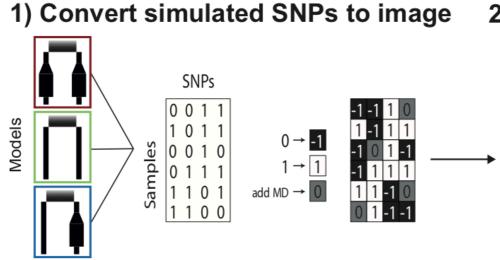
# Redes neuronales como alternativa a modelos probabilísticos en inferencia filogenética

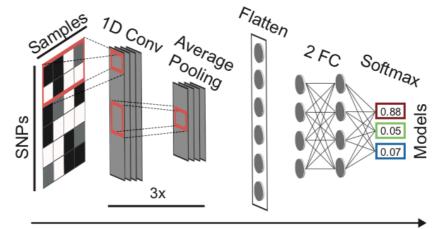
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- **Phylogenetic inference** is considered a **non-polynomial time problem**: e.g., the set or property of problems for which no polynomial-time algorithm is known and for which the only NPalgorithms require a number of steps which grow exponentially with the size of the problem (e.g., MCMC inference).
- Many commonly used models of evolutionary inference have issues with **non-identifiability**: different model parameters induce the same probability distributions and are mathematically or "practically" undistinguishable.
- **Deep learning neural networks** have been proposed as an alternative to likelihood-based approaches to tackle these issues.

# Deep learning in microevolution



#### 2) Train CNN with images from all models

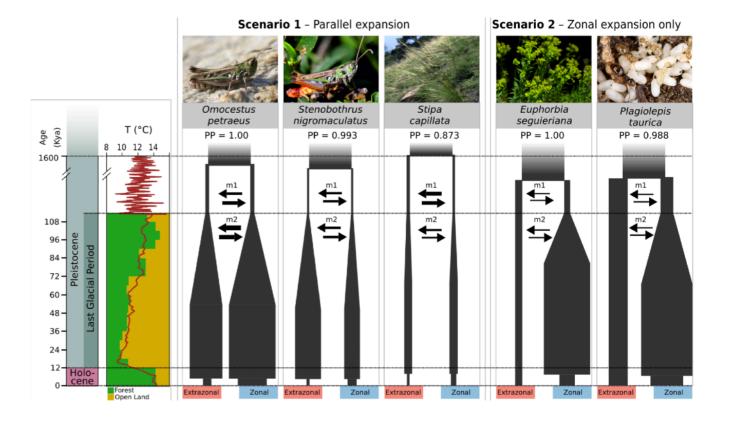


### **Convolutional Neural Network** (CNN) trained with simulated single-site

polymorphism (SNP) genomic data.

**Replaces summary statistics** (ABC): CNN uses **image pattern recognition** to capture site variance/covariance patterns in the data.

**Higher discriminatory** power between "nonidentifiable" demographic models: populations-size bottleneck vs. positive selective sweep; incomplete lineage sorting vs. secondary contact + migration, etc.



### Deep Learning in macroevolution

**Convoluted neural networks (CNN)** trained with simulated diversification scenarios: time trees.

Instead of image recognition, trees are decomposed into **vector information** (nodes, tips, tree height) to capture topology and branch lengths.

**Higher discriminatory** power between "non-identifiable" models of diversity generation: evolutionary stasis + accelerated speciation vs. mass extinction; exponentially increasing extinction vs. diversity-dependence, etc.

