

STATISTICAL ANALYSIS PIPELINE ADMIXTURE DATA FROM A HUMAN POPULATION SETTLEMENT MODEL

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MASSEY
UNIVERSITY
TE KUNENGA KI PŪREHURUA

UNIVERSITY OF NEW ZEALAND

Université
de BORDEAUX

INTRODUCTION

- ▶ Internship at Massey University (New Zealand)
- ▶ Computational Biology Research Group
- ▶ Part of a 2 years project
- ▶ Research assistant for the project:
 - ▶ François Vallée
- ▶ Supervisors:
 - ▶ Murray Cox
 - ▶ Marie Noelle Beurton-Aimar

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Context

- Geological and anthropological context
- Previous papers
- Model

Measures and comparisons

Pipeline

Statistical analysis





**FIRST SETTLEMENT WAVE
AROUND 45,000 YEARS AGO**

- ▶ First humans
- ▶ Ancestral Melanesian population
- ▶ Hunter-gatherers



**SECOND SETTLEMENT WAVE
AROUND 4,500 YEARS AGO**

- ▶ “Austronesian expansion”
- ▶ Two possible waves
- ▶ Admixture between populations
- ▶ What started it?
 - ▶ Agriculture knowledge?
 - ▶ Better navigation?

CONTEXT

PREVIOUS PAPERS

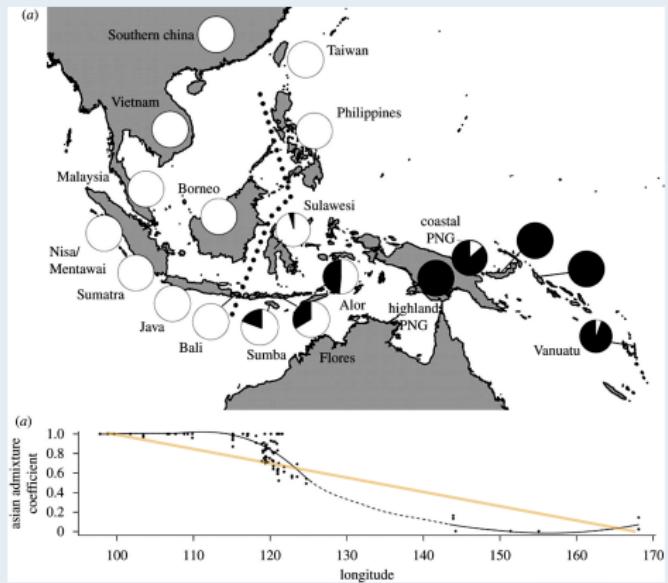
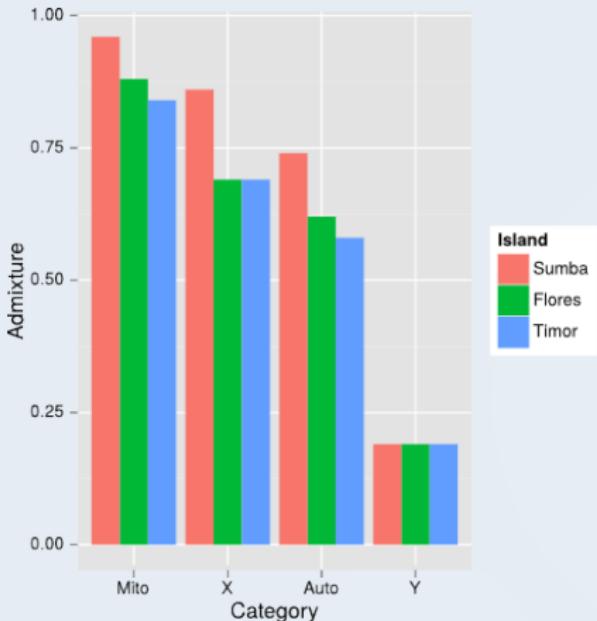


Figure : Cox et al. [2010]. *Proceedings of the Royal Society of London B: Biological Sciences*, modified

- ▶ Admixture measured on each island
- ▶ Expected: linear admixture change
- ▶ Observed: Non-linear admixture changes

CONTEXT

PREVIOUS PAPERS



- ▶ Difference of admixture by category of DNA
- ▶ Sex-biased admixture
- ▶ Implicit marriage rule?
- ▶ Melanesian ♂ — Asian ♀ marriages favoured?

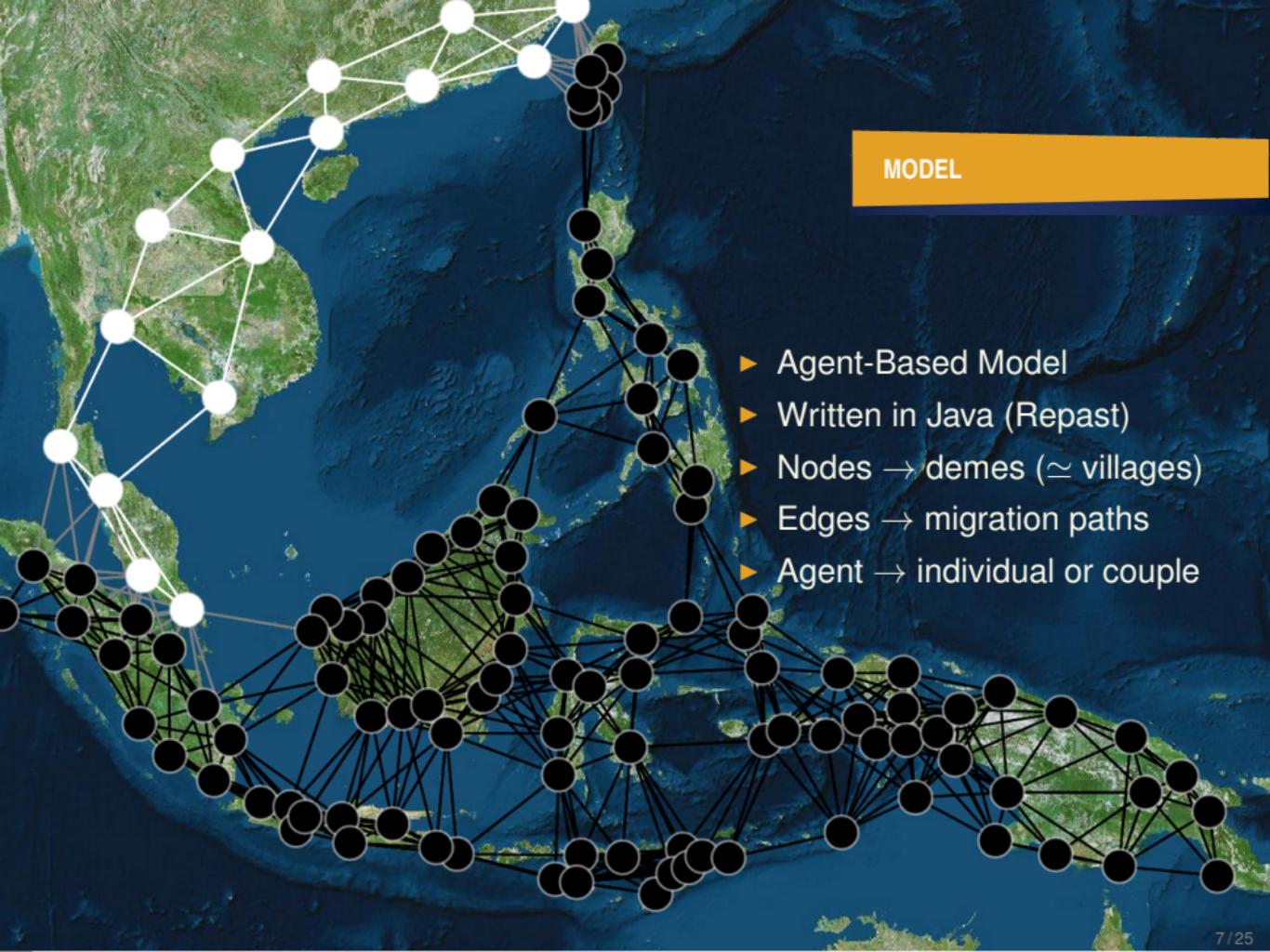
Figure : Data from Lansing et al. [2011]. *Journal of Anthropological Archaeology*

