

# T-cell repertoire annotation and motif discovery

An AIRR-Seq data analysis tutorial in R

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# Outline

Introduction

Setting

Interactive part

Concluding remarks

# Aims of this tutorial

**Aim1** Learn how to infer T-cells specific to certain epitopes and extract T-cell receptor (TCR) sequence motifs from high-throughput sequencing data (AIRR-Seq).

**Aim2** Get familiar with VDJdb database, VDJtools software and some useful R templates for TCR sequence analysis.

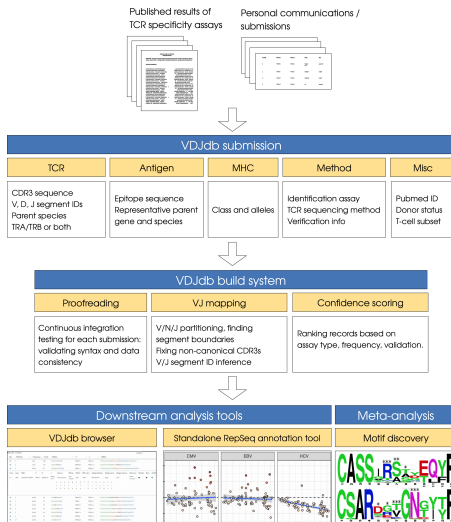
**Disclaimer** This tutorial will not cover AIRR-Seq data processing and basic<sup>1</sup> analysis.

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<sup>1</sup>Repertoire diversity analysis, segment usage, etc. See **Examples** section of VDJtools docs for this.

# VDJdb database

VDJdb is a curated database of T-cell receptor sequences of known antigen specificity that can be accessed at <http://vdjdb.cdr3.net>



# Clonotype tables

We define a clonotype as a unique combination of Variable (V) and Joining (J) segment and CDR3nt sequence observed in our sequencing data.

Index	Frequency	Count	CDR3AA	V	D	J	CDR3NT
1	1.0%	3913	CSAGGLGSTDQYF	TRBV20-1	TRBD1	TRBJ2-3	TGCAGTGCTGGGGGGCTCGGTAGCACAGATACGCAGTATTTT
2	0.90%	3440	CASNSSSYNEQFF	TRBV5-1	TRBD2	TRBJ2-1	TGCGCCAGCAATAGCGGGAGCTCTACAATGAGCAGTCTTC
3	0.79%	3021	CSARQGNQPHF	TRBV20-1	TRBD1	TRBJ1-5	TGCAGTGCGCGACAGGGGAATCAGCCCCAGCATTTT
4	0.65%	2490	CASSQEPGGEQFF	TRBV4-1	TRBD2	TRBJ2-1	TGCGCCAGCAGCCAAGAGCCGGGCGGGGAGCAGTCTTC
5	0.61%	2336	CASSYGMNTEAFF	TRBV6-6	TRBD2	TRBJ1-1	TGTGCCAGCAGTTACGGGATGAACACTGAAGCTTTCTTT
6	0.52%	1992	CASSQGGRAPTHQYF	TRBV4-3	TRBD2	TRBJ2-3	TGCGCCAGCAGCCAAGGGGGAGGGCCCCCATACGCAGTATTTT
7	0.49%	1871	CASSQSGGSYEQYF	TRBV5-1	TRBD1	TRBJ2-7	TGCGCCAGCAGCAAAGTCAAGGGGGGTCTCTACGAGCAGTACTTC
8	0.48%	1847	CASSRPKSGRSGELFF	TRBV11-2	TRBD2	TRBJ2-2	TGTGCCAGCAGCCGACCCAAGAGCGGGAGAAAGTGGGGAGCTGTTTTTT

# TCR motif inference

Motif inference in present tutorial is based on the TCR neighbor enrichment test (TCRNET) implemented in VDJtools.

TCRNET scans TCR sequence graph from a sample of interest and detects nodes having a degree higher than would be expected from placing a given node in the control sample.

# Test for TCR neighbor enrichment

Let  $n_i^s$  be the number of clonotypes in sample  $s$  that differ from  $i^{\text{th}}$  clonotype by no more than  $d = 1$  substitutions in the CDR3aa sequence.<sup>2</sup>

Let  $N_i^s$  be the total number of clonotypes having the same V/J segments as  $i^{\text{th}}$  clonotype in sample  $s$ .

Select clonotypes with more neighbors than expected by chance by assuming that

$$n_i^s \stackrel{H_0}{\sim} \text{Poisson} \left( N_i^s \frac{n_i^c}{N_i^c} \right) \quad (1)$$

where  $c$  is the control sample.

