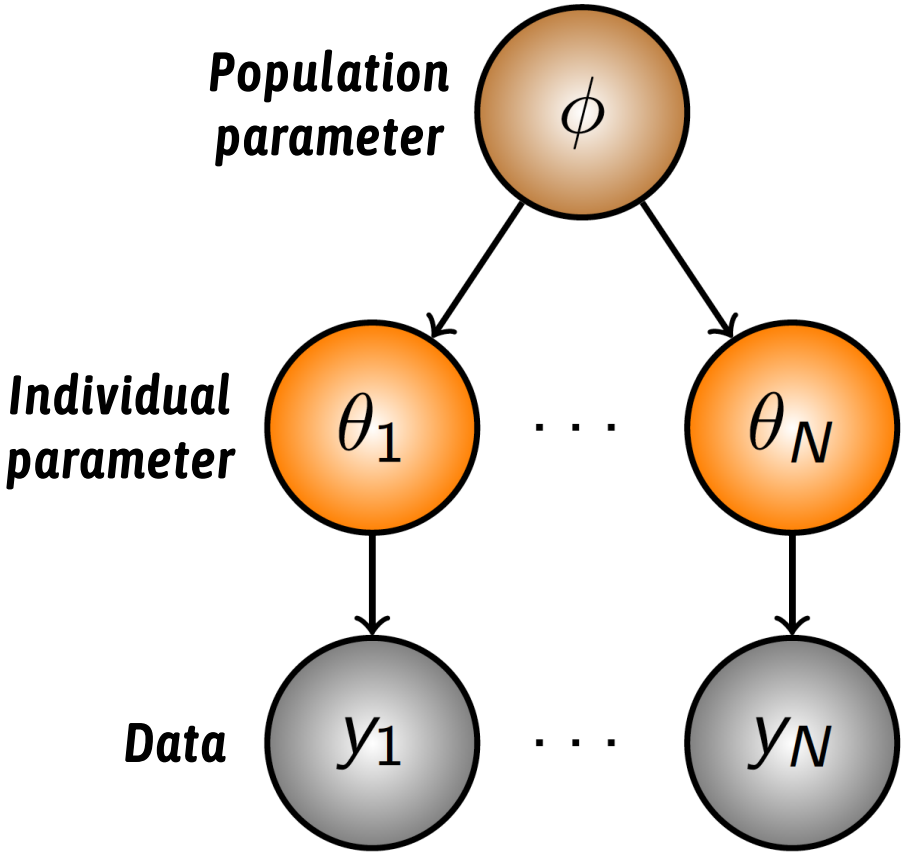

Data inform factor-level parameters, θ…

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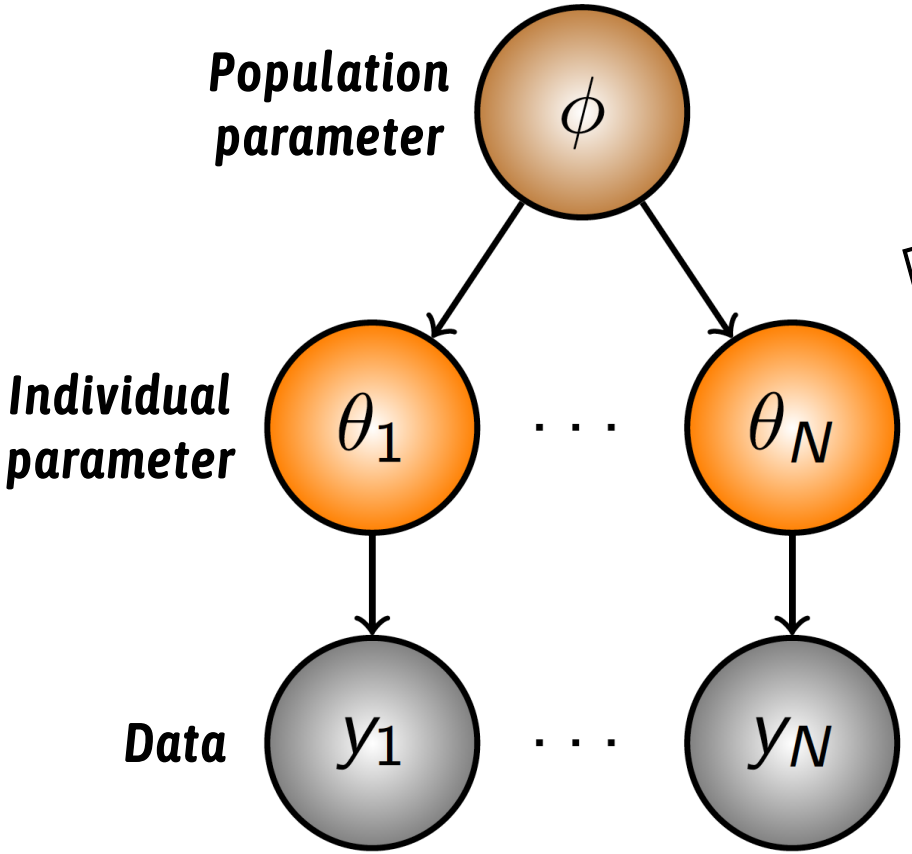
HIERARCHICAL MODELS

