COWW-Covid in WasteWater Analysis

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Rationale

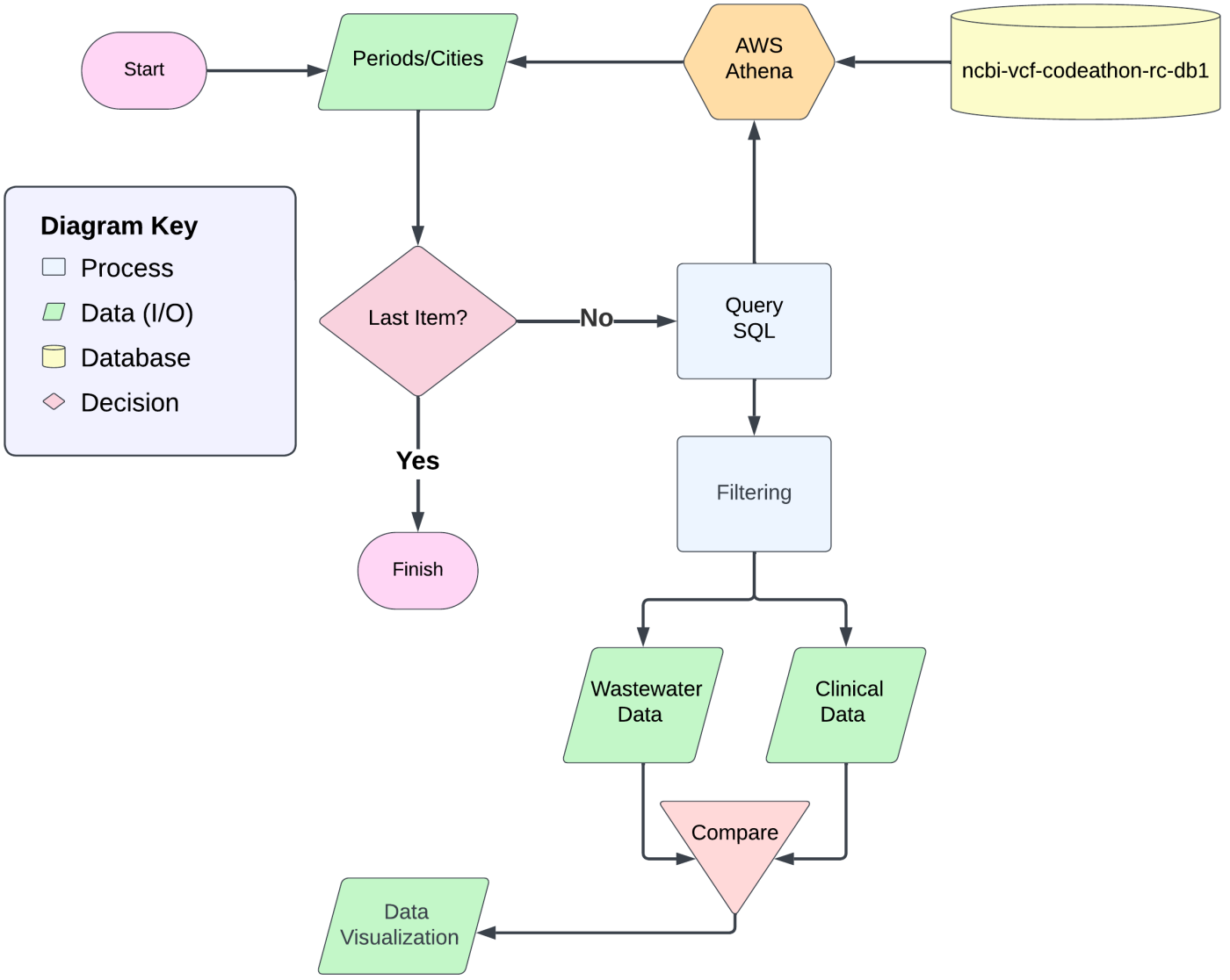
- Clinical isolate limitations:
  - Primarily represents severe cases, not fully capturing milder infections.
- Wastewater sequencing advantages:
  - Broad representation of circulating strains, including asymptomatic and mild cases.
  - Avoids bias towards severe cases.
- Wastewater sequencing challenges:
  - RNA degradation in wastewater may underestimate minor alleles or variants.
  - Includes non-infectious viral RNA, requiring careful interpretation.