PREVIOUS PAPERS

Questions:

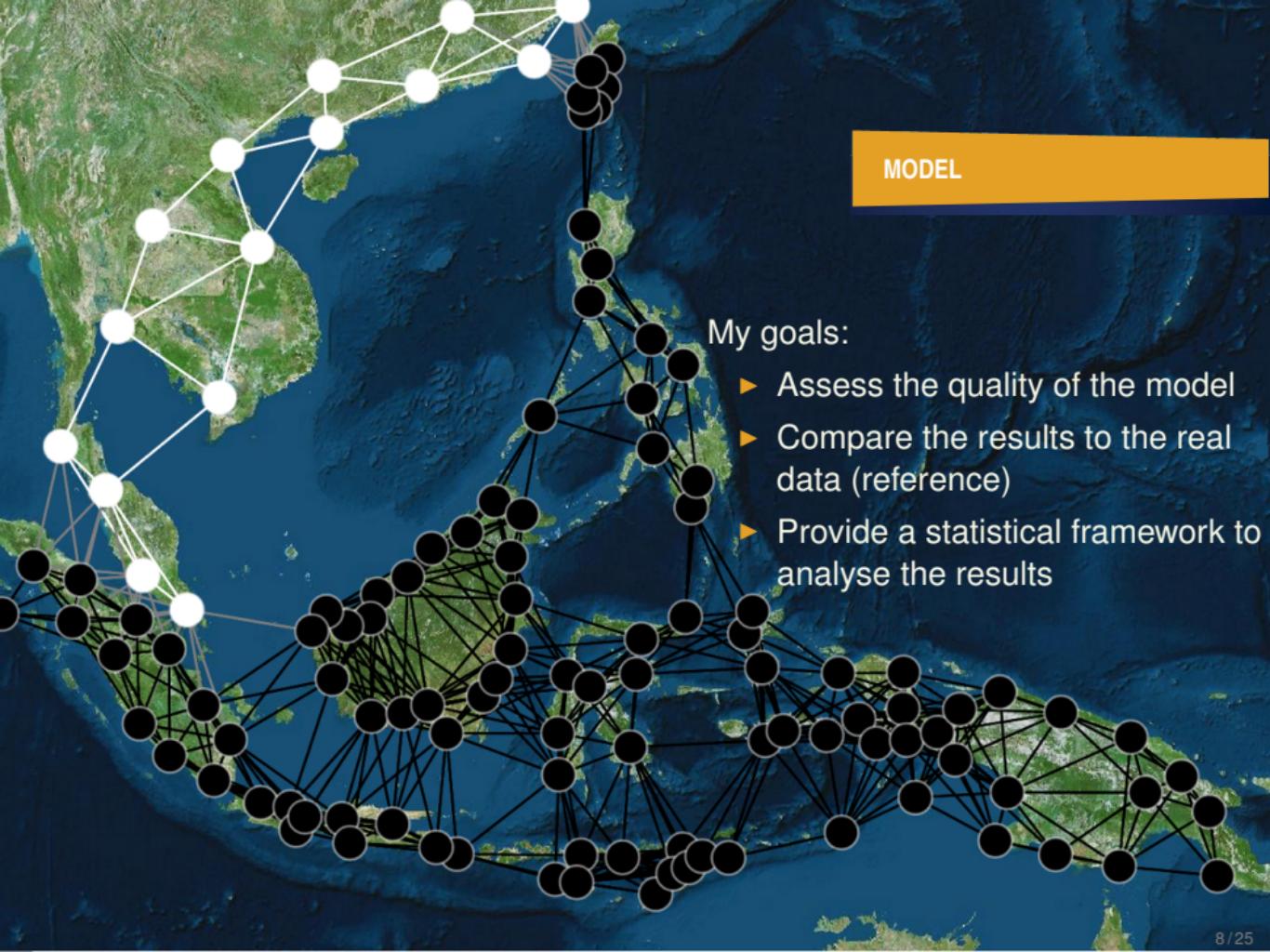
- ▶ Why the steep admixture gradient?
- ▶ Why the sex-biased admixture?
- ▶ What differences between the populations?

First step towards understanding → reproduce the scenario



MODEL

- ▶ Agent-Based Model
- ▶ Written in Java (Repast)
- ▶ Nodes → demes (\simeq villages)
- ▶ Edges → migration paths
- ▶ Agent → individual or couple



MODEL

My goals:

- ▶ Assess the quality of the model
- ▶ Compare the results to the real data (reference)
- ▶ Provide a statistical framework to analyse the results

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Context

Measures and comparisons

Observed data

Parameters

Comparison functions

Mean Square Distance

Partial Mantel Correlation

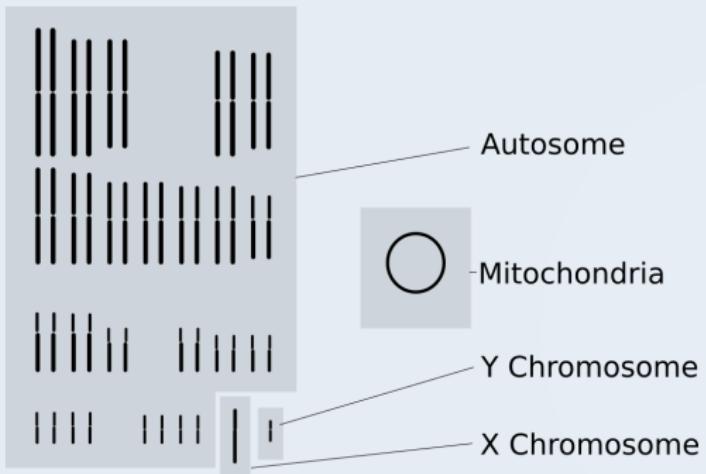
Summary statistics

Pipeline

Statistical analysis

MEASURES & COMPARISONS

OBSERVED DATA



- ▶ Discriminant markers
- ▶ Different parts of the DNA
- ▶ Associated with different origins
- ▶ Inside the model: values by agent
- ▶ Output of the model: values by deme

