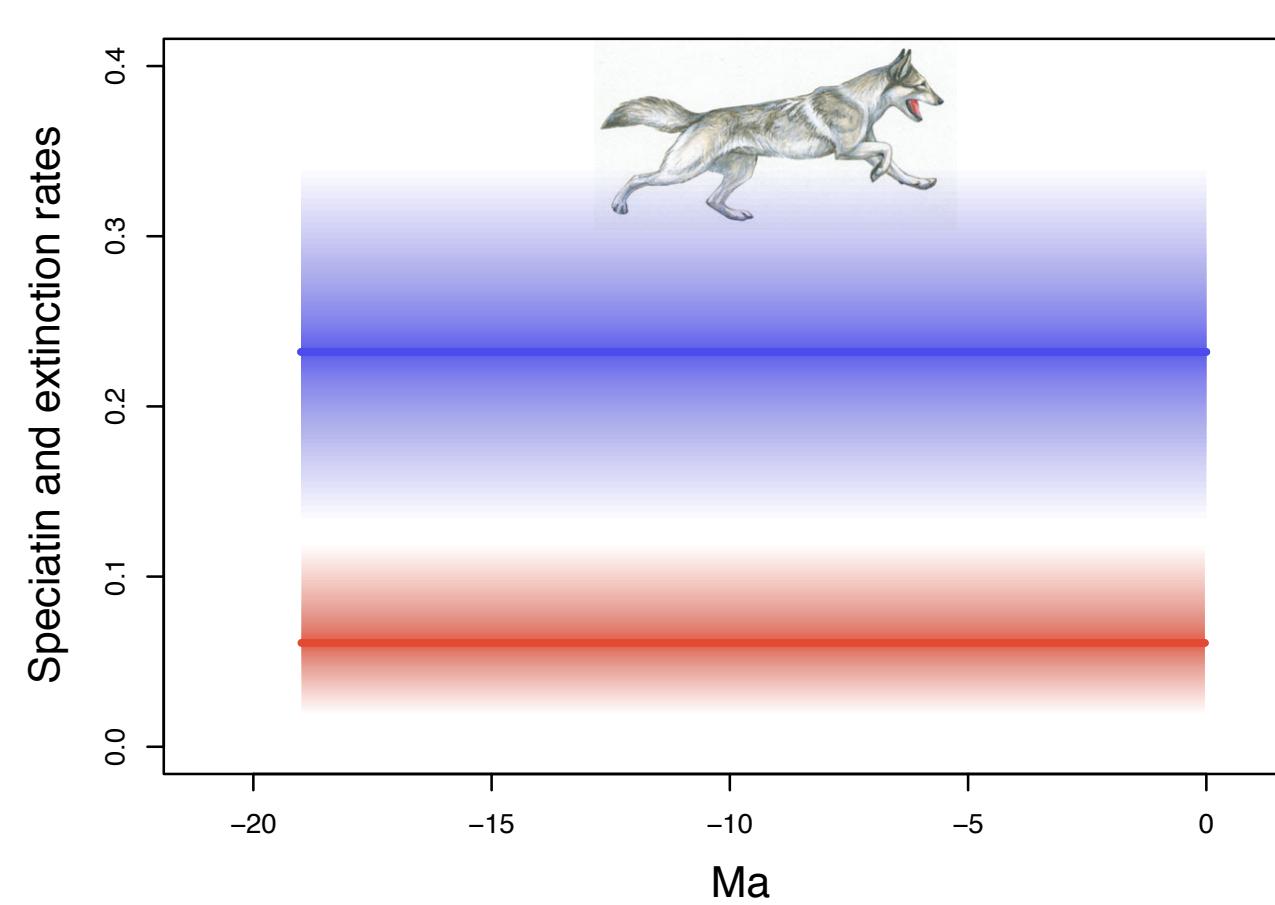
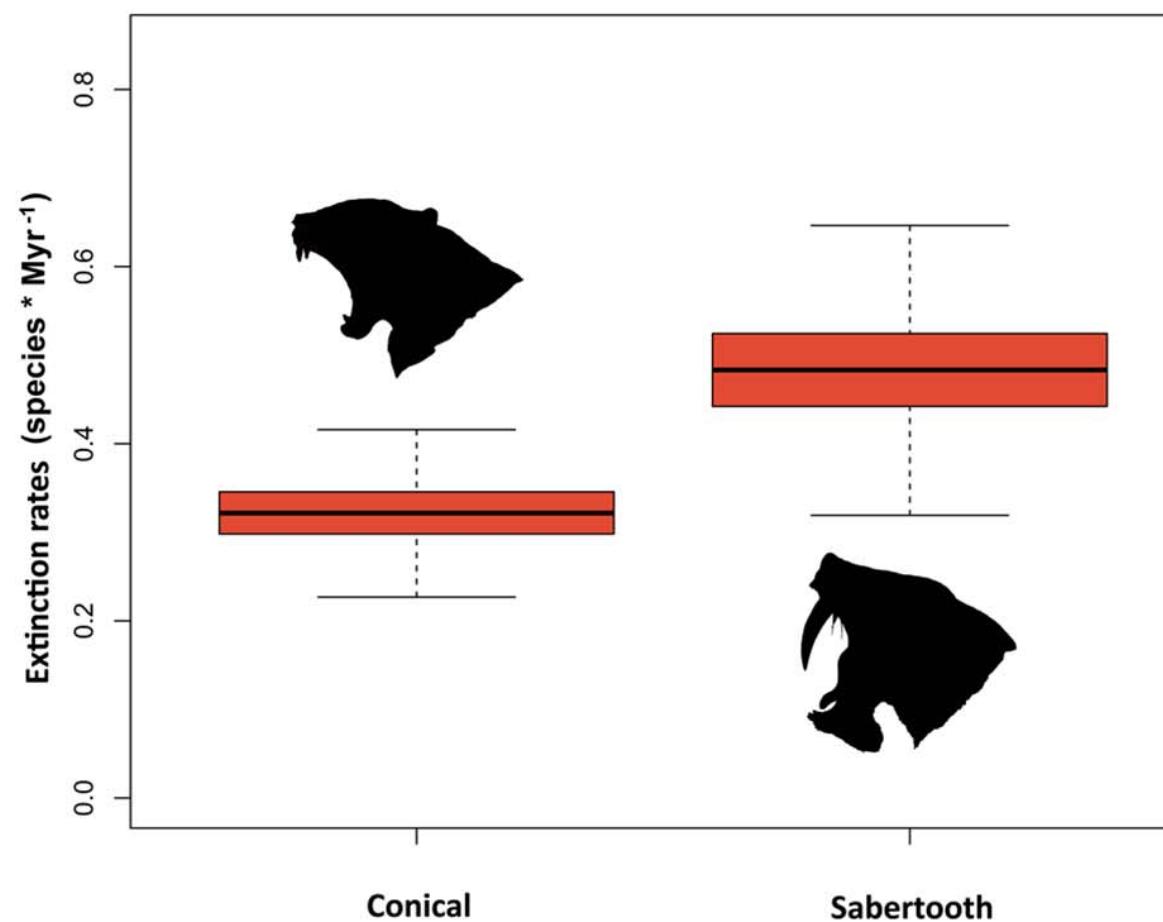


So many flavors of the birth-death model...

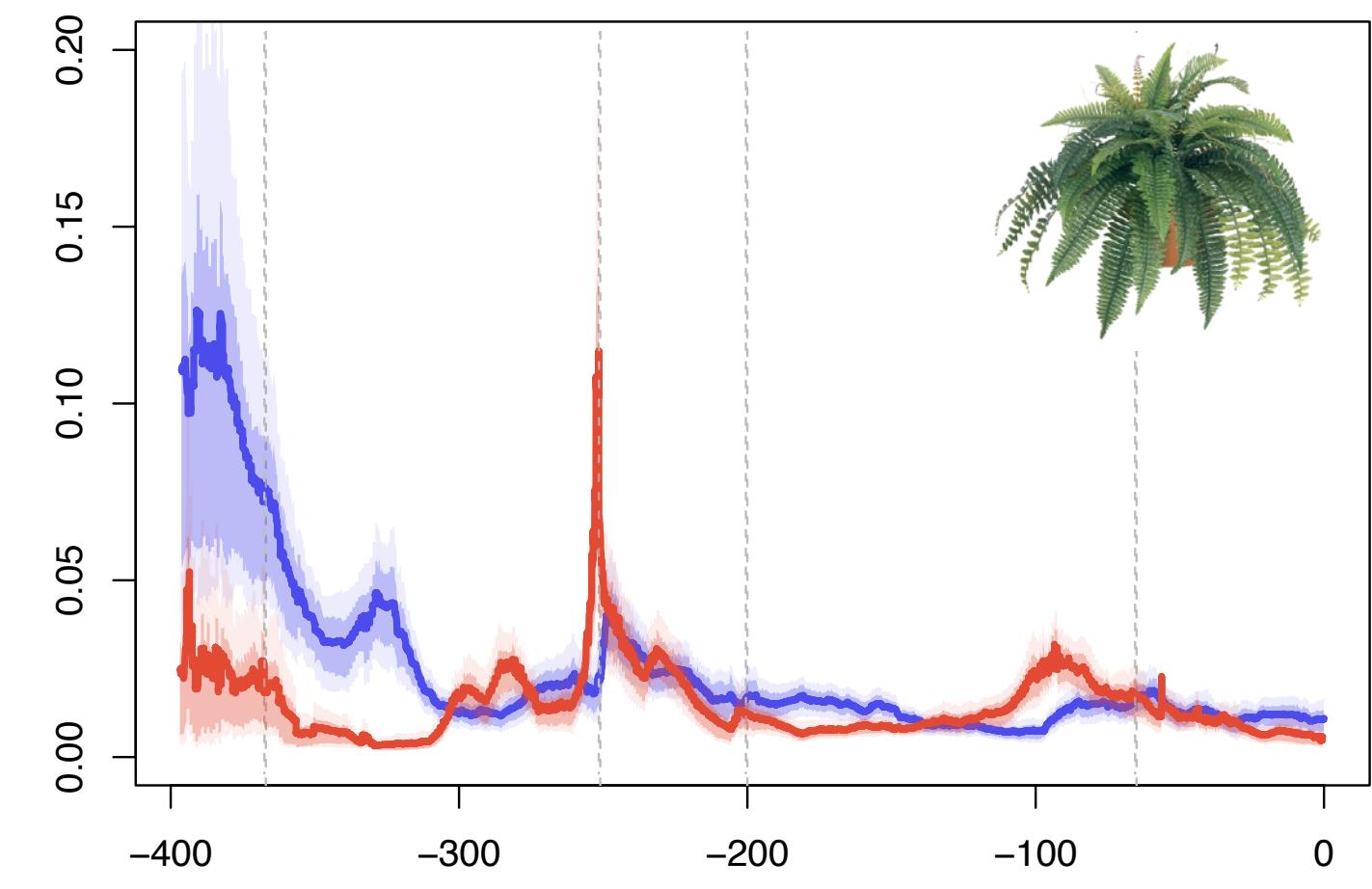
Constant rate



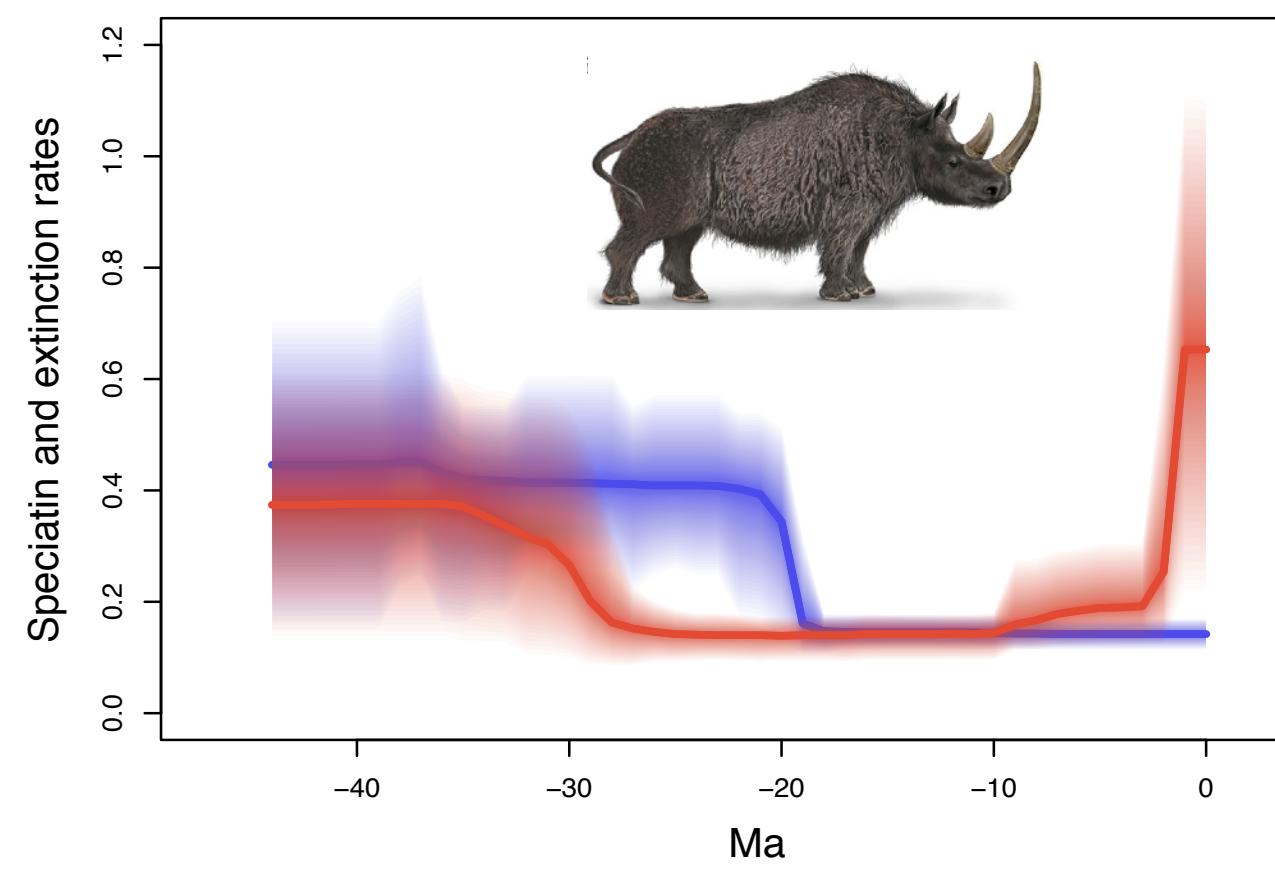
Trait-dependent extinction



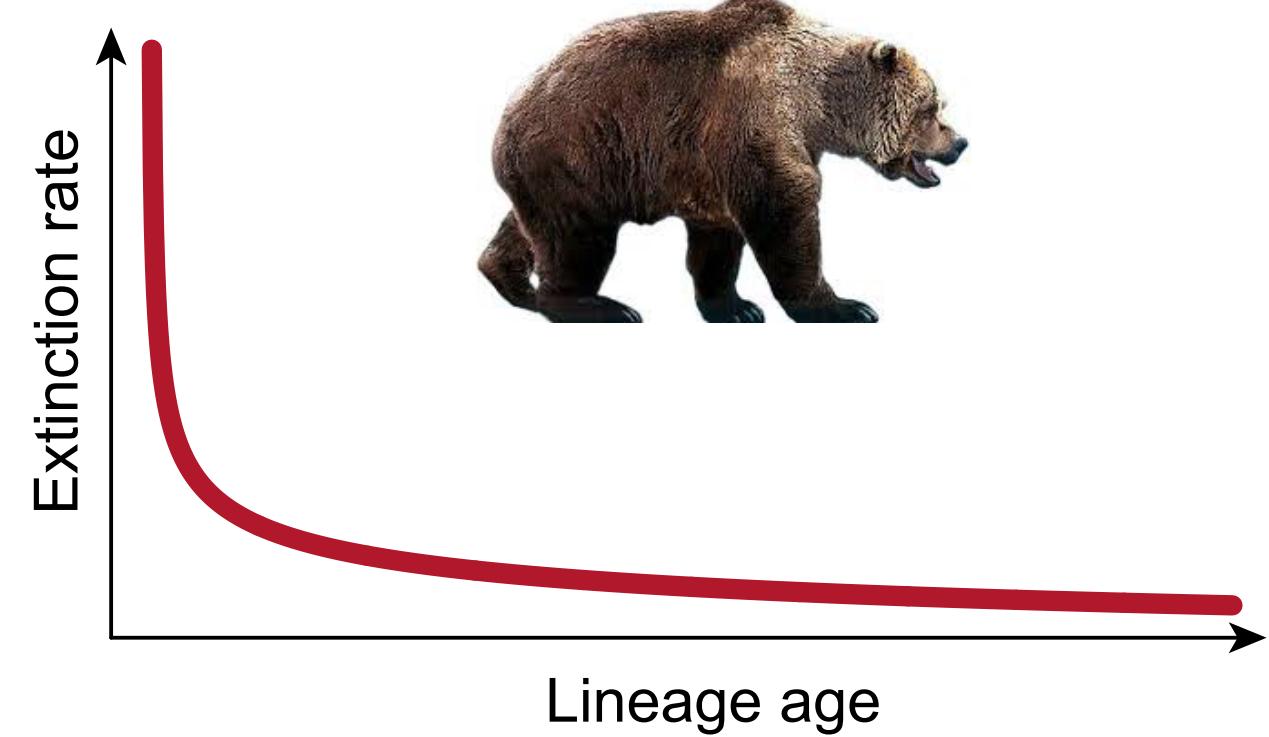
Multivariate BD model



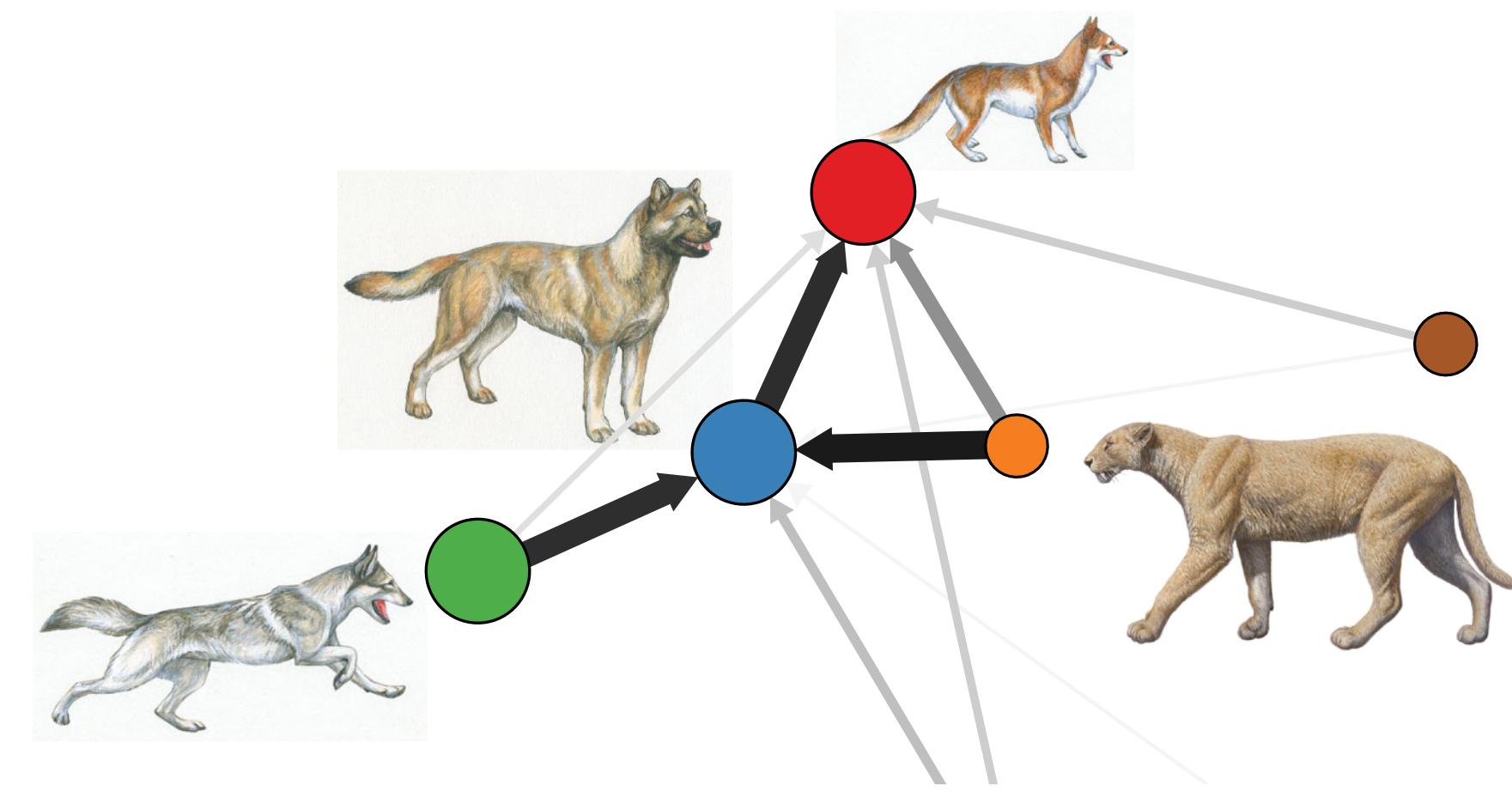
Time-variable rate



Age dependent extinction models

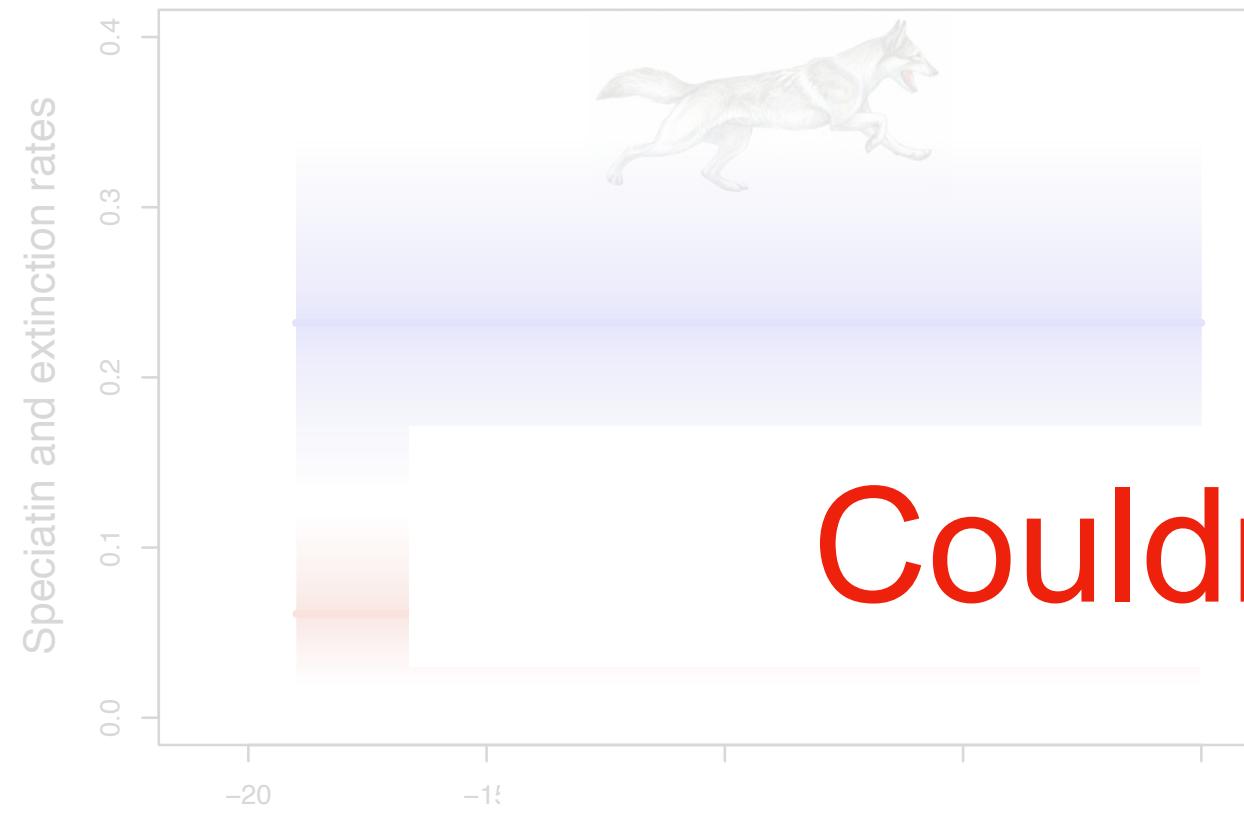


Diversity dependence within and between clades



So many flavors of the birth-death model...

Constant rate



Trait-dependent extinction



Multivariate BD model

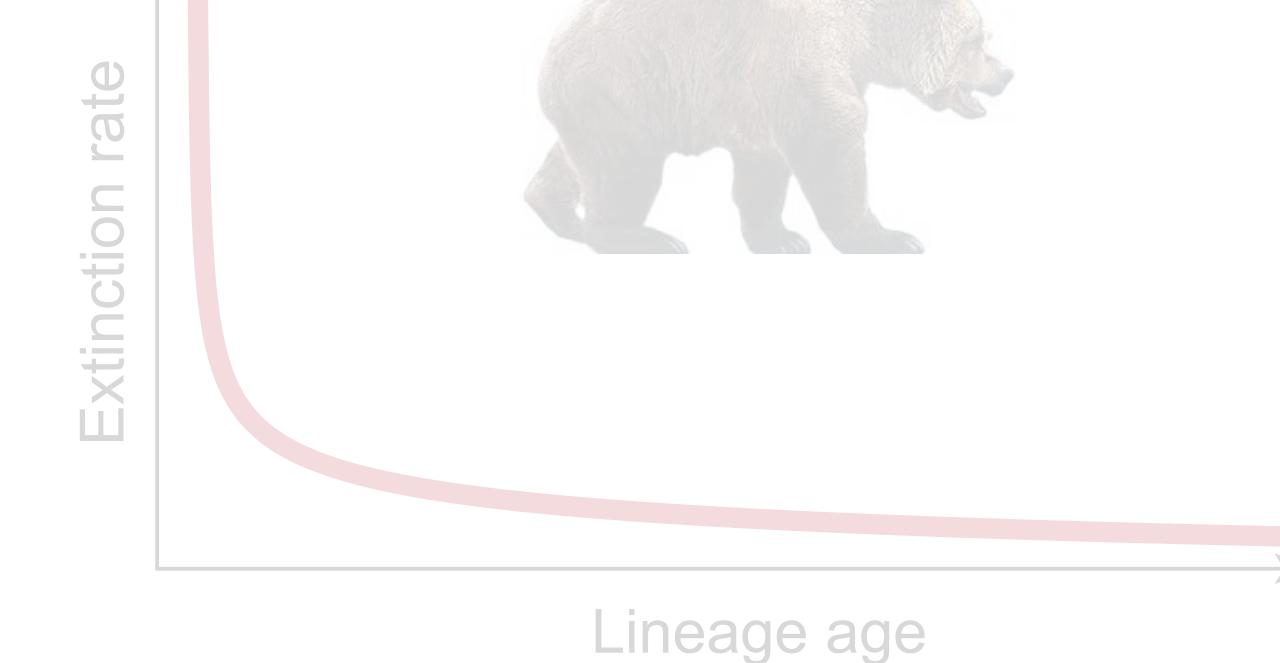
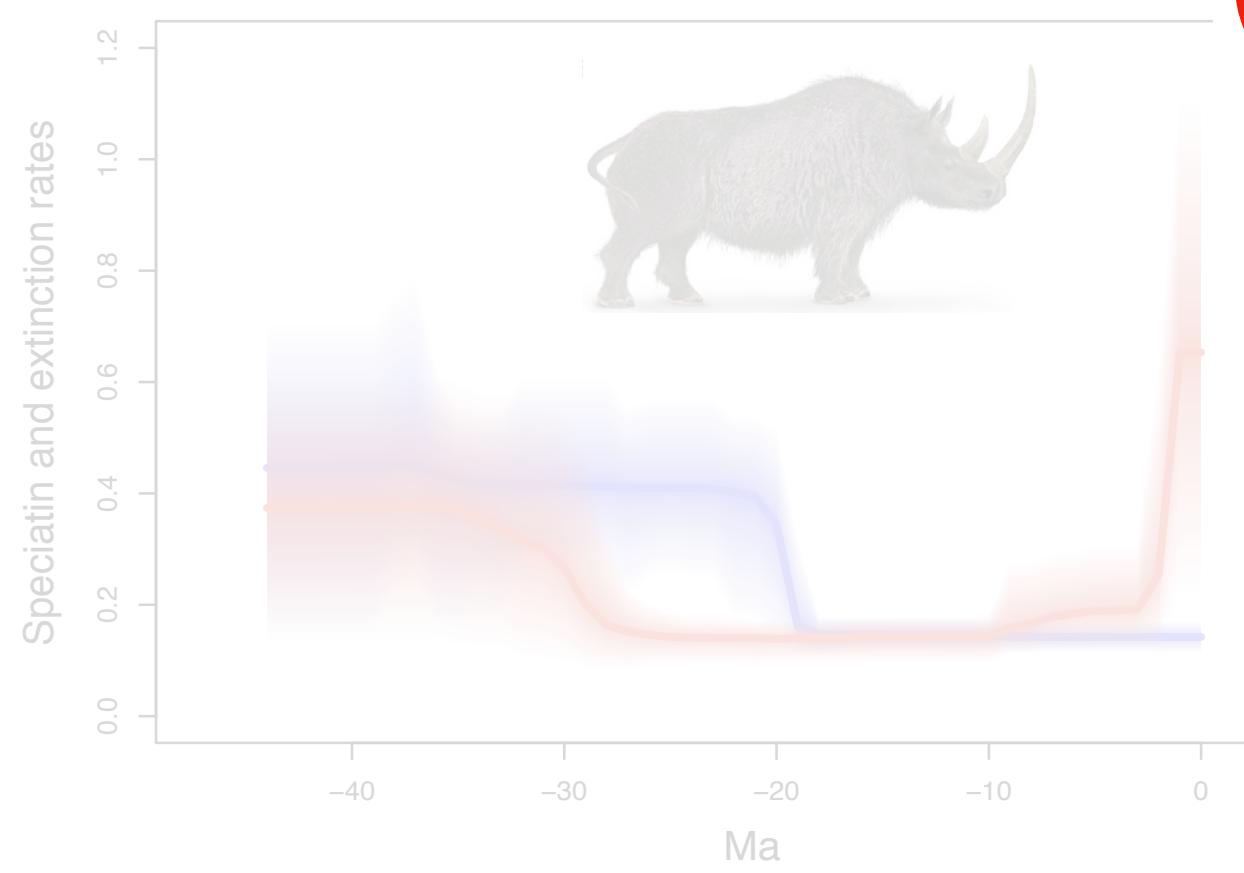


Couldn't we have one model that does it all? 🤔

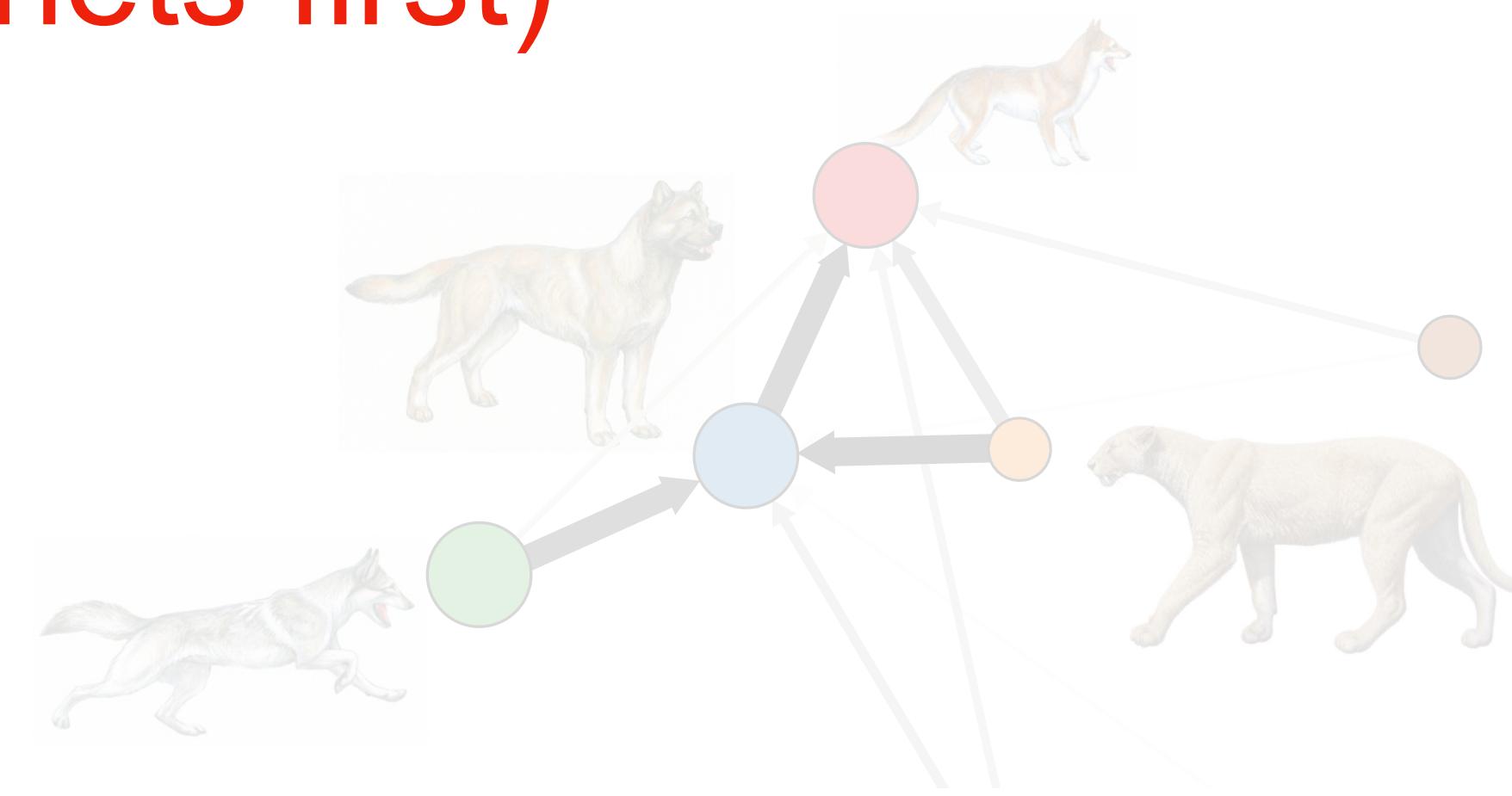
Well, perhaps we can... 🦄

(but let's talk about neural nets first)

