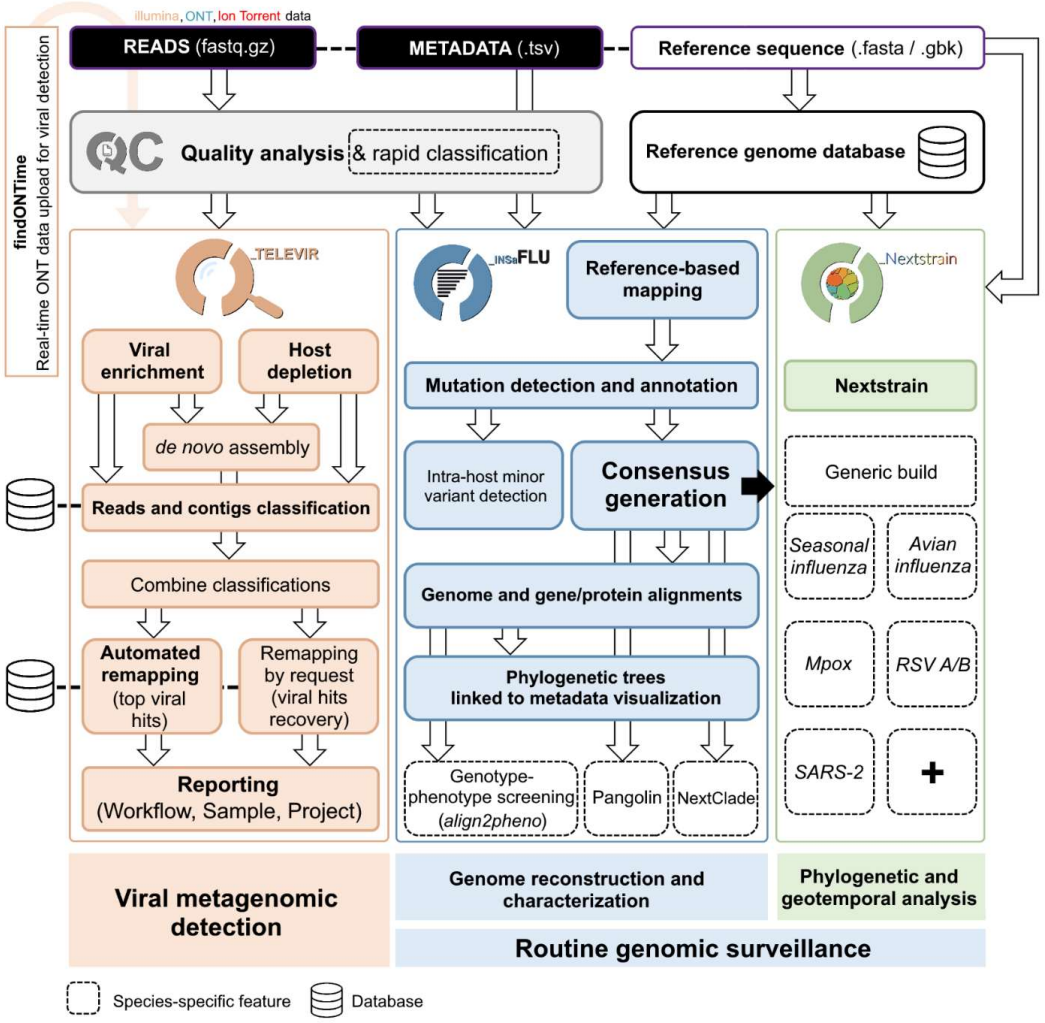
Concluding remarks

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**

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

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

In summary

During this webinar, we hope you have had **opportunity to learn:**

1. the **foundations of metagenomics for pathogen detection**
2. the associated **bioinformatics workflows**, namely the one implemented in the **TELEVIR module for viral metagenomics detection**
3. how to perform TELEVIR **hypothesis-free viral detection** using metagenomic sequencing data
4. how TELEVIR integrates **multiple classification** and **validation steps** to ensure robust virus detection
5. **key metrics** to consider for **validation and interpretation of viral detection results** (e.g. coverage, read support, consistency across classifiers)
6. how to conduct complementary analysis, like **targeted viral searches/validations**, including specific viruses or user-defined viral panels
7. **practical examples** illustrating real-world use cases of viral metagenomics detection using TELEVIR

INSaFLU-TELEVIR

Recommended material to explore further

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

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

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

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

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

Contact: insaflu@insa.min-saude.pt

References

INSaFLU-TELEVIR publications:

- Borges, V., Pinheiro, M., et al. Genome Medicine (2018) (https://doi.org/10.1186/s13073-018-0555-0)
- Santos, J.D., et al. Genome Medicine (2024) (https://doi.org/10.1186/s13073-024-01334-3)

Other tools connected to / embedded within INSaFLU and Nextstrain modules:

- Rambaut, A., Holmes, E.C., et al. Nature Microbiology. (2020) (https://doi.org/10.1038/s41564-020-0770-5)
- O'Toole, Á., et al. Vírus Evolution. (2021) (https://doi.org/10.1093/ve/veab064)
- Hadfield, J., et al. Bioinformatics. (2018) (https://doi.org/10.1093/bioinformatics/bty407)
- Aksamentov I., et al. (2021) (https://doi.org/10.21105/joss.03773)
- Santos, J.D., et al. (2022) (https://github.com/insapathogenomics/algn2pheno)
- Santos, J.D., et al. (2023) (https://github.com/INSaFLU/findONTime)
- Giussani, E., Sartori, A. et al. Virus Evolution (2025). (https://doi.org/10.1093/ve/veaf011) https://izsvenezie-virology.github.io/FluMut/

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Other tools connected to / embedded within TELEVIR module:

- Wood, D. E., Lu, J., & Langmead, B. (2019). *Genome Biology* (**https://doi.org/10.5281/zenodo.3520278**)
- Kim, D., Song, L., Breitwieser, F. P., & Salzberg, S. L. (2016). *Genome Research* (**https://www.genome.org/cgi/doi/10.1101/gr.210641.116**)
- Buchfink, B., Xie, C., & Huson, D. H. (2015). *Nature Methods* (**https://doi.org/10.1038/nmeth.3176**)
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- Li, H., Durbin, R. (2010). Bioinformatics (**https://doi.org/10.1093/bioinformatics/btp698**)
- Tithi, S. S., Aylward, F. O., Jensen, R. V., & Zhang, L. (2018). PeerJ (**https://doi.org/10.1089/cmb.2022.0**)
- Robinson, J. T., et al (2011). Nature Biotechnology, (**https://doi.org/10.1038/nbt.1754**)

INSaFLU-TELEVIR

Recommended material to explore further

Online training resources - AURORAE

- For a detailed demonstration of the whole **INSaFLU-TELEVIR** 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

- For more information about **avian influenza genomic analyses**, please enroll the **AURORAE Webinar** "Avian influenza in human specimens – genomic analyses and experiences from the field" available at the ECDC Learning Portal:

  https://learning.ecdc.europa.eu/course/view.php?id=1079

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Thank you

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