

Sample Upload

(Input, Single *versus* Batch upload, Settings, Automate QC and Classification)

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Main input files

Sequencing reads (FASTQ)

.fastq.gz (gzip compressed files)



- **1 or 2 files *per* sample**
- Maximum file size:
 - Online: 400 Mb
 - Local: user-defined

Sample information (metadata table)

.tsv/.csv file



- Template file
- **Mandatory fields:** "sample name" and "fastq1" [and fastq2, if paired-end reads].

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



Settings | Quality Control

Before uploading new Samples, if needed:

- **Users can change software settings to fit the parameters to the experimental conditions.**

Note: Settings are applicable to the whole account, but specific Settings can be applied for any sample / project later on.



Settings | Quality Control

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

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Virus Detection
From Reads to viral detection

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

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

News

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

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

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May 6, 2020 by Miguel Pinheiro

A Docker-compose version of INSaFLU, which eases the manual

More information

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Settings



Reads QC,
improvement and
classification

From reads to quality-processed reads and rapid classification

Settings

Settings | Quality Control

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Settings

QC

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Settings | Quality Control

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Settings

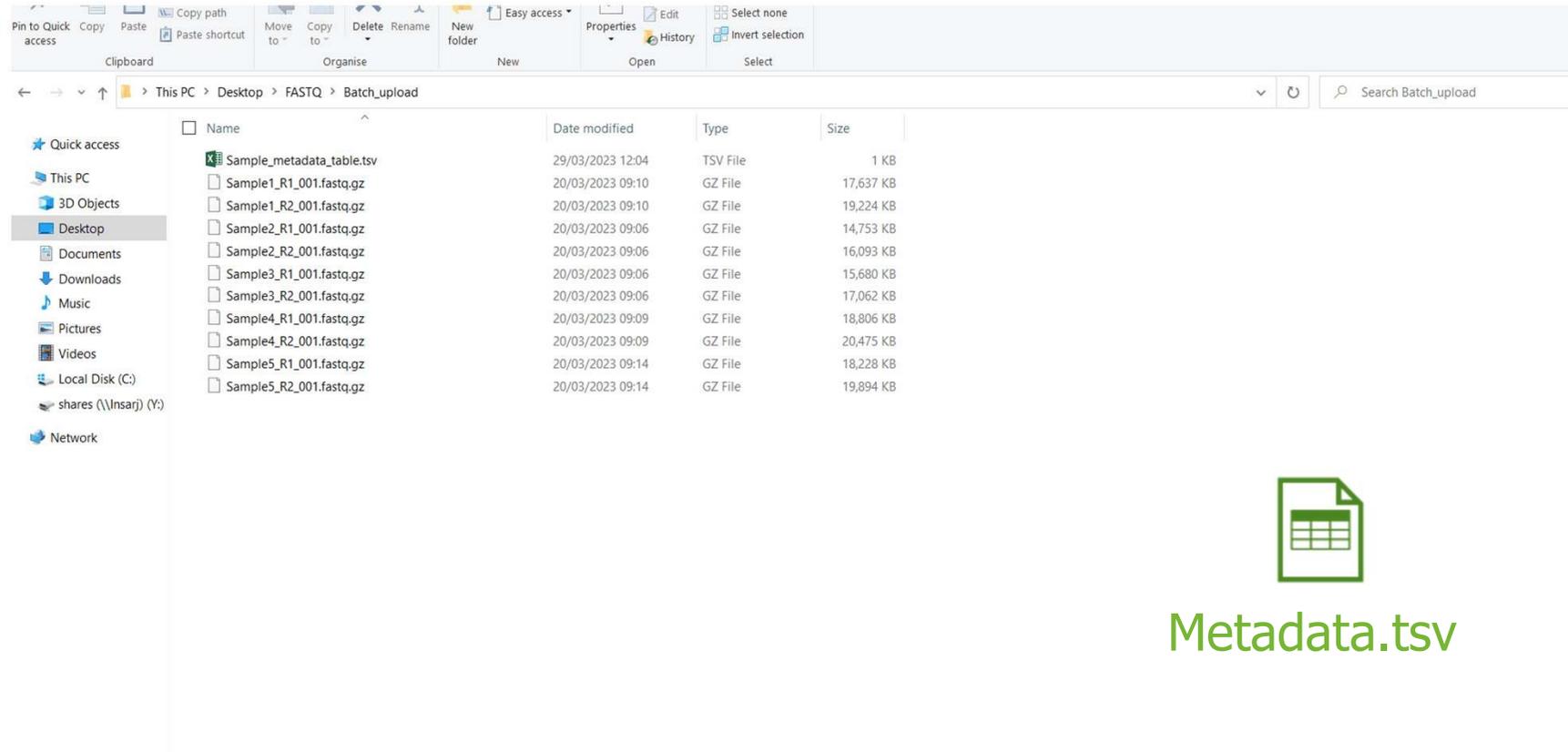


Reads QC,
improvement and
classification

From reads to quality-
processed reads and
rapid classification

