

Vidjil, une plateforme web pour l'étude de populations lymphocytaires par NGS

Aurélien Béliard, Marc Duez, Mathieu Giraud, Ryan Herbert,
Tatiana Rocher, Mikaël Salson, Florian Thonier



Bonsai bioinformatics
CRISAL (Université Lille, CNRS), Inria, GBMHM/Inca

Hôpital Rennes
GBMHM/Inca

June 23, 2017
contact@vidjil.org

Conflicts of interest

MS : Novartis funded his living expenses for a 2-day workshop in Dieppe, France

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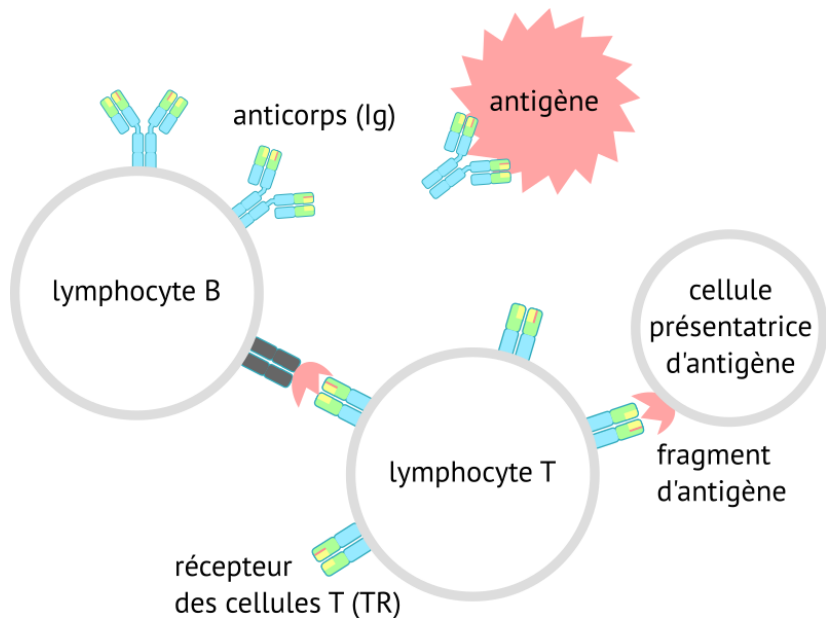
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Immune Repertoire Sequencing (RepSeq)

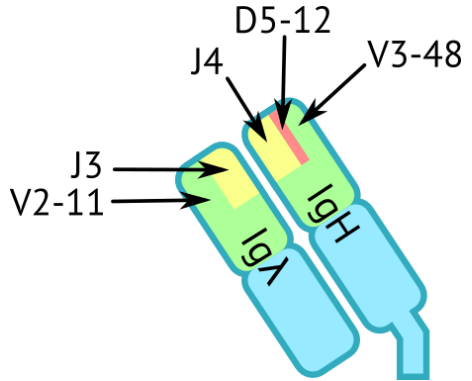
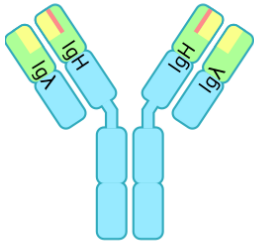
1. Monitor the immune response (vaccine, immunotherapy)

2. Identify markers for leukemia stratification and follow-up

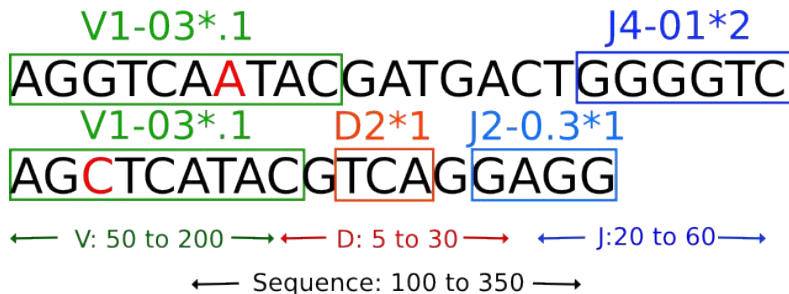
The Adaptive Immune System



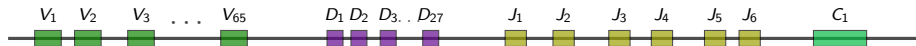
TCR and Antibody Specificity – V(D)J Recombination



