

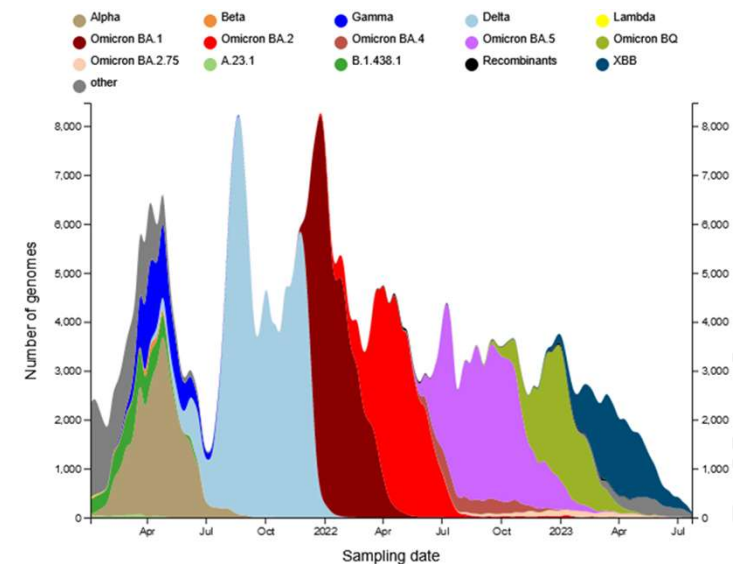


DUOTANG

**A Genomic Epidemiology Analyses and
Mathematical Modelling Notebook**

Duotang

- Web notebook for genomic epidemiology analysis and mathematical modelling designed originally for SARS-CoV-2.
- Semi-automated report generation with expert review.
- Includes multiple, interactive, plots for analysis of frequency changes, estimating selection on variants, phylogenetics, and more.
- **Goal:** investigate SARS-CoV-2 evolution and spread within the country and to spur scientific discussion and communication with public health authorities.

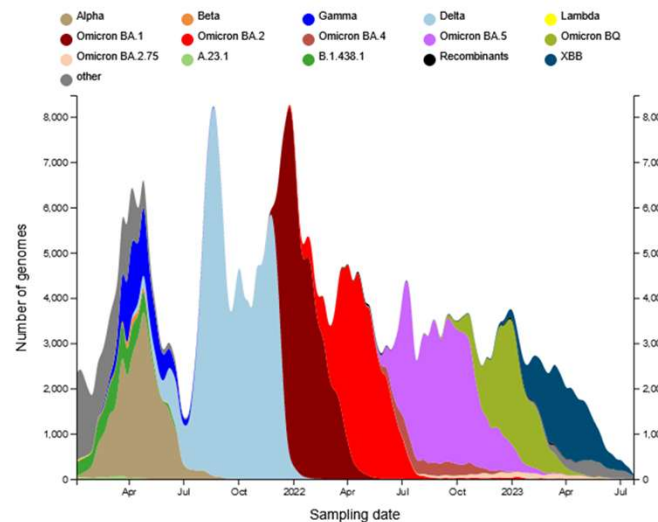
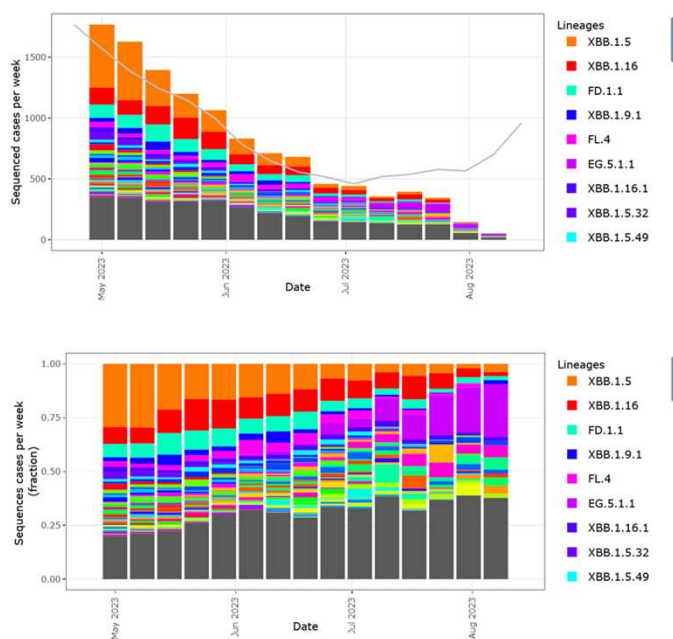




