



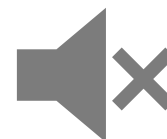
The 2024 Immucantation Users Group Meeting will take place on **January 25th, 2024**.

*Note that all times shown here use ET.*

Start	End	Speaker	Title
10:00 am	10:15 am	Kleinstein lab, Yale University	Welcome
10:15 am	10:35 am	Mr. Easton E. Ford, University of Louisville	<a href="#">Defining Immunogenomic Signatures in B Cell-Mediated Autoimmunities</a>
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1:10 pm	1:25 pm	Kleinstein lab, Yale University	Wrap up



The meeting will start shortly.



To reduce noise, everyone is muted upon entry and during the presentation.



Use the chat to submit your questions.



# 2024 Immcantation Users Group Meeting

Kleinstein Lab

# Immucantation turns 10!



2014 - ?

## **BIOINFORMATICS APPLICATIONS NOTE** Vol. 30 no. 13 2014, pages 1930–1932 doi:10.1093/bioinformatics/btu138

Sequence analysis

Advance Access publication March 10, 2014

### **pRESTO: a toolkit for processing high-throughput sequencing raw reads of lymphocyte receptor repertoires**

Jason A. Vander Heiden<sup>1,†</sup>, Gur Yaari<sup>2,3,†</sup>, Mohamed Uduman<sup>1,3</sup>, Joel N.H. Stern<sup>4,5,6</sup>, Kevin C. O'Connor<sup>5,6</sup>, David A. Hafler<sup>5,6</sup>, Francois Vigneault<sup>7</sup> and Steven H. Kleinstei<sup>1,3,\*</sup>

Sequence analysis

Bioinformatics, 31(20), 2015, 3356–3358

doi: 10.1093/bioinformatics/btv359

Advance Access Publication Date: 10 June 2015

Applications Note

OXFORD

### **Change-O: a toolkit for analyzing large-scale B cell immunoglobulin repertoire sequencing data**

Namita T. Gupta<sup>1,†</sup>, Jason A. Vander Heiden<sup>1,†</sup>, Mohamed Uduman<sup>2</sup>, Daniel Gadala-Maria<sup>1</sup>, Gur Yaari<sup>3</sup> and Steven H. Kleinstei<sup>1,2,\*</sup>

