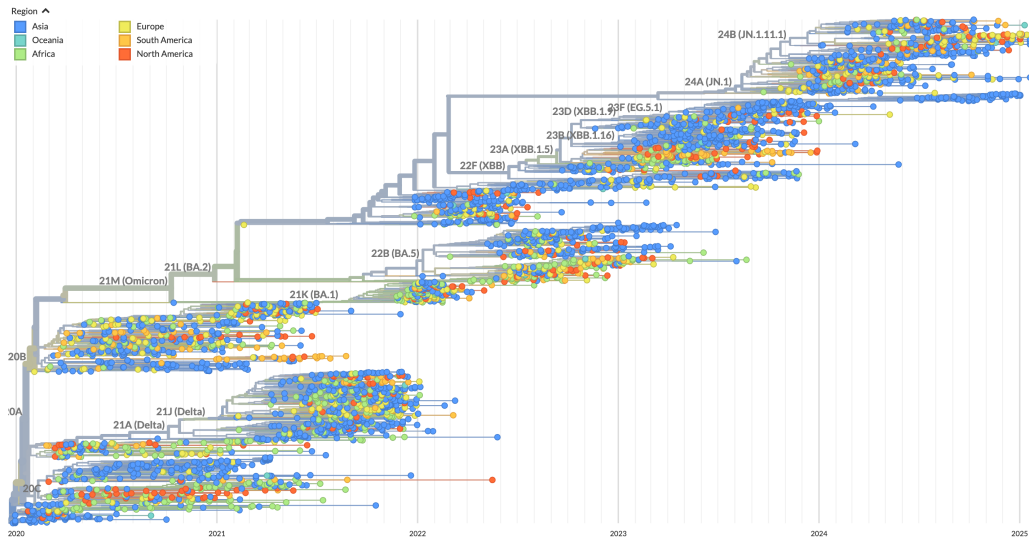


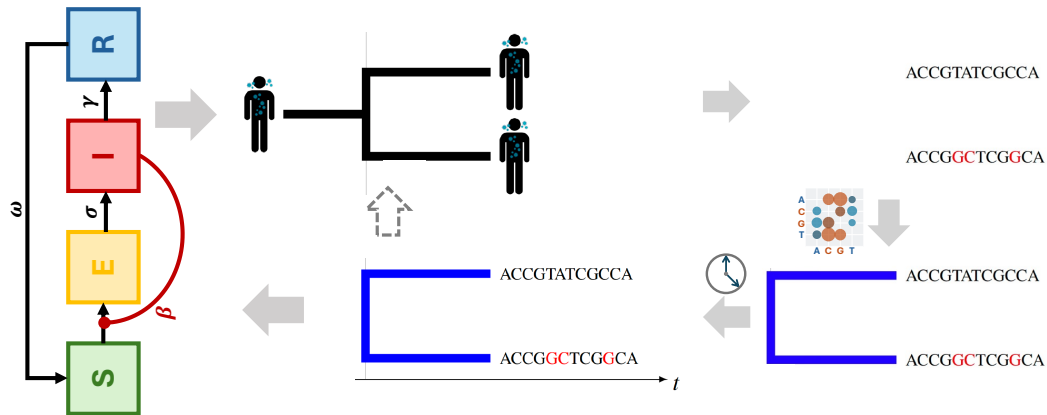
phylopomp: an R package for POMP inference on genealogies

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Background: genomic sequences & phylogenetic tree



Background: phylogenetics & phylodynamics



The goal of phylopomp is to infer the partially observed epidemiological dynamics, formulated by compartmental models, using the genealogy/phylogeny, reconstructed from sampled genomic sequences.

Installation

The github repo for phylopomp is on <https://github.com/kingaa/phylopomp/>. We can install the latest released version from github using devtools.

```
library(devtools)  
install_github("kingaa/phylopomp@0.14.8.0")
```

To confirm the package is installed successfully,

```
packageVersion("phylopomp")
```

```
[1] '0.14.8.0'
```

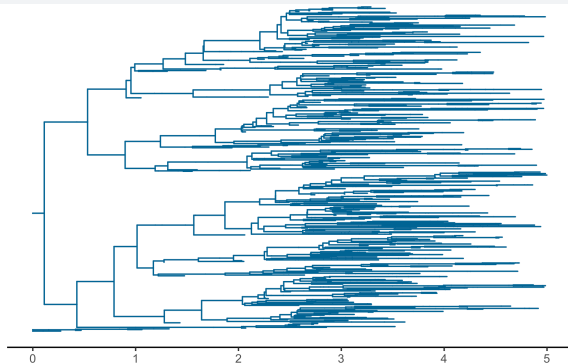
```
library(phylopomp)
```

Simulation and inference

- ▶ The first useful function of `phylomp` is to build customized models and simulate genealogies from it. Pre-defined models are included: linear birth-death model (`lbdp`), moran model, SIR, SEIR, two-class SIR model with super-infection (`si2r`), two-strain SIR model (`siir`), etc.
- ▶ The second is to infer the models given genealogies using `pomp`. This function is currently under development, while a few models are available: `lbdp`, `moran`, `sir`, and `seir`.

