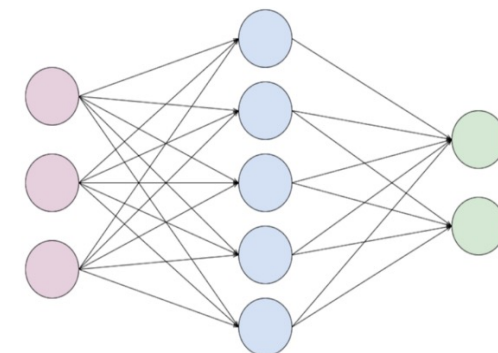
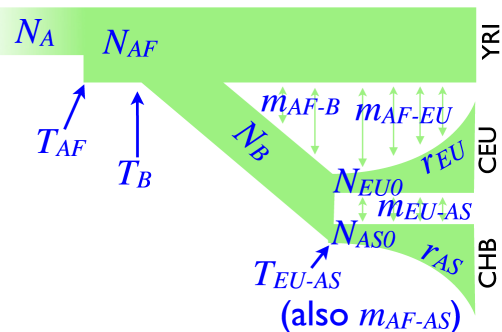


Computationally Efficient Demographic Inference with

Supervised Machine Learning



Linh N. Tran, Connie Sun, Mathews Sajan, Ryan Gutenkunst

University of Arizona

SMBE everywhere GS2

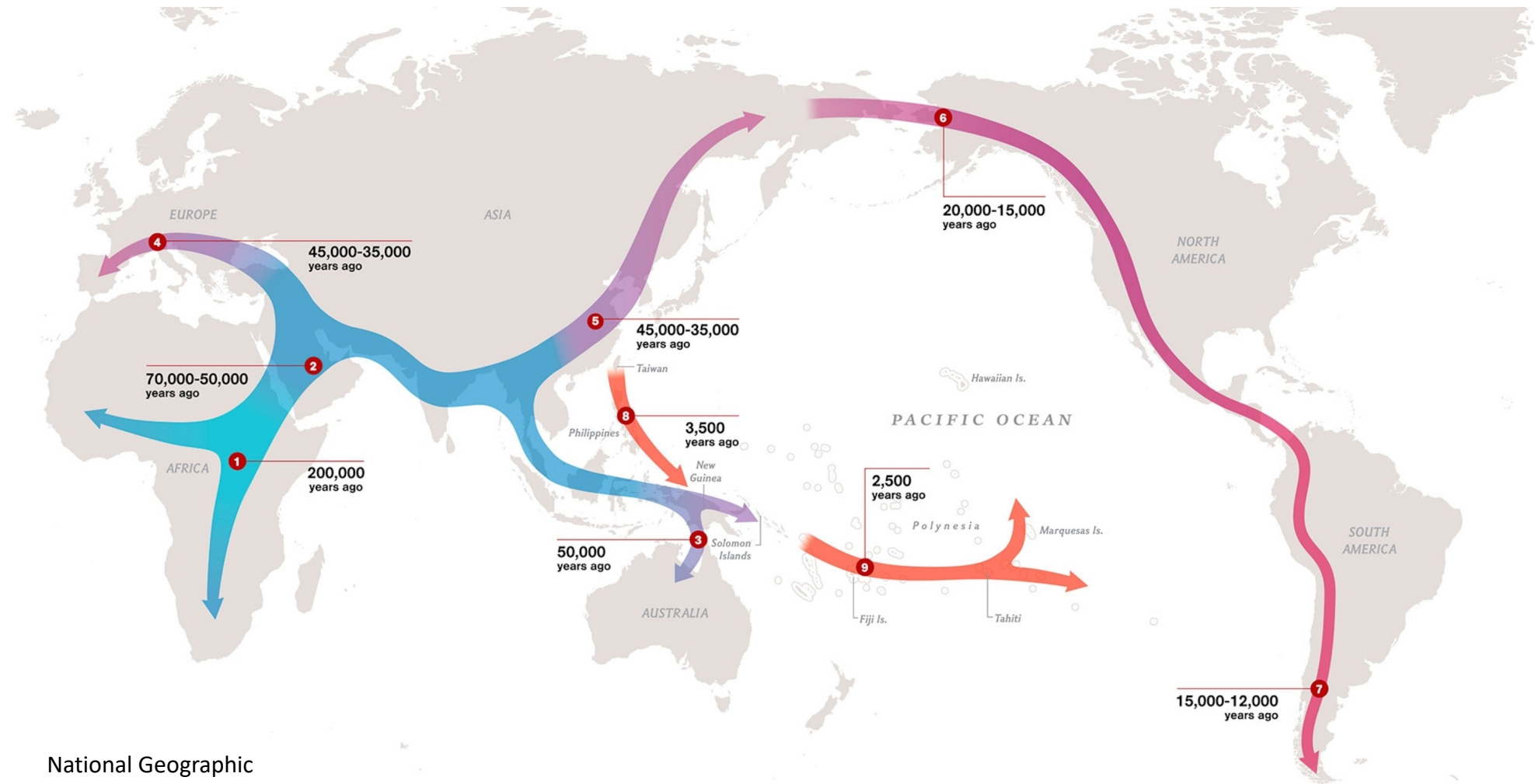
July 12, 2022



THE UNIVERSITY
OF ARIZONA

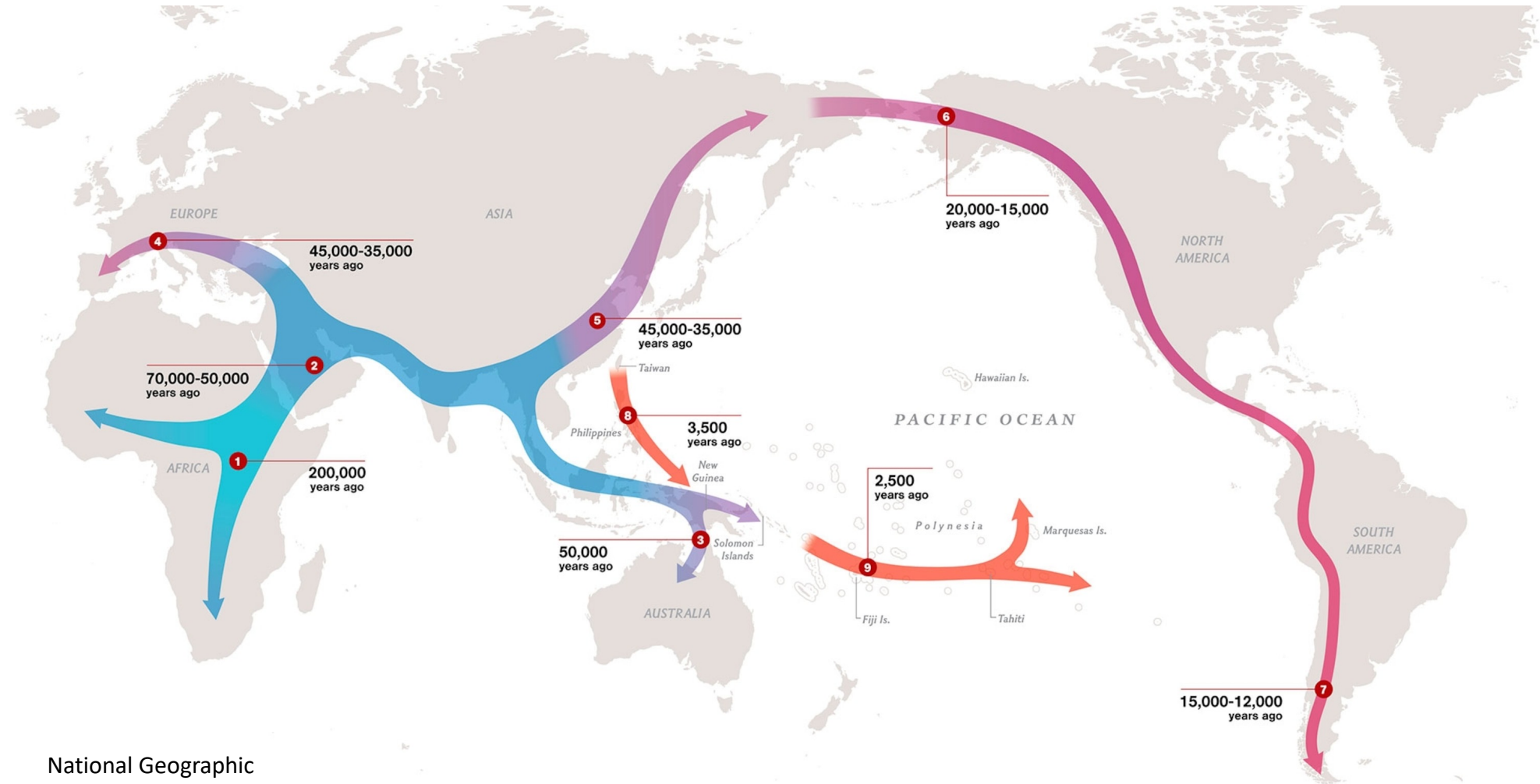


Demographic history inference



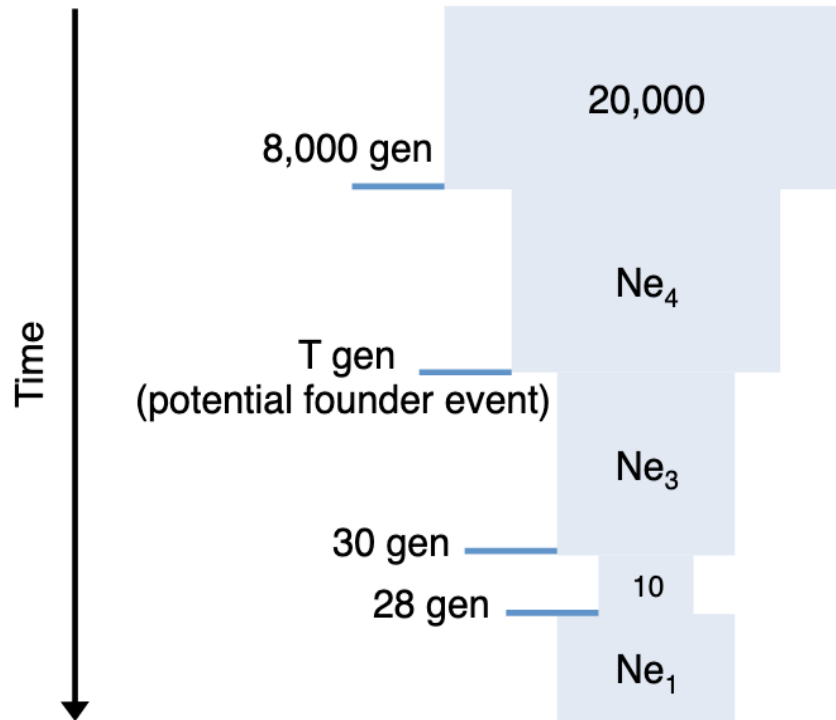
Demographic history inference – Motivation

- Understand population history: bottlenecks, gene flow, etc.



