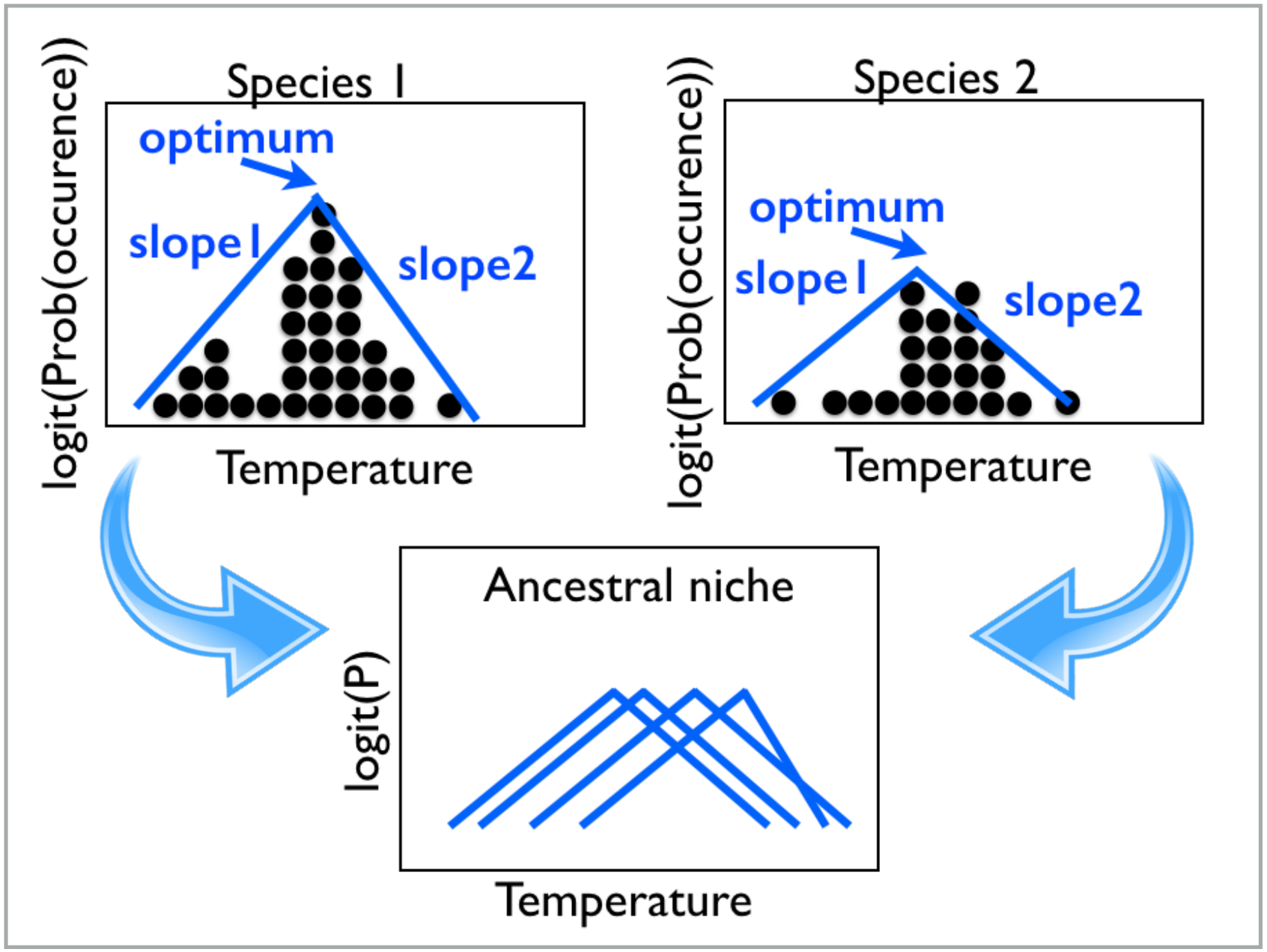
Putting Evolution Into Ecological Niche Modelling: Background and Paths Forward



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Evolution 2016
Sunday, June 19, 8:15 - 11:45 am, Ballroom C

Thanks for support from:

SSB Symposium: Putting Evolution Into Ecological Niche Modelling

1. **Nick Matzke —** Introduction to Symposium; and phyloSDM with joint Bayesian estimation
2. **Dan Warren —** Incorporating evolutionary information into niche and distribution models: learning to love terrible SDMs
3. **Erin Saupe —** A Tale Of Two Sisters: Ecological & Evolutionary Divergence In Geminate Species Pairs
4. **Kaitlin Maguire —** The fossil record and projecting species distribution models through time
5. **Jenny McGuire —** Evolution and epigenetics: unraveling error in niche models
6. **COFFEE BREAK**
7. **Renee Catullo —** Extending spatial modelling of climate change responses beyond the realized niche: estimating, and accommodating, physiological limits and adaptive evolution
8. **Matt Van Dam —** Environmental Niche Trackers and Nice Adapters Revealed Through Fine Scale Phenological Niche Modeling
9. **Dan Rosauer —** Distribution models for intraspecific lineages – which method is best?
10. **Laura Pollock —** Protecting evolutionary history into the future
11. **All presenters —** Panel discussion and further questions

<u>Outline</u>:

1. **Ecological Niche Modelling/ Species Distribution Modelling methods**
   - and common critiques

2. **Phylogenetic Comparative Methods**
   - and common critiques

3. **Phylogenetic Niche Conservatism methods**
   - and less common critiques

4. **Joint Bayesian modelling: a way forward?**

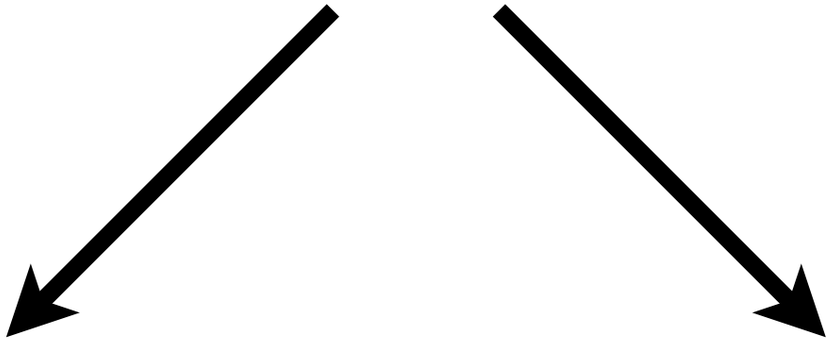
<u>Definitions</u>:

ENM: Ecological Niche Modelling

SDM: Species Distribution Modelling

PCMs: Phylogenetic Comparative Methods

Biogeography:
The geography of life



Ecological biogeography

Historical biogeography

Biogeography:
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Ecological biogeography

- Focus: Environmental controls on distribution
- Ecological interactions
- Timescale: the Recent

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- **Methods revolution: SDM/ENM**

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Historical biogeography

- Focus: Evolutionary history of distributions
- Dispersal/vicariance events
- Timescale: Millions of years

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- **Methods revolution: Phylogenetics, PCMs**

Phylogenetics in the scientific literature

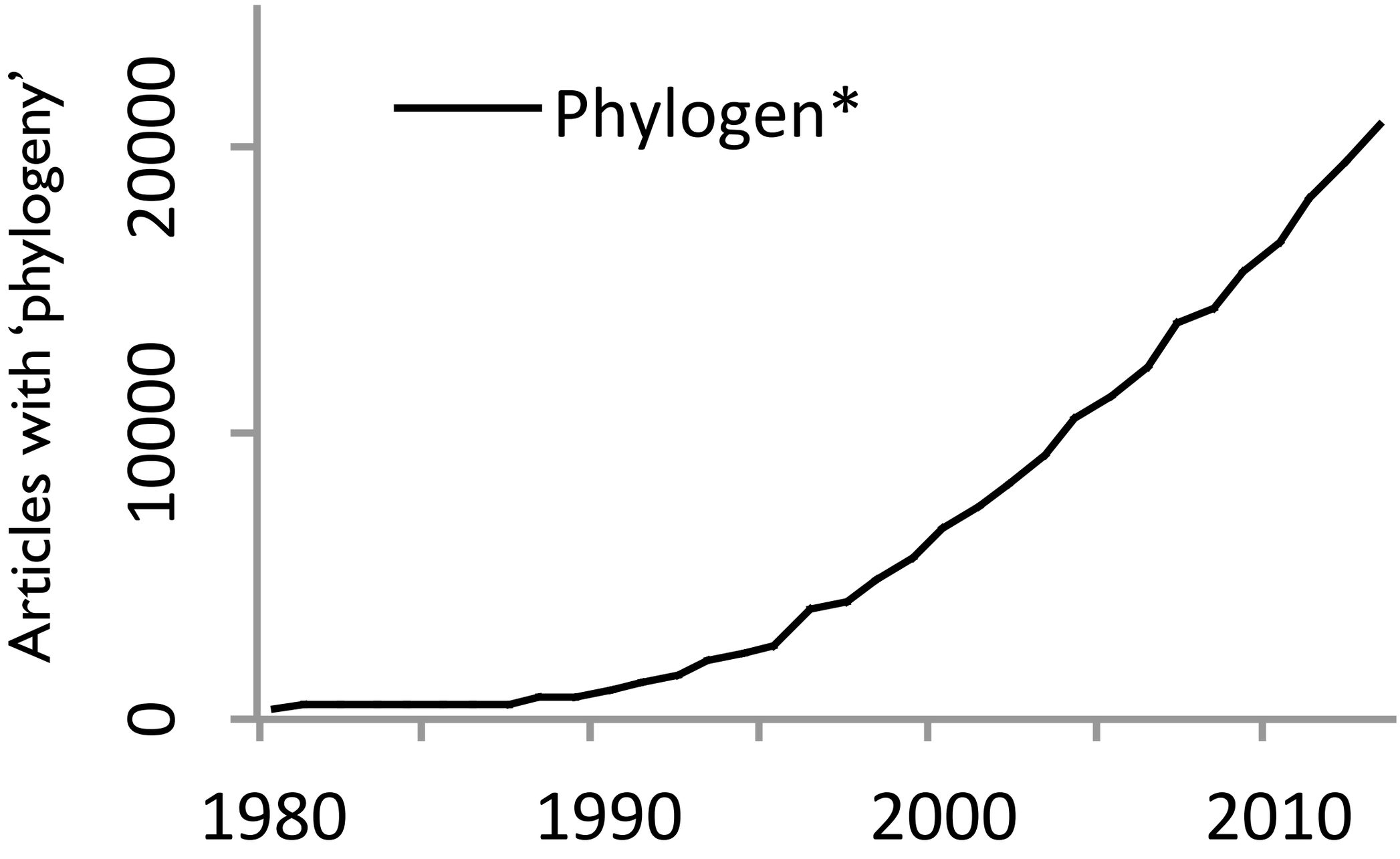
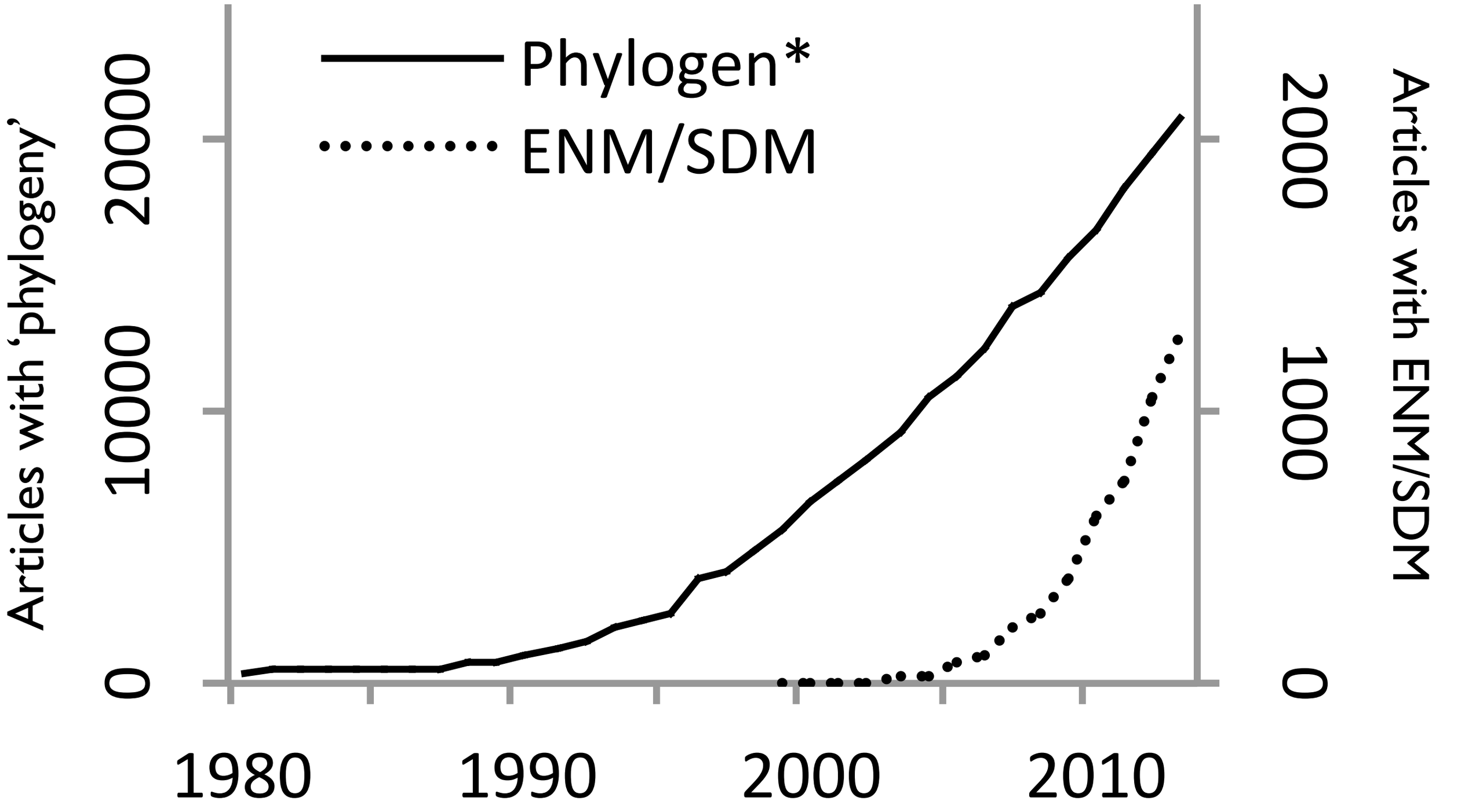


Figure. Growth in phylogenetics studies. By 2013, studies involving phylogenies were ~1% of all published science (David Hillis, pers. comm.).

Data: Scopus search, 2014

ENMs in the scientific literature



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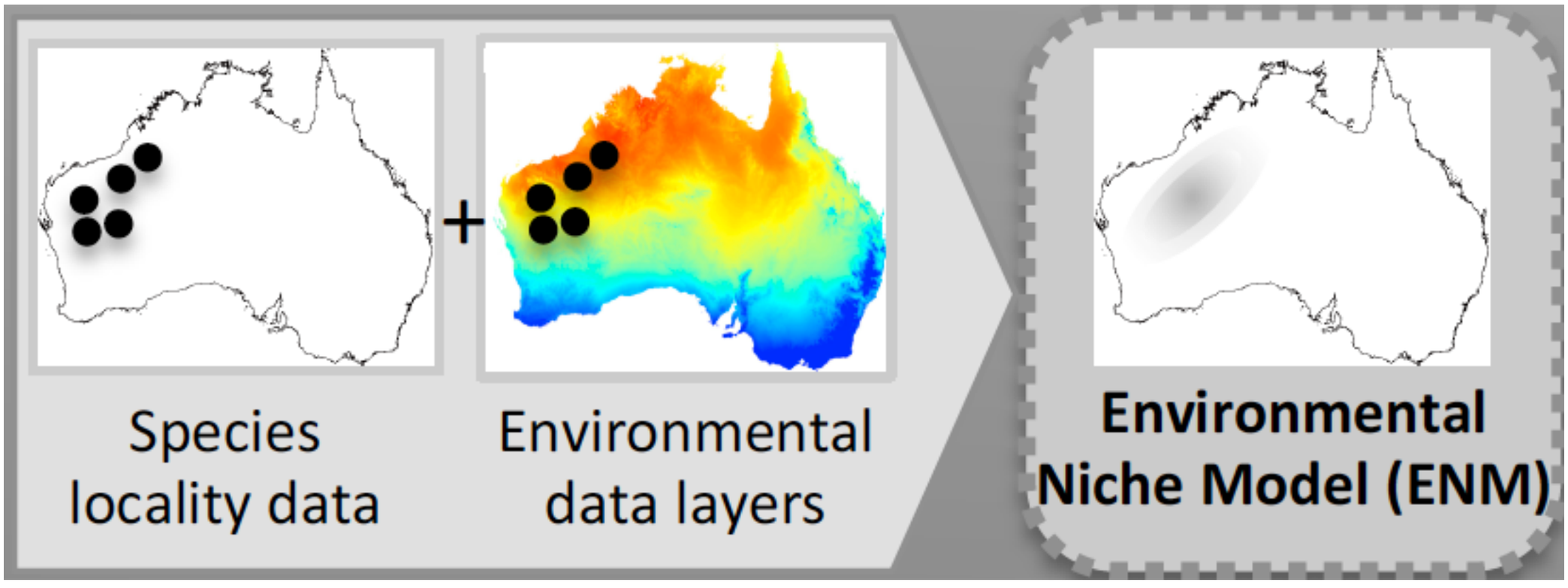
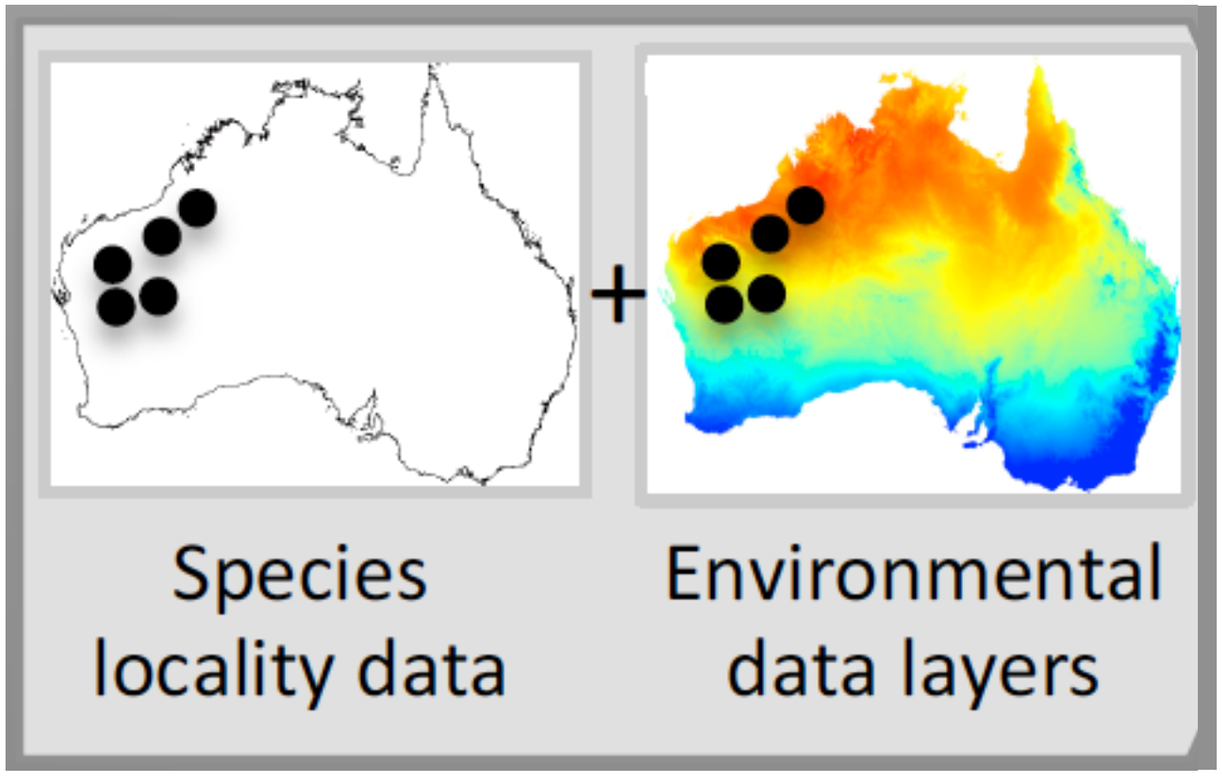
Ecological Niche Modelling (ENM)/ Species Distribution Modelling (SDM):

A brief introduction



Niche modelling: basic procedure



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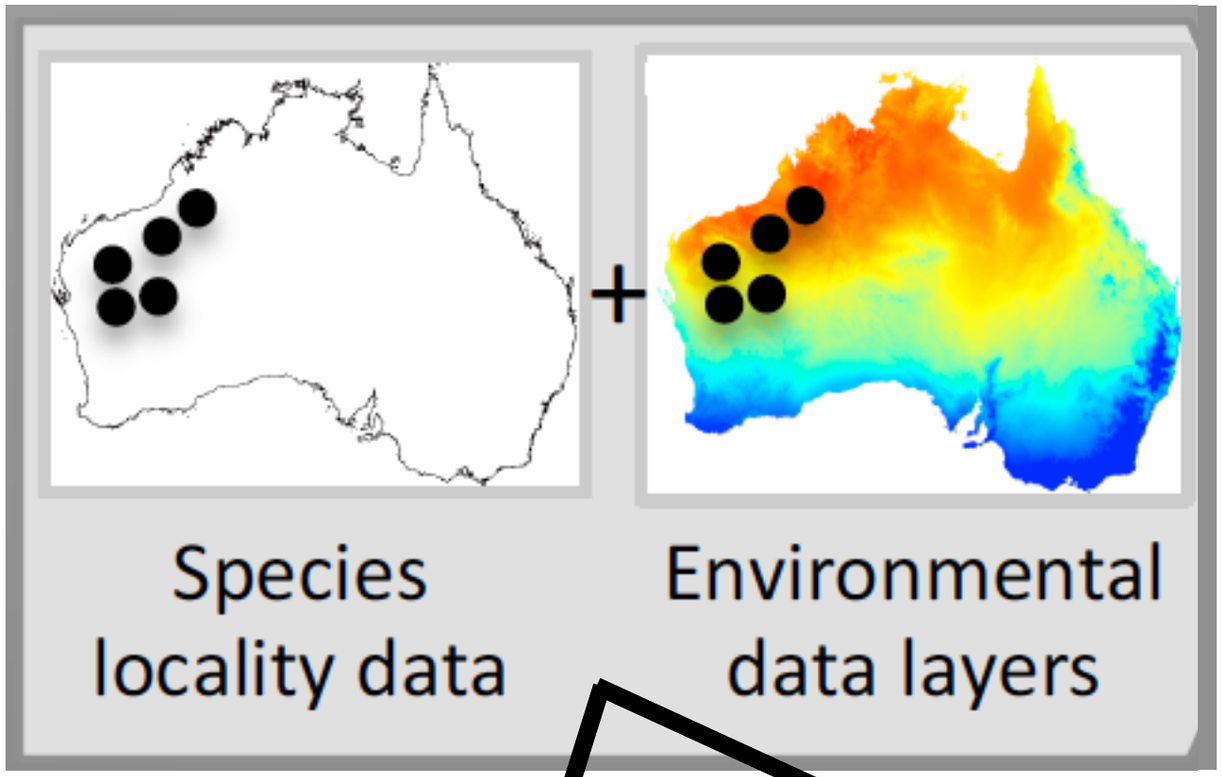

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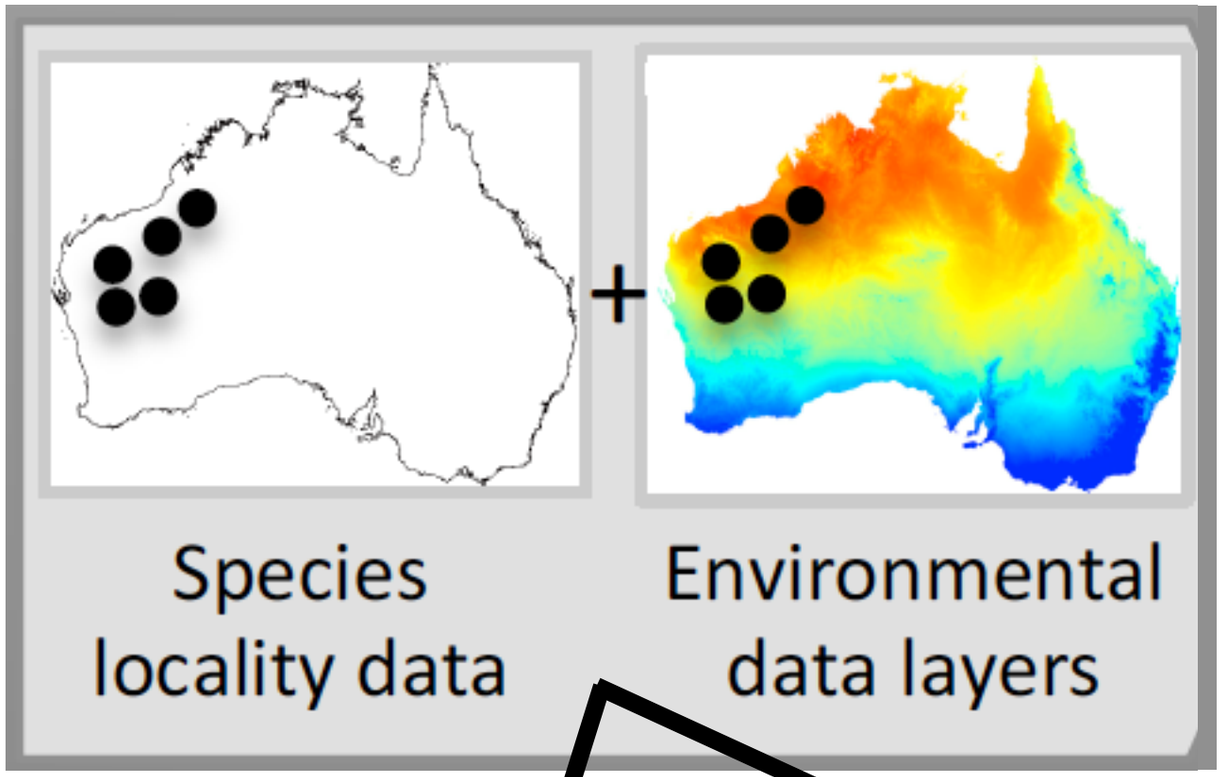

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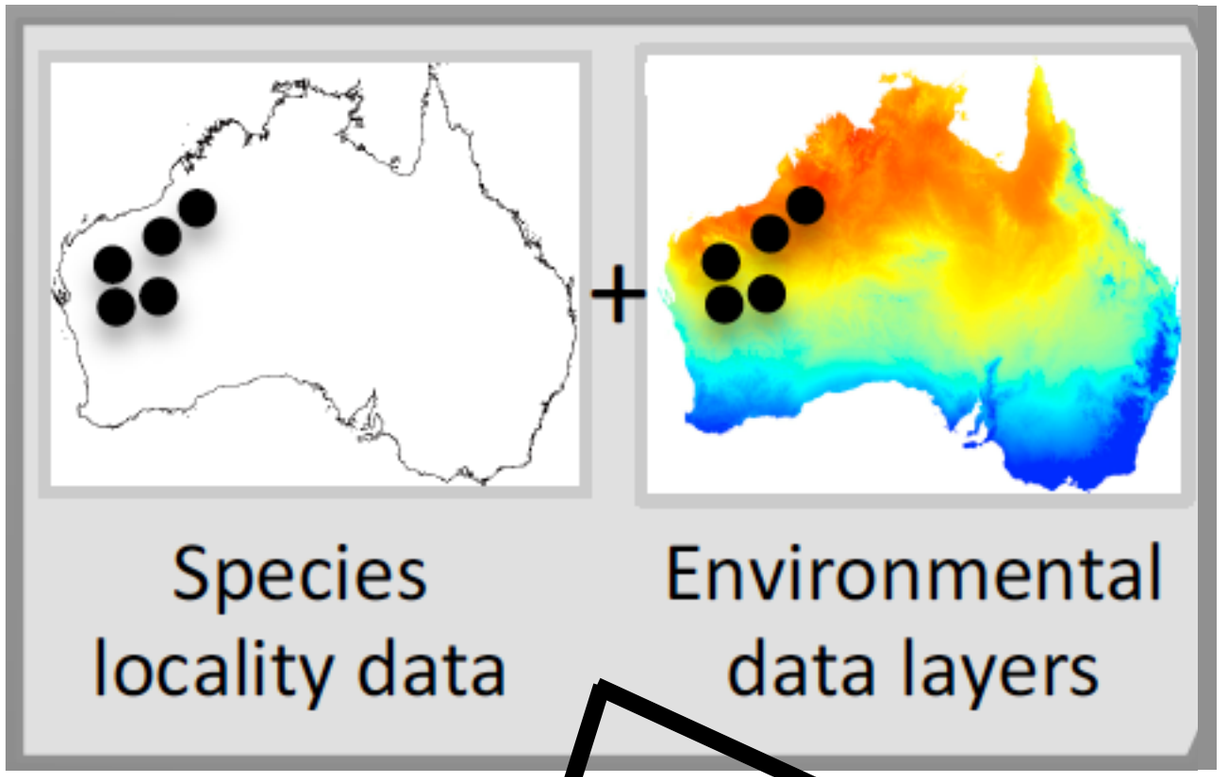

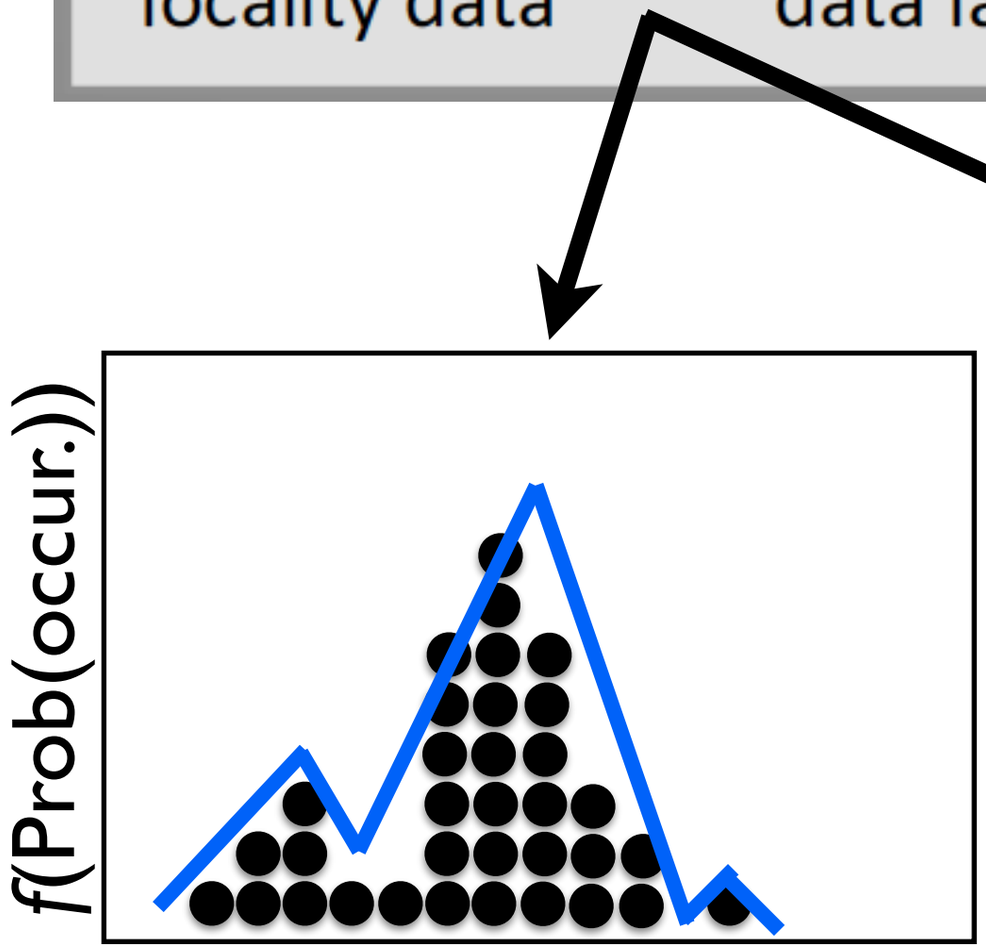

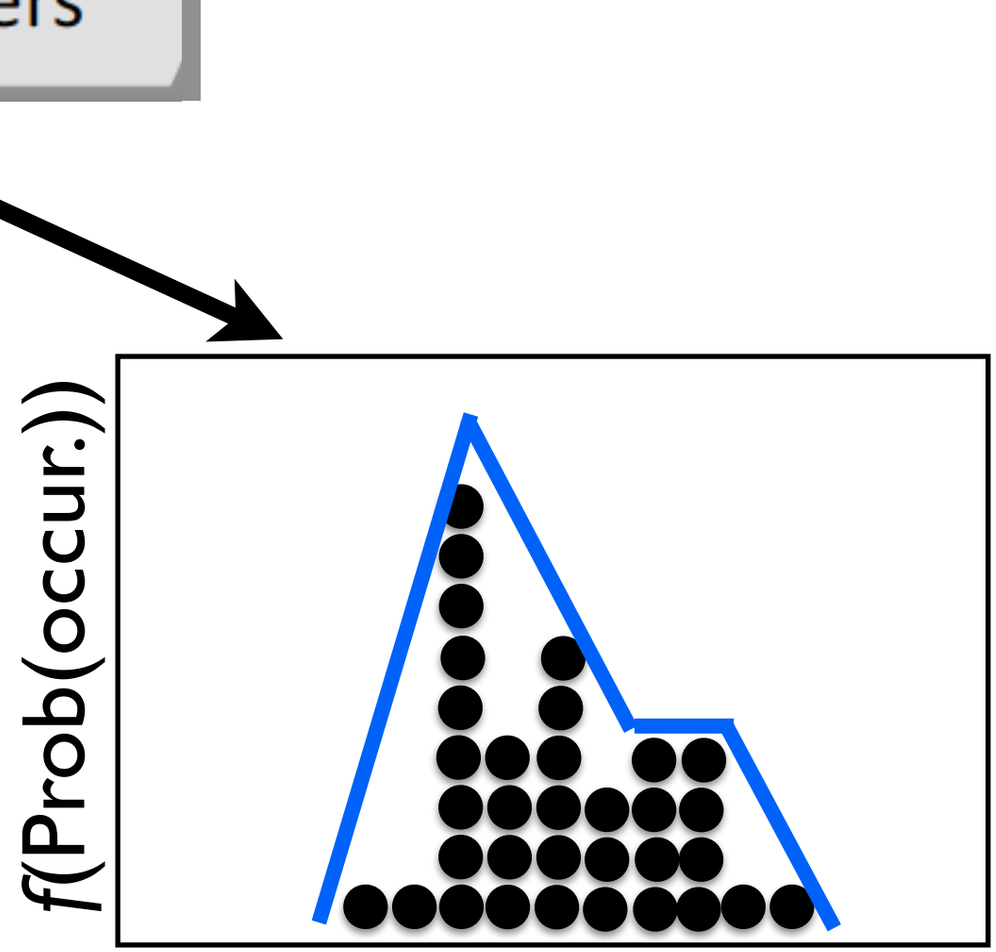

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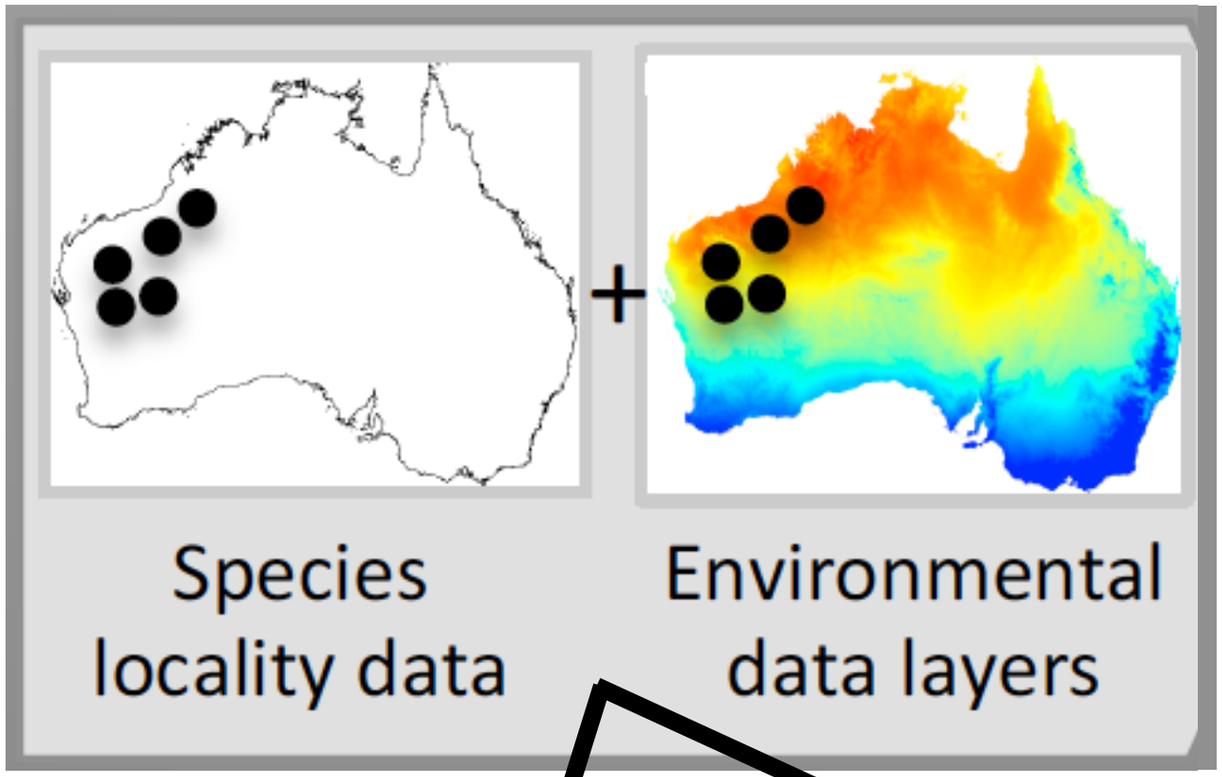
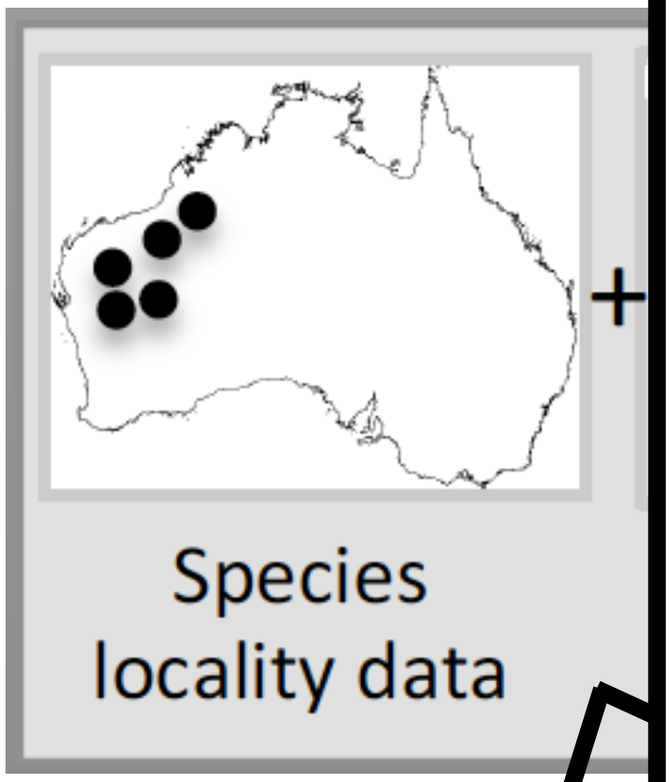
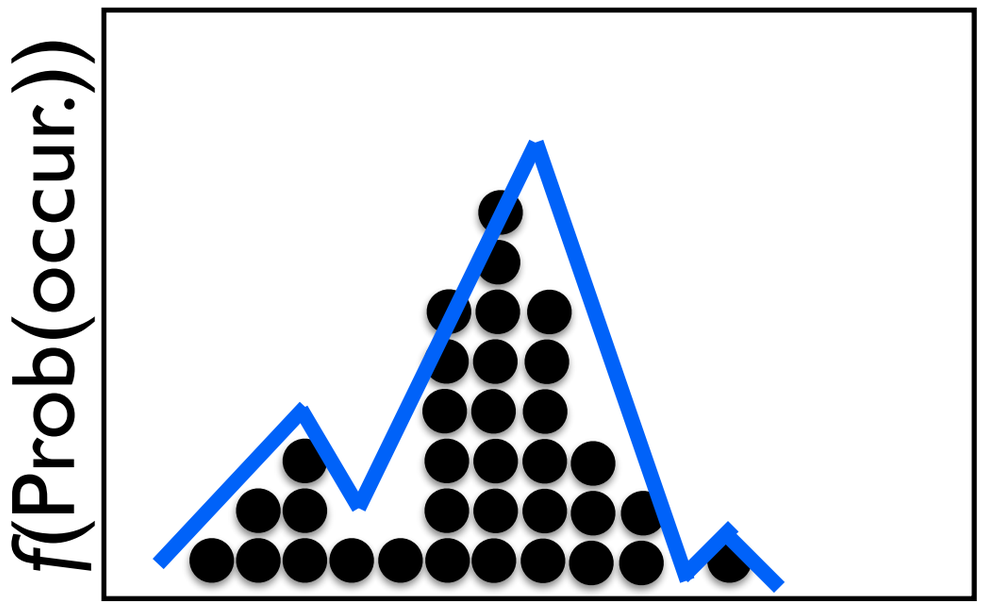
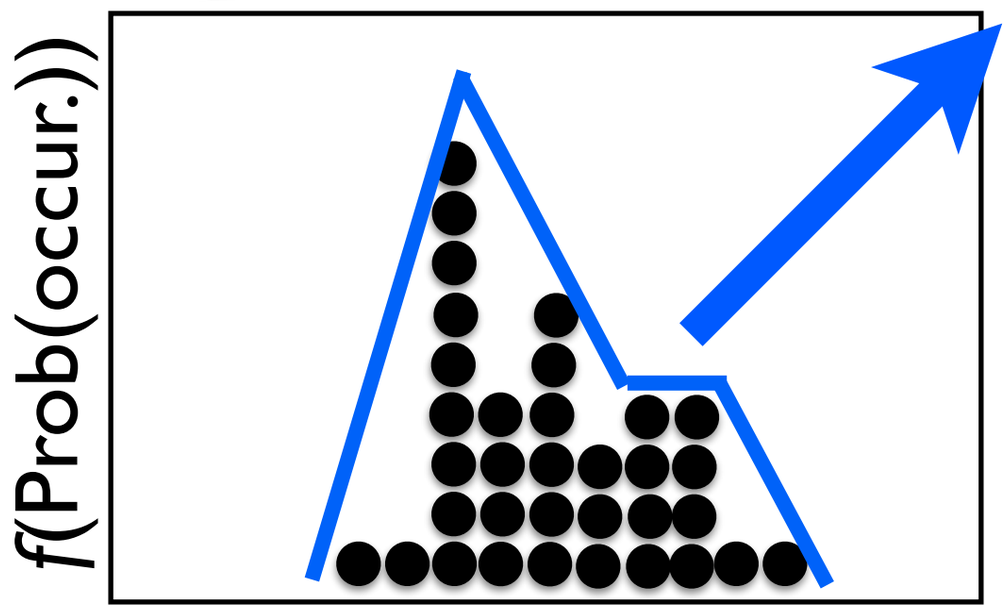




