Sample Upload

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

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Genomics and Bioinformatics Unit

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

Instituto_Nacional de Saúde Doutor Ricardo Jorge

ecdc EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

Main input files

Sequencing reads (FASTQ)

.fastq.gz (gzip compressed files)

FASTQ

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

+

Sample information (metadata table)

.tsv/.csv file

TSV

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

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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.

Reads QC, improvement and classification

From reads to quality-processed reads and rapid classification

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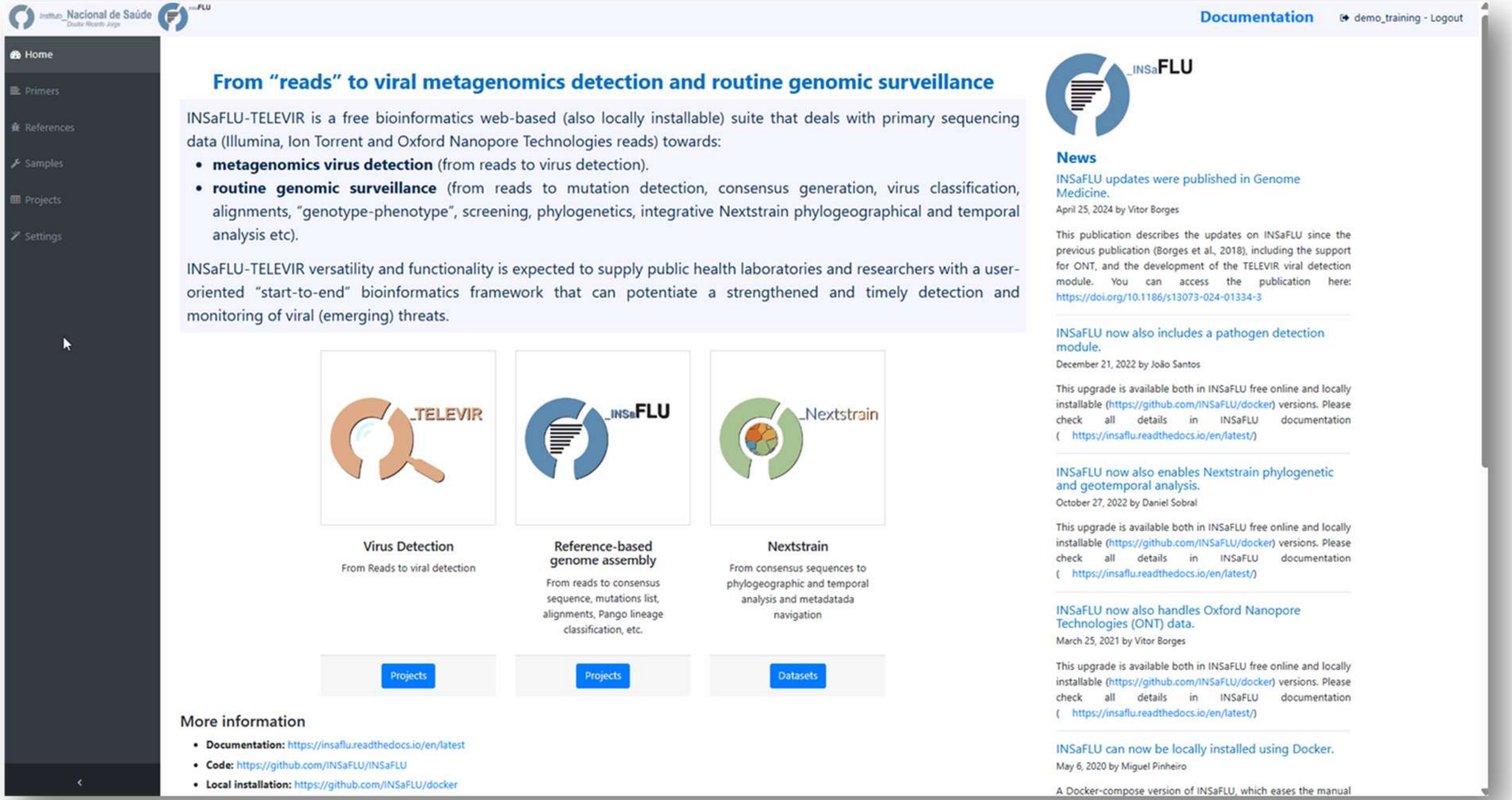
Settings | Quality Control



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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 metadatada navigation
Datasets

More information

- **Documentation:** https://insaflu.readthedocs.io/en/latest
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April 25, 2024 by Vitor Borges

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May 6, 2020 by Miguel Pinheiro

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Documentation: https://insaflu.readthedocs.io/en/latest/bioinformatics_pipeline.html?highlight=settings#user-defined-parameters

