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Project report: TITLE

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Contents

Introduction

Two groups of populations can be identified in the Islands of South-East Asia (ISEA), one is composed of the Melanesians, whose ancestors settled in these islands during the first human settlement, around 45 thousand years ago. The other arrived more recently during a period often called the Austronesian expansion, between 5 and 4 thousand years ago, when people from mainland China settled in the islands. Nowadays, people living in this area have mixed genomic ancestry and markers can be identified and defined as either from an Asian ancestry or a Melanesian one. These markers are based on single nucleotid polymorphisms (SNPs) located in different chromosomes and 52 markers can be used to define accurately the admixture of the Asian ancestry in every individuals [Cox et al., 2010].

The choice of these SNPs is a result of previous studies at Massey University, the University of Arizona, the Santa Fe Institute, and the Eijkman Institute that sequenced 1430 individuals from 60 populations. This set of SNPs is defined as highly informative and allows to define the ancestry of a person based on a small quantity of markers that are highly discriminant.

Two specific patterns can be seen [Lansing et al., 2011]. One is the non-linear gradient of Asian admixture along the longitudinal axis in the different islands in the area, that could correspond more or less to how the Austronesian expansion wave propagated from the mainland. The second is the difference of admixture when looking at specific parts of the genomes associated with male or female ancestry, implying a possible gender-biased expansion.

Chapter 1

Project presentation

The project consists of developing a model of the Austronesian expansion throughout the ISEA that could reproduce the same two patterns observed in the real data. The first pattern can be seen in the figure 1.1 and is a non-linear gradient in Asian admixture that declines abruptly around the eastern part of Indonesia. The second one, represented in the figure 1.2, shows the differences of admixtures on distinct parts of the DNA for different islands. These differences would tend to appear in a context where marriages between Asian women and Melanesian men would be favoured.

The whole idea of the project is thus to try to reproduce the same patterns and to determine which sets of parameters led to outputs similar to what is observed. The model is set to run from the beginning of the Austronesian expansion, around 4.500 years ago, to nowadays.

1.1 Values observed

The observed values from the model will be the admixtures of every deme, a deme being the generic name for a single unit of space corresponding to a populated area, this can be assumed similar to a village. The admixtures will be measured for five parts of the DNA, the whole DNA, the mitochondrial DNA, the autosomal DNA and the X and the Y-chromosomal DNA. These admixtures values will only be for the last step of the simulation, since they

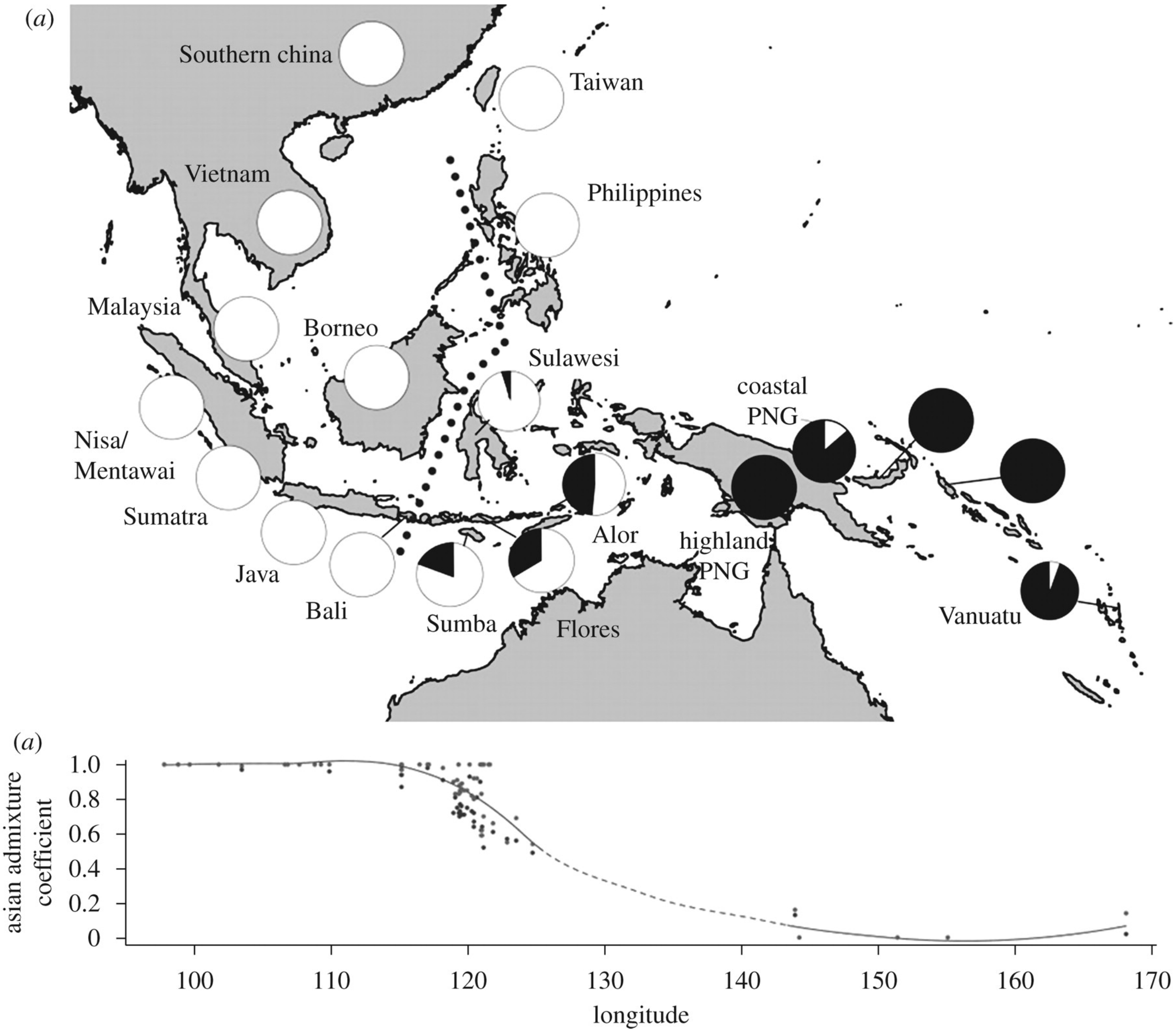


Figure 1.1: Local admixture rates across the Indo-Pacific region. (a) Pie charts showing mean regional admixture rates (Asian component in white; Melanesian component in black). Wallace's biogeographic line is shown as a dotted line. Regional admixture rates are shown for data reduction purposes; (b) Change in Asian admixture rates calculated from all SNPs combined (black line). Regions with no data indicated by a dashed line (exact gradient unknown). Asian admixture estimated from autosomal and X-chromosomal SNPs are indicated by black and grey points, respectively. Note the decline in Asian admixture beginning in eastern Indonesia, as well as preferential retention of X-chromosomal (grey) versus autosomal (black) diversity. Reproduced unmodified from [Cox et al., 2010].

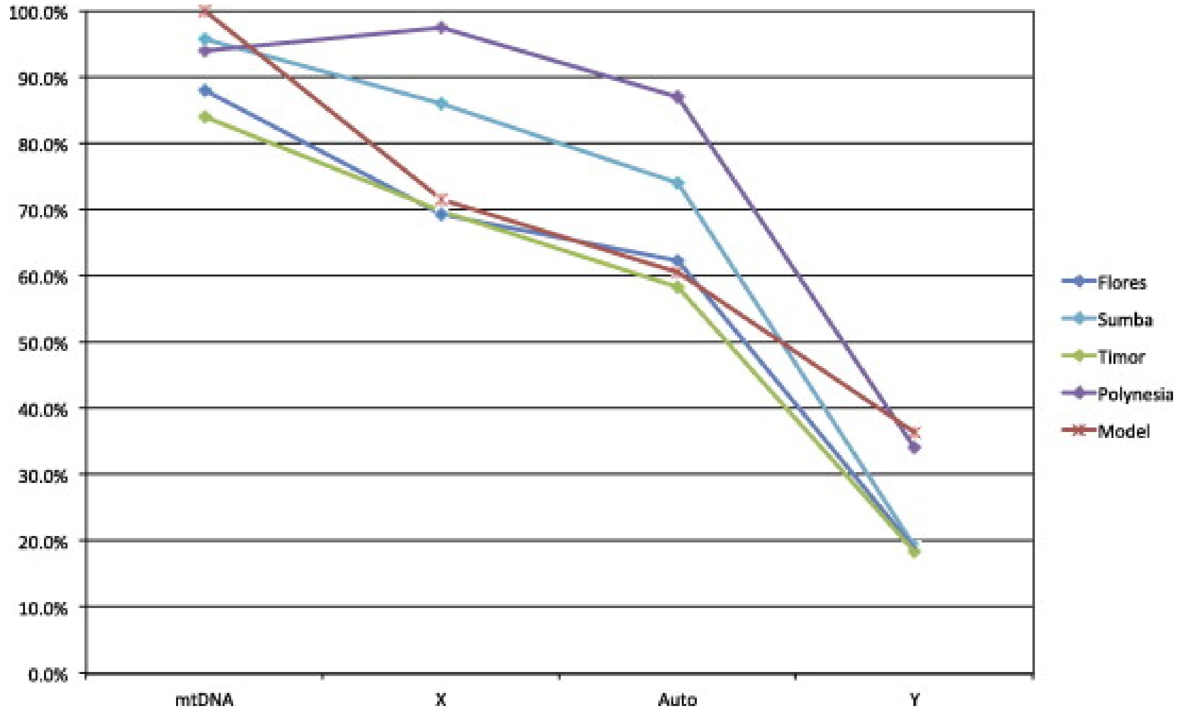


Figure 1.2: Fraction of Asian DNA in four genetic systems compared with model results for $\alpha = 0.02$ and 50 generations. Sample sizes: Flores = 453, Sumba = 639, Timor = 529. Reproduced unmodified from [Lansing et al., 2011].

will be the only values comparable to the real observed admixtures.

