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

Oct 1st 2012 – Mar 2016

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I. State of the art

Sep 2015	Oct 2015

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

Nov 1st 2015 → Nov 15th 2015	Nov 15th 2015 → Nov 30th 2015

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

Dec 1^{st} 2015 → Dec 15^{th} 2015	Nov 15^{th} 2015 → Nov 30^{th} 2015

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. Disease control by reinforcement learning

Dec 15th 2015 → Dec 30th 2015

V. Conclusion and perspective

Jan 1st 2016 → Jan 15th 2016