AIRR Community

AIRR Community FOCiS 2021 Symposium Agenda
"How immune repertoires can inform human immunology"
June 8th, 2021 12:30 - 4:00 PT / 15:30 - 19:00 PM ET / 21:30 - 1:00 (June 9th) CET

The AIRR Community (AIRR-C) is a grass-roots group of immunologists, bioinformaticists, computer scientists, and experts in legal, ethics and IP issues, who are developing guidelines and standards for the generation, annotation and storage of high-throughput AIRR-seq data to facilitate its use by the larger research community.

12:30 - 12:35	Encarnita Mariotti-Ferrandiz, Sorbonne Université, France - Symposium Chair ***Symposium Learning Objectives***
12:35 - 12:45	Lindsay Cowell, University of Texas Southwestern Medical Center, USA ***Introduction to The AIRR Community***
12:45 - 13:10	Victor Greiff, Oslo University, Norway ***Computational and machine learning approaches for identifying antigen-specific information in adaptive immune receptor repertoires***
13:10 - 13:35	Encarnita Mariotti-Ferrandiz, Sorbonne Université, France ***TCR signatures as biomarkers of autoimmune diseases***
13:35 - 14:00	Lindsay Cowell, University of Texas Southwestern Medical Center, USA ***Biophysicochemical Motifs in T Cell Receptor Antigen Binding Regions as Potential Biomarkers of Cancer***
14:00 - 14:15	***Break***
14:15 - 14:40	Nina Luning Prak, University of Pennsylvania, USA ***B cell clonal networks: lessons learned from SARS-CoV-2***
14:40 - 15:05	Corey Watson, University of Louisville, USA ***Characterizing germline variation in adaptive immune receptor genes***
15:05 - 15:30	Christian Busse, German Cancer Research Center (DKFZ), Germany ***AIRR Community Data Standards - Past, Present and Future***
15:30 - 15:55	Brian Corrie, Simon Fraser University, Canada ***The AIRR Data Commons - towards FAIR AIRR-seq data***
15:55 - 16:00	Encarnita Mariotti-Ferrandiz, Sorbonne Université, France ***Final questions and closing***

Symposium Learning Objectives

- Learn about AIRR-seq data, how they are generated, and how they inform the biology of human immune responses.
- Learn what to do, and not do, when studying AIRRs (wet & dry lab aspects), as well as remaining challenges.
- Learn about new tools for AIRR-seq data modeling, sharing, and storage.
- Learn about the history, contributions, and initiatives of The AIRR Community (AIRR-C).
- Learn where to find partners and collaborators in this field.

Lindsay Cowell

Abstract: Deep sequencing of adaptive immune receptor repertoires (AIRRs) has long been considered a useful tool for the prognostication of cancer patients and the monitoring of immunotherapy responses. We hypothesized that AIRR sequencing may also enable early detection of cancer by detecting T cell receptors (TCRs) that are part of the antitumor immune response. To this end, we compared tumor and healthy tissue repertoires and identified biophysicochemical motifs that distinguish early stage breast cancer repertoires from healthy breast tissue repertoires, colorectal cancer repertoires from healthy colorectal tissue repertoires, and high grade serous ovarian cancer repertoires from the ovarian repertoires of cancer-free women with accuracies ranging from 93-95%. We have shown that the breast cancer motifs can be found in the blood of breast cancer patients. The motifs identified for the three cancer types are distinct, suggesting that they could not only indicate the presence of cancer but also point to the cancer type. Using cervical cancer as a source of pre-neoplasic lesions, we have also demonstrated motifs that predict the likelihood of spontaneous lesion regression.