1.2 Model used

The model will be a graph of nodes, each node corresponding to a deme, and each edge corresponding to a possible migration route between demes (see figure 1.3). People will live in the graph, in every node, and these agents will be able to migrate and to form families. The graph and the agents living in it will respond to a set of basic rules regulated by parameters and the goal is then to observe the emerging behaviours arising from it.

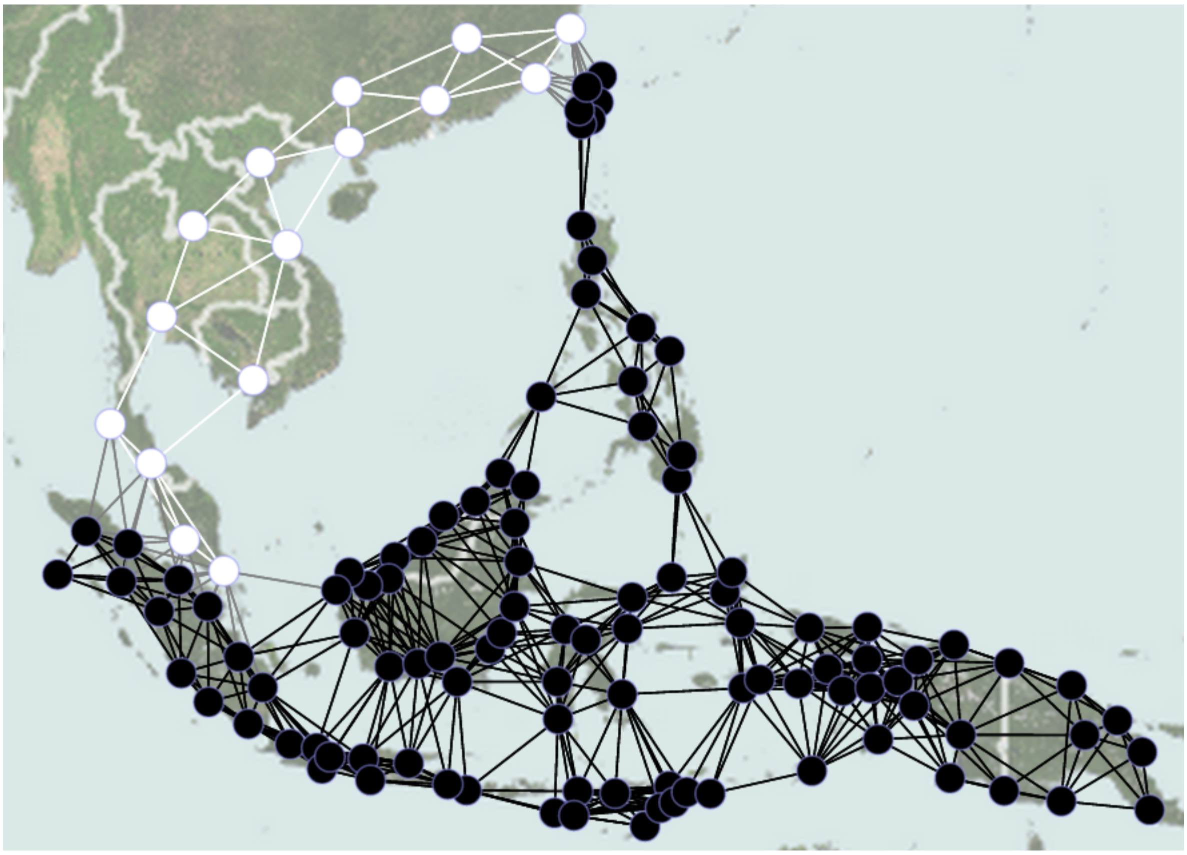


Figure 1.3: Nodes of a model superimposed on the map of the modelled region. White nodes are the Asian nodes at the beginning of the simulation and black nodes are the Melanesian ones, according to one of the starting distributions used as parameter

Because of the stochasticity of the model, and because the parameters used might not be viable, a simulation can end up having non-usable outputs. For example, if an island ends up being completely empty, the admixture values yielded by this specific simulation will be the value `NaN` (not a number). In such extreme cases, the model can be considered as "failed" and can either be discarded or given the worst possible score, depending on the current analysis. Arbitrarily, two rules have been set to define that a simulation has failed:

- If a deme has a population of less than 10% of the most populous deme in the network, it is considered as empty;
- If more than 25% of the demes in any of the islands are empty, the simulation is considered as failed.

Comparison to other models

This model is one of the types of models that could have been chosen. For example, other models can have the single unit of time defined as a generation (roughly equivalent to 20 years), here the unit of time has been defined as one year to have more precise time steps in the model and to be closer to the reality due to the higher time resolution.

Coalescent models also exist, they take the problem the other way around by trying to rebuild the past, the ancestry of the individuals, based on present data. They do it this way to try to reduce the amount of computation needed, they therefore don't have to simulate agents whose line would have ended up extinct. It is not really suited for this agent-based model though because parameters vary among agents and this is not trivial to do with coalescence.

Parameters

Numerous parameters can be set in the model. A lot have been set in the code and are immutable without actually updating the code but this have been done to simplify the actual use of the model by limiting the number of

Parameter	Values	Estimated	Comment
Migration prob.	$\mathbb{R}_{0\leq x\leq 1}$	$\mathbb{R}_{0<x\leq 0.8}$	prob. to start migrating for a Melanesian agent
Migration prob. ratio	$\mathbb{R}_{\geq 0}$	$\mathbb{R}_{1\leq x\leq 4}$	corresponding ratio for an Asian agent
Fecundity	$\mathbb{R}_{\geq 0}$	$\mathbb{R}_{2.3<x<6}$	Poisson law mean for a Melanesian agent
Fecundity ratio	$\mathbb{R}_{\geq 0}$	$\mathbb{R}_{1\leq x\leq 1.5}$	corresponding ratio for an Asian agent
Marriage threshold	$\mathbb{R}_{0\leq x\leq 1}$	$\mathbb{R}_{0<x<0.5}$	affects marriages rules
Growth rate	$\mathbb{R}_{0\leq x\leq 1}$	$\mathbb{R}_{0<x<0.001}$	limiting rate of pop. growth
Number of agents	$\mathbb{Z}_{\geq 0}$	$\mathbb{Z}_{50<x<400}$	pop. size in each deme, initially
Graph	{...}	{...}	composition of the graph (nodes and edges)
Starting distribution	{...}	{...}	distribution of pop. in the graph

Table 1.1: Summary of the model parameters

parameters to set and because some actually could not change or changing them would not hold any meaning nor output realistic values.

The parameters that can actually be adjusted are listed in the table 1.1 and can be put into different groups. Most of them are continuous parameters, whose values are numbers, and a few of them are discrete. The discrete parameters are the graphs used and the starting distributions. While the former corresponds to the topography of the graph used in the model, comprising the nodes and the edges between them, the latter is the distribution of the Melanesian and Asian populations in the graph at the initial step of the model.

The model can actually work with a lot of different parameter values, those corresponds to the "values" columns in the table 1.1, but knowing what we are dealing with and the context of the model, an estimation of possible realistic values can be found easily and will need to be refined later on during the analysis processes (see 2.3) and based on values suggested by other anthropological studies.

1.3 Statistical analysis framework

Given that the model will be run numerous times, with a lot of different changing values for the parameters, a robust statistical analysis framework needs to be implemented in order to be able to extract meaningful information from the high quantity of generated data.

Recently, a fairly recent statistical analysis framework has been used more and more in the context of population simulations. This framework is called ABC, standing for Approximate Bayesian Computation. Its use is recommended when the high quantity of data and the high dimensionality of it makes difficult the use of standard statistical framework. It still relies highly on standard statistical tools but instead of giving one best result, it tries to give a distribution of best possible parameters. It answers the question of, given a set of parameter distribution, that are called “priors”, what are the distributions, subsets of the priors, that gives best results. This set of outputted distributions are then called “posteriors”.

Its use has been increasing recently and some examples of papers using the ABC in similar contexts are [Guillot et al., 2015] or [Kehdy et al., 2015].

Chapter 2

Implementation

The model itself has been developed in Java using the Repast Simphony framework [North et al., 2013], a cross-platform framework made to write flexible agent-based models. The agents corresponds either to a single person or a couple that evolve in the demes. Each deme is a node in a graph and possible migration path between demes are edges of this graph. Therefore, the implementation consists of agents evolving in a graph.

The different parts of the implementation are detailed in the next sections. A global overview of the pipeline is available in the figure 2.3.

2.1 Run management

The fact that many simulations are required to be able to infer meaningful information from the model imply that they cannot be run sequentially on a single desktop computer. In fact, if one decided to do so, the time to run enough simulations to be statistically relevant could be counted in years. Luckily, every simulation being independent from the others, there are multiple ways to generate more results in less time. Firstly, since nowadays most of the computers have multiple processors, one computer can run multiple simulation concurrently. Also, a cluster of computers can be used and the simulations needed can be dispatched among the nodes of the cluster so that they each run the simulations they were assigned. When all of the nodes have ended their runs, their outputs can be aggregated and/or stored.

