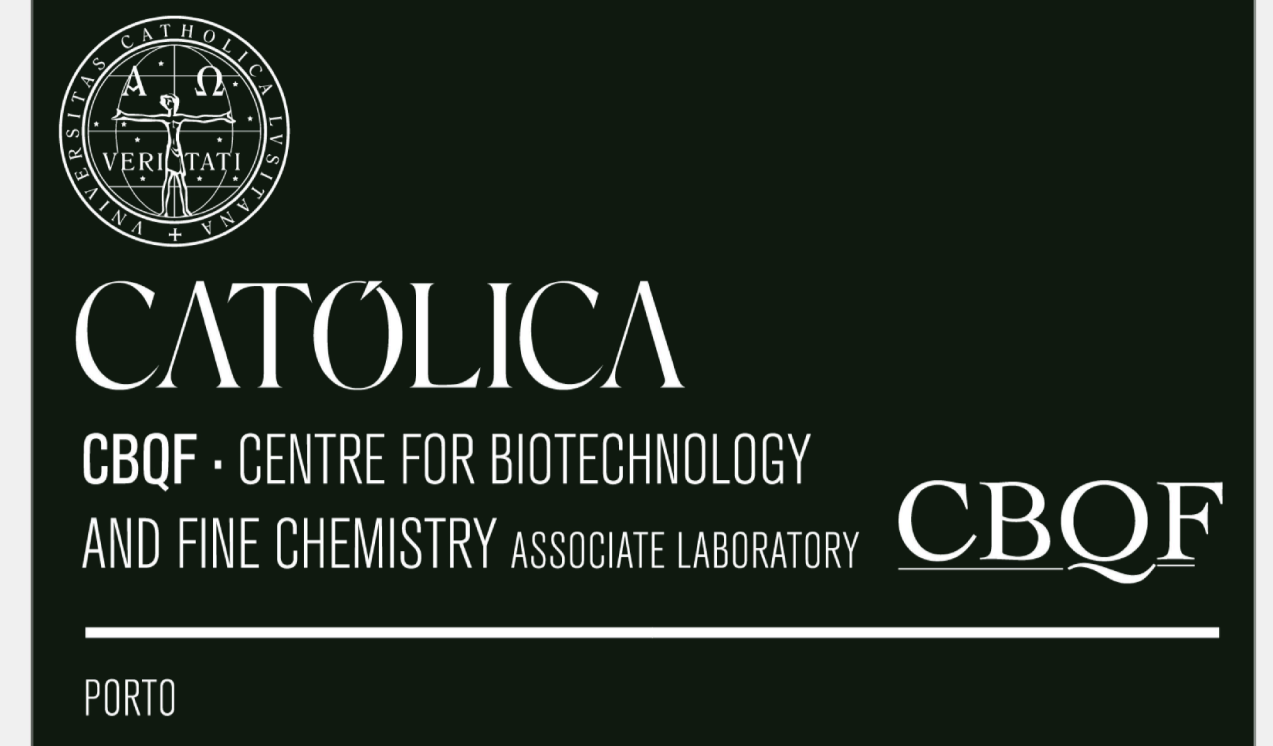
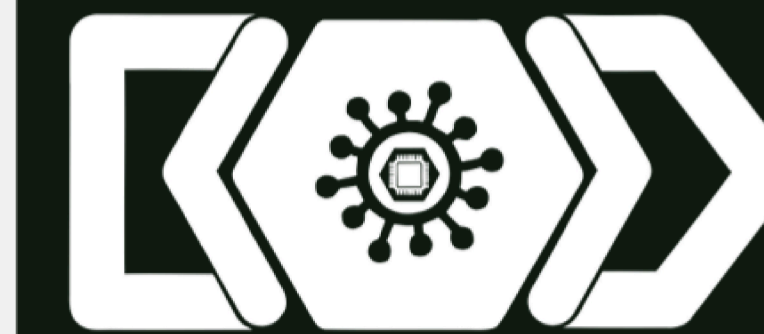


# VirusScope

An Integrated Pipeline for Literature-Driven and In Silico Viral Primer Design



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## Introduction

Viral diagnostics and surveillance depend critically on **robust primer design**, yet existing workflows for retrieving, generating, and validating viral primers are often **fragmented** across **heterogeneous tools** and **formats**. **VirusScope** is a Python based command line framework that unifies:

- literature mining;
- in silico primer generation, scoring, annotation;
- downstream analysis

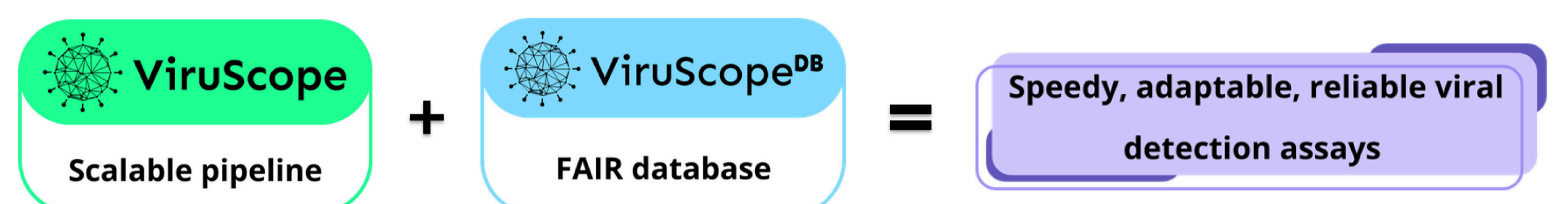
into a **single reproducible pipeline**.

