



MARE-Madeira 2025

# *Population-level inferences*

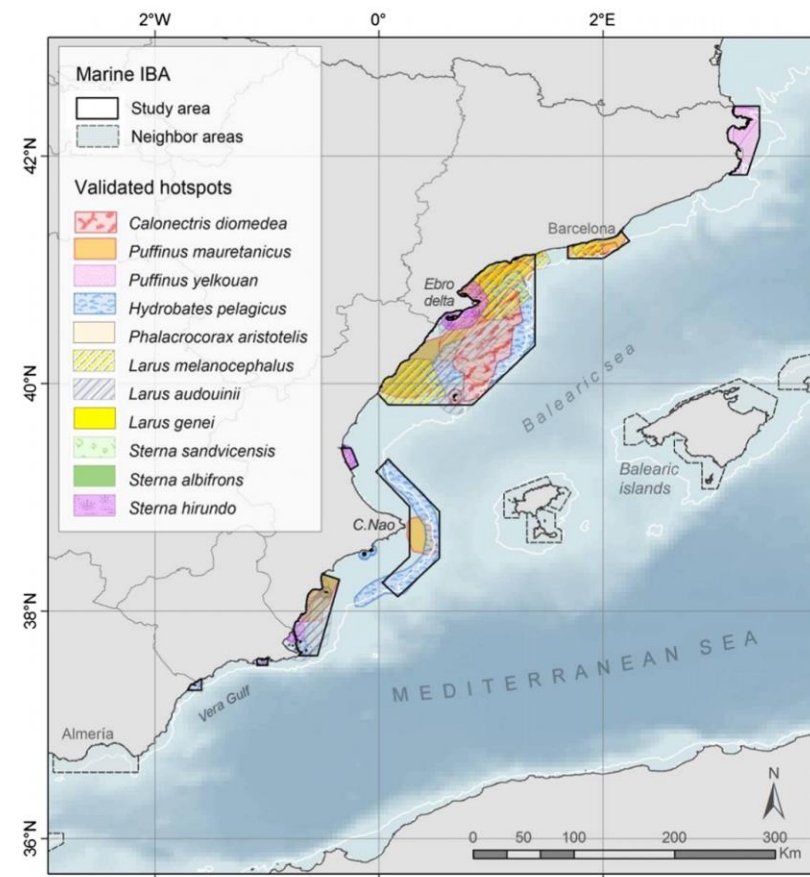
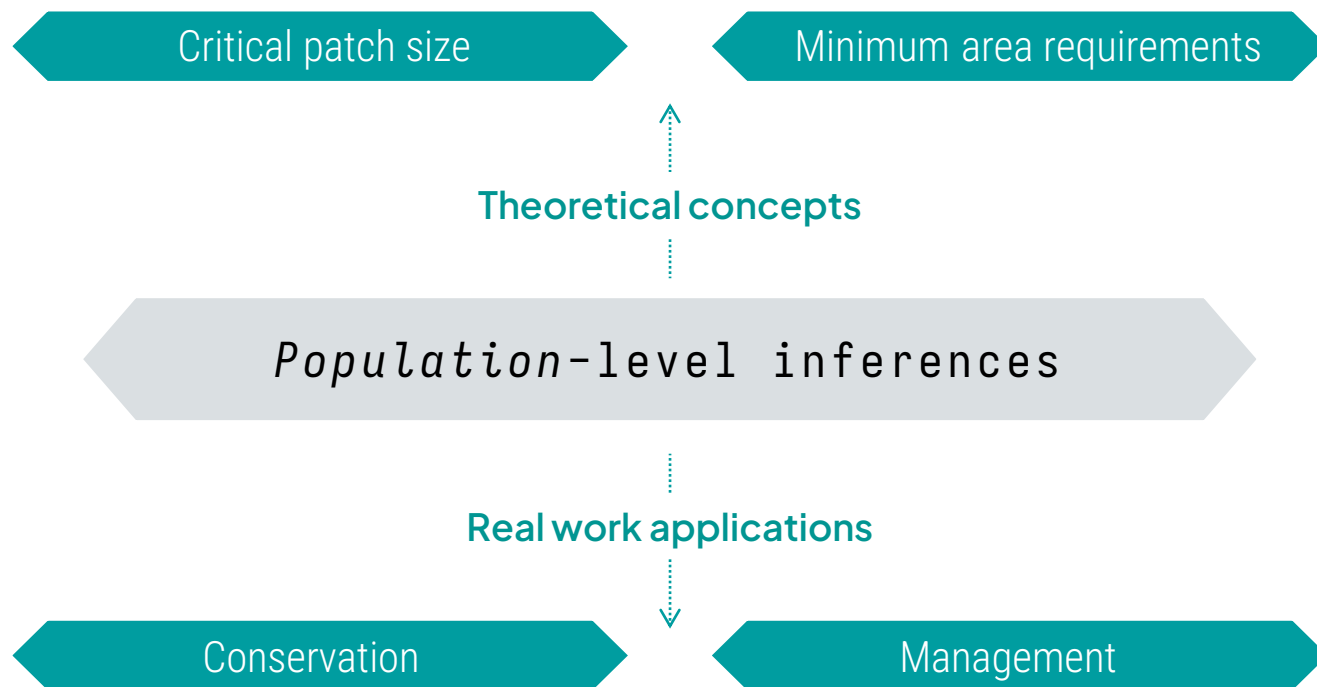
Using the 'ctmm' R package




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Using foraging hotspots of pelagic seabirds to identify marine **Important Bird Areas (IBAs)** in Spain.

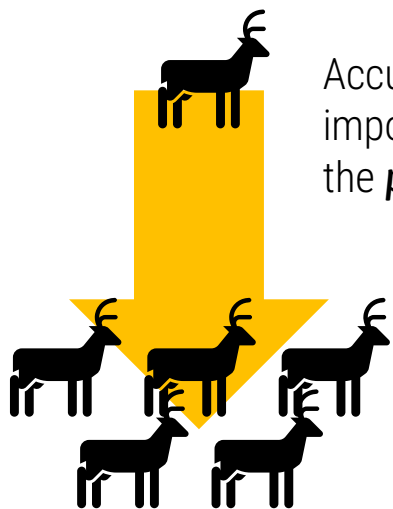


 **Arcos *et al.* (2012)**  
DOI: 10.1016/j.biocon.2011.12.011

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



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



We want to quantify the effect of covariates, such as **species**, **sex**, **body size**, **age**, **habitat**, **anthropogenic impact**, etc...