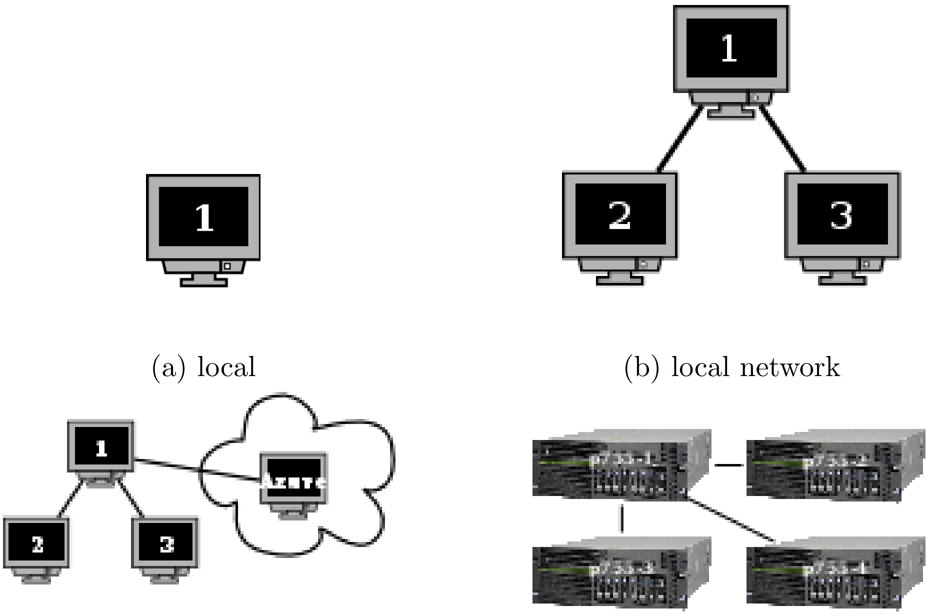
Different levels have been used. First, running the simulations locally (figure 2.1a), on a single computer, then using the three computers in the office as a cluster of compute nodes (figure 2.1b), for more heavy batches. Also, since Massey University just made an agreement with Microsoft Azure, that provides computing “in the cloud”, simulations have been run transparently adding virtual machines on the Microsoft Azure system to the cluster of computers in the office (figure 2.1c). Finally, when the computation requirements were to high, for really huge batches, the NeSI[1]'s High Performance Computing (HPC) facilities have been used (figure 2.1d). They provide servers specially designed for scientific computation and can be tasked with hundreds of parallel jobs at a time and multiple batches can be queued so they will be run as soon as computational power is available. Each node is an IBM Power755 machine.

The most powerful level used for this study is obviously using the HPC but a trade-off of using this system is that, since it is shared by multiple users and is managed by a third-party, it requires specific settings and it cannot be used exactly as can be a custom cluster of computers. The batches have to be submitted to a load leveller to the system and thus slight changes have been made to the way the model and the Repast framework are launched. Simulations run on this HPC use several nodes (usually around 4), with each of these nodes having 32 threads available for the simulations. This configuration leads to the parallel simulation of more than a hundred of scenarios at the same time.

2.2 Data processing, storage and query

Since running a lot of simulations, with a lot of different parameters, can generate a lot of output files whose original parameters can be hard to track, a way to keep them organised was needed. Doing so, it would also be possible to use results from different batches and to analyse them together, thus

[1] New Zealand eScience Infrastructure



(a) local

(b) local network

(c) local network and Azure

(d) NeSI

Figure 2.1: Different set-ups to run the model

avoiding to redo simulations for parameter values already tested.

The organised way to store this is naturally in a database. The choice has been made to use a relational database, specifically MariaDB (a fork of Oracle's MySQL). The structure and indices have been designed so that the parameters can be efficiently queried. The tables and relations between them can be seen in the figure 2.2. It has first been developed and tested locally and then, once it was working properly, it was deployed on a database server provided by Massey University for research purposes.

The use of the database can be done through phpMyAdmin but two scripts have been done to interact with it, one that adds the model outputs to the database and an other one that queries the database. The scripts have been written in Python3, using the PyMySQL module to access the MariaDB database, and internally using an other script, in R, that treats the data before adding them to the DB.

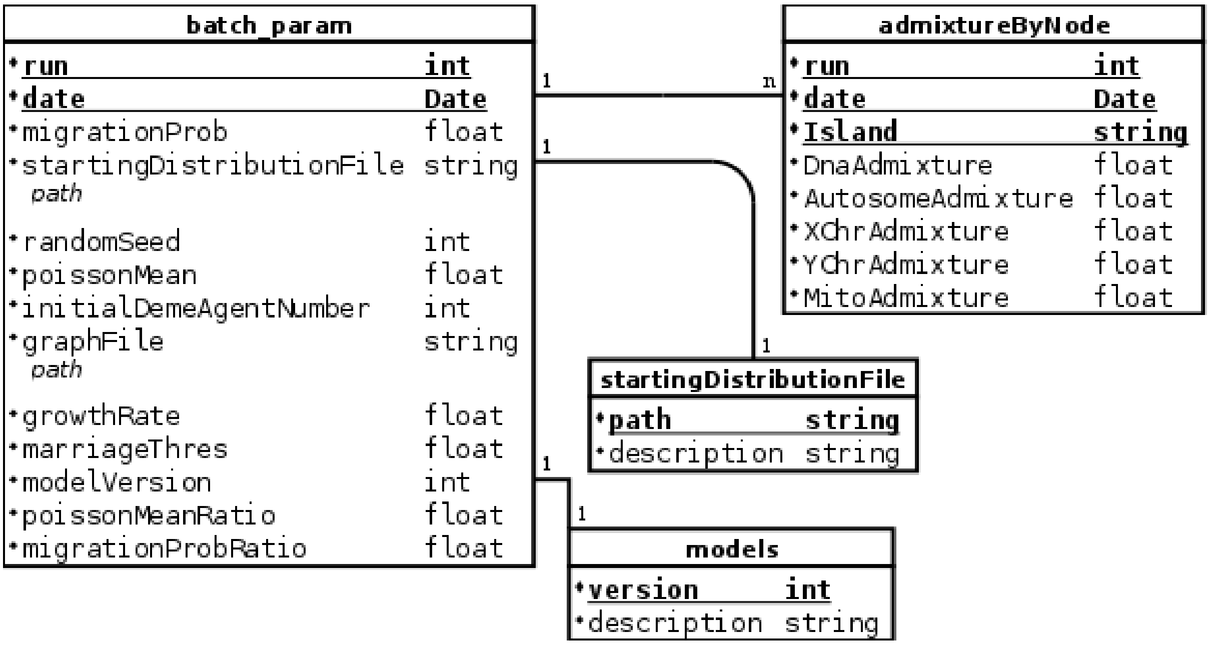


Figure 2.2: Structure of the database storing the results of the simulations and the corresponding parameters

2.3 Analysis

2.3.1 Comparisons

To be able to compare two different scenarios, one has to define comparison functions that will be able to provide a value of similarity or dissimilarity when provided with observable values that characterise the scenarios. In this case, the comparison is done between the real observed data and the output of one simulation. Every simulation output has to be treated to be of the same form than the observed data. Doing so allows them to be compared. The observed data does not include values for specific islands that are included in the simulations, namely Alor, Tanimbar and Aru in eastern Indonesia. The admixture values for mitochondrion and Y-chromosome are also not available for every island. Those values in the models can then be dropped as they cannot be compared.

Many different comparison functions have been tested. Two functions have been selected that can hold different information about a comparison.

The mean square distance (MSD) and the partial Mantel test have been selected as they do not have a good correlation when applying them to random admixture values, thus meaning that they do not carry the same information. They are complementary, and using them both gives a better overview of the comparison.

Mean square distance

The mean square distance is the mean value of all of the distances between observed and simulated values of admixture for every n island.

$$MSD = \frac{\sum_{i=1}^{n}(AdReal_i - AdSim_i)^2}{n} \tag{2.1}$$

where $AdReal$ is the array of admixture data observed in the real values and $AdSim$ the corresponding values in the simulated model.

It gives a distance value, with 0 meaning that the two observed values are absolutely identical. In this specific context, with the fact that the compared values are admixture values, ranging from zero to one, and because of the values observed in the real data, the higher possible MSD value will be around 0.8 (see reference cases lines in the upper part of figure A.5).

Partial Mantel test

The Mantel tests have been developed to be able to compare two matrices with the same information. the partial Mantel test is one of them that also uses a third matrix, holding geographical distances of the cells of the matrices to be able to weight the values according to the actual geographical distance of the points [Smouse et al., 1986].

In this case, the matrices contain the values of distances of admixtures between every islands in the graph and a matrix M is calculated as

$$M = \begin{bmatrix} d(Ad_0, Ad_0) & \cdots & d(Ad_0, Ad_n) \\ \vdots & \ddots & \vdots \\ d(Ad_n, Ad_0) & \cdots & d(Ad_n, Ad_n) \end{bmatrix} \tag{2.2}$$

where d is the function returning the distance between the two arguments and A the admixtures of the n islands of the graph. With the corresponding matrices for the simulation data, the real data and also the geographical distances, the partial Mantel test can be done as such

$$correlation = partial.Mantel(M_{Simulated}, M_{Real}, M_{geographical}) \tag{2.3}$$

The partial Mantel test returns a correlation value that is between -1 and 1 with a value of 0 meaning that the two matrices are not correlated at all and of 1 if they are completely correlated.