MEASURES & COMPARISONS

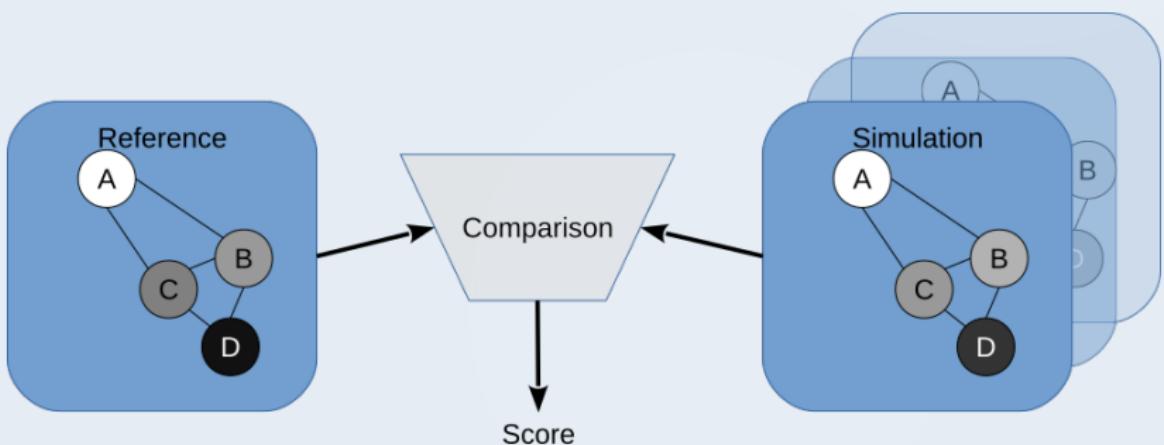
PARAMETERS

| Parameter | Estimated | Comment |
|-----------------------|------------------------|--|
| Migration prob. | $0.0 < x \leq 1.0$ | for a Melanesian agent |
| Migration prob. ratio | $1.0 \leq x \leq 4.0$ | corresponding ratio for an Asian agent |
| Fecundity | $2.5 < x < 8.0$ | for a Melanesian agent |
| Fecundity ratio | $1.0 \leq x \leq 2.0$ | corresponding ratio for an Asian agent |
| Marriage threshold | $0.0 \leq x \leq 0.25$ | affects marriages rules |
| Growth rate | $0.0 < x < 0.001$ | limiting rate of pop. growth |
| Number of agents | $100 \leq x < 400$ | pop. size in each deme, initially |
| Graph | {...} | nodes and edges of the graph |
| Starting distribution | {...} | distribution of pop. in the graph |

Table : Summary of the changing model parameters.

MEASURES & COMPARISONS

COMPARISON FUNCTIONS



MEASURES & COMPARISONS

COMPARISON FUNCTIONS

Mean Square Distance

$$MSD = \frac{\sum_{i=1}^n (AdRef_i - AdSim_i)^2}{n}$$

$$0 \leq MSD \leq 1$$

MEASURES & COMPARISONS

COMPARISON FUNCTIONS

Mean Square Distance

$$MSD = \frac{\sum_{i=1}^n (AdRef_i - AdSim_i)^2}{n}$$

$$0 \leq MSD \leq 1$$

Example

| Island | A | B | C | D |
|-----------|-----|-----|-----|-----|
| Reference | 1.0 | 0.5 | 0.4 | 0.0 |
| Simulated | 1.0 | 0.4 | 0.3 | 0.2 |
| Distance | 0.0 | 0.1 | 0.1 | 0.2 |

$$MSD = 0.1$$

MEASURES & COMPARISONS

COMPARISON FUNCTIONS

Mantel Partial Correlation

$cor = \text{mantel.partial}(M_{\text{Simulated}}, M_{\text{Reference}}, M_{\text{geographical}})$

$$-1 \leq cor \leq 1$$

MEASURES & COMPARISONS

COMPARISON FUNCTIONS

Mantel Partial Correlation

$cor = \text{mantel.partial}(M_{\text{Simulated}}, M_{\text{Reference}}, M_{\text{geographical}})$

$$-1 \leq cor \leq 1$$

Example

$$\text{mantel.partial} \left(\begin{bmatrix} 0.0 & 0.5 & 0.6 & 1.0 \\ 0.5 & 0.0 & 0.1 & 0.5 \\ 0.6 & 0.1 & 0.0 & 0.4 \\ 1.0 & 0.5 & 0.4 & 0.0 \end{bmatrix}, \begin{bmatrix} 0.0 & 0.6 & 0.7 & 0.8 \\ 0.6 & 0.0 & 0.1 & 0.2 \\ 0.7 & 0.1 & 0.0 & 0.1 \\ 0.8 & 0.2 & 0.1 & 0.0 \end{bmatrix}, \begin{bmatrix} 0.0 & 300 & 250 & 400 \\ 300 & 0.0 & 120 & 150 \\ 250 & 120 & 0.0 & 100 \\ 400 & 150 & 100 & 0.0 \end{bmatrix} \right)$$

$$cor = 0.72$$

MEASURES & COMPARISONS

COMPARISON FUNCTIONS

Summary statistics:

- ▶ Mean Square Distance
 - ▶ Autosomal admixture
 - ▶ X-Chromosomal admixture
- ▶ Partial Mantel Correlation
 - ▶ Autosomal admixture
 - ▶ X-Chromosomal admixture