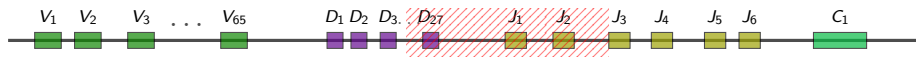
TCR and Antibody Specificity – V(D)J Recombination



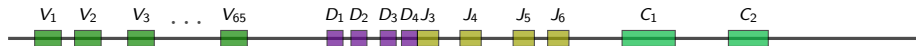
V(D)J recombinations are responsible for receptor diversity



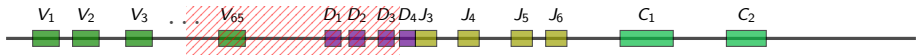
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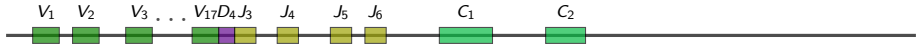
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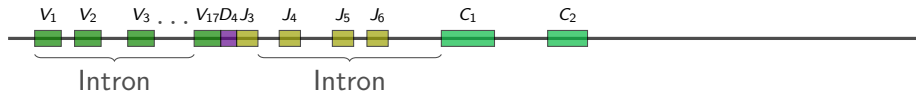
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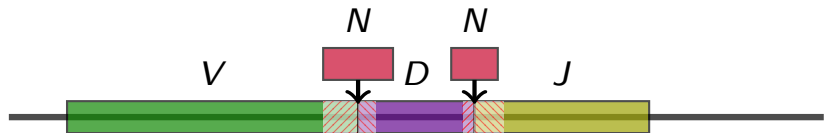
V(D)J recombinations are responsible for receptor diversity



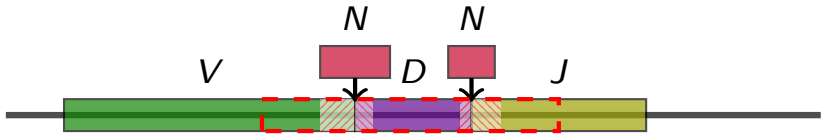
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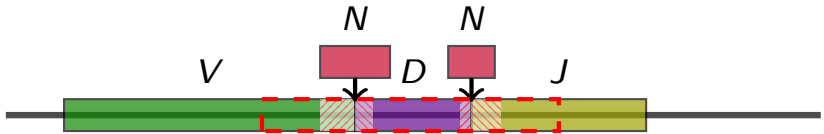


V(D)J recombinations are responsible for receptor diversity

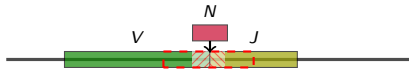


Diversity region

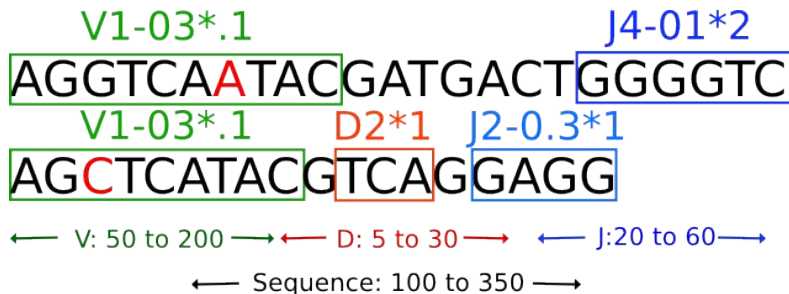
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Diversity region

