

International Statistical Ecology Conference 2024

The scale-dependency of biotic interactions species associations in the eyes of integrated species distribution models

Florencia Grattarola, Gurutzeta Guillera-Arroita,
José Lahoz-Monfort, and Petr Keil



Czech University
of Life Sciences Prague

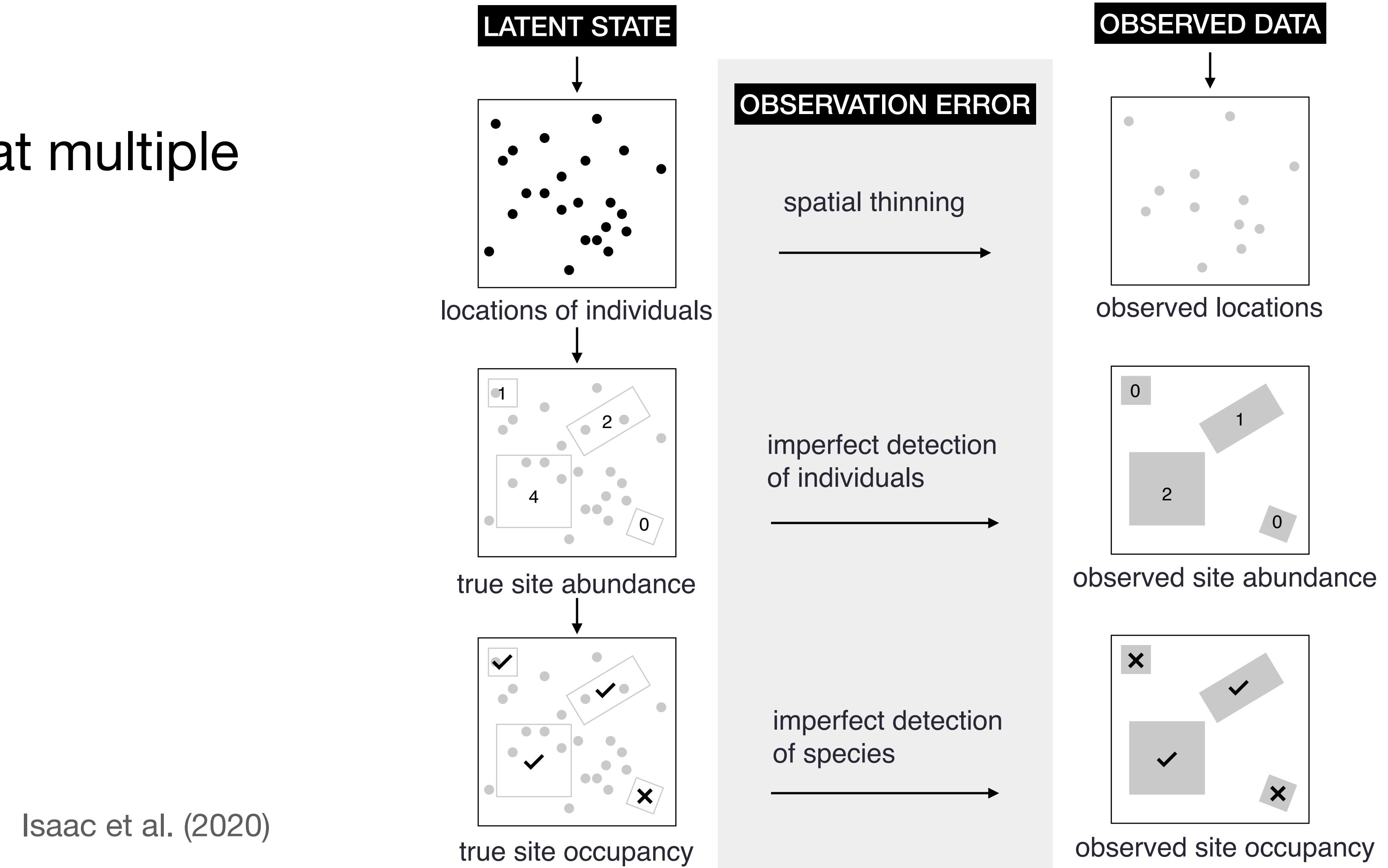


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Pirenaico
de Ecología

Integrated species distribution model

ISDM

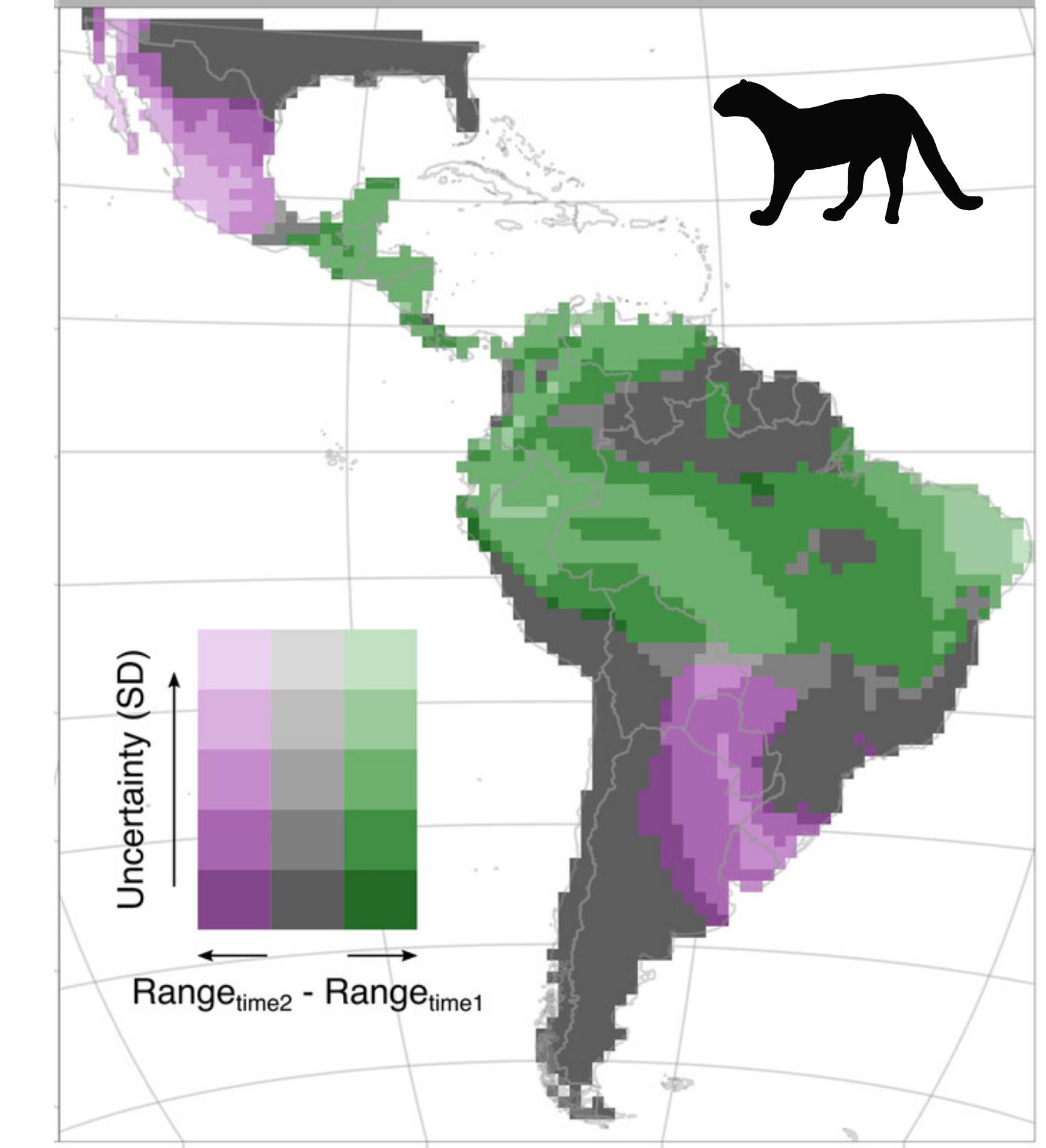
- Multiple data sources at multiple scales



jaguarundi (*Herpailurus yagouaroundi*)



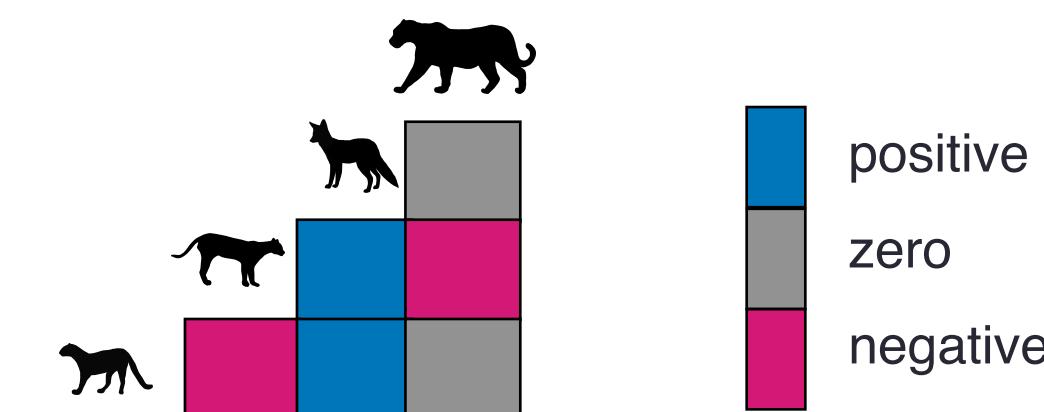
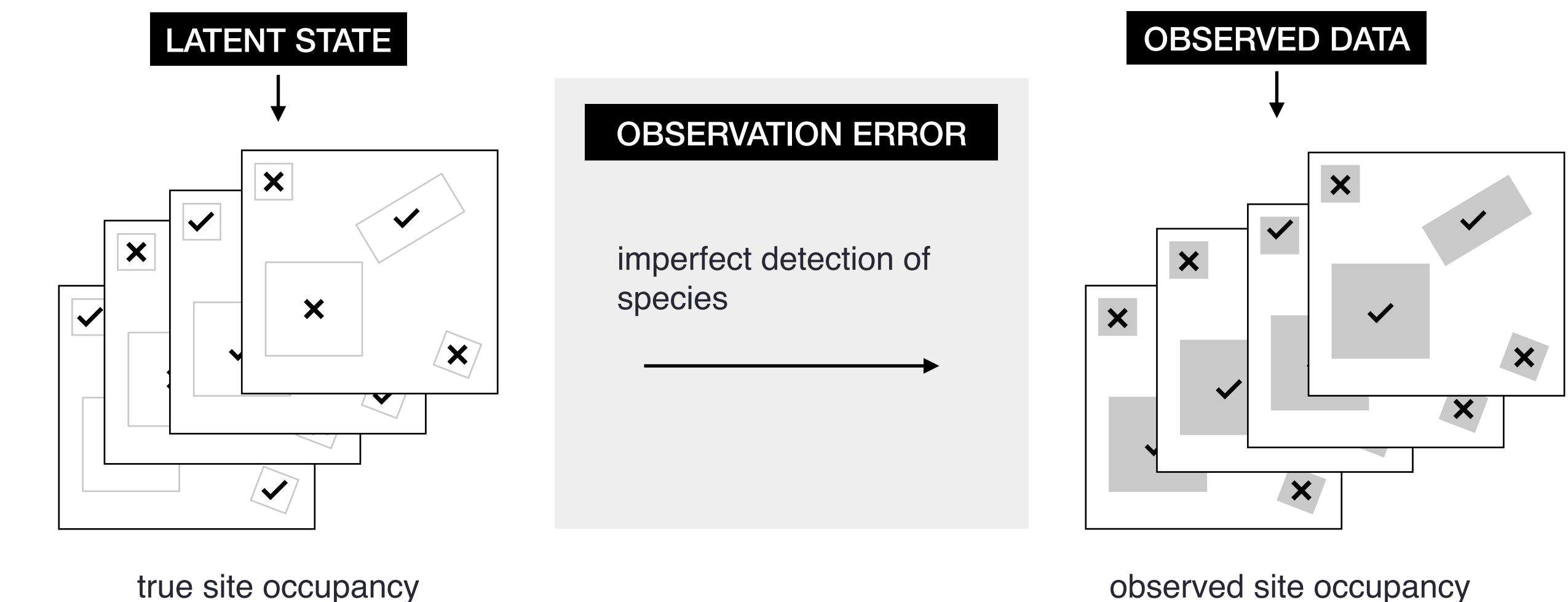
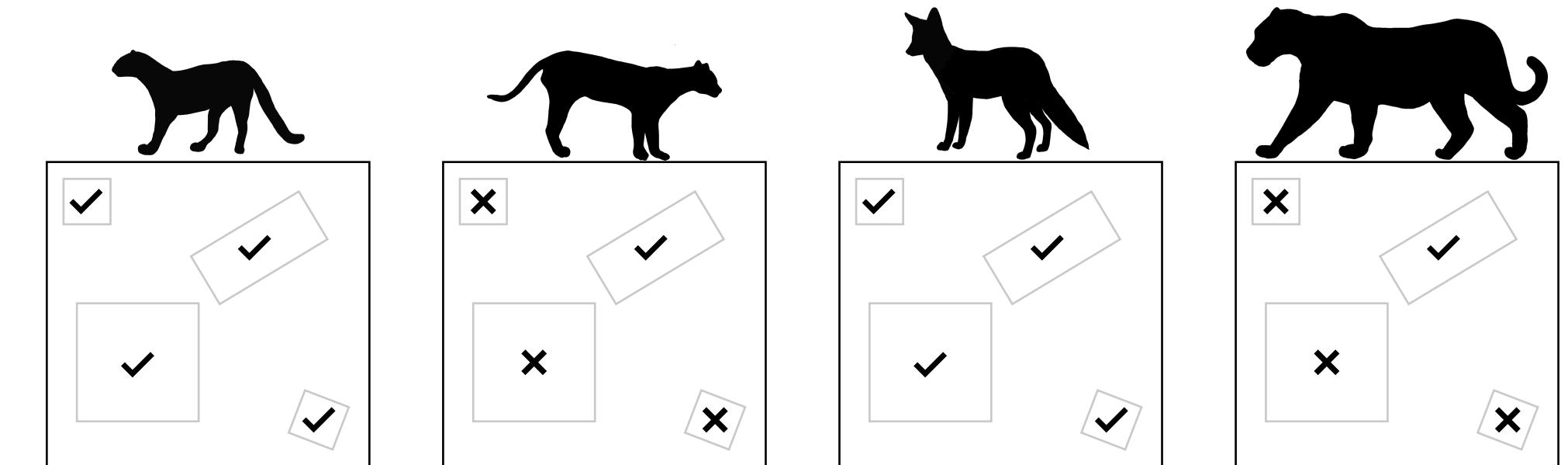
$\text{Range}_{\text{time}2} - \text{Range}_{\text{time}1}$ by SD



Joint species distribution model

JSDM

- Multiple species (co-occurrence)



Warton et al. (2015)

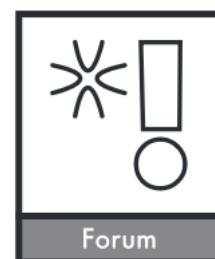
**GfÖ**GfÖ Ecological Society of Germany,
Austria and Switzerland

Basic and Applied Ecology 13 (2012) 371–379

**Basic and
Applied Ecology**

www.elsevier.com/locate/baae

Patterns of coexistence of two species of freshwater turtles are affected by spatial scale

P. Segurado^{a,b,*}, W.E. Kunin^c, A.F. Filipe^d, M.B. Araújo^{a,e,f}**Ecography 37: 406–415, 2014**

doi: 10.1111/j.1600-0587.2013.00643.x

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Subject Editor: Carsten Rahbek. Accepted 21 October 2013

The geographic scaling of biotic interactions

Miguel B. Araújo and Alejandro Rozenfeld

Global Ecology and Biogeography, (Global Ecol. Biogeogr.) (2015) 24, 750–761

**RESEARCH
PAPER**

Empirical evidence for the scale dependence of biotic interactions

Jonathan Belmaker^{1,*†}, Phoebe Zarnetske^{2,3†}, Mao-Ning Tuanmu⁴,
Sara Zonneveld^{3,5}, Sydne Record^{2,6}, Angela Strecker⁷ and Lydia Beaudrot⁸

ECOGRAPHY

Forum

Do joint species distribution models reliably detect interspecific interactions from co-occurrence data in homogenous environments?

