International Statistical Ecology Conference 2024

The scale-dependency of ~~biotic interactions~~ species associations

in the eyes of integrated species distribution models

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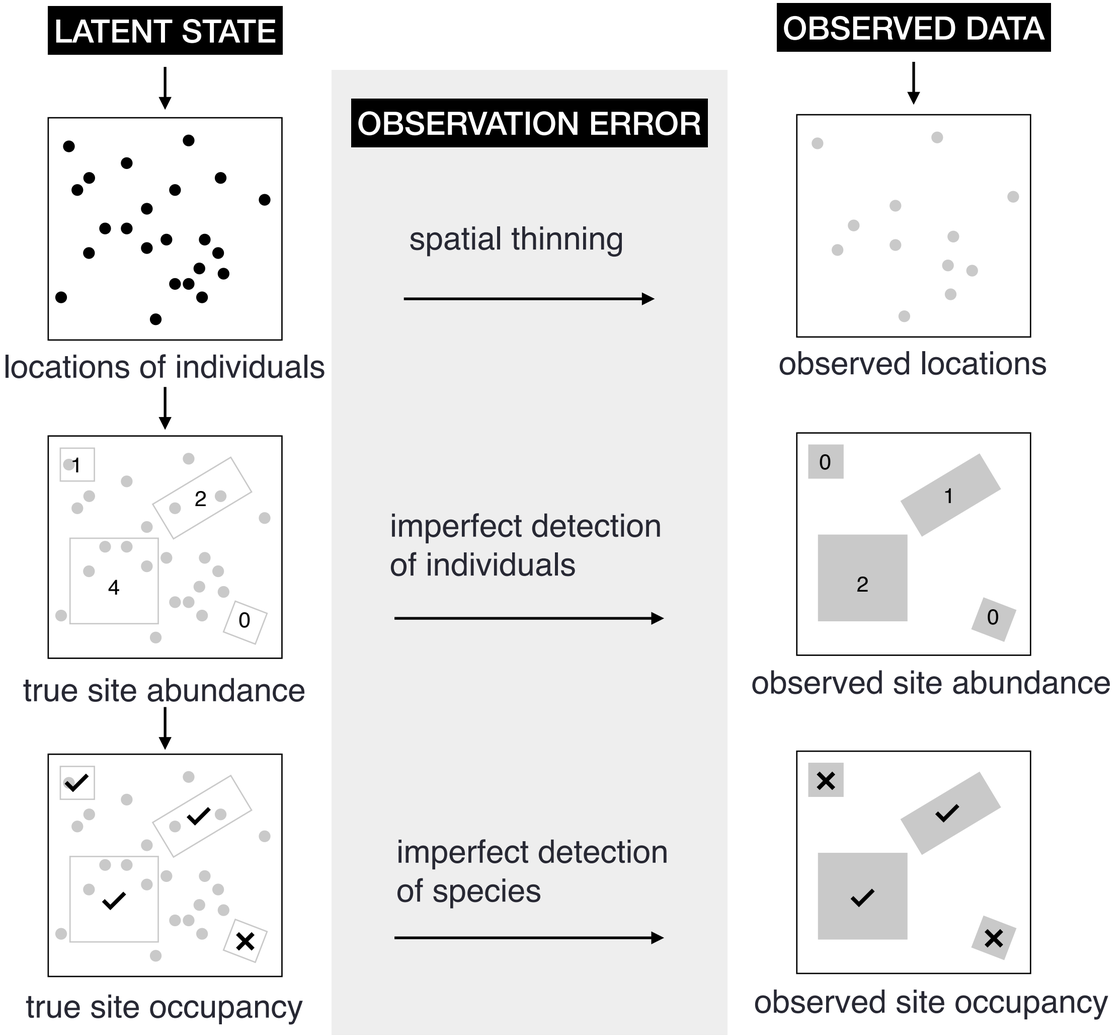
Integrated species distribution model

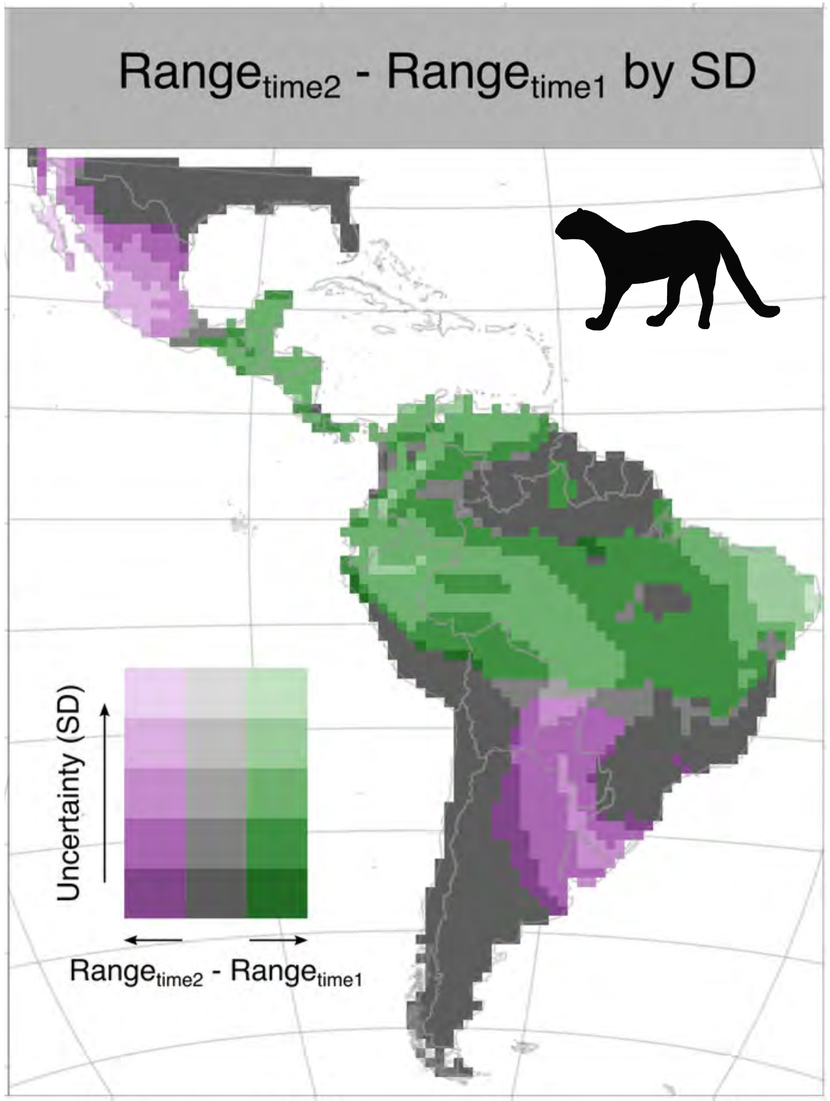
ISDM

- Multiple data sources at multiple scales



Isaac et al. (2020)

jaguarundi (*Herpailurus yagouaroundi*)

