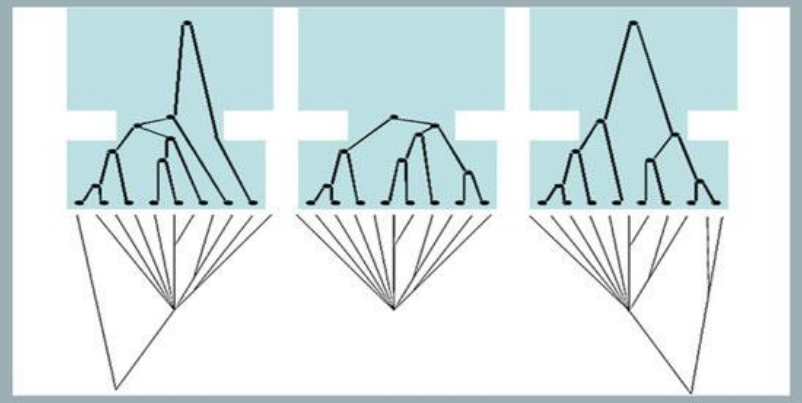

Deep learning methods in population genomics and phylogeography

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sites.google.com/site/manolofperez

Goals

- Conceive and simulate genetic data under competing demographic scenarios 

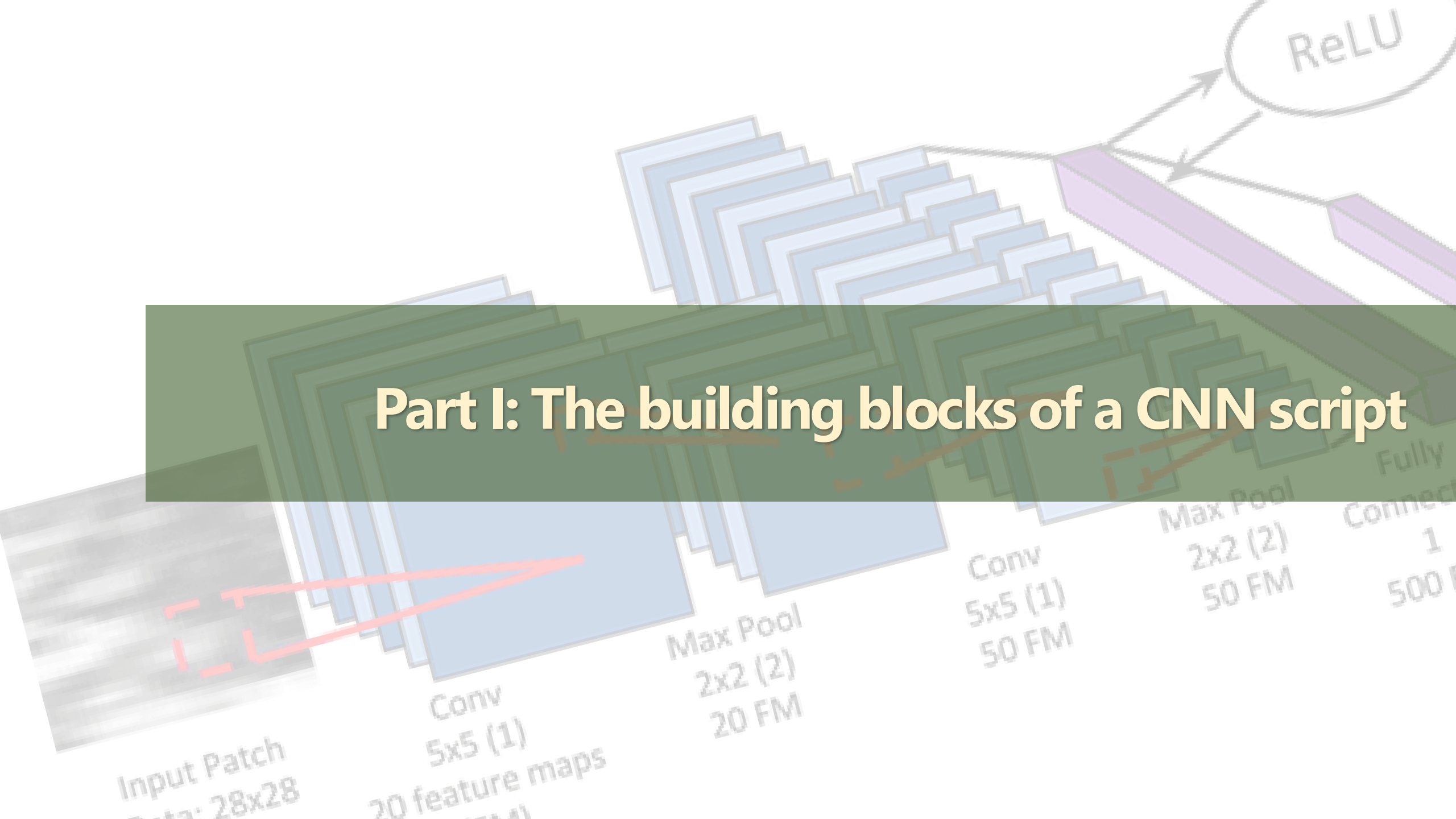
- Understand deep learning background and how a CNN works 

- How to use deep learning to compare demographic scenarios

Program

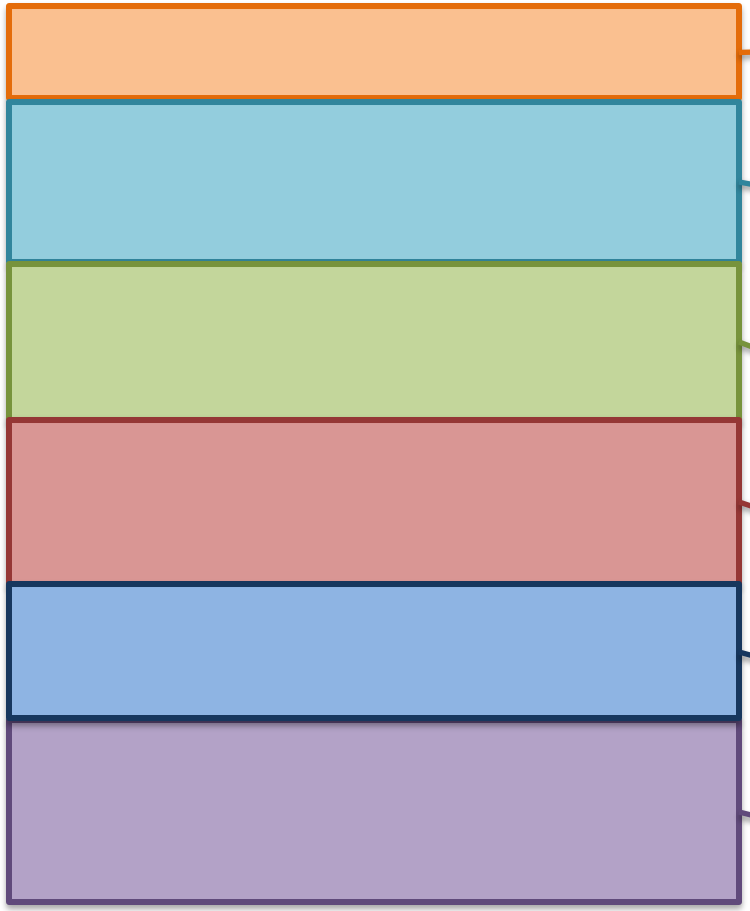
Program

- *Part I: - The building blocks of a CNN script.*
- *Practical: Comparing demographic scenarios with deep learning.*
- *Part II: Quick overview of other applications and future perspectives.*
- *Part III: Wrapup.*



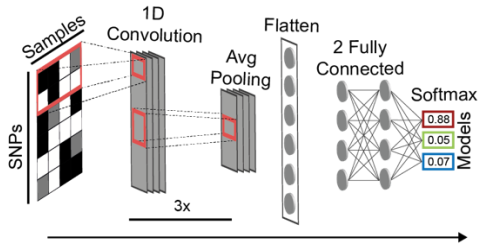
Part I: The building blocks of a CNN script

CNN Script



required python modules.

Define the CNN architecture.



Load and process the training data.

Train the network.

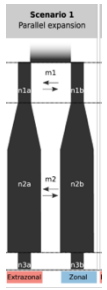
Load the test data and perform cross-validation.