Damaris Zurell, Laura J. Pollock and Wilfried Thuiller

RESEARCH ARTICLE**Journal of Ecology**

Scale dependence of ecological assembly rules: Insights from empirical datasets and joint species distribution modelling

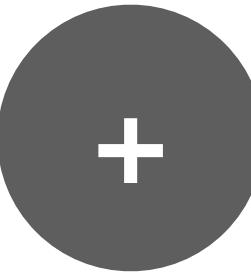
Heidi K. Mod^{1,2} | Mathieu Chevalier¹ | Miska Luoto² | Antoine Guisan^{1,3} **RESEARCH ARTICLE****Journal of
Biogeography****WILEY**

Species associations in joint species distribution models: from missing variables to conditional predictions

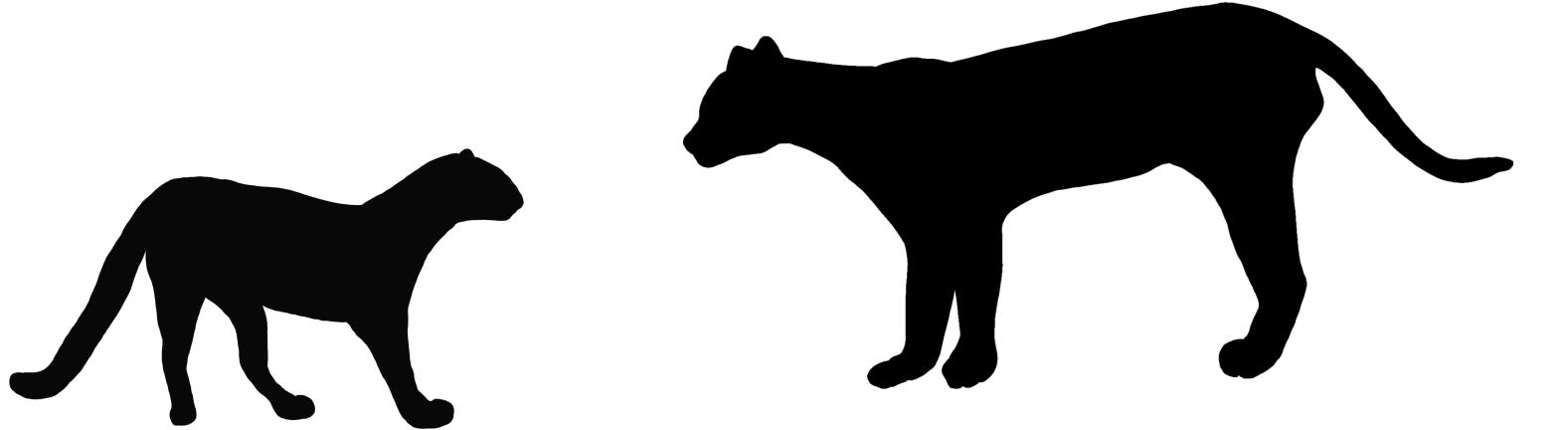
Clément Vallé¹ | Giovanni Poggiato^{2,3} | Wilfried Thuiller² | Frédéric Jiguet¹ | Karine Princé¹ | Isabelle Le Viol^{1,4}

Our goal

ISDM + JSDM



Can fine-scale associations be detected using coarse-grain data with IJSDMs?



Methods



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Methods

1. Data simulation:
 - A. Environmental predictor
 - B. Species data
2. Fit an IJSDM
3. Check the identifiability and coverage of model parameters

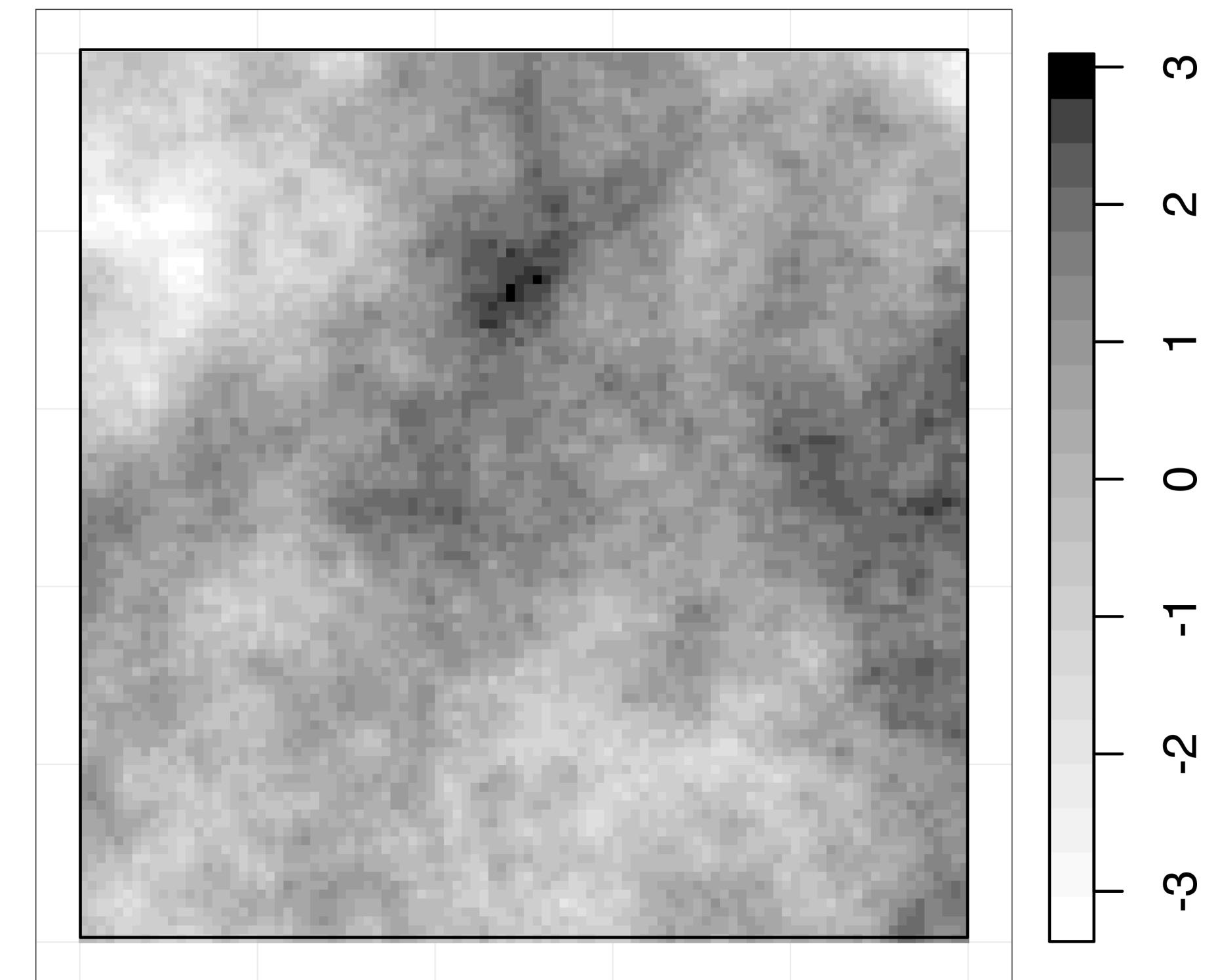
Data simulations

Environmental predictor

- We simulated a hypothetical **temperature** predictor as a spatially autocorrelated environmental raster at a resolution of 100x100 grid cells (fine-grain).

Note: We used the same raster for all simulations

temperature



Data simulations

Species data

Point pattern

$$\lambda_1 = \exp^{(\alpha_1 + \beta_1 \times \text{temp} + e_1)}$$

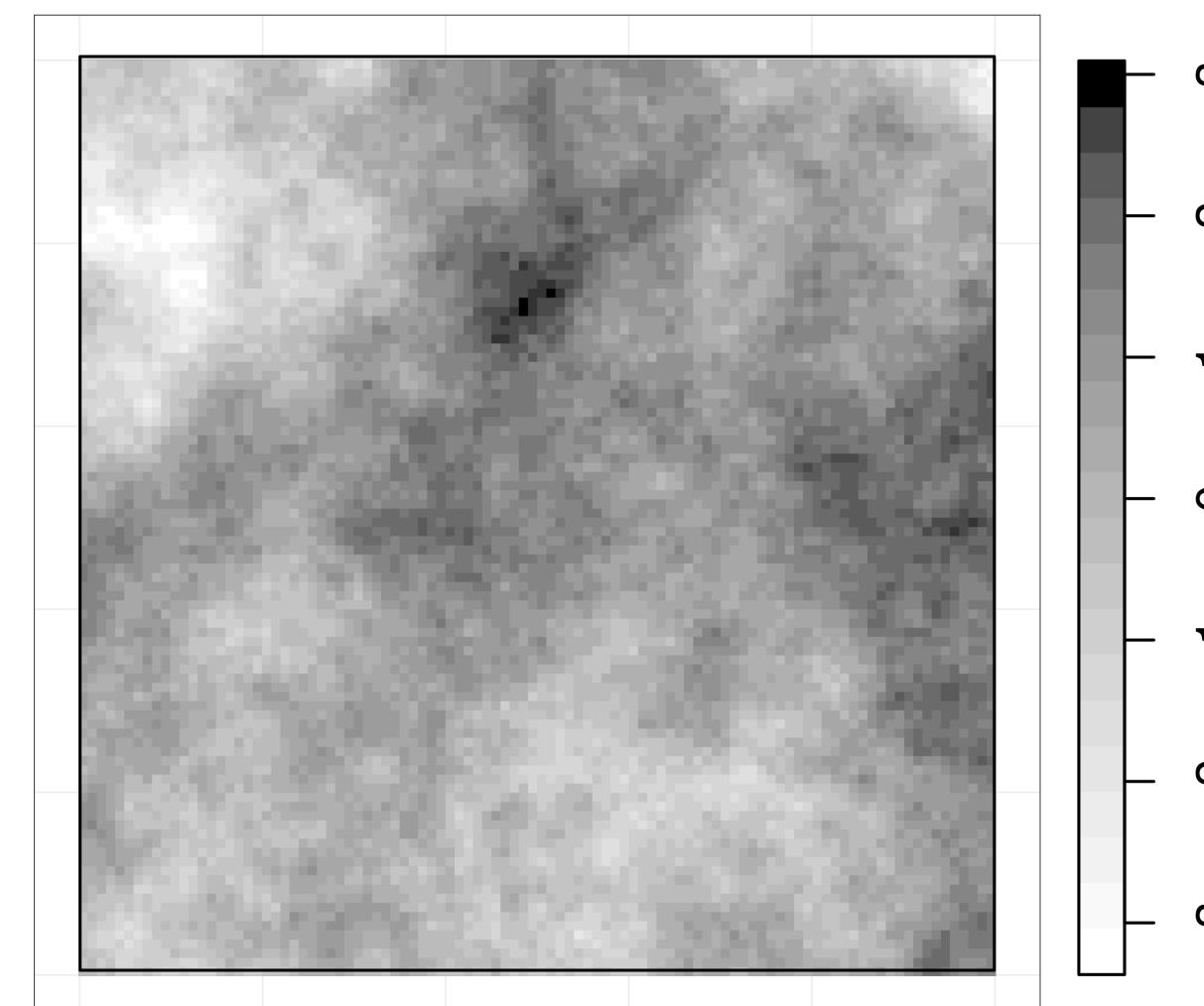
$$\lambda_2 = \exp^{(\alpha_2 + \beta_2 \times \text{temp} + e_2)}$$

Correlated error

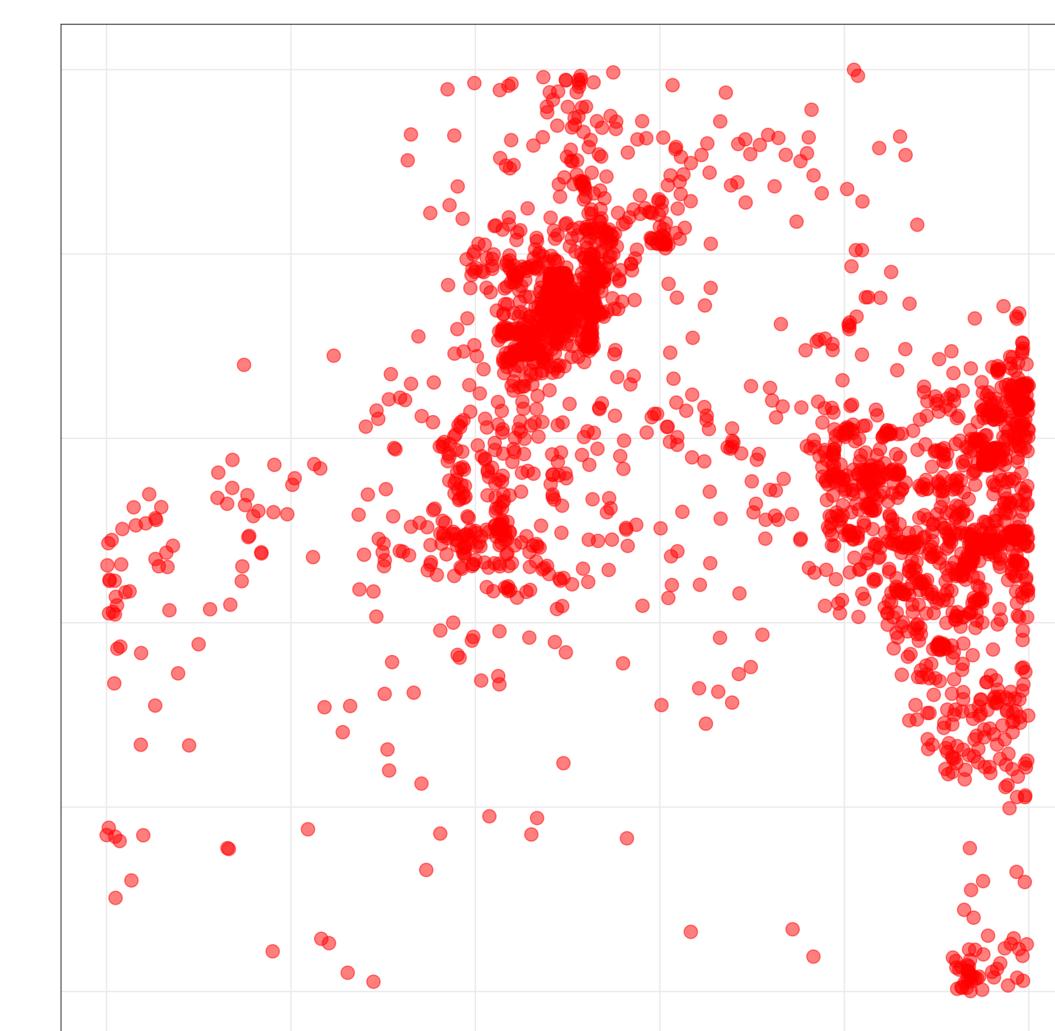
$$e_{ij} \sim \text{MVN}(0, \Sigma)$$

$$\Sigma = \begin{bmatrix} var_1 & cov_{1,2} \\ cov_{2,1} & var_2 \end{bmatrix}$$