Plots: Frequency Changes

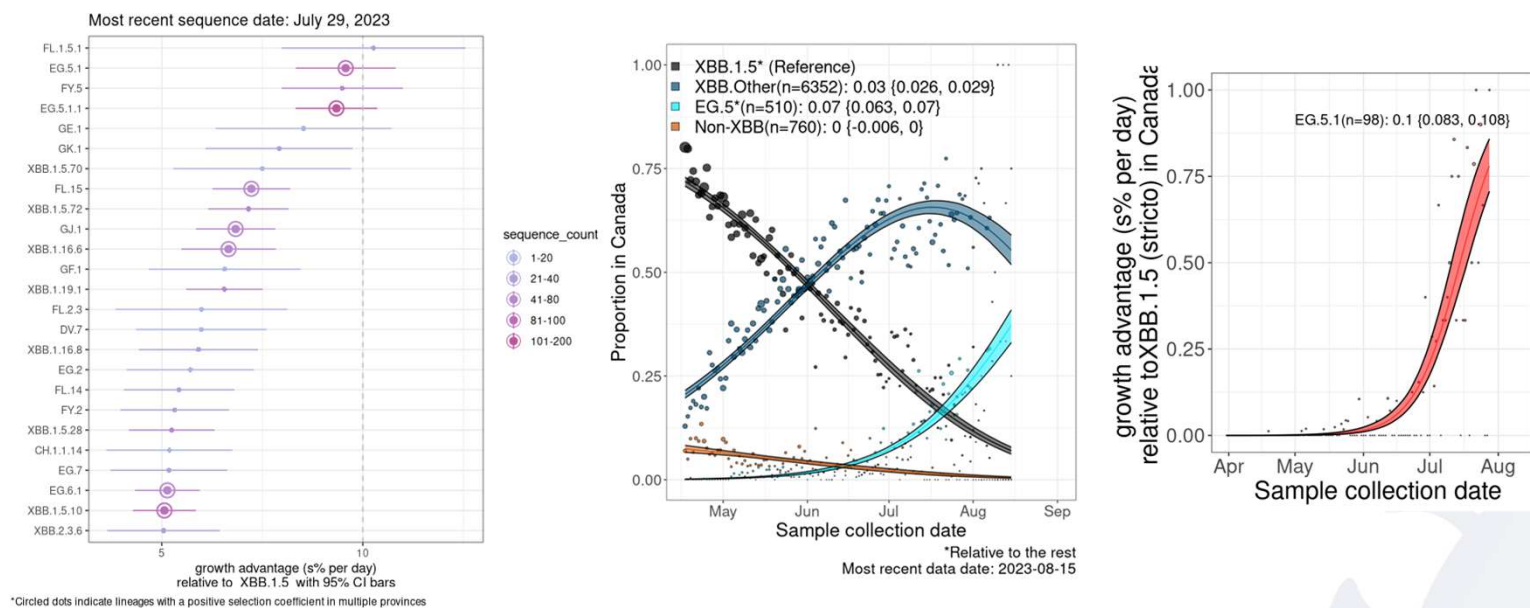
Last 120 days BA.1 BA.2 BA.4 BA.5 Recombinants

Last 120 days sublineages starting from 2023-04-17 (Frequency Table Download)