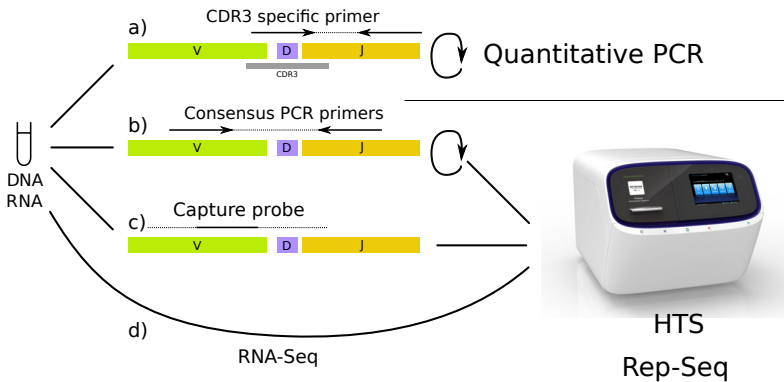


TCR and Antibody Specificity – V(D)J Recombination



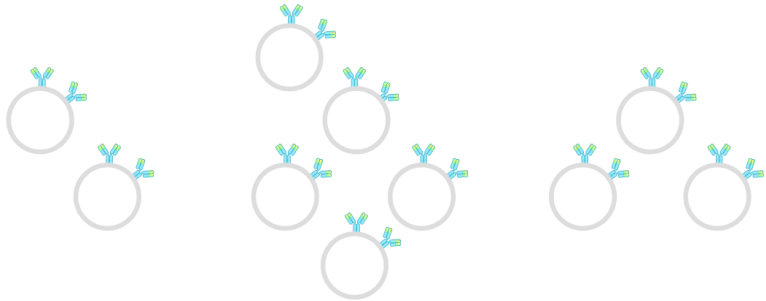
Immune Repertoire Sequencing (RepSeq)

Strategies – Sequencing millions of V(D)J recombinations from T-cells or B-cells



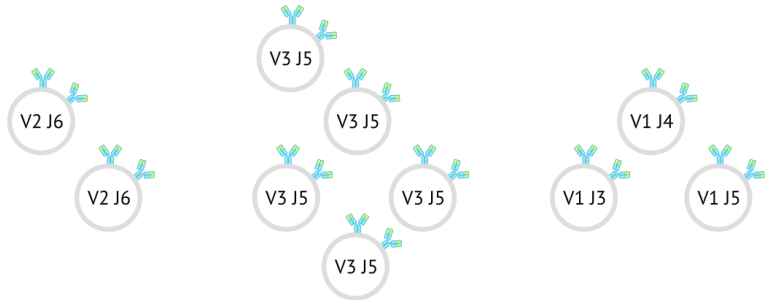
Immune Repertoire Sequencing (RepSeq)

Identification of all VDJ recombinations



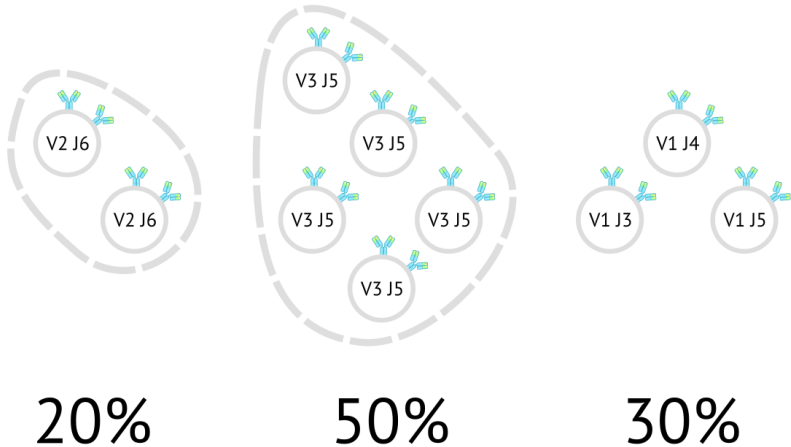
Immune Repertoire Sequencing (RepSeq)

