AIRR Community Meeting VII

Learnings and Perspectives

June 3 - 6, 2024

Gold

Silver

Bronze

Travel Award

Hosting Partner

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Welcome from the AIRR-C Meetings Sub-Committee and the AIRR-C Executive Chair

Welcome to the seventh meeting of the Adaptive-Immune Receptor Repertoire Community (AIRR-C) of The Antibody Society, hosted at Faculty of Engineering, University of Porto, Portugal - AIRR-C Meeting VII: Learnings & Perspectives.

The AIRR-C is committed to developing standards and/or recommendations for:

i. Generating, analyzing, curating, and sharing AIRR-sequencing (AIRR-seq) data;
ii. Using and validating tools for analyzing AIRR-seq data;
iii. Relating AIRR-seq data to other "big data" types, such as microarray, flow cytometric, and single-cell gene-expression data; and
iv. Legal and ethical matters associated with the use and sharing of AIRR-seq data derived from human sources.

Through its Working Groups, Sub-Committees, and meetings, the AIRR-C has developed and published recommendations and action plans to maximize the generation, use, and sharing of AIRR-seq data within the scientific community for the benefit of humanity.

AIRR-C meetings are the premier event for research on adaptive immune-receptor repertoires. They are also the primary location where the AIRR-C's Working Groups and Sub-committees come together in one location to discuss how to push standardization in AIRR-seq data and analysis forward. All attendees are welcome to participate in the Working Group and Sub-Committee Future Plans session, when achievements and work plans for the coming year of each of the Working Groups, Sub-committees, and Review-Committees will be presented and ratified.

The AIRR-C VII Meeting focused on ***Learnings & Perspectives*** through two themed "Challenge Sessions" and two "Science Sessions":

i. ***Germline Challenge Session:*** Using IG and TR germline resources for advancing immunobiology
ii. ***Machine Learning Challenge Session:*** Machine Learning applied to AIRR-seq data
iii. ***Basic Science:*** Advances in AIRR-sequencing: Addressing Fundamental Biological Processes
iv. ***Biomedical Science:*** Advances in AIRR-sequencing: Addressing Human Diseases

Through a diverse and original array of activities, the AIRR-C VII Meeting provided opportunities for investigators, industry professionals, and early career researchers to network (three events), to participate in AIRR-C Working Groups and Sub-Committee meetings (three events), and to learn at the workshop sessions (The Fundamentals of Immunology and AIRR-seq data: Processing and Analysis), poster sessions, software demonstrations, and deep dive tool tutorials.

Last but not least, the AIRR-C Challenge and Science Sessions gathered an outstanding line up, including keynote lectures by Jeffrey Gray, Nicholas Provine, Bill Schief, and Hedda Wardemann, invited presentations and short presentations chosen from the submitted poster abstracts.

For this AIRR-C VII Meeting, the AIRR-C was awarded a travel grant from the European Federation of Immunological Societies (EFIS) – European Journal of Immunology to help junior faculty members, post-

docs, and students to attend the AIRR-C VII Meeting. Priority was given to applicants from middle to low-income countries.

All meeting documents and video recordings can be found on the AIRR-C YouTube channel under the AIRR-C7 playlist (click here for link).

Thank you for your participation and we invite you to become an active member of the AIRR-C, if you are not one already! Consider joining a Working Group, Sub-Committee, or Review-Committee. It is a great way to get involved in an interdisciplinary network of basic and biomedical scientists, bioinformaticians, ethicists, and legal experts from academia and industry who are all working toward a greater good!

Sincerely the members of the Meetings Sub-Committee:

Ademar Aguiar (PT); Edel Aron (US); Justin Barton (UK); Pam Borghardt (CA, Co-Lead); Lorissa Corrie (CA); Encarnita Mariotti-Ferrandiz (FR, Co-Lead); and Corey Watson (US)

Thank you to the Executive and Communications Sub-Committees and Working Group Co-leads and volunteers from Sorbonne Université and Oslo University!

The Meeting at a Glance

The event drew a diverse global audience with 182 in-person attendees and 31 remote participants from 26 countries, marking an increase from 2022. The success of AIRR-C VII was bolstered by the generous support of our 19 sponsors and partners, whose contributions were instrumental. Our exceptional program featured 16 invited speakers, 10 contributed talks, 96 research posters, 11 Working Group and Sub-Committee posters, three early career events with over 50 early career researchers and 20 mentors participating, and a dynamic mix of sessions including four themed scientific or challenge sessions, two workshops, 10 lightning demos, and nine deep dive tutorials.

Our four session themes featured two science (Basic and Biomedical Science) and two challenge (Germline and Machine Learning) sessions with a keynote, invited speakers, contributed talks, and posters exploring the diverse array of research occurring in these areas in the AIRR-C. The sessions were described as follows:

- Basic Science: Advances in AIRR-sequencing - Addressing Fundamental Biological Processes
- Biomedical Science: Advances in AIRR-sequencing - Addressing Human Diseases
- AIRR-C Challenge Session: Using IG and TR germline resources for advancing immunobiology
- AIRR-C Challenge Session: Machine Learning applied to AIRR-seq data

Additionally, participants engaged in hands-on, one-hour “deep dive” tutorials and short 10-minute “lightning” demonstrations of innovative software and tools, enhancing their technical skills and knowledge. These demonstrations included tutorials and walkthroughs, question and answer periods, and discussion on what users would like to see in future software and tool development.

Early career researchers and students actively participated in career development activities alongside the scientific program. “Networking is in the AIRR” featured a speed networking event connecting early career scientists with established AIRR researchers, fostering invaluable connections across sectors and research areas. A “Service as an Early Career Researcher: The rewards of being active in the AIRR-C” presentation by Chaim Schramm discussed how his experience in the AIRR-C helped shape his career. A career development panel discussion offered insights into diverse career paths within AIRR research, complementing the scientific sessions and providing opportunities for direct engagement with experts.

As part of the Industry Networking Reception, a special “hot topics in the field” round table session provided a unique opportunity for industry partners and scientific researchers to engage in exciting discussions. Moderated by pairs of AIRR-C Working Group Co-leaders and Industry Partners, these sessions focused on future needs and challenges in key areas such as “Antibody Discovery,” “AIRR-seq epitope / antigen annotation,” “Datasets and applications / tools for mining the repertoire,” “Biological Standards / Controls / Methods,” and “Data sharing & data standards for AIRR analysis and software.” The goal of these discussions was to gather input and ideas to shape the future of AIRR research.

Sponsors

The AIRR-C warmly thanks all our meeting sponsors for their generous financial support. It is their contribution that made this meeting possible, laying the foundation for an exciting and stimulating scientific exchange. Please take a moment and inform yourself about the ground-breaking work and services our sponsors provide and make sure to engage with them during the Industry Networking session on June 5th, during the daily Sponsor Exhibit opportunities, and Lunch & Science, Tools and Technology Gold Sponsor Presentations session on June 5th.

You will find below a list of the meeting sponsors and access to their websites.

Gold	
Cellecta	cellecta.com
Imprint	www.imprint.org
MIXCR	milaboratories.com
PipeBio	pipebio.com
Takara Bio	www.takarabio.com
Silver	
ENPICOM	enpicom.com
genmab	www.genmab.com
GSK	www.gsk.com/en-gb
Antibody Society	www.antibodysociety.org
Voredos	www.airrdb.com
Bronze	
FairJourney Biologics	fjbio.com
ImmuneWatch	www.immunewatch.com
Infinimmune	www.infinimmune.com
Infinity Bio Inc	www.infinitybio.com
MAbSilico	www.mabsilico.com
NaturalAntibody	naturalantibody.com
UCB	www.ucb.com
Hosting Partner	
INESCTEC	www.inesctec.pt/en
Travel Award	
EFIS – European Journal of Immunology	www.efis.org/journals/european-journal-of-immunology

The AIRR-C Online

know more about the AIRRC

join the AIRRC

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On AIRR an AIRRC podcast

AIRRC youtube channel

AIRRC merchandizing

The AIRR-C on Social Media

x.com/airr_community

www.linkedin.com/company/the-AIRRCommunity/

AIRR-C Sub-Committees and Working Groups Contact Information

Communications Sub-Committee (SC): communications@AIRRCommunity.org

Executive SC: exec@airrc.antibodysociety.org

Inferred Allele Review SC: iarc@AIRRCommunity.org

Meetings SC: meetings@AIRRCommunity.org

Strategic Planning SC: strategic-planning@AIRRCommunity.org

Biological Resources Working Group (WG)*: biological-resources@AIRRCommunity.org

Common Repository WG: common-repository@AIRRCommunity.org

Diagnostics WG: diagnostics@AIRRCommunity.org

Germline WG: germline-database@AIRRCommunity.org

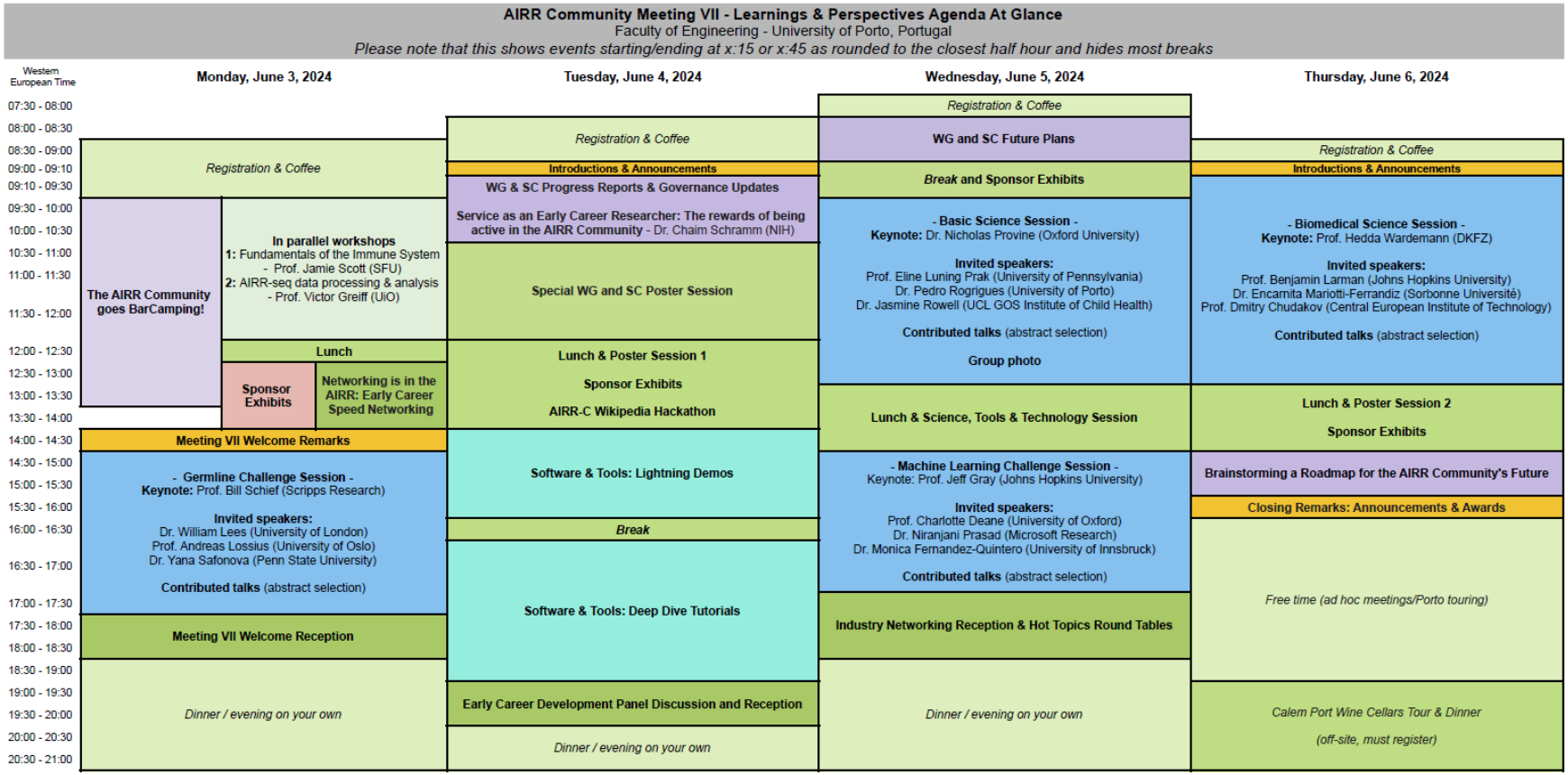
Legal & Ethics WG*: legal-ethics@AIRRCommunity.org

Software WG: software@AIRRCommunity.org

Standards WG: standards@AIRRCommunity.org

*These WGs reached their aims and are no longer active. Their disband has been proposed and voted on at the AIRR-C Meeting VII General Assembly.

Agenda at glance



AIRR Community Meeting VII - Learnings & Perspectives Agenda At Glance
Faculty of Engineering - University of Porto, Portugal
Please note that this shows events starting/ending at x:15 or x:45 as rounded to the closest half hour and hides most breaks

Western European Time	Monday, June 3, 2024	Tuesday, June 4, 2024	Wednesday, June 5, 2024	Thursday, June 6, 2024
07:30 - 08:00			*Registration & Coffee*	
08:00 - 08:30		*Registration & Coffee*	**WG and SC Future Plans**	
08:30 - 09:00	*Registration & Coffee*			*Registration & Coffee*
09:00 - 09:10		**Introductions & Announcements**		**Introductions & Announcements**
09:10 - 09:30		**WG & SC Progress Reports & Governance Updates**	***Break* and Sponsor Exhibits**	
09:30 - 10:00	**The AIRR Community goes BarCamping!**	**Service as an Early Career Researcher: The rewards of being active in the AIRR Community** - Dr. Chaim Schramm (NIH)	**- Basic Science Session -** **Keynote:** Dr. Nicholas Provine (Oxford University)	**- Biomedical Science Session -** **Keynote:** Prof. Hedda Wardemann (DKFZ)
10:00 - 10:30			**Invited speakers:** Prof. Eline Luning Prak (University of Pennsylvania) Dr. Pedro Rogrigues (University of Porto) Dr. Jasmine Rowell (UCL GOS Institute of Child Health)	**Invited speakers:** Prof. Benjamin Larman (Johns Hopkins University) Dr. Encarnita Mariotti-Ferrandiz (Sorbonne Université) Prof. Dmitry Chudakov (Central European Institute of Technology)
10:30 - 11:00	**In parallel workshops** **1:** Fundamentals of the Immune System - Prof. Jamie Scott (SFU) **2:** AIRR-seq data processing & analysis - Prof. Victor Greiff (UiO)	**Special WG and SC Poster Session**		
11:00 - 11:30				
11:30 - 12:00			**Contributed talks** (abstract selection)	**Contributed talks** (abstract selection)
12:00 - 12:30	**Lunch**	**Lunch & Poster Session 1**	**Group photo**	
12:30 - 13:00	**Sponsor Exhibits** / **Networking is in the AIRR: Early Career Speed Networking**	**Sponsor Exhibits**		
13:00 - 13:30		**AIRR-C Wikipedia Hackathon**	**Lunch & Science, Tools & Technology Session**	**Lunch & Poster Session 2**
13:30 - 14:00				**Sponsor Exhibits**
14:00 - 14:30	**Meeting VII Welcome Remarks**	**Software & Tools: Lightning Demos**		
14:30 - 15:00	**- Germline Challenge Session -** **Keynote:** Prof. Bill Schief (Scripps Research)		**- Machine Learning Challenge Session -** Keynote: Prof. Jeff Gray (Johns Hopkins University)	**Brainstorming a Roadmap for the AIRR Community's Future**
15:00 - 15:30				
15:30 - 16:00				**Closing Remarks: Announcements & Awards**
16:00 - 16:30	**Invited speakers:** Dr. William Lees (University of London) Prof. Andreas Lossius (University of Oslo) Dr. Yana Safonova (Penn State University)	***Break***	**Invited speakers:** Prof. Charlotte Deane (University of Oxford) Dr. Niranjani Prasad (Microsoft Research) Dr. Monica Fernandez-Quintero (University of Innsbruck)	
16:30 - 17:00		**Software & Tools: Deep Dive Tutorials**		*Free time (ad hoc meetings/Porto touring)*
17:00 - 17:30	**Contributed talks** (abstract selection)			
17:30 - 18:00	**Meeting VII Welcome Reception**		**Industry Networking Reception & Hot Topics Round Tables**	
18:00 - 18:30				
18:30 - 19:00	*Dinner / evening on your own*	**Early Career Development Panel Discussion and Reception**	*Dinner / evening on your own*	*Calem Port Wine Cellars Tour & Dinner* *(off-site, must register)*
19:00 - 19:30				
19:30 - 20:00		*Dinner / evening on your own*		
20:00 - 20:30				
20:30 - 21:00				

AIRR Community

ANTIBODY SOCIETY

Full Agenda

Event Agenda

AIRR Community Meeting VII - Learnings and Perspectives

Mon, Jun 03, 2024

8:30 AM - 9:30 AM
Registration & Coffee
Location: FEUP - Building A - Registration desk – level 1 & Exhibition Hall – ground floor

9:00 AM - 1:30 PM
The AIRR Community Goes BarCamping!
Location: FEUP - Building I - Room I-105 – Ground floor

9:30 AM - 12:00 PM
Workshop I: Fundamentals of the immune system
Location: FEUP - Building B - Noble Ampitheater B032 – level 1
Speaker: Jamie Scott

9:30 AM - 12:00 PM
Workshop II: AIRR-seq data generation, preprocessing and analysis
Location: FEUP - Building A - Auditorium – level 1
Speaker: Victor Greiff

10:45 AM - 11:00 AM
Coffee Break brought to you by Voredos
Location: FEUP - Building A - Exhibition Hall – Ground floor

12:00 PM - 2:00 PM
Lunch Activities: Sponsor Exhibits, Early Career Networking

Lunch brought to you by GenMab
12:00 PM - 12:45 PM
Location: FEUP - Building A - Exhibition Hall – Ground floor