Settings

Upload | Batch upload



The screenshot shows a Windows File Explorer window with the following table of files:

Name	Date modified	Type	Size
Sample_metadata_table.tsv	29/03/2023 12:04	TSV File	1 KB
Sample1_R1_001.fastq.gz	20/03/2023 09:10	GZ File	17,637 KB
Sample1_R2_001.fastq.gz	20/03/2023 09:10	GZ File	19,224 KB
Sample2_R1_001.fastq.gz	20/03/2023 09:06	GZ File	14,753 KB
Sample2_R2_001.fastq.gz	20/03/2023 09:06	GZ File	16,093 KB
Sample3_R1_001.fastq.gz	20/03/2023 09:06	GZ File	15,680 KB
Sample3_R2_001.fastq.gz	20/03/2023 09:06	GZ File	17,062 KB
Sample4_R1_001.fastq.gz	20/03/2023 09:09	GZ File	18,806 KB
Sample4_R2_001.fastq.gz	20/03/2023 09:09	GZ File	20,475 KB
Sample5_R1_001.fastq.gz	20/03/2023 09:14	GZ File	18,228 KB
Sample5_R2_001.fastq.gz	20/03/2023 09:14	GZ File	19,894 KB

The web interface on the right shows a 'Samples' section with a search bar and a list of actions: 'Add Samples', 'Add One Sample', 'Add Multiple Samples', 'Add Fastq Files', and 'Update metadata'. The 'Add Multiple Samples' and 'Add Fastq Files' buttons are highlighted with a green box.



Metadata.tsv

Documentation: https://insaflu.readthedocs.io/en/latest/uploading_data.html#option-1-batch

INSaFLU-TELEVIR

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



Upload | Batch upload

The screenshot shows the INSaFLU-TELEVIR web interface. The main content area features a news article titled "From 'reads' to viral metagenomics detection and routine genomic surveillance". The article describes INSaFLU as a free bioinformatics web-based suite for handling primary sequencing data. It lists two main features: metagenomics virus detection and routine genomic surveillance. Below the article are three logos: TELEVIR, INSaFLU, and Nextstrain. On the right side of the interface, there is a "Documentation" section with a "demo_insaflu - Logout" link. The interface also includes a sidebar with navigation options like Home, References, Samples, Projects, and Settings.

Reads
- fastq.gz

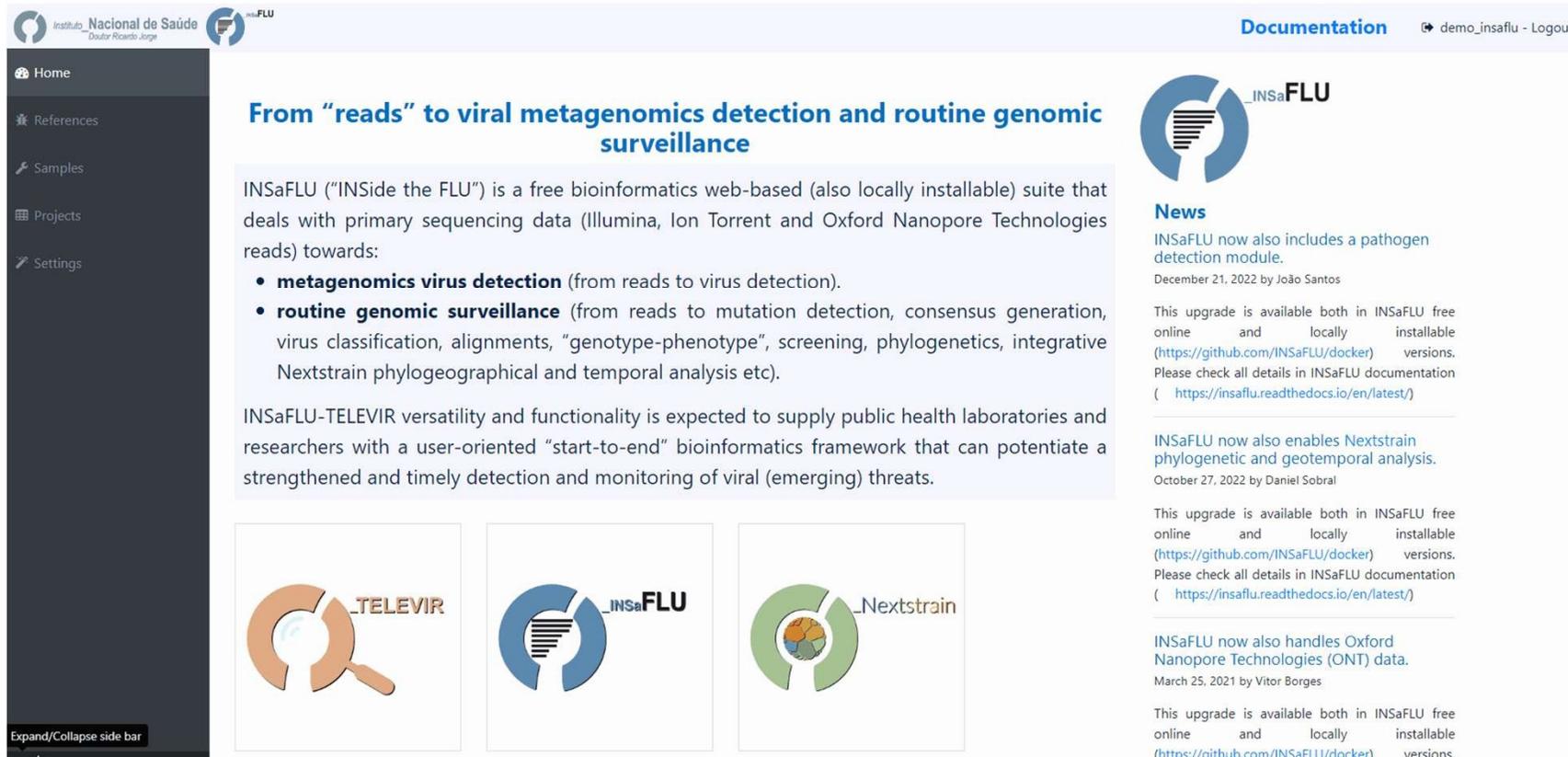
R1 (R2)



1 or 2 files
per sample

Documentation: https://insaflu.readthedocs.io/en/latest/uploading_data.html#option-1-batch

Upload | Batch upload



The screenshot shows the INSaFLU-TELEVIR web interface. On the left is a dark sidebar with navigation options: Home, References, Samples, Projects, and Settings. The main content area features a header with the INSaFLU logo and a navigation menu with 'Documentation' and 'demo_insaflu - Logout'. The central article is titled 'From "reads" to viral metagenomics detection and routine genomic surveillance'. It describes INSaFLU as a free bioinformatics web-based suite for primary sequencing data. A list of features includes metagenomics virus detection and routine genomic surveillance. Below the text are three icons for TELEVIR, INSaFLU, and Nextstrain. On the right, a 'News' section lists updates, including a pathogen detection module and Nextstrain integration.