Demographic history inference – Motivation

- Understand population history: bottlenecks, gene flow, etc.
- Conservation: historical genetic diversity of endangered species

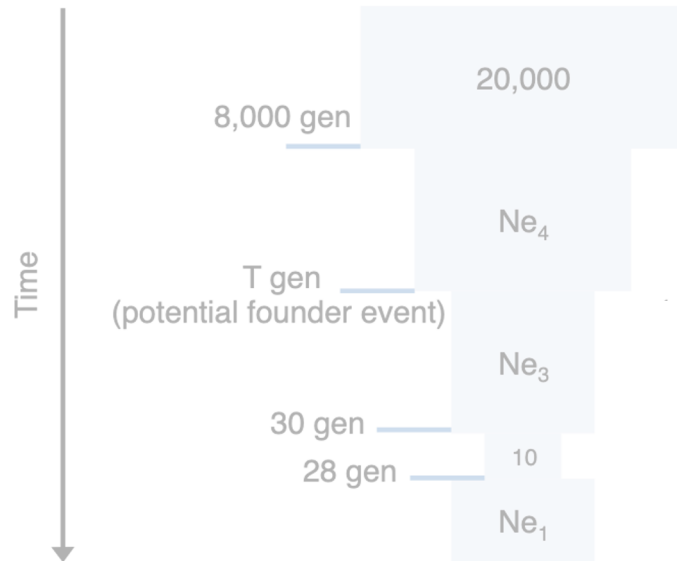


Robinson et al. (2016) *Current Biology*

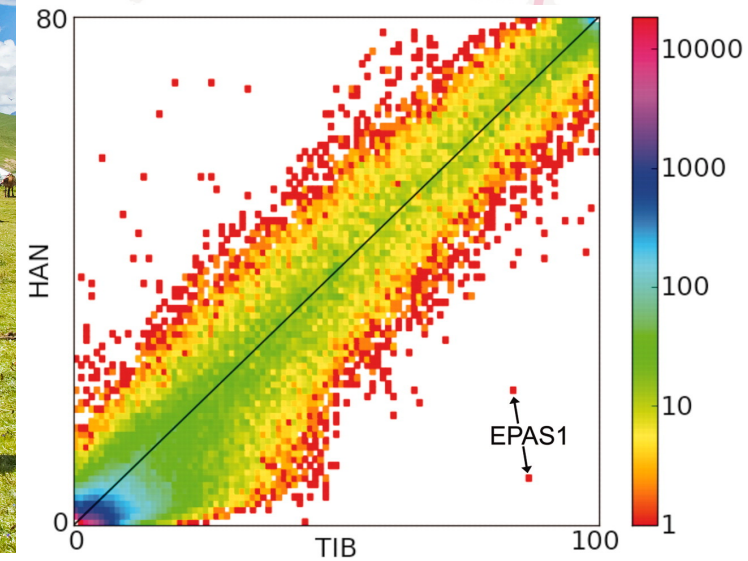


Demographic history inference – Motivation

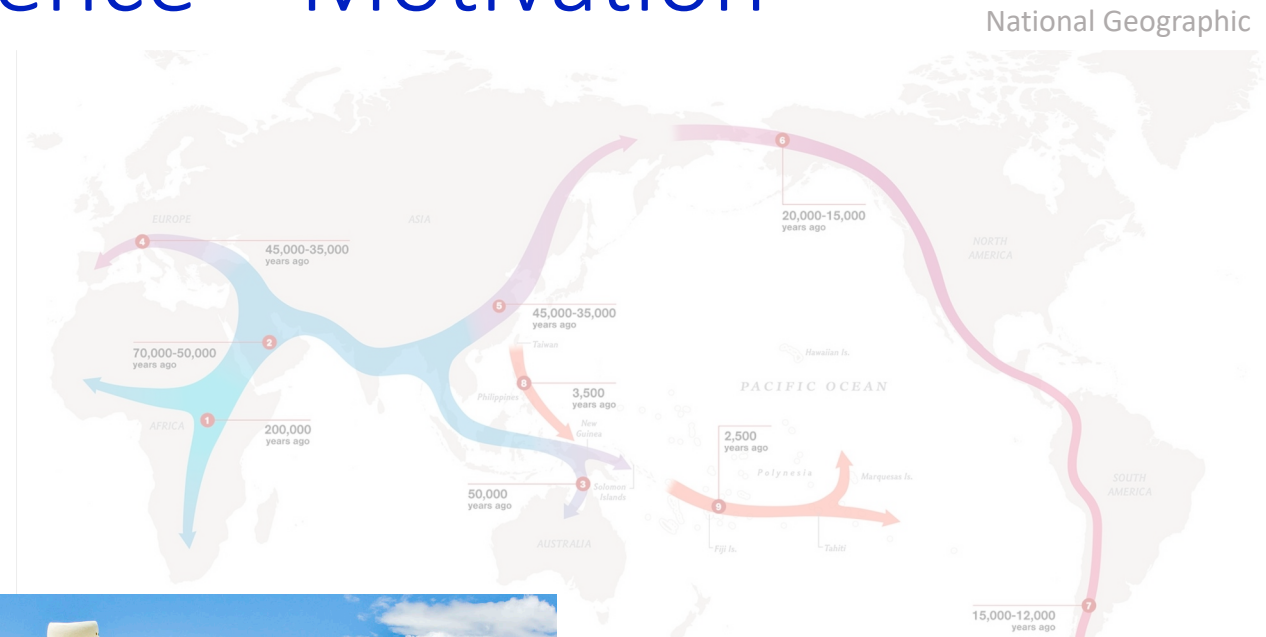
- Understand population history: bottlenecks, gene flow, etc.
- Conservation: historical genetic diversity of endangered species
- Selection: sets neutral background for detecting adaptation



Robinson et al. (2016) *Current Biology*



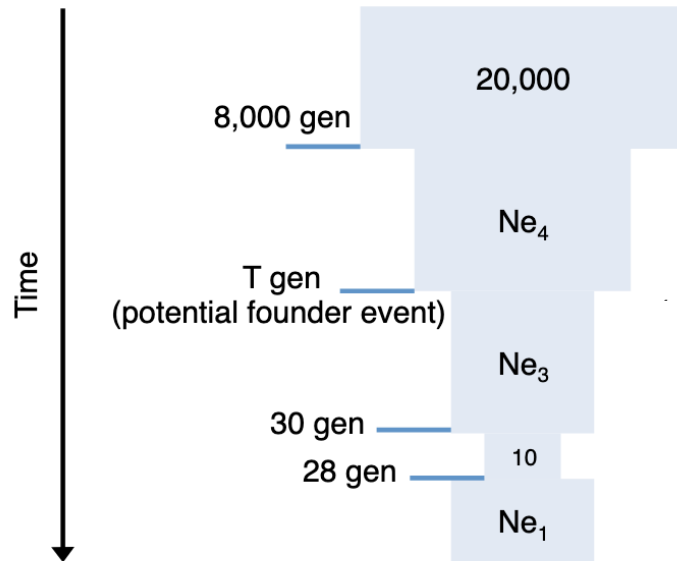
Yi et al. (2010) *Science*



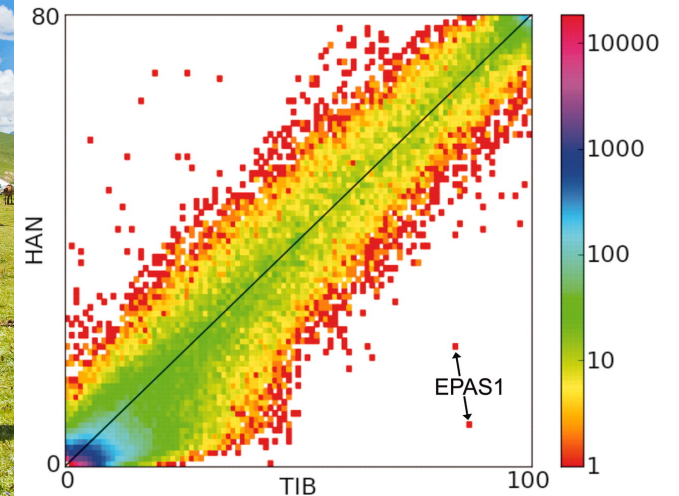
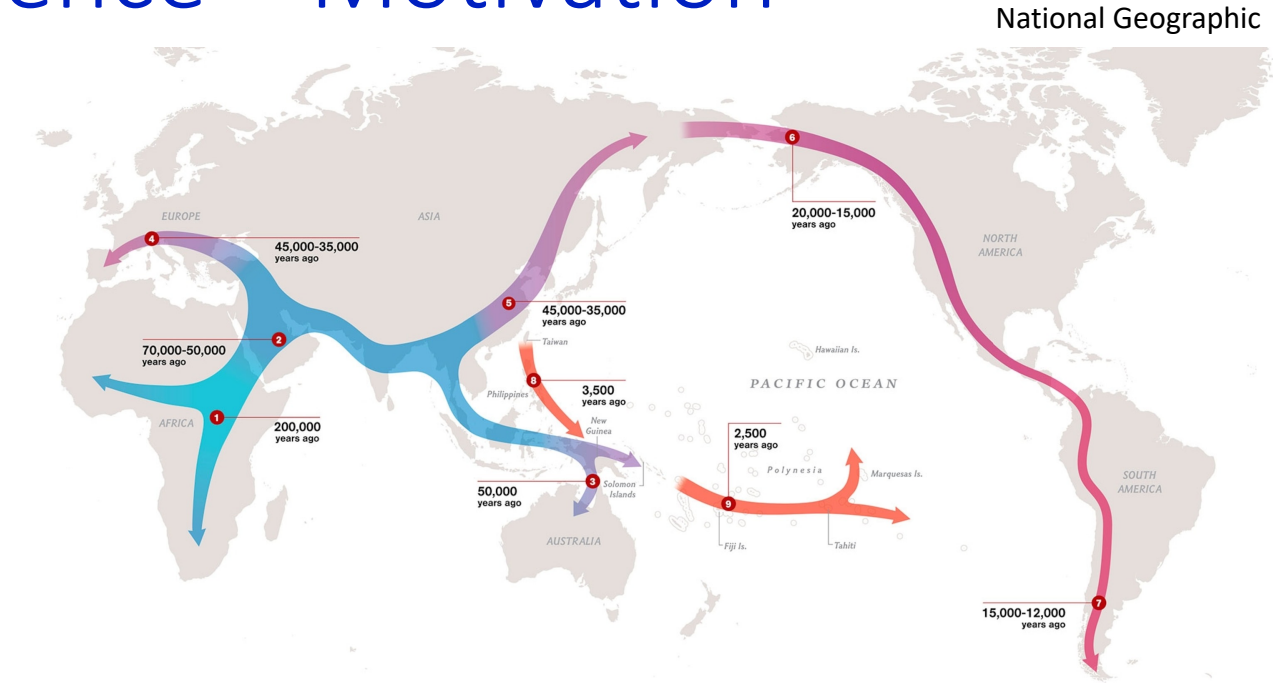
National Geographic

Demographic history inference – Motivation

- Understand population history: bottlenecks, gene flow, etc.
- Conservation: historical genetic diversity of endangered species
- Selection: sets neutral background for detecting adaptation

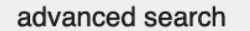


Robinson et al. (2016) *Current Biology*



Yi et al. (2010) *Science*

Diffusion approximation for demographic inference (dadi)



 OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Inferring the Joint Demographic History of Multiple Populations from Multidimensional SNP Frequency Data

Ryan N. Gutenkunst , Ryan D. Hernandez, Scott H. Williamson, Carlos D. Bustamante

Published: October 23, 2009 • <https://doi.org/10.1371/journal.pgen.1000695>

1,286
Citation

8
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 Groups

☆ dadi-user 391 members

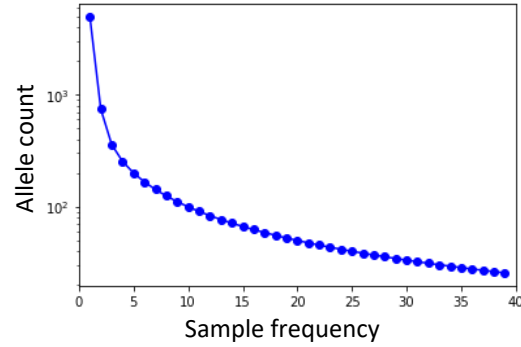
Diffusion approximation for demographic inference (dadi)

Data

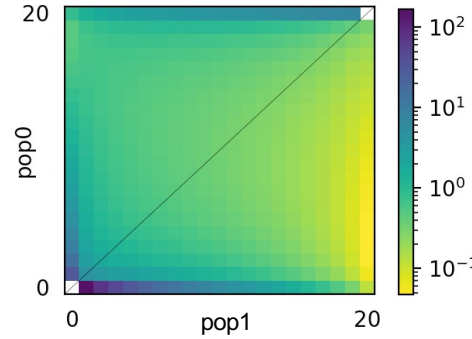
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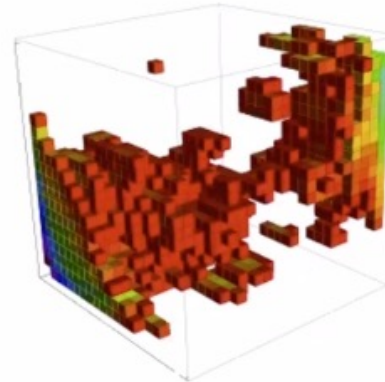
Data Summary