Visit the Sponsor Exhibits!
12:30 PM - 1:45 PM
Location: FEUP - Building B - Panoramic corridor - Ground Floor

(MENTOR RSVP) Early career event: Networking is in the AIRR
12:30 PM - 1:45 PM
Location: FEUP - Building I - Room I-105 (lawn) – Ground floor

(MENTEE RSVP) Early career event: Networking is in the AIRR
12:30 PM - 1:45 PM
Location: FEUP - Building I - Room I-105 (lawn) – Ground floor

12:45 PM - 1:45 PM
Registration Open
Location: FEUP - Building A - Registration desk – level 1

2:00 PM - 2:10 PM
Welcome by the Chair of the AIRR Community and by Gabriel David, University of Porto
Location: FEUP - Building A - Auditorium – level 1
Moderator: Victor Greiff

2:10 PM - 2:20 PM
AIRR-C Germline Challenge Session: Using IG and TR germline resources for advancing immunobiology
Location: FEUP - Building A - Auditorium – level 1
Moderator: Corey Watson

2:20 PM - 3:10 PM
Stepping toward an HIV vaccine
Location: FEUP - Building A - Auditorium – level 1
Speaker: Bill Schief

3:10 PM - 3:20 PM
Break brought to you by the Antibody Society
Location: FEUP - Building A - Exhibition Hall – Ground floor

3:20 PM - 3:50 PM
The rapidly changing world of IG/TR germline gene databases
Location: FEUP - Building A - Auditorium – level 1
Speaker: William Lees

3:50 PM - 4:20 PM

Immunoglobulin heavy-chain constant gene polymorphisms in multiple sclerosis
Location: FEUP - Building A - Auditorium – level 1
Speaker: Andreas Lossius

4:20 PM - 4:50 PM

Comparative Analyses of Immunoglobulin Loci in Mammalian Genomes
Location: FEUP - Building A - Auditorium – level 1
Speaker: Yana Safanova

5:00 PM - 5:30 PM

AIRR-C Germline Challenge Session: Short Contributed Talks
Location: FEUP - Building A - Auditorium – level 1

The Hidden Diversity of Antibody Heavy Chains: Implications for Autoantibody Mediated Disease
5:00 PM - 5:15 PM
Speaker: Easton Ford

Full-length assembly and immunogenetic analysis of immunoglobulin and T cell receptor loci from Mauritian cynomolgus macaques
5:15 PM - 5:30 PM
Speaker: Chaim Schramm

5:30 PM - 6:30 PM

AIRR Community Meeting VII Welcome Reception
Location: FEUP - Building I - Room I-105 (lawn) – Ground floor

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Tue, Jun 04, 2024

8:00 AM - 9:00 AM

Registration & Coffee brought to you by Cellecta
Location: FEUP - Building A - Registration desk – level 1 & Exhibition Hall – ground floor

9:00 AM - 9:10 PM

Welcome & Announcements
Location: FEUP - Building A - Auditorium – level 1
Speakers: Victor Greiff, Janine Schuurman

9:10 AM - 9:35 AM

Presentation: AIRR Community WG / SC Progress Reports Overview
Location: FEUP - Building A - Auditorium – level 1
Session Presenter: Victor Greiff

9:35 AM - 10:00 AM

Presentation: AIRR Community Governance v23 updates
Location: FEUP - Building A - Auditorium – level 1
Session Presenter: Christian Busse

10:00 AM - 10:15 AM

Service as an Early Career Researcher: The rewards of being active in the AIRR Community
Location: FEUP - Building A - Auditorium – level 1
Session Presenter: Chaim Schramm

10:15 AM - 10:30 AM

Coffee Break brought to you by IMPRINT
Location: FEUP - Building A - Exhibition Hall – Ground floor

10:30 AM - 12:00 PM

Special Poster Session by AIRR-C Working Groups & Sub-Committees
Location: FEUP - Building A - Exhibition Hall – Ground floor

12:00 PM - 2:00 PM

Lunch Activities: Poster Session 1, Sponsor Exhibits, AIRR-C Wikipedia Hackathon

Lunch brought to you by GSK
12:00 PM - 12:40 PM
Location: FEUP - Building A - Exhibition Hall – Ground floor

Poster Session I
12:30 PM - 1:45 PM
Location: FEUP - Building B - Panoramic corridor - Ground Floor

Visit the Sponsor Exhibits!
12:30 PM - 1:45 PM
Location: FEUP - Building B - Panoramic corridor - Ground Floor

AIRR-C Wikipedia Hackathon
1:40 PM - 2:00 PM
Location: FEUP - Building A - Exhibition Hall – Ground floor

12:45 PM - 1:30 PM

Registration Open
Location: FEUP - Building A - Registration desk – level 1

2:00 PM - 4:10 PM — **Software & Tools - Lightning Demos**
Location: FEUP - Building A - Auditorium – level 1

ImmuneWatch DETECT
2:10 PM - 2:20 PM
Speaker: Sander Wuyts

LZGraphs
2:20 PM - 2:30 PM
Speaker: Thomas Konstantinovsky

AbSolution
2:30 PM - 2:40 PM
Speaker: Rodrigo García Valiente

AnalyzAIRR
2:40 PM - 2:50 PM
Speaker: Vanessa Mhanna

ACE Configurator for ELIspot
2:50 PM - 3:00 PM
Speakers: Dhuvi Karthikeyan, Jin Seok (Andy) Lee

Break
3:00 PM - 3:10 PM
Location: Lobby - Ground Floor

reportAIRR
3:10 PM - 3:20 PM
Speaker: Ayelet Peres

ALIGaToR
3:20 PM - 3:30 PM
Speaker: Chaim Schramm

Immcantation
3:30 PM - 3:40 PM
Speaker: Steven Kleinstein

MAbFactory
3:40 PM - 3:50 PM
Speaker: Anne Poupon

RepCred
3:50 PM - 4:00 PM
Speaker: Ayelet Peres

3:00 PM - 3:00 PM — **AIRR Community Voting Opens**
Location: FEUP - Building A - Auditorium – level 1

4:10 PM - 4:30 PM — **Coffee Break brought to you by Genmab**
Location: FEUP - Building A - Exhibition Hall – Ground floor

4:30 PM - 5:30 PM — **Software & Tools - Deep Dive Tutorials - Session A**

Digger (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B022 – Ground Floor
Speaker: William Lees

Dowser (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B031 – Ground Floor
Speaker: Kenneth Hoehn

Immcantation and nf-core/airrflow (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B033 – Ground Floor
Speakers: Gisela Gabernet, Susanna Marquez

immuneML (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B025 – Ground Floor
Speakers: Lonneke Scheffer, Charlotte Würtzen

ImReP (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B034 – Ground Floor
Speaker: Erik Huang

iReceptor Gateway - Tool Integration (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B024 – Ground Floor
Speaker: Brian Corrie

pyTCR (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B030 – Ground Floor
Speaker: Serghei Mangul

STEGO.R (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B027 – Ground Floor
Speaker: Kerry Mullan

TCRex and ClusTCR (Session A)
4:30 PM - 5:30 PM
Location: FEUP - Building B - Amphitheater B028 – Ground Floor
Speaker: Pieter Meysman

5:30 PM - 5:50 PM — **Break & move to Deep Dive Tutorial B**

5:50 PM - 6:50 PM — **Software & Tools - Deep Dive Tutorials - Session B**

Digger (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B022 – Ground Floor
Speaker: William Lees

Dowser (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B031 – Ground Floor
Speaker: Kenneth Hoehn

Immcantation and nf-core/airrflow (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B033 – Ground Floor
Speakers: Gisela Gabernet, Susanna Marquez

immuneML (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B025 – Ground Floor
Speakers: Lonneke Scheffer, Charlotte Würtzen

ImReP (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B034 – Ground Floor
Speaker: Erik Huang

iReceptor Gateway - Tool Integration (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B024 – Ground Floor
Speaker: Brian Corrie

pyTCR (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B030 – Ground Floor
Speaker: Serghei Mangul

STEGO.R (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B027 – Ground Floor
Speaker: Kerry Mullan

TCRex and ClusTCR (Session B)
5:50 PM - 6:50 PM
Location: FEUP - Building B - Amphitheater B028 – Ground Floor
Speaker: Pieter Meysman

6:50 PM - 8:00 PM — **Early Career Development Networking Reception & Panel Discussion**
Location: FEUP - Building I - Room I-105 – Ground floor
Speakers: Janine Schuurman, Nina Luning Prak, Nina Senna, Pieter Meysman, Steven Kleinstein

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Wed, Jun 05, 2024

7:30 AM - 8:00 AM — **Registration & Coffee brought to you by MiLaboratories**
Location: FEUP - Building A - Registration desk – level 1 & Exhibition Hall – ground floor

8:00 AM - 8:05 AM — **Welcome & Announcements**
Location: FEUP - Building A - Auditorium – level 1
Speaker: Victor Greiff

8:05 AM - 9:10 AM — **Presentation: Working Group & Sub-Committee: Future Plans**
Location: FEUP - Building A - Auditorium – level 1
Speakers: Victor Greiff, Brian Corrie, Pieter Meysman, William Lees, Justin Barton, Christian Busse, Encarnita Mariotti-Ferrandiz, Ulrik Stervbo, Mats Ohlin, Pam Borghardt, Simon Schaefer

9:10 AM - 9:30 AM — **Break brought to you by Takara Bio & Visit the Sponsor Exhibits!**
Location: FEUP - Building A - Exhibition Hall – Ground floor

Visit the Sponsor Exhibits!
9:10 AM - 9:30 AM
Location: FEUP - Building B - Panoramic corridor - Ground Floor

9:30 AM - 9:40 AM — **Basic Science Session: Advances in AIRR-sequencing: Addressing Fundamental Biological Processes**
Location: FEUP - Building A - Auditorium – level 1
Moderator: Jamie Scott

9:40 AM - 10:30 AM — **Leveraging single-cell TCR-sequencing to investigate mucosal-associated invariant T cell biology**
Location: FEUP - Building A - Auditorium – level 1
Speaker: Nicholas Provine

10:30 AM - 11:00 AM

Identification of pathogenic B cells in type 1 diabetes.
Location: FEUP - Building A - Auditorium – level 1
Speaker: Nina Luning Prak

11:00 AM - 11:20 AM

Coffee Break & Group Photos
Location: FEUP - Building A - Exhibition Hall – Ground floor

11:20 AM - 11:50 AM

The molecular principles underlying T cell selection in the thymus and their implications for protective immune responses
Location: FEUP - Building A - Auditorium – level 1
Speaker: Pedro Rodrigues

11:50 AM - 12:20 PM

Investigating the foetal and young adult T Cell Receptor (TCR) thymic repertoires
Location: FEUP - Building A - Auditorium – level 1
Speaker: Jasmine Rowell

12:20 PM - 1:05 PM

Basic Science Session: Short Contributed Talks
Location: FEUP - Building A - Auditorium – level 1

MHC Heterozygosity Prunes the Numbers of Different T Cell Receptors Expressed in CD4 T Cells
12:20 PM - 12:35 PM
Speaker: Alex Brown

Exploring Sex Disparities in the generation and selection of T Cell Receptor repertoires
12:35 PM - 12:50 PM
Speaker: Hélène Vantomme

Unraveling the Complex T Cell Receptor-Microbiome Interaction Network in the Colon Through Advanced Computational Analysis
12:50 PM - 1:05 PM
Speaker: Romi Vandoren

1:05 PM - 2:30 PM

Lunch & Science, Tools and Technology Gold Sponsor Presentations
Moderator: Felix Breden

Lunch
1:05 PM - 1:30 PM
Location: FEUP - Building A - Exhibition Hall – Ground floor

Gold Sponsors - Science, Tools & Technologies - Cellecta
1:30 PM - 1:40 PM
Location: FEUP - Building A - Auditorium – level 1
Speaker: Alex Chenchik

Gold Sponsors - Science, Tools & Technologies - IMPRINT
1:40 PM - 1:50 PM
Location: FEUP - Building A - Auditorium – level 1
Speaker: Victor Greiff

Gold Sponsors - Science, Tools & Technologies - Mi Laboratories
1:50 PM - 2:00 PM
Location: FEUP - Building A - Auditorium – level 1
Speaker: Stanislav Poslavsky

Gold Sponsors - Science, Tools & Technologies - PipeBio
2:00 PM - 2:10 PM
Location: FEUP - Building A - Auditorium – level 1
Speaker: Jannick Bendtsen

Gold Sponsors - Science, Tools & Technologies - Takara Bio
2:10 PM - 2:20 PM
Location: FEUP - Building A - Auditorium – level 1
Speaker: Shaveta Goyal

2:30 PM - 2:40 PM

AIRR-C Challenge Session: Machine Learning applied to AIRR-seq data
Location: FEUP - Building A - Auditorium – level 1
Moderator: Justin Barton

2:40 PM - 3:30 PM

Artificial Intelligence Tools for Antibody Engineering
Location: FEUP - Building A - Auditorium – level 1
Speaker: Jeffrey Gray

3:30 PM - 4:00 PM

Building the toolkit for computational antibody design
Location: FEUP - Building A - Auditorium – level 1
Speaker: Charlotte Deane

4:00 PM - 4:20 PM

Coffee Break brought to you by Enpicom
Location: FEUP - Building A - Auditorium – level 1

4:20 PM - 4:50 PM	**Decoding the adaptive immune system using deep generative models.** Location: FEUP - Building A - Auditorium – level 1 Speaker: Niranjani Prasad
4:50 PM - 5:20 PM	**Modelling Conformational Dynamics of Antibodies - Consequences for Biophysical Properties** Location: FEUP - Building A - Auditorium – level 1 Speaker: Monica Fernandez-Quintero
5:20 PM - 5:50 PM	**Machine Learning Challenge Session: Short Contributed Talks** Location: FEUP - Building A - Auditorium – level 1 **Methods for antigen-specificity prediction applied to BCR-seq data** 5:20 PM - 5:35 PM Speaker: Eve Richardson **Leveraging Large Language Models to Enrich Clone Selection and Characterization in Antibody Discovery** 5:35 PM - 5:50 PM Speaker: Wing Ki Wong
6:00 PM - 7:30 PM	**Industry Networking Reception & Hot Topics Round Table** Location: FEUP - Building I - Room I-105 (lawn) – Ground floor Moderator: Encarnita Mariotti-Ferrandiz, Corey Watson

Thu, Jun 06, 2024

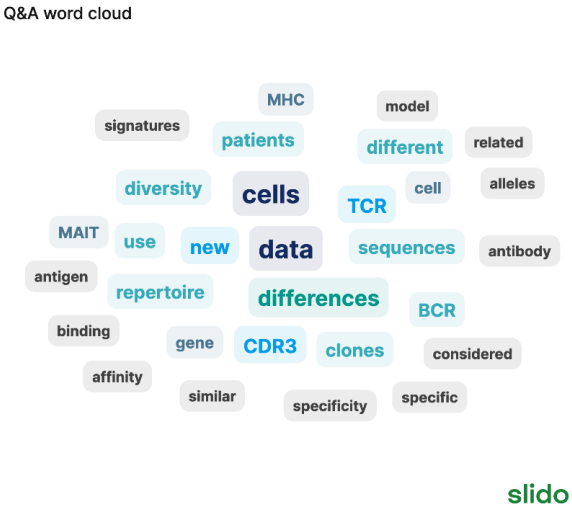
8:30 AM - 9:00 AM	**Registration & Coffee brought to you by GSK** Location: FEUP - Building A - Registration desk – level 1 & Exhibition Hall – ground floor
9:00 AM - 9:10 AM	**Welcome & Announcements by AIRR-C Chair-Elect** Location: FEUP - Building A - Auditorium – level 1 Moderator: Encarnita Mariotti-Ferrandiz
9:10 AM - 9:20 AM	**Biomedical Science Session: Advances in AIRR-sequencing: Addressing Human Diseases** Location: FEUP - Building A - Auditorium – level 1 Moderator: Nina Luning Prak
9:20 AM - 10:10 AM	**Single-cell based antigen-receptor gene and function analyses to instruct vaccine designs** Location: FEUP - Building A - Auditorium – level 1 Speaker: Hedda Wardemann
10:10 AM - 10:40 AM	**Antibody reactome profiling via self-assembling libraries of DNA barcoded antigens** Location: FEUP - Building A - Auditorium – level 1 Speaker: Ben Larman
10:40 AM - 11:00 AM	**Coffee Break brought to you by PipeBio** Location: FEUP - Building A - Exhibition Hall – Ground floor
11:00 AM - 11:30 AM	**Unveiling the Potential of Blood T Cell Receptor Repertoire as Biomarkers for Autoimmune and Inflammatory Diseases** Location: FEUP - Building A - Auditorium – level 1 Speaker: Encarnita Mariotti-Ferrandiz
11:30 AM - 12:00 PM	**Aging and autoimmunity as accumulated errors of adaptive immunity** Location: FEUP - Building A - Auditorium – level 1 Speaker: Dmitry Chudakov

12:00 PM - 12:45 PM	**Biomedical Science Session: Short Contributed Talks** Location: FEUP - Building A - Auditorium – level 1 **Understanding the role of T-cell receptor repertoire in T1D status** 12:00 PM - 12:15 PM Speaker: Puneet Rawat **The regulatory T-cell receptor repertoire as an early predictor of SLE disease progression and response to immunotherapy** 12:15 PM - 12:30 PM Speaker: Martin Pezous **Decoding the T-Cell Receptor Repertoire in Chronic Autoimmune Arthritis** 12:30 PM - 12:45 PM Speaker: Vincent Van Deuren
12:45 PM - 1:00 PM	**AIRR Community Voting Closing Reminders** Location: FEUP - Building A - Auditorium – level 1
1:00 PM - 2:30 PM	**Lunch Activities: Poster Session II & Sponsor Exhibits** **Lunch brought to you by Enpicom** 1:00 PM - 1:40 PM Location: FEUP - Building A - Exhibition Hall – Ground floor **Poster Session II** 1:15 PM - 2:15 PM Location: FEUP - Building B - Panoramic corridor - Ground Floor **Visit the Sponsor Exhibits!** 1:15 PM - 2:15 PM Location: FEUP - Building B - Panoramic corridor - Ground Floor
2:30 PM - 3:30 PM	**Brainstorming a Roadmap for the AIRR Community's Future** Location: FEUP - Building A - Auditorium – level 1
3:30 PM - 4:00 PM	**AIRR Community Meeting VII Closing Remarks: Announcements & Awards** Location: FEUP - Building A - Auditorium – level 1 Moderator: Victor Greiff, Encarnita Mariotti-Ferrandiz
4:00 PM - 6:45 PM	**Free Time**
6:45 PM - 9:30 PM	**Cálem Port Wine Cellars Tour & Dinner - SOLD OUT!** Location: Avenida Diogo Leite, 344 Vila Nova de Gaia

Attending Virtually

The AIRR-C Meetings SC is pleased to provide a Virtual Attendance option for AIRR-C Meeting VII through the Whova Application.