Common ENM tools

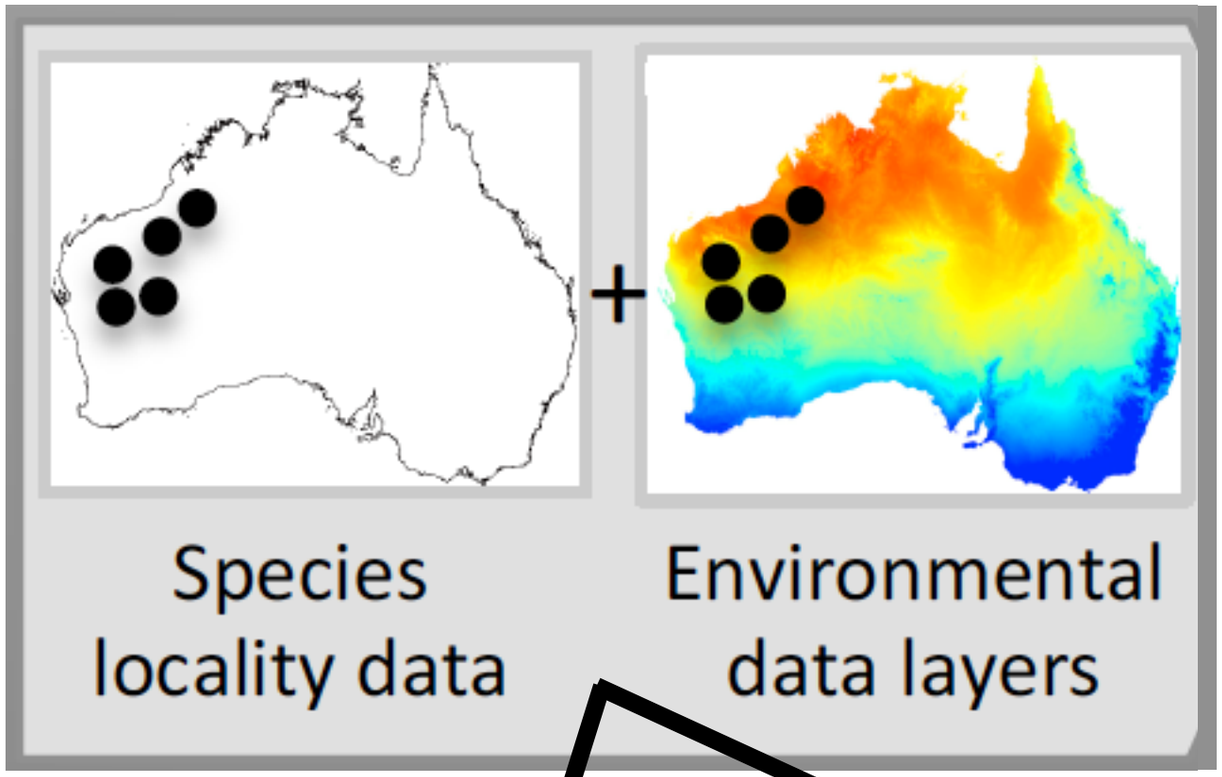
- BioClim (min/max)
- GLMs
- GAMs
- MaxEnt
- MARS
- RandomForest





Ecological niche model

Niche modelling: basic procedure



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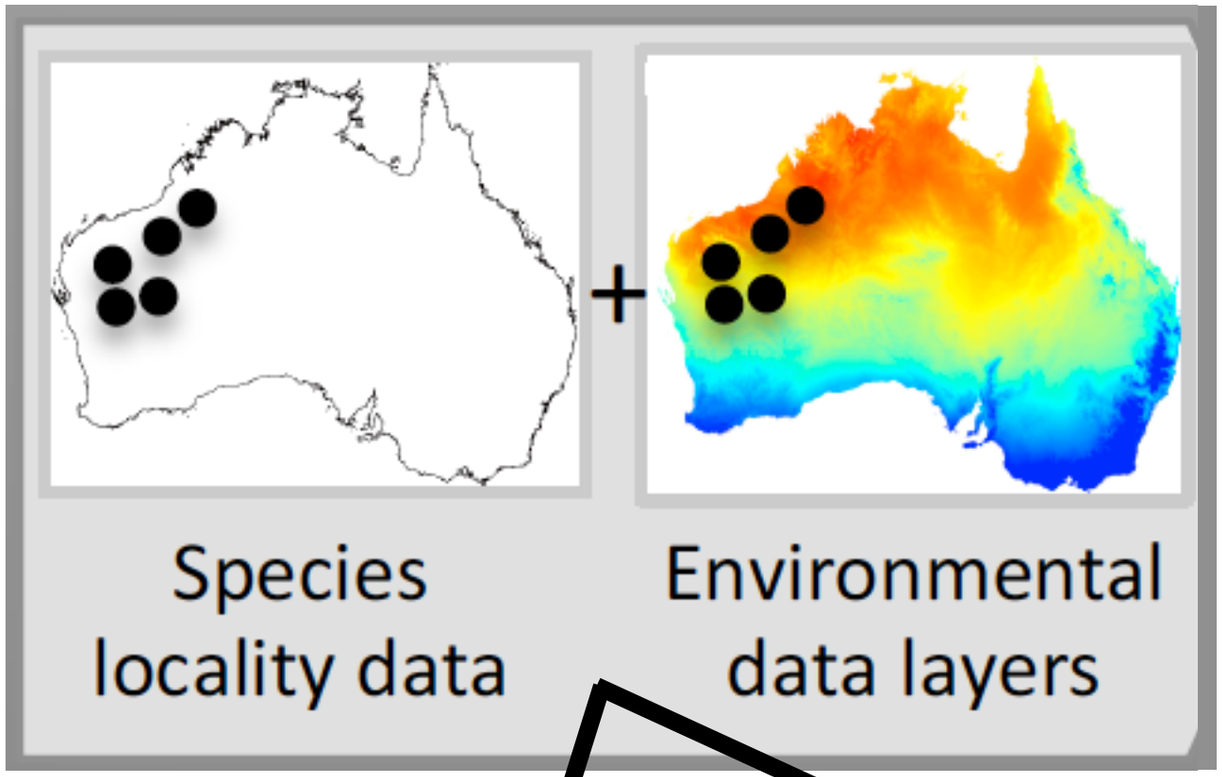

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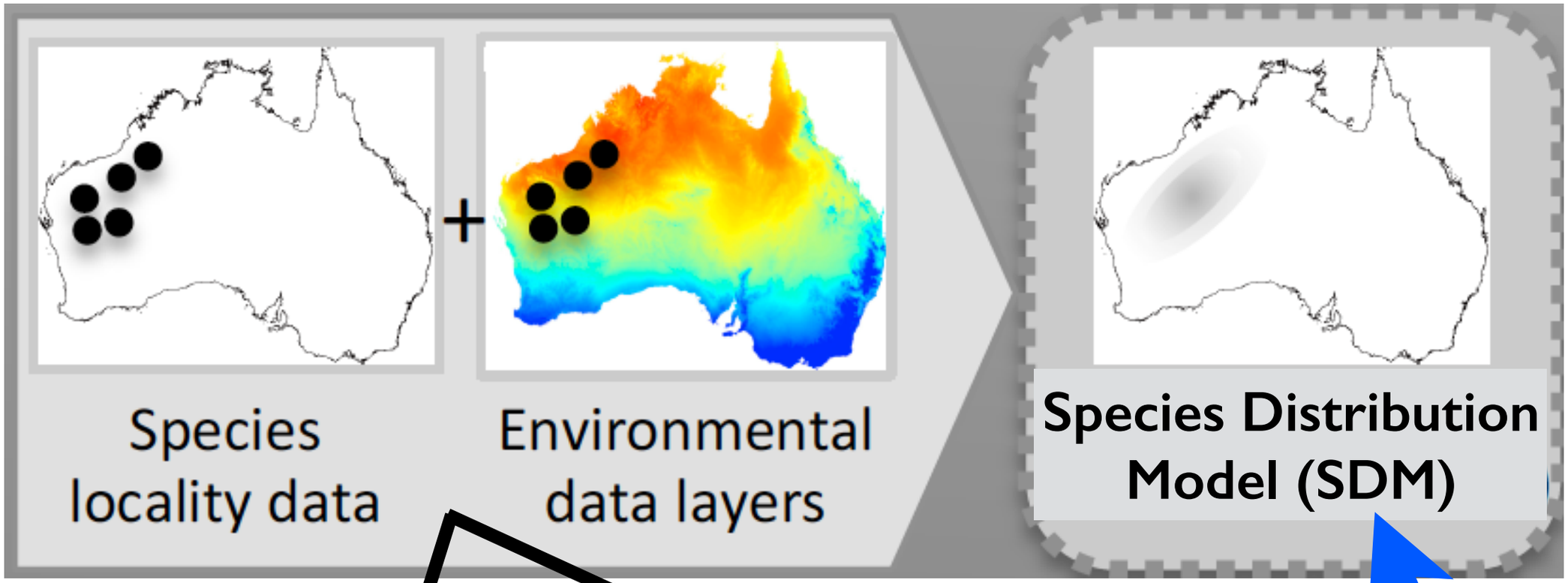

ENM procedure

Occurrence data

+

Environmental Data

=

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Ecological niche model

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Projection onto map

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* **Presence-only data**
* **Sampling issues**

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***correlation vs. causation**

***overfitting**

***poor extrapolation ability**

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Projection into space assumes:

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***correlation vs. causation**

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Projection into space assumes:

* **Niche model equals true niche**
* **Niche is wholly environmental**
* **Equilibrium**
* **No dispersal limitation**
* **No competition, etc.**

Nevertheless:

All models are wrong, but some models are useful

ENMs/SDMs are clearly useful, even if imperfect

Let's take them more seriously, as statistical *models*

PCM procedure

Tip data

+

Phylogeny

=

PCM procedure

Tip data

+

Phylogeny

=

Fit continuous trait model(s)

PCM procedure

Tip data

+

Phylogeny

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Fit continuous trait model(s)

1. **Estimate ancestral states**
2. **Test hypotheses about processes, rates**

PCM procedure

Tip data

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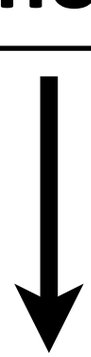

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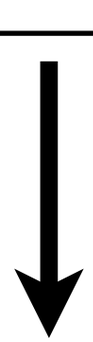

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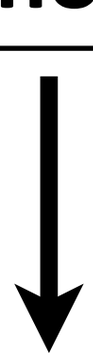

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PCM procedure

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Phylogeny

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Fit continuous trait model(s)

Common PCM models

- Brownian motion
- OU process
- Early Burst
- Trend
- Multiple regimes, shifting means, etc.

(fit with ML or Bayes)

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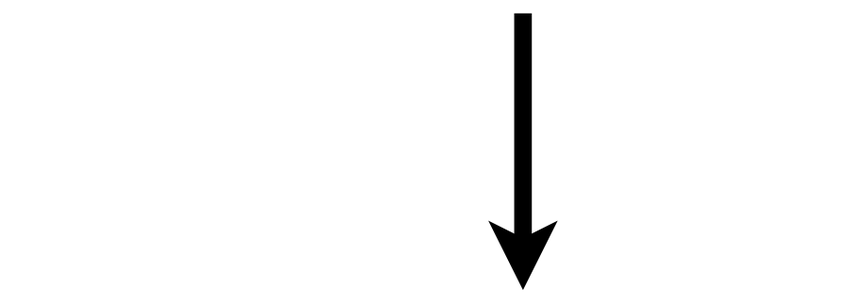

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Common critiques

* **Tip data have error**
* **Phylogeny, branch lengths have error**
* **Identifiability**
* **Without paleo: weighted averaging**
* **Interpretation**
* **Fitting multiregime models, overfitting issues**

Nevertheless:

All models are wrong, but some models are useful

Models of continuous trait evolution are useful and can be improved

1

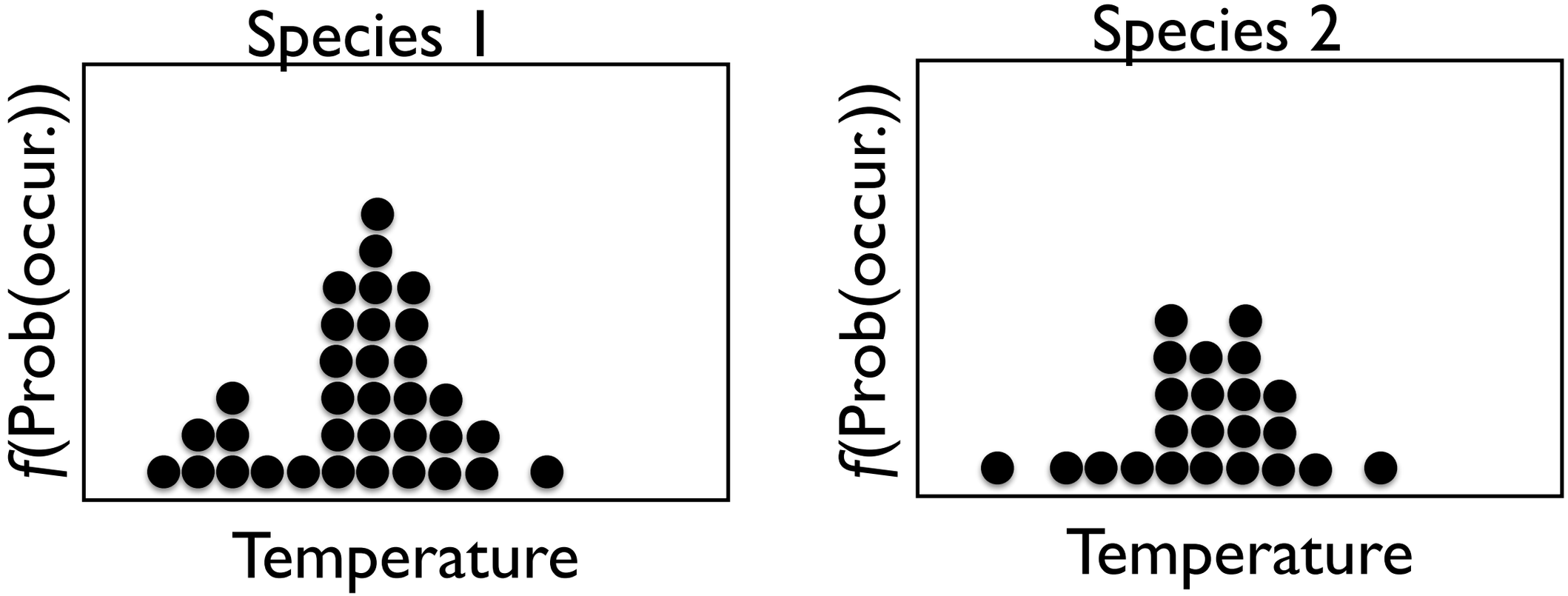
2

Combining ENMs and PCMs

ENM+PCM: use the mean?

1. Fit a niche model

2a. Sample from curve:



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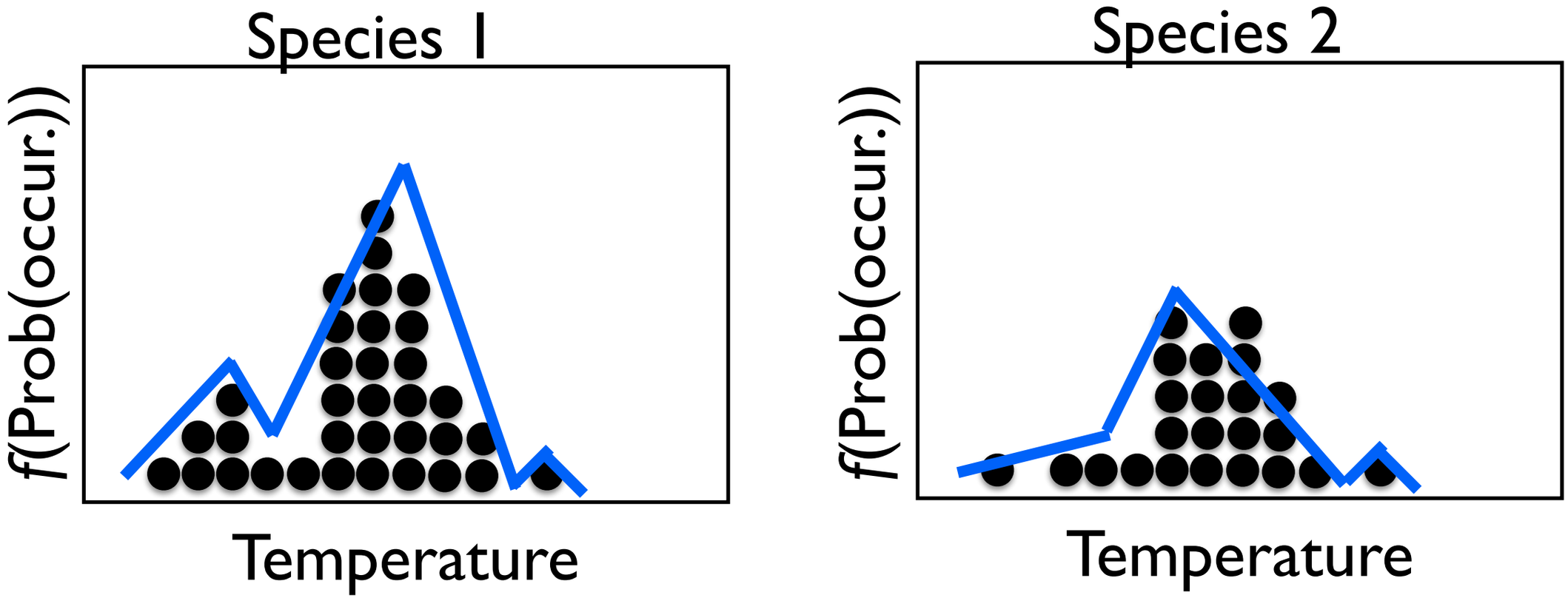

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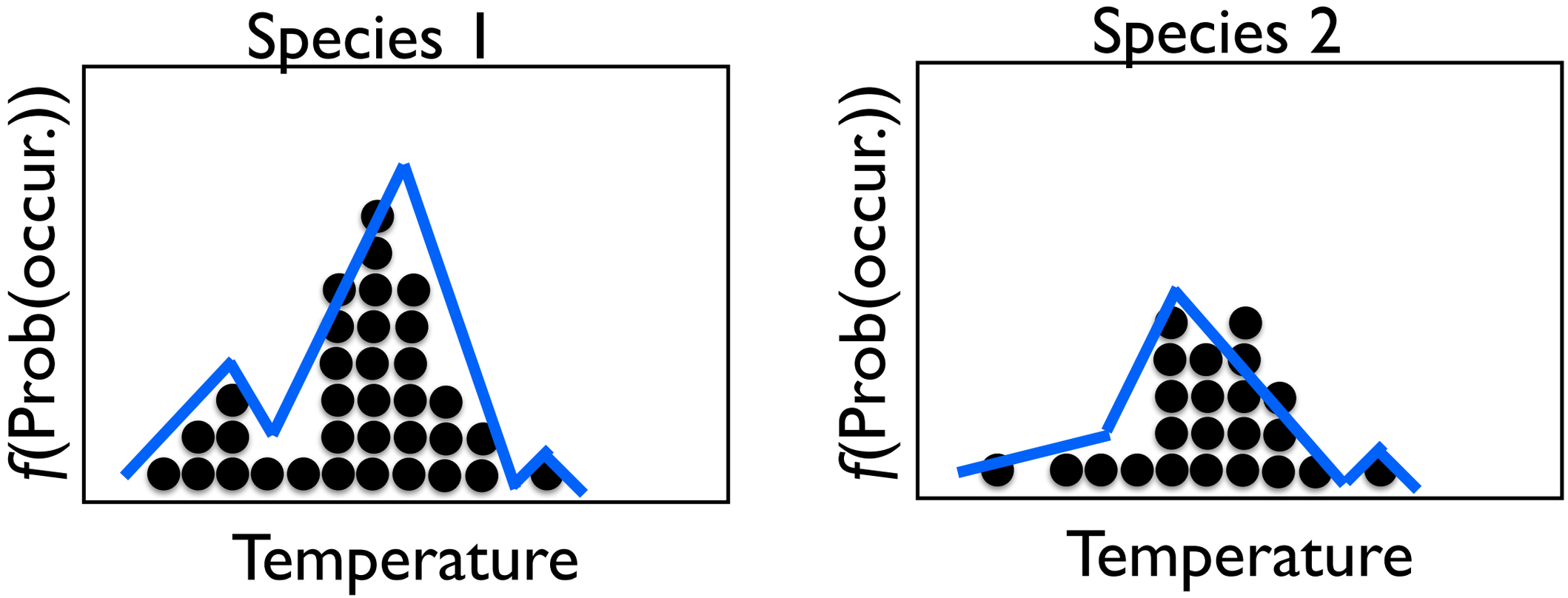

2b. Ancestral states w. Brownian:

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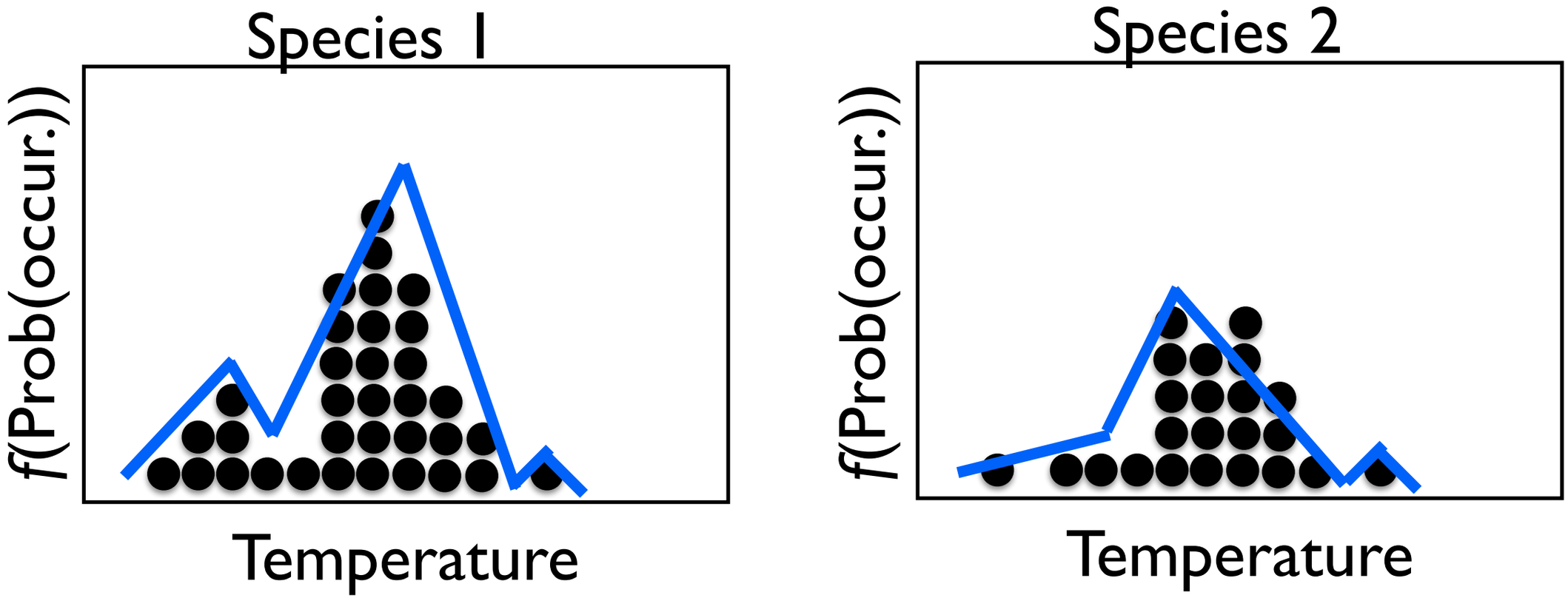

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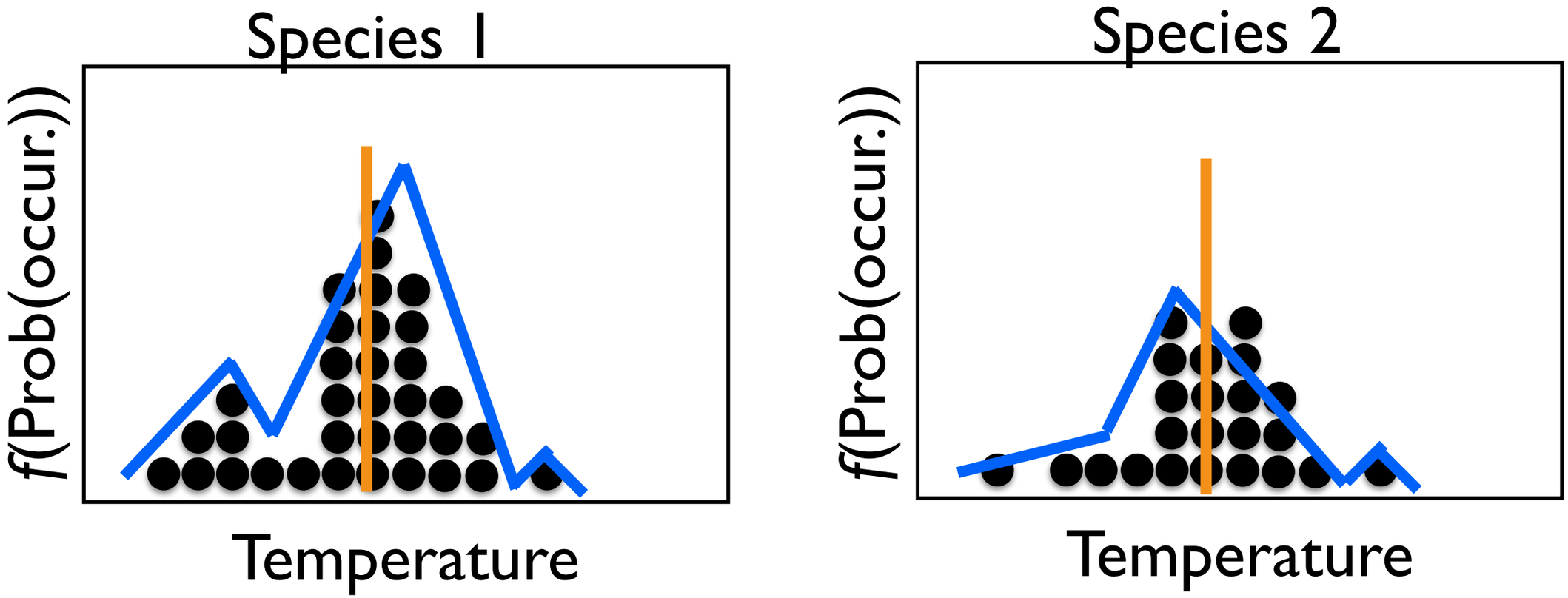

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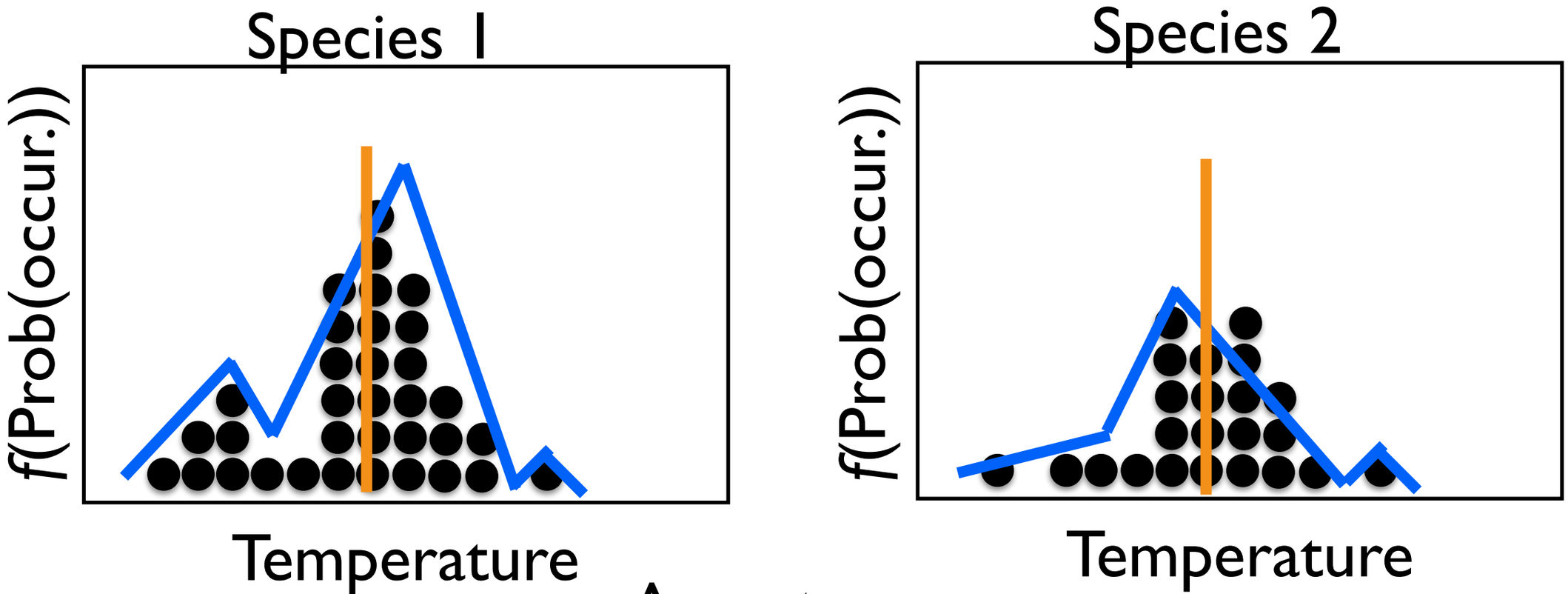

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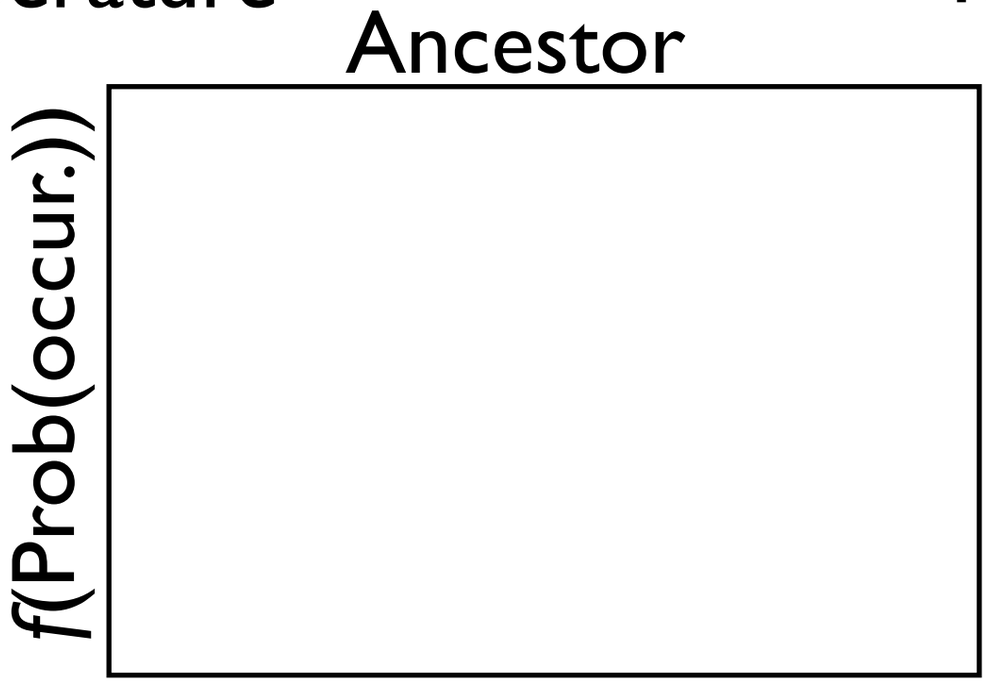