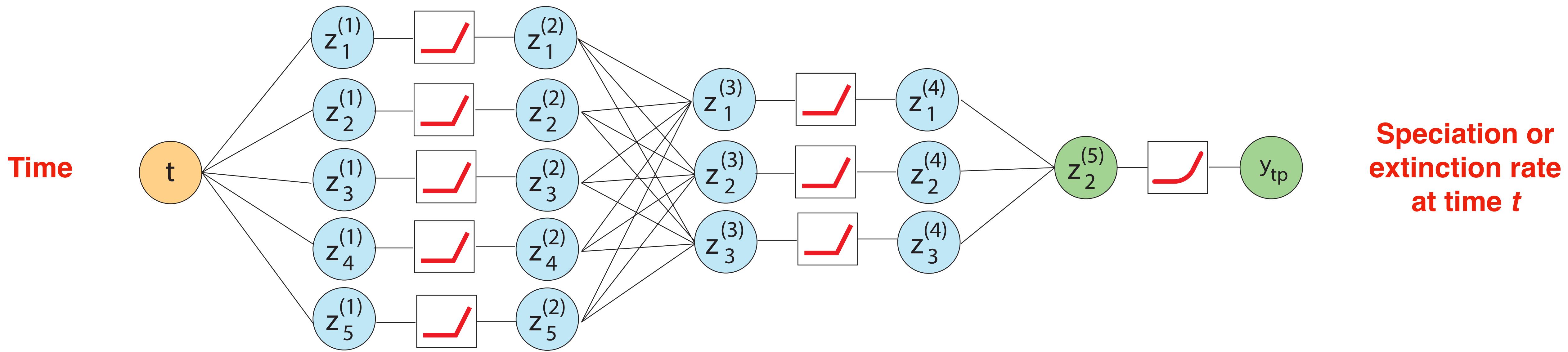
Time-variable rate



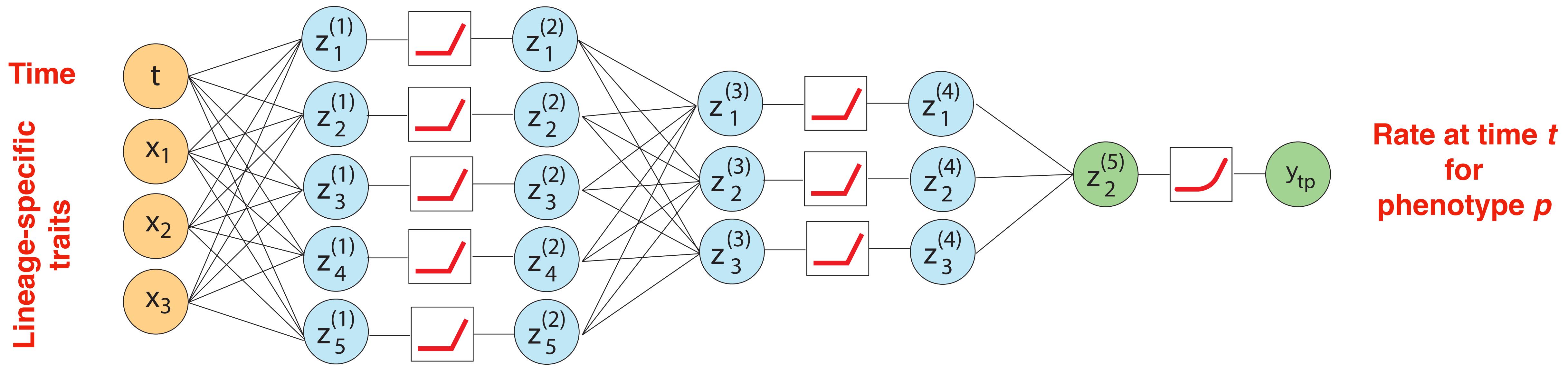
ice within and between clades



Time-dependent Birth-Death-NN model

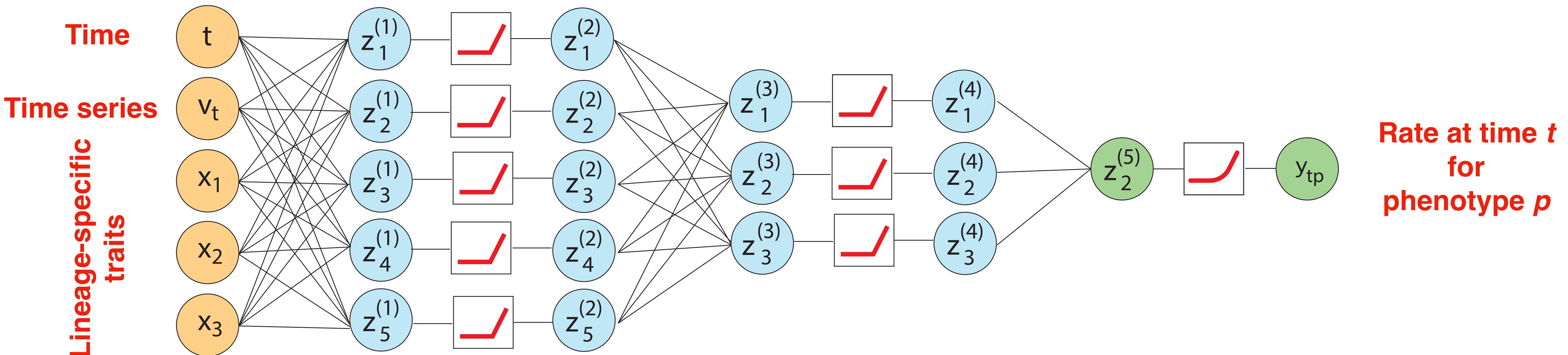


Time-dependent and trait-dependent BDNN model



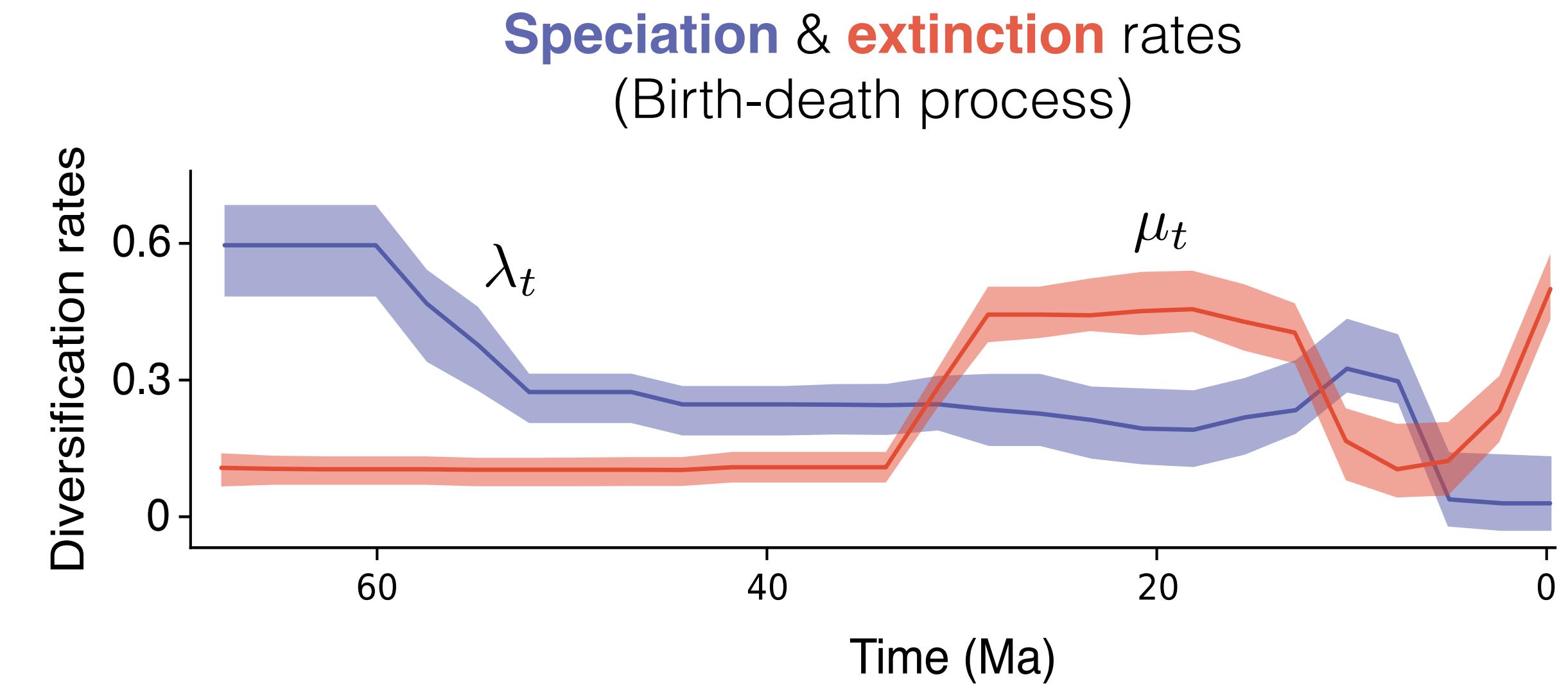
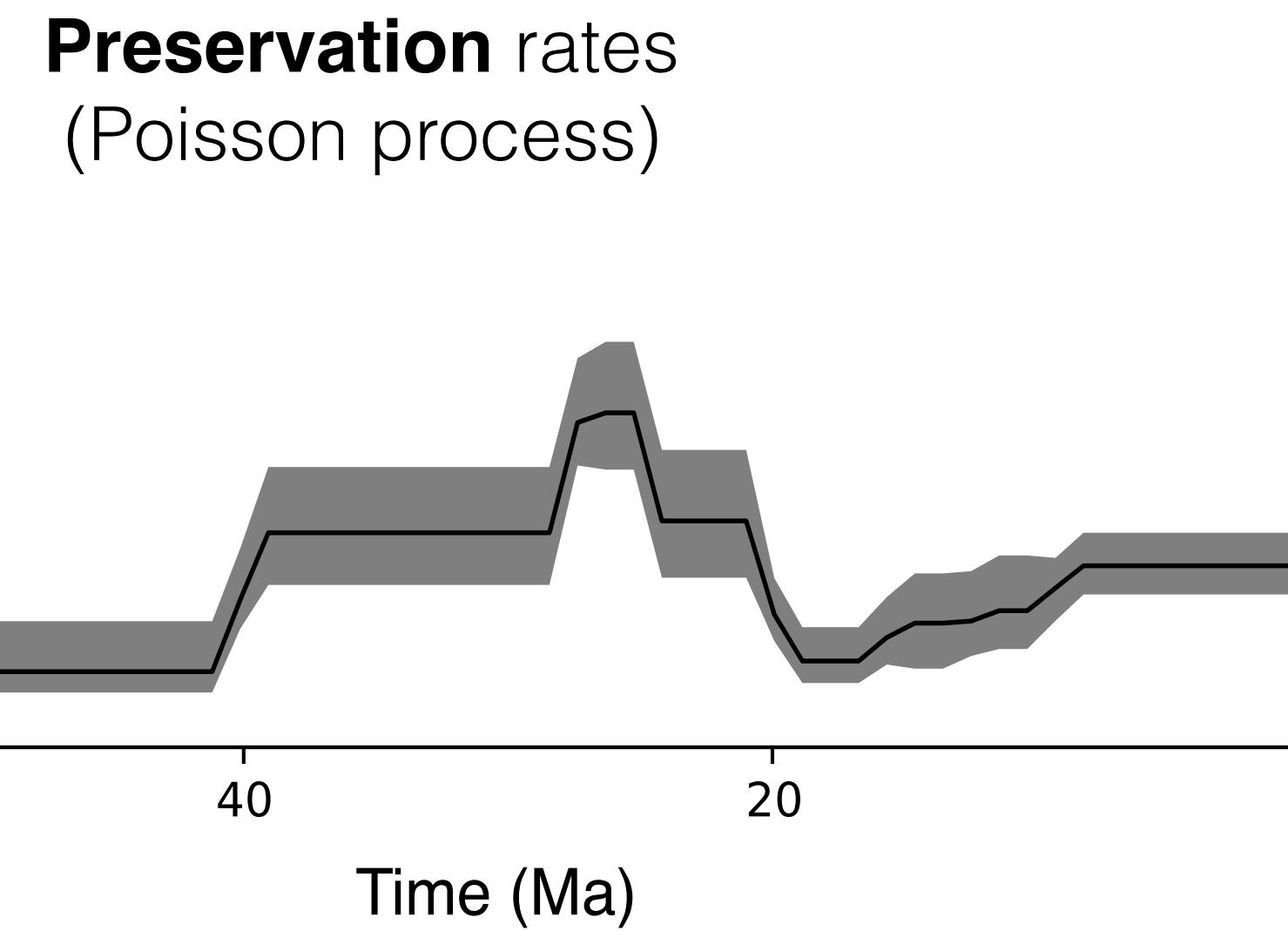
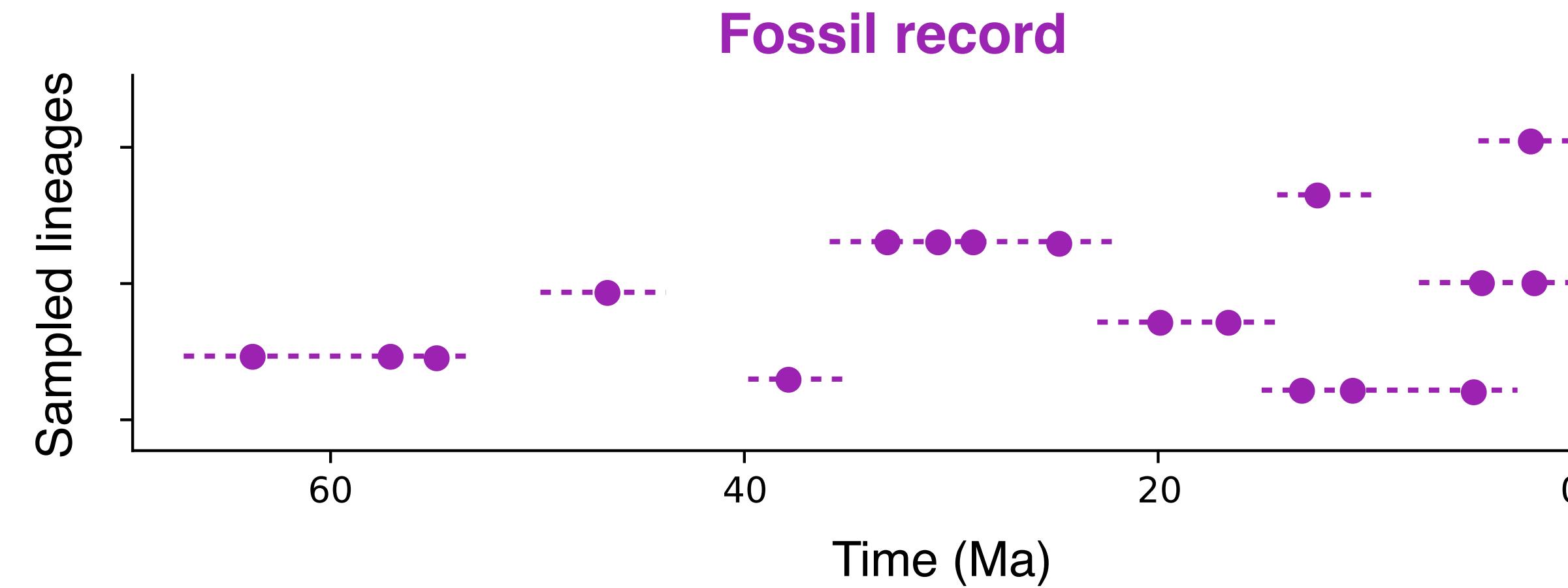
The model can include (continuous and discrete) traits and allows for species-specific rates

Time-dependent and trait-dependent BDNN model

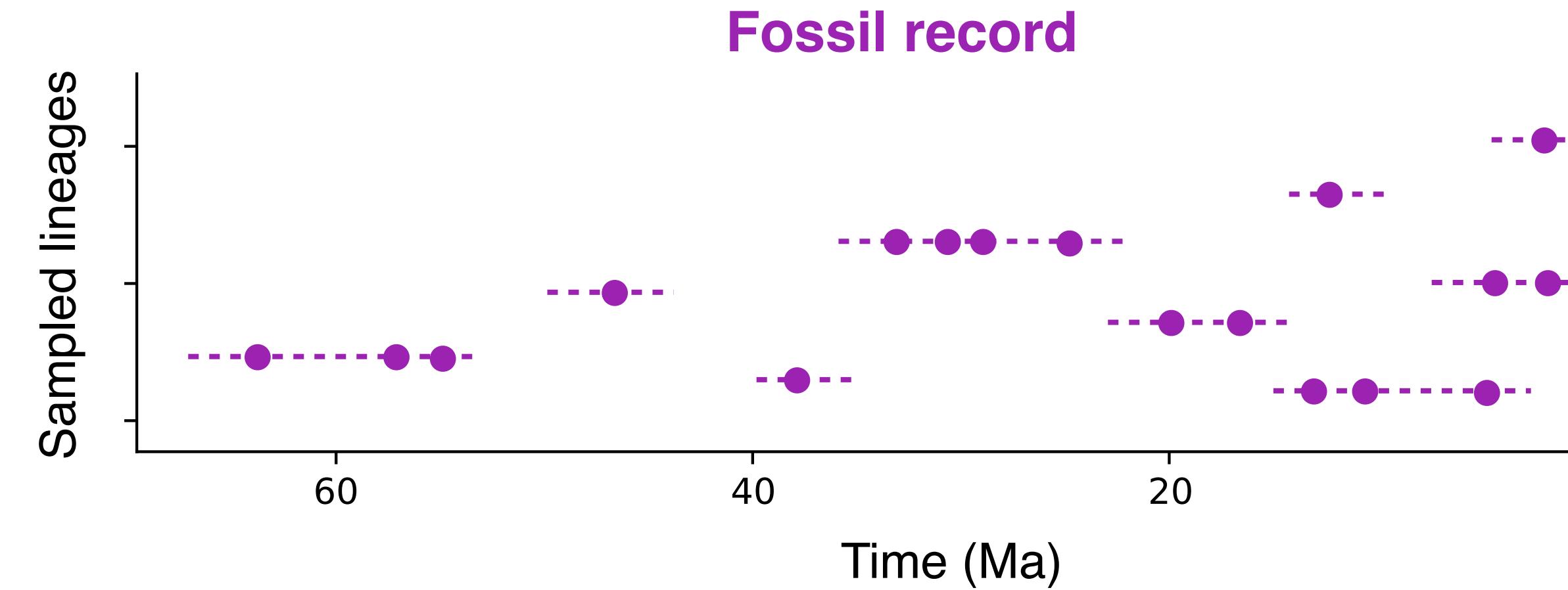


The model can include (continuous and discrete) traits and time series

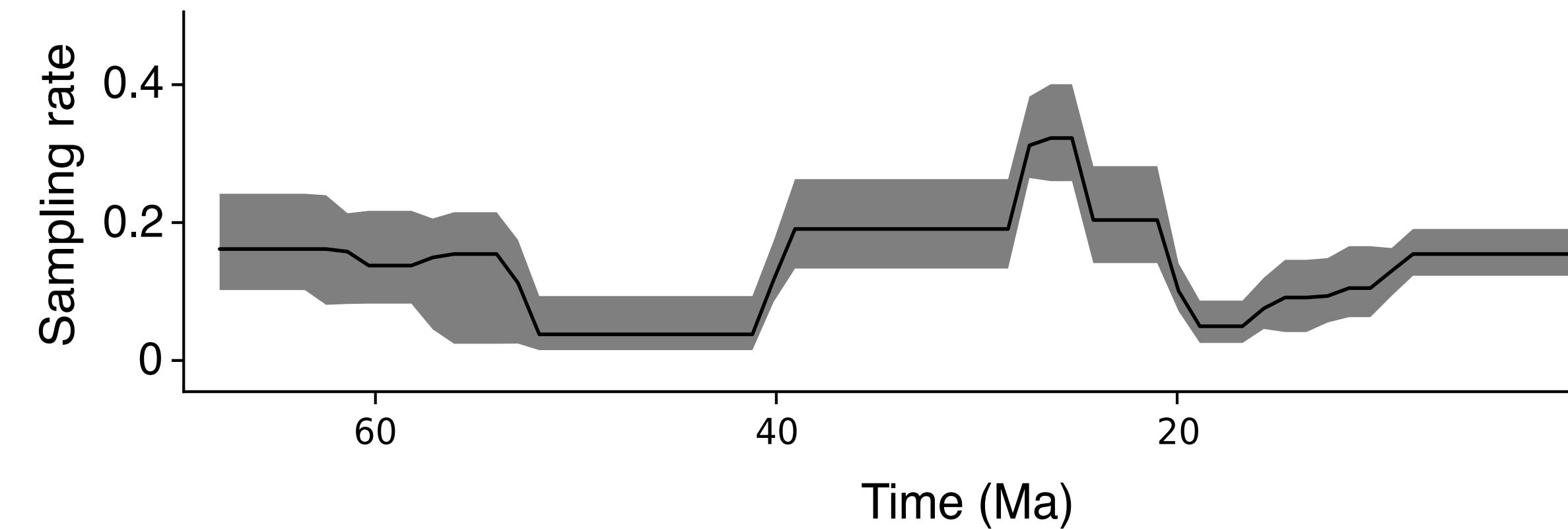
Bayesian (unsupervised) estimation of speciation and extinction rates from fossils



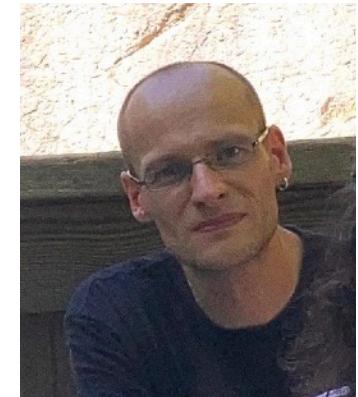
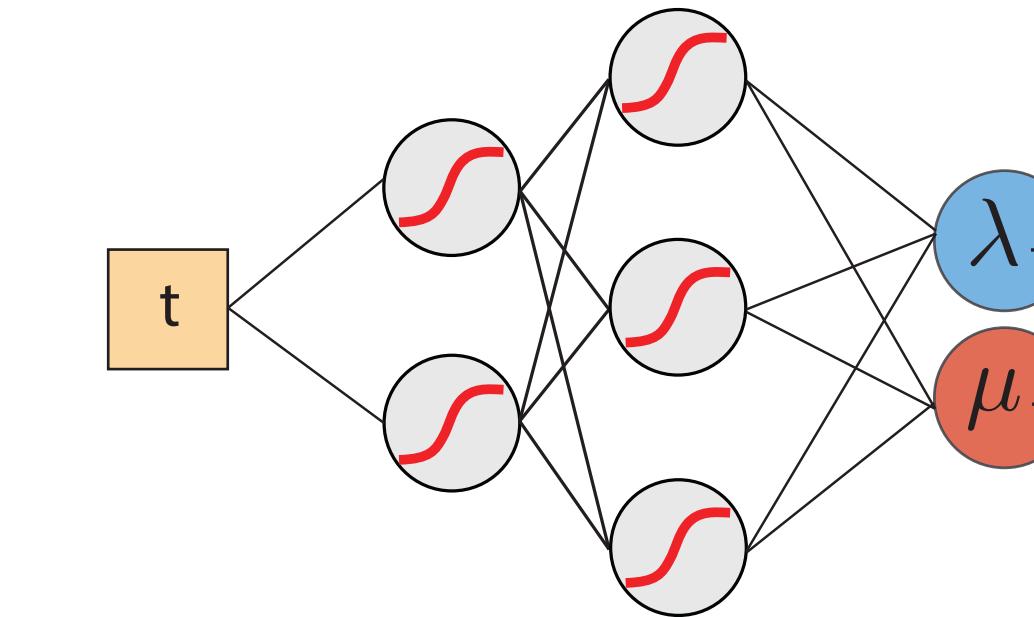
A birth-death neural network model of speciation and extinction



Preservation rates

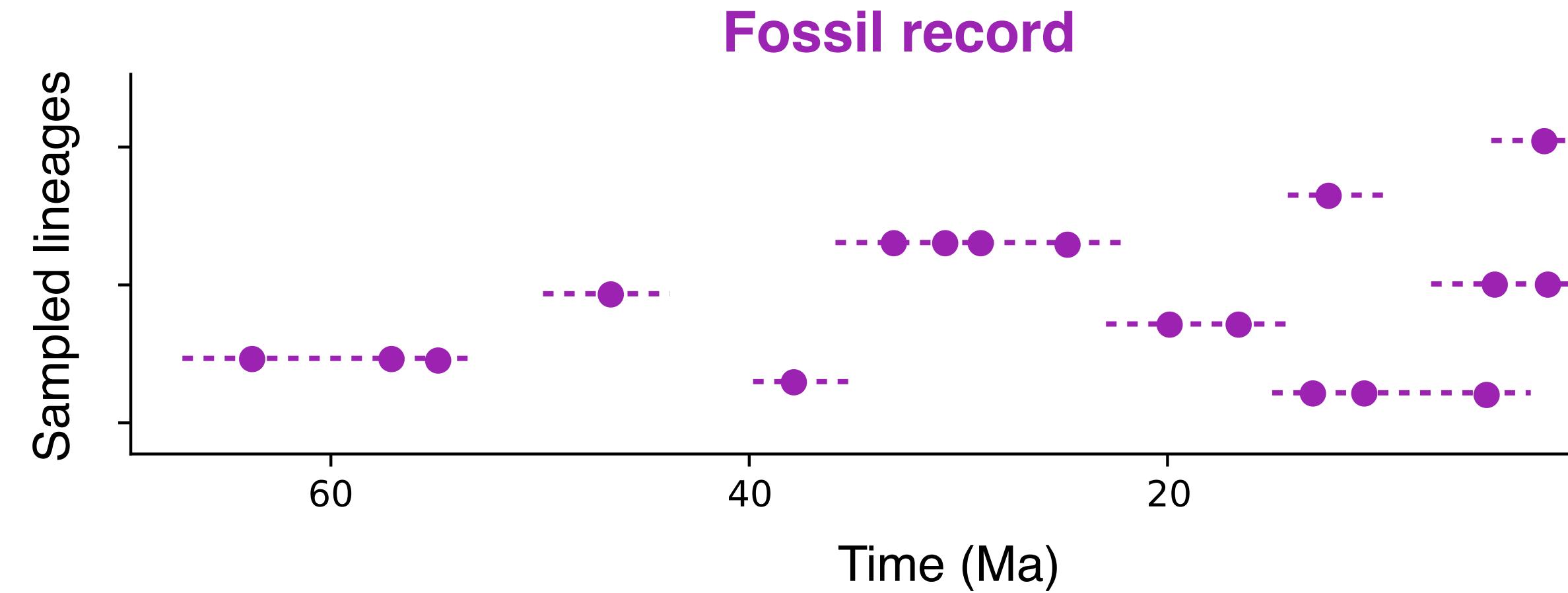


Time-varying **Speciation** & **extinction**
rates modeled by a NN

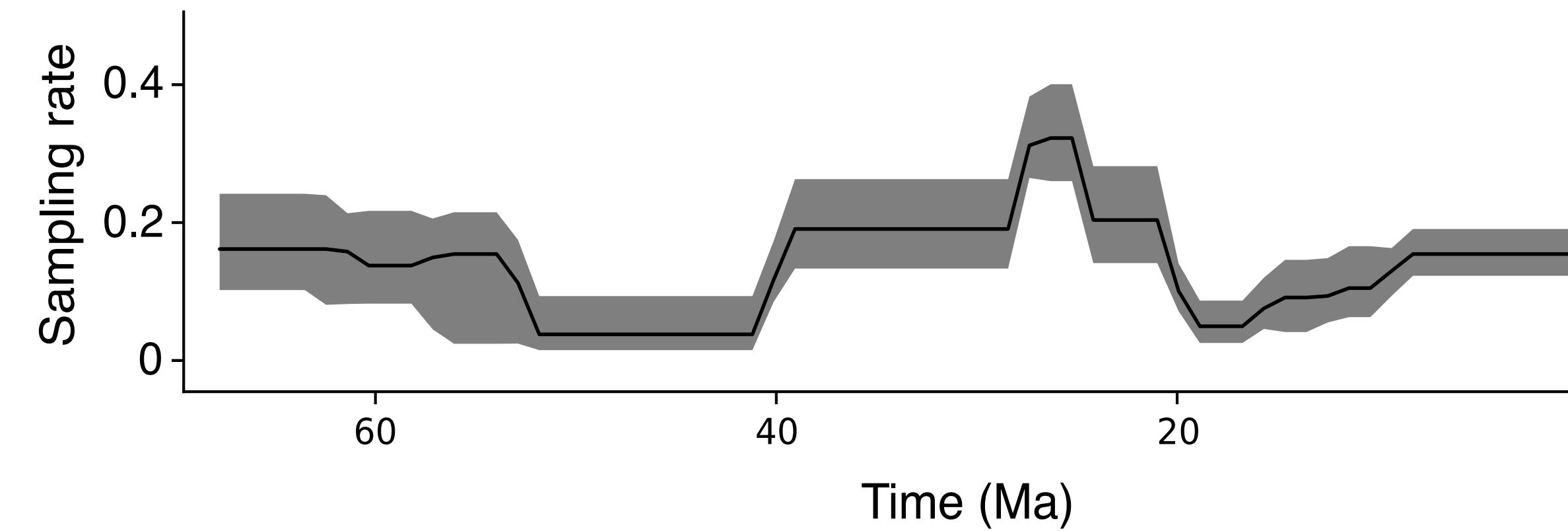


T Hauffe

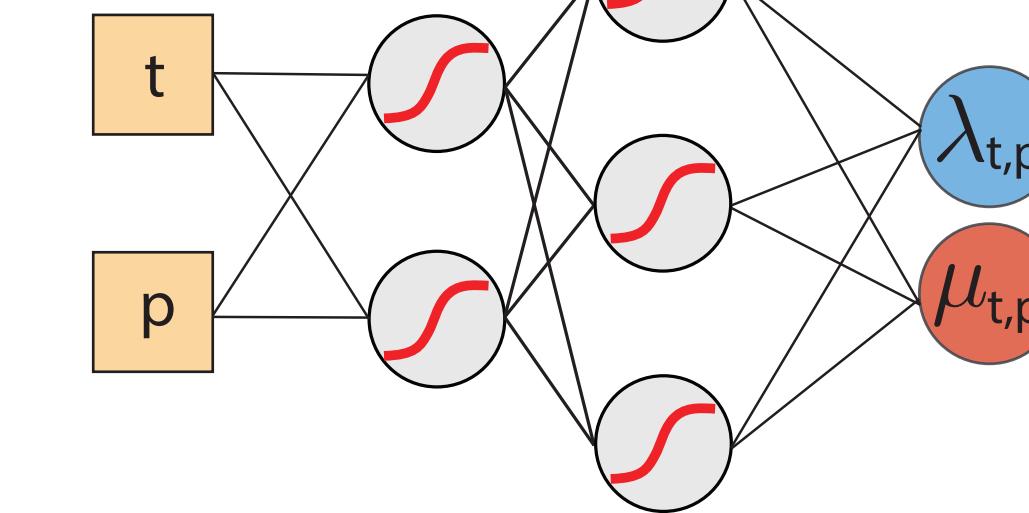
A birth-death neural network model of speciation and extinction



Preservation rates



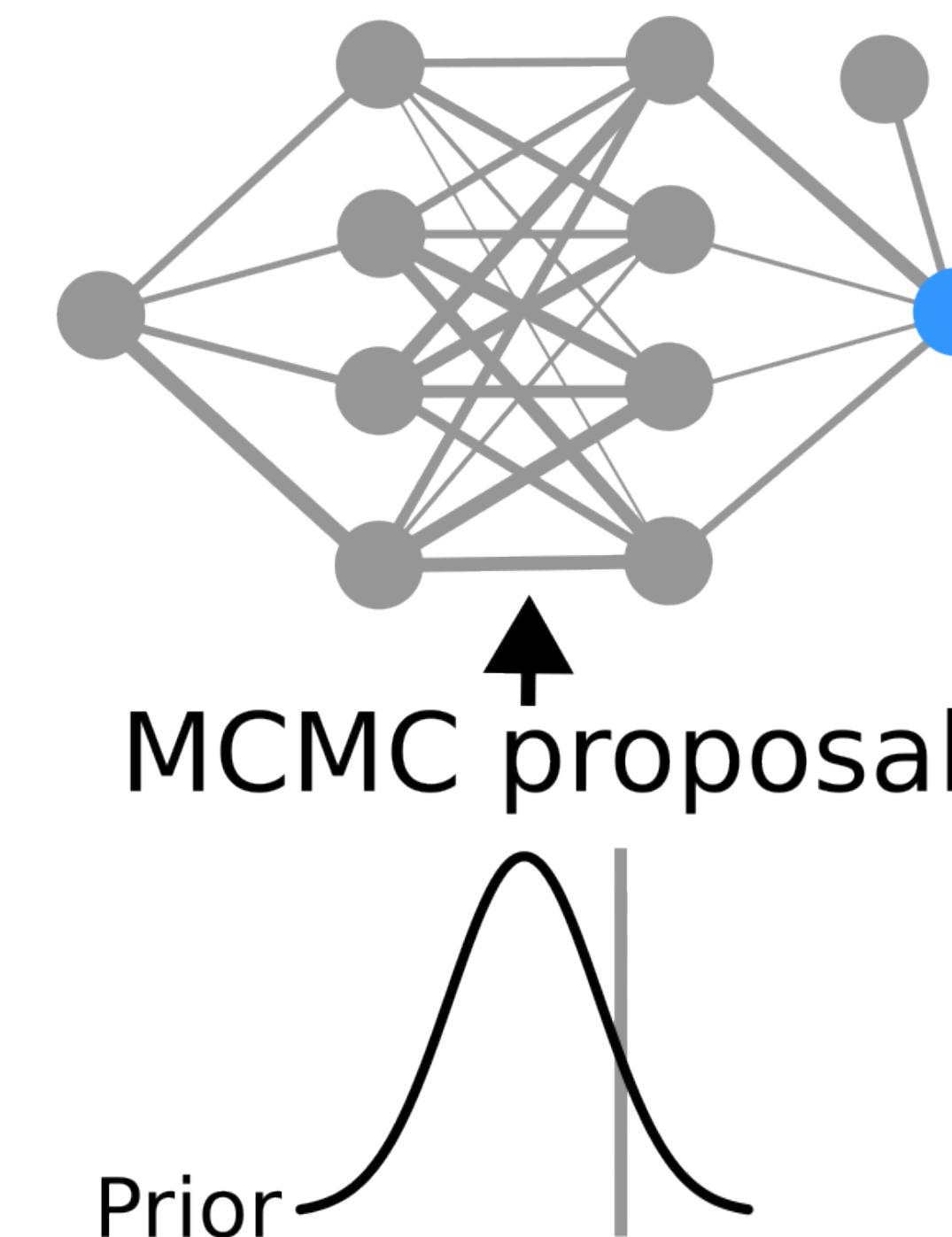
Species-specific and time-varying
Speciation & extinction rates