How does data inform parameters?



…which are governed by some additional parameter, ϕ.

Data inform factor-level parameters, θ…

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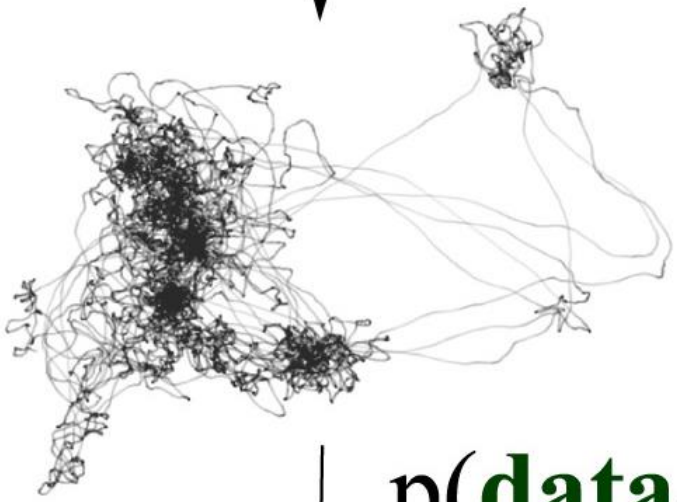
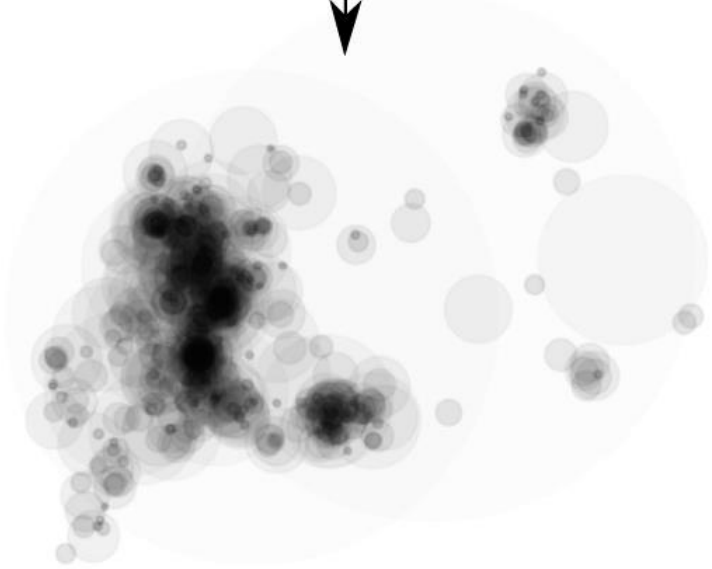
$p(\mathbf{r}_i|\boldsymbol{\theta}_i)$

Trajectory



$p(\mathbf{data}_i|\mathbf{r}_i)$

Data



χ^2 *inverse-Gaussian meta-analysis*

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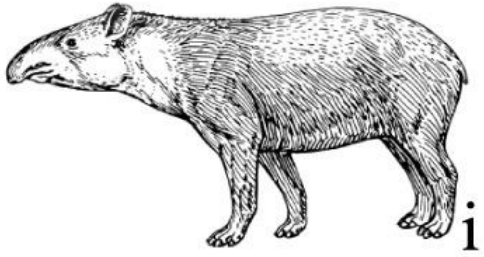
Individual