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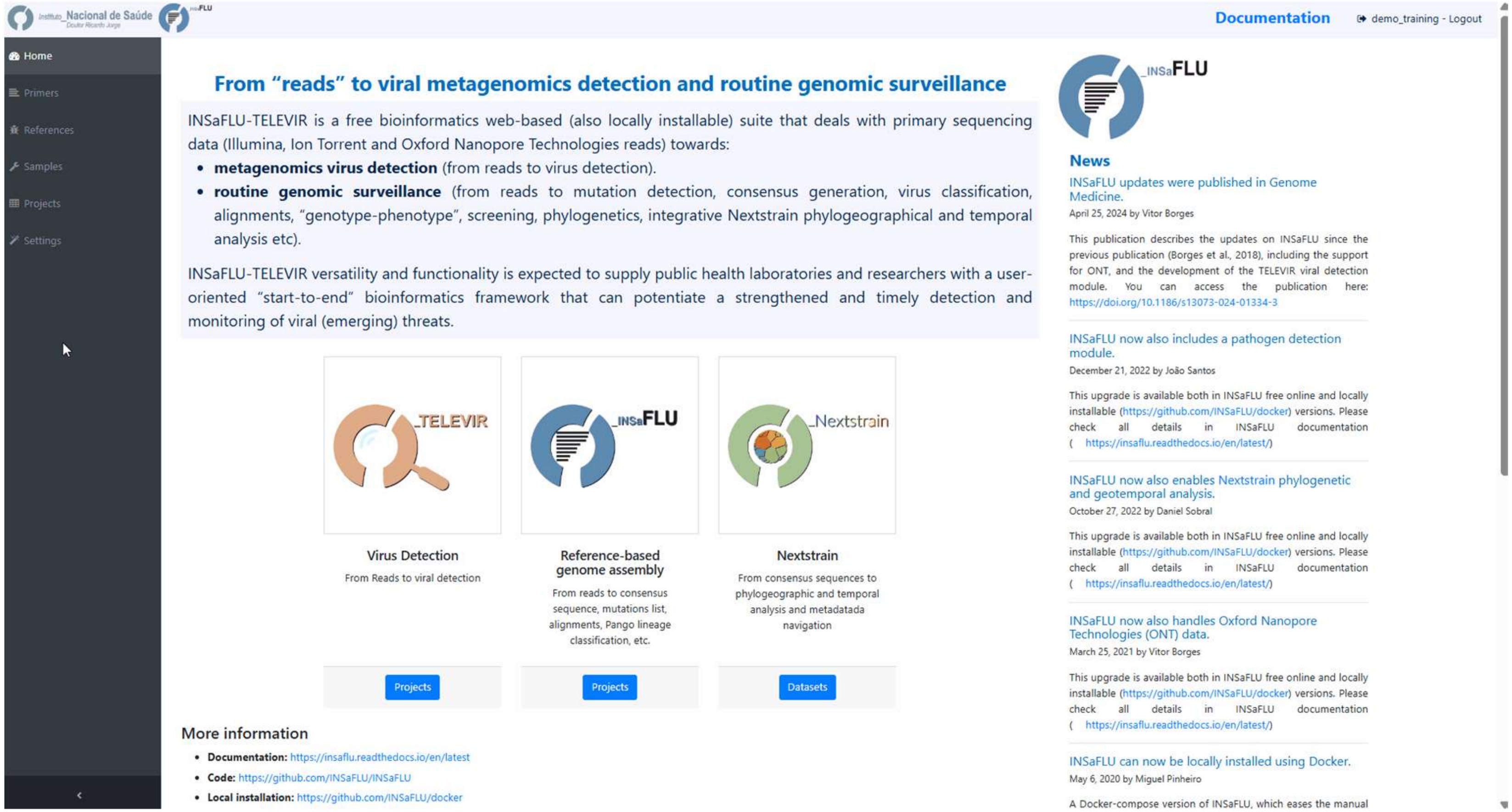
Settings | Quality Control