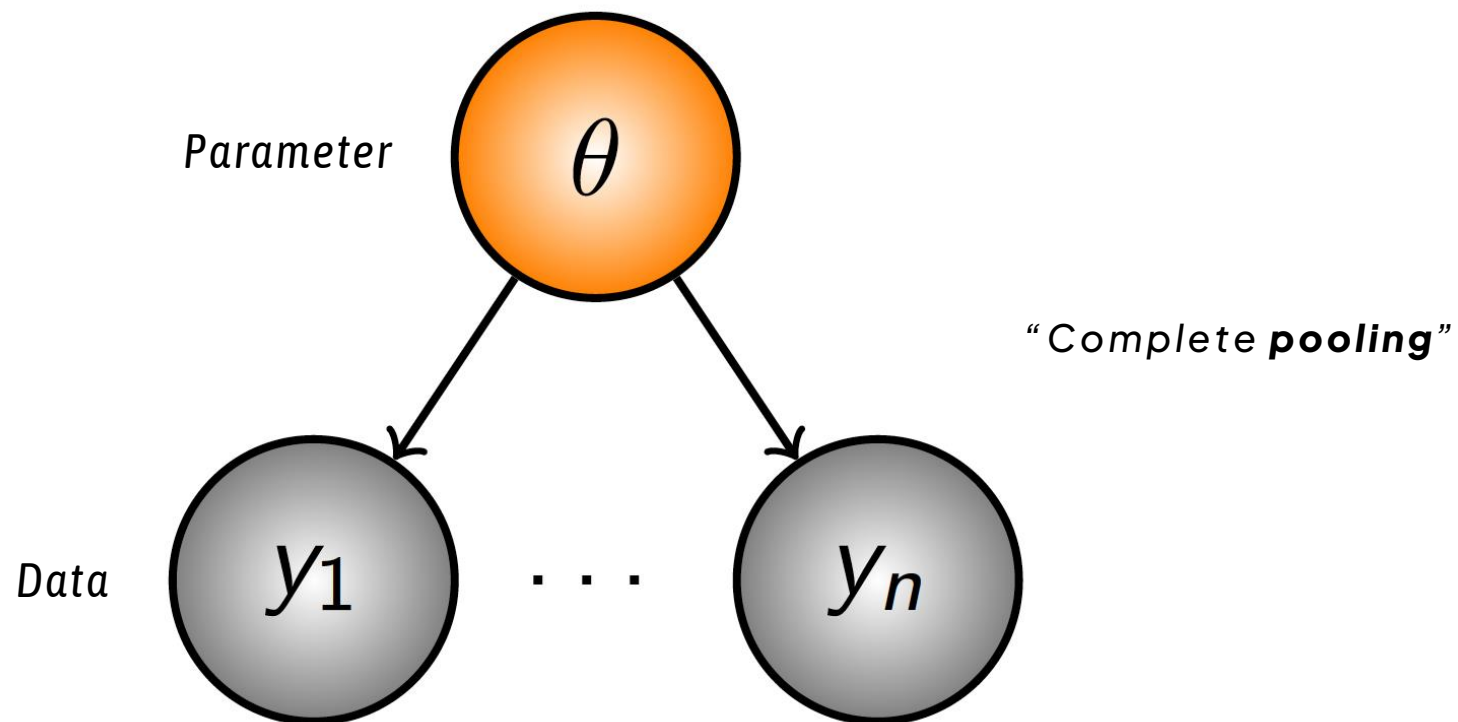
...even if we are comparing different populations with different **movement behaviors** or **sampling schedules**.





## NON-HIERARCHICAL MODELS

How does data inform parameters?

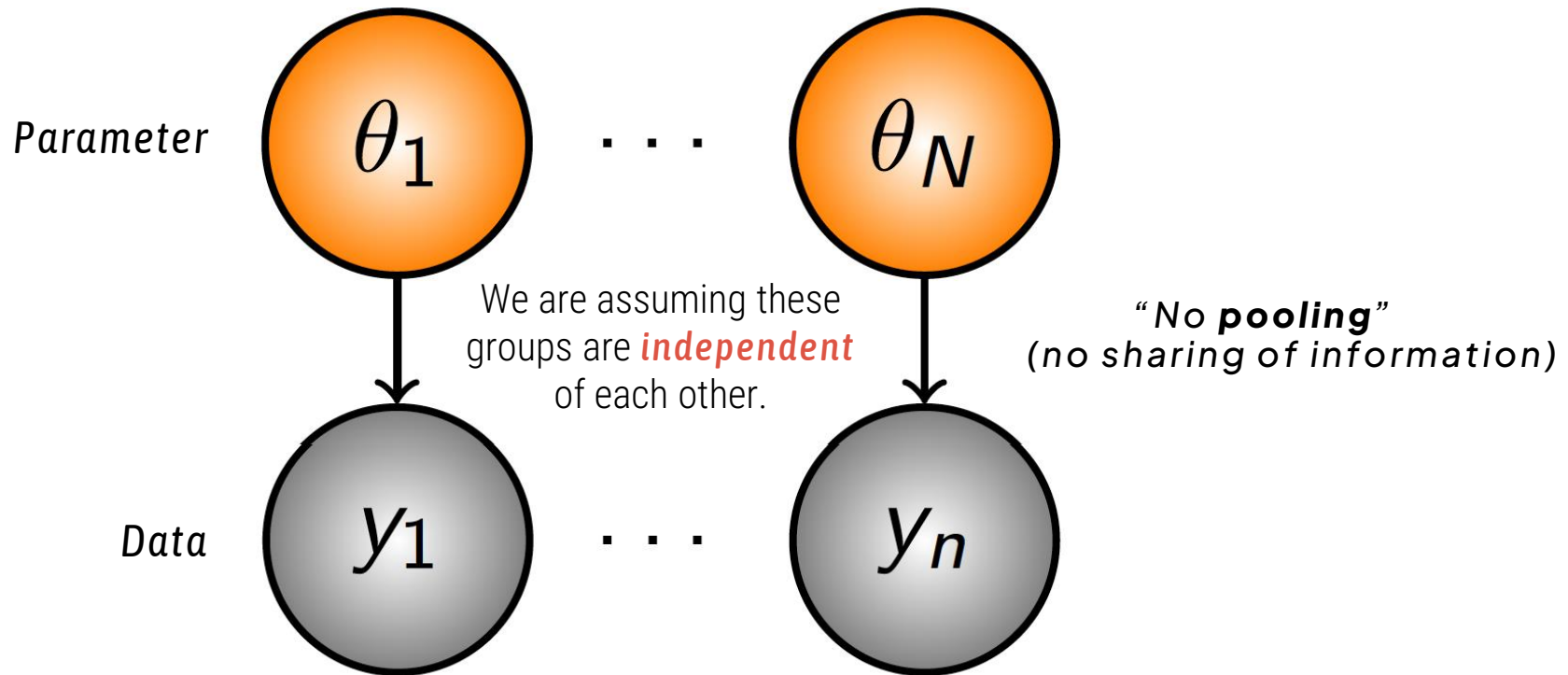


Adapted from Midway (2008)



## NON-HIERARCHICAL MODELS

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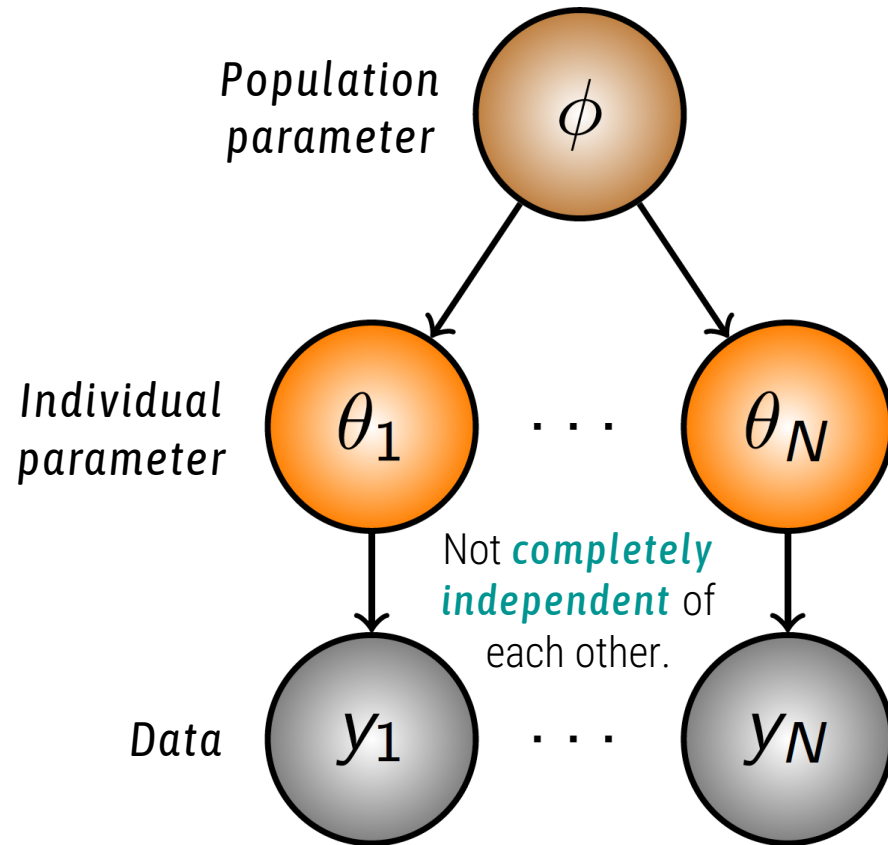