temperature

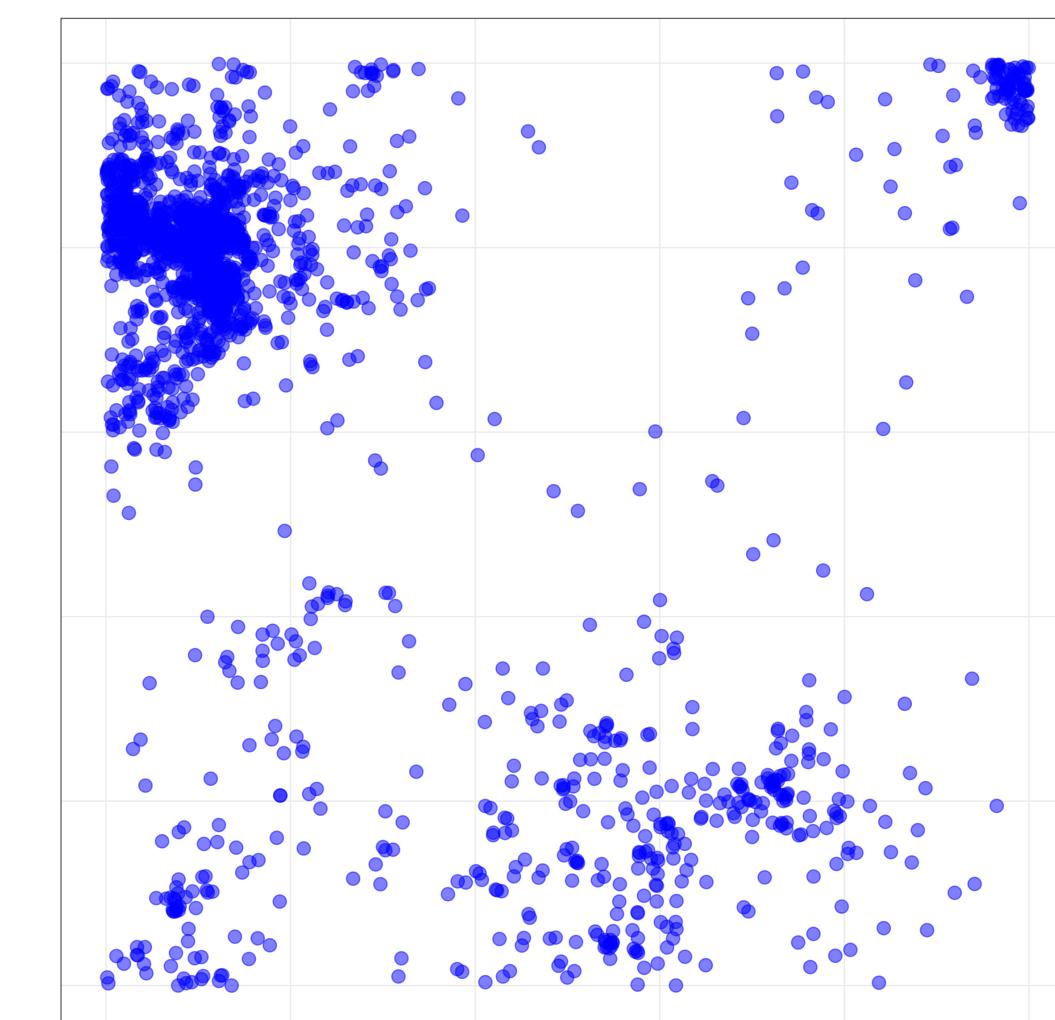


point pattern of species₁



$\alpha_1 = 5$
 $\beta_1 = 2.5$
 $\text{cov}_1 = 0.9$

point pattern of species₂

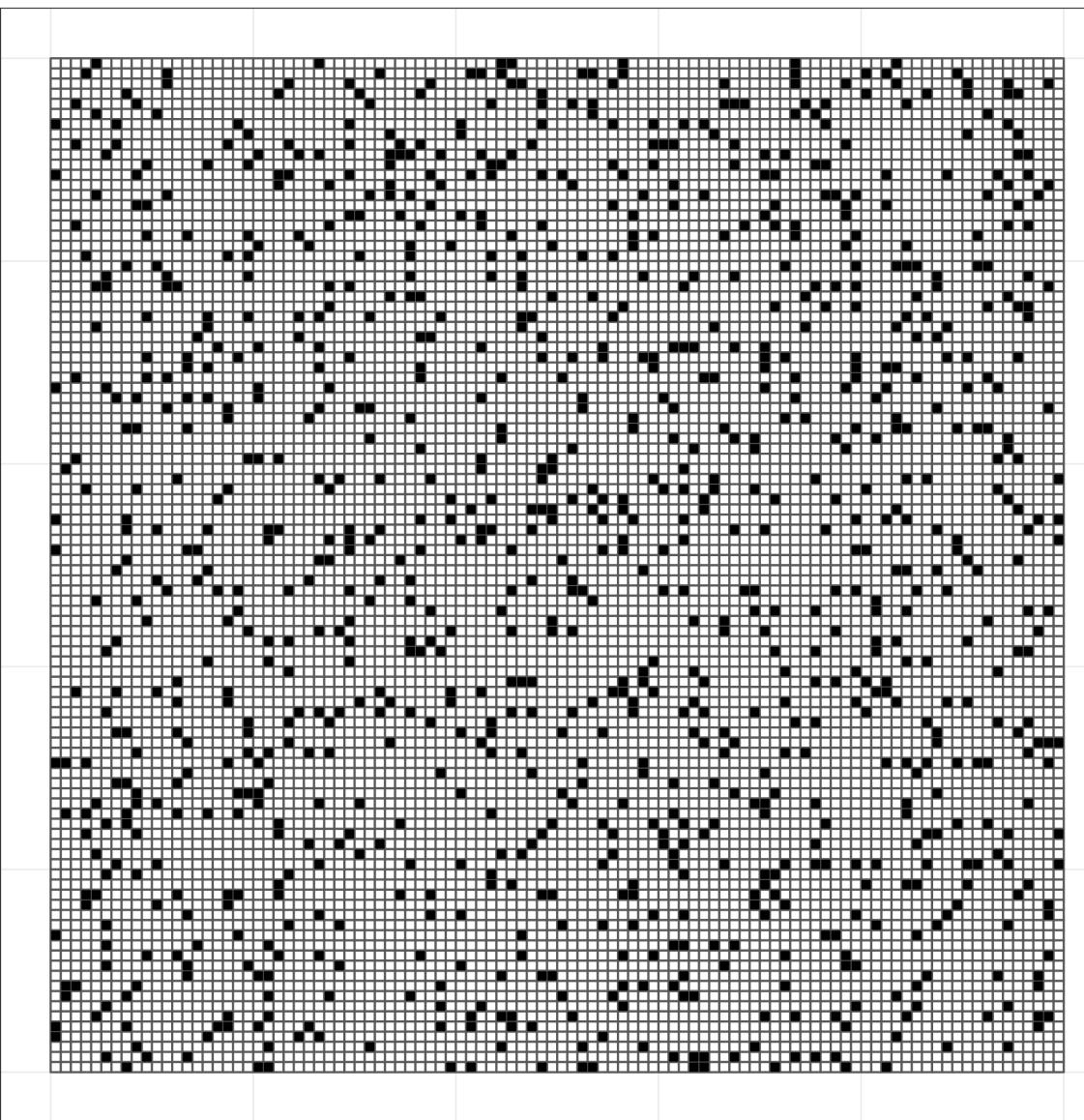


$\alpha_2 = 5$
 $\beta_2 = -2$
 $\text{cov}_2 = 0.9$

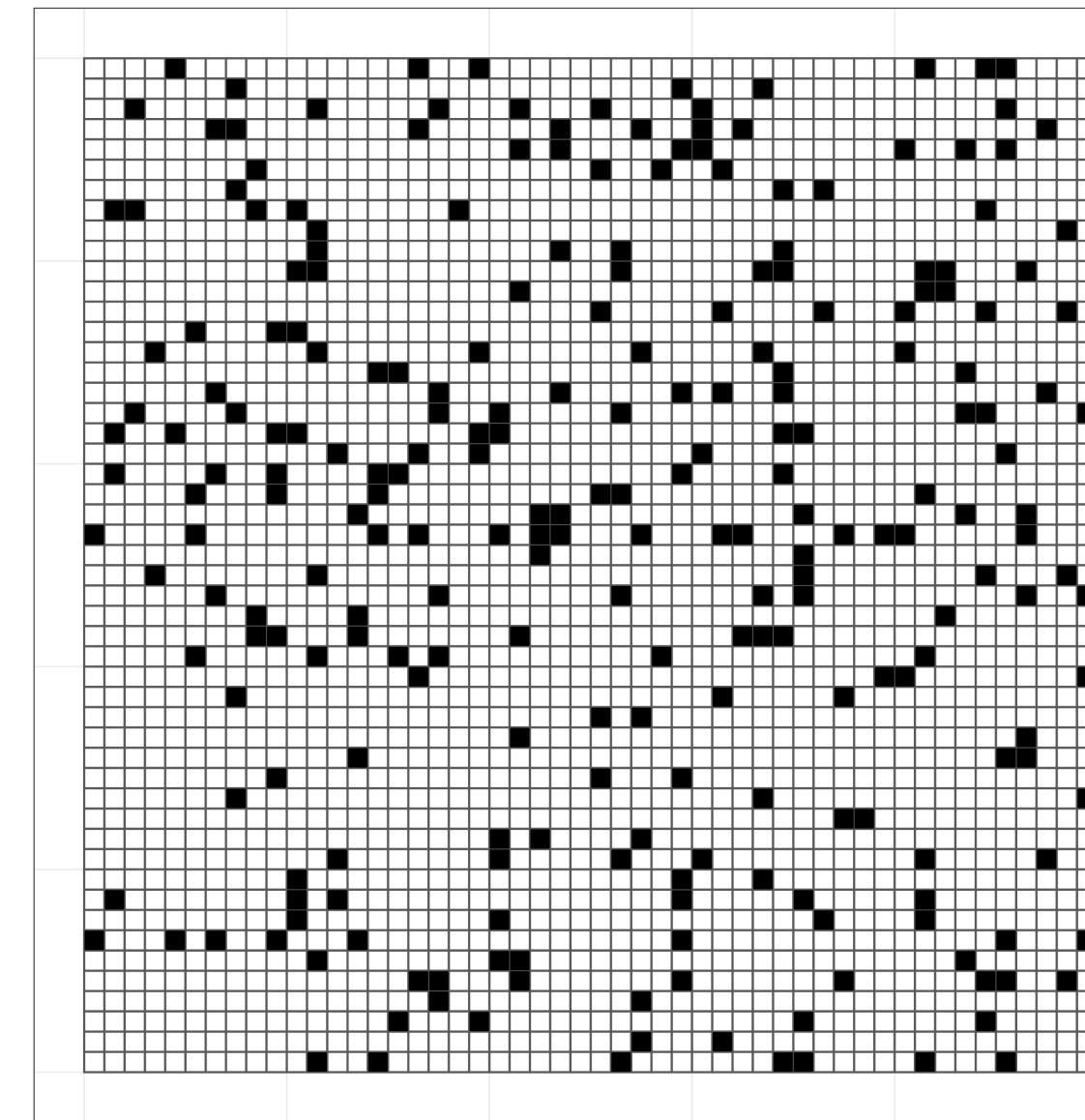
Data simulations

Sampling sites of varying grain size

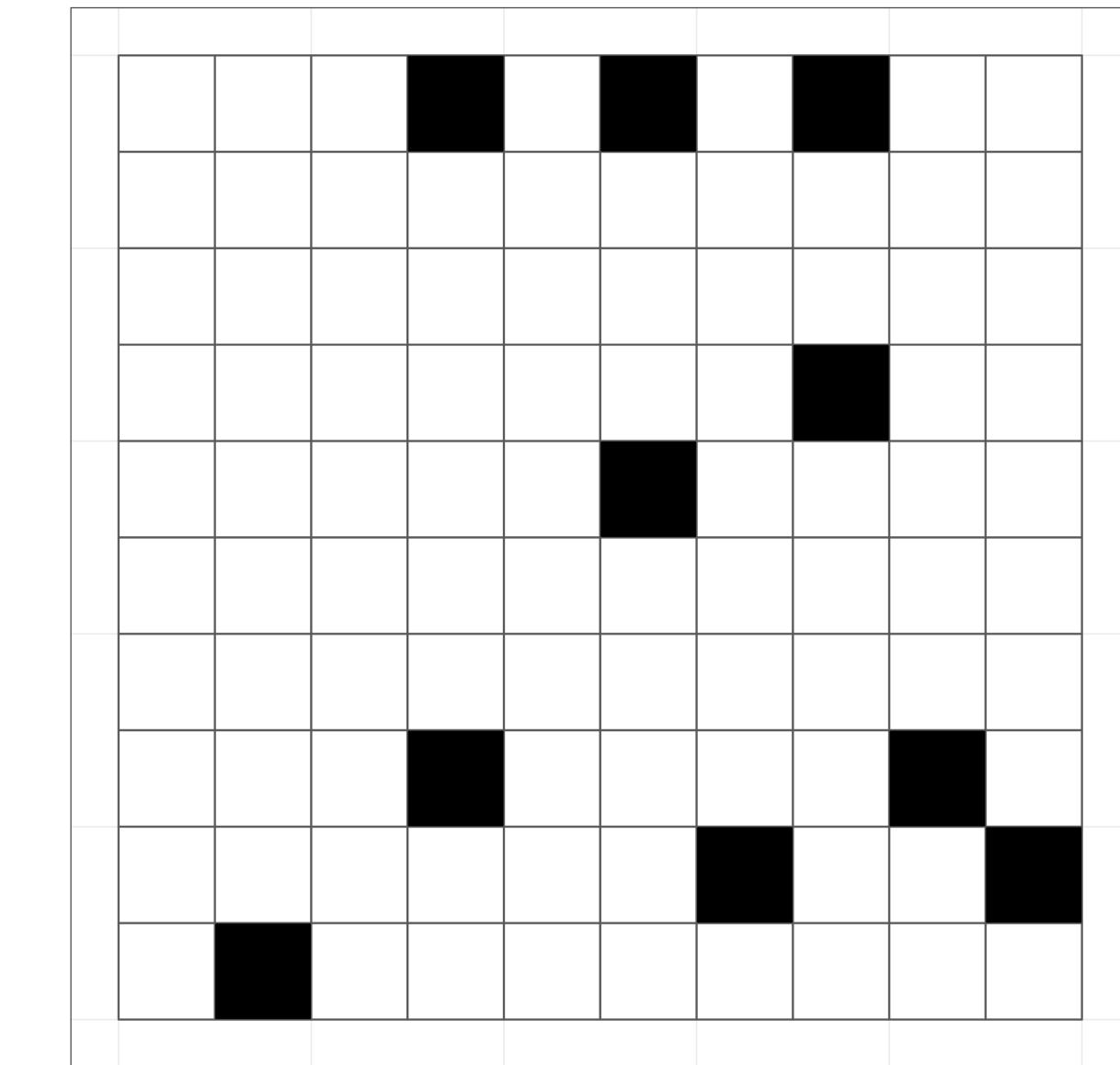
sampling sites at
100x100 grain



sampling sites at
50x50 grain



sampling sites at
10x10 grain



black cells are 10% of cells, representing hypothetical discrete sampling sites

IJSMD

Abundance

OBSERVED DATA

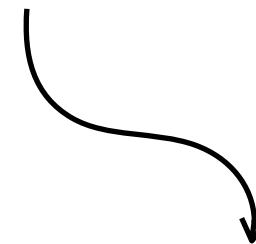
$$AB_{i,j} \sim \text{Poisson}(\phi_{i,j})$$

sites, i , where $i \in 1 : n_i$
species, j , where $j \in 1 : n_j$

LATENT STATE

$$\begin{aligned} \log(\phi_{i,1}) &= \alpha_1 + \beta_1 \times \text{temp}_i + e_{i,1} + \log(\text{area}_i) \\ \log(\phi_{i,2}) &= \alpha_2 + \beta_2 \times \text{temp}_i + e_{i,2} + \log(\text{area}_i) \end{aligned}$$

area of each grid cell



$$\begin{aligned} e_{i,j} &\sim \text{MVN}(0, \tau) \\ \tau &= \Sigma^{-1} \end{aligned}$$

IJSMD

Presence-absence

OBSERVED DATA

$$PA_{i,j} \sim \text{Bernoulli}(\psi_{i,j})$$

sites, i , where $i \in 1 : n_i$
species, j , where $j \in 1 : n_j$

area of each
grid cell

LATENT STATE

$$\begin{aligned} cloglog(\psi_{i,1}) &= \alpha_1 + \beta_1 \times temp_i + e_{i,2} + log(area_i) \\ cloglog(\psi_{i,2}) &= \alpha_2 + \beta_2 \times temp_i + e_{i,2} + log(area_i) \end{aligned}$$

$$\begin{aligned} e_{i,j} &\sim \text{MVN}(0, \tau) \\ \tau &= \Sigma^{-1} \end{aligned}$$

Methods

Data simulations: parameter set

540 combinations repeated 10x, resulting in 5,400 simulation runs

Parameter	Description	Values in the simulation
α	Intercept (always $\alpha_1 = \alpha_2$)	5 (fixed)
<u>β_1</u> and <u>β_2</u>	The species-specific effect (slope) of the environmental predictor driving the point process intensity	-3, -2.5, -2, 2.5, 3, 3.5
<u>var</u>	Residual variance (with $var_1 = var_2$)	1 (fixed)
<u>cov</u>	Residual covariance (with $cov_{1,2} = cov_{2,1}$) representing species association	-0.9, -0.5, 0, 0.5, 0.9
<u>$grid$</u>	The grain at which we sampled the species data	10x10, 50x50, 100x100