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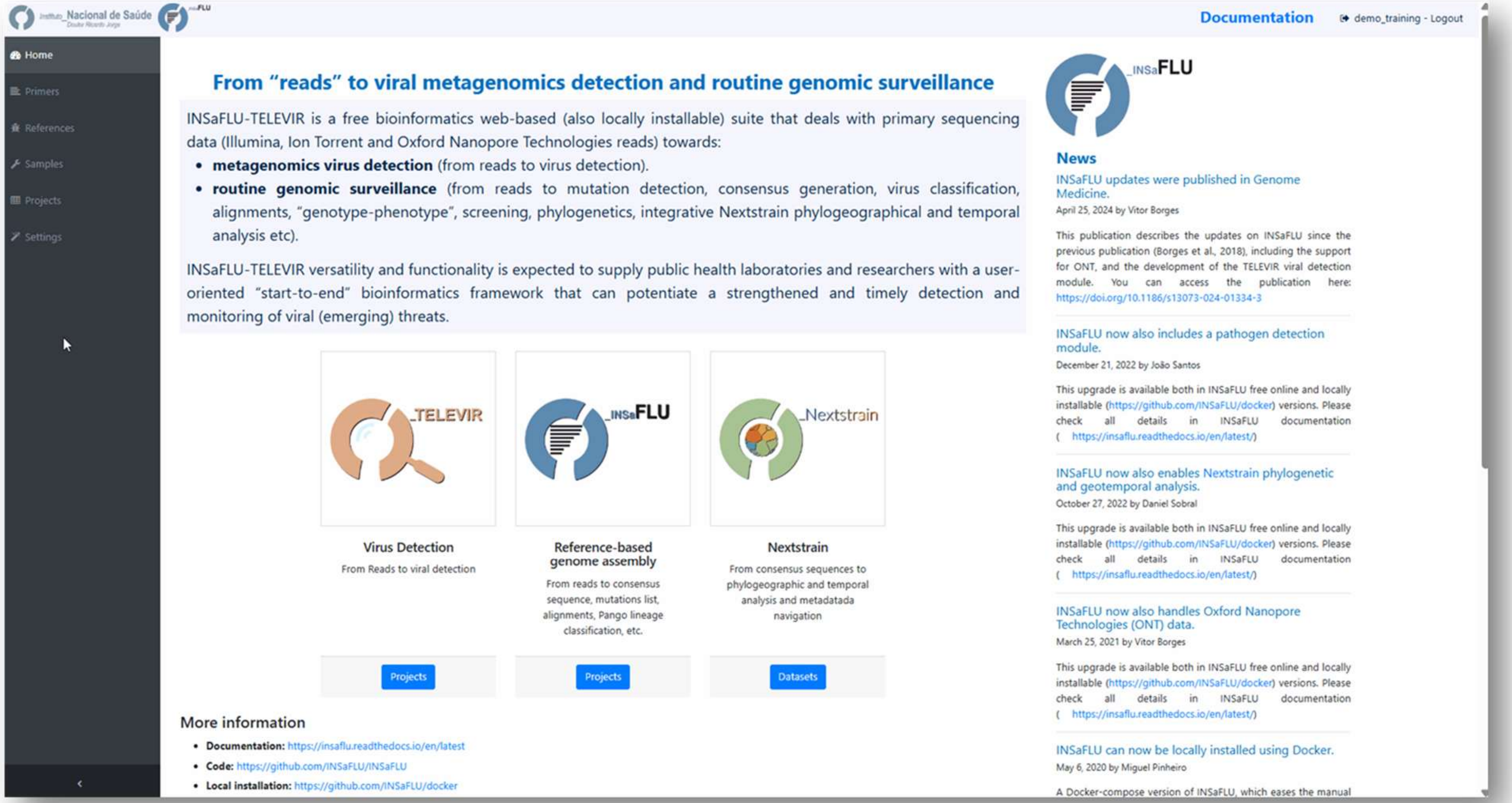

