ICS Summer School 2012

Scientific Trends at the Interfaces Biomathematics – Bioinformatics

Organisers: Alessandra Carbone, Jean-Pierre Françoise, Pascal Frey

July 16th – August 10th, 2012, Roscoff - France





Science at the interfaces







A multidisciplinary way of learning

Improve your curriculum Discover the challenges of tomorrow

Welcome to ICS Summer School

The Institute for Scientific Computation and Simulation (ICS) at University Pierre et Marie Curie (UPMC, Paris) is proud to launch the first edition of its Summer School from July 16th to August 10th 2012.

About the Summer Schools

Experience a multidisciplinary way of learning, explore courses outside your major and experience campus life at the Roscoff Marine Station, a renowned research and training centre. Ideally located on the Brittany coast of the English Channel, the research centre is jointly operated by the French National Centre for Scientific Research (CNRS) and the Pierre & Marie Curie University (UPMC).

ICS Commitment to Teaching

Our unique four weeks summer program offers challenging academics and experiments for talented and intellectually curious undergraduate students, who like to discover new topic areas.

We are committed to provide the best level of teaching and academic environment for our students, in view of creating a community beyond the classroom and build life lasting friendships. "Interdisciplinary programmes are a unique opportunity to achieve scientific breakthroughs in numerical simulations"

Pascal Frey, Programme Director, ICS Summer School

Interdisciplinary Summer School

Biomathematics Bioinformatics

A stimulating experience

ICS invites motivated undergraduate students (or recent graduates) to apply for admission to ICS Summer School Programme. We select students who have excellent academic results and who like to experience a different style of learning with world-class faculty.

The Summer School Programme allows students to focus on their academic interests and explore areas at the interfaces between disciplines, involving scientific computation and simulation. In addition to daily classes, students are invited to attend seminar series with invited speakers from other institutions worldwide.

ICS also organizes shorter programs, seminars and conferences at his main campus at heart of the city of Paris.

Eligibility

Our courses are intended for advanced Bachelor's degree, Master's degree (L3-M2 levels). Applicants should have completed at least two years of university studies. ICS summer school is open to students from all over the world.

Language requirements

All courses are taught in French or English, depending on the audience. Applicants are expected to be fluent in either language or both in order to follow the lectures and participate in classrooms discussions.

Application and registration

In order to secure your participation, we advise you to submit your application form as soon as possible. Registration fees must accompany all applications. Registration form can be downloaded from the ICS web site: http://www.ics.upmc.fr/en/events/summer_school.html

Scholarships

ICS is able to grant a limited number of full or partial scholarships. A full scholarship covers the tuition fees and transportation expenses between Paris and Roscoff.

Accommodation in 2012

All Summer School students have the opportunity to live on campus hotel, space permitting. Rooms include breakfast, lunch and evening meals (except on Saturdays and Sundays).

2012 Edition Programme

The four weeks 2012 edition programme will cover two challenging yet attractive topics from Monday, July 16 until Friday, August 10.

Term I: 16 – 27 July, **biomathematics** Term II: 30 July – 10 August, **bioinformatics**

Summer School Terms I and II are interdisciplinary courses and are independent: students may enrol for either or both. Both courses consist of morning plenary sessions, afternoon numerical simulation hands-on activities and evening lectures.

All courses are limited to 50 participants.

Two areas of intellectual challenge

The largely interdisciplinary field of mathematical and computational biology encompasses four major subfields: biological mathematical modelling, relational complex systems biology, bioinformatics and computational biomodelling.

Biomathematics

Mathematical biology focuses on the mathematical representation, treatment and modelling of biological processes, using a wide range of applied mathematical methods. The description of the behaviour of a biological system over time is converted into a set of equations, the model. This allows its behaviour to be simulated, and properties to be predicted, that might not be accessed through experiment. Biomathematics has both theoretical and practical applications in biological, biomedical and biotechnology research.

Keynote speakers

Adel Blouza, Assistant Professor, Rouen; Yannick Deleuze, PhD, UPMC; Mathieu Desroches, researcher, INRIA; Linda El Alaoui, Assistant Professor, Paris-Nord; J.-Pierre Françoise, Professor, UPMC; Alexandre Genadot, PhD, UPMC; Michèle Thieullen, Professor, UPMC; Marc Thiriet, researcher, CNRS; Alexandre Vidal, Assistant Professor, Evry;

Bioinformatics

Bioinformatics is the application of computer science and information technology to the field of biology and medicine. Bioinformatics primarily focuses on developing computationally intensive techniques to increase the understanding of biological processes. This involves dealing with algorithms and computation theory, artificial intelligence, image and signal processing, discrete mathematics, control and system theory, databases and information systems, and statistics. Bioinformatics impacts several major research areas: sequence analysis, genome annotation, computational evolutionary biology, analysis of complex dynamical systems such as genetic regulatory networks and signal transduction pathways, for example.

Keynote speakers

Gregory Batt, researcher, INRIA; Francois Bertaux, PhD, UPMC; Vincent Hakim, director of research, ENS; Bogdan Mirauta, PhD, UPMC; Hugues Richard, Assistant Professor, UPMC; Marc Santolini, PhD, ENS; Martin Weigt, professor, UPMC.



