VirHunter: a deep learning-based method for detection of novel viruses in plant sequencing data

Grigorii Sukhorukov, Macha Nikolski

VirHunter: a deep learning-based method for detection of novel viruses in plant sequencing data

Sukhorukov Grigorii, Macha Nikolski

IBGC/CNRS and CBiB, Bordeaux University, France

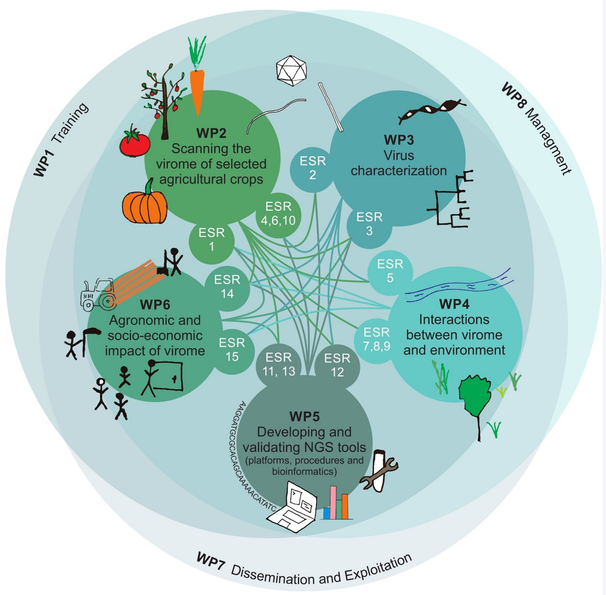
grigorii.sukhorukov@u-bordeaux.fr

Plant viruses in our lives

- **Plant Viruses cause 50% of the emerging plant diseases** and pose an important threat to many agricultural crops worldwide, **they are responsible for production losses estimated at € 15 to 45 billion per year.**

MSCA ITN INEXTVIR

- Network for Next Generation Training and Sequencing of Virome classification
- Our research: Bioinformatics pipelines development for virome classification

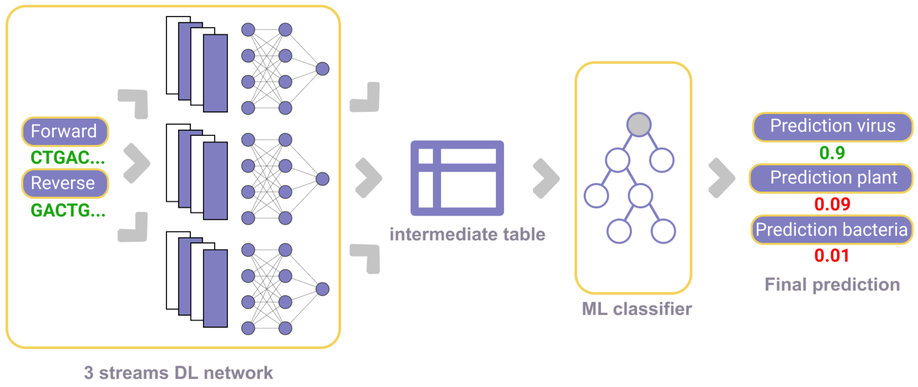


INEXTVIR project landscape

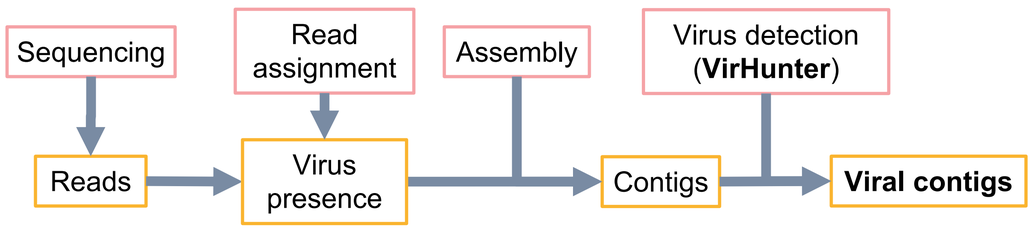
VirHunter idea

- Develop deep learning approach to detect novel plant viruses from assembled contigs of plant virome sequencing data
- Leverage multiple models that rely on different k-mer sizes
- Enable multi-class approach to deal with contamination problem (virus, plant, bacteria)
- Validate the approach on leave-out datasets (family, genus, specie levels)

Network architecture



Novel virus detection workflow

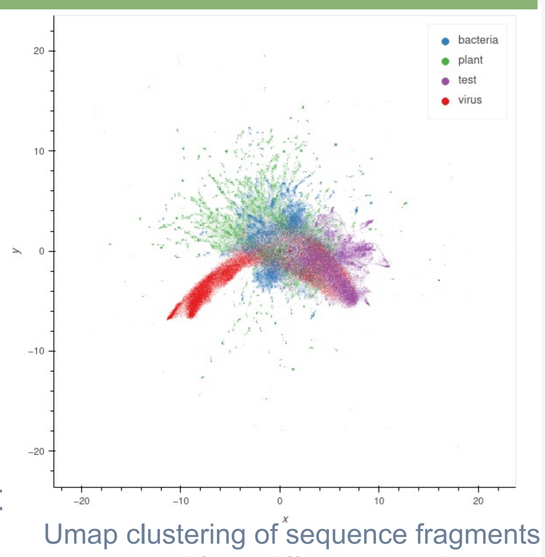


What makes VirHunter special

- Highly accurate novel virus identification
- Deals with contamination
- Can be easily integrated in standard pipelines
- Uses novel hybrid architecture (deep learning + standard machine learning)