2.3.2 Visualisations

As said in [Weissgerber et al., 2015], it is easy to represent data but hard to represent it so that the person visualising it does not need to dig into the huge quantity of data again to understand what is happening. It is important to represent it well so that it is useful to the user. A trade-off has been found between showing as much data as possible and doing visualisations easy to understand and showing what it is expected from a specific type of visualisation.

For this, an important part was to try to avoid simplistic visualisations when they would not show enough information. For example, a simple mean value is not enough when there are alternative ways to represent this data. Whenever possible, box-plots were used to really try to show the distributions and shapes of the data. In certain cases, too much box-plots would overwhelm the user so as an alternative, mean values are used but with additional error bars to be able to evaluate quickly the significance of the differences between the displayed values.

To let the viewer easily grasp diverse data, even though the values are and work differently, they share a single color theme. For example, low distance values and high correlation values are both displayed in green colors, as a way to signal “good” values. Inversely, high distances and low or opposite correlations are displayed in red shades as a way to show that they represent “bad” values in the specific context of this project.

Examples are available in the appendix (see A) and are made in R using the ggplot2 library [Wickham, 2009] to get nice looking graphs while having simpler code and thus more maintainable code. They will be detailed while presenting the results in chapter 3.

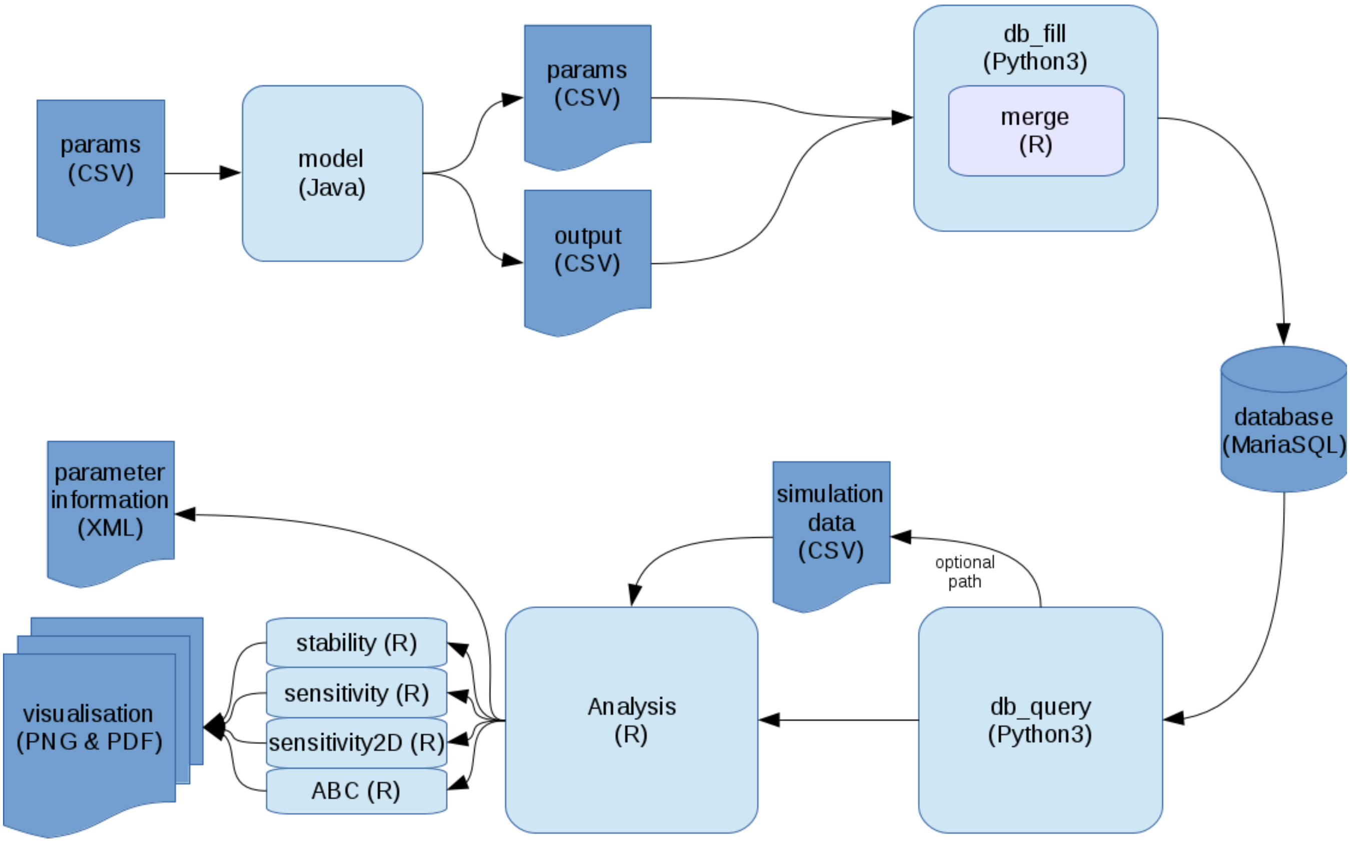


Figure 2.3: Visual representation of the different parts of the treatment and analysis pipeline. Dark colours represents data and the way it is stored and light colours represent programs and scripts and the language in which they have been written

Chapter 3

Results

3.1 Grid search analysis

In order to reduce the parameter space, a grid search as been done. It consists of going through the possible parameter sets by setting parameter values at regular steps throughout the space and to run n multiple simulations for every point in the space in order to have statistically meaningful results for every point. One hypothetical parameter grid search can be seen in figure 3.1.

Depending on the number of parameters and the size of the value steps, this holds an important computational cost. This has been considered a necessary step though, in order to reduce the parameter space for the next analysis, the ABC analysis, that would be even more computationally consuming if run over a huge parameter space. The resulting parameter space that will be used after the grid search analysis is defined manually after selecting interesting and meaningful values that can either be a smaller space or a specific value, thus making a parameter a non-changing parameter.

Stability analysis

There was multiple ways to analyse outputs from simulations with grid searches. The first one was to look at a specific point of the grid and assess the stability of the output generated with this parameter set.

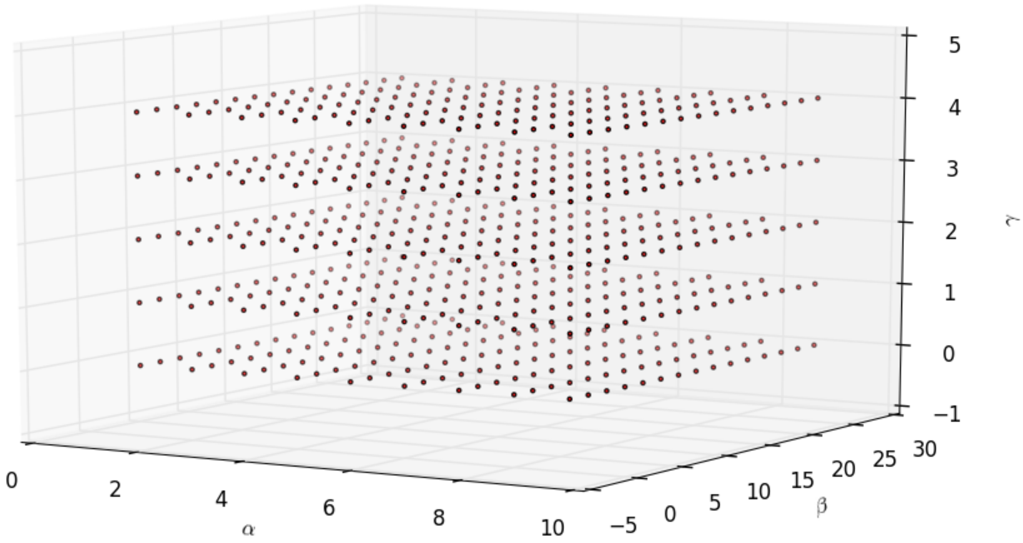


Figure 3.1: Visual representation of a grid search on three hypothetical parameters, α, β and γ. Each point represents a set of those parameters, that will be used for n different simulations

The stability analysis outputs different views on the data for this point in the grid. The first ones are 4 graphs, one for each type of observed DNA, wherein box-plots for the admixture values of each island are displayed (fig. A.1). The size and spread of the box-plots represent the variability of the data among the different simulations with the same input parameters. With "correct" parameters, the admixtures are supposed to be less stable in the contact zones than in the extremities of the graph. Less stability is also expected when looking at admixtures values comprising less markers (mitochondrial and Y-chromosomal admixtures). Any other behaviour leads to believe that the parameter set it comes from is not realistic, thus inducing abnormal model behaviours.

An other view that is outputted by the stability analysis is the graph of admixture values as a function of the types of DNA, and this for every island (fig. A.2). This graph aims at resembling the figure 1.2 from [Lansing et al., 2011] as a way to compare the real data in this paper to the data generated in the simulations.

Sensitivity analysis

When looking at lines or planes of the grid, one can analyse the sensitivity of the output to the changes in the corresponding parameters. At first, this analysis was done by looking at a single parameter changing while the others were fixed at one value, this was called a one-dimensional sweep and corresponds to parameters values aligned on a one-dimensional line in the grid. Then, this could be done on a two-dimensional sweep, corresponding to a plane. Even though it was technically possible, no higher dimension was analysed because of the difficulty to further visualise the results. Indeed, the visualisation choices would have needed three or higher-dimensional visualisations and those are less straightforward to analyse.