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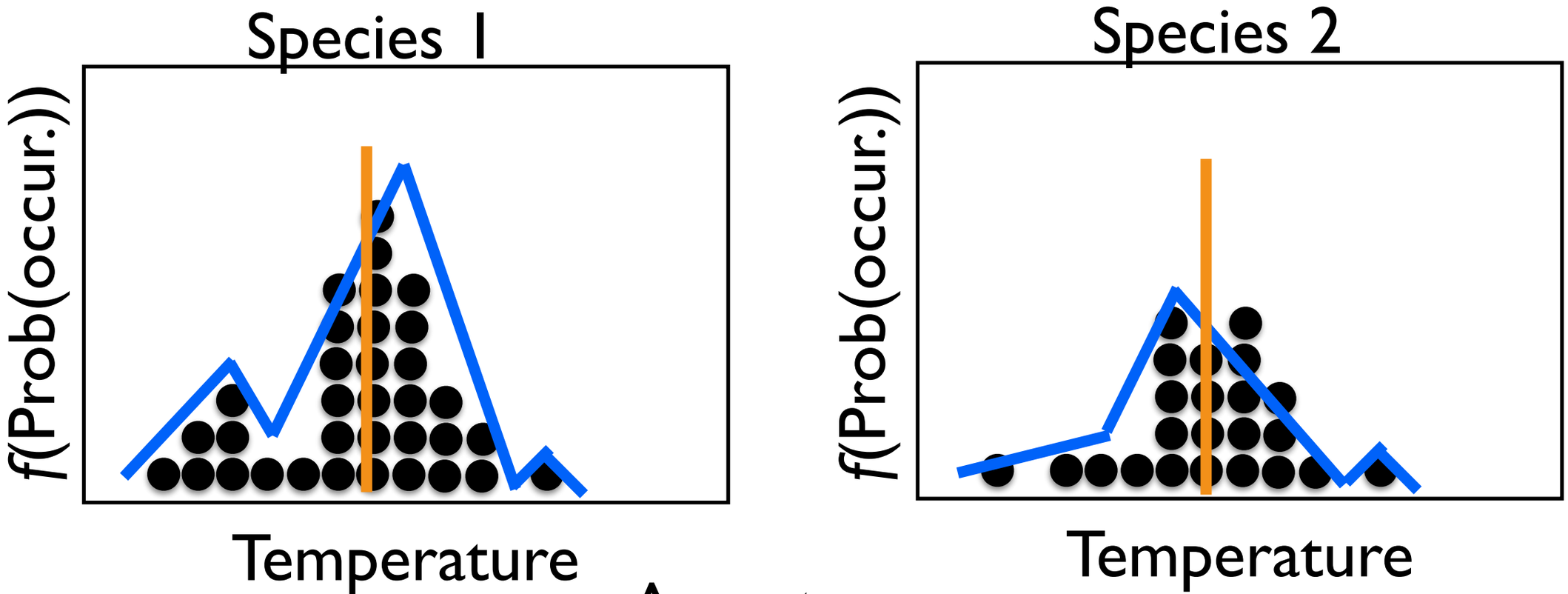

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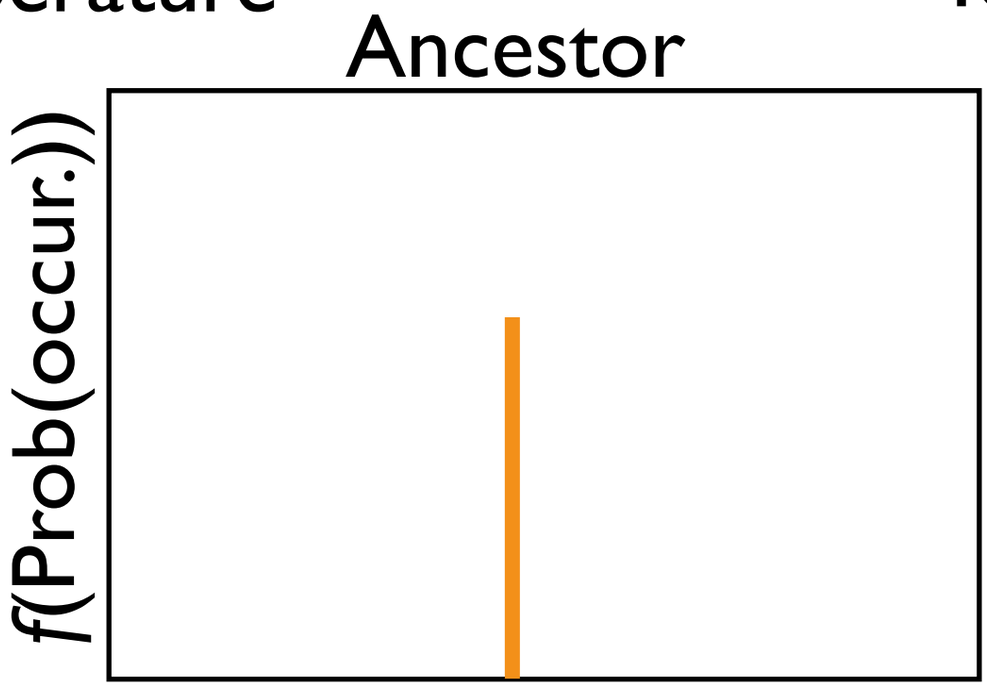

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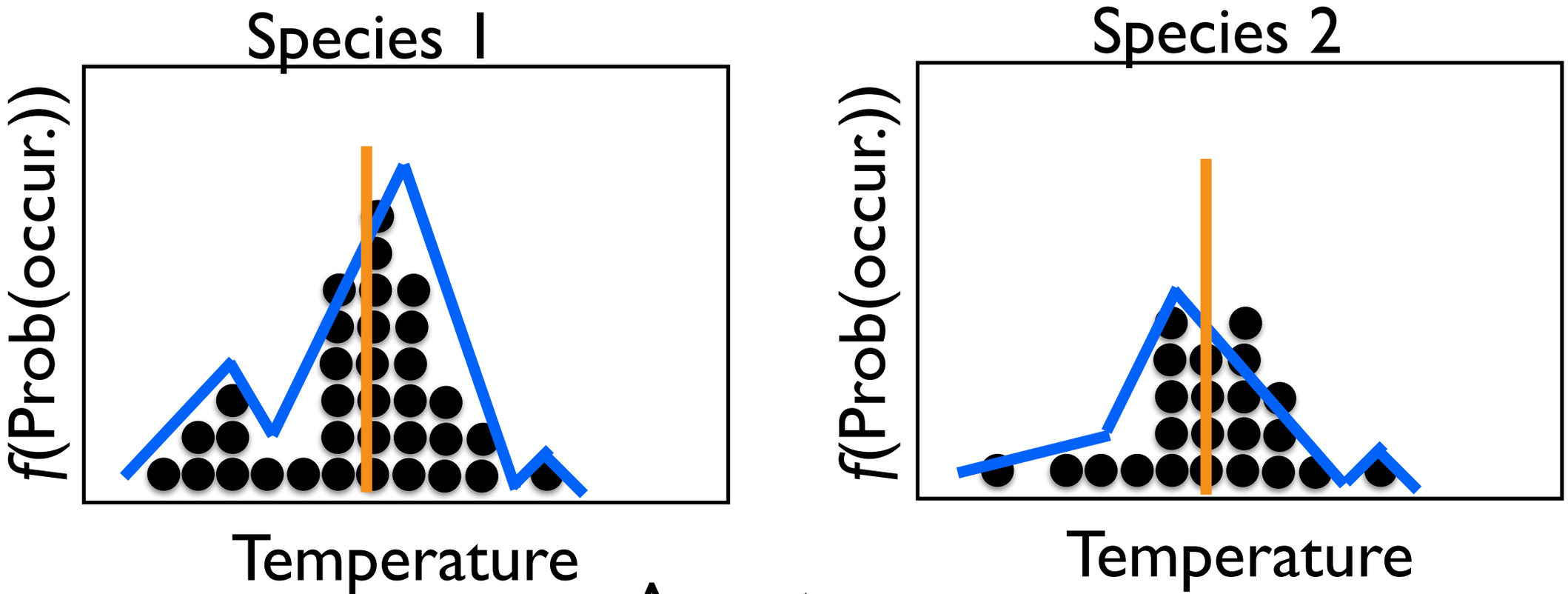

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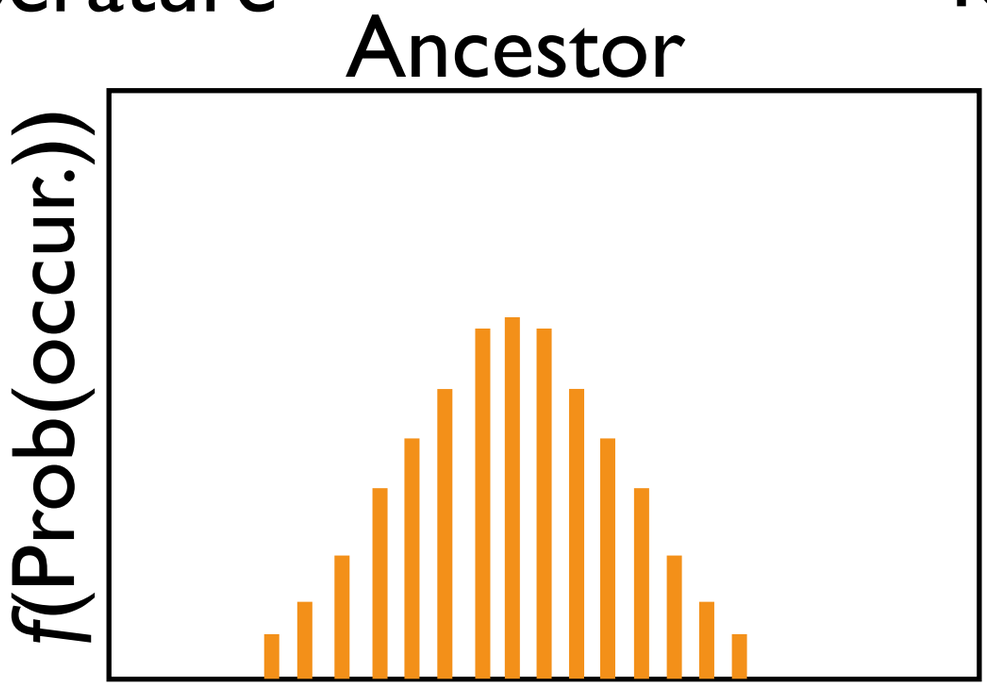

ENM+PCM: use the mean?

Critiques of the mean approach:

1. Mean is *inferred* from an *inferred* model (2 steps from data)
2. Is distribution gaussian?
3. Limits might be crucial

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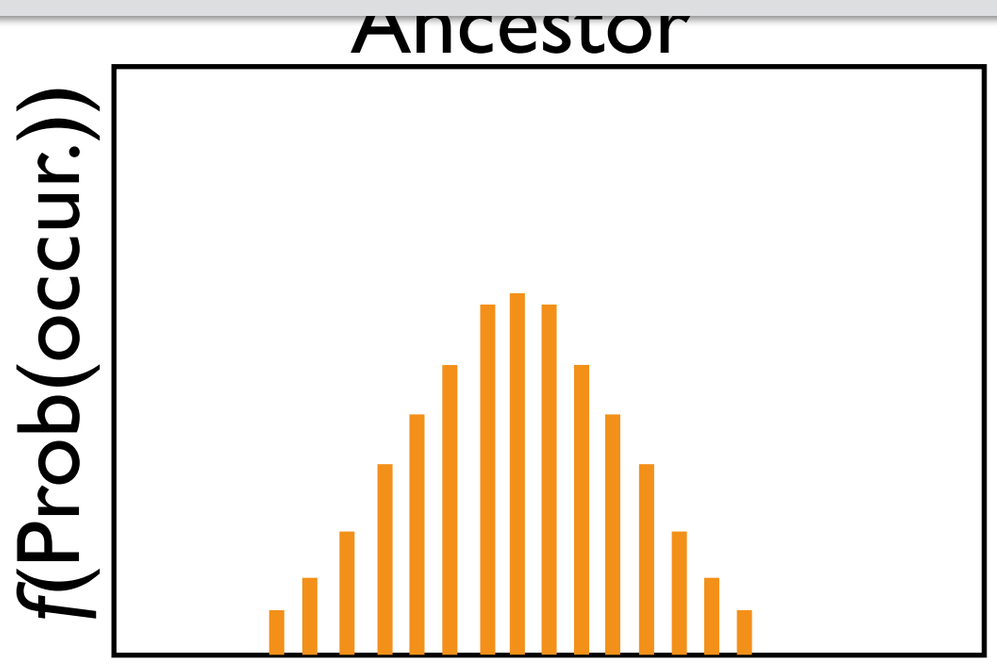

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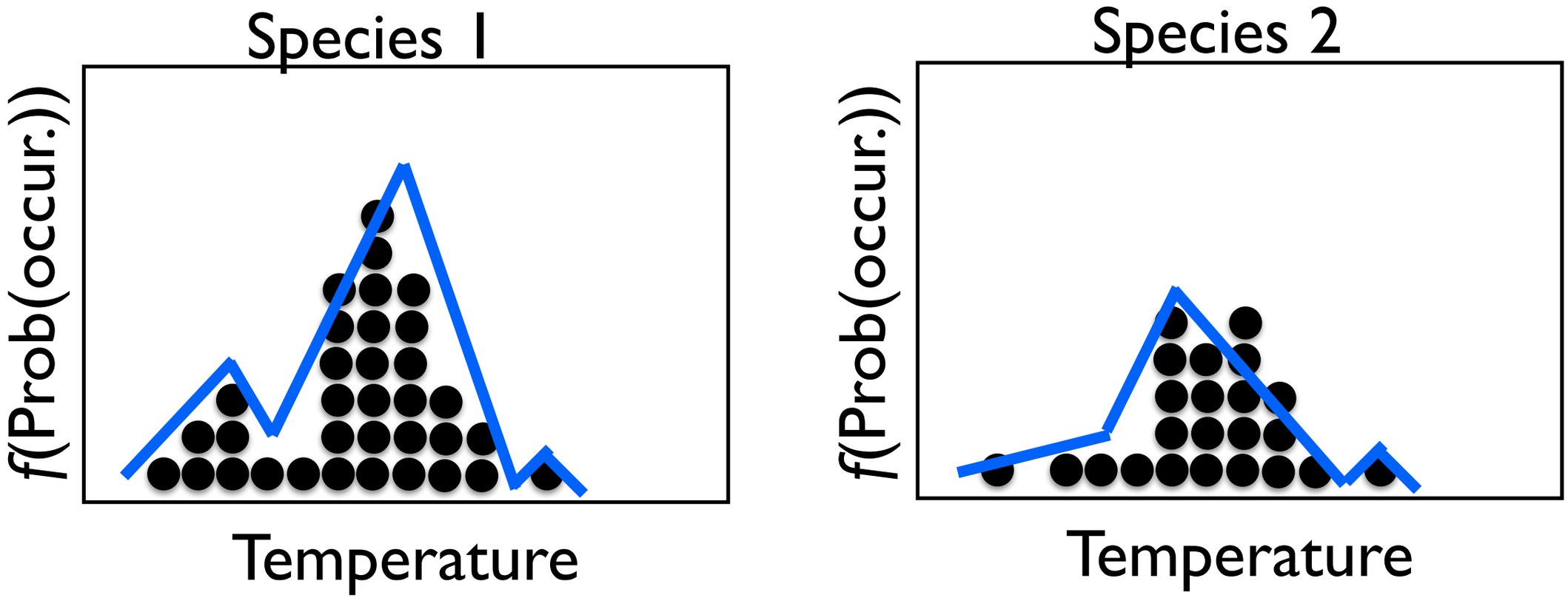

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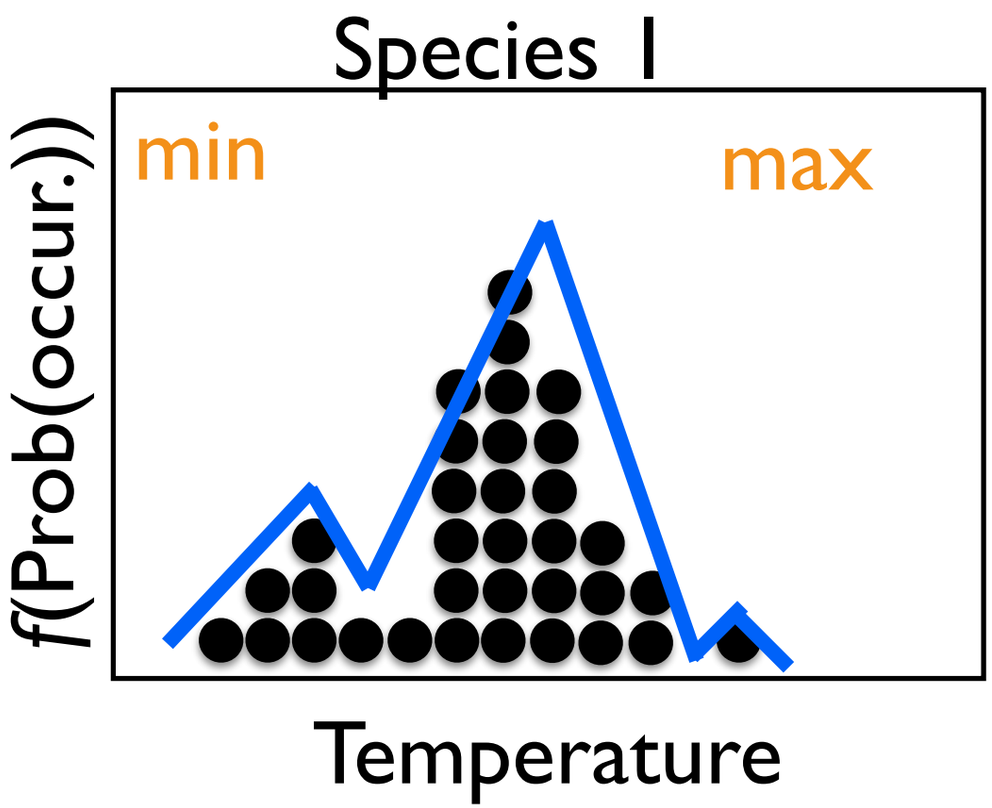

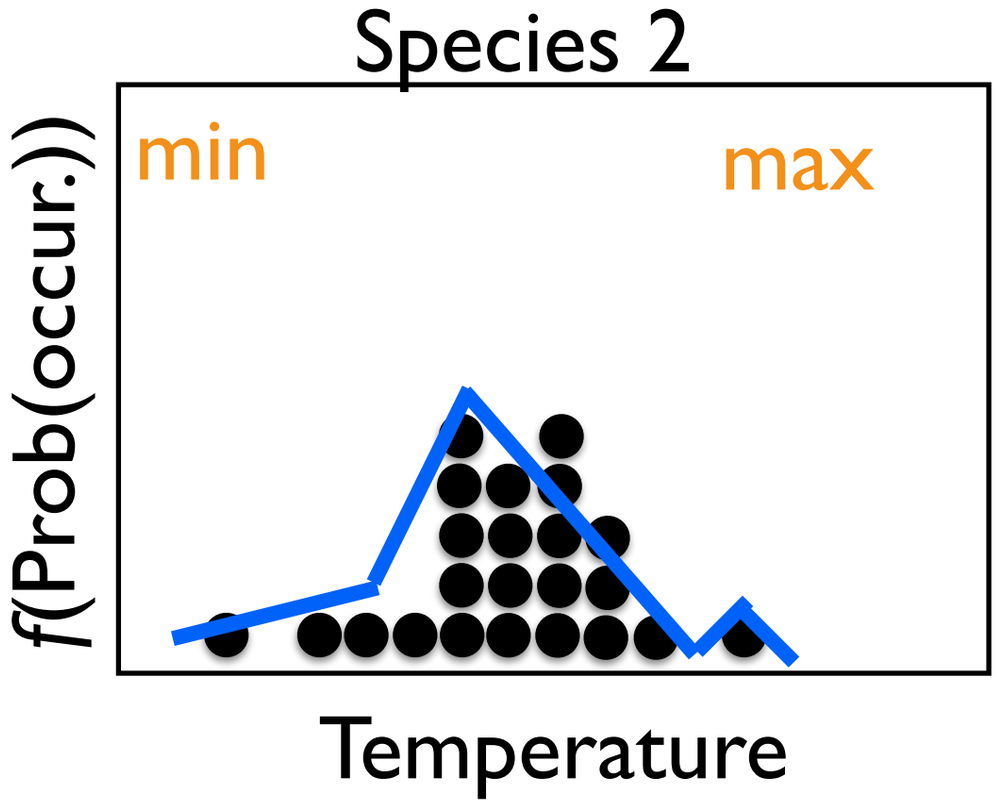

ENM+PCMs: Min-max approach

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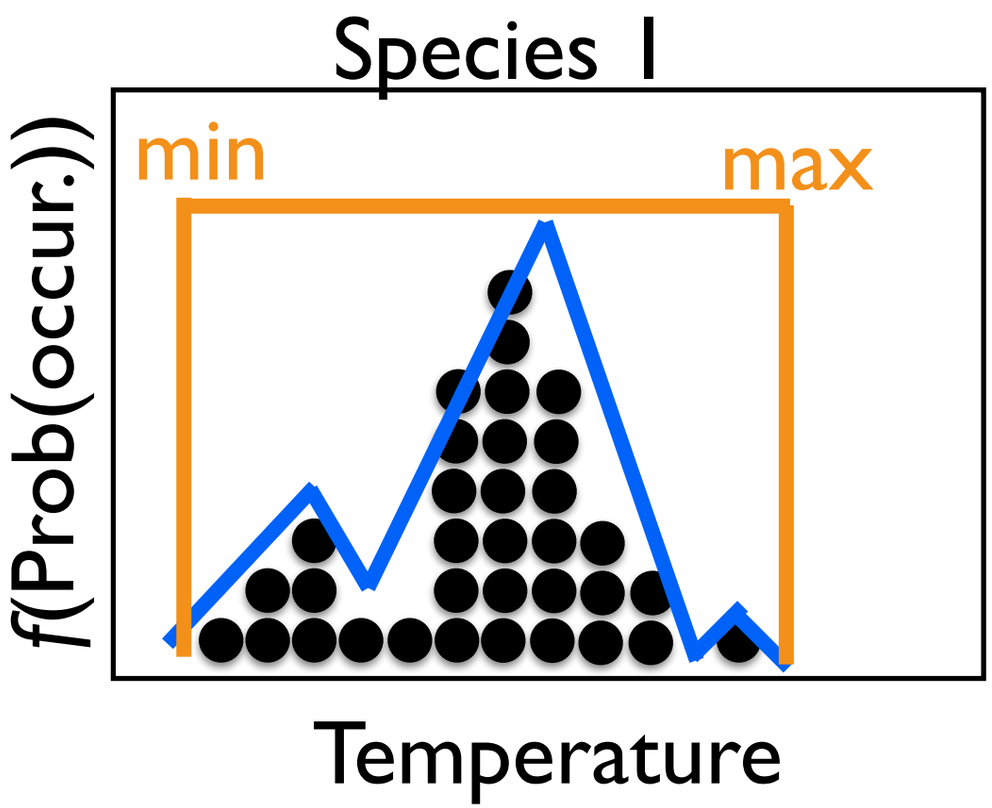

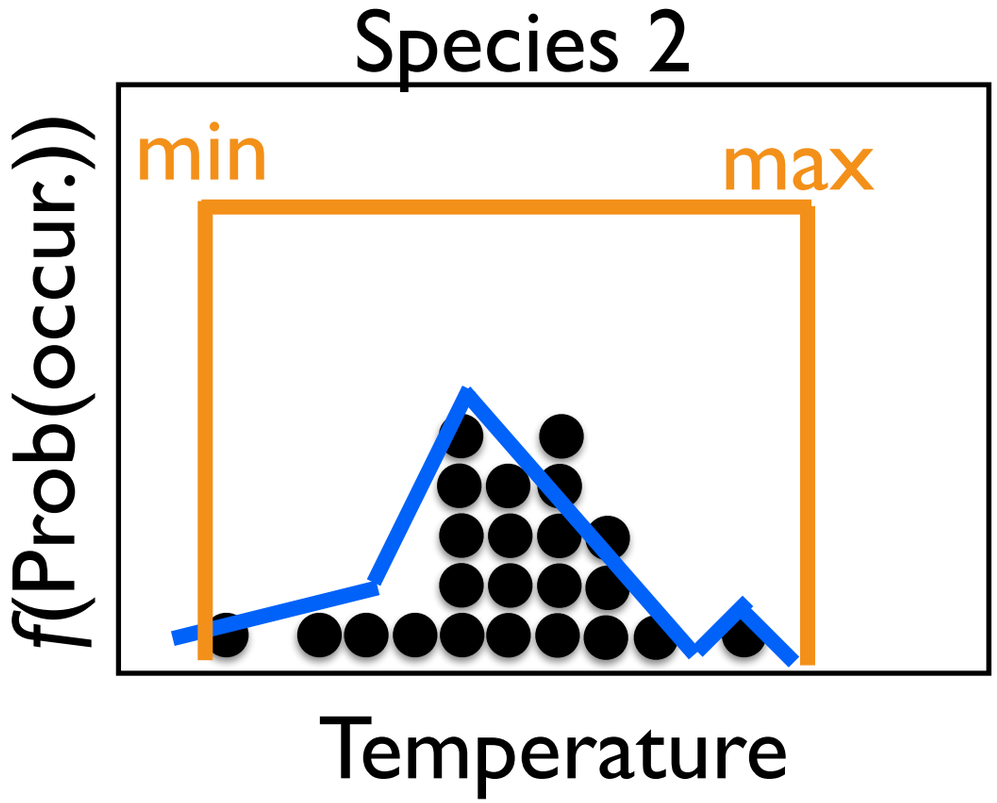

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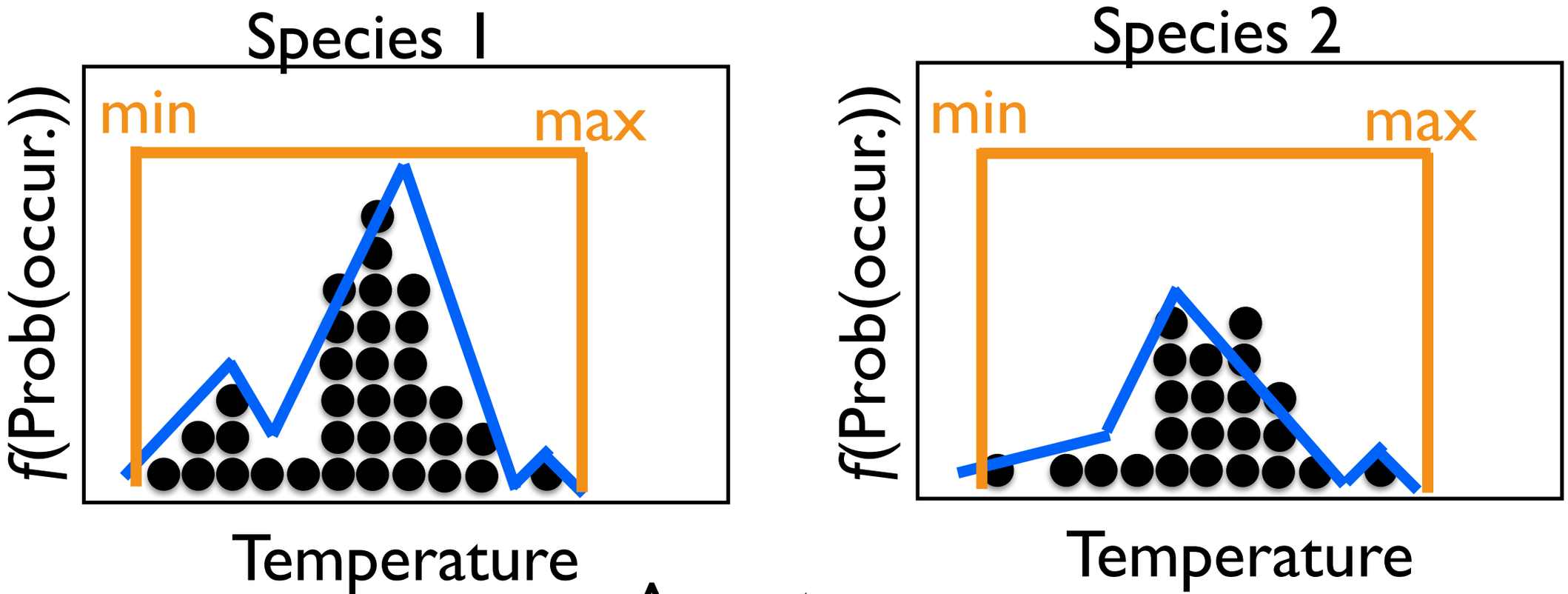

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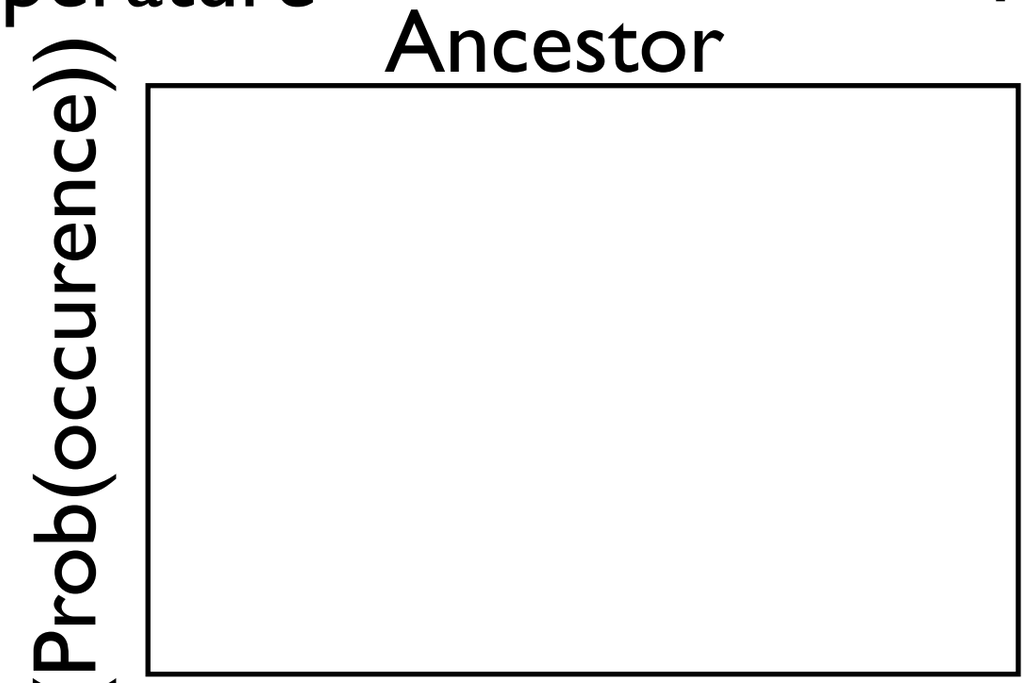

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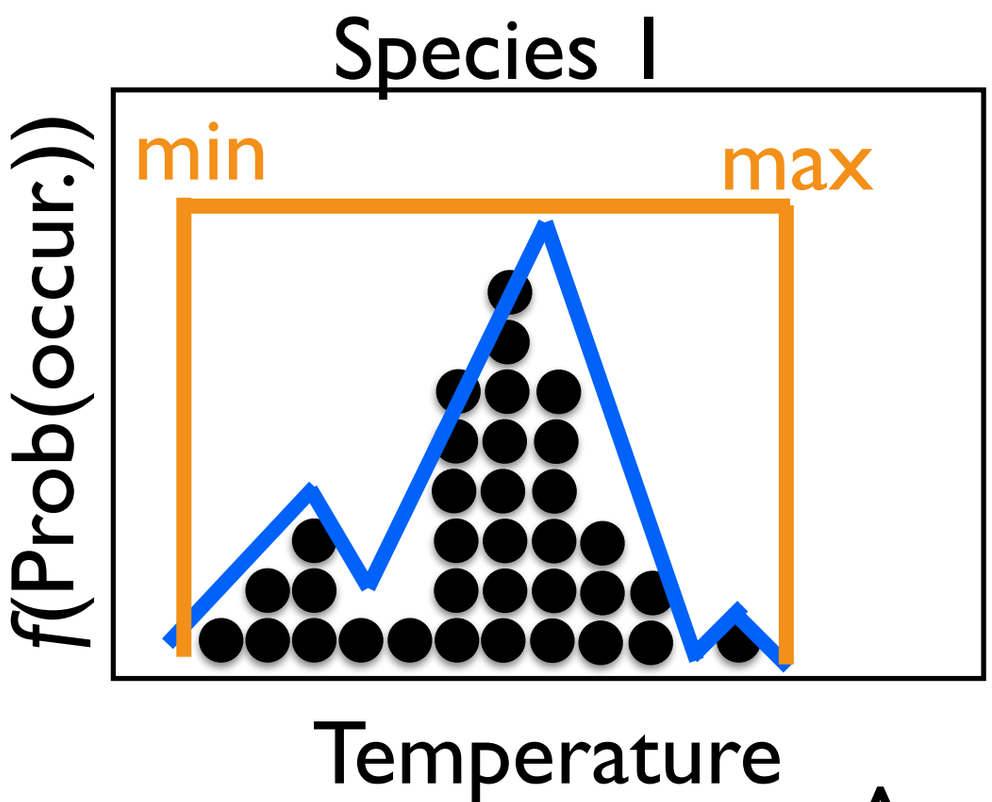

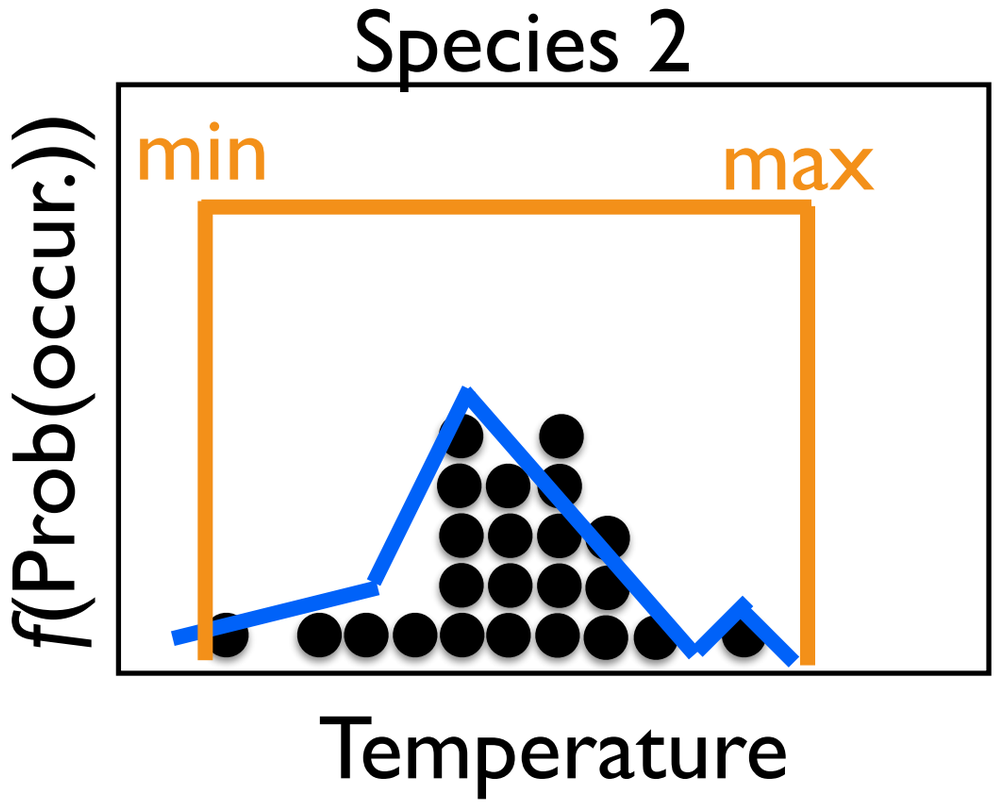

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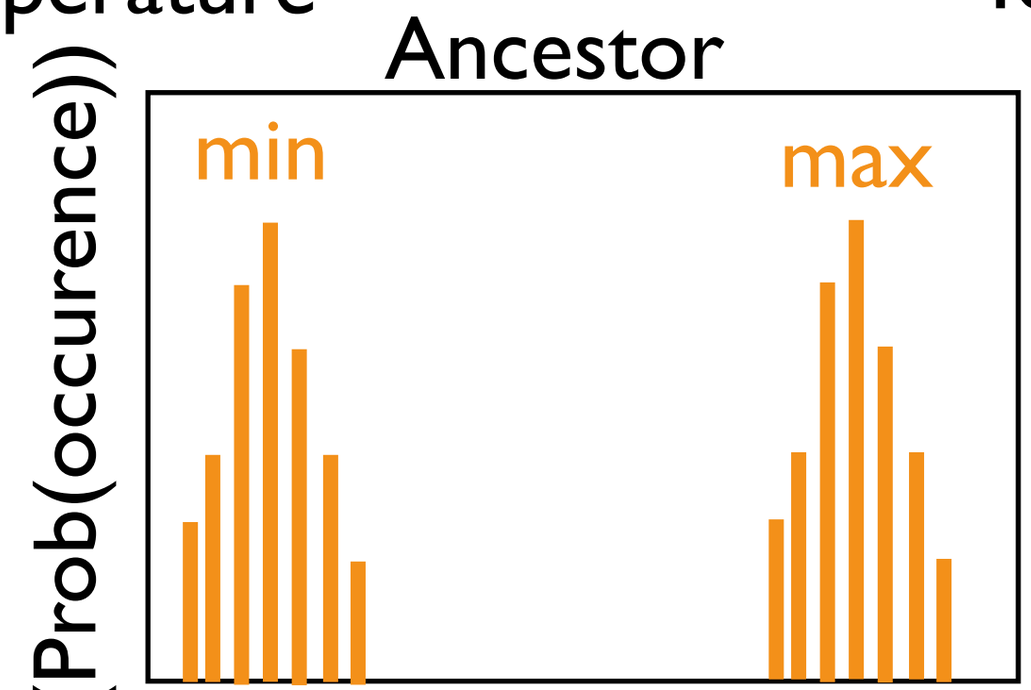

ENM+PCMs: Min-max approach

Critiques of the min/max approach:

1. Min/max are inferred estimates, not data
2. Min and max could cross over under Brownian motion
3. No model choice

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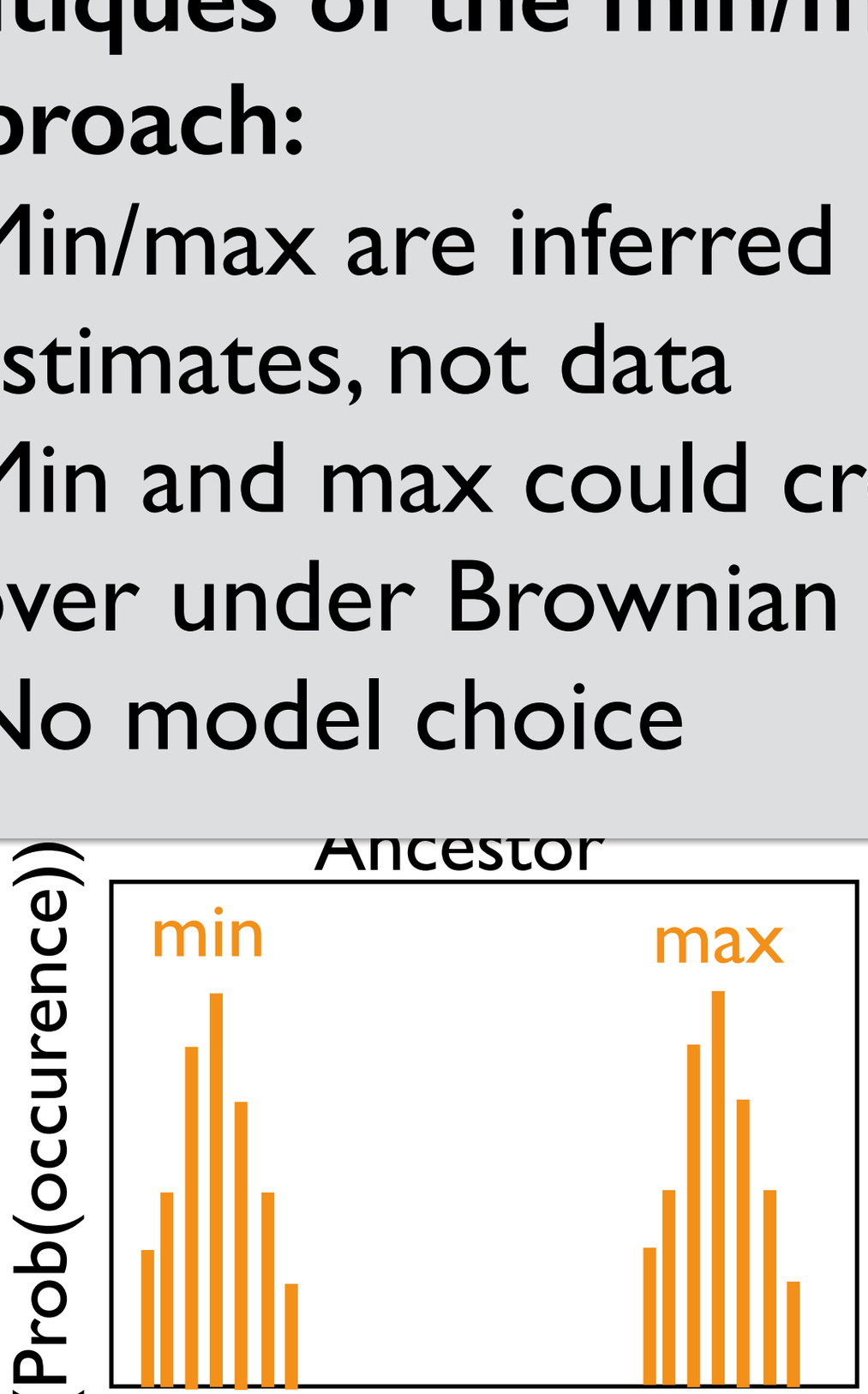

ENM+PCMs: Sampling approach

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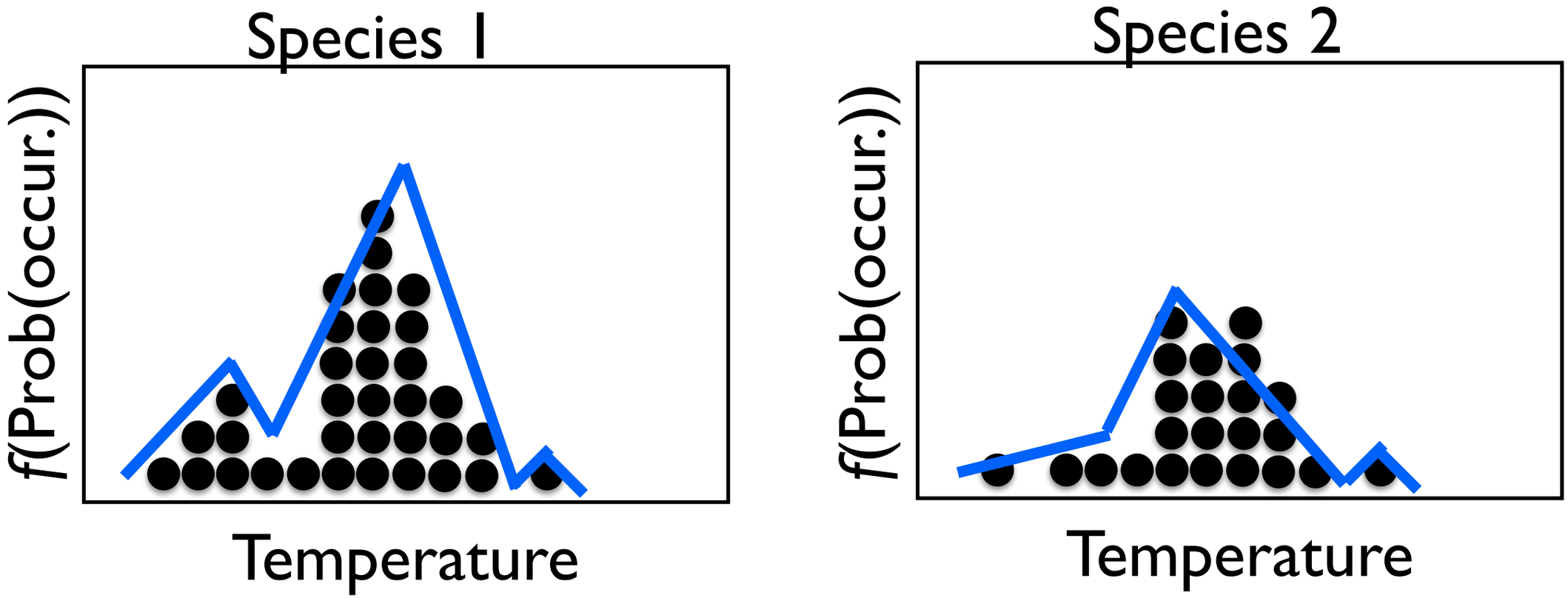
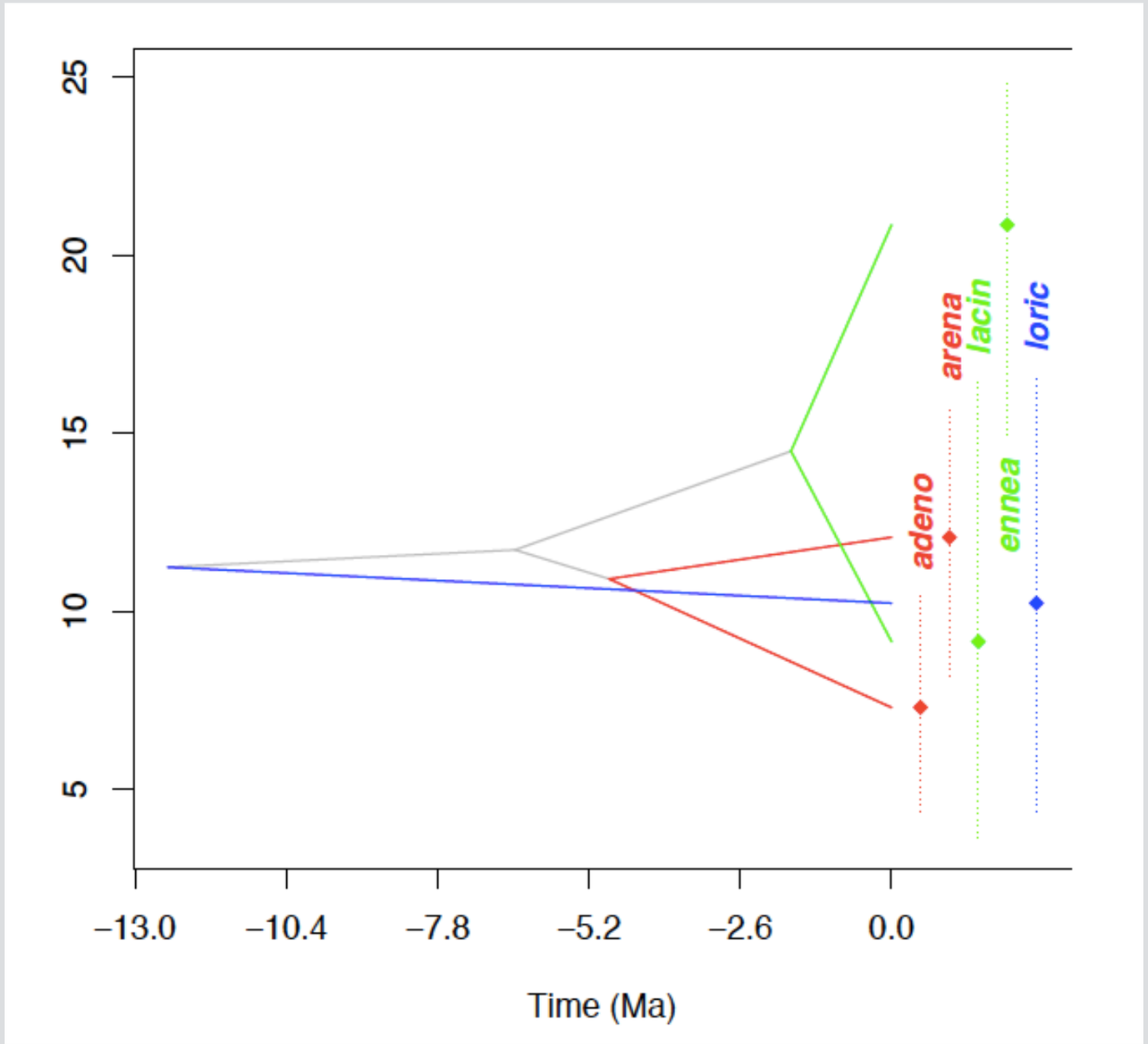


ENM+PCMs: Sampling approach

Pioneered by Evans et al. (2009); Available in phyloclim R package



(example dataset from Heibl's phyloclim R package)

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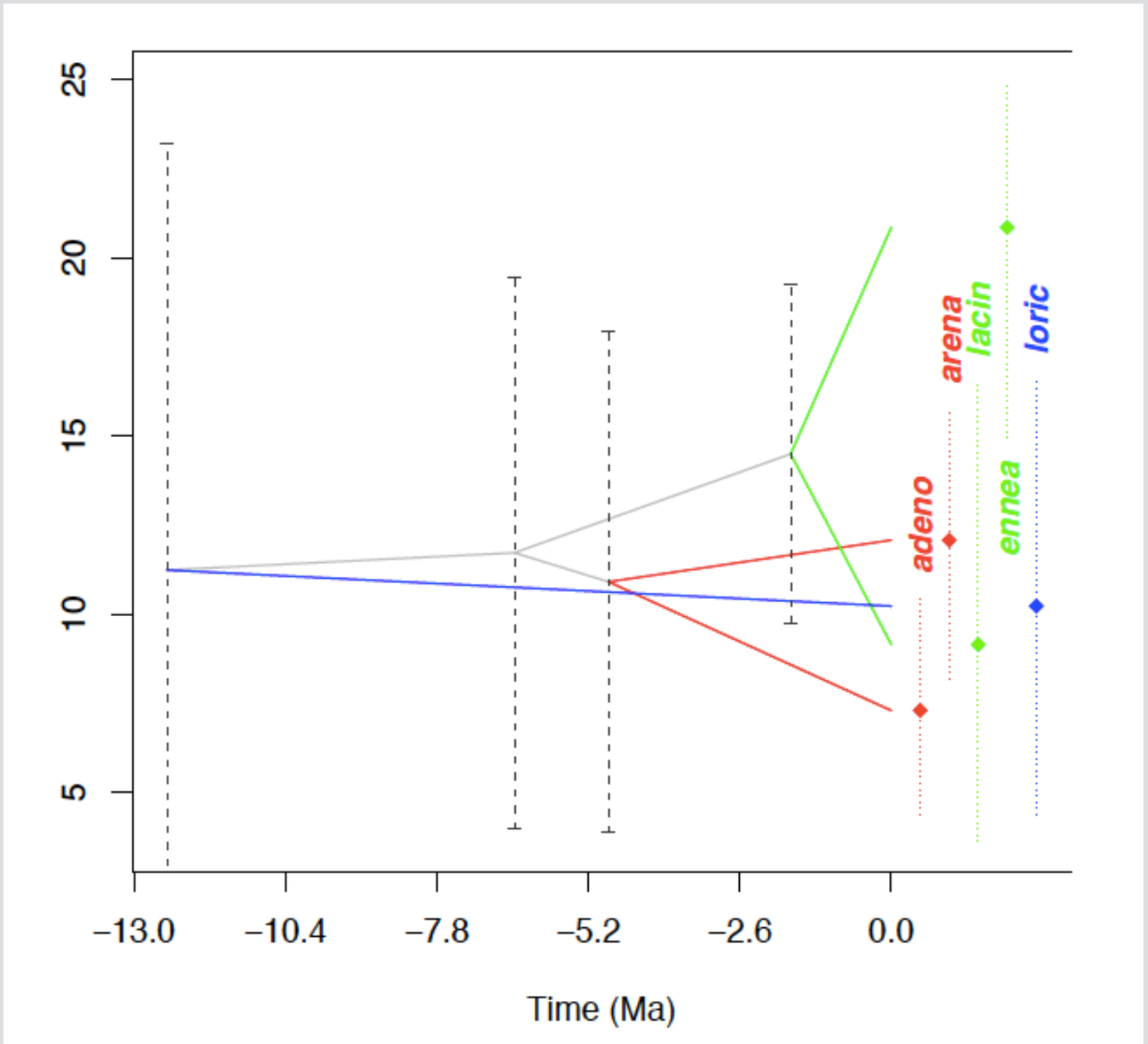

(example dataset from Heibl's phyloclim R package)

(adding the 95% CIs on ancestral means)

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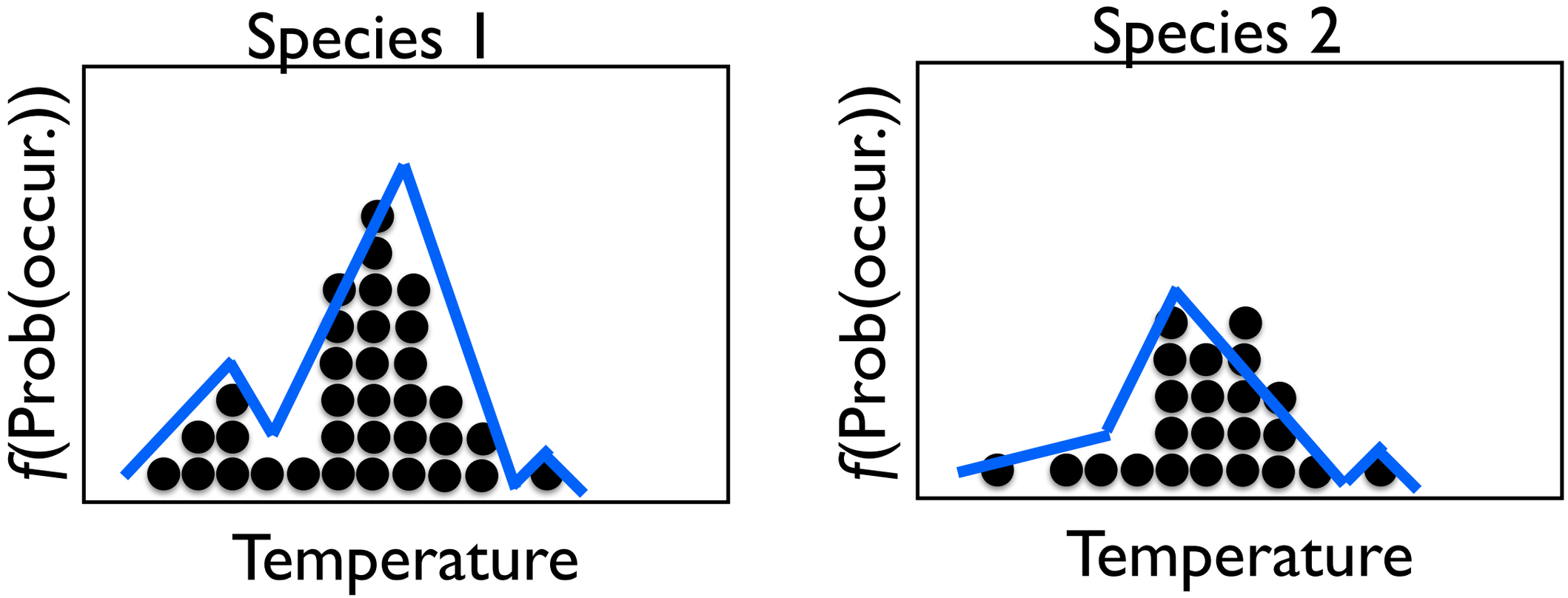

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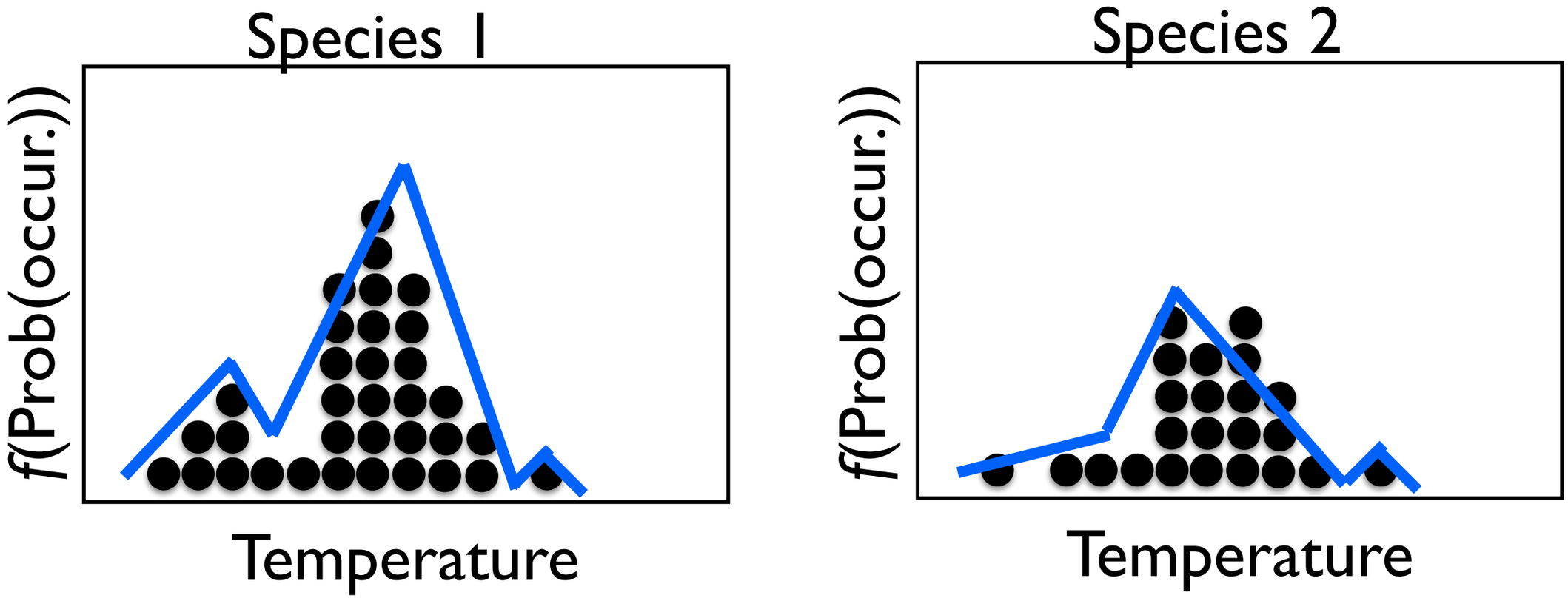

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ENM+PCMs: Sampling approach

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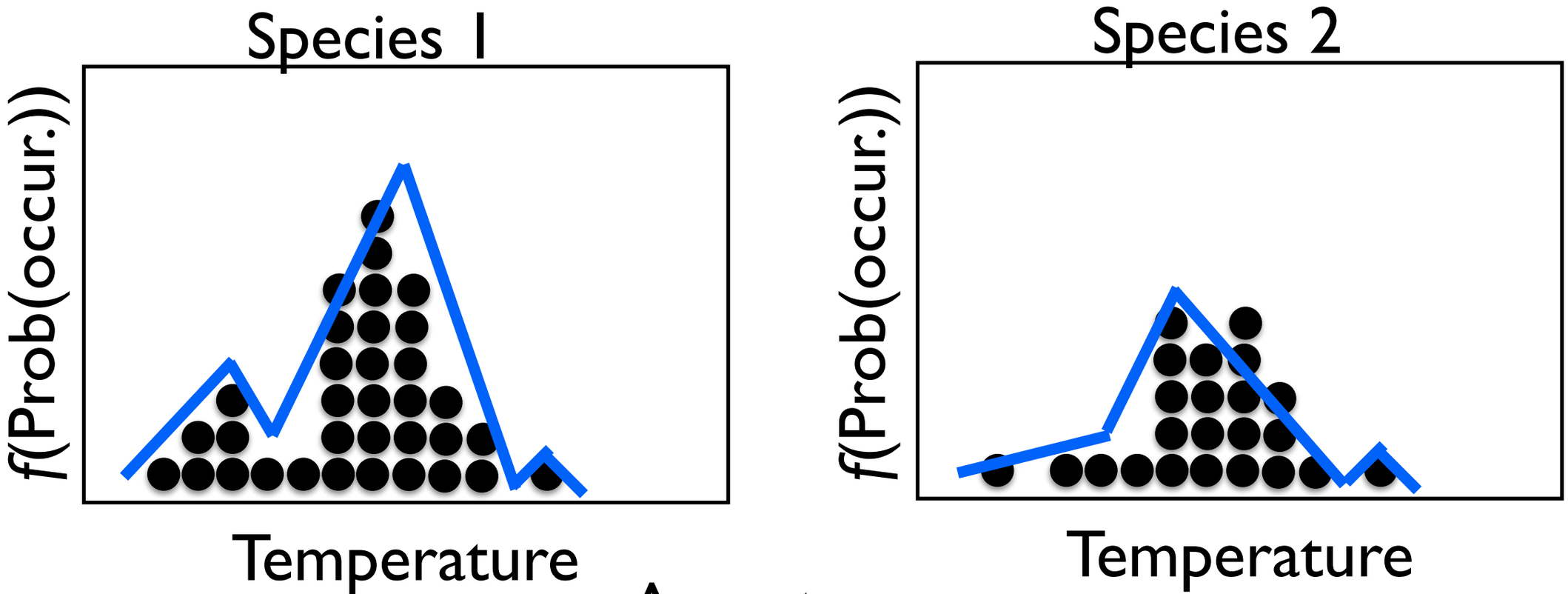

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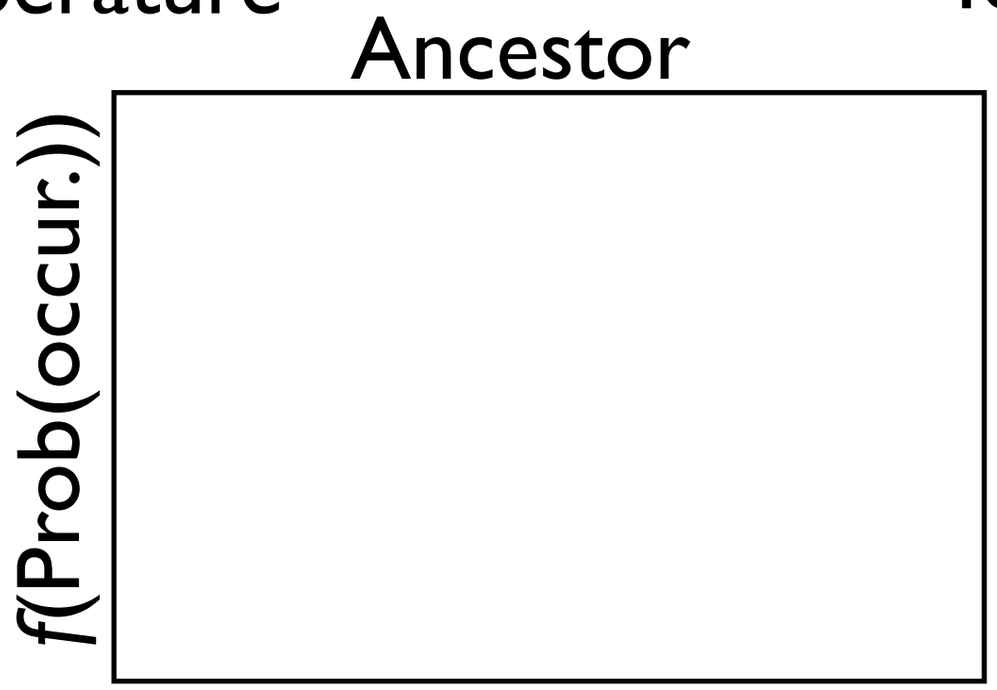

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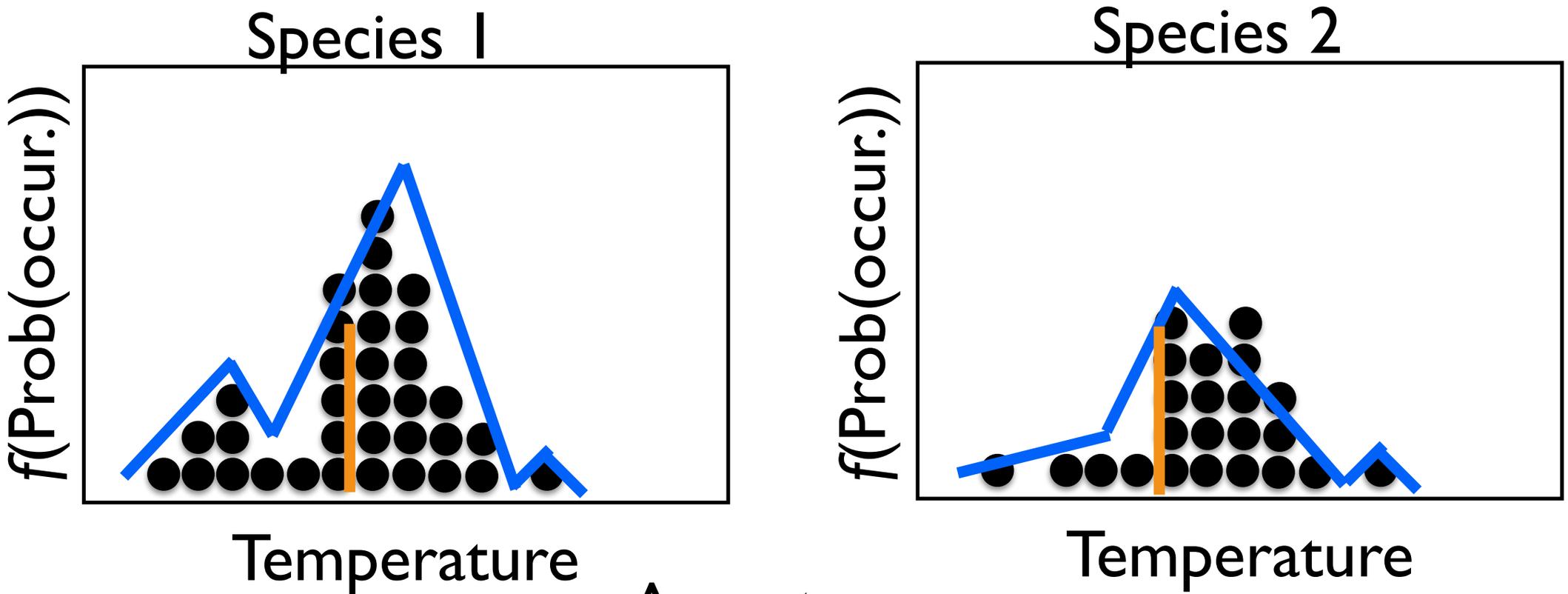

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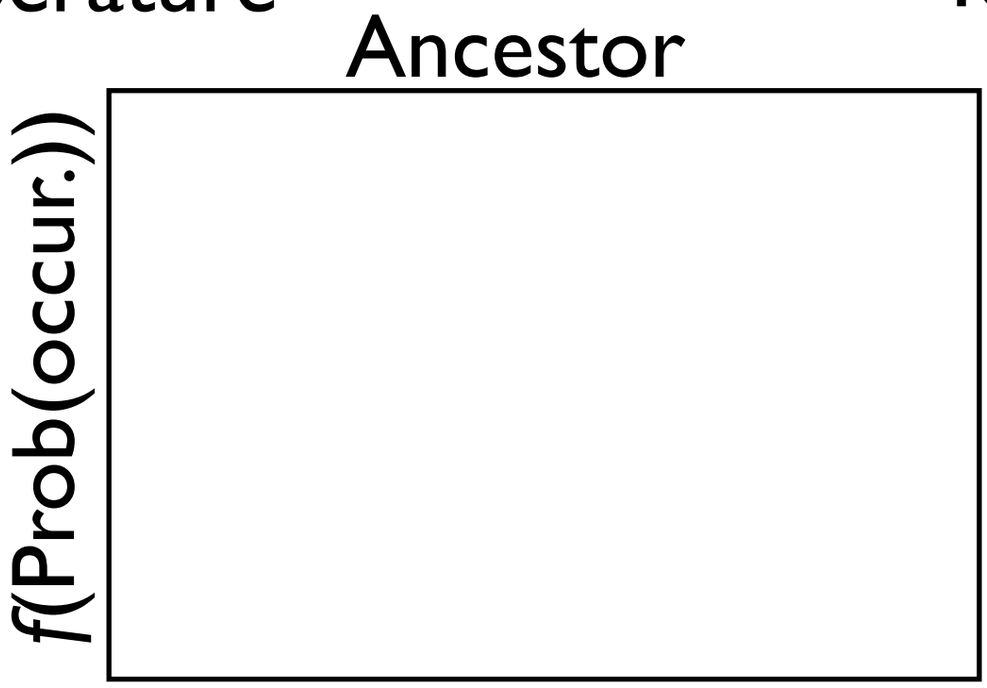

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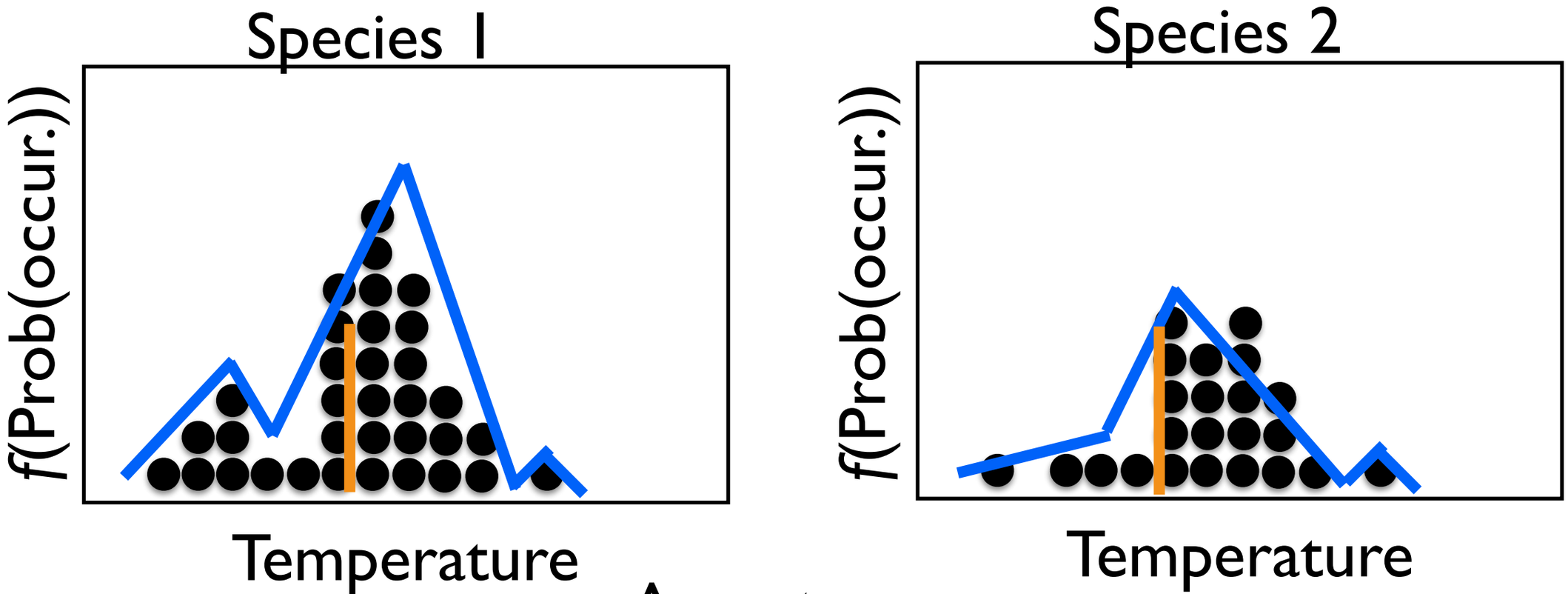

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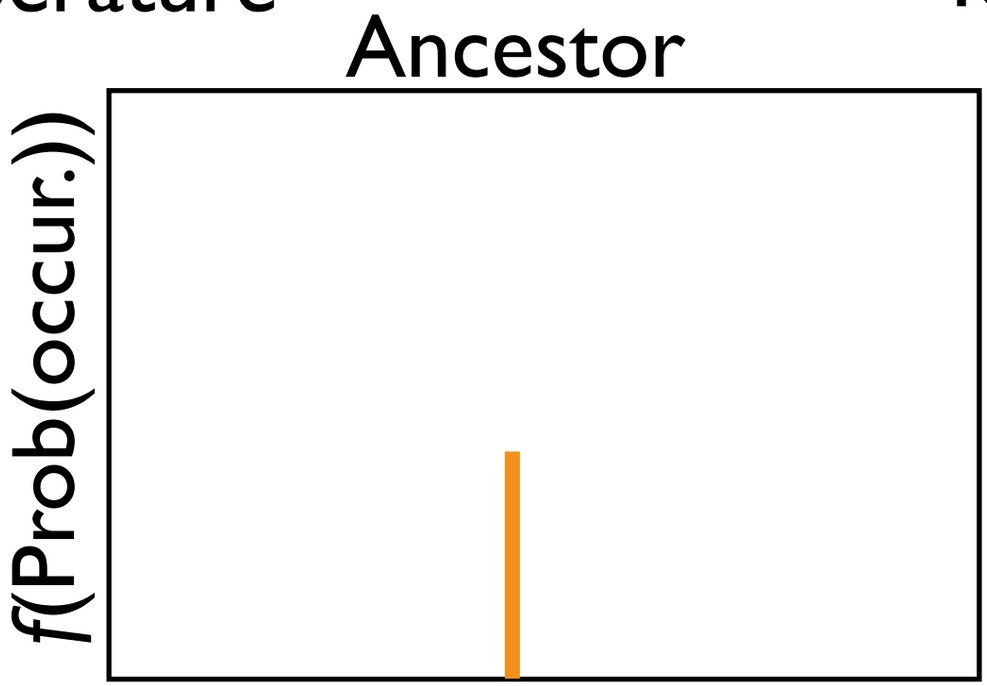

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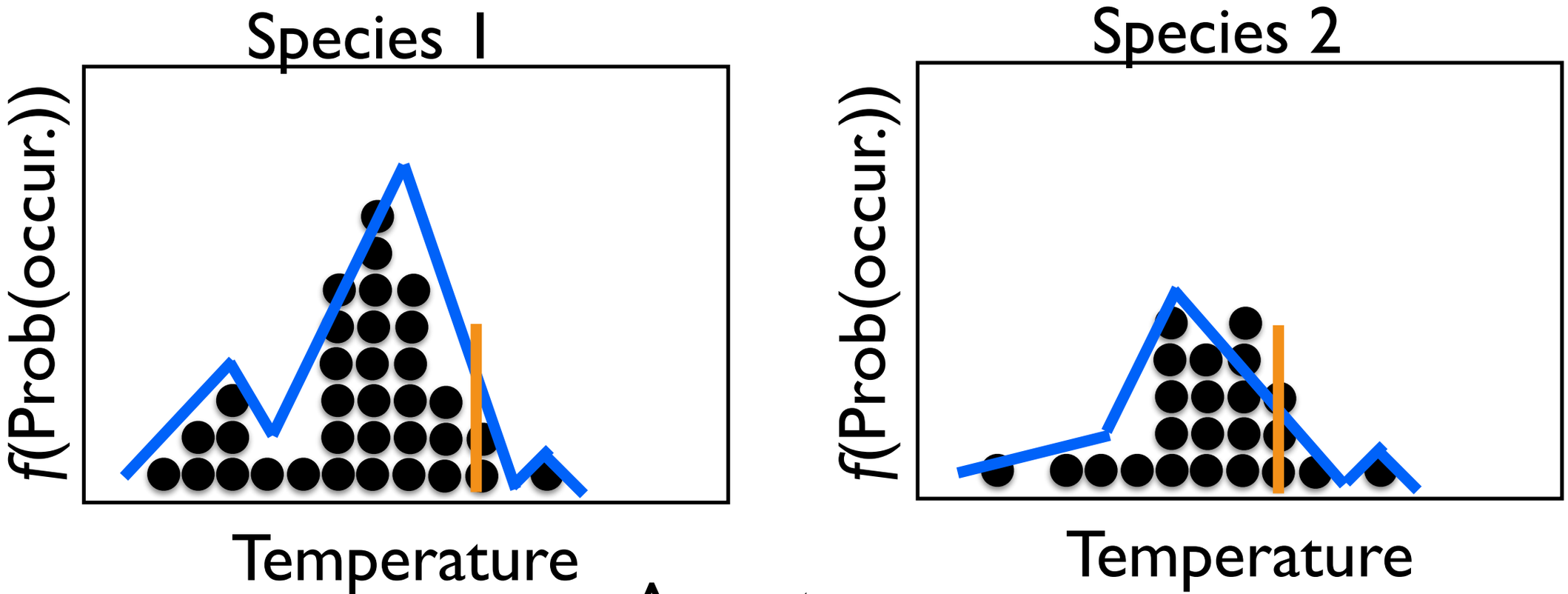