Plots: Estimating Selection

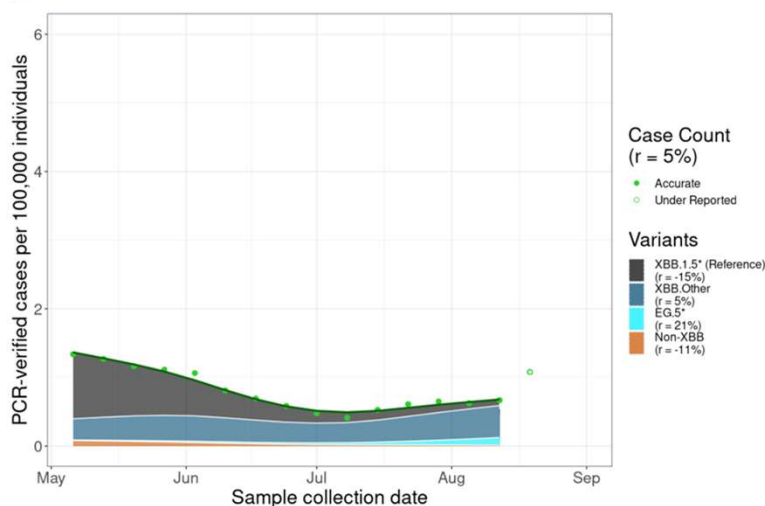


148 named lineages have been circulating in Canada over the last month. Measuring the selective advantage of each relative to XBB.1.5, the fastest growing lineages in multiple provinces and with sufficient data is EG.5.1 ($s \sim 10\%$).



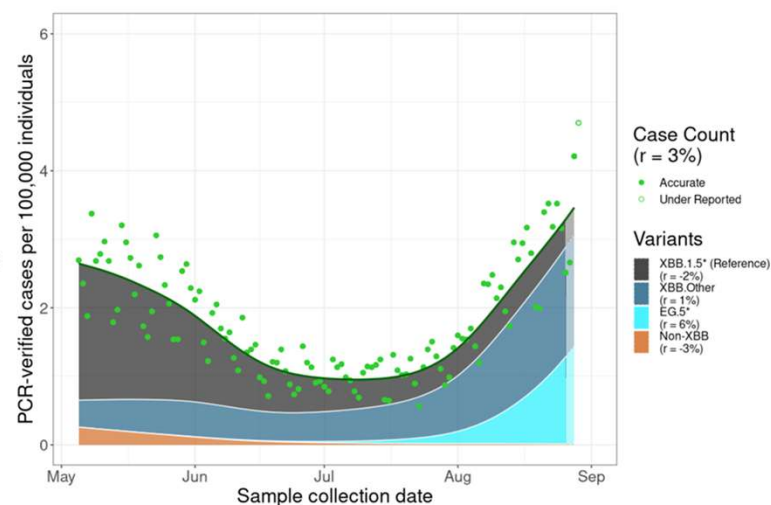
Plots: Estimating Case Counts

Ontario



iter shade represents per lineage case counts estimated using available genomics data
Last day of genomic data is 2023-08-19
Last day of accurate case counts is 2023-08-12

