



Instituto Nacional de Saúde
Doutor Ricardo Jorge



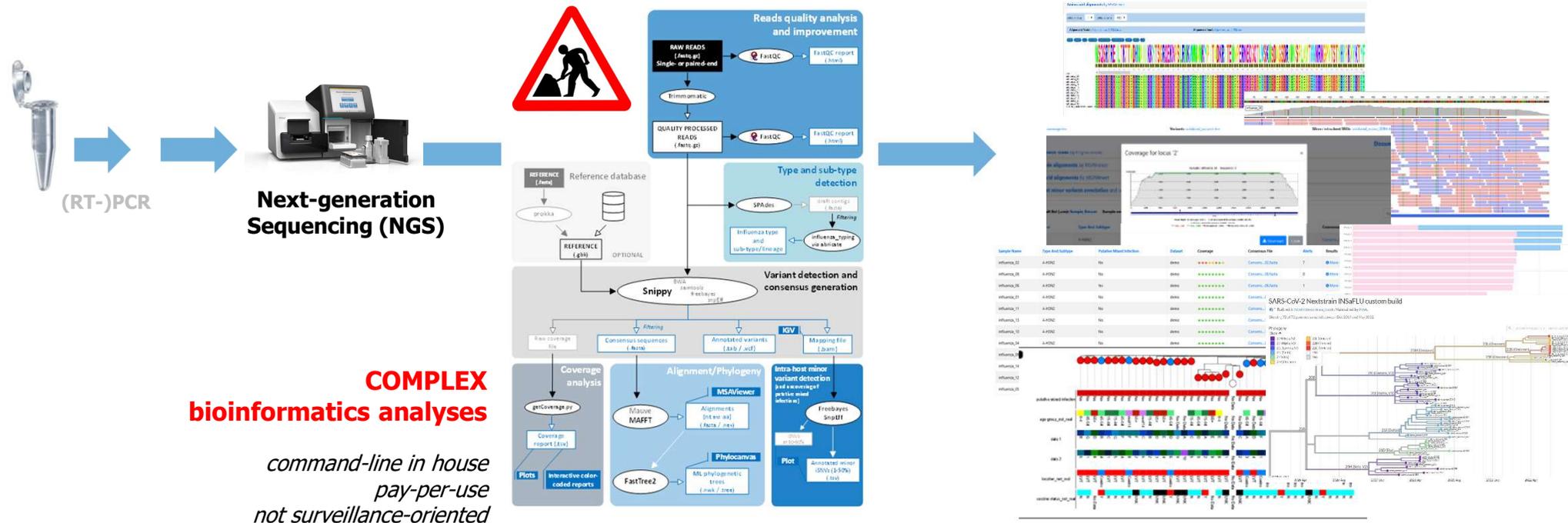
INSaFLU-TELEVIR platform

Vítor Borges

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Department of Infectious Diseases
Genomics and Bioinformatics Unit

New era of virus detection and surveillance

Next-generation sequencing



Key challenges in adopting the new methodology include handling large data volumes that require advanced bioinformatics tools, infrastructure and expertise, etc.

New era of virus detection and surveillance

Next-generation sequencing



(RT-)PCR



Next-generation
Sequencing (NGS)



illumina®

iontorrent

Oxford
NANOPORE
Technologies



Documentation

From "reads" to WGS-based first-line influenza laboratory surveillance

INSaFLU (INSaFLU the FLU) is an influenza-specific, bioinformatics free web-based suite that deals with primary data (reads) towards the automatic generation of the output data that are actually the core first-line 'genomic requests' for effective and timely influenza laboratory surveillance (e.g. type and sub-type, gene and whole-genome consensus sequences, variants annotation, alignments and phylogenetic trees). Data integration is continuously scalable, fitting the need for a real-time epidemiological surveillance during the flu epidemics.