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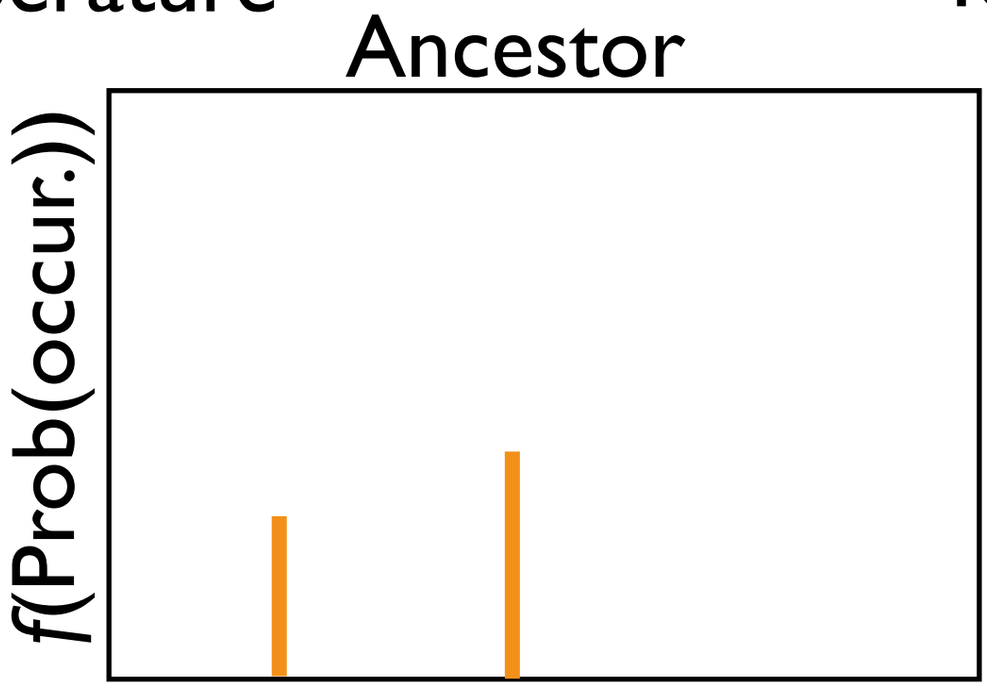

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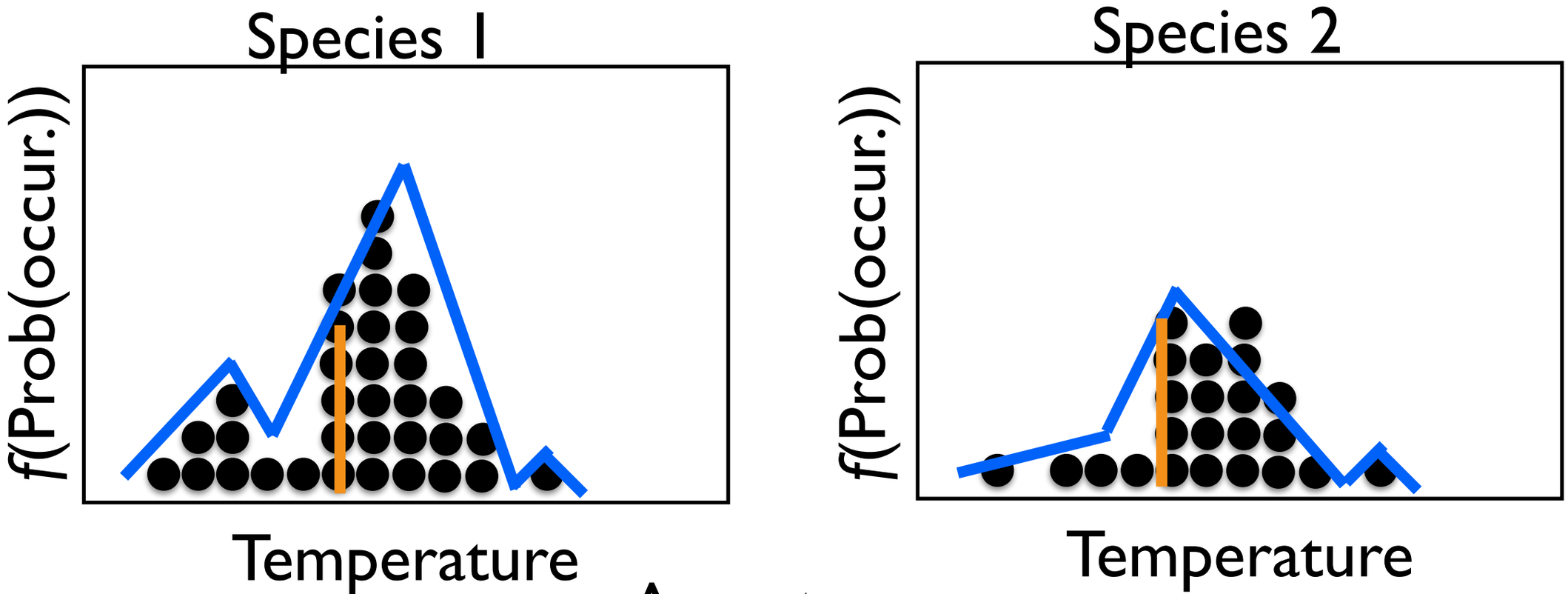

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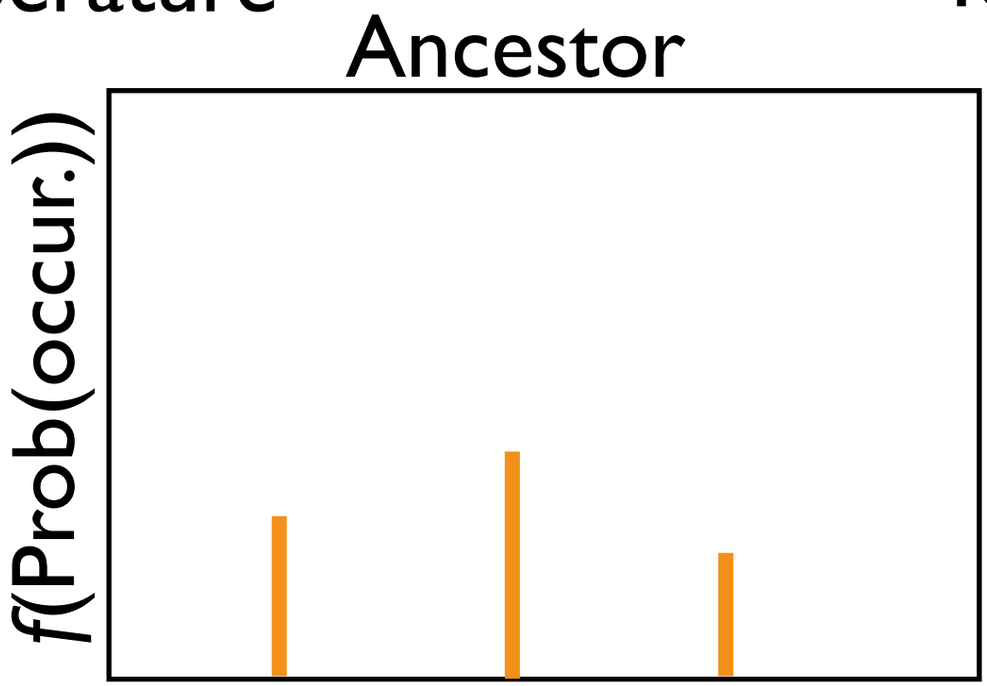

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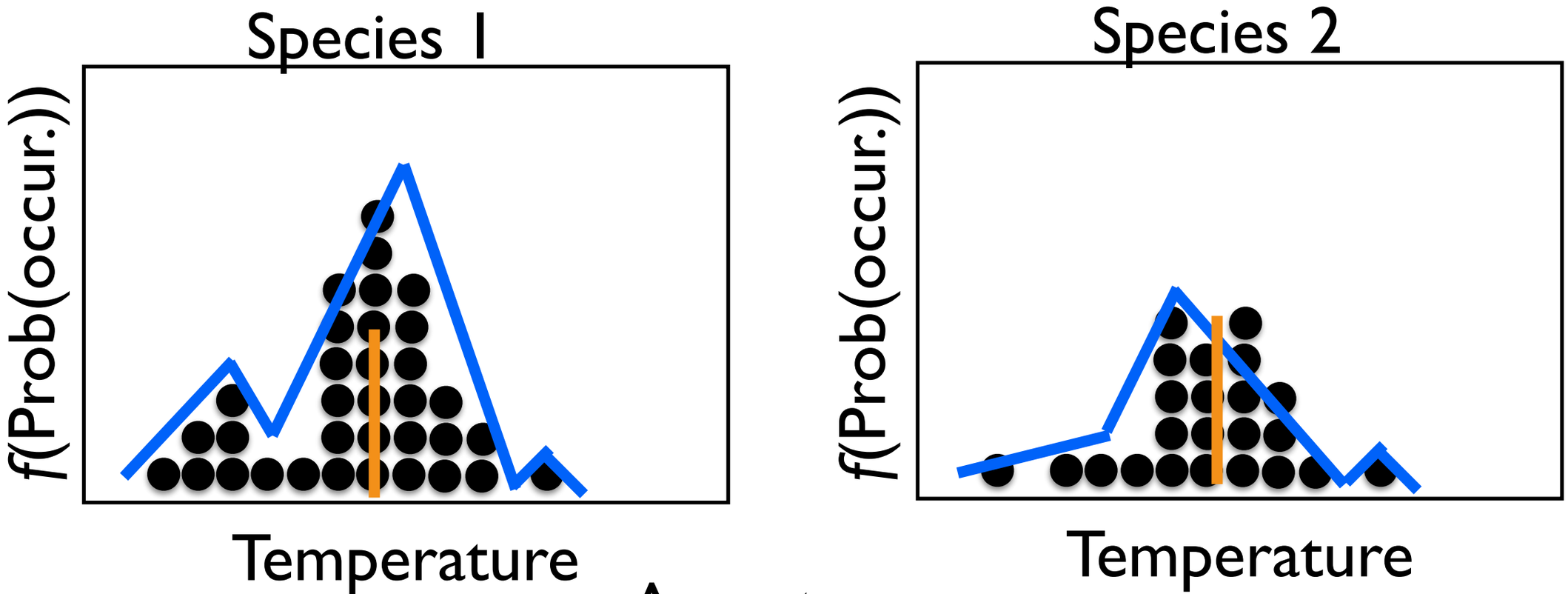

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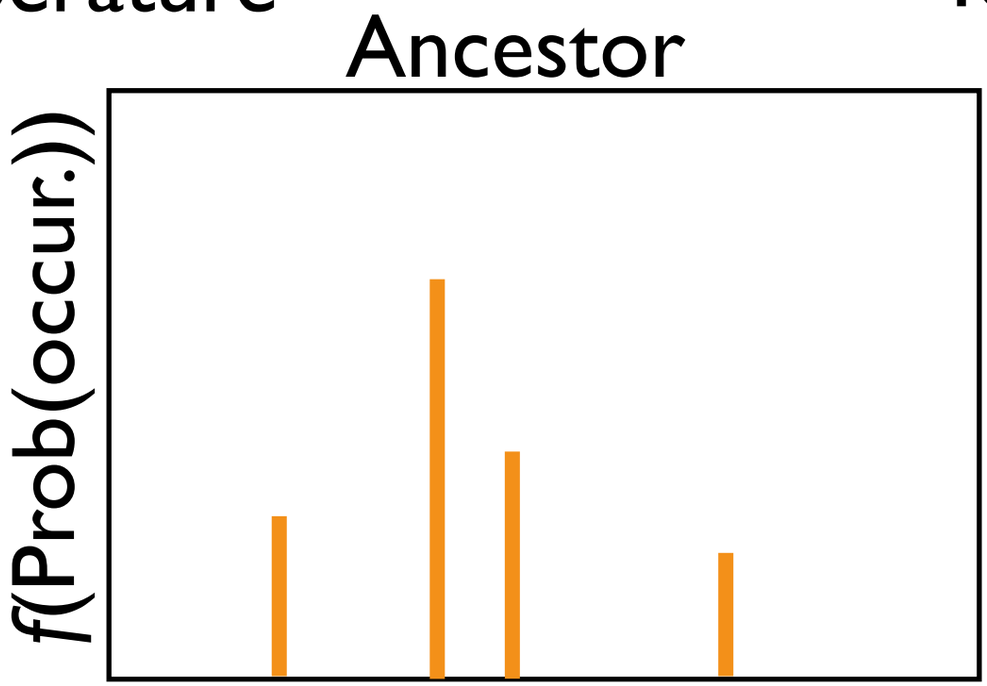

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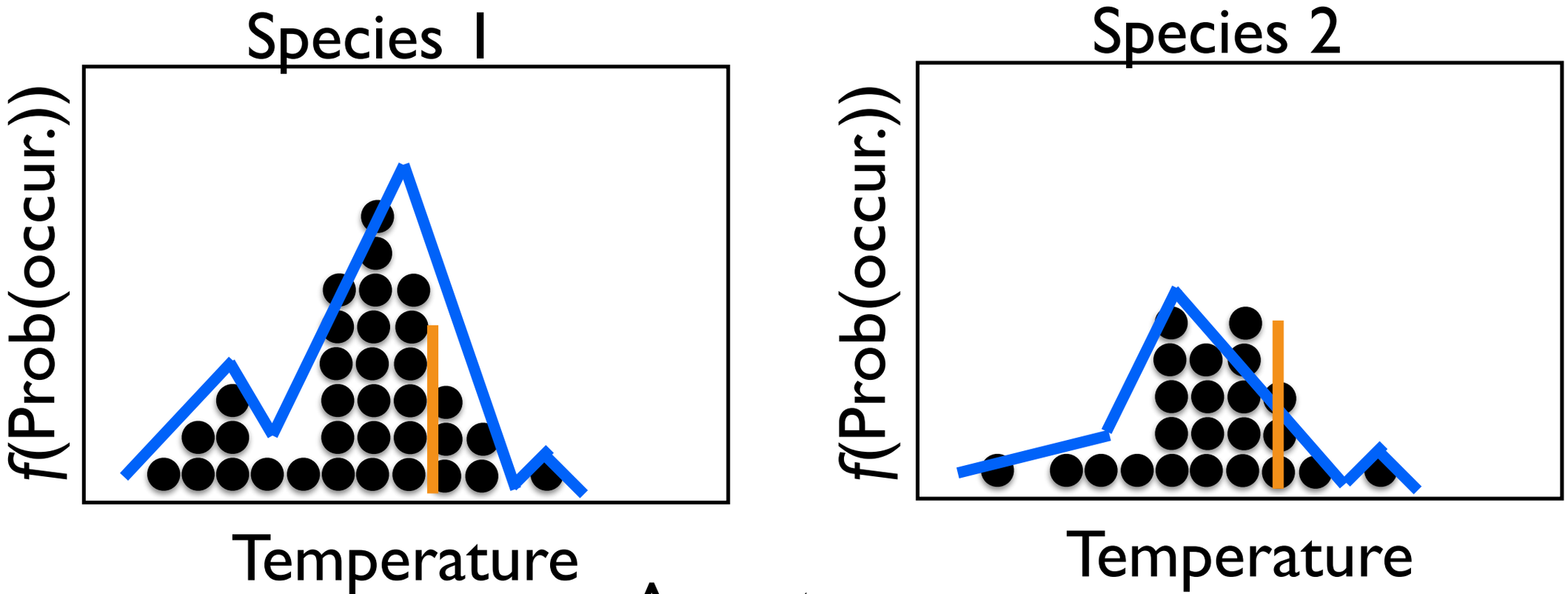

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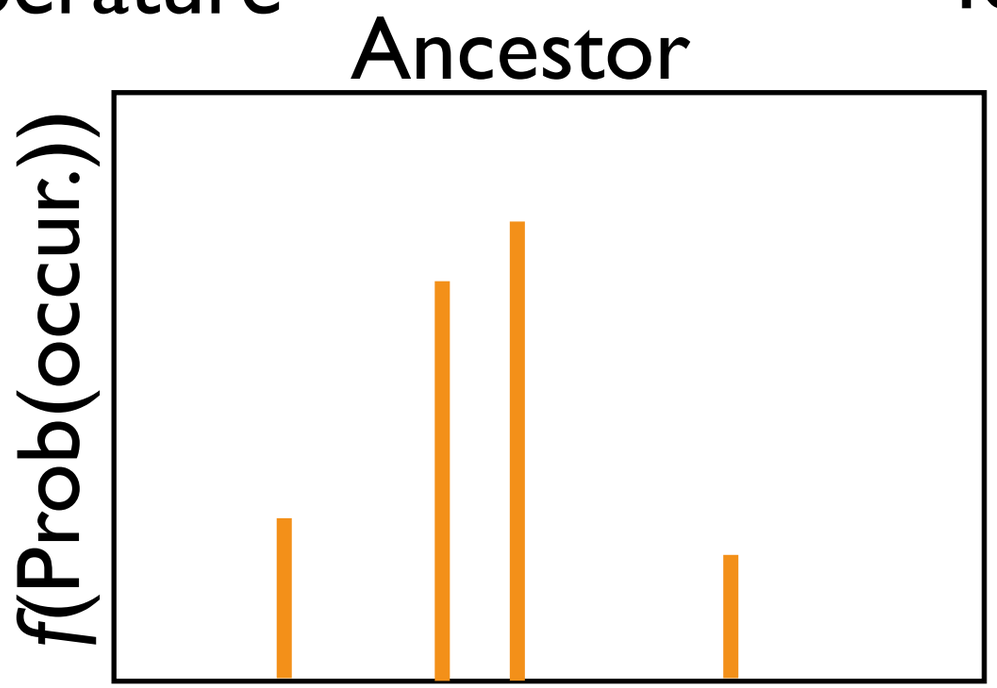

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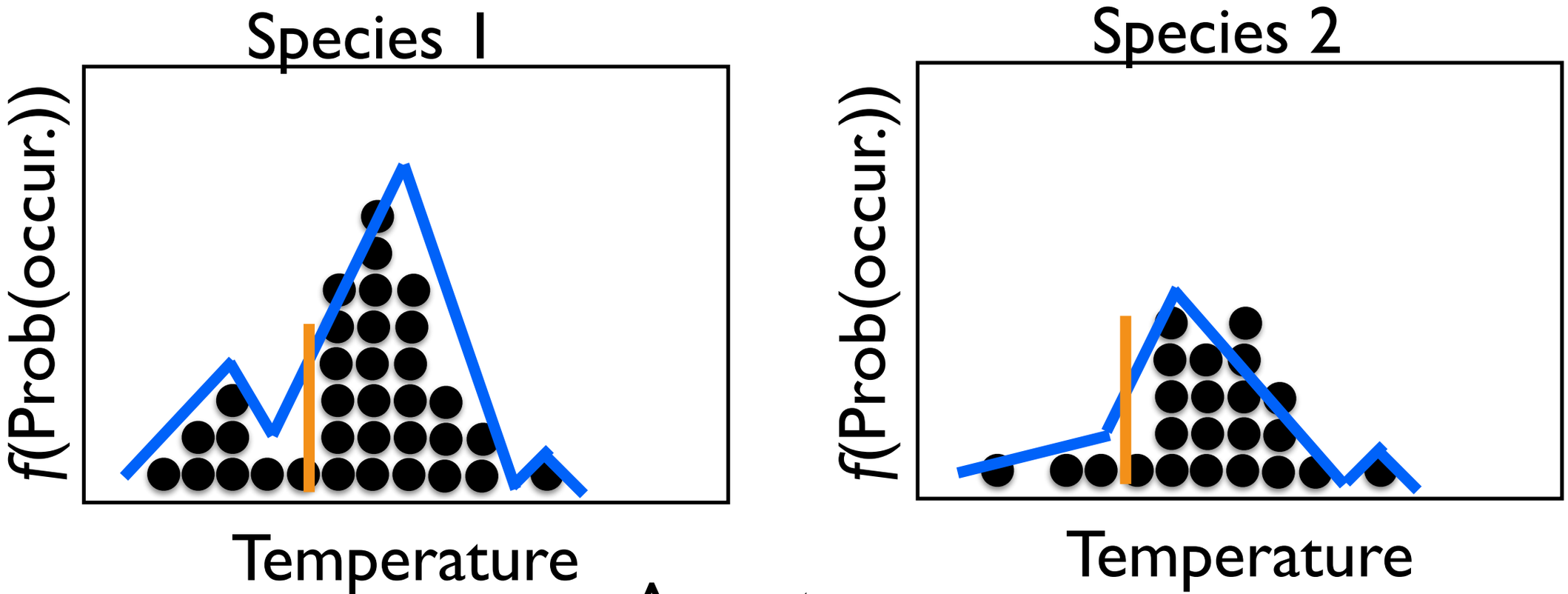

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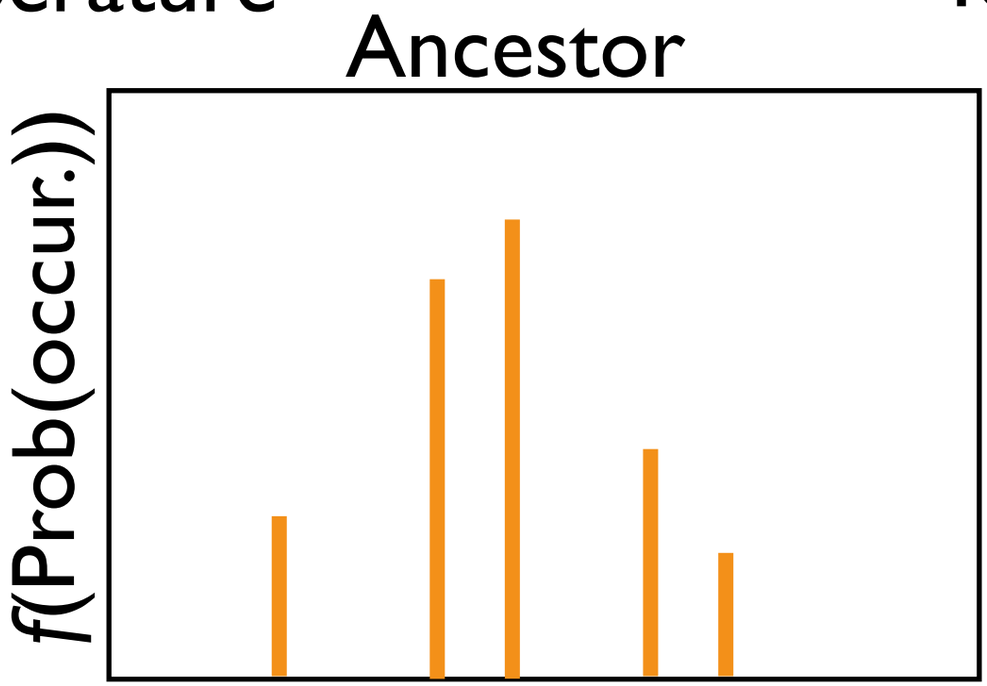

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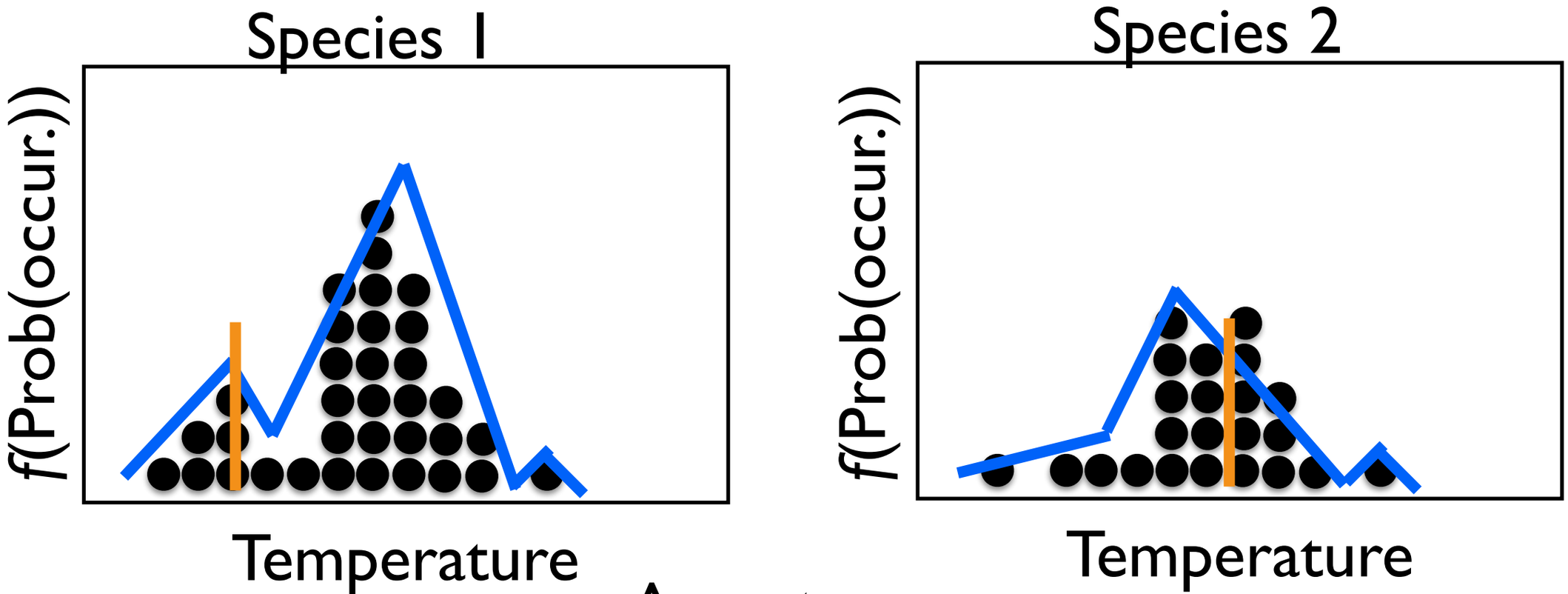

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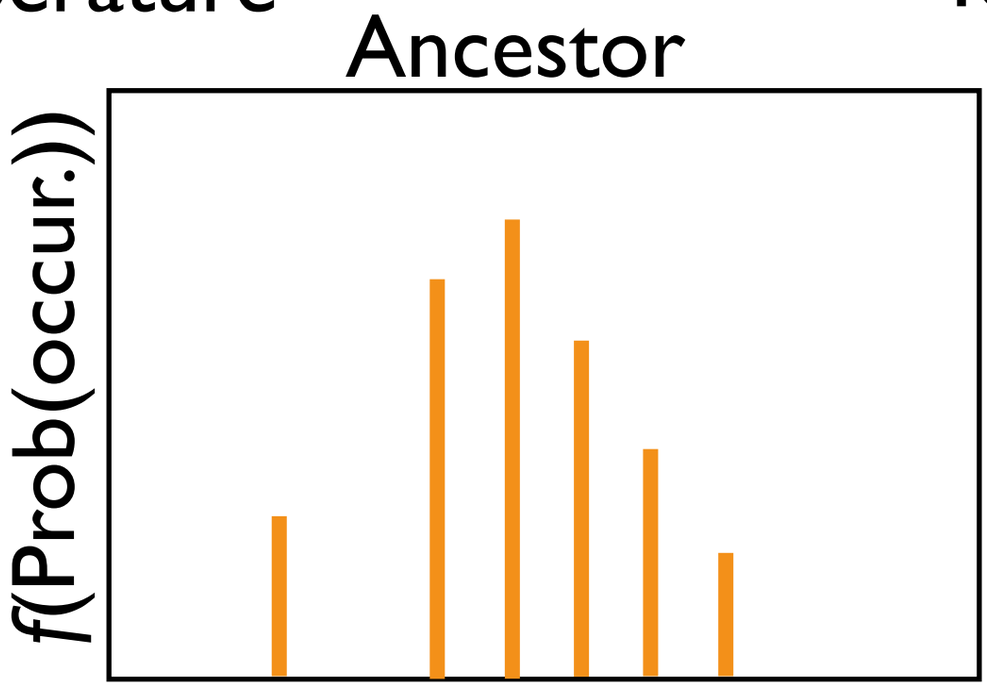

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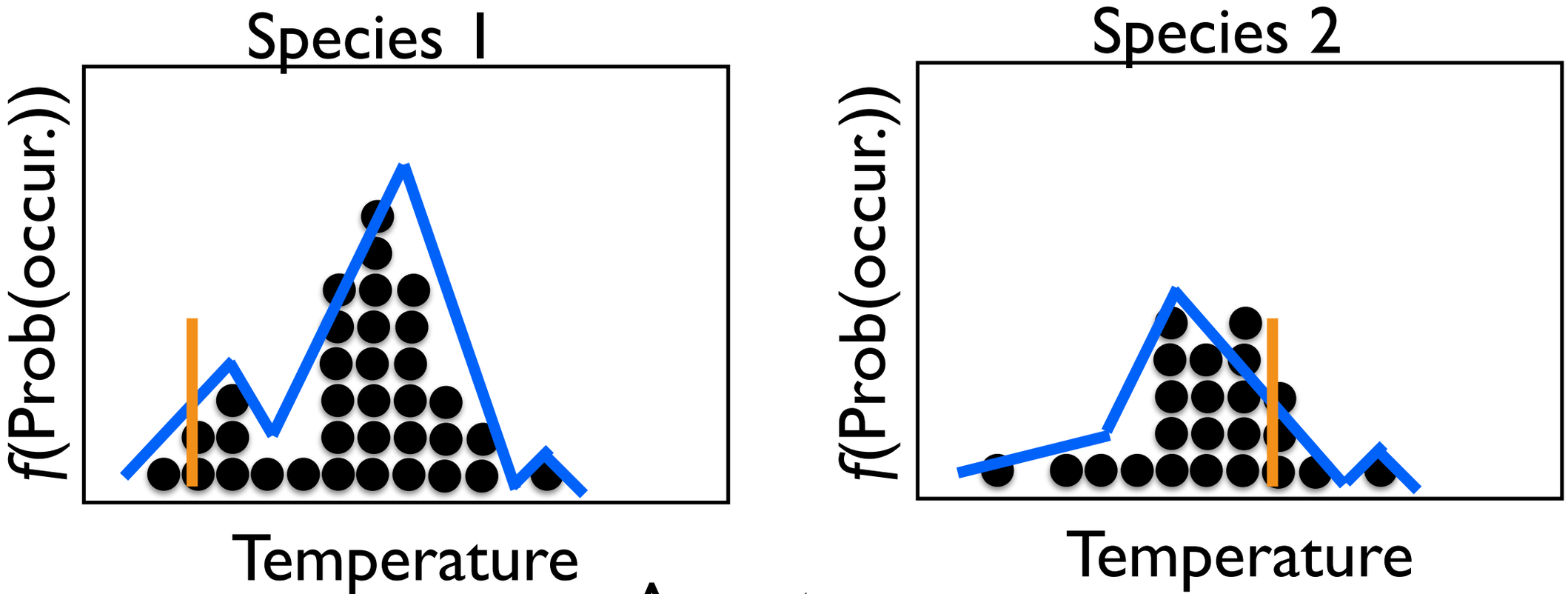

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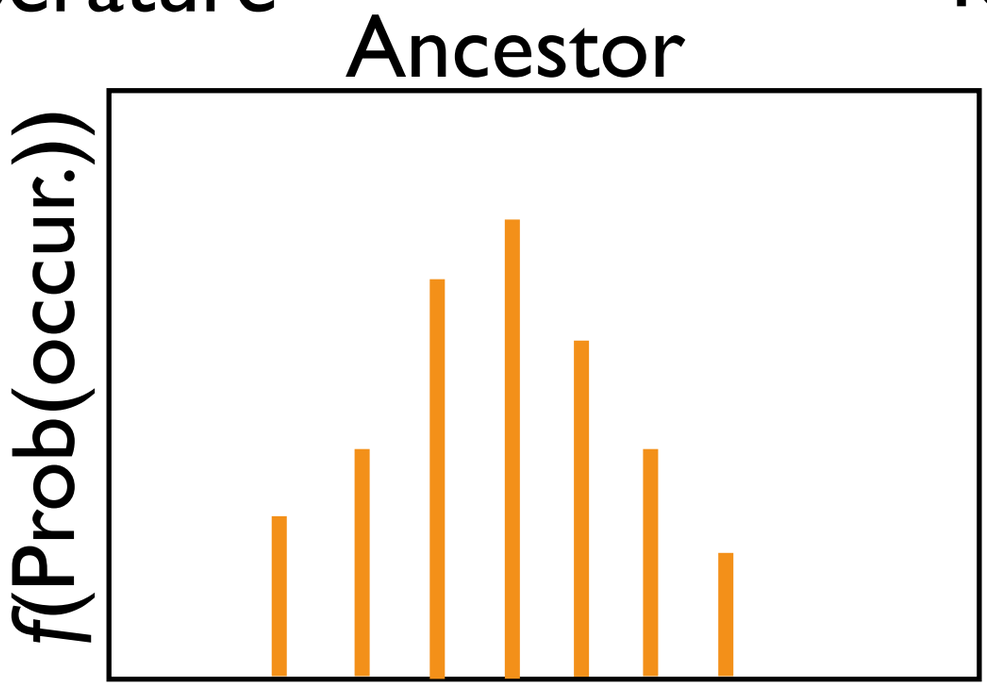

ENM+PCMs: Sampling approach

Critiques:

1. Niche curves are inferred estimates, not data
2. Sampling from the curves adds variance
3. No model choice

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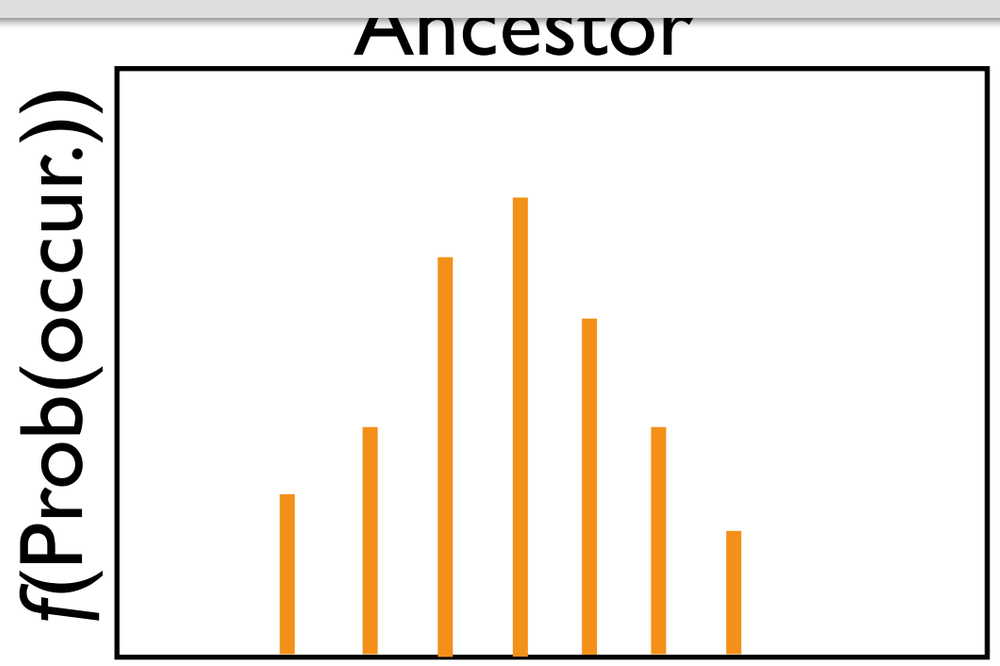

Combining ENMs and PCMs

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How *should* we link ENMs/SDMs and PCMs?