Predict the most likely model for the empirical data

CNN Script

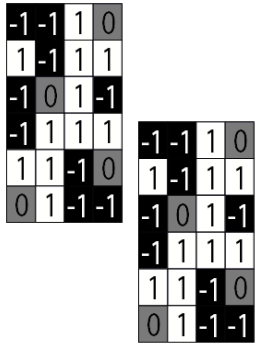
Inputs:

Scenario 1

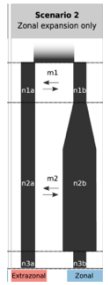


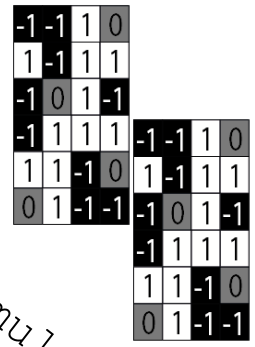
Samples

SNPs

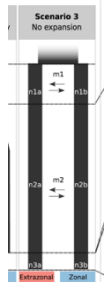


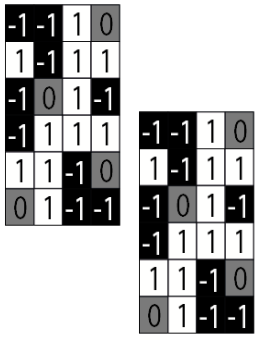
Scenario 2

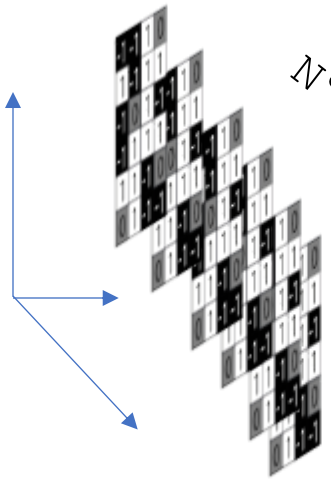




Scenario 3







N° of simulations

3-D Numpy array

Parameters

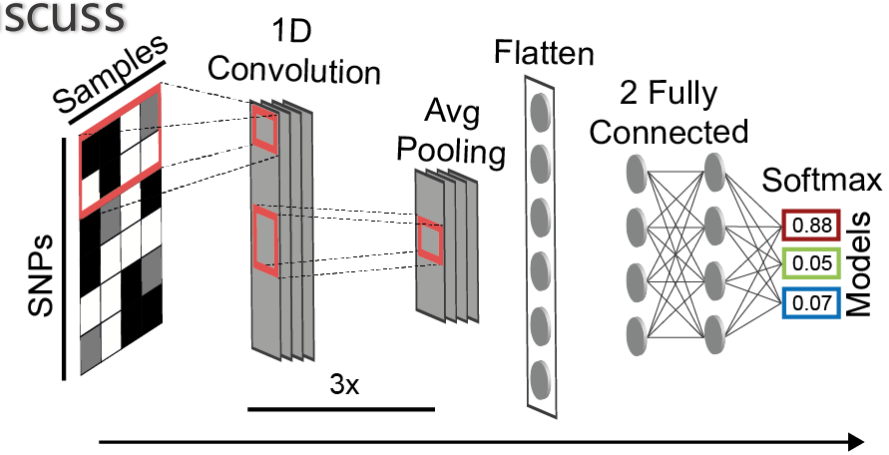
	Theta	T1	T2	T3	Ne
Sim1					
Sim2					
Sim3					
Sim4					

- **Practical Exercise 1:**

- Go through Section 1 of the notebook: https://drive.google.com/file/d/1dA2GWzG5I7m0NbInxtE7-LL_Os0Ytmql/view?usp=sharing

- We will try to recognize all the elements of the network. Do you remember the function of each of those elements? Remember that you can add annotations to the code using # and add information that might help you when you get back to the script in the future.

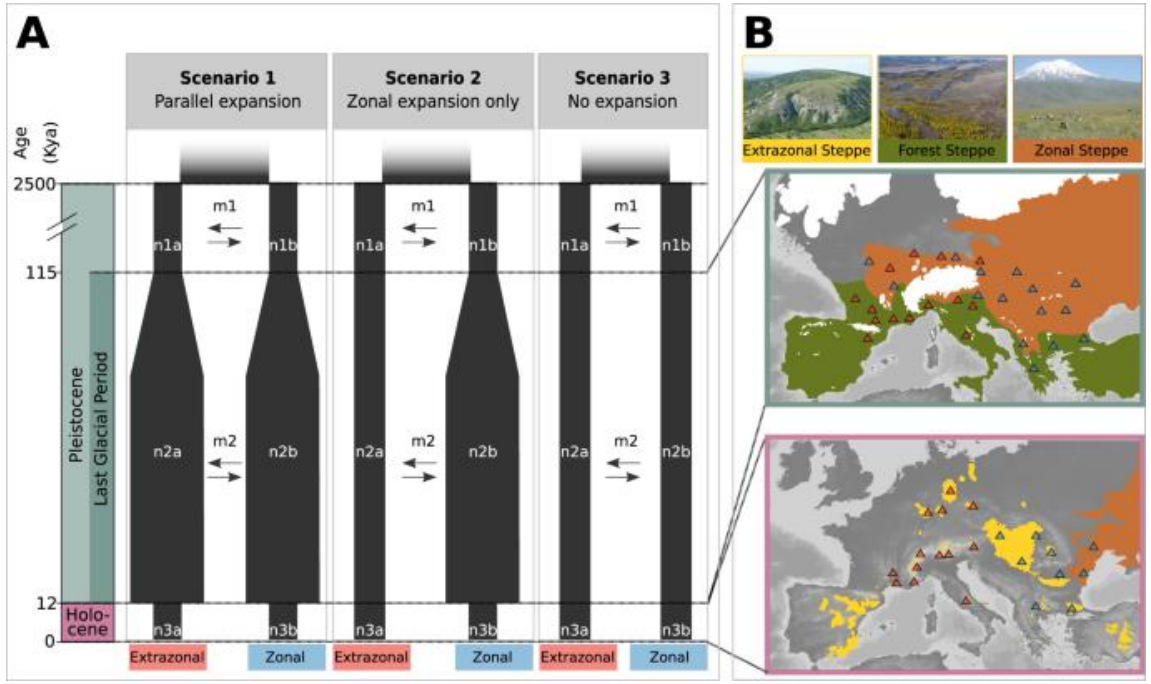
- Now run all the cells until you reach the end of section 2. Your network will be training, so now we will have some time to discuss and do a quick review on the CNN elements.

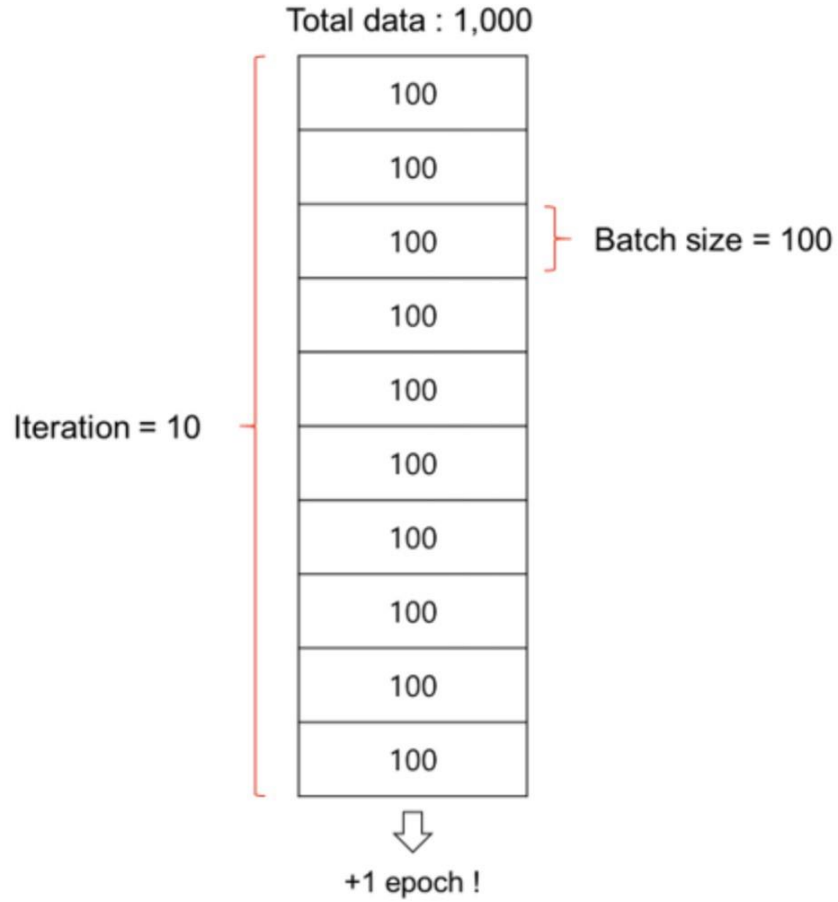


CNN Script

```
# Define parameters for the CNN run.
batch_size = 128
### how much interations to train the network
epochs = 50

###n of models
num_classes = 3
```



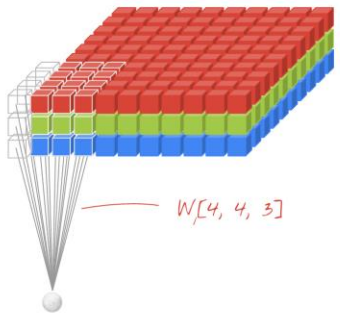


https://jerryan.medium.com/batch-size-a15958708a6

Kirschner et al. (2022) *Nat Comm*

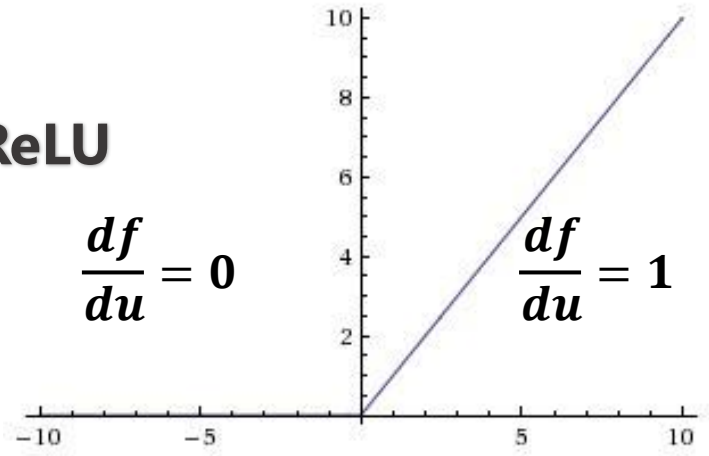
CNN Script

```
# Define the CNN architecture.
def create_cnn(xtest):
  inputShape = (xtest.shape[1], xtest.shape[2])
  ## image size. images need to have EXACTLY the same size
  inputs = Input(shape=inputShape)
  x = inputs
  ## 1D convolution - less computational intensive and is also invariant to the samples order;
  x = Conv1D(256, kernel_size=2, activation='relu',input_shape=(xtest.shape[1], xtest.shape[2]))(x)
  ### Enables the network to learn more complex features / shapes.
  x = AveragePooling1D(pool_size=2)(x)
  x = BatchNormalization()(x)
```