Adapted from Midway (2008)



## HIERARCHICAL MODELS

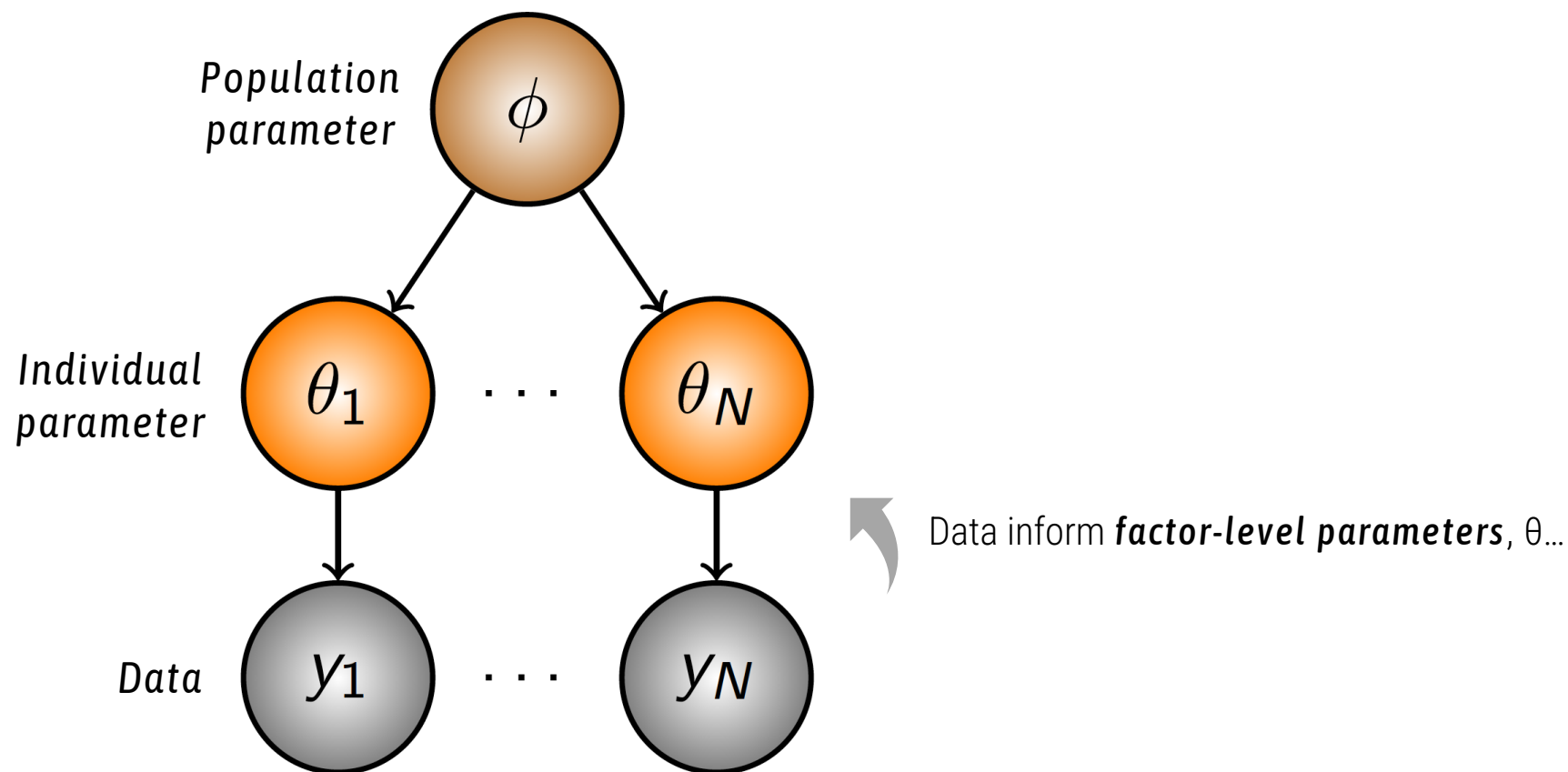
How does data inform parameters?



Adapted from Midway (2008)

## HIERARCHICAL MODELS

How does data inform parameters?



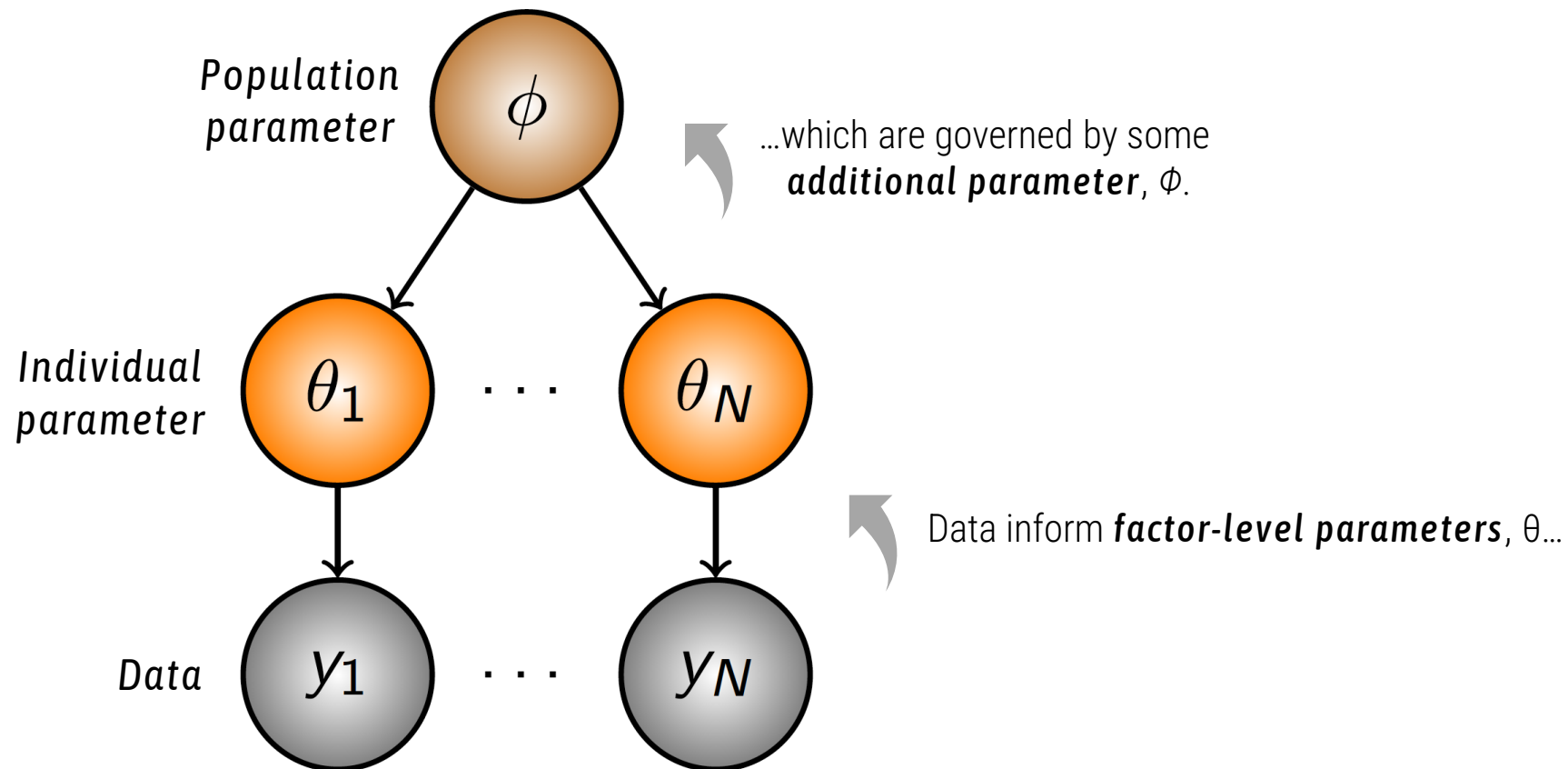
 Adapted from Midway (2008)