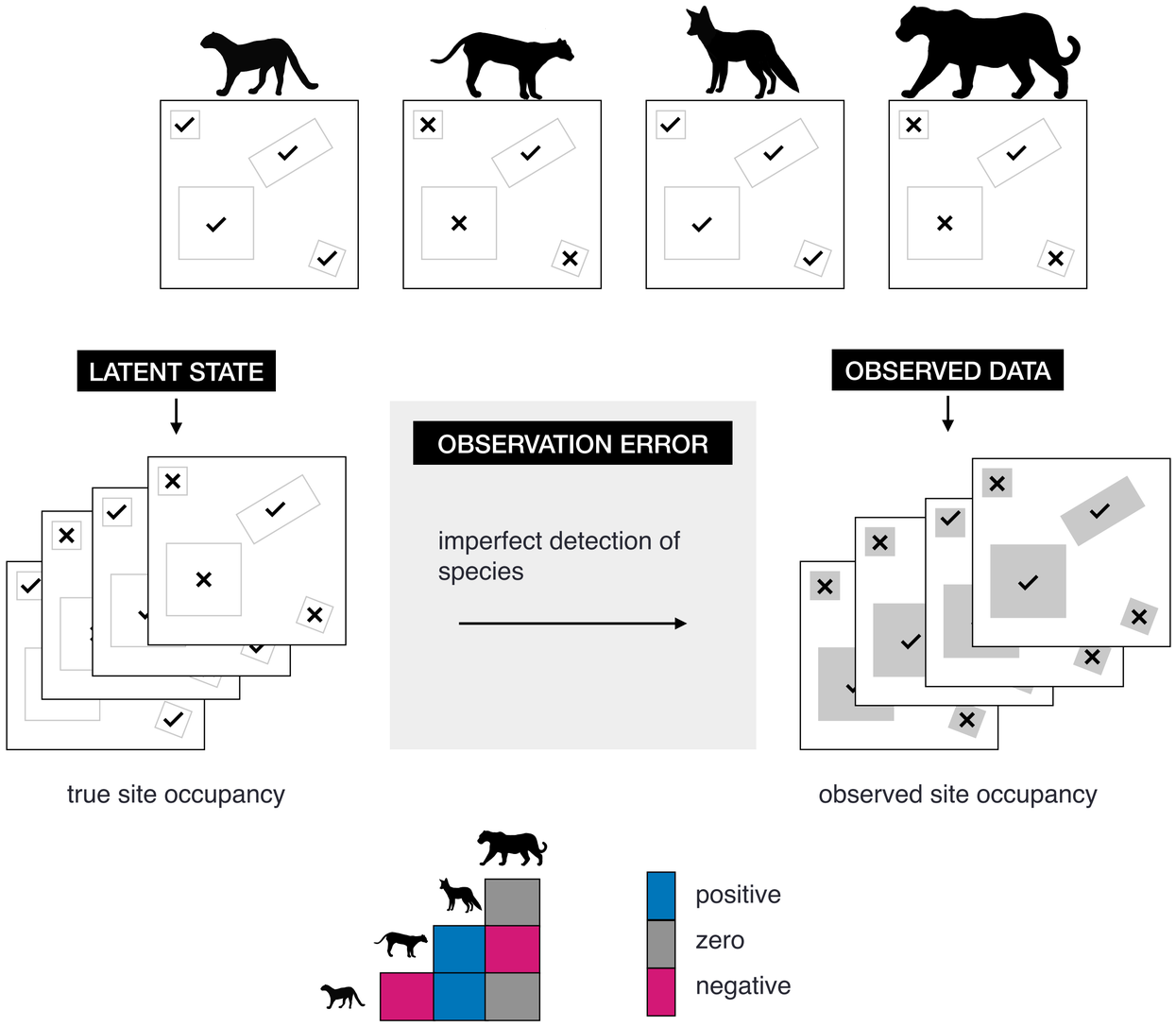


Grattarola, Florencia, Diana E. Bowler, and Petr Keil. 2023. 'Integrating Presence-Only and Presence–Absence Data to Model Changes in Species Geographic Ranges: An Example in the Neotropics'. Journal of Biogeography 50(9): 1561–75. doi:10.1111/jbi.14622.

Joint species distribution model

JSDM

- Multiple species (co-occurrence)



Warton et al. (2015)

ELSEVIER

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]

Forum

Ecography 37: 406–415, 2014
doi: 10.1111/j.1600-0587.2013.00643.x

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 Tuanmu[4], Sara Zonneveld[3,5], Sydne Record[2,6], Angela Strecker[7] and Lydia Beaudrot[8]

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
BRITISH ECOLOGICAL SOCIETY

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

Heidi K. Mod[1,2] | Mathieu Chevalier[1] | Miska Luoto[2] | Antoine Guisan[1,3]

RESEARCH ARTICLE

Journal of Biogeography
WILEY

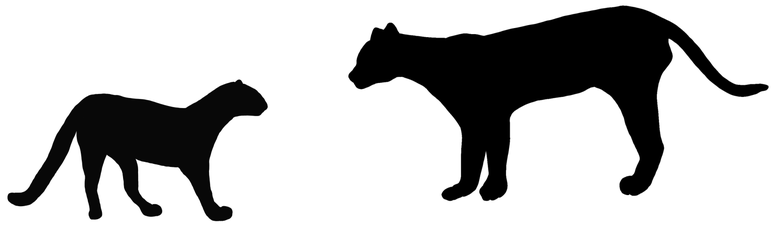
Species associations in joint species distribution models: from missing variables to conditional predictions

Clément Vallé[1] | Giovanni Poggiato[2,3] | Wilfried Thuiller[2] | Frédéric Jiguet[1] | Karine Princé[1] | Isabelle Le Viol[1,4]

Our goal

ISDM + JSDM

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



Methods

Methods

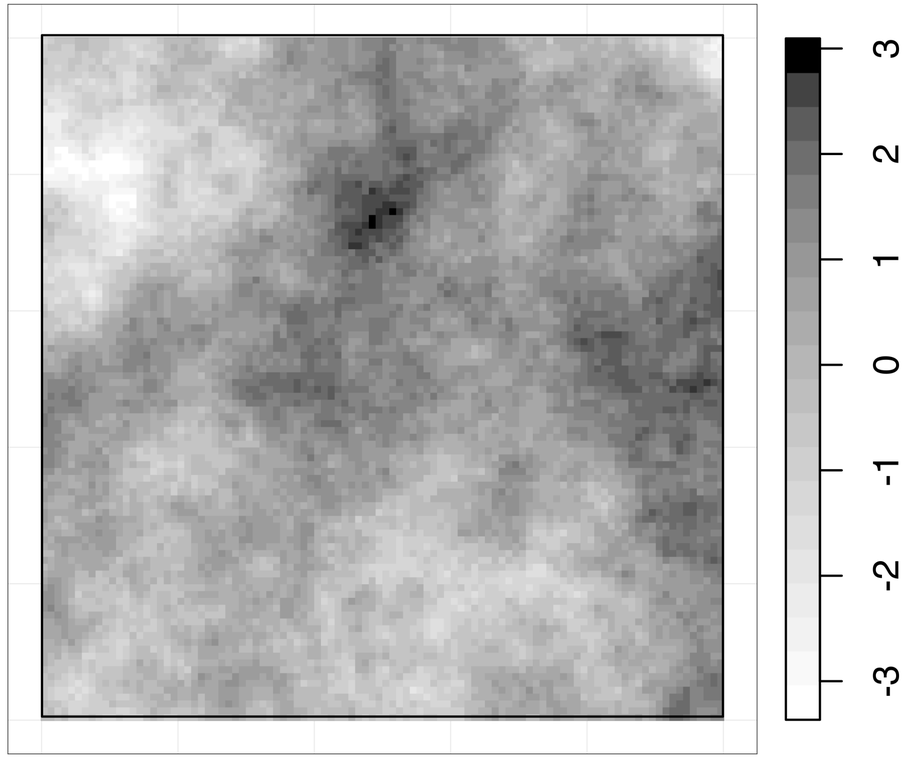
1. Data simulation:
    A. Environmental predictor
    B. Species data
2. Fit an IJSDM
3. Check the identifiability and coverage of model parameters

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).