Speaker Bio: Dr. Lindsay Cowell is an Associate Professor in the Department of Population and Data Sciences and the Department of Immunology at UT Southwestern Medical Center. She is broadly interested in understanding the mechanisms of adaptive immunity and their role in infectious diseases, autoimmune diseases, cancer, and vaccine responses. Research in the Cowell group is currently directed toward advancing understanding of (1) the molecular mechanisms by which adaptive immune receptor genes are somatically generated and diversified, (2) the role of these mechanisms in disease, and (3) the dynamics of adaptive immune receptor repertoires in the context of various states of human health and disease. In addition to our basic science research, the group has pursued clinical applications in the areas of autoimmune disease (*e.g.,* multiple sclerosis), infectious disease (*e.g.,*Staphylococcus aureus), and cancer (*e.g.,* ovarian cancer, HPV-related cancers, particularly cervical cancer, and design of chimeric antigen receptors for cancer therapy).

Dr. Cowell is the Chair of the AIRR-C Executive Sub-committee and the former Co-lead of the AIRR-C Common Repository Working Group.

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Victor Greiff

Abstract: The adaptive immune system recognizes antigens via an immense array of antigen-binding antibodies and T-cell receptors, the adaptive immune receptor repertoire. The interrogation of immune repertoires is of high relevance for interpreting the adaptive immune response in disease and infection (e.g., autoimmunity, cancer, HIV) and the conception of immunotherapeutics. I will present our recent work on developing novel systems immunology and machine learning methods for deciphering how specificity is encoded into repertoires and how we can potentially use this information to predict patient immune state and immune receptor-antigen binding.

Speaker Bio: Dr. Victor Greiff is an Associate Professor for Systems Immunology at the University of Oslo. His group develops machine learning, computational and experimental tools for analyzing antibody and T-cell repertoires to develop immune-repertoire-based immunodiagnostics and immunotherapeutics.

Dr. Greiff is the Chair-elect of the AIRR-C Executive Sub-committee and an active member of the AIRR-C Communications Sub-committee.

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Encarnita Mariotti-Ferrandiz

Abstract: With the advances in next-generation sequencing and data modelling, T-cell receptor repertoire is now believed to provide biomarkers of diagnostics. In the race of methods and tools development, it is important to ensure the reliability of such complex biological components characterized by an uneven diversity. After introducing our recent comparative study that evaluated the performances of various molecular biology methods commonly used in the field, I will introduce our method and results of TCR signatures identification in several autoimmune diseases.

Speaker Bio: Dr. Encarnita Mariotti-Ferrandiz is an Associate Professor for Systems Immunology at Sorbonne Universite (Paris, France). Her group, part of the i3 laboratory, studies T-cell repertoires in physiological and pathological contexts, from sample to data modelling. The main objectives being to (i) better understand T-cell selection and tissue homing and (ii) to identify biomarkers of disease status.

Dr. Mariotti-Ferrandiz is the former Co-lead and still member of the AIRR-C Biological Resources Working Group, a member of the AIRR-C Executive Sub-committee, the AIRR-C Meetings Sub-committee and the AIRR-C Diagnostics Working Group.

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Nina Luning Prak

Abstract: We are interested in how B cells generate protective vs. maladaptive immune responses. In the past year, we have focused most of our efforts on the analysis of B-cell responses to SARS-CoV-2. I will discuss some of our recent studies of B-cell responses in COVID-19 patients using next-generation sequencing of antibody gene rearrangements. I will describe longitudinal studies of clonal expansion and somatic hypermutation in recovered patients and individuals who have received one or both doses of an mRNA vaccine. I will also provide an update on our efforts to map expanded clones across different tissues and B-cell subsets. These studies provide insights into how primary and memory B-cell responses are organized in space and time.

Speaker Bio: Dr. Nina Luning Prak is a Professor of Pathology and Laboratory Medicine in the Perelman School of Medicine at the University of Pennsylvania. Dr. Luning Prak directs an NIH-funded research lab that studies human B cells and immune repertoires in health and disease. She also serves as the Director of the Human Immunology Core and Associate Director of the Clinical Immunology Laboratory at the Hospital of the University of Pennsylvania.

Dr. Luning Prak is the past chair of the Executive Sub-committee, the former Co-lead of the Standards Working group, as well as now a member of the AIRR-C Executive Sub-committee, the AIRR-C Diagnostics Working Group and the AIRR-C Biological Resources Working Group.