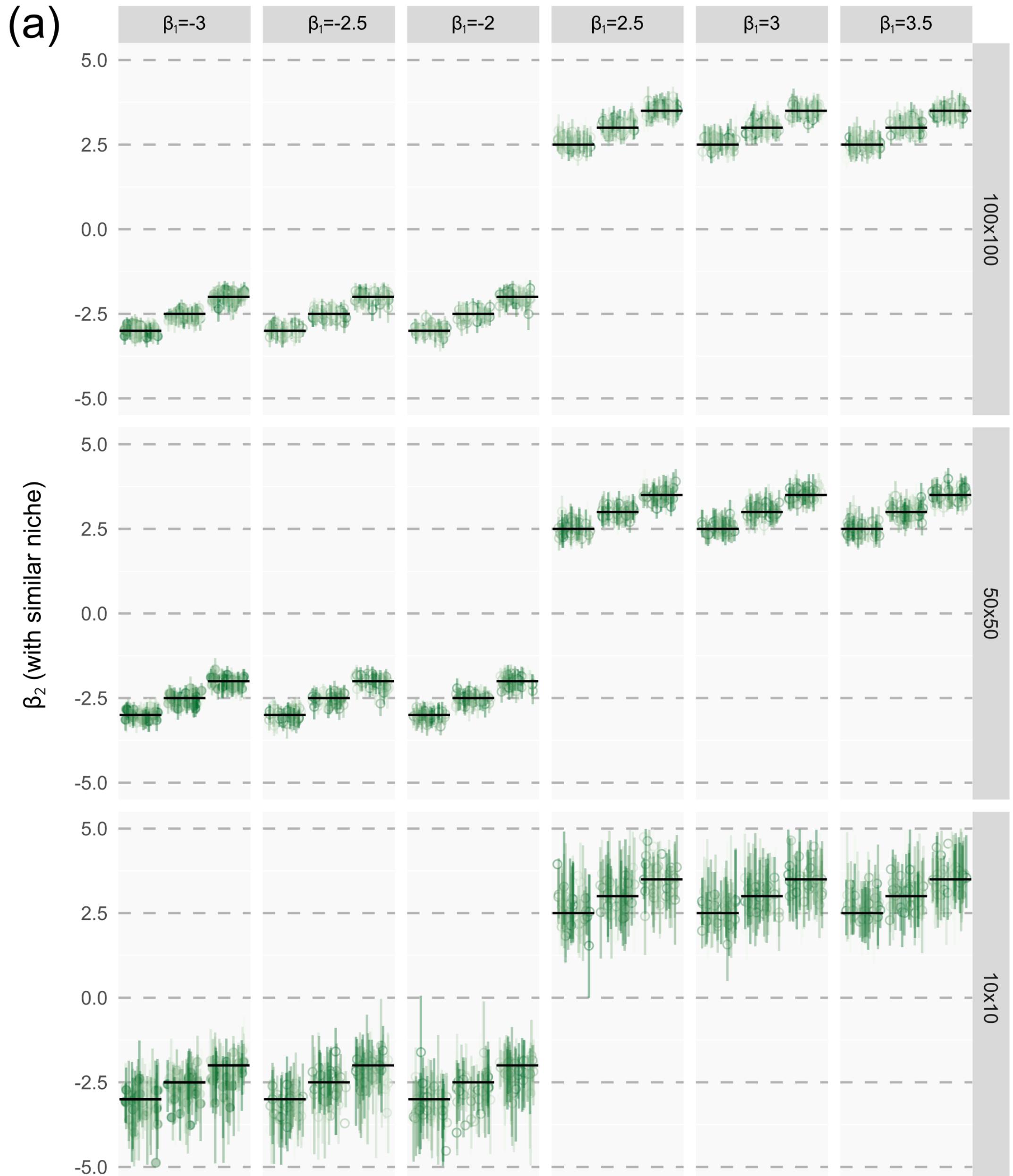
Note: using 200 cores, the abundance model took 10 hours to run, and the presence-absence model took 23 hours

Results

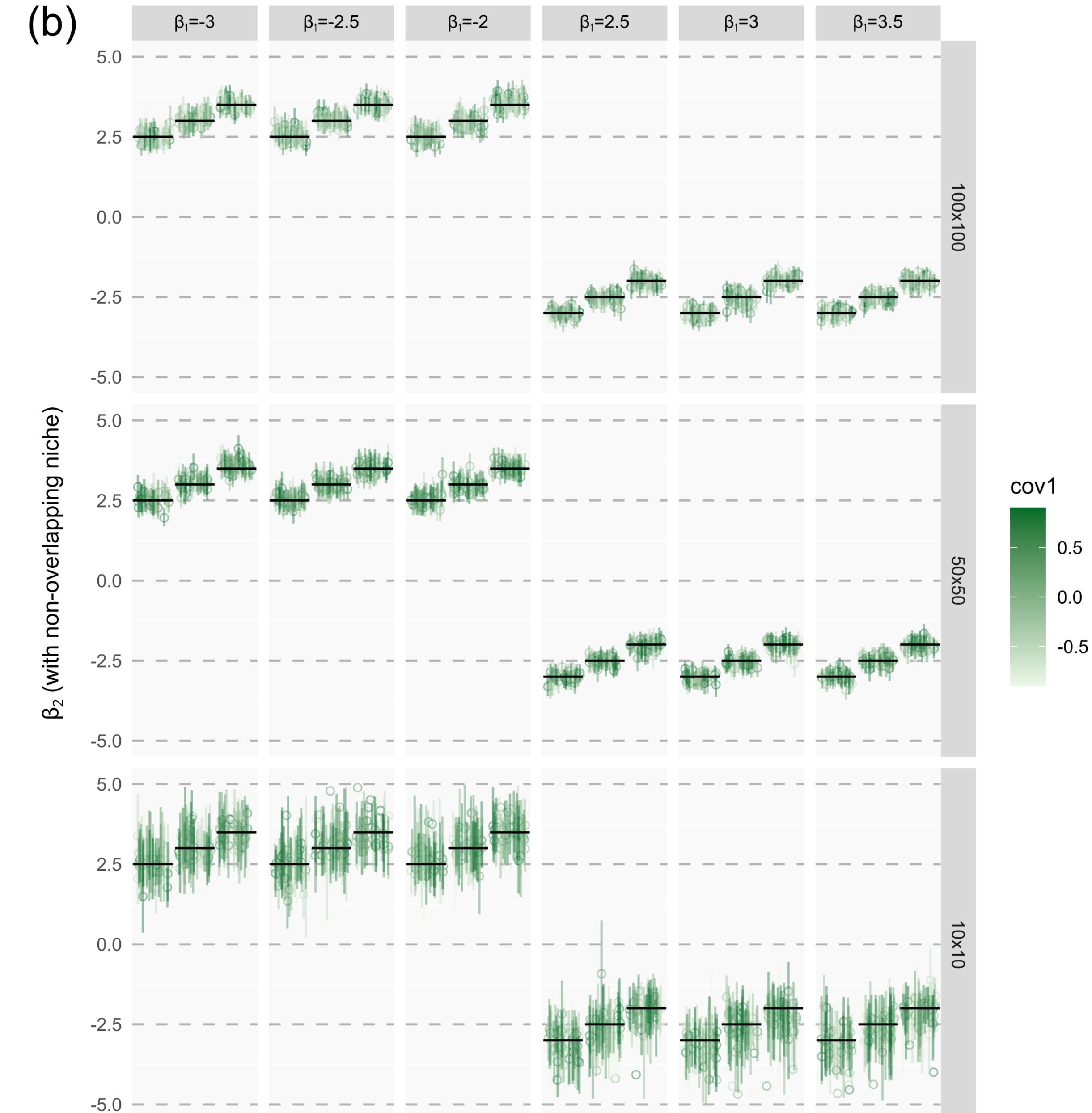


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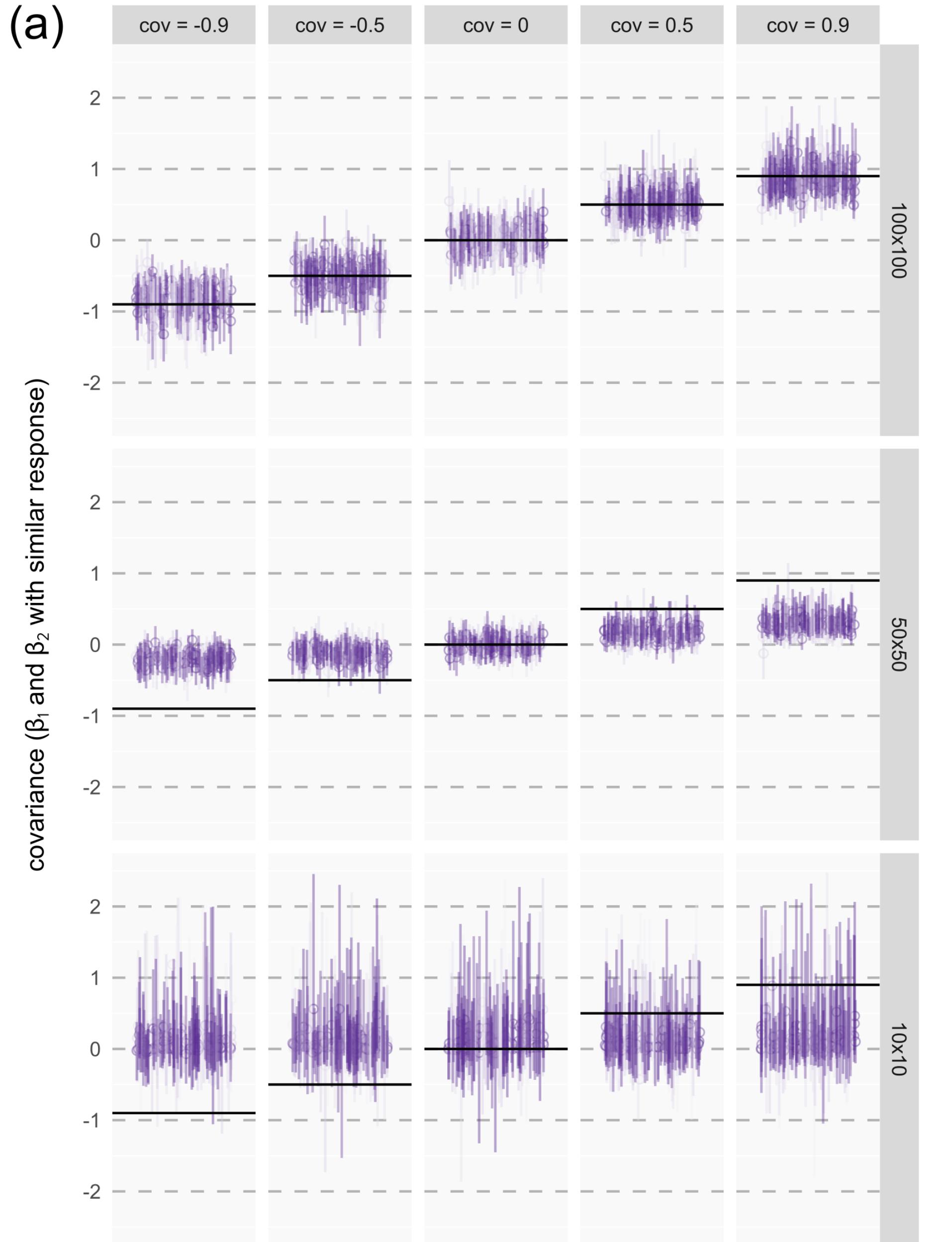
with similar niche



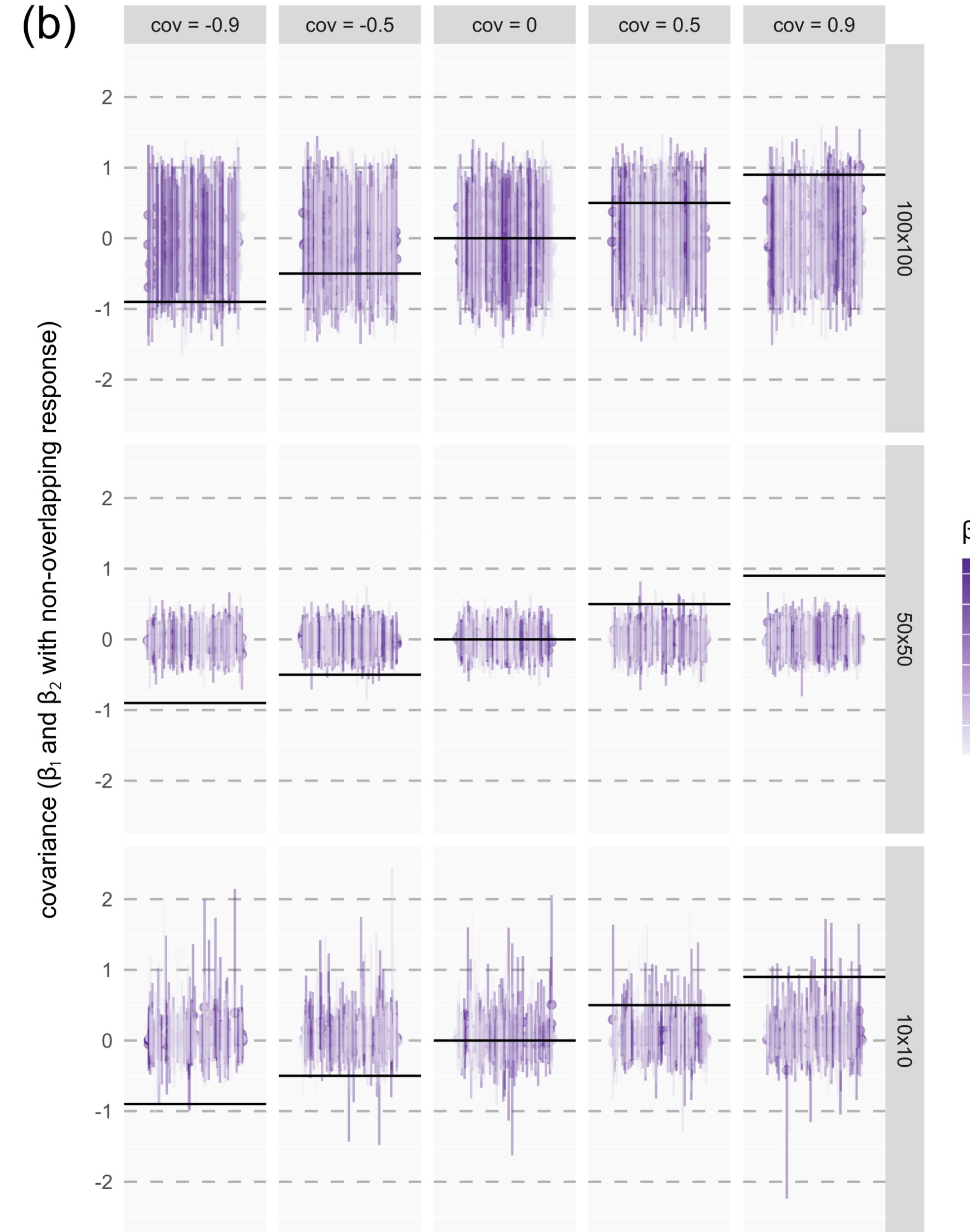
with non-overlapping niche



with similar niche



with non-overlapping niche



Discussion



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Discussion

Can fine-scale associations be detected using coarse-grain data with IJSDMs?