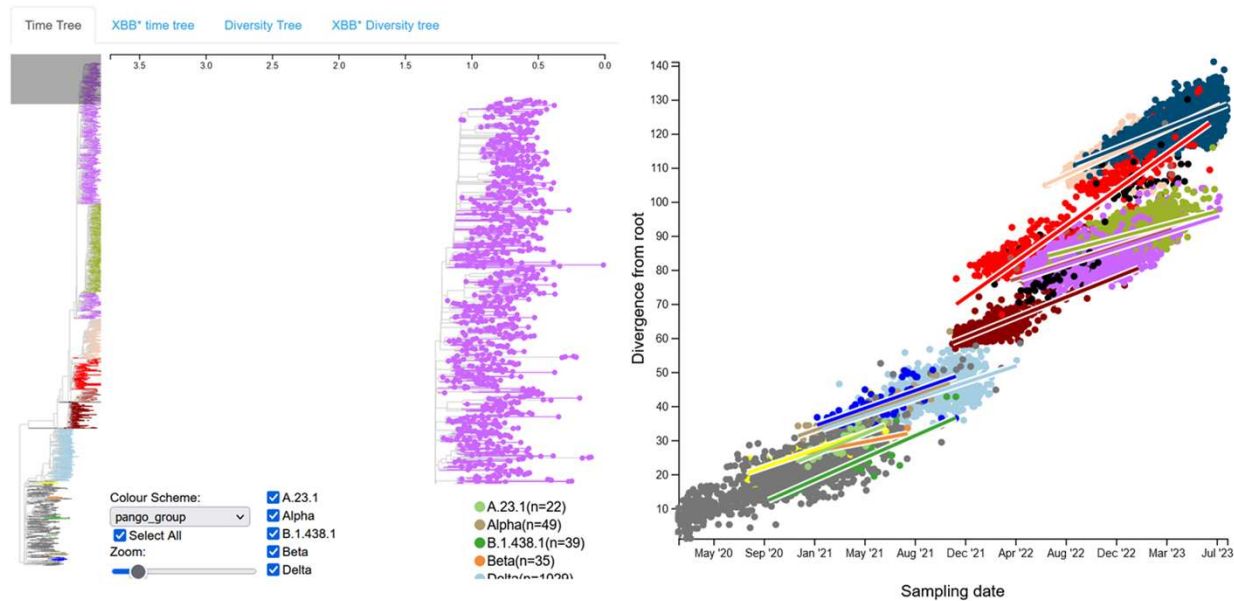
Quebec



iter shade represents per lineage case counts estimated using available genomics data
Last day of genomic data is 2023-08-26
Last day of accurate case counts is 2023-08-28

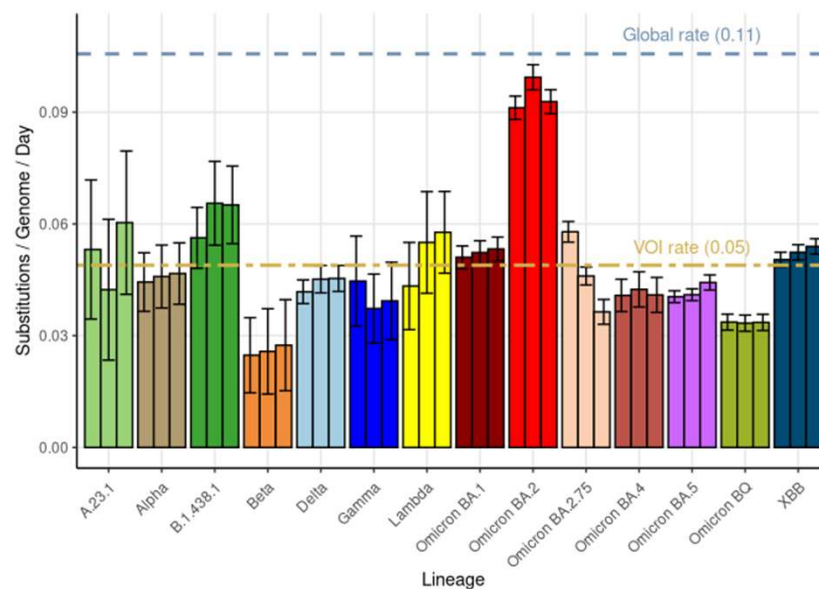


Plots: Phylogeny and Estimating Substitution Rates





Plots: Phylogeny and Estimating Substitution Rates





Other Information

- Weekly updates on the current SARS-CoV-2 landscape in Canada (Current Situation)
- Searchable lineage descriptions and ancestry information
- Detailed methodologies and source information
- Archive of past notebooks
- Open source, freely available.