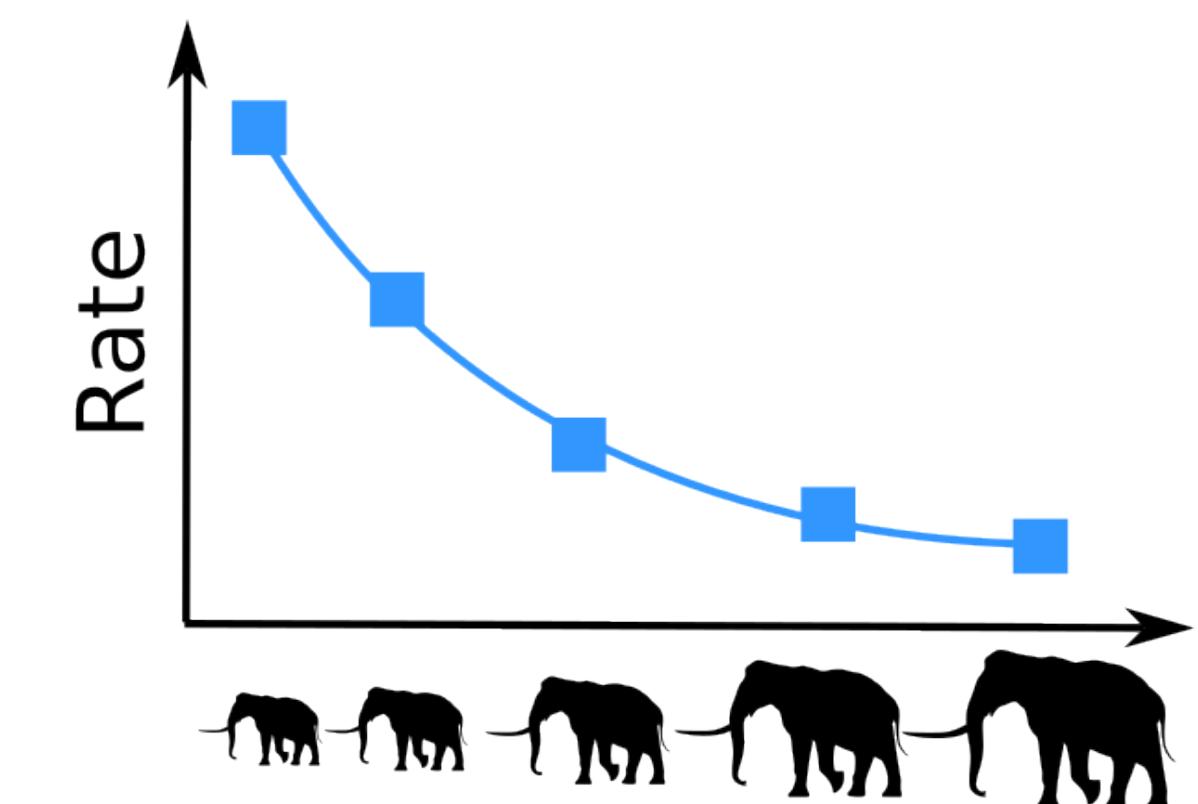
T Hauffe

1. Predictors

Sp1 Sp2 Sp3 Sp4 Sp5

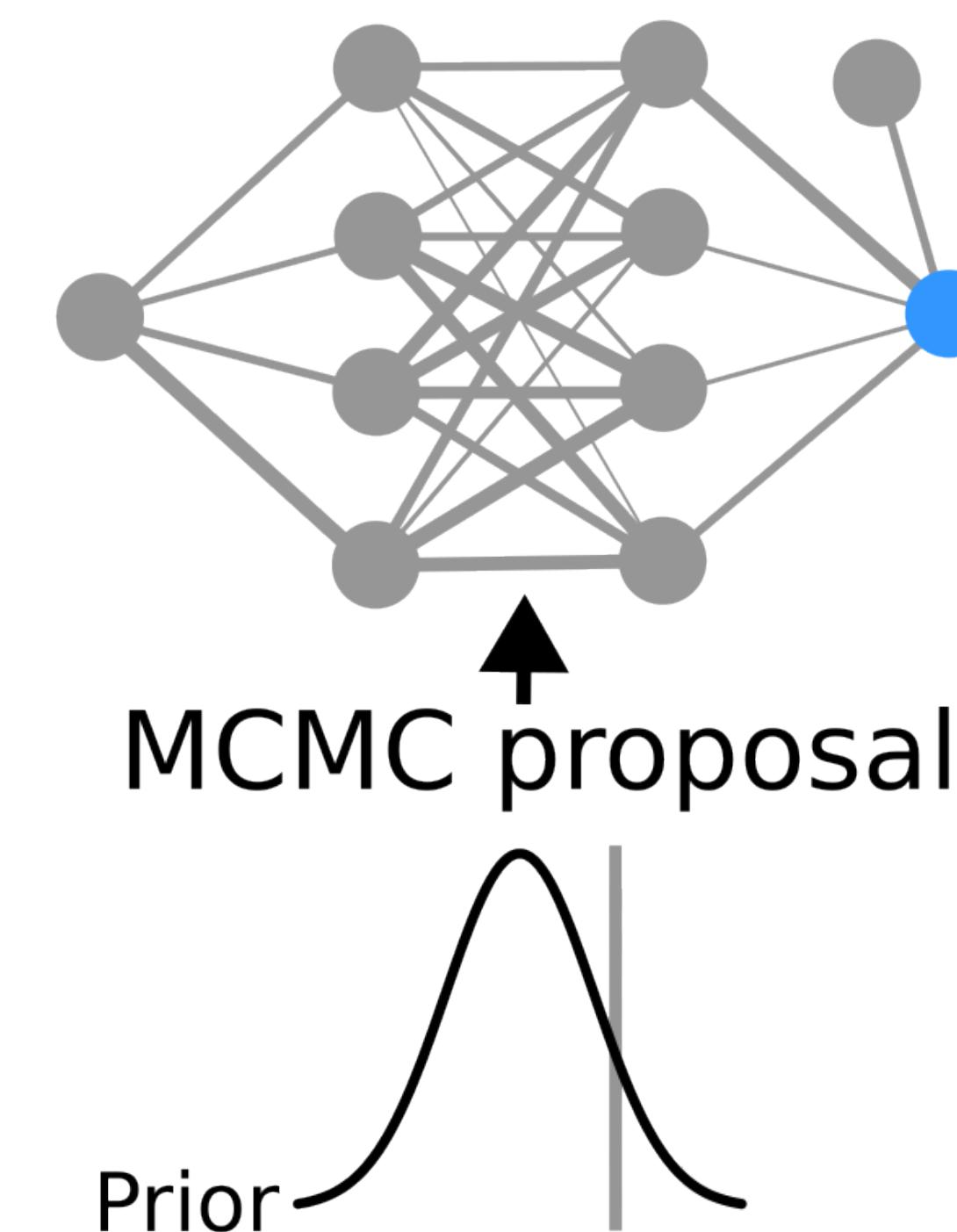


2. Transformation

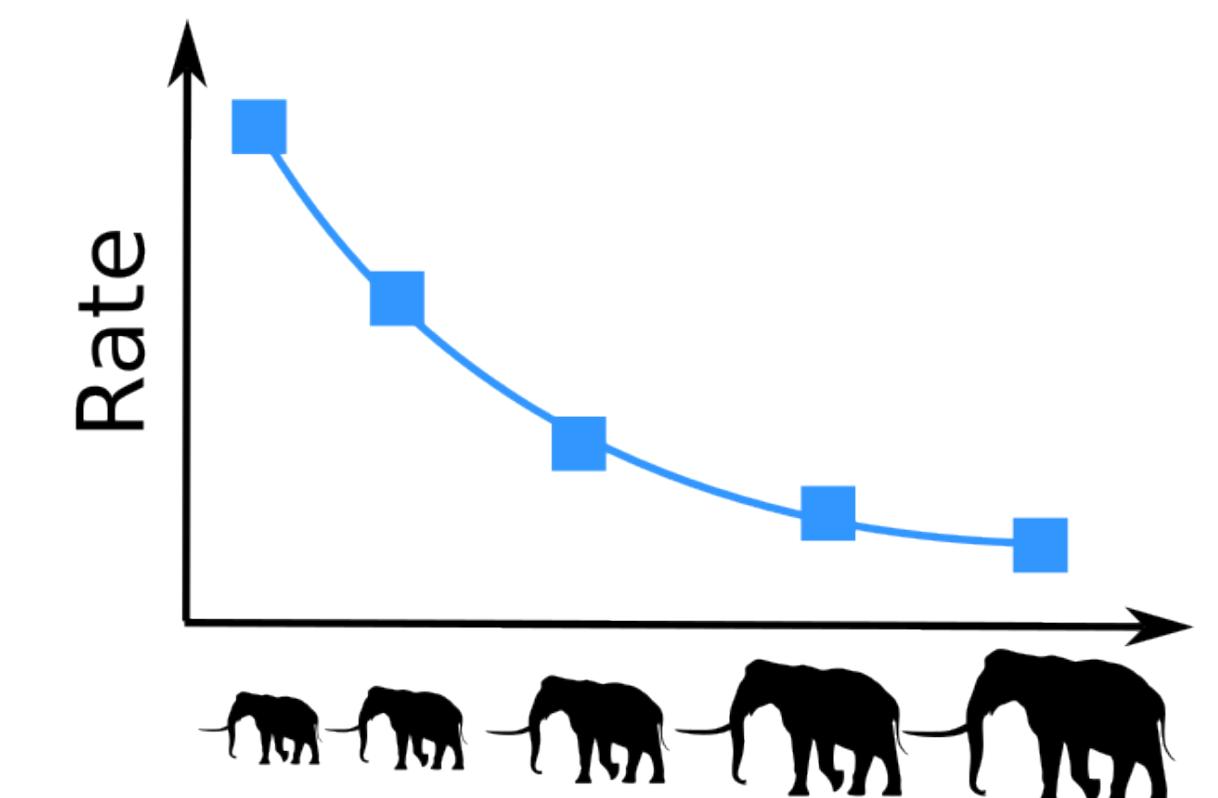


1. Predictors

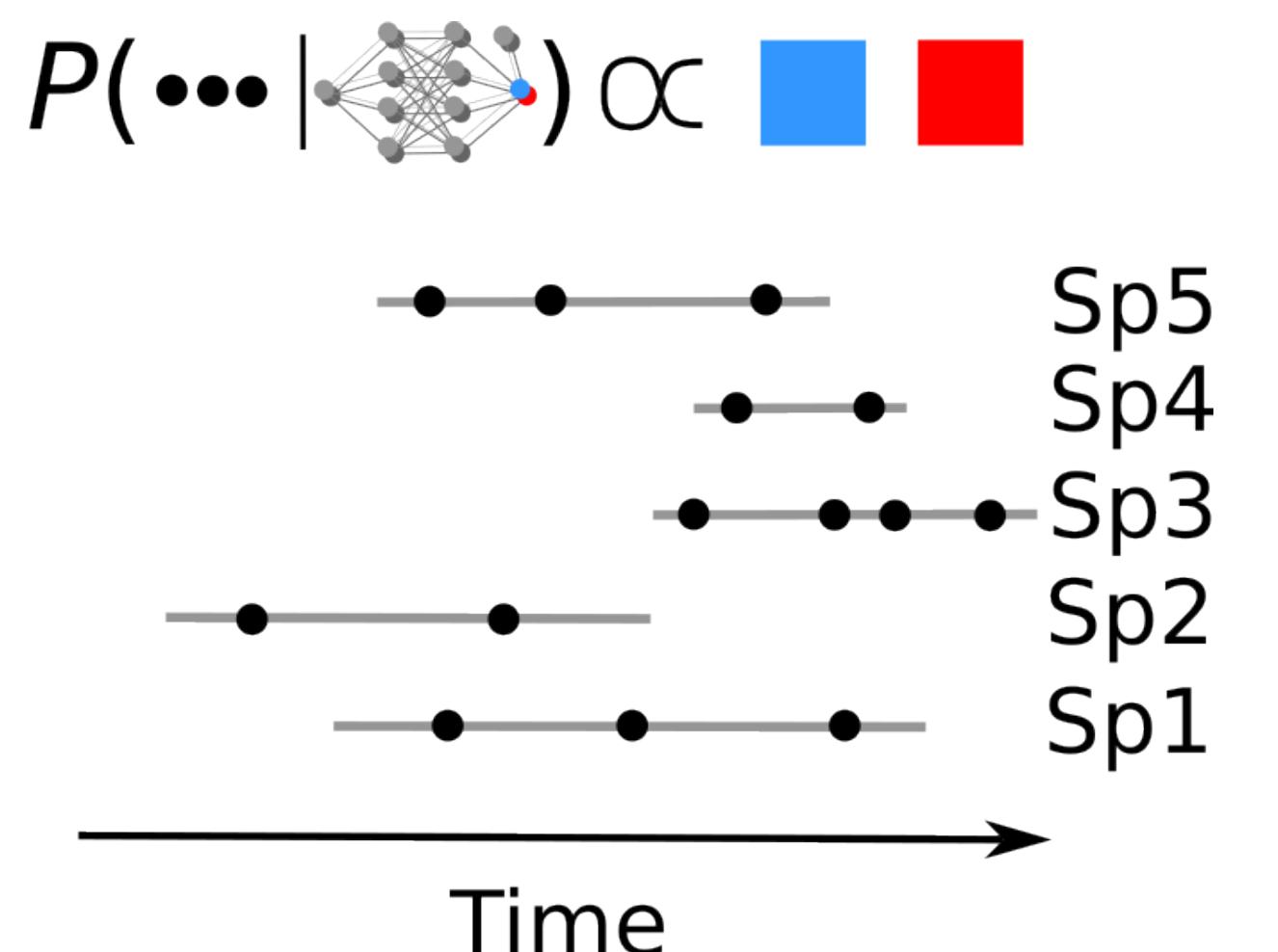
Sp1 Sp2 Sp3 Sp4 Sp5



2. Transformation

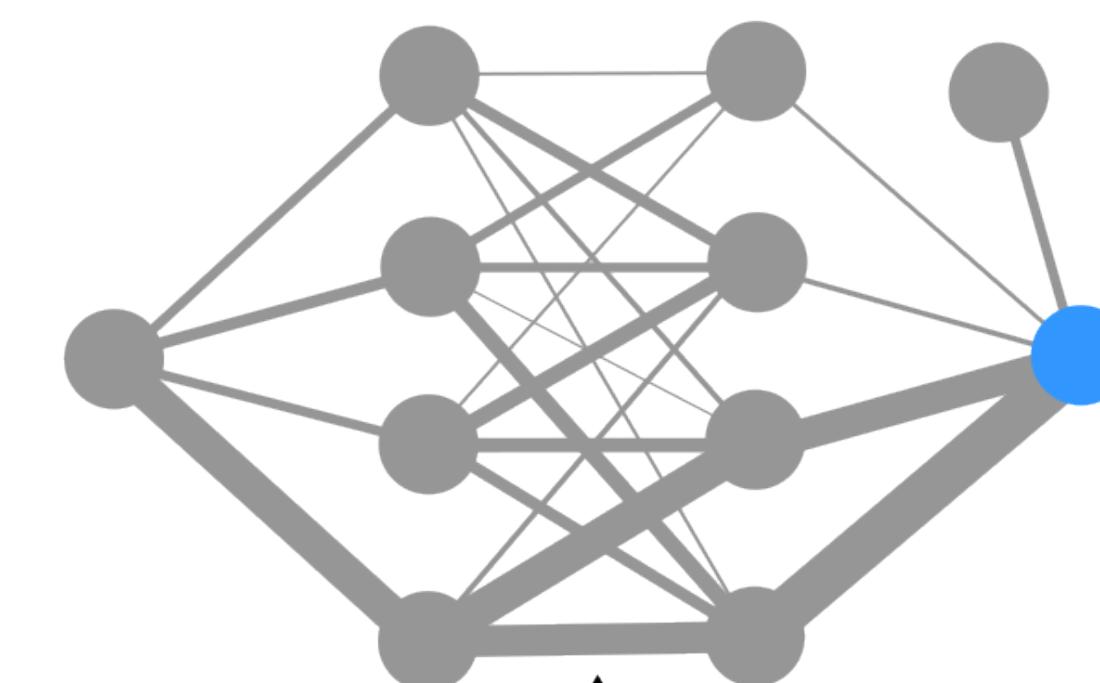


3. Likelihood



1. Predictors

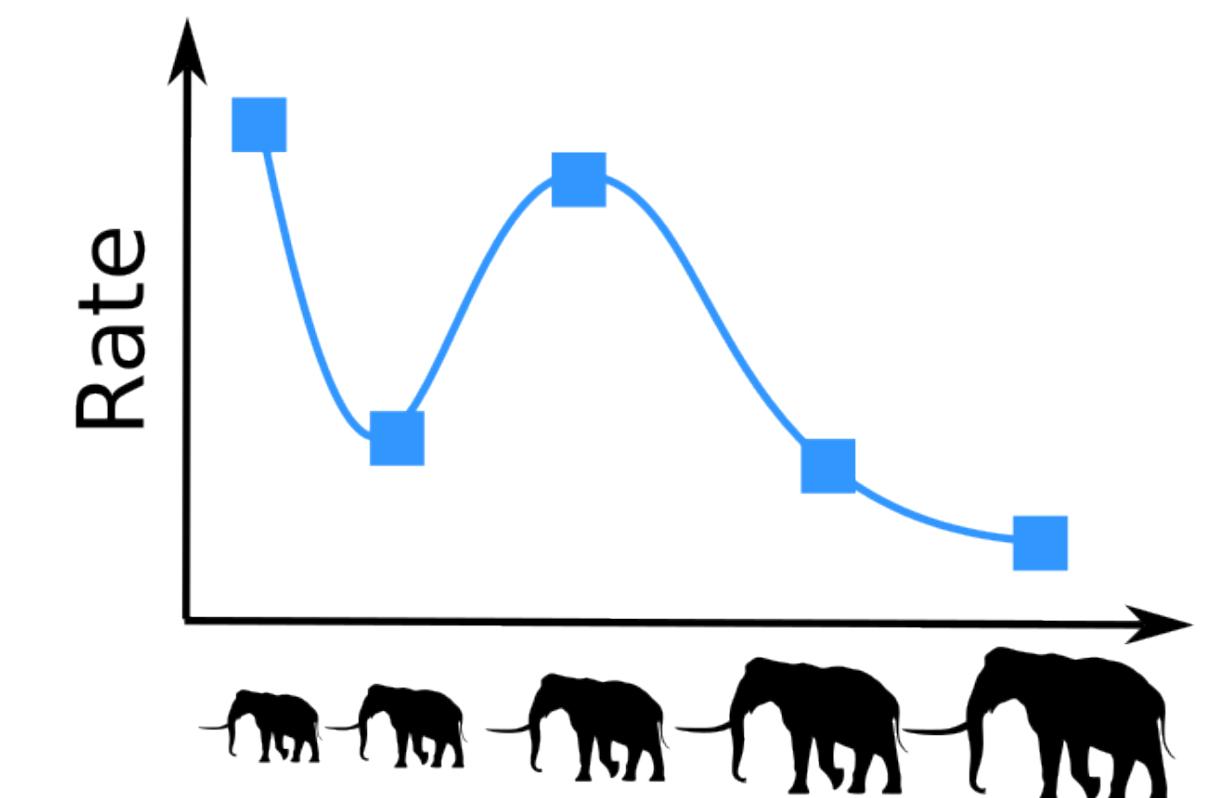
Sp1 Sp2 Sp3 Sp4 Sp5



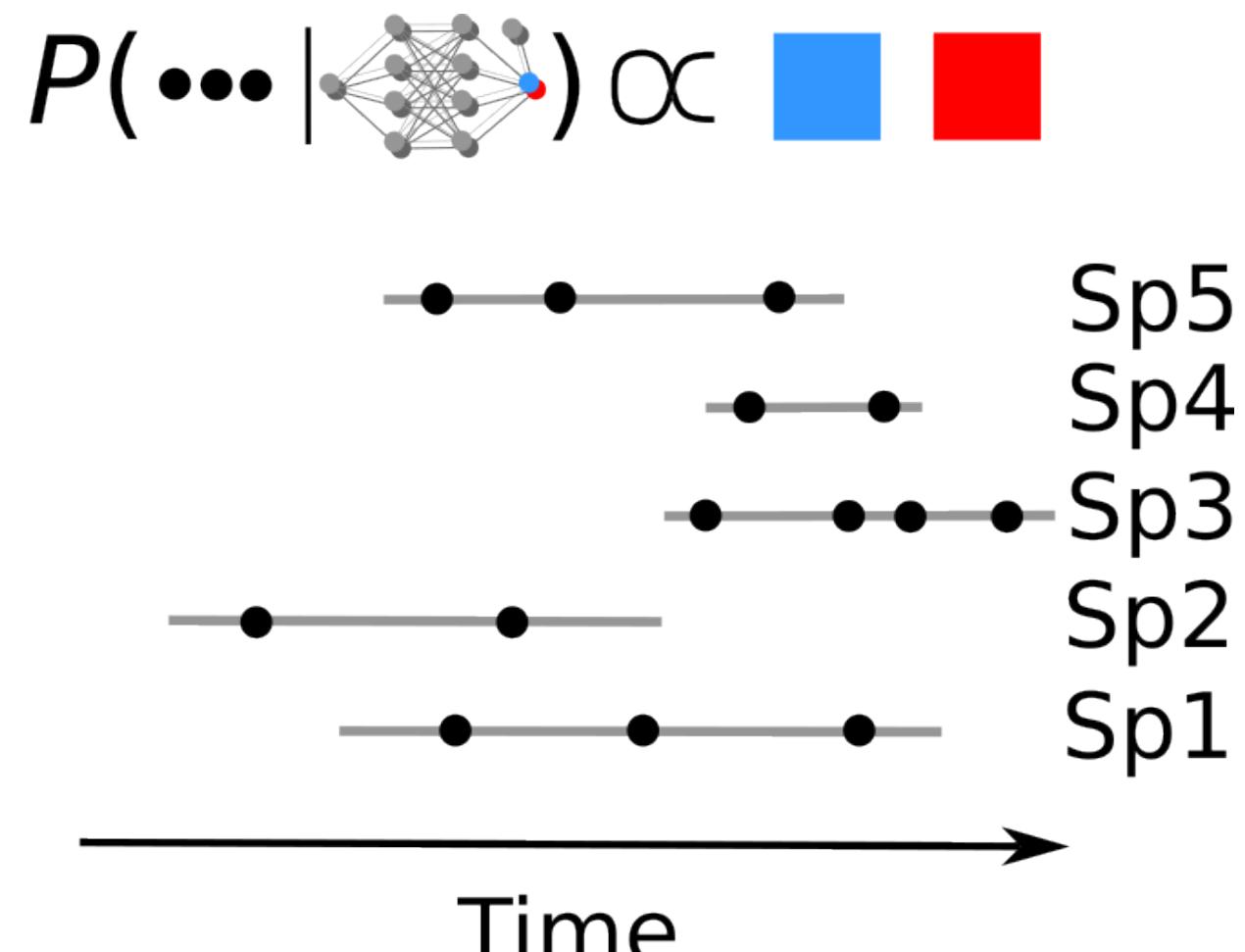
MCMC proposal

Prior

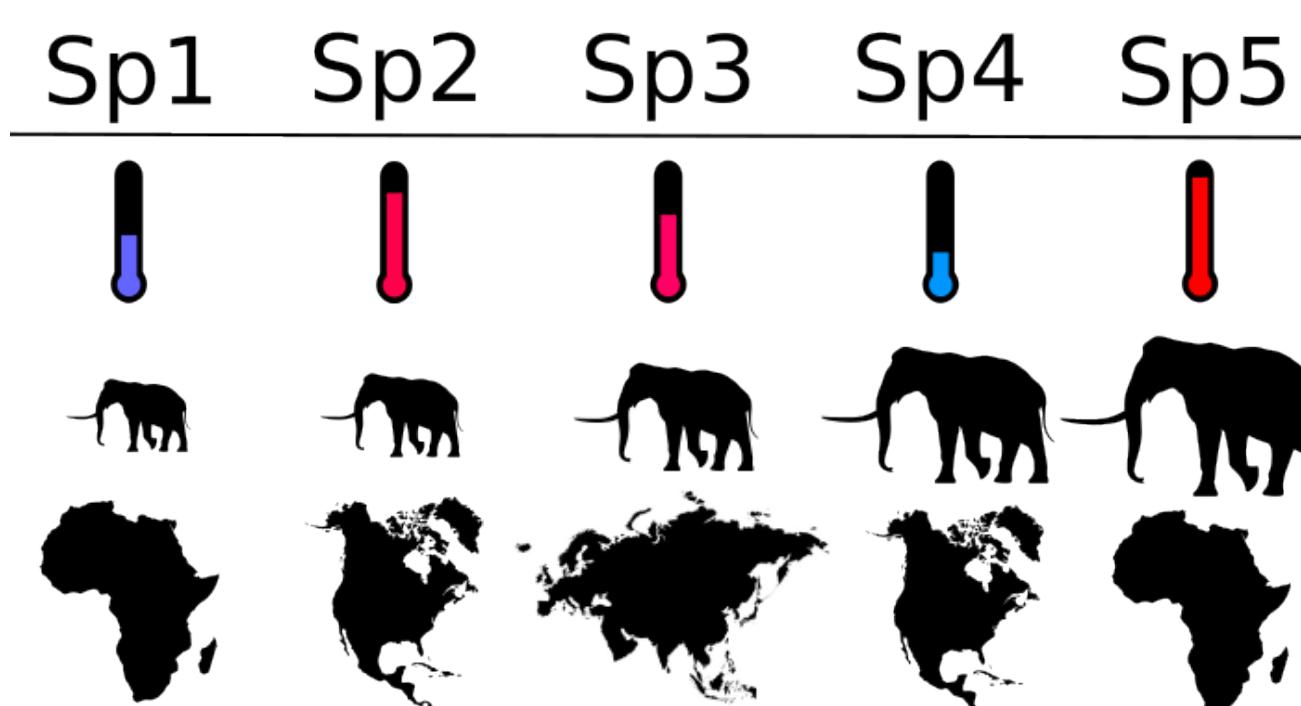
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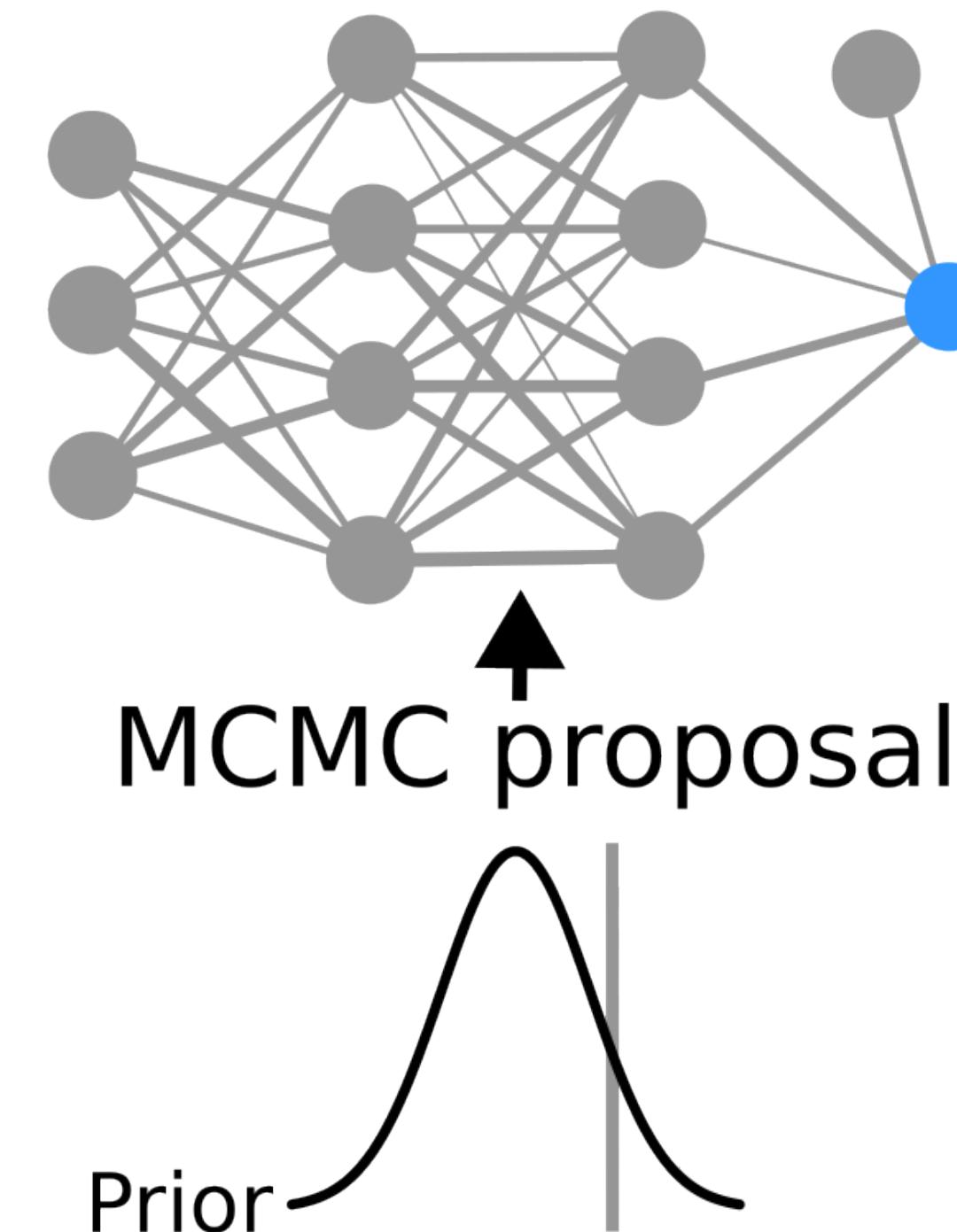
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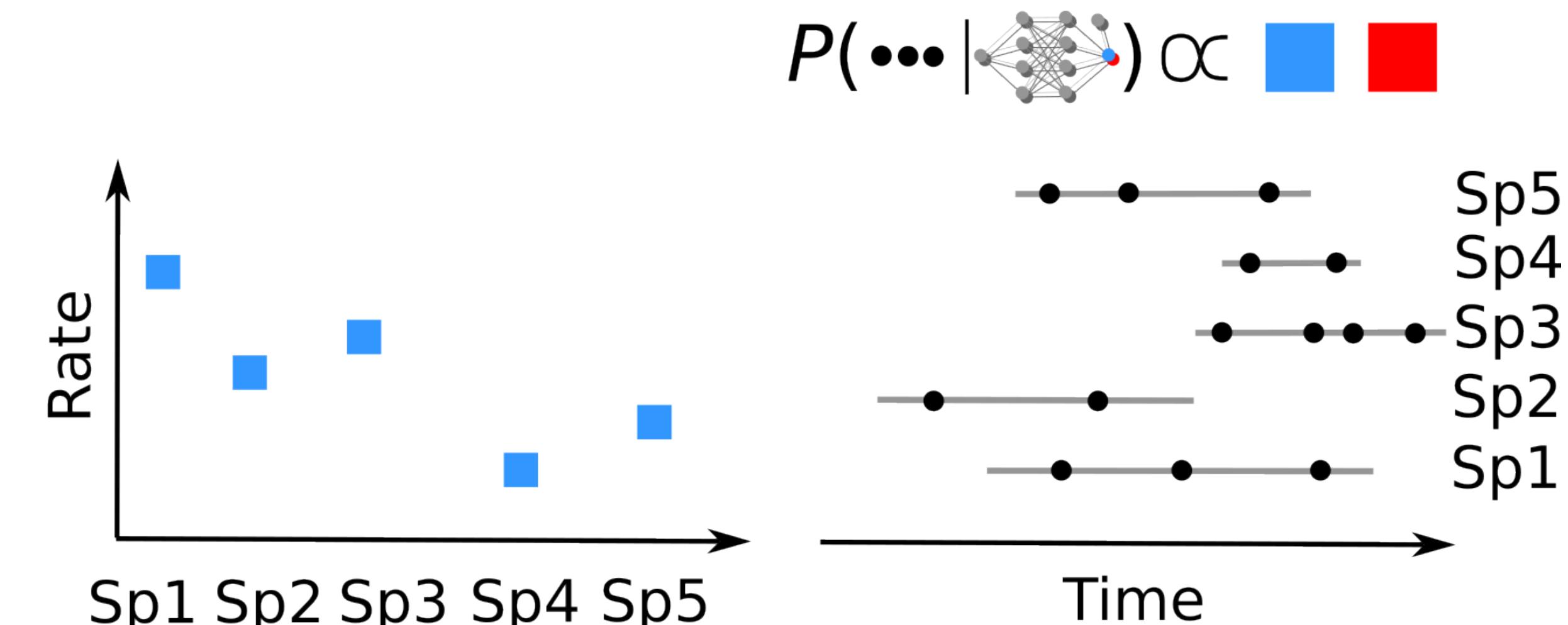
1. Predictors



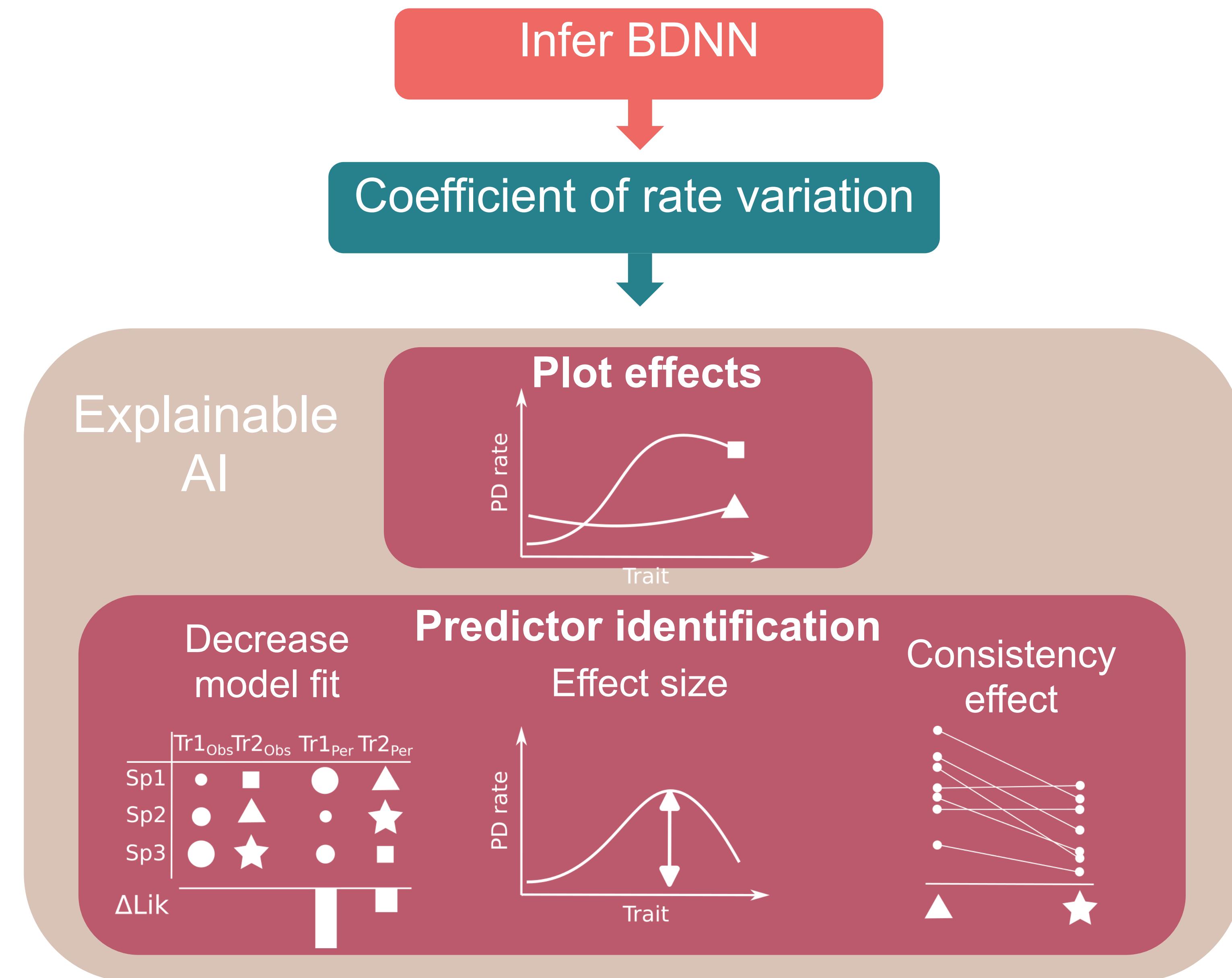
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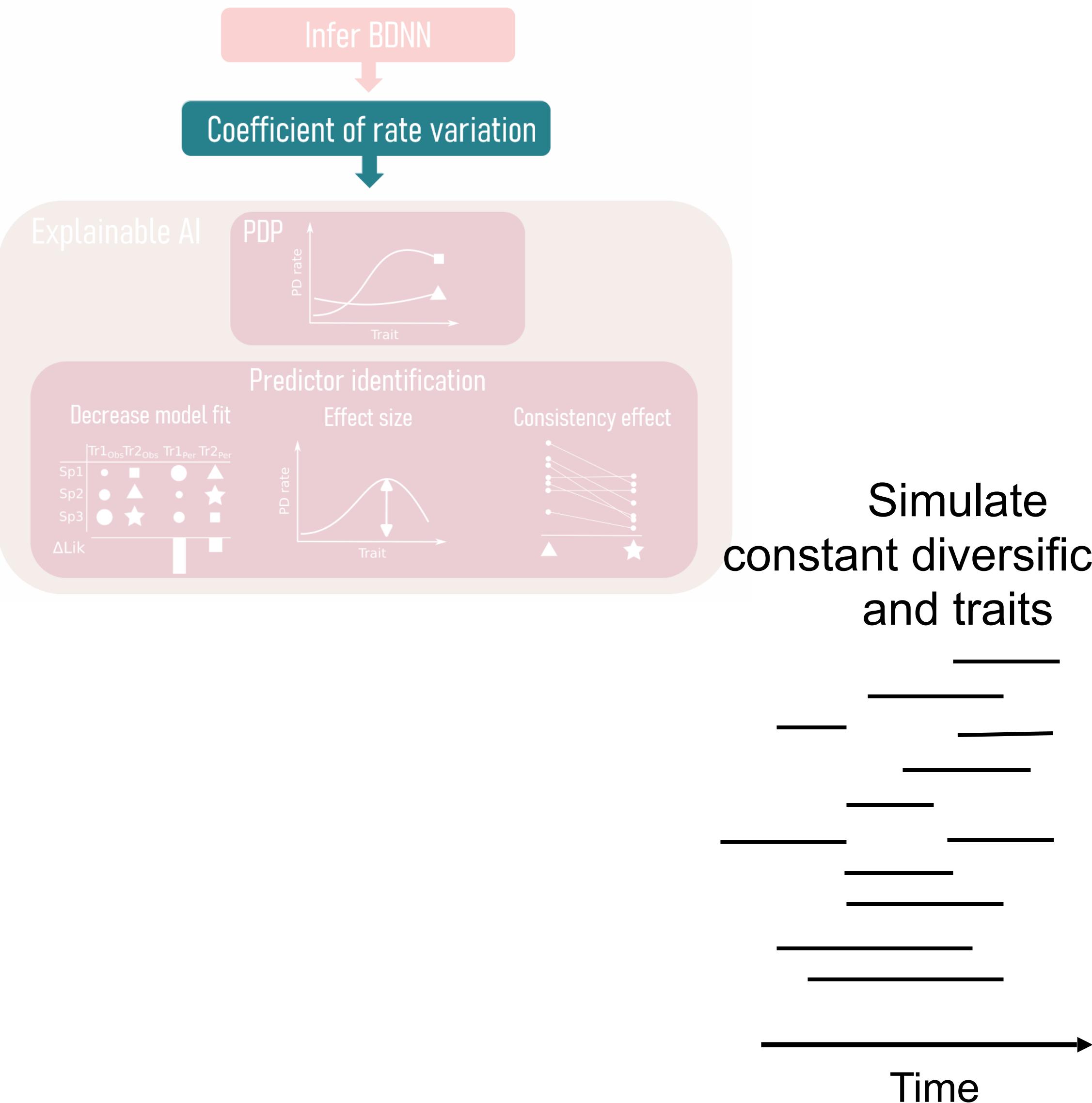
3. Likelihood



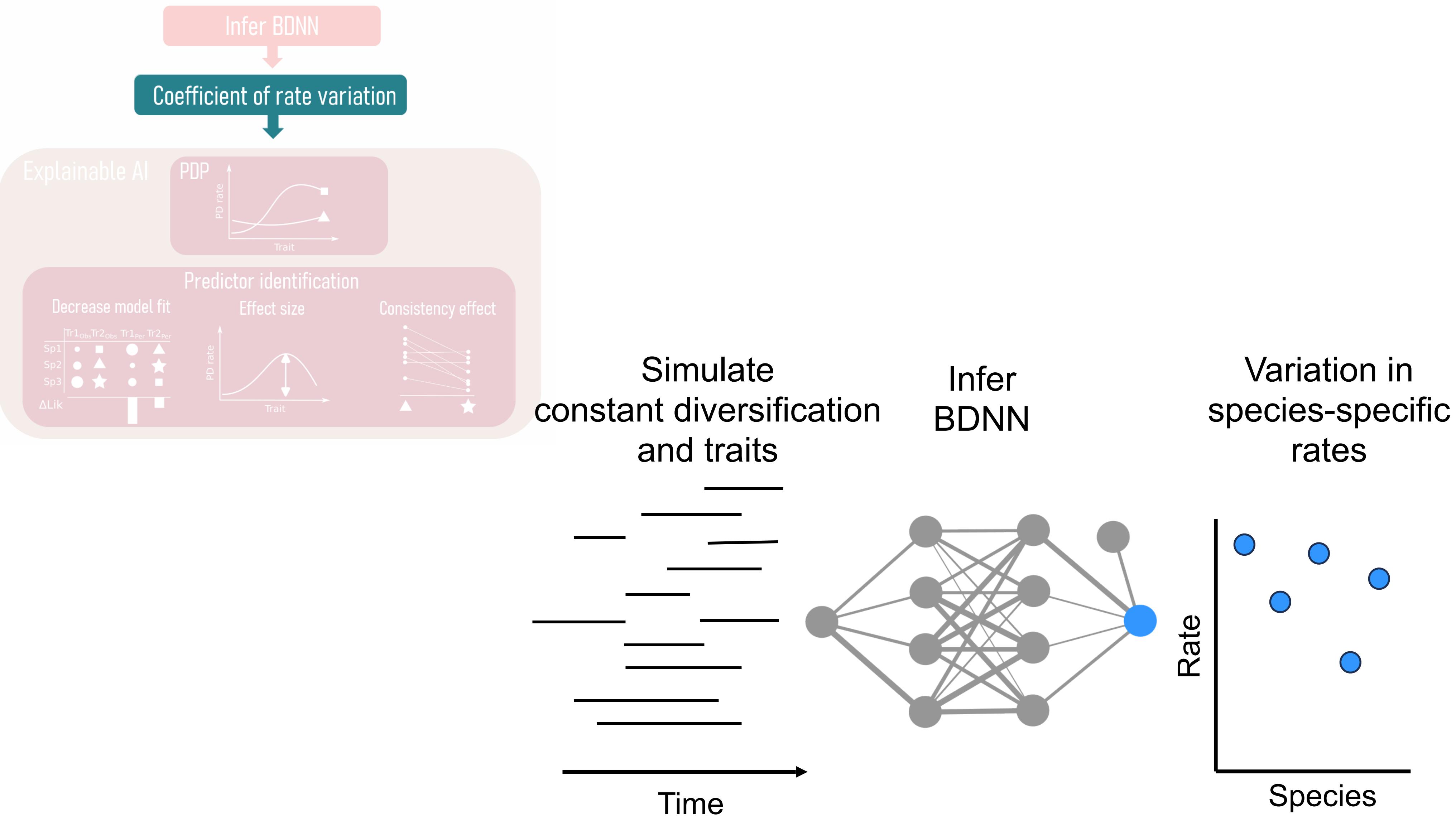
Unsupervised Bayesian neural networks and xAI to infer factors governing diversification



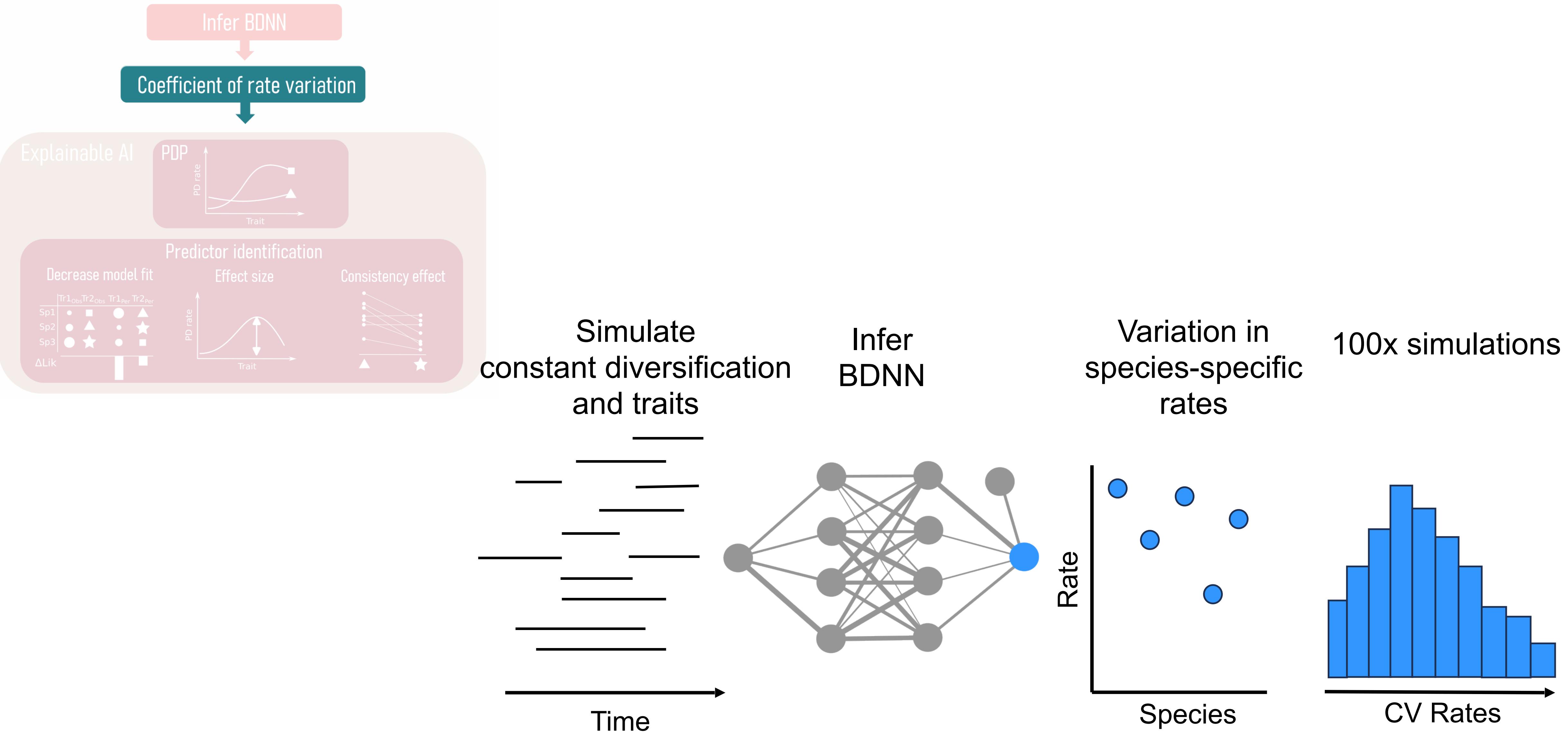
Should we dig deeper into factors? Threshold for variation in species-specific rates



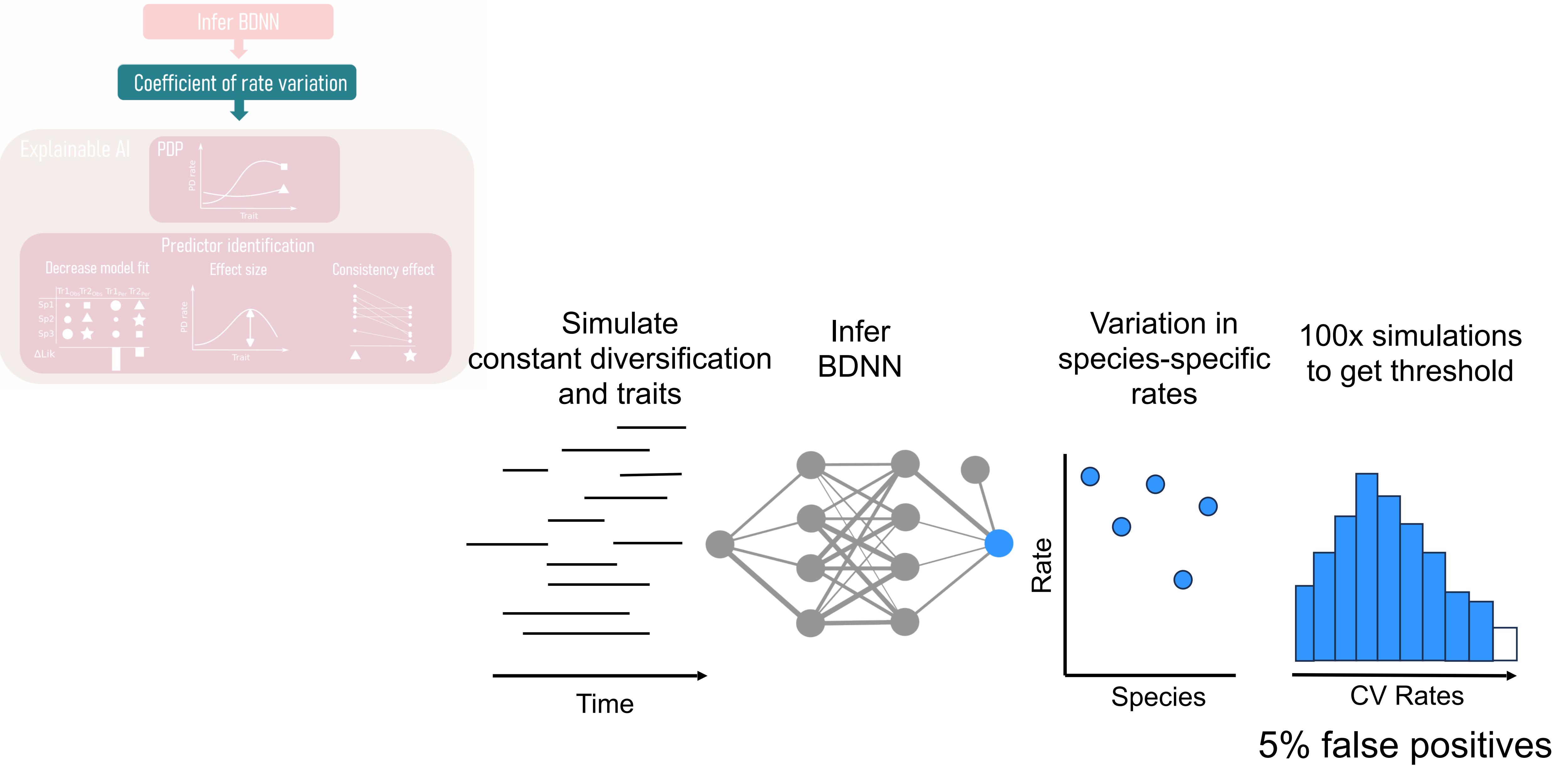
Should we dig deeper into factors? Threshold for variation in species-specific rates



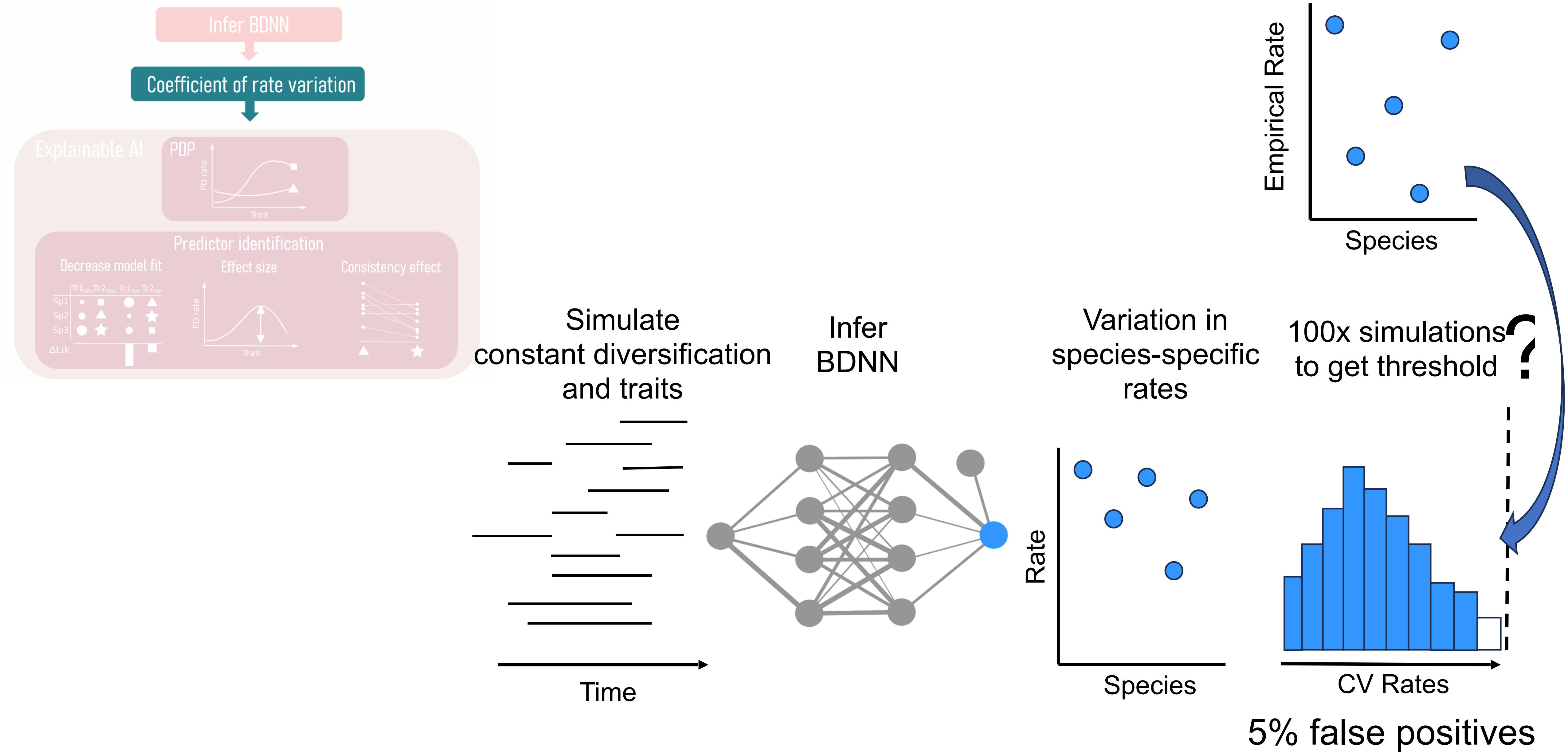
Should we dig deeper into factors? Threshold for variation in species-specific rates