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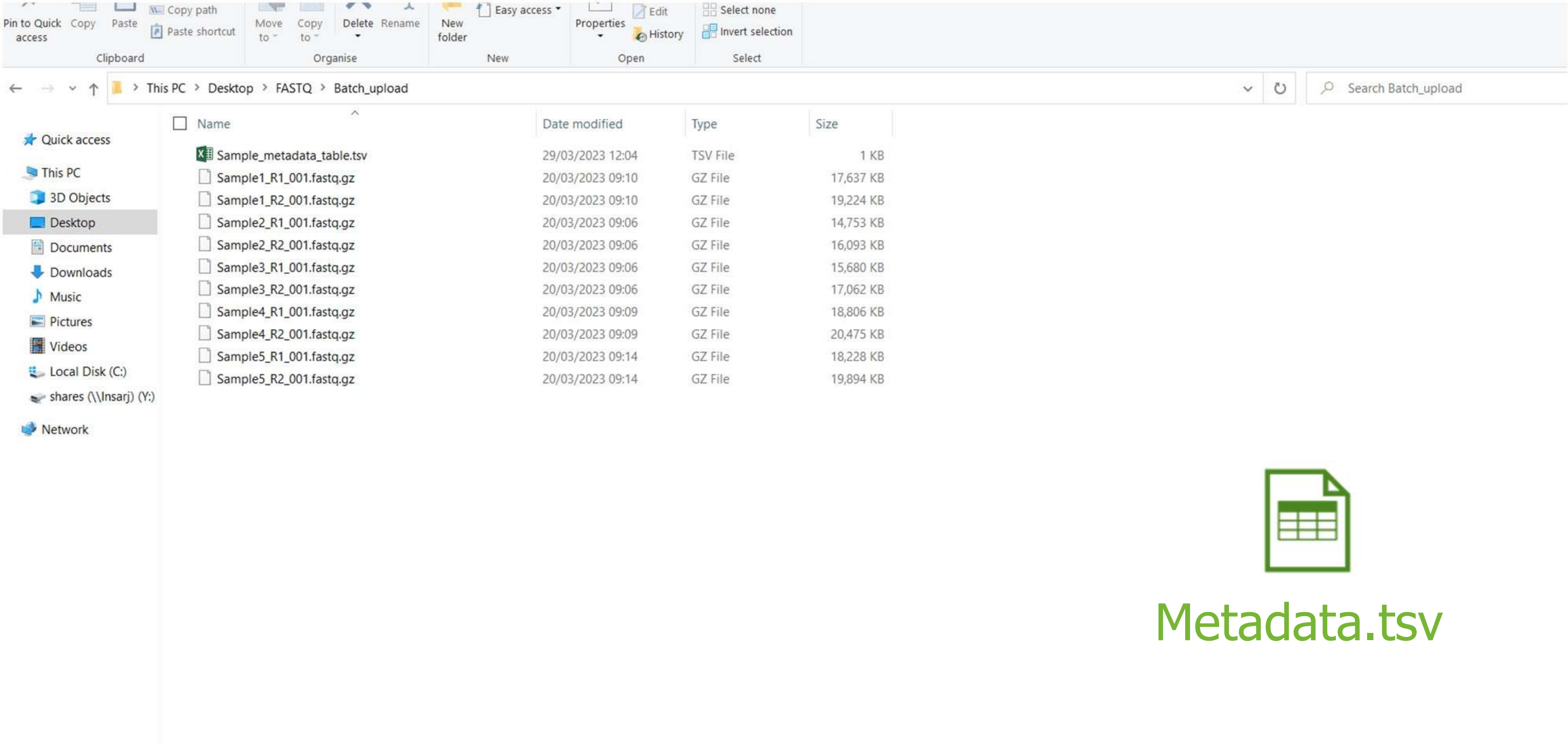
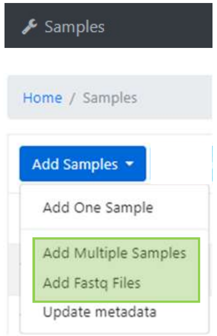
Upload | Batch upload