ReLU

$$\frac{df}{du} = 0 \qquad \frac{df}{du} = 1$$



https://www.kaggle.com/code/dansbecker/rectified-linear-units-relu-in-deep-learning/notebook

Kirschner et al. (2022) *Nat Comm*

CNN Script

```
# Define the CNN architecture.
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```

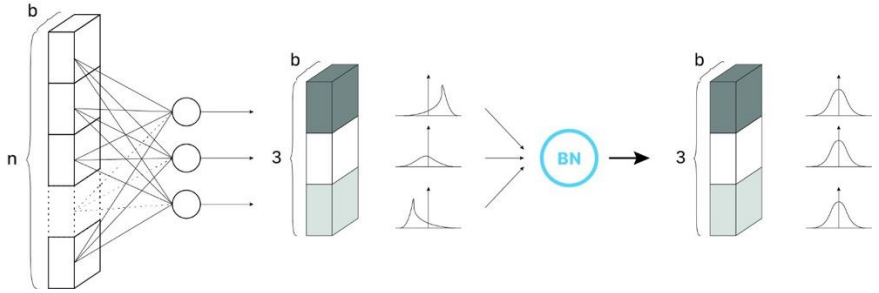

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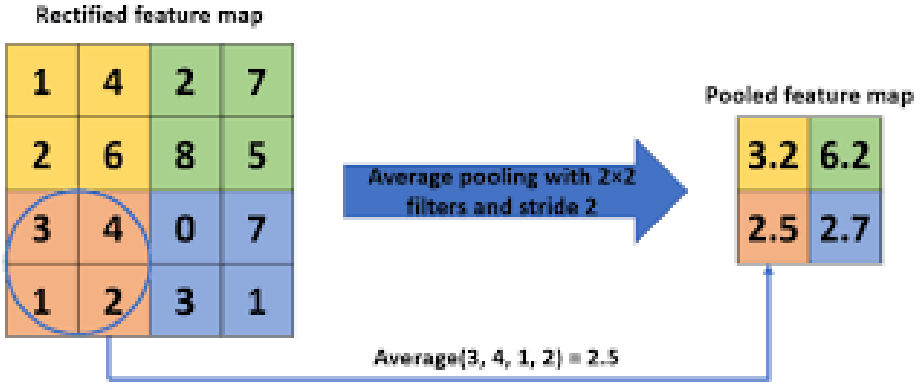
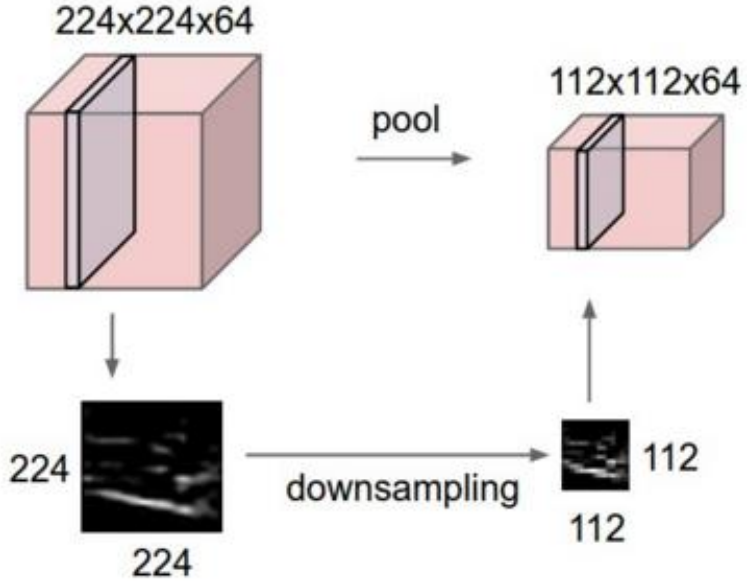




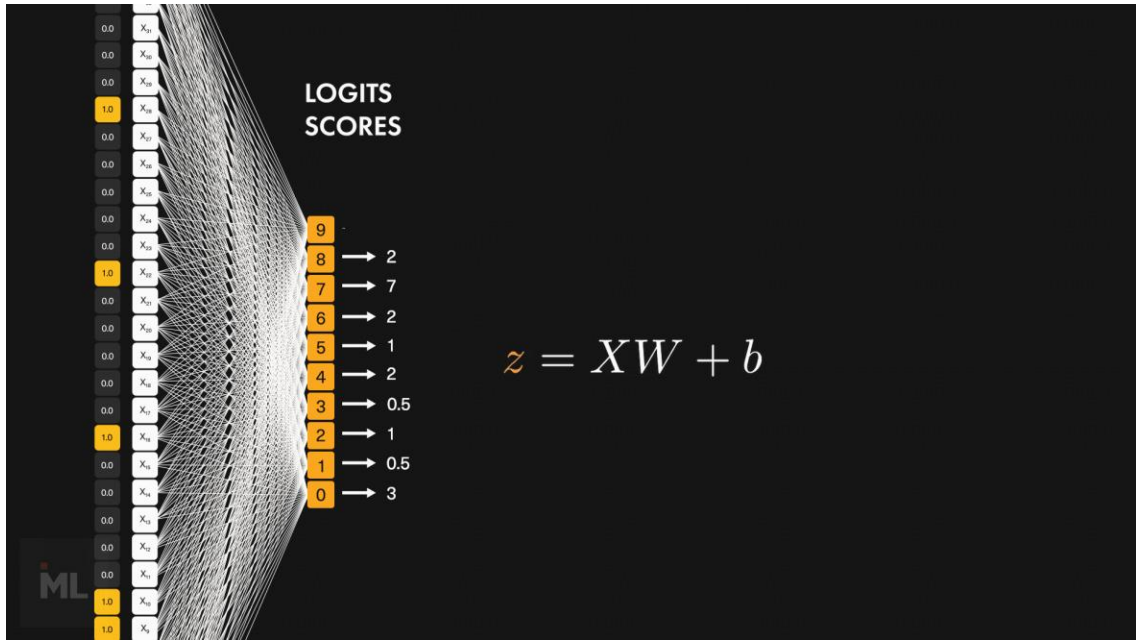
https://leonardoaraujosantos.gitbook.io/artificial-inteligence/machine_learning/deep_learning/pooling_layer

Gholamalinezhad & Khosravi (2020) *arXiv*

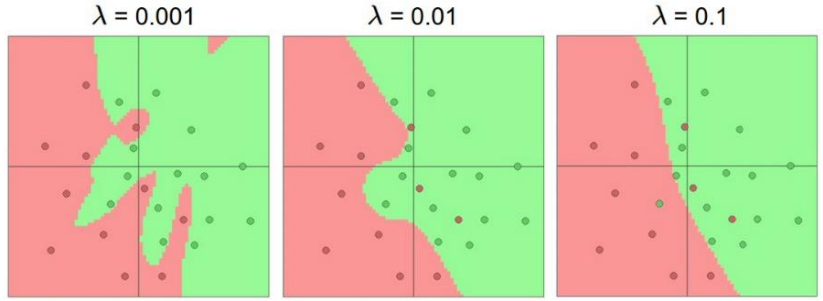
Kirschner et al. (2022) *Nat Comm*

CNN Script

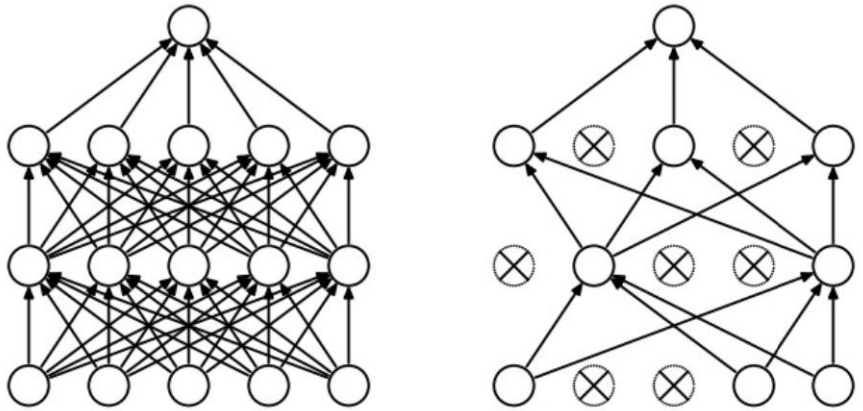
```
### Linearising the image as in the initial step.
x = Flatten()(x)
x = Dense(128, activation='relu')(x)
x = Dropout(0.5)(x)
x = Dense(128, activation='relu')(x)
x = Dropout(0.5)(x)
x = Dense(num_classes, activation="softmax")(x)
```



Regularization



Options:



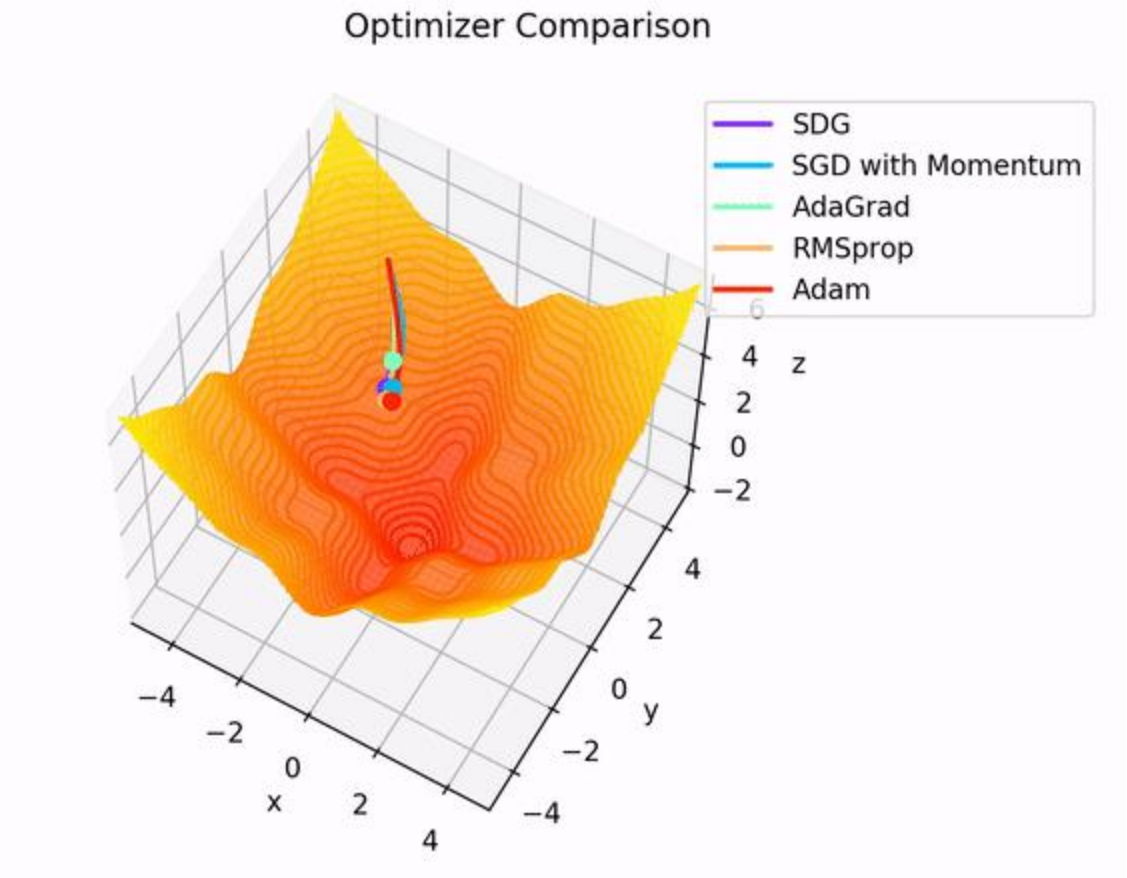
(a) Standard Neural Net

(b) After applying dropout.

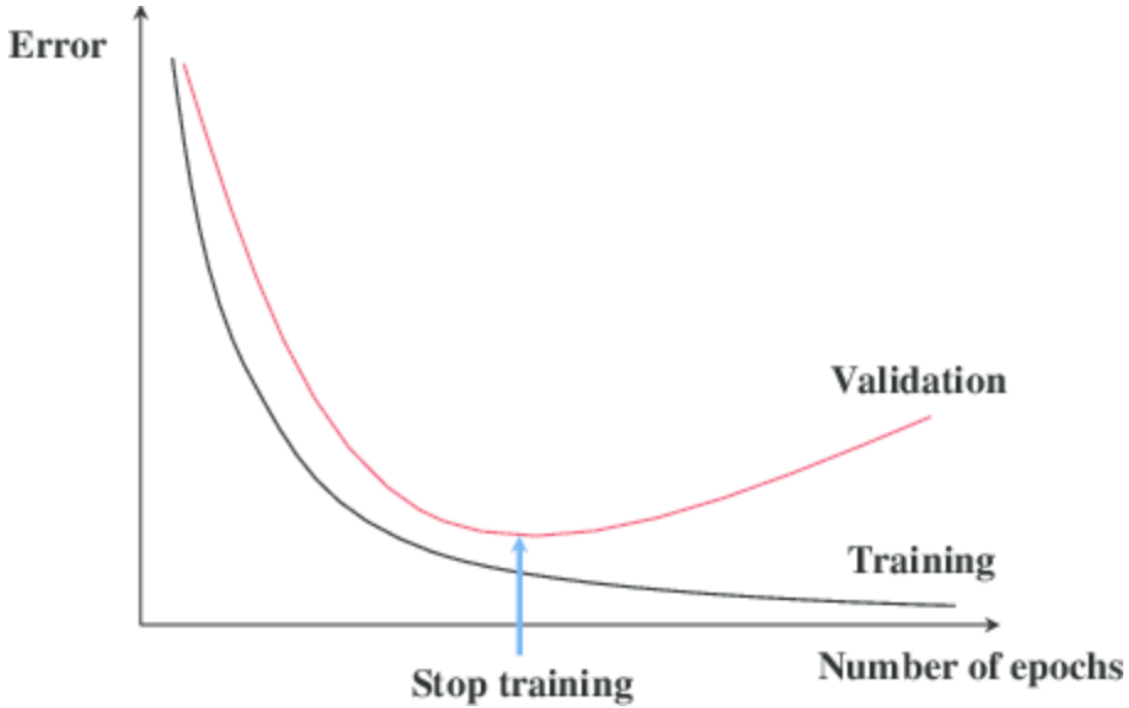
CNN Script

