

# Supplementary File S1: Computational & Rapid Verification Protocol

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## Purpose

End-to-end reproduction of Bayesian haplogroup inference, cultural continuity calculations, and figure generation referenced in the main manuscript.

## 1 Rapid Verification (30 minutes)

1. Verify Hebrew lexemes in BDB/HALOT/DCH.
2. Audit Hawass et al. (2012) Supplementary Table 4.
3. Filter SlaveVoyages manifests.
4. Inspect Equiano page scan.

## 2 Computational Reproduction

### 2.1 Prerequisites

Python 3.10+, R 4.3+, Git, Make.

### 2.2 One-line Execution

```
git clone https://example.org/EphraimConvergence.git
cd EphraimConvergence
make all
```

### 2.3 Manual Steps

```
python -m venv .venv && source .venv/bin/activate
```

```
pip install -r requirements.txt
python code/haplogroup_bayes.py --str data/hawass_table4.csv \
    --priors data/priors_uniform.json --out results/haplogroup_bayes.json
Rscript code/kappa_calculator.R data/cultural_coding.csv results/cultural_stats.csv
python code/make_figures.py --haplo results/haplogroup_bayes.json \
    --culture results/cultural_stats.csv --outfig figs/
```

### 3 Repository Structure

```
/data
    hawass_table4.csv
    cultural_coding.csv
    priors_uniform.json
/code
    haplogroup_bayes.py
    kappa_calculator.R
    make_figures.py
/figs
    bayesian_pipeline_flowchart.png
    cultural_retention_map.png
/results
    haplogroup_bayes.json
    cultural_stats.csv
```

### 4 Figures (Tagged)

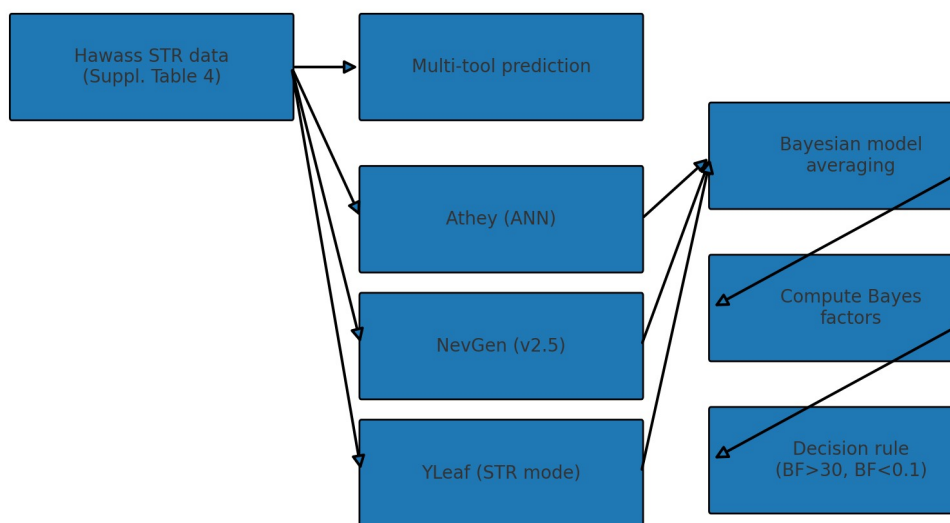


Figure 1: Bayesian multi-predictor genetic pipeline used in reproduction.

### Cultural Retention Rates in African Diaspora Locations

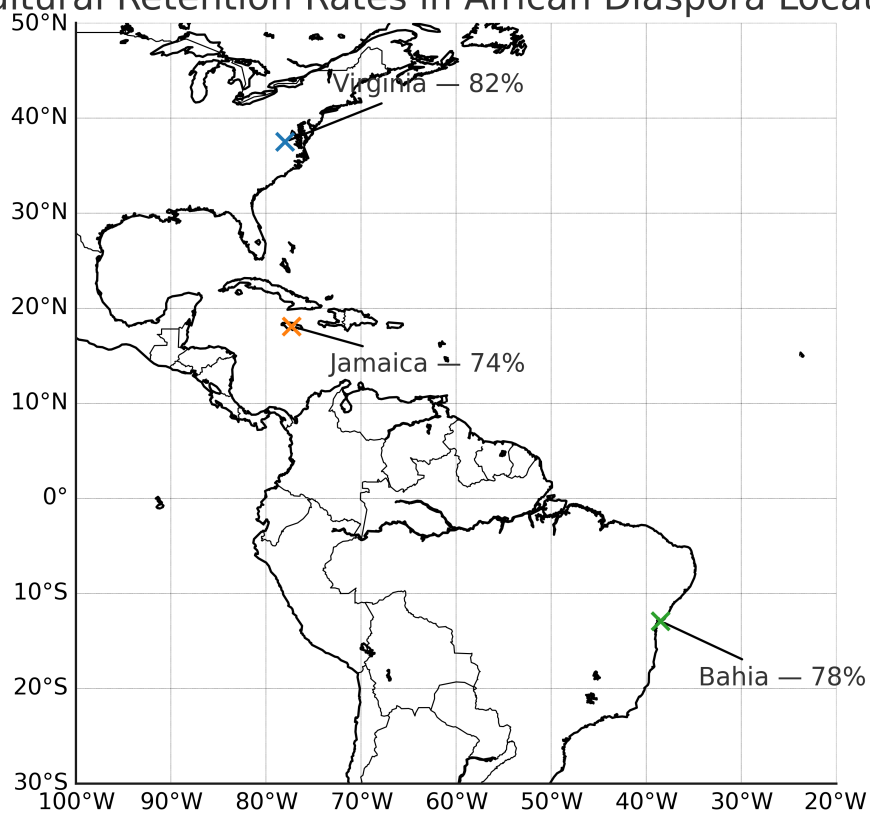


Figure 2: Map used for rapid verification of cultural retention rates.

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