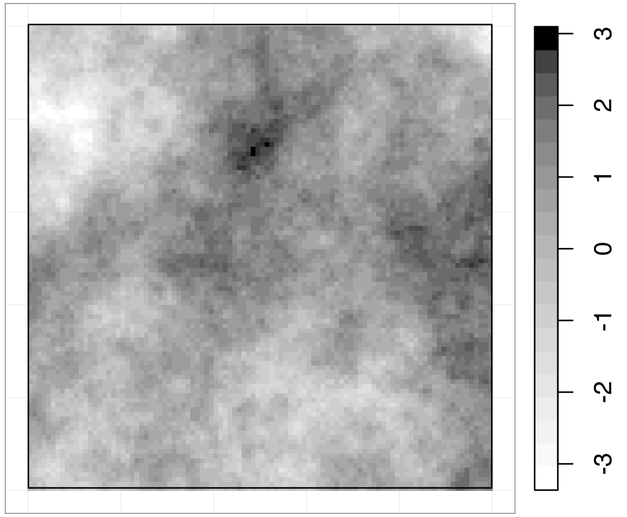
Note: We used the same raster for all simulations



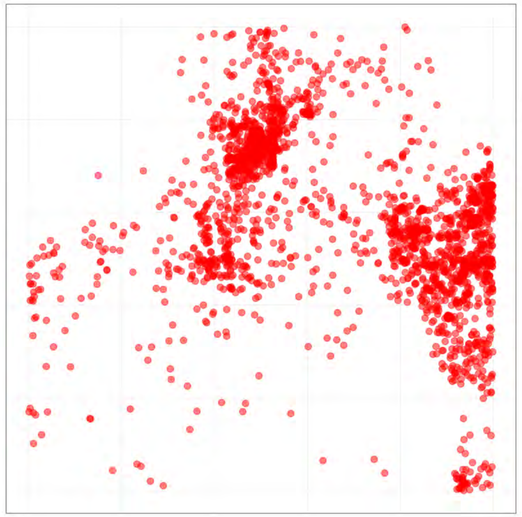
Data simulations

Species data

temperature



point pattern of species$_1$



$\alpha_1 = 5$
$\beta_1 = 2.5$
$cov_1 = 0.9$

Point pattern

$$\lambda_1 = exp^{(\alpha_1 + \beta_1 \times temp + e_1)}$$
$$\lambda_2 = exp^{(\alpha_2 + \beta_2 \times temp + e_2)}$$

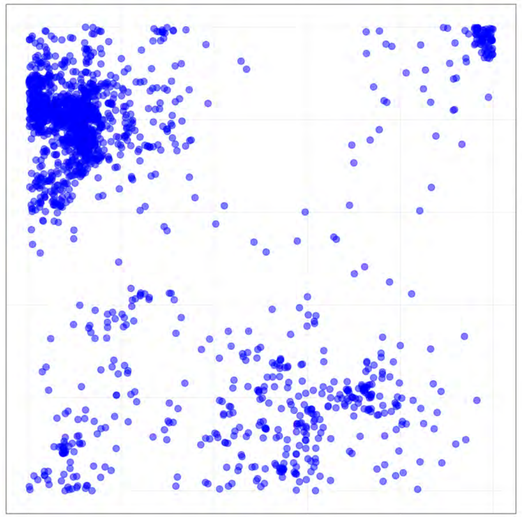
Correlated error

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

covariance (degree of species association)

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

point pattern of species$_2$

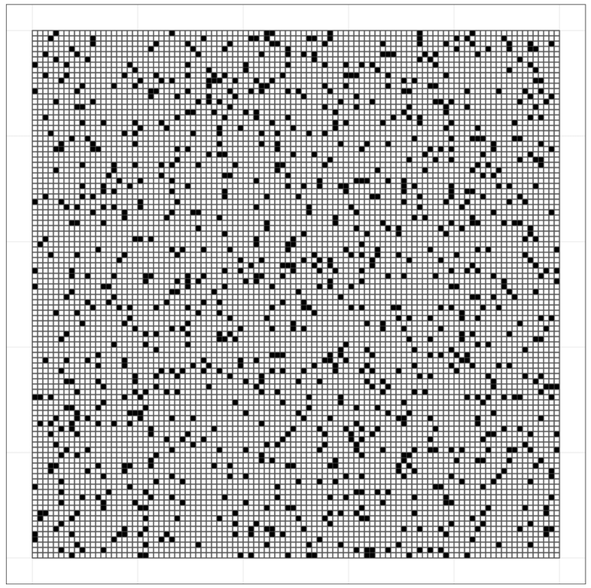


$\alpha_2 = 5$
$\beta_2 = -2$
$cov_2 = 0.9$

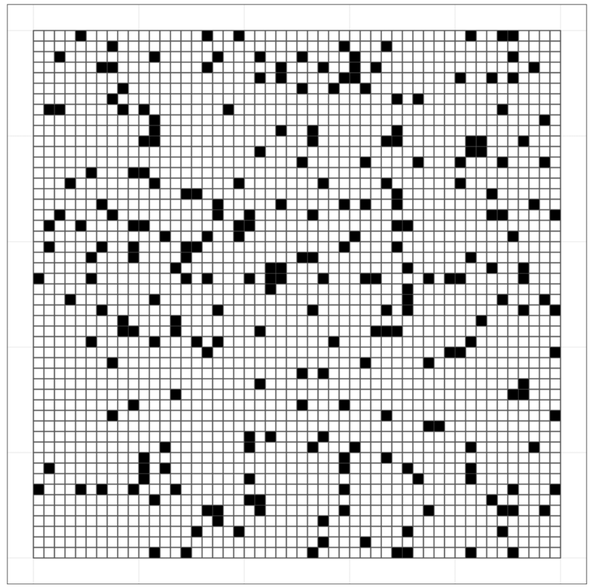
Data simulations

Sampling sites of varying grain size

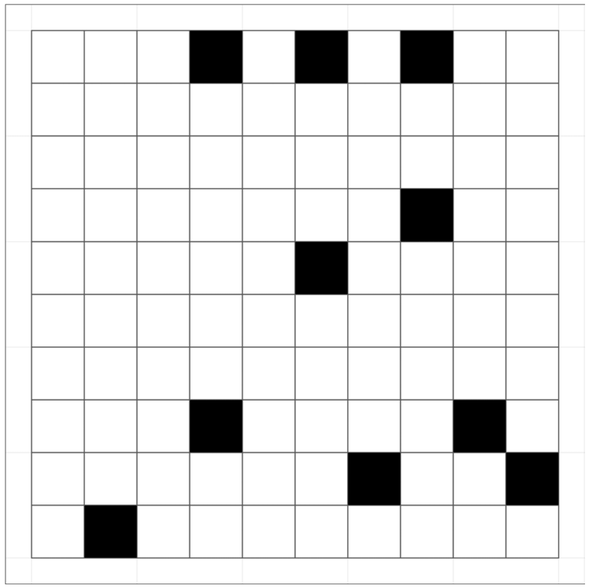
sampling sites at
100x100 grain



sampling sites at
50x50 grain



sampling sites at
10x10 grain



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

IJSDM

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

area of each grid cell

$$log(\phi_{i,1}) = \alpha_1 + \beta_1 \times temp_i + e_{i,1} + log(area_i)$$
$$log(\phi_{i,2}) = \alpha_2 + \beta_2 \times temp_i + e_{i,2} + log(area_i)$$

$$e_{i,j} \sim \text{MVN}(0, \tau)$$

$$\tau = \Sigma^{-1}$$

Based on ideas from Bowler et al. (2019), Grattarola et al. (2023), and Pollock et al. (2014)