```
# Compile the CNN.
model.compile(loss=keras.losses.categorical_crossentropy,
                optimizer='Adam',
                metrics=['accuracy'])

# We will use early stopping and save the model with the best val_accuracy.
earlyStopping = EarlyStopping(monitor='val_accuracy', patience=25, verbose=0, mode='max', restore_best_weights
### stop training when validation error increases (wait 25 epochs to see if there is any improvement).
```



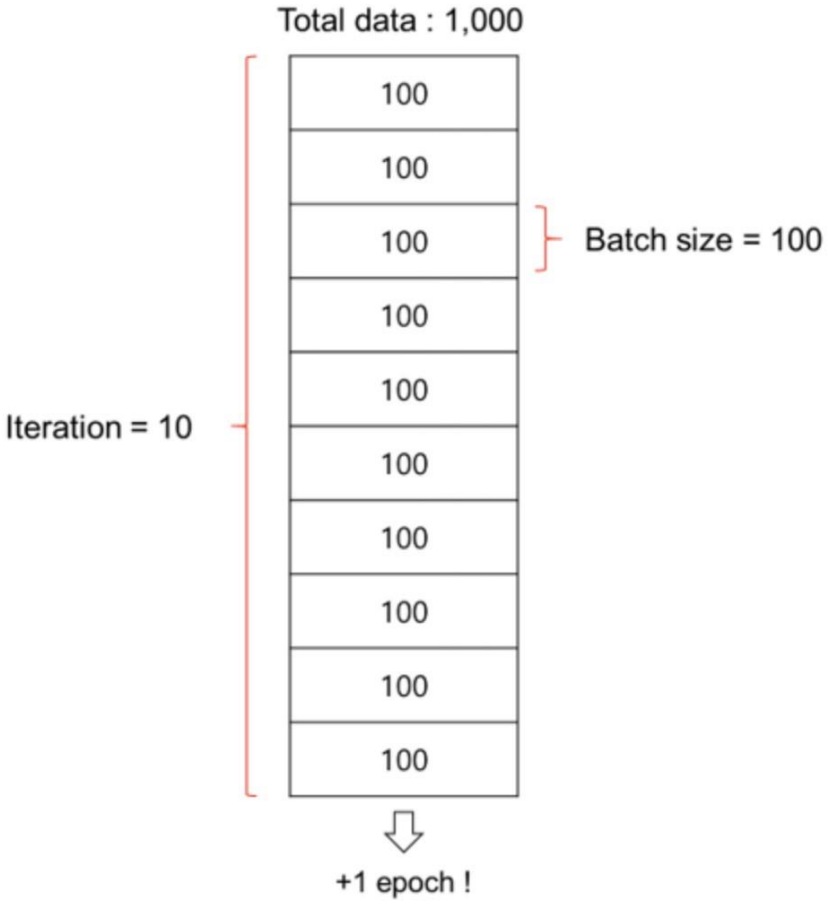
https://towardsdatascience.com/complete-guide-to-adam-optimization-1e5f29532c3d

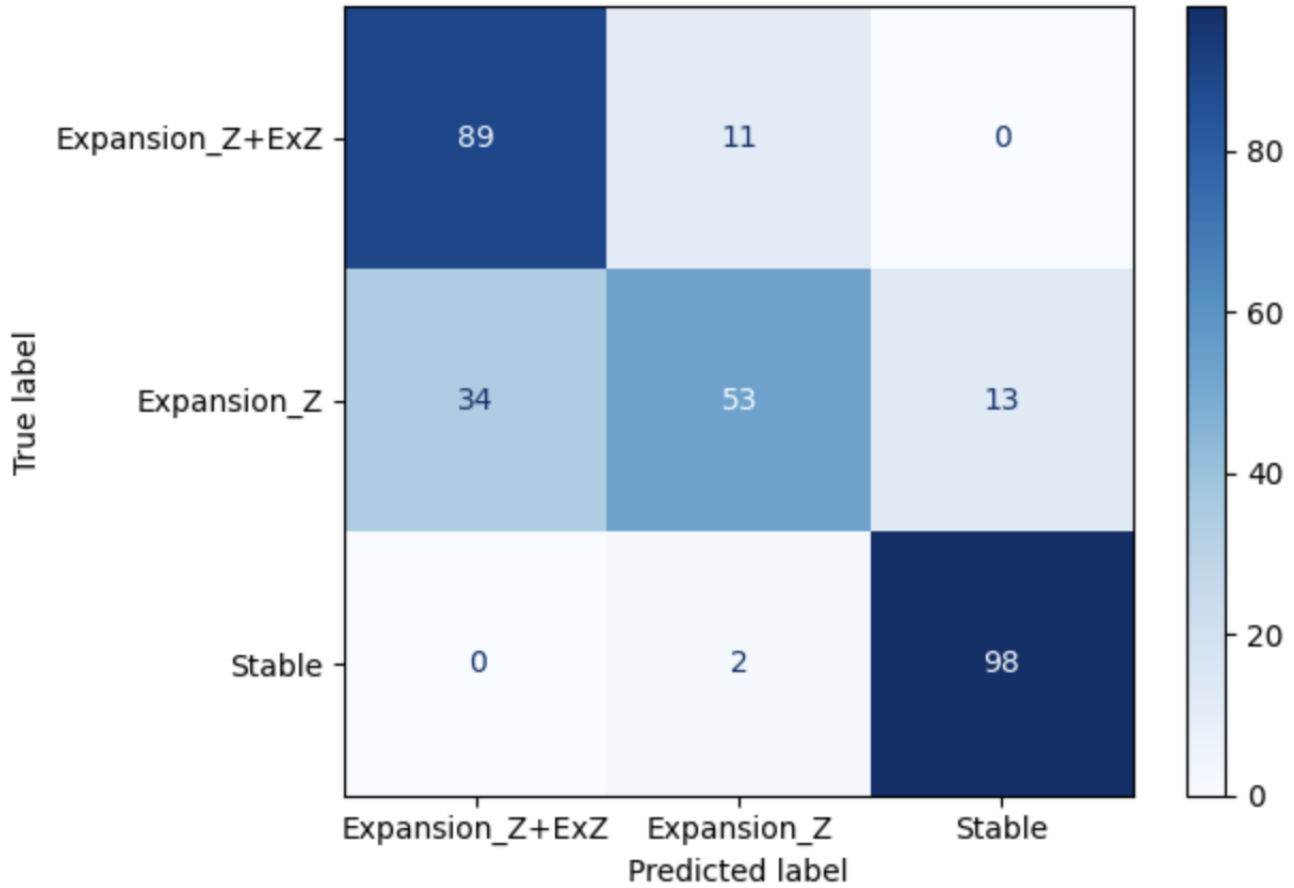


https://towardsdatascience.com/a-practical-introduction-to-early-stopping-in-machine-learning-550ac88bc8fd

CNN Script