The first thing checked is the count of simulations for every point in the grid, so that one can be sure that during the further steps, similar number of simulations are compared. Otherwise, and especially when there are low numbers of simulations, results can be biased and the standard deviations can be not comparable. Example of this visualisation can be seen in figures A.3 and A.4.

Then, comparisons to the real data are done, for both the Autosomal and X-Chromosomal DNA data (see 2.3.1) and the resulting values are displayed so they can be analysed by the user as seen in figures A.5 and A.6.

3.2 ABC Framework

Once an interesting subspace of parameters have been defined, it can be used to feed the ABC framework used later on. ABC stands for Approximate Bayesian Computation and, instead of a standard Bayesian analysis where one can infer one best value for every parameter, here the ABC gives a posterior distribution of parameters corresponding to the best values. This lets appreciate the shape of the distributions and allows better understanding of the output values of highly stochastic models ran a high number of times. This technique, although quite recent, has been described in numerous studies ([Sunnåker et al., 2013], [Csilléry et al., 2010]).

Here, after using the R package “ABC” [Csillery et al., 2012], custom code inspired by it has been written but adapted to the specifics of this project.

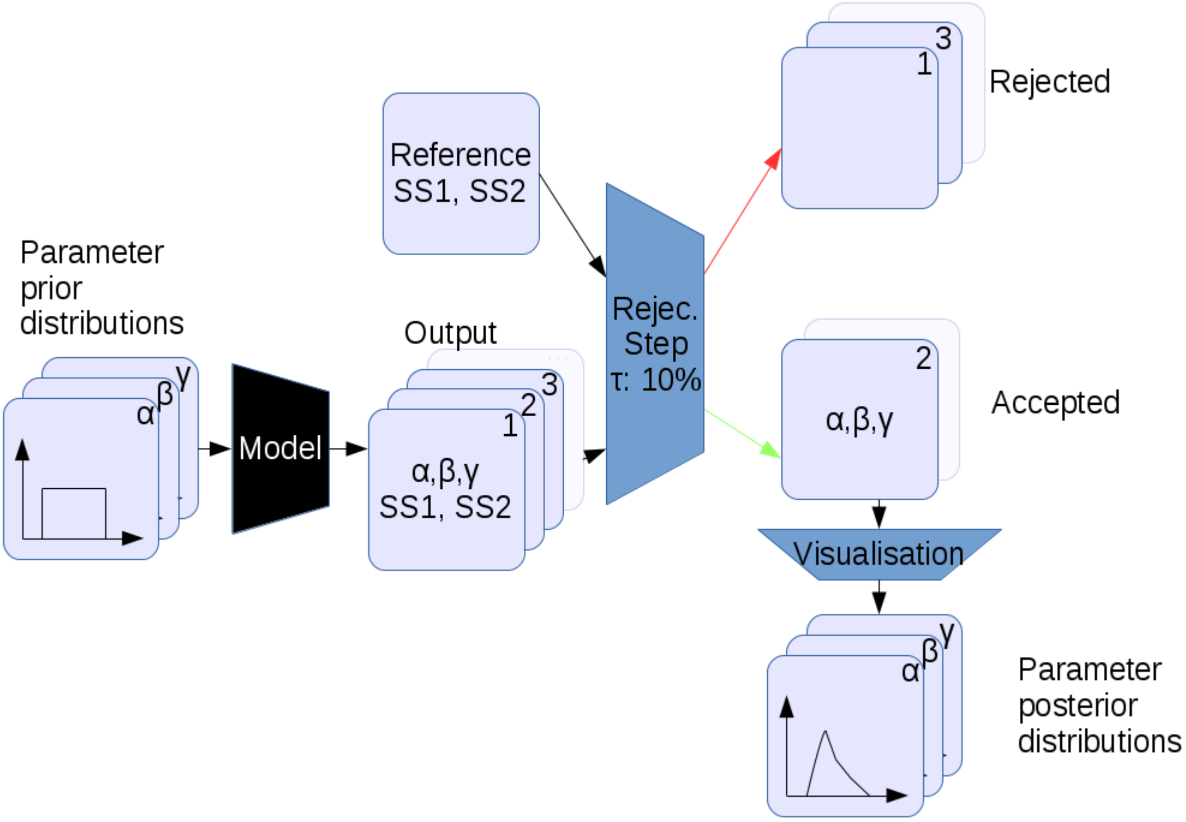


Figure 3.2: Visual representation of the different steps of an ABC inference framework

The whole framework encompasses the steps from the choice of the parameter sets to the inference of the posterior distributions. The figure 3.2 summarises the successive steps of this process with hypothetical parameters α, β and γ and summary statistics $SS1$ and $SS2$. In this project, the parameters used are the ones defined in the table 1.1 even though, the ones set after the grid search analyses will be ignored as they are defined once and will not change. The summary statistics will be the 4 results of the comparison functions defined in the section 2.3.1. These are the MSD and the correlation for both the X-chromosome and for the autosome.

3.2.1 Prior distributions and corresponding posterior distributions

The priors are defined as a set of distributions, one for each observed parameter. The distributions can be of any type but it is necessary to know them when doing the inference of the posterior distributions since, depending on the type chosen, they can induce a bias that will need to be corrected. Here, the distributions chosen are all uniform and the only bias can be if the correct parameters lay outside of the boundaries of the distributions (thus the importance of the previous grid search analysis). A visualisation of the hypothetical simulation parameter sets that can be generated by the first step of an ABC framework can be seen in the figure 3.3.

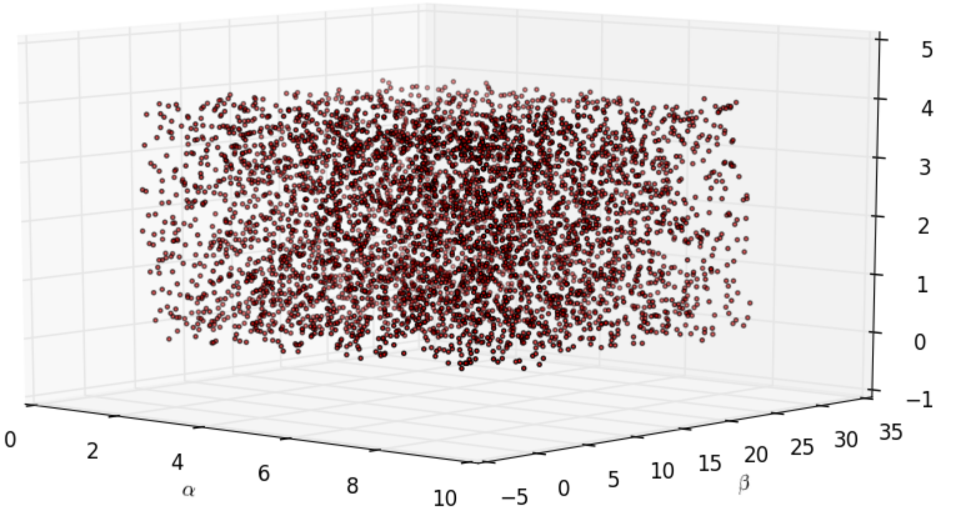


Figure 3.3: Visual representation of 5.000 sets of three hypothetical parameters, α, β and γ drawn from independent uniform distributions, as a result the points are evenly spread inside a cuboid. Each point represents one set of parameters that will be used for one single simulation

Chapter 4

Discussion

4.1 Importance of randomness

One important aspect that has been discovered while working with the Repast framework was the way it handles randomness. For a stochastic simulation, randomness is key, since starting two simulations with the same random seed and the same parameters would lead to the same succession of events in the simulation and thus to the same outcome. These two simulations would actually be the same one.

When looking at the results with a statistical point of view, one cannot use two identical simulations as two distinct values, that would simply make no sense and lead to biased interpretations of the values.

The problem with Repast is that it uses the current time to generate a random seed. This can be acceptable when the program is run on one thread on a single computer, since the time at which one simulation starts will always be different from one to an other simulation. It might lead to problems if the simulations are run in parallel using multiple threads on the same machine and/or using different machines and they happen to start at the same time. The risk of both the random seed and the parameter set used for the simulations colliding, while not probable, is still possible and thus not acceptable. Actually, even though the random seed is supposed to be a 32 bits signed integer, meaning that there are more that 4 billions possibilities, collisions happened more than once during this project.

The first way to handle this has been to alert the user when this happened, letting him remove the specific simulations if needed. Secondly, a way has been found to generate the random seeds for the ABC analysis beforehand using Unix's random source, `/dev/urandom/`, that can generate pseudo-random values which can be used for cryptographic purposes, meaning that it is good enough in this case to avoid collision.

4.2 Optimisations

Some key steps in the analysis framework need to be efficient enough so that time is not lost waiting for results to be treated or for graphs to be plotted and that the computation can be done without needing a supercomputer. This project has seen a few important refactoring steps to be able to cope with the quantity of data to be treated. The most important one has been to start treating the simulation results as a stream of values instead of loading the whole dataset in memory. This changed the memory complexity from linear to constant and it actually improved the time complexity from sub-quadratic to linear for the treatment part and from sub-quadratic to linearithmic for the analysis part. The improvement in time has been made possible by assuming that the results of one simulation are always together in the result stream, that way saving the cost of searching results in a big block of memory when they are actually next to each other. Actual execution times have been recorded and can be seen in the appendix B in the graphs B.1 for the treatment step and B.3 for the analysis step. The corresponding maximum memory use values are in the graphs B.2 and B.4.