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Measures and comparisons

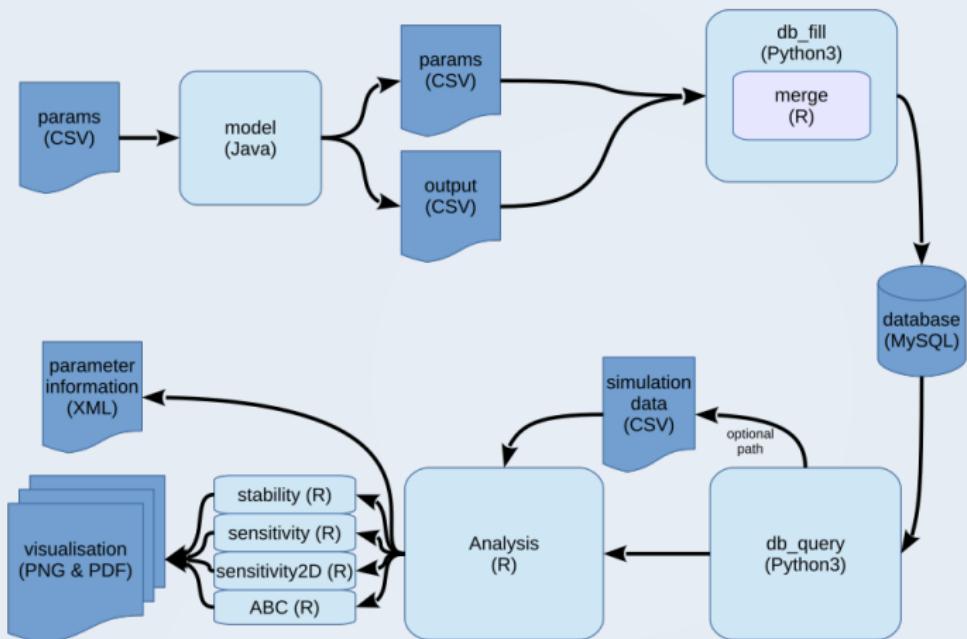
Pipeline

Overview

Statistical analysis

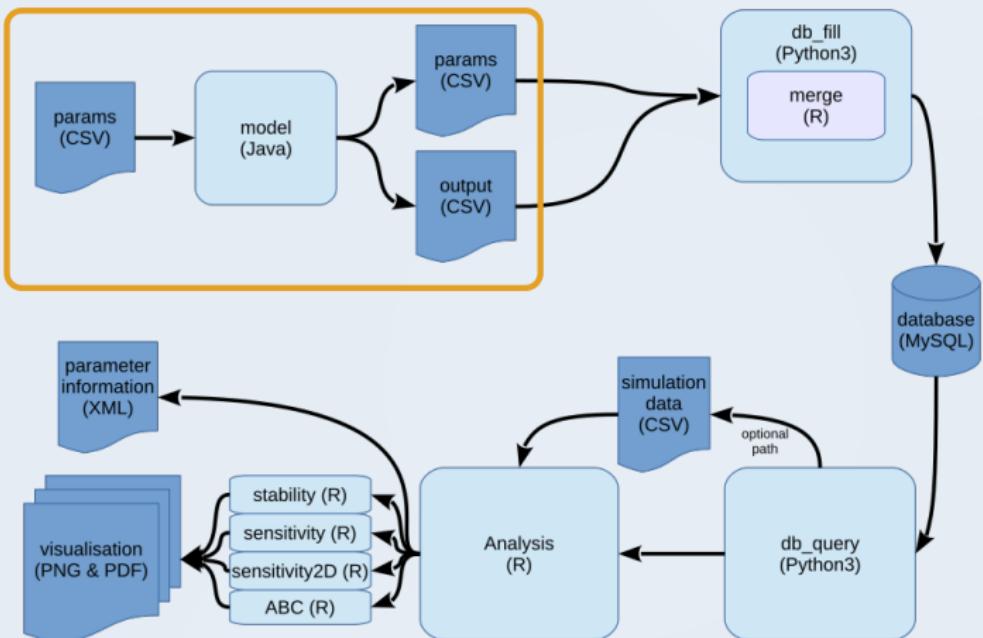
PIPELINE

OVERVIEW



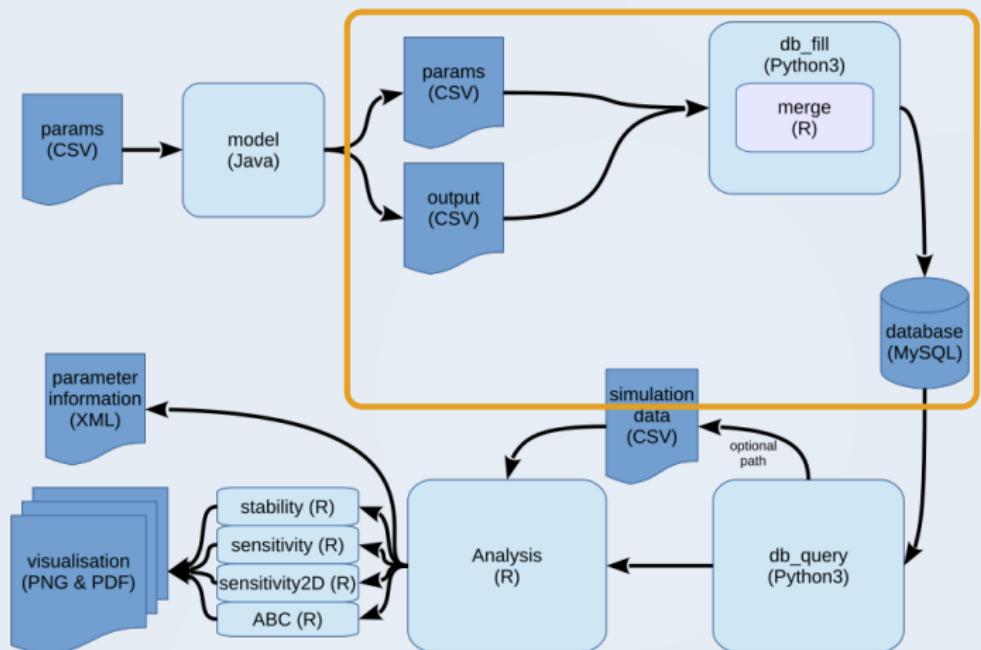
PIPELINE

MODEL RUNS



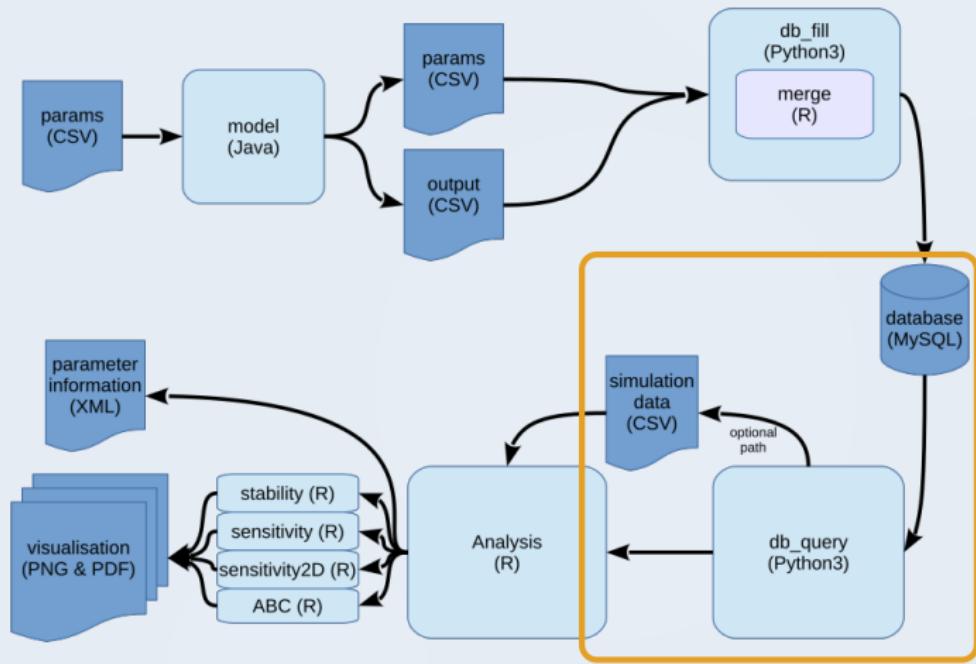
