

# Biomathematics

## — A Thematic Line Proposal —

Delfim F. M. Torres

delfim@ua.pt

Center for Research and Development in Mathematics and Applications (CIDMA)  
Department of Mathematics, University of Aveiro  
3810-193 Aveiro, Portugal

CIDMA, DMat, University of Aveiro  
December 7, 2017

# BioMath: What is it?

- It is an interdisciplinary scientific research field with a range of both theoretical and practical applications.
- The field is sometimes also called *mathematical biology*.
- It focuses on the use of mathematical tools to study biological systems.
- Aims: mathematical representation, treatment and modeling of biological processes, using techniques and tools of applied mathematics.
- Mathematical biology employs many components of mathematics, and has also contributed to the development of new techniques.

Describing systems in a quantitative manner means their behavior can be better simulated, and hence properties can be predicted that might not be evident to the experimenter. This requires precise mathematical models.

# Researchers of CIDMA interested in the subject

Current Figures (Dec 6, 2017)

## 15 researchers from 4 Research Groups of CIDMA

- Probability and Statistics (PS)
- Systems and Control Group (SC)
- Algebra and Geometry (AG)
- Optimization, Graph Theory and Combinatorics (OGTC)

- 1 6 from PS: Adelaide Freitas, Vera Afreixo, Pedro Sá Couto, Magda Monteiro, Marco Costa, Ana Helena Tavares
- 2 5 from SCG: Delfim F. M. Torres, Isabel Brás, Cristiana J. Silva, Sofia Rodrigues, Ana Pedro Lemos Paião
- 3 2 from AG: Manuel António Martins, Daniel Oliveira Figueiredo
- 4 2 OGTC: Cristina Requejo, Olga Oliveira

# Topics of Research

- Population Dynamics
- Mathematical Epidemiology
- Biostatistics
- Molecular Biology
- Epigenetics
- Joint-modeling
- Hybrid Systems (Biological networks, etc.)

And other topics that involve mathematics, systems and control theory, statistics and scientific computing as scientific support.

## Useful Mathematics Tools

- Modelling
- Applied Statistics
- Differential dynamic logics
- Fuzzy models
- Optimal control (Boolean dynamics, etc.)

# Research done by CIDMA members on BioMath

- Follows some illustrative examples of problems on Biomathematics already investigated by CIDMA members
- The list is far from exhaustive and is definitely not updated!
- We give examples from different groups of CIDMA

CIDMA has a rich and consolidated publication record on Biomathematics since 2010, as well as several Master and PhD thesis supervised in the area.

Some journals where we have published:

- Math. Biosci.
- Bull. Math. Biol.
- J. Theoret. Biol.
- Math. Comput. Modelling
- Math. Popul. Stud.
- Math. Model. Nat. Phenom.
- Ecological Complexity ...

# Biological network design

- The study of biological networks, their modeling, analysis, and visualization are important tasks in life science.
- Important goals of their study are the understanding of the overall structure of the network and the understanding of the interactions between network elements.
- Important networks closely related to molecular biology are gene regulatory, signal transduction, protein-protein interaction, metabolic networks and phylogenetic trees.
- Phylogenetic trees are an application of the Minimum-Weight Tree Reconstruction problem. A phylogenetic tree represents the evolutionary relationships of a set of species and is often built on information from molecular biology such as DNA or protein sequences.

## Keywords

combinatorial optimization, mixed integer programs, algorithms

Topics where the Probability and Statistics group have contributed:

- Development of new statistical methodologies to explore large data set in DNA context.
- Development of novel statistical methods to compare distributions of very large samples, with application in characterizing the phenomenon of symmetry in intra-strand DNA (the distribution of a given word distribution vs the distribution of the corresponding symmetric word) and similarities in word distance-distributions in DNA sequences.
- Exploring the data from the 1000 genomes project, to develop/apply statistical methods to better describe genetic variations.

# Identification of patterns or homogeneous groups

- The increasing number of sequenced genomes and the large amount of complex data emerging from DNA microarray technologies have created new challenges
- The Iterative Signature Algorithm (ISA) has become very attractive to detect co-regulated genes from microarray data matrices
- We investigated the effect of several modifications on the performance of the biclustering algorithm and a new biclustering algorithm, called ISA-median was constructed.
- All these biclustering algorithms were implemented in the software platform Anaconda

## Keywords

bicluster, biclustering algorithms.



# Correction and normalization on microarray data

Different statistical methodologies are possible for the detection of differentially expressed genes in microarray experiments.

- The effect of 36 preprocessing strategies resultant of combination of one background correction method with one normalization method on three published microarray data sets are already classified by cancer type.
- The rate of differentially expressed genes incorrectly detected depends strongly on the data set and the selected preprocessing method.
- Investigations show that the proportion of differentially expressed genes commonly identified by different methods is not so high as would be expected.

## Keywords

microarray; differentially expressed gene; Background correction; Normalization; False discovery rate; SAM; Biplot.

# Mathematical Modeling, Optimization and Control

- Epidemiological modeling
- Optimal control
- Numerical optimization
- Infectious diseases

Cristiana J. Silva, Post-doc

Title of the Project: Optimal control applied to epidemiological models

Fellowship from FCT: SFRH/BPD/72061/2010

Ana P. Lemos-Paião, PhD student

Thesis: Optimal Control and Mathematical Models in Epidemiology

Fellowship from FCT: PD/BD/114184/2016

# Epidemics on human or animal populations

- The development of new modeling approaches for the analysis of the spread of infectious diseases in modern societies is driven by an increasing necessity of predicting the impact of outbreaks of new emerging diseases.
- Some of these are reintroduced by migratory flows of animals and persons, while others emerge from the evolution of biological pathogens.

## Goal

To capture human/animal behavior in epidemic modeling, outbreak analysis and optimal control.

# Meetings being organized by CIDMA members at DMat-UA

- 1 Annual Workshop on Molecular Logic, since 2014  
<https://molecularlogic2017.weebly.com>
- 2 4th International Conference on Algorithms for Computational Biology, AlCoB 2017, Aveiro, Portugal, June 5-6, 2017.  
<http://grammars.grlmc.com/AlCoB2017>
- 3 5th International Conference on Complex Dynamical Systems in Life Sciences: Modeling and Analysis, University of Aveiro, Portugal, 10th to 12th May 2018.  
<https://sites.google.com/view/5thiccds2018/home>
- 4 III Encontro Luso-Galaico de Biometria, Department of Mathematics, University of Aveiro, 28–30 June 2018.  
<http://ebio2018-pt.weebly.com>
- 5 2nd Portuguese Meeting in Biomathematics, Department of Mathematics, University of Aveiro, July 19 and 20, 2018.  
<http://epb2018.weebly.com>