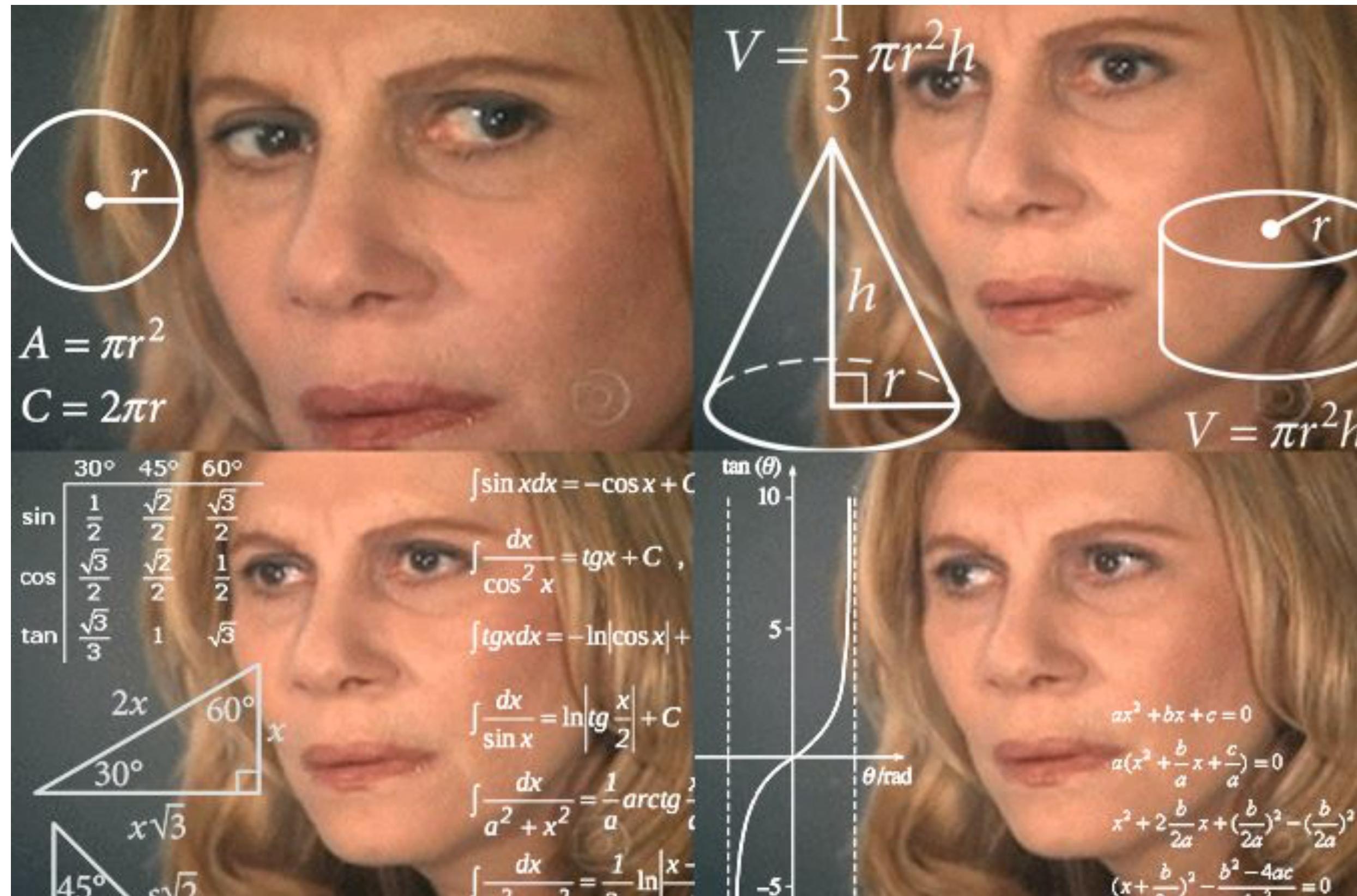
The correct species associations can **only** be detected using:

1. fine-grain data (at the grain of the simulated interaction) and
2. when both species respond similarly to the environment.

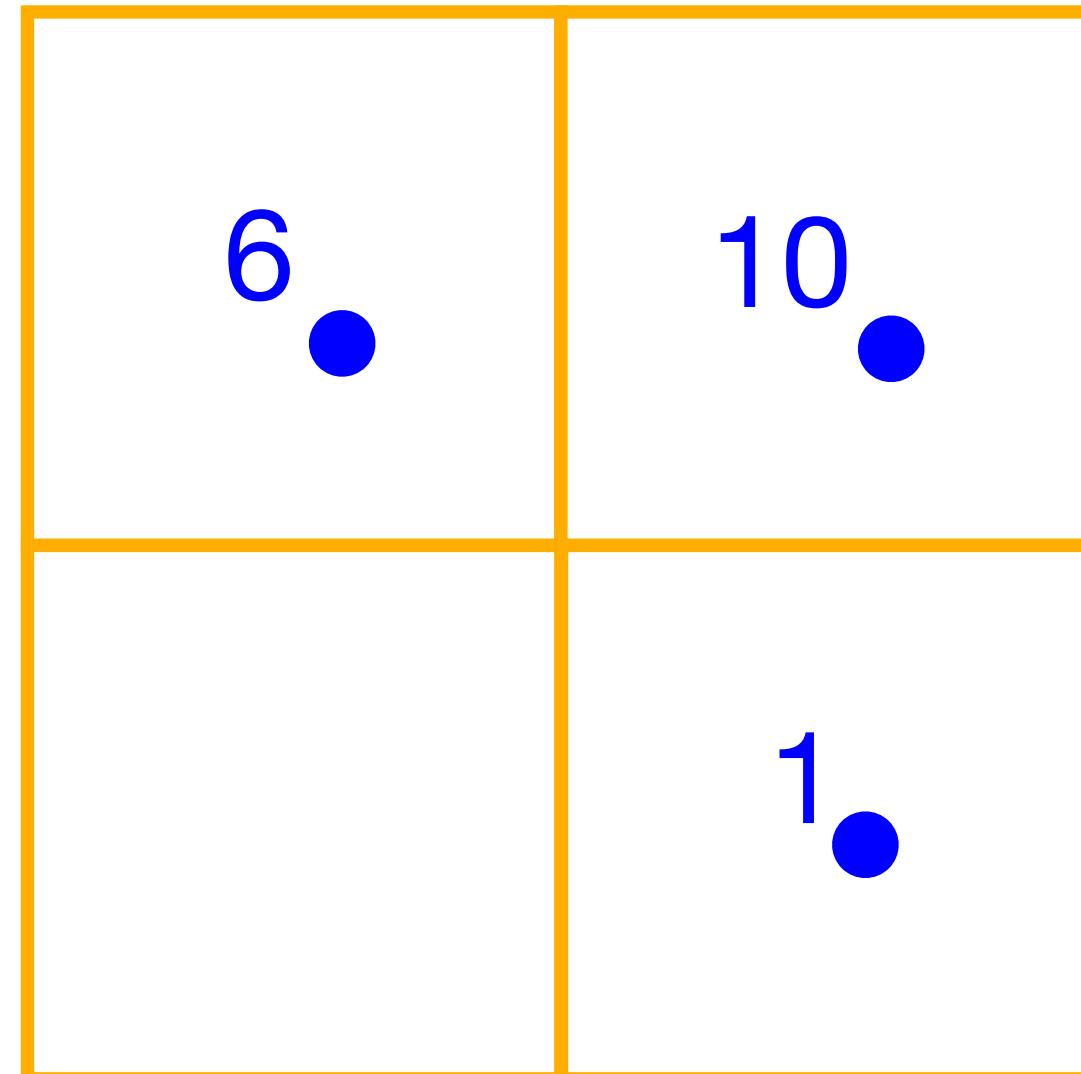
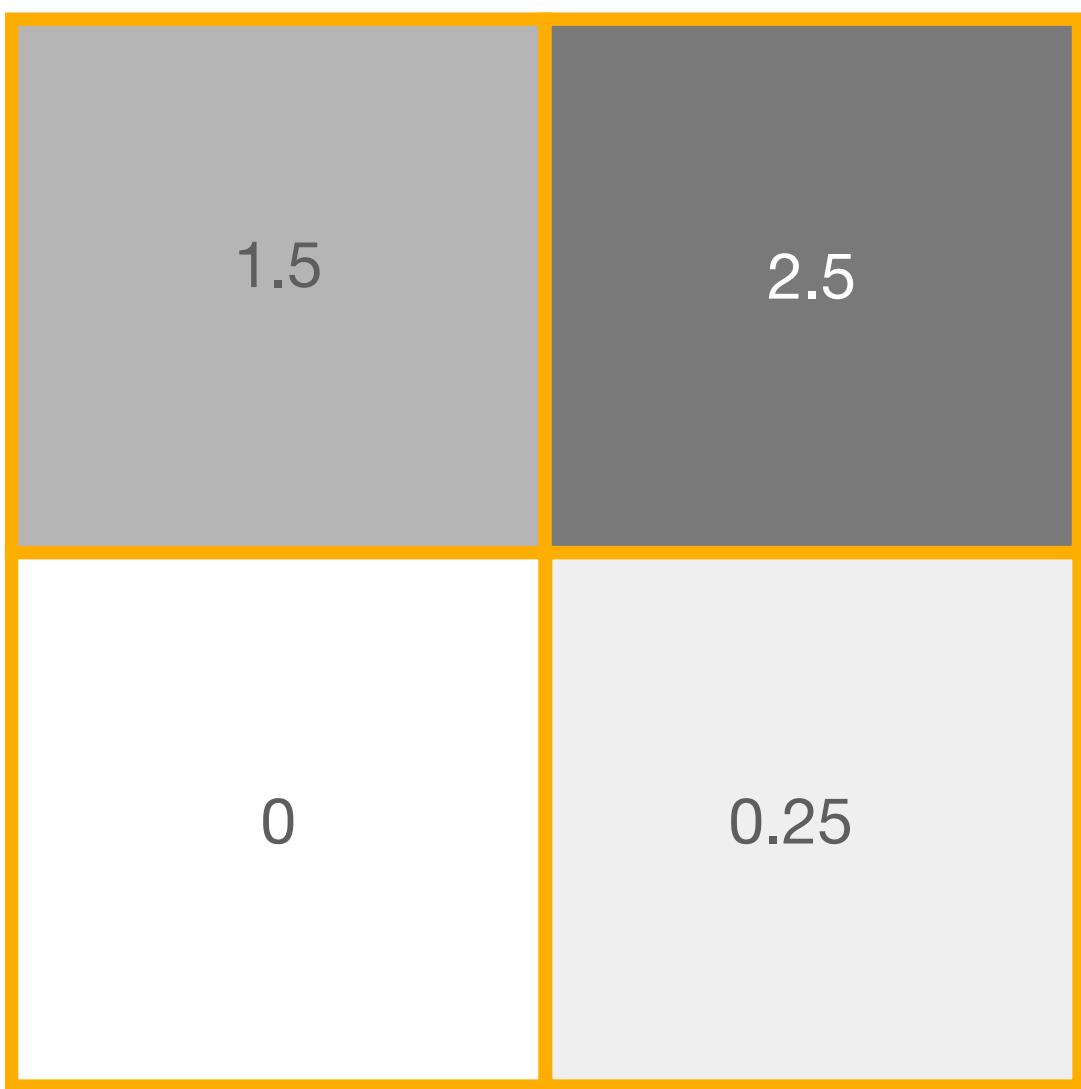
Thus, running the IJSDM with data sources at coarse resolutions can provide incorrect estimates of the species' associations.

Discussion

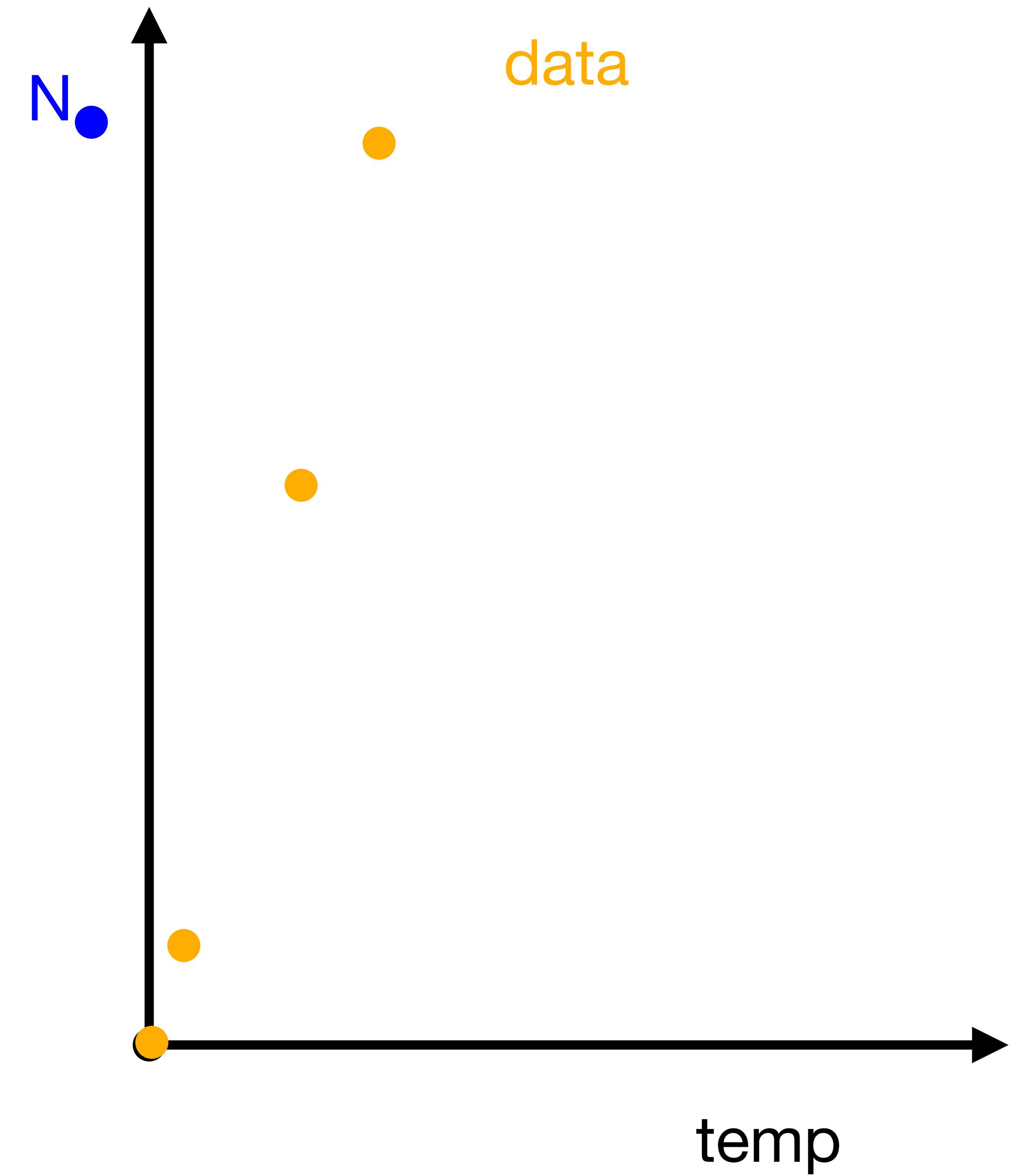
Why does the association disappear towards coarse grains?