# Users Statistics



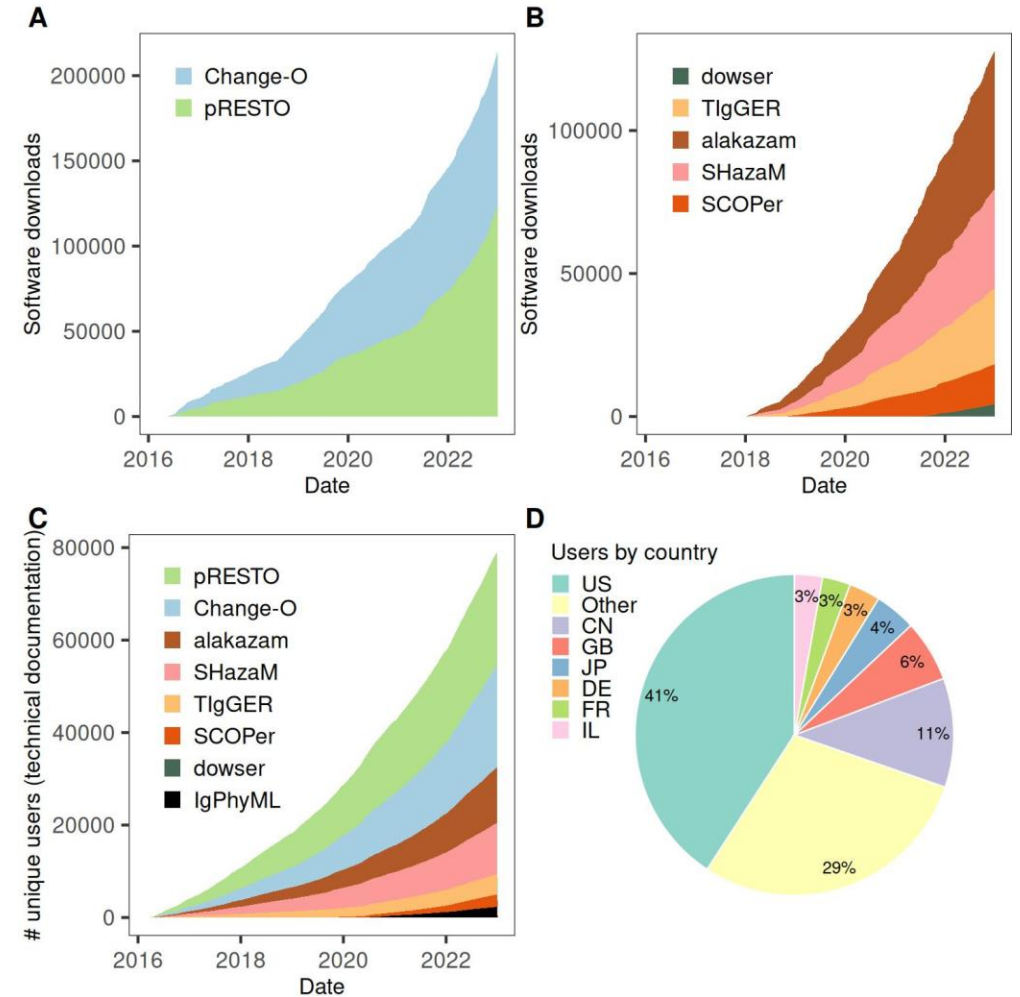
"Keep up the good work eh!"

"I am implementing BCR analysis into a python package and want to know more about current methods."

"Be familiar with how to analyze single cell data"

"I am using Immcantation for my master's thesis"

"Looking forward to learn more about how the community applies Immcantation"



# Immucantation Team

Paraskevas Filippidis  
Jason Vander Heiden  
Susanna Marquez  
Ang Cui Nima Nouri Gisela Gabernet  
Moriah Cohen Mohamed Uduman  
Edward Lee Gur Yaari Tony Melillo  
Julian Zhou Namita Gupta  
Ruoyi Jiang Mamie Wang Chris Bolen  
Cole Jensen Burhan Sabuwala  
Hailong Meng Noah Yann Lee  
Kenneth Hoehn Steven Kleinstein  
Daniel Gadala-Maria Edel Aron  
Collaborators Funding



National Institute of  
Allergy and  
Infectious Diseases

## Welcome to the Kleinstein Lab



We are a computational immunology group with a combination of "big data" analysis and immunology domain expertise. Our interests include both developing new computational methods and applying these methods to study human immune responses. Specific areas of focus include:

- High-throughput B cell receptor (BCR) repertoire profiling (AIRR-seq or Rep-seq)
- Immune signature of human infection and vaccination responses