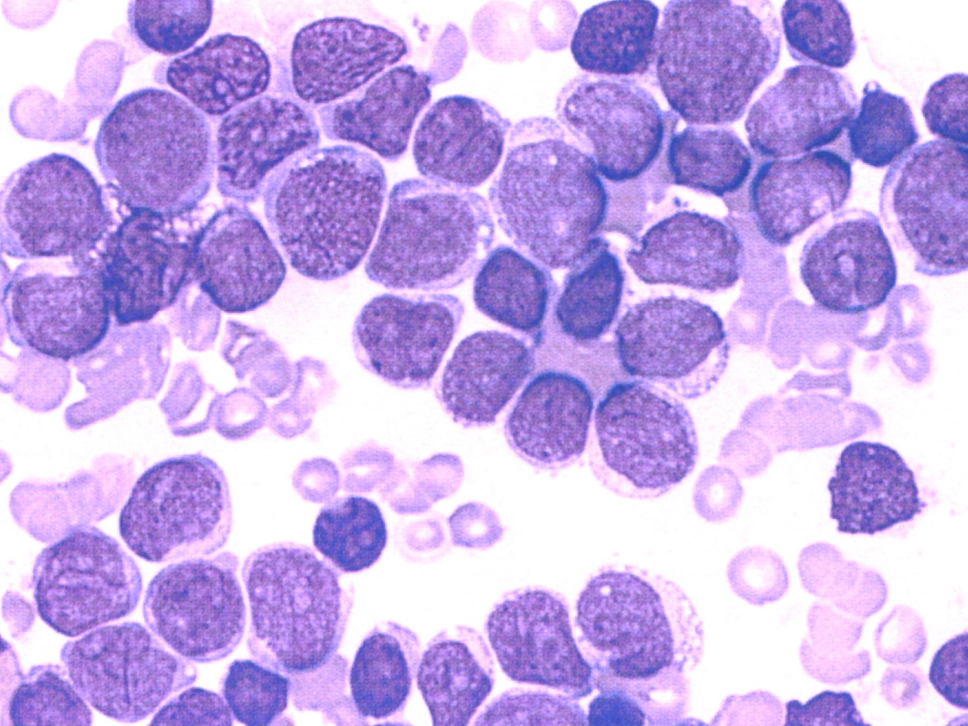
Identification of all VDJ recombinations



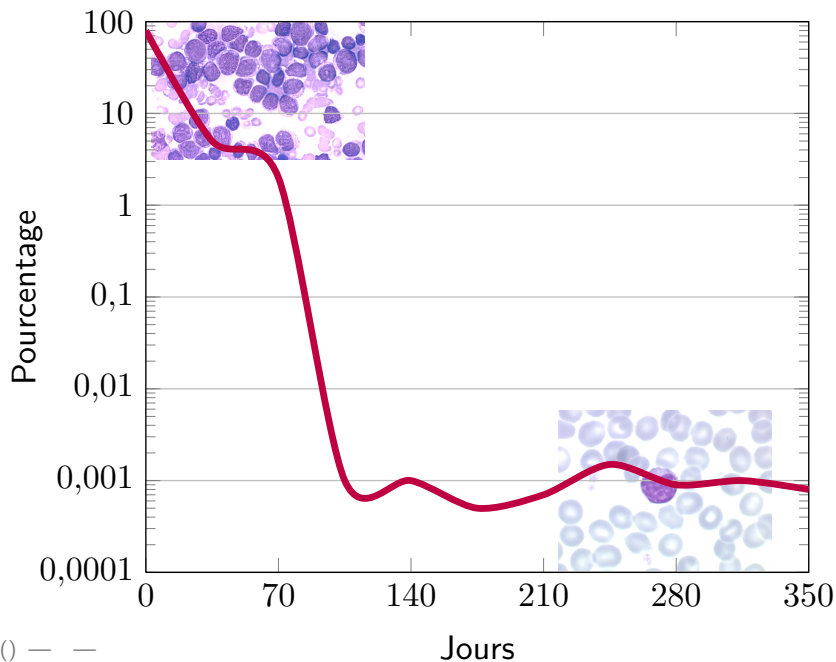
Immune Repertoire Sequencing (RepSeq)