AIRR-C Meeting VII was streamed live through Zoom and the Whova Application. Virtual attendees were able to follow all the scientific sessions seeing the slides and listening to the speakers. Virtual and in-person attendees also had the chance to anonymously ask questions via Slido during the Q&A portion of each session. A total of 243 questions were asked during the event (see below for Q&A word cloud).



All recorded sessions will be available on the AIRR-C YouTube after the meeting.

Keynote Speakers

Keynote Speakers

Listed in alphabetical order

Machine Learning	**Jeffrey Gray** (Professor, Johns Hopkins University)

Artificial Intelligence Tools for Antibody Engineering

Advances in artificial intelligence (AI) have unlocked tremendous possibilities in biomolecular science. However, many leading methods are limited in their ability to predict and design antibody structures, likely because loop structures are less well represented and data on the coevolution of antibodies and their antigens is scarce. In this talk, I will share AI-based methods that we have developed for antibody engineering, mostly based on antibody data sets. Neural network models outperform physical models for antibody structure prediction, and generative language models offer multiple promising routes for design of antibody therapeutics. Docking methods reveal biological mechanisms and may someday allow for screening. I will use the docking case to show how AI methods differ from physics-based approaches, suggesting ways to benefit from their combination. Finally, I will share data from antibody design studies from both physics and AI-based approaches.

Basic Science	**Nicholas Provine** (Group Leader, University of Oxford)

Leveraging single-cell TCR-sequencing to investigate mucosal-associated invariant T cell biology

Mucosal-associated invariant T (MAIT) cells are innate-like T cells that are abundant in human blood and non-lymphoid tissues. MAIT cells recognize microbial metabolites through a semi-invariant T cell receptor (TCR) and can be activated in a TCR-independent manner by cytokines. Correlative and mechanistic studies have implicated a role for MAIT cells in an expanding array of infectious and inflammatory diseases. However, major questions remain regarding the extent of human MAIT cell functional and clonal diversity, particularly the minor interleukin (IL)-17-producing fraction. To address these questions, we analyzed the single-cell transcriptome and TCR repertoire of blood and liver MAIT cells and developed functional RNA-sequencing (fRNA-seq), a method to integrate function and TCR clonotype at single-cell resolution. Despite a semi-invariant TCR, MAIT cell clonal diversity was comparable to conventional memory T cells, with private TCR repertoires shared across matched tissues. Baseline functional diversity was low and largely related to tissue site. Transcriptional responses in vitro were stimulus-specific, with cells positioned along gradients of activation. Clonal origin influenced resting and activated transcriptional profiles, but intriguingly was not associated with the capacity to produce IL-17. Instead, clonal tracking suggested equal capacity of cells to make IL-17 under appropriate conditions. Overall, MAIT cells at rest exhibit diverse donor-specific TCR repertoires linked to their phenotype, and functional diversity according to both clonotype and stimulus. These data reinforce the utility of single-cell TCR-sequencing to contextualize phenotypic and functional analysis of T cell populations.

Germline	**Bill Schief** (Professor, Scripps Research Institute, Moderna)

Stepping toward an HIV vaccine

Dr. Schief is Vice President for Antigen Design and Selection at Moderna, as part of the Infectious Diseases Research Team. He is also a Professor at the Scripps Research Institute in the Department of Immunology and Microbiology, and Executive Director of Vaccine Design at The Scripps Research Institute's IAVI Neutralizing Antibody Center. Dr. Schief's research focuses on the design of novel immunogens and immunization strategies that aim to induce protective immunity against a wide range of pathogens.

Biomedical Science	**Hedda Wardemann** (Bill-and-Melinda Gates Foundation)

Single-cell based antigen-receptor gene and function analyses to instruct vaccine designs

Adaptive immune responses are characterized by the clonal selection and expansion of antigen-reactive cells. Using paired antigen-receptor gene information as natural barcodes, we track the clonal evolution of adaptive immune responses in response to vaccination in naïve mice and humans to define how antigen-receptor reactivity determines cell differentiation and fate. The long-term goal is to use this information for the design of optimized vaccination strategies with a specific focus on malaria.

Invited Speakers

Invited Speakers

Listed in alphabetical order

Biomedical Science	**Dmitry Chudakov** (CEITEC)

Aging and autoimmunity as accumulated errors of adaptive immunity

I will try to link the logic between adaptive immunity functioning, malfunctioning, and memory, as well as inflammation, cancer, age-related disease and modern understanding of what we call immunotherapy.

Machine Learning	**Charlotte Deane** (Professor of Bioinformatics, Head of the Oxford Protein Informatics Group, University of Oxford)

Building the toolkit for computational antibody design

Antibodies play a key role in the immune system and our response to vaccines, and have shown great promise as biotherapeutics. The development of new biotherapeutics typically takes many years and requires over $1bn in investment. Computational methods and in particular, machine learning, have shown great promise for increasing the speed and reducing the cost of biotherapeutic development. In this talk I will describe some of the novel computational tools and databases we are pioneering in biotherapeutics, from accurate rapid structure prediction to the prediction of their affinity and binding, looking at both their promise and limitations.

Machine Learning	**Monica Fernandez-Quintero** (Staff Scientist, The Scripps Research Institute)

Modelling Conformational Dynamics of Antibodies - Consequences for Biophysical Properties

Describing an antibody's binding site using only one single static structure limits the understanding of the antibody's function. To improve antibody structure prediction and to take the strongly correlated loop and interface movements into account, antibody paratopes should be described as interconverting states in solution. Therefore, the definition of kinetically and functionally relevant states can be successfully used to improve the accuracy and enhance the understanding of antibody-antigen recognition. Accounting for the high conformational diversity of antibodies by considering them as conformational ensembles can additionally advance the antibody development process, as the identification of potential liabilities and optimization of biophysical properties, such as hydrophobicity and electrostatics, can be facilitated. Even the low population states, that occur more frequently near hydrophobic surfaces, can contribute to understand processes such as aggregation or chemical modifications. In fact, these interactions with hydrophobic surfaces can result in a population shift towards more hydrophobic conformations, which are more likely to aggregate. In addition, we also test state-of-the art structure prediction tools, emphasize the importance of reliable protein structure models, in terms of structural and physical accuracies and the influence of predicted antibody structures on biophysical properties and recognition.

Biomedical Science	**Ben Larman** (Associate Professor, Johns Hopkins University)

Antibody reactome profiling via self-assembling libraries of DNA barcoded antigens

The Larman laboratory creates sequencing-based technologies for detailed characterization of serum antibodies at cohort scale. Phage ImmunoPrecipitation Sequencing (PhIP-Seq) and Molecular Indexing of Proteins by Self Assembly (MIPSA) are two examples that will be discussed. I will provide an overview of our current antibody profiling capabilities, recent findings, and ongoing developmental efforts that seek to overcome current limitations of high throughput antibody reactome profiling.

Germline	**William Lees** (Researcher, Bar-Ilan University, and University of Louisville)

The rapidly changing world of IG/TR germline gene databases

There is growing evidence that allelic polymorphism in germline receptor genes can impact immunoglobulin and T cell receptor response to immune challenge. Recent studies, for example, have highlighted significant impacts of known polymorphisms on the reactivity of published Abs and bnAbs, and have demonstrated that TRBV polymorphism can predict the likelihood of immune-related adverse effects to cancer therapy. There is therefore a pressing need for an accurate understanding of germline gene polymorphism, both at the population level, and within sub-populations. Current germline sets are based on limited data and are known to be incomplete, many sets for non-human species being based on the sequencing of a single specimen. With the advent of high-fidelity long-read genomic sequencing, the data landscape is changing quickly, with sequencing from many thousands of samples becoming available.

For curators, the new wealth of data poses challenges of scale, requiring automated pipelines, and wider community involvement to take on the work of annotating the many species of interest. The degree of

complexity discovered in receptor loci is also driving the development of new methods, and reinforcing the potential significance of acknowledged, but often overlooked, shortcomings in current approaches.

For researchers studying AIRR-C repertoires, enhanced germline sets can improve signal and reduce noise, providing a clearer picture of mutation levels, clonal structure, and response specificity. With these benefits come concerns: what are the best sources of germline sets to work with, and how can their applicability for a particular study be confirmed?

Germline	**Andreas Lossius** (University of Oslo)

Immunoglobulin heavy-chain constant gene polymorphisms in multiple sclerosis

Multiple sclerosis (MS) is a chronic inflammatory disorder of the brain and spinal cord. B cells seem to play a critical role in the pathogenesis, as B cell depletion has proven to be efficacious. It is known that clonally related antibody-secreting cells (ASCs) infiltrate the brain, meninges, and cerebrospinal fluid of patients. However, the mechanisms driving the B-cell response and shaping the immunoglobulin repertoires remain unclear.

The humoral immune response in the cerebrospinal fluid of MS patients is dominated by the IgG1 subclass. Using antibodies against allelic markers of the IgG1 constant heavy chain, we investigated the ASCs in the cerebrospinal fluid of patients carrying the IGHG1*02 and IGHG1*03 alleles. Surprisingly, we found that patients carrying both alleles had an almost exclusive enrichment of ASCs expressing the IGHG1*02 allele in their cerebrospinal fluid. This contrasted with the distribution of these cells in the blood, where the ASCs were evenly distributed between the two alleles, as expected from random allelic exclusion. We confirmed the preferential usage of this allele at the transcript level using single-cell RNA-seq, and for intrathecally secreted antibodies by investigating oligoclonal IgG1 bands on isoelectric focusing gels. We did not observe such a preferential utilization of a particular heavy chain allele in patients with Lyme neuroborreliosis or Varicella Zoster Virus encephalitis, which are infectious diseases of the central nervous system with humoral immune responses directed against the causative agents. Further investigation of the immunoglobulin variable gene repertoire in the IGHG1*02-expressing ASCs in MS patients revealed a preferential pairing of the IGHV4 gene family with the IGKV1 gene family. The IGHV4-39 gene, in particular, showed the highest frequency of pairing with IGKV1-5 and IGKV1(D)-33.

These findings collectively suggest an interplay between genetic factors in shaping the B-cell response in MS. They highlight the importance of considering constant gene polymorphisms and allele-specific responses in the context of autoimmune and infectious diseases. We are currently using long-read sequencing to map the IGHC genes in MS patients and to construct haplotype-resolved de novo assemblies of the patients' IGH locus.

Biomedical Science	**Encarnita Mariotti-Ferrandiz** (Associate Professor, Sorbonne University)

Unveiling the Potential of Blood T Cell Receptor Repertoire as Biomarkers for Autoimmune and Inflammatory Diseases

Autoimmune and inflammatory diseases (AIDs) pose a significant societal burden due to their chronic and debilitating nature. Addressing the need for disease-specific treatments, curative interventions, and enhanced prognostic markers is imperative. While T and B lymphocytes play pivotal roles in autoimmune disorders by targeting tissues, their involvement in inflammatory conditions appears less specific, although some diseases exhibit tissue specificity. To bridge this gap, we conducted an analysis

of the T-Cell Receptor (TCR) repertoire using next-generation sequencing in patients across various AID contexts.

TCR sequencing was performed on total blood or sorted CD4 T effector cells (Teff), CD4 T regulatory T-cells (Treg), and CD8 T-cells from the blood in different clinical trials. By employing a combination of classical and descriptive diversity analyses along with innovative machine learning (ML) techniques, our objectives were to provide an atlas of AIDs based on the TCR repertoire and identify TCR repertoires alterations across the autoimmune and inflammatory spectrum and within each condition.

We developed several TCR signature strategies adapted to the different datasets available and validated on publically available datasets classically used for ML method benchmarking.

We applied one of these strategies to (i) tissue-specific autoimmune disorders like type 1 diabetes (T1D) and rheumatoid arthritis (RA) in adult patients, (ii) sequential samples from lupus patients undergoing low-dose IL-2 treatment, and (iii) inflammatory diseases such as myocardial infarction and osteoarthritis. Through these analyses, we identified TCR signatures capable of predicting disease onset (in i), clinical response to treatment (in ii), or disease outcomes (in iii). Validation of these signatures on external datasets further supports their reliability.

In summary, our findings demonstrate that peripheral blood TCR repertoires harbor valuable disease-specific information that can serve as biomarkers to enhance the diagnosis, prognosis, and management of AIDs, ultimately improving patient care.

Finally, this study underscores the potential of ML approaches for classification purposes, highlighting their promise in the realm of biomarker discovery. However, it also emphasizes the critical need for high-quality and harmonized data sharing initiatives. By facilitating access to standardized datasets, we can refine ML methods and deepen our biological understanding of ML-based biomarkers. Such collaborative efforts hold the key to unlocking the full potential of ML in biomedical research and clinical applications.

Basic Science **Nina Luning Prak** (Professor, University of Pennsylvania)

Identification of pathogenic B cells in type 1 diabetes

In type 1 diabetes (T1D), T cells, helped by autoreactive B cells, destroy the insulin-producing beta cells in the pancreas. The identification of pathogenic B cells could facilitate earlier disease detection and intervention that may delay or prevent autoimmune attack before organ damage. To that end, we are using immune repertoire profiling approaches to identify and characterize tissue-based B cells in organ donors with and without T1D. Leveraging tissue samples and extensively phenotyped organ donors from the human pancreas analysis program, we are studying clonal networks of B cells in pancreatic lymph node (PLN), mesenteric lymph node and spleen of organ donors with and without T1D to identify and characterize tissue-resident B cell populations. This analysis has generated thousands of tissue-spanning clones and candidate clones of interest that are large and enriched in PLN. Coupled with cell sorting and single cell analysis, we are further studying clones that reside in memory B cell subsets. In parallel, we are studying autoantigen-enriched B cell populations and isolating monoclonal antibodies of autoantigen-binding B cells. Finally, we are tracking candidate clones derived from both of these approaches through immune repertoires of different individuals to search for repertoire motifs that may distinguish T1D autoimmunity from health.

Machine Learning **Niranjani Prasad** (Microsoft Research)

Decoding the adaptive immune system using deep generative models

Recent advances in high-throughput sequencing of the adaptive immune system have unlocked a new path to diagnosing diseases, from viral infection to autoimmune disease and cancer. To do so, we need to learn the mapping from observed immune response to specific disease antigens. This poses a number of challenges in practice: immune repertoires are highly diverse---with much of the signal specific to individuals---and are influenced by various genetic, environmental and experimental factors beyond the disease of interest.

In this talk, I present the Adaptive Immune Repertoire-Invariant Variational Autoencoder (AIRIVA), a generative model that learns a low-dimensional, interpretable, and compositional representation of TCR repertoires to disentangle such systematic effects in repertoires. We apply AIRIVA to two infectious disease case-studies: COVID-19 (natural infection and vaccination) and the Herpes Simplex Virus (HSV-1 and HSV-2), and empirically show that we can disentangle the individual disease signals. We further demonstrate AIRIVA's capability to: learn from unlabelled samples; generate in-silico TCR repertoires by intervening on the latent factors; and identify disease-associated TCRs validated using TCR annotations from external assay data.

I will go on to describe some of the ongoing work to translate such generative models to learning meaningful representations of the TCR sequence space, tackling the extreme diversity of TCRs. These models hold promise not only for improving diagnostic performance, particularly in diseases with highly heterogenous response, but also for advancing our understanding of the binding interactions between TCRs and pMHC complexes, which can be crucial to the development of new therapeutics.

Basic Science **Jasmine Rowell** (Research Fellow, University College London)

Investigating the foetal and young adult T Cell Receptor (TCR) thymic repertoires

The thymus is essential for T cell development and TCR repertoire selection. It undergoes several fluctuations in output and function during the life of a mouse. In our study, we compared the αβTCR repertoire generated in the foetal thymus to that of the young adult, to investigate how these life-stages impact the TCR repertoire, in particular variable (V) and joining (J) gene segment usage, and repertoire diversity and distribution. To achieve this, we TCR sequenced FACS-sorted CD4+CD8+ double positive (DP), CD4+CD8- single positive (SP4) and CD4-CD8+ (SP8) foetal and young adult thymocyte populations.

We found that the foetal TCRβ repertoire was less diverse, less evenly distributed, with fewer non-template insertions, and all foetal populations contained more clonotypic expansions than young adult. Life-stage had a greater impact on TCRβ and TCRα gene segment usage than cell-type. Foetal repertoires showed bias towards 3'TRAV and 5'TRAJ rearrangements in all populations, whereas adult repertoires used more 5'TRAV gene segments, suggesting that progressive TCRα rearrangements occur less frequently in foetal DP cells. To examine the influence of the rate of differentiation on VJ gene usage, we synchronized the differentiation of adult DP thymocytes by treating young adult mice with hydrocortisone to deplete the adult thymus of all but the most mature cells. After hydrocortisone treatment, the new recovering DP thymocyte population showed more foetal- like 3'TRAV and 5'TRAJ gene segment usage. Thus, differences between foetal and control young adult TCRαV-J rearrangements in DP cells may be the result of slower differentiation in the adult thymus, allowing more time for multiple rounds of TCRαV-J rearrangements in the DP population.