temp_{coarse}

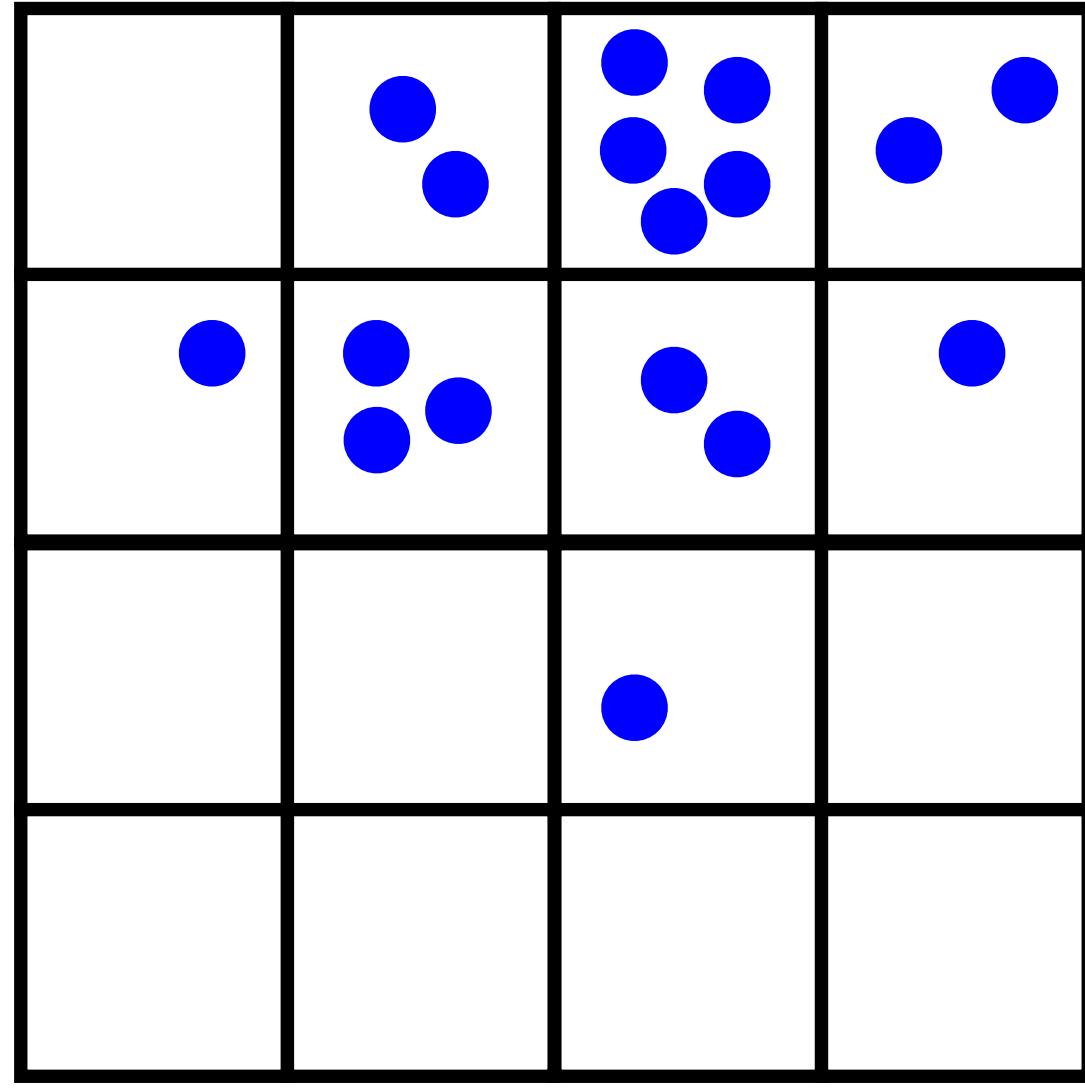
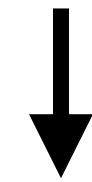


data



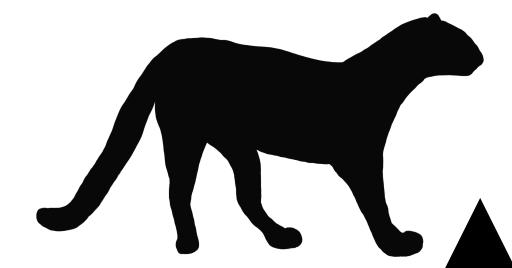
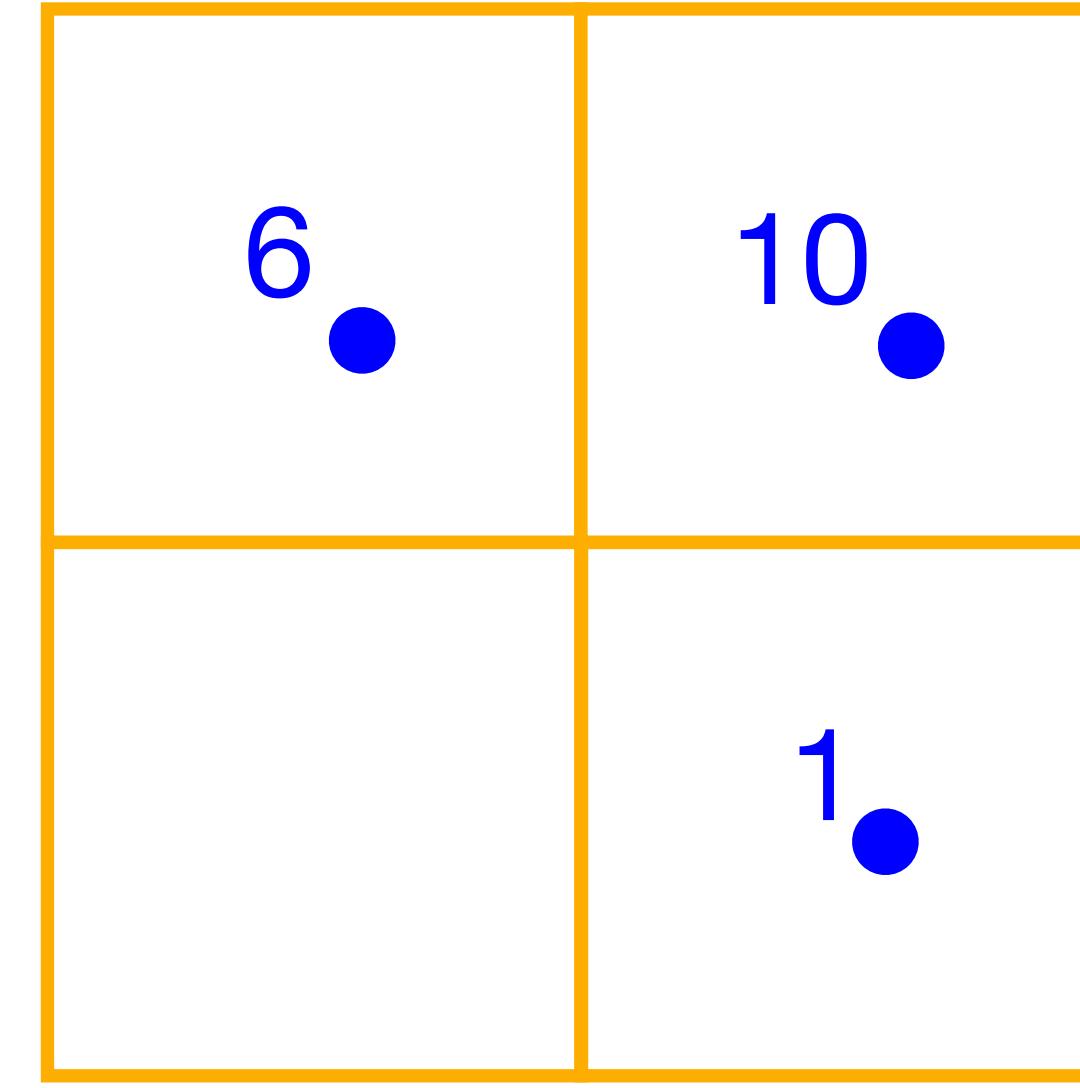
$\text{temp}_{\text{fine}}$

0	2	4	2
1	3	2	1
0	0	1	0
0	0	0	0



$\text{temp}_{\text{coarse}}$

1.5	2.5
0	0.25



N

data



N

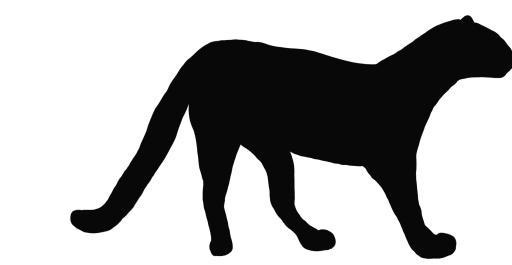
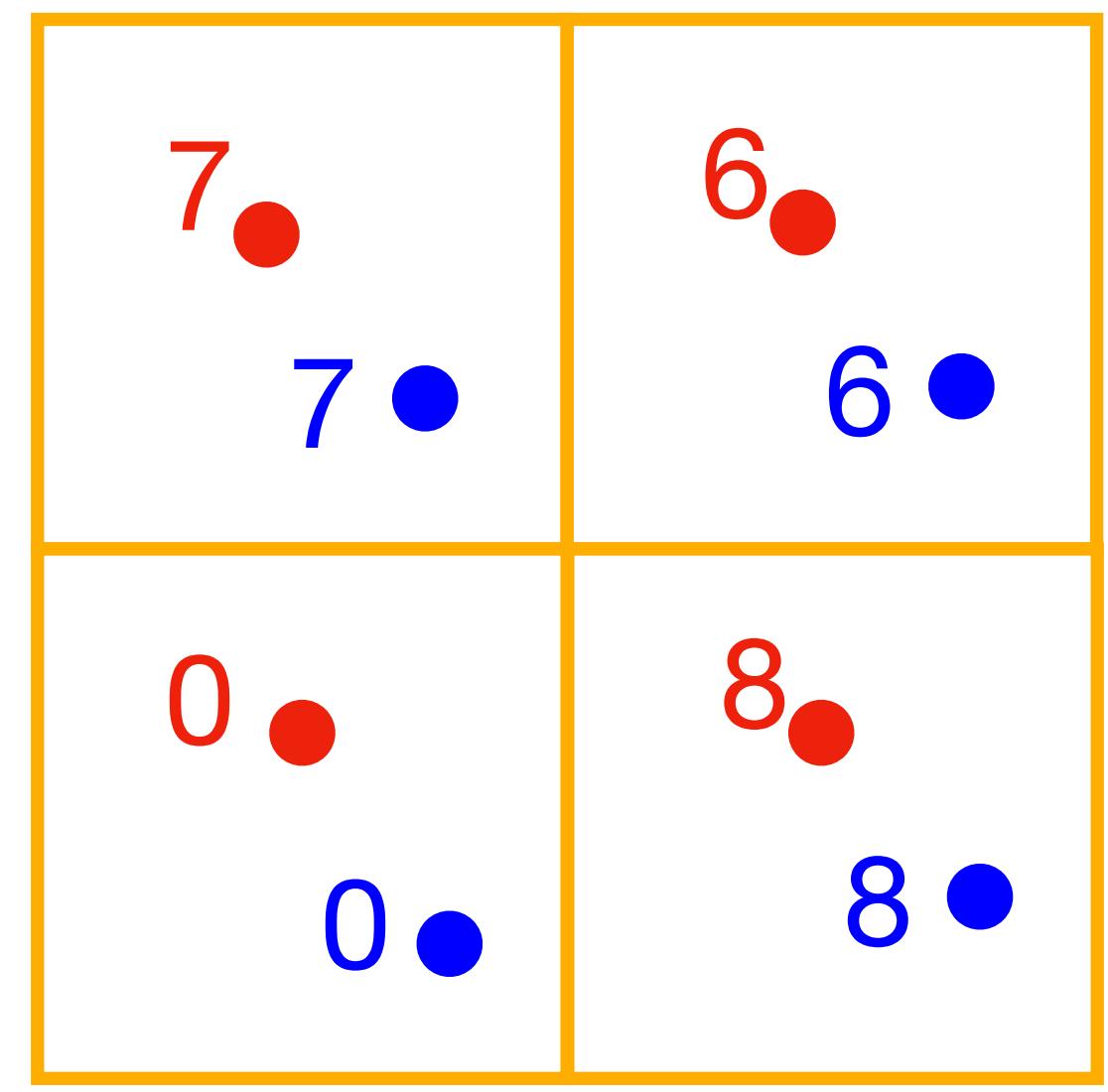
latent state