```
#Run the CNN
history = model.fit(xtrain, ytrain, batch_size=batch_size,
          epochs=epochs,
          verbose=1,
          validation_data=(xval, yval),callbacks=[earlyStopping])
```





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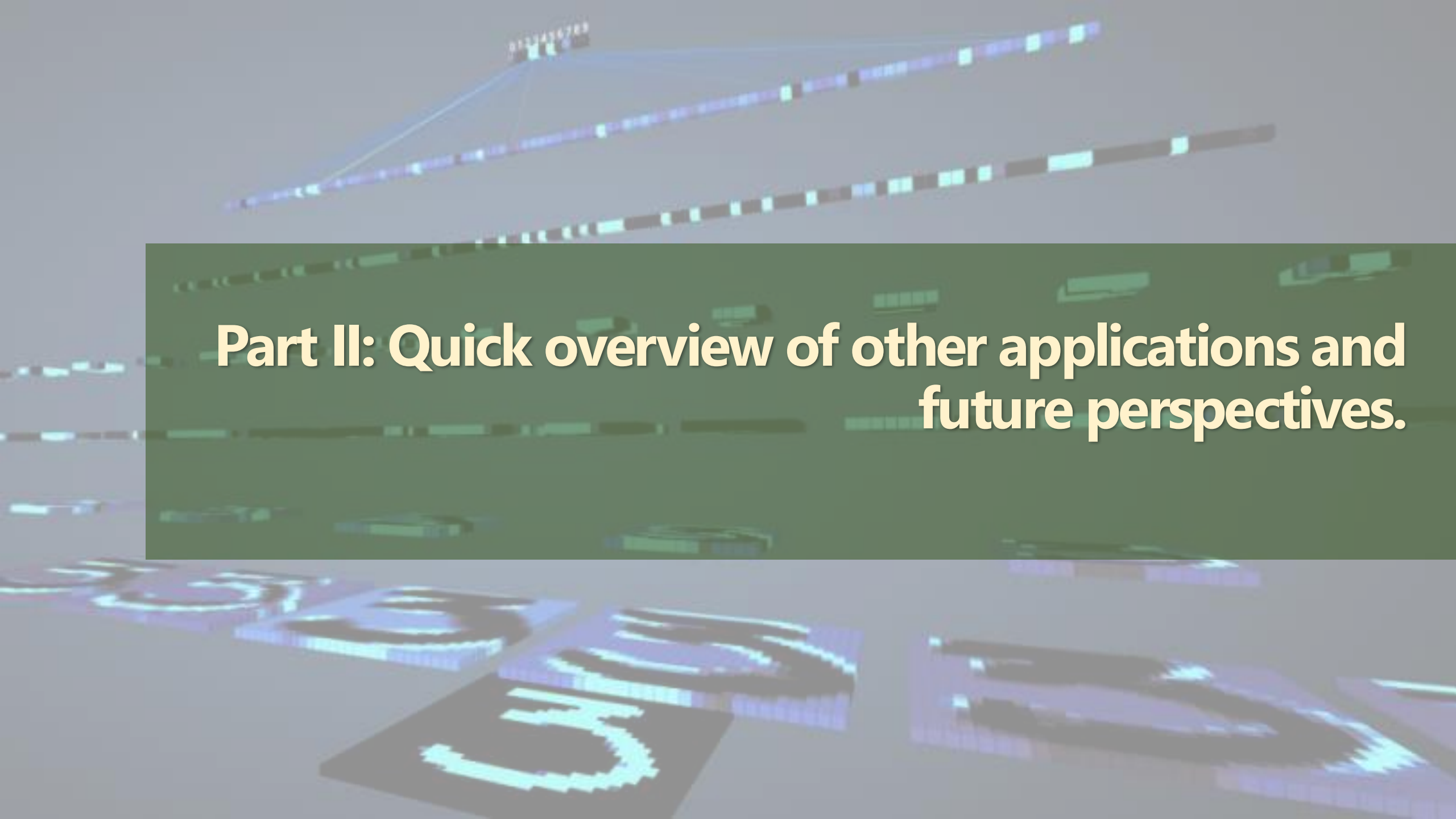


Part II: Quick overview of other applications and future perspectives.

GBE

Deep Learning in Population Genetics

Kevin Korfmann[1], Oscar E. Gaggiotti[2], and Matteo Fumagalli [3,*]

[1]Professorship for Population Genetics, Department of Life Science Systems, Technical University of Munich, Germany
[2]Centre for Biological Diversity, Sir Harold Mitchell Building, University of St Andrews, Fife KY16 9TF, UK
[3]Department of Biological and Behavioural Sciences, Queen Mary University of London, UK

*Corresponding author: E-mail: m.fumagalli@qmul.ac.uk.

Accepted: 16 January 2023

The Unreasonable Effectiveness of Convolutional Neural Networks in Population Genetic Inference

Lex Flagel,[1,2] Yaniv Brandvain,[2] and Daniel R. Schrider*[,3]
[1]Monsanto Company, Chesterfield, MO
[2]Department of Plant and Microbial Biology, University of Minnesota, St. Paul, MN