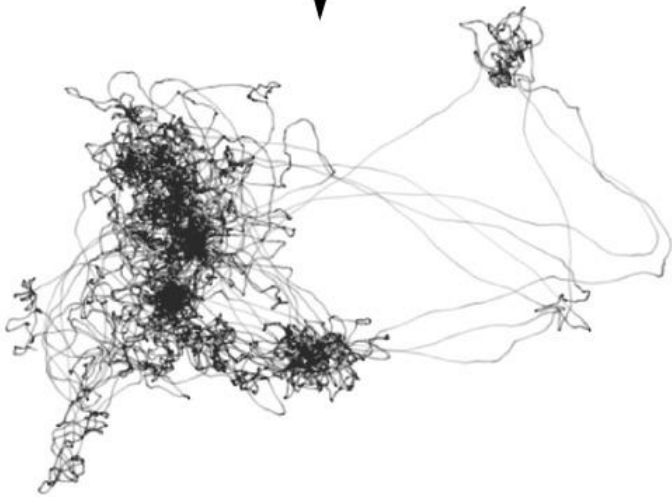
$p(\theta_i|\Theta)$



i

$p(r_i|\theta_i)$

Trajectory



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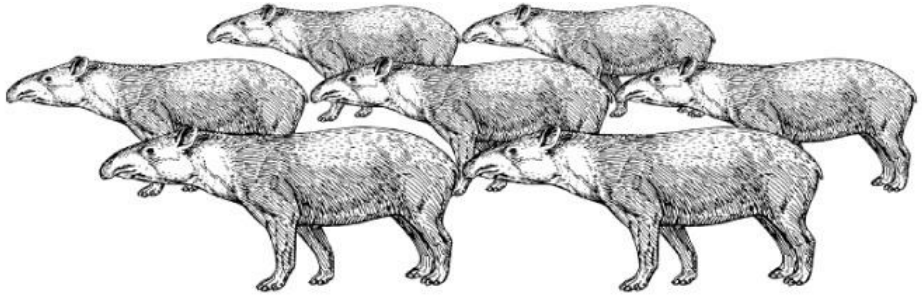
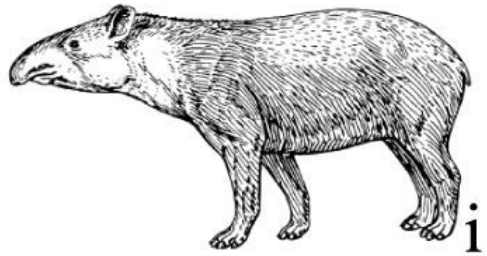
Population