Duotang as a Framework & Service

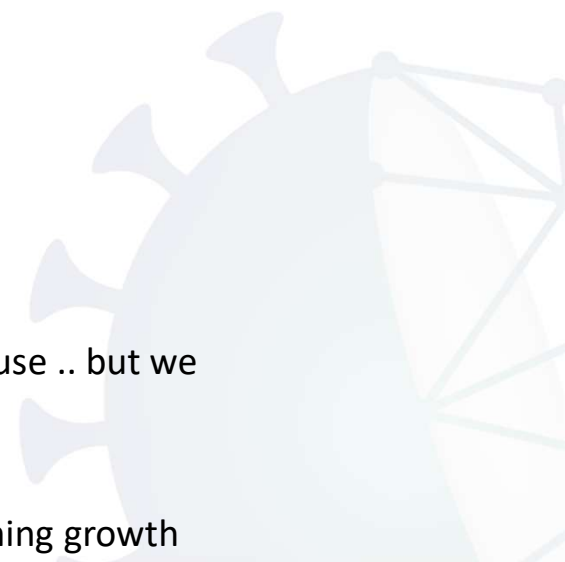
- Expansion of tools and methodologies learned from SARS-CoV-2 into other emerging viruses and data types.
- Enable rapid and automated deployment for visualization of custom datasets without requiring an in-house bioinformatician.
- Can serve as a framework for other jurisdictions interested in open, collaborative sequence data sharing and analysis.





Usage Example

- E.g. seeing BA.2 lineage contains multiple more divergent lineages based on the high substitution rate of the group.
- Find robust growth rates not so alarming versus international tools
- Alert both when there is a problem but also when there isn't a problem.
- Identify lineages of note specifically in the Canadian context.
- Notes from chat:
 - I like those use cases — when there is, and when there isn't, a problem
 - Maybe a concrete example: we knew that [whatever] was a problem because .. but we could see that [whatever else] was not because [..]
- BA.2.86 is not growing really notably anywhere, so avoid referring to alarming growth





Duotang Can Be Virus Agnostic

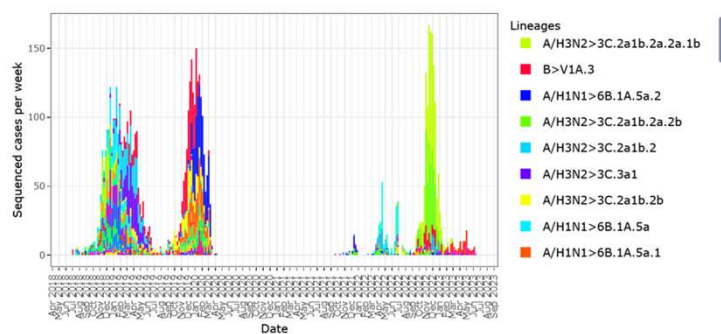


CoVaRR⁺Net

CAMEO - Fluotang

Fluotang, a genomic epidemiology analyses and mathematical modelling notebook. For Flu!

Influenza In Canada

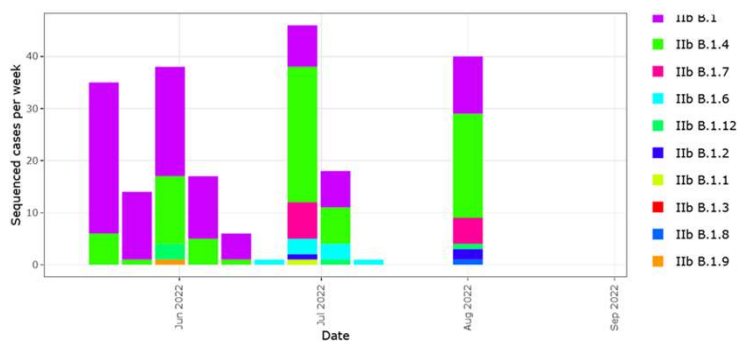


CoVaRR⁺Net

CAMEO - MPuotang

MPuotang, a genomic epidemiology analyses and mathematical modelling notebook. For Monkey Pox!

