

Using **deep learning** for unifying **genomic data** and **traits** in species delimitation

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Introduction

Different **species concepts** - distinct strategies to **identify species boundaries** (de Queiroz 2007). It is important to adopt a **multidisciplinary approach**, by assessing **different sources of evidence** (Carstens et al. 2013).

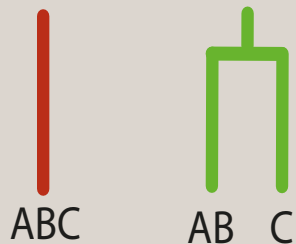
Most approaches consist in analyzing **genomic and phenotypical/geographical information separately**, followed by **visual/qualitative comparison**. Methods that actually **integrate** different data are **limited** to up to a few hundreds of loci and **simple models** of evolution (Solís-Lemus et al. 2015).

We present a method based on **simulated data and deep learning**, that combines both **genomic and trait** information in a unified framework.

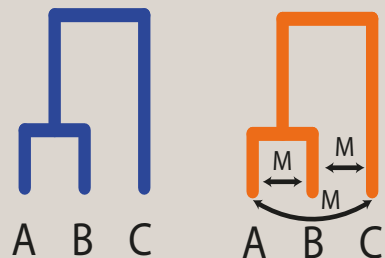
Methods

Simulate SNPs & trees with ms (Hudson 2002)

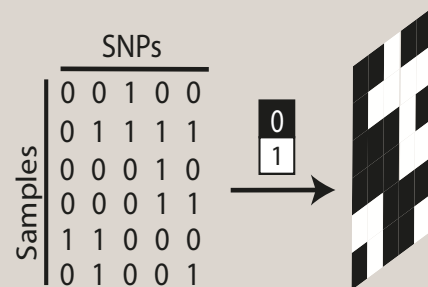
Model 1 Model 2



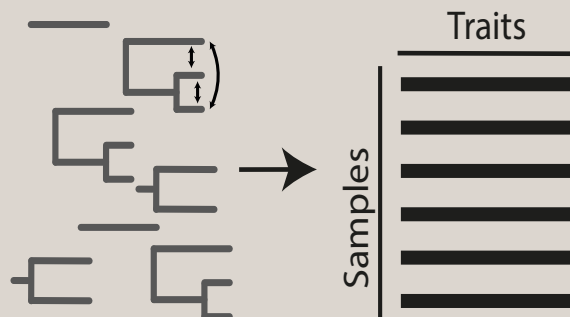
Model 3 Model 4



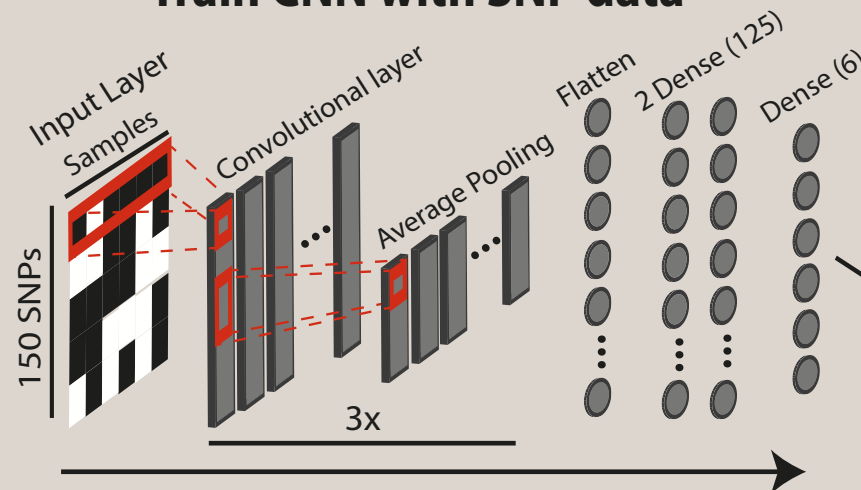
Transform SNPs to image



Simulate traits (discrete, BM and OU) from trees



Train CNN with SNP data



Combine the Dense layers from both networks

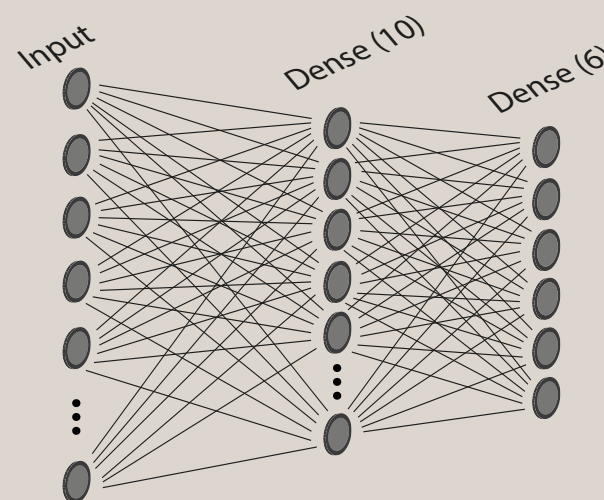
ReLU

Dense (6)