1D – 1 population

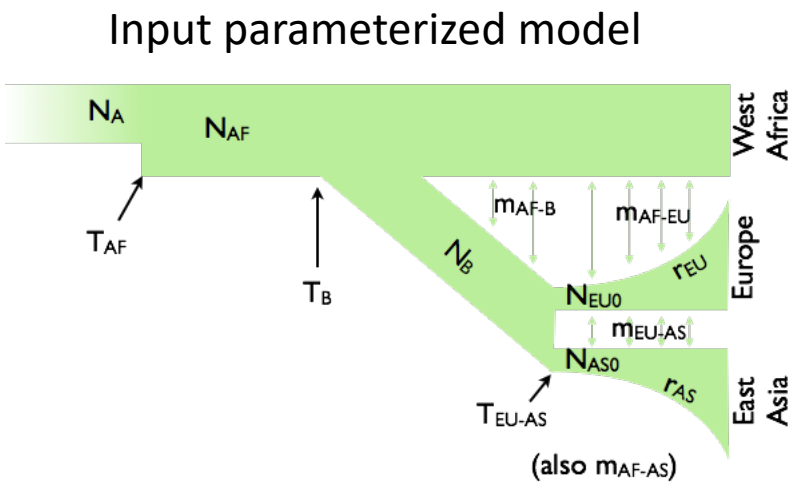
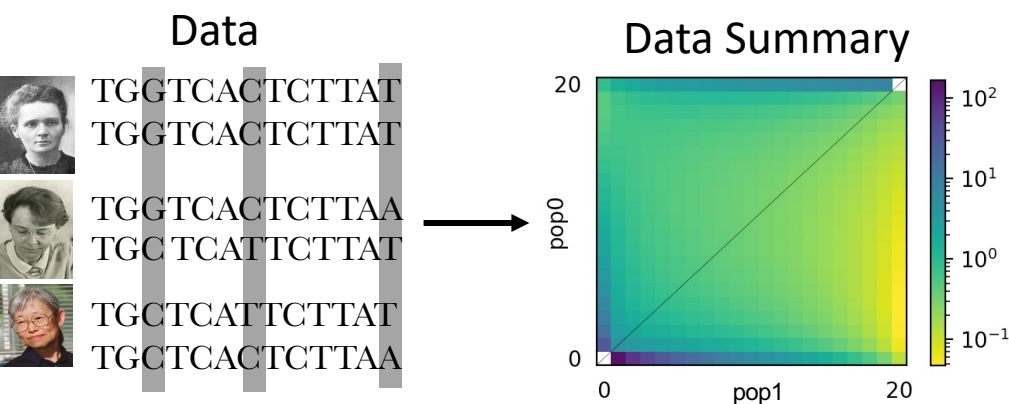


2D – 2 populations

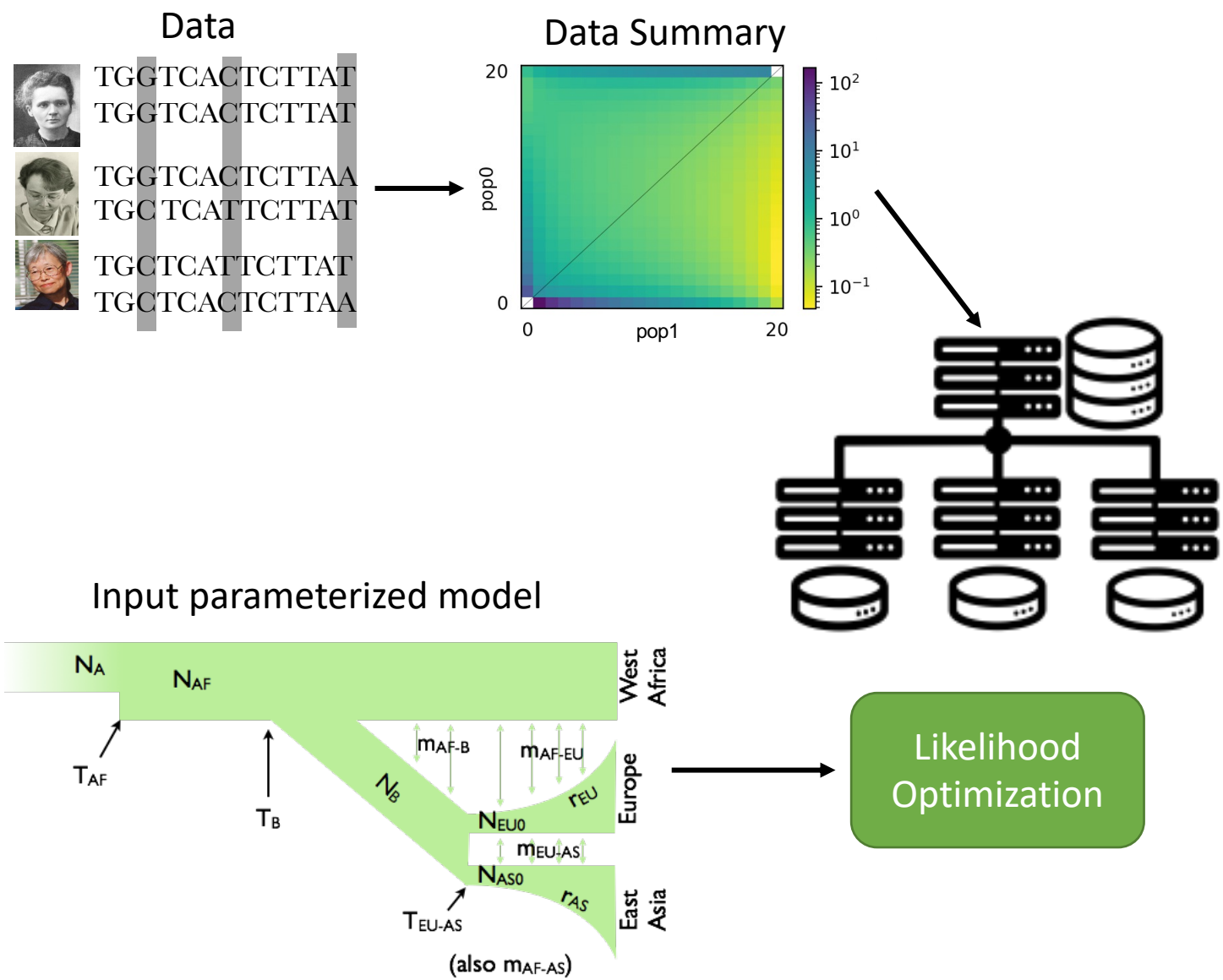


3D – 3 populations

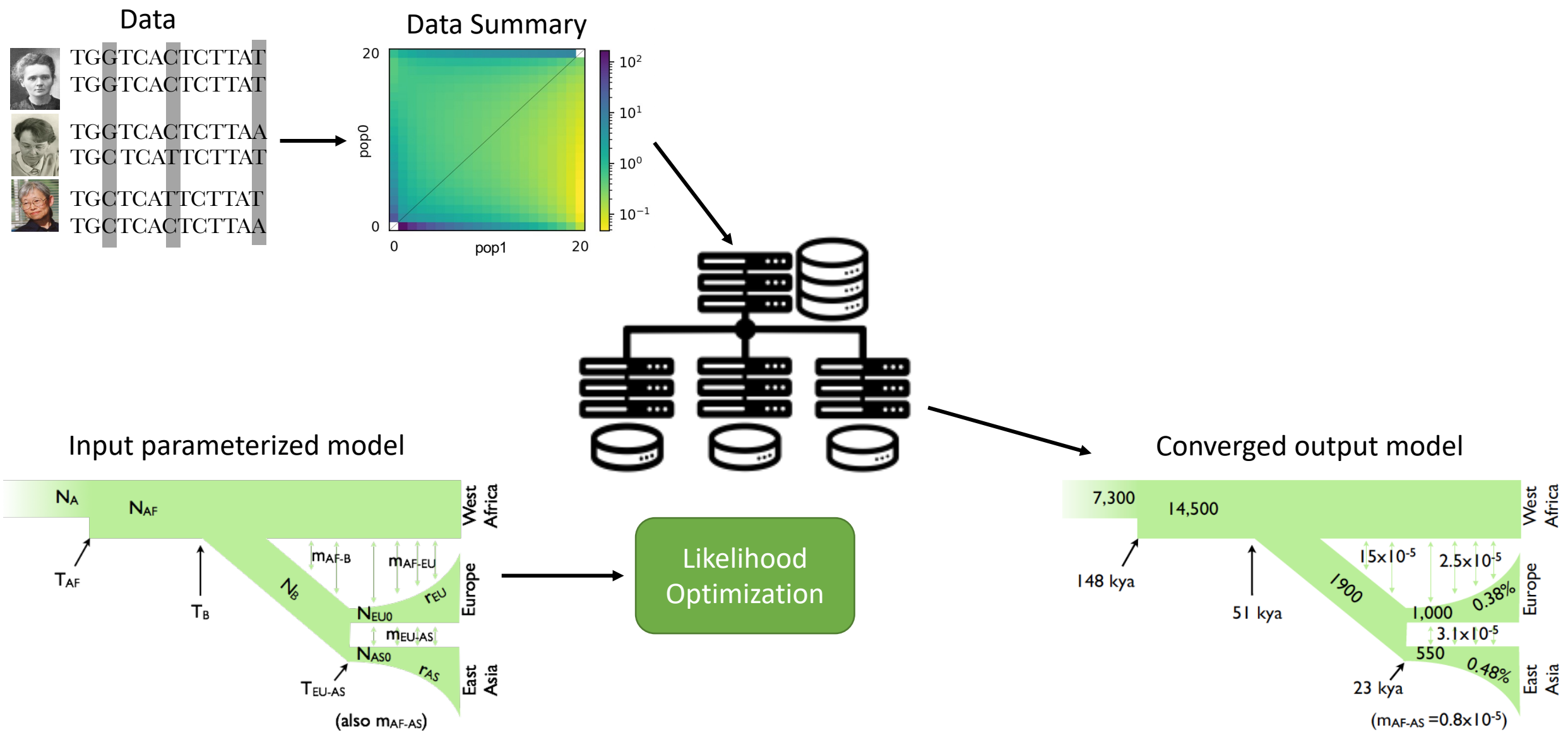
Diffusion approximation for demographic inference (dadi)



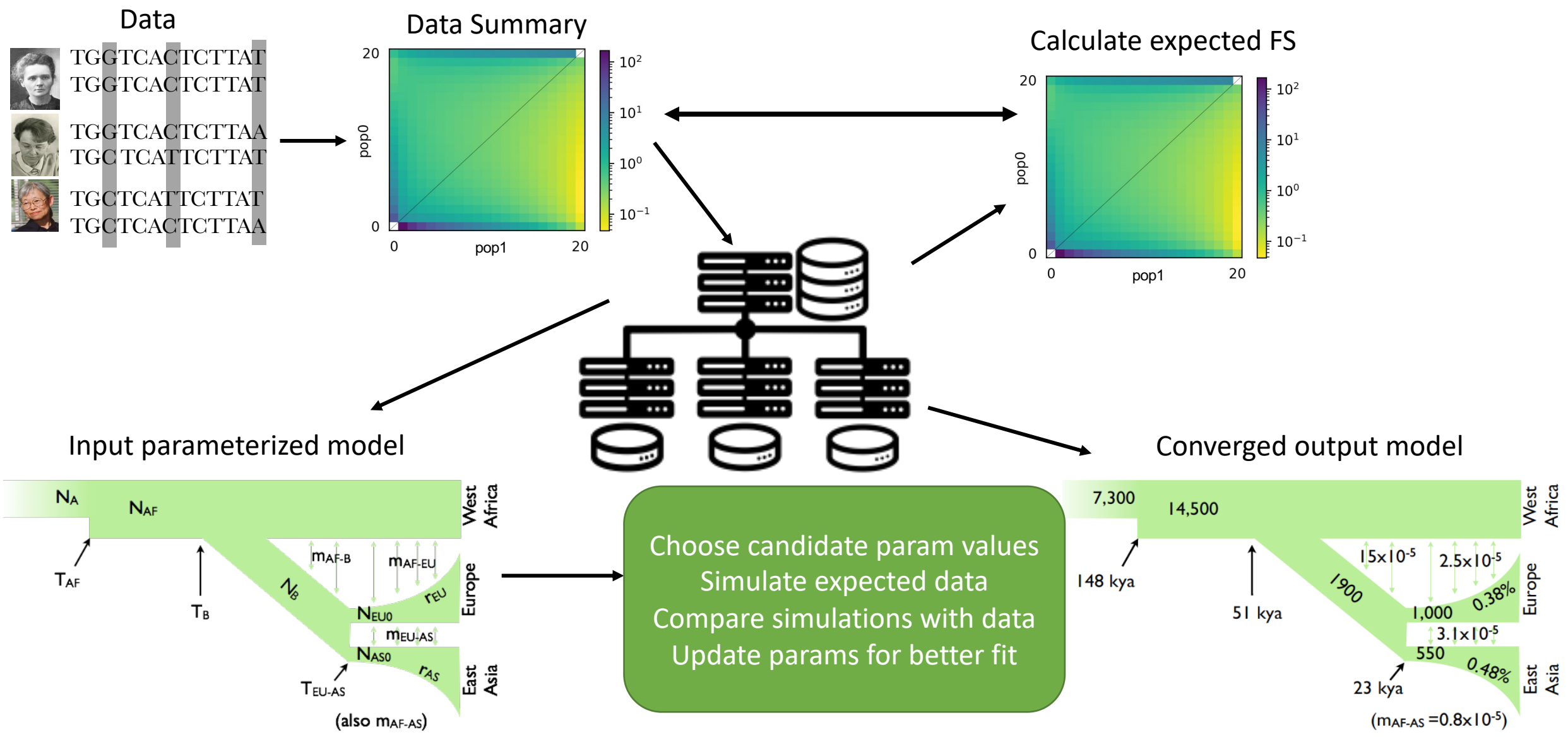
Diffusion approximation for demographic inference (dadi)



