





COST Action CA21135 IMMUNO-model

Computational immuno-genomics Summer School

11-13 June 2024

Zaragoza, Spain

In line with the Immuno-model COST Action goals, this training school aims at providing an introduction to key computational strategies to study the reciprocal interactions between the tumour and its microenvironment, with a specific focus on the immune compartment. Trainees will attend lectures and hands-on sessions, to enable them to incorporate such methods in their research activities. The training school will additionally be the opportunity to launch the collection of immuno-omic datasets to later generate and publish a publicly available resource.

Eligibility

Applicants must be part of a PhD programme, or a postdoctoral fellow or should be employed by an institution or organization performing research.

- The Home institution of the applicant should be any of the below.
 - Legal Entity in a COST Full Member/ COST Cooperating Member
 - Legal Entity in a COST Near Neighbour Countries (NNC)
 - Specific European RTD Organisation

Please see Appendix 1 for details and the **COST ANNEX I – LEVEL A. COUNTRY AND ORGANISATIONS TABLE**.

In light of the topics covered in the training school, applicants are expected to have.

- Basic/good knowledge of either R, Python or a similar language
- Basic knowledge on omics data generation and analysis (i.e. RNA-sequencing, whole exome sequencing).

While practical exercises will be executed in a server, students should attend with a laptop. Link and credentials to server will be provided in advance.

Application Process (Deadline April 5th, 2024)

Please fill in the form at this link.

https://forms.gle/9qG37kgT7PJU5Emn7







Once the applicant is determined to be eligible, applications will be accepted on a first come first served basis for a maximum of 15 trainees. Please be aware that the organisers reserve the right to reject applications if their computational background or the motivation to participate are considered inadequate.

Selected participants will receive an official invitation from e-COST.

Please find Frequently Asked Questions regarding Training Schools here.

Reimbursement

<u>After the event</u>, trainees will be reimbursed for travel expenses (up to $400 \in$) and will receive a daily allowance of $192 \in$ per day to cover expenses of meals, accommodation and short-distance travel (below 101 kms).

For more information please see the COST Travel Reimbursement Rules.

Please contact <u>ghm_immunomodel@igtp.cat</u> for further details and any other issues pertaining to travel costs.

Acknowledgements

This training school is supported by COST (European Cooperation in Science and Technology). COST is a funding agency for research and innovation networks. Their Actions help connect research initiatives across Europe and enable scientists to grow their ideas by sharing them with their peers. This boosts their research, career and innovation (www.cost.eu).







Training School Schedule

DAY 1 (11th June)

IMMUNOGENOMICS OVERVIEW AND ANALYSIS OF PRE-CLINICAL MODELS

9 – 9.30 h.	Welcome and introductions (teachers / students)
9.30 – 10.30 h.	Immunogenomics overview (Rebeca Sanz-Pamplona)
10.30 – 10.45 h.	Coffee Break
10.45– 11.30 h.	Analysis of CyTOF single cell data (Maurizio Callari)
11.30 – 11.45 h.	Coffee Break
11.45 – 12.30 h.	Practical exercises (Maurizio Callari)
12.30- 14.00 h.	Lunch
14.00 – 15.15 h.	How to deal with sequencing data from hetero-species models
	(Maurizio Callari)
15.15 – 15.45 h.	Coffee Break
15.45 - 17.00 h.	Practical exercises (Maurizio Callari)

DAY 2 (12th June)

CHARACTERISING THE TUMOUR MICROENVIRONMENT AND PREDICTING CANCER NEOANTIGENS FROM BULK SEQUENCING

9 – 10.30 h.	Deconvoluting immune populations from bulk RNA-seq data (Sandra García-Mulero)
10.30 – 11.00 h.	Coffee Break
11.00 – 12.30 h.	Practical exercises (Sandra García-Mulero)
12.30- 14.00 h.	Lunch
14.00 – 15.30 h.	Neoantigen prediction from somatic genomics data (Roberto Fornelino)
15.30 – 16.00 h.	Coffee Break
16.00 - 17.00 h.	Practical exercises (Roberto Fornelino)

DAY 3 (13th June)

STUDYING THE CROSSTALK BETWEEN CANCER AND IMMUNE CELLS

9 – 10.00 h.	Mathematical models of the interactions between cancer and the immune system (Peter Rashkov)
10.00 – 10.15 h.	Coffee Break
10.15-11.15 h.	Practical exercises (Peter Rashkov)
11.15 – 11.30 h.	Coffee Break