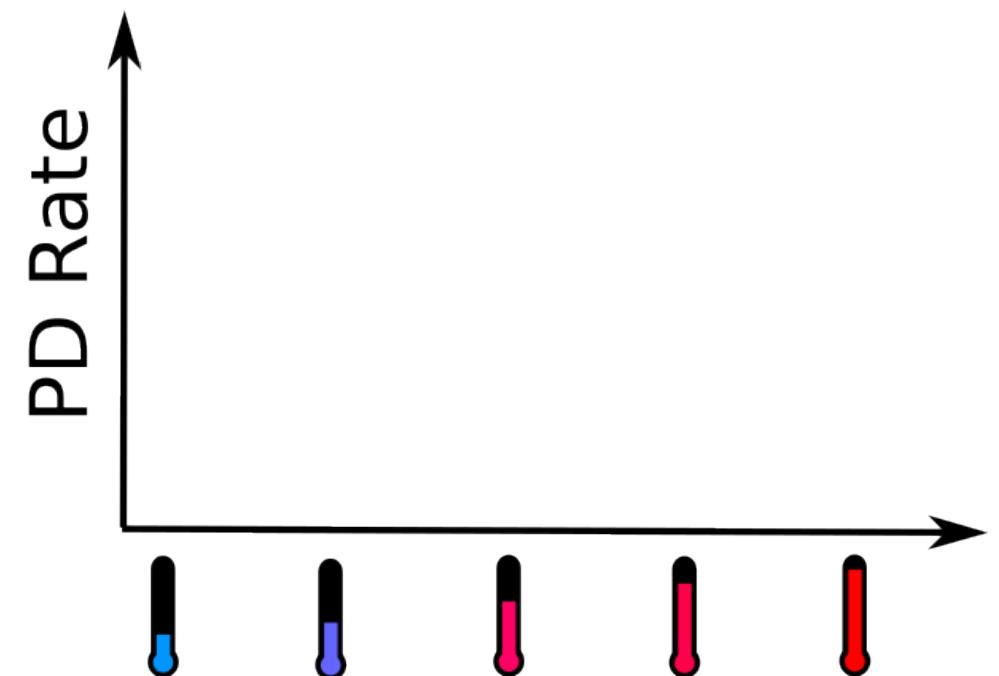
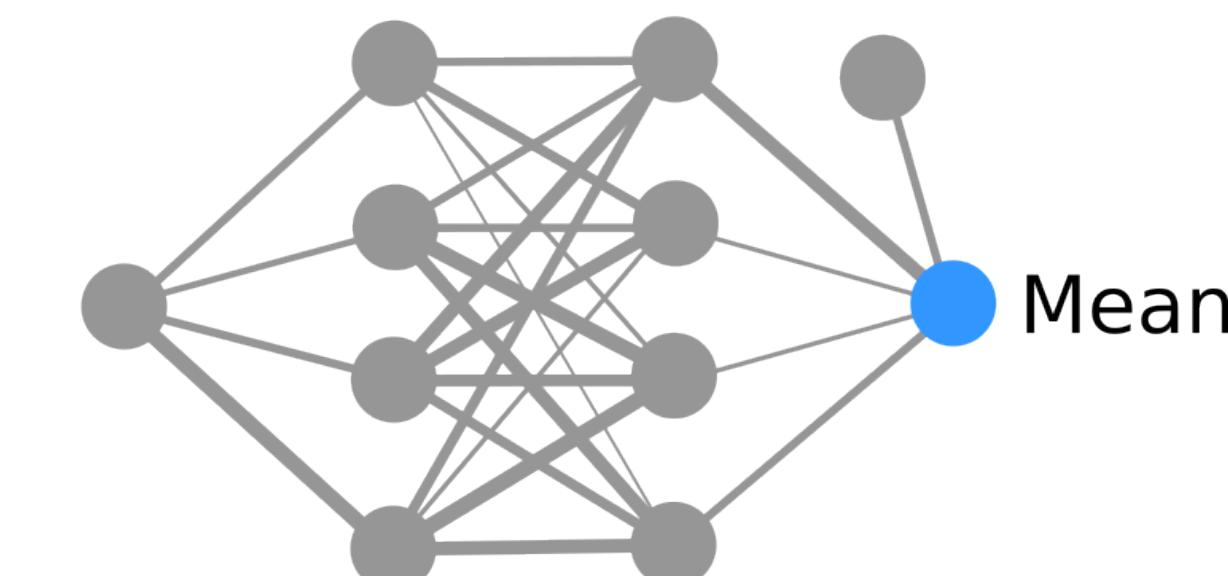
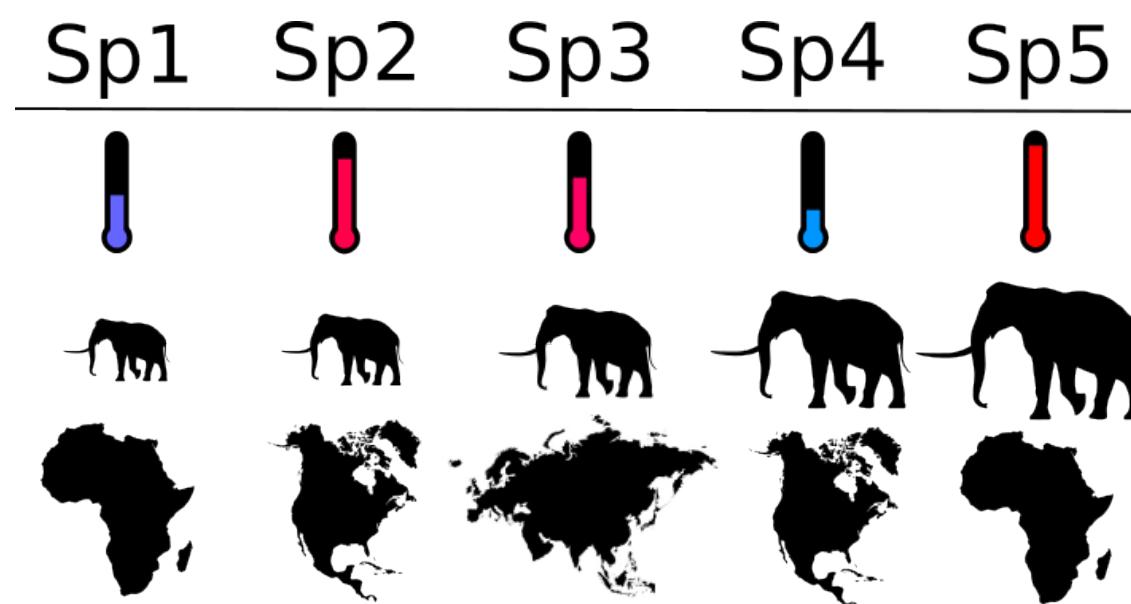
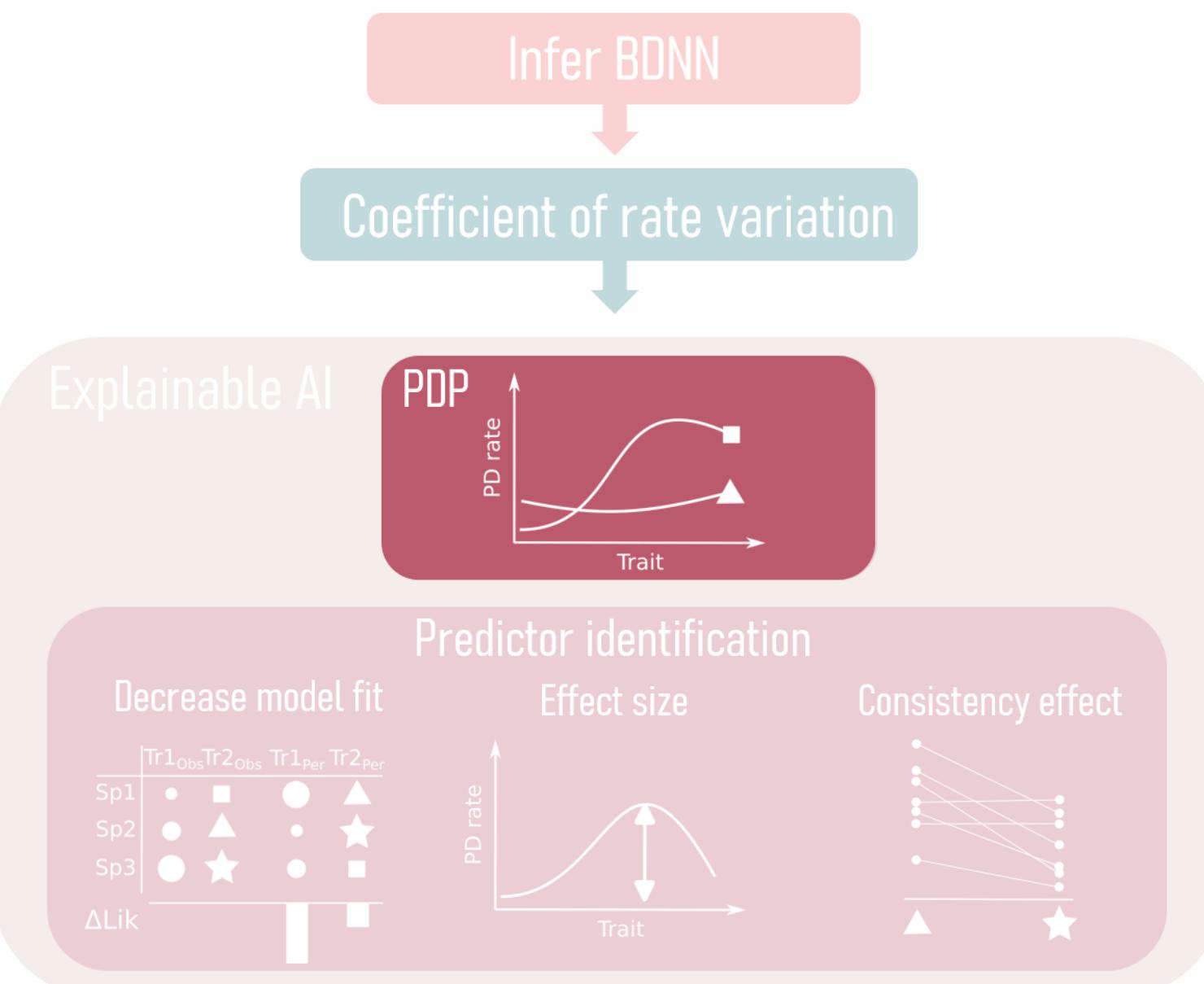
Should we dig deeper into factors? Threshold for variation in species-specific rates



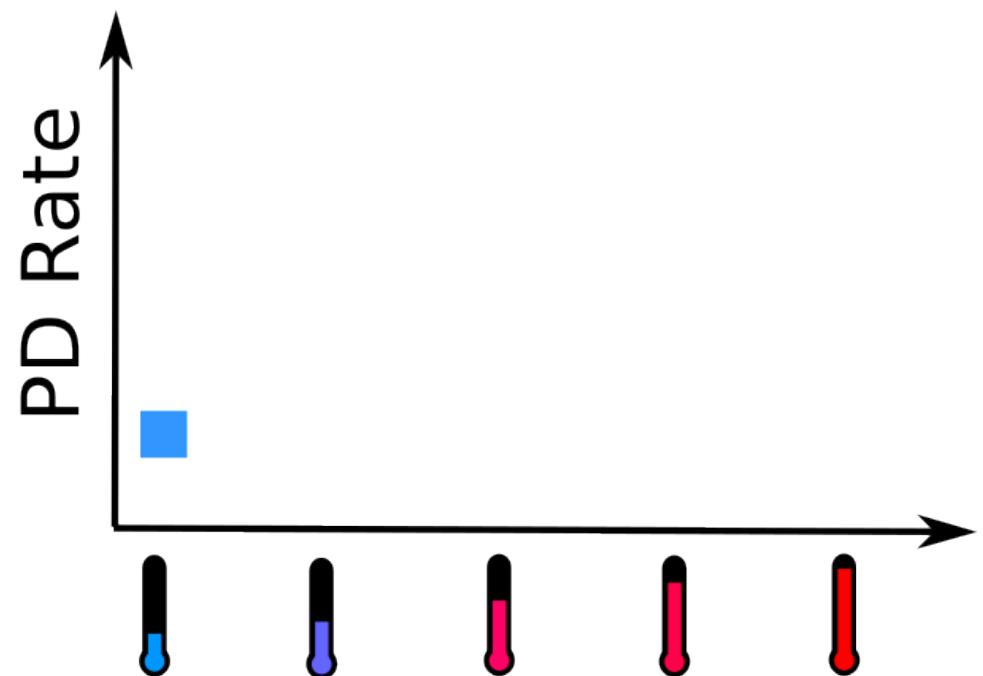
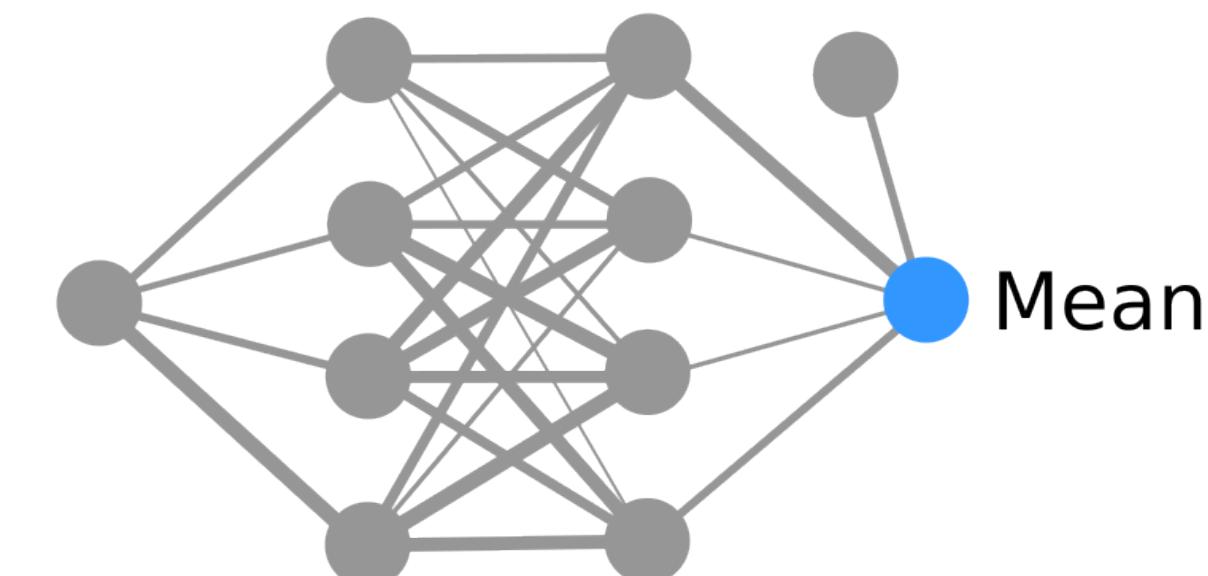
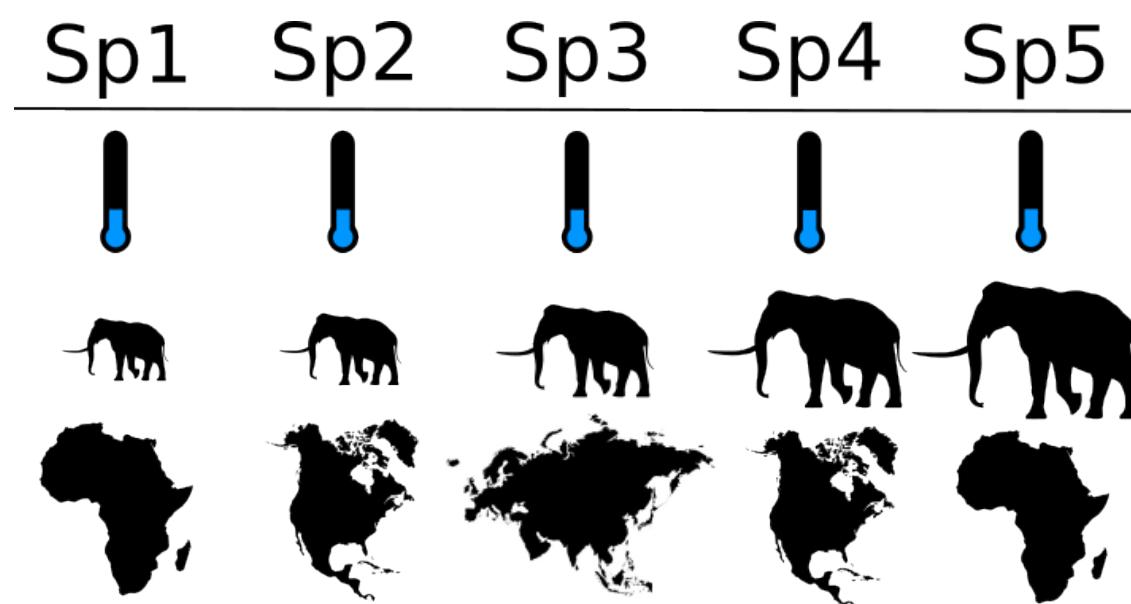
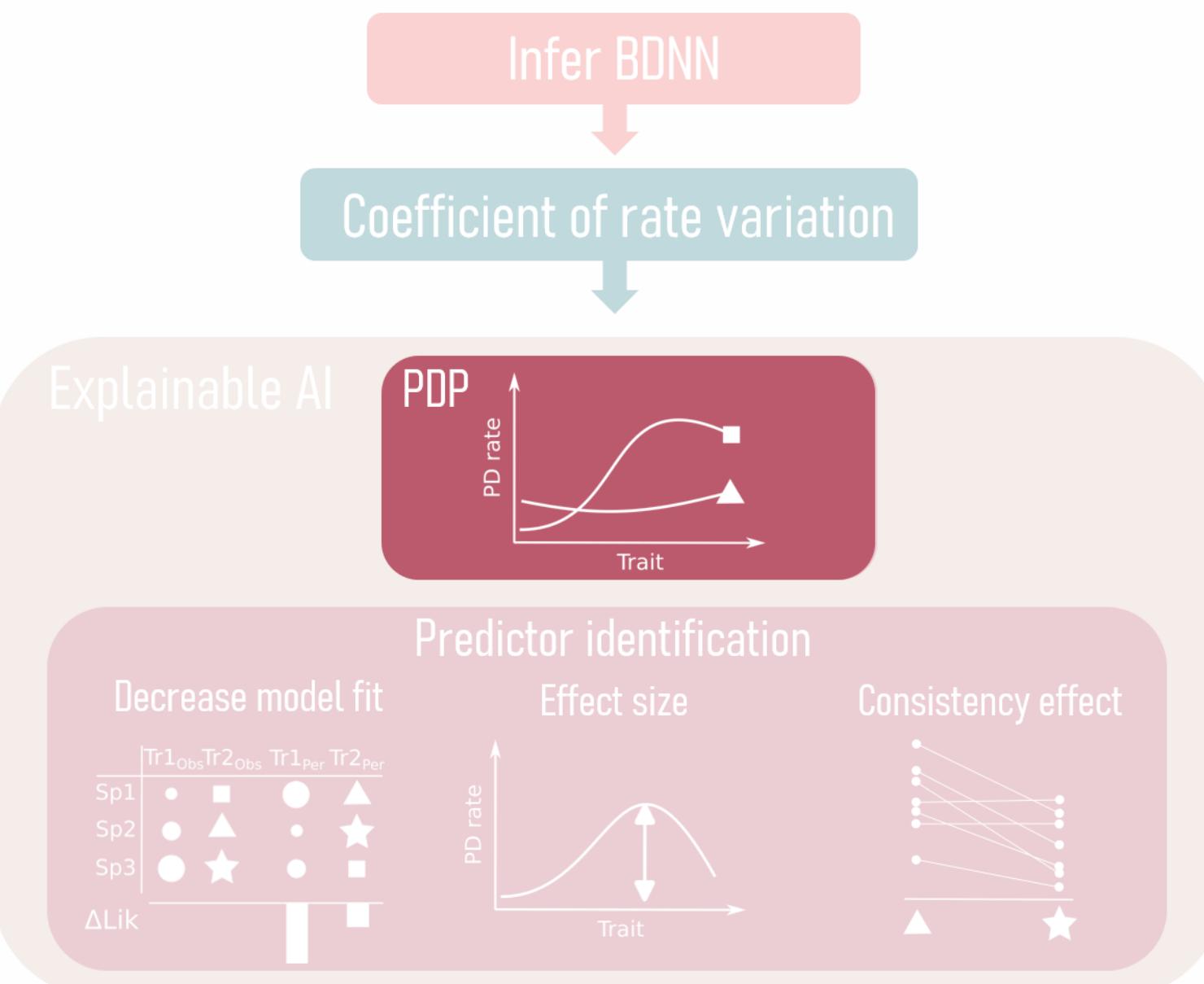
Should we dig deeper into factors? Threshold for variation in species-specific rates



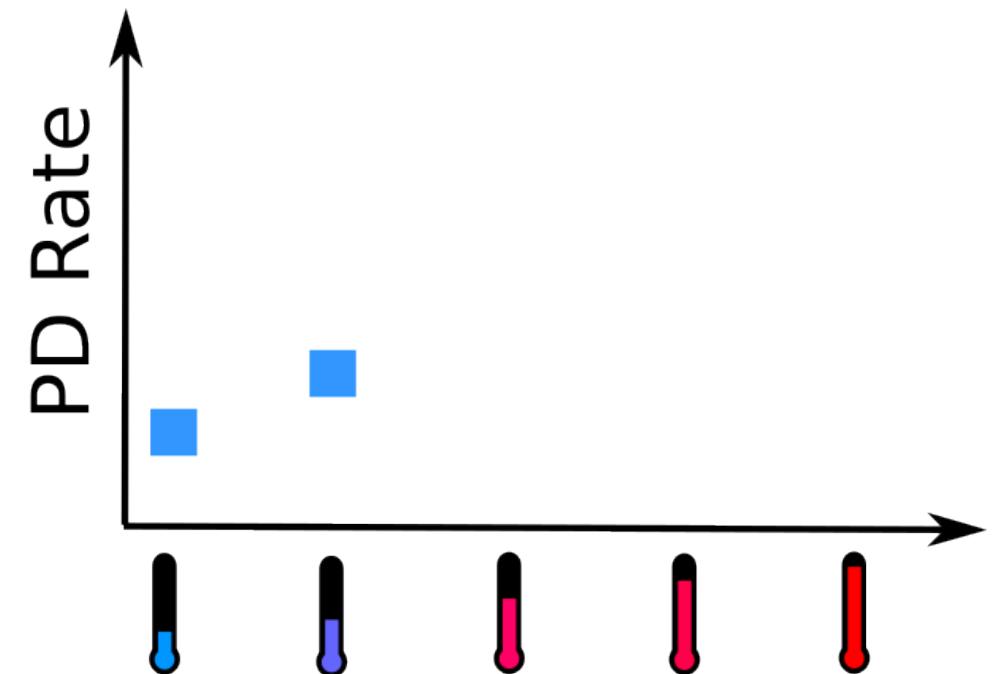
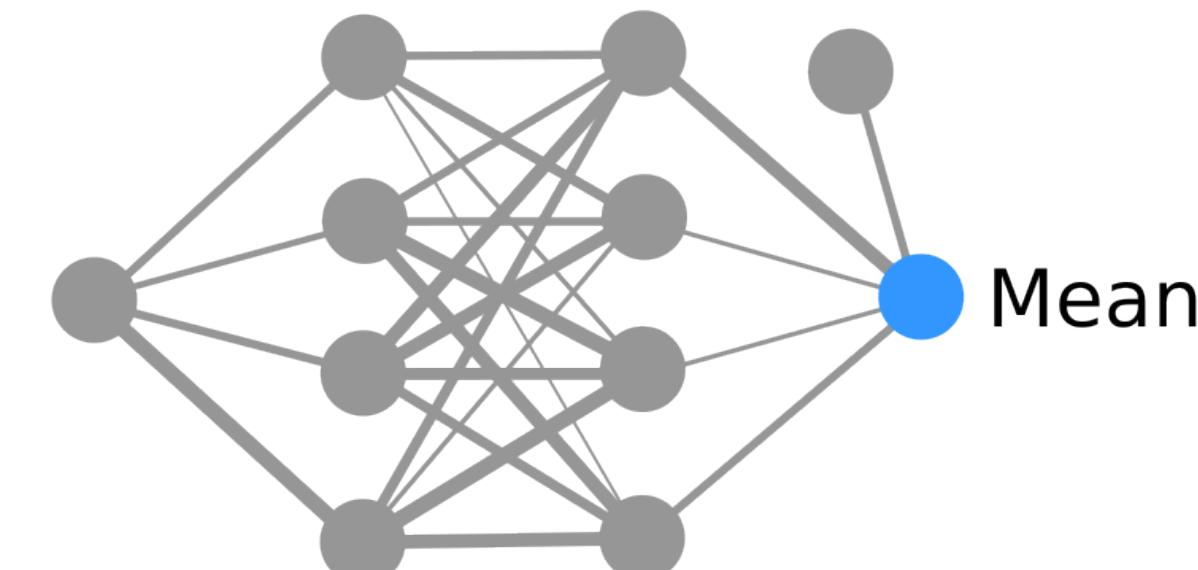
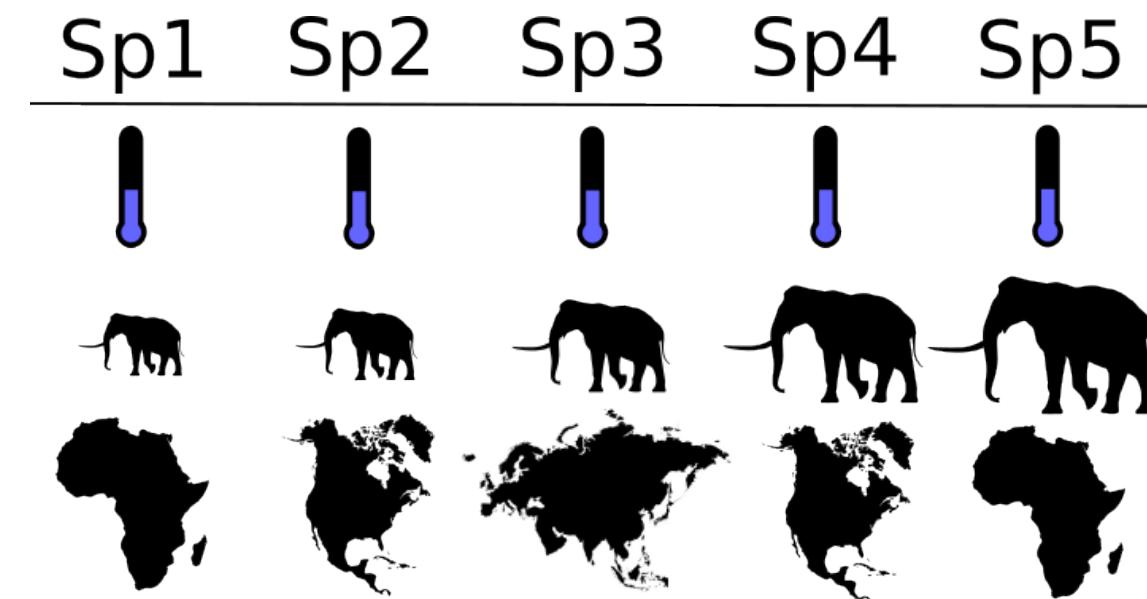
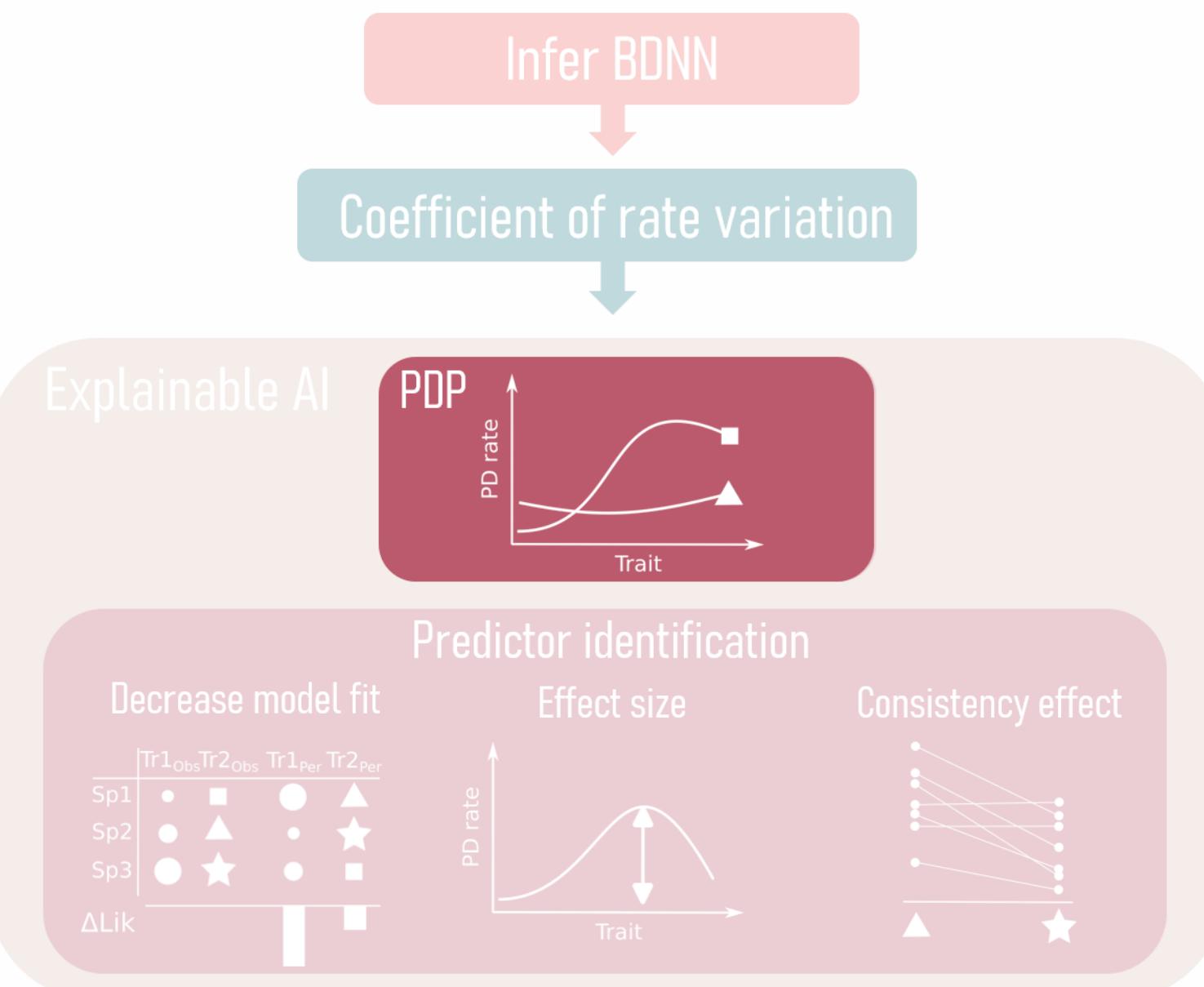
Visualize effect on rates



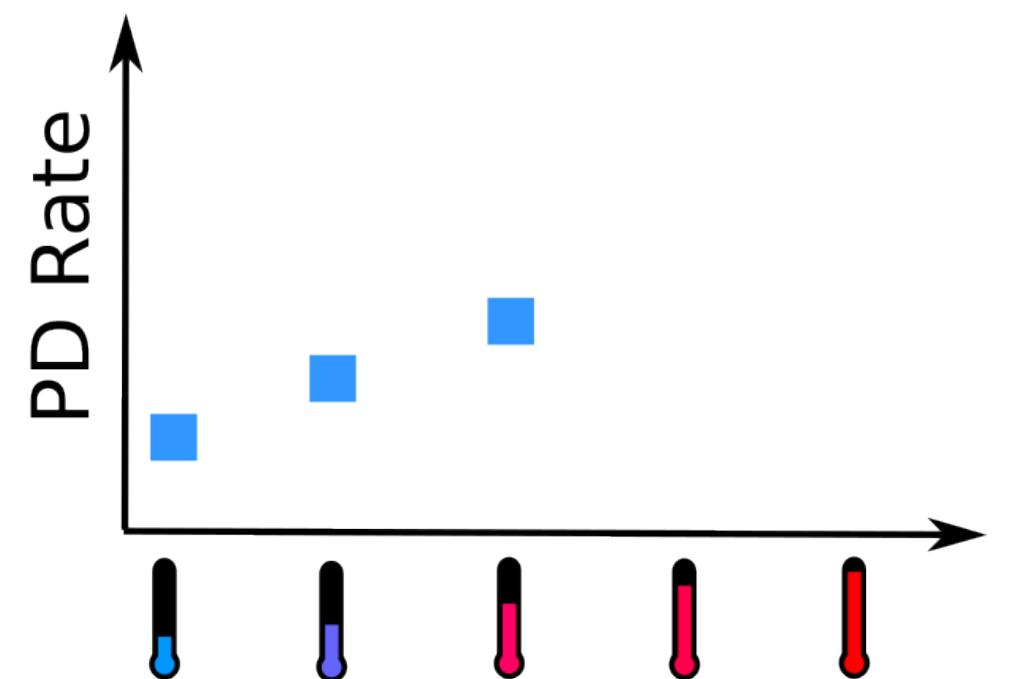
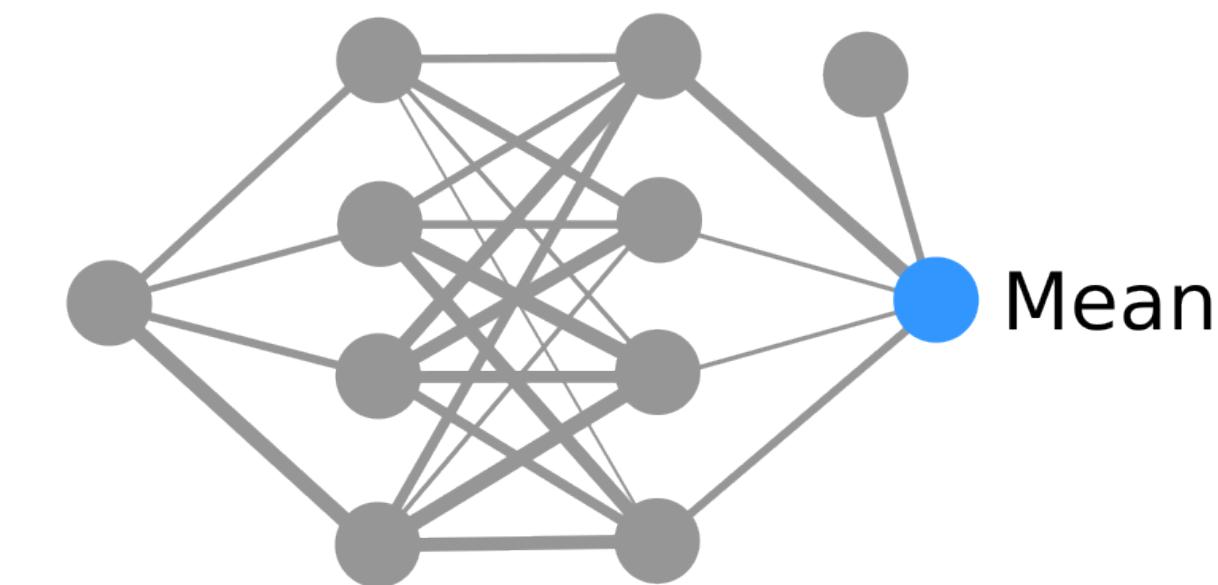
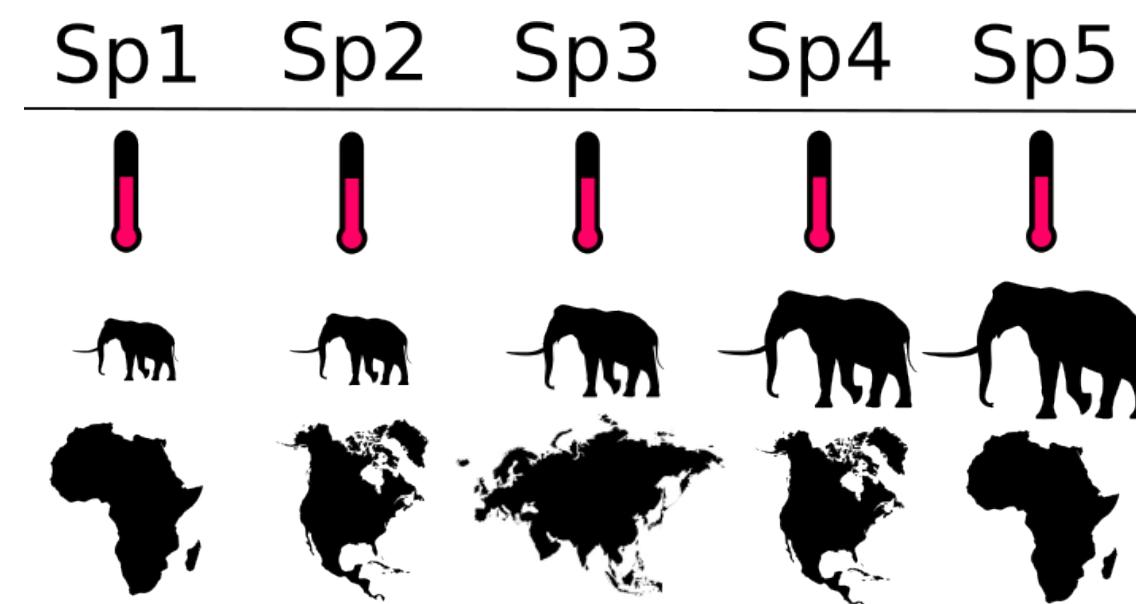
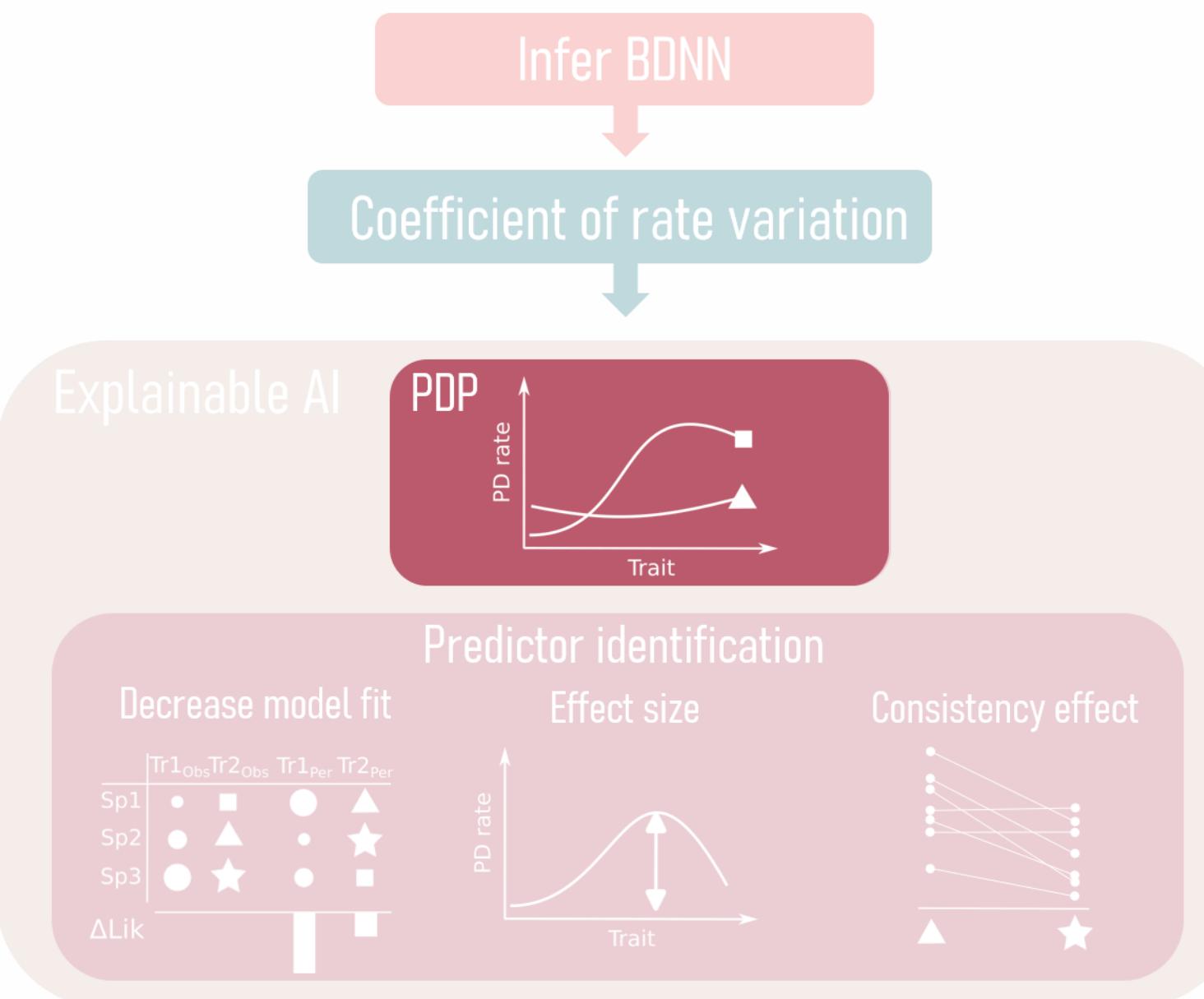
Visualize effect on rates



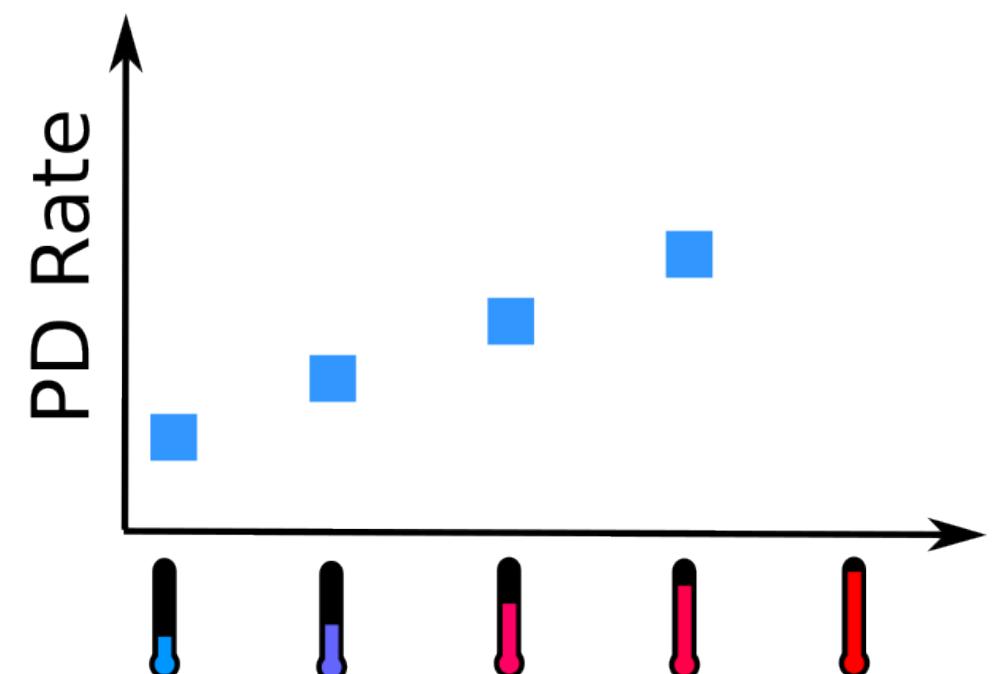
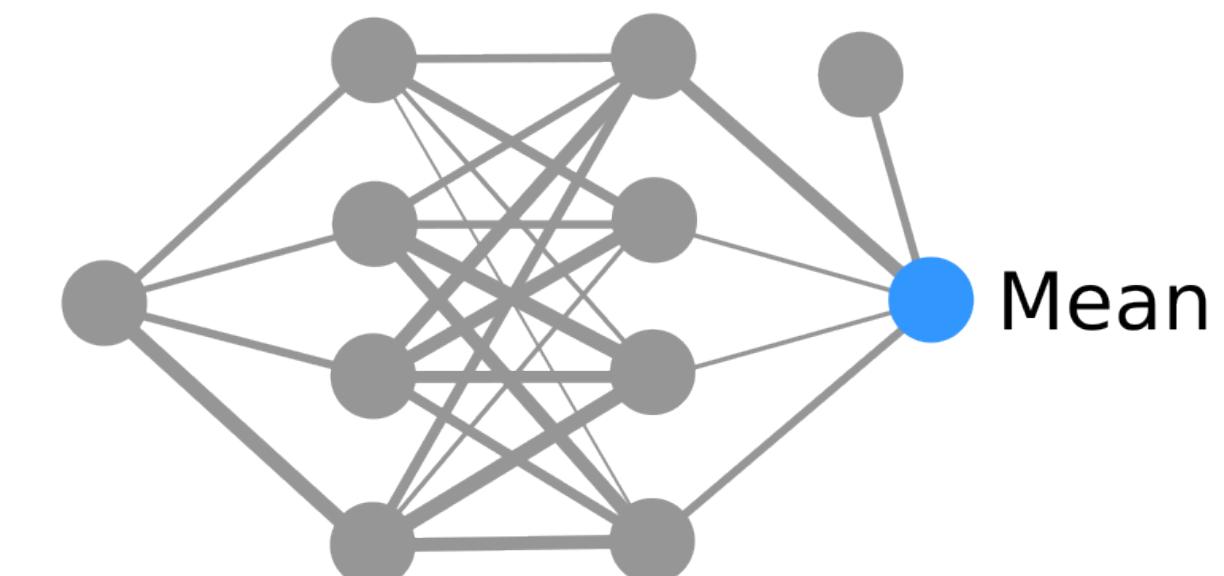
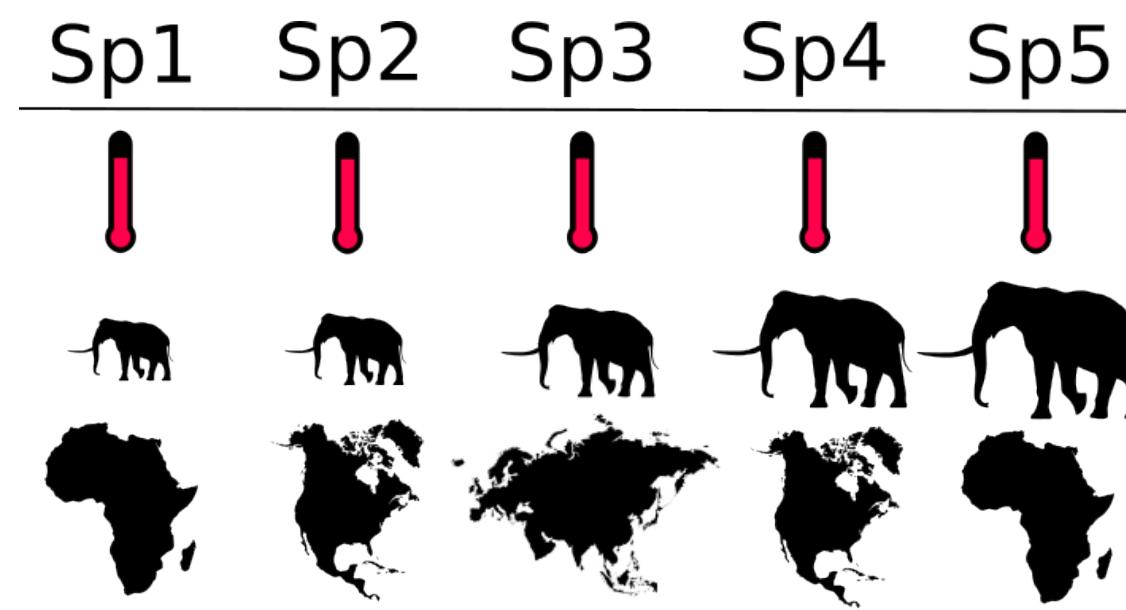
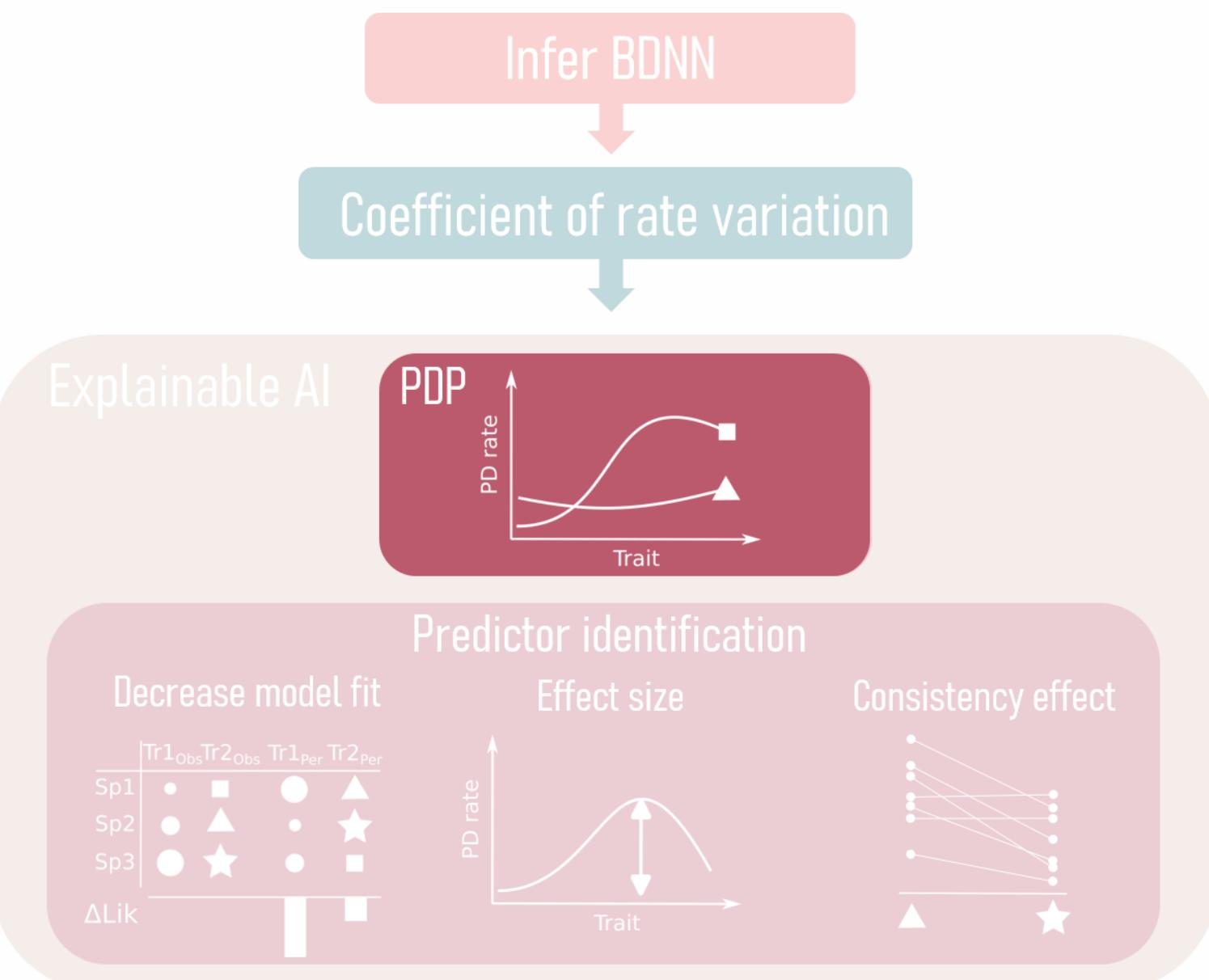
Visualize effect on rates