There is effectively still a great amount of room to improve in memory usage, especially seeing that the base memory usage is between 60 and 200 MiB just when loading libraries, functions, global variables and set-up code.

The stream approach also allows the different steps of an analysis to be run simultaneously, by piping each step to the next, effectively making the whole process runnable in parallel. This is useful only if the computer used has at least n cores if n processes need to be run in parallel. In this case, the time of the whole process is the time needed to run the longest step.

4.3 Other visualizations

The visualisations done were made and adapted on the run so that they could be used to help make decisions and choices. They can still change and be adapted to new needs and that is supposed to be made easier through the use of adapted R libraries like ggplot2 and other useful ones. They added a layer of abstraction that could have added performance problems but the choice of already mainly used ones limited this and also made it easier to evolve even though the person writing the code changed. The code responsible for the visualisations is also restricted to specific parts of the pipeline, making it highly modular and easy to change or to replace.

Until now, the graphs generated were limited to two-dimensional graphs, mainly for easier understanding and integrating in papers, but one way to add more information can be through the use of three-dimensional graphs or animated graphs so that a higher number of model parameters can be visualised at the same time. It is important though that those new visualisations keep a certain level of readability that can easily be lost with higher dimensional graphs.

4.4 More complex model

The model can also be changed and, hopefully, improved. The problem of adding complexity would be to add enough complexity to keep the model relevant while still being computationally simple enough so that it could be run in an acceptable amount of time.

Several aspects can be changed, ranging from the structure of the family and how it is managed in the model, to higher level things like the integration of resource management at different scales of the model to try to be more accurate and have more realistic behaviours.

Conclusion

This internship has been the opportunity to work on a real research problem, to think about it and to decide what approach would be best to answer the questions raised by this problem. In order to do so, different pieces of software have been developed and will be reusable to continue the research in the same direction. The languages of the different scripts have been chosen in order to use the ones adapted to a specific task, for example all the heavy data handling as been done in R. The code produced aims to easily handle the data generated by the model used for this project and to represent it in a way that conclusions can be made by looking at the visualisations of the data and not having to manually analyse the huge quantity of data generated by the numerous iterations of the model. All the data has been handled in a recent but recognised statistical context, an ABC framework, that guarantees that the interpretations made are not biased and can be found again using other implementations of the same statistical framework.

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Appendix A

Examples of visualisation

This appendix presents different visualisation examples that are generated by the developed scripts.

I Stability

II Sensitivity

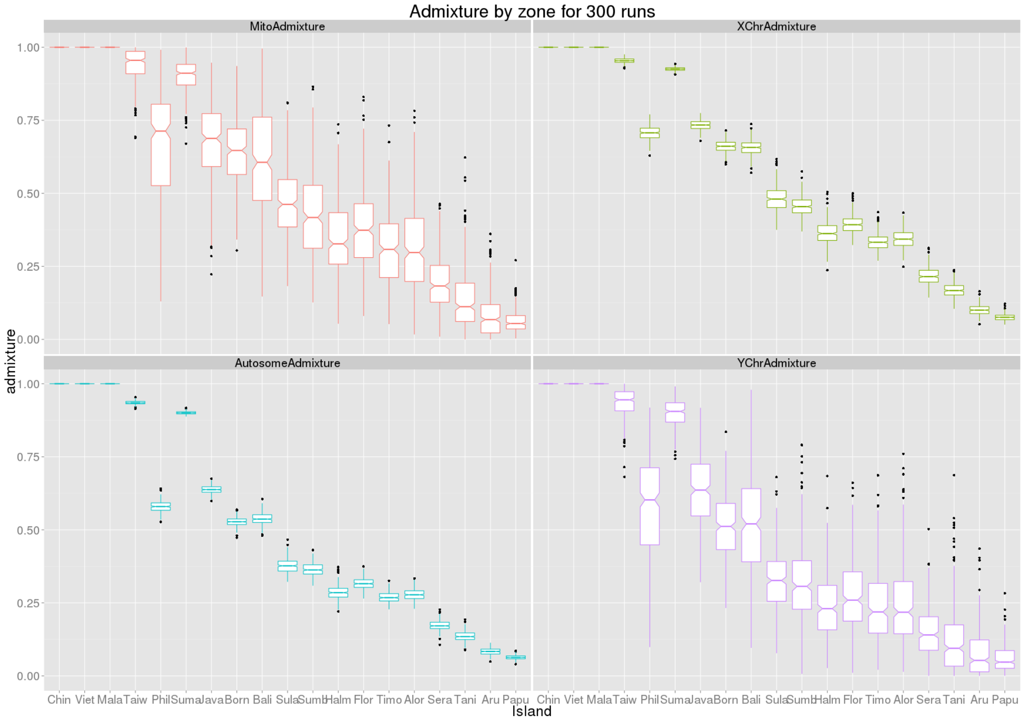


Figure A.1: box-plots of admixtures by island, separated by type of DNA

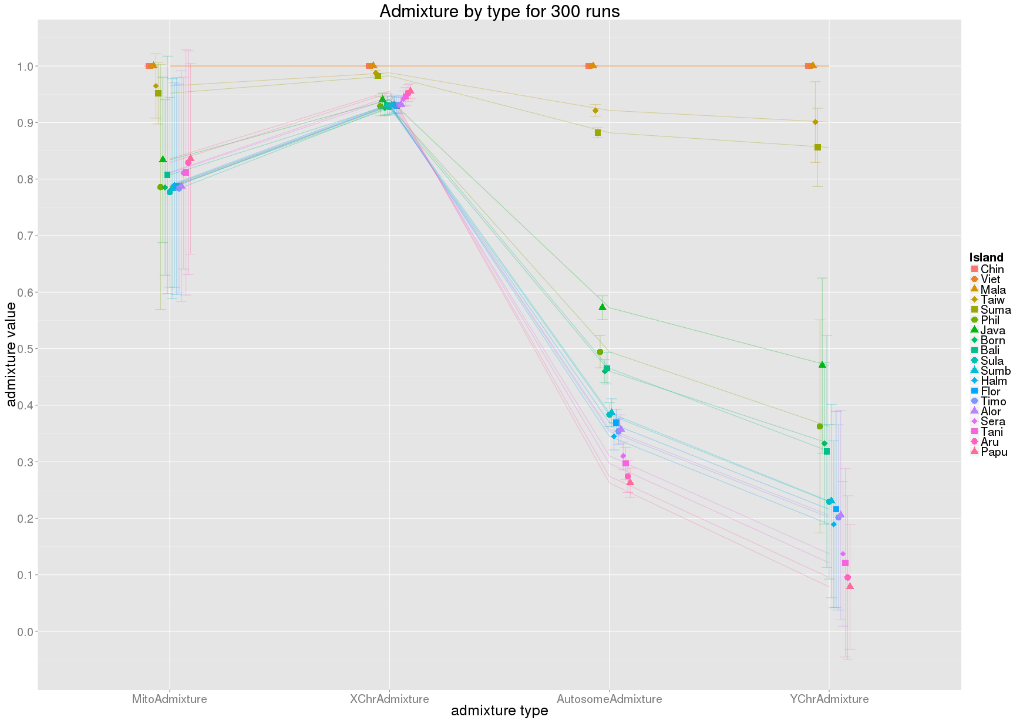


Figure A.2: admixture values by type of DNA, for every island

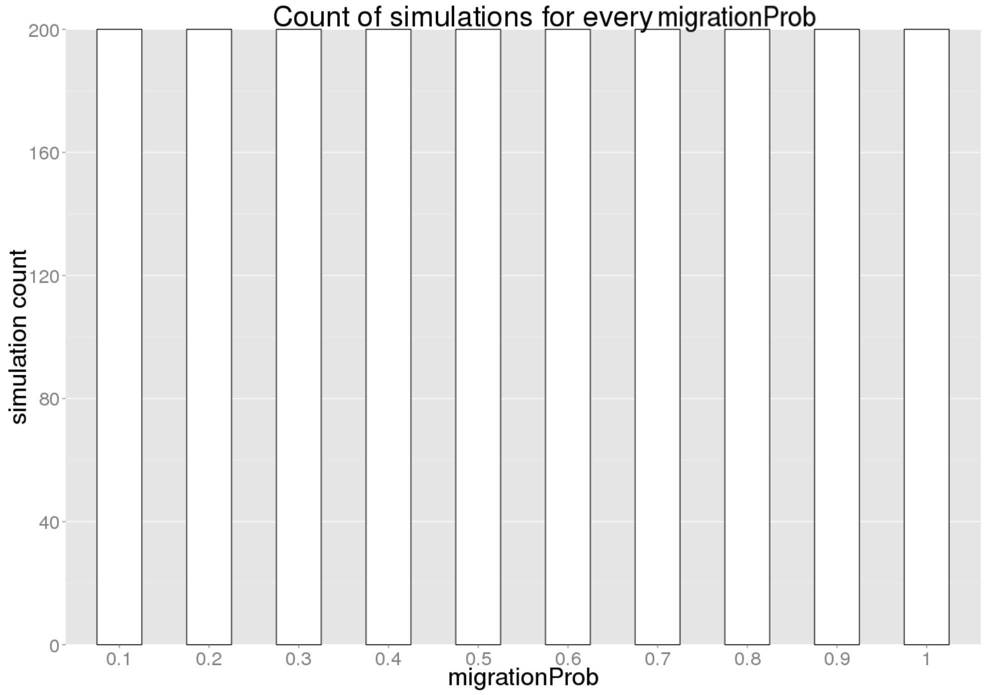


Figure A.3: Histogram of counts of simulations for a one-dimensional sweep of migrationProb values