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<sup>2</sup>They don't have to have the same V/J segments

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# Dataset

We'll use AIRR-Seq data from Emerson et al. Nat Genet 2017

<b>Sample</b>	<b>ID</b>	<b>a1</b>	<b>a2</b>	<b>b1</b>	<b>b2</b>	<b>status</b>
B35+	HIP02877	A*26	A*33	B*14	B*35	CMV-
CMV+	HIP13994	A*02	A*02	B*07	B*44	CMV+
Control-1	HIP03484	A*02	A*02	B*07	B*58	CMV-
Control-2	HIP03592	A*02	A*32	B*07	B*39	CMV-
Control-3	HIP04532	A*02	A*24	B*07	B*51	CMV-
Control-4	HIP04576	A*02	A*30	B*07	B*18	CMV-

# Experiment - 1

Comparing B35+ sample versus samples without this allele

<b>Sample</b>	<b>ID</b>	<b>a1</b>	<b>a2</b>	<b>b1</b>	<b>b2</b>	<b>status</b>
B35+	HIP02877	A*26	A*33	B*14	B*35	CMV-
CMV+	HIP13994	A*02	A*02	B*07	B*44	CMV+
Control-1	HIP03484	A*02	A*02	B*07	B*58	CMV-
Control-2	HIP03592	A*02	A*32	B*07	B*39	CMV-
Control-3	HIP04532	A*02	A*24	B*07	B*51	CMV-
Control-4	HIP04576	A*02	A*30	B*07	B*18	CMV-

## Experiment - 2

Comparing CMV+ and CMV- samples for A\*02 and B\*07

<b>Sample</b>	<b>ID</b>	<b>a1</b>	<b>a2</b>	<b>b1</b>	<b>b2</b>	<b>status</b>
B35+	HIP02877	A*26	A*33	B*14	B*35	CMV-
CMV+	HIP13994	A*02	A*02	B*07	B*44	CMV+
Control-1	HIP03484	A*02	A*02	B*07	B*58	CMV-
Control-2	HIP03592	A*02	A*32	B*07	B*39	CMV-
Control-3	HIP04532	A*02	A*24	B*07	B*51	CMV-
Control-4	HIP04576	A*02	A*30	B*07	B*18	CMV-

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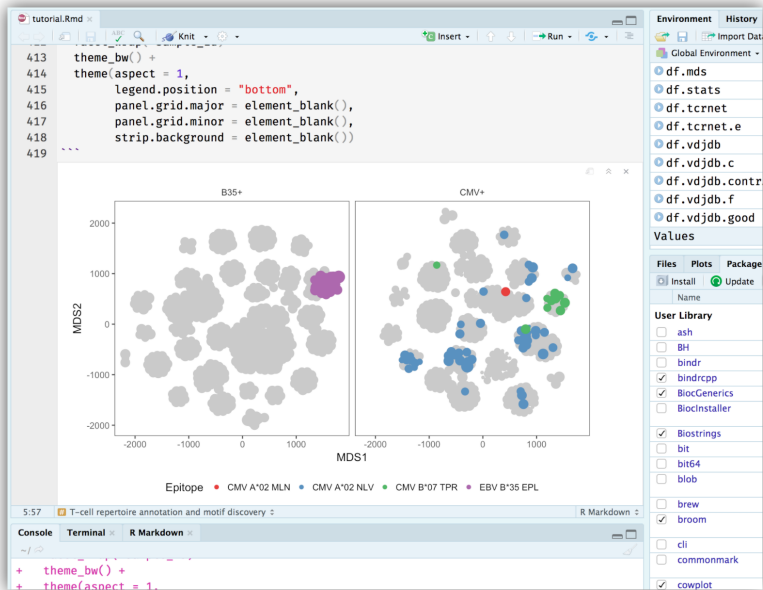
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# Interactive part



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# Overview

- ▶ Annotated our samples with VDJdb and quality-filtered results
- ▶ Filtered annotation results based on our allele of interest (HLA-B35) or donor status (CMV+)
- ▶ Inferred antigen-specific clonotype groups using TCRNET algorithm in VDJtools
- ▶ Overlapped VDJdb annotations and TCRNET results and extract CDR3 sequence motifs

# Potential pitfalls

- ▶ Repertoires are extremely diverse making TCR annotation an imbalanced classification problem. Even when matching against VDJdb with high specificity<sup>3</sup> one will observe many false-positives.

Use proper controls, e.g. naive T-cells

- ▶ TCRNET will fail in some cases simply because the repertoire of T-cells specific to a given antigen is dominated by a single hyperexpanded clonotype.

Always annotate and check large clonotypes

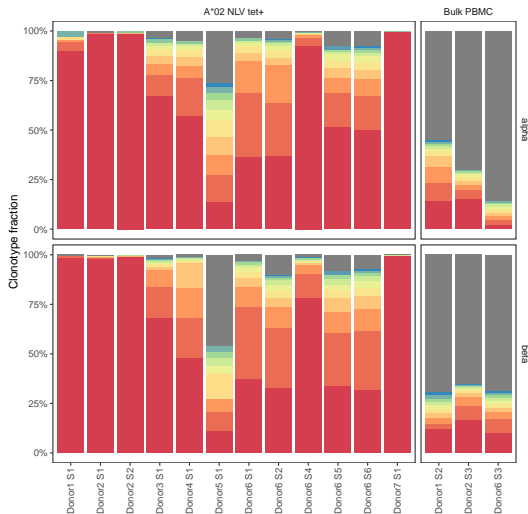
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<sup>3</sup>According to VDJdb benchmark odds of matching the same epitope given 1 substitution in CDR3 $\beta$  are around 200+ to 1



# Note on CMV-specific clonotypes

Diverse repertoire of dissimilar TCRs, individuals are likely to carry a single hyperexpanded clonotype with no subvariants



*Thank you for listening!*

## Contacts



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