PIPELINE

DATA MERGING, AGGREGATING AND STORAGE



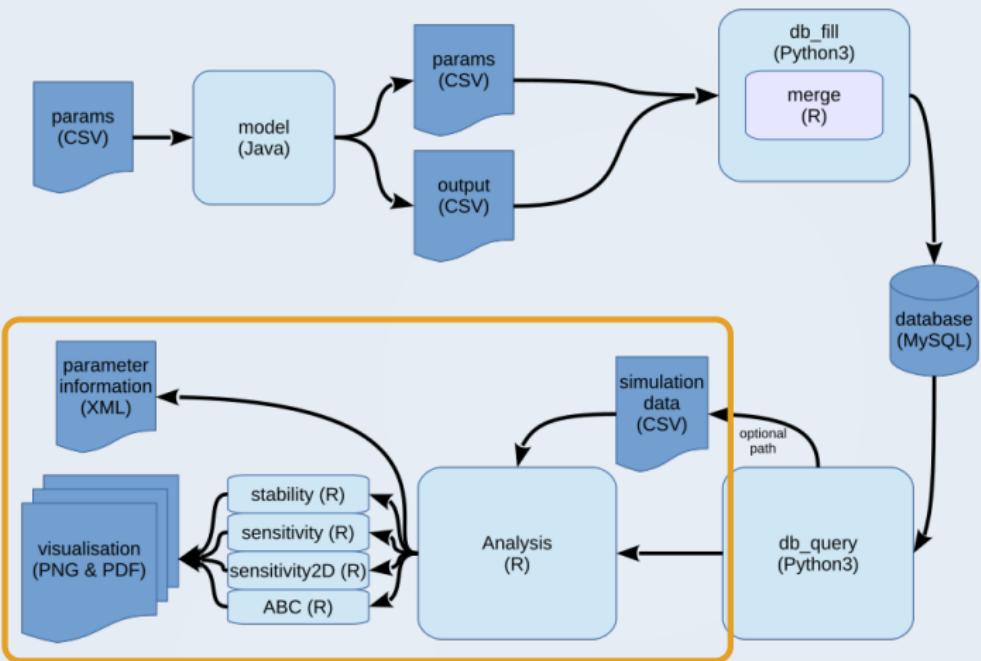
PIPELINE

DATA QUERYING



PIPELINE

ANALYSES



PIPELINE

OVERVIEW

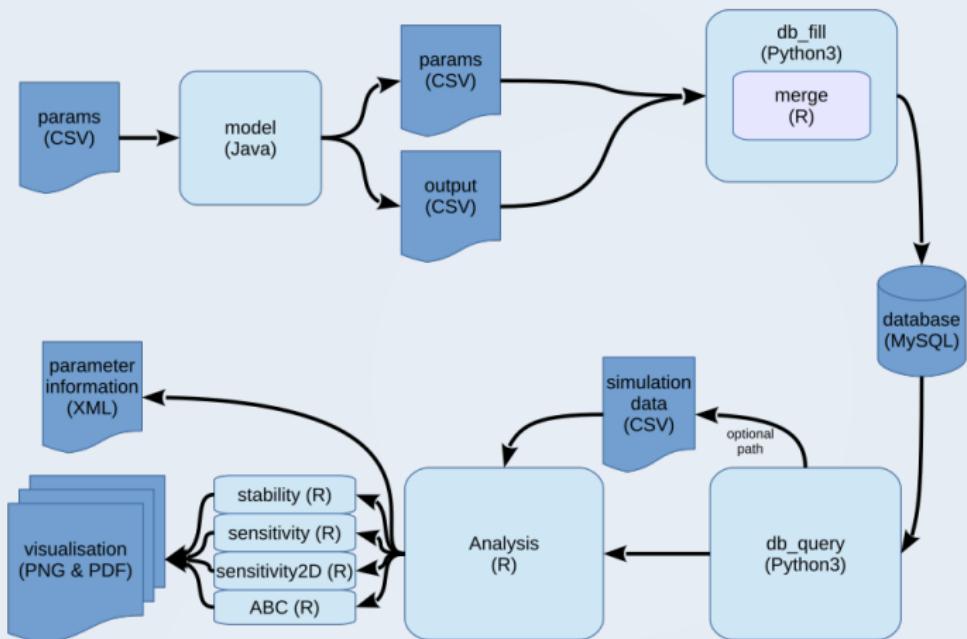


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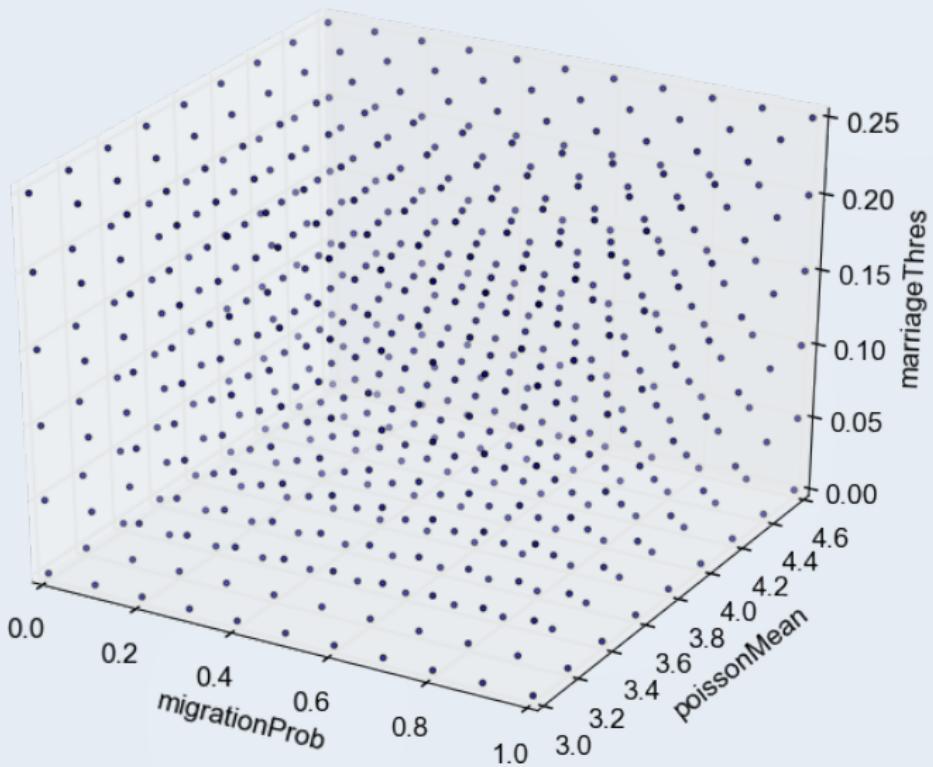
Statistical analysis