$p(\theta_i|\Theta)$

Individual



i

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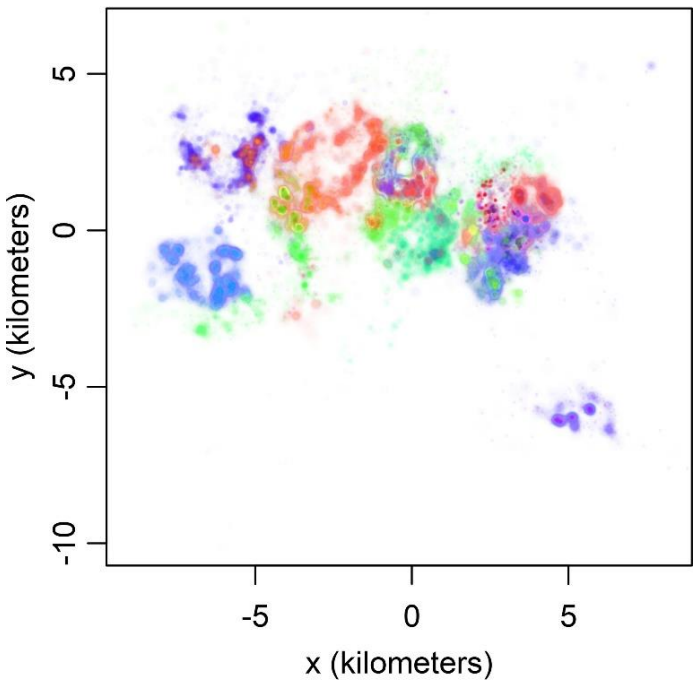
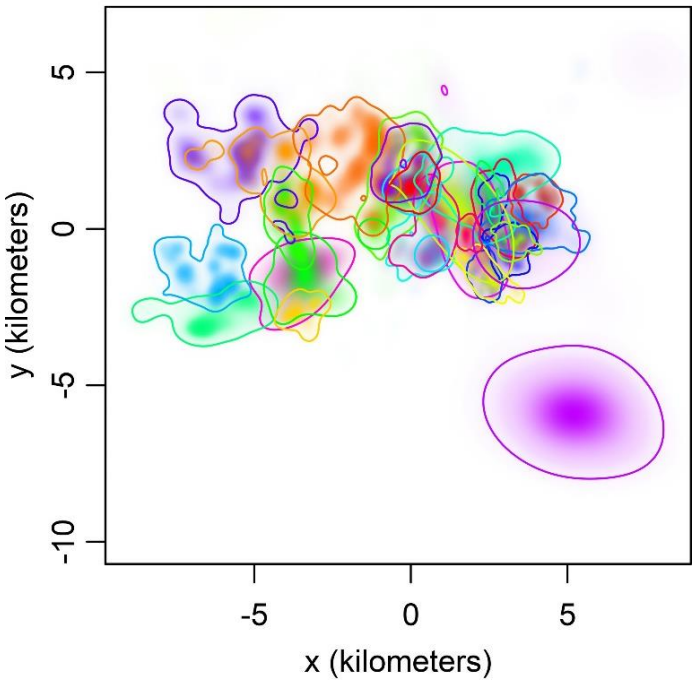
Population-level inferences