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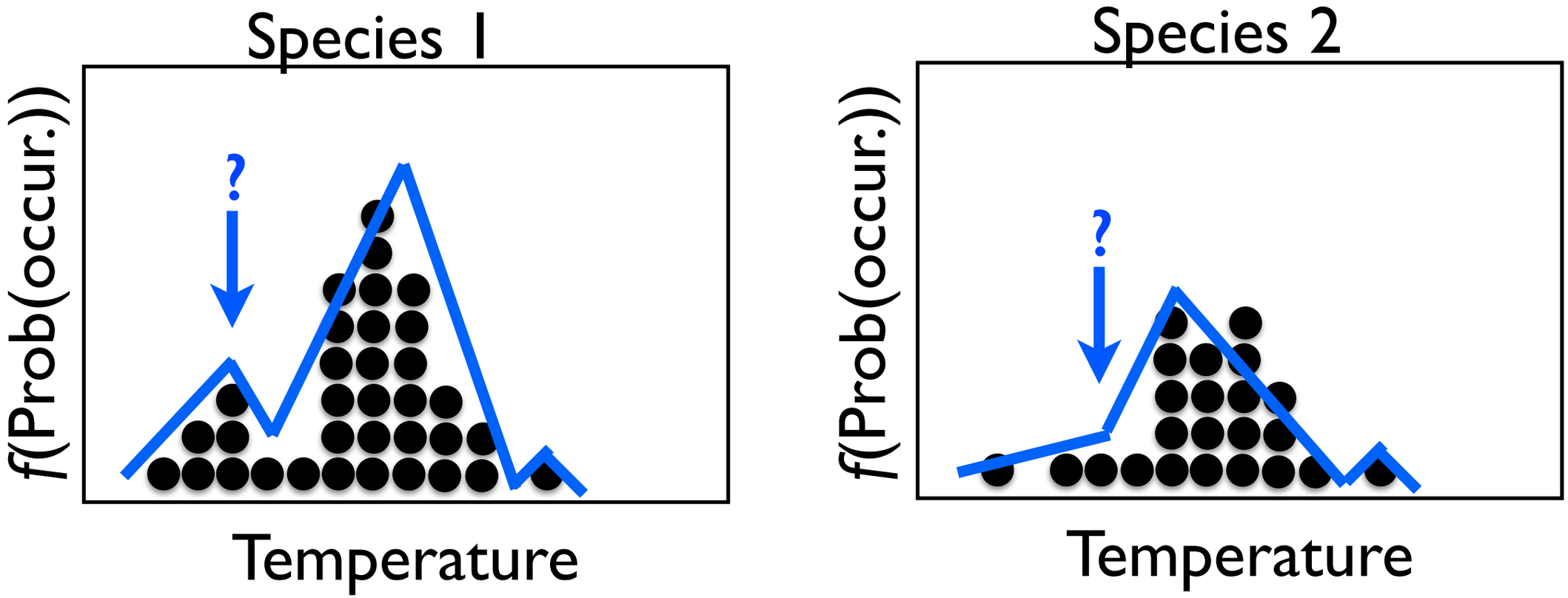
Unsolved problem: how are niches *homologous?*



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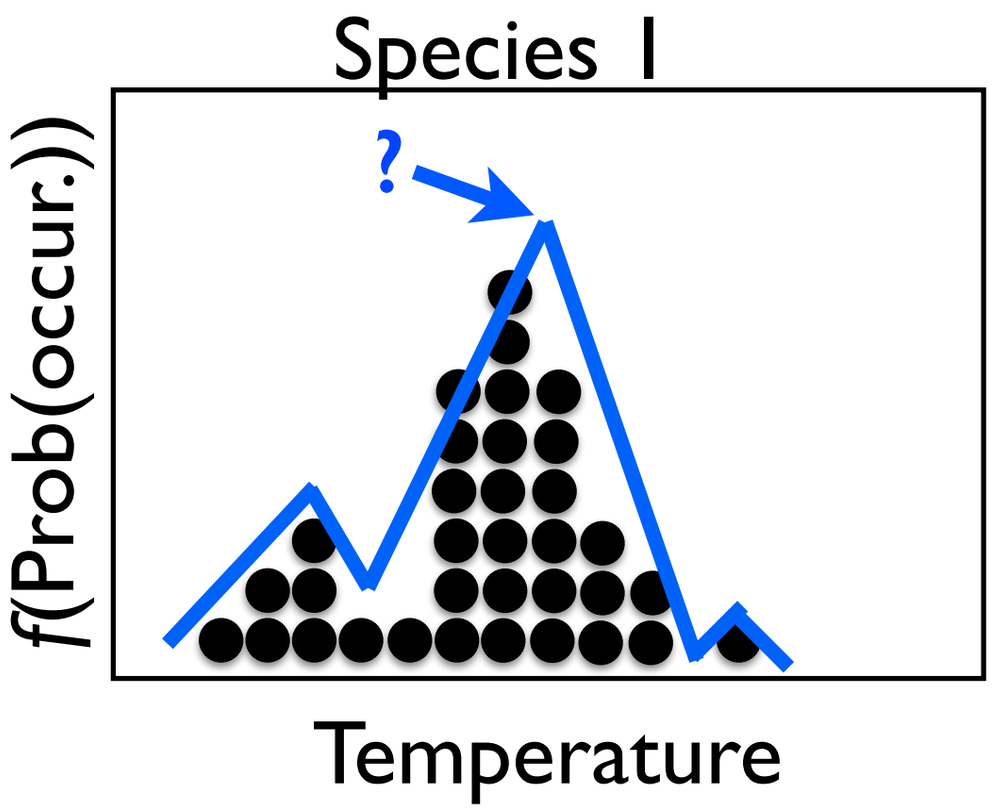

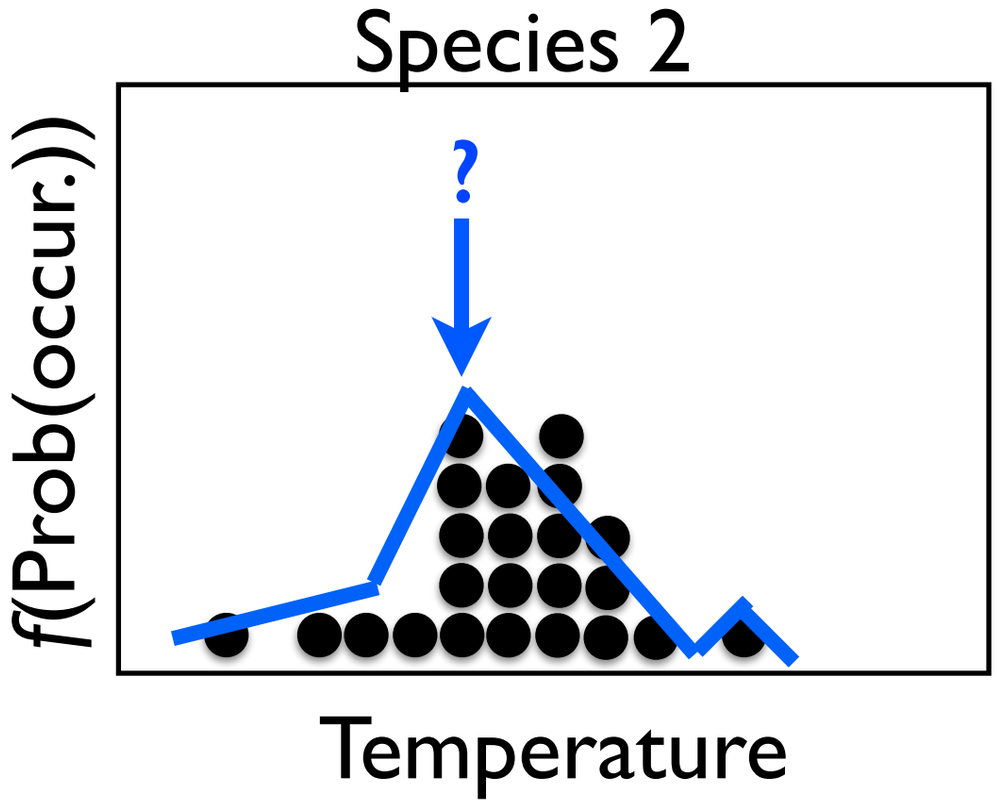

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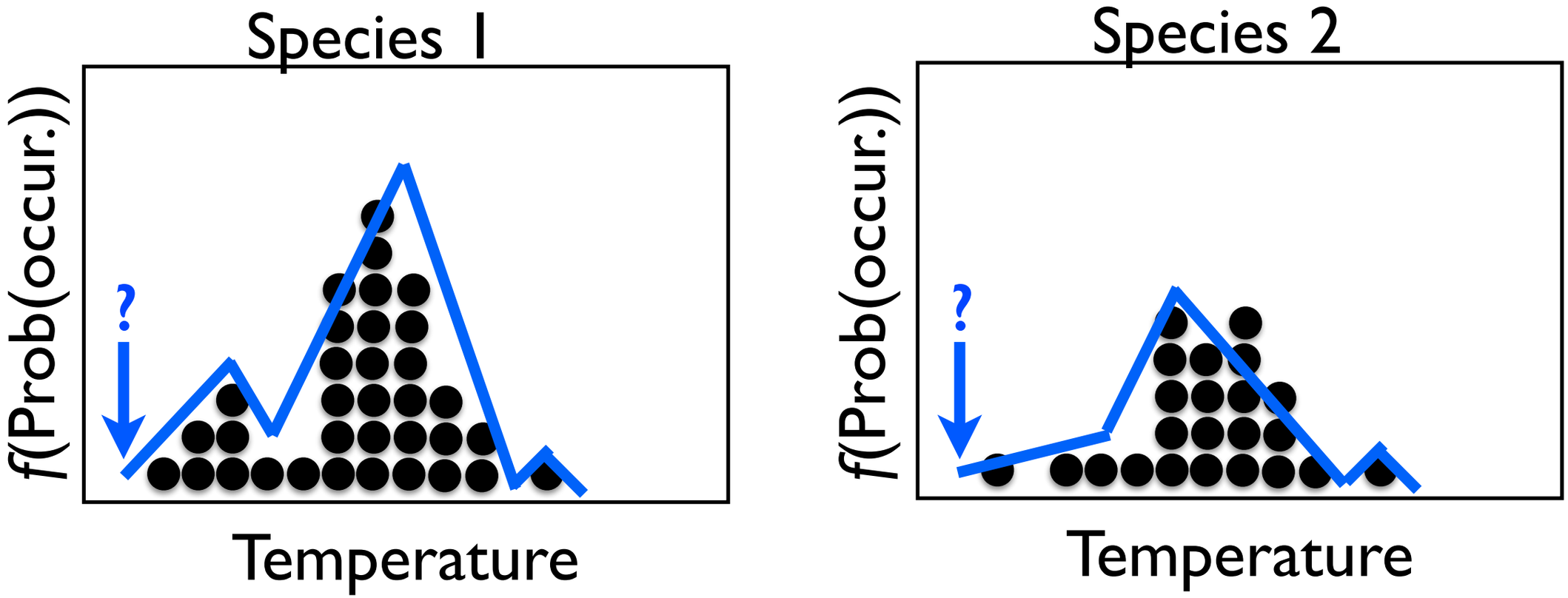

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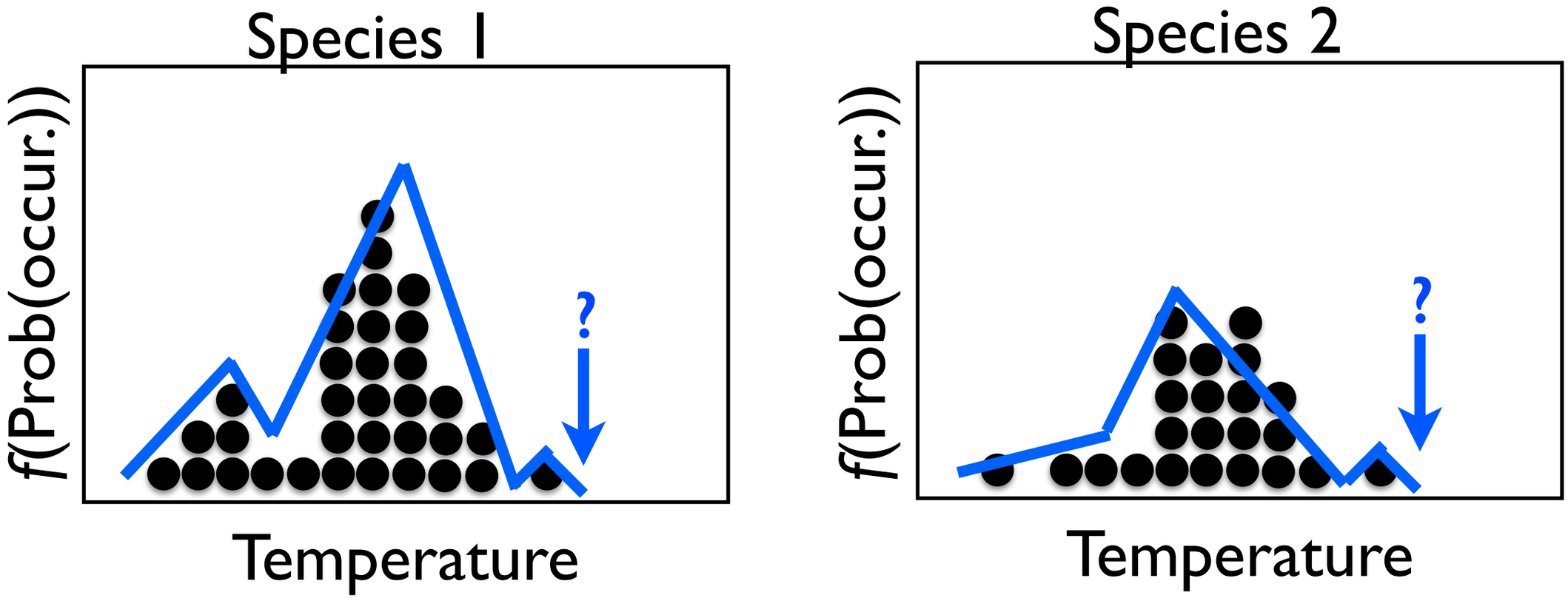

How *should* we link ENMs/SDMs and PCMs?

Homology problem: standard Niche Modelling tools won't give identical niche models between methods

…or even between random number seeds

Common ENM tools

- BioClim (min/max)
- GLMs
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- MARS
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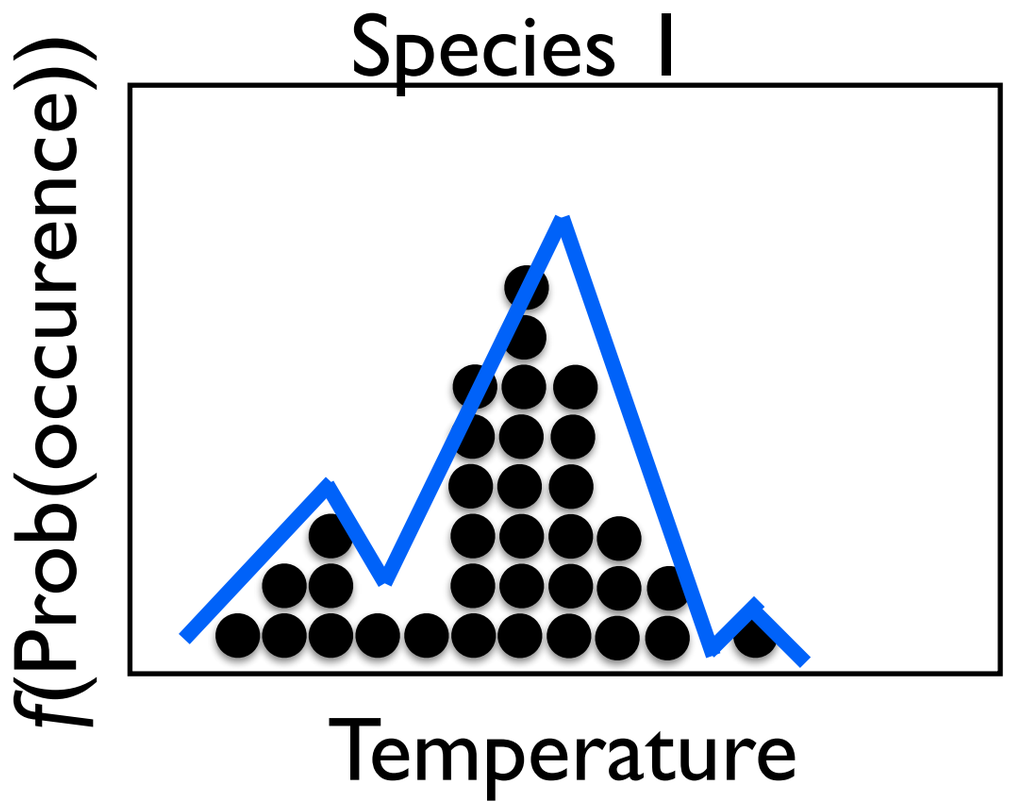

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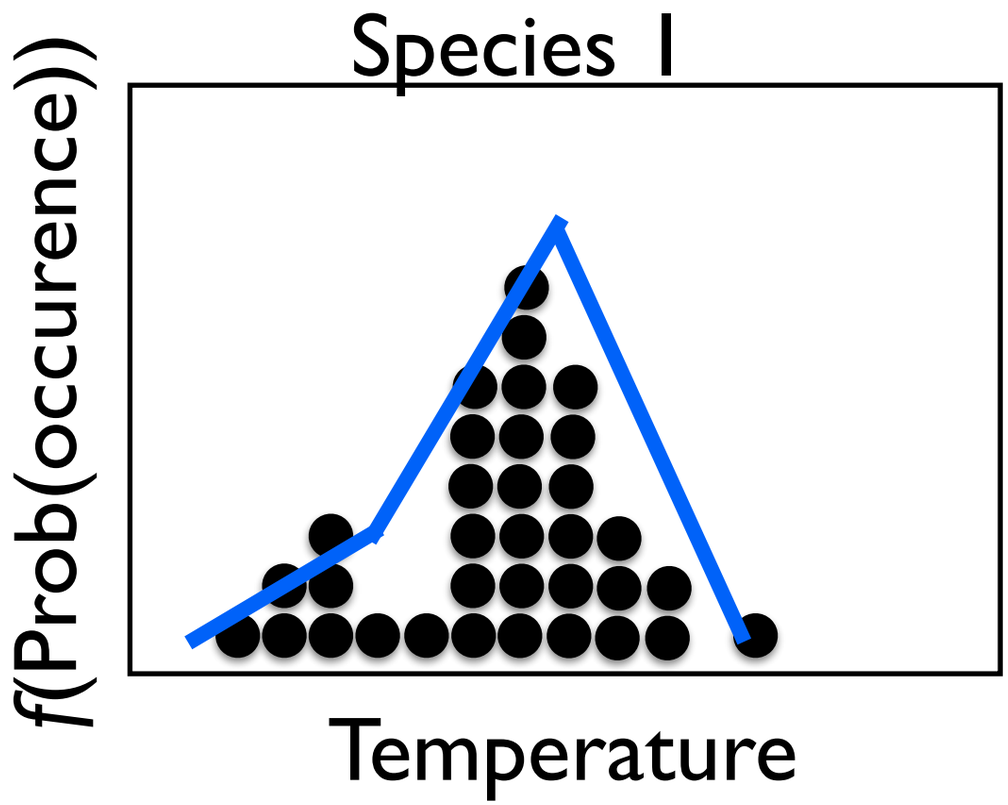

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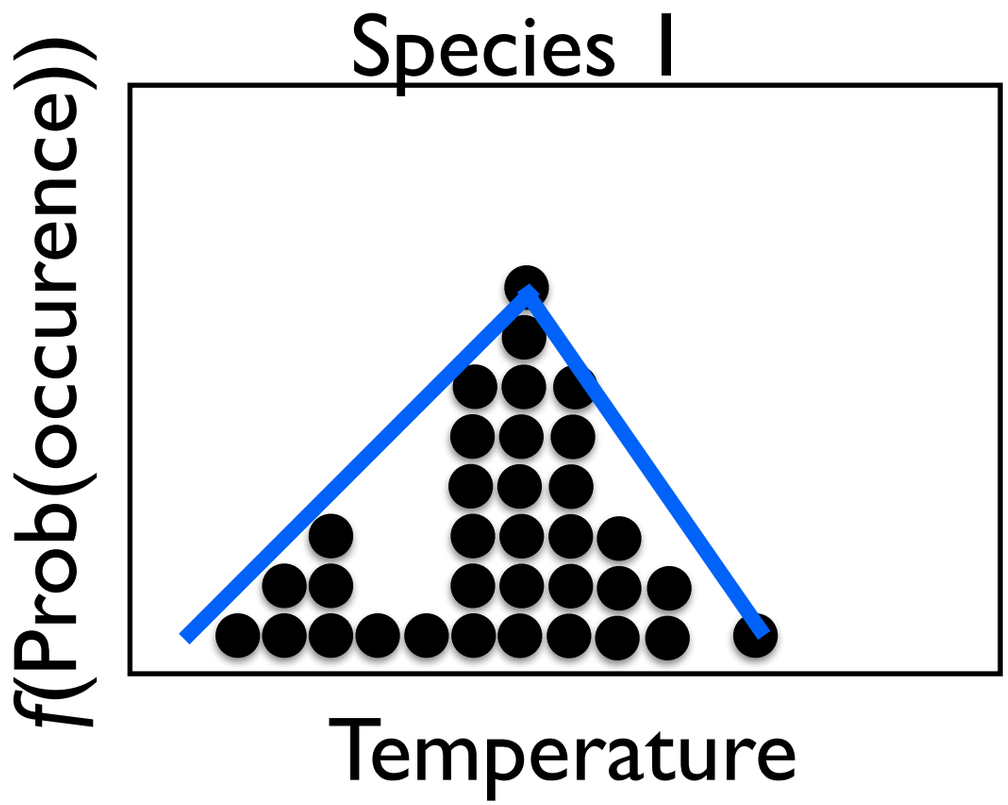

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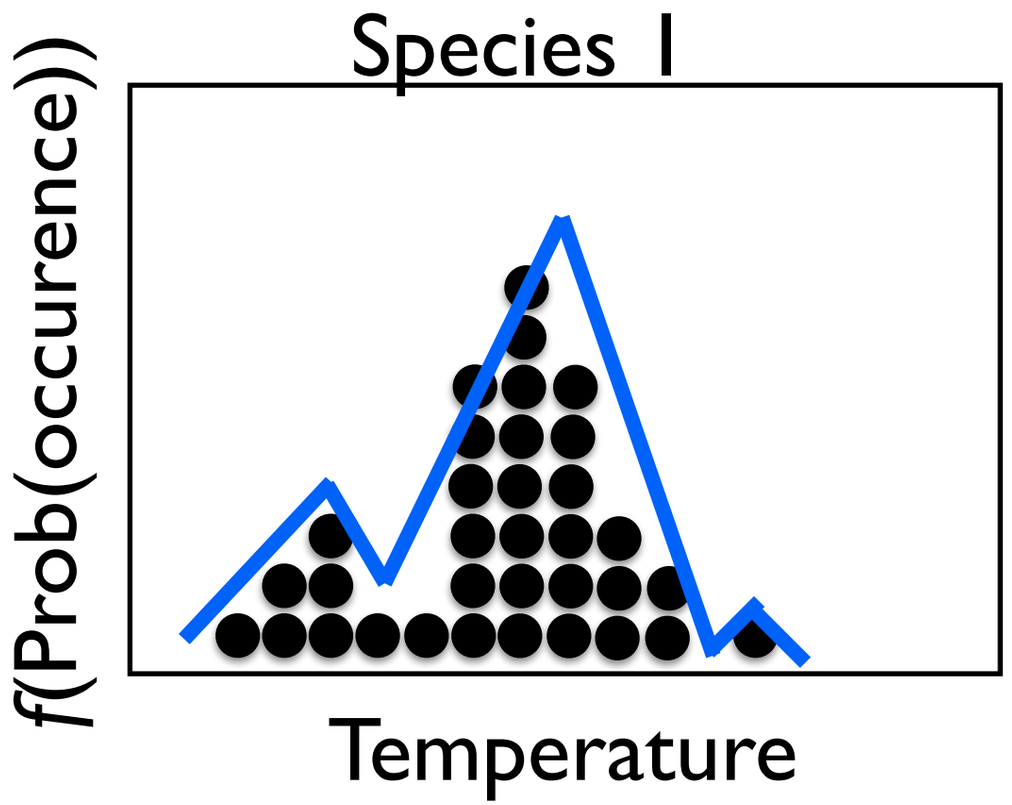

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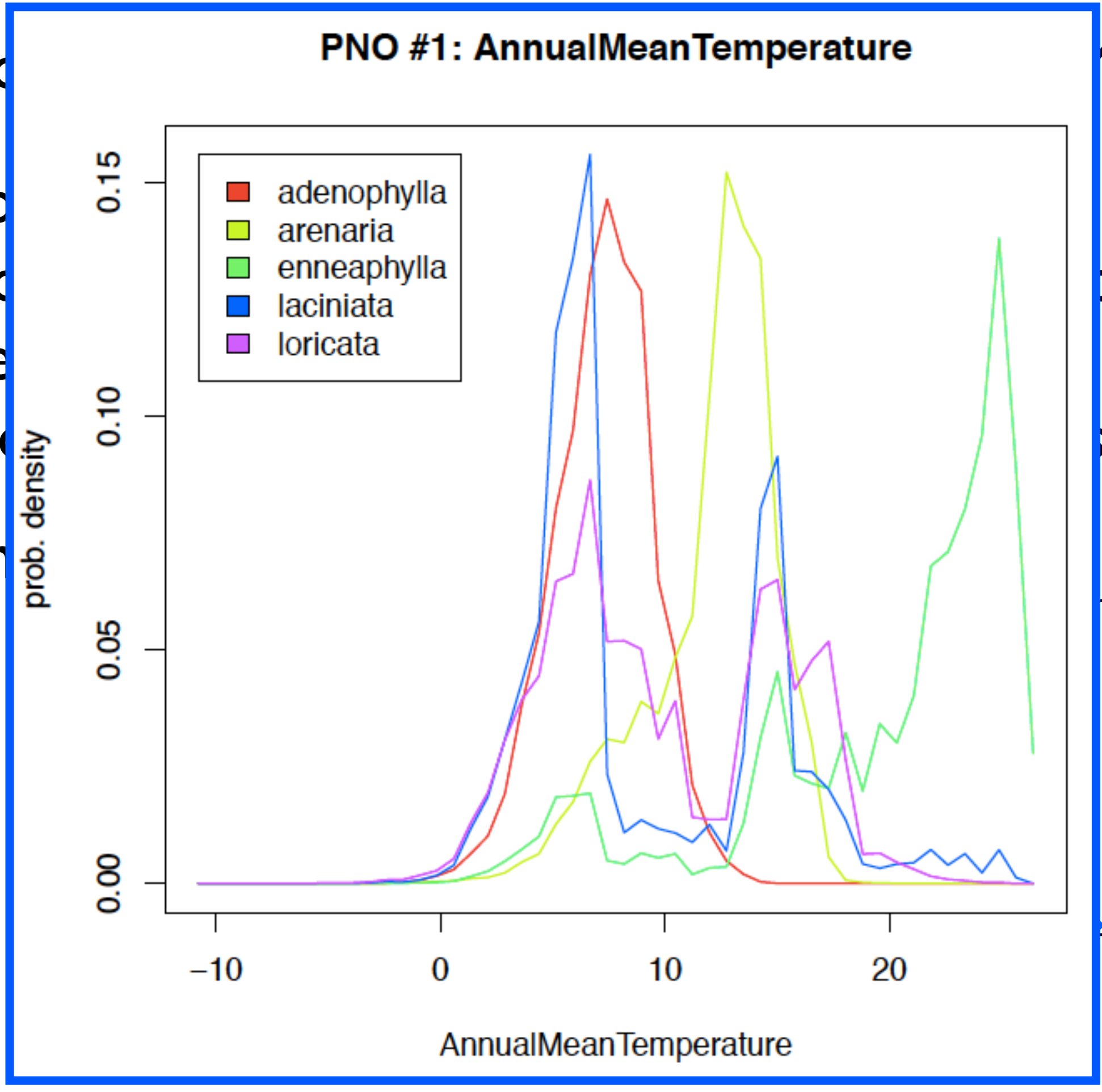

(example dataset from Heibl's phyloclim R package)

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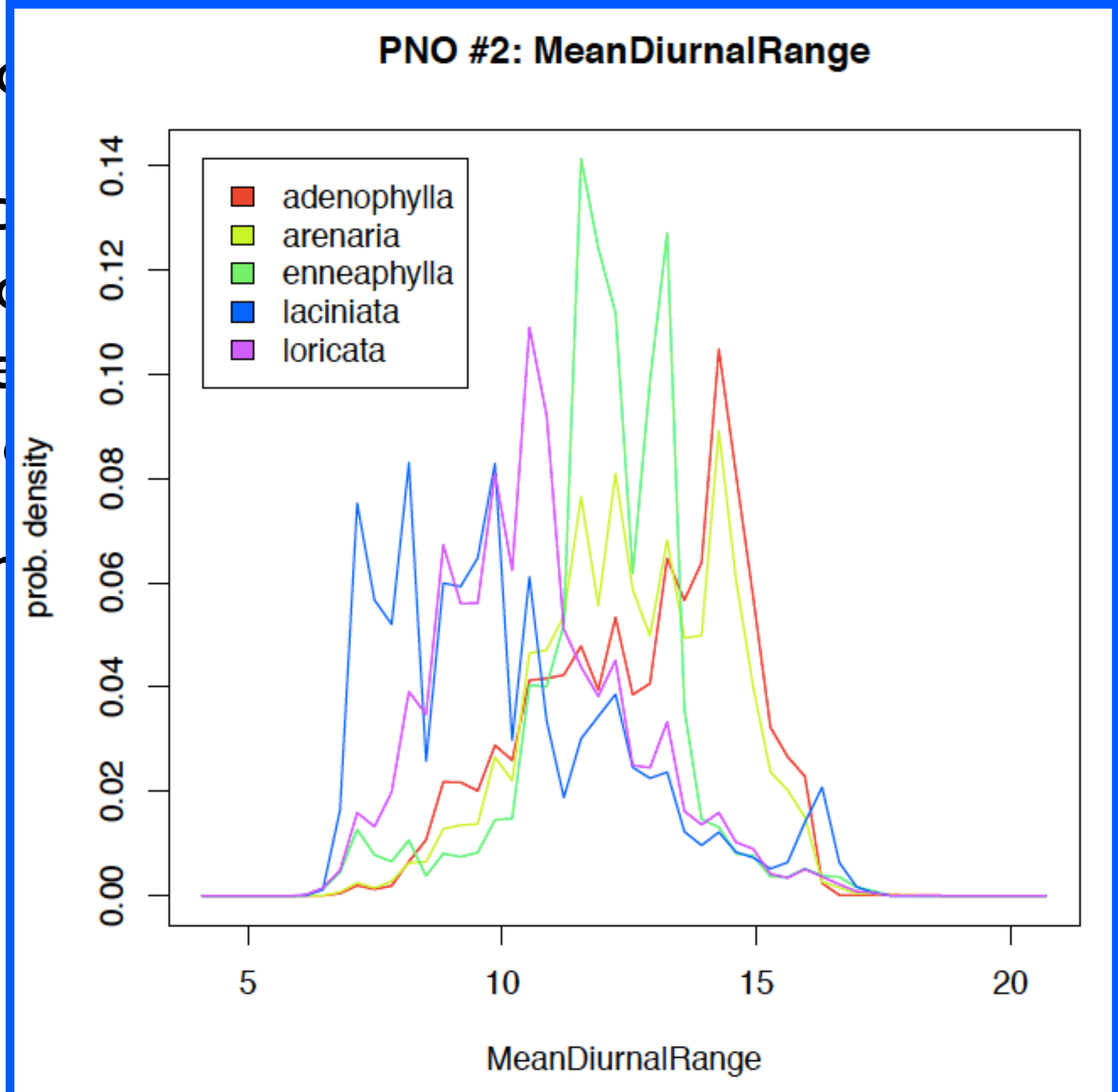

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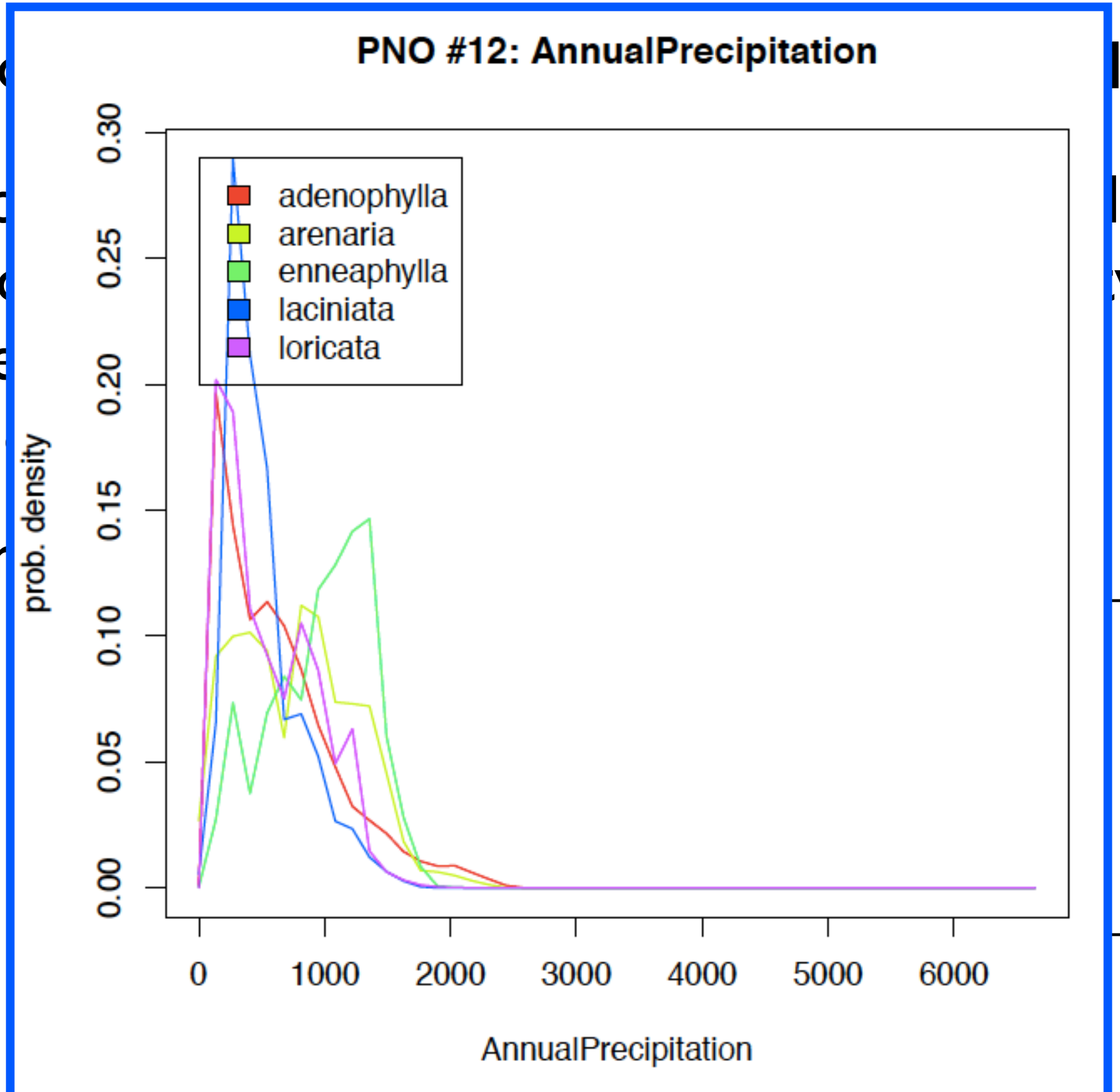

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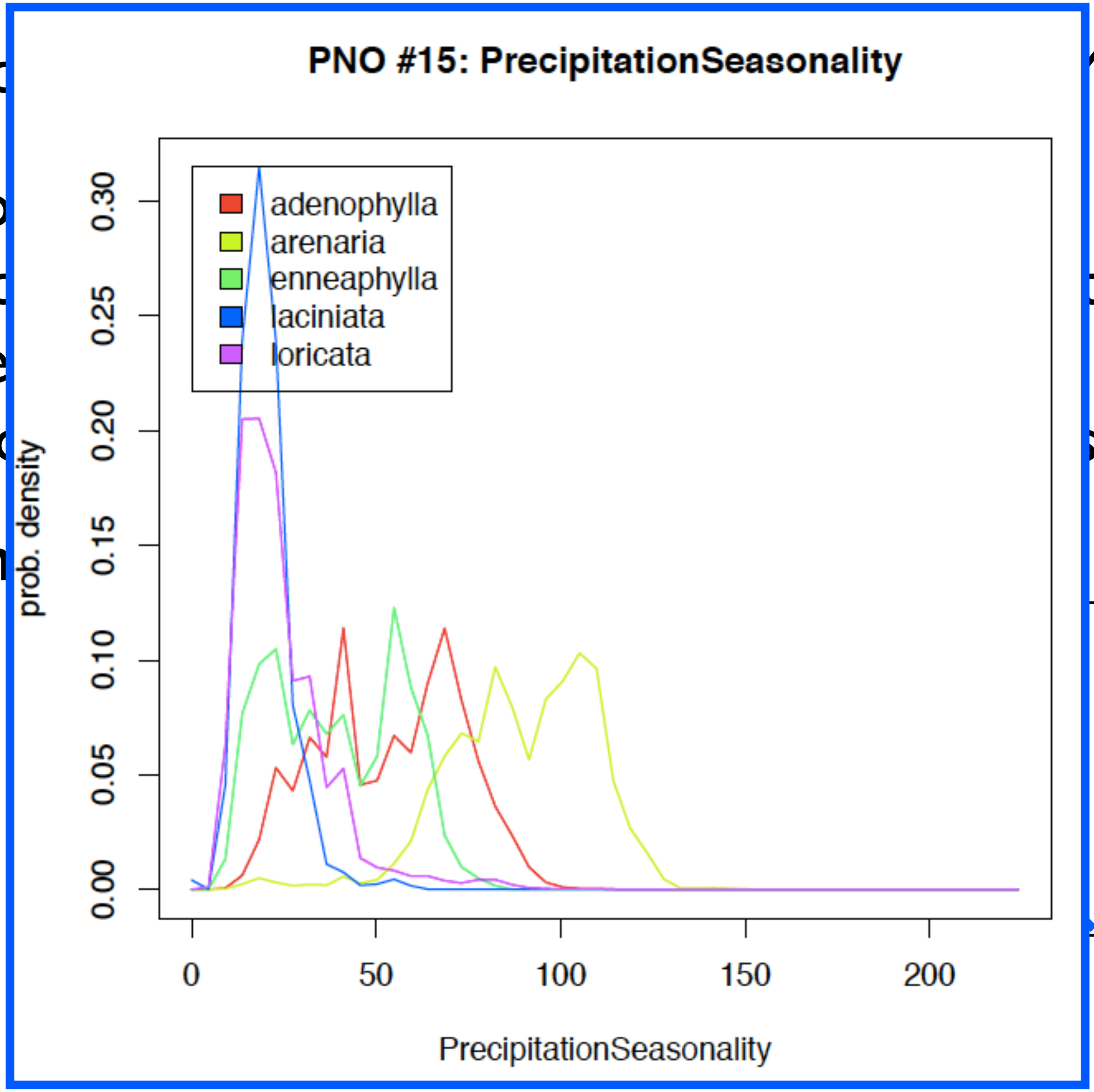
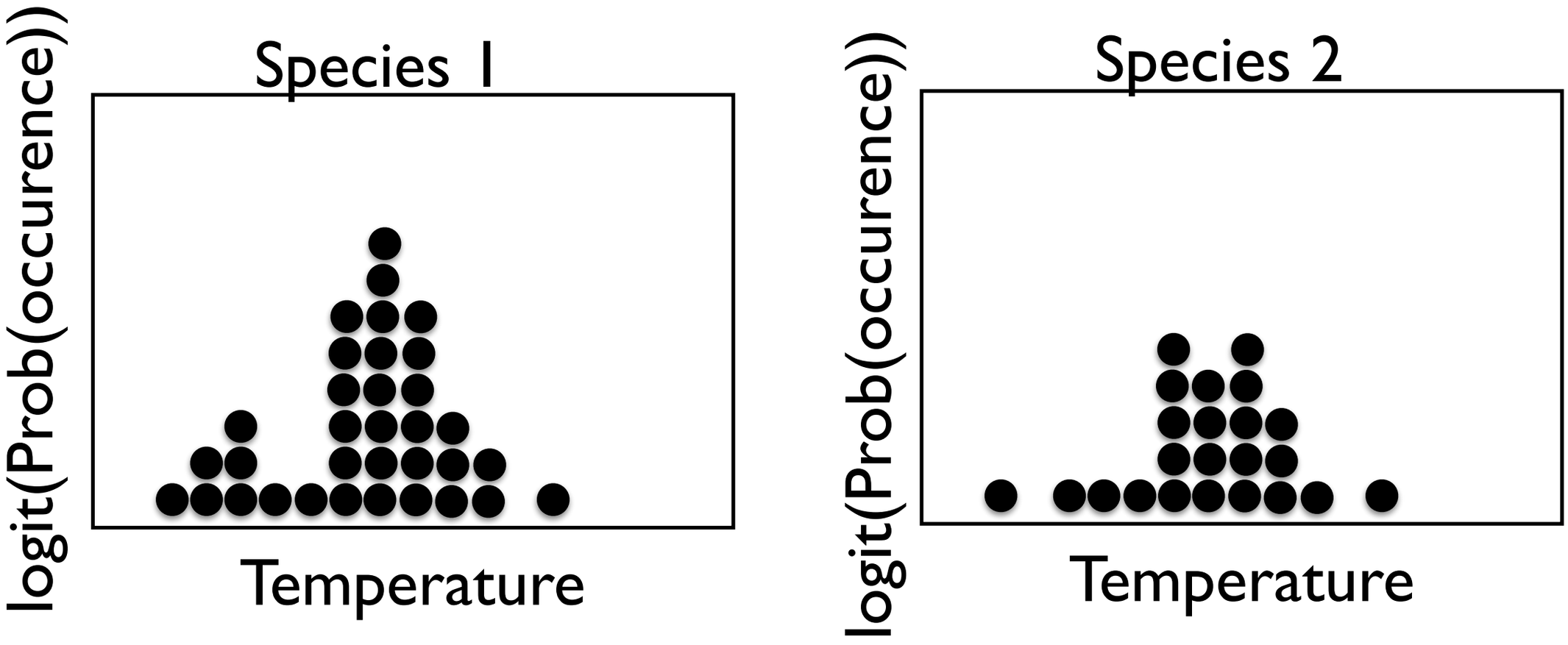


