iReceptor+

Sharing AIRR-seq data

Promoting Human Immunological Data Sharing to Improve Development of Novel Vaccines, Cancer Immunotherapies and Autoimmune Treatments.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 825821 and the Canadian Institutes of Health Research (CIHR).

+ iReceptor Plus will

Unleash the power of the Adaptive Immune System to treat disease via personalized immunotherapy

Provide a queriable set of AIRR-seq data repositories following FAIR (findable, accessible, interoperable, and reusable) principles and the AIRR Community's data standards for sharing AIRR-seq data

Make it easy for researchers in immune genetics to use advanced research computing (ARC) infrastructure
without becoming ARC experts

Big Data

AIRR Data Commons
Distributed repositories based on standards developed by the international AIRR Community

Computer Power

Advanced AIRR-seq Analysis
Data staging, job management and complex data analysis.

Integation of large computational resource to perform complex analyses

The iReceptor Plus Approach

Job Management
Analysis Results

Data Federation
Data Query

iReceptor+ Platform

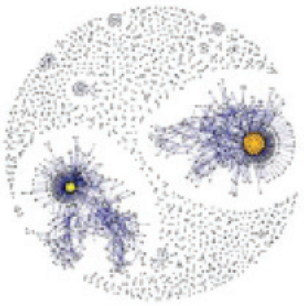
iReceptor+ Scientific Gateway
Interactive data discovery, exploration, and analytics

Web based portal that hides the complexity of data federation across many repositories

+ iReceptor Plus will

Perform the Complete Research-Development-Innovation Cycle to achieve. Immunotherapy for Cancer, Infections, & Autoimmune Disease

- Immunotherapy harnesses the power of the adaptive immune system to **develop treatments** for:
  - Cancer (e.g., anti-checkpoint therapy)
  - Infectious diseases (e.g., vaccines)
  - Autoimmune diseases (e.g., therapeutic monoclonal antibodies to suppress MS)
- **iReceptor Plus platform** enables integration of large scale AIRR-seq genomics data (deep-sequenced antibody/B-cell or T-cell receptor repertoires) with extensive health data. This will be critical to advances in immunotherapy
- Patterns in AIRR-seq data may be used as **biomarkers** to stratify patients and predict outcome to therapies
- AIRR-seq data is already being used in clinics to **monitor minimum residual disease (MRD)**



CLL sample 5
26,086 sequences total
48.0 % maximum cluster

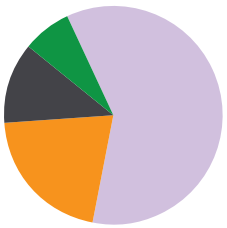
Healthy donor
1 12,316 sequences total 0.49 % maximum cluster

Figure 1: Mapping related clones using AIRR-seq data shows extreme expansion of malignant B-cells in Chronic Lymphocytic Leukemia (CLL) compared to human healthy controls. Such expansions can be used to diagnose patients, monitor response to immunotherapy, and test for relapse of disease (Bashford-Rogers, et al., 2013)

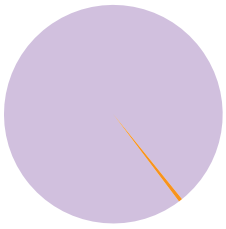
+ The iReceptor Gateway

iReceptor federates more than 2 billion sequences and 1,184 repertoires from 6 remote repositories and 26 research labs.

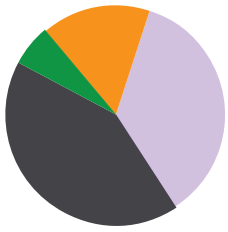
The 6 Repositories include:



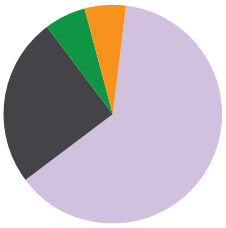
12 STUDY TYPES



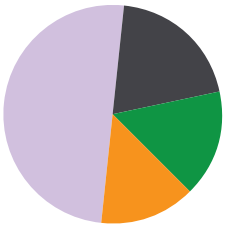
2 ORGANISMS



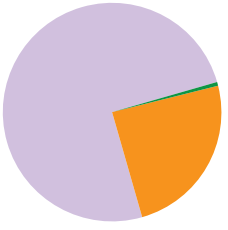
43 DISEASE STATES



22 TISSUES



22 CELL SUBSETS



3 TARGET SUBSTRATES

+ iReceptor Plus Consortium

Composed of 19 academic, biopharma, and clinical institutions from 9 countries. Their goal is to provide a data integration platform to share, compare and analyze Adaptive Immune Receptor Repertoire (AIRR-seq) data.

To connect your data repository and use the iReceptor Plus platform and tools, contact us at www.ireceptor-plus.com

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