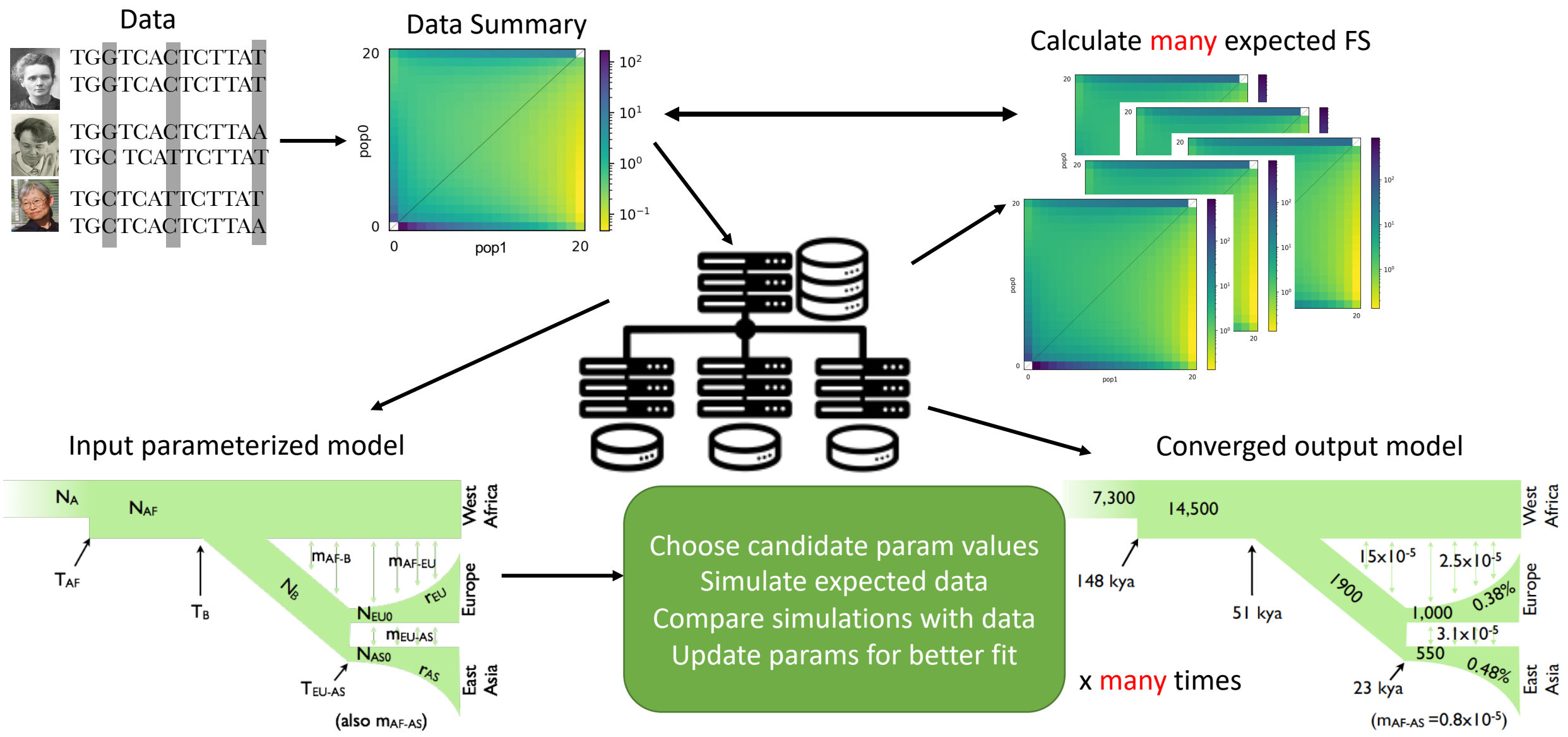
Diffusion approximation for demographic inference (dadi)



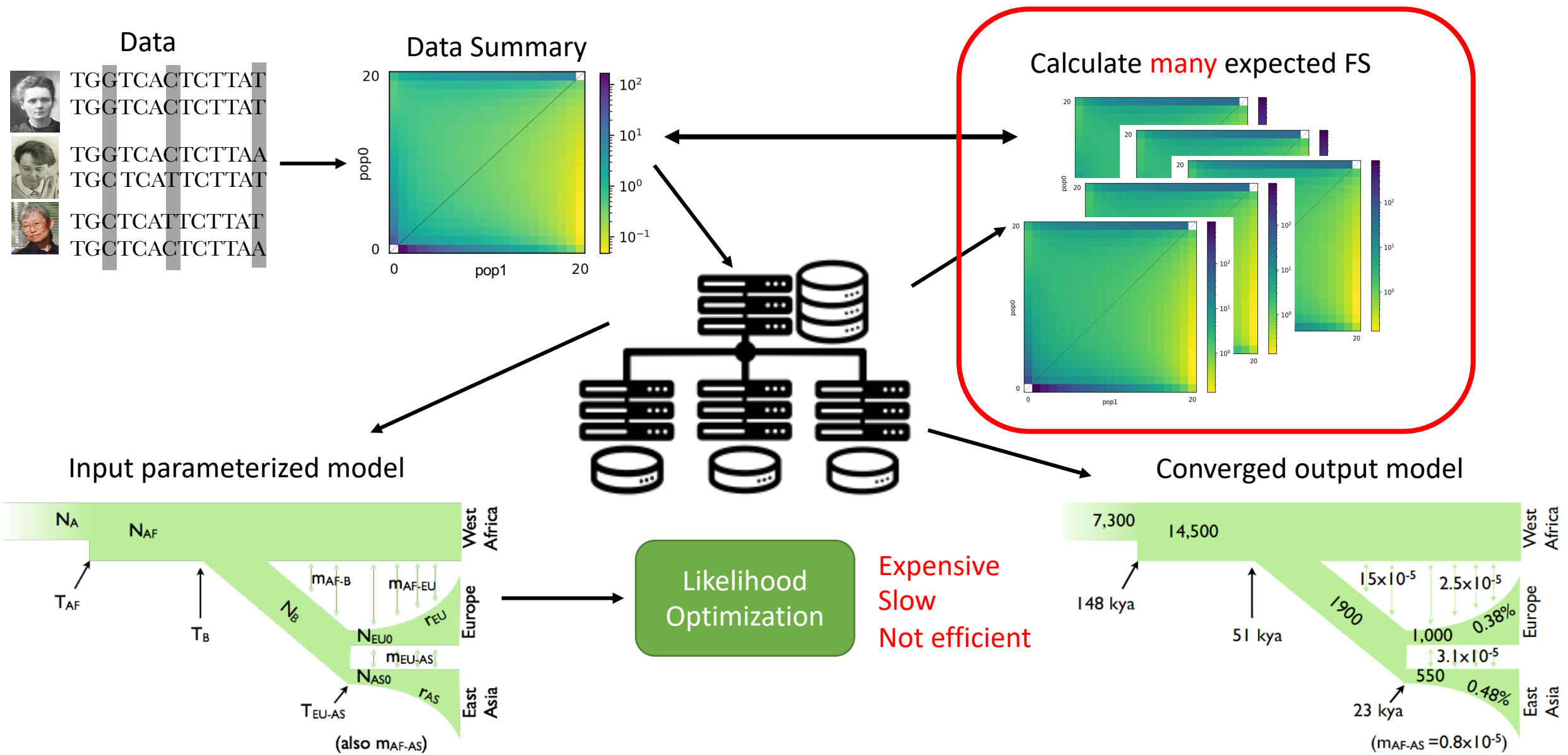
Diffusion approximation for demographic inference (dadi)



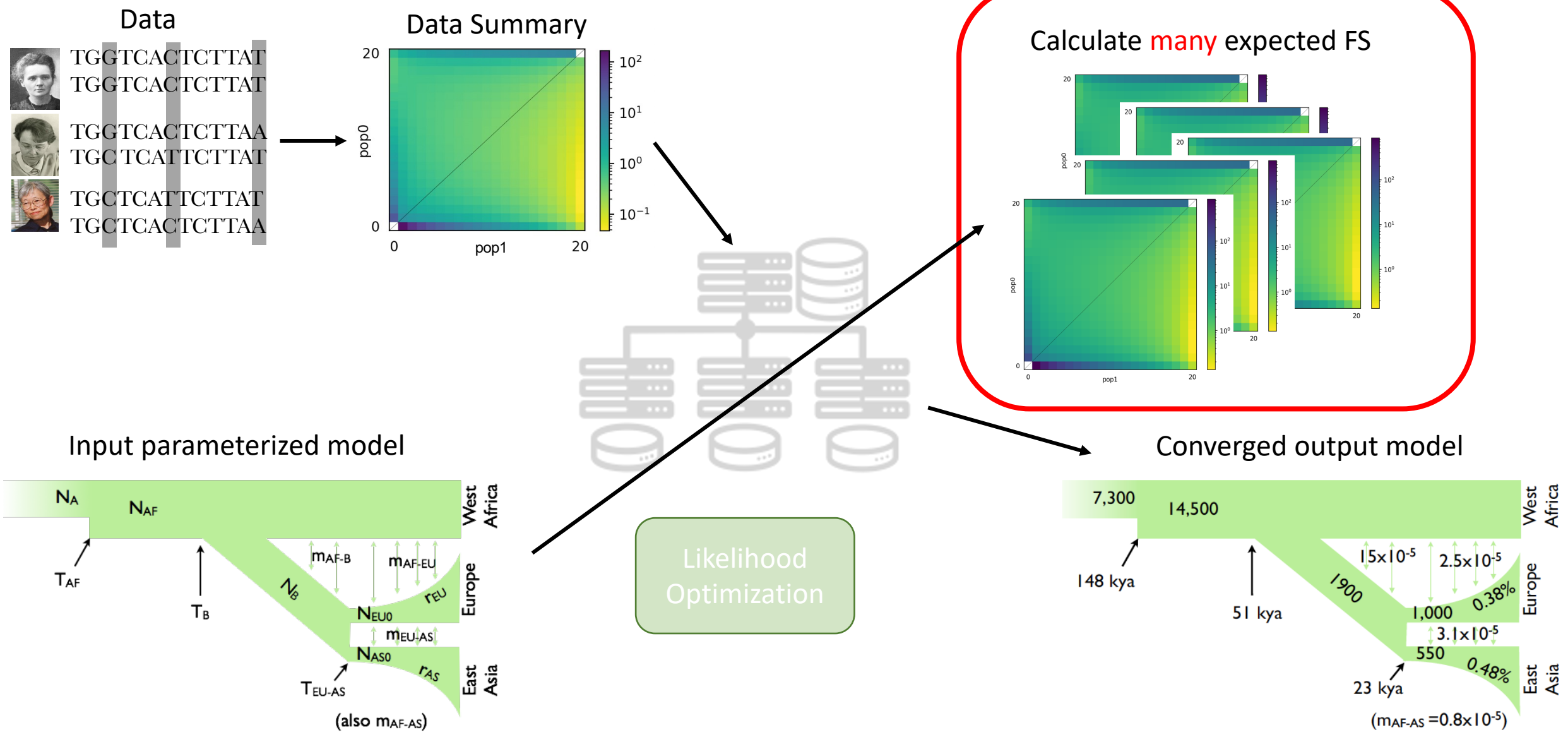
Diffusion approximation for demographic inference (dadi)