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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NEWS

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Reads
. fastq.gz



1 or 2 files
per sample



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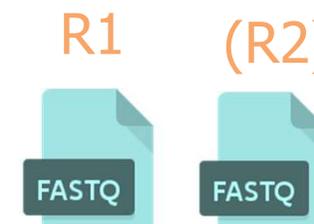
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Upload | Batch upload

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Reads
- fastq.gz



1 or 2 files
per sample

Documentation: https://insaflu.readthedocs.io/en/latest/uploading_data.html#option-1-batch

INSaFLU-TELEVIR

First outputs | Quality Control

"All Samples" QC
statistics, software details
and metadata

Number of reads
and size (post-QC)

[More info](#)

Home / Samples

[Add Samples](#) [Download](#)

Name, Type, Date, Tech

Sample Name	Uploaded Date	#Fastq Files	Technology	Classification	Data Set	Alerts	#Quality Seq. (Fastq1)-(Fastq2)	Extra Info
exercise_C_NegCtrl_meta	01-07-2025 23:21	2	Illumina/IonTorrent	NA (not applicable)	exercise_C_meta	0	🚫 (11564/75.0)-(11564/75.0) (23128)	🔗 + More Info
exercise_C2_meta	01-07-2025 23:21	2	Illumina/IonTorrent	NA (not applicable)	exercise_C_meta	0	🚫 (72618/75.0)-(72618/74.7) (145236)	🔗 + More Info
exercise_C1_meta	01-07-2025 23:21	2	Illumina/IonTorrent	NA (not applicable)	exercise_C_meta	0	🚫 (401370/74.9)-(401370/74.6) (802740)	🔗 + More Info
exercise_B_NegCtrl_meta	01-07-2025 23:20	1	ONT	NA (not applicable)	exercise_B_meta	0	🚫 (39721/748.8) (39721)	🔗 + More Info
exercise_B2_meta	01-07-2025 23:20	1	ONT	NA (not applicable)	exercise_B_meta	0	🚫 (229315/892.3) (229315)	🔗 + More Info
exercise_B1_meta	01-07-2025 23:20	1	ONT	NA (not applicable)	exercise_B_meta	0	🚫 (184341/1006.9) (184341)	🔗 + More Info
exercise_A6_amplicon	01-07-2025 23:13	2	Illumina/IonTorrent	NA (not applicable)	exercise_A_amplicon	0	🚫 (1015315/117.5)-(1015315/114.3) (2030630)	🔗 + More Info
exercise_A5_amplicon	01-07-2025 23:13	2	Illumina/IonTorrent	NA (not applicable)	exercise_A_amplicon	0	🚫 (1111117/119.1)-(1111117/115.8) (2222234)	🔗 + More Info
exercise_A4_amplicon	01-07-2025 23:13	2	Illumina/IonTorrent	NA (not applicable)	exercise_A_amplicon	0	🚫 (2055614/118.9)-(2055614/115.7) (4111228)	🔗 + More Info

Documentation: https://insaflu.readthedocs.io/en/latest/routine_genomic_surveillance.html#a-go-to-samples-menu-and-check-the-reads-quality-reports-and-typing-data

INSaFLU-TELEVIR

First results | Quality Control

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INSaFLU-TELEVIR

First results | Quality Control

INSaFLU

Home / Samples

Add Samples Download Remove ALL samples

Name, Type, Data set, Tec Search

Sample Name	Uploaded Date	#Fastq Files	Technology	Classification	Data Set	Alerts	#Quality Seq. (Fastq1)-(Fastq2)	Extra Info
exercise_C2_meta	01-07-2025 23:21	2	Illumina/IonTorrent	NA (not applicable)	exercise_C_meta	0	(72618/75.0)-(72618/74.7) (145236)	More Info
exercise_C1_meta	01-07-2025 23:21	2	Illumina/IonTorrent	NA (not applicable)	exercise_C_meta	0	(401370/74.9)-(401370/74.6) (802740)	More Info
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exercise_A3_meta	01-07-2025 23:11	2	Illumina/IonTorrent	NA (not applicable)	exercise_A_meta	0	(645200/74.9)-(645200/74.7) (1290400)	More Info
exercise_A2_meta	01-07-2025 23:11	2	Illumina/IonTorrent	NA (not applicable)	exercise_A_meta	0	(1209448/74.9)-(1209448/74.5) (2418896)	More Info

Extra Info

[More Info](#)

[Video tutorial](#)

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INSaFLU-TELEVIR

First results | Quality Control



Documentation demo_training - Logout

Extra Info

[More Info](#)

Home
Primers
References
Samples
Projects
Settings

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Questions from chat