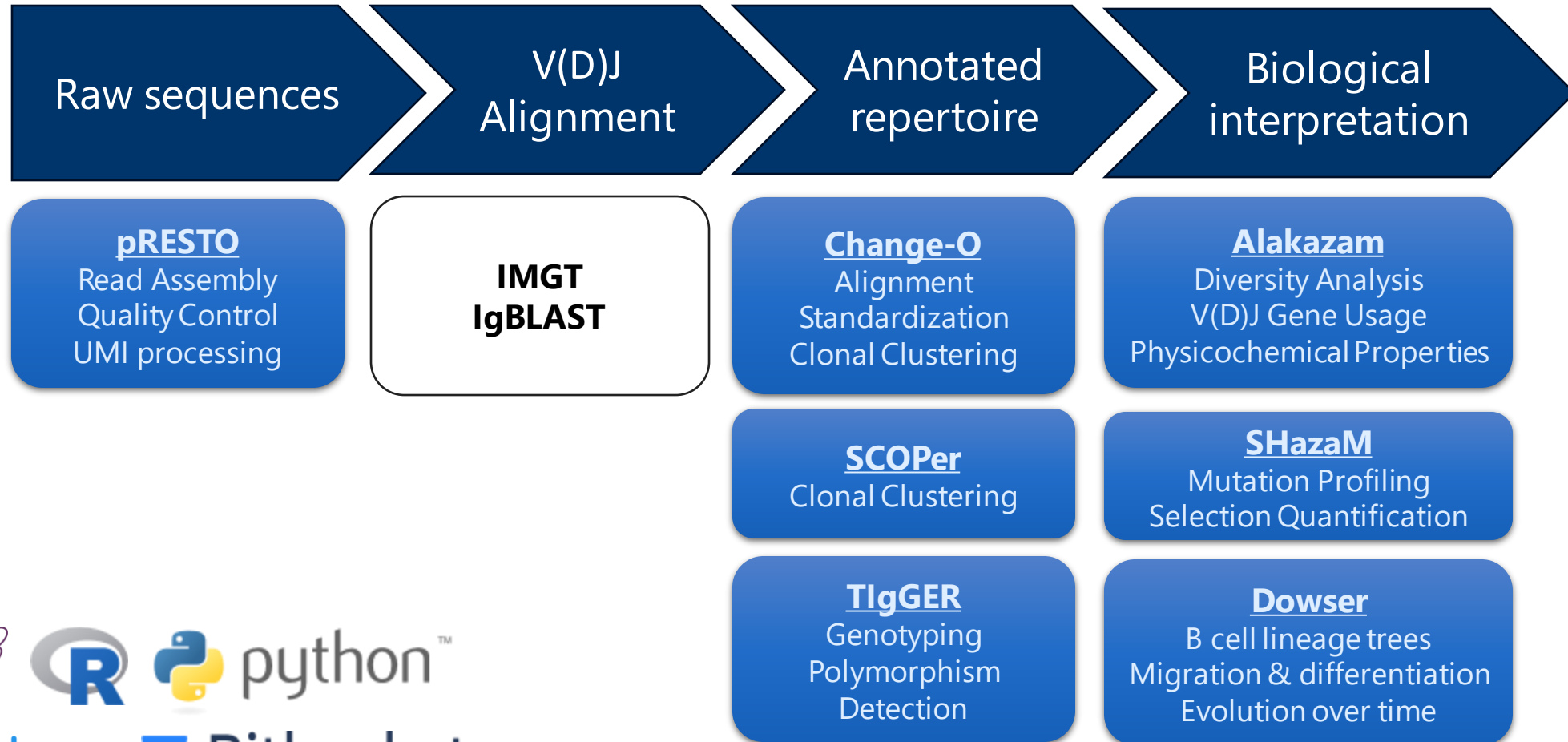
We are always open to new collaboration opportunities with basic science and clinical research groups. Please send us an email if interested. For research updates, follow us on twitter ([@skleinstein](https://twitter.com/skleinstein)).

[Read more about our research](#)

Yale SCHOOL OF MEDICINE

<https://medicine.yale.edu/lab/kleinstein>

# Start-to-finish analytical ecosystem



python™



[immcantation.org](http://immcantation.org) | [immcantation@googlegroups.com](mailto:immcantation@googlegroups.com) | <http://airr-community.org>