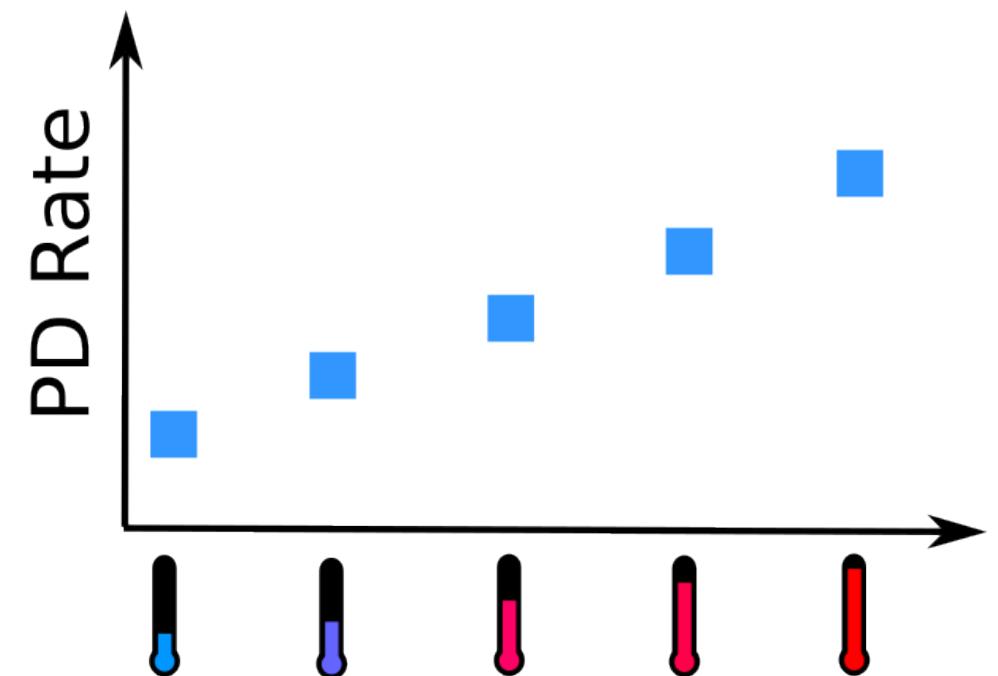
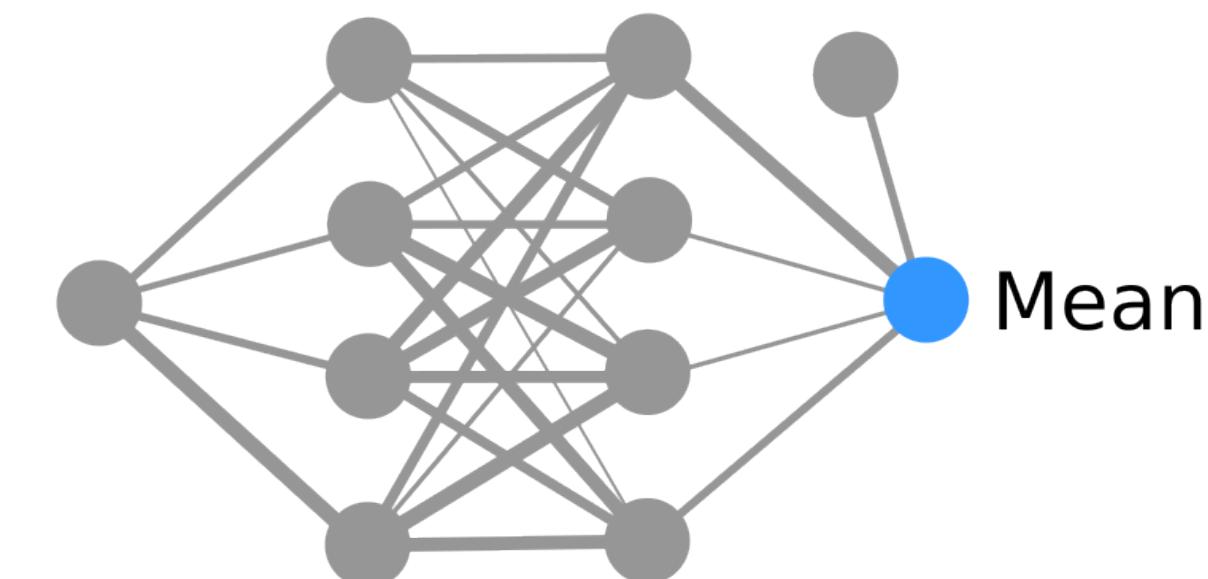
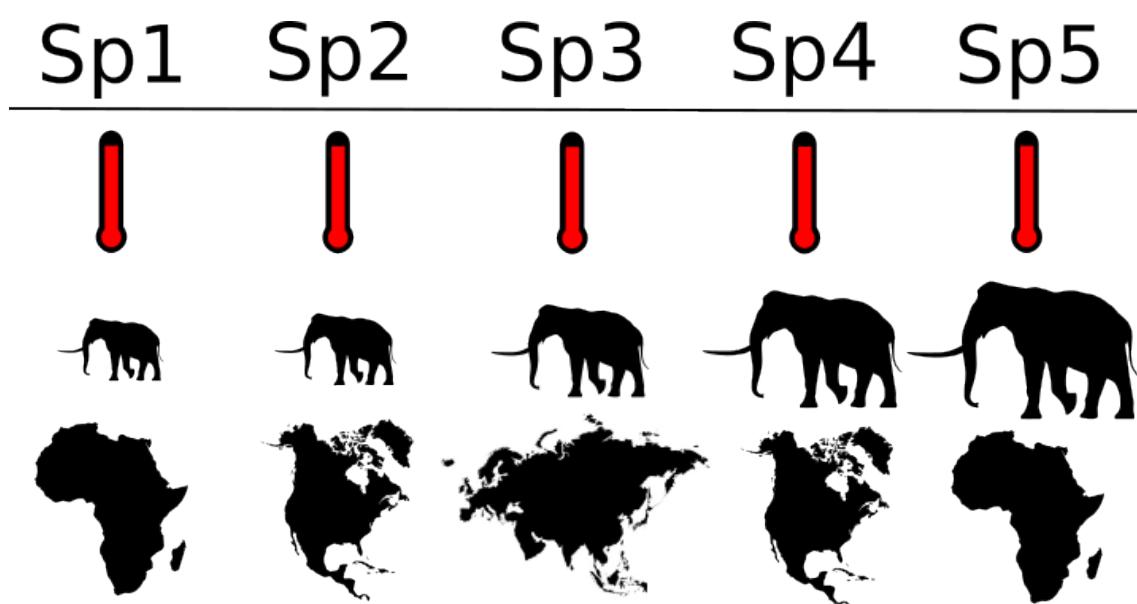
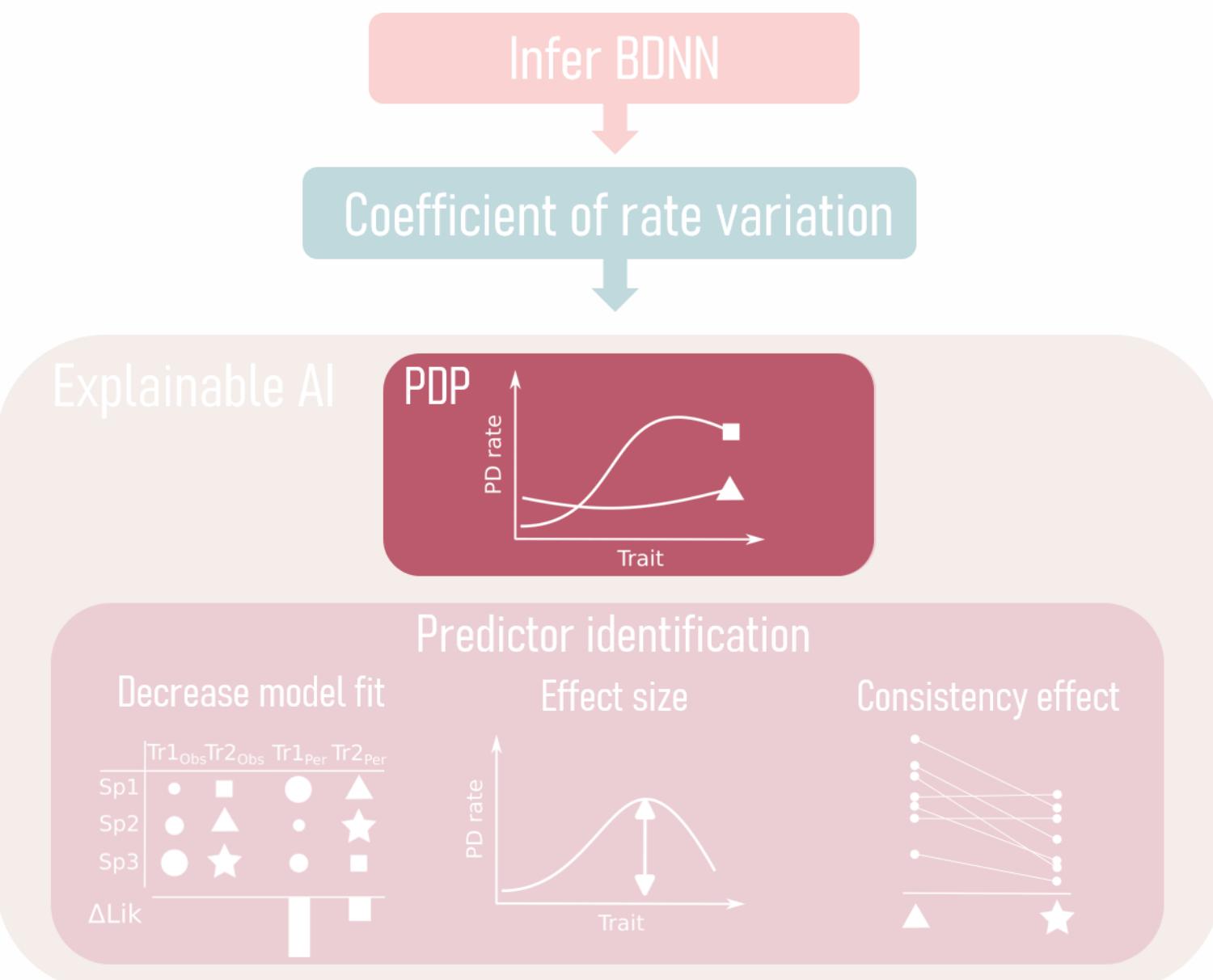
Visualize effect on rates



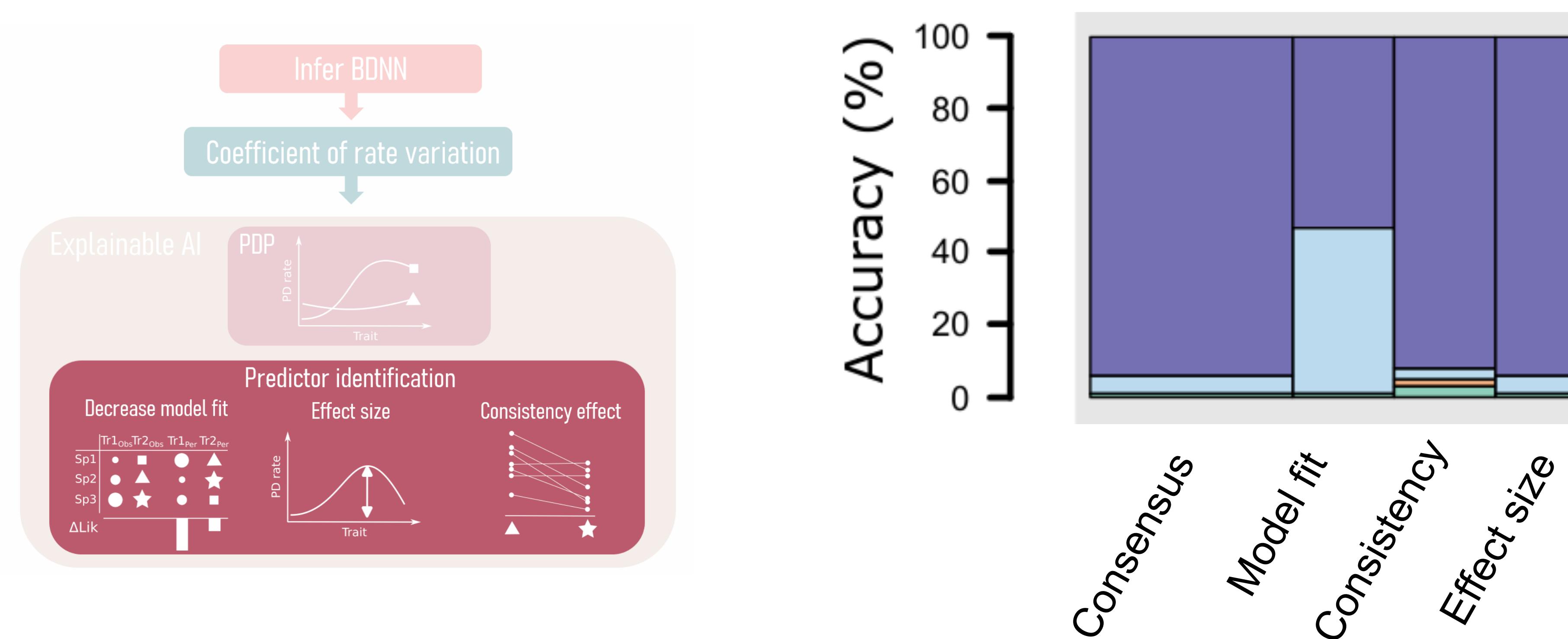
Visualize effect on rates



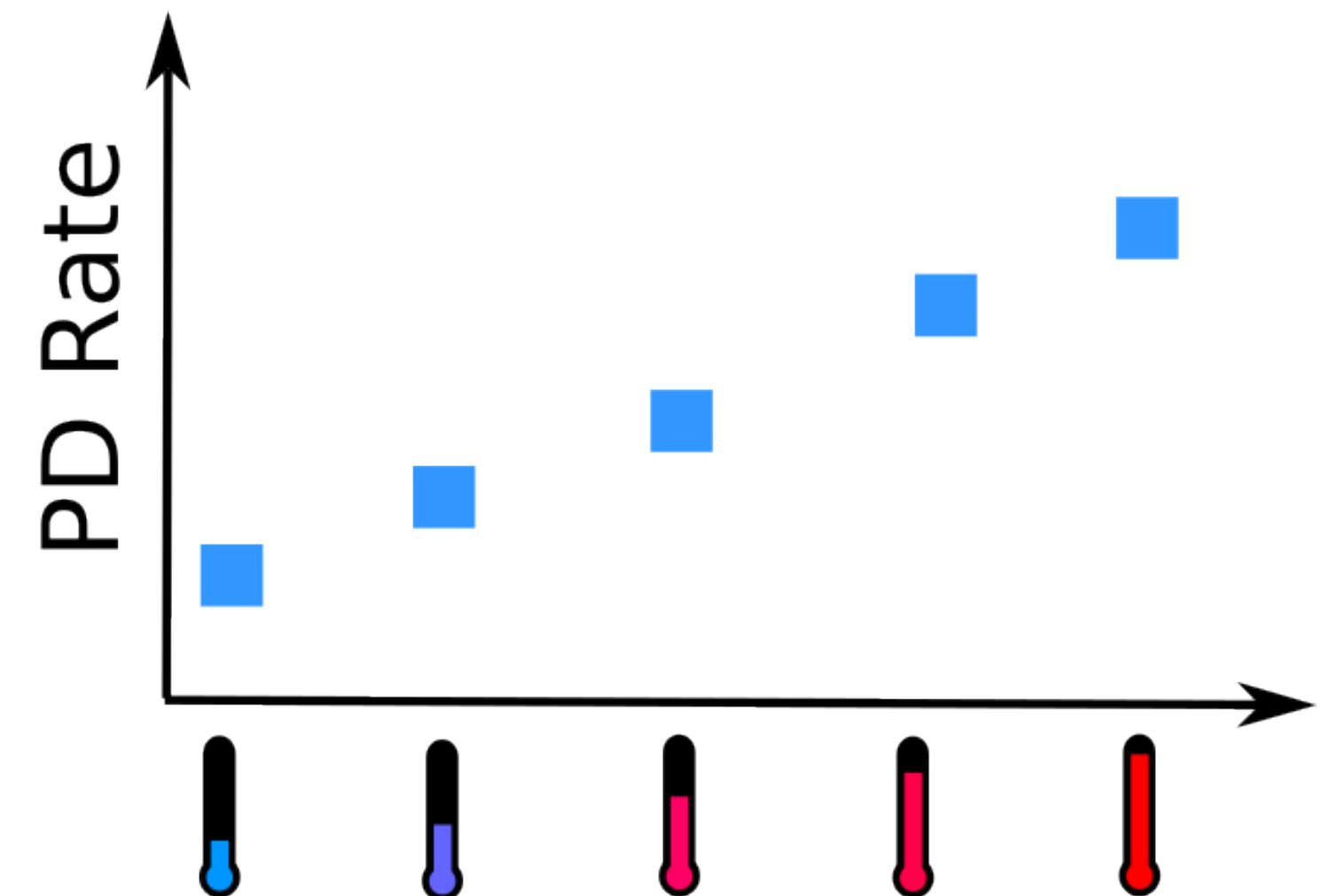
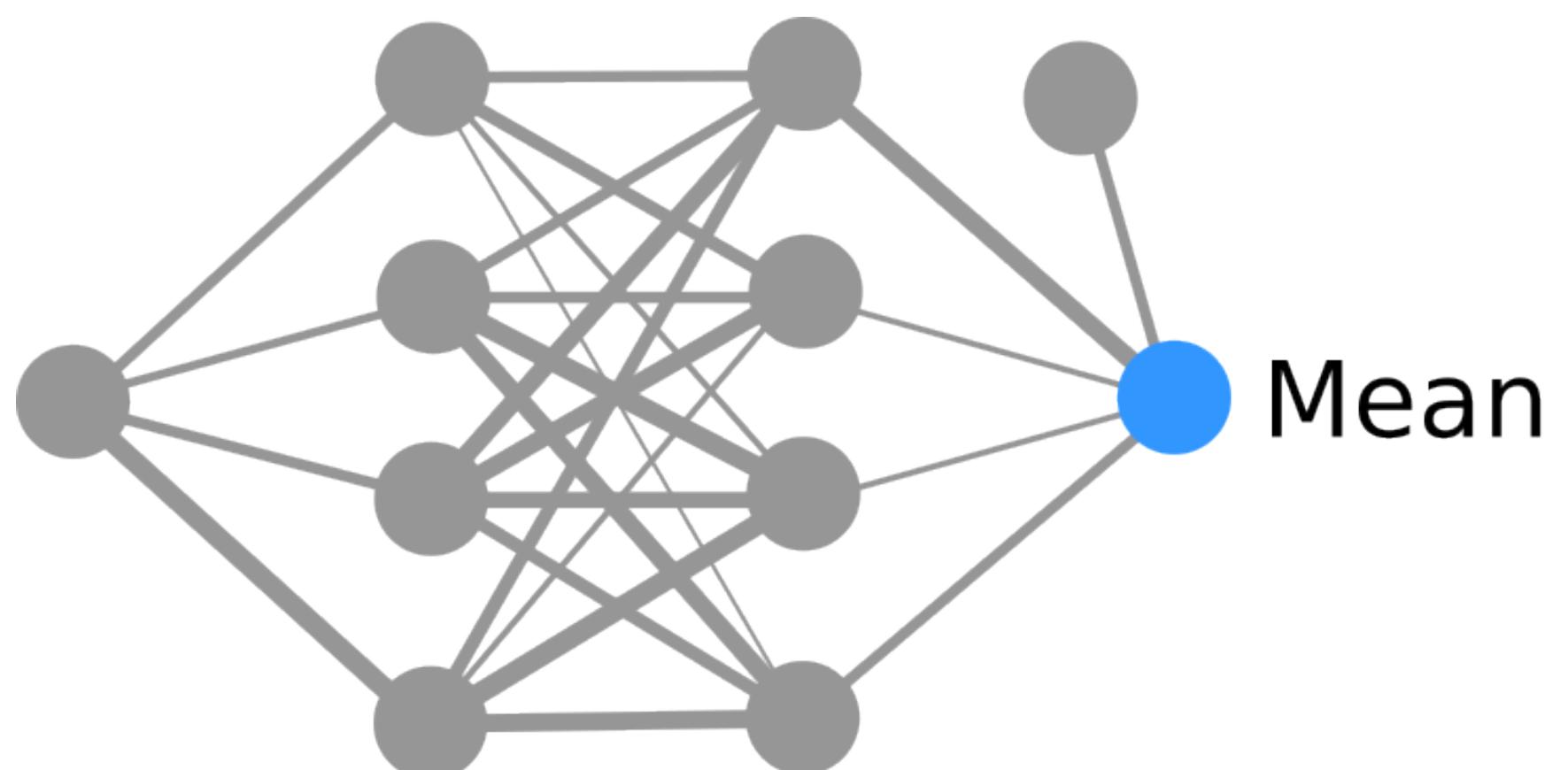
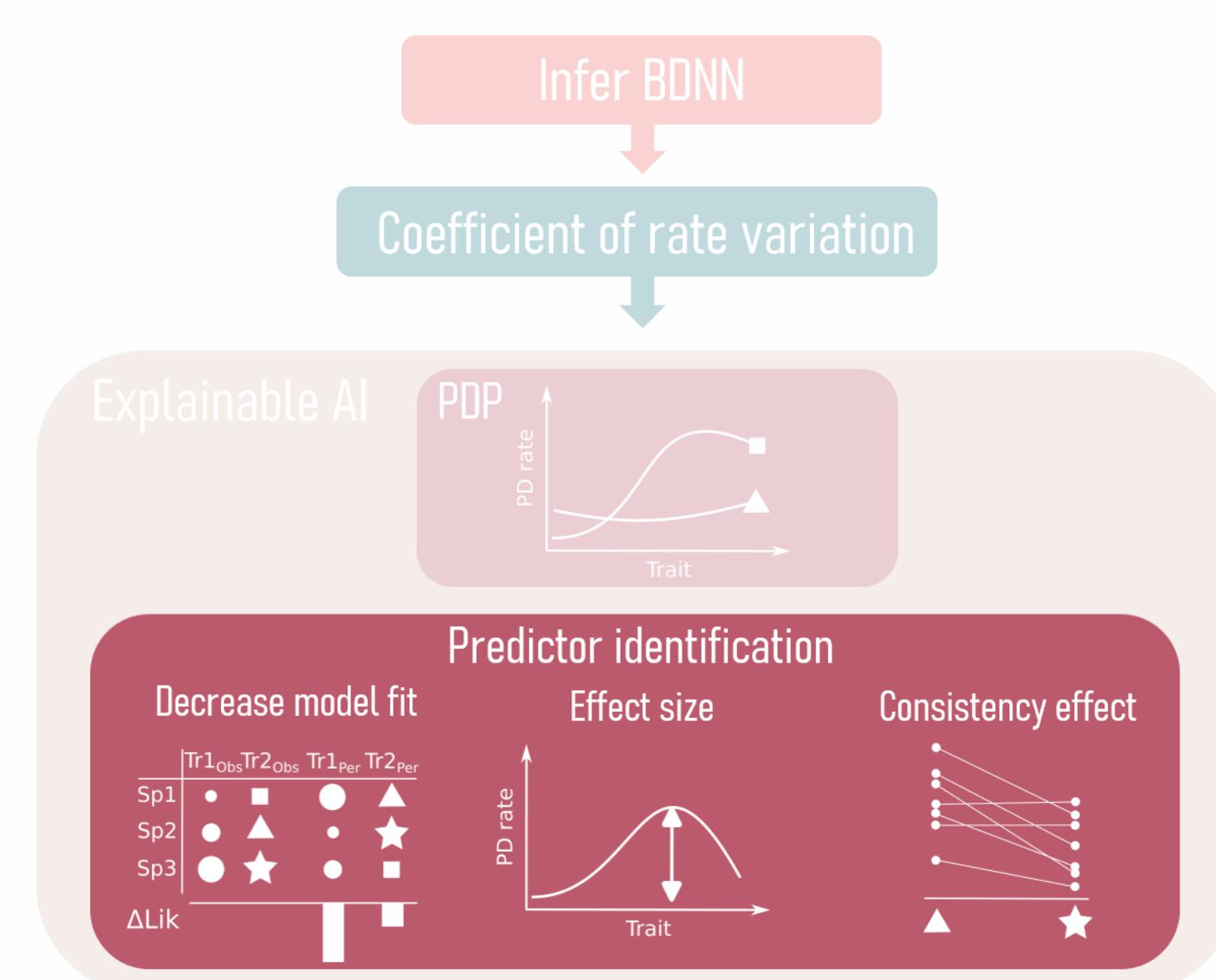
Visualize effect on rates



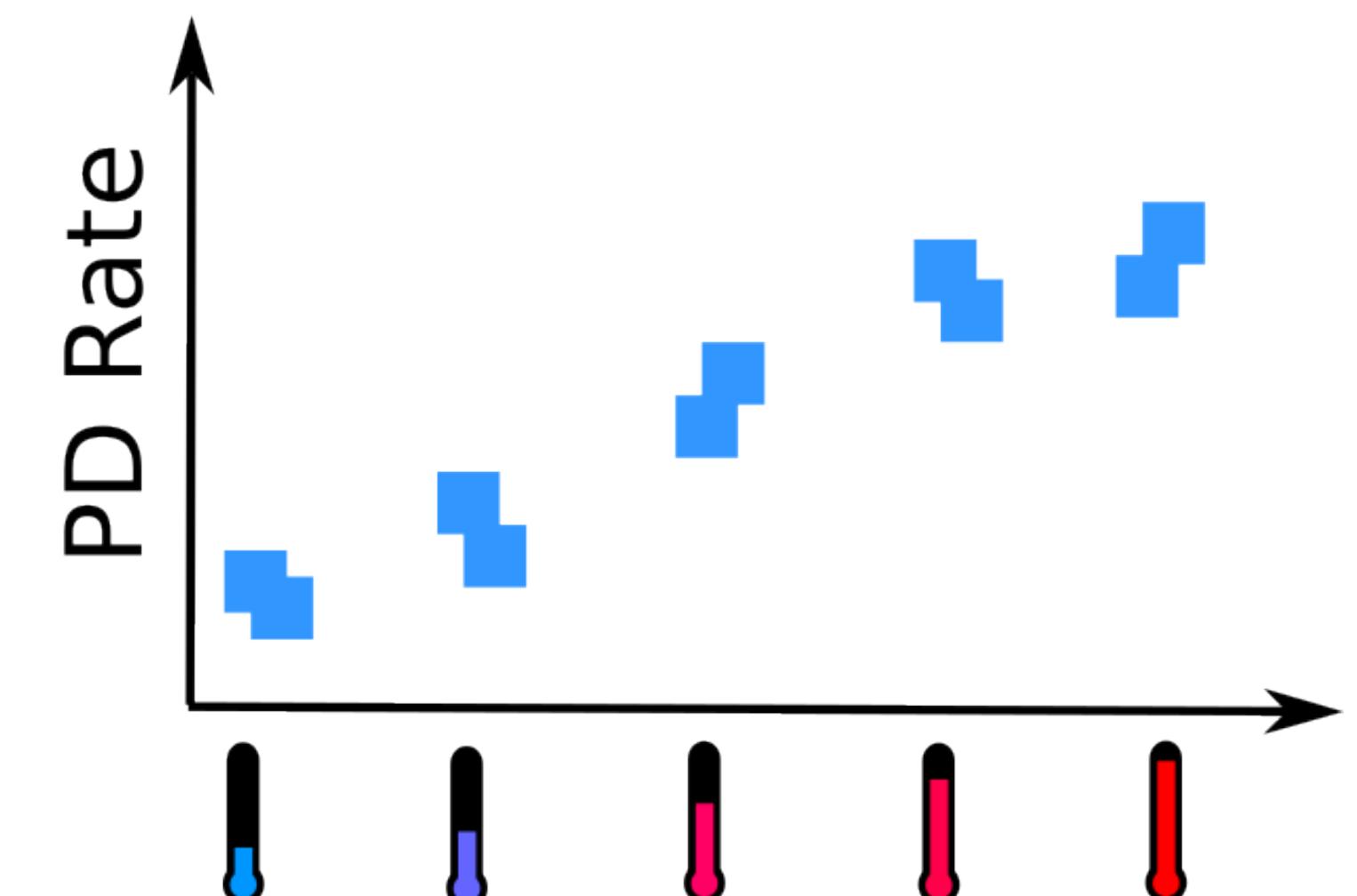
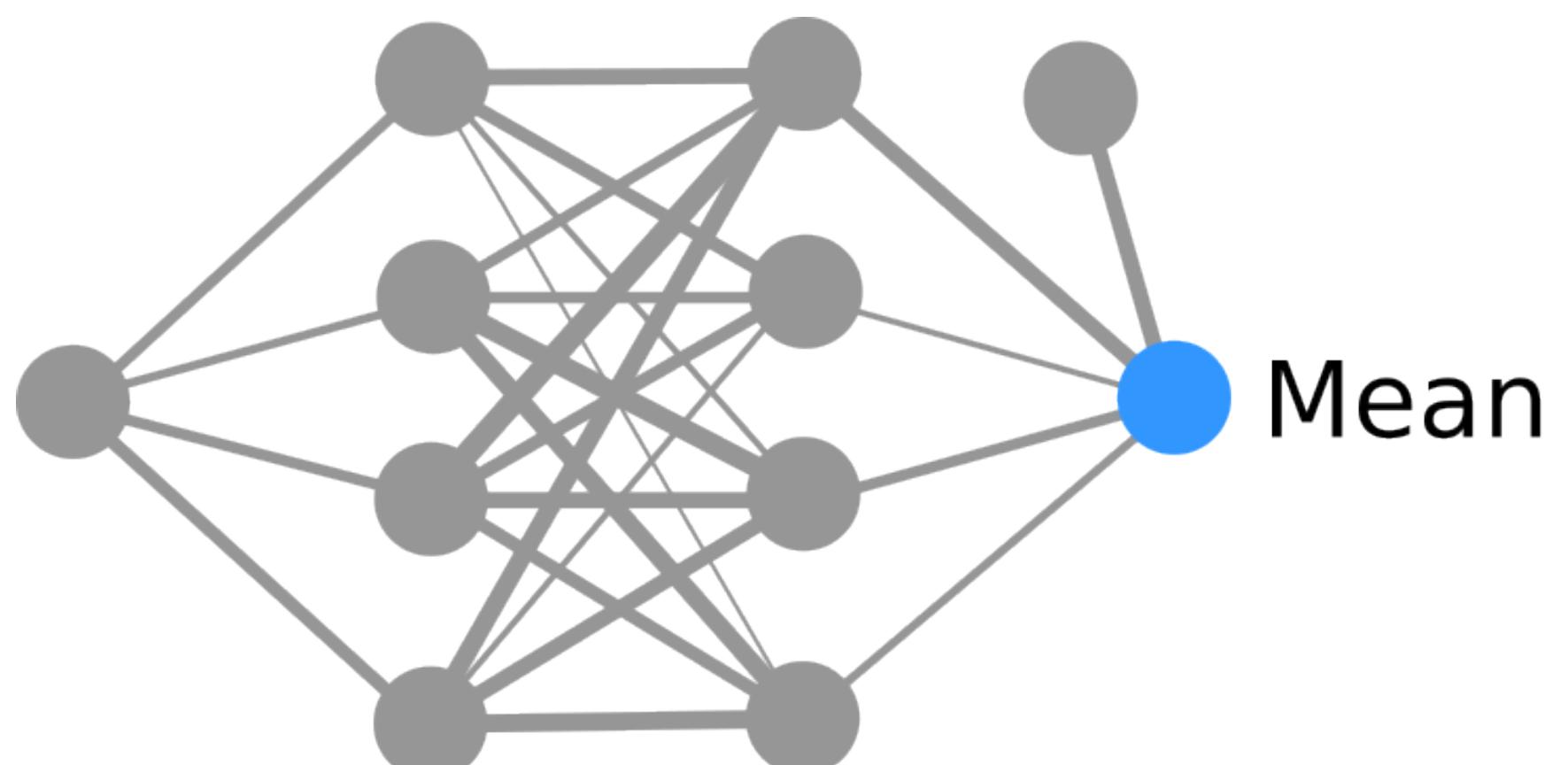
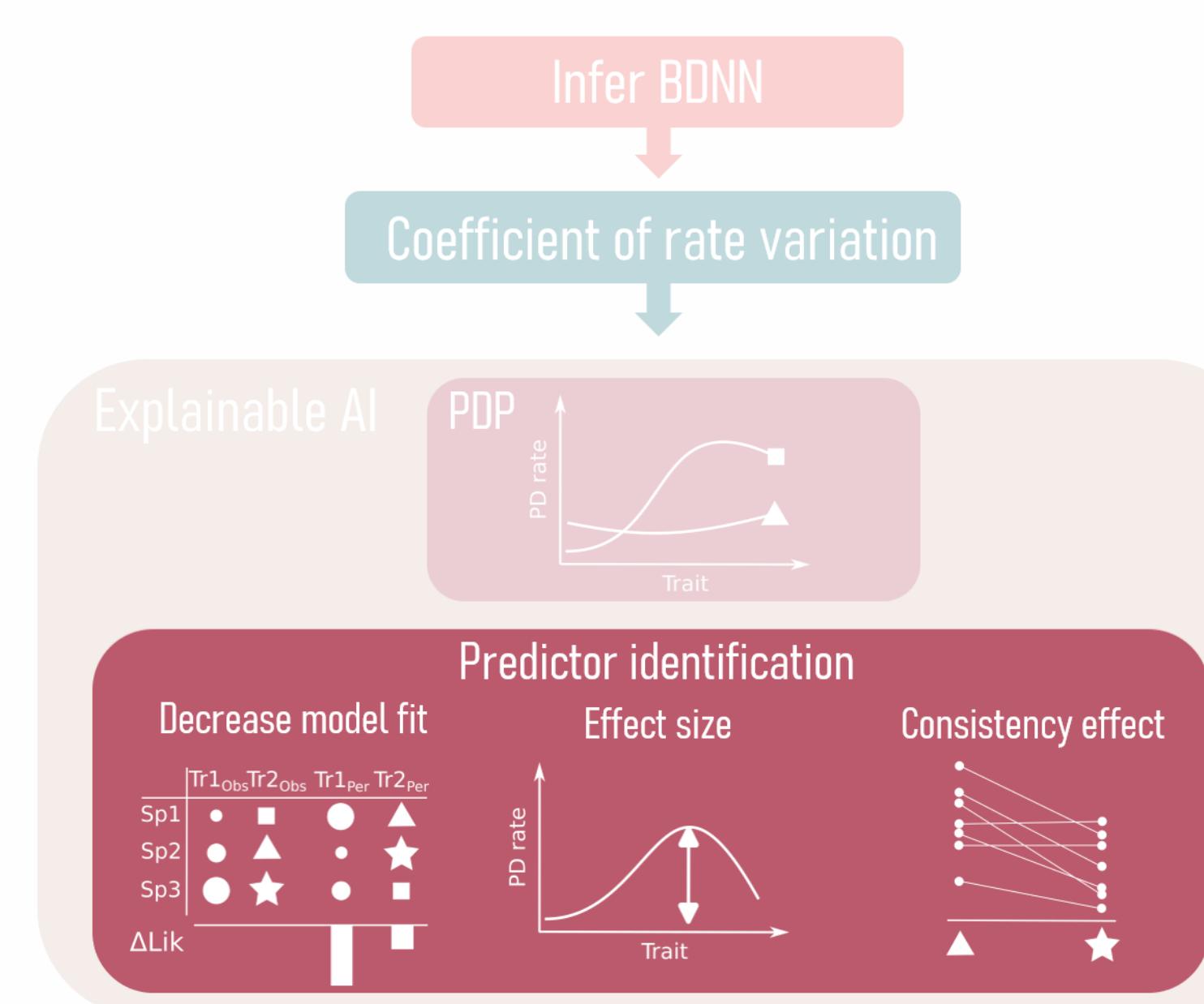
Identify rate predictors with consensus among xAI approaches