Future DIRECTIONS

How to cite

Contacts

Useful links

<https://insaflu.insa.pt>

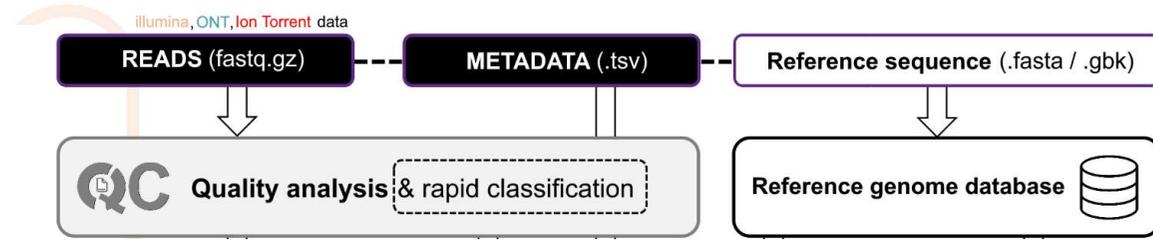


Borges V et al., (2018) Genome Medicine; 10:46
<https://doi.org/10.1186/s13073-018-0555-0>

GOAL: To supply public health laboratories and researchers around the world with an open and user-friendly bioinformatics framework for virus NGS data analysis.



<https://onehealthjp.eu/jrp-tele-vir/>



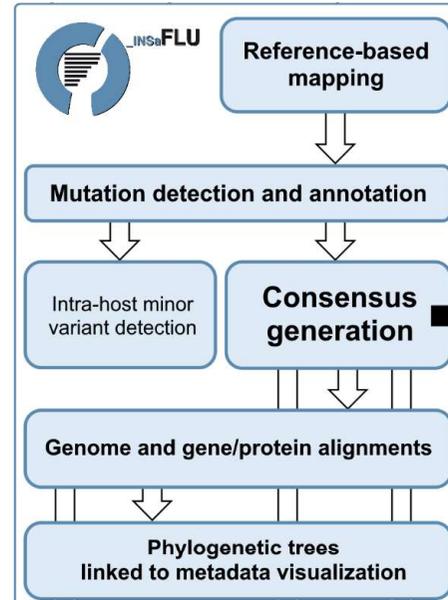
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Dourado Santos V et al., (2024) Genome Medicine; 16:61
<https://doi.org/10.1186/s13073-024-01334-3>

INSaFLU Upgraded "INSaFLU"

- ONT pipeline, alternative to Illumina pipelines
- Rapid Classification of key pathogens (influenza, Mpox, CoVs, RSV, DENV)
- Automate Nextclade linkage
- Algn2pheno
- Avian influenza mutation detection (FLUmut)

etc



New module Nextstrain



TELEVIR New module TELEVIR

- Released findONTIME



Species-specific feature Database



INSaFLU-TELEVIR

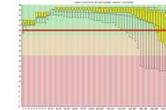
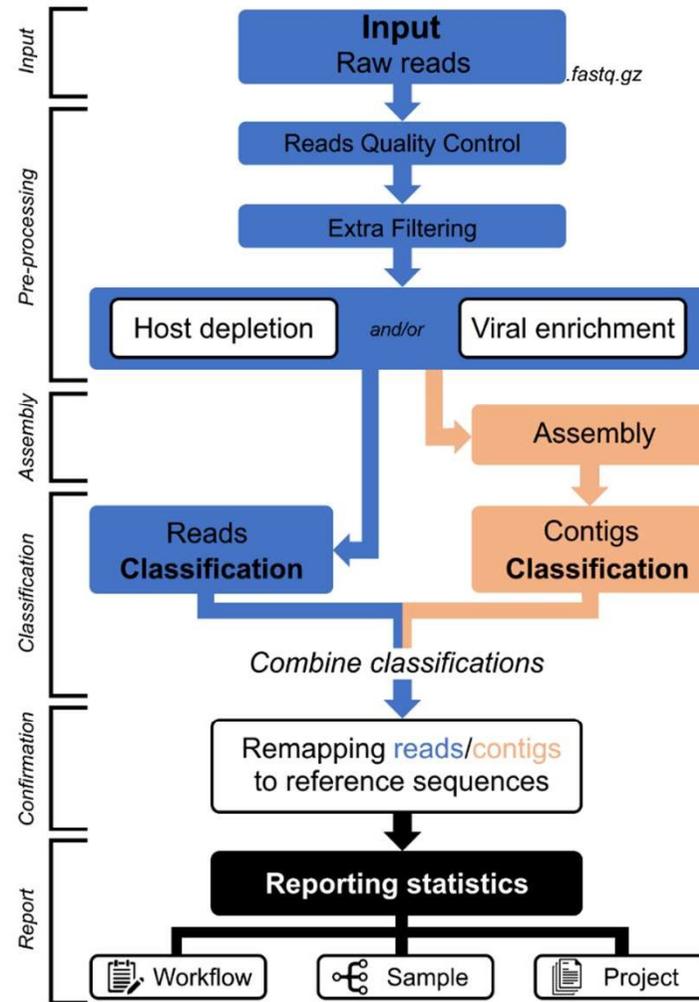
<https://insaflu.insa.pt/>



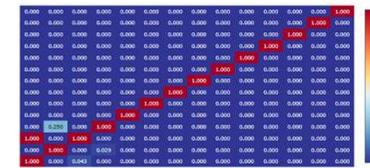
illumina

iontorrent

Oxford NANOPORE Technologies



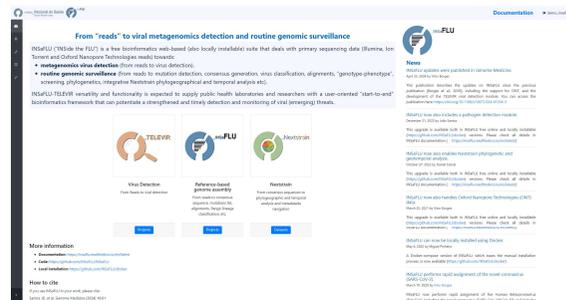
Contig 1: ATGGACGAGTAGGGTATGAAGTATTCTGGAACGAGACACTCAGCGATACGGAGTGAAT
 Contig_2: ACAGTAGAAACTATTCTCATGTAGTTCGACGACTTTAAACATTCGTATTGATCTAAAGI
 Contig_3: TGCTGAAAAGTAAAGTTCAGATTCAATCCGCTAGGGCGTAGACACTGAATTCGATGGGGA
 Contig_4: ATGAGCCCGCTCGACTCGATCGACTGACGCTATCTGTATCTAGCTATGCGTACTCTGC
 Contig_5: AAGAGGTTATTCAAATAAAAAAACACGCTCTATTTTTTCGACGTTGACTGCTCAAGGAGI



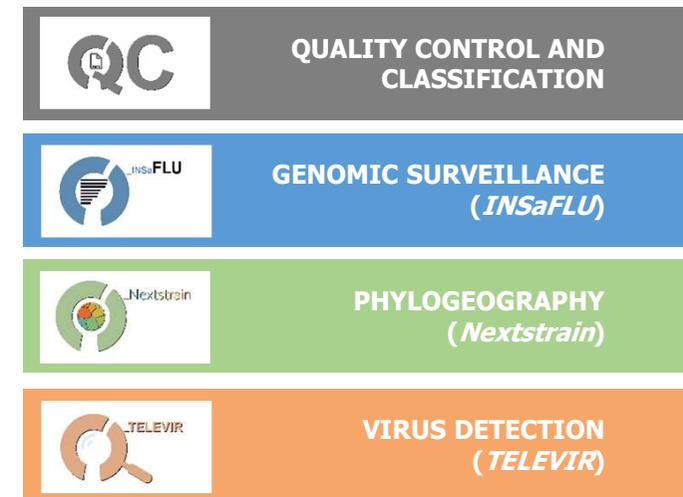
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New era of virus detection and surveillance

Metagenomics diagnosis and Whole-genome sequencing



<https://insaflu.insa.pt>

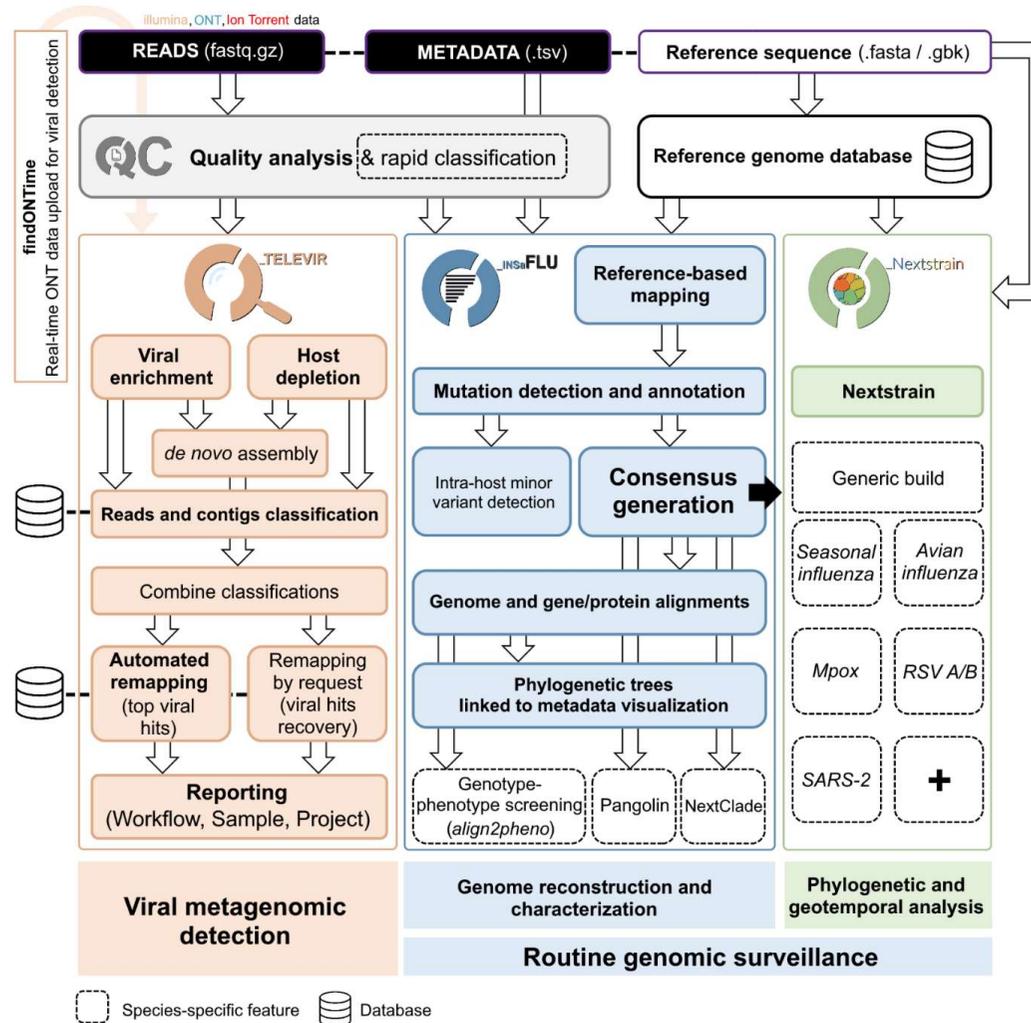


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GOAL: To supply public health laboratories and researchers around the world with an **open and user-friendly bioinformatics framework** for **viral metagenomic detection** and **routine genomic surveillance**

INSaFLU-TELEVIR

<https://insaflu.insa.pt/>



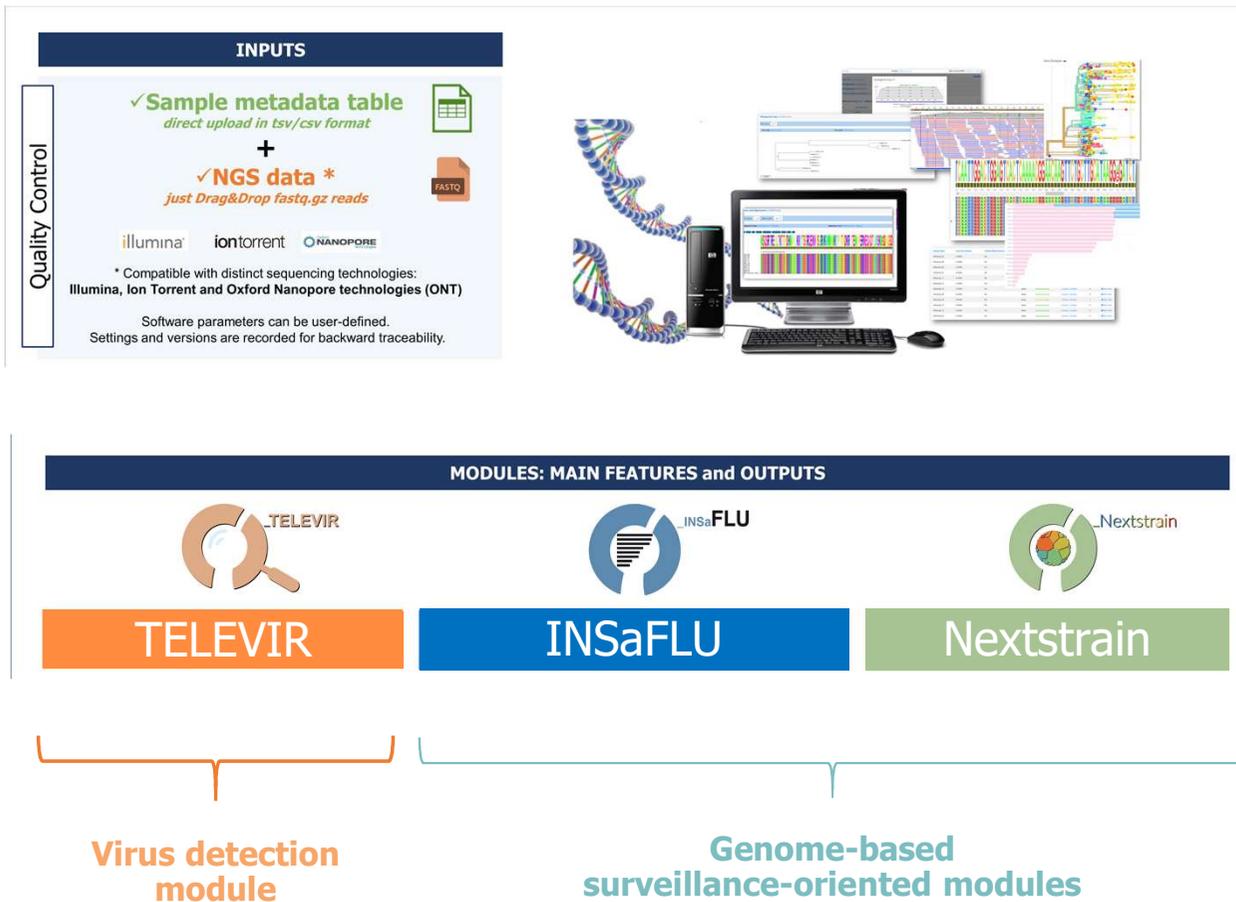
- **Online** (also installable locally)
- **Free** (confidential accounts)
- **User- and surveillance-oriented**
- **Compatible with main sequencing technologies**
- **Multiple features and workflows**