(example dataset from Heibl's phyloclim R package)

Proposal: PhyloSDM

1. Niche model: simple spline, 3 parameters/species/trait



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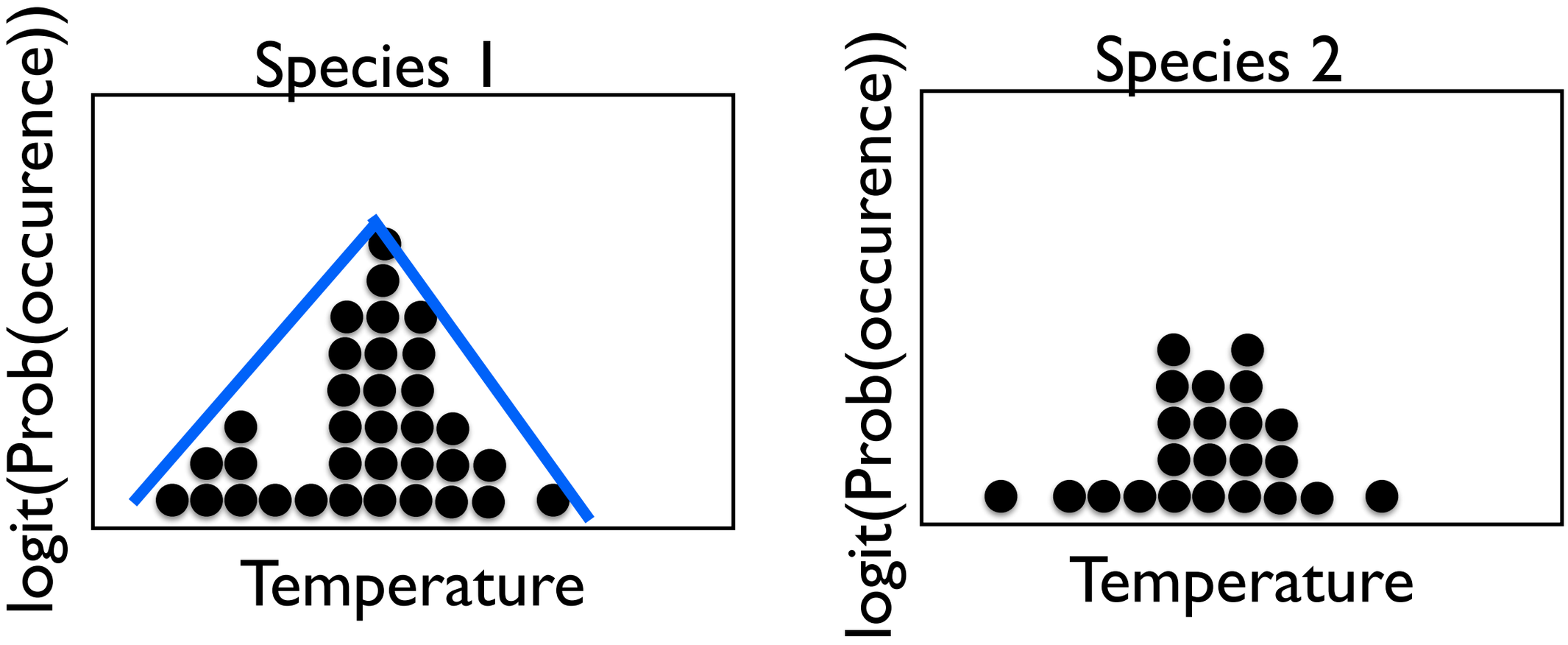

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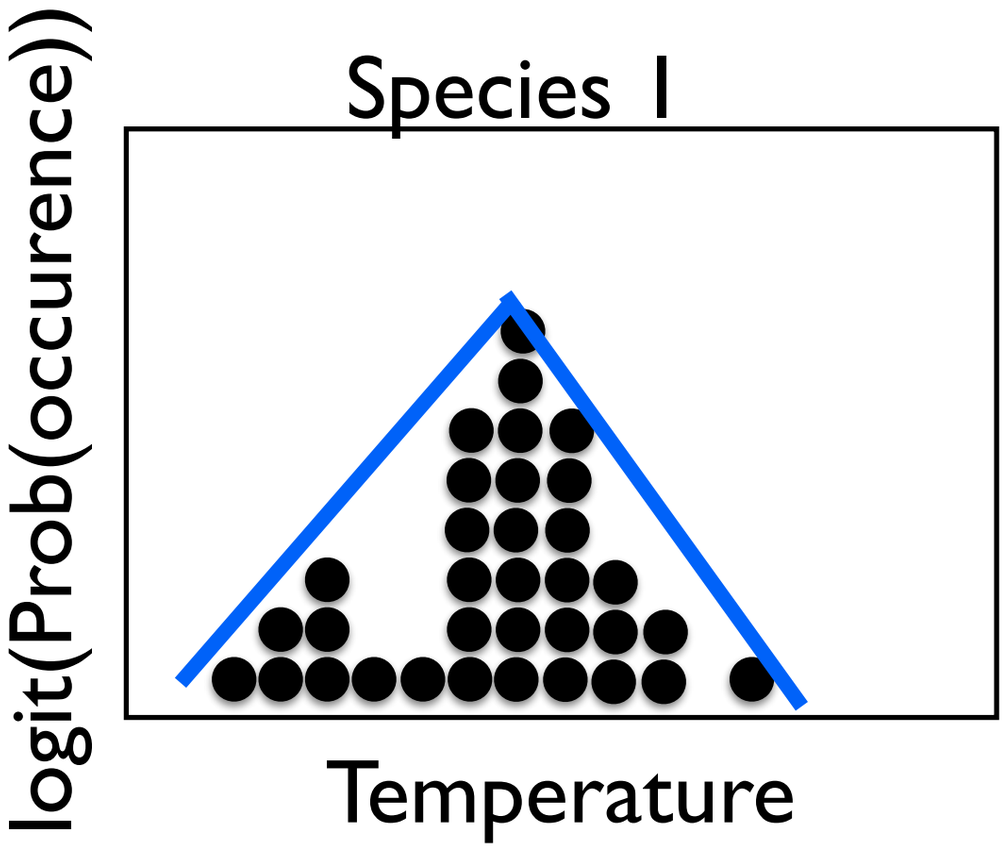

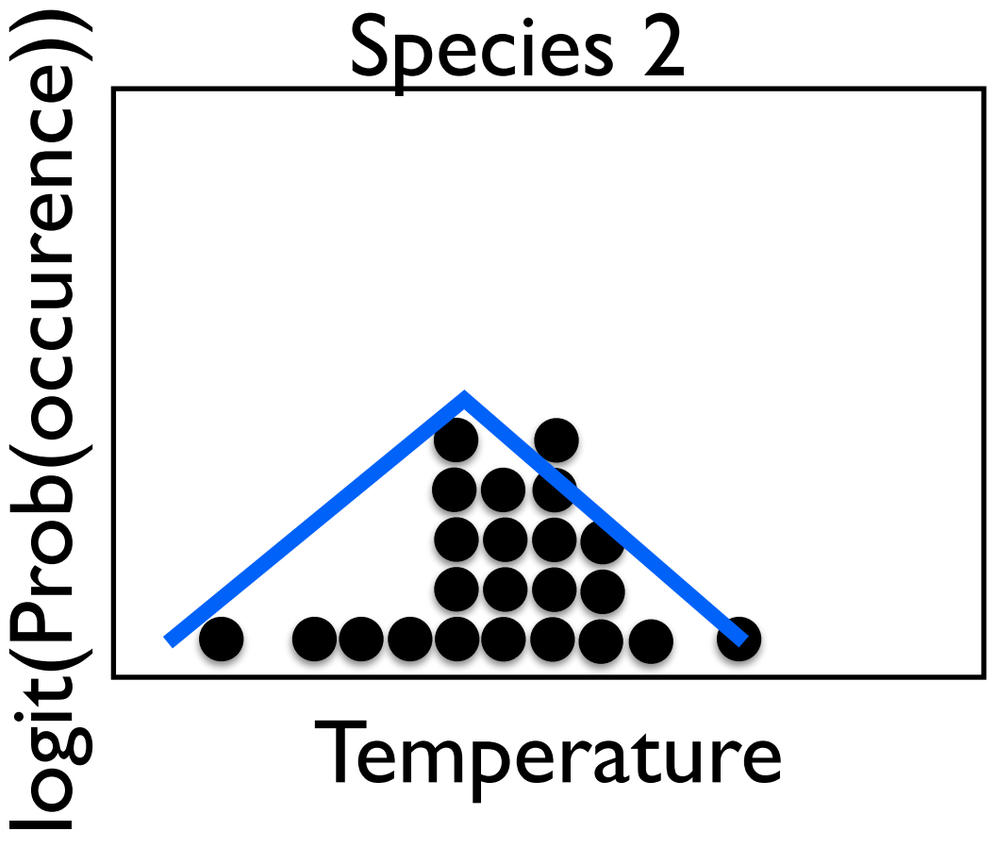

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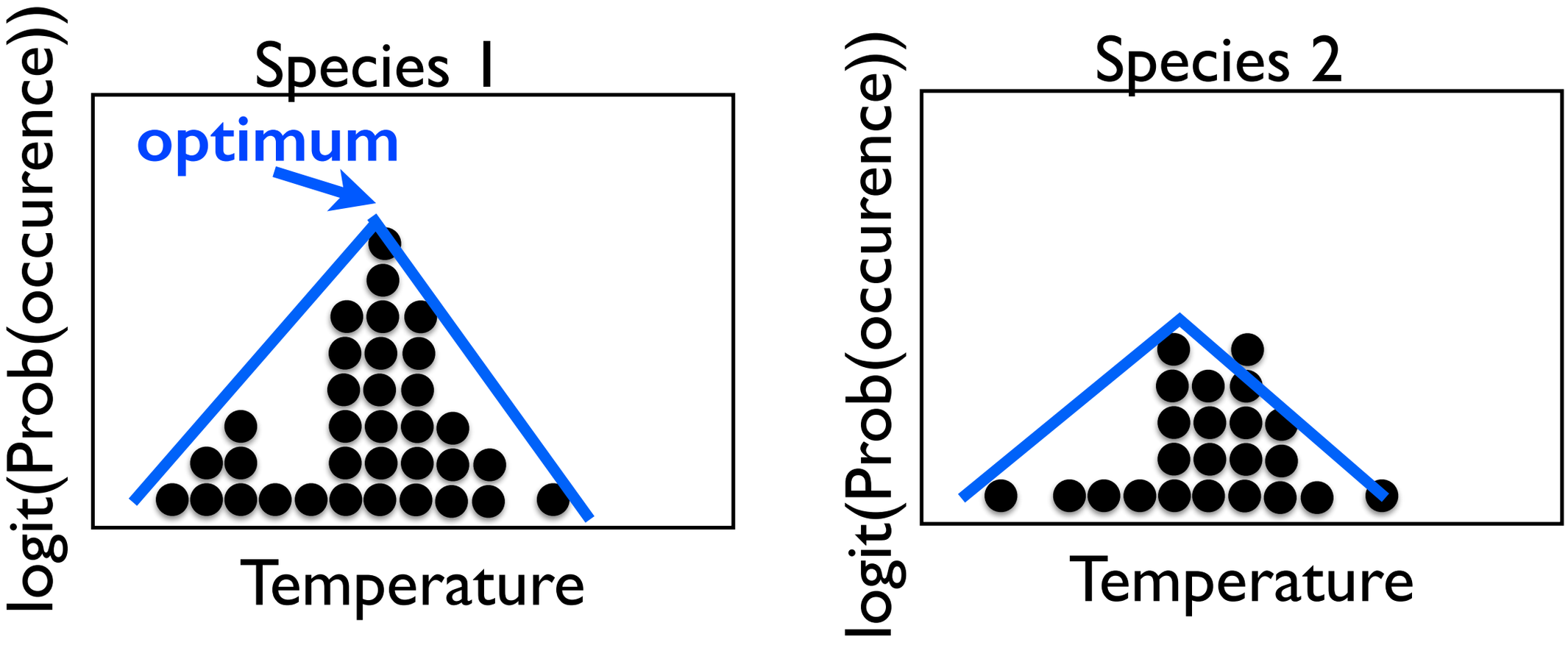

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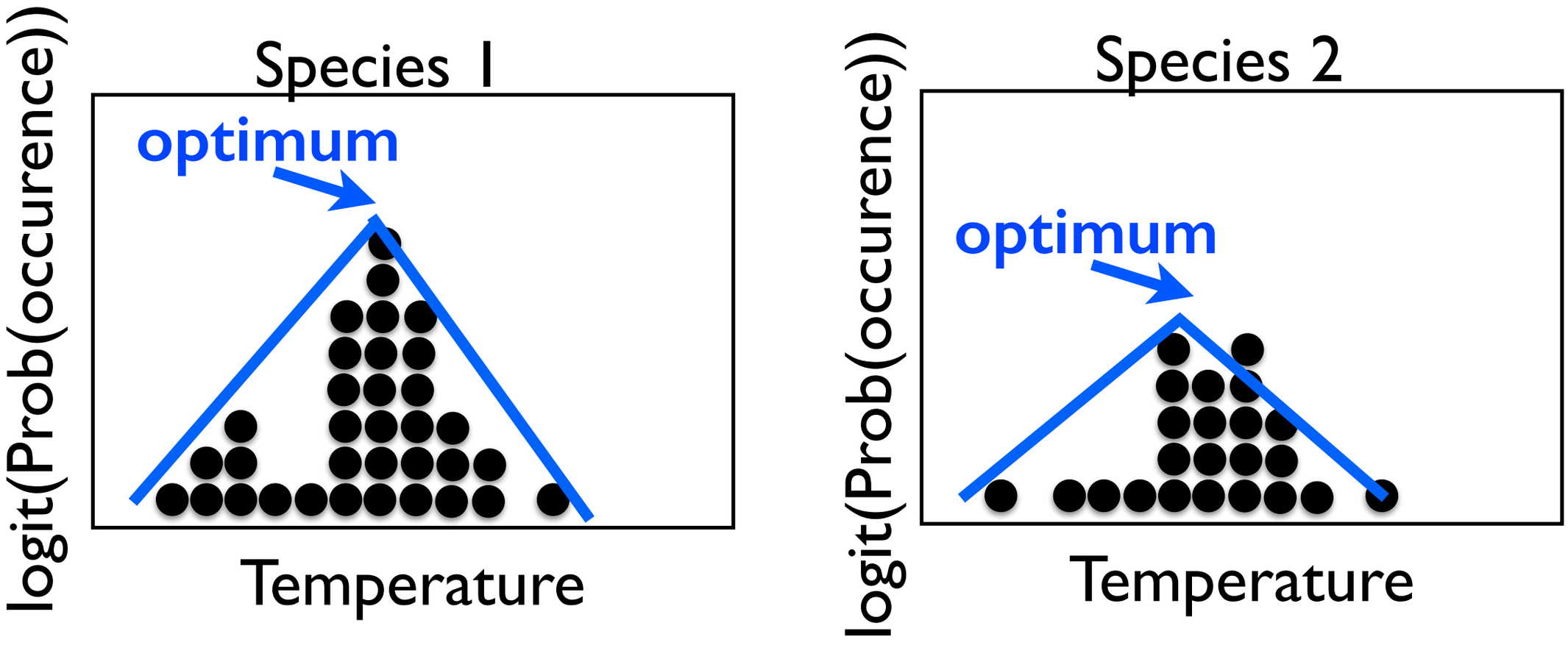

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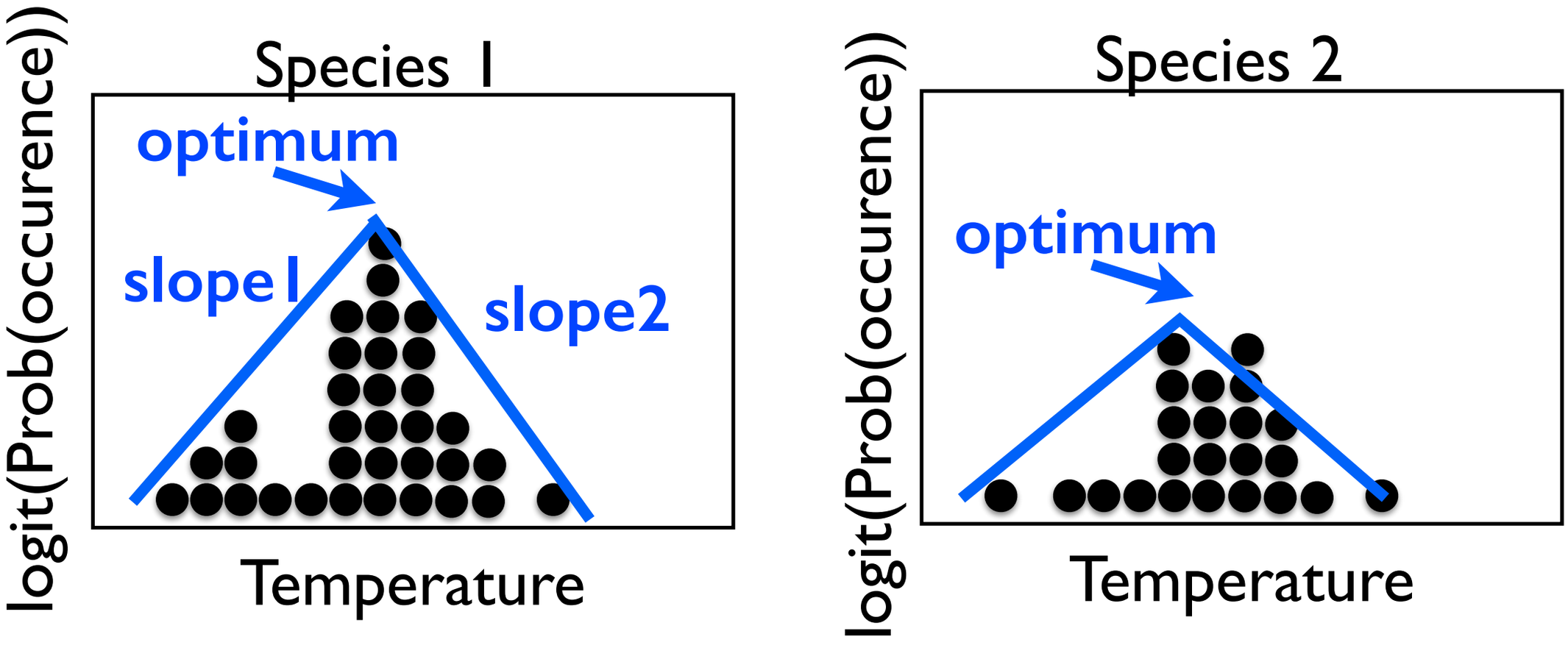

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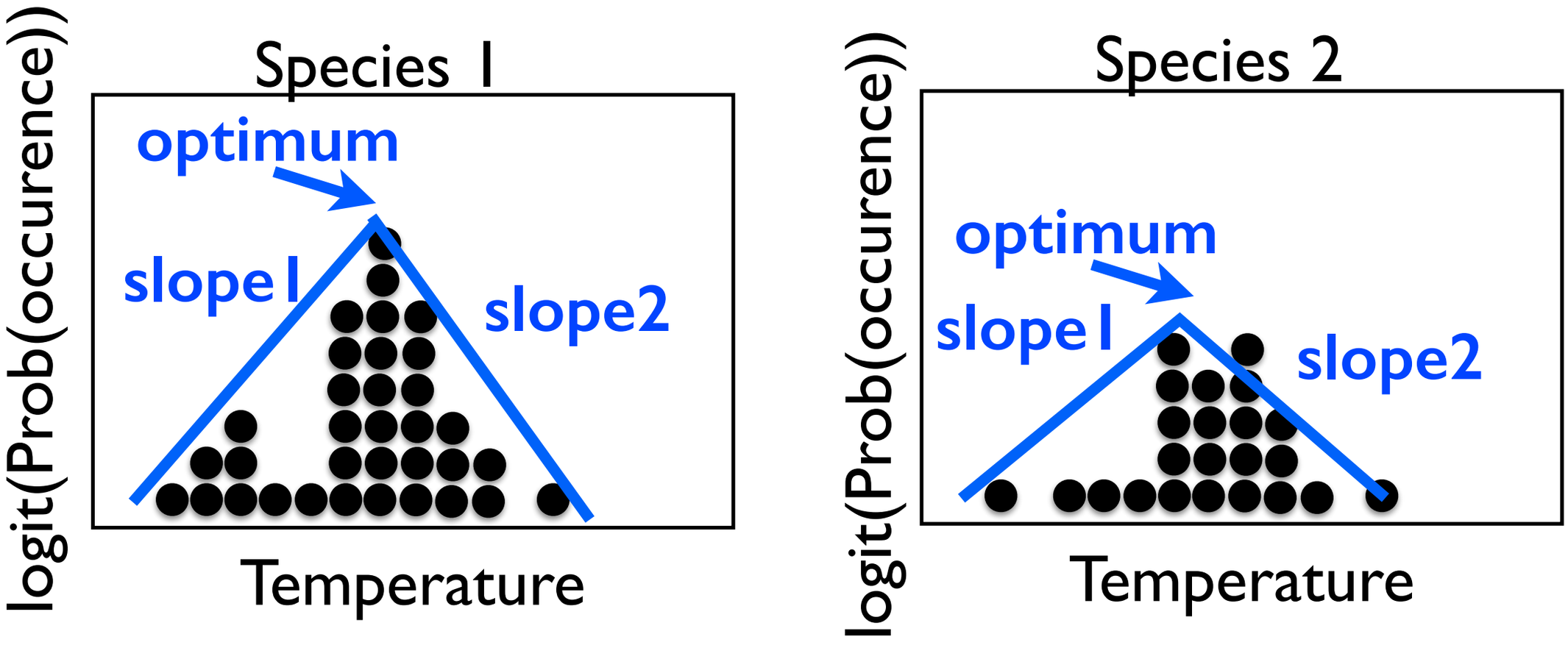

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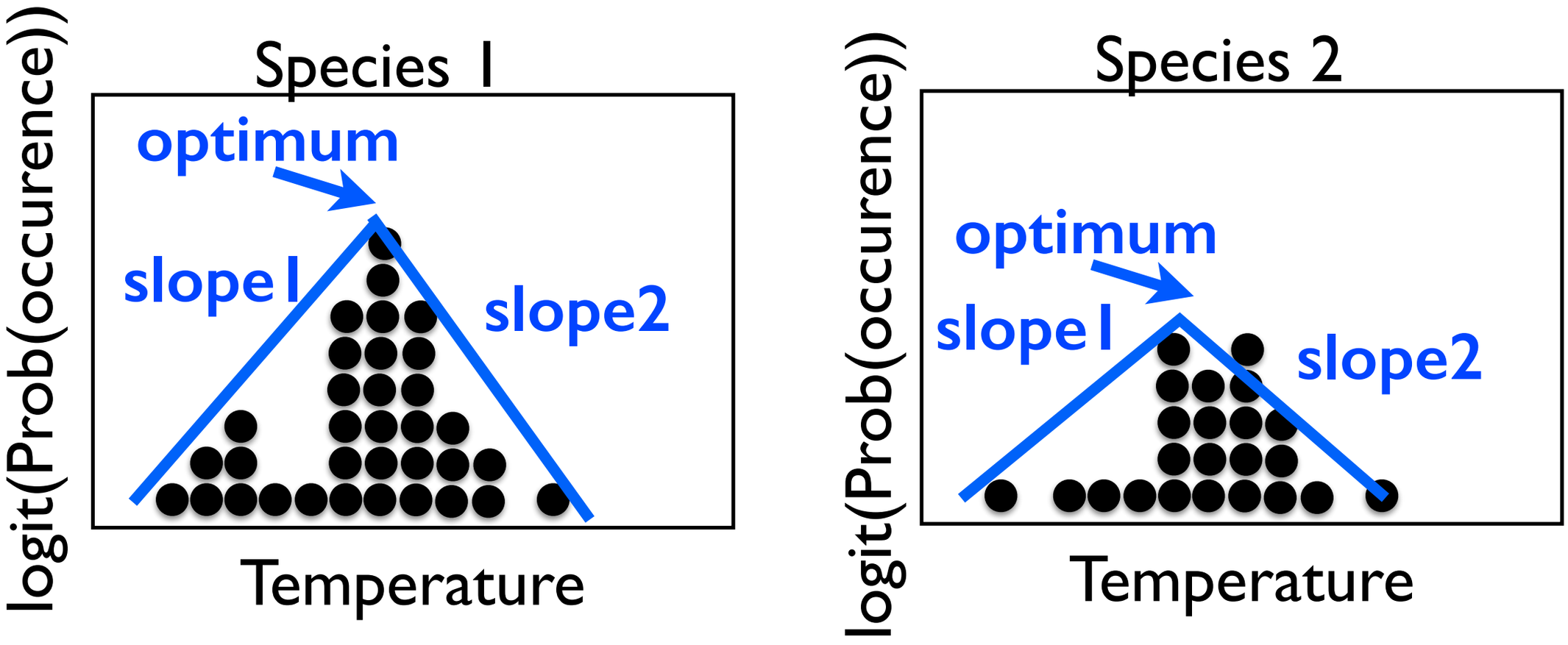

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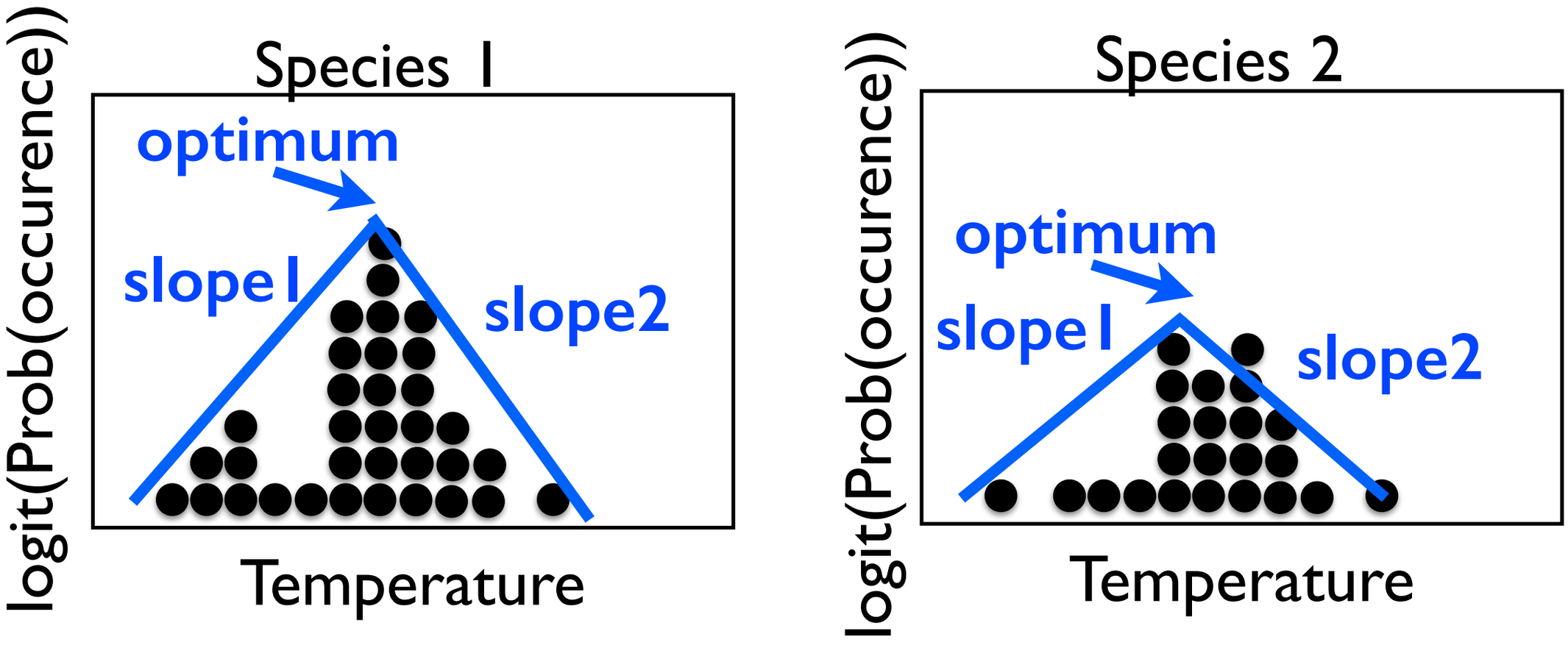

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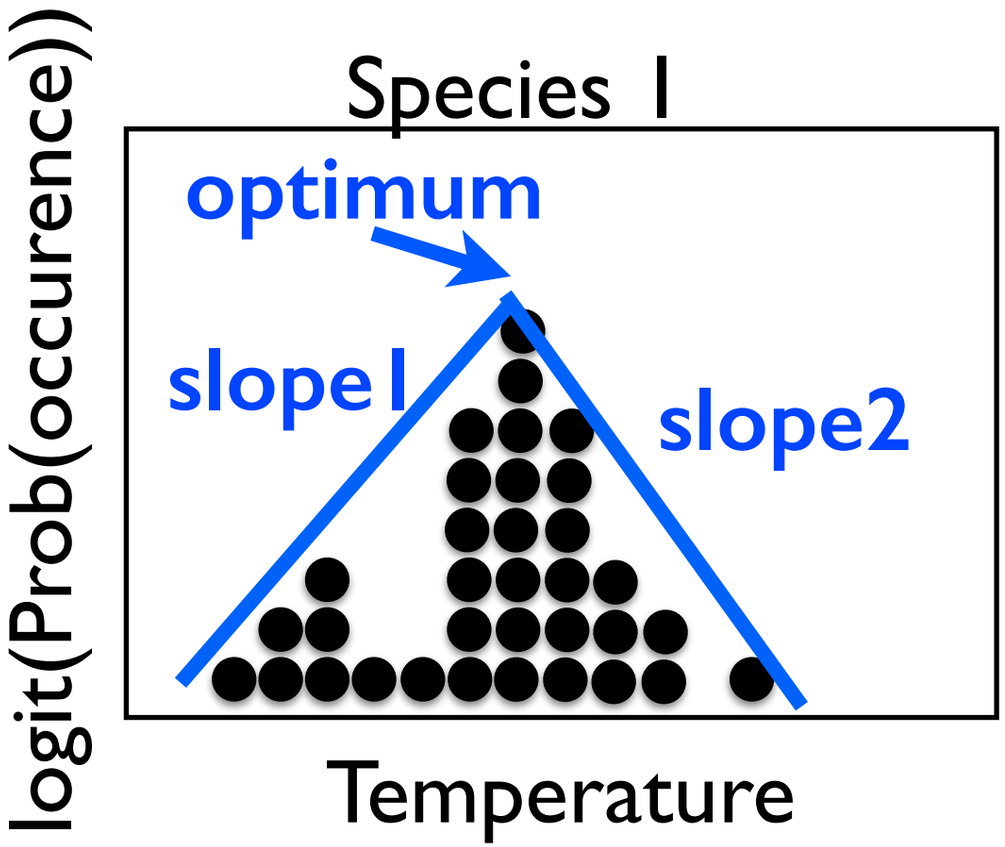

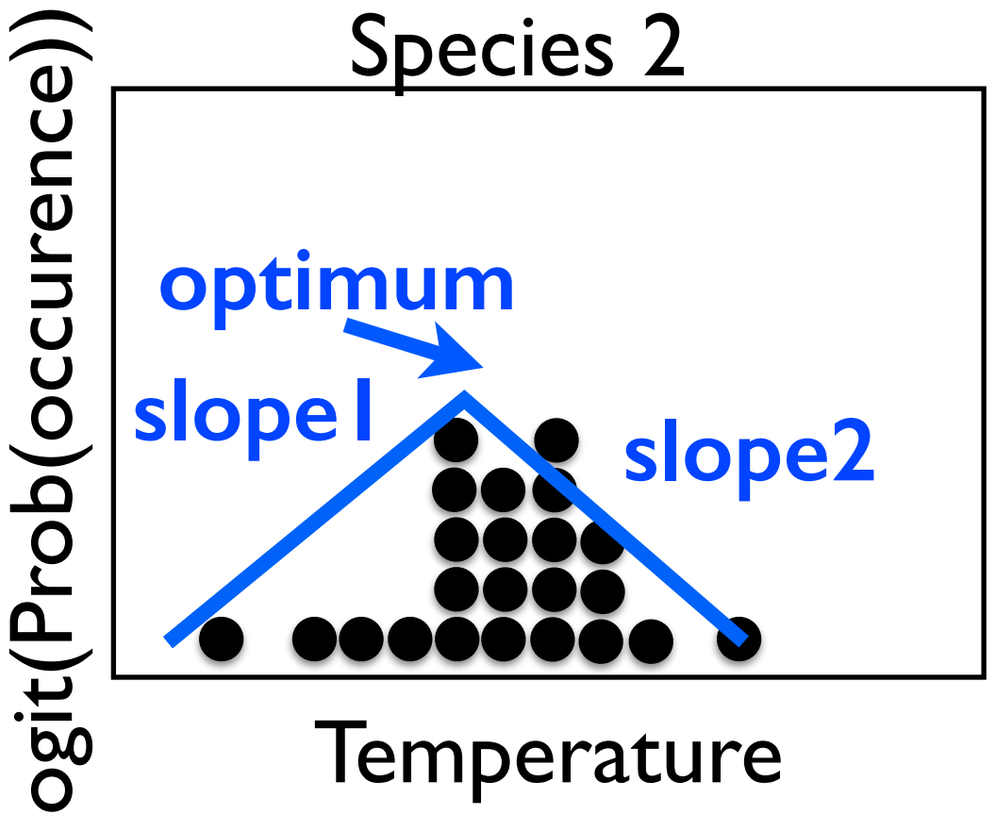

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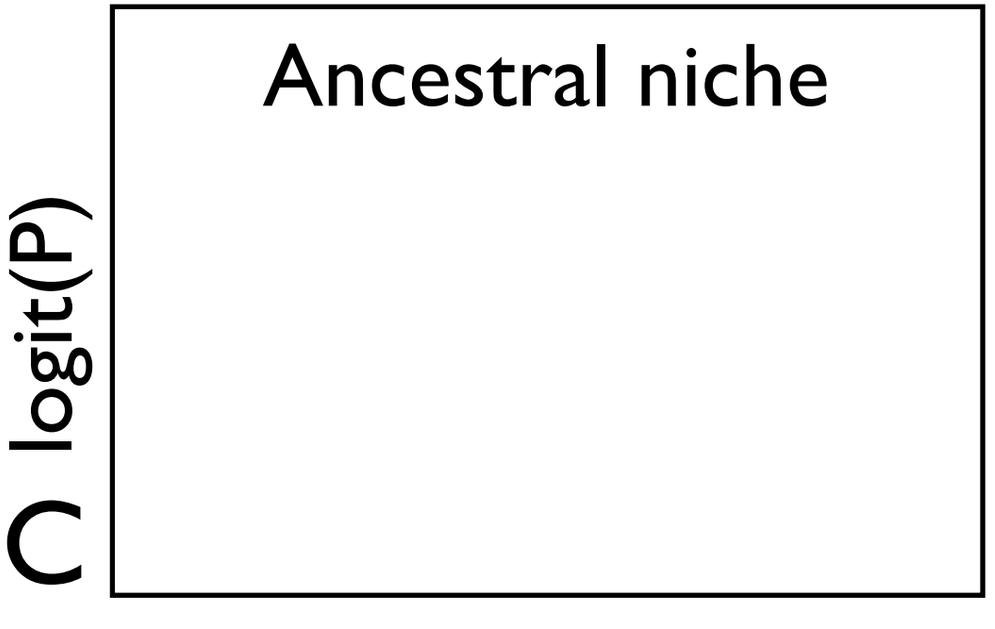