Links to:  
Online Shiny APP demo  
Zenodo dataset  
GitHub (CLI and GUI repositories in the profile)  
Ana Lima's LinkedIn, ResearchGate and email address

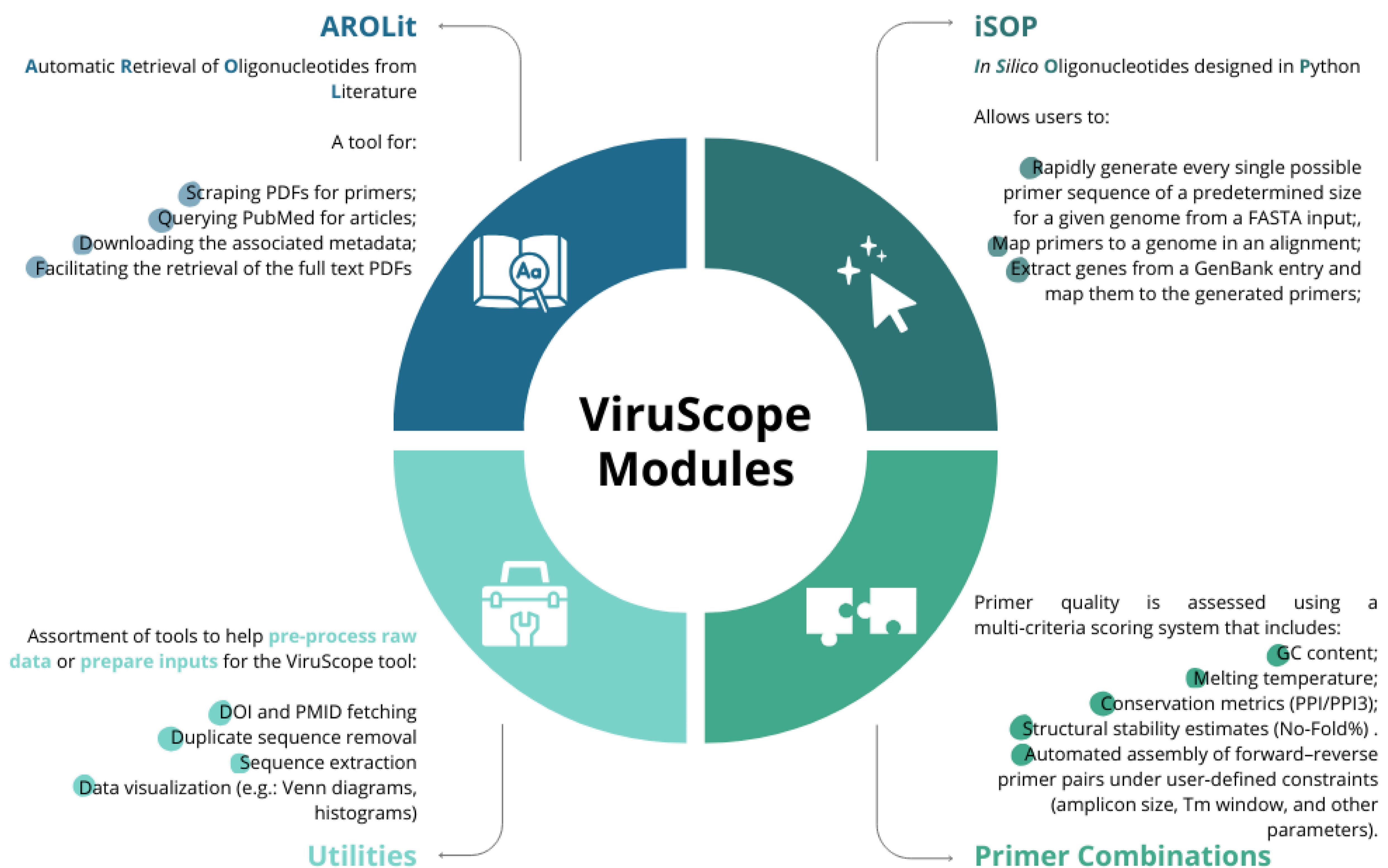


## Objectives

1. **Automated sequence mining** from viral genomes;
2. **Literature text mining** for validated primers/probes;
3. **In silico primer generation and validation** across strains;
4. **Automated scoring & export** of reliable primer sets;
5. **Database creation and extension**;



## Methods and Results



## Conclusions

VirusScope is suited for both **literature curated** and **purely computational** primer discovery scenarios, including **emerging** or **poorly characterized viruses**, **outbreak response**, and **assay re-evaluation** under viral evolution.

The tool is openly available at: <https://github.com/anasplima/VirusScope> and can be installed using standard Python virtual environments and requirement files, making it straightforward to **adopt in research and diagnostic settings**. A **GUI version** is also available in the repositories of the same GitHub user. Other important links and resources can be accessed by scanning the **QR code** on this poster.

## Acknowledgements

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