IJSDM

Presence-absence

OBSERVED DATA

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

sites, i, where $i \in 1 : n_i$

species, j, where $j \in 1 : n_j$

LATENT STATE

area of each grid cell

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

$$e_{i,j} \sim \text{MVN}(0, \tau)$$

$$\tau = \Sigma^{-1}$$

Based on ideas from Bowler et al. (2019), Grattarola et al. (2023), and Pollock et al. (2014)

Methods

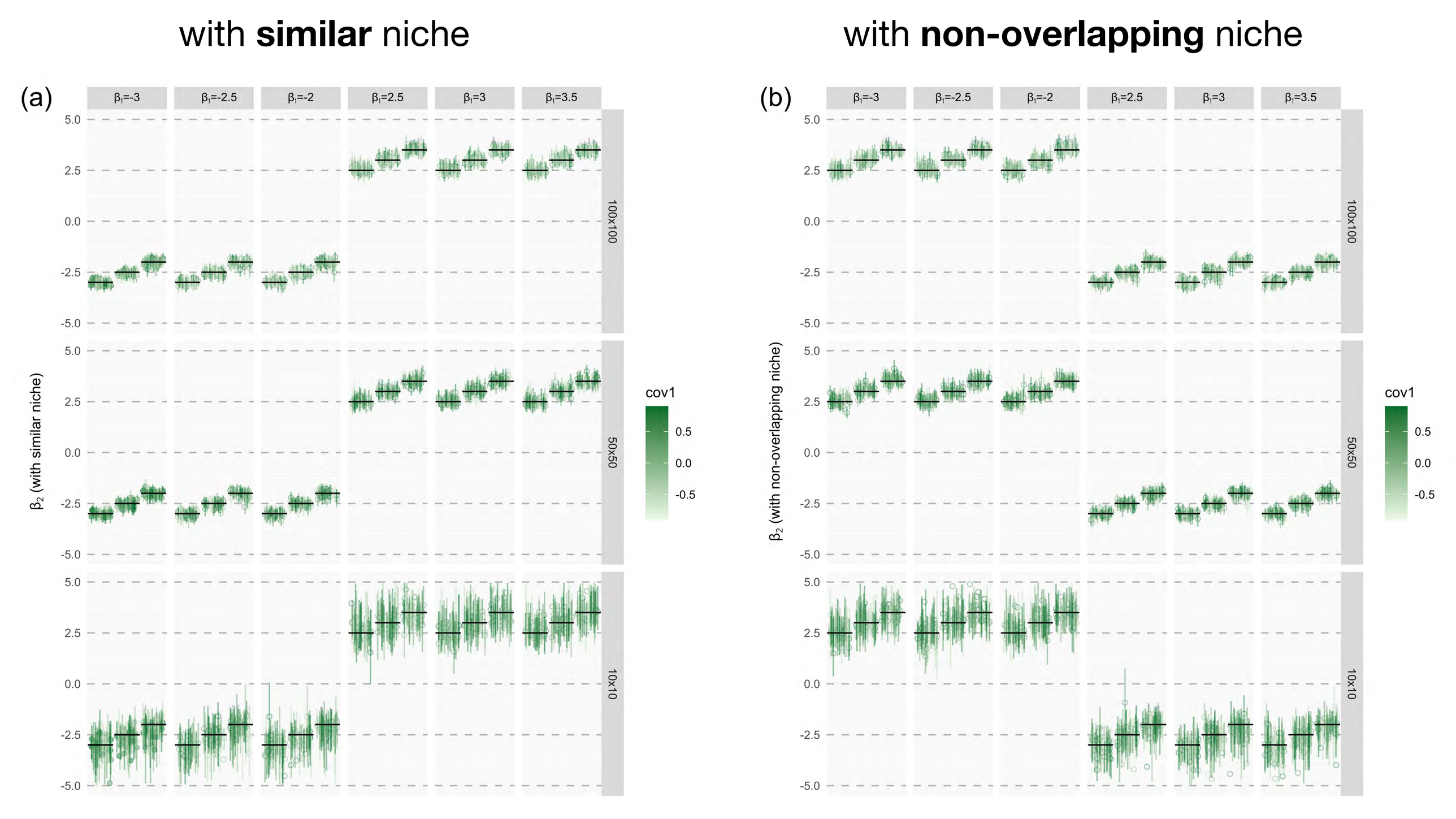
Data simulations: parameter set

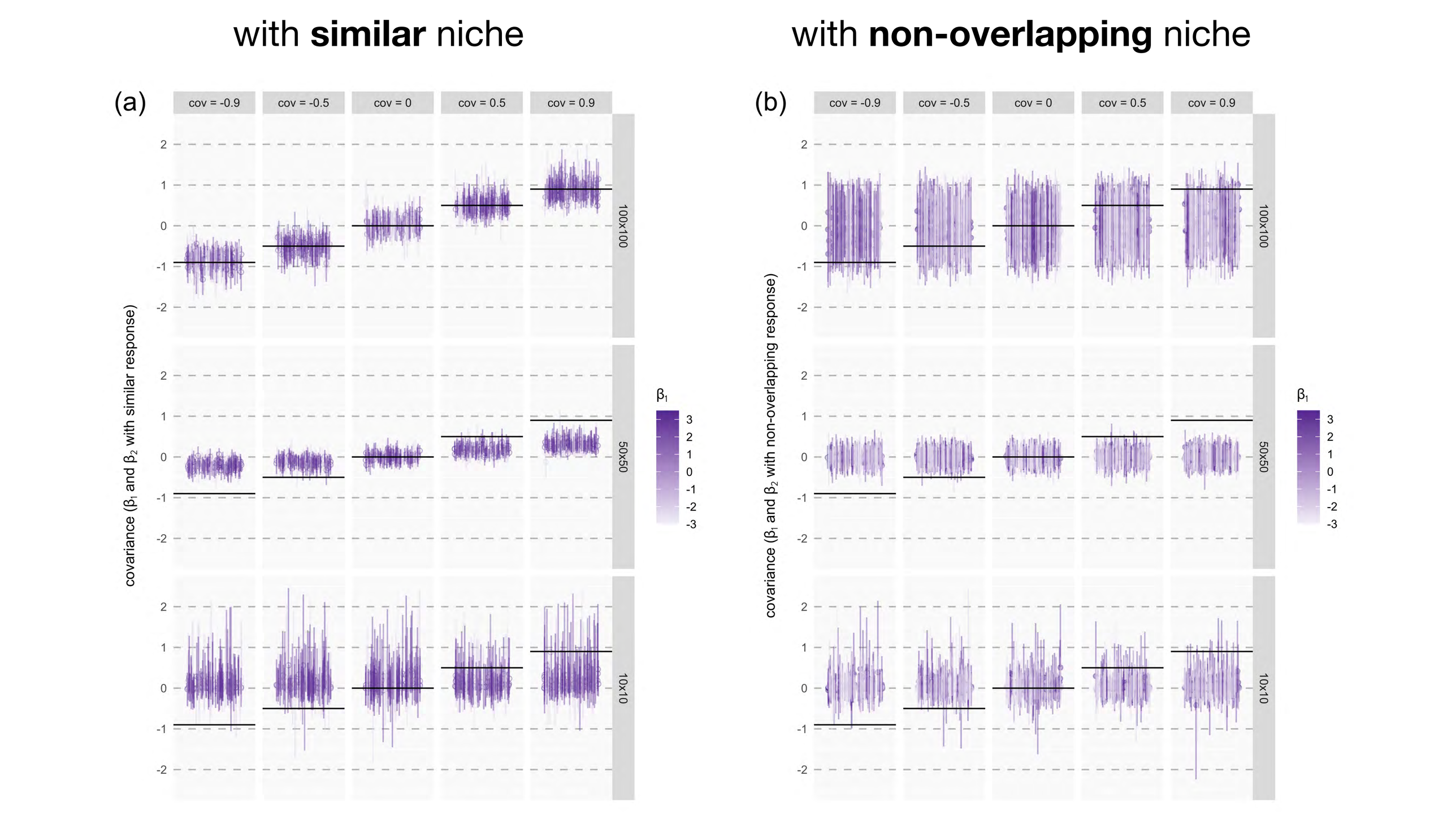
540 combinations repeated 10x, resulting in 5,400 simulation runs