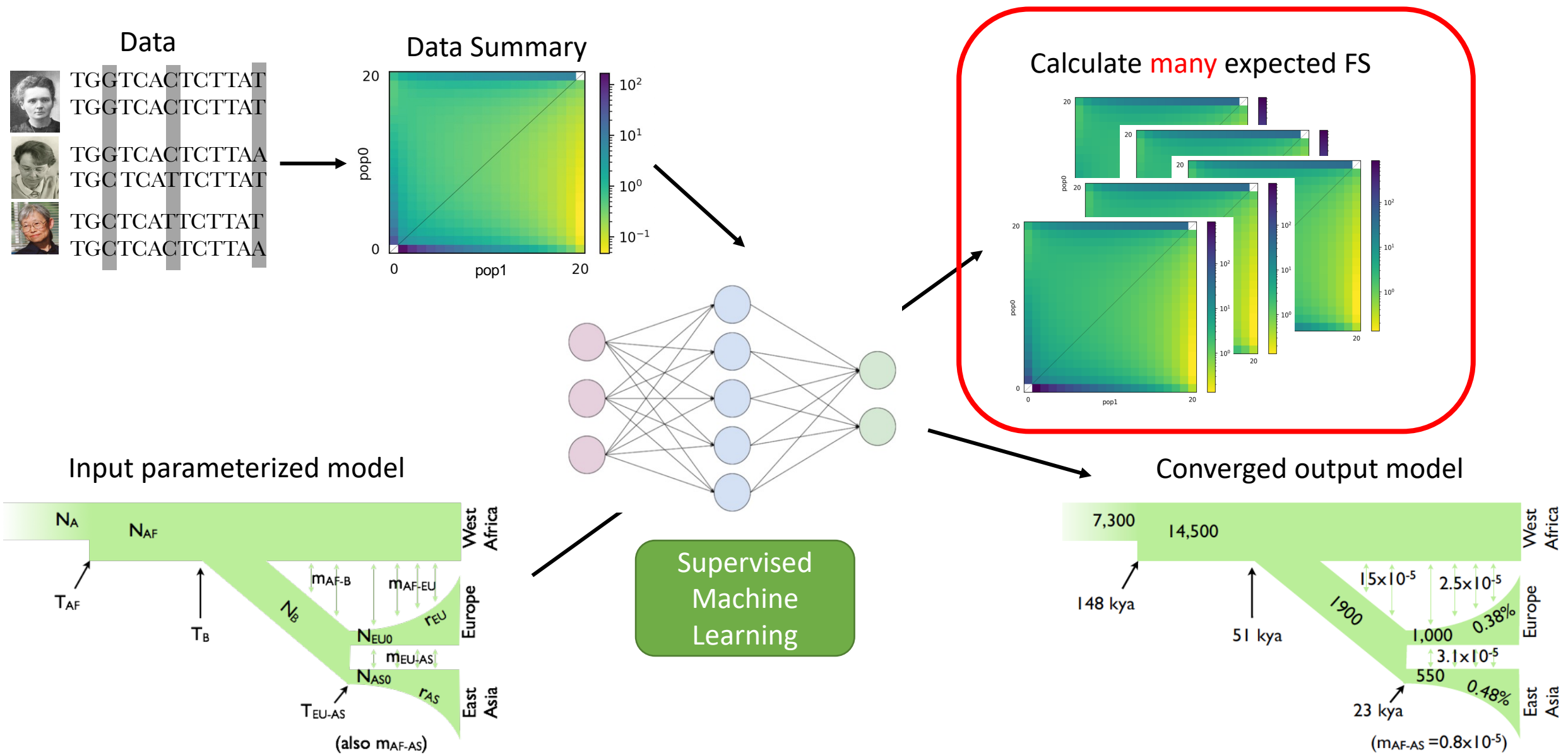
Diffusion approximation for demographic inference (dadi)



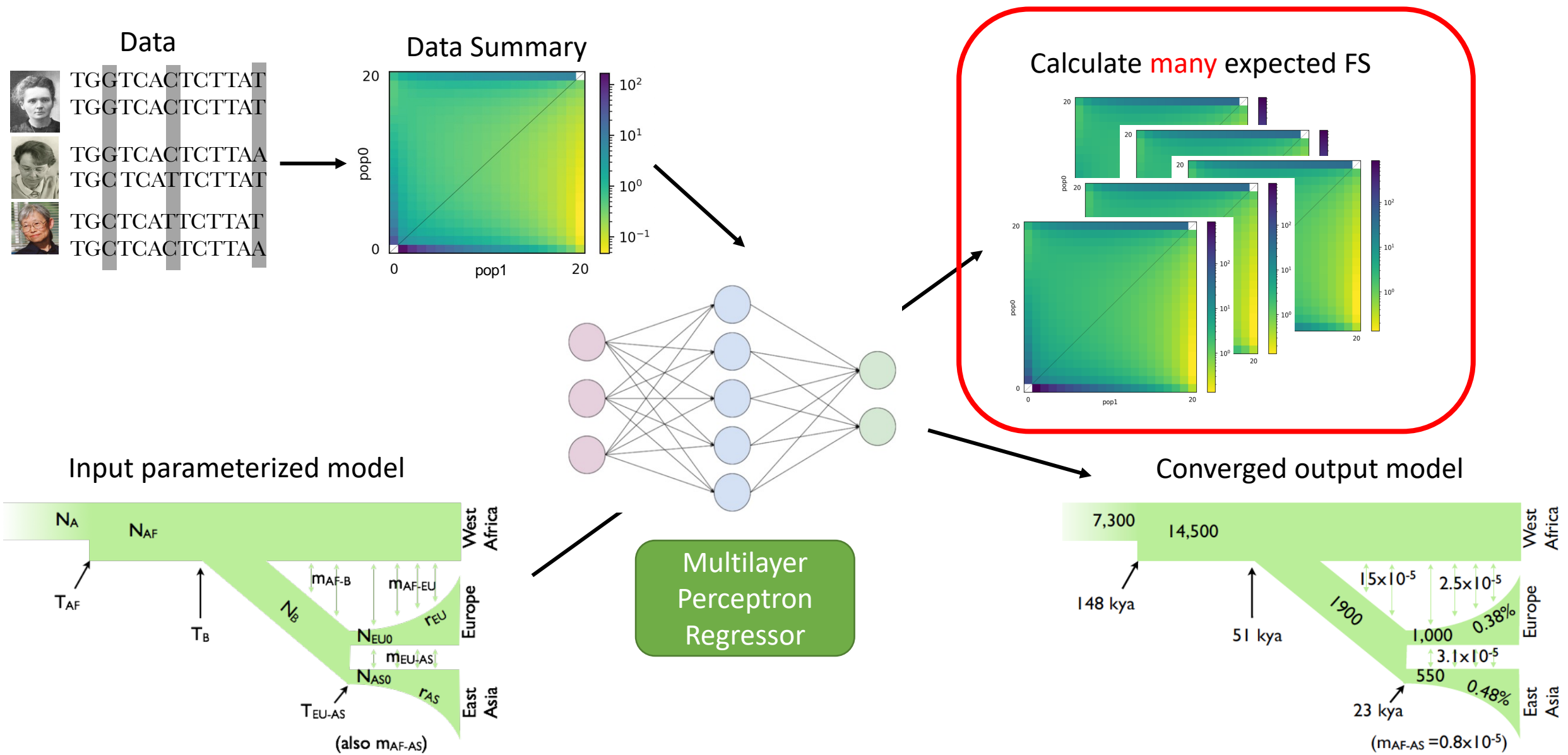
Diffusion approximation for demographic inference (dadi)



Diffusion approximation for demographic inference (dadi)



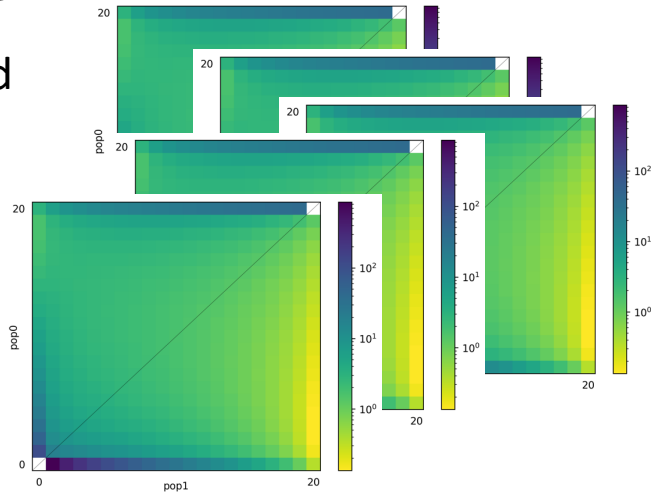
Diffusion approximation for demographic inference (dadi)



dadi-machine learning workflow

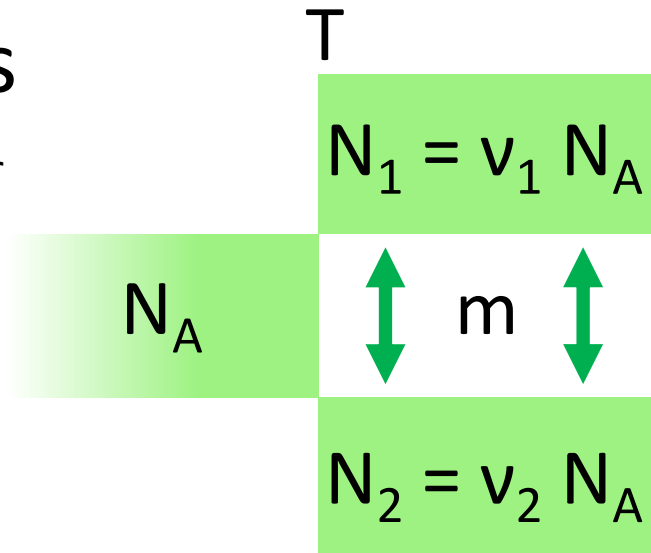
Training data

dadi-simulated
spectra
(1000)



Labels

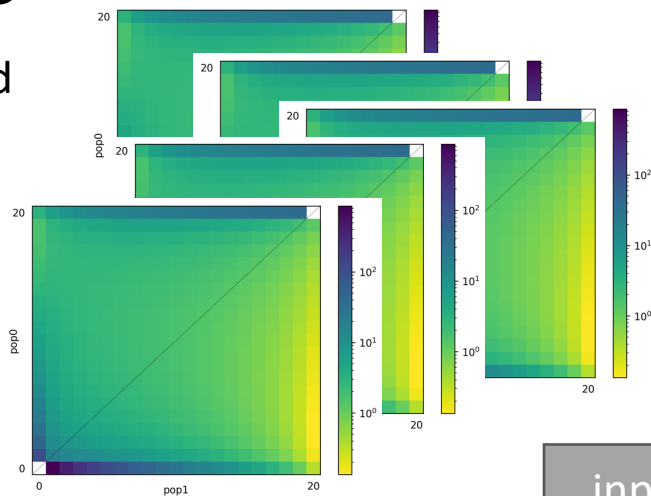
parameter
values



dadi-machine learning workflow

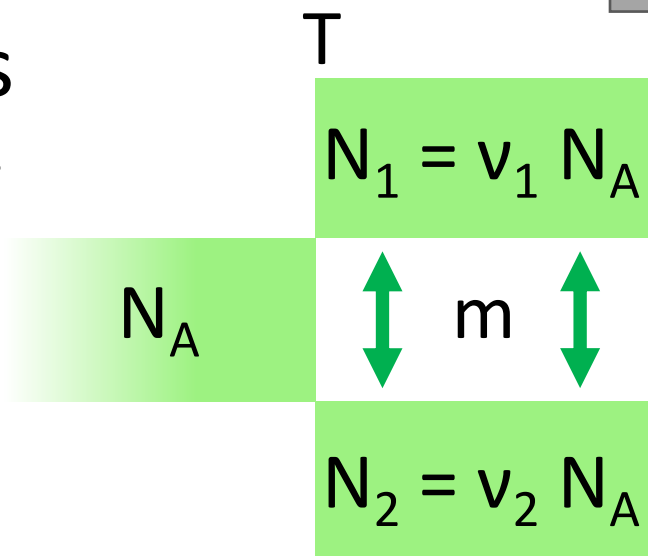
Training data

dadi-simulated
spectra
(1000)