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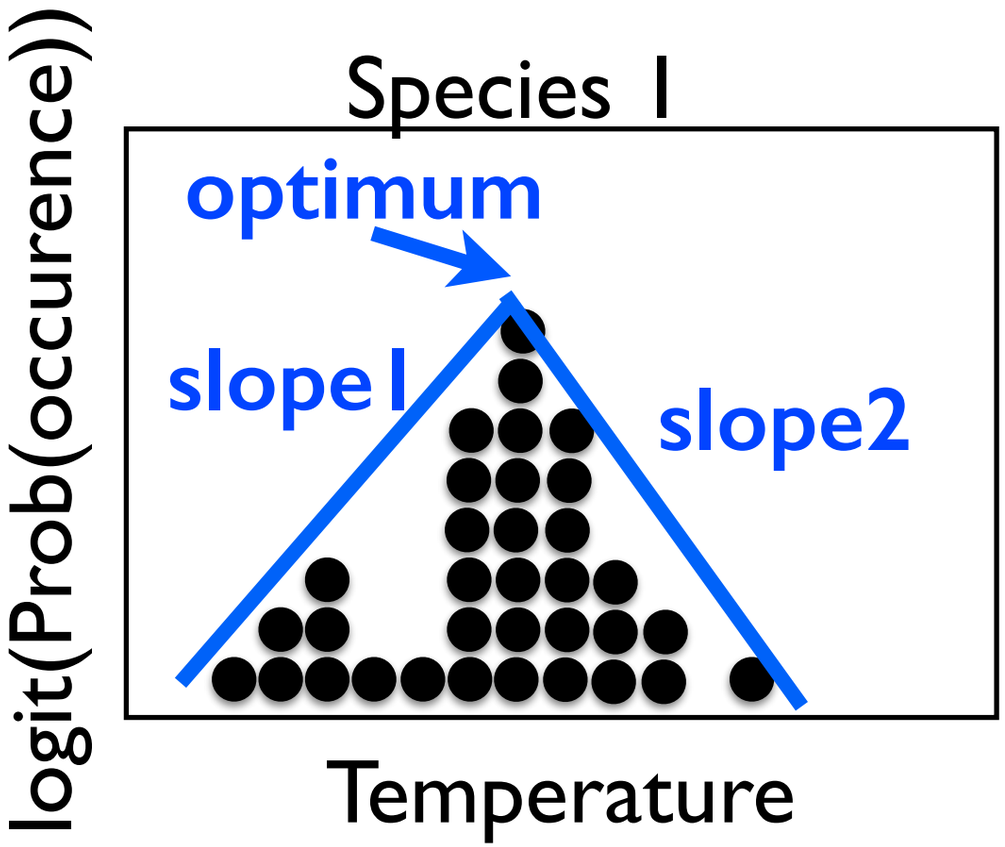

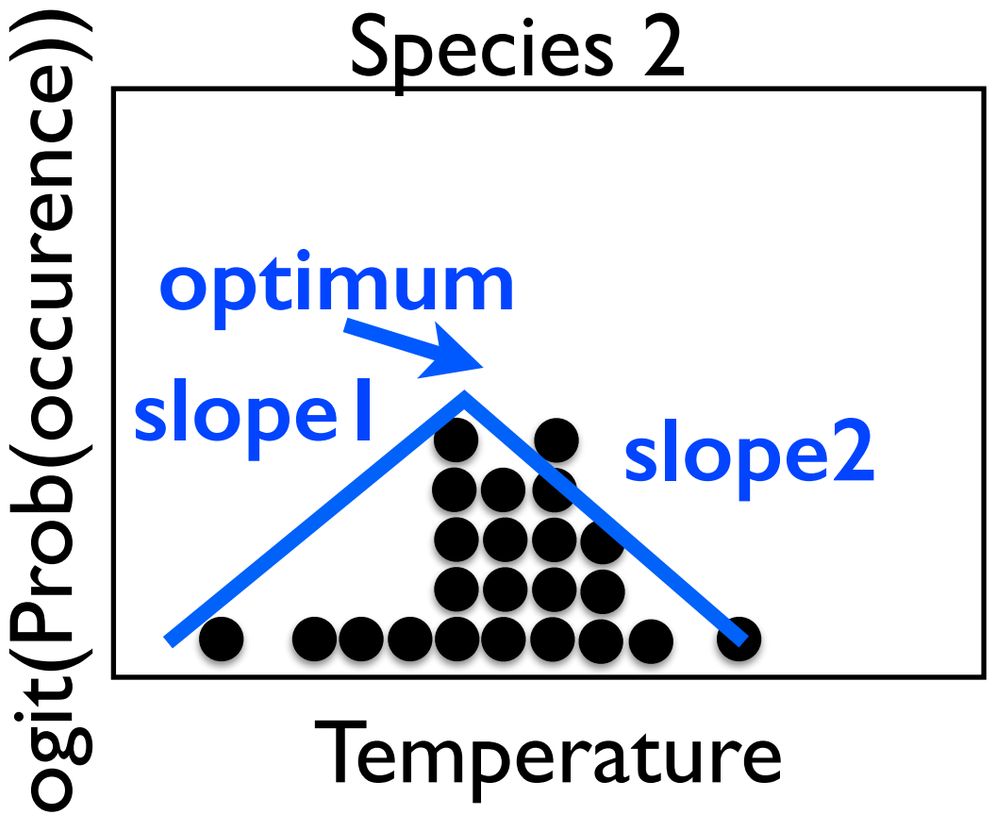

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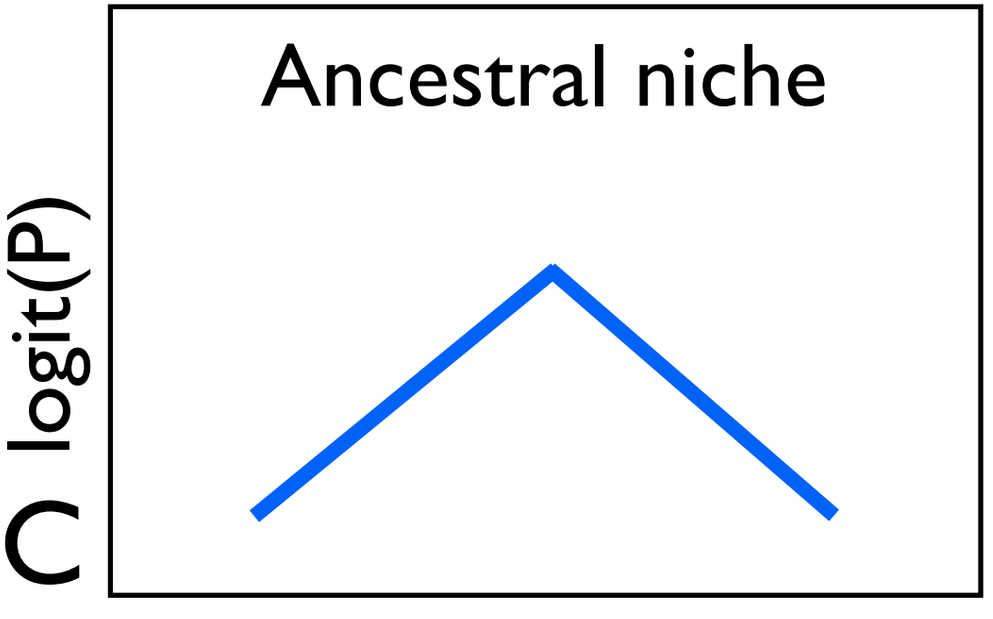

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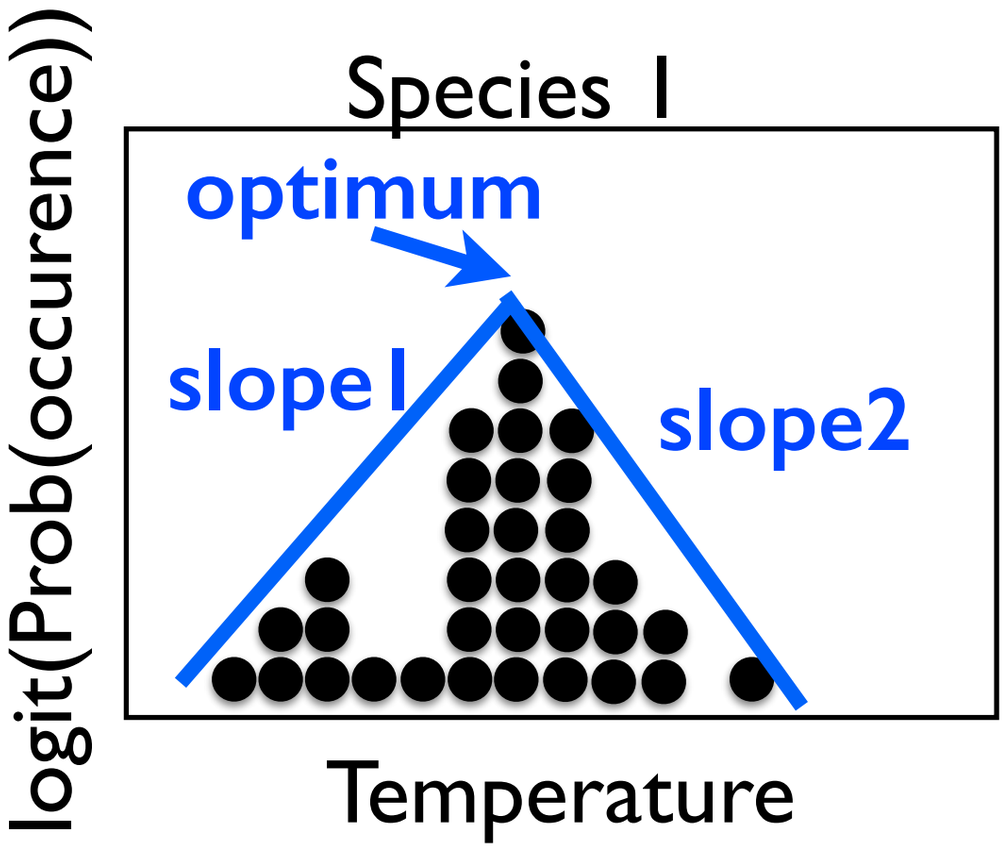

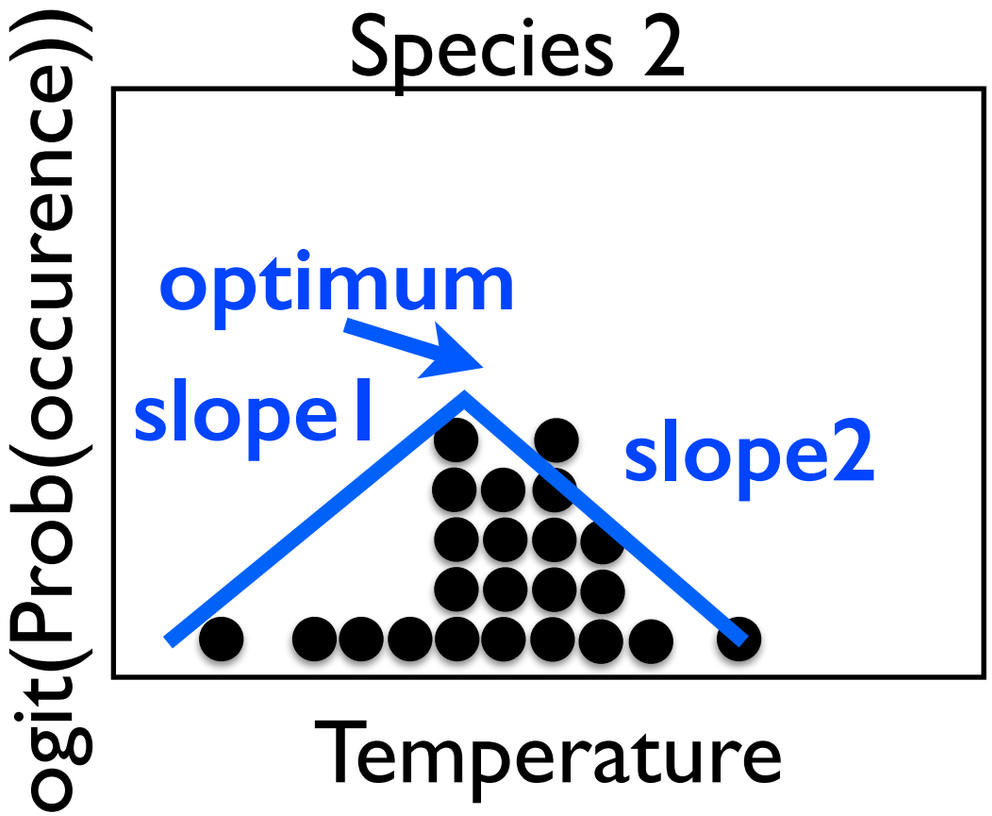

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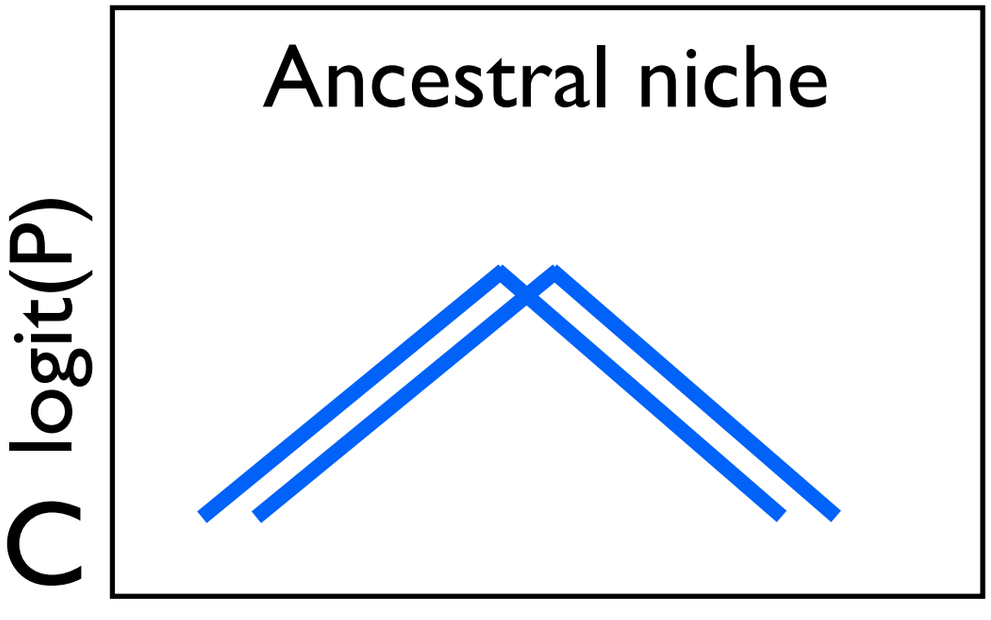

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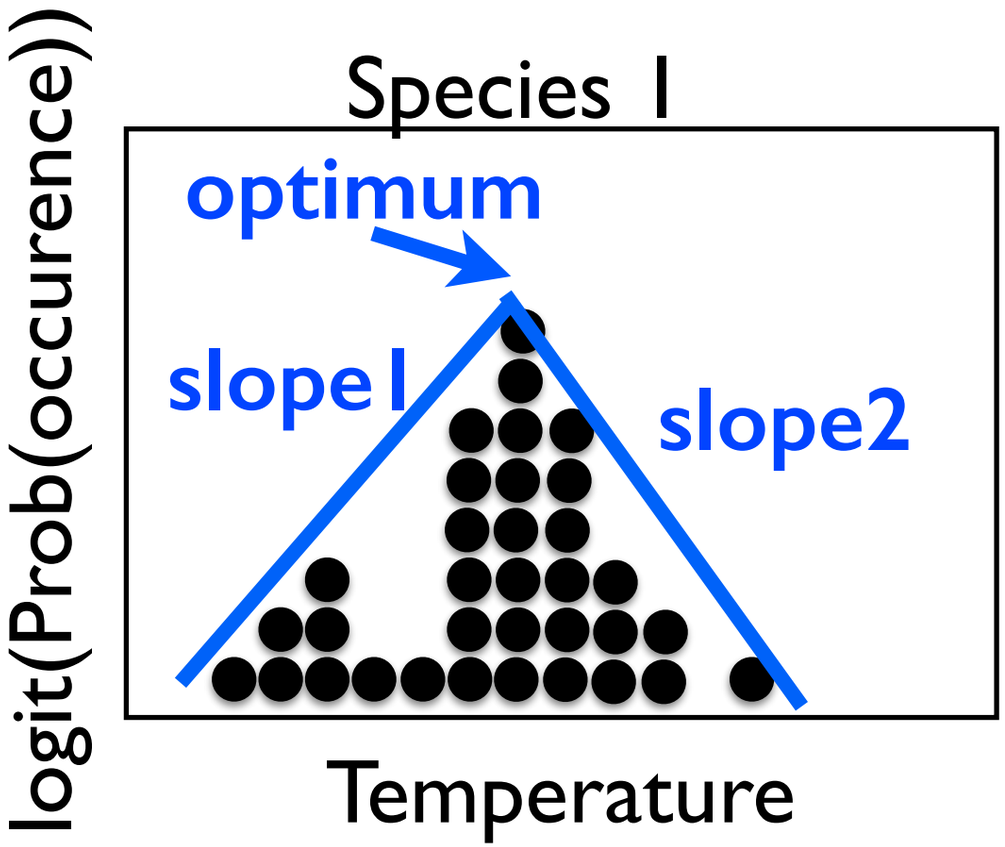

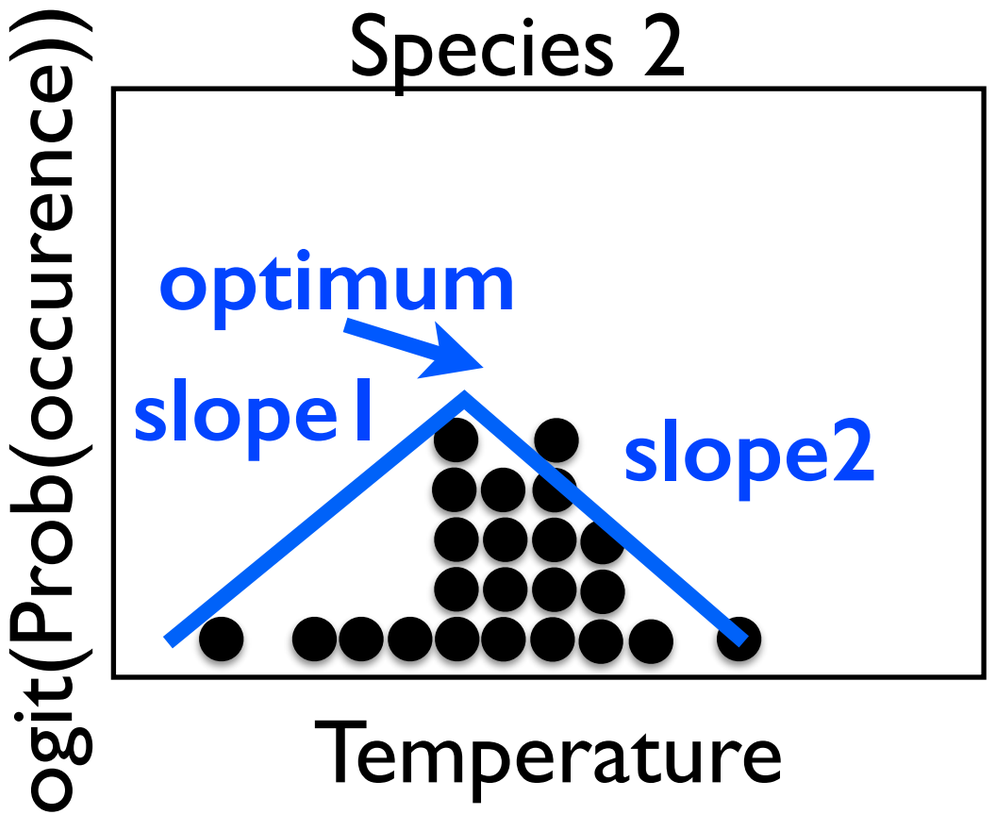

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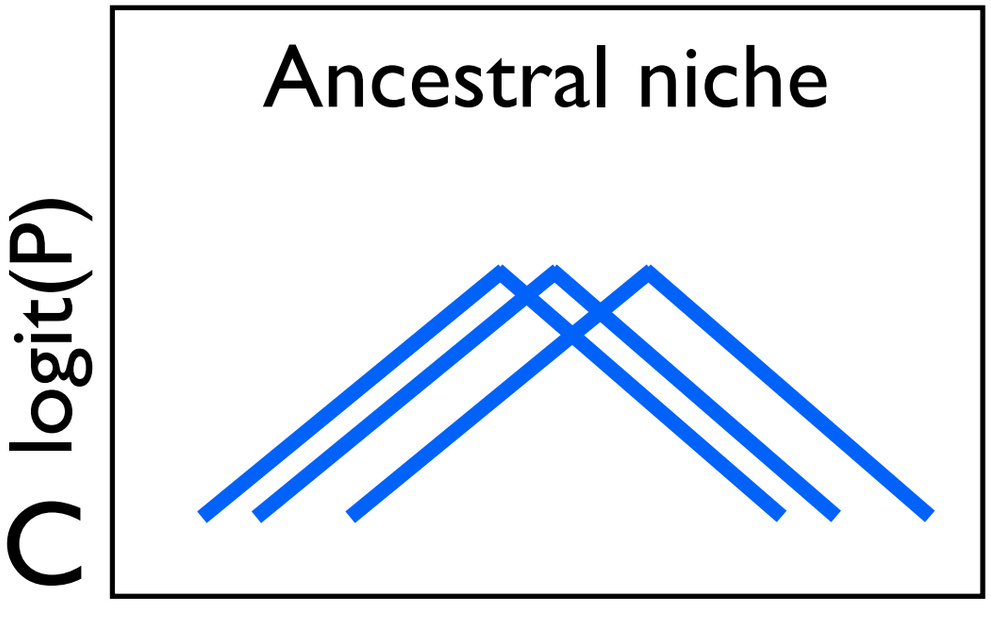

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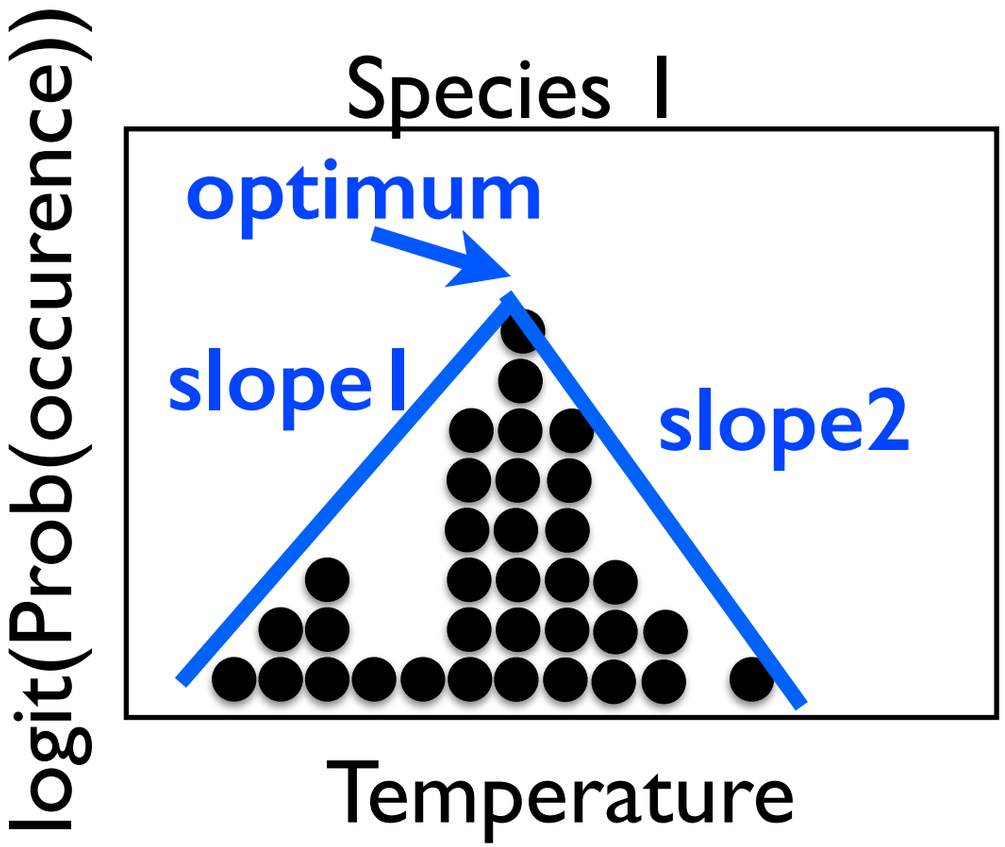

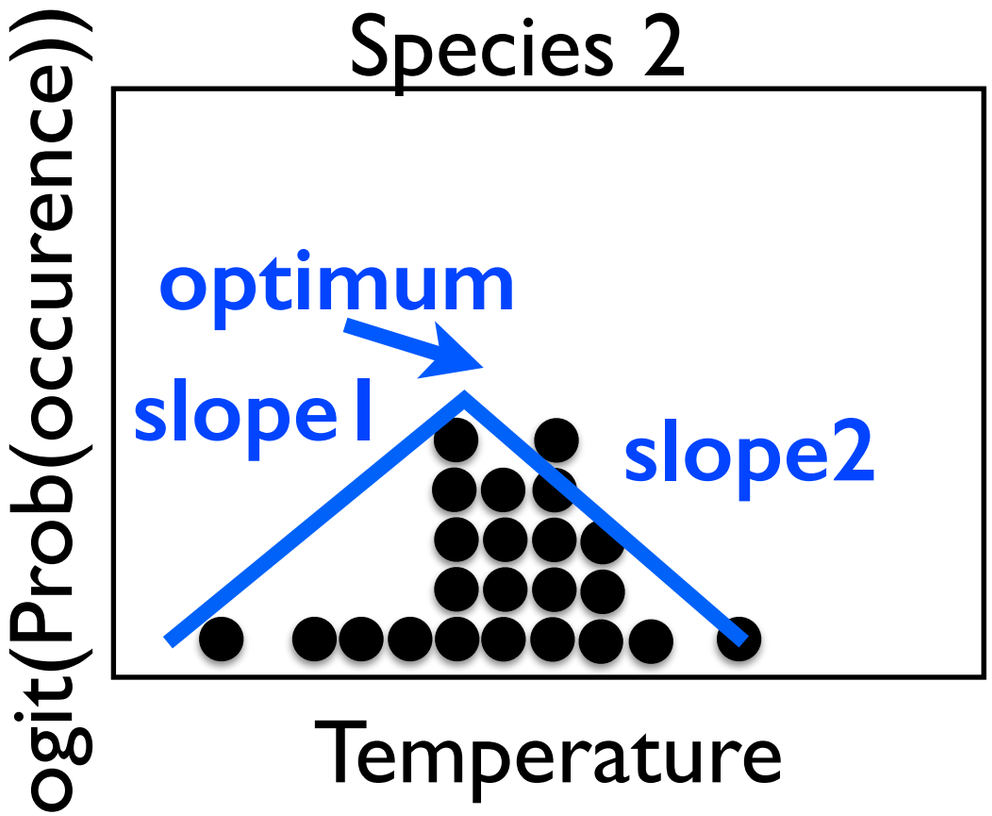

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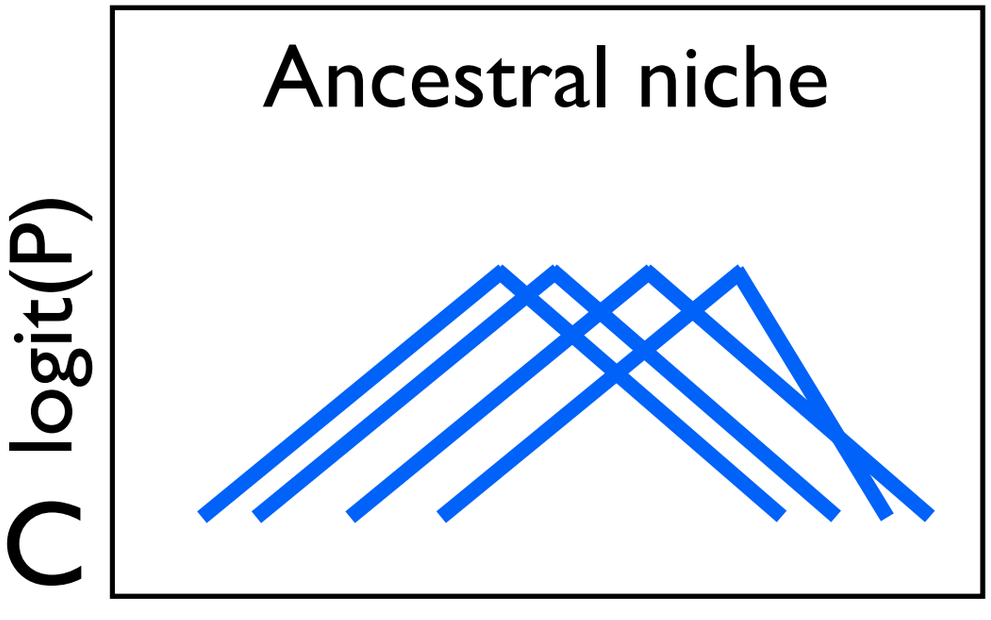

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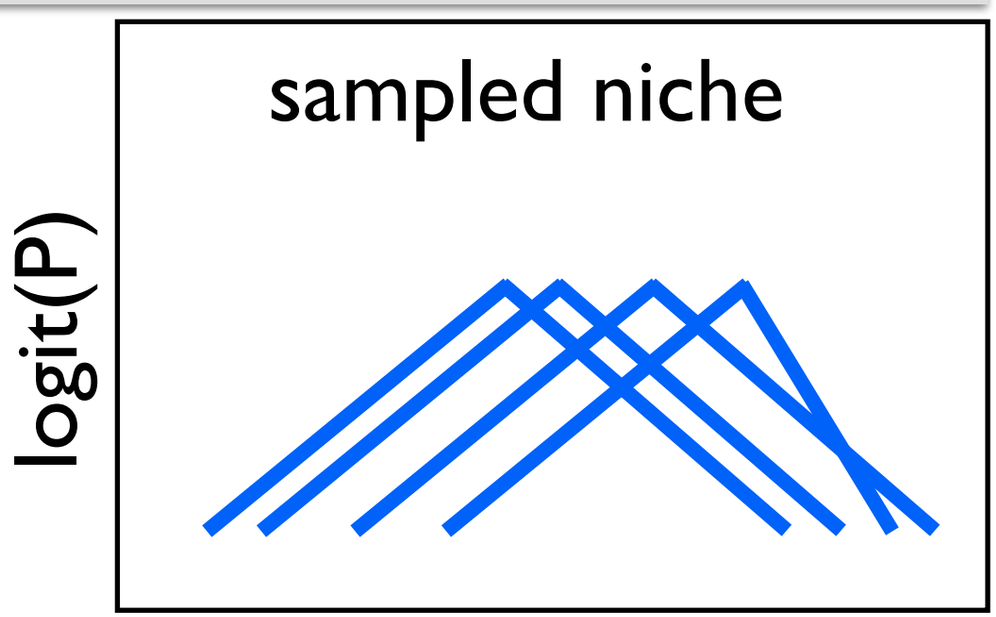
3. Evaluation metrics - unexplored

Current status of phyloSDM

Programming in JAGS / R2jags:

- Detection model: P(detect|presence)
- Niche model: P(presence|environ, params)
- Evolutionary model: P(params|evo. model)
- E.g. OU process with shifting means (using a stochastically mapped trait)
- Sample from distrib. of trees, maps

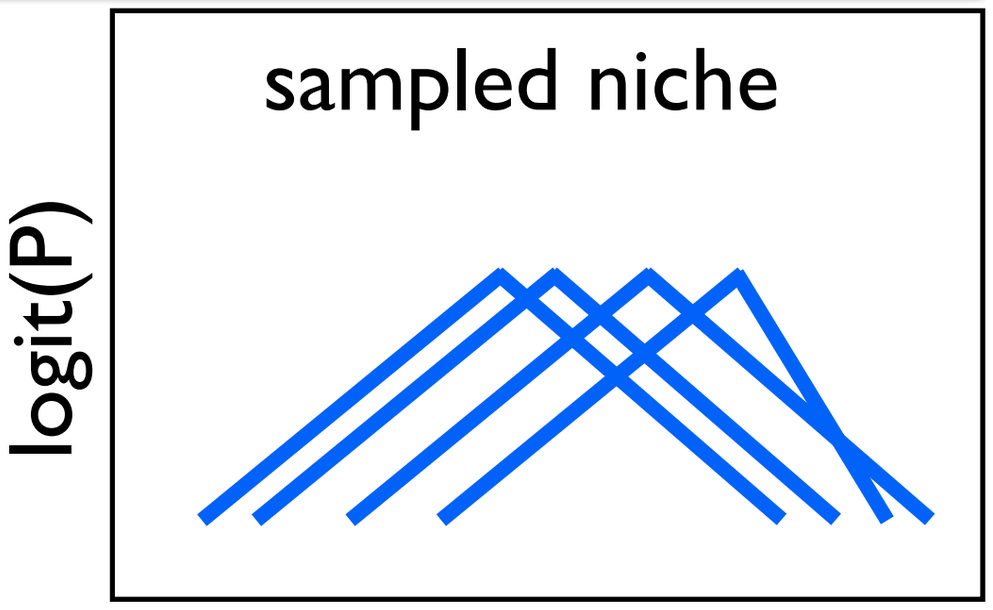
MCMC sampling of possible niche models



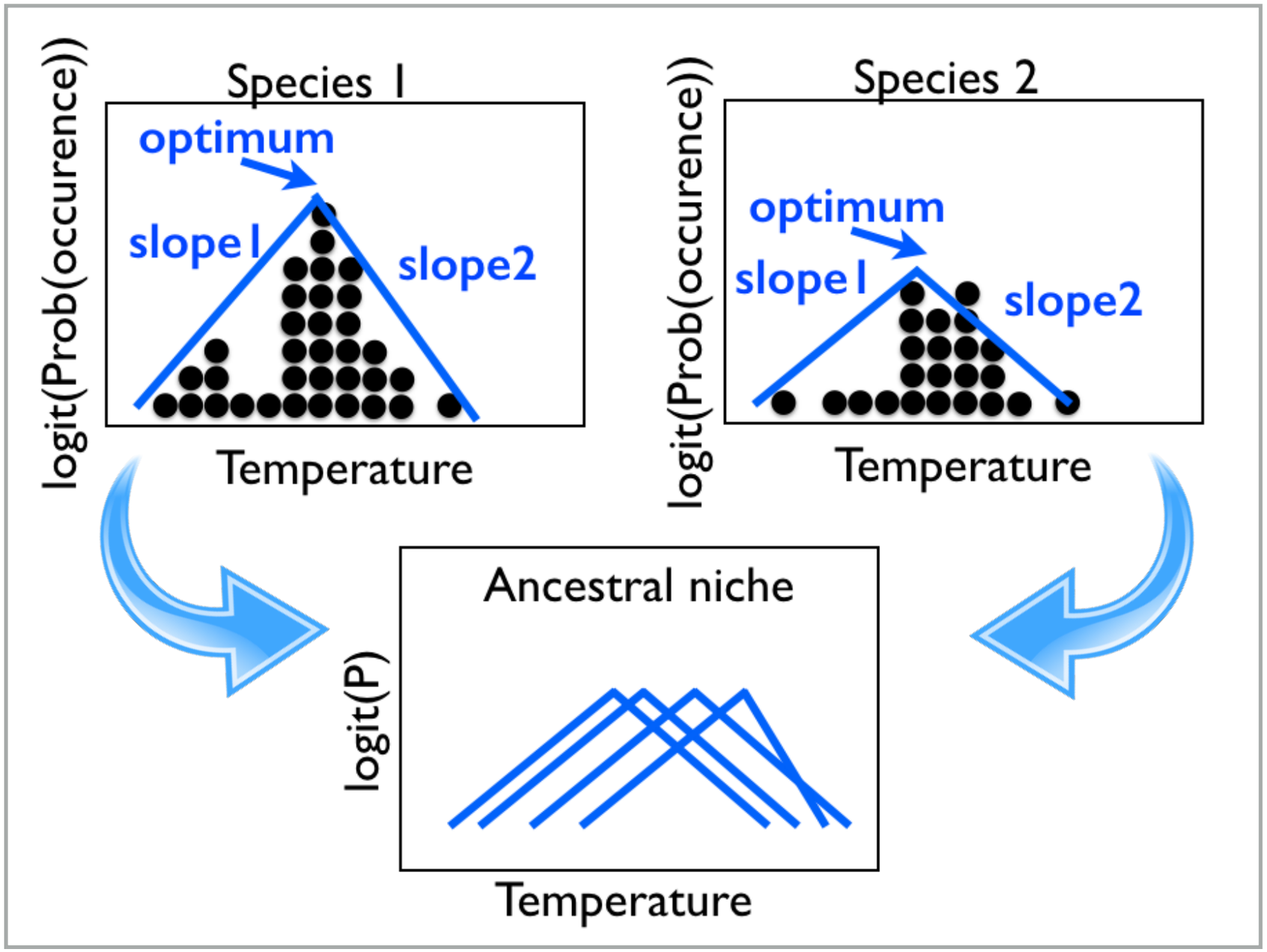
Open questions for symposium

- What do we miss in ENM if we leave out evolution/phylogeny?
- How can we include paleontological information?
- How can we combine models of ecological niche, and niche evolution?

MCMC sampling of possible niche models



Putting Evolution Into Ecological Niche Modelling: Background and Paths Forward



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Division of Ecology, Evolution, and Genetics
Research School of Biology
The Australian National University
phylo.wikidot.com/nicholas-j-matzke

Evolution 2016
Sunday, June 19, 8:15 - 11:45 am, Ballroom C

Thanks for support from: