

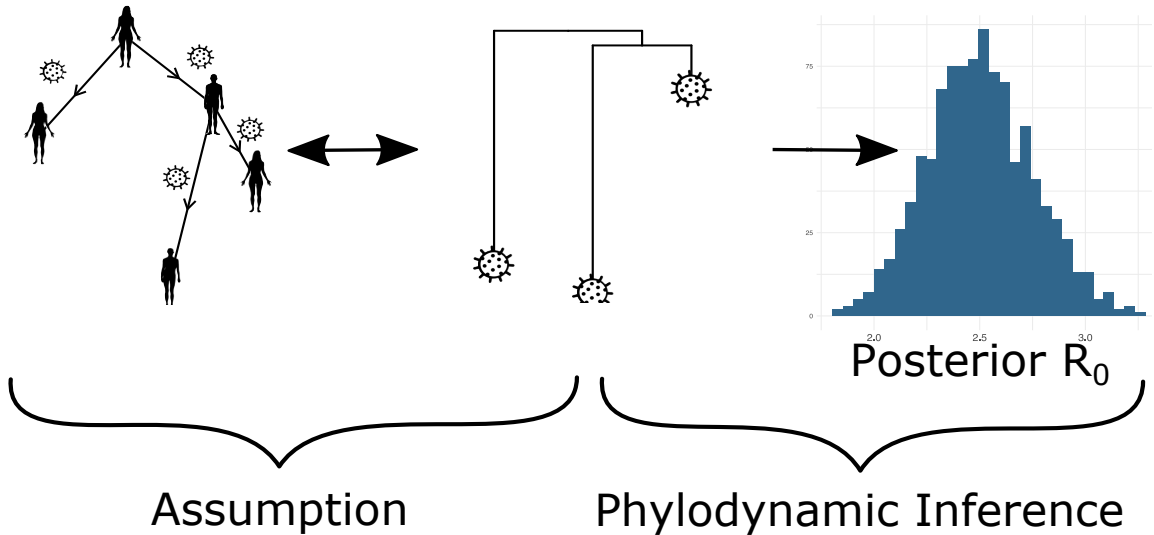
Assessing the effects of date and sequence data in phylodynamics

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Phylodynamics workflow



Isolating data effects

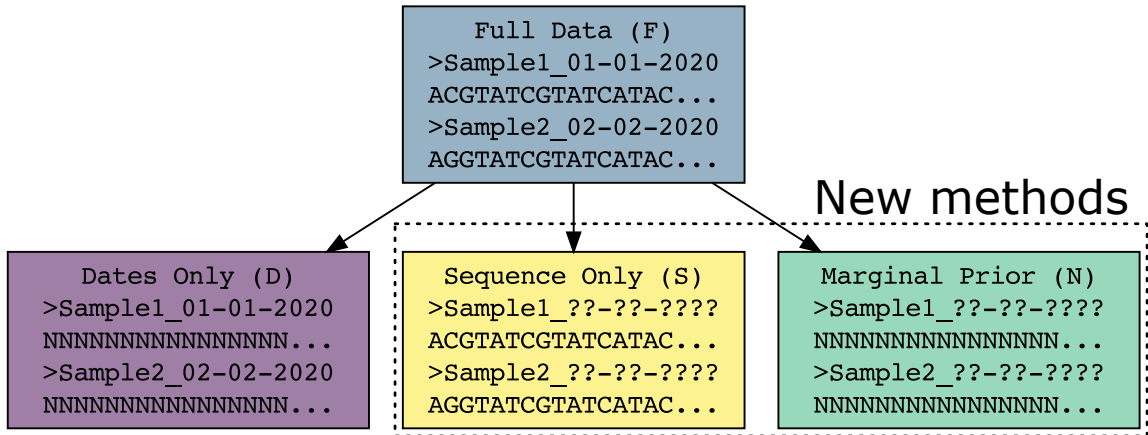
```
Full Data (F)
>Sample1_01-01-2020
ACGTATCGTATCATAC...
>Sample2_02-02-2020
AGGTATCGTATCATAC...
```

Isolating data effects

Full Data (F)
>Sample1_01-01-2020
ACGTATCGTATCATAAC...
>Sample2_02-02-2020
AGGTATCGTATCATAAC...

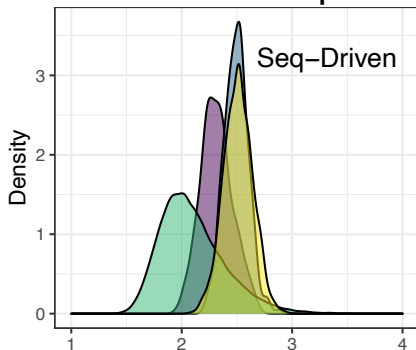
Dates Only (D)
>Sample1_01-01-2020
NNNNNNNNNNNNNNNNNN...
>Sample2_02-02-2020
NNNNNNNNNNNNNNNNNN...

Isolating data effects

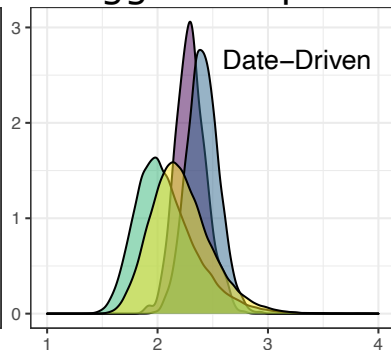


Simulated Data Example

More mutation
Smaller sample



Less mutation
Bigger sample

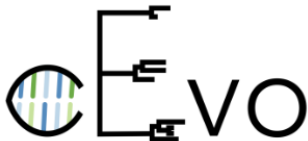


■ Date Data ■ Full Data ■ Marginal Prior ■ Sequence Data

Acknowledgments



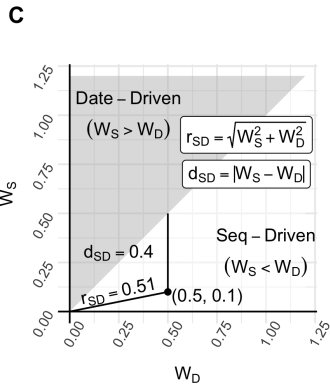
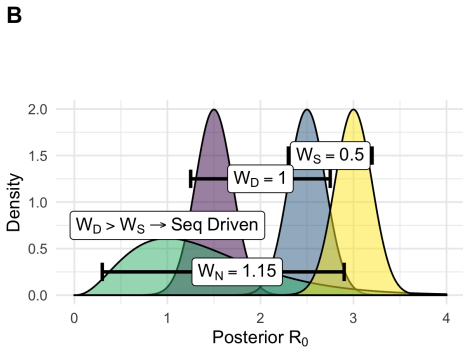
ETH zürich



Outstanding supervisors: Dr. Sebastian Duchene (UoM) and Dr. Tim Vaughan (ETH)

Since you asked :)

A	Marginal Prior (N)	Dates Only (D)	Full Data (F)	Sequence Only (S)
	<pre>>Sample1_???? NNNNNNNNNN... >Sample2_???? NNNNNNNNNN...</pre>	<pre>>Sample1_2020 NNNNNNNNNN... >Sample2_2021 NNNNNNNNNN...</pre>	<pre>>Sample1_2020 ACGTATCGTA... >Sample2_2021 AGGTATCGTA...</pre>	<pre>>Sample1_???? ACGTATCGTA... >Sample2_???? AGGTATCGTA...</pre>



Empirical SARS-CoV-2 Example