Project Goals

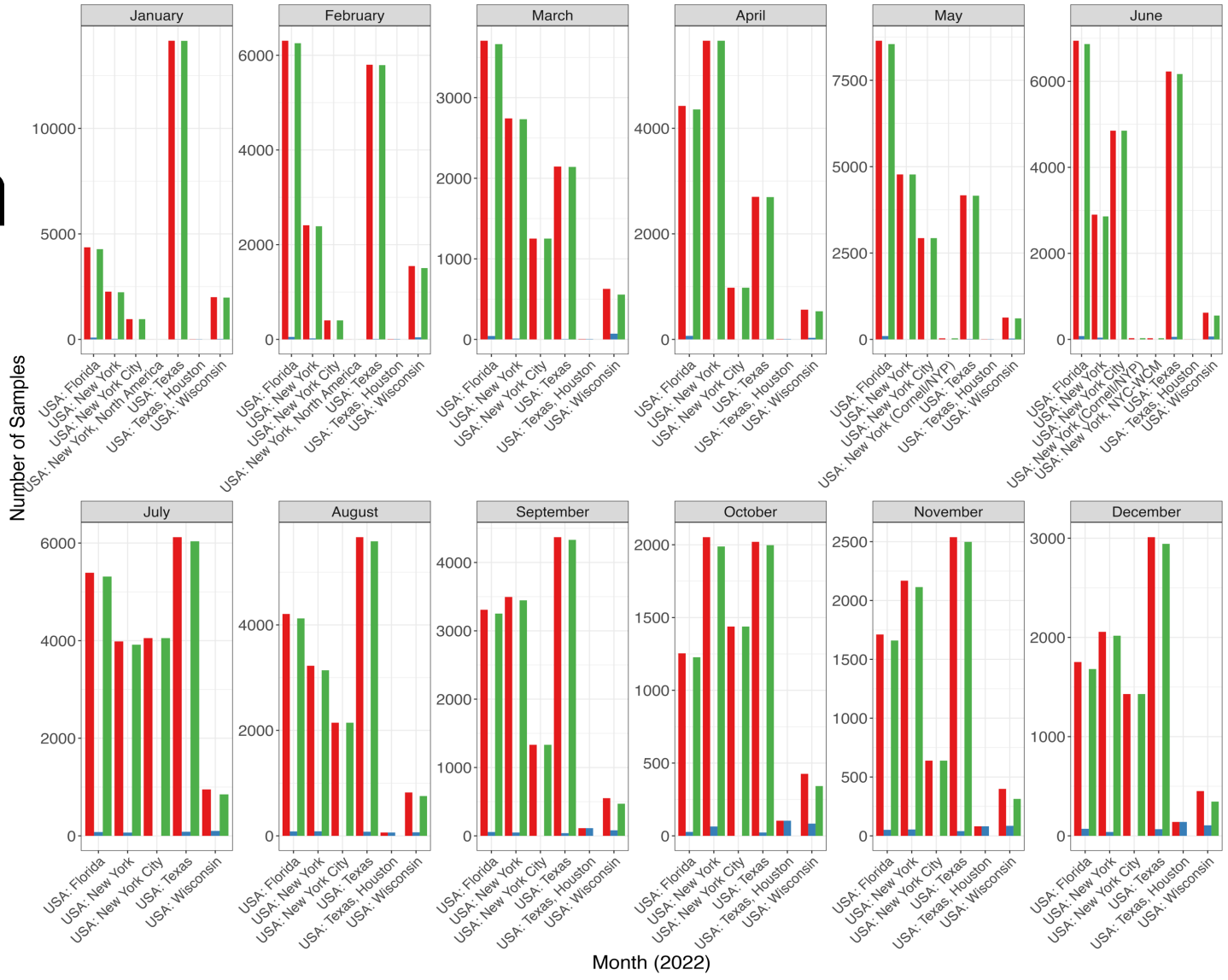
- Compare wastewater sequencing with clinical isolates of SARS-CoV-2 at specific geographical locations and time points.
- Evaluate representativeness of each approach for circulating viral strains.
- Gain insights into diversity and prevalence of SARS-CoV-2 in specific subsets.
- Understand strengths and limitations of wastewater and clinical isolate approaches.