[3]Department of Genetics, University of North Carolina, Chapel Hill, NC

***Corresponding author:** E-mail: drs@unc.edu.

Associate editor: Yuseob Kim

Review Article | Published: 04 September 2023

Harnessing deep learning for population genetic inference

Xin Huang, Aigerim Rymbekova, Olga Dolgova, Oscar Lao & Martin Kuhlwilm

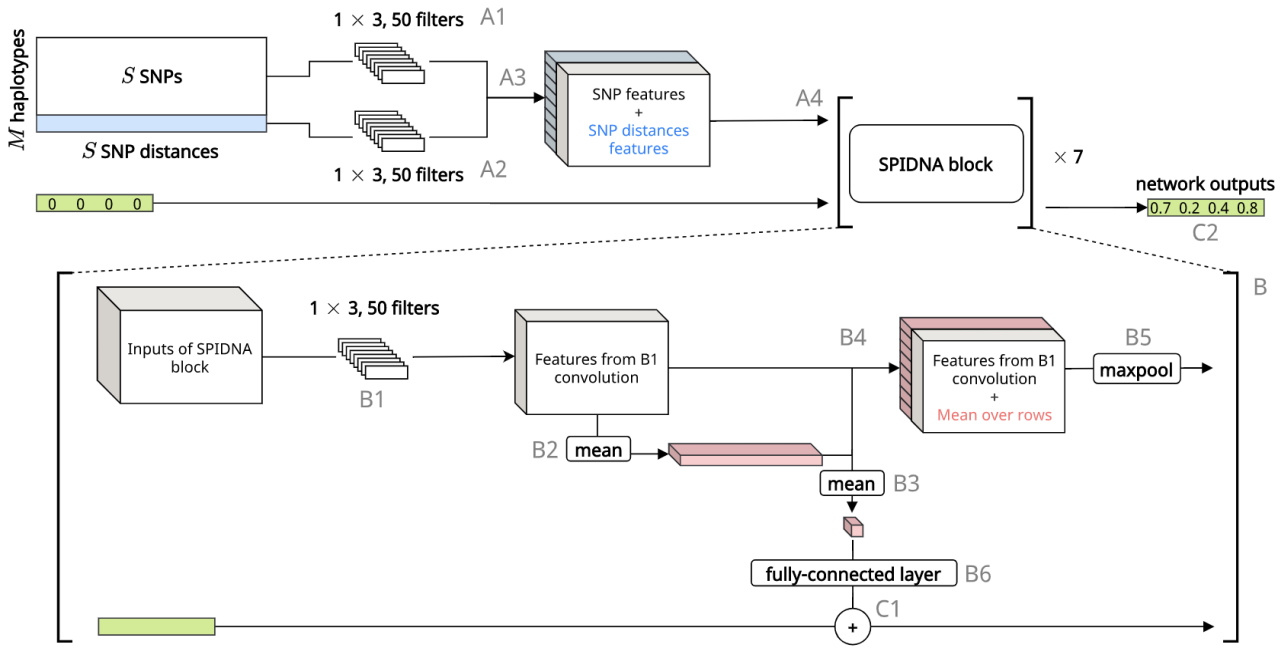
Nature Reviews Genetics **25**, 61–78 (2024) | Cite this article

SPECIAL ISSUE ARTICLE

MOLECULAR ECOLOGY RESOURCES WILEY

Deep learning for population size history inference: Design, comparison and combination with approximate Bayesian computation

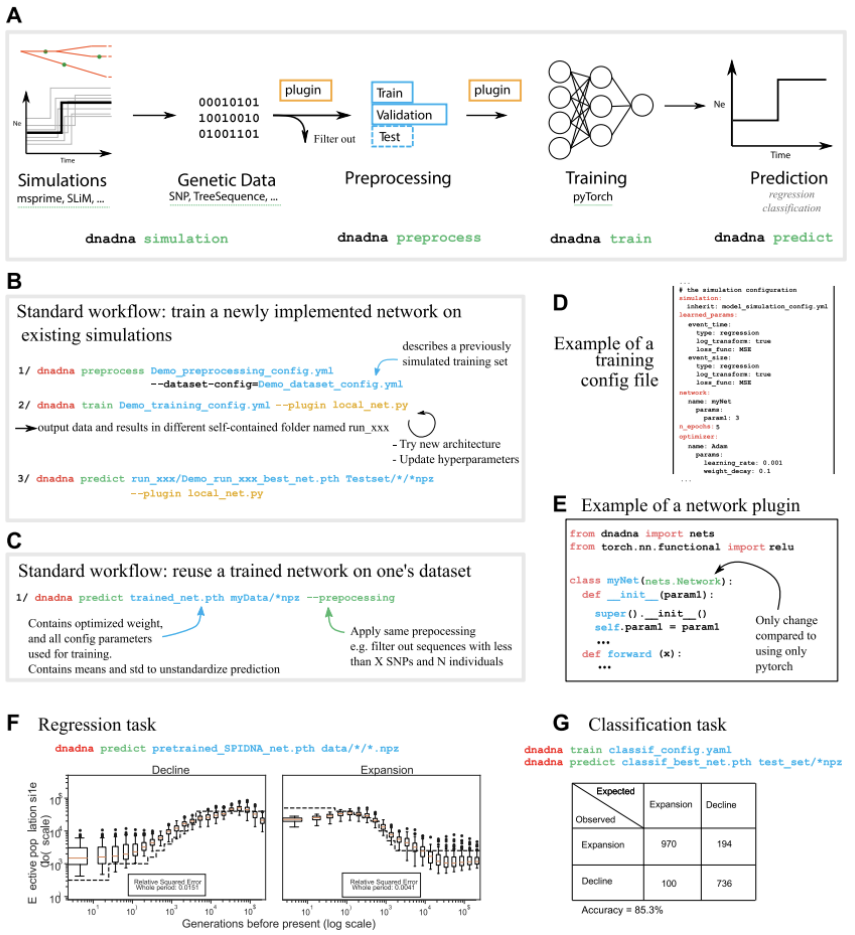
Théophile Sanchez | Jean Cury | Guillaume Charpiat | Flora Jay



Genetics and population analysis

dnadna: a deep learning framework for population genetics inference

Théophile Sanchez[1†], Erik Madison Bray[1†], Pierre Jobic[1,2], Jérémy Guez[1,3], Anne-Catherine Letournel[1], Guillaume Charpiat[1], Jean Cury[1,4*‡] and Flora Jay[1*‡]

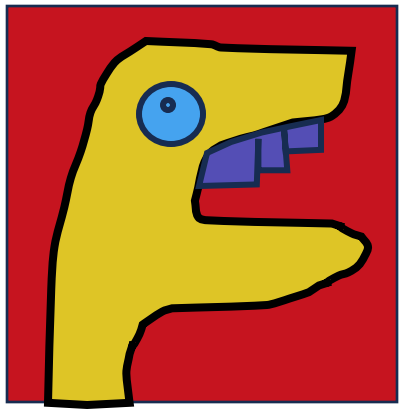


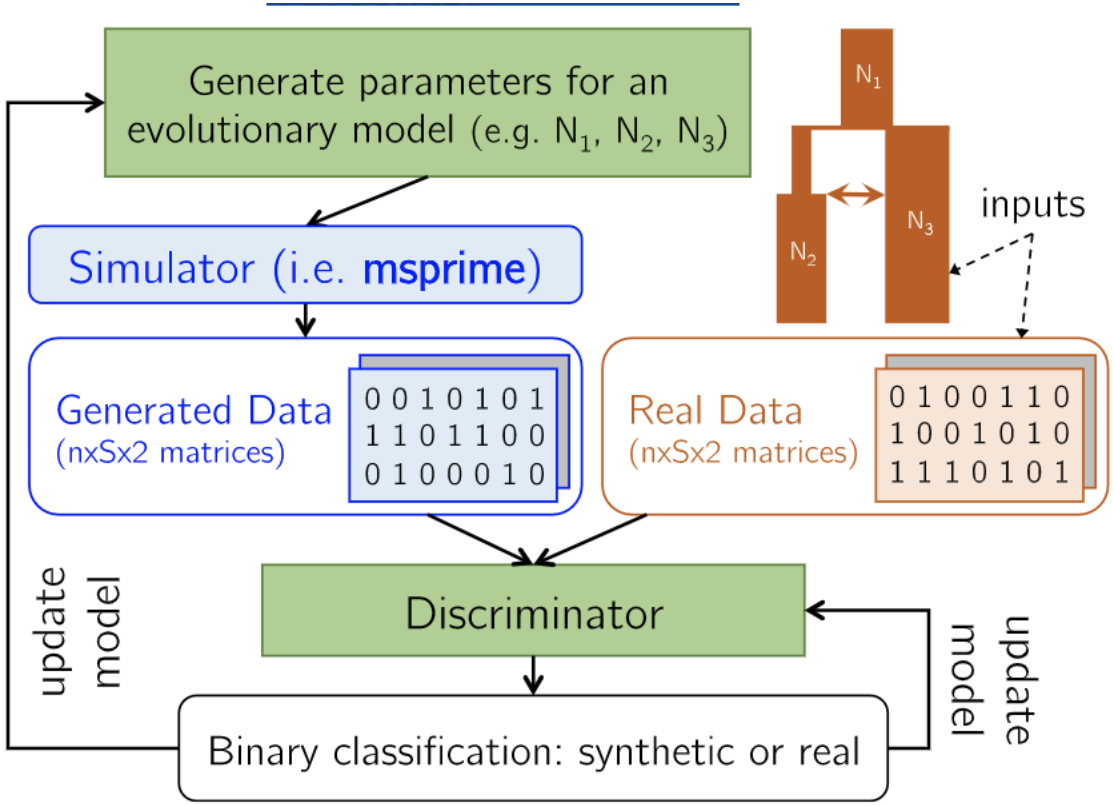
SPECIAL ISSUE