Grid search

Approximate Bayesian Computation

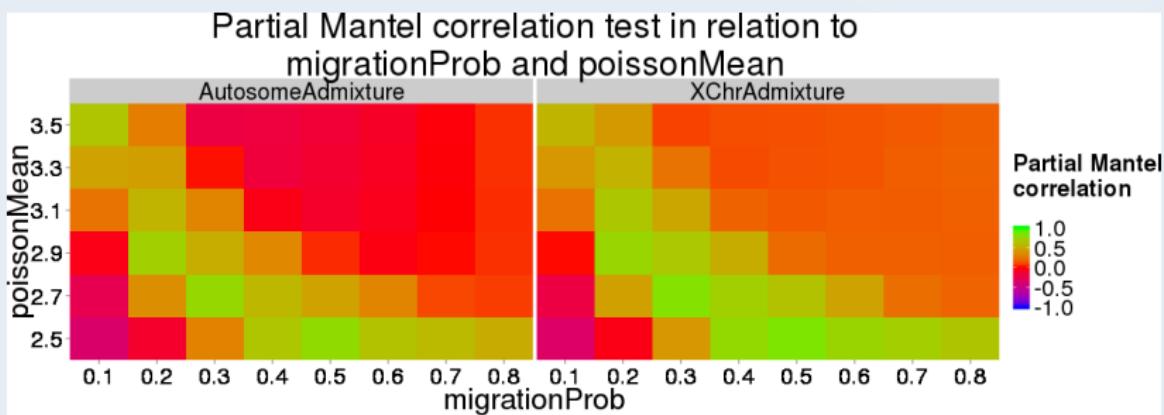
STATISTICAL ANALYSIS

GRID SEARCH



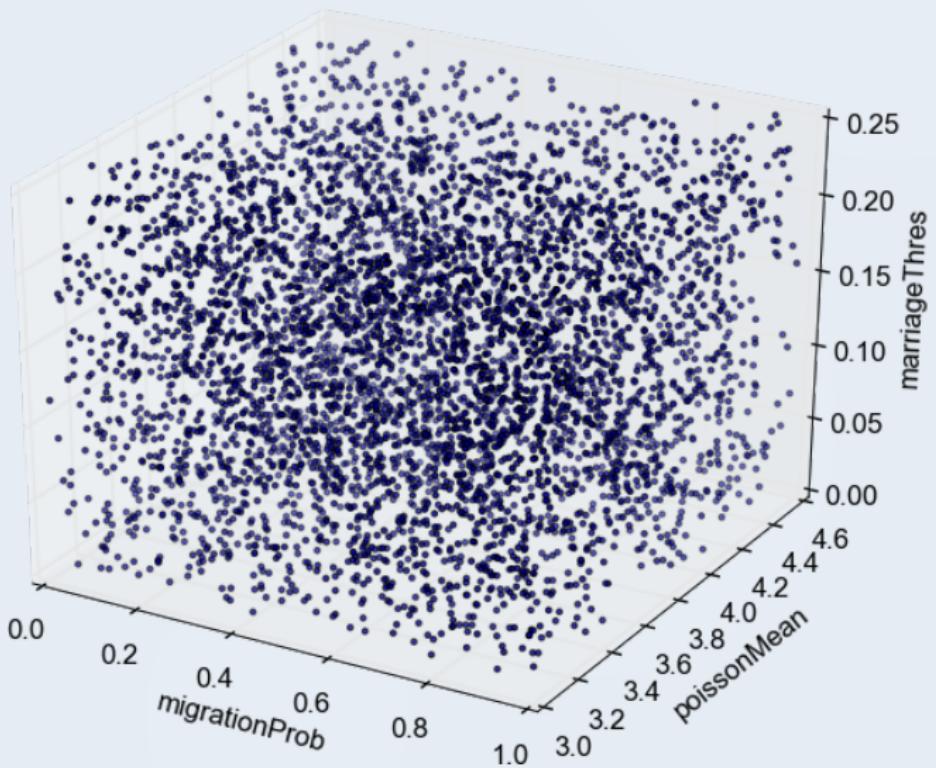
STATISTICAL ANALYSIS

GRID SEARCH



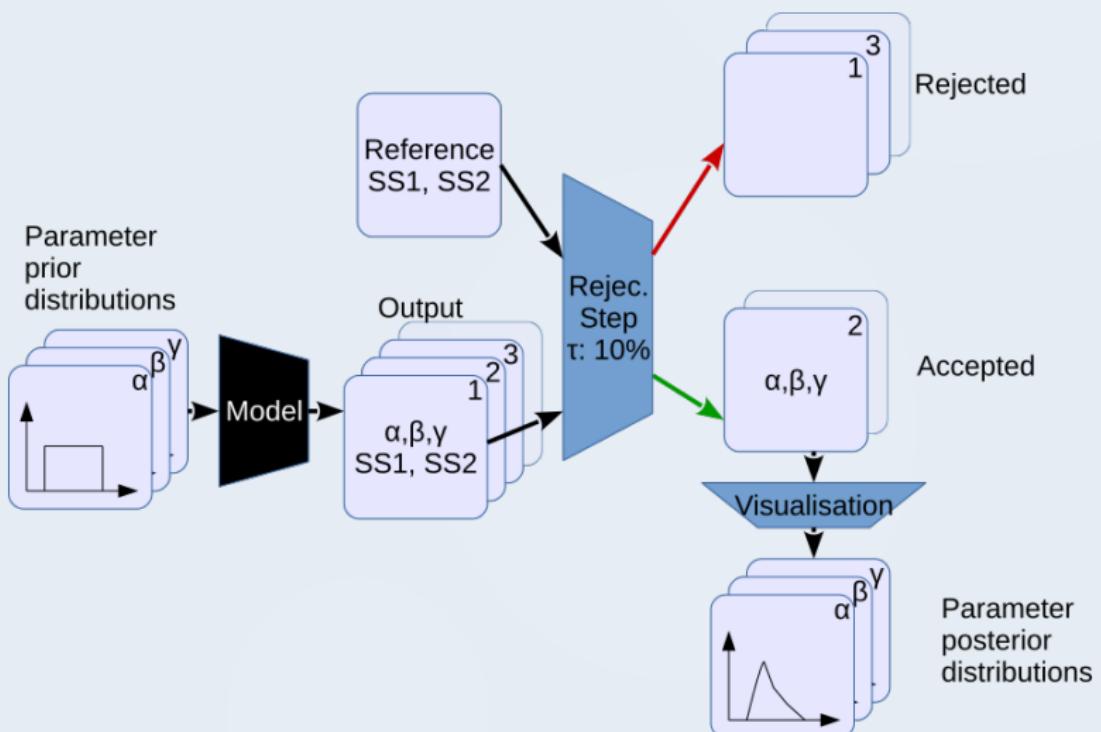
STATISTICAL ANALYSIS

APPROXIMATE BAYESIAN COMPUTATION



STATISTICAL ANALYSIS

APPROXIMATE BAYESIAN COMPUTATION



STATISTICAL ANALYSIS

APPROXIMATE BAYESIAN COMPUTATION

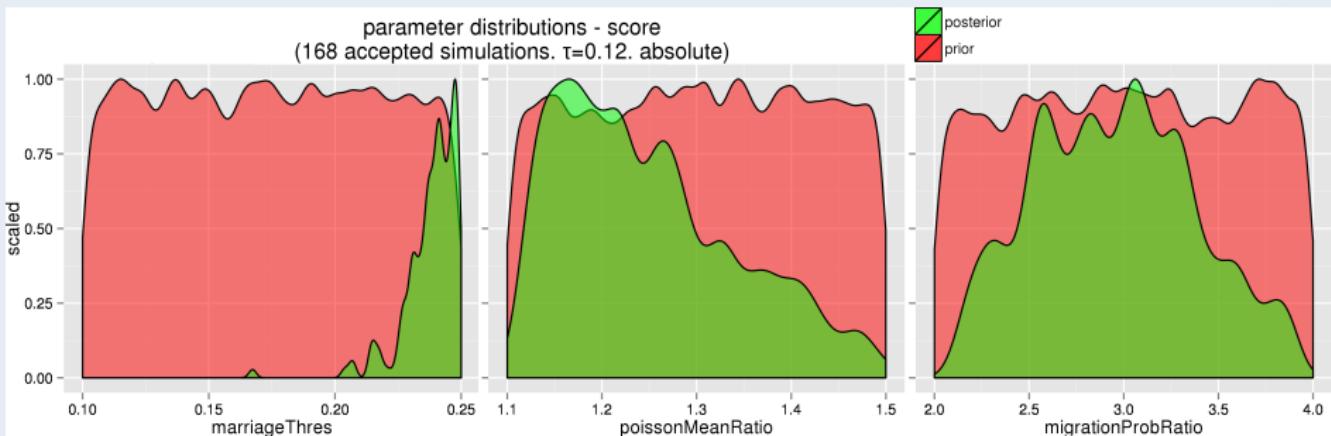


Figure : Example output from an ABC analysis

CONCLUSION

- ▶ Pipeline:
 - ▶ Modular pipeline
 - ▶ Stream processing
 - ▶ Database use
- ▶ Statistically powerful approach:
 - ▶ Approximate Bayesian Computation
 - ▶ Accept good results
 - ▶ Discard bad results
- ▶ “Austronesian Expansion”:
 - ▶ Higher fecundity
 - ▶ Higher migration rates
 - ▶ Melanesian ♂ — Asian ♀ marriages favoured

