# Modélisation, Simulation multi-niveau pour l'optimisation de politiques de vaccination

## Oct 1st 2012 – Sep 2016

**TRAN Thi Cam Giang, Jean Daniel ZUCKER, Marc CHOISY, Yann CHEVALEYRE**

## I. State of the art

1. Epidemiology (and monitoring)
    1. Epidemiology
    2. Control
2. Dynamics/ spatial structures (théorie métapopulations, réseaux, etc. . . )
3. Stochastic simulation Algorithms
    1. Exact stochastic simulation
        1. First reaction method (FRM)/Direct method (DM)/Next Reaction Method (NRM)
        2. Compare the direct method (DM) to the next reaction method (NRM), which algorithm is most efficient?
    2. Approximate methods
        1. $\tau$ − leaping method
        2. Adaptive tau-leaping method
    3. Hybrid and multiscale methods
4. Reinforcement learning

## II. DIZZYS : Description du modèle

1. Epidemiological models
    1. SIR model
    2. SEIR model
2. Infection force proposed by YANN
3. The equilibrium state for the SEIR model.
4. Improvement on the exact method "DIRECT METHOD" of a single population to a metapopulation of n subpopulations
5. DIZZYS : Description of package dizzys
    1. Introduction

2. Methods
    1. Deterministic SEIR model:
    2. Stochastic models:
        1. Direct method
        2. Adaptive tau-leaping algorithm
    3. Transformation SEIR model into SIR model
3. Example
    1. Example 1
    2. Example ….
4. Comparison between the package “dizzys” and other packages
5. Conclusion

## III. Relation structure/ spatial dynamics and persistence

1. Introduction
2. Material and methods
    1. Material
        1. Deterministic model for many subpopulations
        2. Stochastic model for many subpopulations
        3. Spatial structures
    2. Methods
        1. Stationary distribution in metapopulation
        2. Global persistence in a metapopulation
        3. Characterization of synchrony
3. Plan of experience
    1. Quantifying disease persistence in the simplest metapopulation
    2. Quantifying global extinction and asynchrony level φ max
    3. Influence of other parameters on the mass extinction rate
    4. Stochastic metapopulation simulations
4. Results
    1. Quantifying disease persistence in the simplest metapopulation
    2. Quantifying global extinction rate and asynchrony level φ max
    3. Influence of other parameters on global extinction rate

1. Number of subpopulation in a metapopulation
2. Influence of the metapopulation size
3. Coupling rate

5. Discussion and Conclusion

## IV. CCS against disease persistence

| May 25th 2016 → May 30th 2016 |
|---|

## V. Disease control by reinforcement learning

| June 1th 2016 → June 10th 2016 |
|---|

## VI. Conclusion and perspective

| Jun 11st 2016 → Jun 20th 2016 |
|---|