MOLECULAR ECOLOGY RESOURCES WILEY

Automatic inference of demographic parameters using generative adversarial networks

Zhanpeng Wang[1] | Jiaping Wang[1] | Michael Kourakos[2] | Nhung Hoang[2] | Hyong Hark Lee[2] | Iain Mathieson[3] | Sara Mathieson[1]





SPECIAL ISSUE

MOLECULAR ECOLOGY RESOURCES WILEY

Automatic inference of demographic parameters using generative adversarial networks

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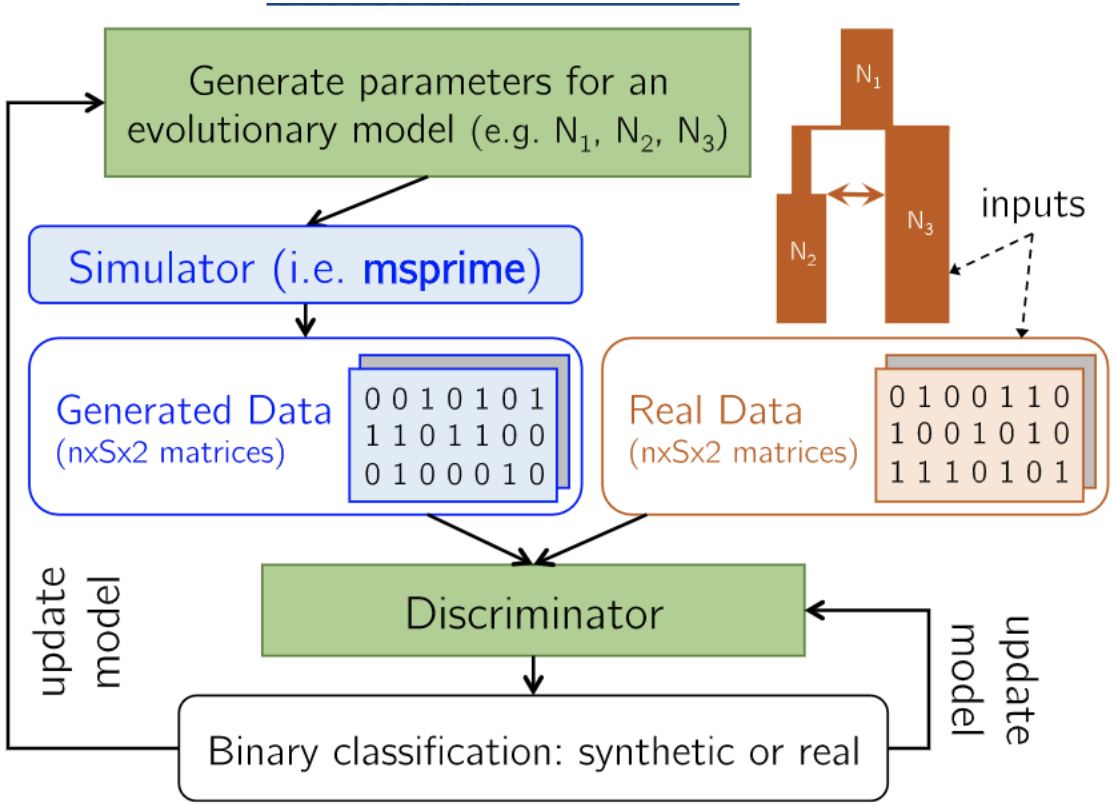
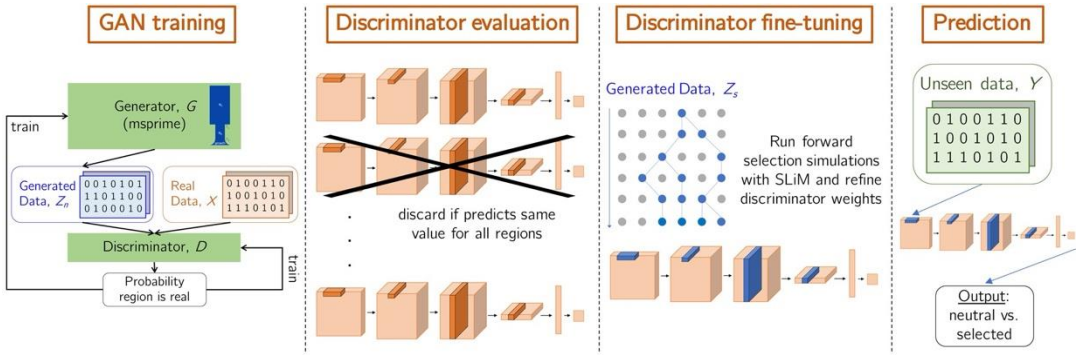
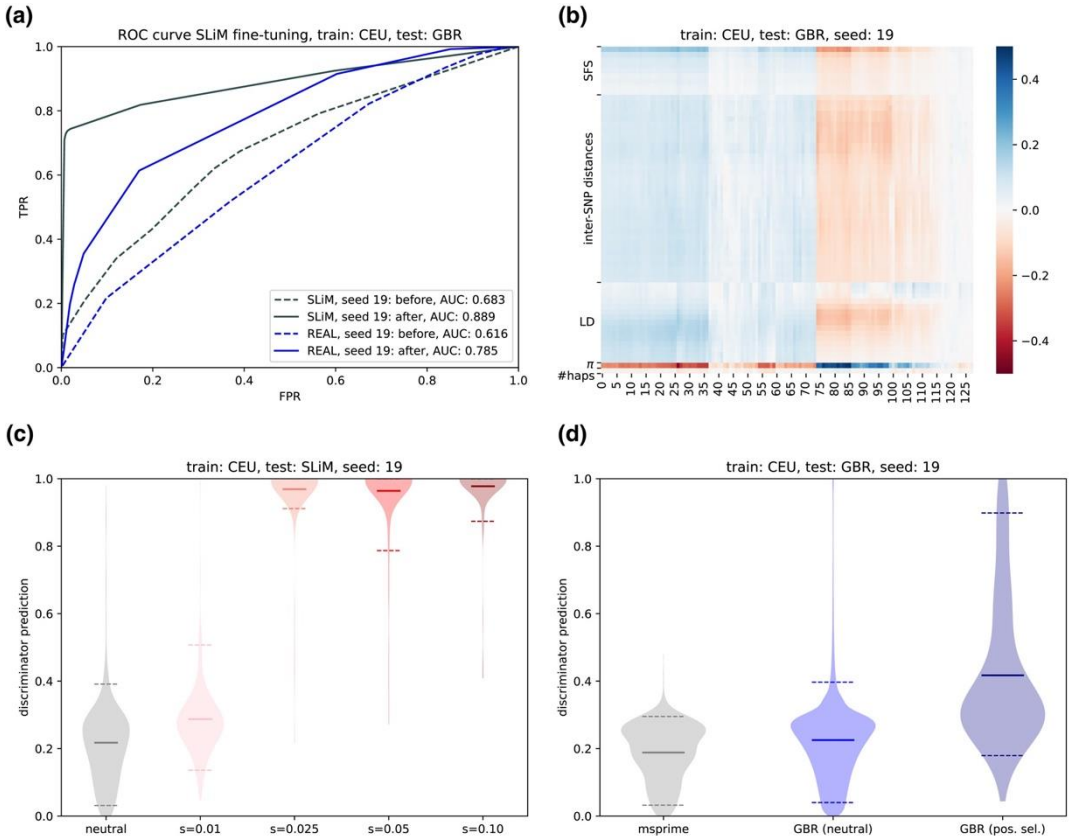


Neural Network for Genomic data





Riley et al (2024) *Genetics*

Peer Community Journal

Section: Evolutionary Biology

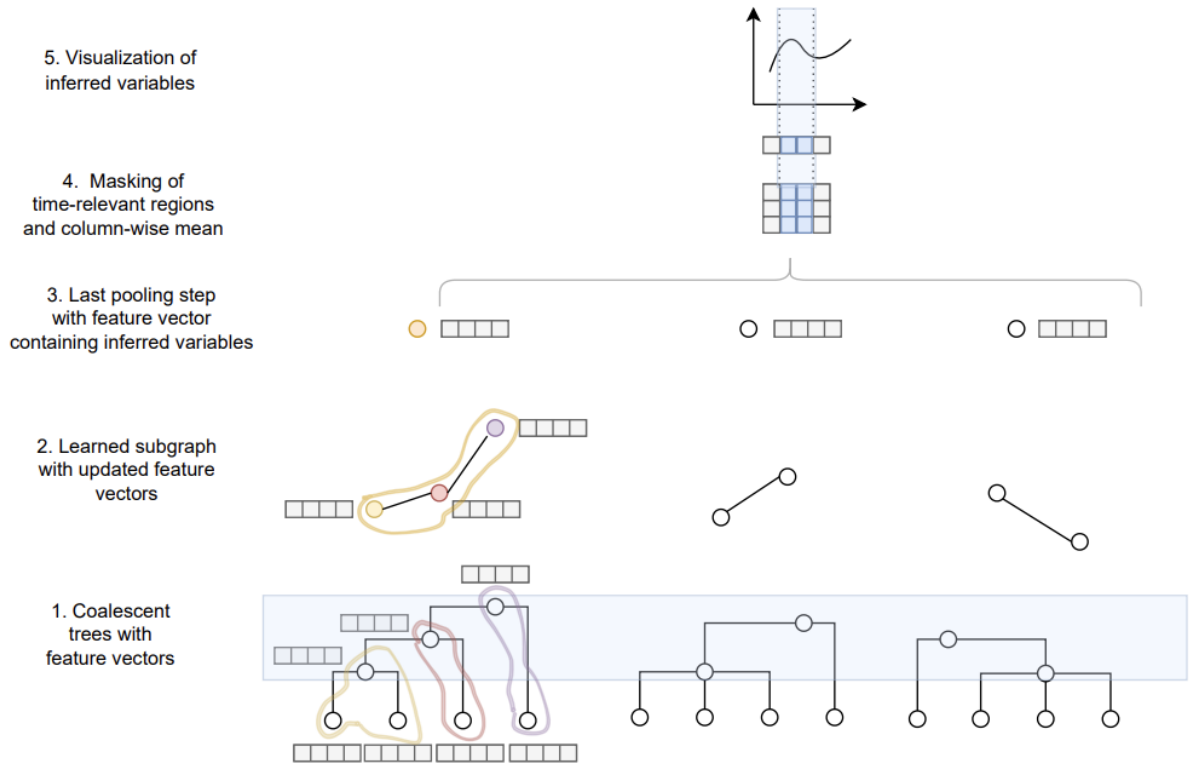
Research article

Published
2024-03-18

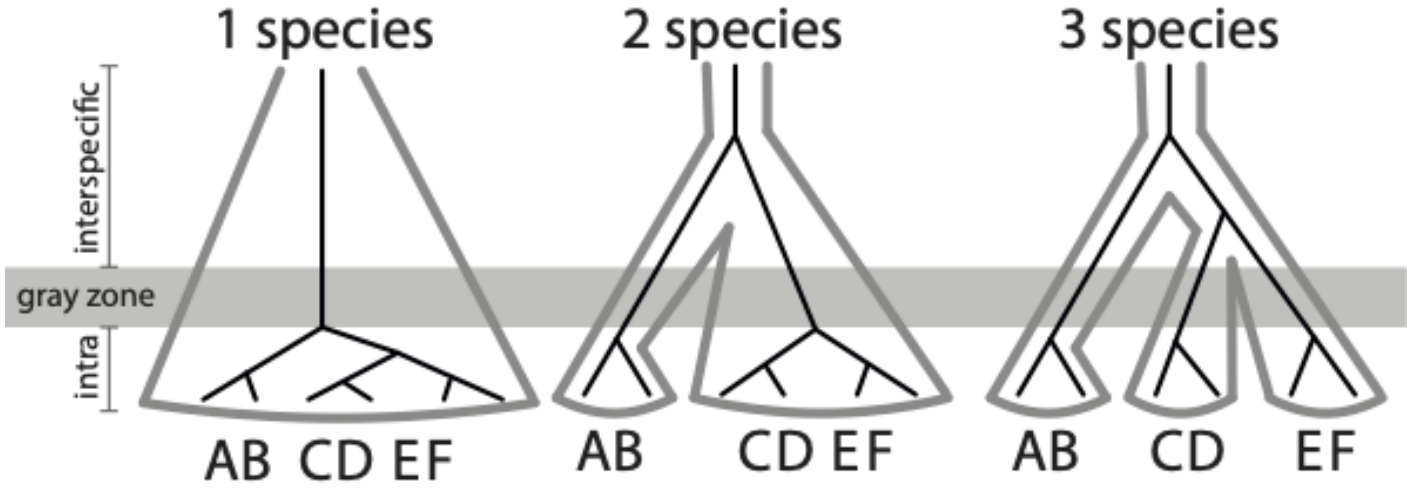
Cite as
Kevin Korfmann, Thibaut Paul Patrick Sellinger, Fabian Freund, Matteo Fumagalli and Aurélien Tellier (2024) *Simultaneous Inference of Past Demography and Selection from the Ancestral Recombination Graph under the Beta Coalescent*, Peer Community Journal, 4: e33.

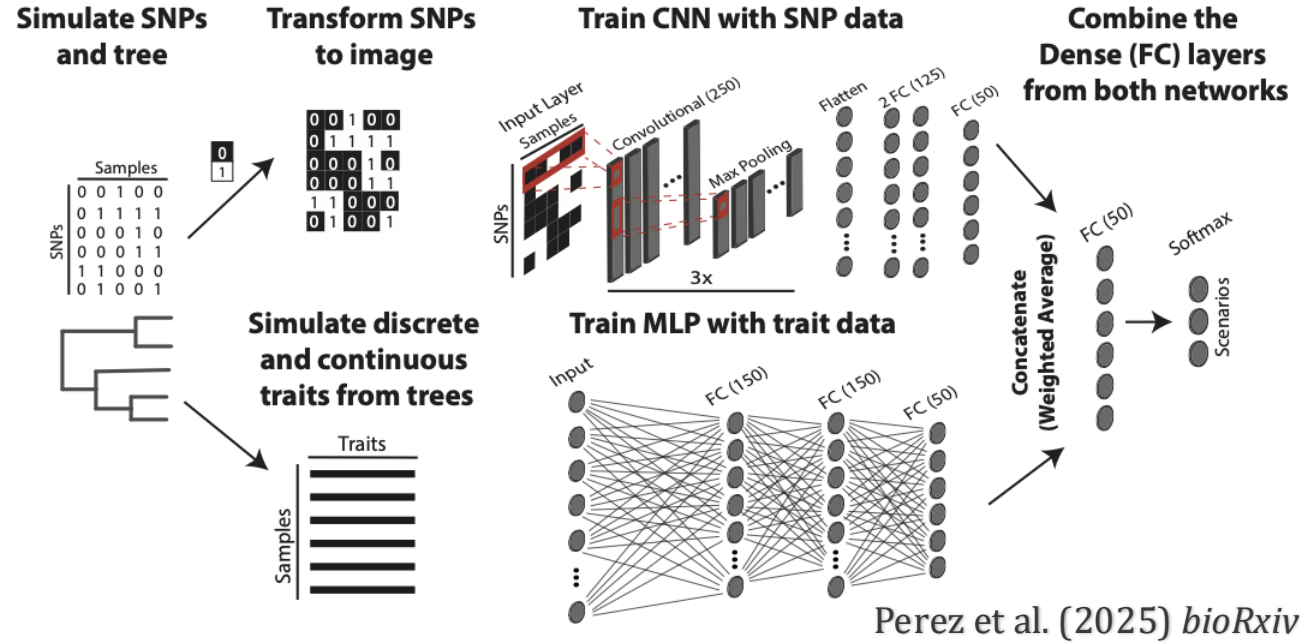