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

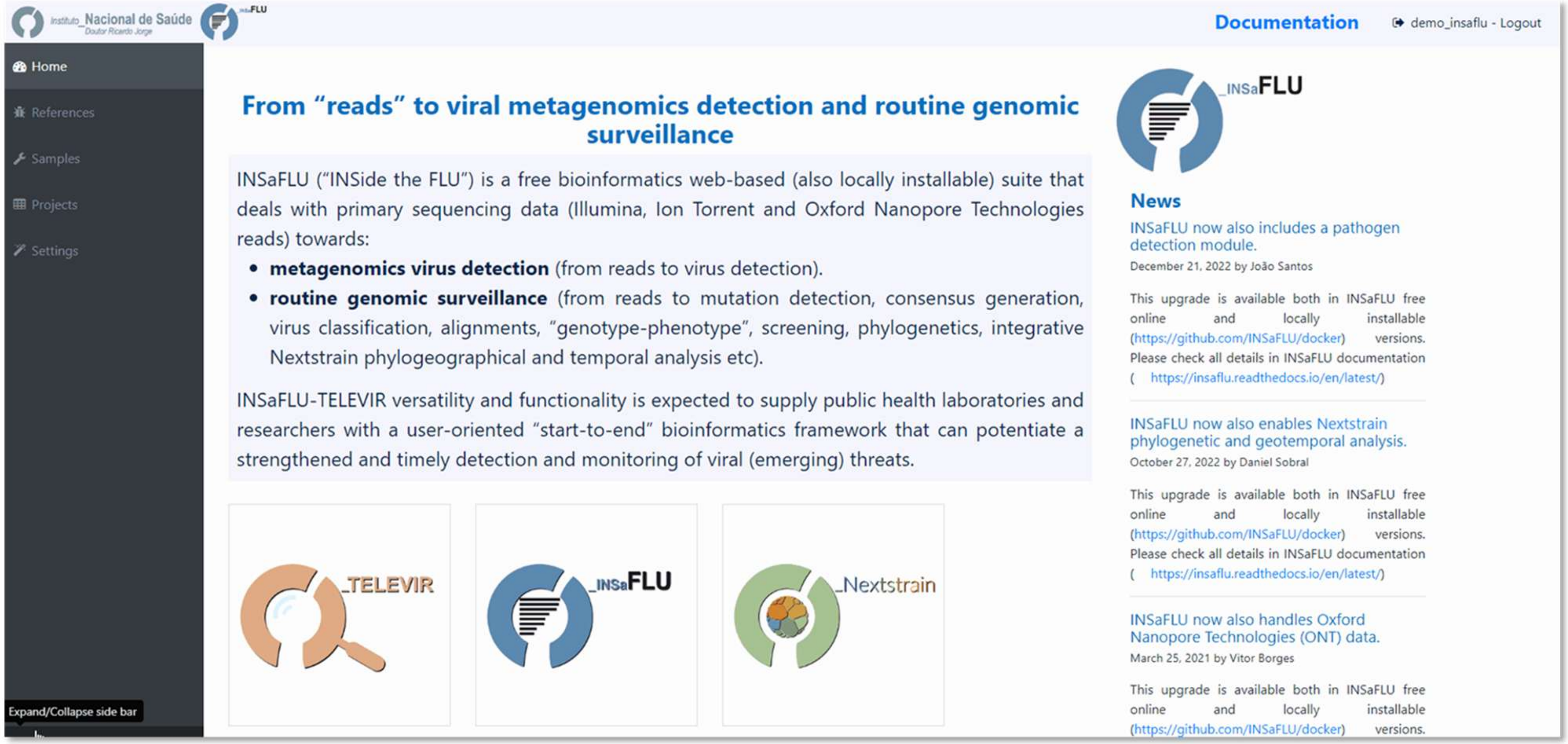


Metadata.tsv

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

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

Upload | Batch upload



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Reads

. fastq.gz

R1 (R2)

FASTQ FASTQ

1 or 2 files
per sample

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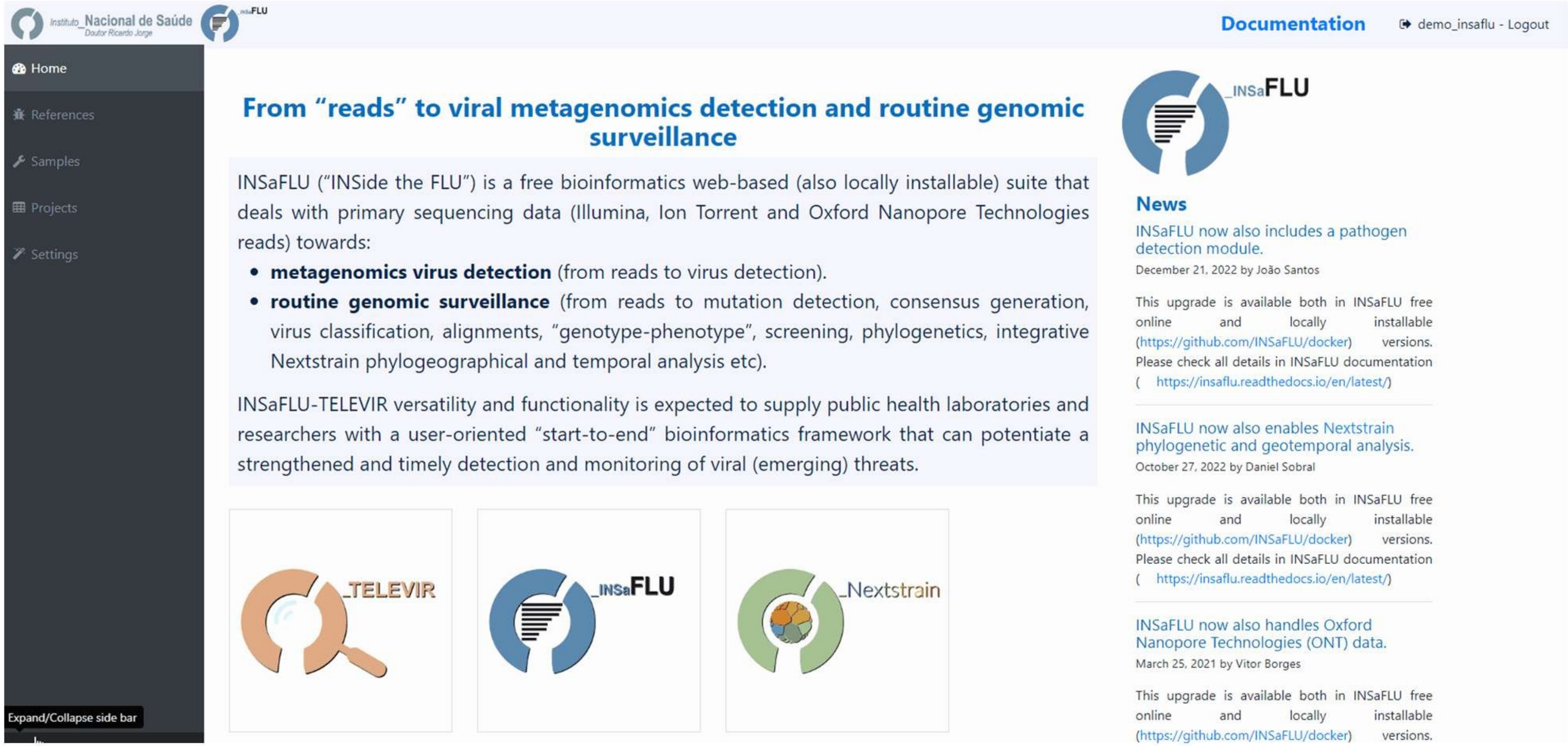