$\beta = 1.125$



temp

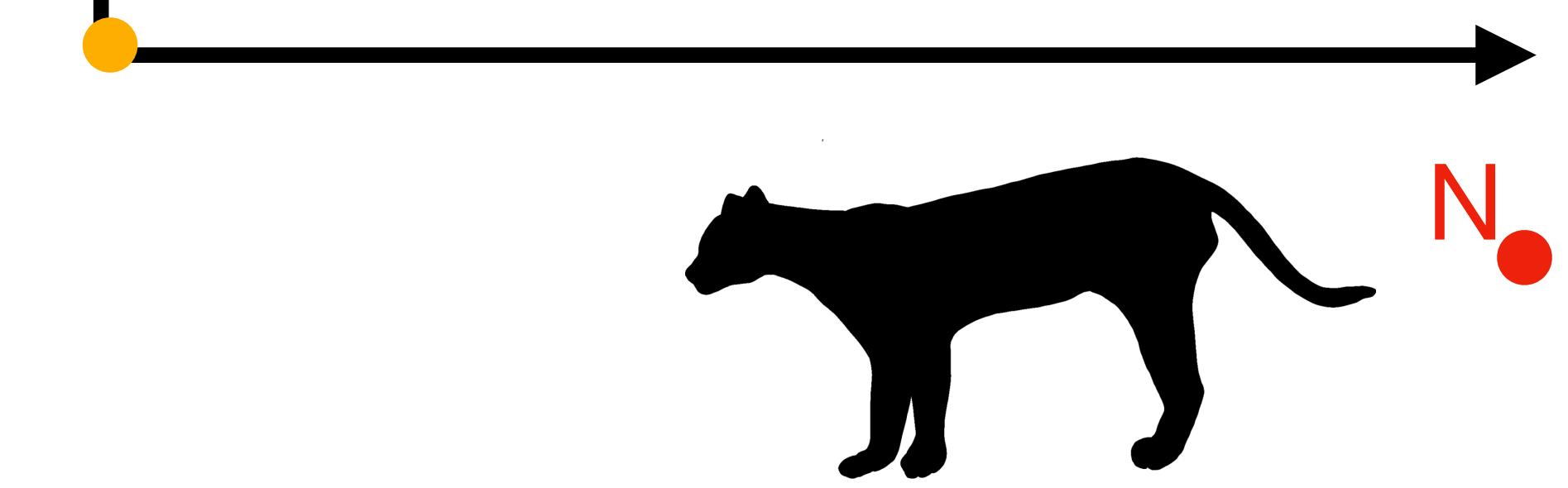
data



N

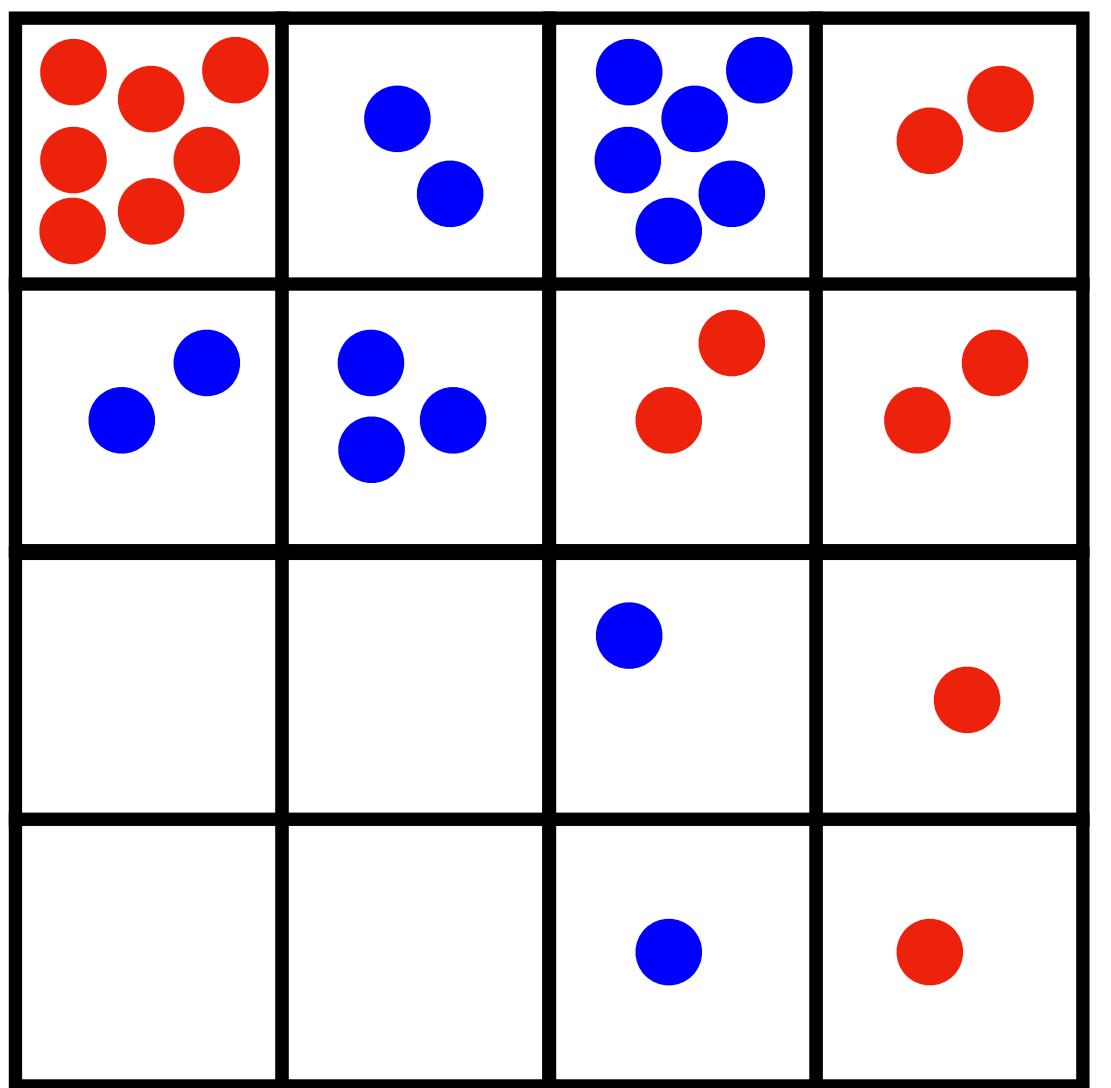


data

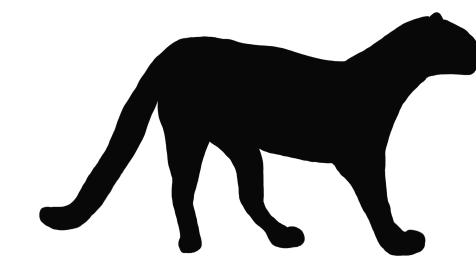
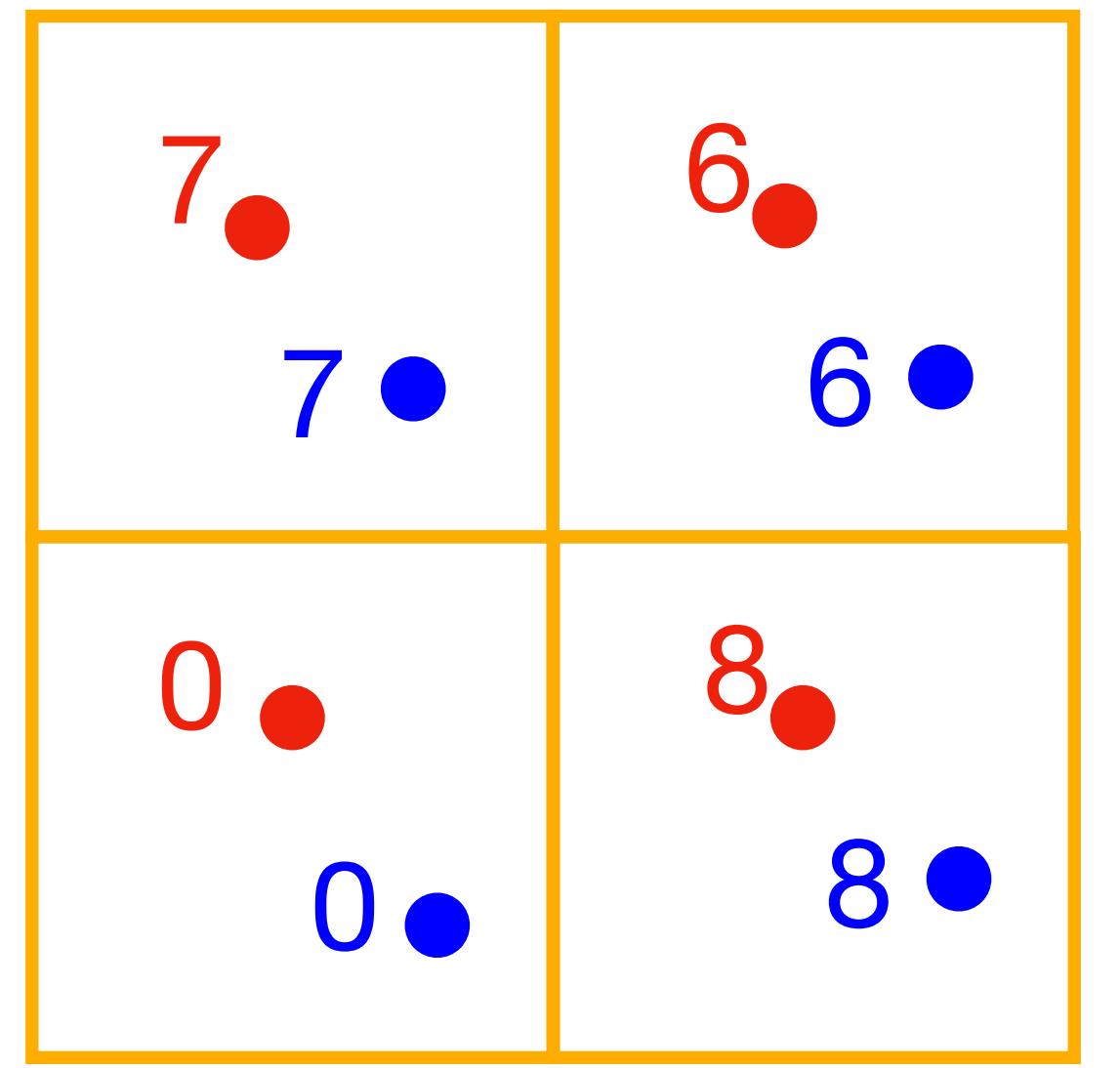


$cov(-)$

latent state

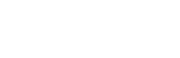


data



N

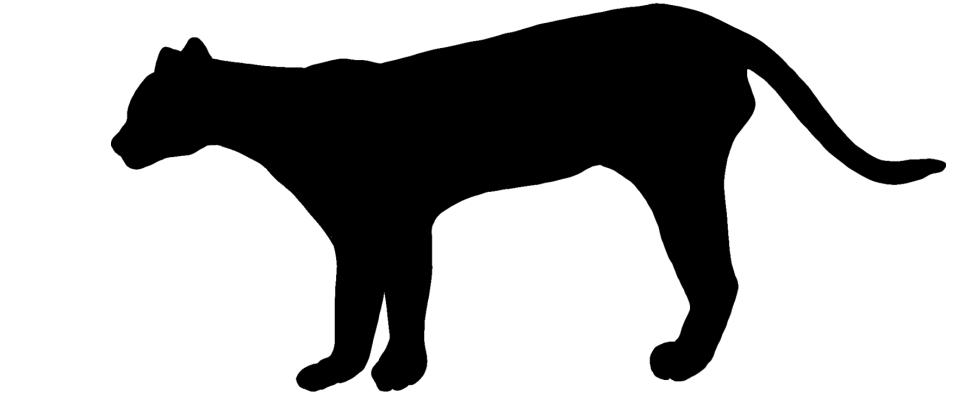
data

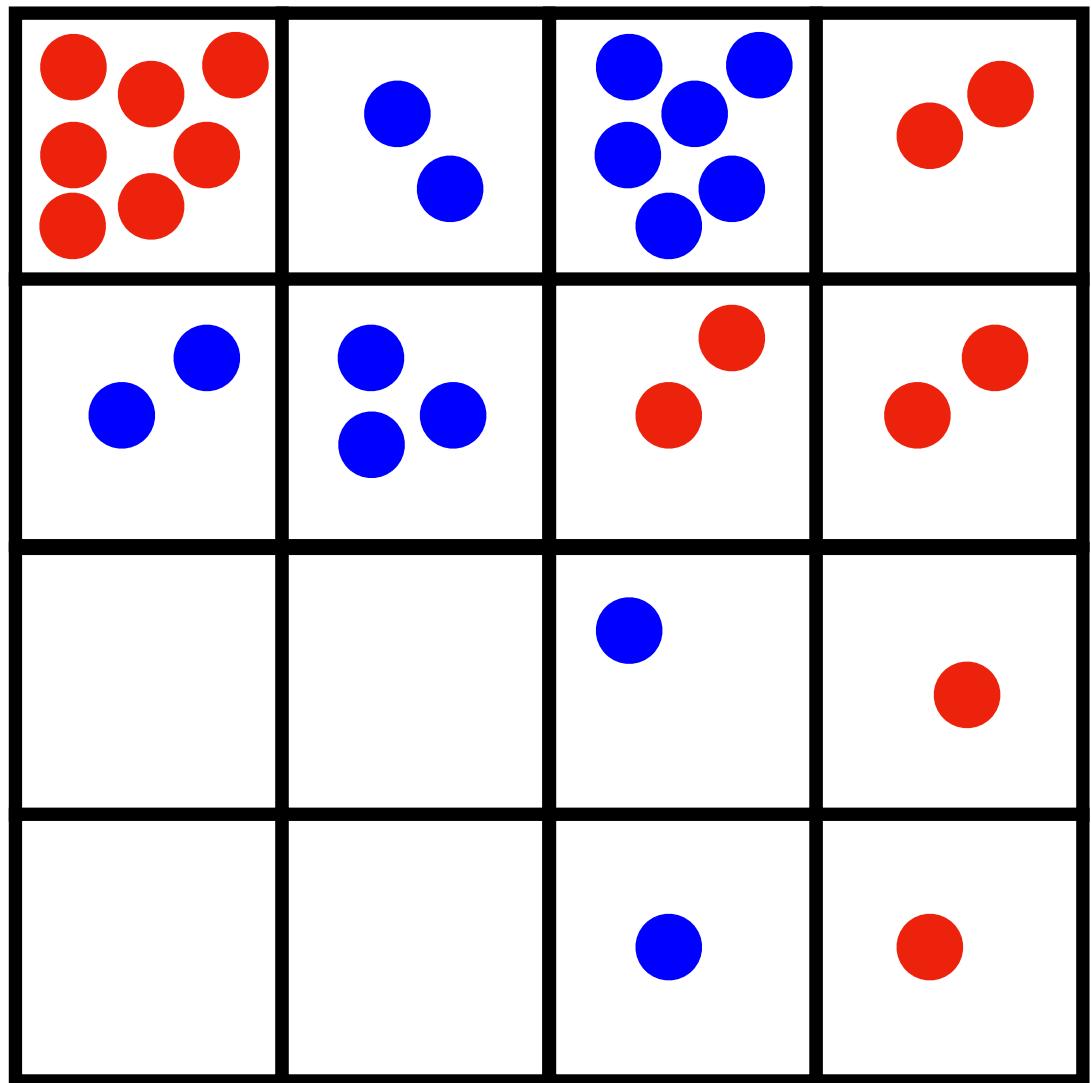


$cov(-)$

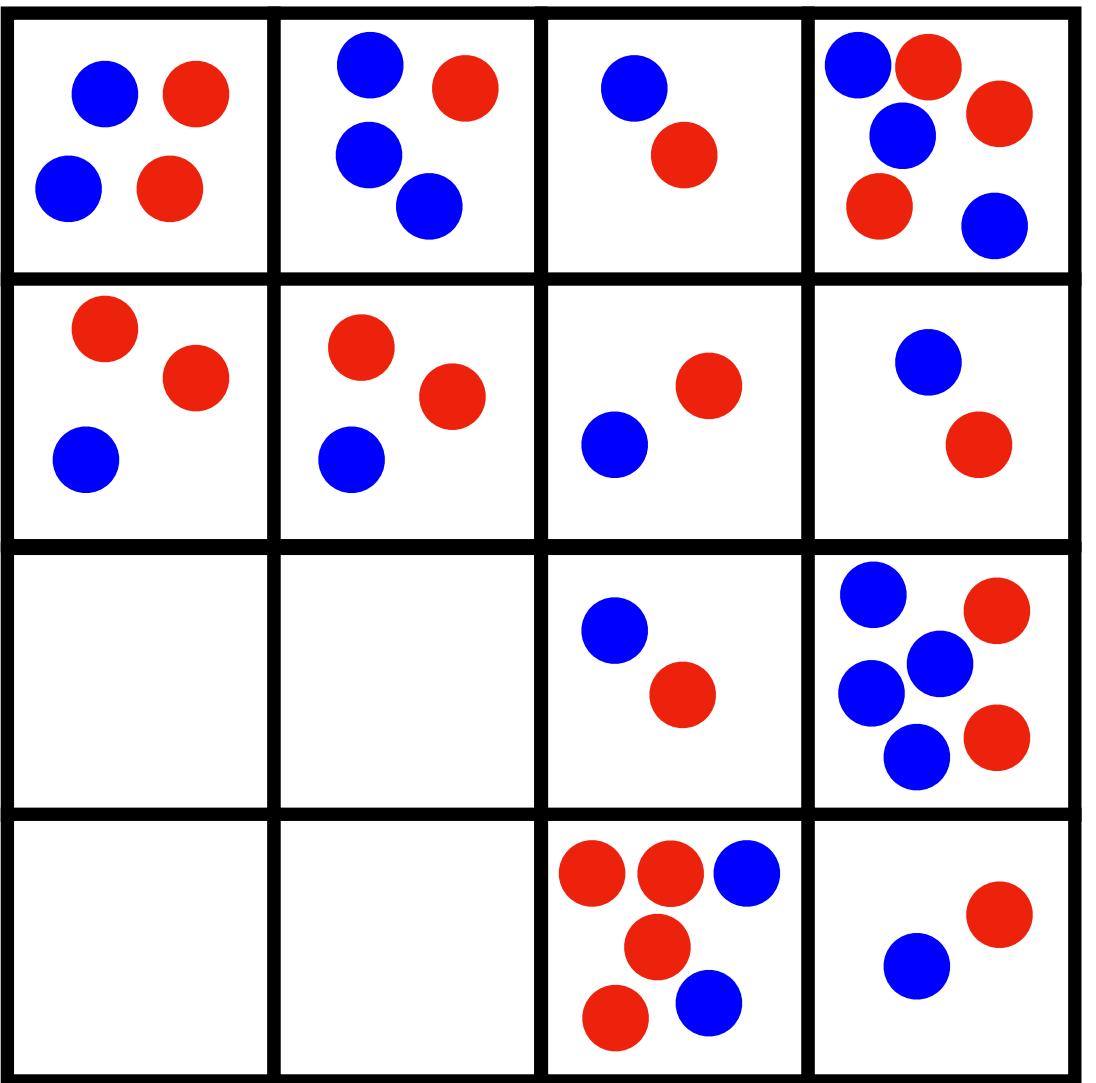
latent state

N

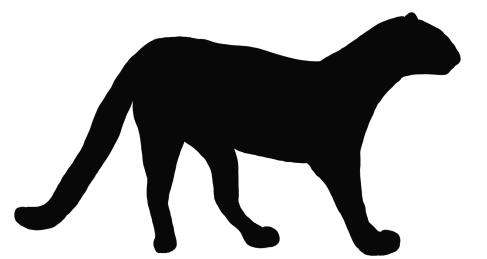
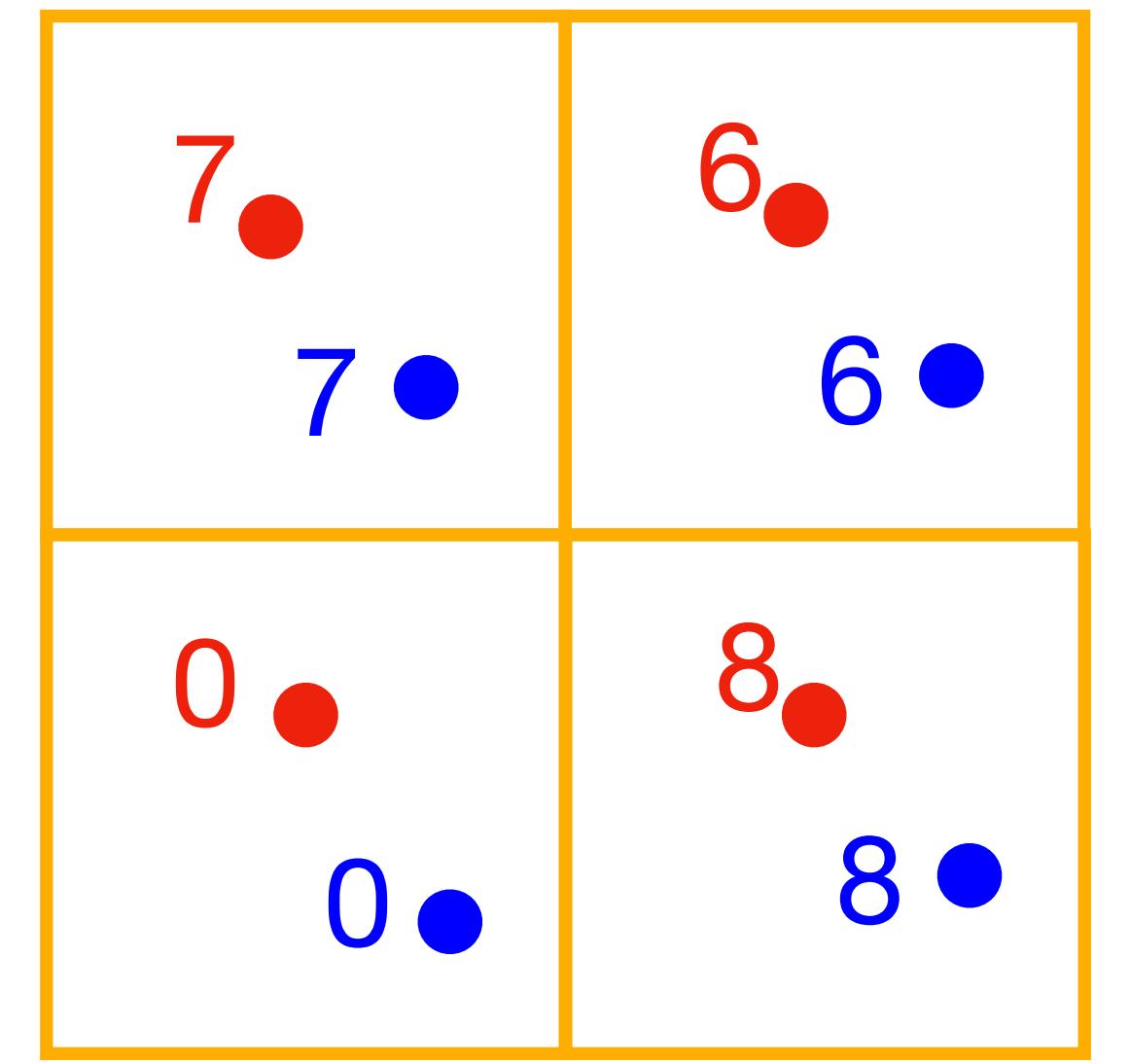