Identification of all VDJ recombinations

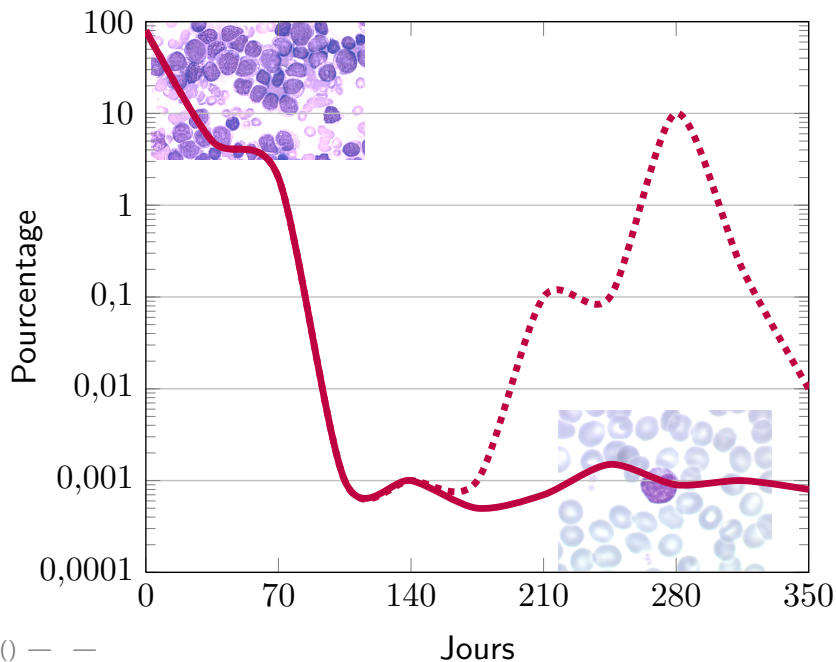


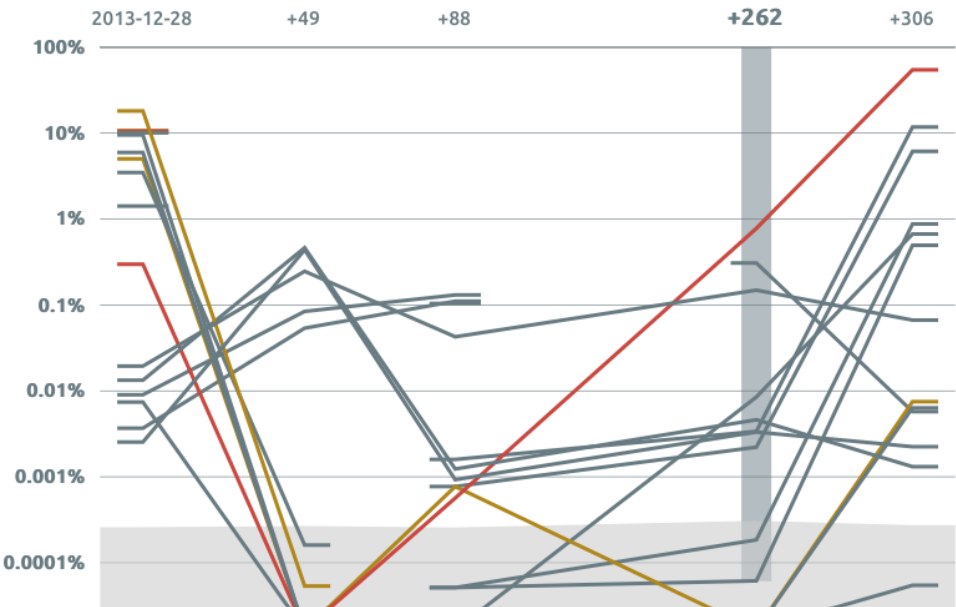


Concentration du lymphocyte cancéreux



Concentration du lymphocyte cancéreux





A strong collaboration with Lille hospital since 2011

M. Figeac

TTATTATAAG

S. Sebda

A. Caillault

N. Duployez

N. Grardel

C. Preudhomme

V8 CCTG

AGG

CTGGGAC

V8 CCT

CCTGGGAC

V4

CCTGGGGATGGG

V2

CCTGG

V5

CCTGGGGG

V3

CCTGGGAT

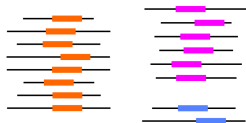
Vidjil Platform

High-throughput Repertoire Sequencing (RepSeq) analysis

Web Application

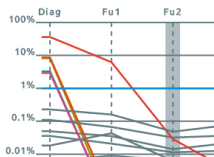
Patient database
Server

Algorithm

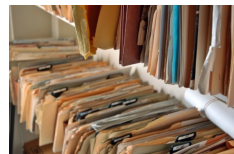


C++

Client



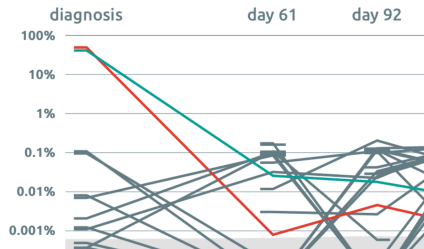
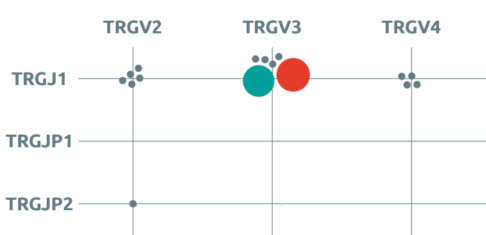
Javascript, d3.js