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FASTQ FASTQ

1 or 2 files *per* sample

Video tutorial

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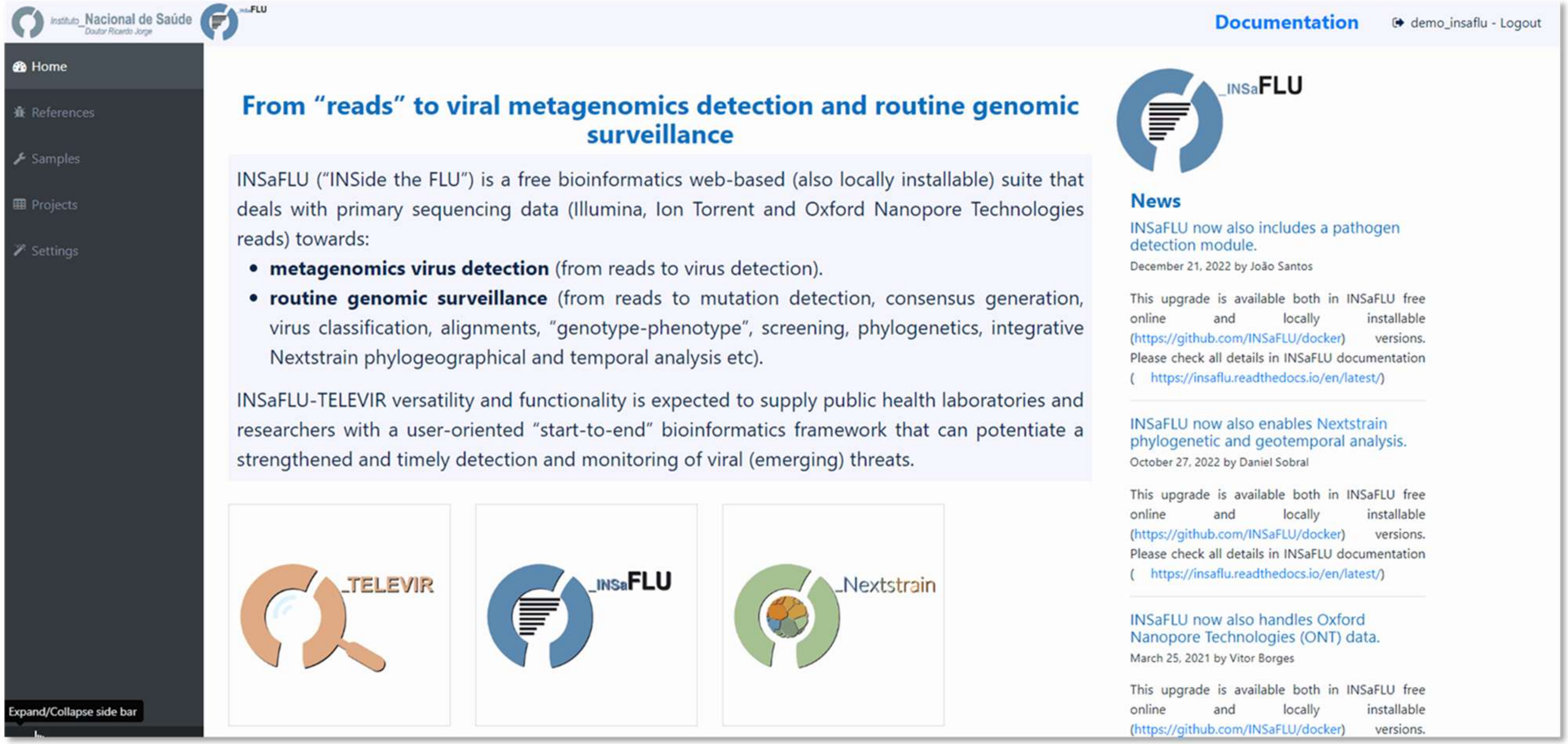

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Reads

. fastq.gz

R1 (R2)