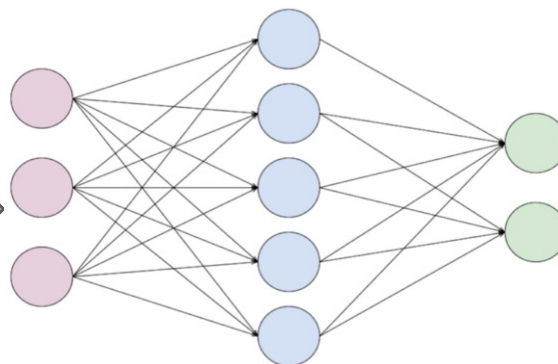


Labels

parameter
values



MLP Regressor
algorithm

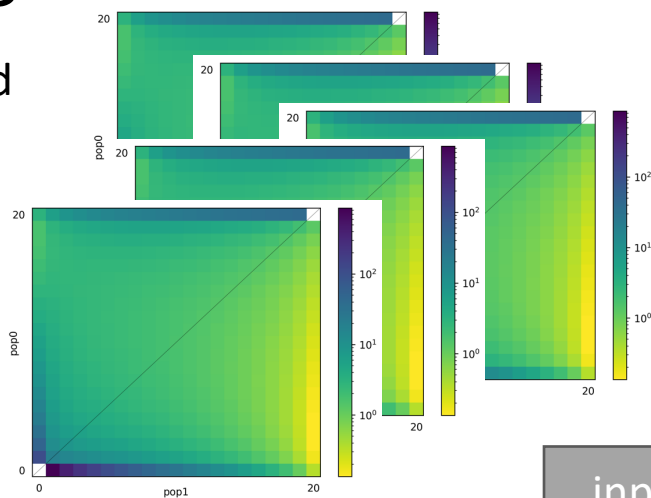


Learns:
Finds pattern
of association

dadi-machine learning workflow

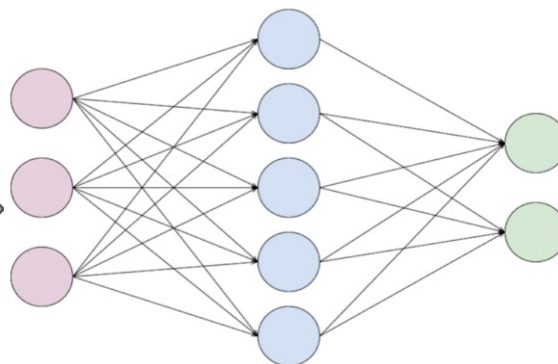
Training data

dadi-simulated
spectra
(1000)



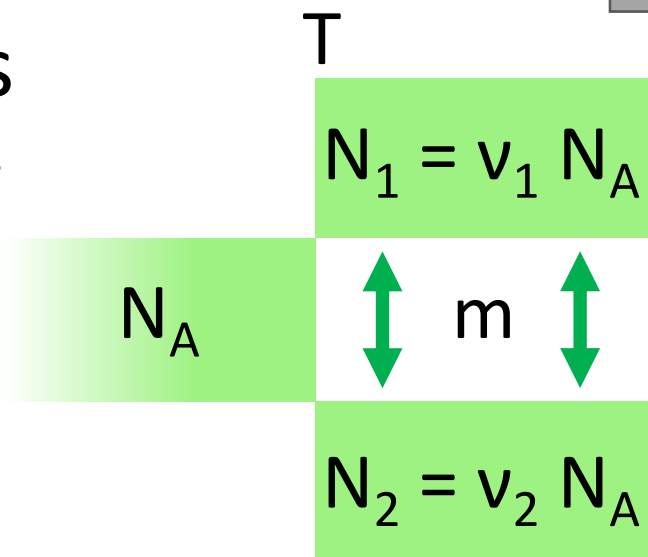
input

Trained MLP
Regressor



Labels

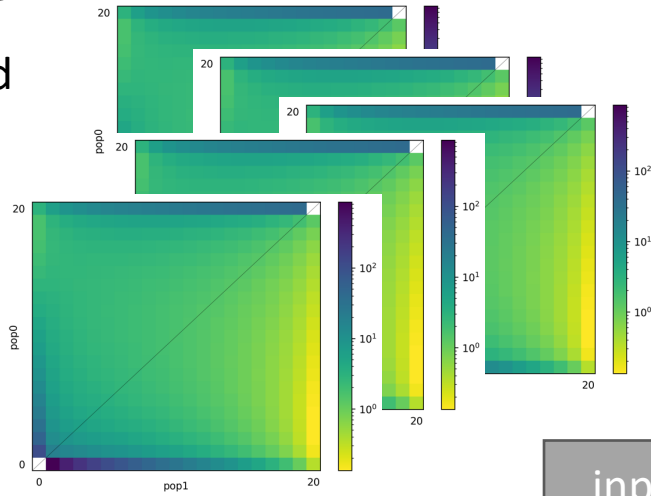
parameter
values



dadi-machine learning workflow

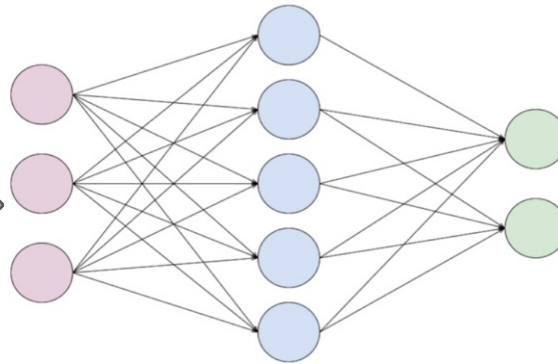
Training data

dadi-simulated
spectra
(1000)



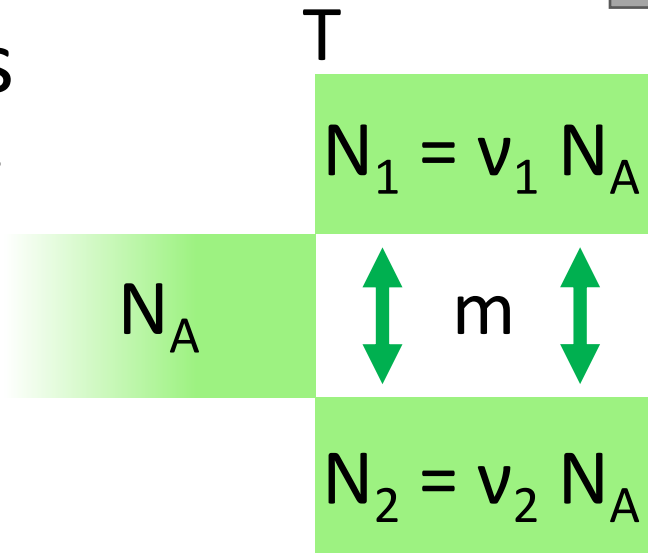
input

Trained MLP
Regressor



Labels

parameter
values



Strength of frequency spectra simulation with dadi:

- Faster and less expensive than coalescent simulations
- Organism-agnostic and transferability

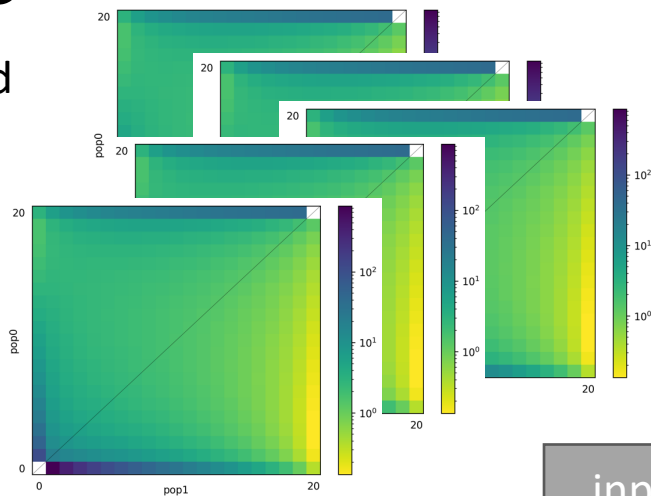
Weakness:

- Ignores linkage

dadi-machine learning workflow

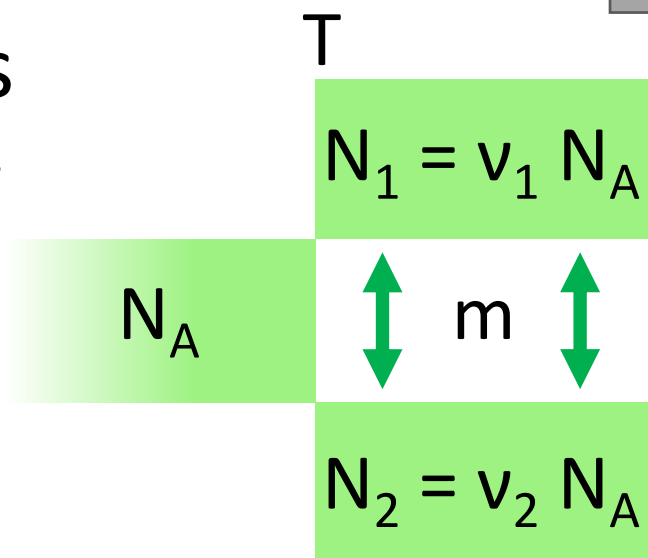
Training data

dadi-simulated
spectra
(1000)

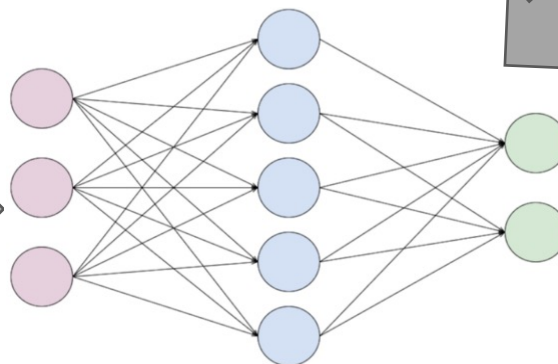


Labels

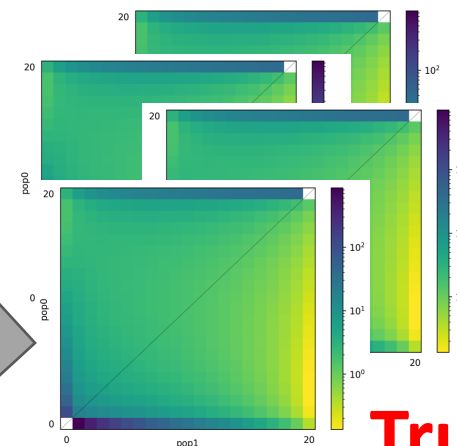
parameter
values



Trained MLP
Regressor



Test data



dadi- and
msprime-
simulated
spectra
(100-200)

True params:
set aside for
comparison

Strength of frequency spectra simulation with dadi:

- Faster and less expensive than coalescent simulations
- Organism-agnostic and transferability

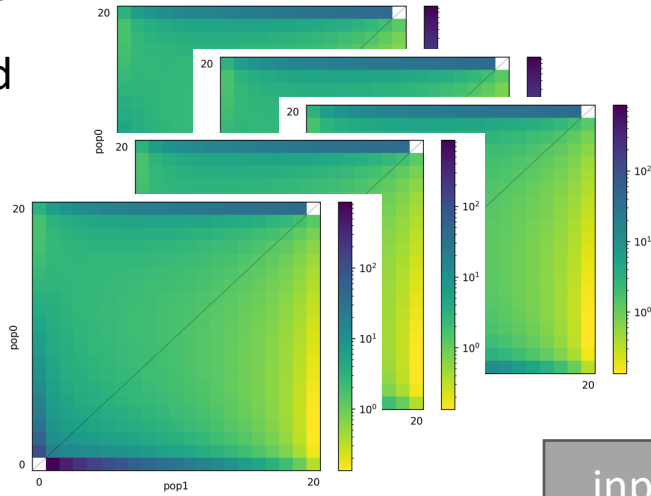
Weakness:

- Ignores linkage

dadi-machine learning workflow

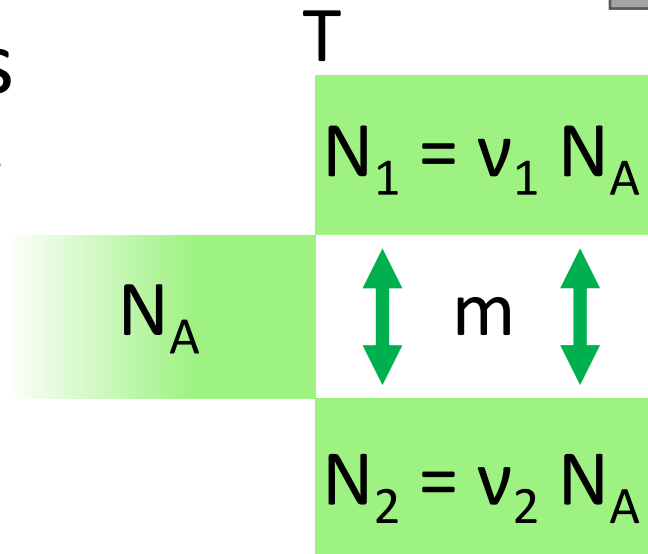
Training data

dadi-simulated
spectra
(1000)

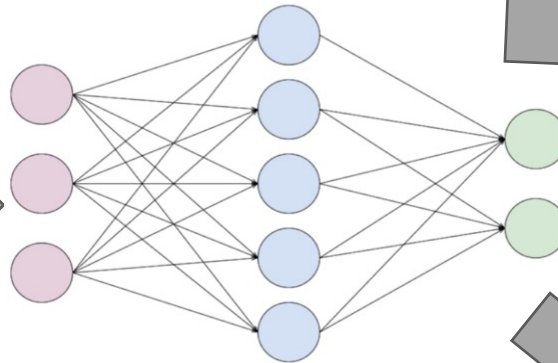


Labels

parameter
values

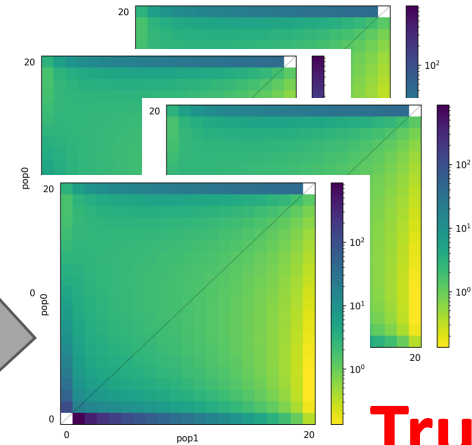


Trained MLP
Regressor



Test data

dadi- and
msprime-
simulated
spectra
(100-200)



True params:
set aside for
comparison

Prediction

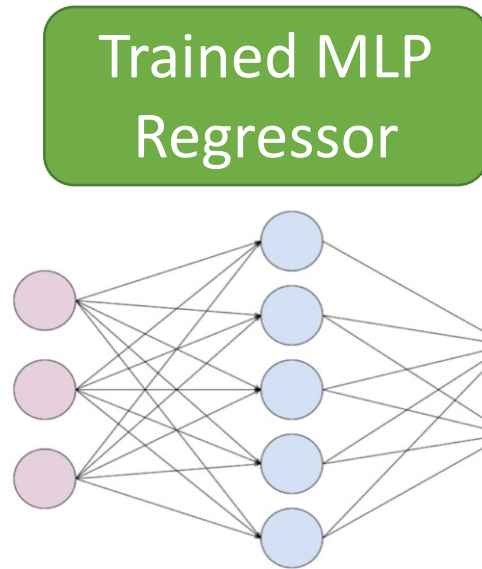
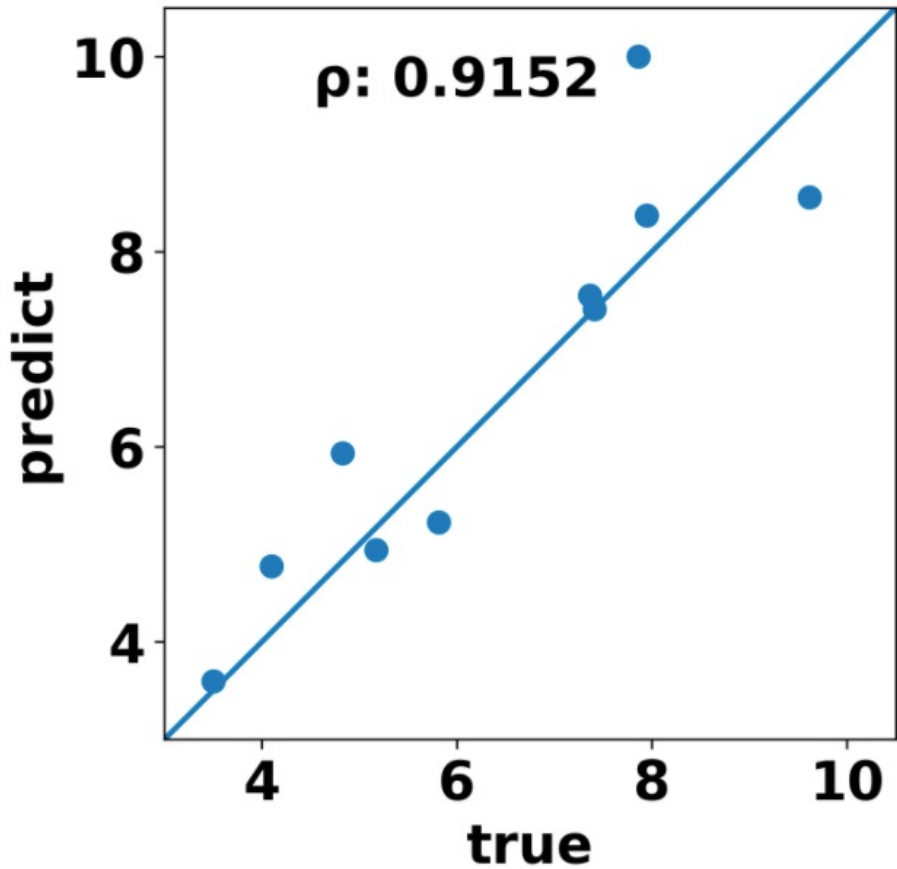
param values for
each test spectrum

Predict :

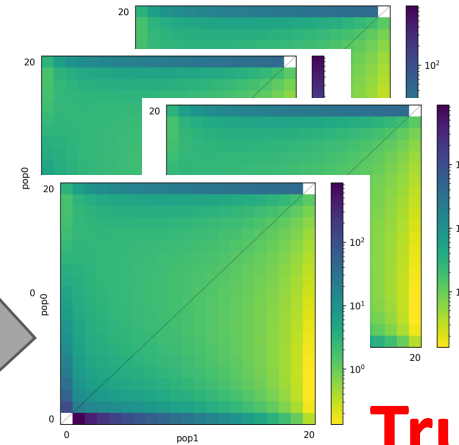
- $v_1 = 0.1$
- $v_2 = 0.5$
- $T = 1.3$
- $m = 5$

Testing and validation

Prediction accuracy



Test data



dadi- and
msprime-
simulated
spectra
(100-200)

True params:
set aside for
comparison

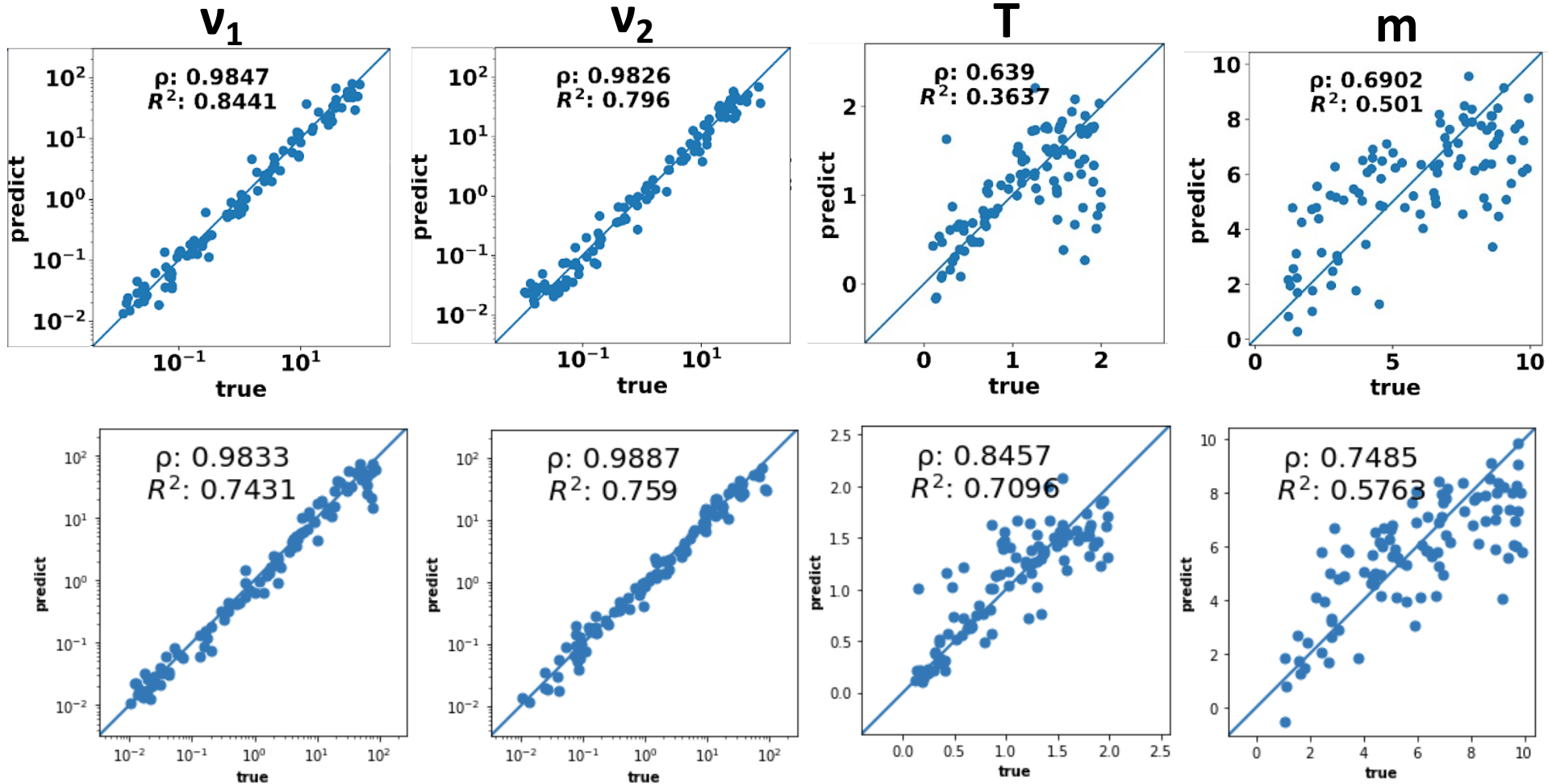
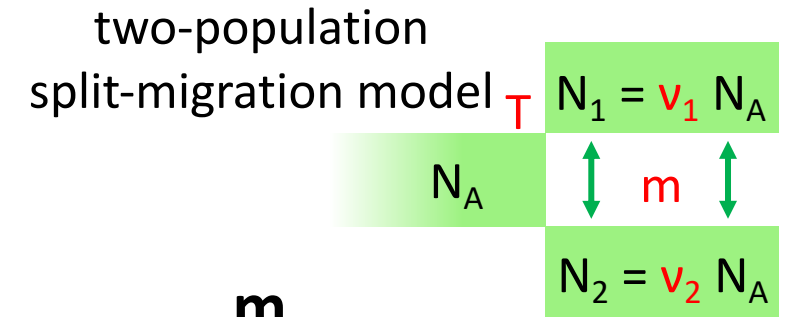
Prediction