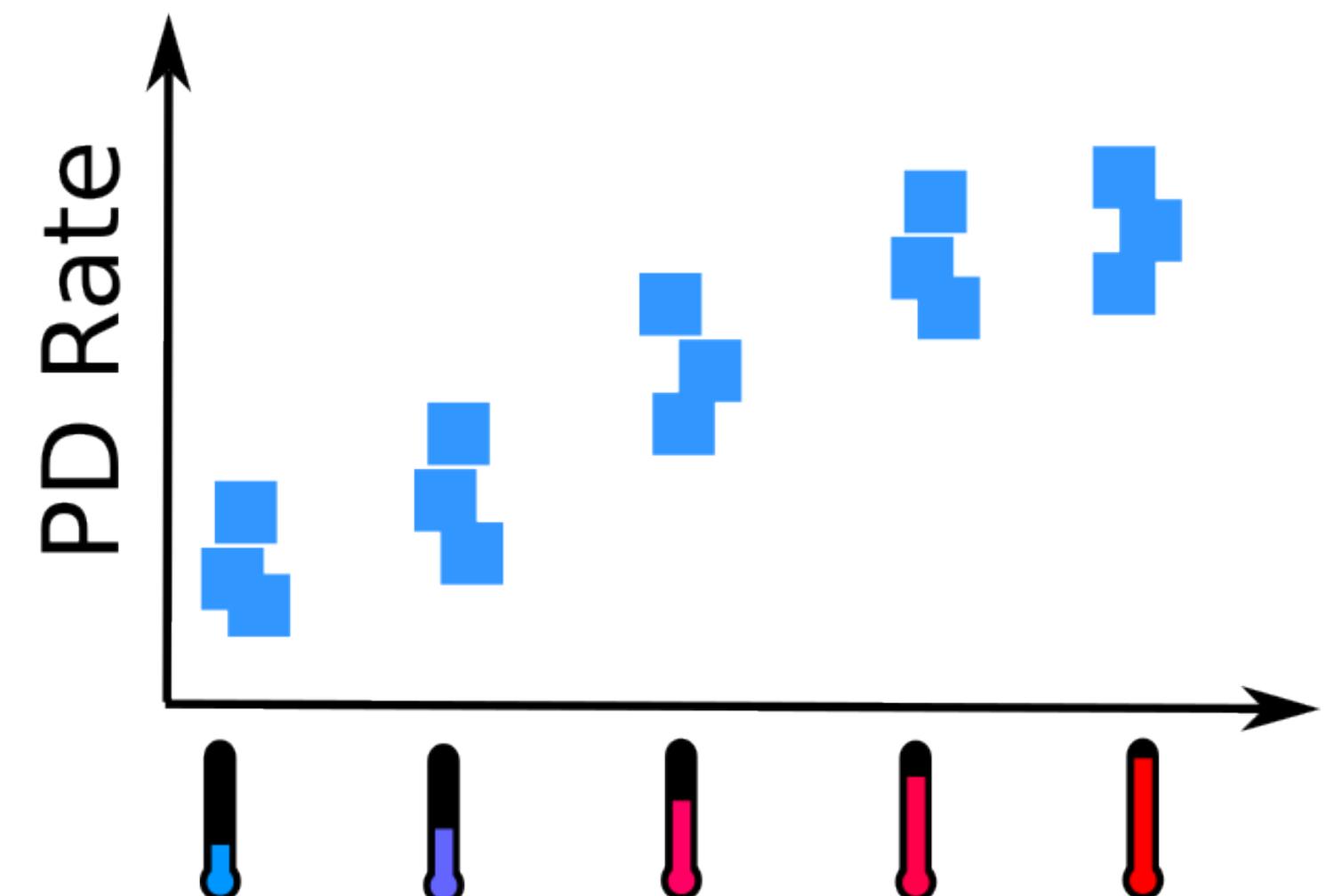
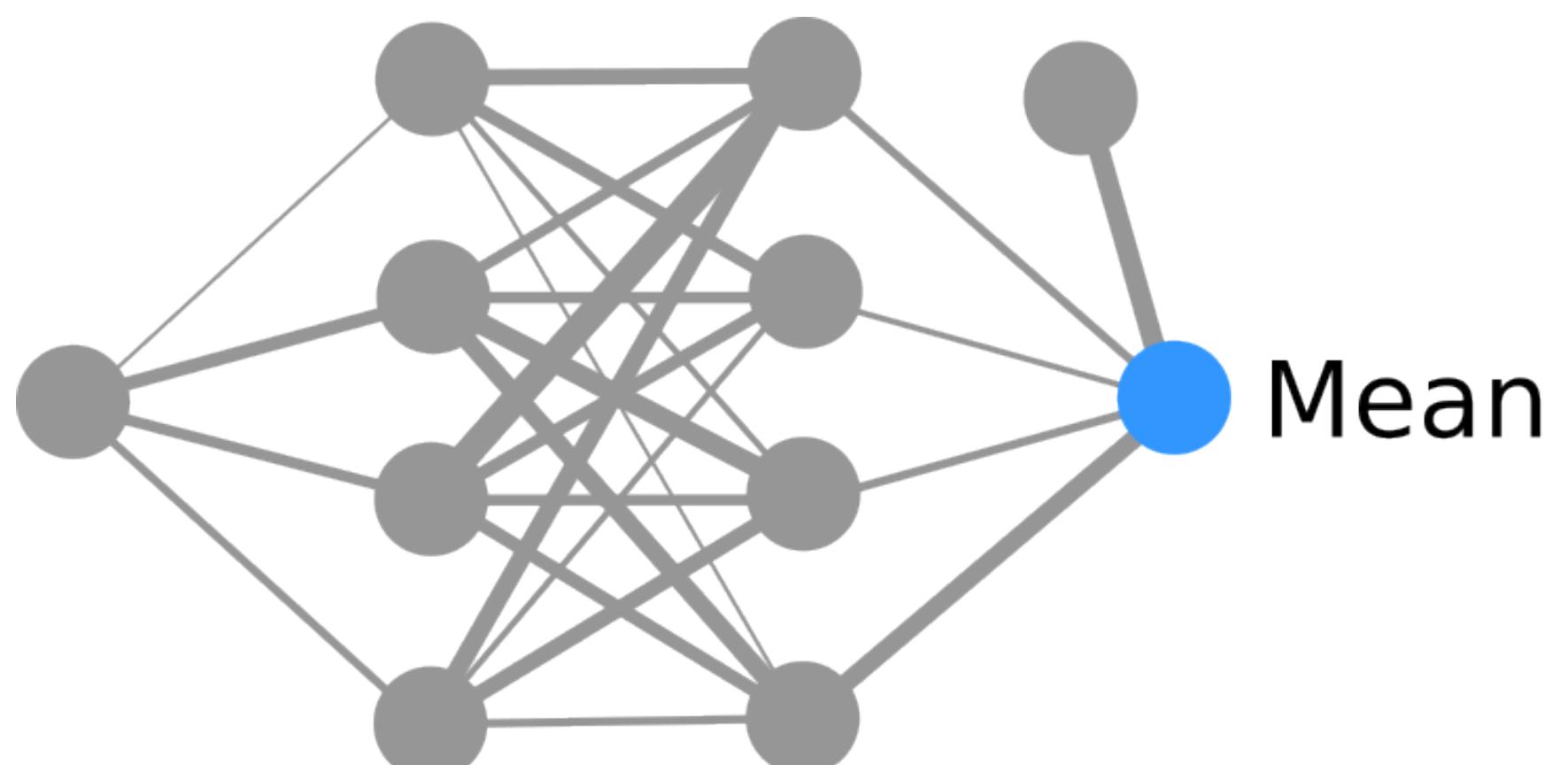
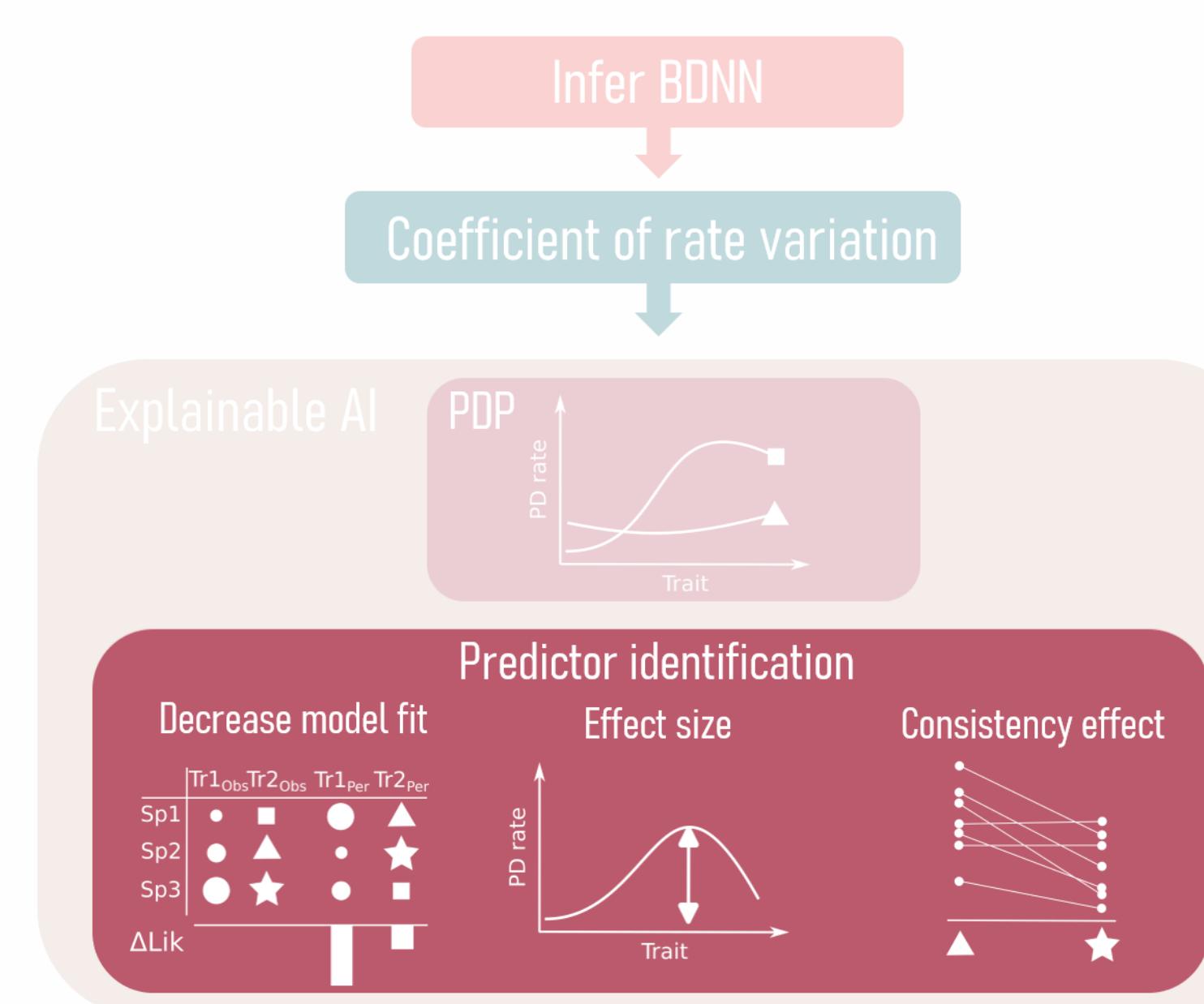
xAI: Consistency through posterior probability



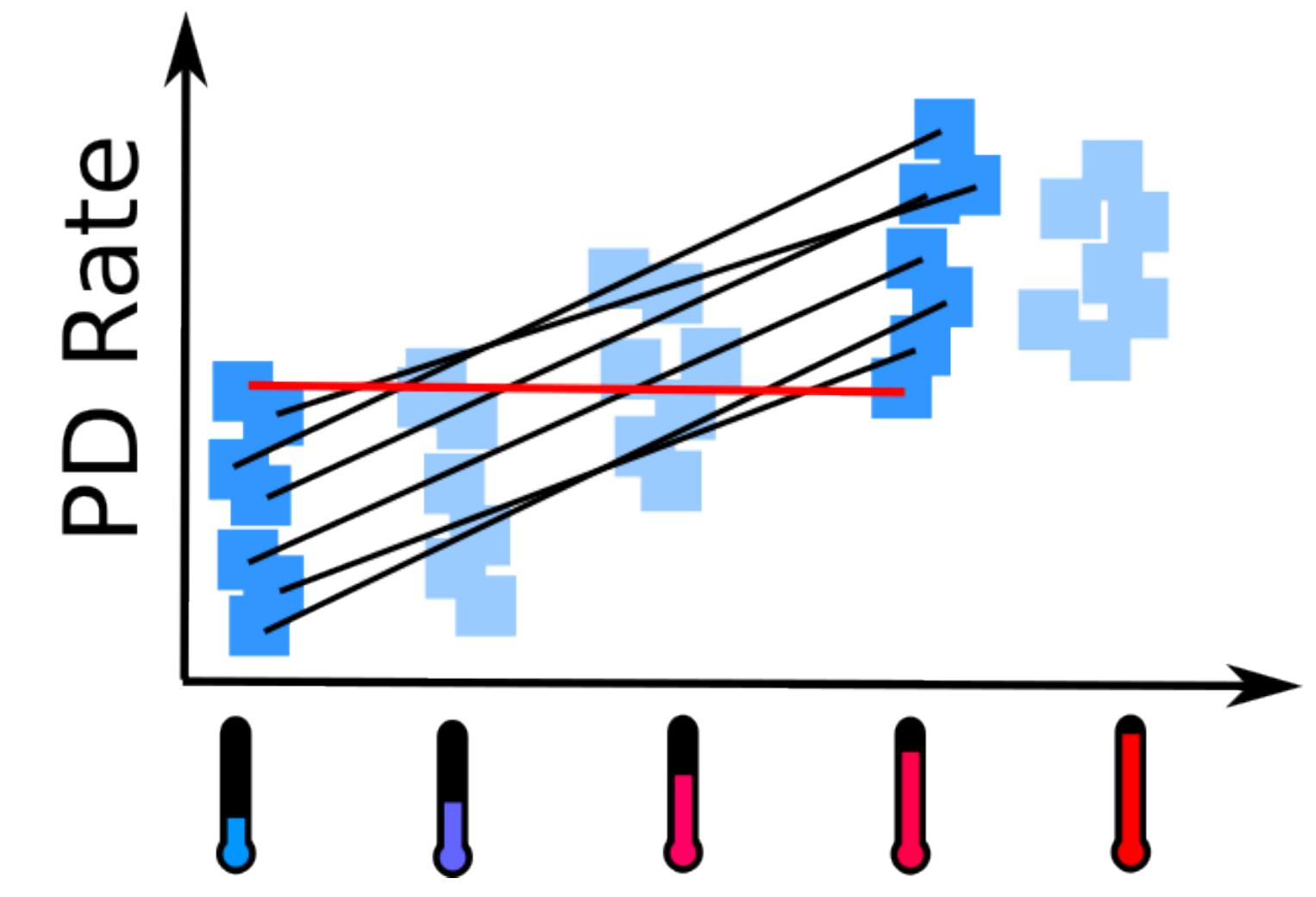
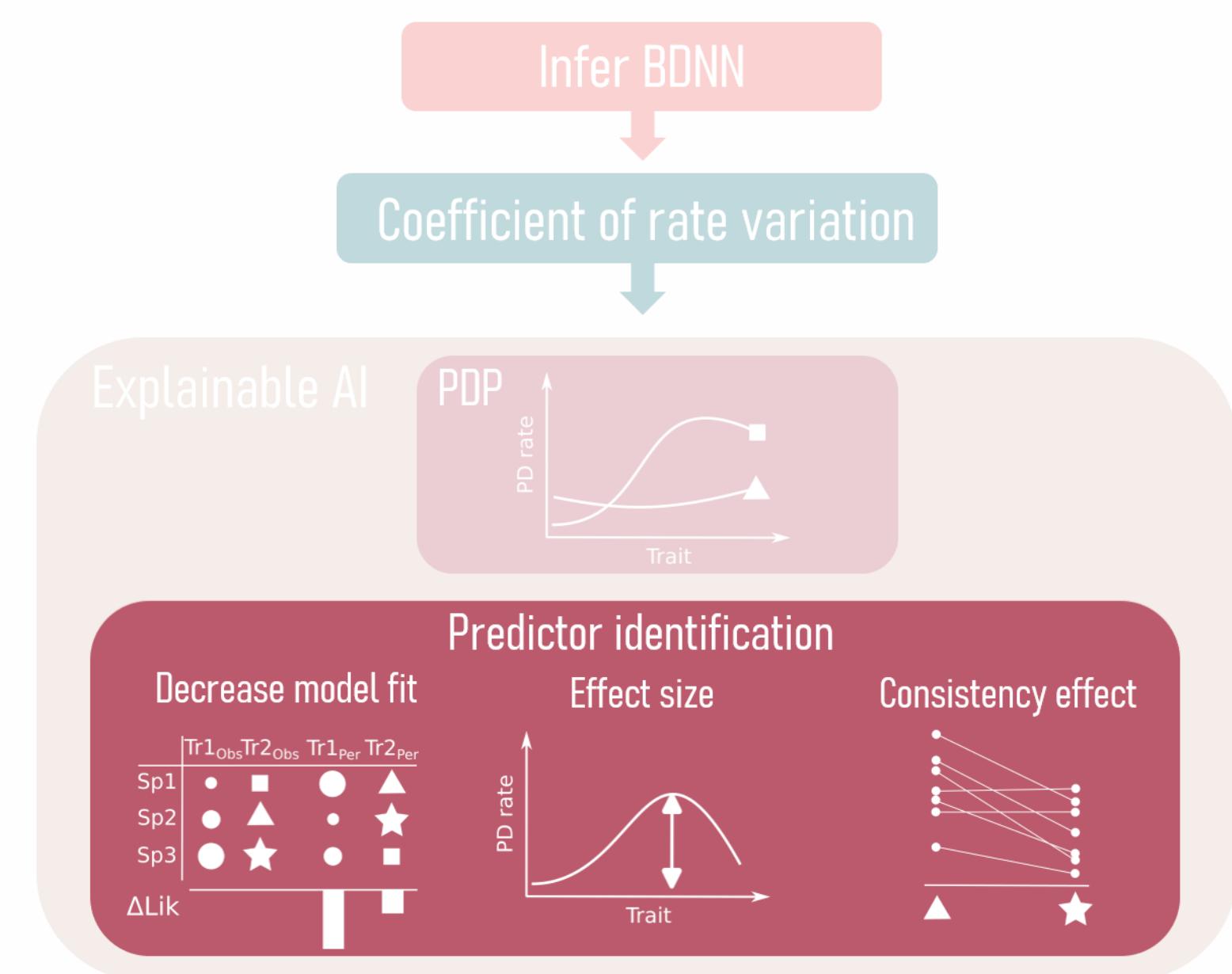
xAI: Consistency through posterior probability



xAI: Consistency through posterior probability

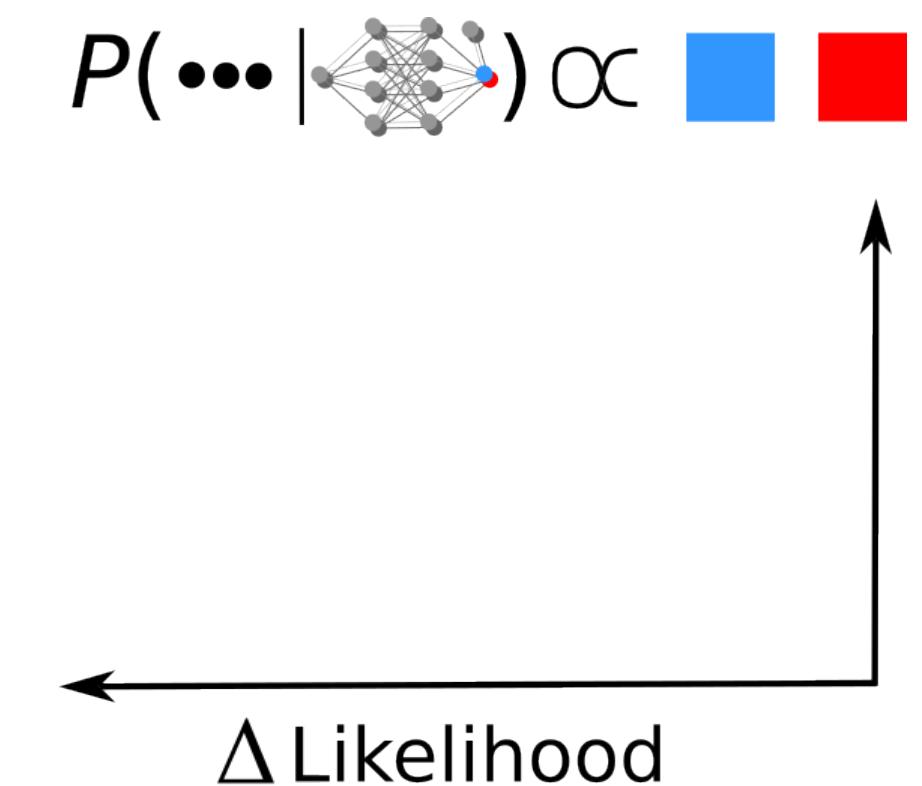
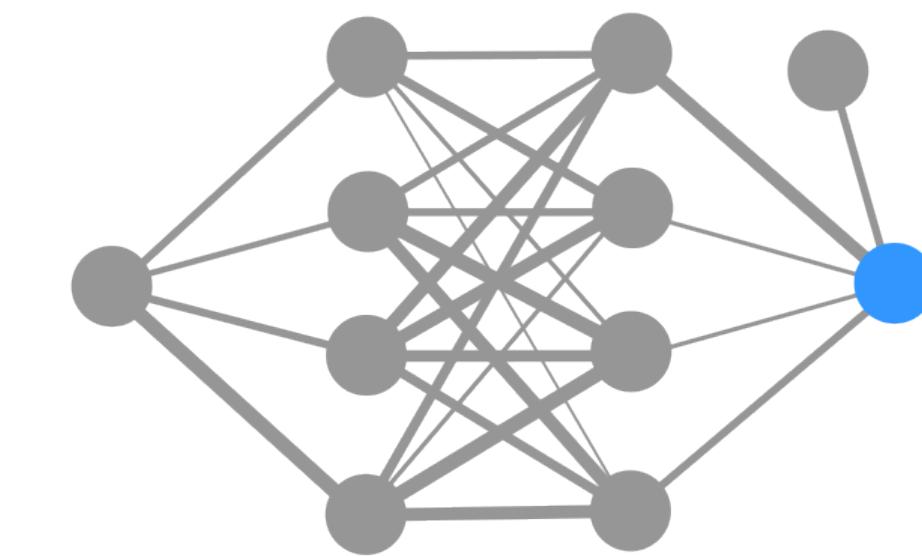
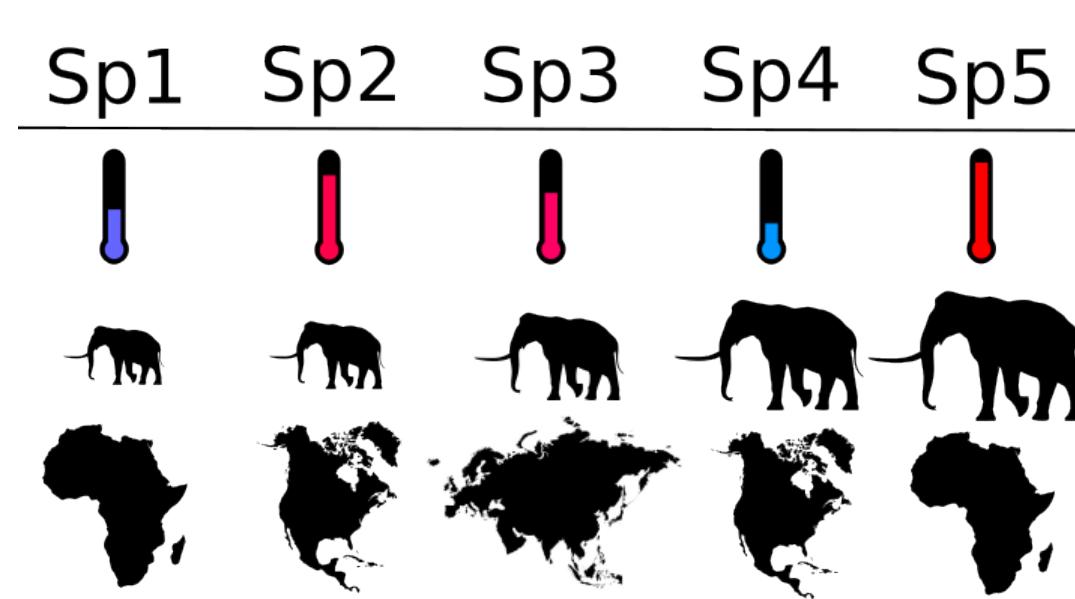
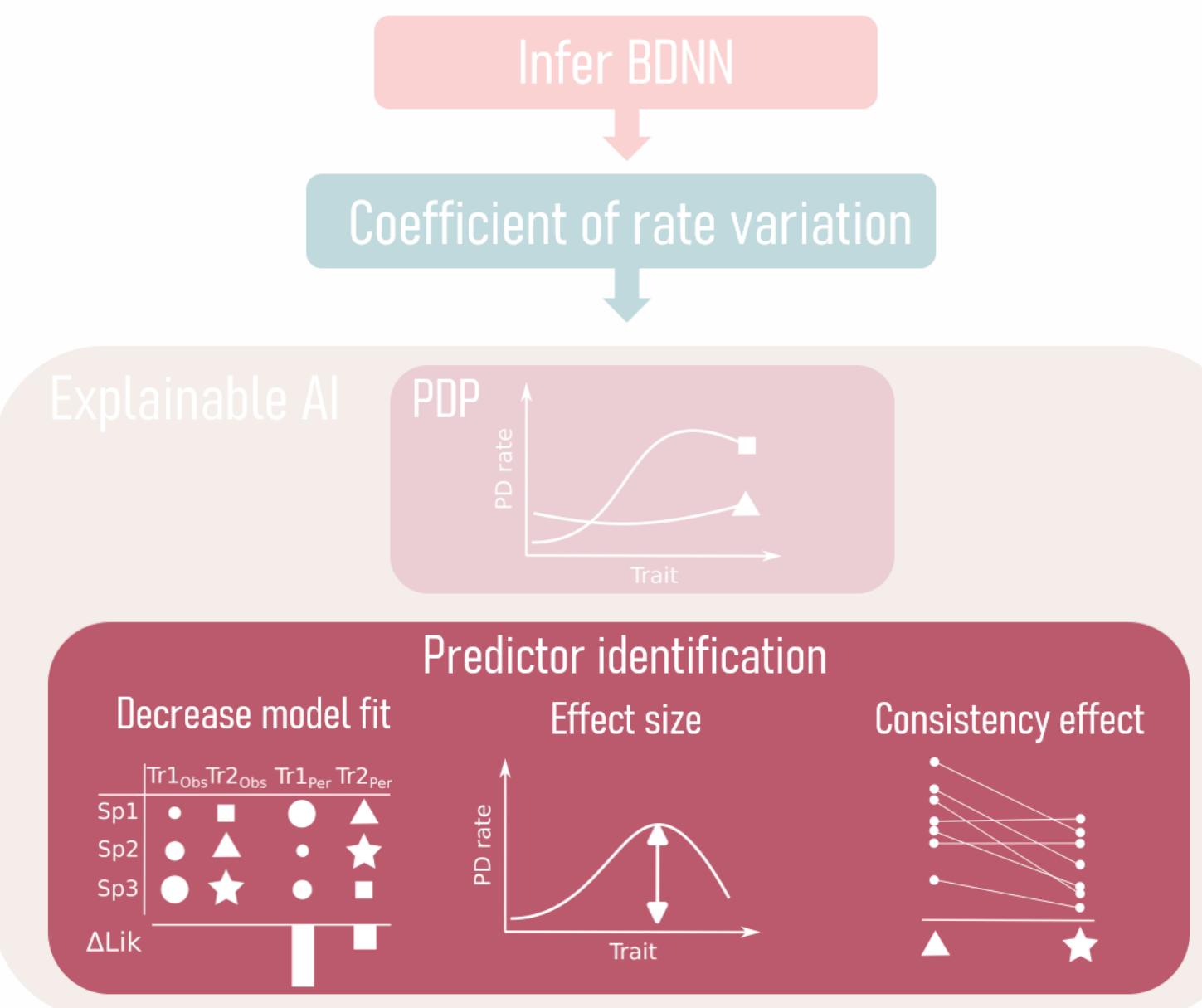


xAI: Consistency through posterior probability

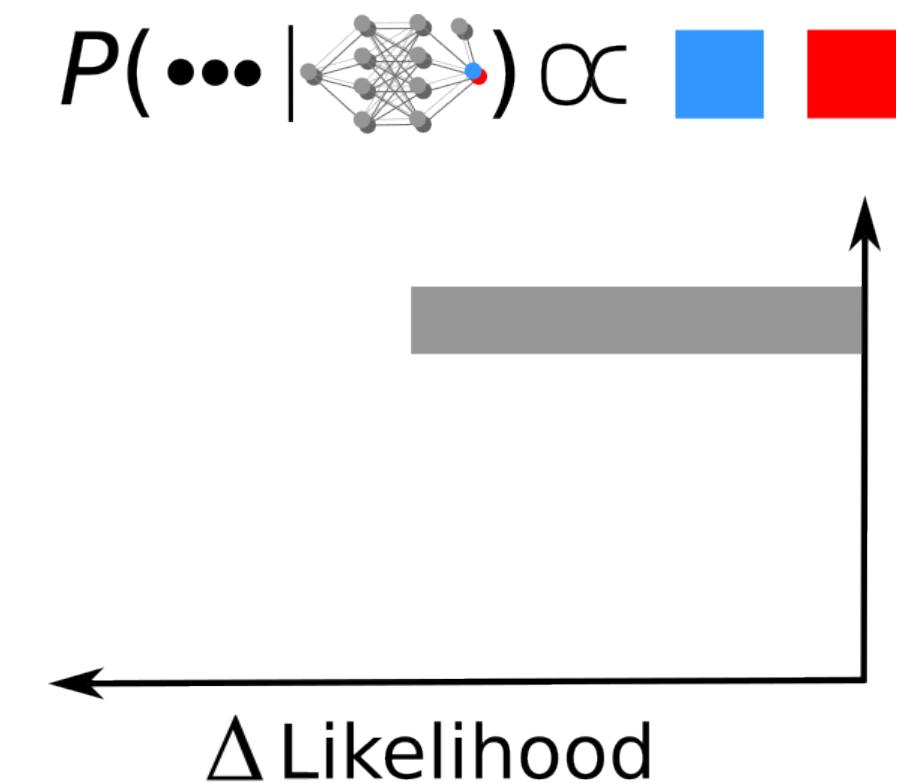
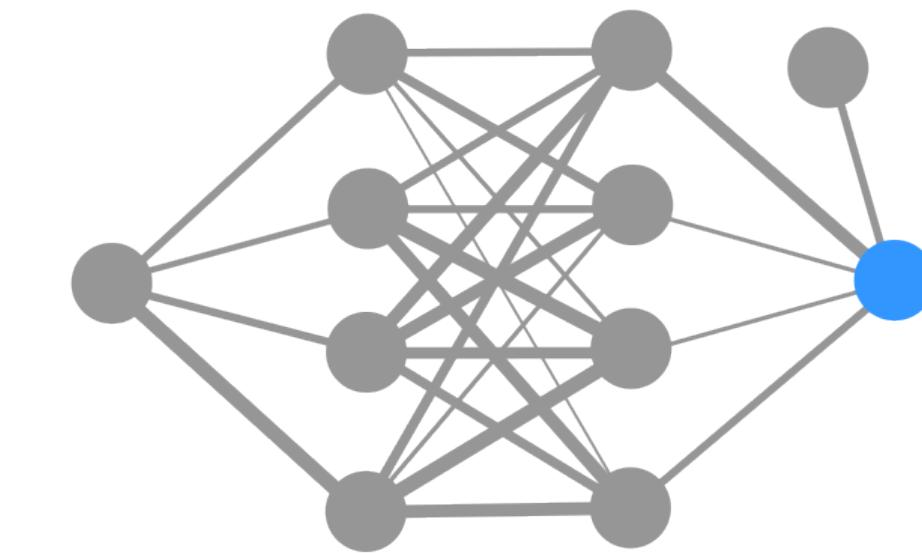
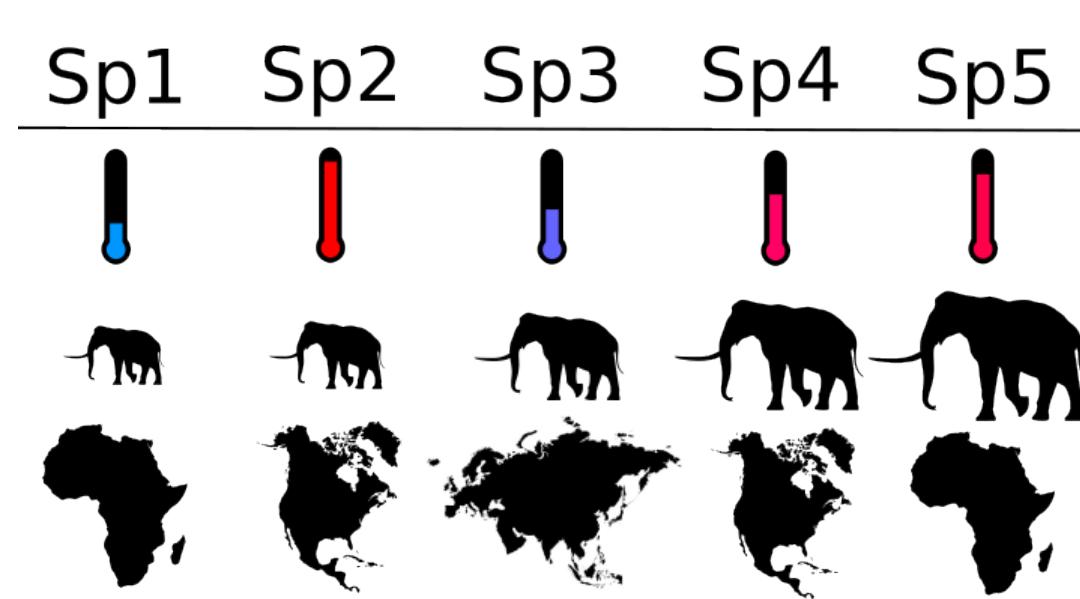
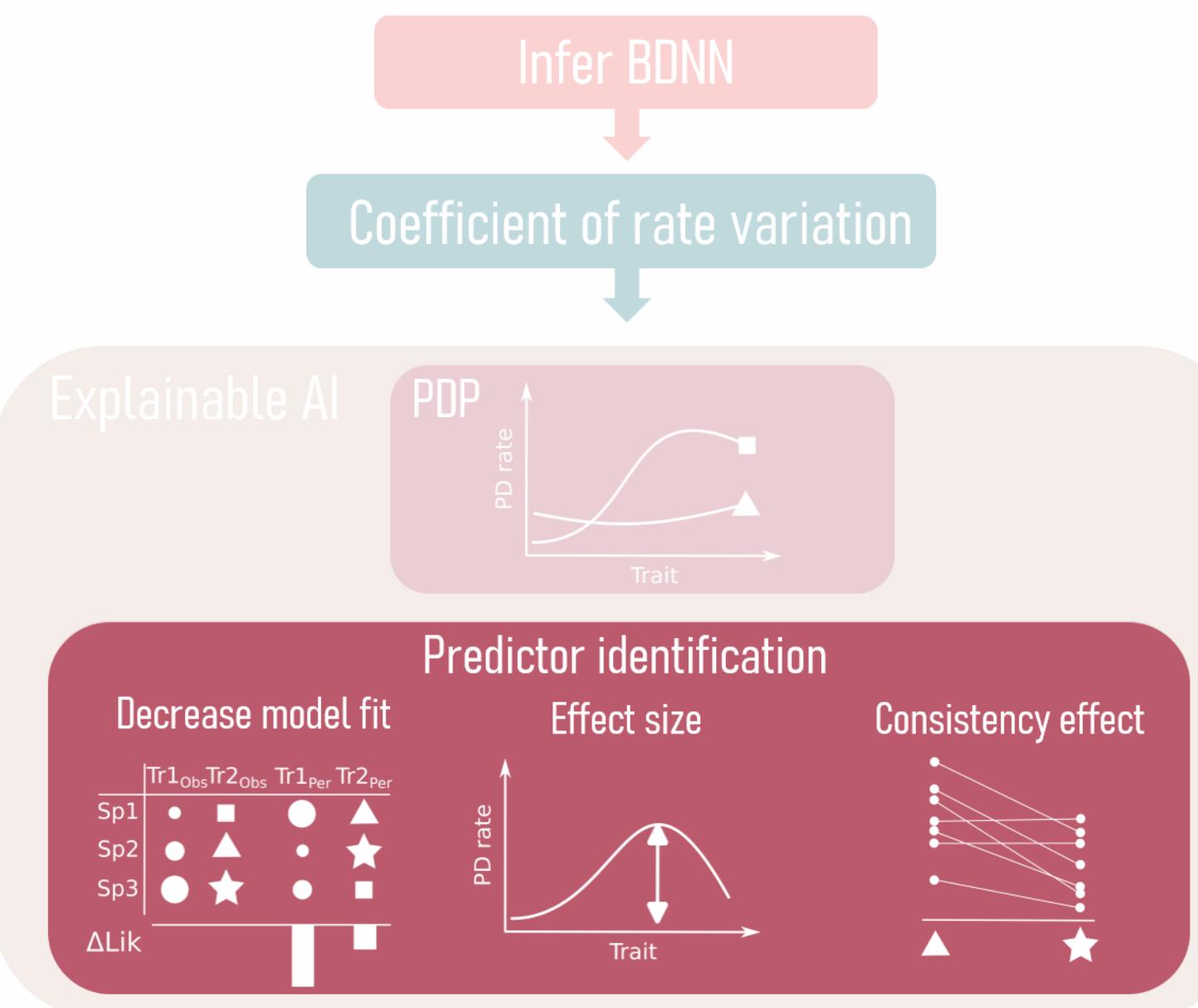


85 % of PD rates are greater than comparative temperature

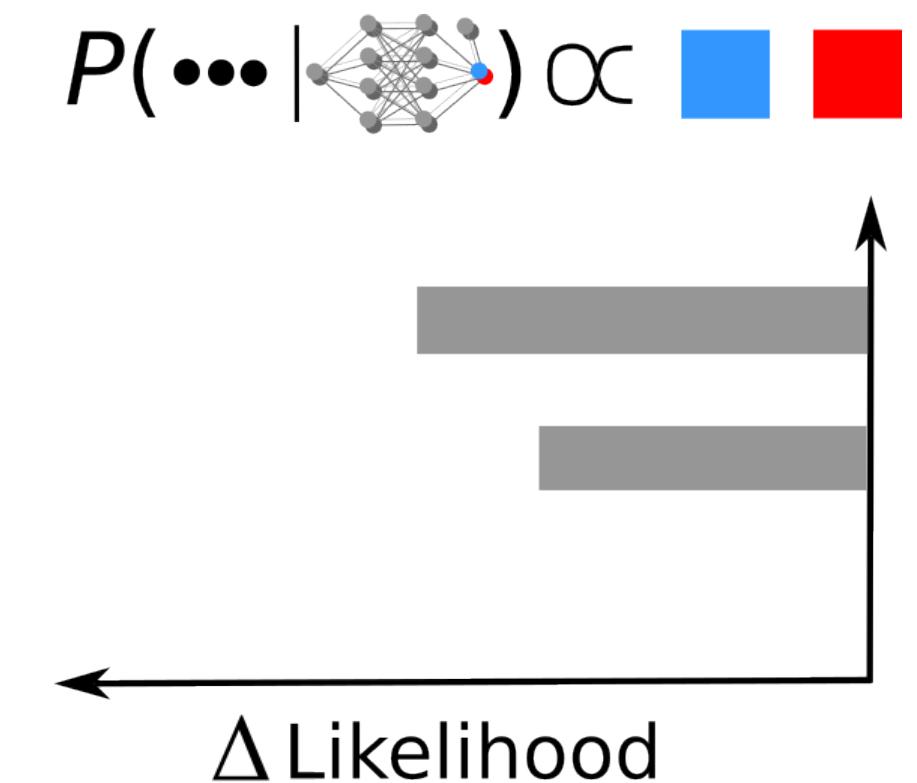
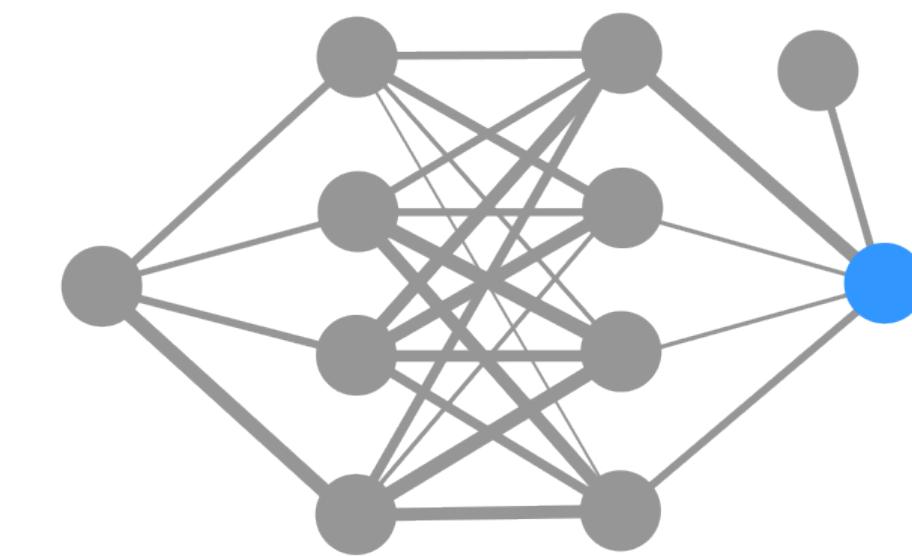
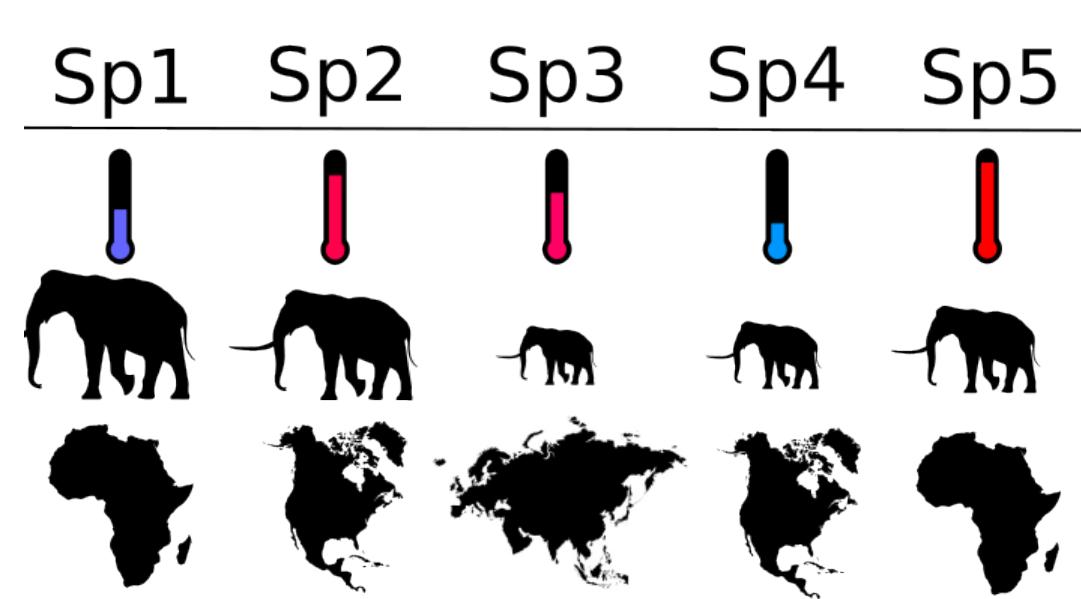
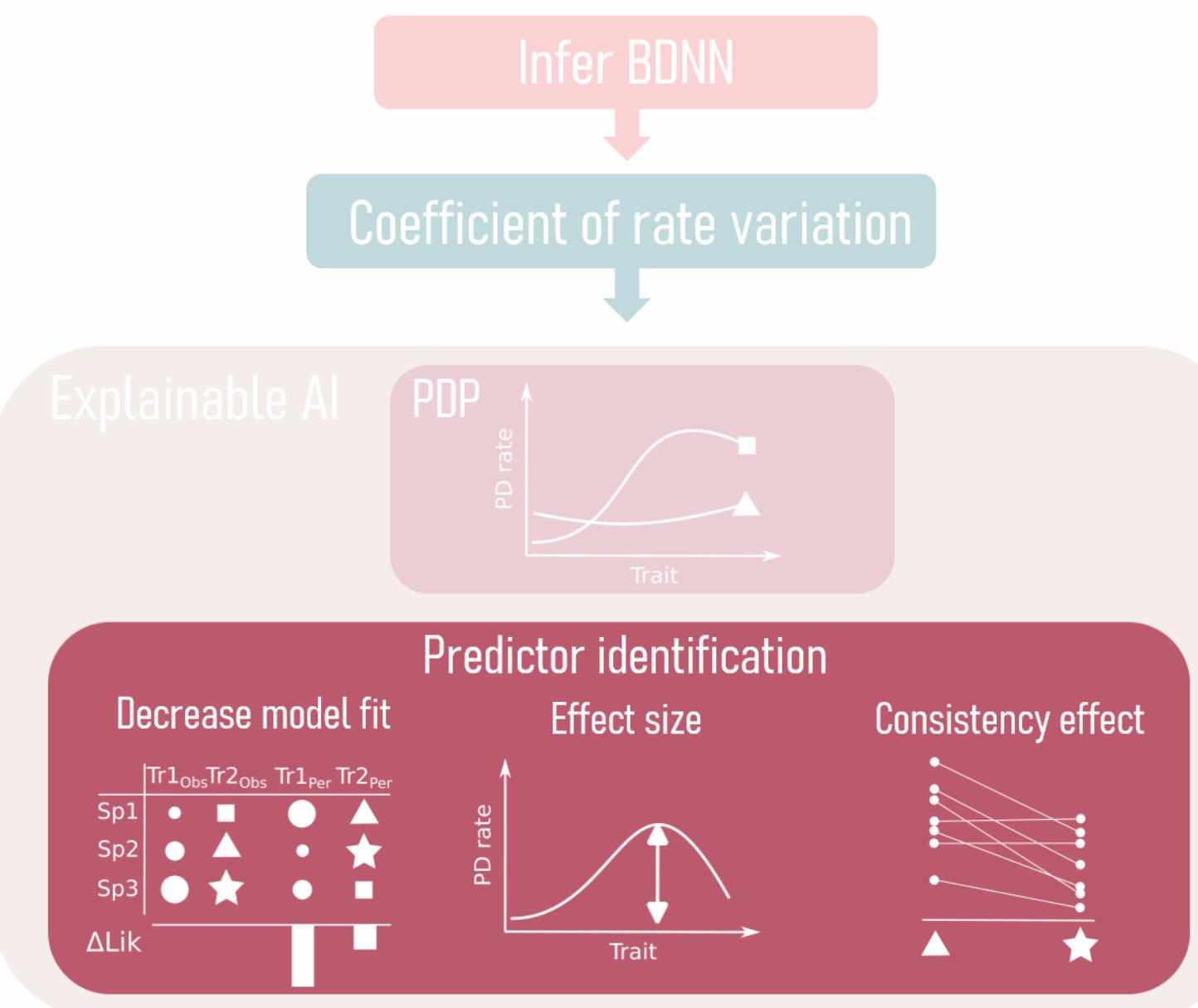
xAI: Decrease in model likelihood when permuting features