11.30 – 12.30 h.	Crosstalk between cancer cells and immune cells. spatial transcriptomics, TALKIEN and other technologies (Rebeca Sanz-
	Pamplona)
12.30- 14.00 h.	Lunch
14.00- 15.00 h.	Practical exercises (Rebeca Sanz-Pamplona)
15.00 – 15.15 h.	Coffee Break
15.15 – 15.45 h.	Exploiting public data repositories and the immunogenomic data collection initiative (Maurizio and Rebeca)
15.45 – 16.00 h.	Coffee Break
16.00 – 16.45 h.	Kick-off of the immunogenomic data collection initiative (Maurizio and Rebeca)
16.45 – 17.00 h.	Closing







Venue. University Hospital Lozano Blesa. Health Research Institute Aragon, Zaragoza, Spain

Travel. There are flights to Zaragoza from some EU cities and direct speed train from Madrid and Barcelona (both cities directly connected by air with direct flights).

Accommodation. Options will be provided by local organizers.

Health Research Institute Aragon (IISA)

The IIS Aragón Foundation is the Health Research Institute of the Hospital Complex made up of the Teaching and University Hospitals "Hospital Clínico Universitario Lozano Blesa" and "Hospital Universitario Miguel Servet" and Primary Health Care. The University of Zaragoza and the Aragonese Institute of Health Sciences are associated with this Hospital Complex through different legal instruments.

The purposes of the IIS Aragón are:

- Approximate basic and applied research, clinical and health services.
- Create a quality research, care and teaching environment to which health professionals, training specialists, graduate and undergraduate students are exposed, to constitute the ideal place for the recruitment of talent and the location of the large scientific-technological facilities.

IIS Aragón is a Health Research Institute established according to the model proposed by the Ministry of Health and Consumer Affairs in its Royal Decree 339/2004 and updated to the draft Royal Decree currently in the consultation phase.

The Aragon Health Research Institute was accredited according to the Order of May 6, 2015, issued by the Secretary of State for Research, Development and Innovation of the Ministry of Economy and Competitiveness, according to the joint accreditation proposal of the Director of the Institute of Salud Carlos III and the Minister of Health, Social Welfare and Family of the Government of Aragon, after the previous favorable report issued by the Commission for the Evaluation of Accreditations of the Carlos III Health Institute.







Appendix 1 – Eligibility (Please refer to the <u>COST ANNEX I – LEVEL A. COUNTRY AND</u> <u>ORGANISATIONS TABLE</u>)

COST Full Members

The 41 COST Full Members are: Albania, Armenia, Austria, Belgium, Bosnia and Herzegovina, Bulgaria, Croatia, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Georgia, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Republic of Moldova, Montenegro, The Netherlands, The Republic of North Macedonia, Norway, Poland, Portugal, Romania, Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Turkey, Ukraine, and United Kingdom.

COST Cooperating Member

Israel is a Cooperating Member. A Cooperating Member implies non-voting rights in the COST CSO. However, researchers from COST's Cooperating Member enjoy member rights in COST Action participation.

COST Partner Member

South Africa is a Partner Member of COST. A Partner Member implies no rights to attend the COST CSO. However, researchers from COST's Partner Members enjoy observer rights in COST Action participation.

COST Near Neighbour Countries

Algeria, Azerbaijan, Belarus, Egypt, the Faroe Islands, Jordan, Kosovo3, Lebanon, Libya, Morocco, Palestine, Syria, and Tunisia.

European RTD Organisations (please see the <u>COST ANNEX I – LEVEL A. COUNTRY AND</u> ORGANISATIONS TABLE)







Appendix 2 – Trainers' biosketch and relevant publications.

Dr. Maurizio Callari

Graduated in Functional genomics and Bioinformatics at the University of Milan in 2007. He completed his PhD in Biomedical Sciences and Oncology in 2014 at Istituto Nazionale dei Tumori in Milan and University of Turin, working on the identification of prognostic/predictive signatures in breast cancer. In 2014 moved to the CRUK Cambridge Institute to work on breast cancer genomics and single-cell data to study tumour heterogeneity. Since 2021 leads the computational biology activities at Fondazione Michelangelo in Milan, Italy, focusing on the identification of multi-dimensional biomarkers in breast cancer and the study of molecular dynamics under treatment.