## HIERARCHICAL MODELS

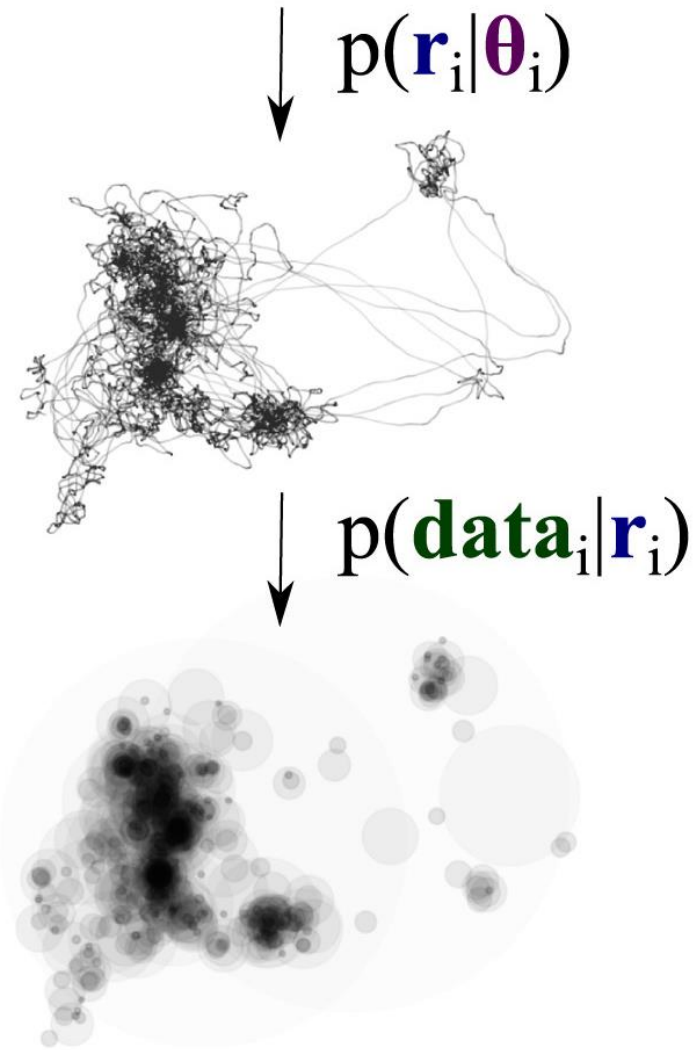
How does data inform parameters?



Adapted from Midway (2008)