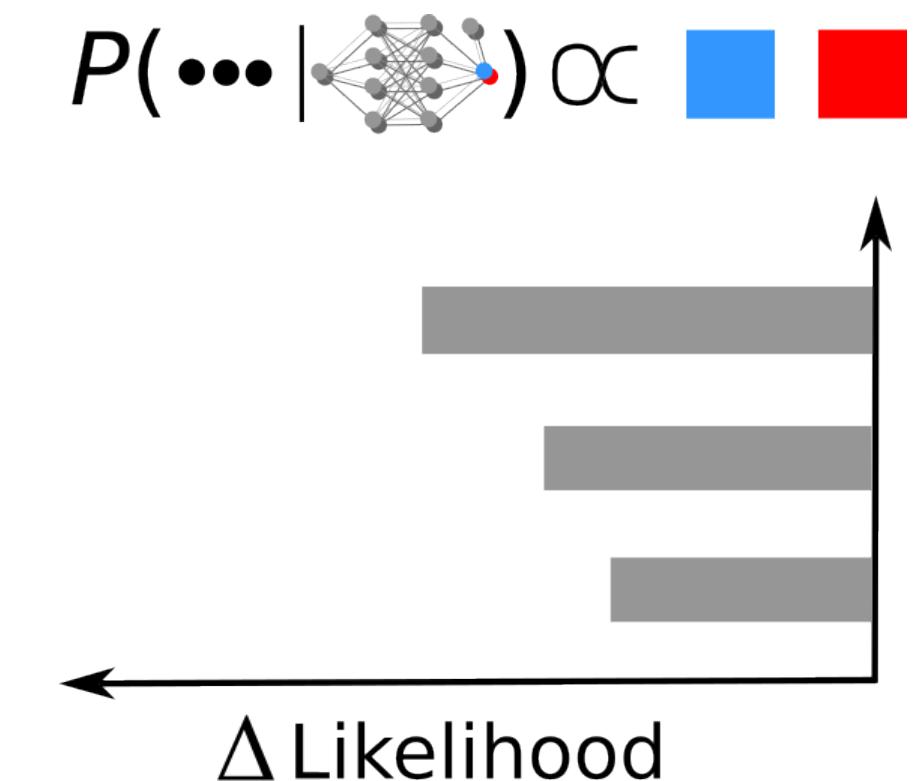
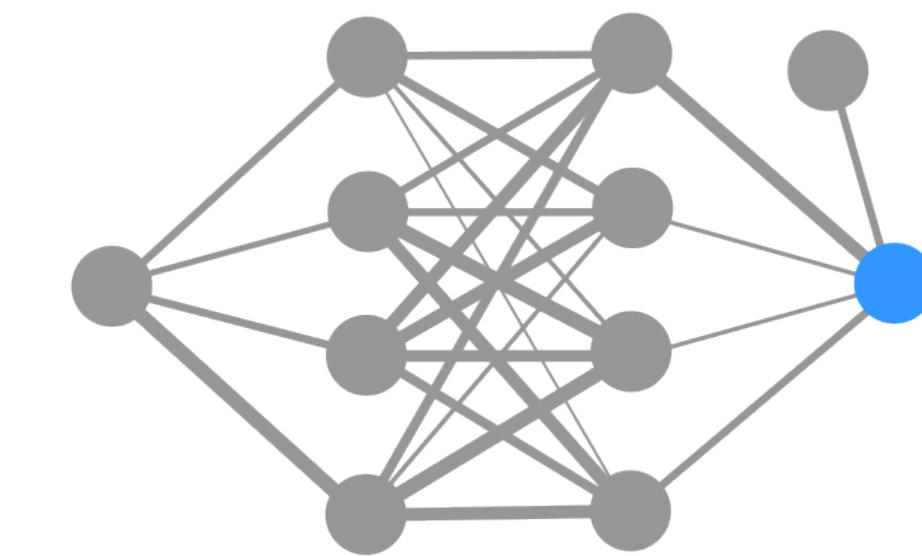
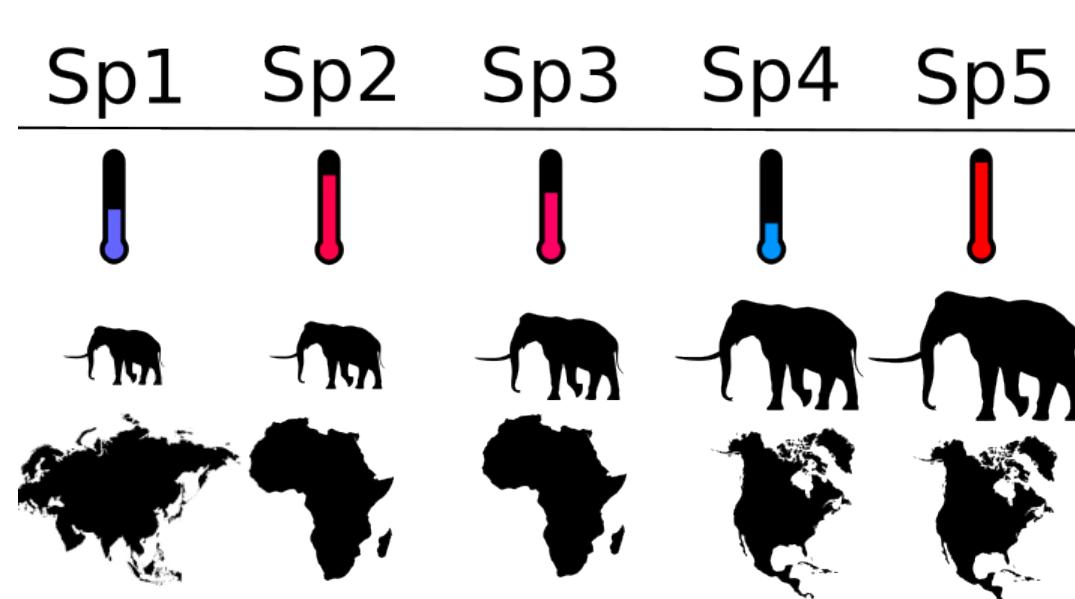
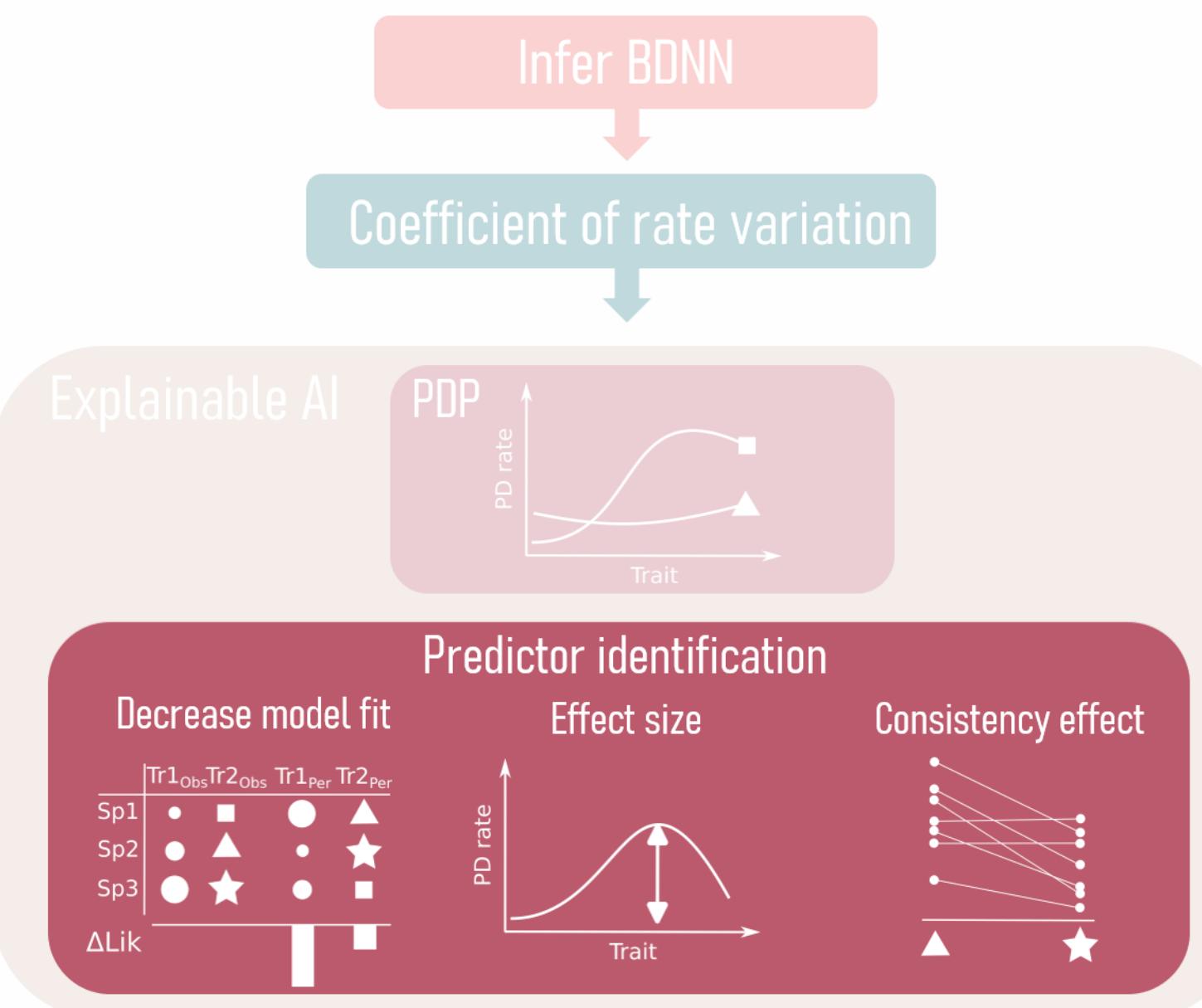
xAI: Decrease in model likelihood when permuting features



xAI: Decrease in model likelihood when permuting features

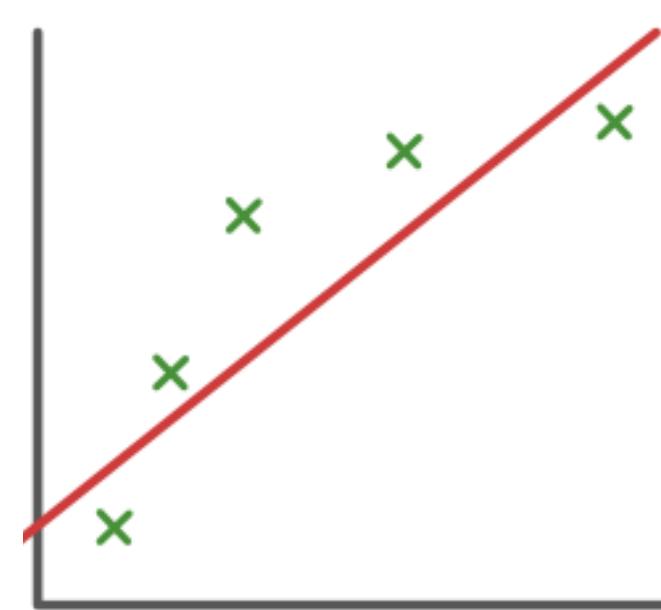


xAI: Decrease in model likelihood when permuting features

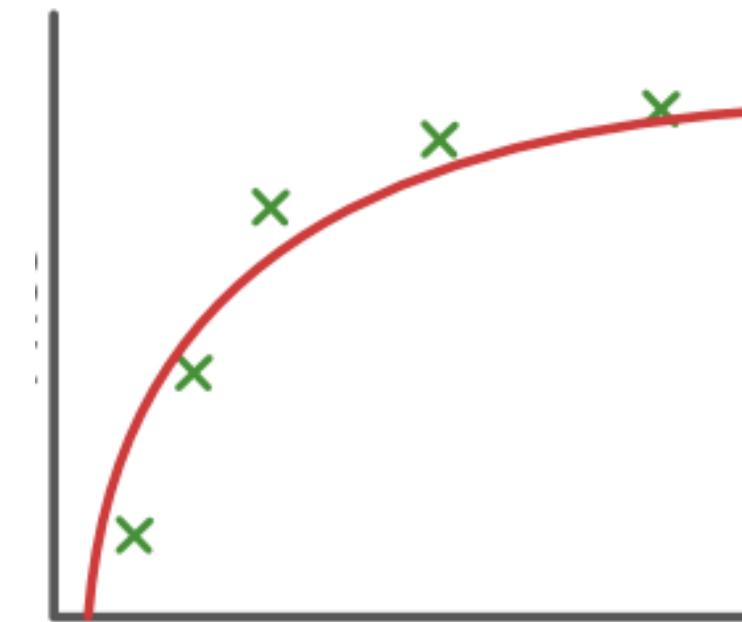


What about overfitting? 🤔

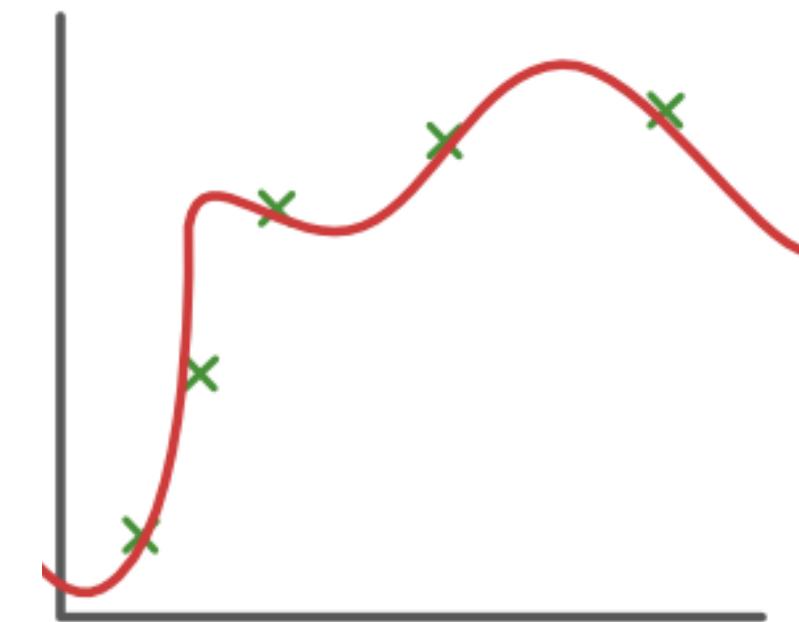
Under-fitting



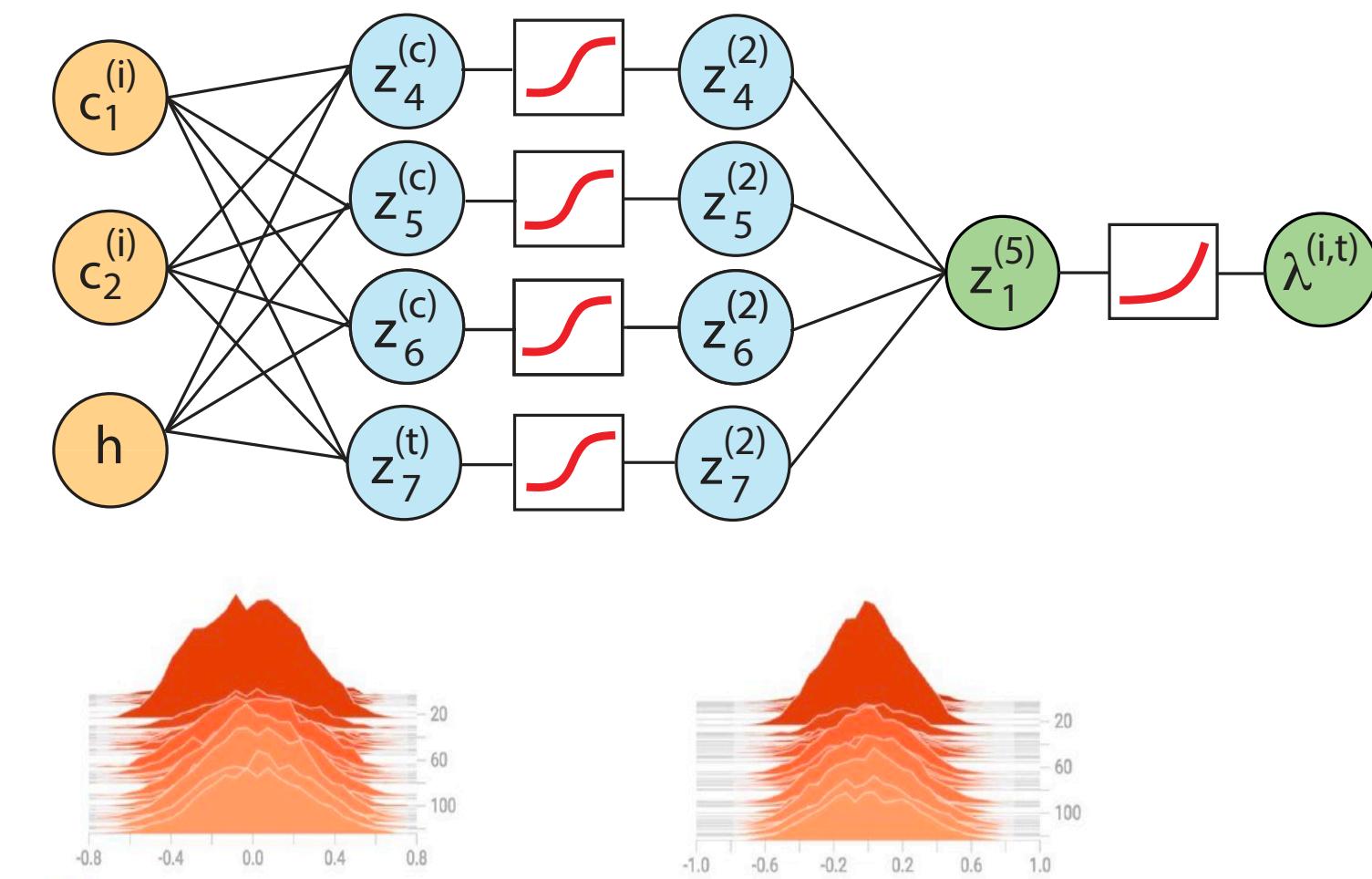
Just right



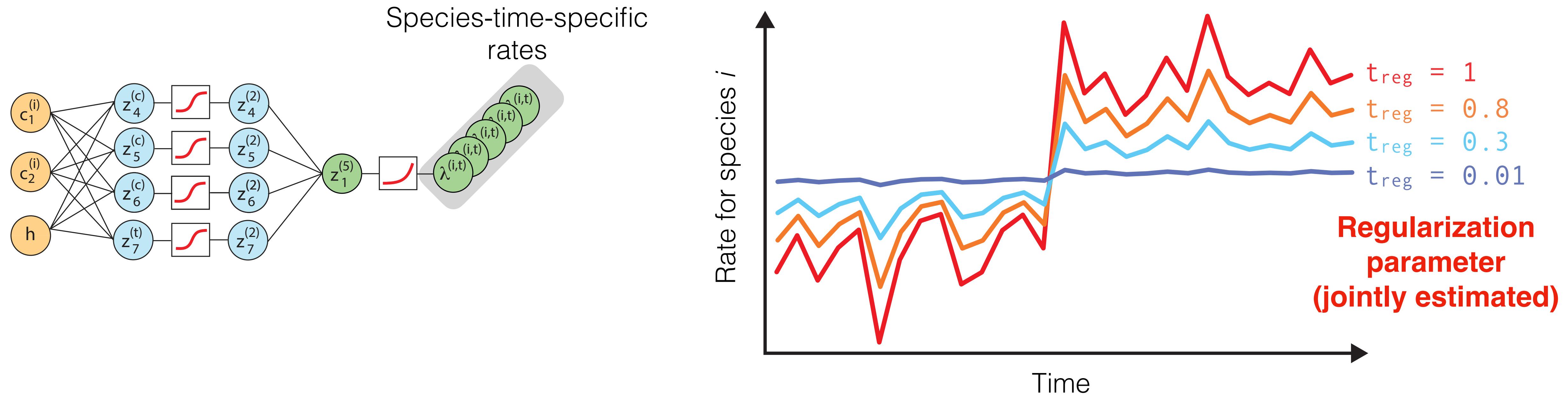
Over-fitting



Model regularization #1 - priors on NN weights

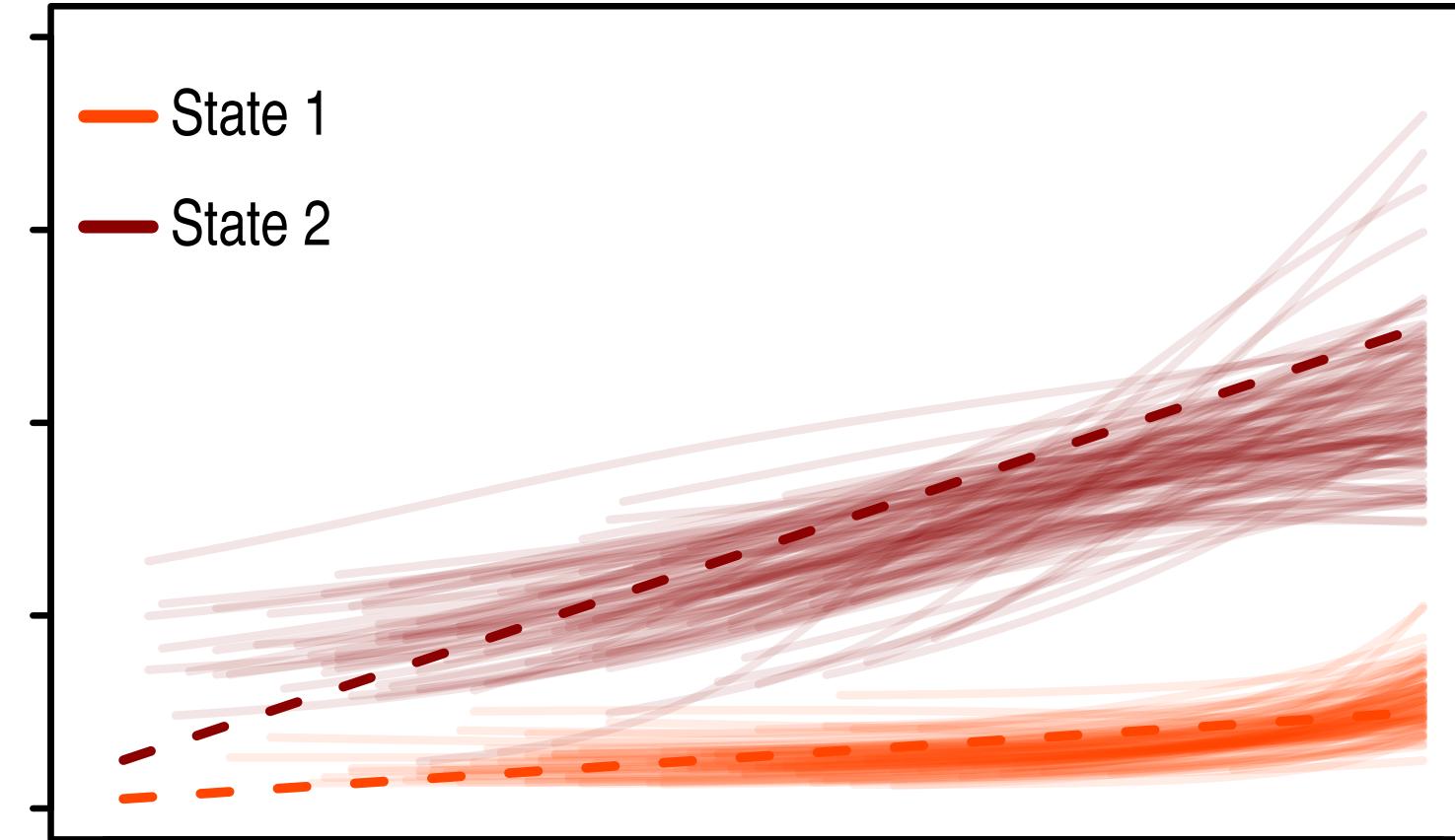


Model regularization #2 – Bayesian shrinkage



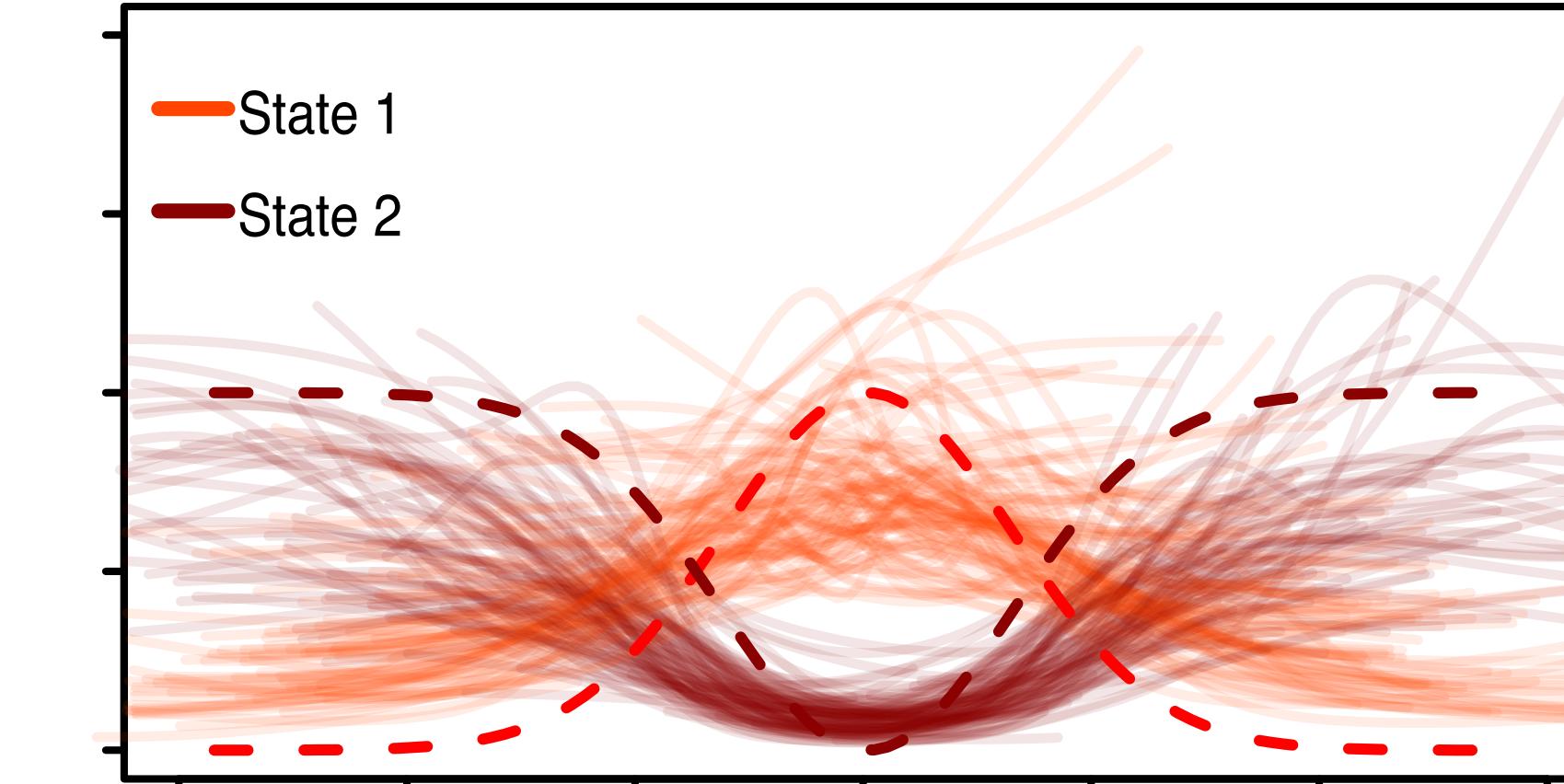
Time-dependent and trait-dependent BDNN model