Furthermore, in foetus we identified distinct β-chain combinatorial VxJ usage and predicted α and β CDR1xCDR2 usage in SP compared to adult, indicating that MHC-restriction is governed by a differing set of rules in the foetal TCR repertoire. These data reinforce the idea that foetal and adult αβT-cells have distinct properties and functions, with foetal T cell repertoires using differing gene segments, less diversity and higher clonotypic expansions and more closely encoded by genomic sequence than the adult.

Germline **Yana Safanova** (Assistant Professor, Pennsylvania State University)

Comparative Analyses of Immunoglobulin Loci in Mammalian Genomes

A central challenge faced by all organisms is defending themselves against pathogens, including those that are often rapidly evolving. Early in the lineage leading to jawed vertebrates, evolution devised an ingenious solution in the adaptive immune system – in which sets of germline immunoglobulin (IG) genes, collectively called the IG loci, undergo a process called V(D)J recombination that generates an immensely diverse collection of antibodies (antibody repertoire) with a potential to recognize a huge variety of pathogens. We have a remarkably limited understanding of what the IG loci, and the resulting antibodies look like for essentially all (non-model) species — these loci are among the parts of the genome left on the cutting-room floor when reference genomes are released. This is because until very recently, the IG loci had been nearly impossible to assemble as the structural complexity of the regions thwarted standard assemblers designed for short-read sequences. It is only with the advent of long-read sequencing platforms and specialized assembly algorithms over the last several years that researchers were able to reliably conduct population level sampling and variant curation. Recent studies pioneered techniques for estimating the IG gene content from existing genome assemblies and produced the first estimate of the number of V, D, and J genes in a phylogenetically diverse set of mammals. While these methods are a substantial advance, many challenges related to detection of highly diverged IG genes, IG gene verification, IG gene naming, and comparative analysis remain practically unaddressed. In this talk, we will present the state-of-the-art solutions to annotation and comparative analysis of highly diverged IG loci and discuss open immunogenomics questions.

AIRR Community

AIRR Community Meeting VII

Learnings and Perspectives

June 3 - 6, 2024 | Porto, Portugal

ANTIBODY SOCIETY

Early Career Activities

Join us for our early career events focusing on networking opportunities and learn how being involved in the AIRR community can help your career.

Monday, June 3rd

Networking is in the AIRR: A speed networking early career event

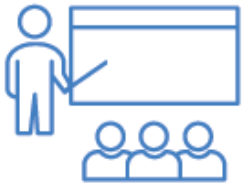
12:00 pm to 2:00 pm

This event gives early career scientists the opportunity to interact with professionals from various sectors including academia, industry, and non-profit. Mentors will be grouped by sector at different tables and mentees will have the opportunity to rotate through and chat with them as lunch progresses. As this event occurs early on in the conference schedule, it is a great way to begin making connections with other attendees and to share experiences.

Tuesday, June 4th

Service as an Early Career Researcher: The rewards of being active in the AIRR Community

10:00 am to 10:15 am



Early Career Development Panel Discussion

6:50 pm to 8:00 pm

Listen to a panel of experts discuss how they got to where they are now! With a focus on career paths, this event is a great opportunity to hear about the many ways to be involved and work in the AIRR Community, as well as to ask questions from career scientists from a variety of sectors and areas of research. This event will begin with a series of short introductions, and presentations followed by an open question and answer period.

Three early career and student events were hosted at the AIRR-C Meeting VII:

i. **Networking is in the AIRR: A speed networking early career event!** This event gave early career scientists the opportunity to interact with professionals from various sectors including academia, industry, and non-profit. Mentors were grouped by sector at different tables and mentees had the opportunity to rotate through as lunch progressed. Discussions were informal with an emphasis on helping early career scientists understand what options may be available to them in their career trajectories. Each table was provided with a few questions to help start the conversation. *Moderated by Lorissa Corrie and Edel Aron.*

ii. **Service as an Early Career Researcher: The rewards of being active in the AIRR Community.** "I need to focus on papers so I can get a good postdoc/faculty position/tenure!" or "I don't know enough to contribute meaningfully!" Everyone has lots of reasons to not become an active member of the AIRR-C, and early career researchers face some extra barriers. However, there are rewards to participation that are specific to early career researchers, as well. I first joined the AIRR-C as a postdoc nearly a decade ago and will share my experiences and how it has helped shape my career. *Presentation by Chaim Schramm*

iii. **Early Career Development Panel Discussions:** A panel of academic and industry experts discussed how they got to where they are now! With a focus on career paths, this event was a great opportunity to hear about the many ways to be involved and work in the AIRR-C, as well as to ask questions from career scientists from a variety of sectors and areas of research. This event began with a light reception, followed by a series of short introductions and an open question and answer period. *Panelists*: *Janine Schuurman, Nina Luning Prak, Nina Senna, Pieter Meysman, and Steven Kleinstein. Moderated by Lorissa Corrie and Edel Aron.*

The early career events were a huge success with more than 50 early career participants and 20 mentors (including five panelists and one speaker) participating.



Industry Networking Reception & Hot Topics Round Table

As part of the Industry Networking Reception there was a 'hot topics in the field' round table session. This session offered a unique opportunity for industry partners and scientific researchers to engage in an exciting discussion.

The tables were moderated by pairs of AIRR-C WG Co-leaders and Industry Partners. Corey Watson was the chair of the session with the help of the co-chairs Nina Luning Prak, Ulrik Stervbo, William Lees, Bjoern Peters, Eve Richardson, and Brian Corrie, as well as the industry partners Henk-Jan van den Ham (Enpicom), Andrew Farmer (Takara Bio), and Alex Chenchik (Cellecta).

The goal of this session was to foster discussion about the future needs and challenges in current and future 'hot topics in the field.' The following five topics were chosen:

i. Antibody Discovery
ii. AIRR-seq epitope / antigen annotation
iii. Datasets and applications / tools for mining the repertoire
iv. Biological Standards/Controls / Methods
v. Data sharing & data standards for AIRR analysis and software (from annotation to modeling)

AIRR-C 2024 EFIS Travel Awards

The AIRR-C was successful receiving a travel award from the EFIS - European Journal of Immunology - to help junior faculty members, post-docs, and students to attend the AIRR-C VII Meeting. We are delighted to recognize the Meeting VII travel award recipients.

From left to right:

1. Lonneke Scheffer (NO)
2. Easton Ford (US)
3. Ayelet Peres (IL)
4. Alexandra Elsakova (EE)
5. Vanessa Mhanna (FR)
6. Farzaneh Meimandi Parizi (NL)
7. Romi Vandoren (BE)
8. Cole Jensen (US)
9. Eric Franciskovic (SE)
10. Yu Ning Huang (US)

Lightning Demonstrations

Software & Tools - Lightning Demonstrations

June 4, 2024

2:00 pm to 4:10 pm

ImmuneWatch DETECT	Sander Wuyts

ImmuneWatch DETECT is a reliable and fast TCR-epitope interaction annotation tool. It can annotate the most likely epitope candidate for a full TCR repertoire in under a minute. Its great performance was recently demonstrated in the IMMREP23 challenge, in which it ended in first place. We are now planning to release a publicly available version, so that the whole research community can make use of it. In this demo, we will provide the audience with an overview of the main functionalities of the new DETECT platform as well as some specific use cases on how it can generate novel insights.

LZGraphs	Thomas Konstantinovsky

The LZGraph is a graph-based model for analyzing adaptive immune receptor repertoires, where the nodes represent unique sub-patterns and edges connect sequential sub-patterns. The weights of the edges are proportional to the transition events between the connected nodes, normalized by the out-degree of each node. The graph can also include information on the V and J gene usage of the sequences contributing to each edge. Three main graph types are presented in the paper, including “Naive,” “Nucleotide Double Positional,” and “Amino Acid Positional” graphs, with the latter two appending positional information to the nodes. This ensures that the resulting LZGraph is a directed acyclic graph, which allows for constant flow from the root node to the terminal node, avoiding self-loops or cycles. The inclusion of positional information enhances the interoperability of the graph, as each node can be associated with a specific position in the CDR3 sequence.

AbSolution	Rodrigo García Valiente

AbSolution is an R Shiny tool for interactive analysis and exploration of Ig-Fab-sequence features. It is built on the principles of accessibility, flexibility and scalability. Through its interface, the user can access and process the data, interact with it and explore its behaviour at different levels in a customizable way. It works with memory-mapping techniques to provide an environment able to handle numerous and diverse datasets at once.

AnalyzAIRR	Vanessa Mhanna

AnalyzAIRR is an R package developed to analyze bulk Ig/TCR repertoire datasets. It allows a general data exploration to evaluate the homogeneity within defined groups, identify outliers and filter them out. Moreover, it proposes a set of diversity measures and statistical metrics applicable at any level of granularity. Thus, single-sample repertoire explorations or in-depth cross-comparisons of AIRR datasets can be conducted leading to ready-to-publish visualization graphics. AnalyzAIRR is complemented with a guided workflow to help users in their analytical strategy, and a Shiny web application making it user-friendly for biologists with little or no background in bioinformatics.

ACE Configurator for ELIspot	Dhuvi Karthikeyan and Jin Seok (Andy) Lee

ACE Configurator for ELISpot (ACE) is a standalone GUI AND CLI program that facilitates sequence-aware ELISpot assay design and deconvolution of immunogenic peptides end-to-end. It uses a fine-tuned ESM-2 to predict epitope similarity and we leverage this novel axis of optimization to enhance multiplexed ELISpot efficiency. We demonstrate ACE's robustness by rigorous benchmarking on various real-world scenarios.

reportAIRR	Ayelet Peres

reportAIRR is an interactive app for exploring adaptive immune receptor repertoire quality, facilitates easy comparison of features across repertoires through multi-sample reporting. Additionally, the tool enables in-depth qualitative exploration using the interactive single-sample report, complete with convenient note-taking capabilities. Key features include:

- Processing Step Insight: Comprehensive quality control for each processing step.
- Outlier Identification: Effortless spotting of potential outliers through dynamic statistical surveys.
- Dual Viewing Modes: Compare repertoires in multi-sample reports and explore qualitatively in single-sample reports with note-taking.
- Structured Database: Fast and easy repertoire data querying with a robust database structure.
- Revolutionizing Quality Observation: Gain insights into repertoire quality throughout processing steps

ALIGaToR	Chaim Schramm

ALIGaToR ("Annotator of Loci for ImmunoGlobulins and T Receptors") is a tool for the automated de novo annotation of V, D, J, and C genes in (unrearranged) genomic sequences. ALIGaToR works with contigs covering all or part of the locus and classifies identified genes as functional, ORF, or pseudogenes based on the presence/absence of predicted RSS and expected splicing motifs.

Immcantation	Steven Kleinstein

The Immcantation framework provides a start-to-finish AIRR-compliant analytical ecosystem for high-throughput AIRR-seq datasets. Beginning from raw reads, Python and R packages are provided for pre-processing, population structure determination, and repertoire analysis. Over the past decade, the widely-used Immcantation framework has continued to grow to adapt to the evolving high-throughput Adaptive Immune Receptor Repertoire sequencing (AIRR-seq) methods. The most recent techniques allow the joint identification of the adaptive immune receptors and the inspection of the transcriptional status at the single-cell resolution. This demo will provide an overview of the broad range of capabilities that Immcantation provides, with a special focus on the recent methods that use single-cell information to improve clonal relationships detection, lineage tree building, integration of transcriptomics gene expression, and incorporation of additional metadata and annotations.

MAbFactory	Anne Poupon

MAbFactory offers easy and fast access to a comprehensive range of antibodies-related data and tools. Whether you need to search for anteriority landscape, patentability or evaluate the interest of a target, our solution will save you time and increase your productivity. MAbFactory can benefit to a large range of customers working in biology, life sciences, and in particular in antibody drug discovery and biologics development.

RepCred	Ayelet Peres

Adaptive immune receptor repertoire sequencing (AIRR-seq) data provides a wealth of biological and clinical insights, including identifying therapeutic monoclonal antibodies, assessing vaccine responses, and monitoring disease status. However, both experimental and computational problems can radically skew annotation and key repertoire statistics, including gene usage, somatic hypermutation levels, and clonal structure. Evaluating the quality of the processed AIRR-seq data is thus a critical initial step in data analysis. Here we present RepCred, an easy-to-use R package that takes an AIRR-formatted rearrangements TSV file as input and produces a graphical report that can be used to quickly appraise repertoire credibility and identify potential problems. RepCred can be installed from https://github.com/airr-community/rep-cred and is also available as a Docker image and as an analysis tool in the iReceptor Gateway (**https://gateway.ireceptor.org/)**.

Deep Dive Tutorials

Software & Tools – Deep Dive Tutorials

June 4, 2024

Session A: 4:30 pm to 5:30 pm and Session B: 5:50 pm to 6:50 pm

Digger	William Lees

Digger is a toolkit for the automatic annotation of V, D and J genes and associated features in IG/TR genomic loci. In the hands-on tutorial I will briefly explain the features of these 'unrearranged' sequences and show how you can use the tool to annotate single sequences or entire loci. The talk will be interesting to anyone working with species that are poorly covered by existing reference sets, and anyone who would like to understand more about the regulatory regions of V, D and J sequences, and their possible biological significance.

Dowser	Kenneth Hoehn

Dowser is an R package for building, visualizing, and analyzing lineage trees using B cell receptor sequences. The goal of this tutorial is to demonstrate how to build B cell lineage trees and use them to understand B cell dynamics using longitudinally-sampled single B cell sequence data. This tutorial will cover each of these topics, with emphasis on newly developed methods for building trees using paired heavy and light chain sequences from single cell sequencing data. We will also briefly cover topics like identifying B cell clones when analyzing single cell data using other packages in the Immcantation framework, which is a start-to-finish ecosystem of BCR analysis packages.

Immcantation and nf-core/airrflow	Gisela Gabernet and Susanna Marquez

Currently available tools to reconstruct B cell and T cell receptor sequences from AIRR-seq data and to infer clonal relationships offer limited parallelization across samples, scalability or portability to HPC infrastructures. In this tutorial, we will introduce nf-core/airrflow, an end-to-end bulk and single-cell AIRR-seq processing workflow with Nextflow and Immcantation. The Immcantation Framework (immcantation.org) is an open source AIRR-compliant comprehensive toolset, which allows the processing of bulk and single-cell AIRR-seq data from raw read processing to clonal inference and lineage reconstruction. nf-core/airrflow is written in Nextflow and is part of the nf-core project, which collects community contributed and curated Nextflow workflows for a wide variety of bioinformatics analysis. nf-core/airrflow has already been applied to a variety of studies, and the community of users is flourishing. With airrflow, we have validated and extended previously reported findings of convergent antibody responses to SARS-CoV-2 with data from 97 COVID-19 infected individuals and 99 healthy controls retrieved from iReceptor through the AIRR Data Commons web API. In this tutorial, we will introduce this new powerful tool to the participants and will demonstrate how to install nf-core/airrflow, how to configure it for different compute environments, and how to execute an example analysis. nf-core/airrflow is open source, and available free of charge, under the MIT license at https://github.com/nf-core/airrflow. Detailed documentation and example results are available on the nf-core website at https://nf-co.re/airrflow. Users can join the nf-core dedicated airrflow slack channel (https://nf-co.re/join) for questions and feature requests.

immuneML	Lonneke Scheffer and Charlotte Würtzen

The powerful ability of machine learning (ML) to analyse sequence data has sparked a surge of AIRR ML studies. But besides the challenge of developing new ML algorithms, setting up the computational pipelines to thoroughly (and correctly) benchmark new methods against existing solutions is a large and complex task. As a result, independently developed methods may be evaluated under different conditions, resulting in a lack of transparency regarding which ML method(s) are optimal for a given AIRR prediction problem.

We therefore developed immuneML (https://immuneml.uio.no), a software platform for ML-based analysis of adaptive immune receptors and repertoires. immuneML supports the development, introspection and reproducible benchmarking of classifiers for immune repertoire-disease status and immune receptor-antigen binding prediction.

At the previous AIRR-C meeting VI workshop we explained how to run immuneML analyses. This time around, we will demonstrate how to integrate new ML algorithm components into immuneML, and benchmark them. This workshop will in particular be of interest for researchers developing new immune receptor or repertoire classifiers.

ImReP	Erik Huang

ImReP is a computational approach designed to reconstruct adaptive immune receptor repertoires accurately using AIRR-Seq and RNA-Seq data. The method efficiently extracts TCR and IG-derived reads and assembles corresponding hypervariable region sequences, particularly excelling in assembling CDR3 sequences despite sequencing errors and short read lengths. ImReP outperforms existing methods in precision and recall rates, as demonstrated through simulations with varying read lengths and coverage depths. ImReP facilitates the creation of a systematic atlas of immune sequences across diverse human tissues, forming one of the largest collections of CDR3 sequences and tissue types. This atlas serves as a valuable resource for comparative analysis and has the potential to enhance studies in immunology, contributing to the development of diagnostic tools and therapies for human diseases. The advantages of ImReP include the simultaneous capture of clonotype populations from all chains in a single run and the ability to detect overall transcriptional responses of the adaptive immune system. The scalability of the atlas using large-scale AIRR-Seq and RNA-Seq datasets holds promise for providing insights into immune responses across autoimmune diseases, allergies, and cancers.

iReceptor Gateway - Tool Integration	Brian Corrie

iReceptor is a platform for finding and analyzing AIRR-seq data in the AIRR Data Commons. In this tutorial we will explore the new and advanced features of iReceptor's ability to integrate external open source tools into the platform for analysis. We will discuss the platforms ability to integrate advanced analysis techniques such as single-cell analysis, epitope prediction, and ML approaches, as well as discuss tools that we anticipate adding in the near future.
Log in to the iReceptor Science Gateway to access your free account and start exploring!

pyTCR	Serghei Mangul

pyTCR, a computational notebook-based solution for comprehensive and scalable TCR-Seq data analysis. Computational notebooks, which combine code, calculations, and visualization, are able to provide users with a high level of flexibility and transparency for the analysis. Additionally,

computational notebooks are demonstrated to be user-friendly and suitable for researchers with limited computational skills. Our tool has a rich set of functionalities including various TCR metrics, statistical analysis, and customizable visualizations. The application of pyTCR on large and diverse TCR-Seq datasets will enable the effective analysis of large-scale TCR-Seq data with flexibility, and eventually facilitate new discoveries.