Monkey Pox In Canada





Expansion Into Emerging Pathogens

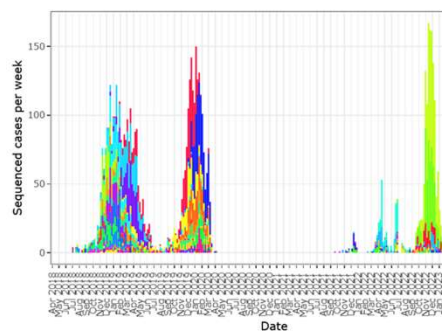


CoVaRR

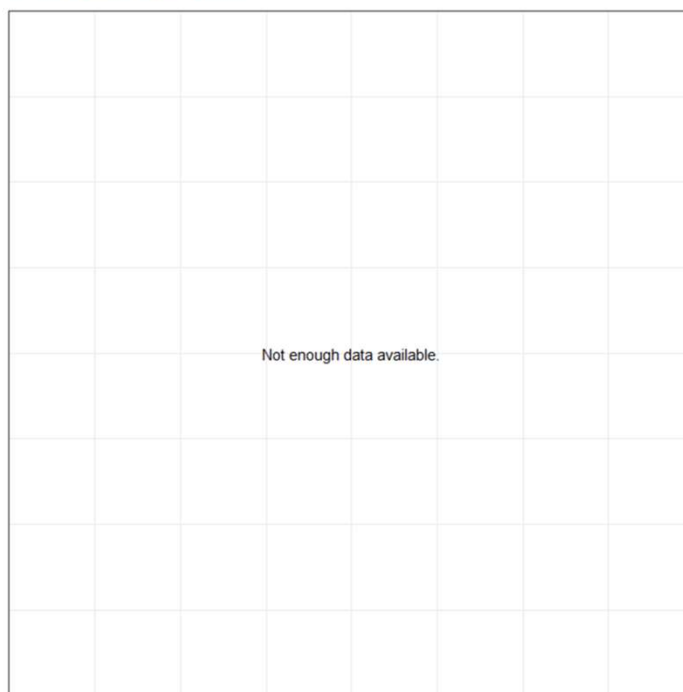
CAMEO - Fluotang

Fluotang, a genomic epidemiology analysis notebook. For Flu!

Influenza In Canada



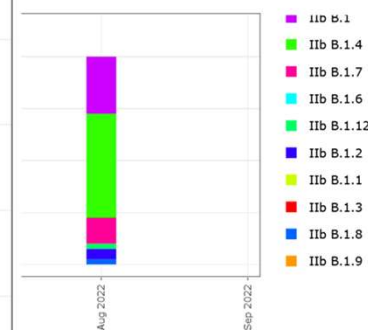
Plot single lineages in Canada *



RNet

analyses and mathematical modelling

ada





Duotang Can Be Data Agnostic



CAMEO - Duotang-GSD

Duotang-GSD, a genomic epidemiology analyses and mathematical modelling notebook. With GSD Data!

Code ▾



CAMEO - WWuotang

WWuotang, a genomic epidemiology analyses and mathematical modelling notebook. Using Metagenomics Data!