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Corey Watson

Abstract: Adaptive immune receptor genes (immunoglobulins and T cell receptors) are critical to the immune system. These genes represent large, expanded gene families and reside within the most complex regions of mammalian genomes. The complexity of these loci have hindered our ability to characterize the extent of genetic diversity across species and populations. This has had practical implications for data analysis approaches and has hindered our ability to determine the influence of germline variation on the immune response. I will talk about our ongoing work to develop approaches to more comprehensively curate adaptive immune receptor gene diversity in humans and various animal models, and discuss how these approaches can be leveraged to more fully explore features of B and T cell mediated immunity.

Speaker Bio: Dr. Corey Watson is an Assistant Professor in the Department of Biochemistry and Molecular Genetics at the University of Louisville School of Medicine. His group is interested in determining how germline polymorphism within adaptive immune receptor genes contributes to variation in the immune response, and how this information can be leveraged to better our understanding of disease susceptibility and clinical health outcomes.

Dr. Watson is a Co-lead of the AIRR-C Germline Database Working Group and a member of both the AIRR-C Inferred Allele Working Group and the AIRR-C Meetings Sub-committee.

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Christian Busse

Abstract: Adaptive Immune Receptor Repertoire sequencing (AIRR-seq) is a heterogeneous set of NGS-based technologies that provide information on immunoglobulins (Ig) and T-cell receptors (TCR). Over the last five years, the AIRR Community Standards Working Group and its predecessors have developed a set of standards, representations and interfaces to simplify the exchange and reuse of such data sets. This talk will provide an overview about the current standards maintained by the working group, a brief summary of their development since 2016 and the future directions and challenges on the way towards a strongly interconnected and FAIR data ecosystem.

Speaker Bio: Dr. Christian Busse is a project lead at the German Cancer Research Center (DKFZ). He has a background in experimental immunology, with a focus on single-cell applications. Together with his team, he is currently developing concepts, tools and interfaces to facilitate the creation, sharing and reuse of FAIR immunological research data within an open and sustainable infrastructure.

Dr. Busse is a Co-lead of the AIRR-C Standards Working Group, a member of the AIRR-C Executive Sub-committee, the AIRR-C Common Repository Working Group and the AIRR-C Germline Database Working Group.

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Brian Corrie

Abstract: The AIRR Community has established the AIRR Data Commons (ADC) [Christley et al.], a network of geographically distributed AIRR compliant repositories that adhere to the AIRR Standards. The AIRR Community and the ADC adheres to the FAIR principles of data sharing (Findable, Accessible, Interoperable, and Reproducible). The AIRR Data Commons web API is a web based query API that makes AIRR-seq studies and their associated annotated sequence data in the ADC findable and accessible (the FA in FAIR). Because the ADC API utilizes the MiAIRR Standards and AIRR file formats, the ADC also promotes and facilitates interoperability and data reuse (the IR in FAIR), thereby supporting both reproducibility and meta-analysis.

The AIRR Data Commons has grown from just under 400 million sequence annotations in two distributed repositories in late 2018 to its current size of five distributed repositories with over 60 studies, 6000 repertoires, and 4 billion sequence annotations available for exploration and analysis. Of the four distributed repositories, there are two community repositories in Canada (the iReceptor Public Archive (IPA) and iReceptor COVID-19 repositories managed by iReceptor), one community repository in the US (managed by VDJServer) and one research group-specific repository VDJBase repository at Bar Ilan University in Israel.

Speaker Bio: Dr. Brian Corrie is the Technical Director for the iReceptor Project, the Technical Manager for iReceptor Plus Project. Brian has a background in computer science with a focus on data visualization, computational science, and scientific collaboration.

Dr. Corrie is a Co-lead of the AIRR-C Common Repository Working Group and a member of the AIRR-C Standards, Diagnostics, and Software Working Groups.

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