Selected publications:

- 1. Wang XQ, Danenberg E, Huang CS, Egle D, Callari M, Bermejo B et al. Spatial predictors of immunotherapy response in triple-negative breast cancer. Nature. 2023 Sep;621(7980):868-876. doi: 10.1038/s41586-023-06498-3. Epub 2023 Sep 6.
- 2. Georgopoulou D, Callari M, Rueda OM, Shea A, Martin A, Giovannetti A et al. Landscapes of cellular phenotypic diversity in breast cancer xenografts and their impact on drug response. Nat Commun. 2021 Mar 31;12(1):1998. doi: 10.1038/s41467-021-22303-z.
- 3. Callari M, Batra AS, Batra RN, Sammut SJ, Greenwood W, Clifford H, et al. Computational approach to discriminate human and mouse sequences in patient-derived tumour xenografts. BMC Genomics. 2018 Jan 5;19(1):19. doi: 10.1186/s12864-017-4414-y.
- 4. Bruna A, Rueda OM, Greenwood W, Batra AS, Callari M, Batra RN et al. A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell. 2016 Sep 22;167(1):260-274.e22. doi: 10.1016/j.cell.2016.08.041. Epub 2016 Sep 15.
- Callari M, Cappelletti V, D'Aiuto F, Musella V, Lembo A, Petel F et al. Subtype-Specific Metagene-Based Prediction of Outcome after Neoadjuvant and Adjuvant Treatment in Breast Cancer. Clin Cancer Res. 2016 Jan 15;22(2):337-45. doi: 10.1158/1078-0432.CCR-15-0757. Epub 2015 Sep 30.

Roberto Fornelino Gonzalez

Roberto obtained his BSc in Biology in 2018, followed by an MSc in Bioinformatics and Biostatistics in 2021. He is currently working in the private sector as a bioinformatician, specializing in the development of cancer immunotherapies. His main field of expertise focuses on applying structural modeling and artificial intelligence techniques for neoantigen and antibody discovery.

Selected publications:

1. García-Mulero S, Fornelino R, Punta M, Sanz-Pamplona R, et al. (1/14). Driver mutations in GNAQ and GNA11 genes as potential targets for precision immunotherapy in uveal melanoma patients. Oncoimmunology. 2023 Oct 24;12(1):2261278.







Dr. Sandra García-Mulero

Graduated in biological sciences (2015), with a PhD in molecular biology (2022), she is currently working as bioinformatician specialized in cancer and bioinformatics. Her research interest focus in the study of the immunogenomic profiling of solid tumors by bioinformatics tools. Her main field of expertise is the analysis of genomic and transcriptomic data from different sequencing platforms, characterization of tumor-immune system interaction, and discovery of biomarkers of cancer prognosis and therapy resistance.

Selected publications

- 1. <u>García-Mulero S</u>, Fornelino R, Punta M, Sanz-Pamplona R, et al. (1/14). Driver mutations in GNAQ and GNA11 genes as potential targets for precision immunotherapy in uveal melanoma patients. Oncoimmunology. 2023 Oct 24;12(1):2261278.
- Mur P, Viana-Errasti J, <u>García-Mulero S</u>, Valle L, et al. (3/10). Recommendations for the classification of germline variants in the exonuclease domain of POLE and POLD1. Genome Med. 2023 Oct 17;15(1):85.
- Marín-Jiménez JA, <u>García-Mulero S</u>, Matías-Guiu X, Piulats JM. (2/4). 2022. Facts and Hopes in Immunotherapy of Endometrial Cancer. Clinical Cancer Research. 2022 Nov 14;28(22):4849-4860.
- <u>García-Mulero S</u>, Alonso MH, Del Carpio LP, Sanz-Pamplona R, Piulats JM. (1/5). 2021. Additive Role of Immune System Infiltration and Angiogenesis in Uveal Melanoma Progression. Int J Mol Sci (Basel). 2021 Mar 6;22(5):2669.
- <u>García-Mulero S</u>, Alonso MH, Pardo J, Sanz-Pamplona R, et al. (1/9). 2020. Lung metastases share common immune features regardless of primary tumor origin Journal for Immunotherapy of Cancer. The Journal for ImmunoTherapy of Cancer. 2020 Jun;8(1):e000491.

Dr. Peter Rashkov

Dr. Peter Rashkov obtained his doctoral degree in Mathematics at the Jacobs University in Bremen, Germany in 2010 in the field of time-frequency analysis. He moved to the field of mathematical modelling in biology as a postdoc at the LOEWE Centre for Synthetic Microbiology in Marburg, Germany between 2010 and 2014, where he worked on models for regulatory networks for cell polarity. During a second postdoc at the University of Exeter, UK, he worked on a project with AstraZeneca on pharmacodynamical models for kinase inhibitors in the context of cancer. After returning to my home country Bulgaria in 2017, he obtained his habilitation at the Institute of Mathematics and Informatics in Sofia. He also teaches part-time at the Faculty of Mathematics and Informatics and chronic inflammatory diseases.