AIRR-C sw-tools v1 compliant



# New in 4.5.0

## Version updates

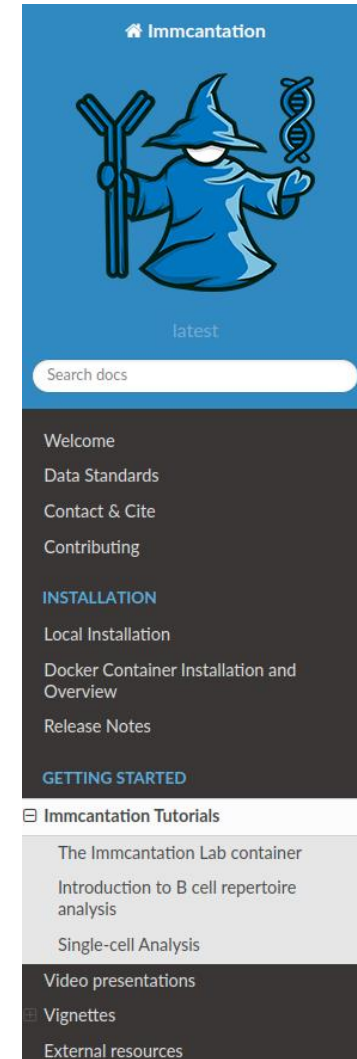
- alakazam: 1.3.0
- presto: 0.7.2
- shazam: 1.2.0
- tigger: 1.1.0
- scoper: 1.3.0
- dowser: 2.1.0

## .Rmd tutorials

- Introduction to B cell repertoire analysis
- 10x Genomics V(D)J Sequence Analysis with Immcantation
- Integration of BCR and GEX data