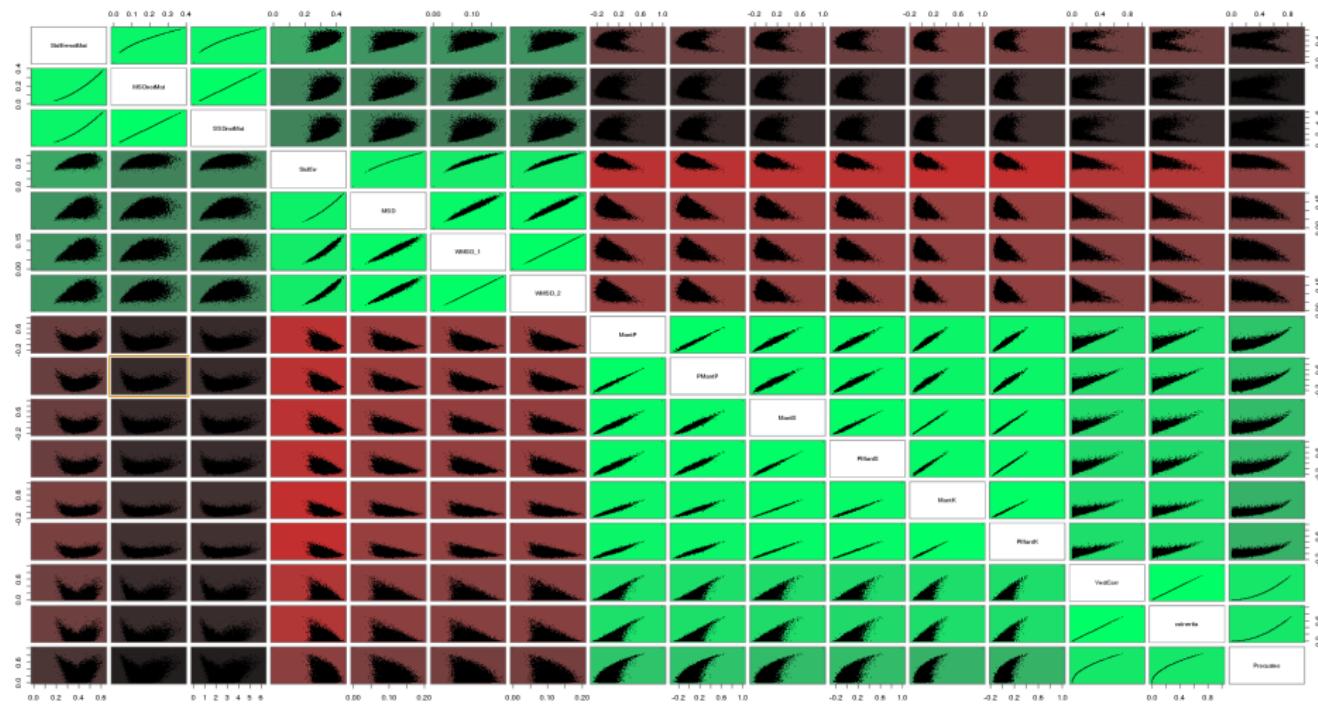
THANK YOU

Questions?

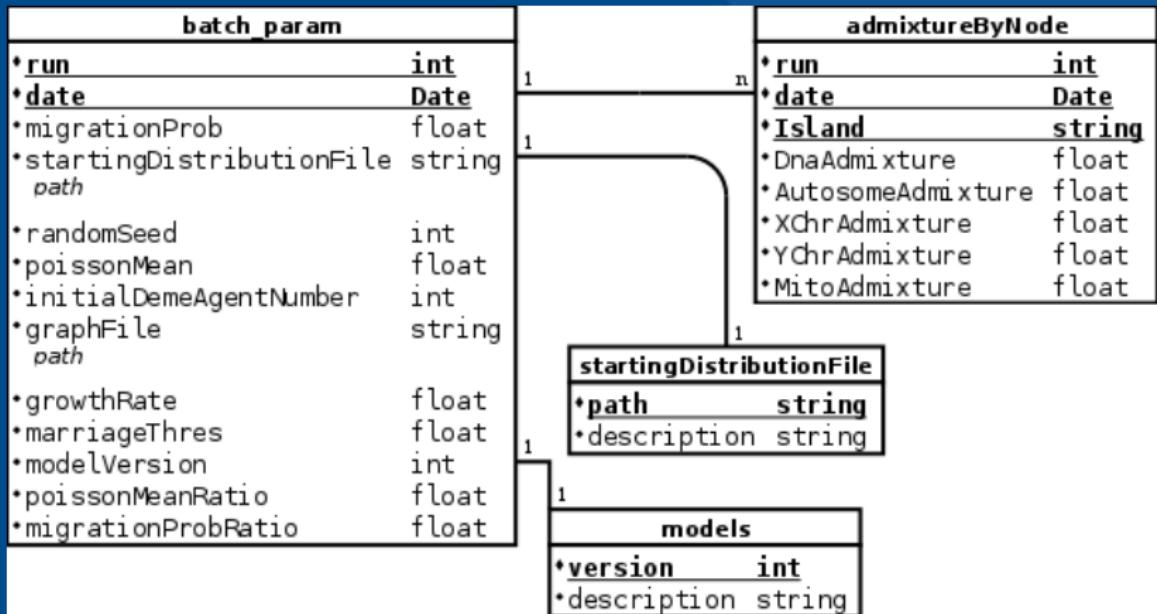
map backgrounds from “HERE Satellite”