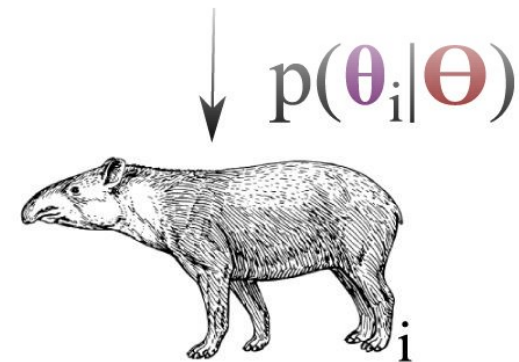
**Trajectory**



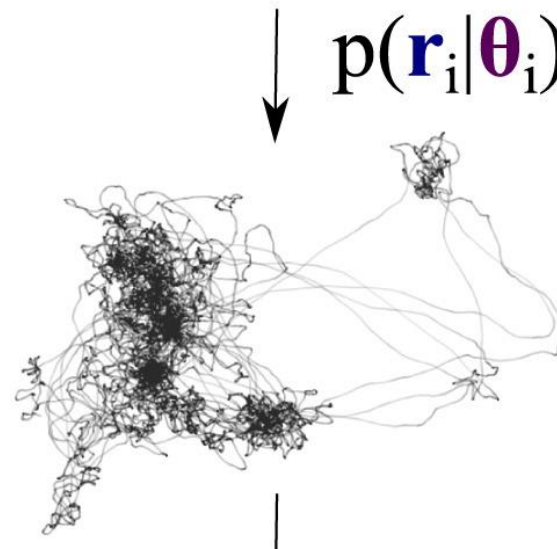
**Data**



**Individual**

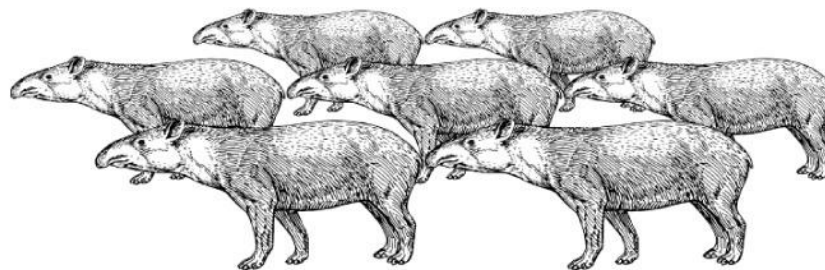


**Trajectory**



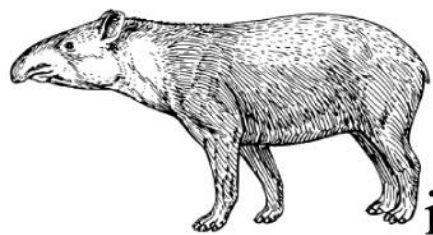


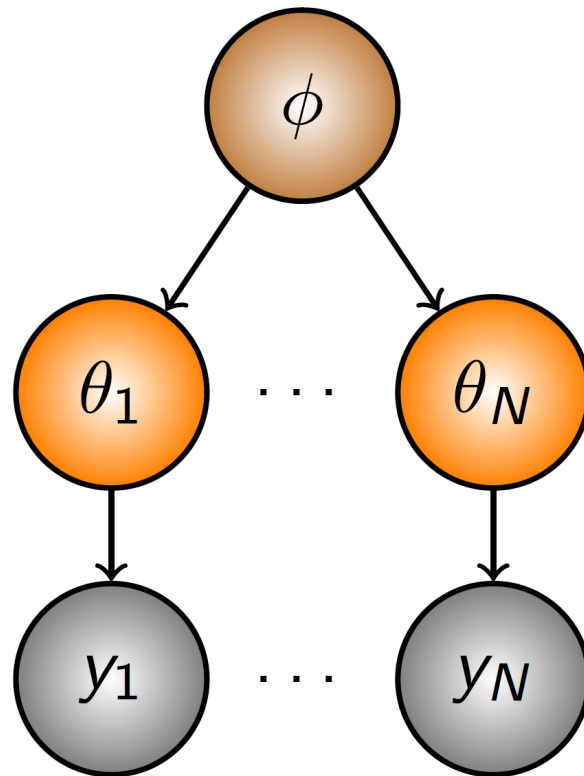
**Population**



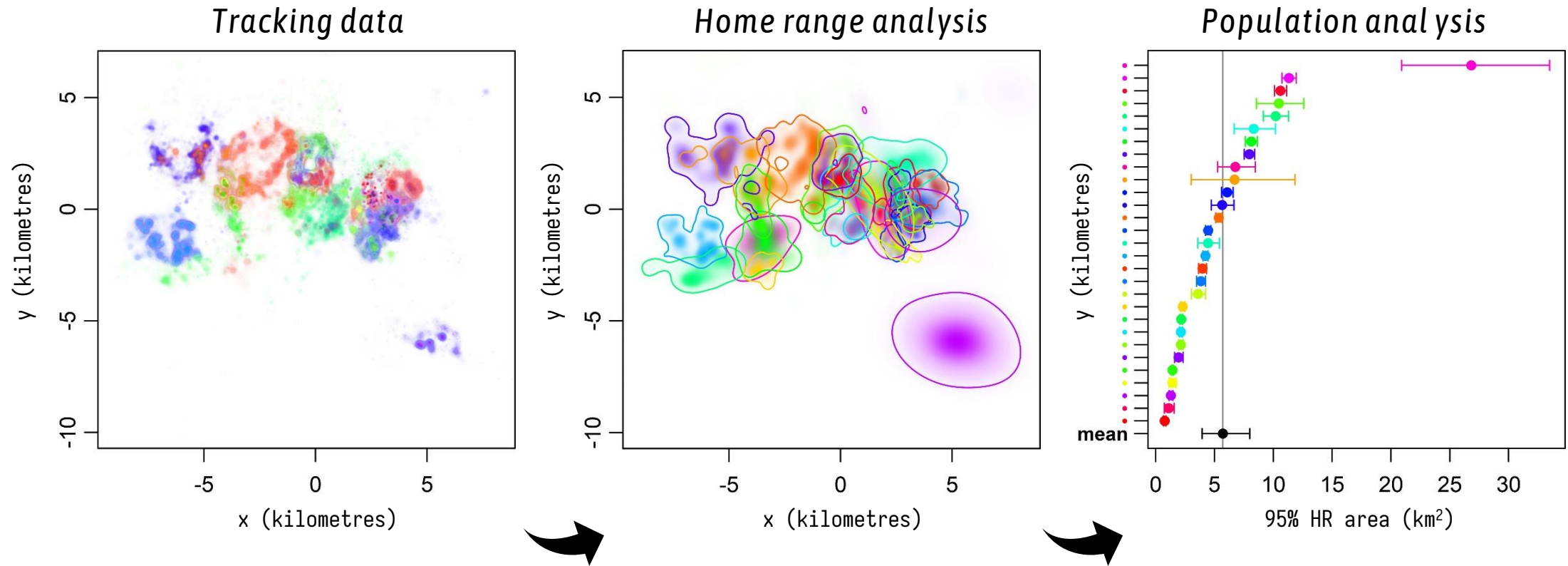
$$p(\theta_i | \Theta)$$

**Individual**





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



Home range area estimates follow a  $\chi^2$  sampling distribution

Population of home-range areas follows an inverse-Gaussian distribution

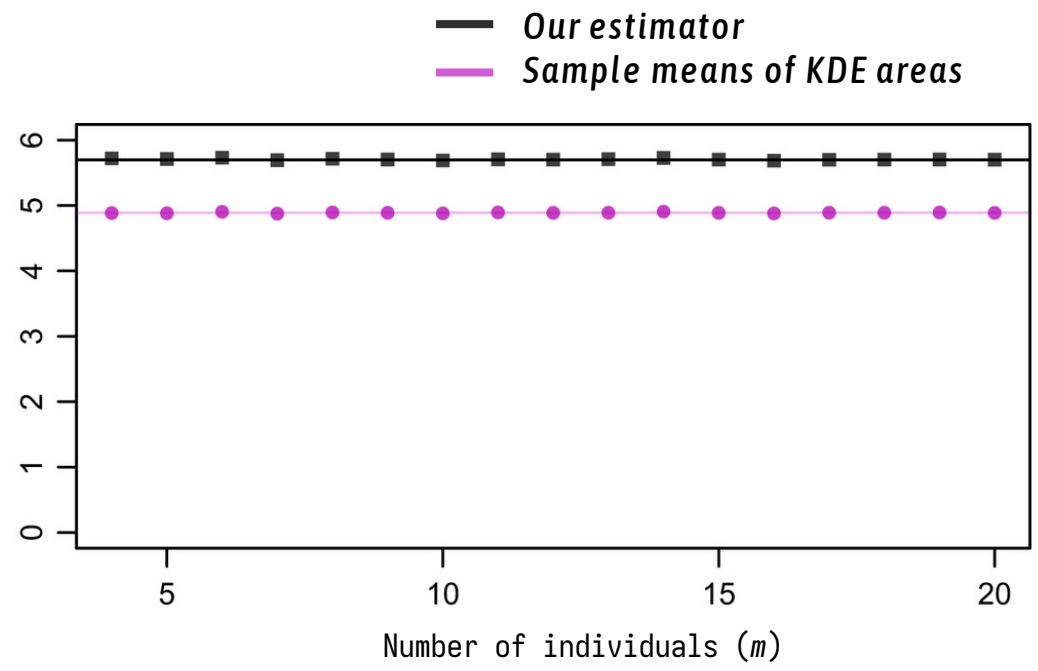
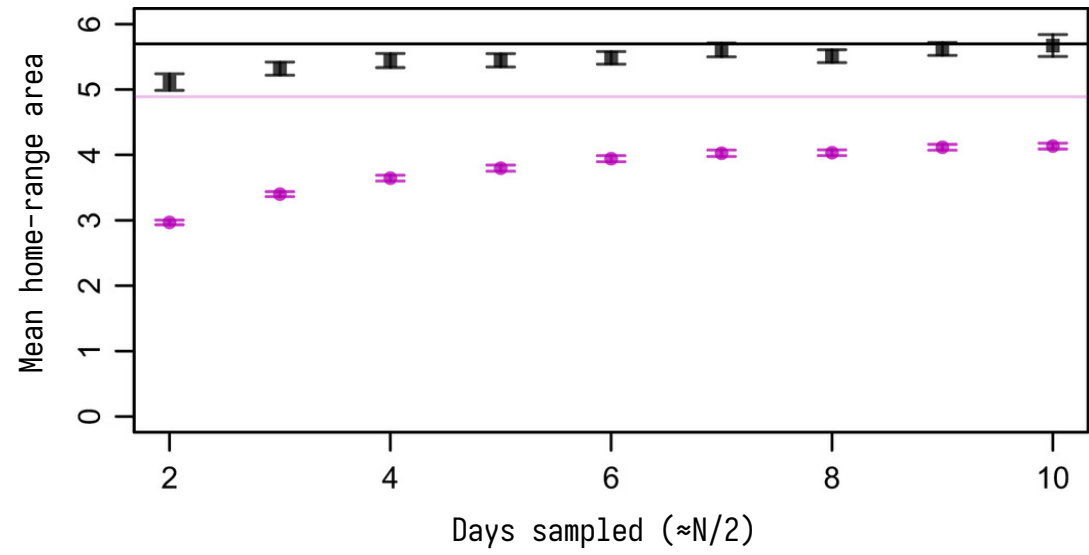
A statistically efficient estimator will **downweight** uncertain estimates relative to more certain estimates in such a way that the estimated mean has a smaller variance.



