

# Multi-layered model of individual HIV infection progression and mechanisms of phenotypical expression

## *Appendix C: Source Code*

On this CD, you will find the source code for the three layers of the model presented in this Thesis. This code was tested on several platforms. Apart from the MPI library, it does not require installation of extra software. Unless stated otherwise, all files are written by Dimitri Perrin.

### **1. Agent-based lymph network model**

All files required for the main model layer are located in the “HIV” folder. For random number generation, we provide an interface with Mersenne Twister, and this generator is included in the folder, (“mersenne-twister.h”). This is to avoid requirements for SPRNG installation.

### **2. Microarray biclustering**

#### **2.1. Weighting scheme**

All files required for weights generation are available in the “Weights” folder, in “Microarray”. As an exemple, we also provide a dataset ready to use, (“MIT.txt”), and the corresponding weights obtained (“weights-MIT.txt”). In this folder, the file “main.c” is the only one directly referring to the work implemented in this Thesis. The other files exclusively deal with data storage, through a matrix structure implemented by Nicolas Aunai.

#### **2.2. Parallel genetic algorithm**

All files required for weights generation are located in the “GA” folder, in “Microarray”. In this folder, the files “genetic.c” and “main.c” are the only ones directly referring to the work implemented in this Thesis. Other files were developed by Christophe Duhamel, remain his property, and are only provided here because they are required to compile and run the genetic algorithm.

As an exemple, we also provide a set of weights, (“DATA/weights-MIT.txt”). Using the makefile provided, compile with “make release”.

### **3. Epigenetic model**

All files required for the epigenetic model are available in the “Crypt model” folder.