Computational Biology Research Group: massey.genomicus.com

COMPARISON FUNCTIONS

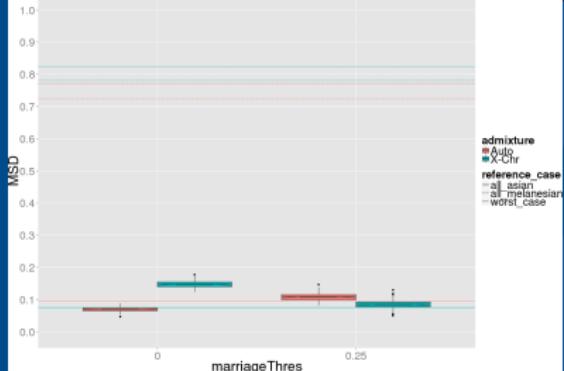


DATABASE STRUCTURE

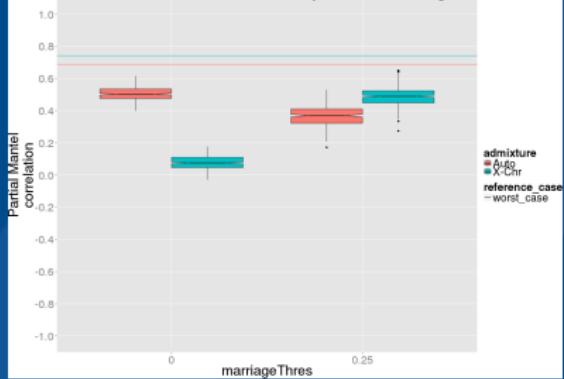


SENSITIVITY 1D - COMPARISONS

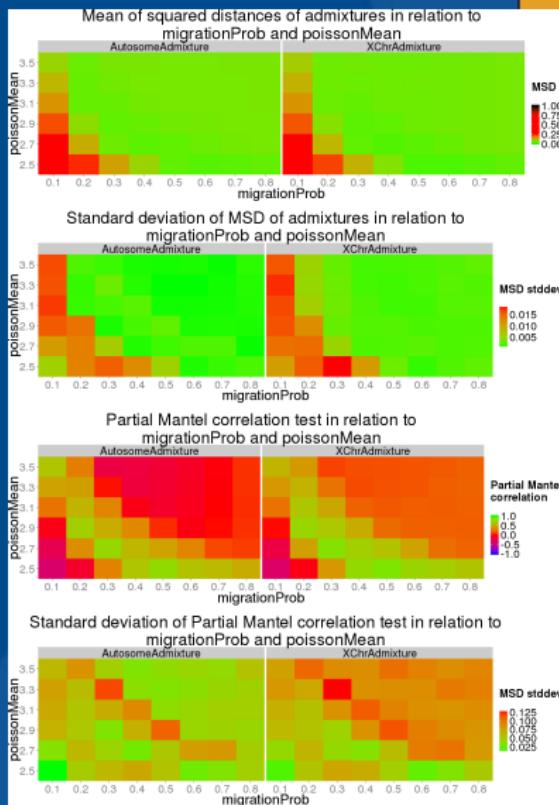
Mean of squared distances of admixtures for every different marriageThres



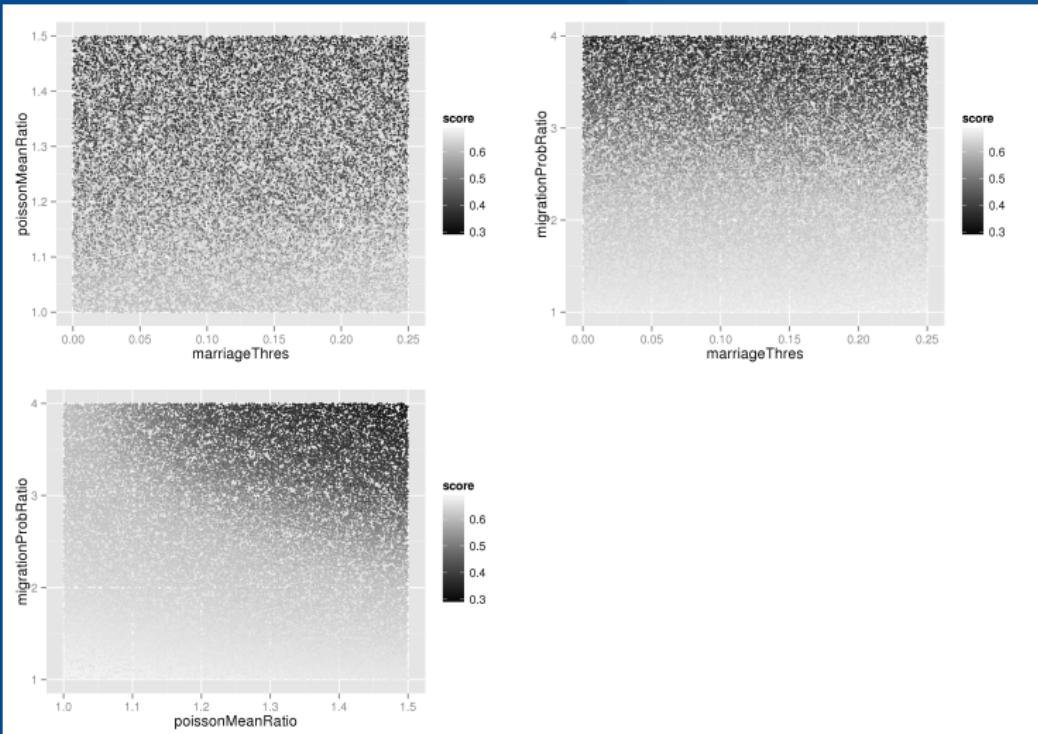
Partial Mantel correlation test for every different marriageThres



SENSITIVITY 2D - COMPARISONS

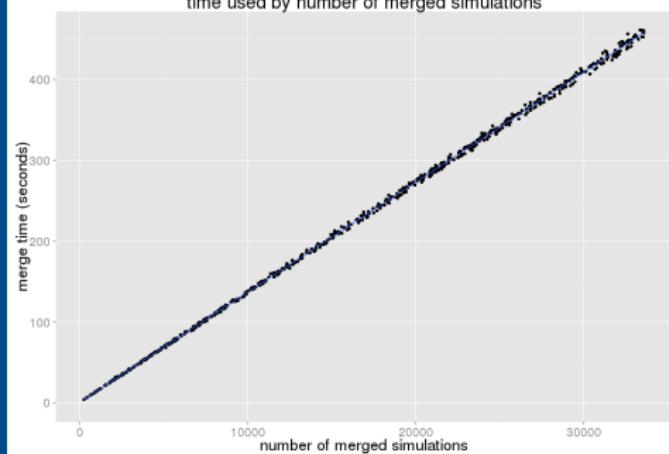


ABC SCATTER SCORE



BENCHMARK MERGE

time used by number of merged simulations

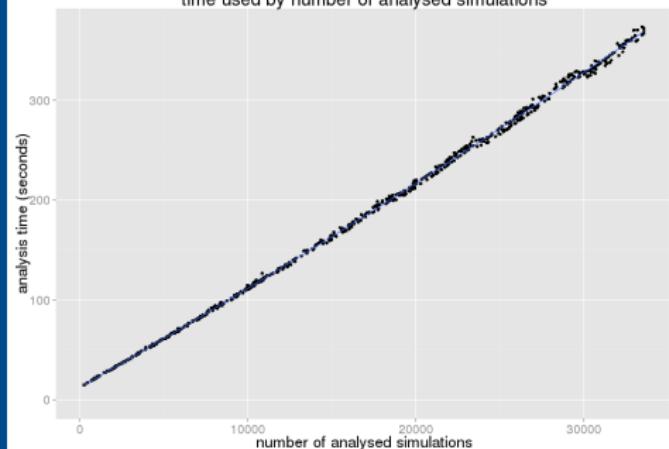


maximum memory used by number of merged simulations



BENCHMARK ANALYSIS & ABC

time used by number of analysed simulations



maximum memory used by number of analysed simulations

