



**SOUTH EAST ASIAN MATHEMATICAL SOCIETY**

**FINAL REPORT**

**MATHEMATICAL MODELLING IN BIOLOGY**

Hanoi, Vietnam  
March 8 – 15, 2017

**Organized by**

Vietnam Institute for Advanced Study in Mathematics (VIASM)  
and  
University of Science, Vietnam National University in Hanoi (VNU-HUS)

**With the support of  
CIMPA, SEAMS, VIASM and HUS**

**2017  
Mathematical Modelling in Biology  
Hanoi, March 8 – 15, 2017**

**I. Summary**

The SEAMS School “Mathematical Modelling in Biology” was organized by Vietnam Institute for Advanced Study in Mathematics (VIASM) and University of Science, Vietnam National University at Hanoi (VNU-HUS). It was held at VIASM from March 8 to March 15, 2017.

There were five lecturers: one from Vietnam, one from France, one from United States, one from Japan and one from Germany. There were 60 participants including 36 from Vietnam and 24 international from Malaysia (1), Cambodia (1), Japan (5), Thailand (4), Philippines (4), Indonesia (4), Singapore (1), France (2), Germany (1), USA (1).

The School received generous supports from CIMPA-SEAMS, VIASM and HUS.

The School started on March 8, 2017. The opening ceremony took place on the first morning including speeches given by Prof. Nguyen Huu Du, Director of VIASM. The School ended on Wednesday, March 15 followed by a lecture of Prof. Takasu.

## **II. Scientific Objectives and Rationale for the School**

This school is aimed to provide foundations of Mathematical Modelling in Biology, and to introduce some problems of the subject which are currently in the field of intensive research. The school is addressed to senior undergraduate students and graduate students from Southeast Asia and all over the world. The school is expected to accommodate students with basic knowledge of the subject which will be necessary for further study.

## **III. Organizers and Lecturers**

### **Organizers:**

- Nguyen Huu Du, Vietnam Institute for Advanced Study in Mathematics
- Tran Tat Dat, Max Planck Institute for Mathematics in the Sciences, Germany
- Nguyen Trong Hieu, Hanoi University of Science, University of Science, Vietnam National University at Hanoi

- Nguyen Trung Hieu, University of Science, Vietnam National University at Hanoi
- Nguyen Ngoc Phan, University of Science, Vietnam National University at Hanoi

**Lecturers:**

- Hien Tran, North Carolina State University, USA
- Marc Peigne, Université François Rabelais, President of French Mathematical Society, France
- Fugo Takasu, Nara Women's University, Japan
- Tat Dat Tran, Max Planck Institute for Mathematics in the Sciences, Germany
- Thanh Ha Do, University of Science, Vietnam National University at Hanoi, Vietnam

**IV. The Participants**

(See the attached file)

**V. School Programs**

This Seams School was objected to provide some background necessary for the research in Mathematical Modelling in Biology. The participants were also introduced some research projects which have been attracting the considerable interest of mathematicians in the field.

There were five courses in the school. The titles and abstracts are as follows.

**Course M1: Mathematical Modeling Techniques for Biological Systems**

**Lecturer:** Hien Tran

**Abstract:** This course seeks to provide students with a fundamental understanding of how mathematics and statistics are applied to problems in life sciences. Our approach will be through several “case studies” problems that arise in biological applications. For each case study we will discuss why a model is needed and what goals are to be sought. We will examine the mathematical models both analytically and computationally in order to compare their behavior with that exhibited by the modeled phenomena. Such a comparison can be achieved quantitatively through model verification and validation, which are central to the process of

model development and evaluation for all complex systems. Some computational tools are also presented to simulate the models.

**Course M2: Branching Processes**

**Lecturer:** Marc Peigne

**Abstract:** Galton-Watson branching processes describe the evolution of a population, assuming that individuals reproduce independently of each other to some given offspring distribution. One of the most important question concerns the probability of extinction of the population, with some transition phenomenon from subcriticality to supercriticality in several steps. We will present well known results in two natural generalizations and also recent ones concerning multi-type Galton-Watson processes in random environment. These results rely on a stimulating interplay between branching process theory and random walk theory.

**Course M3: Octave**

**Lecturer:** Thanh Ha Do (female)

**Abstract:** The course will provide an introduction to computing using Octave, the free software. It will teach you how to perform advanced data analysis, solve common numerical linear algebra problems, and simulate the mathematical models for biological systems related to the materials presented in course M1 of Professor Hien Tran.

**Course M4: An introduction to mathematical population genetics**

**Lecturer:** Tat Dat Tran

**Abstract:** This course seeks to provide students

- Mathematical models: Wright-Fisher models, Wright-Fisher models with other evolutionary factors (mutations, selection, recombination, migration), Fleming-Viot models.
- A fundamental knowledge about mathematical population genetics;
- Some advanced methods in studying mathematical population genetics;
- Open problems in mathematical population genetics.

**Course M5: Individual-based modeling of population dynamics**

**Lecturer:** Fugo Takasu

**Abstract:** Models of population dynamics have been usually described by ordinary or partial differential equations. These models describe dynamics of population size or distribution over space as continuous variable at the expense of biological realism of being individual. Individual-based models

assume individuals as "base unit", and thus they are more realistic but at the cost of mathematical tractability; dynamics of population size or distribution over space becomes inherently stochastic and model analysis is not straightforward. The course content will be 1) Introduction of ODE/PDE models used in population ecology, 2) Reconstruction of these models as individual-based models, and 3) Mathematical analysis of these individual-based models.

## **VI. Conclusion**

The School started on March 8 and ended on March 15, 2017. The school included 40.5 hours for lectures and 3.5 hours for discussion and practice in the computer lab. The time of classes were from 8:30 to 11:45 in the morning and from 13:30 to 17:15 in the afternoon. The schedule is located at here:

<http://viasm.edu.vn/en/hdkh/seams2017?userkey=program>

All lectures were nicely represented and the participants attended the school seriously. The school rendered not only helpful backgrounds in Mathematical Modelling in Biology, but also provided useful professional connections for participants.

## **VII. Financial Report**

### 1. Financial supports received

CIMPA – SEAMS	EURO	5000
VIASM	EURO	5000
HUS	EURO	1500

### 2. Total expenses by CIMPA grantees (see the attached files)