Simultaneous Inference of Past Demography and Selection from the Ancestral Recombination Graph under the Beta Coalescent

Kevin Korfmann [#,1], Thibaut Paul Patrick Sellinger [#,2,1], Fabian Freund [3,4], Matteo Fumagalli [5,6], and Aurélien Tellier [1]



Integrative Deep Learning species delimitation



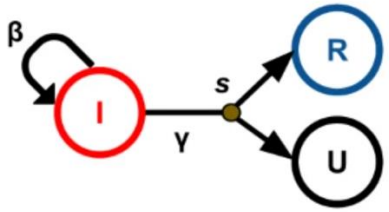


Perez et al. (2025) *bioRxiv*

Deep Learning for **phylodynamics** and **macroevolution**

Perez & Gascuel (2025) *bioRxiv*

BD



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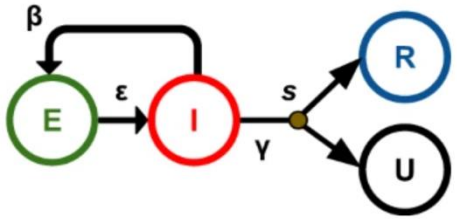

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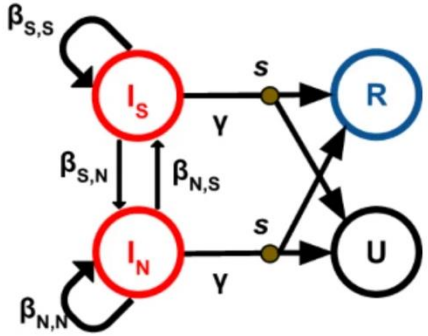
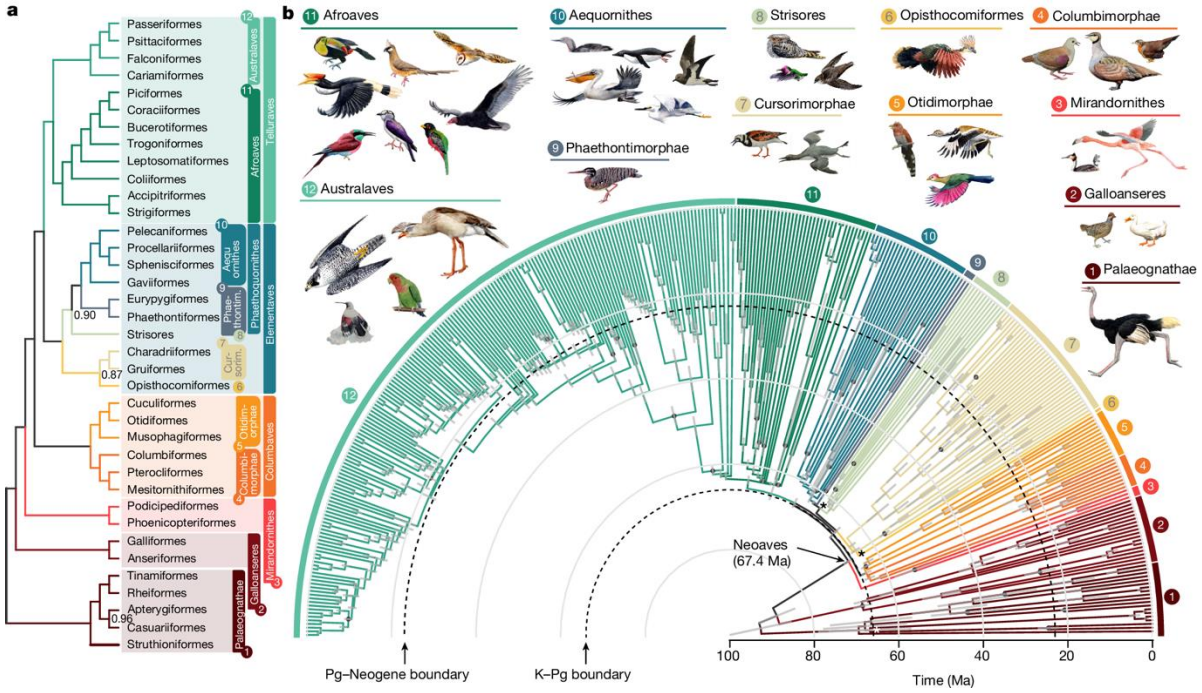
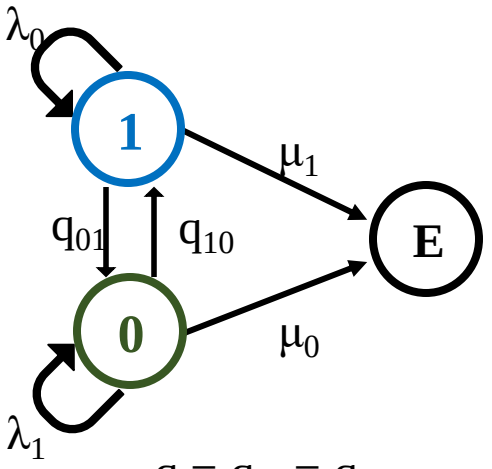


Voznica et al. (2022) Nat Comm

Stiller et al 2024 Nature





$q = q_{01} = q_{10}$

$\varepsilon = \mu_0 / \lambda_0 = \mu_1 / \lambda_1$

Perez et al. (2025) *bioRxiv*

What's next?

Part III: Wrapup.

Goals

- Conceive and simulate genetic data under competing demographic scenarios 

- Understand deep learning background and how a CNN works 

- How to use deep learning to compare demographic scenarios