Link to the publication: https://www.frontiersin.org/articles/10.3389/fimmu.2022.954078/full

STEGO.R	Kerry Mullan

Introduction: T cells are critical to protect against a broad array of aberrant cells including pathogens and cancer. The hypervariable T cell receptor (TCR), created through recombination of the variable, Diversity, and Junction genes, is what allows for recognition of a diverse array of antigens. We can now capture both single cell expression data (scRNA-seq) with the paired single cell TCR sequencing (TCR-seq) data to further understand the role of T cells. Many of the current strategies examine the gene expression (GEx) and then describe the TCR repertoire. There is limited focus on the specific clones, which may be missing important and actionable features. Here we developed STEGO (Single cell TCR and Expression Grouped Ontologies) Shiny R application that focuses on the TCR and then the associated GEx profile.

Program parameters: STEGO.R application can process 10x Genomics data and BD Rhapsody. The application includes the Seurat quality control (QC) process, merging with Harmony, followed by annotations with scGate. The program also includes TCR clustering (ClusTCR2) and analysing the predicted epitopes from TCRex. The TCR → GEx section is broken down into four sections: Top clonotype, expanded clonotypes, Clustering and epitope. The Shiny R interface also facilitates the program and is accessible to novice R coders. We have also automated downloading of prioritised lists of the clonotypes (Single- and Multi-sample), clustering and epitope section. https://github.com/KerryAM-R/STEGO.R.

Novel findings using STEGO when re-analyzing GSE144469, a colon inflammation due to melanoma therapy, did not include any scRNA-seq with scTCR-seq analysis. STEGO.R identified limited private clonal expansion. Therefore it was ideal to preference the sequence similarity. This process identified two TRBV6-2 colitis specific clusters as well as identified TRGV4 cluster specific to the melanoma cases. Therefore, this highlighted several actionable TCR for experimental validation.

TCRex and ClusTCR	Pieter Meysman

In this brief tutorial, we aim to give a hands-on tutorial on how to analyse processed TCR clonotypes with unsupervised clustering (using ClusTCR) and epitope annotations (using TCRex). ClusTCR is a python package that is designed to rapidly group highly similar sequences across full TCR repertoires. It uses a two-step process, wherein first likely candidates are grouped, followed by a slower but more accurate clustering. The identified TCR clusters can then be used for further in-depth analysis of shared properties across samples.

The TCRex webtool is able to annotate TCR–epitope binding for AIRR-compliant human full TCR repertoires using TCR beta chain information, i.e. the CDR3 amino acid sequence and the corresponding V/J genes. It is based on random forest classifiers trained on epitope-specific TCR data collected from the manually curated catalogue of pathology-associated T cell receptor sequences (McPAS-TCR), the VDJ database (VDJdb) and the ImmuneCODETM database. In total prediction models for 100 different epitopes, consisting of 93 viral and 7 cancer epitopes, are provided.

Posters

			Session #	
Full Name	Title	Poster #	1	2
Aengus Officer	Genetic basis for recognition of transglutaminase 2 and gluten peptides in celiac disease	1	x	
Akshay Tiwari	Biophysical Model Predicts Optimal Antigen Valency for Tuning Antibody Responses	35	x	
Alex Chenchik	A Streamlined 96-Well Plate Method for Single-cell TCRa/b and TCRg/d Immune Receptor and Immunophenotyping Analysis	2	x	
Alex Chenchik	Synthetic RNA TCR/BCR Spike-In Controls for Assessing Immune Receptor Profiling Assay Accuracy	3		x
Alexander Brown	MHC heterozygosity reduces the T cell receptor repertoire	3	x	
Alexandra Elsakova	Discovering the T-Cell Receptor Repertoire in APECED Patients	4	x	
Alexandra Sharland	Characterisation of directly-alloreactive CD8 T cell repertoires	5	x	
Anastasia Minervina	Ensuring Epitope Space Coverage: The Role of TCR alpha beta chain pairing	42	x	
Anna Postovskaya	Expanding annotation of TCR antigen specificity by accounting for diverse epitope-specific TCRs	6	x	
Areen Shtewe	A model for defining health state by examining repertoire diversity from multiple high throughput B cell receptor sequencing experiments	43	x	
Areen Shtewe	ImmuneDB Stats (IS) API - A novel API for AIRR-seq meta analysis across immune repertoires: an example analysis of the repertoire differences related to COVID-19 infection severity and outcome	47		x
Ayelet Peres	Guidelines for Reproducible Analysis of Adaptive Immune Receptor Repertoire Sequencing Data: Examples from VDJbase	7	x	
Benjamin McMaster	Quantifying conformational changes of TCR CDR loops and pMHC interactions	8	x	
Bjoern Peters	A systems vaccinology resource to develop and test computational models of immunity	4		x
Bjoern Peters	The IEDB and CEDAR as repositories of antigen-specific adaptive immune receptors	9	x	
Celine AlBalaa	Conversing with Immune Guardians	10	x	
Chaim Schramm	Full-length assembly and immunogenetic analysis of immunoglobulin and T cell receptor loci from Mauritian cynomolgus macaques	1		x
Cole Jensen	Inferring B cell phylogenies from paired heavy and light chain BCR sequences with Dowser	11	x	
Corey Watson	Genome poises antibody repertoire from early B cell development	36	x	
Damon May	Discovering public immune signatures of dozens of exposures from tens of thousands of T-cell repertoires	12	x	
Dana Moreno	Exploring the footprints of T-cell receptor generation rules in single-cell TCR repertoire data	44	x	
Dani Marinelli	Discovery and Characterization of Human Anti-Astrovirus Antibodies for Vaccine Design	13	x	

Henk-Jan van den Ham	Comparison of sequence- and structure-based antibody clustering approaches on simulated repertoire sequencing data	40	x	
Jessie Fielding	Simulating B cell evolution and differentiation with Simble	27	x	
Jonas Schuck	Exploring clonal dynamics of adaptive immune cell infiltrates in solid tumors	28	x	
Jonathan Hurtado	Single-cell analysis of temporal antibody repertoire patterns among circulating B cells from healthy individuals	45		x
Joshua S. Martin Beem	ARMADiLLO: a web server for analyzing antibody mutation probabilities	7		x
Karenna Ng	Focused learning by antibody language models using preferential masking of non-templated regions	8		x
Katalin Voss	Using simulations to assess the performance of methods for B-cell clonal family assignment	9		x
Kelvin Tuong	AIRR analysis considerations and concepts for single-cell data	10		x
Kevin Wiehe	Mutation-guided Vaccine Design: A Strategy for Developing Boosting Immunogens for HIV Broadly Neutralizing Antibody Induction	11		x
Khang Le Quy	Systematic analysis and validation of mass spectrometry in serum antibody repertoire profiling	12		x
Krishna M. Roskin	The Immune Receptor Antigen Database (IRAD): an AIRR Knowledge Commons Initiative	13		x
Leslie Adda	Investigating EBV-Specific TCR dynamics in Longitudinal Samples from Patients with Multiple Sclerosis Relapses	34	x	
Lewis Chinery	Baselining the Buzz. Trastuzumab-HER2 Affinity, and Beyond!	14		x
Li C. Xue	AI-boosted three-dimensional modelling for cancer immunotherapy design	15		x
Lindsay Cowell	Adaptive Immune Receptor Repertoire Knowledge Commons: large-scale knowledge for research and innovation	16		x
Lindsay Cowell	Data Harmonization across the AIRR Data Commons and Data Repositories for AIR Specificity and Germline Data: an AIRR Knowledge Commons Initiative	29	x	
Margarida Victoriano	Evaluation of level of trust in AIRR simulation approaches for real-world machine learning application - a literature review	17		x
Marie Bonnet-Di Placido	Combining antibody single cell and whole repertoire sequencing to identify cross-serotype reactive antibodies against Foot-and-Mouth Disease Virus in cattle	18		x
Mariia Zakharova	The analysis of autoimmune T cell repertoire from Lupus patients	19		x
Martin Pezous	The regulatory T-cell receptor repertoire as an early predictor of SLE disease progression and response to immunotherapy	20		x
Maxim Zaslavsky	Disease diagnostics using machine learning of immune receptors	21		x
Michael Jarman	Immunoinformatic workflows to annotate and cluster single cell and whole B cell repertoire antibody sequences in cattle	22		x
Mikhail Pogorelyy	TRTLseq: Open source high-throughput paired TCR repertoire sequencing approach	48		x
Noah Yann Lee	Naive B Cell Classifier for Single-Cell BCR Genotype Inference	23		x

Daria Balashova	Active learning for Antibody-Antigen binding prediction	14	x	
Dawit A. Yohannes	Exploring the TCR-specificity profiles in patients with multiple sclerosis	15	x	
Dhuvarakesh Karthikeyan	ACE configurator for ELISpot: optimizing combinatorial design of pooled ELISpot assays with an epitope similarity model	16	x	
Dylan Duchen	Scalable genotyping and variant calling across immunoglobulin loci using sequence variation graphs and short-read sequencing data	17	x	
Easton Ford	The Hidden Diversity of Antibody Heavy Chains: Implications for Autoantibody Mediated Disease	37	x	
Edel Aron	Single Cell Profiling of the Host Immune Response in Lyme Disease	44		x
Eglantine Hector	SeQuoIA: a novel bioinformatic pipeline for tracking B cell selection dynamics in germinal centers through quantitative analyses of integrated single-cell datasets	45	x	
Elisa Rosati	The IUIS TR-IG nomenclature review committee for facilitating the annotation of IG/TR genes: towards transparent and community-shared policies	18	x	
Elizabeth Van Itallie	Analysis of BCR Repertoires from Rearranging BnAb Knockin Mice Models with a Newly Developed Bioinformatics Pipeline	19	x	
Ella Schwab	Comparative Evaluation of T-Cell Receptor Repertoire Sequencing Methods	5		x
Ella Schwab	reAIRR: a unified repository for robust, rigorous, and reproducible analysis of AIRR-Seq data	20	x	
Eric de Sousa	Characterization of T-cell receptor repertoires of ex vivo expanded TIL from patients with pancreatic ductal adenocarcinoma	21	x	
Eric Franciskovic	Allergen-specific human antibodies - a multi-omics approach	22	x	
Eve Richardson	Methods for antigen-specificity prediction applied to BCR-seq data	38	x	
Farzaneh M. Parizi	Efficient Computational Rigid-body Docking of TCR:pMHC-I Complexes Using Restricted Rotation Matrices and Distance Restraints	23	x	
Fatima A. Davila-Hernandez	Benchmarking of Developability Property Oracles and Deep Learning Sequence and Structure Generation Methods for Efficient Antibody Camelization	39	x	
Felix Breden	A Comprehensive Evaluation of Long-read Whole-Genome Assembly Quality in the Immunoglobulin (IG) Loci Across Diverse Vertebrate Species	6		x
Felix Breden	The iReceptor Project Promotes Data Reuse by Providing Access to the AIRR Data Commons	24	x	
Felix Drost	Benchmarking T cell receptor - Epitope predictors with ePytope-TCR	25	x	
Gisela Gabernet	nf-core/airrflow: an adaptive immune receptor repertoire analysis workflow employing the Immcantation framework	26	x	
Giulio Isacchini	Model-based quantification of the individual variability of adaptive immune receptor repertoires	49		x
Helene Vantomme	Exploring Sex Disparities in the generation and selection of T Cell Receptor repertoires	2		x

Paul Diehl	Dynamic Immunological Profiling Reveals Transcriptomic Changes in Response to Immunization and Therapeutic Intervention	24		x
Paul Stys	TCR atlas of multiples auto-immune diseases	25		x
Pei-Lung Chen	Identification of 307 Novel Human T Cell Receptor (TR) Alleles in 44 Subjects from the Human Pangenome Reference Consortium (HPRC) Using gAIRR Suite	26		x
Pragati Sharma	Exploring Pre-Pandemic SARS-CoV-2-Specific B Cell Responses in the West African Population	46		x
Puneet Rawat	Understanding the role of T-cell receptor repertoire in T1D status	27		x
Rachel Waterworth	Deconstructing the T cell response to COVID-19 vaccines using single-cell RNA sequencing	30	x	
Robert Frank	Attribution analysis for deep-generative antibody sequence models	28		x
Romi Vandoren	Unraveling the Complex T Cell Receptor-Microbiome Interaction Network in the Colon Through Advanced Computational Analysis	29		x
Sander Wuyts	Epitope-specific tracking of cancer vaccine response using TCR-epitope annotations	41	x	
Sarah Burbach	Improving antibody language models with natively paired sequences	30		x
Sarah Robinson	Computational methods for in silico epitope binning	31		x
Sebastiaan Valkiers	Detection of convergent immune responses through quantification of the T-cell receptor similarity space	32		x
Serghei Mangul	VDJHunter, a method to infer TCR alleles from RNA-seq data	33		x
Shaveta Goyal	Evaluation of SMART-Seq Human BCR (with UMIs) for unbiased BCR repertoire profiling	31	x	
Simon Schaefer	Integrating molecular barcoding and single cell sequencing to unveil spike protein-specific immune responses	34		x
Simone Spandau	Predicting natural somatic hypermutations with protein and antibody language models	35		x
Sofia Krasik	Identification of naturally protective antibodies in the repertoires of resilient individuals	36		x
Sujatha Seenu	Computational characterization of public BCR clonotypes in response to influenza vaccination	32	x	
Susana Magadan	T cell receptor loci in salmonids: from genomics to comparative immune repertoire analysis	33	x	
Susanna Marquez	Immcantation: A start-to-finish AIRR-compliant analytical ecosystem for AIRR-seq	37		x
Tadeusz Satlawa	LAP: Liability Antibody Profiler by sequence & structural mapping of natural and therapeutic antibodies	38		x
Thomas Konstantinovsky	AlignAIRR: Deep Learning Based Adaptive Immune Receptor Sequence Alignment	39		x
Vincent Van Deuren	Decoding the T-Cell Receptor Repertoire in Chronic Autoimmune Arthritis	40		x
William Gibson	Long-read sequencing of the immunoglobulin light chain lambda locus from 222 individuals reveals extensive genetic diversity and novel population signatures	41		x
Wing Ki Wong	Leveraging Large Language Models to Enrich Clone Selection and Characterization in Antibody Discovery	42		x
Yu Ning Huang	Rigorous benchmarking of TCR allele reconstruction tools	43		x

Reports at a Glance

AIRR Community

ANTIBODY SOCIETY

AIRR Community Meeting VII:
« Learnings & Perspectives »
Summary of Working Group and Sub-Committee Reports

Porto, Portugal
June 3rd to 6th, 2024

Questions?:
meetings@airr-community.org

AIRR Community

Special Poster Session by AIRR-C Working Groups & Sub...

10:30 AM – 12:00 PM

FEUP - Building B - Panoramic corridor - Ground Floor

AIRR-C General Assembly Event | In Person Only

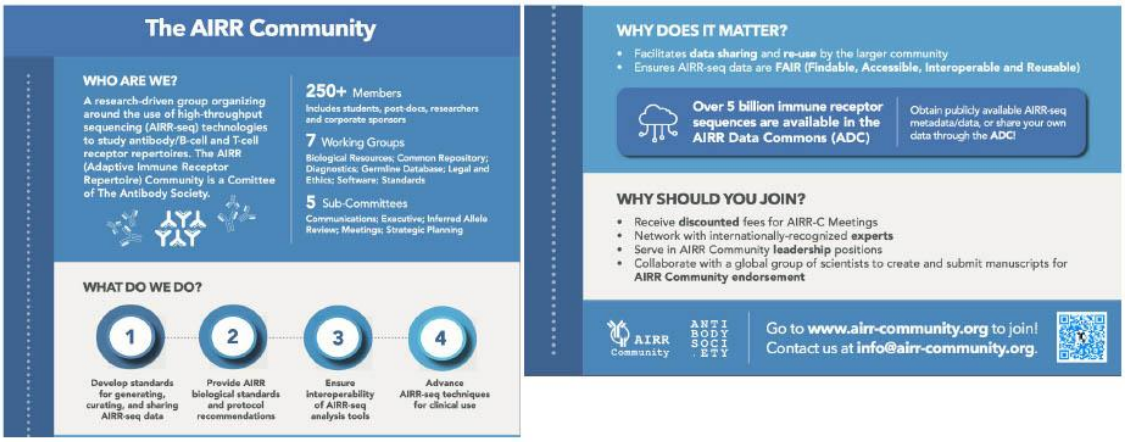
+ Add Sub-session

Join this special poster session and learn about the AIRR Community Working Group (WG) and Sub-Committee (SC) activities and goals.

All WG's and SC's are looking for new people to join. If there is an initiative or conversation that sparks your interest, please be sure to let the WG/SC co-leads or organizers know of your interest, we will help get you connected.

2

Introduction to AIRR-C



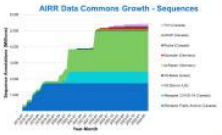
- Ability to share AIRR-seq data greatly increases the **value** of any one data set:
- Each researcher may have small N, large amount of data per sample
- Increase sample sizes, statistical power
- Facilitate comparisons between affected/controls/multiple disease states

AIRR Community Working Groups are focused on specific questions and are expected to disband when their stated goals are accomplished.

AIRR-C Working Groups products

1. **Biological Resources** – Biological calibrators and reagents for evaluation of AIRR-seq data (≈3–10 participants)
   - On AIRR podcast on MRD (and other clinical applications of AIRR-seq)
   - AIRR Community webinar on QC pipelines for AIRR-seq data (Encarnita and Nina)
   - Participation in FDA BCR-SEQC initiative

2. **Common Repository** – Data Commons for AIRR-seq data, following FAIR principles (≈9 participants)
   - Release of AIRR Data Commons API 1.2
   - AIRR Data Commons Registry (initial specification completed)



3. **Diagnostics** – Facilitate development of diagnostics and markers for disease (≈19 participants)
   - AIRR-C podcast (growing number of subscribers)
   - Special event 2023: AIRR-seq into the clinic

4

AIRR Community

AIRR Community Working Groups are focused on specific questions and are expected to disband when their stated goals are accomplished.