Parameter	Description	Values in the simulation
α	Intercept (always $\alpha_1 = \alpha_2$)	5 (fixed)
1 β_1 and β_2	The species-specific effect (slope) of the environmental predictor driving the point process intensity	-3, -2.5, -2, 2.5, 3, 3.5
var	Residual variance (with $var_1 = var_2$)	1 (fixed)
2 *cov*	Residual covariance (with $cov_{1,2} = cov_{2,1}$) representing species association	-0.9, -0.5, 0, 0.5, 0.9
3 *grid*	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


with **similar** niche
with **non-overlapping** niche
(a)
(b)
β_1=-3
β_1=-2.5
β_1=-2
β_1=2.5
β_1=3
β_1=3.5
100x100
50x50
10x10
5.0
2.5
0.0
-2.5
-5.0
β_2 (with similar niche)
β_2 (with non-overlapping niche)
cov1
0.5
0.0
-0.5


with **similar** niche
with **non-overlapping** niche
(a)
(b)
cov = -0.9
cov = -0.5
cov = 0
cov = 0.5
cov = 0.9
100x100
50x50
10x10
covariance (β_1 and β_2 with similar response)
covariance (β_1 and β_2 with non-overlapping response)
β_1
3
2
1
0
-1
-2
-3

Discussion

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Discussion

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

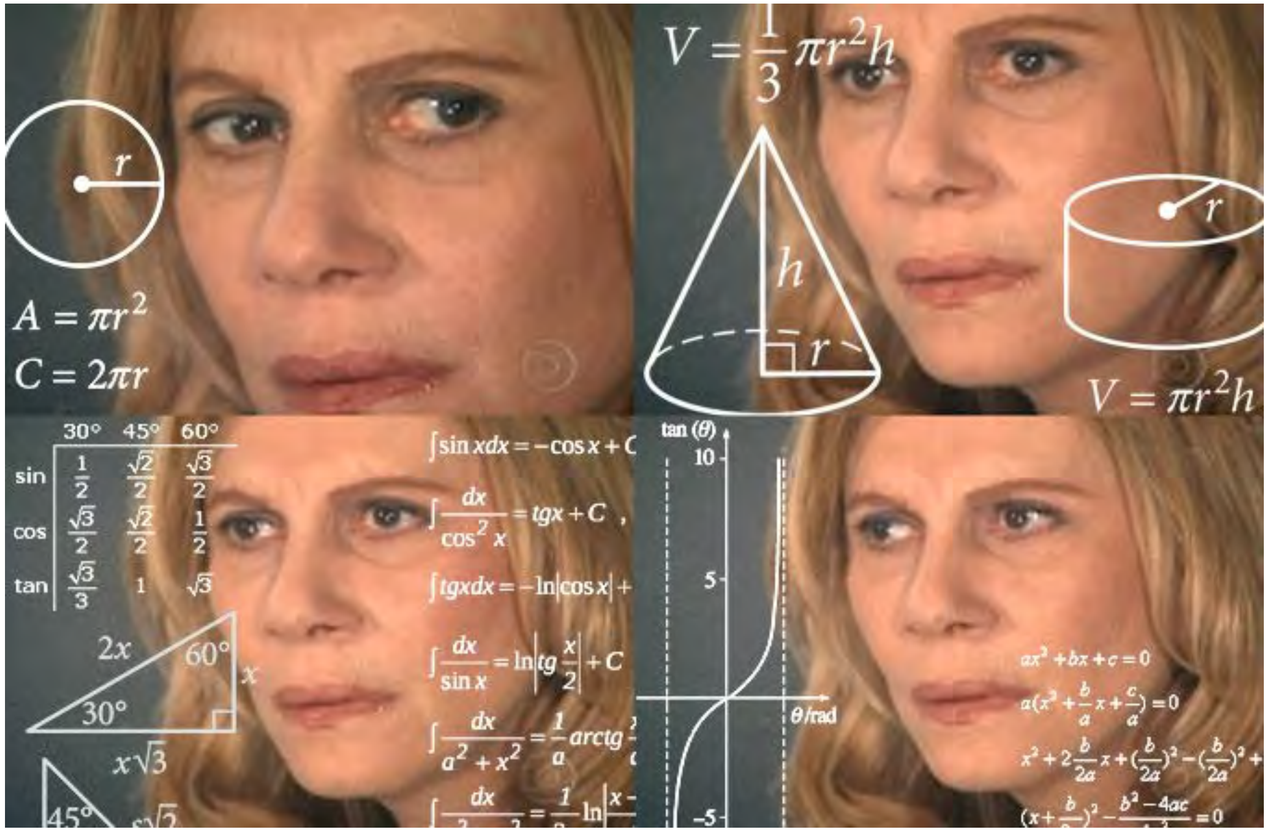
The correct species associations can **only** be detected using:

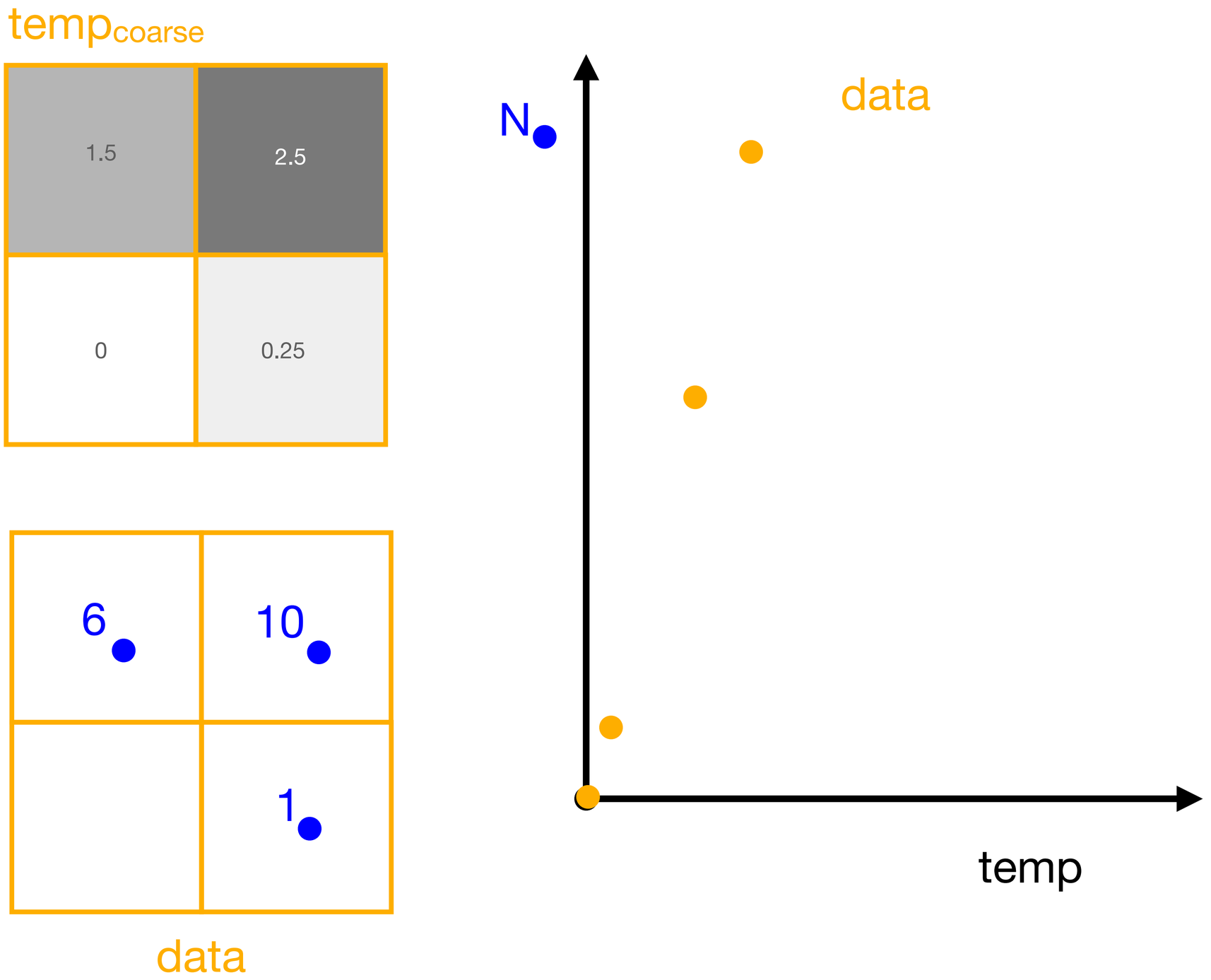
1. fine-grain data (at the grain of the simulated interaction) and
2. when both species respond similarly to the environment.

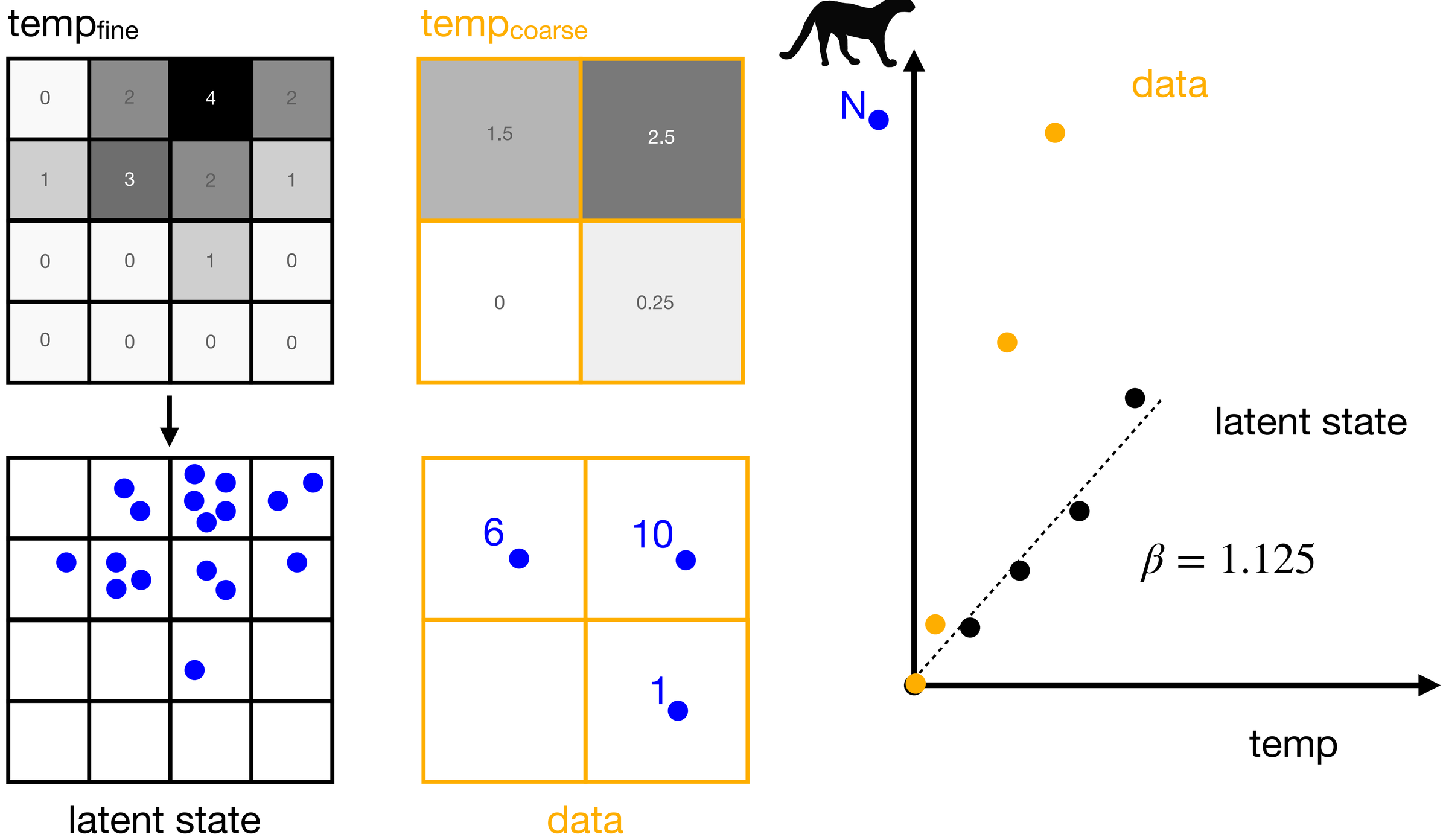
Thus, running the IJSDM with data sources at coarse resolutions can provide incorrect estimates of the species' associations.