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 INSaFLU

Documentation Login

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- Projects
- Settings

From "reads" to viral metagenomics detection and routine genomic surveillance

INSaFLU-TELEVIR is a free bioinformatics web-based (also locally installable) suite that deals with primary sequencing data (Illumina, Ion Torrent and Oxford Nanopore Technologies reads) towards:

- **metagenomics virus detection** (from reads to virus detection).
- **routine genomic surveillance** (from reads to mutation detection, consensus generation, virus classification, alignments, "genotype-phenotype", screening, phylogenetics, integrative Nextstrain phylogeographical and temporal analysis etc).

INSaFLU-TELEVIR versatility and functionality is expected to supply public health laboratories and researchers with a user-oriented "start-to-end" bioinformatics framework that can potentiate a strengthened and timely detection and monitoring of viral (emerging) threats.



Virus Detection
From Reads to viral detection

Projects



Reference-based genome assembly
From reads to consensus sequence, mutations list, alignments, Pango lineage classification, etc.

Projects



Nextstrain
From consensus sequences to phylogeographic and temporal analysis and metadata navigation

Datasets

Walkthrough INSaFLU by logging into the "demo" account

More information

- **Documentation:** <https://insaflu.readthedocs.io/en/latest>

INSaFLU

News

INSaFLU updates were published in Genome Medicine.
April 25, 2024 by Vitor Borges

This publication describes the updates on INSaFLU since the previous publication (Borges et al., 2018), including the support for ONT, and the development of the TELEVIR viral detection module. You can access the publication here: <https://doi.org/10.1186/s13073-024-01334-3>

INSaFLU now also includes a pathogen detection module.
December 21, 2022 by João Santos

This upgrade is available both in INSaFLU free online and locally installable (<https://github.com/INSaFLU/docker>) versions. Please check all details in INSaFLU documentation (<https://insaflu.readthedocs.io/en/latest/>)

INSaFLU now also enables Nextstrain phylogenetic and geotemporal analysis.
October 27, 2022 by Daniel Sobral

This upgrade is available both in INSaFLU free online and locally installable (<https://github.com/INSaFLU/docker>) versions. Please check all details in INSaFLU documentation (<https://insaflu.readthedocs.io/en/latest/>)

INSaFLU now also handles Oxford Nanopore Technologies (ONT) data.
March 25, 2021 by Vitor Borges

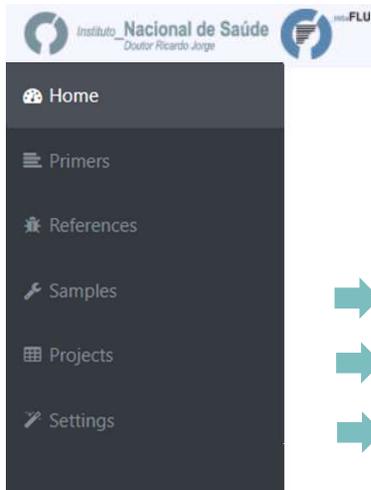
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INSaFLU can now be locally installed using Docker.
May 6, 2020 by Miguel Pinheiro

A Docker-compose version of INSaFLU which eases the manual

INSaFLU-TELEVIR

<https://insaflu.insa.pt/>



Documentation

Login

Login, please.

Please, use the browsers Firefox, Safari or Chrome for better view experience.

User name/Email*

demo

A valid user name or email

Password*

Demo login. Make a demo login. Only can view predefined data.