Python, web2py,
AJAX

- ▶ all the Vidjil components are open-source (GPL v3)
- ▶ code on <http://www.vidjil.org/> and on GitHub
- ▶ continuous integration, > 2,000 unit and functional tests

Duez et al., PLOS One, 2016



merge align > to IMGT/V-QUEST > to IgBlast > to Blast

4 clones, 738 494 reads (90.53%)

× TRGV3 1/11/2 J1	49.30%	★ i	GCCACCTGGGACAGCTCCC-TT-GTTC--ATTATAAGAAACTCTTTGGCAGTG
× TRGV3 4/1/2 J1	41.23%	★ i	GCCACCTGGG--A--T--A--T---T---ATTATAAGAAACTCTTTGGCAGTG
× TRGV3 3/16/3 J1	0.0021%	★ i	GCCG-CTTGGGA-ACCCCAATTTGGTACGGGTATAAGAAACTCTTTGGCAGTG
× TRGV3 5/4/2 J1	+	★ i	GCCACCTGGG---GC--CA-A-T---T---A-TA--AGAAACTCTTTGGCAGTG

Web application: traceability– Reports for medical records

Sample info (IonXpress_086)

Filename: IonXpress_086.L1413629.fastq
Sample date: 2014-12-19
Software used: vidjil dev 0cf35de (2015-02-17)
Parameters: -i -g germline -c clones -z 100 -r 1
Analysis date: 2015-02-17 21:50:09

User note

PCR avec 250ng d'ADN, Ion Fgt+ 50µL

Reads distribution

total

segmented

■ TRG
■ IGK+
■ VdJa
■ IGH
■ TRD+

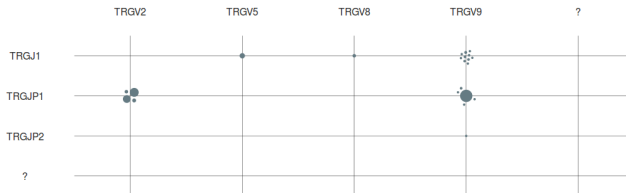
IonXpress_086

632 686

88%

29%
55%
7%
5%
5%

IonXpress_086 – TRG



>TRGV9*01 -8/10/-3 TRGJP1*01

13.44% (45.99% of TRG)

CGGCACTGTCAGAAAGGAATCCGGCATTCCGTCAGGCAAAATTTGAGGTGGATAGGATACCTGAAACGTCTACATCCACTCTCAACATTGAGAGAAACAGGACATAGCT
ACCTACTACTGTGCGCTGT CTTACAGAGGG CCACTGGTTGGTTCAAGATATTTGCTGAAGGGACTAAGCTCATAGTAACTTCGCGCTGGTAA

>TRGV2*01 -9/6/-1 TRGJP1*01

5.062% (17.32% of TRG)

GGAAAGGCCCAACAGCTCTTCAGTACTATGACTCTCAAACTCCAAGGTTGTGTGGAAATCAGGAGTCAGTCCAGGGAAGTATTATACCTTACGCAAGCACAAGGAACAACCTGAG
ATTGATACCTCGAAATCTAAATTGAAATGACTTTGGGGTCTATTACTGTGCCACC CCTGG TACCACCTGGTTGGTTCAAGATATTTGCTGAAGGGACTAAGCTCATAGTAA
CTTCGCGCTGGTAA



Patient database and server

Autonomous RepSeq analysis pipeline in a clinical/research lab



Patient database and server

Autonomous RepSeq analysis pipeline in a clinical/research lab



Upload

upload list

L1413893.fasta



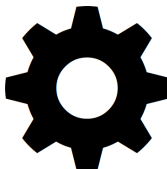


Patient database and server

Autonomous RepSeq analysis pipeline in a clinical/research lab



Upload



Process

upload list

L1413893.fasta



last processing status

2015-02-09

RUNNING

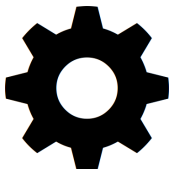


Patient database and server

Autonomous RepSeq analysis pipeline in a clinical/research lab



Upload



Process



Analyze

upload list

L1413893.fasta



last processing status

2015-02-09

RUNNING

see the result:

[multi](#)

2015-02-09

Web Application, October 2014 to June 2017

Public test server app.vidjil.org, >100 users, including **30 regular users**

10,000
samples

Web Application, October 2014 to June 2017

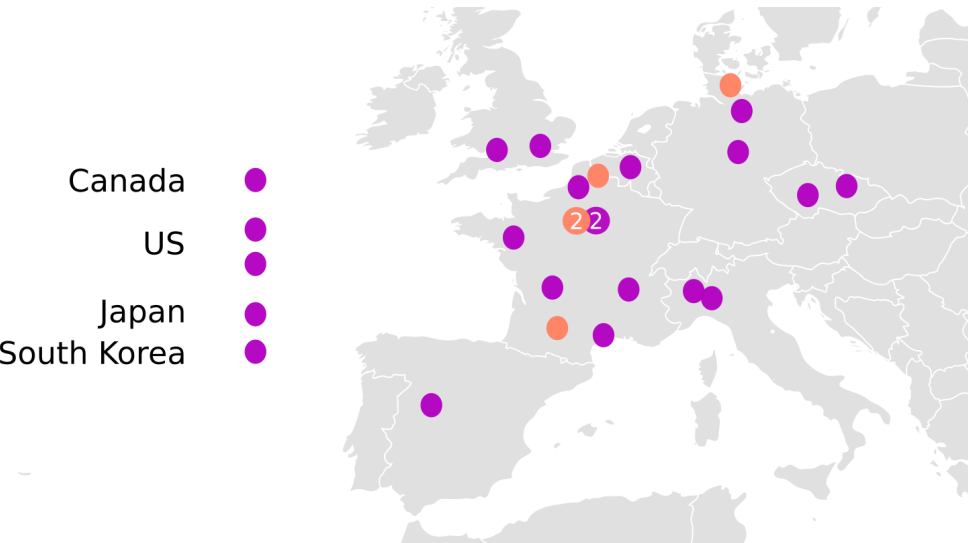
Public test server app.vidjil.org, >100 users, including **30 regular users**

1,000

ALL/CLL patients at diagnosis in 5 labs

Web Application, October 2014 to June 2017

Public test server app.vidjil.org, >100 users, including **30 regular users**



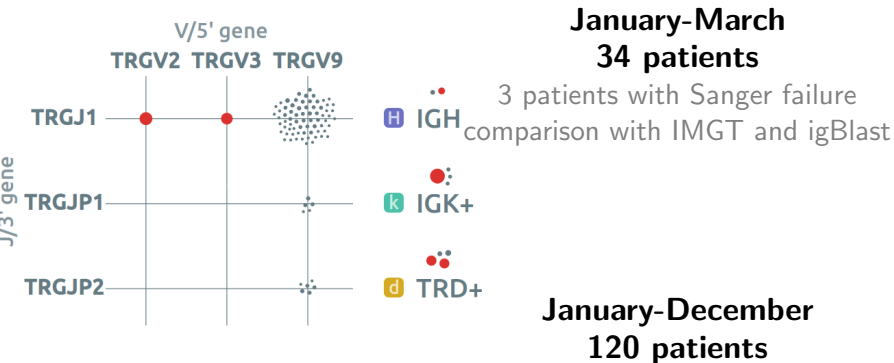
Web Application, October 2014 to June 2017

Public test server app.vidjil.org, >100 users, including **30 regular users**



Lille, 2015: routine diagnosis of patients with ALL

5 tubes, mainly BIOMED-2 primers



Analyze your immune repertoire data with **Vidjil**

Interactively process all lymphocyte receptors

Ready-to-use platform to handle HTS/RepSeq data

1. Upload, 2. Process, 3. View and Annotate

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Open-source software

Feel free to use: `app.vidjil.org`

Feel free to contribute: `git.vidjil.org`

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New academic and industrial collaborations

ALL/CLL diagnosis and follow-up, other pathologies

Immunological studies, immune monitoring