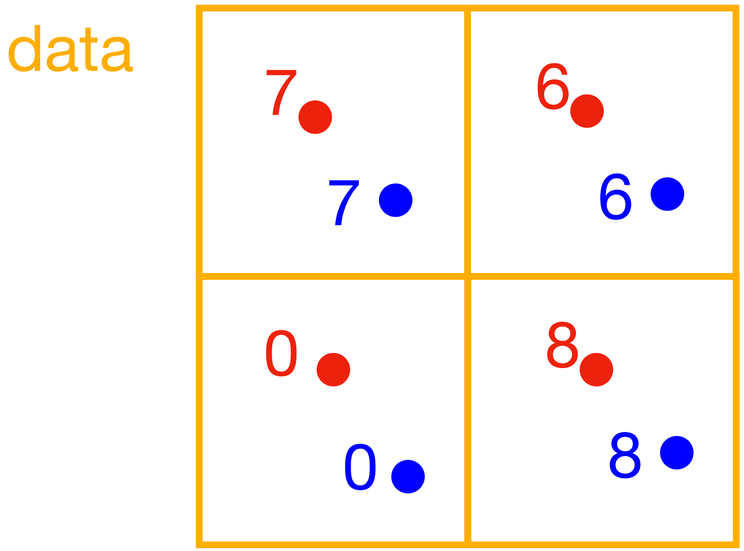
Discussion

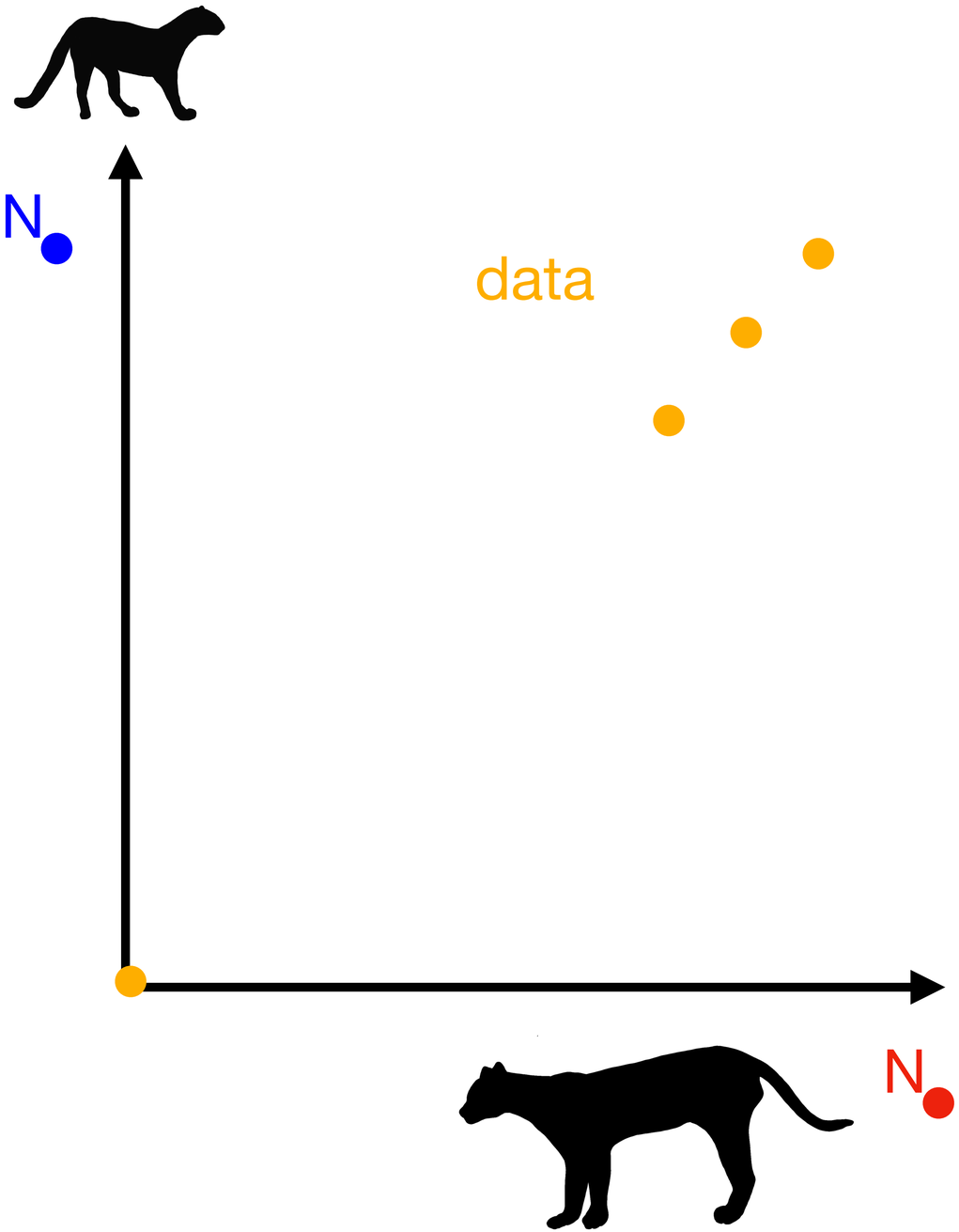
Why does the association disappear towards coarse grains?