Selected Publications

- 1. B.W. Kooi, P. Rashkov, E. Venturino (2023), Multi-strain host-vector dengue modeling: dynamics and control, Chapter 6 in: P. Ghaffari (ed.), Bio-mathematics, Statistics, and Nano-Technologies: Mosquito Control Strategies, Chapman and Hall/CRC.
- 2. P. Rashkov, B.W. Kooi (2021), Complexity of host-vector dynamics in a two-strain dengue model. J. Biol. Dynam. 15: 35-72.
- 3. M. Borisov, G. Dimitriu, P. Rashkov (2019), Modelling the host immune response to mature and immature dengue viruses. Bull. Math. Biol. 81(12): 4951-4976.
- 4. P. Rashkov (2018), Competition for resources and space contributes to the emergence of drug resistance in cancer. Studies in Computational Intelligence 728: 169-183.
- P. Rashkov, I.P. Barrett, R.E. Beardmore, C. Bendtsen, I. Gudelj (2016), Kinase inhibition leads to hormesis in a dual phosphorylation-dephosphorylation cycle. PLoS Comput. Biol. 12 (11): e1005216.

Dr. Rebeca Sanz Pamplona

Her research focus is to understand cancer progression and metastasis taking into account both tumor heterogeneity and molecular crosstalk between malignant cells and their microenvironment. After obtaining her Biology Degree at University of Barcelona (2003), she did a PhD studying breast cancer metastasis (2009). In 2010, granted with a high competitive Spanish national fellowship (AECC post-doctoral), she joined to Colorectal Cancer Group at IDIBELL (Barcelona) in which she learnt bioinformatic and biostatistics techniques. In March 2020 she was named as the Coordinator of the Unit of Biomarkers and Susceptibility at ICO (Catalan Institute of Oncology). In 2022, she moved to IISA (Aragon Institute of Health Research) to start consolidating her own research group focus on immunomics and cancer heterogeneity.

Publications

- 1. García-Mulero S, Fornelino R, Punta M, Lise S, Varela M, Del Carpio LP, Moreno R, Costa-García M, Rieder D, Trajanoski Z, Gros A, Alemany R, Piulats JM, Sanz-Pamplona R. Driver mutations in GNAQ and GNA11 genes as potential targets for precision immunotherapy in uveal melanoma patients. Oncoimmunology. 2023 Oct 24;12(1):2261278.
- Lanuza PM, Alonso MH, Hidalgo S, Uranga-Murillo I, García-Mulero S, Arnau R, Santos C, Sanjuan X, Santiago L, Comas L, Redrado S, Pazo-Cid R, Agustin-Ferrández MJ, Jaime-Sánchez P, Pesini C, Gálvez EM, Ramírez-Labrada A, Arias M, Sanz-Pamplona R*, Pardo J*. Adoptive NK Cell Transfer as a Treatment in Colorectal Cancer Patients: Analyses of Tumour Cell Determinants Correlating With Efficacy In Vitro and In Vivo. Front Immunol. 2022 Jun 7;13:890836.
- 3. García-Mulero S, Alonso MH, Pardo J, Santos C, Sanjuan X, Salazar R, Moreno V, Piulats JM, Sanz-Pamplona R. Lung metastases share common immune features regardless of primary tumor origin. J Immunother Cancer. 2020 Jun;8(1):e000491.







- Moratalla-Navarro F, Moreno V, Sanz-Pamplona R. TALKIEN: crossTALK IntEraction Network. A web-based tool for deciphering molecular communication through ligandreceptor interactions. Mol Omics. 2023 Oct 30;19(9):688-696. doi: 10.1039/d3mo00049d. PMID: 37403821.
- Sanz-Pamplona R, Melas M, Maoz A, Schmit SL, Rennert H, Lejbkowicz F, Greenson JK, Sanjuan X, Lopez-Zambrano M, Alonso MH, Qu C, McDonnell KJ, Idos GE, Vignali M, Emerson R, Fields P, Guinó E, Santos C, Salazar R, Robins HS, Rennert G, Gruber SB, Moreno V. Lymphocytic infiltration in stage II microsatellite stable colorectal tumors: A retrospective prognosis biomarker analysis. PLoS Med. 2020