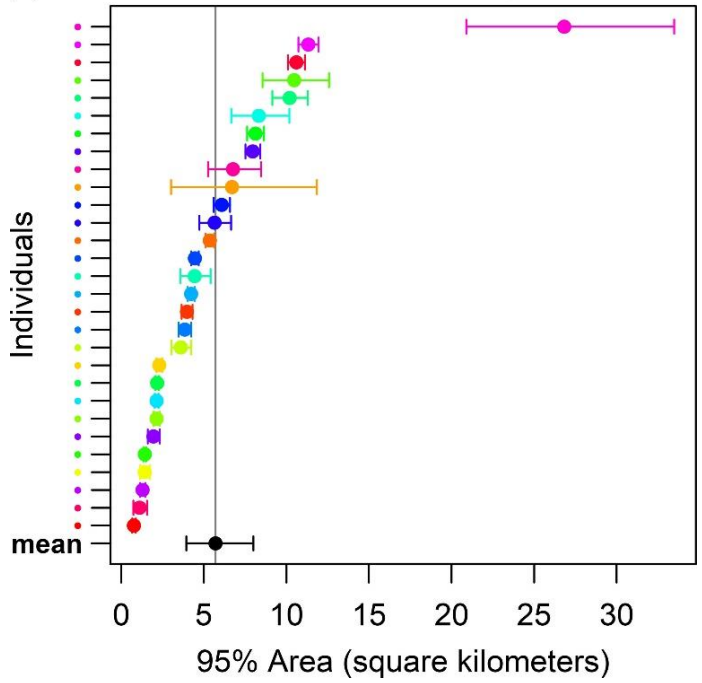
Tracking data



Home range analysis



Population analysis



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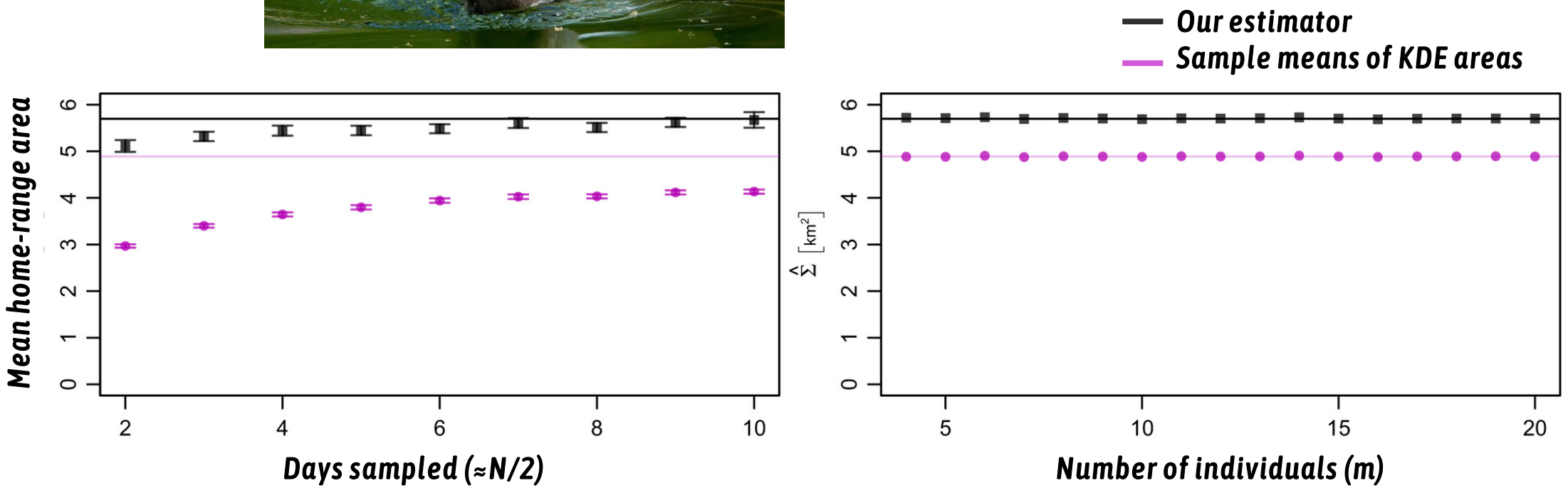
LOWLAND TAPIR

TAPIRUS TERRESTRIS

VU

Tapirs have HR crossing times (τ_p) of 0.72 days, ranging from 0.05 to 12.8 days.



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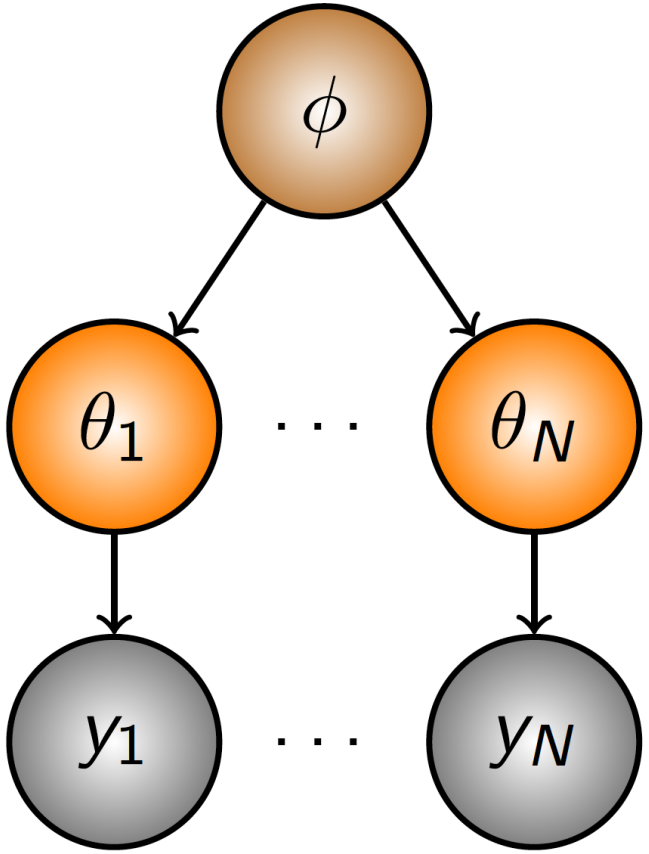

This framework facilitates population-level inference with as few as ***2–3 observed home range crossings*** (τ_p) and similarly small ***number of individuals (m)***.

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