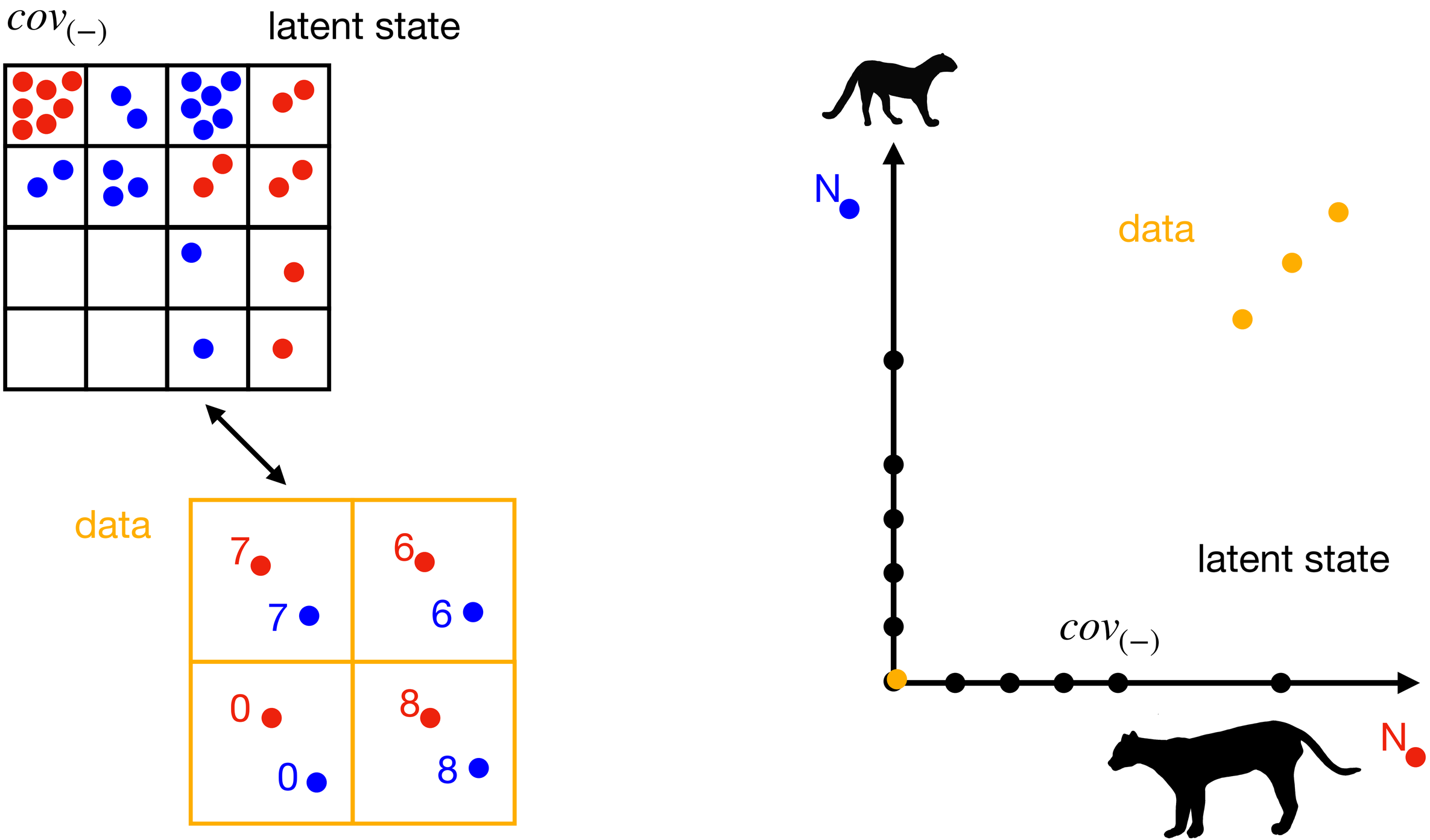


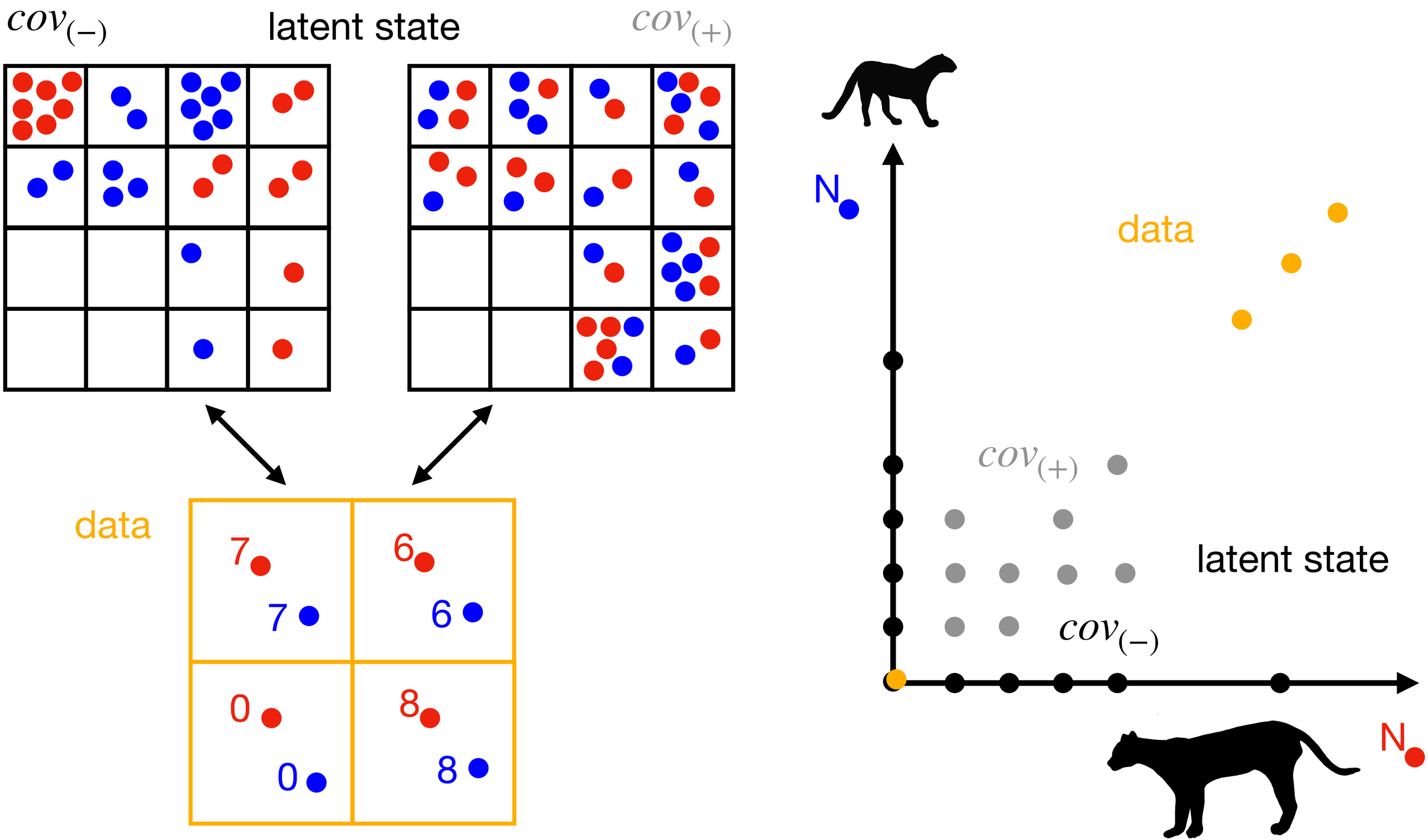

temp coarse
1.5
2.5
0
0.25
6
10
1
data
N
data
temp


temp_fine
0 2 4 2
1 3 2 1
0 0 1 0
0 0 0 0
latent state
temp_coarse
1.5 2.5
0 0.25
6 10
1
data
N
data
latent state
$\beta = 1.125$
temp


data
7
7
6
6
0
0
8
8

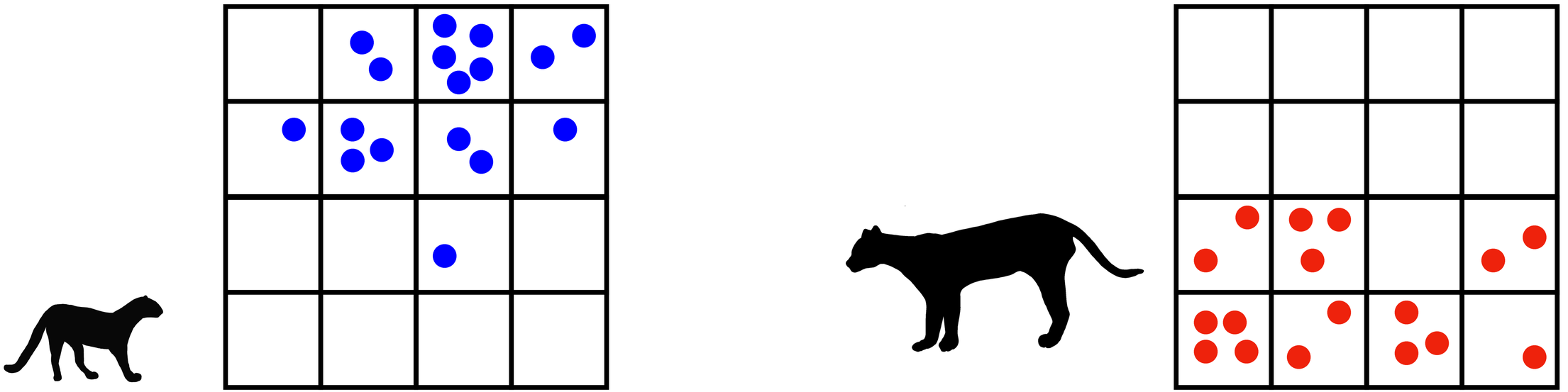

N
data
N


$cov_{(-)}$
latent state
data
7
7
6
6
0
0
8
8
N
data
latent state
$cov_{(-)}$
N


$cov_{(-)}$
latent state
$cov_{(+)}$
data
7
7
6
6
0
0
8
8
N
data
$cov_{(+)}$
latent state
$cov_{(-)}$
N

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.

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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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European Research Council
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