$cov(-)$ 

latent state

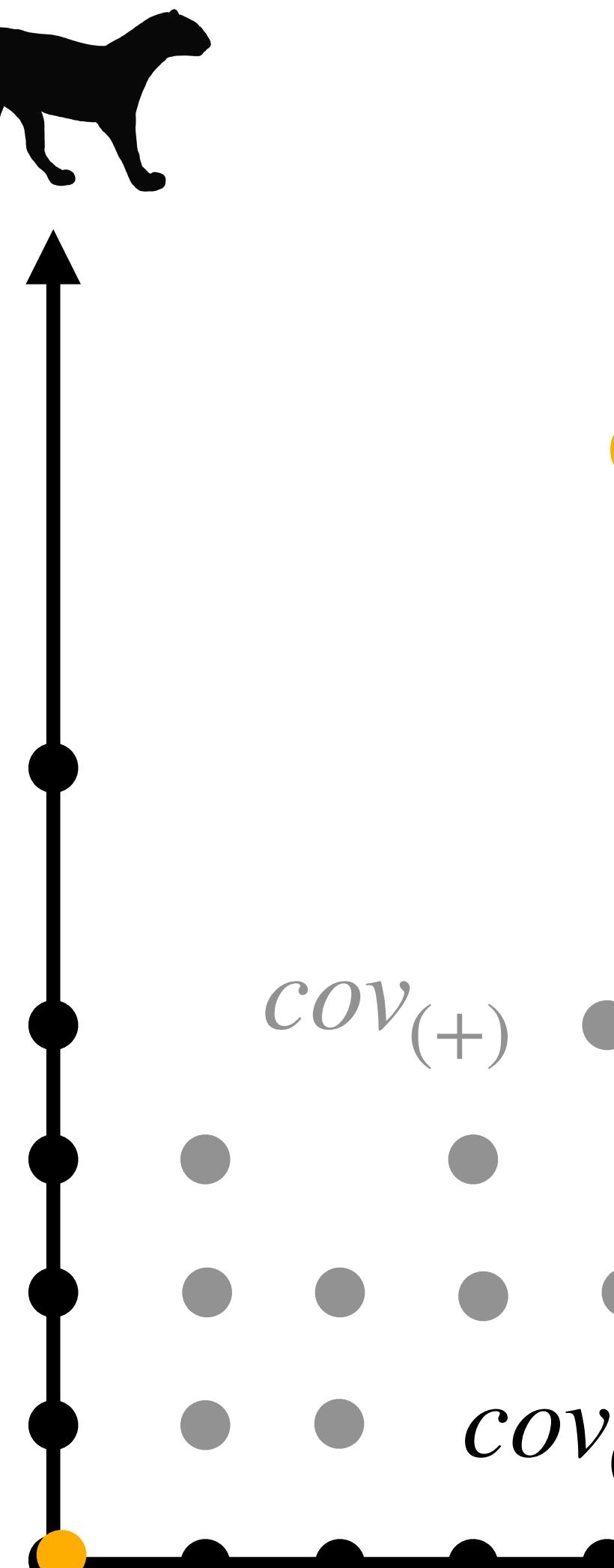
 $cov(+)$ 

data

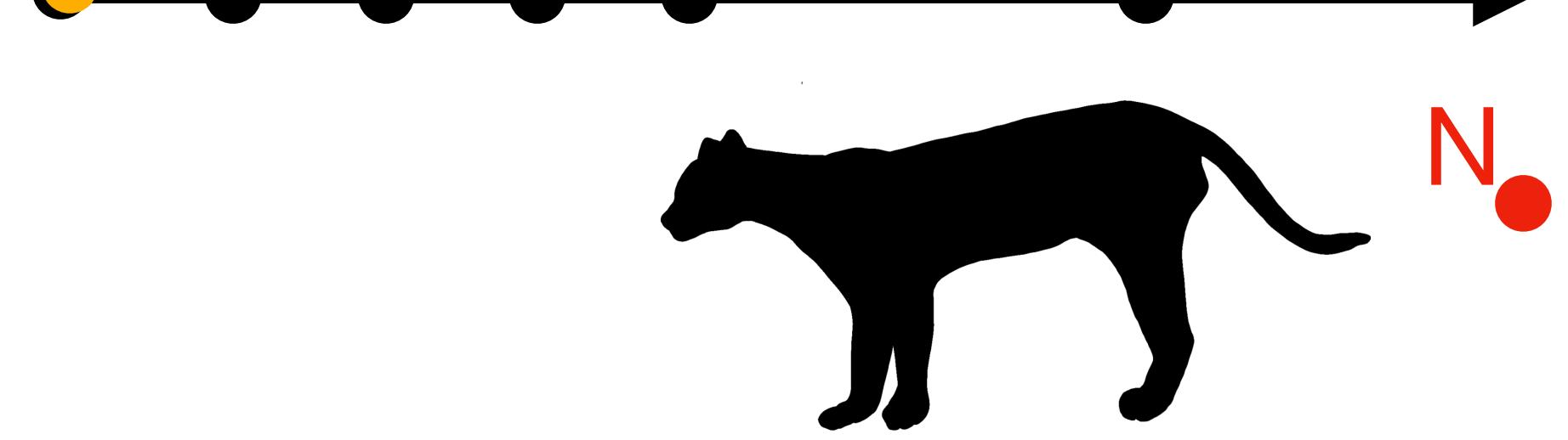


N

data

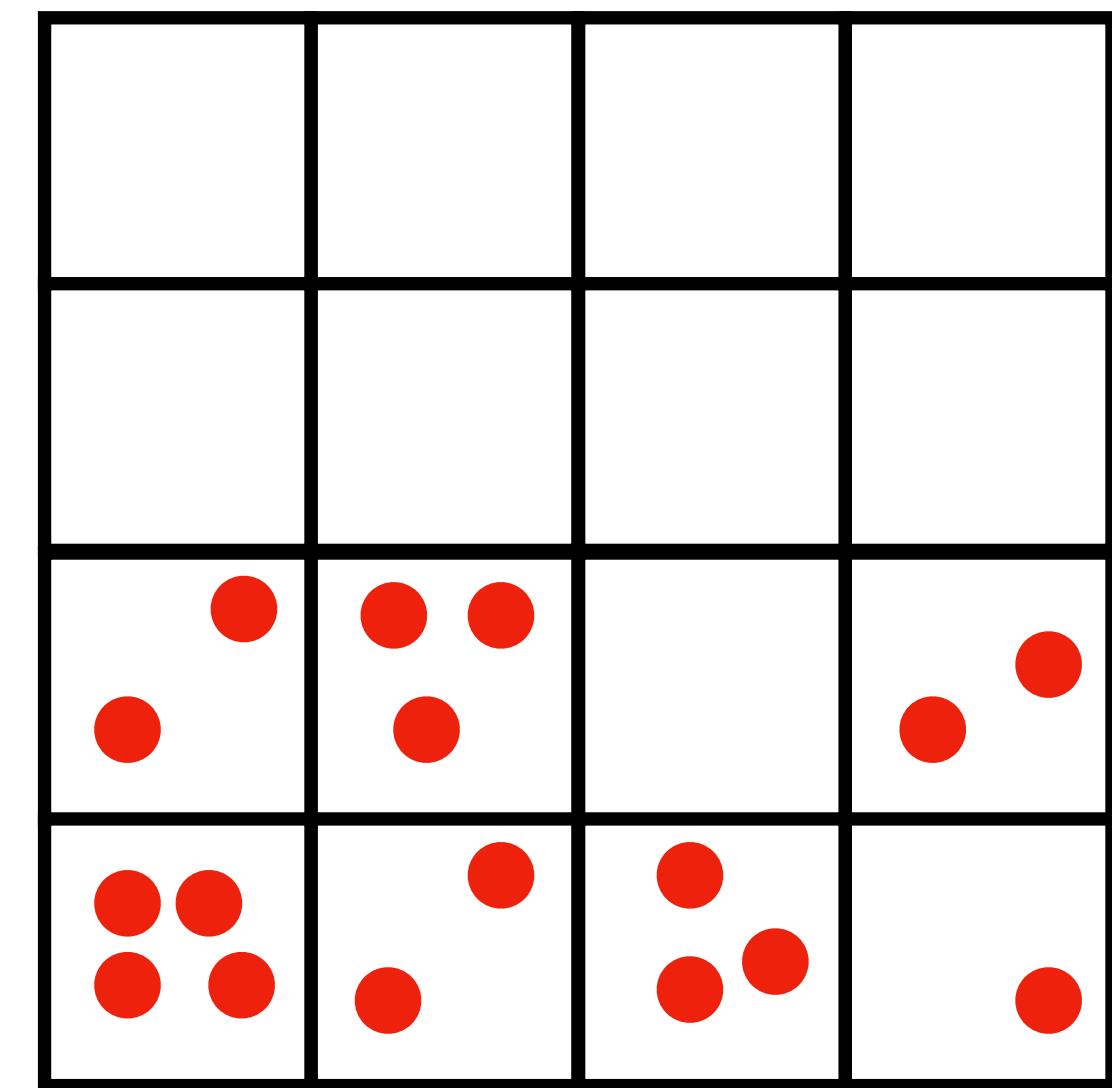
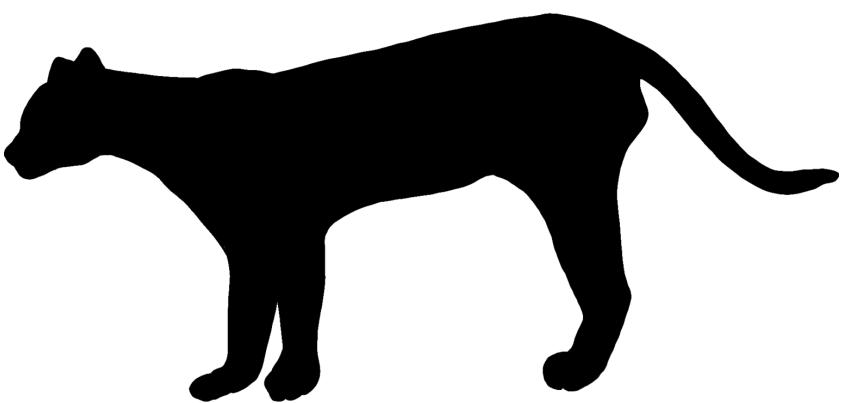
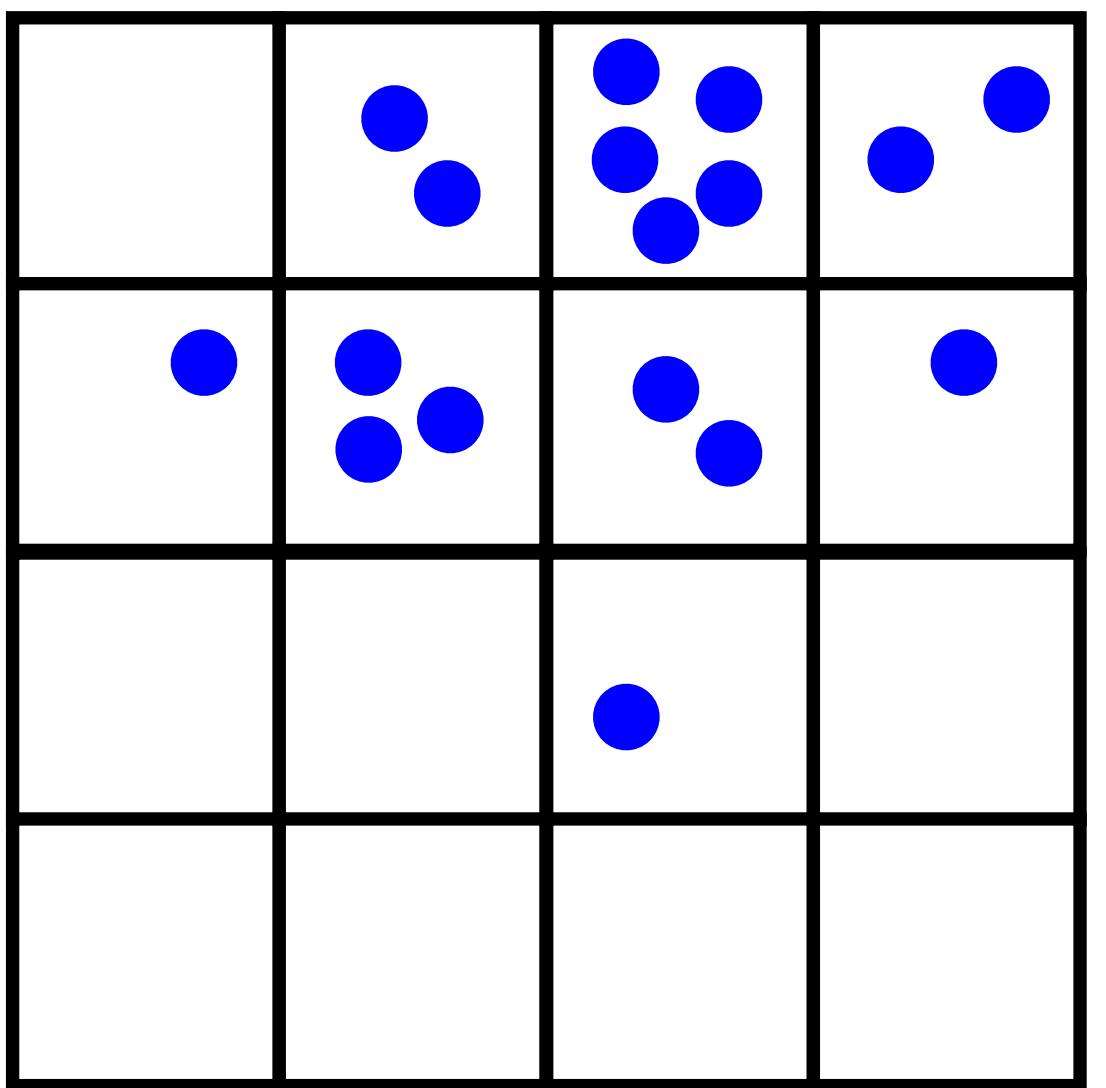
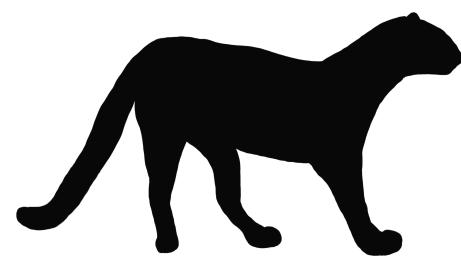
 $cov(+)$ 

latent state

 $cov(-)$ 

Discussion

The effect of similar vs opposite niche



Take-home messages

IJSDMs

1

It's not possible to get the fine-grain species associations from coarse-grain data using IJSDMs.

2

Perhaps by including some fine-scale data in the IJSDM, the model can correct itself by borrowing information.

¡Gracias!



Czech University
of Life Sciences Prague



MOBI
Lab



BEAST
Project

**Thanks to my co-authors: Gurutzeta Guillera-Arroita,
José Lahoz-Monfort, and Petr Keil**

Acknowledgements

Thanks to Gabriel Ortega Solís for helping with the MOBI Lab server.

Funding

European Research Council. Grant Number: 101044740

Credits

Photos jaguraundi (*Herpailurus yagouaroundi*) by hhulsberg (CC-BY-NC) and ocelot (*Leopardus pardalis*) by quiltedquetzal (CC-BY-NC) via iNaturalist. Silhouettes by Gabriela Palomo-Muñoz (CC BY-NC) and Margot Michaud (CC0), via PhyloPic.



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