Lowland tapir  
(*Tapirus terrestris*)



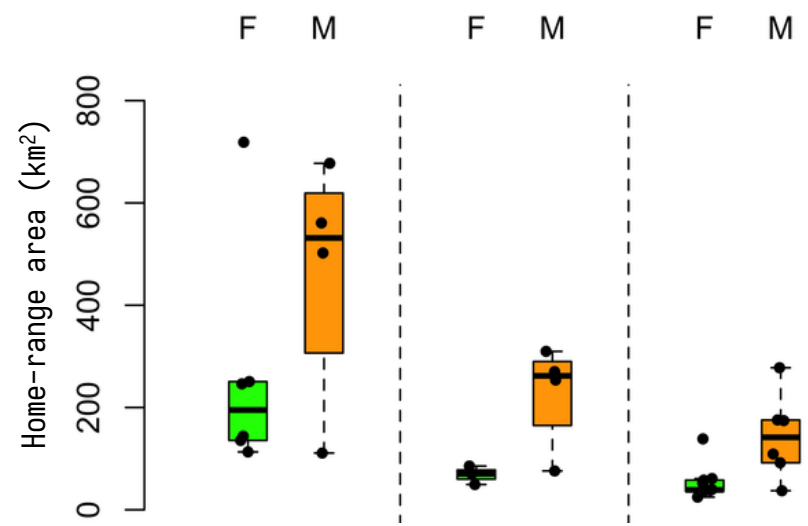
Tapirs have **home range crossing times** ( $\tau_p$ ) of 0.72 days,  
(ranging from 0.05–12.8 days)







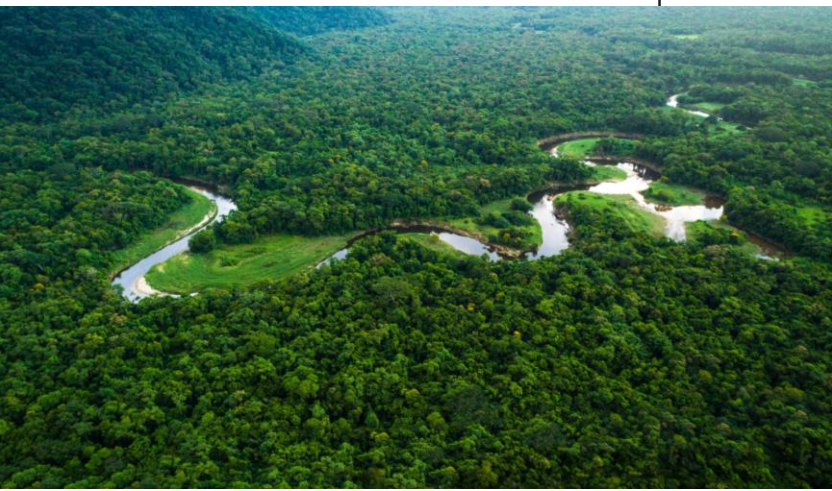
✍ **Morato *et al.* (2016)**  
DOI: 10.1093/jmammal/gyab068



Atlantic forest

Amazon

Pantanal



**Jaguar**  
(*Panthera onca*)

📷 Pete Wilcox

📷 Frans Lanting



What's the **mean home range area**?

Average area used by individuals in a sample

What's the **population distribution**?

Spatial extent of the population as a whole

*Methods:*

- (A)KDE of population?
- Union of (A)KDEs?
- Mean of (A)KDEs?