Plenary lectures

Plenary lectures are held on weekday mornings and will propose talks on a wide range of topics from the modelling of biological systems (e.g., the theory of dynamical systems in ecology), to the design of algorithms for genomics.

Full details about the lecturers and speakers will appear in the daily timetable you receive upon registration.

Evening lectures

During the sessions, a few topicrelated lectures will take place on evenings, given by invited speakers and faculty members.

These sessions are aimed to enhance your understanding and enjoyment of the programme. Speakers are experts in their field: senior figures from within and beyond the University, Course Directors, and Guest Lecturers.

Hands-on simulations

These sessions are meant to be interactive, educational and, possibly fun. They will provide various concrete experiences and insights into educational software packages (Matlab; FreeFEM++) by letting participants play and learn by doing, under the guidance of experts.

Students can develop their intuition and skills by interacting with experienced users in a user-friendly environment. Students are encouraged to assist and participate actively.

ICS Summer School Term 1

Biomathematics

Classes are held from Monday 16 July to Friday 27 July, every morning, 9.00am – 11.30am, in the main conference room.

The objective is to introduce the basic knowledge required to understand modelling in biomathematics (from nano to mesoscopic and macroscopic scales. This is a true multidisciplinary approach that involves biology, rheology, mechanics, physics and chemistry, and mathematics notions and concepts.

	Session A.1: Dr. Marc Thiriet (UPMC, INRIA) 16 - 19	Iuly
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Modelling and simulation of biological phenomena

Outline of the lecture

1) Modelling of cellular signaling

2) Cardiac Electrophysiology

3) Mechanics of biofluids, Navier-Stokes, Womersley solution

4) Biofluid-biostructure interactions and biomechanical modelling.

Session A.2: Dr. Adel Blouza (Univ. Rouen)

Modelling and simulation of the antibiotic proportioning in the processing of bacterial infections

Outline of the lecture

- 1) Introduction to biofilms
- 2) Mathematical modelling of the bacterial growth
- 3) Numerical methods for solving the problem
- 4) Numerical simulations using Matlab/Scilab

Keywords: Bacteria, Biofilm, Ordinary Differential Equations (ODE), Finite Differences Method



Session A.3: Pr.	<i>Jean-Pierre Francoise</i>	(UPMC)	24 - 25 July
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Mathematics for oscillations

Outline of the lecture

20 - 23 July

The aim is to introduce students to numerical techniques and to the bifurcation theory of systems with interfaces to biological modelling: numerical techniques for extending solutions of ODEs; introduction to AUTO and XPP-aut; search for slow varieties of multi-scale systems; application to ectopic focus-transition-conduction block in heart disease and complex rhythms of neuro-endocrine, to systemstritrophic ecology and population dynamics

Session A.4: Dr. Michèle Thieullen (UPMC)

26 - 27 July

Deterministic and stochastic modelling of systems of chemical reactions

Outline of the lecture

- 1) Introduction to chemical kinetics
- 2) The cycle of cell division
- 3) Numerical methods
- 4) Numerical experiments with Matlab



ICS Summer School Term 2

Bioinformatics

Classes are held from Monday 30 July to Friday 10 August, every morning, 9.00am – 11.30am, in the main conference room.

Bioinformatics, inspired by approaches coming from the fields of computer science, mathematics, statistics, statistical physics, focuses on problems whose solutions aim to understand biological processes interesting for both biology and medicine. Bioinformatics impacts major research areas: sequence analysis, genome annotation, computational evolutionary biology, analyses of gene and protein expression, etc.

Session B.1: Dr. Gregory Batt (INRIA)

5 - 10 August

Computational methods for the analysis of the functioning of biological systems at the molecular level

The emphasis of this course will be given on the modelling work, and on simple but important analysis methods. Such methods include state space analysis, global optimization for parameter search, sensitivity analysis for robustness assessment and stochastic simulation techniques.

Statistical Modelling of Biological Sequences

The course aims at giving an introduction into statistical methods for the description and algorithmic analysis of biological sequence data (e.g. DNA sequences, amino-acid sequences):

- 1) Binding sites for DNA-binding proteins: Position-specific weight matrices
- 2) Sequence alignments: Hidden Markov models
- 3) Modelling protein families: Profile Hidden Markov models
- 4) Detecting protein co-evolution: Covariance analysis

Session B.3: Dr. Vincent Hakim (ENS) 30 july -3 August

Deciphering the structure of genetic networks

Understanding how genomic information is encoded and how it gives rise to different cell identities and behaviours is a central biological question. Computational modelling usefully complements experiments that are currently producing an impressive amount of data. The following topics will be addressed in this session:

- 1) Transcription factor-DNA interaction : basics
- 2) From data to network structures : identification of transcription factor binding sites

From function to network structure : evolutionary design of networks with specified functions

Session B.4: Dr. Hugues Richard	(UPMC) 5 -10 August
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Analysis of high throughput sequencing data, from sequences to biological interpretation

The dramatic fall in costs for DNA-sequencing technologies over the last years (over 10,000 fold) is revolutionizing many experimental approaches in biology, medicine or ecology. This lecture will first introduce latest technological developments and then present statistical and computational methods for the analysis of high throughput sequencing data.



Institute for Scientific Computation and Simulation

Université Pierre et Marie Curie 4, place Jussieu, 75005 Paris, France

www.ics.upmc.fr