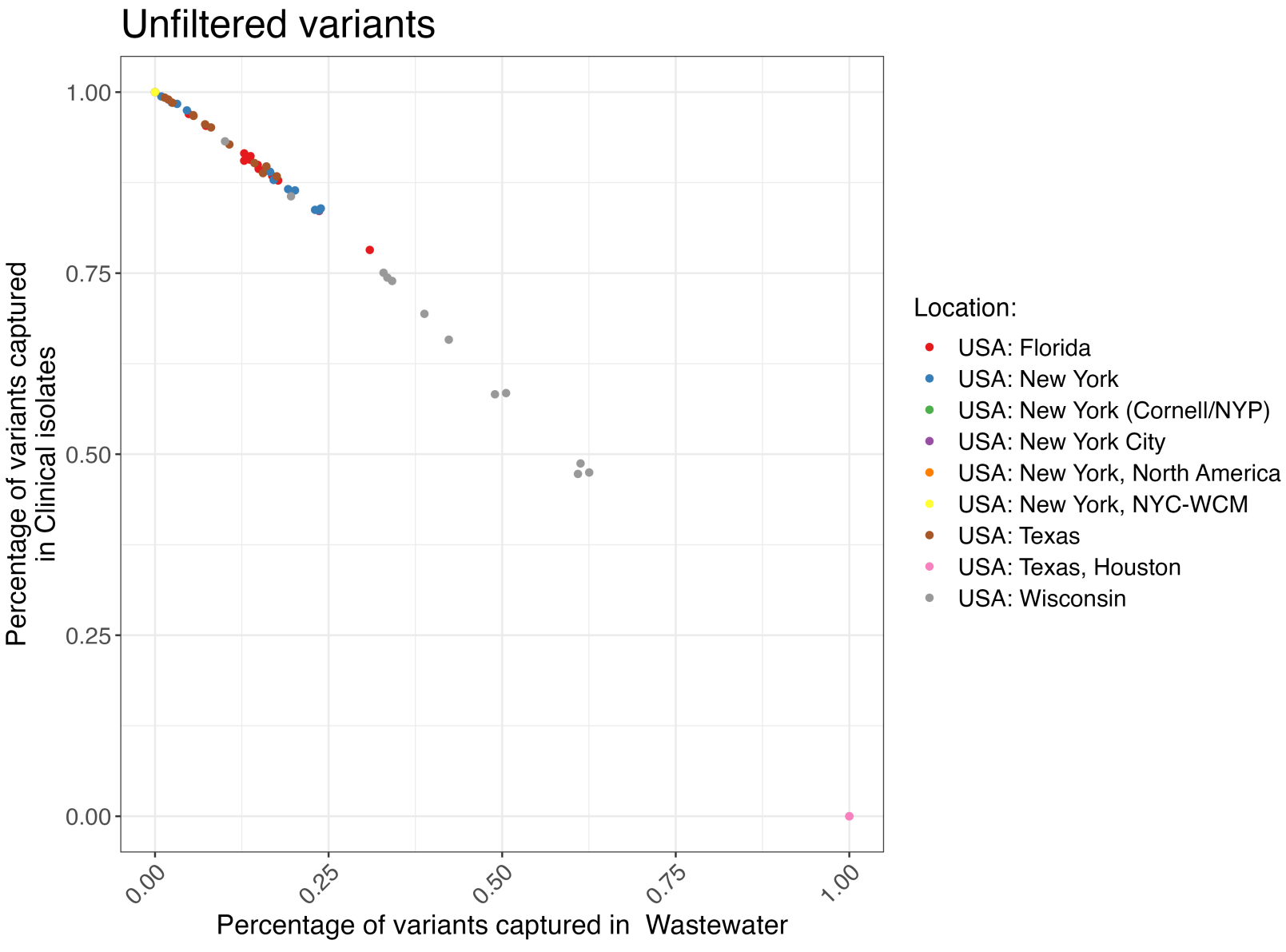
Approach

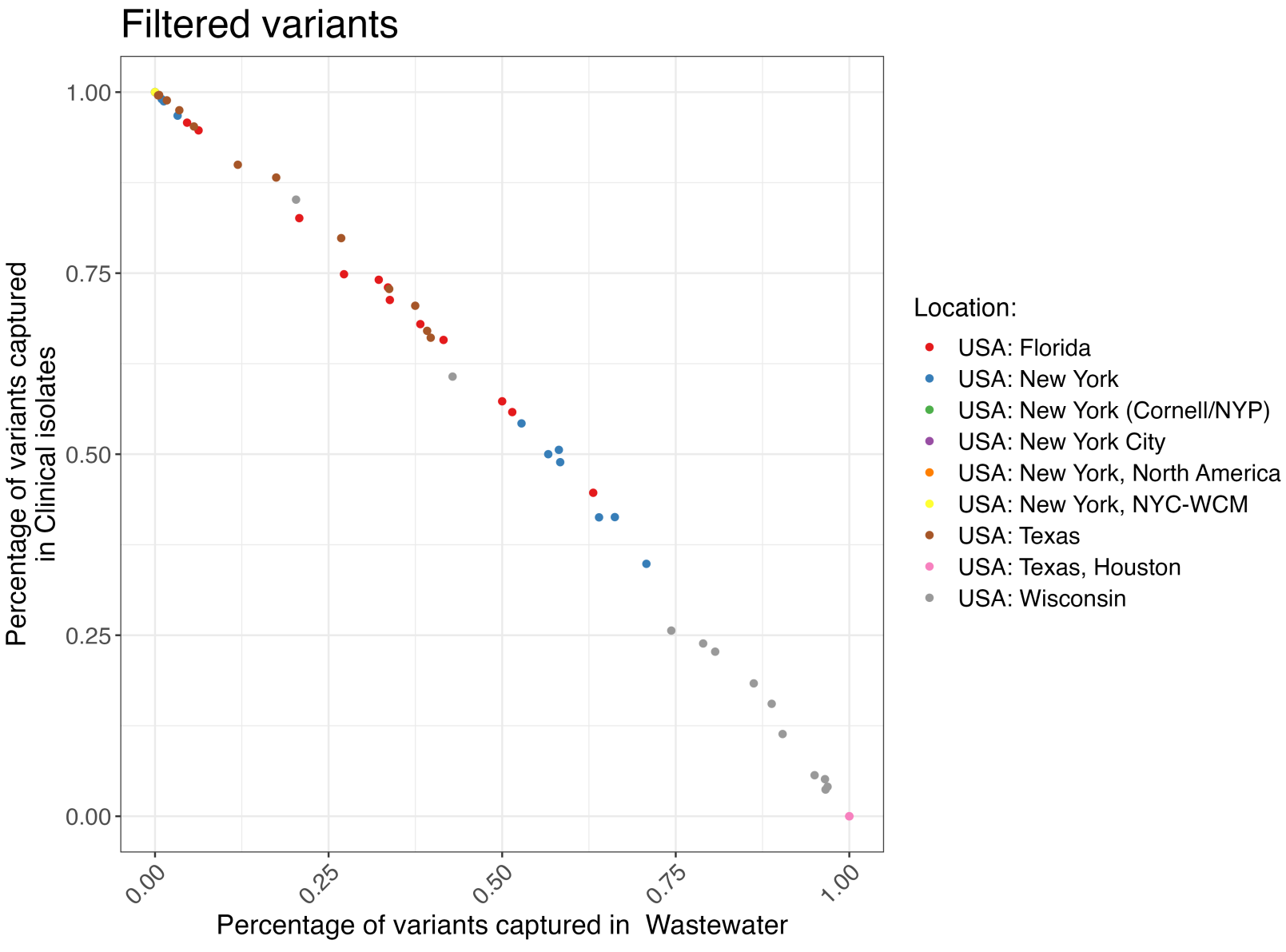
- Filters used
  - Synonymous and intergenic variants were removed.
  - Allele frequency cut-off ≥ 0.4



Sample Distribution




Unfiltered variants
Percentage of variants captured in Clinical isolates
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
Percentage of variants captured in Wastewater
Location:
USA: Florida
USA: New York
USA: New York (Cornell/NYP)
USA: New York City
USA: New York, North America
USA: New York, NYC-WCM
USA: Texas
USA: Texas, Houston
USA: Wisconsin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USA: Wisconsin

Conclusions

- When analyzing filtered variants, Wasterwater and Clinical data seems to have little overlap in our comparison.
- A possible cause may be the short time period of the analysis (1 month).
- For most locations, under sampling of Wastewater could be an issue.

Future directions

- Use different time windows.
- Understand the strengths and limitations of wastewater and clinical isolate approaches in terms of temporal alignment.
- https://github.com/NCBI-Codeathons/vcf-4-population-genomics-team-agustinho/tree/main