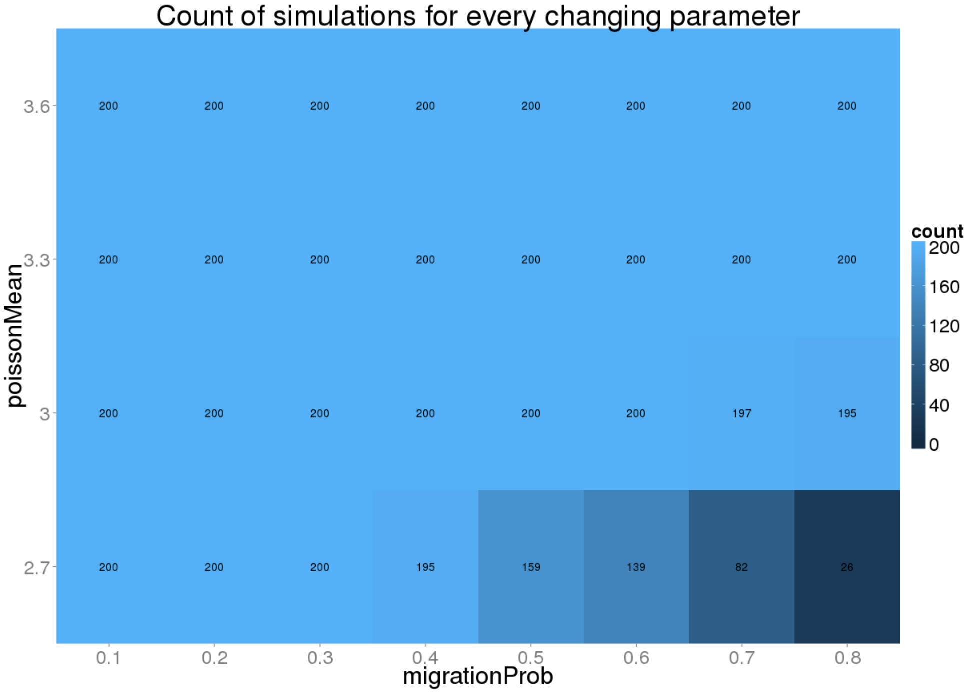


Figure A.4: Heat-map of counts of simulations for a one-dimensional sweep of migrationProb and poissonMean values. Failed simulations are revealed for both high migrationProb and low poissonMean values

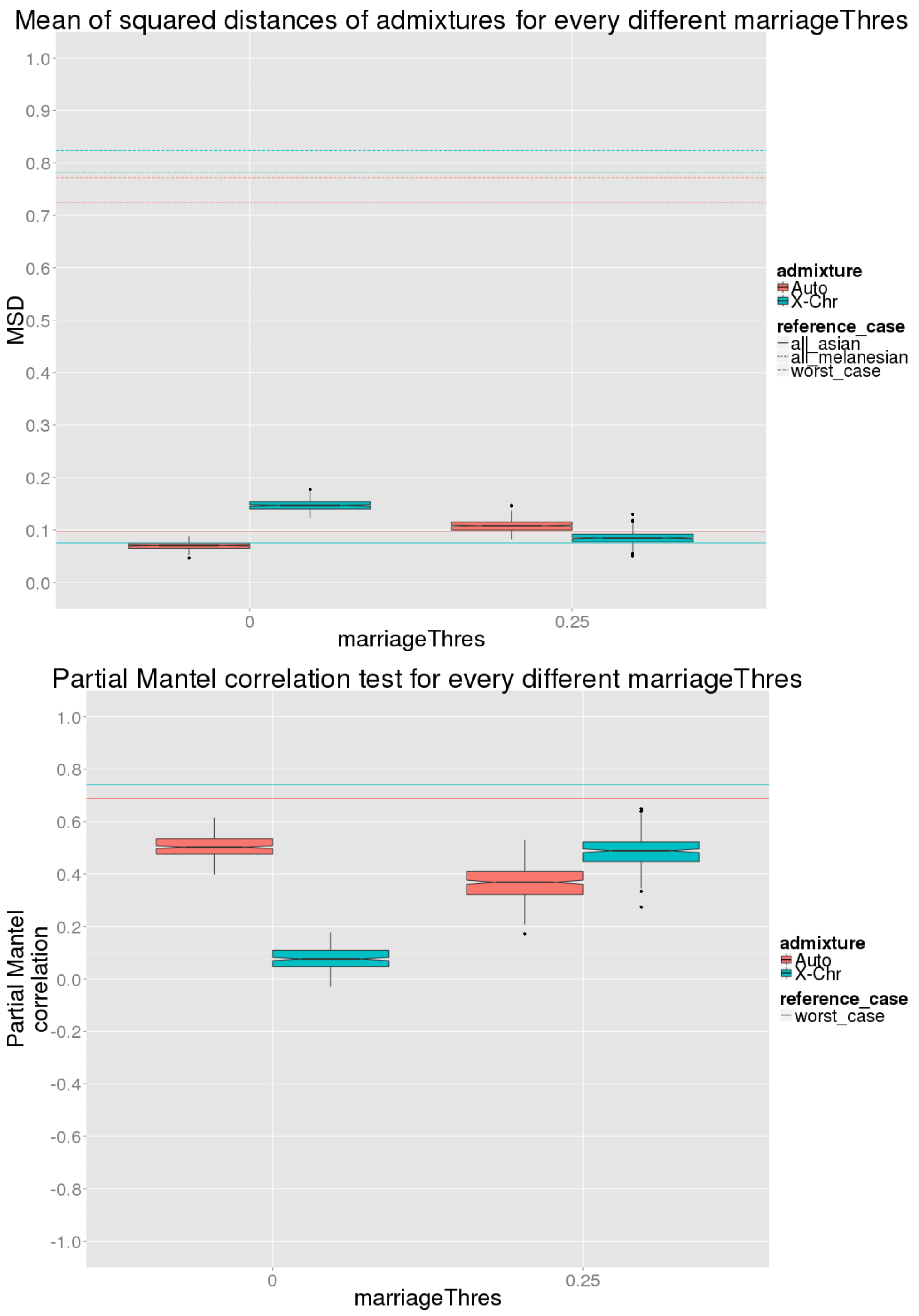
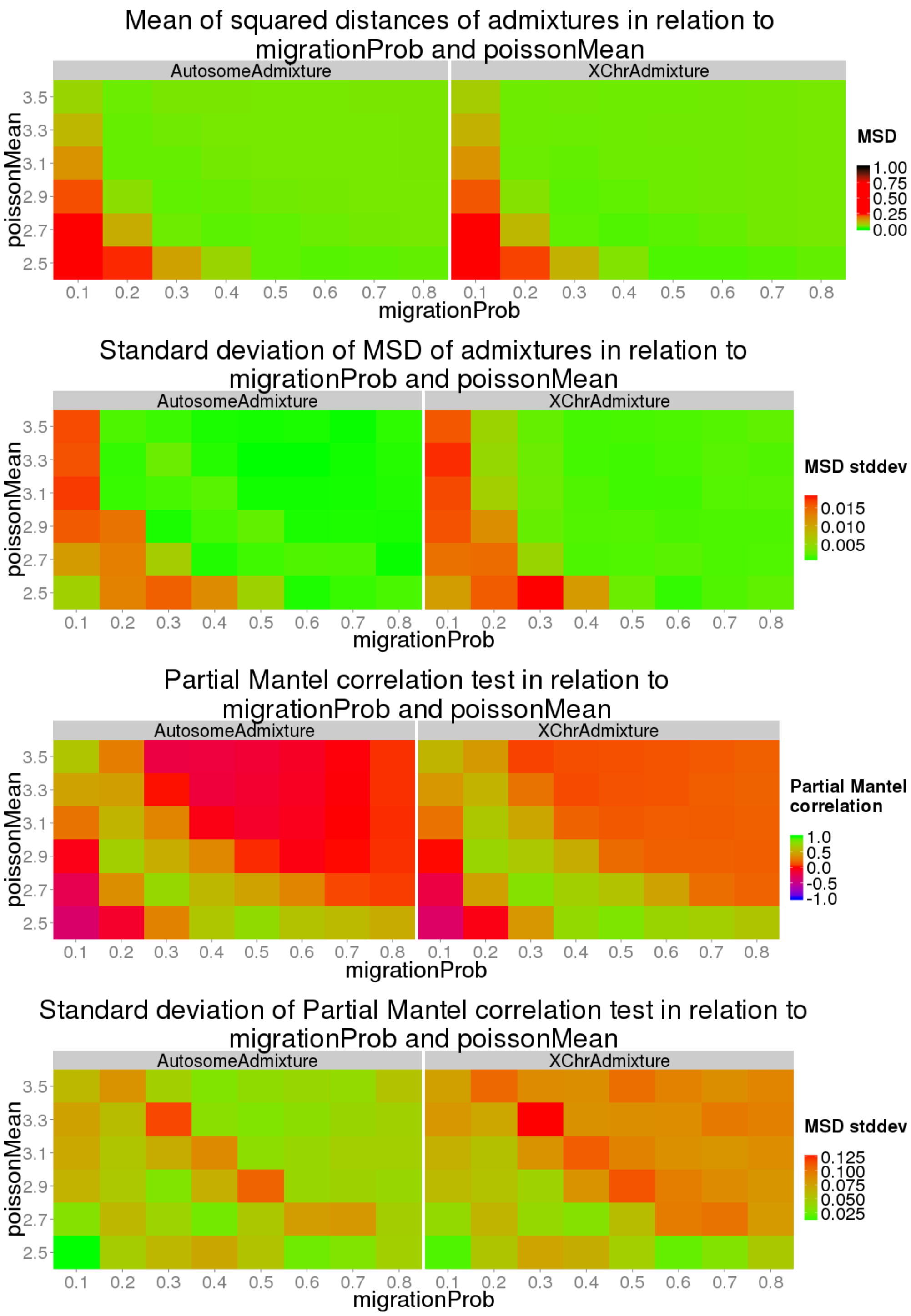