AIRR-C Working Groups products

4. **Germline Database** – Germline gene inference from AIRR-seq data (≈27 participants)
   - Progress on large-scale rhesus macaque genomic sequencing at Emory and Louisville has been shared with the group. 'Beta' consolidated set was circulated within the subgroup in March 2024.
   - No additional progress on mouse sets in this period: the current sets are available from OGRDB.

5. **Legal and Ethics** – Standards for human subjects (≈4 participants)
   - Manuscript

6. **Software** – Interoperability of analysis software (≈6-7 participants)
   - Repcred is now functional
   - Approved 4 software tools as AIRR compliant (total now: 11)

7. **Standards** – For publishing or depositing AIRR-seq data (MiAIRR) (≈6 participants)
   - Release of AIRR data standards 1.4 and 1.5 (release of experimental schemas for paired chain, receptor, germline gene database, abandoning of Python2)

5

AIRR Community

AIRR Community Sub-Committees are formally established groups within the AIRR Community to address continuous or repetitive duties of high organizational relevance to the AIRR Community.

AIRR-C Sub-Committee products

1. **Communications** – Communicating activities of the AIRR-C to both the AIRR Community and the general research community. (≈5 participants)
   - AIRR-C Poster and Infographic
   - Comms about AIRR-C news
   - Seminar Series and Webinar (TAbS)

   - Online presence: X, mastodon, linkedin, bluesky, youtube, web, B-T.CR, store, slack. In progress: Wikipedia

2. **Executive** – Provides leadership (e.g., oversees manuscript endorsements, receives reports from WG's and other SC's, manages votes and elections, drafts proposals regarding governance, facilitates dispute resolution, and other services to the WG's and other SC's). (7 participants)
   - Streamlining of AIRR-C operations (e.g., governance Exec)
   - Facilitating WG interaction (manuscript endorsements, SPSC, biannual WG/SC updates
   - Outreach (sponsor acquisition, promote interaction with IUIS, FDA, Euroclonality)

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AIRR Community

AIRR Community Sub-Committees are formally established groups within the AIRR Community to address continuous or repetitive duties of high organizational relevance to the AIRR Community.

AIRR-C Sub-Committee products

3. **IARC (Inferred allele review committee) –** Responsible for judging the validity of germline immunoglobulin and TCR genes inferred from AIRR-Seq and genomic data and submitting their findings to the IUIS T-cell Receptor and Immunoglobulin Nomenclature Review Committee. (≈9 participants)
   - Novel alleles have been affirmed and forwarded to the nomenclature committee/TR-IG.
   - Human and mouse reference sets have been established (in collaboration with other WG) and published. Can now be selected in the online IgBlast tool.
   - Consolidation of the human TCR IARC process.

4. **Meetings –** Responsible for the initiation and planning of AIRR-C related meetings. (≈5 participants).
   - 2x Meetings (AIRR-C Special Event 2023, AIRR-C Meeting VII, Porto 2024)

5. **Strategic Planning –** Develop plans for AIRR-C standard adoption, sustainability and scientific visibility. (≈6 participants)
   - Delivery of report to the AIRR-C Community (you have all received it, please read it!, will be discussed on Thursday!)

7

AIRR Community

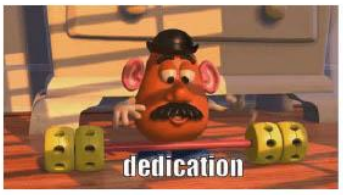
AIRR-C Working Group Manuscripts 2022 - 2024

- Human IG Reference Set published on OGRDB:
  Collins *et al.* (2024) AIRR-C IG Reference Sets: curated sets of immunoglobulin heavy and light chain germline genes. *Frontiers in Immunology*
- AIRR-C paper on germline set development:
  Lees, Christley *et al*. (2023) AIRR community curation and standardised representation for immunoglobulin and T cell receptor germline sets. *ImmunoInformatics*
- 5 chapters in 2022 Springer Methods in Molecular Biology Immunogenetics Issue
- Manuscript on Database Directive and its implications for biological data (Legal and ethics)
  - Bernier, A., Busse, C. & Bubela, T. Public Biological Databases and the Sui Generis Database Right. IIC 54, 1316–1358 (2023).
  - DOI: https://doi.org/10.1007/s40319-023-01373-0

8

AIRR-C WG and SC: strengths

Dedication



AIRR-C WG and SC: challenges

Sustainability and Outreach

9

Individual Reports

Common Repository WG

Common Repository WG Report

AIRR-C Meeting VII
June 2024

Common Repository WG Current goals

- Purpose
  - ***To promote and facilitate deposit, access, and sharing/reuse of IG and TCR AIRR-seq datasets*** through the creation of common repositories that enable:
    - standardized queries of processed AIRR-seq data.
    - re-analysis of raw and processed AIRR-seq data utilizing repository analysis tools.
    - download of raw and processed AIRR-seq data for offline re-analysis.
  - Create, sustain, evolve the ***AIRR Data Commons*** (ADC)

- 2022 Plans
  - ✓ Adapting recommendations as required
  - ✓ Continuing to focus on promoting and advancing the AIRR Data Commons
  - ✓ Evolution of AIRR Standards and the ADC API
  - ✓ Create a searchable programmatic AIRR Repository ADC registry

2

Common Repository WG - Organizational

Co-leads: Brian Corrie, Artur Rocha

Active Members: George Blanck, Felix Breden, Christian Busse, Scott Christley, Karishma Chhugani, Lindsay Cowell, Ulrik Stervbo

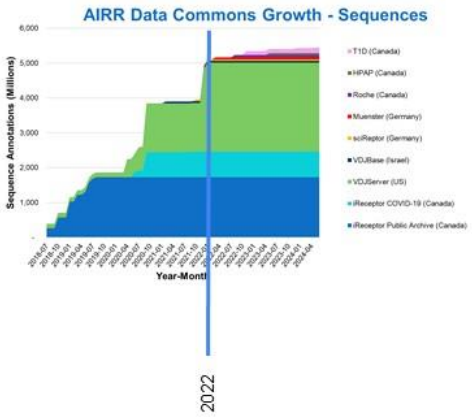
Other Members: Significant number of people on the mailing list

3

Common Repository WG Achievements 2022-2024

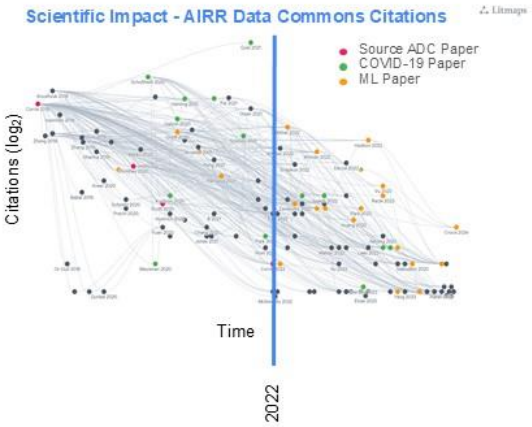
AIRR Data Commons API

- Release of ADC v1.2 (Sep 2022)
- Based on AIRR Standard v1.4



AIRR Data Commons Registry

- Initial specification completed
- Initial governance for registry defined



4

Diagnostics WG

Diagnostics WG Report

AIRR-C Meeting VII

June 2024

Diagnostics WG Current goals

- *Produce and extend reach of additional episodes of the podcast "onAIRR" through support and and direct contribution*
- *Renew funding from the antibody society for microphones, design, sound editing etc. once it's available*
- *Plan and hold a single meeting with diagnostics as a focal point, with support of the AIRR-C Communications SC, Legal and Ethics WG, and Meetings SC.*
- *Review: Immunoinformatics for Precision Diagnostics of Infectious Diseases (in preparation)*
  - *Coordinate a white paper response to regulatory bodies*

2

Diagnostics WG Organizational

Co-leads: Susanna Marquez & Ulrik Stervbo

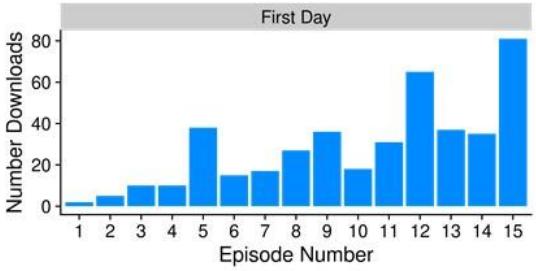
Active members: 19, Mailing list: ~ 60

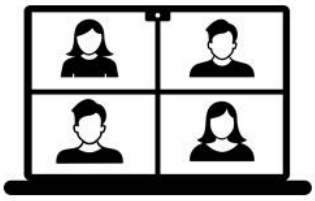
3

Diagnostics WG Achievements 2022-2024

ON AIRR
AN AIRR-C PODCAST

A growing number of subscribers





Bringing AIRR-Seq to the clinic – mapping the challenges (Zooming in to the Community II)

40 participants, 300 YouTube views

4

Germline Database WG

Germline Database WG Report

AIRR-C Meeting VII
June 2024

GLDB Current goals

- Continue to develop appropriate IG Reference Sets for human, various mouse strains, and for rhesus macaque, building upon recent efforts by integrating genomic data currently being generated by multiple groups. This integrated effort should result in robust germline sets for these species that could serve as useful models for other non-human organisms. ✓
- Continue the development and implementation of the germline database schema. ✓
- Collaborate with VDJbase to further develop features for cataloguing and sharing non-coding variation. ✓
- Create an outreach subgroup to identify academic and commercial partners involved in the generation and use of germline data, as a means to encourage broader inclusion of key stakeholders. Specifically, we want to: ✗
    - Improve the provision of datasets from additional species
    - Identify stakeholders and integrate them into community efforts
    - Promote the uptake of germline sets and schema in tools
    - Develop a plan for sustainability through ongoing funding

2

GLDB Organizational

Felix Breden	William Gibson	Katherine Jackson
Mansun Law	Pierre Boudinot	Eric Engelbrecht
Mats Ohlin	Andrew Collins	Mohammed Vahed
Jamie Scott	Andrew Buchanon	Scott Christlie
Swati Saha	Christian Busse	Yu Ning Huang
Amit Upadhyay	Pei-Lung Chen	Gur Yaari
Oscar Rodriguez	Ivana Milocziova	Susana Magadan
Eve Richardson	Jesus Martinez	
Chaim Schramm	Barnetche	co-leads:
Corey Watson	Steven Bosinger	**Jamie Heather**
		William Lees

quarterly meetings (duplicated in 2 timezones; monthly subgroup calls

3

GLDB Achievements 2022-2024

- Human IG Reference Set published on OGRDB:
  Collins *et al.* (2024) AIRR-C IG Reference Sets: curated sets of immunoglobulin heavy and light chain germline genes. *Frontiers in Immunology*
- AIRR-C paper on germline set development:
  Lees, Christley *et al.* (2023) AIRR community curation and standardised representation for immunoglobulin and T cell receptor germline sets. *Immunoinformatics*

3 sequences are submitted by researchers. The second is a sub-sequence of the first.		2 alleles are identified from the 3 sequences		The two alleles are established to be from the same gene.		Further confirmation becomes available and the sequences are sent to IUIS. IUIS ratifies the gene and alleles and assigns names	
label		**label**	**alias**	**label**	**alias**	**label**	**alias**
IGHV-A5B2		IGHV-A5B2	IGHV-C89D	IGHV-A5B2*01	IGHV-C89D	IGHV3-189*01	IGHV-A5B2*01, IGHV-A5B2, IGHV-C89D
IGHV-C89D		IGHV-KZO5		IGHV-A5B2*02	IGHV-KZO5	IGHV3-189*01	IGHV-A5B2*02, IGHV-KZO5
IGHV-KZO5							

Rhesus macaque subgroup has met monthly. IG sequences have been compiled from various sources and tested against a collection of repertoires.

- Progress on large-scale rhesus macaque genomic sequencing at Emory and Louisville has been shared with the group. 'Beta' consolidated set was circulated within the subgroup in March 2024.
- No additional progress on mouse sets in this period: the current sets are available from OGRDB.
- Outreach, especially industry outreach, is recognised as important, particularly with the delivery of the first AIRR-C germline sets, but it needs focussed effort which WG members have not been able to provide.

4

Software WG

Software WG Report

AIRR-C Meeting VII
June 2024

Software WG Current goals

- Complete RepCred
- Align benchmarking and gold-standards dataset with PrecisionFDA activities - *proceeding on an individual basis*
- Survey our AIRR-C membership for key focus areas (particular emphasis on industry needs) - *dropped*
- Support the Communications WG industry initiative by drawing on WG members' knowledge of the tools marketplace - *dropped*

Software WG Organizational

Co-leads: William Lees and Chaim Schramm

6-7 other members who regularly join calls

Software WG Achievements 2022-2024

RepCred is now functional (come to the demo by Ayelet Peres!) though some polish is still needed.

4

Standards WG

Standards WG Report

AIRR-C Meeting VII
June 2024

Standards WG - Current goals

Goals for 2022-2023 interval:

- Focus on refining current schema
  - Release AIRR Schema v1.4 & ADC API v1.2
  - Release AIRR Data Standards v2.0
- Draft a manuscript to accompany the v2.0 release describing new standards development since the original Minimal Standards (2017) and Data Representations (2018) publications
- Continue community outreach

Standards WG - Organizational

- Co-leads: Jason Vander Heiden, Christian Busse
- Number of Participants: 6
- Diversity: Well… there is room for improvement ;-)

Standards WG - Achievements 2022-2024

- Release of AIRR Data Standards v1.4:
  - Experimental release of the germline database schemas
  - Experimental release of the single-cell schemas
  - Experimental release of the receptor schema
  - Updates to abundance fields to account for new technologies
  - Support for additional schemas in the R and python libraries
  - Abandonment of Python v2 support
  - Various minor improvements to field definitions and documentation
- Release of AIRR Data Standards v1.5:
  - Revision of schema to harmonize structure of objects
  - Revision of schema to harmonize naming and style and attributes and enums

4

Communications SC

Communications SC Report

AIRR-C Meeting VII
June 2024

Communications Current goals

- Finalize an AIRR-C adoption and sustainability strategy to be developed in collaboration with AIRR-C Exec and with input from other SC/WG members.
- Improve our communication strategy and networking with industry members.
- Collaborate with Diagnostics WG, Legal and Ethics WG, and Meetings SC in organizing an event covering AIRR+AI/ML+legal+regulatory aspects.
- Continue to:
  - Organize webinars and seminars
  - Support the Meeting SC in dissemination and communication for AIRR-C Meeting VII
  - Create an AIRR-C-related news showcase post on each WG after significant WG milestones are met
  - Continue to support the AIRR Community in all communication and dissemination activities: website, social media, podcasts…
- Bring more members to the Communications SC. If you want to join: communications@airr-community.org

2

Communications Organizational

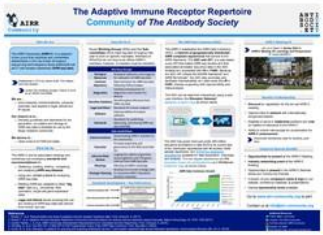
Co-leads: Susanna Márquez, Kira Neller (left the group)

Members:

- Edel Aron
- Pam Borghardt
- Victor Greiff
- Simon Schäfer

3

Communications Achievements 2022-2024



Main highlights:

- AIRR-C poster and infographic
- Communication:
  - AIRR-C VII
  - Bringing AIRR-seq to the Clinic - Mapping the Challenges
  - News
- Seminar Series and Webinar (TAbS)
- Online presence: X, mastodon, linkedin, bluesky, youtube, web, B-T.CR, store, slack. In progress: Wikipedia
- Strengths: dedication. Weaknesses: 5 people

4

Inferred Allele Review Committee

Inferred Allele Review Committee

AIRR-C Meeting VII
June 2024

IARC Current goals (selected examples)

Affirmation of novel human IGHV, IGKV, IGLV, and TRV alleles: Done
Publication of human IGV germline allele sets: Published
Collaboration on consolidation of a macaque IG germline set: Ongoing
Consolidation of the use of temporary labels: Published
Integration of genomic and transcriptomic data: Ongoing
Processes for allele submission / germline gene sets of other species (no activity)
Submission of manuscript(s) on novel alleles and IARC processes: Published
Publication of guidelines for the generation of germline sets: Published
Establishment of funding mechanisms: (individual activities only)
Consolidation of the human TCR IARC process: Done
IARC sustainability: Ongoing

2

IARC Organizational

List the names of Co-leads:
2022-2024: Mats Ohlin

Number of participants: 9

M/F: 7/2

3

IARC Achievements 2022-2024 (selected)

- Novel alleles have been affirmed and forwarded to the nomenclature committee/TR-IG.
- Human and mouse reference sets have been established (in collaboration with other WG) and published. Can now be selected in the online IgBlast tool.
- The principles of temporary labels have been established.
- Genomic data explored and used whenever possible in the affirmation process.
- Consolidation of the human TCR IARC process

List the strengths and weaknesses of the group

+ Dedicated team.
- Sustainability is a challenge.