Softmax

Models

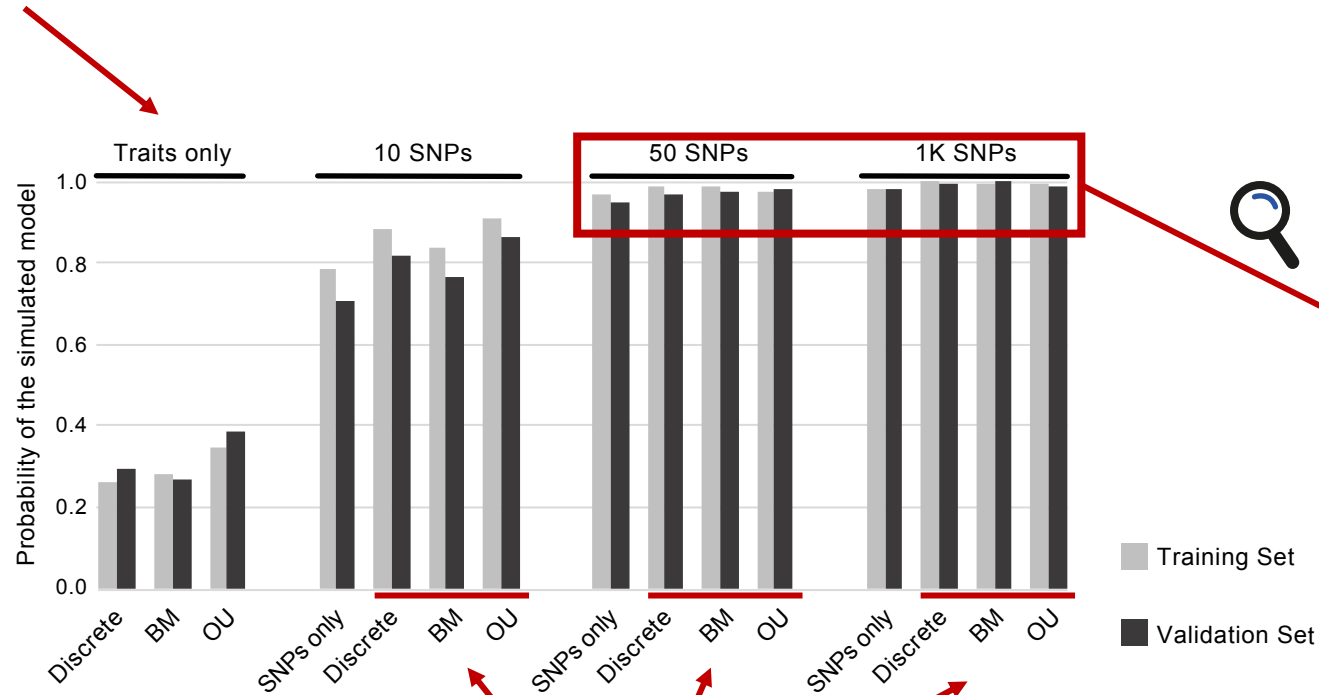
Train MLP with trait data



ReLU

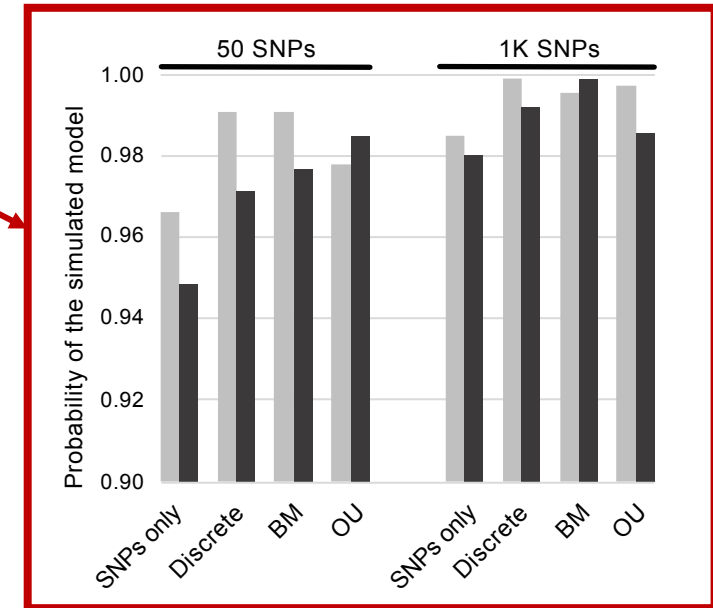
Results

Probabilities are low when using only traits.



Increasing SNPs also raised the probability of recovering the right model.

- little improvement with > 50 SNPs.



Using both genomic and trait data recovered slightly better results than using only SNPs.

Conclusions

The accuracy of our approach was **very high** (confusion matrix with the test set). **Confusion** of model 4 (migration) with model 1 (**one species**).

Incorporating traits resulted in **similar accuracy** to using only SNPs.

Traits incorporate information **complimentary** to genomic data that might be **useful for species delimitation**.