param values for
each test spectrum

Predict :
 $v_1 = 0.1$
 $v_2 = 0.5$
 $T = 1.3$
 $m = 5$

Results – prediction accuracy

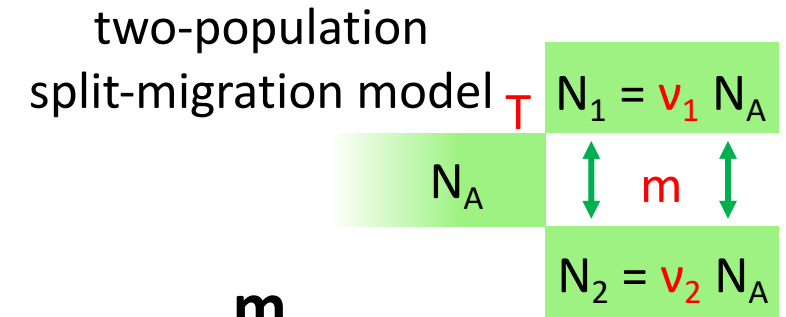
MLPR



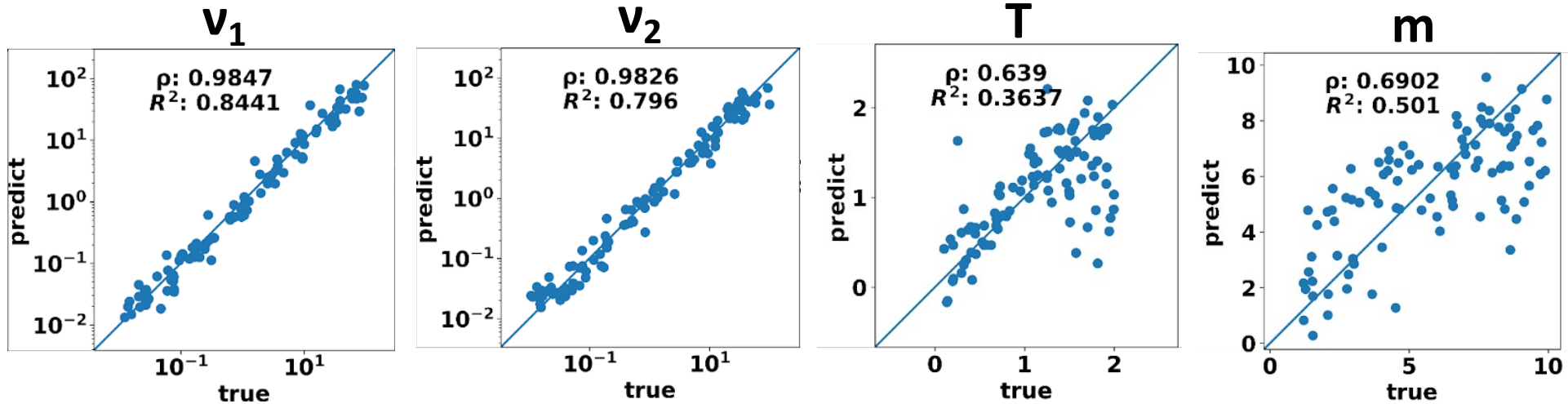
dadi-simulated
data sets

msprime-simulated
data sets

Results – prediction accuracy

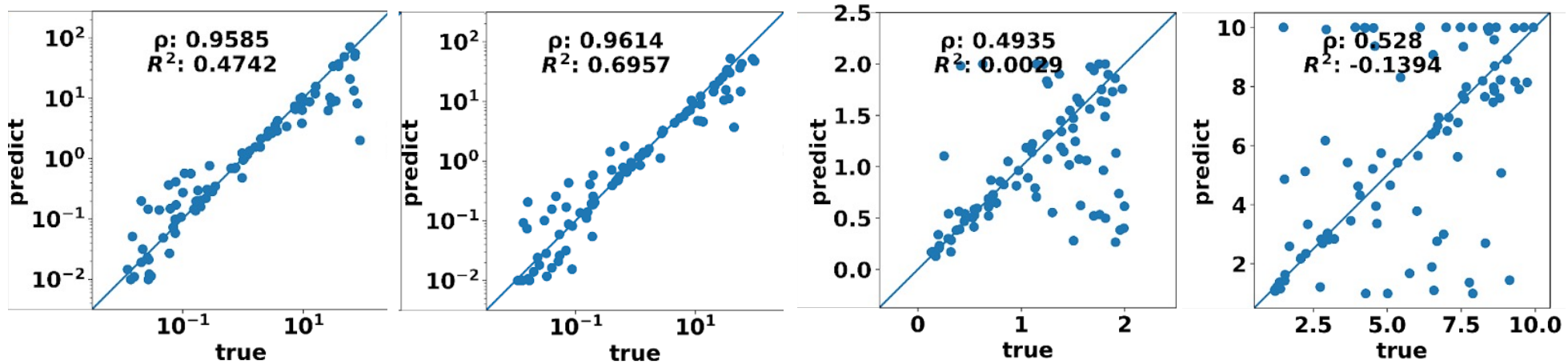


MLPR



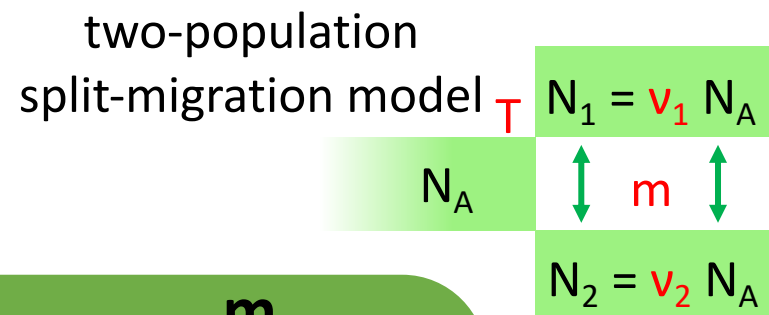
dadi-simulated
data sets

dadi



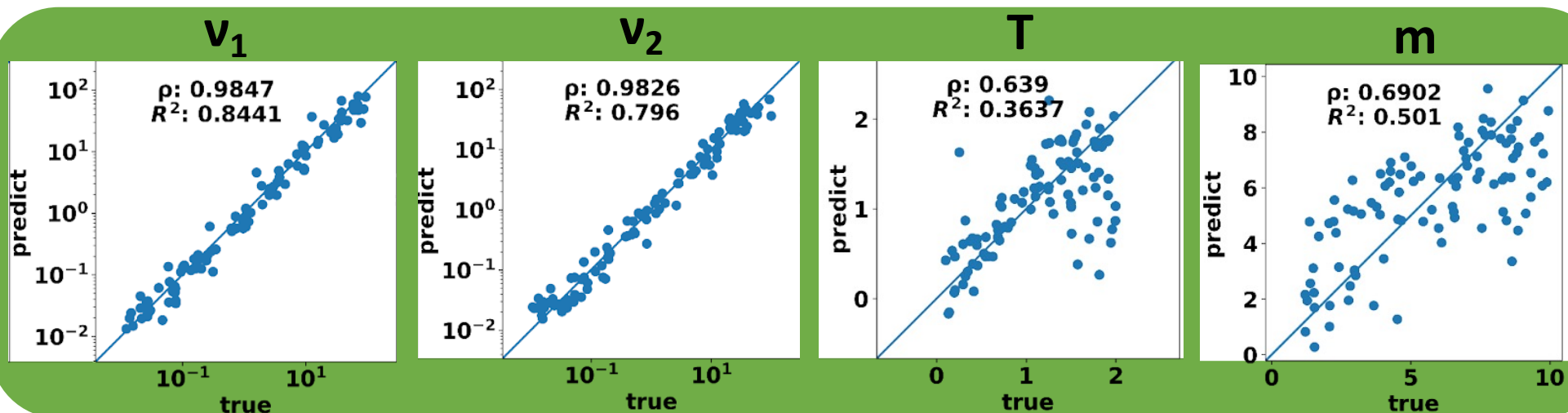
dadi-simulated
data sets

Results – prediction accuracy and computational efficiency



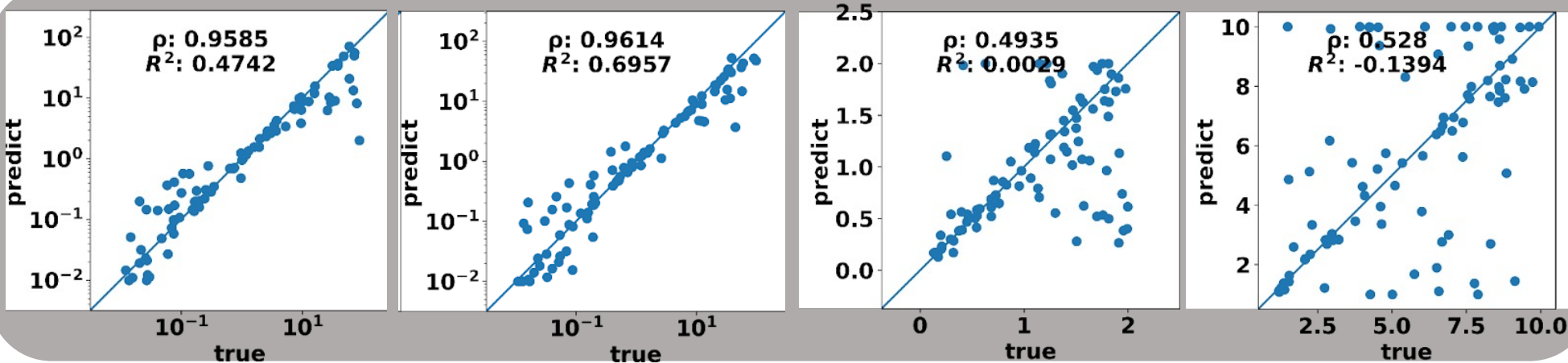
MLPR

instantaneous



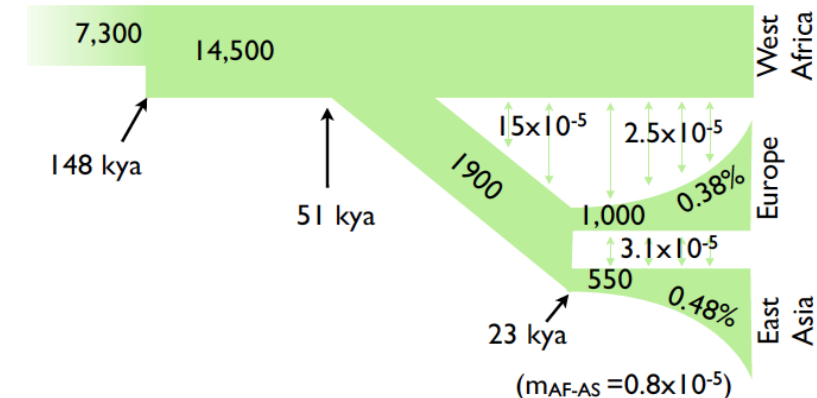
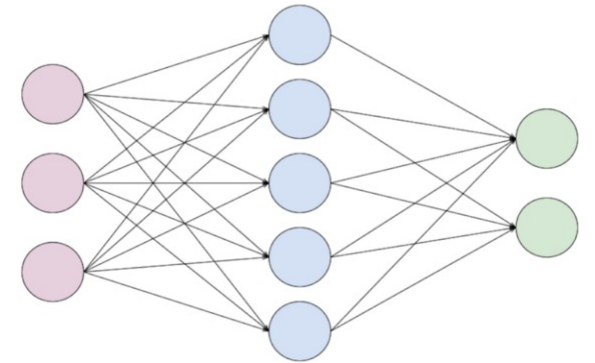
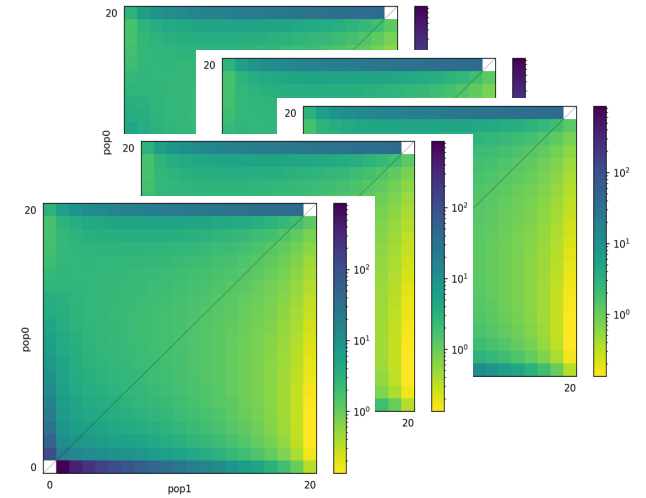
dadi

~13 CPU hours



Summary

- Machine learning approach to improve the computational efficiency of a widely used likelihood-based demographic inference method
- Comparable accuracy with significantly reduced computational cost & complexity
- Robust to test simulations generated with linkage
- Accompanying uncertainty quantification method that provides prediction intervals
- Trained MLPRs for frequently used demographic models and workflow will be distributed



@LnTran26

<http://gutengroup.arizona.edu>