4

Meetings SC

Meetings SC Report

AIRR-C Meeting VII
June 2024

Meetings SC Current goals

- **AIRR-C outreach activities**: participation in other society events
- **AIRR-C annual meeting organization**
  - Zooming in to the AIRR Community Meeting: halfway through the interval meeting - WG/SC reporting session + a dedicated session (in coll. with other WG/SC initiatives)
    Hosted a 2 - ½ day virtual meeting in Sept 2023 in collaboration with the Diagnostics WG
  - Hybrid meeting: end-interval meeting, organised alternately in North America or Europe, includes hosting the General Assembly
    Hosting AIRR Community Meeting VII, June 3-6/24 in Porto, Portugal
- **Host an AIRR-C forum** on conflict of interest, open science, FAIR data principles, diversity, equity and inclusivity in coll. with the Executive SC.
  Scheduling for May/June 2025

2

Meetings SC Organizational

Co-leads: Encarnita Mariotti-Ferrandiz (AIRR-C Chair-Elect, France) & Pam Borghardt (AIRR-C Executive Director, Canada)

Members: 4 full interval members + 1 AIRR-C hybrid meeting member

- Edel Aron, PhD Student, USA;
- Justin Barton, Senior Researcher, Alchemab, UK;
- Lorissa Corrie, Masters (globetrotter student!)
- Corey Watson, Associate Professor, USA
- Ademar Aguiar, Professor, FEUP, Portugal

- **+ : dedicated team**
- **- : small team**

3

Meetings SC Achievements 2022-2024

in coll. with Diagnostics WG

AIRR Community Special Event 2023 – Zooming in to the Community II

September 20 & 21, 2023

7:00 – 10:00 PDT / 10:00 – 13:00 EDT / 16:00 – 19:00 CEST

REGISTER NOW

Building on the success of our two 2020 virtual events (Special Event "Response to COVID-19" and Meeting V – Zooming into the AIRR Community Meeting), the Meetings Sub-committee has partnered with the Executive Sub-committee and the Diagnostics Working Group to create a mid-cycle virtual event. This 2-day virtual meeting includes an interactive session day dedicated to the Working Group and Sub-committee achievements, challenges and updates and a day focused on a special Diagnostics session entitled "**Bringing AIRR-seq to the clinic – mapping the challenges**".

- *WG/SC reporting focusing on achievements, strength & weaknesses*
- *4 Speakers & round-table*
- *Strategic Planning brainstorming*
- *116 Participants*

June 3 - 6, 2024 | University of Porto, Porto, PT

tinyurl.com/airrcmeeting7

- *GA: new format for reporting and discussion*
- *Sponsorship development w/ Executive SC*
- *Organization, speaker invitation, early career sessions…*
  - *19 Sponsors*
  - *16 Invited speakers and 10 short-talk speakers*
  - *239 in-person & virtual participants as of today*

Executive SC

Exec SC Report

AIRR-C Meeting VII

June 2024

Exec-SC Current goals

- Hold monthly meetings with bi-annually special meetings involving leadership of WGs and SCs
- Facilitate and promote the work of the AIRR-C WGs and SCs
- Organization of AIRR-C Seminar
- Contribute to outreach efforts including commercial and academic partnerships that lead to greater sharing, annotation and standardization of AIRR-seq data
- Contribute to the AIRR-C Strategic Plan
- Contribute to sustainability of AIRR-C efforts (funding, sponsors)
- Work on community governance v23
- Represent the AIRR-C on the TAbS Board of Directors and Finance & Audit Committee

2

Exec-SC Organizational

Chair (Victor Greiff), a Chair-Elect (Encarnita Mariotti-Ferrandiz)

Past Chair (Lindsay Cowell), and three elected Members of the AIRR Community (Christian Busse, Nina Luning Prak and Corey Watson).

Executive Director (Pam Borghardt)

Geography: North America (4) / EU (3)

3

Exec-SC Achievements 2022-2024

Streamlining of AIRR-C functioning

- *Governance updates and restructuring (e.g., manuscript endorsements made easier, increase of membership fee, possibility of task forces)*
- *Negotiated interactions with TAbS, including upfated governance*

Facilitating AIRR-C WG interaction

- *Facilitated the formation of the Strategic Planning SC*
- *Organization of bi-annual WG/SC updates*
- *Facilitating of new initiatives within the community (Machine Learning WG, Diagnostics WG, Data Curation Task Force within the Common Repository WG)*
- *Manuscript endorsements*

AIRR-C Meetings and Outreach

- *Contributed to acquiring sponsoring for AIRR-C Meeting VII (industry sponsors, societies, academic partners)*
- *Facilitating and structuring AIRR-C-industry collaborations*
- *Outreach to journals for recognition of AIRR standards*
- *Inauguration of AIRR-C Seminar series*
- *Creation of AIRR-C meeting travel award and selection of travel awardees*
- *Promoted AIRR-C interactions with IUIS, FDA, Euroclonality*

4

Legal and Ethics WG

Legal & Ethics WG Report

AIRR-C Meeting VII
June 2024

Legal & Ethics WG - Goals - Interval 2022-2024

- Finalize and publish Database Directive manuscript and summary
- Plan, conduct and evaluate a survey regarding obstacles to data sharing
- Provide guidance on GDPR issues.
- Develop an ethical framework for patient engagement and studies involving indigenous people.
- Evaluate legal and ethical aspects of current Open Science practices and recommendations in collaboration with other stakeholders (e.g., RDA, IUIS).
- Support the Diagnostics WG and Meetings SC in organizing an event covering AIRR-seq, AI/machine learning and legal/regulatory aspects.

2

Legal & Ethics WG - Organizational

Lead: Tania Bubela

Participants: 4

3

Legal & Ethics WG - Achievements 2022-2024

- Published manuscript on Database Directive and its implications for biological data:
  - Bernier, A., Busse, C. & Bubela, T. Public Biological Databases and the Sui Generis Database Right. IIC 54, 1316–1358 (2023).
  - DOI: https://doi.org/10.1007/s40319-023-01373-0

4

Biological Resources

Biological Resources WG Report

AIRR-C Meeting VII
June 2024

Biological Resources WG - Current goals

Goals

The goal of the working group is to be able to provide AIRR biological standards and protocol recommendations to the scientific and biomedical community. Recommendation of a set of biological standards that can be used for normalization of data sets will allow more direct comparison of data generated by different library prep methods.

For 2022-2024:

- Generation of data from different BCR sequencing methods using three different types of standards: synthetic RNA templates, spleen DNA/RNA and cell line mixtures
- Generation of data from TCR sequencing standards comparison, starting from the methods that performed best in the Nature Biotechnology publication that was led by several of the WG members (Barennes et al., 2021)
- Continued participation in FDA BCR-SEQC initiative
- Continued participation in EuroClonality WG and meetings

Text taken from AIRR-C website

Biological Resources WG - Organizational

- Co-leads: Nina Luning Prak, Johannes Truck, Anne Eugster
- Number of Participants: 3-10, depending on the meeting
- Diversity: Representation from Industry, Institutes (e.g., FDA) and Academia. Recruited a student (Saheli Basu Roy from West Bengal) to the group
- Group is disbanding– Why?
  - Steady attrition in meeting attendance
  - Several of the major goals of the WG have been accomplished– e.g., publication of AIRR standards and QC needs paper (Truck et al. 2021), publication of AIRR-seq methods and data analysis workflows (Methods Mol. Biol. 2022) and publication of T cell AIRR-seq benchmarking paper (Barennes et al. 2021).
  - Much of the work on benchmarking B cell assays has already been performed by the Euroclonality consortium (Knecht et al. 2019; Stewart et al. 2021; Van der Velden et al. 2021 etc.)
  - Much of the work that remains on benchmarking of B cell assays and calibrators is now subsumed under the FDA BCR-SEQC project, which was launched by Dr. Wenming Xiao (who is also a member of the Biological Resources WG)

Biological Resources WG - Achievements 2022-2024

- Publications and Presentations
  - 5 chapters in 2022 Springer Methods in Molecular Biology Immunogenetics Issue
  - On AIRR podcast on MRD (and other clinical applications of AIRR-seq)
  - AIRR Community webinar on QC pipelines for AIRR-seq data (Encarnita and Nina)

- Participation in FDA BCR-SEQC initiative-
  - Evaluation of B cell receptor profiling platforms and analysis tools using next-generation sequencing data. Follows working model of SEQC consortium. Led by Dr. Wenming Xiao.
  - Major goals: 1) detailed characterization of B cell lines; 2) analysis of cell line mixtures using different AIRR-seq assays; 3) benchmarking assays and analysis tools.

4

Future Plans

Common Repository WG

Common Repository WG Future Plans

AIRR-C Meeting VII
June 2024

Common Repository Working Group - Future plans

- ***Goals:***
  - *Continuing to focus on promoting and advancing the AIRR Data Commons*
  - *Evolution of AIRR Standards and the ADC API*
  - *Create a searchable programmatic AIRR Data Commons Repository Registry*
  - *Potential Data Curation "Task Force" or similar being considered*
- ***Products/resources produced:***
  - *AIRR Data Commons*
  - *AIRR Data Commons Registry*
- ***Resource requirements:***
  - *Virtual machine for running AIRR Data Commons Repository Registry*
  - *More people involved in the Working Group*
- ***Elected future WG lead:***
  - ***Brian Corrie (continuing)***

Diagnostics WG

Diagnostics WG Future Plans

AIRR-C Meeting VII
June 2024

Diagnostics WG Future plans

- ***Goals***:

Advance AIRR-Seq for clinical diagnostics & monitoring

1. *Produce and extend reach of On AIRR*
2. *Promote AIRR-Standard*
   a. *Finalize review*
   b. *Initialize review on ML in diagnostic AIRR-Seq - together with new ML WG*
3. *Review AIRR-Standard fields for diagnostic purposes*
4. *Provide a resource for endorsed tools relevant for the use of AIRR in diagnostics*

- ***Products and/or resources:***

Podcast: On AIRR

Review in preparation: Immunoinformatics for Precision Diagnostics of Infectious Diseases

- ***Resource requirements:***

Continuation of

Podcast hosting
Recording software

- ***Elected future WG/SC Co-leads:***

Pieter Meysman | Ulrik Stervbo

Interested in joining?

Scan and email!

Germline Database WG

Germline Database WG Future Plans

AIRR-C Meeting VII
June 2024

GLDB WG Future plans

- ***Goals***:
- Publish a Human TR reference set (in conjunction with IARC)
- Continue work/updates on Human IG reference set
- Publish a Macaque IG reference set (in collaboration with the wider research community)
- Revive the mouse subgroup
- Set up subgroups for other species *provided* there is self-sustaining membership to support them
- Initiate the Outreach subgroup, *provided* we can find a volunteer to lead it

- ***Products and/or resources:***
- Reference sets, as above
- Publications associated with new reference sets

- ***Resource requirements:***
- Volunteers to work on species-specific subgroups - human TR is highest priority
- Volunteer to organise and run the outreach subgroup

- ***Elected future WG/SC Co-leads:***
- Jamie Heather and William Lees are happy to stand for another period, but other nominations are welcome

Software WG

Software WG Future Plans

AIRR-C Meeting VII
June 2024

Software WG Future plans

- ***Sunset***:

We intend to remain formally active as a working group only through submission and ratification of a manuscript. No additional regular WG meetings are planned.

- ***Hand-off:***

Maintenance of the software standards and certification of tools as compliant with them will be passed to the new ML/AI WG. Many of our current members are planning to join that new WG, as well.

Standards WG Future Plans

AIRR-C Meeting VII
June 2024

Standards WG - Future plans (I)

- **Goals**
  - Release AIRR Data Standards v2.0
    - Production release of the germline database schemas
    - Production release of the single-cell schemas
    - Production release of receptor schemas
    - Production release of the lineage schemas
  - Experimental release of a file manifest schema, repertoire grouping schema, and a persistent identifier definition
  - Several small, but backwards incompatible changes
  - Draft a manuscript to accompany the v2.0 release describing new standards development since the original Minimal Standards (2017) and Data Representations (2018) publications
  - Continue community outreach

Standards WG - Future plans (II)

- **Products and/or resources**
  - AIRR Data Standards
  - AIRR Community Docs (shared)
- **Resource requirements**
  - none
- **Elected future WG Co-Leads:**
  - Jason Vander Heiden, Christian Busse

Communications SC Future Plans

AIRR-C Meeting VII
June 2024

Communications SC Future Plans

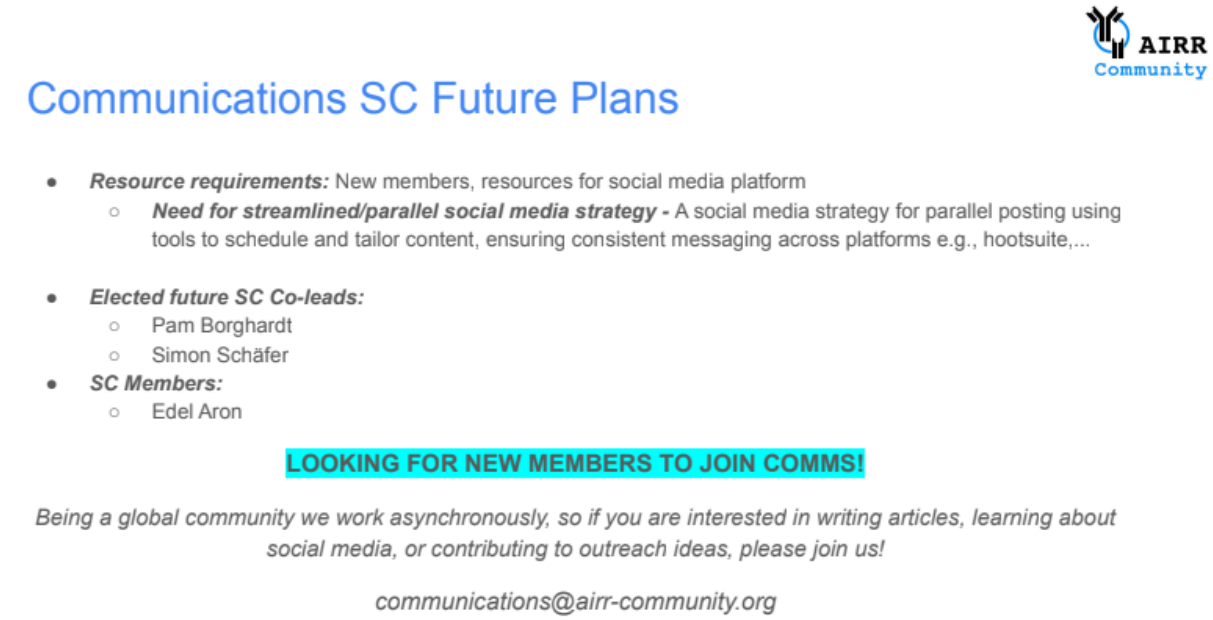
- ***Goals***:

Sustainability. Onboard more members.

Continue to improve internal communications to facilitate project coordination and management within the Community.

  - Support meetings and other outreach activities
  - Organize seminars and webinars
  - Create newsletters, news items and social media posts about AIRR-C initiatives
  - Maintain the online presence
  - Facilitate outreach communication in collaboration w. Exec

- ***Products and/or resources:*** *Newsletter, social media stats*
  - ***Current Information Outlets*** - AIRR-C Website, X/Twitter, Mastodon, Bluesky, LinkedIn, Slack, YouTube, B-T.CR Forum (Audiences vary between outlets and it is time consuming although necessary to send information through all of these channels for maximum engagement within our diverse community.



Inferred Allele Review Committee

IARC Future plans

- ***Goals:***
  - Evolve from SC to review committee
  - Incorporate genomic data in processes; process for larger submissions
  - Consolidate interaction with TR-IG/IUIS nomenclature subcommittee
  - Consolidation of the human TCR IARC process
- ***Products and/or resources:***
  - Publications, reference sets, online tools and resources
- ***Resource requirements:***
  - IT infrastructure
- ***Elected future WG/SC Co-leads:***
  - Mats Ohlin and Ayelet Peres

Meetings SC

Meetings SC Future Plans

AIRR-C Meeting VII
June 2024

Meetings SC Future Plans

- ***Goals**: continue on the same track*
  - **AIRR-C activity outreach**: call for participants, initiatives (FOCIS 2025)
  - **AIRR-C annual meeting organization alternating between virtual and hybrid, Europe and North America**
    - Zooming in to the AIRR Community Meeting May/June 2025
      - Virtual (2 ½ days)
      - General Assembly
      - WG/SC progress reporting session
      - Potential Theme - an AIRR-C Forum on conflict of interest, open science, FAIR data principles, diversity, equity and inclusivity
      - Celebration of 10 years since the first official meeting!
    - AIRR-C Meeting VIII - hybrid meeting: theme title TBD.
      - in North America May/June 2026
      - will try to finalize location before end of 2024 and send out save the dates
      - location suggestions so far:
        - SFU (Vancouver, Canada)
        - UTSW (Dallas, Texas)
        - ***other ideas welcome!***
- ***Products and/or resources:***

  meetings and their recordings
  networking opportunities with industry,
- ***Resource requirements:***

  need to source another meeting platform to replace the Whova meeting platform (becoming cost prohibitive, too many limitations)

Meetings Future Plans

- ***Elected future SC Co-leads:***

  Pam Borghardt (CA) & Encarnita Mariotti-Ferrandiz (FR)
- ***Future SC members:***

  Justin Barton (UK)

  Lorissa Corrie (CA)

  Monica Fernandez-Quintero (US)

  Lonneke Scheffer (NO)

  Corey Watson (US)

  local organizing member (TBD once location established)

  WE NEED YOU!!! Please join the team!

AIRR Community

Executive SC Future Plans

AIRR-C Meeting VII
June 2024

AIRR Community

Executive SC Future Plans

- **Goals**:
  - AIRR-C products adopted and championed more broadly by the immunogenetics and biomedical communities
  - Long-term AIRR-C sustainability (increase third-party partnerships, not necessarily linked only to meetings, increase visibility, increase outreach activities)
  - AIRR-C sponsor outreach
  - Continue to streamline governance
  - Implement Strategic Planning SC recommendations

- **Resource requirements:**
  Funding for community management, technical resources and outreach activities

- **Elected future SC Co-leads and elected Members:**
  Encarnita Mariotti-Ferrandiz, (incoming Chair effective June 7th), Chair-elect (to be elected on June 6th), Victor Greiff (Past Chair as of June 7th) and 3 elected members (to be elected on June 6th)

Machine Learning WG Proposal

OVERVIEW

The purpose of this proposal is to establish a Machine Learning Working Group within the AIRR Community (AIRR-C) with the primary objective of creating and hosting competitions akin to the Critical Assessment of Structure Prediction (CASP) competition that would provide much-needed benchmarks and advance the application of machine learning to AIRR-seq data.