Figure A.5: Box-plots of comparisons of simulations vs. real data for a one-dimensional sweep of marriageThres values. Additional lines corresponding to pre-defined extreme reference cases



Mean of squared distances of admixtures in relation to migrationProb and poissonMean

Standard deviation of MSD of admixtures in relation to migrationProb and poissonMean

Partial Mantel correlation test in relation to migrationProb and poissonMean

Standard deviation of Partial Mantel correlation test in relation to migrationProb and poissonMean

Figure A.6: Heat-maps of comparisons and corresponding standard deviations of simulations vs. real data for a two-dimensional sweep of migrationProb and poissonMean values

Appendix B

Benchmarks

I Merging

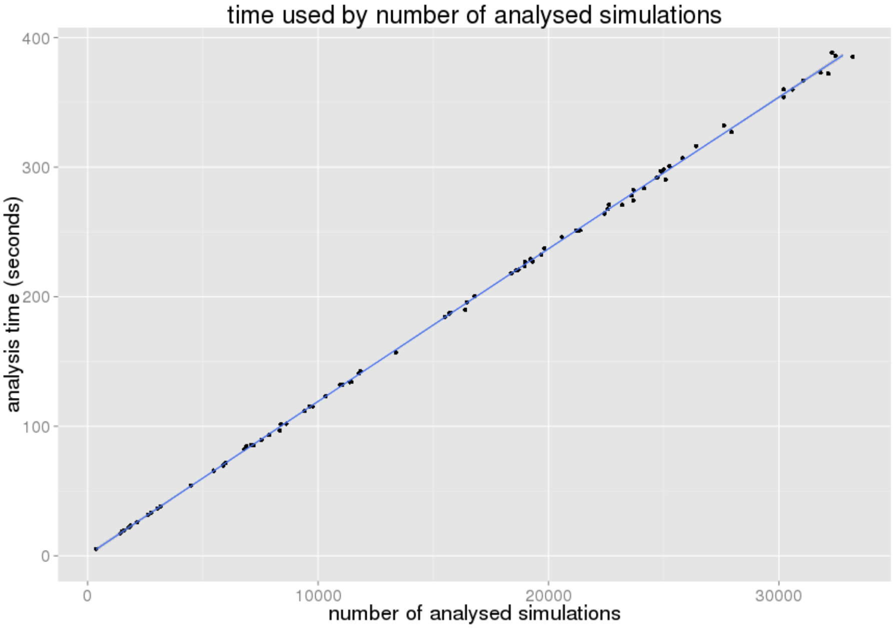


Figure B.1: Time used by the scripts in relation to the number of simulations merged. Corresponding, in the work-flow, to `merge.R`

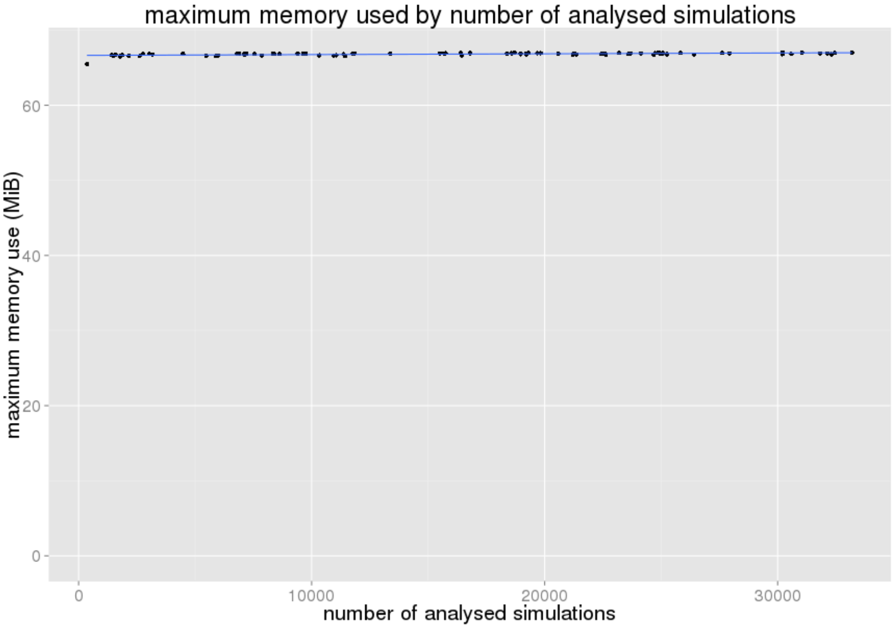


Figure B.2: Maximum memory used by the scripts in relation to the number of simulations analysed. Corresponding, in the work-flow, to `merge.R`

II Analysis

note: update with latest changes (hopefully, better values)

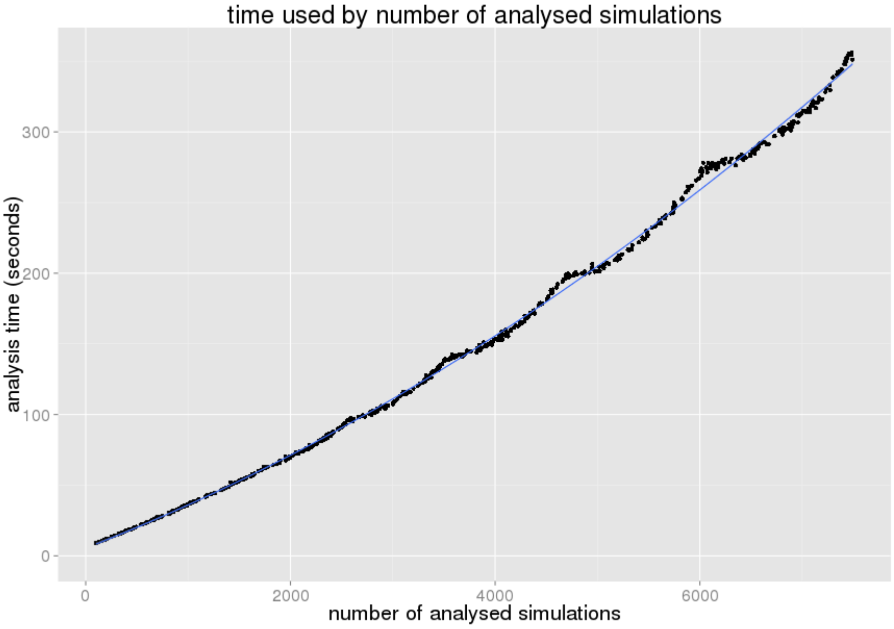


Figure B.3: Time used by the scripts in relation to the number of simulations analysed. Corresponding, in the work-flow, to `analysis.R`, `sensitivity.R` and the creation of the corresponding output files

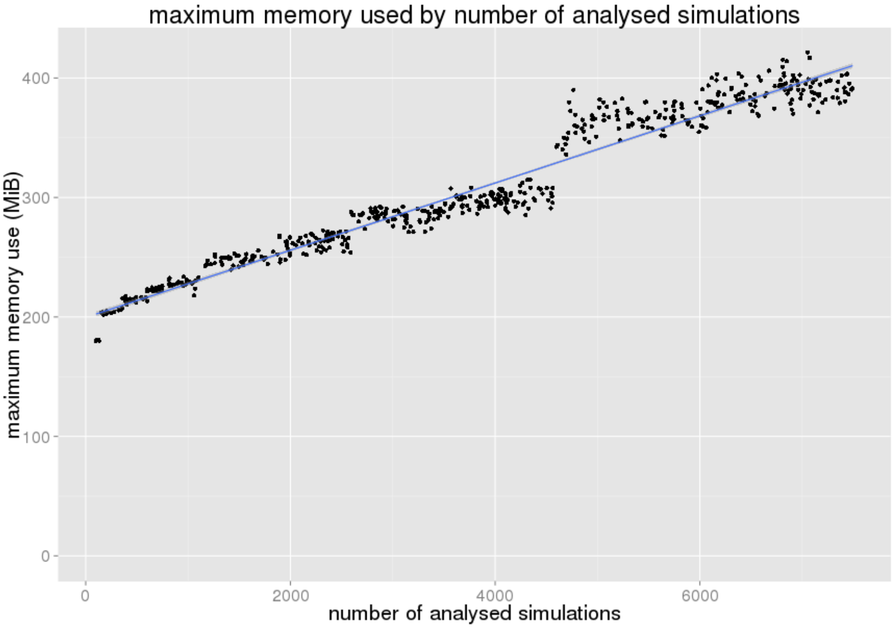


Figure B.4: Maximum memory used by the scripts in relation to the number of simulations analysed. Corresponding, in the work-flow, to `analysis.R`, `sensitivity.R` and the creation of the corresponding output files