

Special session

on

## Computational Biology

### ABSTRACT

When at the turn of this century Joel H. Cohen published his seminal paper “Mathematics is Biology’s Next Microscope, Only Better; Biology is Mathematics’ Next Physics, Only Better”, this was more like a vision, even if a confident one. Nowadays, Mathematical Biology is an established scientific discipline, encompassing both analytical and computational approaches to solving problems at all scales of Bioscience research. The rapid development of Biocomputing, Biomathematics, Biomodelling, and Bioinformatics, all of them representing different facets of this new discipline, not only boosted all areas of biomedical research and drug design, but also provides a variety of opportunities to apply and develop advanced numerical methods, customized solutions, HPC tools and techniques.

The Special Session on Computational Biology at the 10th International Conference on Numerical Methods and Applications (NM&A'22) is devoted to selected topics in mathematical biology, mainly in its computational aspects, illustrating the synergy between mathematics, computing and biology. The program includes but is not limited to:

- Micro-, meso- and macro-system dynamics in Bioscience
- Protein structure, function, and interactions
- Numerical methods in Biomodelling and Bioinformatics
- Topology in protein structure and dynamics
- *In silico* drug design, including within the COVID-19 context