MISSION & GOALS

The mission of the Machine Learning WG is to foster collaboration and innovation in the application of machine learning techniques to AIRR-seq data. The primary goal within the first year of its establishment is to organize a CASP-like competition focused on antibody binding (reactivity) prediction. This competition will serve as a platform for researchers and data scientists to benchmark and advance the state-of-the-art in antibody binding prediction, ultimately contributing to the development of novel computational tools and methodologies in this domain. In collaboration with the Biological Resources WG, the Machine Learning WG will also work to create from this competition an enduring benchmark dataset for each year that the competition is held. This will facilitate common comparison and reproducibility, which are currently lacking in the field.

With the first proof-of-concept of antibody binding challenge established, the Machine Learning WG may then elect to establish a more comprehensive set of benchmark challenges for the community including TCR (currently already underway, this WG will aim to integrate TCR efforts under the AIRR-C umbrella), repertoire, and structure-related prediction challenges that are deemed to be of most value to the community.

A secondary objective of the Machine Learning working group would be to support other AIRR-C WGs (Standards WG and Common Repo WG) in reviewing how to make AIRR-seq data and data repositories more accessible for ML researchers, including data on antigen-enriched B and T cell populations, data sets on individuals with different diseases or therapies, and how to integrate functional data, and any other questions that might benefit from the support of ML subject matter experts.

A further secondary objective of the Machine Learning WG would be to encourage research groups developing models and AIRR-seq analysis tools to seek certification of compliance with the AIRR-C software standard when publishing software. To that end, the WG would maintain the

AIRR-C Software Guidelines, adapting them to the needs of the ML community and certifying compliance of submitted tools.

DELIVERABLES

The Machine Learning WG will plan and execute an open competition with blinded test data, and then subsequently deliver a comprehensive report summarizing the outcomes of the competition, including the evaluation of participating models, identification of best practices, and potential avenues for future research. Additionally, the WG will provide a roadmap for ongoing collaboration and knowledge exchange among participants, aiming to foster continued advancements in immune receptor binding prediction through machine learning. The competition will create enduring materials such as benchmark datasets, evaluation rubrics, and best practices.

TIMELINE

The proposed timeline for the Machine Learning WG is as follows:

AIRR-C Meeting VII (June 2024): Vote to establish the Machine Learning WG amongst the AIRR-C membership.

Month 1-2: Formation of the ML WG, appointment of leadership, and initial planning for the benchmark competition (i.e., planning of specific ML prediction task, test data sets, contacting of industry players to help with experimental validation of ML predictions).

Month 3-6: Solicitation of data, development of evaluation criteria, and establishment of infrastructure for the competition.

Month 7-9: Execution of the competition, data analysis, and model evaluation.

Month 10-12: Compilation of competition results, preparation of the comprehensive report in the form of a publication, and dissemination of findings within the AIRR-C community.

Year 2 and Onwards: The competition(s) would be organized and held on an annual basis to facilitate benchmarking of methods developed within each year and to evolve the benchmarks as methods advance and more data become available.

LEADERSHIP

The ML WG will be led by co-leads with expertise in machine learning, immunology, and computational biology. The co-leads will be responsible for overseeing the planning and

execution of the competition, as well as the subsequent deliverables outlined in this proposal. VG and JB would volunteer to serve as interim organizers until co-leads have been formally elected.

CONCLUSION

The establishment of the Machine Learning Working Group and the organization of a CASP-like competition for antibody binding prediction aligns with the overarching goals of the AIRR Community to promote collaboration, innovation, and data-driven advancements in immunology and antibody research. This initiative has the potential to catalyze significant progress in the field of application of ML to AIRR-seq data, ultimately contributing to the development of more effective therapeutic antibodies and vaccines.

This proposal is presented in accordance with the governance guidelines outlined in v22 of the AIRR-C governance document.

Thank you for your consideration.

Sincerely,
Victor Greiff & Justin Barton

AIRR-C Meeting VII Attendees

Attendee	Affiliation	City / Country
Leslie Adda	Sorbonne University	France
Celine AlBalaa	Sorbonne University	France
Renata Almeida	Takara Bio	
Raymond Alvarez	Imprint Labs	New York City, New York
Sakina Amin		
Catherine Antoine	GSK	
Edel Aron	Yale University	United States
Roos (Rose) Arya-Visser	Genmab	The Netherlands
Daria Balashova	Amsterdam University Medical Centers	The Netherlands
Justin Barton	Alchemab Therapeutics	United Kingdom
Habib Bashour	The University of Oslo (UiO)	
Jannick Bendtsen	PipeBio	Denmark
Spela Binter	RQ Biotechnology	
Nicola Bonzanni	ENPICOM BV	The Netherlands
Pam Borghardt	AIRR Community	Canada
Beck Brachman	IMPRINT	New York, New York, United States
Felix Breden	iReceptor	United States
Frances Breden		
Bryan Briney	Scripps Research	United States
Alex Brown	Roche Diagnostics GmbH	Munich, Bavaria

Attendee	Affiliation	City / Country
Sarah Burbach	Scripps Research	
Jp Burckert	Voredos SRL	
Christian Busse	German Cancer Research Center (DKFZ)	Germany
Monica Campos	imperial College London	
Niccolò Cardente		Italy
Pedro Carmo	FairJourney Biologics	Portugal
Brigite Carvalho	FairJourney Biologics	
Pei-Lung Chen	Graduate Institute of Medical Genomics and Proteomics, National Taiwan University	Taipei
Alex Chenchik	Cellecta, Inc.	Mountain View, California
Maria Chernigovskaya	Karolinska Institute	Sweden
Elena Chernysheva	Cellecta, Inc	United States
Lewis Chinery	University of Oxford	Oxford, England
Scott Christley	UT Southwestern Medical Center	United States
Vicki Christopher-Jones	UCB	
Dmitry Chudakov	CEITEC	
Lorissa Corrie	iReceptor	Canada
Brian Corrie	Simon Fraser University	Summerland, British Columbia
Alexandre Costa	INESC TEC	Portugal
Lindsay Cowell	University of Texas Southwestern Southwestern Medical Center	United States
Bart Cuypers	GSK	Rixensart, Wallonia

Attendee	Affiliation	City / Country
Frederic Davi		
Fatima Davila Hernandez	Johns Hopkins University	Baltimore, Maryland
Eva Dawin	Institut for Translational Neurology, University Clinic Münster, Germany	
Jurrian de Kanter	Genmab	The Netherlands
Emzo de los Santos	UCB	London, England
Taissa de Matos Kasahara	University of Oslo	
Eric de Sousa	Champalimaud Foundation	Portugal
Nicky de Vrij	UAntwerp / Institute of Tropical Medicine	Belgium
Charlotte Deane	University of Oxford	United Kingdom
Marie Di Placido	The Pirbright Institute	Pirbright, England
Paul Diehl	Cellecta, Inc.	Mountain View, California
Felix Drost	Helmholtz Munich	
Dylan Duchen	Yale School of Medicine	United States
Hesham ElAbd	Kiel University	Germany
Alexandra Elsakova	University of Tartu	Estonia
Andrew Farmer	Takara Bio USA, Inc.	San Jose, California
Monica Fernandez-Quintero	The Scripps Research Institute	United States
Filipa Ferreira	FairJourney Biologics S.A.	Porto
Jessie Fielding	Geisel School of Medicine at Dartmouth	Hanover, New Hampshire
Easton Ford	University of Louisville	United States

Attendee	Affiliation	City / Country
Eric Franciskovic	Lund University	Malmö, Skåne
Robert Frank	University of Oslo	Oslo
Javier Freire González	Universidade de Vigo	Vigo
Gisela Gabernet	Yale School of Medicine	United States
Rodrigo García Valiente	Amsterdam UMC	Amsterdam, North Holland
William Gibson	NIH	United States
Sofie Gielis	UAntwerpen	Antwerpen, Flanders
Iria Gomez-Tourino	University of Santiago de Compostela	Santiago de Compostela, Galicia
Shaveta Goyal	Takara Bio USA	San Jose, California
Jeffrey Gray	Johns Hopkins University	Baltimore, Maryland Area
Edward Green	DKFZ	Heidelberg, Baden-Württemberg
Victor Greiff	University of Oslo	Norway
Max Gubert Olivé	PipeBio	Denmark
Ulf Guenther	DKMS Group gGmbH	Germany
Alena Harley	Tempus	USA
Falk Heidenreich	DKMS Group gGmbH	Germany
Lance Hepler	Infinimmune	United States
Kenneth Hoehn	Dartmouth College	United States
Erik Huang	University of Southern California	Los Angeles, California, United States
Jonathan Hurtado Romero	The Scripps Research Institute - La Jolla Campus	United States

Attendee	Affiliation	City / Country
Giulio Isacchini	Imprint Labs	
Katherine Jackson	Garvan Institute of Medical Research	Sydney, New South Wales
Uddalok Jana	University of Louisville	Louisville, Kentucky
Michael Jarman	The Pirbright Institute, UK	
Anitha Jayaprakash	TaKaRaBio	United States
Cole Jensen	Yale University	New Haven, Connecticut
Philippe Joanin	Takara Bio Europe	
Loice Kanda	Kenya AIDS Vaccine Initiative (KAVI-ICR)	Nairobi, Nairobi Area
Dhuvi Karthikeyan	Personalized Immunotherapy Research Lab	San Francisco, California
Dominic Kelly	University of Oxford	
David Klatzmann	Sorbonne University	France
Vered Klein	Bar-Ilan University	Ramat Gan, Tel Aviv
Steven Kleinstein	Yale University	United States
Christian Klesse	DKMS Group gGmbH	Germany
Agnieszka Kolodziejak	Natural Antibody	Poland
Thomas Konstantinovsky	Bar Ilan University	Tel Aviv, Tel Aviv
Sofia Krasik	Alchemab Therapeutics	United Kingdom
Konrad Krawczyk	Natural Antibody	Hamburg, Hamburg, Germany
Jean-Philippe Laine	Infinity Bio, Inc.	United States
Ben Larman	Johns Hopkins University	United States

Attendee	Affiliation	City / Country
Khang Le Quy	University of Oslo	Norway
Noah Lee	Yale University	United States
Jin Seok (Andy) Lee	Personalized Immunotherapy Research Lab (PIRL)	United States
William Lees	Bar-Ilan University, Ramat Gan, Israel and University of Louisville, Kentucky, USA	London, England
Sue Lees		
Auréline Lefèvre	Sorbonne University	France
Stefan Lelieveld	ENPICOM BV	The Netherlands
Julien Limenitakis	Imprint Labs	New York City, New York
Ida Lindeman	Oslo University Hospital	Norway
Laurens Lindenburg	Genmab	Utrecht
Andreas Lossius	University of Oslo	Norway
Cooper Lovano		
Svitlana Lozova	ENPICOM BV	The Netherlands
Nina Luning Prak	University of Pennsylvania	United States
Wim Maes	Leuven University - PharmAbs	Kortrijk, Flanders
Susana Magadan	University of Vigo	Spain
Serghei Mangul	USC	United States
María Marco Salvador		
Daniella Marinelli	Scripps Research	United States
Encarnita Mariotti-Ferrandiz	Sorbonne University	France
Susanna Marquez	Yale University	Valencia, Valencia

Attendee	Affiliation	City / Country
Joshua Martin Beem	Duke University	
Damon May	Adaptive Biotechnologies	Seattle
Wyatt McDonnell	Infinimmune	
Benjamin McMaster	University of Oxford	Oxford
Ramit Mehr	Bar-Ilan University	Petaḫ Tiqwa, Central, Israel
Farzaneh Meimandiparizi	Radboud University Medical Center	Nijmegen, Gelderland
Juan Luis Melero	Omniscope	Spain
Ruth Mercado	Cellecta, Inc.	United States
Shoichi Metsugi	Chugai Pharmacetutical Co., Ltd	Kamakura, Kanagawa
Pieter Meysman	University of Antwerp	
Vanessa Mhanna	Immunology-Immunopathology-Immunotherapy laboratory i3 Sorbonne Université	Paris, Île-de-France
Saheli Mitra	AI Research Engineer	Denmark
Kerry Mullan	University of Antwerp	
Luke Myers	Vanderbilt Vaccine Center	United States
Benjamin Nemoz	Scripps Research	United States
Karenna Ng	Scripps Research	United States
Tim O'Donnell	Imprint Labs	
Aengus Officer		
Mats Ohlin	Lund University	Sweden
Tom Parks	Imperial College London	United Kingdom
Ayelet Peres	Bar Ilan University	Israel

Attendee	Affiliation	City / Country
Jo Peters		
Bjoern Peters	La Jolla Institute for Immunology	United States
Ekaterina Petrova	University of Bern	Switzerland
Martin Pezous	Sorbonne-Université	France
Sabrina Pollastro	Sanquin Research	Amsterdam, North Holland
Lisa Portney	IMPRINT	
Isabel Poschke	German Cancer Research Center	
Olga Poslavskaya		
Stanislav Poslavsky	MiLaboratories Inc.	United States
Lev Poslavsky		
Anna Postovskaya	University of Antwerp	Antwerpen, Flanders
Anne Poupon	MAbSilico	France
Niranjani Prasad	Microsoft Research	United Kingdom
Nicholas Provine	University of Oxford	United Kingdom
Vincent Puard	MabSilico	
Guilhem Pupier	Sorbonne University	France
Tam Quach	Northwell Health System - The Feinstein Institute for Medical Research	Manhasset
Puneet Rawat	University of Oslo	Oslo
Janice Reichert	The Antibody Society	United States
Eve Richardson	La Jolla Institute for Immunology	United States
Sarah Robinson	Genentech	New York
Artur Rocha	INESC TEC	Portugal

Attendee	Affiliation	City / Country
Pedro Rodrigues	University of Porto	Portugal
Elisa Rosati Scalchi	GSK	Rixensart, Wallonia
Krishna Roskin	Cincinnati Children's Hospital Medical Center	Cincinnati, Ohio
Jasmine Rowell	University College London	
Yana Safanova	Pennsylvania State University	United States
Yana Safonova		
Swati Saha	University of Louisville	
James San	DHVI	
Tadusz Satława	Natural Antibody	Poland
Simon Schaefer	FAU Erlangen	
Lonneke Scheffer	University of Oslo	Norway
Bill Schief	Scripps Research Institute, Moderna	United States
Tilman Schneider-Hohendorf	University of Muenster, Germany	Münster
Chaim Schramm	NIH/NIAID/VRC	United States
Jonas Schuck	Goethe University, University Hospital Frankfurt, Neurological Institute (Edinger Institute)	Frankfurt am Main, Hesse
Janine Schuurman	Lust for Life Science	
Nicholas Schwab	University Of Münster	Münster, North Rhine-Westphalia
Ella Schwab	University of Southern California	United States
Jamie Scott	Simon Fraser University	
Sujatha Seenu	US Center for Disease Control and Prevention	United States
Asli Semerci	Bilkent University	Ankara, Ankara

Attendee	Affiliation	City / Country
Nina Senna	Omniscope	Oxford
Alexandra Sharland	University of Sydney	Australia
Pragati Sharma		United States
Troy Sincomb		United States
Andrei Slabodkin	JURA Bio	
Simone Spandau	Scripps Research	
Laura Spector	Specifica	Santa Fe, New Mexico
Roberto Spreafico	Genmab	
Josua Stadelmaier	University of Tübingen	Tübingen, Baden-Württemberg
Ulrik Stervbo	Charité – Universitätsmedizin Berlin	Bochum, North Rhine-Westphalia
Paul Stys	Sorbonne University	France
Vineeth Surendranath	DKMS Life Science Lab	Dresden
Akshay Tiwari	Indian Institute of Science	India
Kelvin (Zewen) Tuong	The University of Queensland	Brisbane, Queensland
Heike Uhlemann	DKMS Group gGmbH	Germany
Sarah Vagner	Takara Bio	
Sebastiaan Valkiers	University of Antwerp	Antwerp
Henk-Jan van den Ham	ENPICOM BV	The Netherlands
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Elizabeth Van Itallie	Duke Human Vaccine Institute	United States

Attendee	Affiliation	City / Country
Romi Vandoren	University of Antwerp	Belgium
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Alexander Walker	DKMS Group gGmbH	Germany
Xinhao Wang		
Hedda Wardemann	Bill-and-Melinda Gates Foundation	Germany
Rachel Waterworth	Simon Fraser University	Vancouver, British Columbia
Corey Watson	University of Louisville School of Medicine	
Simon Watson	RQ Biotechnology Ltd	United Kingdom
Kevin Wiehe	Duke Human Vaccine Institute	
Thomas Wiley	EFIS EJI	
Patrick Wilson		
Wing Ki Wong	Roche Diagnostics GmbH	Munich, Bavaria
Sonia Wrobel	Natural Antibody	
Sander Wuyts	ImmuneWatch	Antwerpen, Flanders
Christian Wünsch	University of Münster	Germany
Charlotte Würtzen	University of Oslo	Norway
Li Xue	Radboudumc	

Attendee	Affiliation	City / Country
Gur Yaari	Bar Ilan University/Yale University	Israel/Unted States of America
Yu-Hsuan Yang	Graduate Institute of Medical Genomics and Proteomics, National Taiwan University	Taipei, Taiwan
Dawit Afework Yohannes	University of Helsinki	
Ian York	US Center for Disease Control and Prevention	United States
Chris Youngston Gray	Johns Hopkins University / Jeff Gray	
Mariia Zakharova	Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry	Russia
Maxim Zaslavsky	Stanford University	United States
Weian Zhao	Aureka Biotechnologies, Inc.	United States
Jahn Zhong	University of Oslo	Norway
Julian Zhou	Washington University in St Louis	Toronto, Ontario
Bojan Zimonja	Simon Fraser University	Canada

Thank you for attending everyone!