Sequenc

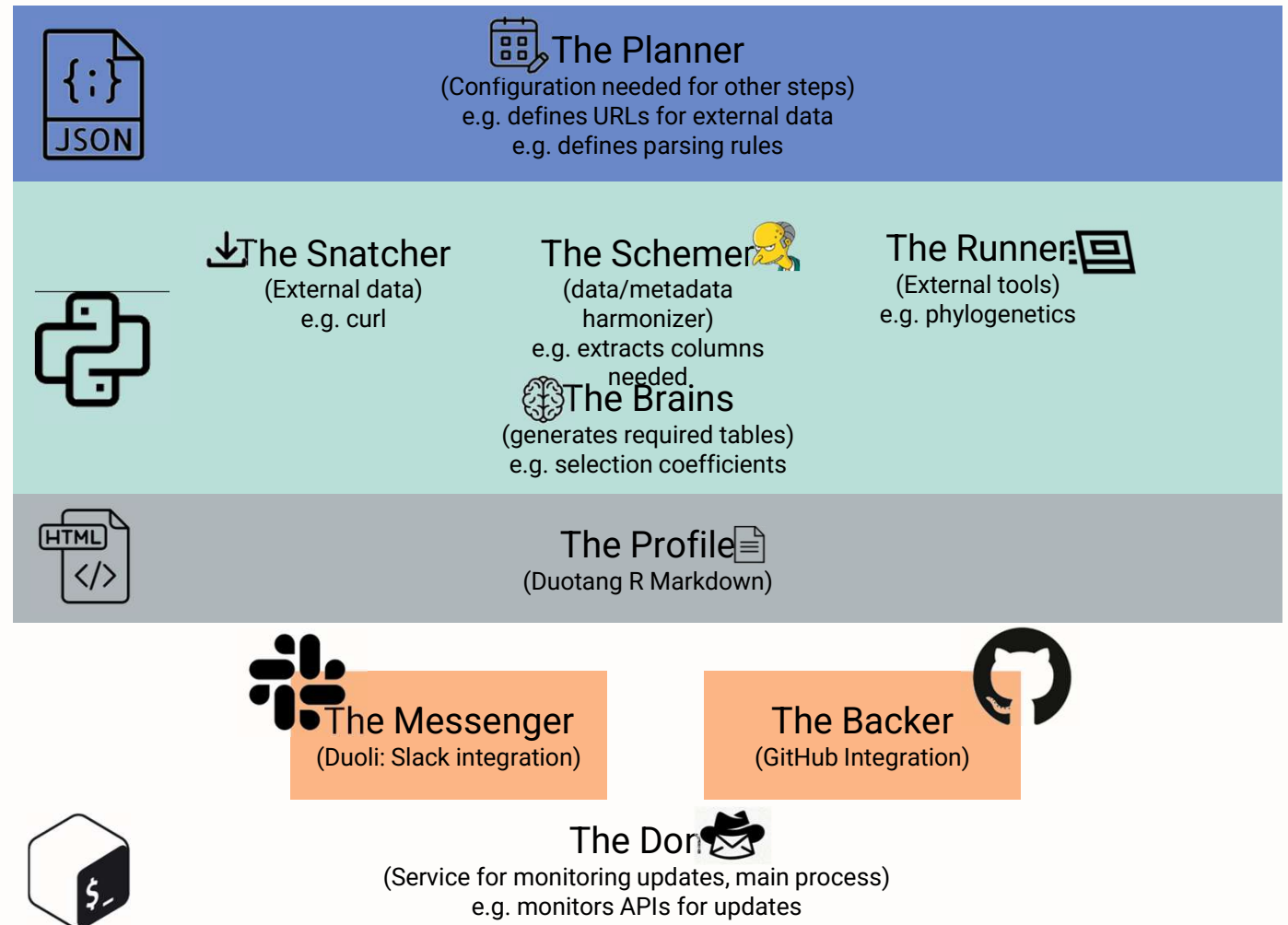


DuoGang (Not actual name)

Modular framework for data-independent Duotang notebooks

Current supported inputs:

- COVID (VirusSeq, GISAID)
 - Duotang
- Flu (GISAID)
 - Fluotang
- Wastewater (Steven/Mock QC)
 - WWuotang





Duotang Notebook Creation Time

- SARS-CoV-2: Years
- Wastewater: Months
- Influenza: Weeks
- Monkey Pox: Days
- Emerging pathogens & Custom datasets: Hours (?)