*Dual challenge:*

Individual temporal autocorrelation  
Population variation

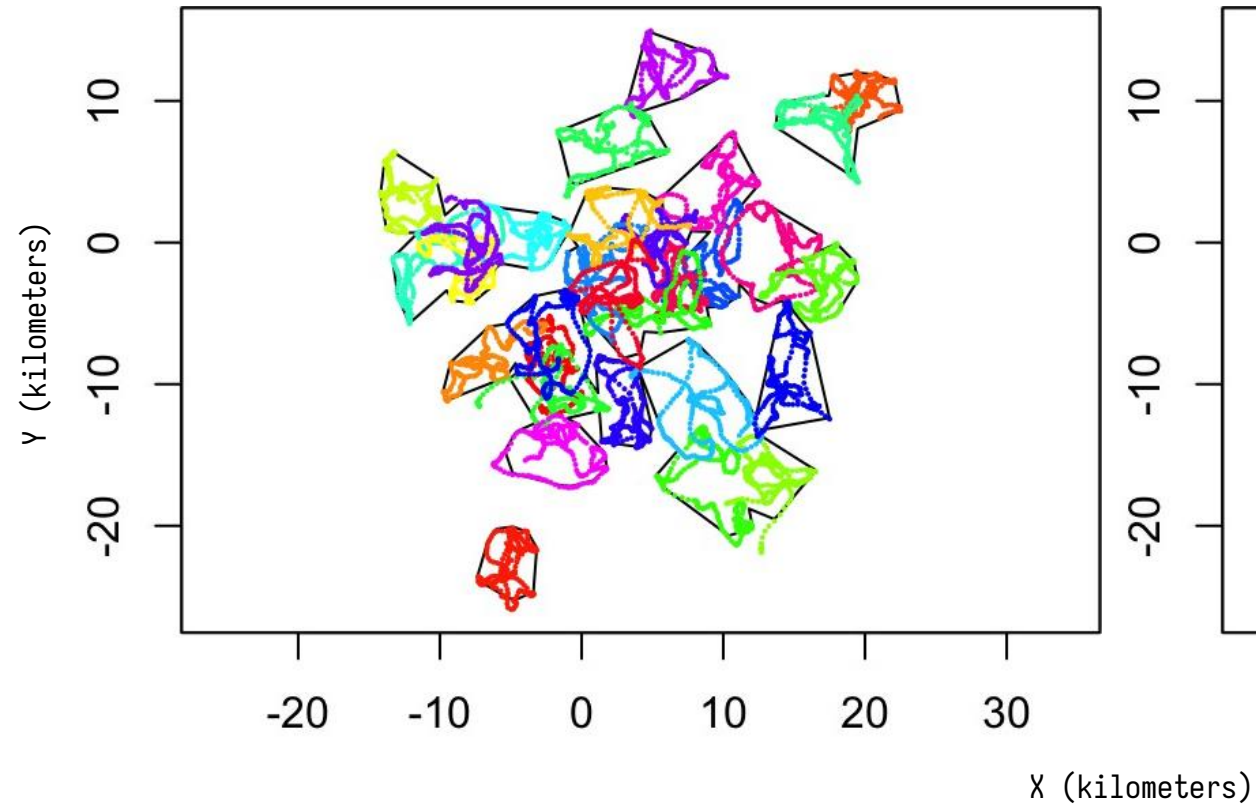
**Sample**  
**Tracked** individuals

**≠**

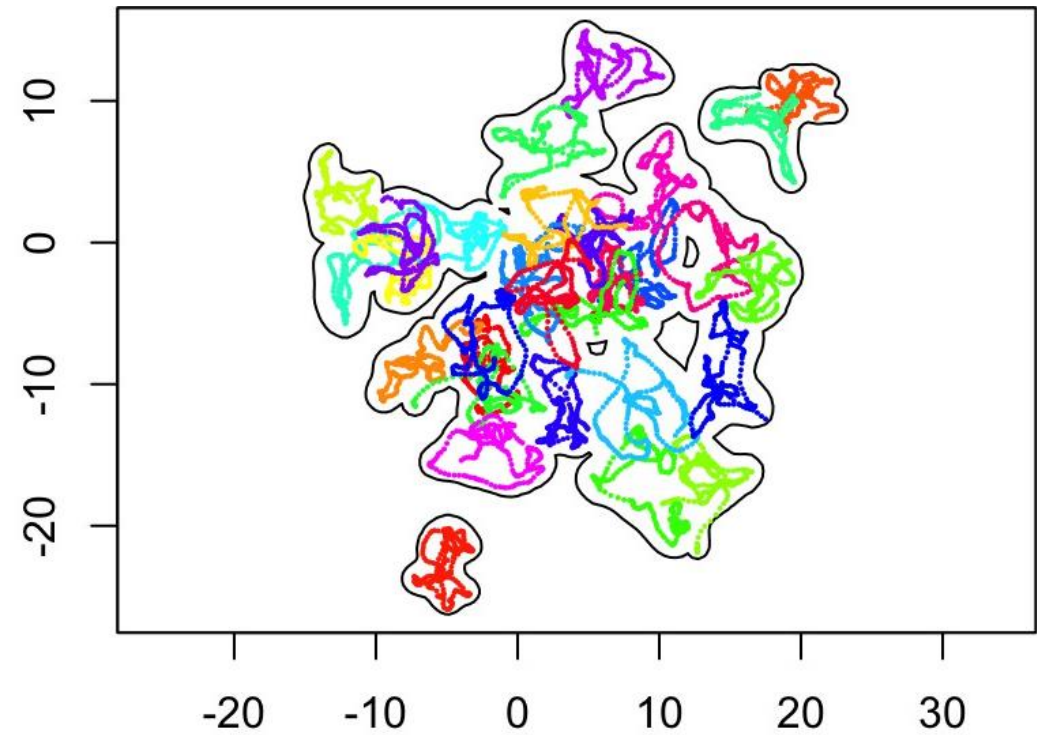
**Population**  
**Tracked + untracked** individuals



Merged **MCP** estimate

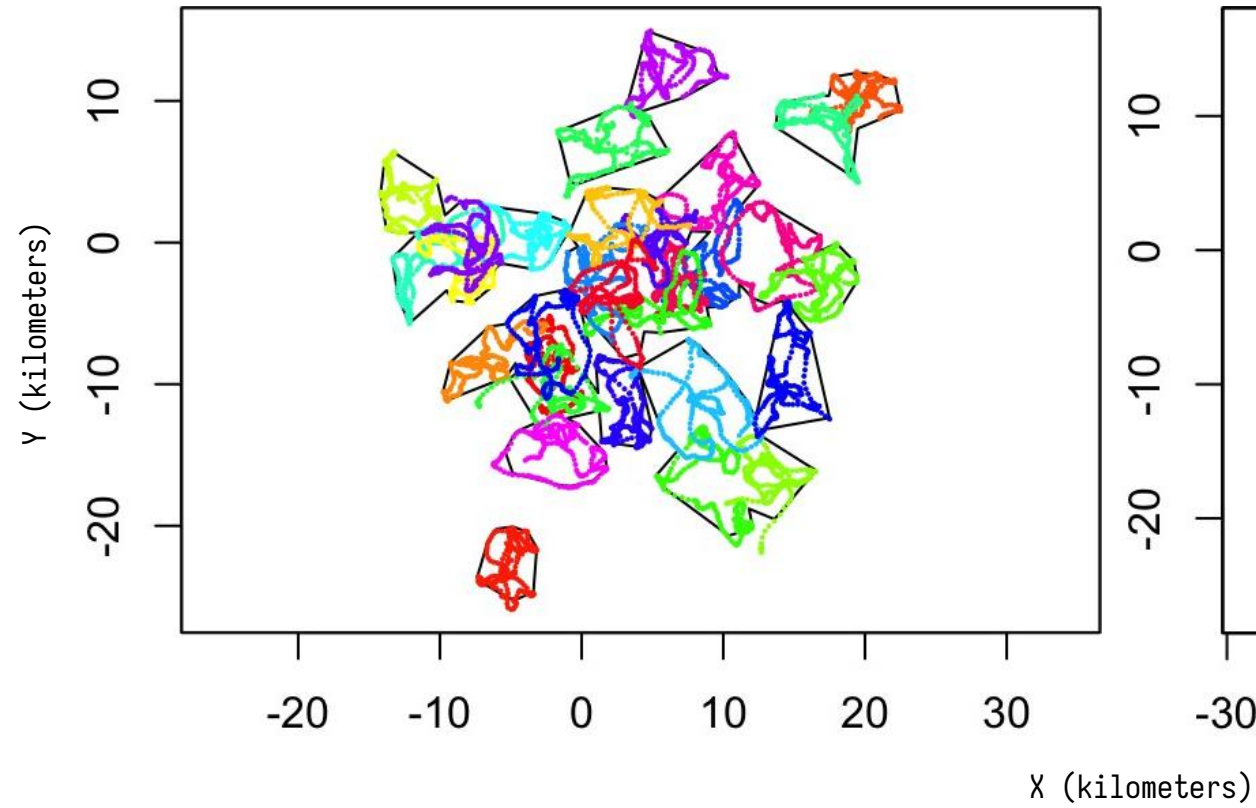


Merged **KDE** estimate

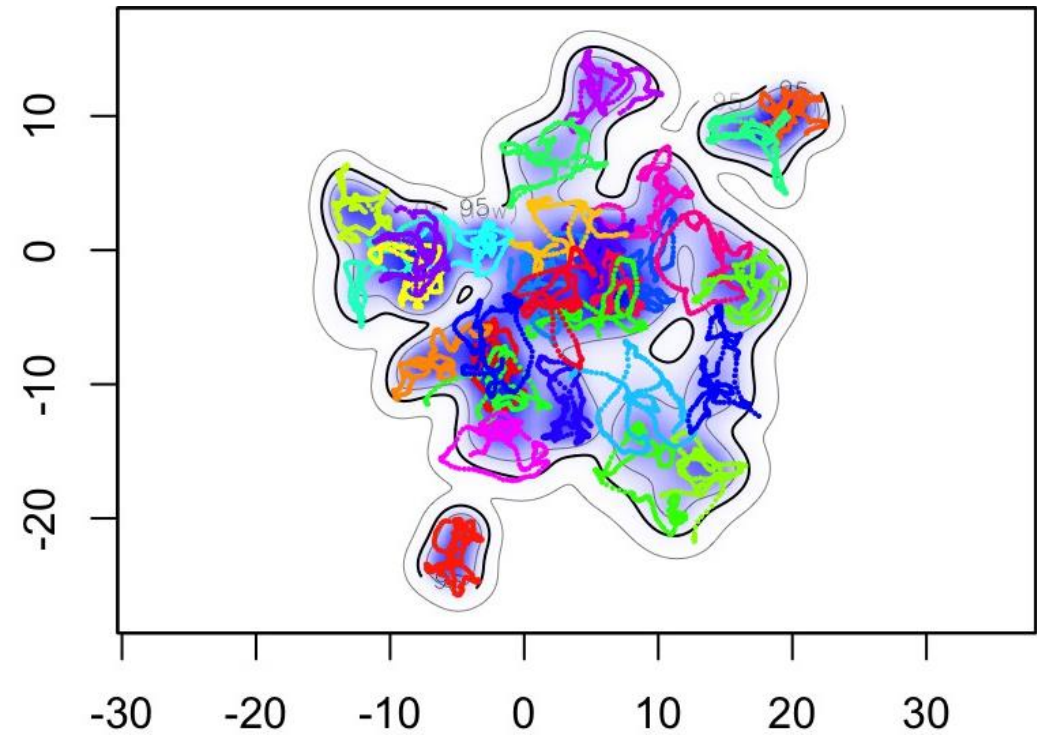




Merged **MCP** estimate



Merged **AKDE** estimate





**KDE** is a weighted average of kernels, where the optimal  $H$  minimizes the MISE:

$$\text{MISE}[\mathbf{H}] = \mathbb{E} \left[ \iint (\hat{p}(\mathbf{x}|\mathbf{H}) - p(\mathbf{x}))^2 d\mathbf{x} \right]$$