FASTQ FASTQ

1 or 2 files *per* sample

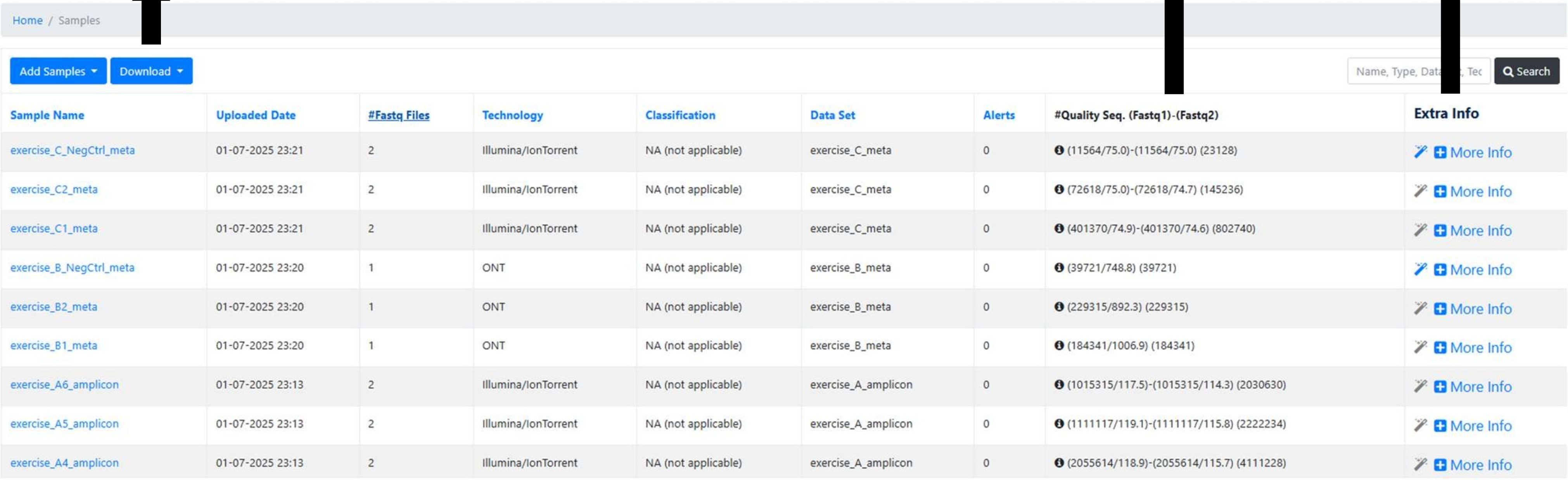
INSaFLU-TELEVIR

First outputs | Quality Control

"All Samples" QC
statistics, software details
and metadata

**Number of reads
and size (post-QC)**

More info



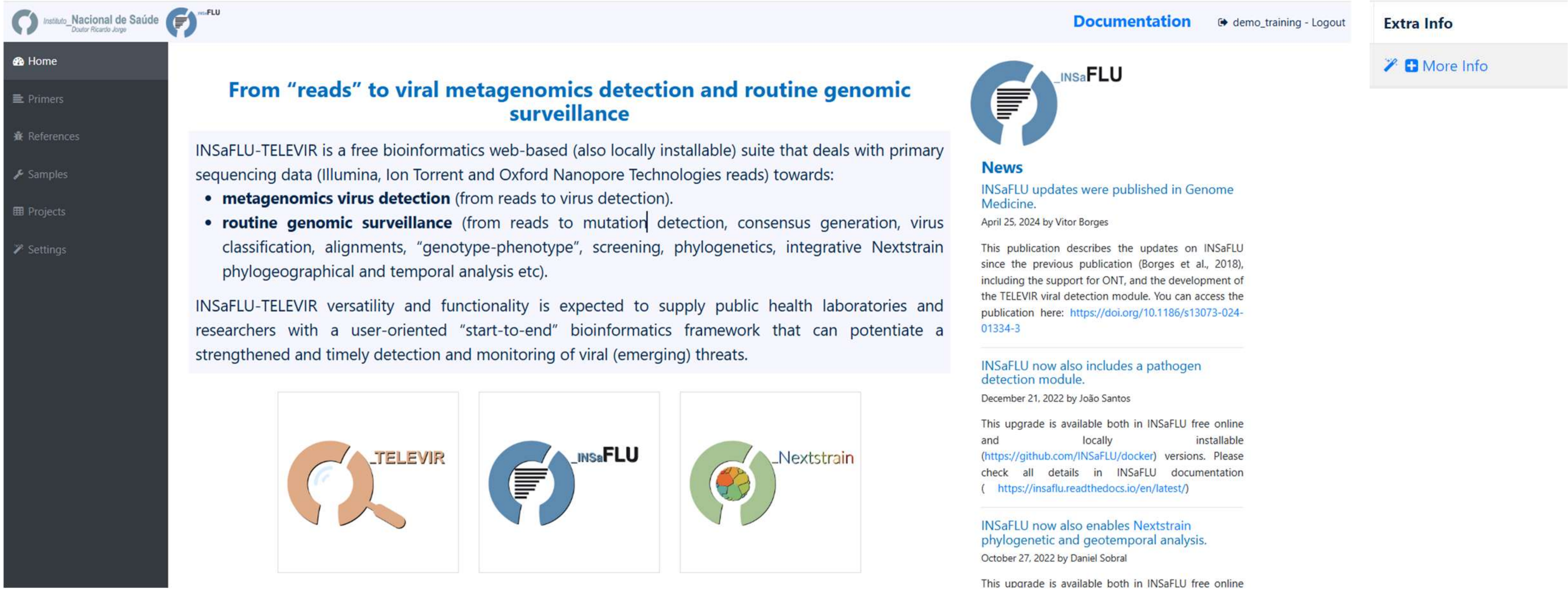
Home / Samples

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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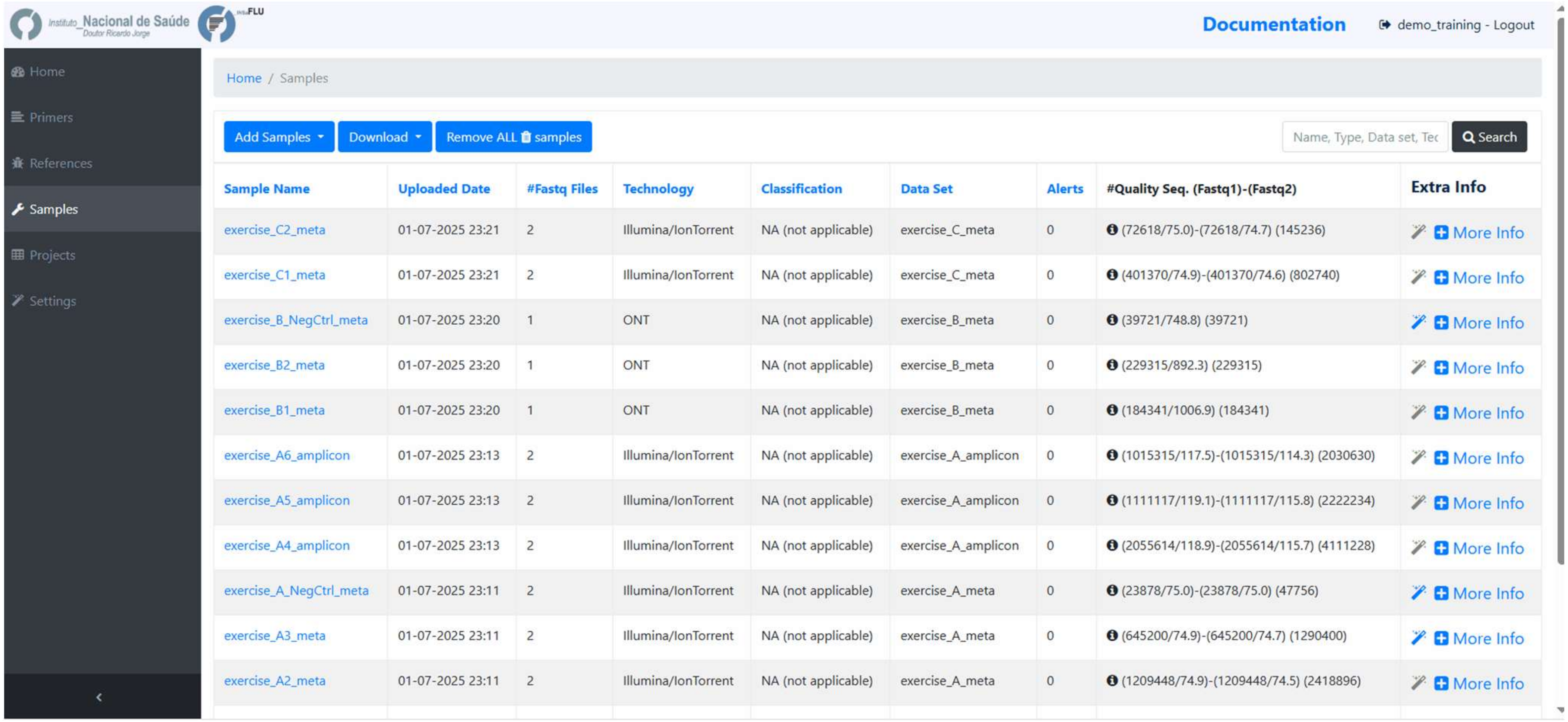

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exercise_A_NegCtrl_meta	01-07-2025 23:11	2	Illumina/IonTorrent	NA (not applicable)	exercise_A_meta	0	(23878/75.0)-(23878/75.0) (47756)	More Info
exercise_A3_meta	01-07-2025 23:11	2	Illumina/IonTorrent	NA (not applicable)	exercise_A_meta	0	(645200/74.9)-(645200/74.7) (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

Video tutorial

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

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.

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

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

Questions from chat