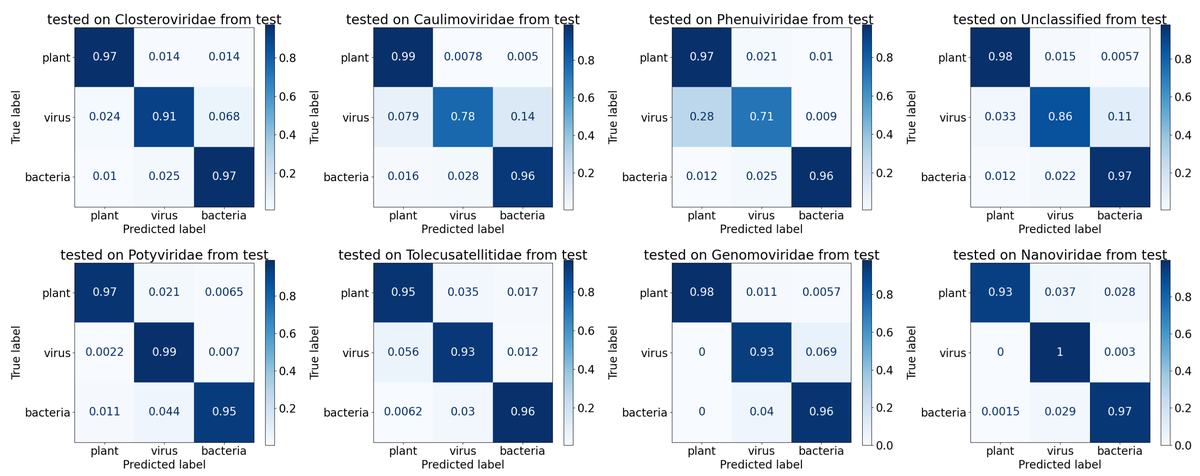
Challenges of novel virus detection

- Virome samples are usually contaminated with bacterial or plant genetic material
- Sequencing technology may disfavor detection of some viruses
- Plant virus families are very dissimilar
- Much of plant viral diversity is not yet described



Umap clustering of sequence fragments sampled from different organisms

Accuracy of novel virus detection

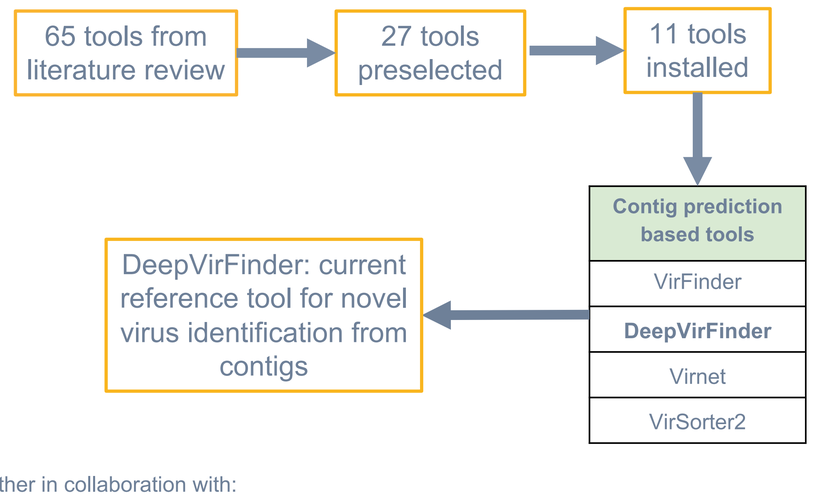


Confusion matrices for viral family leave-out datasets

Tool	% of correctly identified viruses	Weighted average
VirHunter	**(69-91%)**	**85.6%**
DeepVirFinder	(57-83%)	72.5%

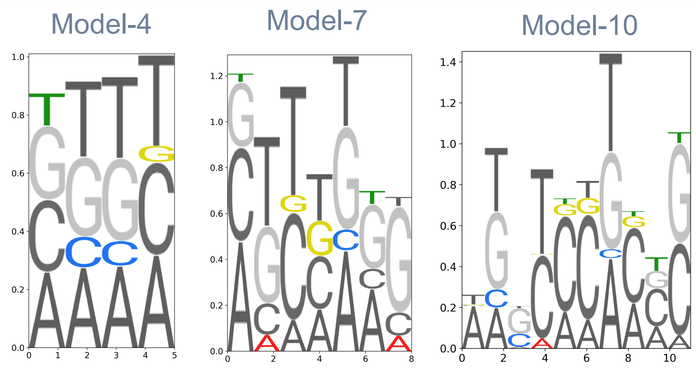
VirHunter outperforms DeepVirFinder!

Existing tools*



* work done together in collaboration with:
University of Ljubljana, Faculty Of Computer And Information Science, Ljubljana, Slovenia
Plant Pathology Laboratory, TERRA, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium

Model interpretability



Examples of motifs learnt by the models.
Letters in color are rewarded, letters in gray are penalized