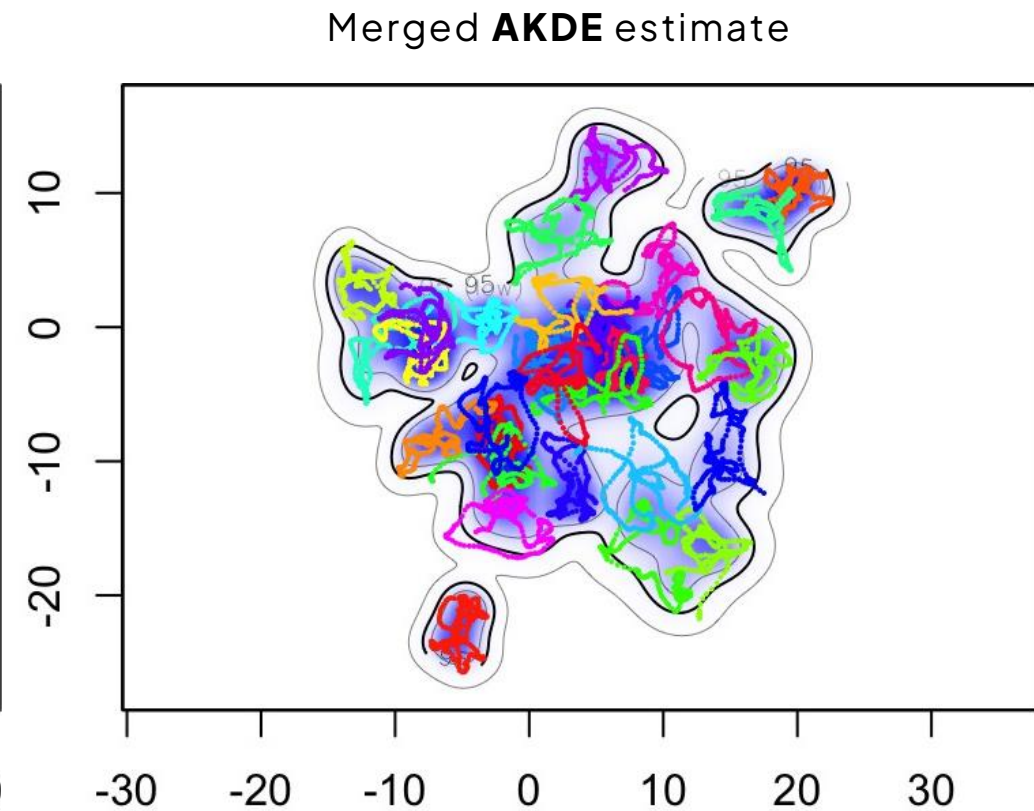
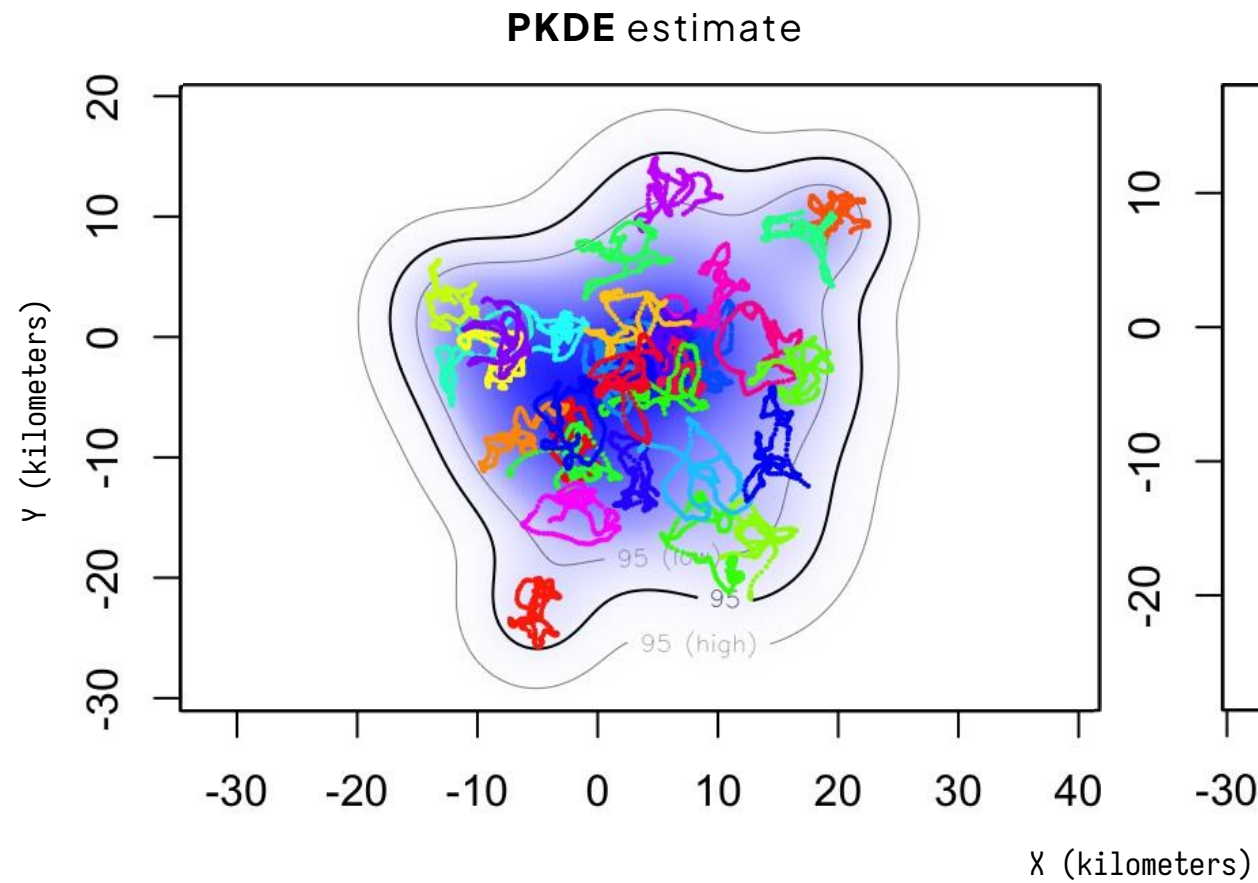
$p(\mathbf{x})$  = approximation (e.g., Gaussian reference function)

**PKDE**

$$\text{MISE}[\mathbf{H}] = \mathbb{E} \left[ \iint (\hat{p}_{\text{pop.}}(\mathbf{x}|\mathbf{H}) - p_{\text{pop.}}(\mathbf{x}))^2 d\mathbf{x} \right]$$

$$\hat{p}_{\text{pop.}}(\mathbf{x}|\mathbf{H}) = \sum_{\text{ind.}} \sum_t w_{\text{ind.}}(t) \kappa(\mathbf{x} - \mathbf{x}_{\text{ind.}}(t) | \mathbf{H}_{\text{ind.}})$$

$p_{\text{pop}}(\mathbf{x})$  requires a hierarchical approximation





Saturation curves