Time and trait dependent rates



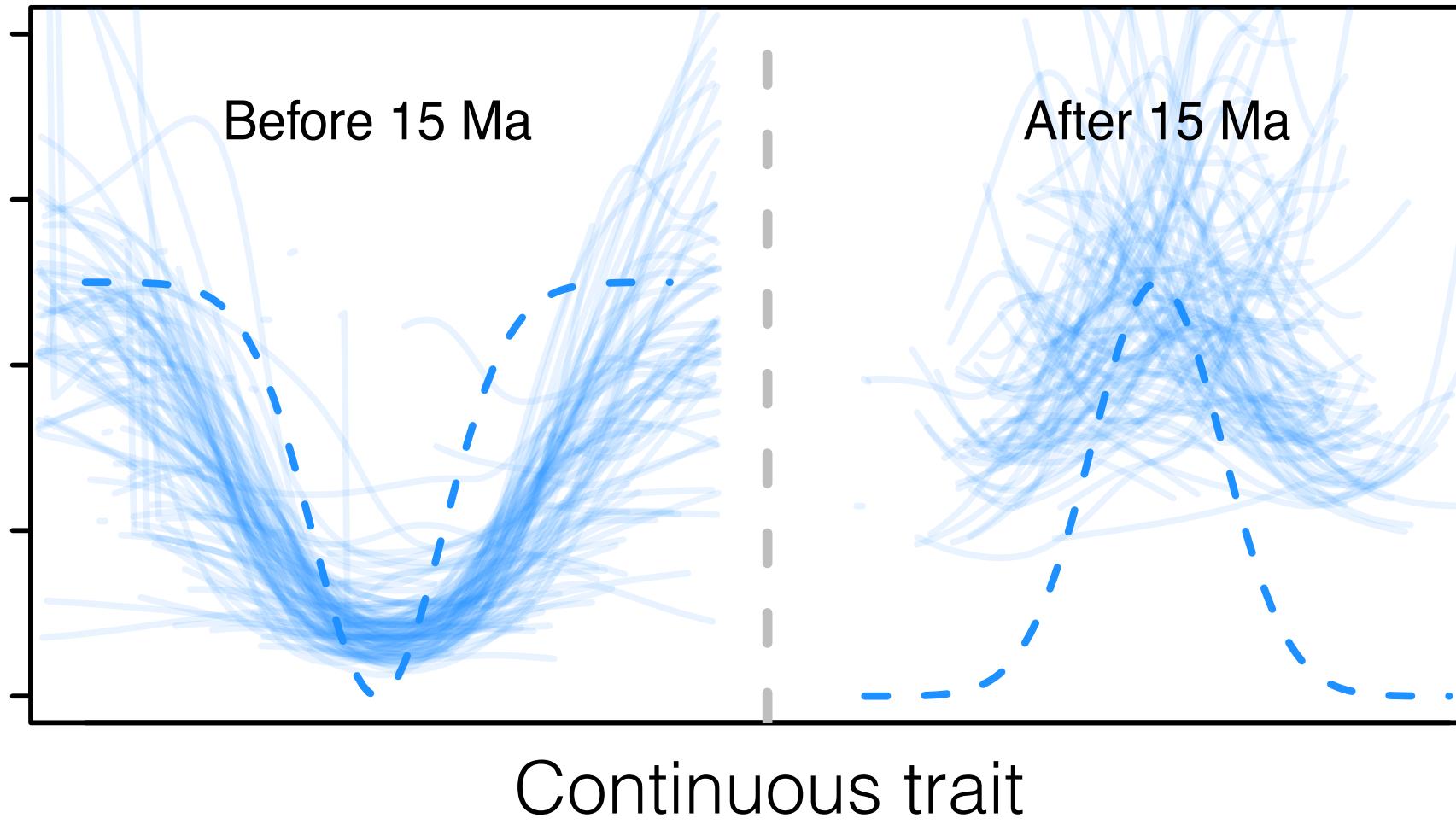
Time

Categorical and continuous trait dependent rates



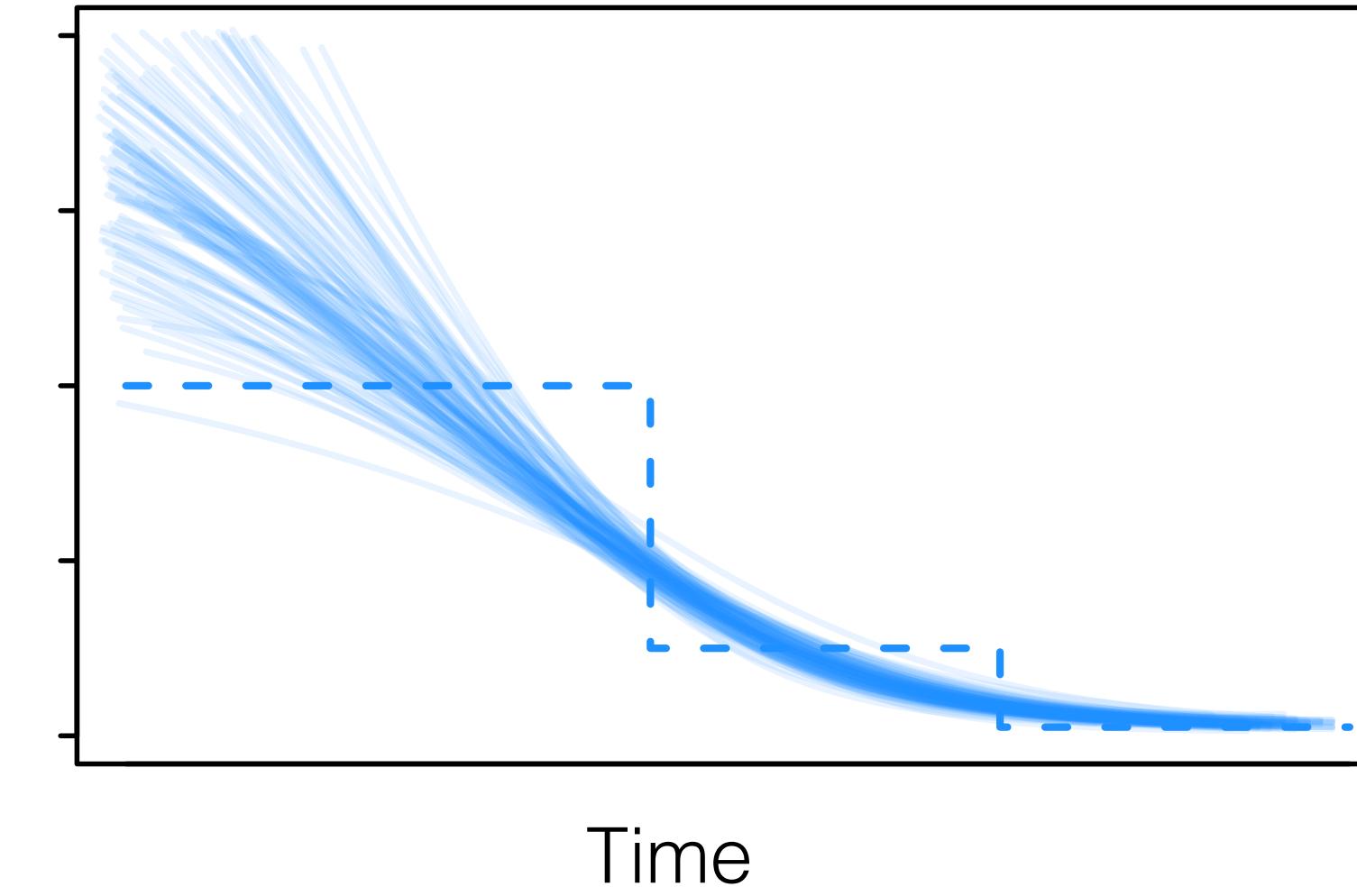
Continuous trait

Time and trait dependent rates



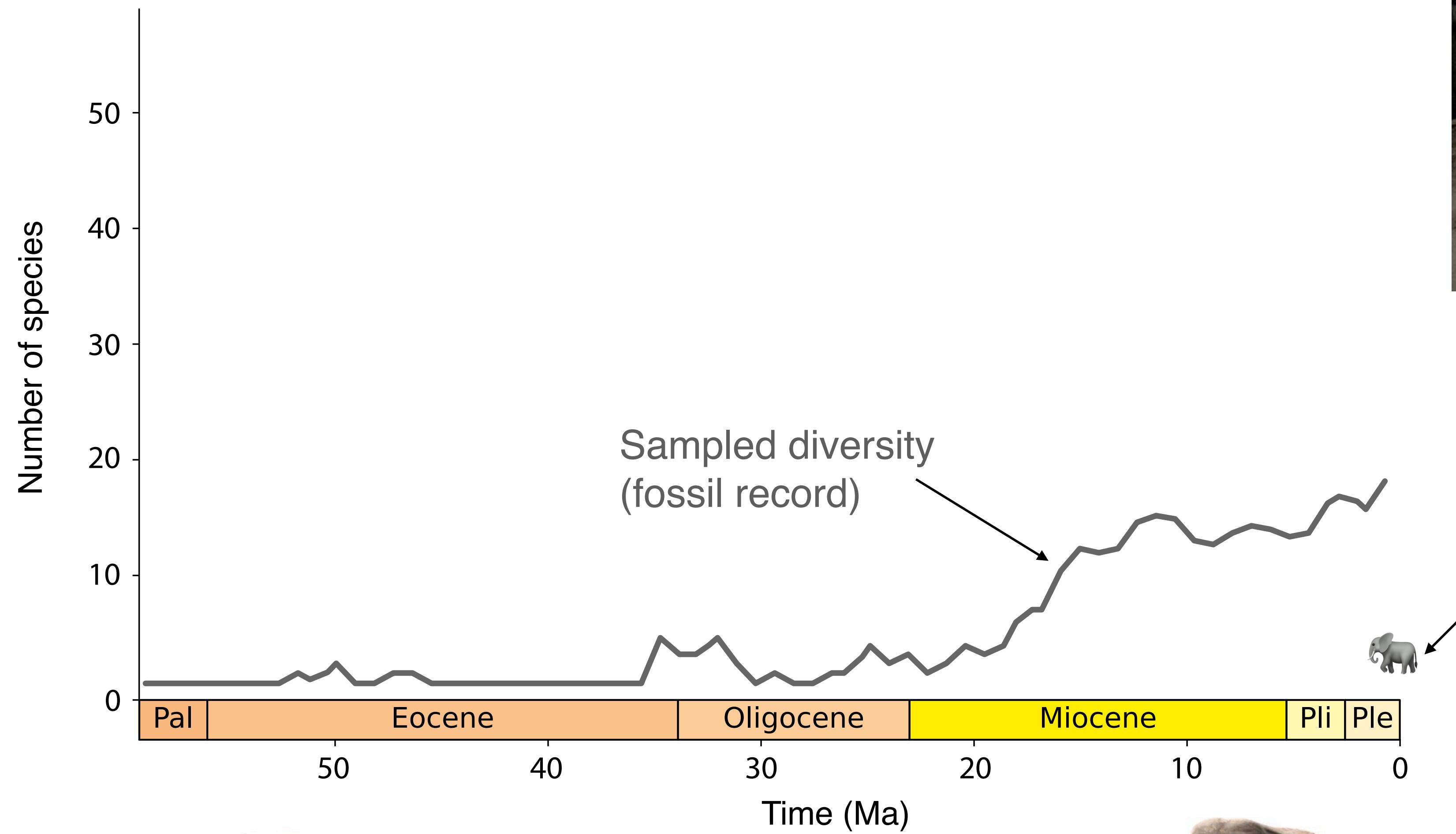
Continuous trait

Time dependent rates



Time

The rise and fall of elephants

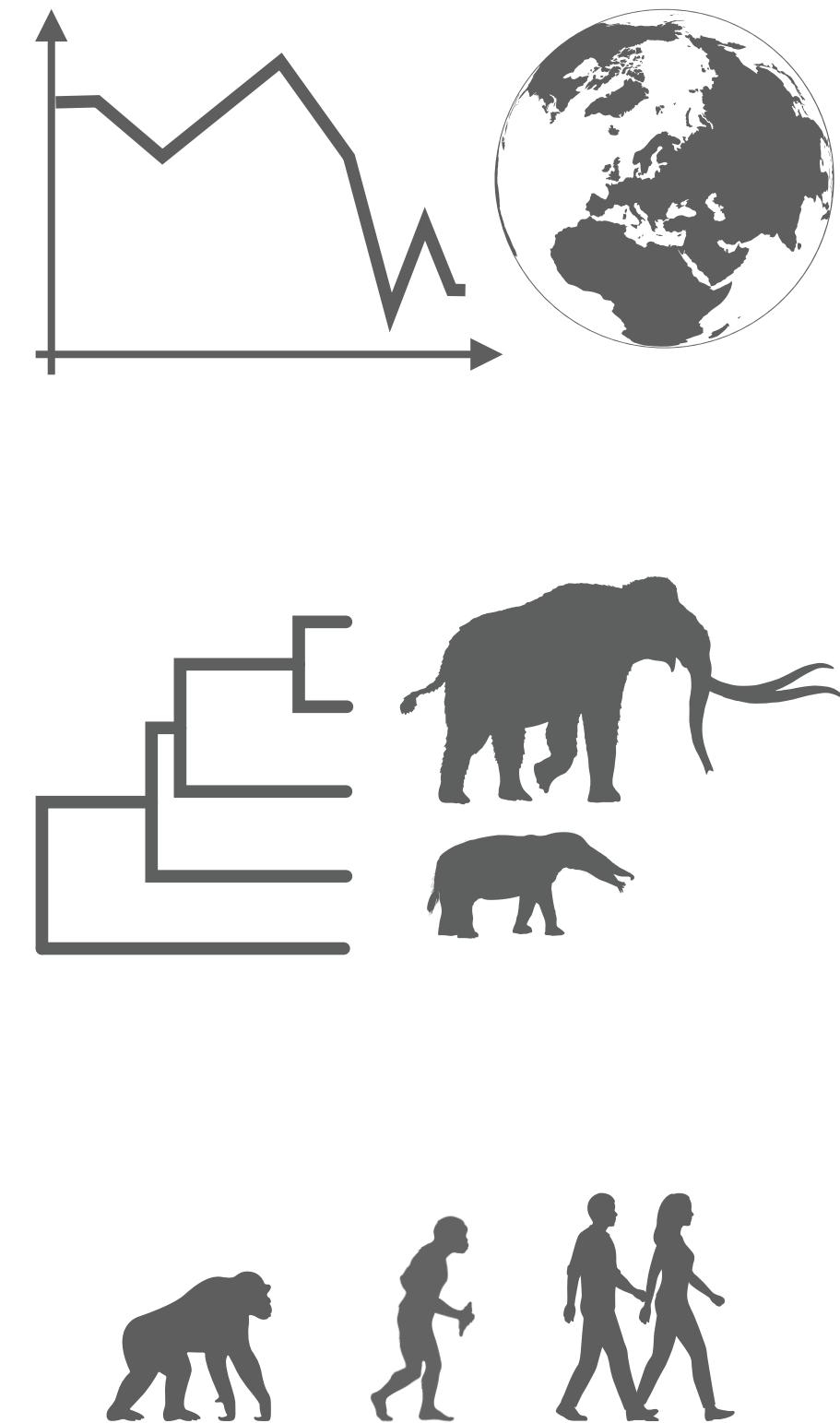


- 2,100 fossil occurrences
- 1,600 localities in 5 continents
- 180 species



Unsupervised Bayesian neural network model of speciation and extinction

Predictors

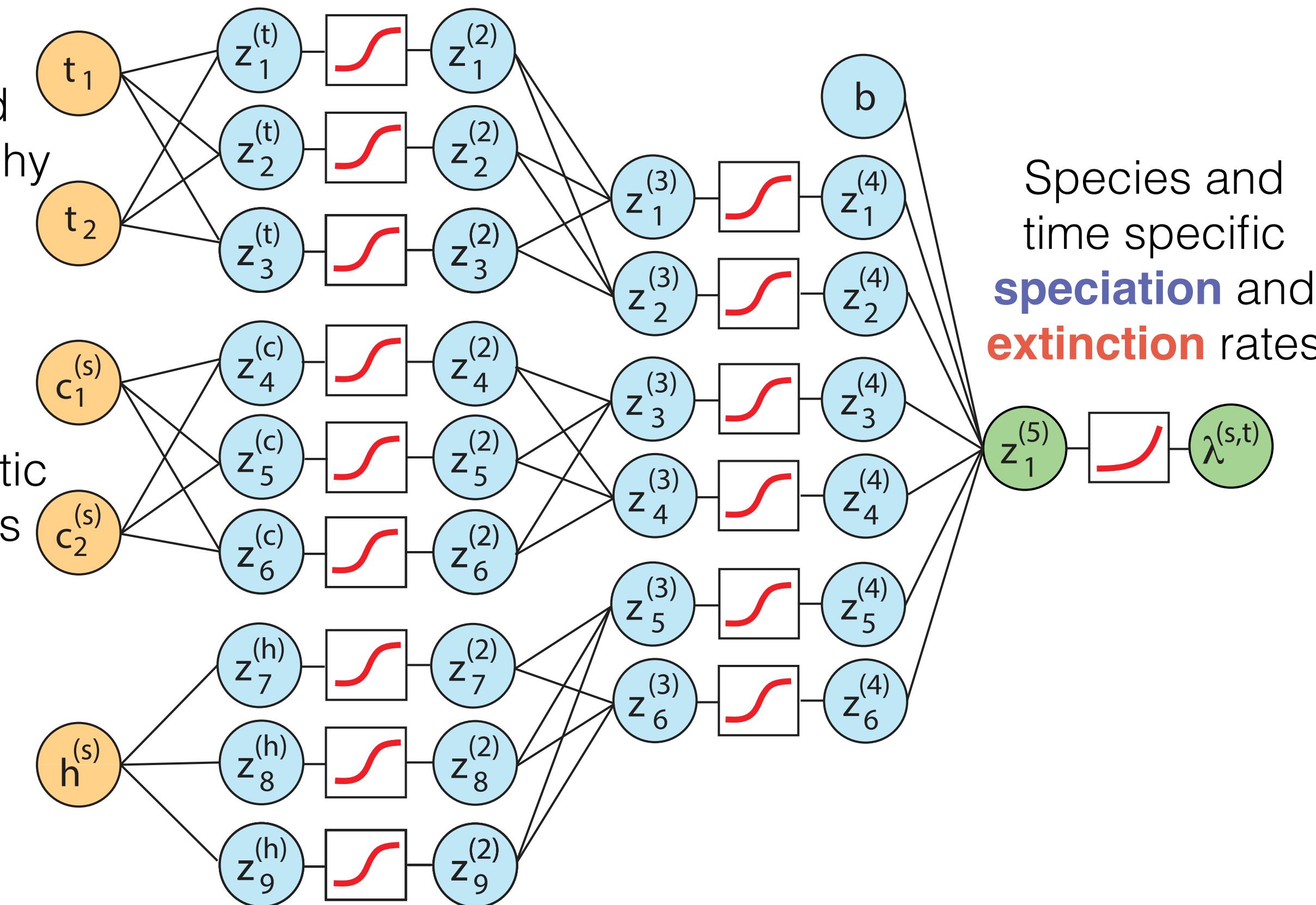


Climate and
biogeography

Traits and
phylogenetic
relatedness

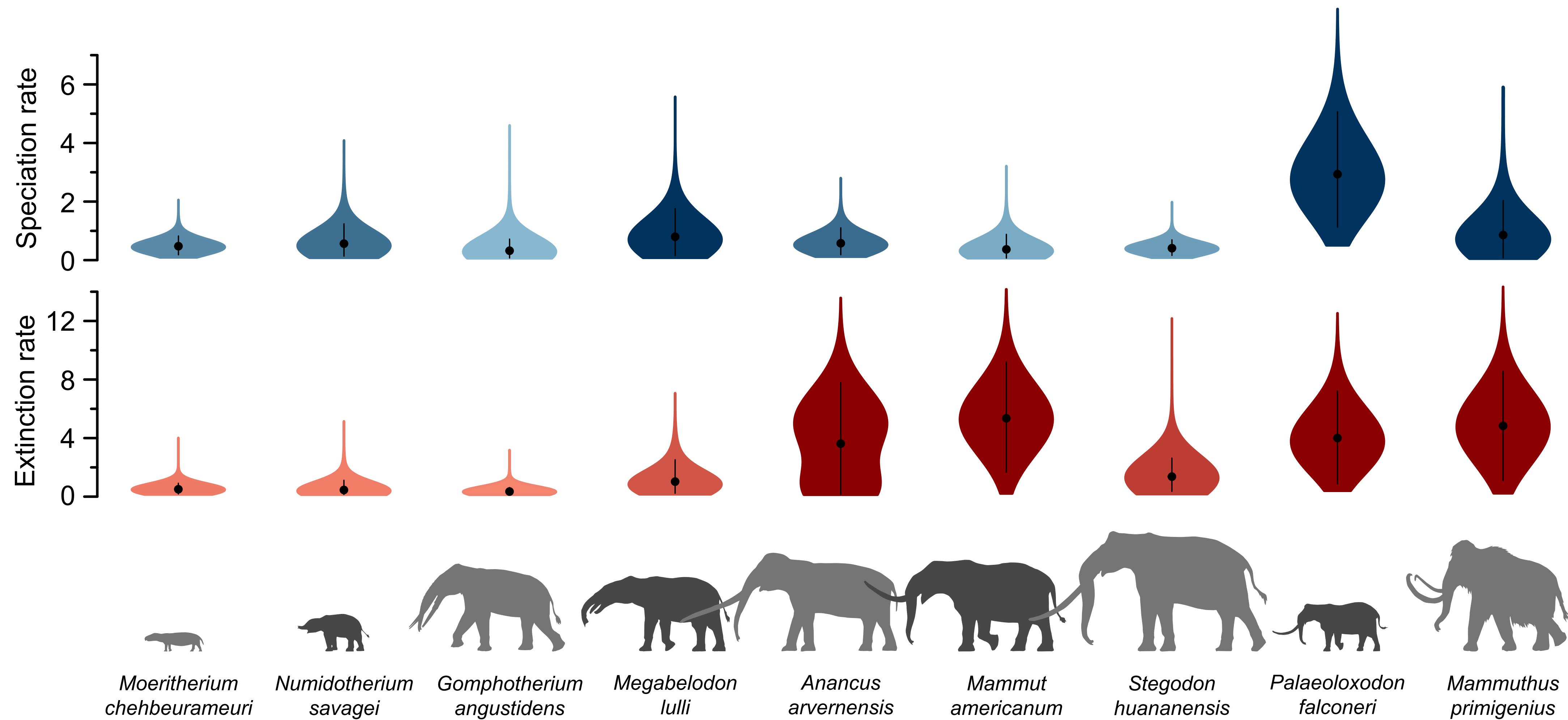
Humans

Resulting rates

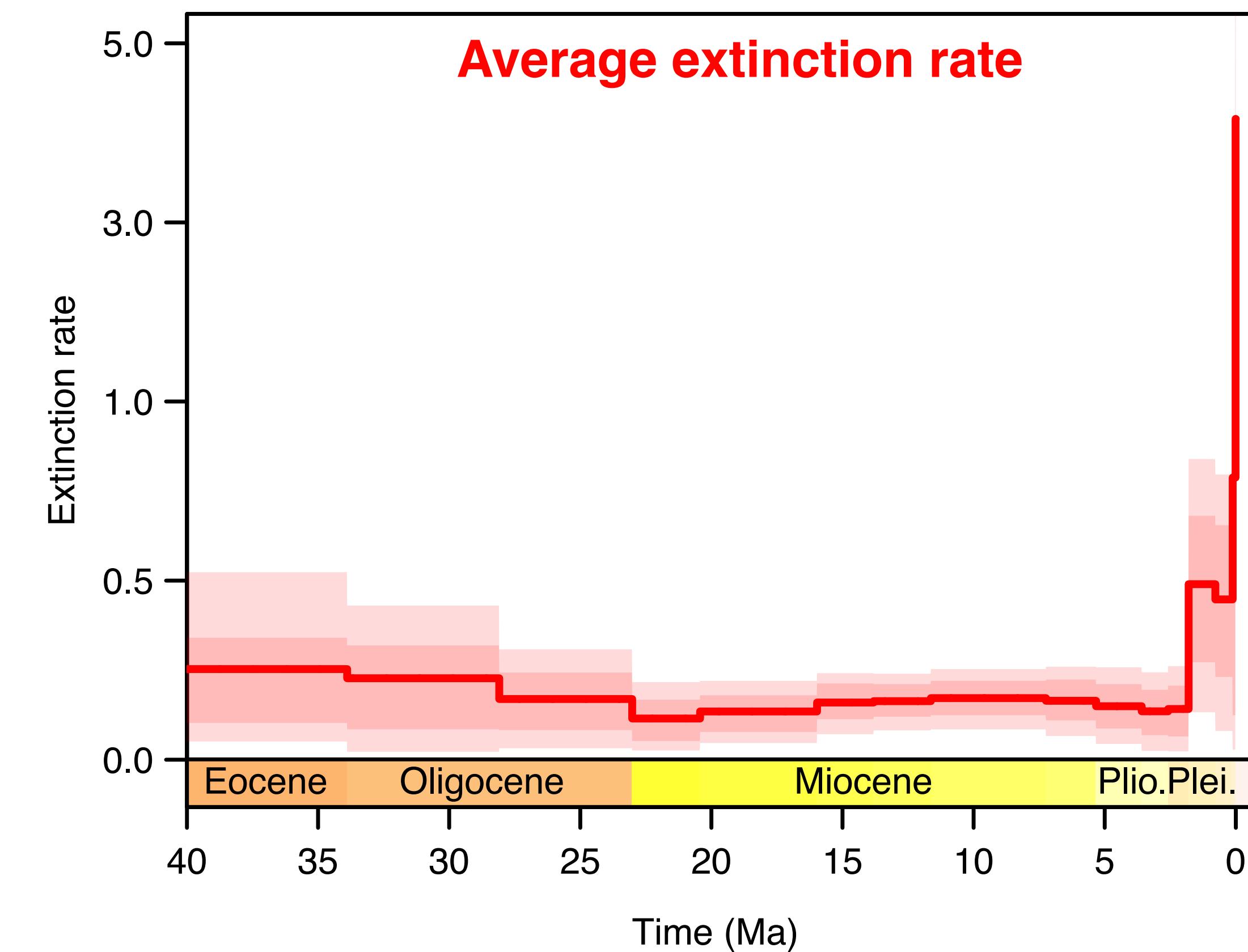
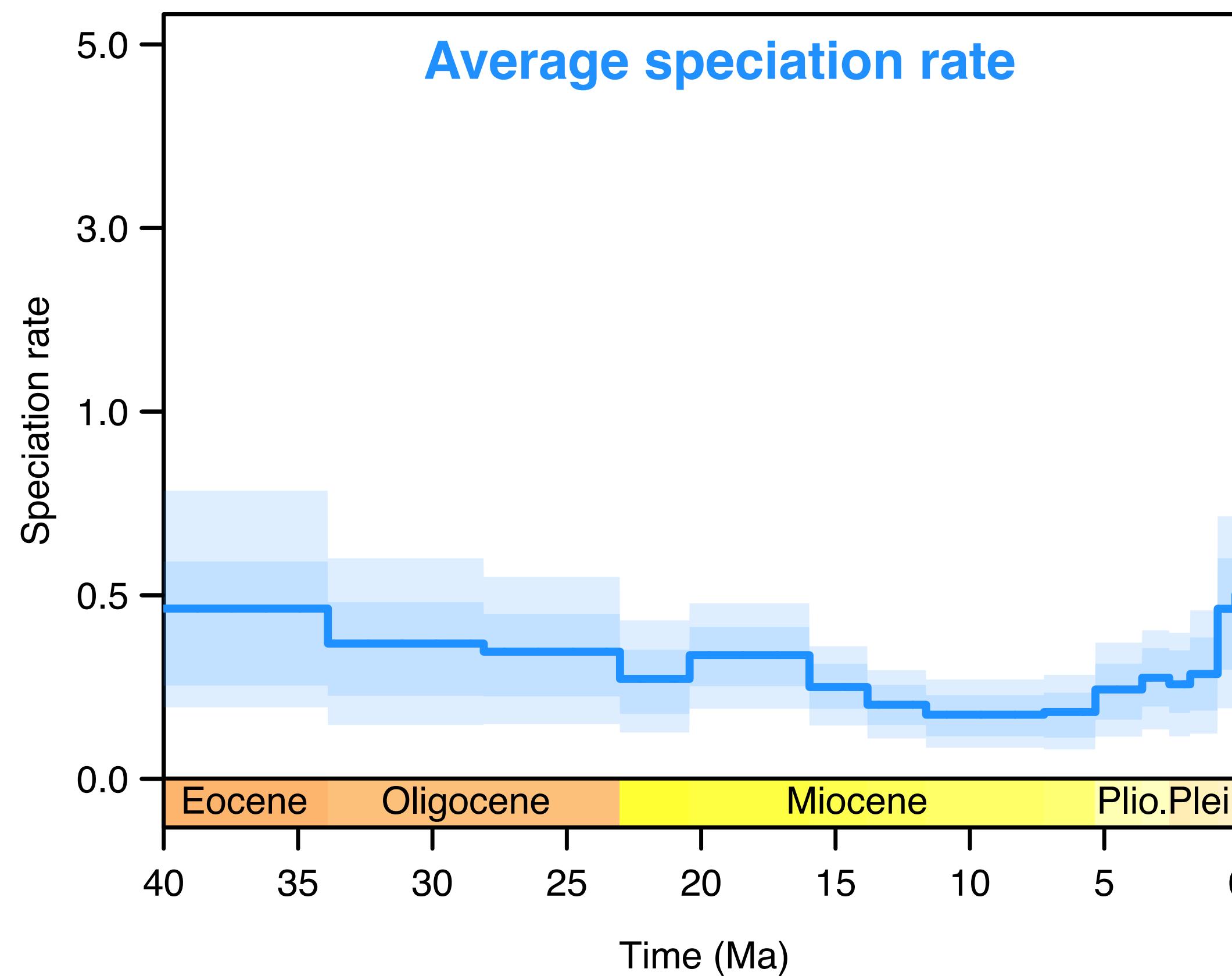


Species and
time specific
speciation and
extinction rates

Marginal per-species speciation and extinction rates

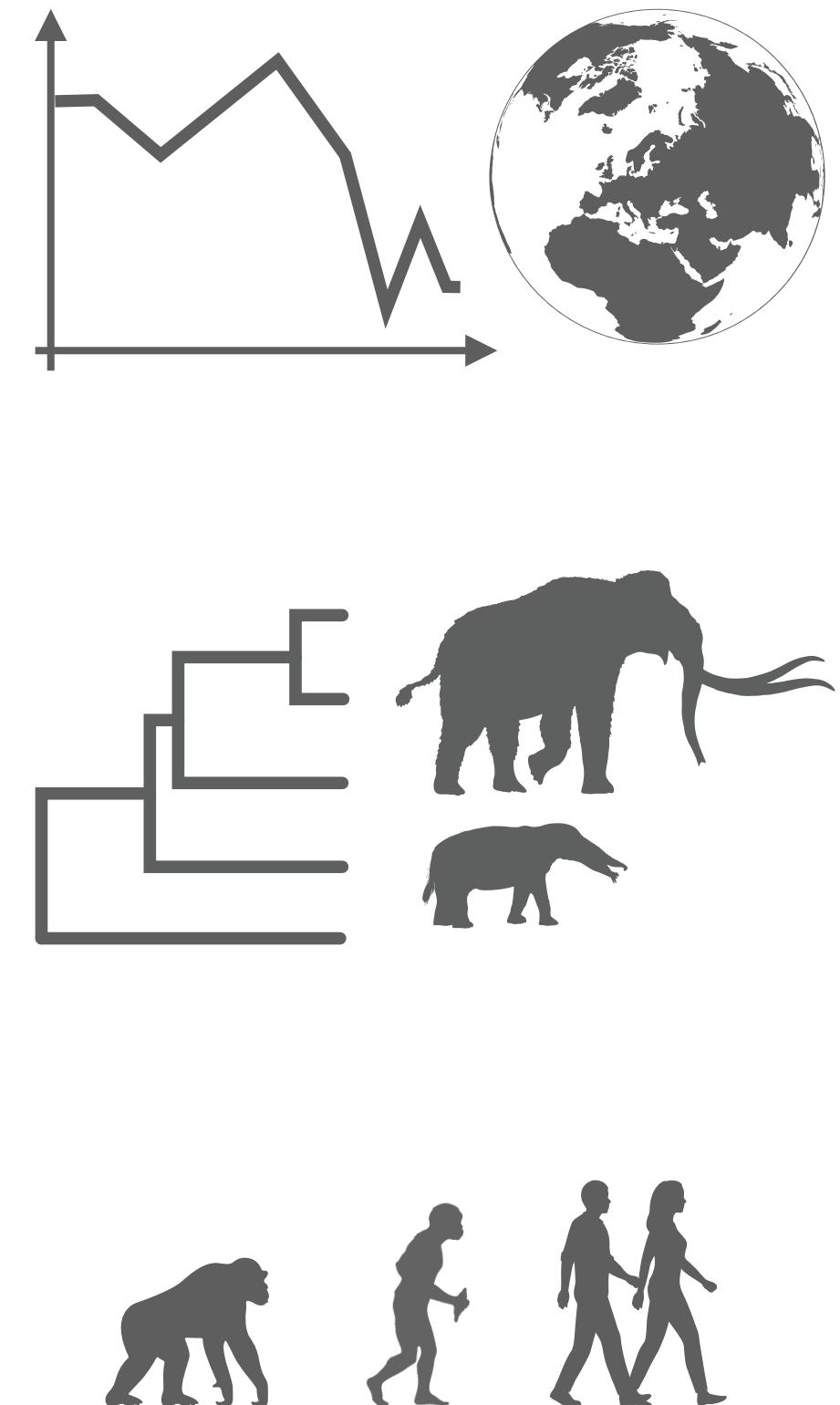


Average speciation and extinction rates through time



Unsupervised Bayesian neural network model of speciation and extinction

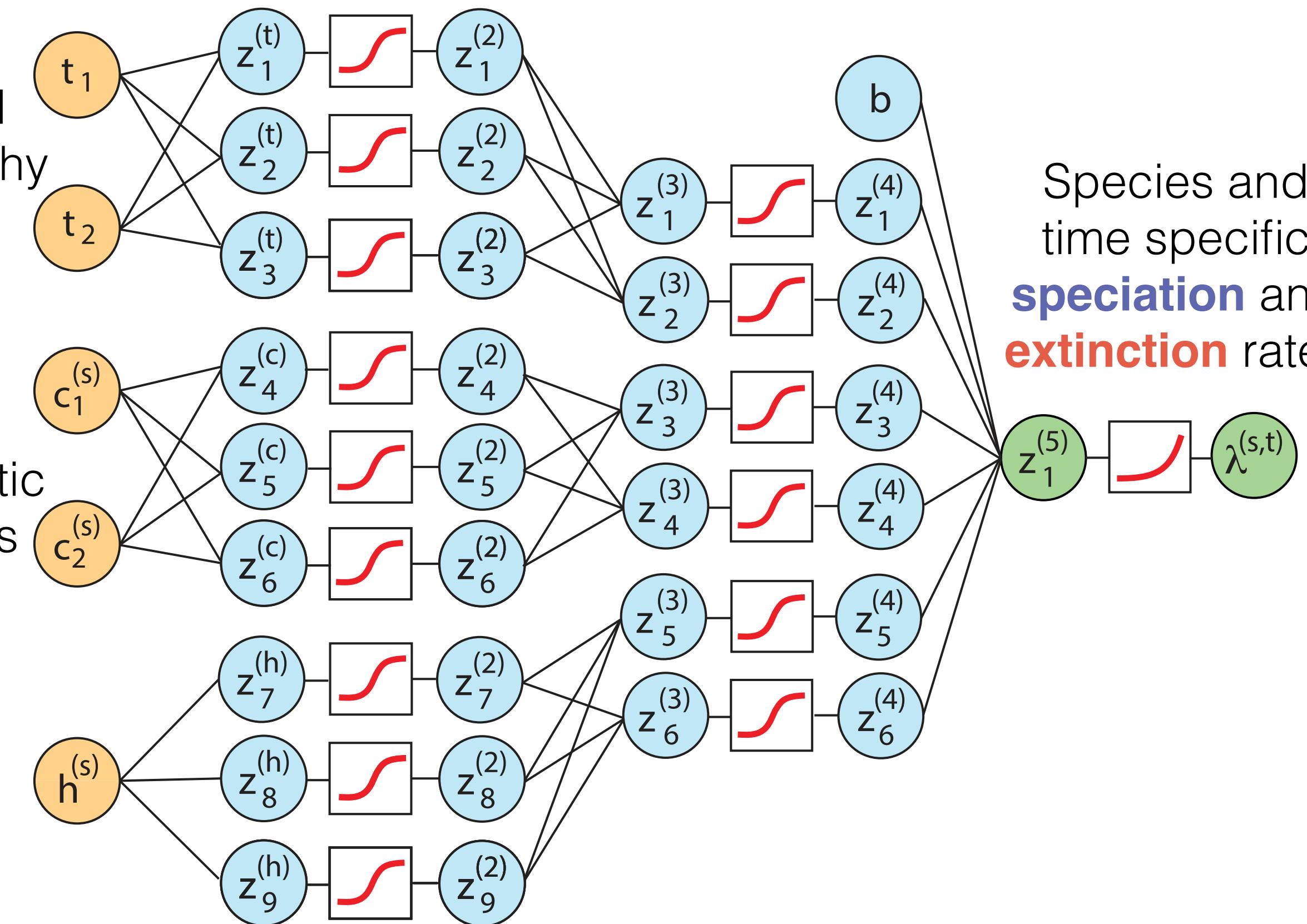
Predictors



Climate and biogeography

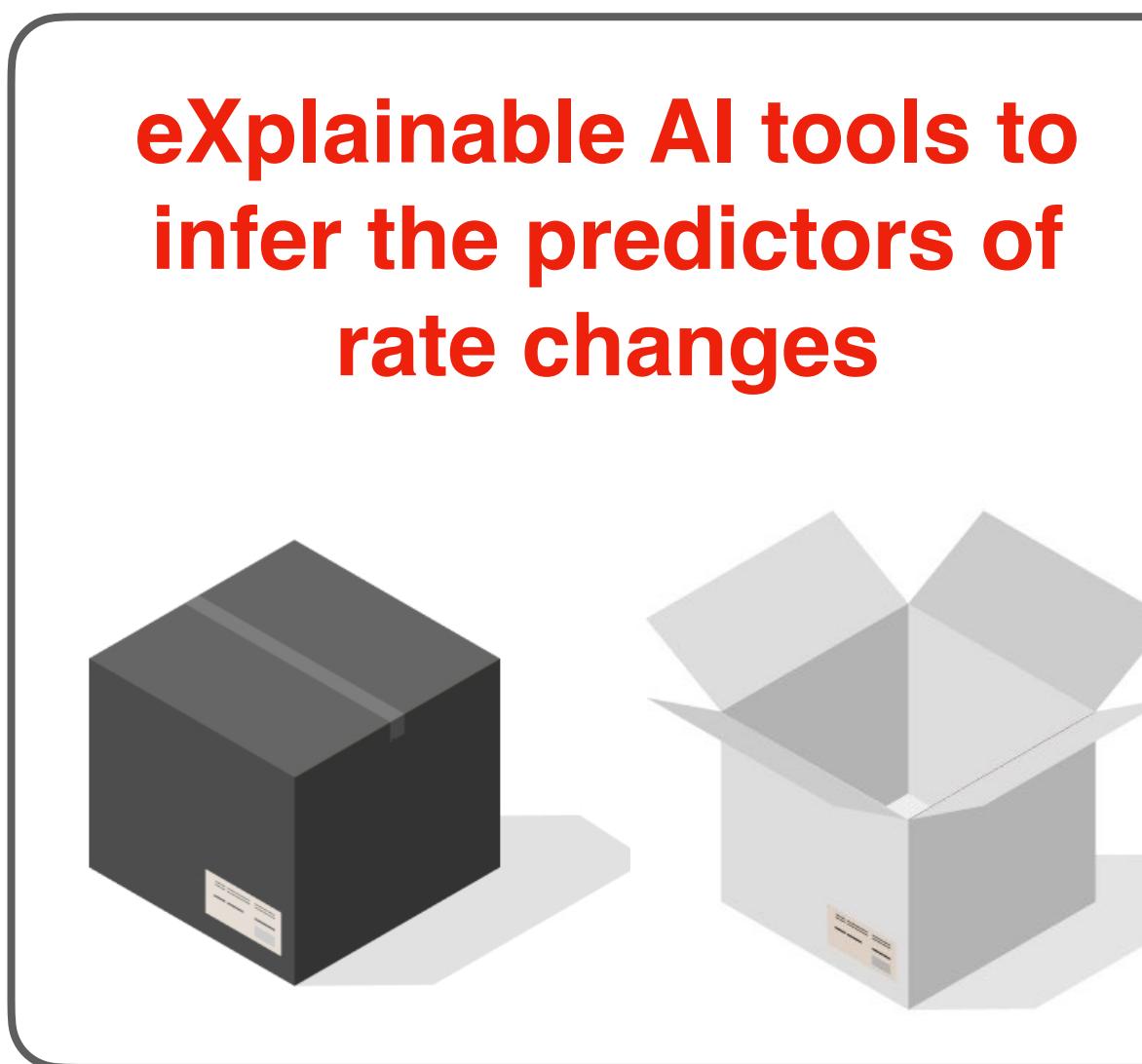
Traits and phylogenetic relatedness

Humans



Resulting rates

Species and time specific **speciation** and **extinction** rates



T Hauffe

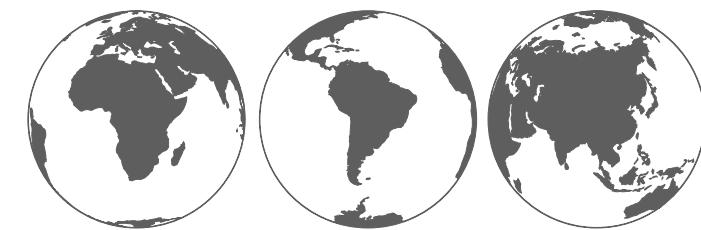
Using tools from Explainable AI to determine the drivers of speciation and extinction

1. Permutations (Partial dependence plots)
2. Marginal probabilities
3. SHAP values (mean absolute deviation from the mean rate across all species caused by a predictor)

Ranking the predictors of speciation



Dietary specialization

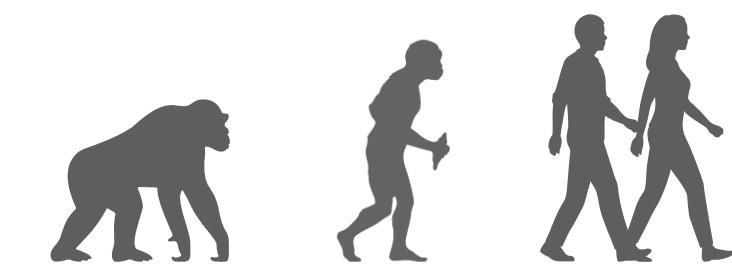


Biogeography

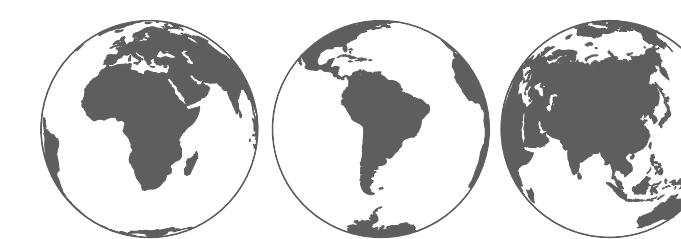


Time

Ranking the predictors of extinction



Human impact

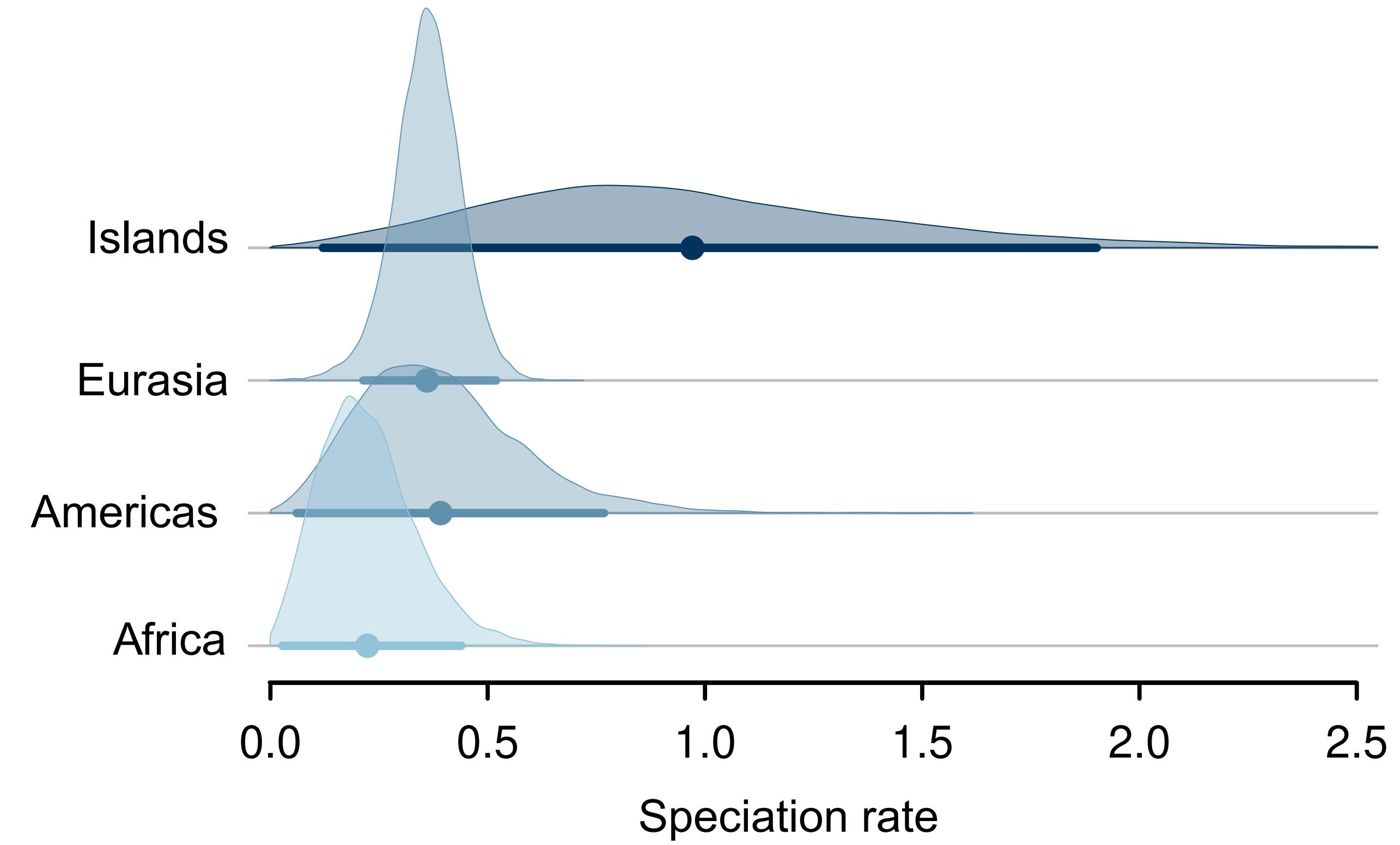
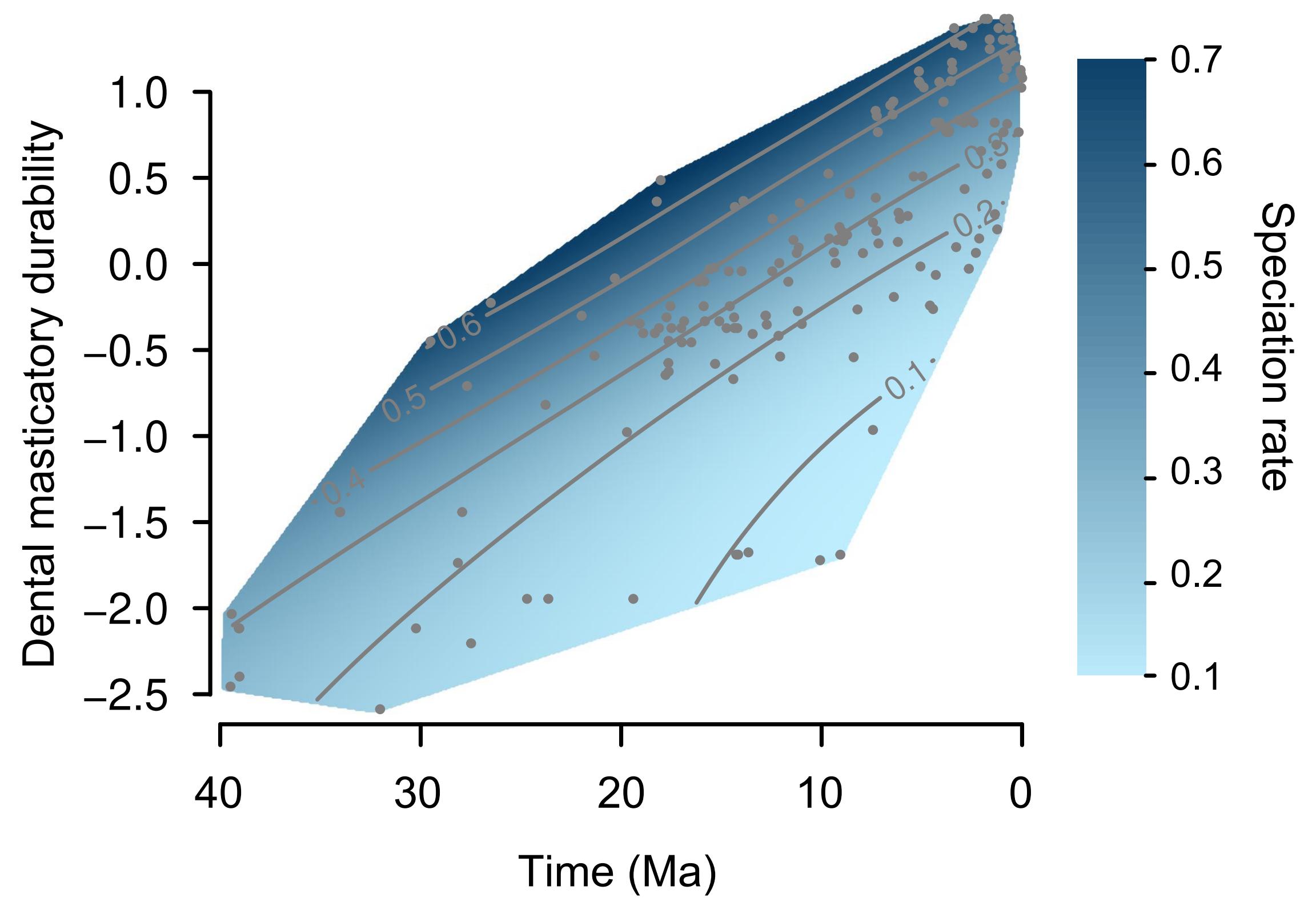


Biogeography

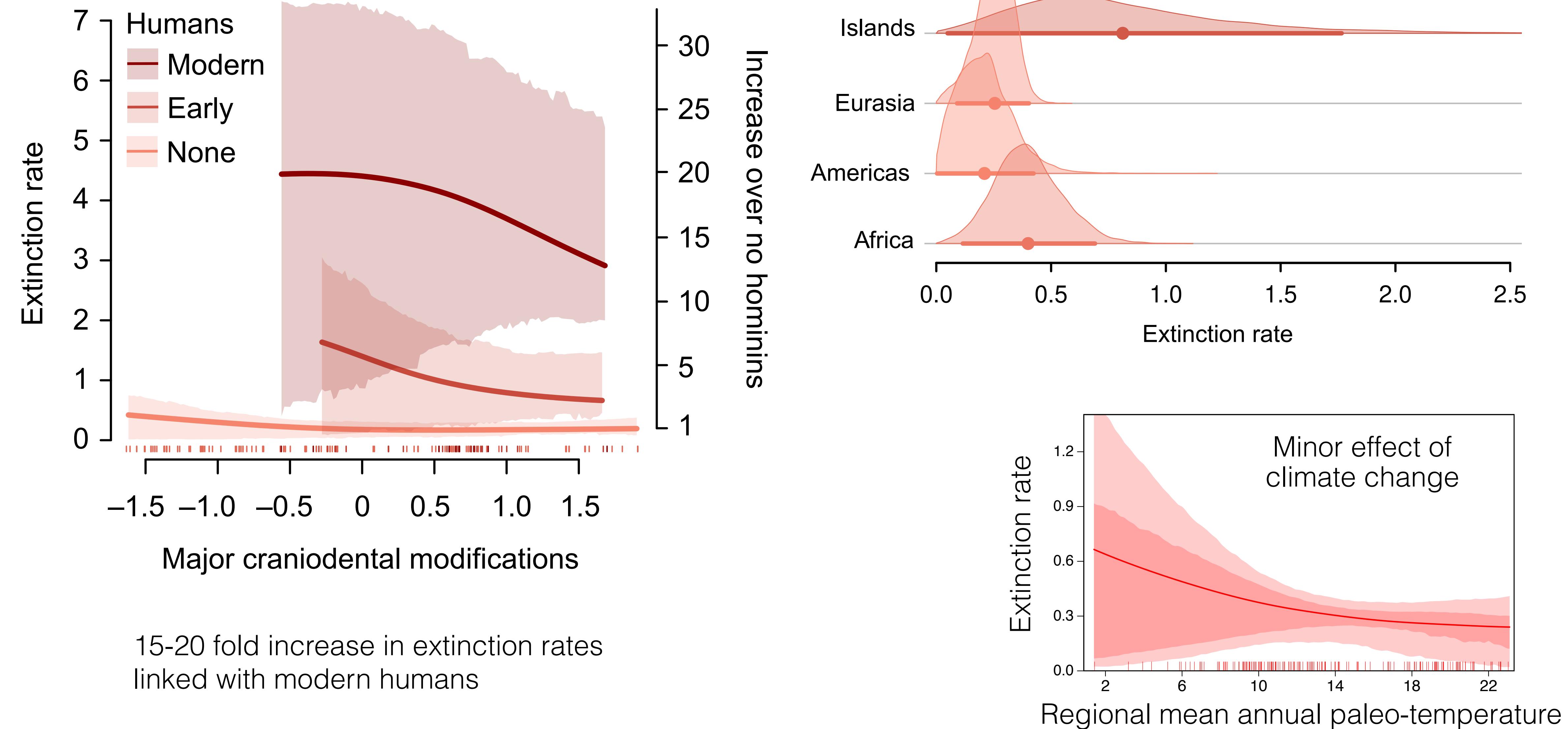


Ecomorphological trait

Speciation rates linked with ecomorphology and biogeography



Extinction rates linked with overlap with humans and biogeography



The BDNN model is available on GitHub (with tutorials)



T Hauffe



The BDNN model

The birth-death neural-network model modulates speciation and extinction rates per lineage and through time as a function of

1. **time**
2. one or multiple **categorical and/or continuous traits** (e.g. diet, body mass, geographic range)
3. one or more **time-dependent variables** (e.g. paleotemperature)
4. **phylogenetic relatedness** (e.g. classification into higher taxa or phylogenetic eigenvectors)

As the function is based on a fully connected feed-forward neural network, it is not based on *a priori* assumptions about its shape. For instance, it can account for non-linear and non-monotonic responses of the rates to variation in the predictors.

It can also account for any interactions among the predictors.

The parameters of the BDNN model are estimated jointly with the origination and extinction times of all taxa and the preservation rates. The output can be used to estimate rate variation through time, across species, and to identify the most important predictors of such variation and their individual or combined effects.

Setting up a BDNN dataset

The BDNN model requires occurrence data in the [standard PyRate format](#). It additionally can use species and time specific data. A table with species-specific trait data can be loaded in the analysis using the `-trait_table` command, while a table with time-series predictors can be loaded using the `-BDNNtimevar` command.

We provide an [example dataset](#) based on [Hauffe et al 2022 MEE](#). This includes genus level occurrence data of northern hemisphere Cenozoic carnivores, a table with a paleotemperature time series, and a table with lineage-specific traits: log-transformed body mass, taxonomic information (family-level classification), and continent of

Is the BDNN a solution to all fossil diversification questions?

The BDNN is data-hungry! (Probably not suitable for poorly sampled fossil clades)

The BDNN is CPU intensive

Formal model testing provides a more direct (arguably) more powerful way to test hypotheses