Login

Register

Reset password

Cancel

Get another confirmation e-mail (check your spam first)

➔ **Samples:** main repository, add/delete samples, inspect / refine QC

➔ **Projects:** TELEVIR, INSaFLU, Nextstrain

➔ **Settings:** user-defined configuration of parameters for reads QC, mapping, mutation validation, consensus generation/masking, virus detection, etc

Try it! Navigate through the demo account

Projects:

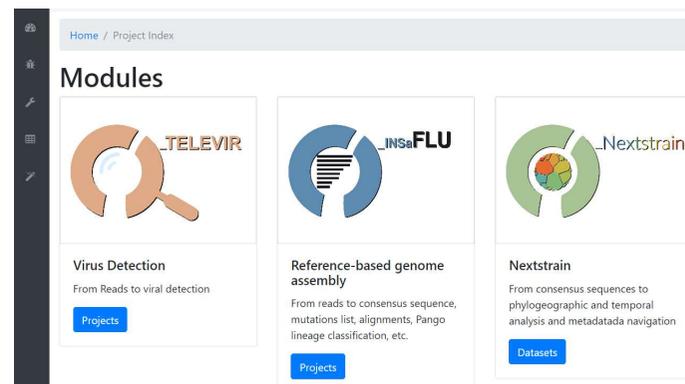
Applicable to:

illumina

iontorrent

Oxford NANOPORE Technologies

- **Online** (also installable locally)
- **Free** (confidential accounts)



Virus detection module

Genome-based surveillance-oriented modules

INSaFLU-TELEVIR

<https://insaflu.insa.pt/>



From “reads” to viral metagenomics detection and routine genomic surveillance

INSaFLU (“INSide the FLU”) is a free bioinformatics web-based (also locally installable) suite that deals with primary sequencing data (Illumina, Ion Torrent and Oxford Nanopore Technologies reads) towards:

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INSaFLU-TELEVIR versatility and functionality is expected to supply public health laboratories and researchers with a user-oriented “start-to-end” bioinformatics framework that can potentiate a strengthened and timely detection and monitoring of viral (emerging) threats.

Applicable to:



Online tool: <https://insaflu.insa.pt>

Documentation / Tutorial: <https://insaflu.readthedocs.io/en/latest/>

Code: <https://github.com/INSaFLU/INSaFLU>

Local installation: <https://github.com/INSaFLU/docker>

INSaFLU
latest

Search docs

Uploading or Updating data

Reference-based genomic surveillance

Metagenomics virus detection

Bioinformatics Pipeline

Frequently Asked Questions (FAQs)

Change log

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 - Updating Sample metadata
 - Uploading Reference data
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- Reference-based genomic surveillance
 - INSaFLU Projects - How to create and scale-up a genomic surveillance project
 - Nextstrain Datasets - How to create and run Nextstrain datasets
 - Output Visualization and Download
- Metagenomics virus detection
 - TELEVIR Projects - How to create and run a metagenomics virus detection project
 - TELEVIR - Output Visualization and Download
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 - Metagenomics virus detection
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- Frequently Asked Questions (FAQs)
 - FAQs
 - Guide for pre-NGS steps
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 - 2024
 - 2023
 - 2022
 - 2021
 - 2020
 - 2019
 - 2018

License: GPL v2

INSaFLU - docker installation

INSaFLU (“INSide the FLU”) is an influenza-oriented bioinformatics free web-based platform for an effective and timely whole-genome-sequencing-based influenza laboratory surveillance.

Hardware Requirements

- Processor: 8 cores (4 minimal);
- RAM: 32GB of memory (16GB minimal);
- Disk Space: 512GB;

INSaFLU-TELEVIR <https://insaflu.insa.pt/>



For a demonstration of the whole platform, please enroll the **AURORAE Webinar** “Introduction to INSaFLU-TELEVIR” available at the **ECDC Learning Portal**:

<https://eva.ecdc.europa.eu/course/view.php?id=983>

Documentation / Tutorial: <https://insaflu.readthedocs.io/en/latest/>

FAQs: <https://insaflu.readthedocs.io/en/latest/>



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