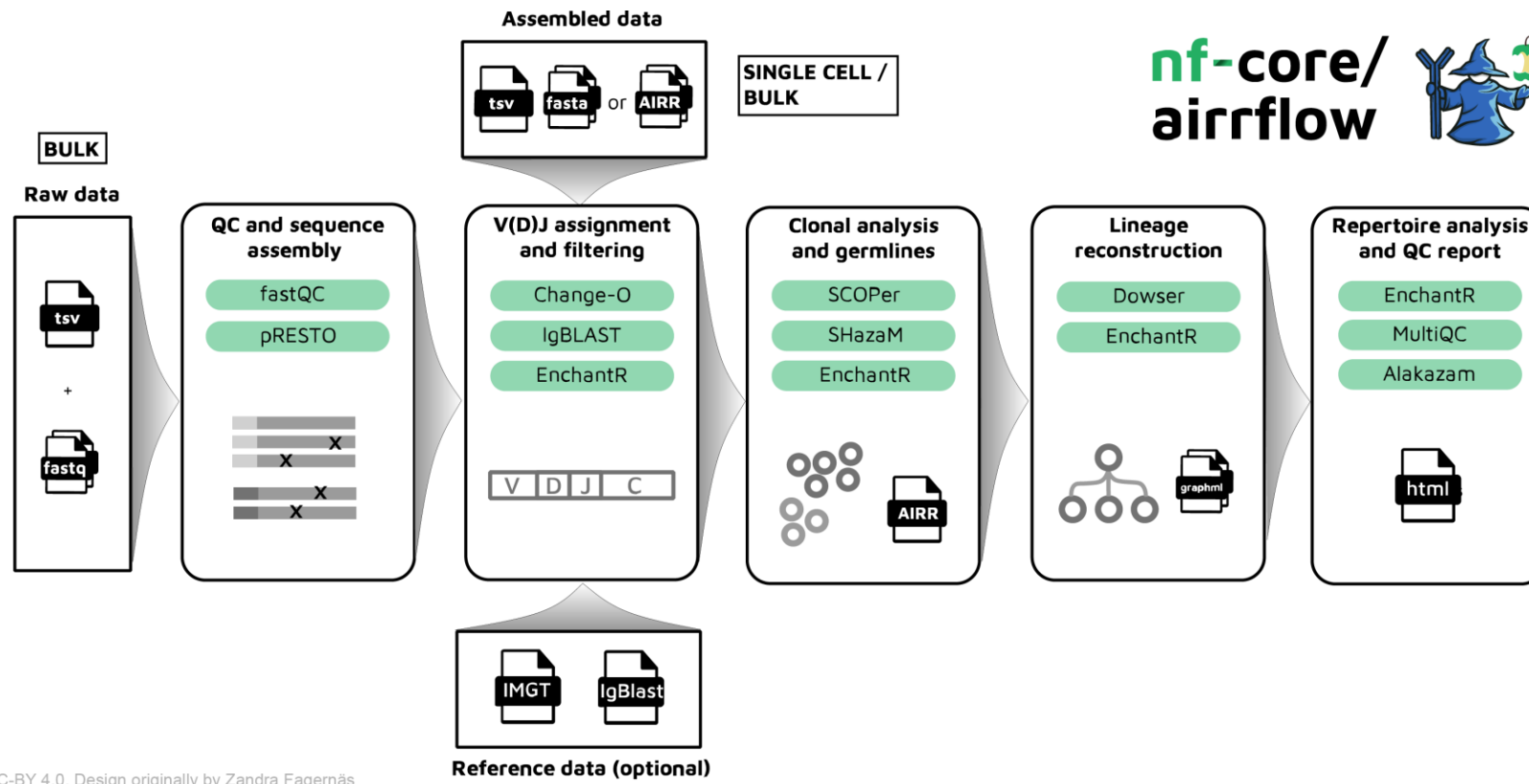
## Future

- Improve and expand single cell methods
- Tutorials
- Documentation
- Integrated analysis with workflows
- Support for spatial (looking for more collaborators)



# nf-core/airrflow: an Immcantation workflow

A best-practices workflow for bulk and single-cell AIRR-seq data analysis





# nf-core/airrflow: an Immcantation workflow

nextflow

**Portable** – supports a variety of computing infrastructures



**Reproducible** – supports multiple container engines



**Continuous checkpoints** – allow pipeline resuming



**Implicit parallelism** – processes samples in parallel



nf-core

Community-curated open-source Nextflow workflows



**Stable releases** – with Zenodo DOI



**Extensive documentation** – on the nf-core site



**Continuous integration tests** – on commits and releases



**Community code review** – of new code

# nf-core/airrflow: single-cell data processing

Example of assembled data processing (single-cell and/or bulk):

```
nextflow run nf-core/airrflow -r 3.2.0 \
-profile <docker/singularity/...> \
--mode assembled \
--input samplesheet.tsv \
--outdir results
```

- Direct output from Cell Ranger (AIRR rearrangement table)
- Assembled sequences in fasta format

Example sample sheet

sample_id	filename	subject_id	species	pcr_target_locus	tissue	sex	age	biomaterial_provider	single_cell
sample01	sample1_AIRR.tsv	Subject2	human	IG	blood	NA	53	sequencing_facility	TRUE
sample02	sample2.fasta	Subject2	human	IG	blood	female	78	sequencing_facility	FALSE

# nf-core/airrflow: future directions

## Future directions

- Common protocols profiles for common sequencing kits

```
nextflow run nf-core/airrflow -r dev \  
-profile NEB,<docker/singularity/...> \  
--input samplesheet.tsv \  
--outdir results
```

- Include TRUST4: extracting BCR/TCR sequences from RNAseq and scRNAseq data
- Contributions and suggestions welcome!

## BioRxiv pre-print



<https://nf-co.re/airrflow>



<https://nf-co.re/join>

**nf-core slack** – #airrflow



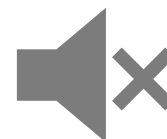
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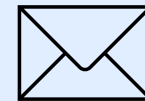
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# Thanks everyone for coming!!

- We will send out speaker answers to unanswered questions as well as a copy of these slides.
- Please fill out the post-event survey (it will be emailed out to all registered people)! We greatly appreciate your feedback.
- The videos (for everyone who agreed to be recorded) will be available online on the Immcantation YouTube.



<https://immcantation.readthedocs.io>



[immcantation@googlegroups.com](mailto:immcantation@googlegroups.com)



# AIRR Community Meeting VII

## LEARNINGS AND PERSPECTIVES



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

[tinyurl.com/airrcmeeting7](https://tinyurl.com/airrcmeeting7)



The deadline for software demonstrations and tutorial abstract proposals is **January 31st, 2024**.

The deadline for posters and short contributed talks is **February 15th, 2024**.