CIN
CNR Immunology Network

FIFTH NETWORKING MEETING

November 16th 2020

Virtual Room GoToMeeting https://global.gotomeeting.com/join/926710469

Accession Code: 926-710-469

10:00-10:10   Greetings and introduction by Maria Rosaria Coscia and Diana Boraschi

Computational and structural immunology

10:10-10:30   Filippo Castiglione (IAC)
Numerical Immunology: a computer model of the immune reponse

10:30-10:50   Claudia Angelini (IAC)
Analysis and integration of omics data with application to biomedical research

10:50-11:10   Paolo Tieri (IAC)
Network medicine and Immunology

11:10-11:30   Christine Nardini (IAC)
Revisiting inflammation: non-communicable disease and the wound healing process

Organ-on-chip: a bridge connecting immunology and mathematical models

11:30-11:50   Luca Businaro (IFN)
Immune system on chip: modelling and measuring the IS under the microscope.

11:50-12:15   **Conclusioni**

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12:30 -14:00   ***Discussione aperta***
* *Organizzazione interna del CIN*
* *Presentazione del CIN alla prossima Conferenza DSB*
* *Nuove iniziative e prospettive future*
* *Varie ed eventuali*

Modera Maria Rosaria Coscia

Abstracts

Filippo Castiglione
Institute for applied mathematics "Mauro Picone" (IAC)

Numerical Immunology: a computer model of the immune response

I will describe a computational model of the immune system that implements a number of immunological theories. It has been developed over the last years and has been used to study the dynamics of few diseases from infections to cancer. I will describe the ideas behind its development, provide examples of its use (one in particular in the field of vaccine development) and discuss further improvements.

Claudia Angelini
Institute for applied mathematics "Mauro Picone" (IAC)

Analysis and integration of omics data with application to biomedical research

Using some illustrative case studies, I will briefly discuss how omics data can be used in current biomedical research and its challenges in terms of data analysis and integration. Then, I will move from bulk analysis to single-cell studies. In particular, I will focus on how single-cell analysis can be useful in the field of immunology. I will describe the main ideas, the steps of the data analysis, and some novel methods. I will conclude by discussing future prospective and open challenges.

Paolo Tieri
Institute for applied mathematics "Mauro Picone" (IAC)

Network medicine and immunology

Network medicine (NM) is the application of network science towards identifying, preventing, and treating diseases. I will briefly introduce basic concepts about NM, its methodologies and objectives, and few case studies in the field of immunology and drug repurposing.

Christine Nardini
Institute for applied mathematics "Mauro Picone" (IAC)

Revisiting inflammation: non-communicable disease and the wound healing process

Non Communicable diseases (NCDs) have represented a silent pandemic long before the dramatic rise of Covid-19. NCDs are well known to be characterized by chronic inflammation and altered wound healing, yet medical approaches leverage only on the former, with virtually no attention to the latter. Investigation of the tight interaction of the role of wound healing in a broader inflammatory perspective may offer additional entry points to treat and prevent the progression of such maladies. I will present hypotheses, preliminary results and perspectives in this direction.

Abstracts

Luca Businaro
Institute for Photonics and Nanotechnologies (IFN)

Immune system on chip: modelling and measuring the IS under the microscope

The immune system is a striking example of an integrated information system, engaged in coordinated host-protective activities. Organs-on-chip approach (OOC) models allow the direct simultaneous observation of hundreds of different cells, moving, interacting and responding to signals coming from the microenvironment nearby, that give access to a number of parameters describing the system that must be properly measured and elaborated. Combining microfluidics with the ability of cellular imaging enable to collect quantitative data from complex biological systems at a single-cell level. When monitoring immune systems, the interplay between different cell types and the impact of functional responses reflect the roles of players and goals, respectively. The case study of onco-immunology on chip, which was our main focus in the past few years, opens a new window to live observation of the host immune response with or without drug treatments, making OOC a cornerstone for dissecting complex biological phenomena and pre-clinical testing of drugs. Smart implementation of image processing algorithms enable to quantify the simultaneous long-time interactions of huge number of cells and accurately solve the practical problems encountered in multi-cell type context. All our results indicate not only the efficacy of the microfluidic based coculture approach, but also show, in our opinion, as organs on chip represent a bridge connecting biology and mathematical models, with piers resting on advanced microscopy and data analysis, but still need to be integrated with other disciplines such as systems biology and agent based models.