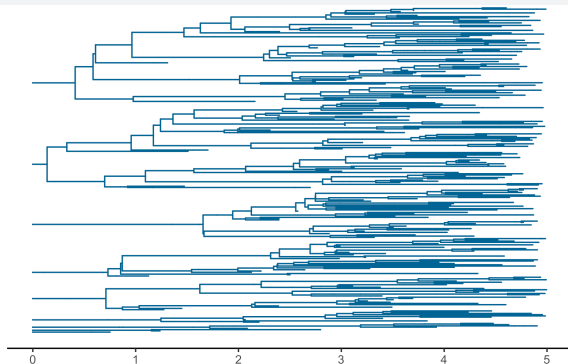
Example: simulation, pre-defined model I

```
set.seed(1234)
simulate("SIR",Beta=2,gamma=1,psi=2,S0=1000,I0=5,time=2) |>
  simulate(Beta=5,gamma=2,time=5,psi=3) -> model.sir # update params
plot(model.sir)
```



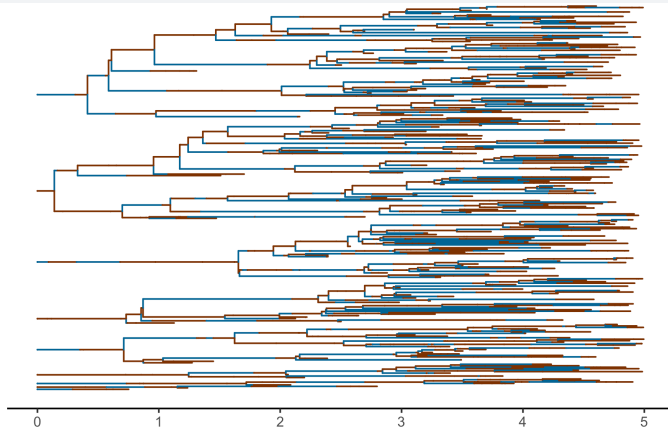
Example: simulation, pre-defined model II

```
set.seed(1234)
simulate("SEIR",Beta=2,sigma=2,gamma=1,psi=2,S0=1000,I0=5,time=2) |>
  simulate(Beta=5,gamma=2,time=5,psi=3) -> model.seir
plot(model.seir)
```



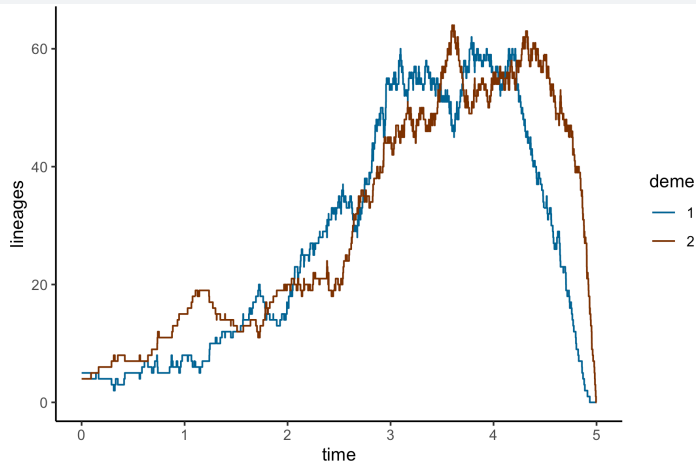
Example: simulation, pre-defined model III

```
plot(model.seir, obscure=FALSE)
```



Example: simulation, pre-defined model IV

```
lineages(model.seir, obscure=FALSE) |> plot()
```



Example: inference, pre-defined model I

```
library(pomp)
set.seed(1234)
# simulate a geneal object from an SIR model
simulate("SIR",Beta=3,gamma=1,psi=2,omega=1,S0=100,I0=5,time=10) -> x
# build a pomp object
x |>
  sir_pomp(
    Beta=3,gamma=1,psi=2,omega=1,
    S0=100,I0=5,R0=0
  ) -> po
po |> pfilter(Np=5000) -> pf

pf |> logLik()


[1] -326.5652
```

Example: inference, pre-defined model II

```
set.seed(1234)
simulate("SEIRS",      # simulate a genealogy from an SEIR model
  Beta=4,sigma=1,gamma=1,psi=1,omega=1,
  S0=100,E0=3,I0=5,R0=100, time=5
) -> G
G |>
  seirs_pomp(
    Beta=4,sigma=1,gamma=1,psi=1,omega=1,
    S0=100,E0=3,I0=5,R0=100
  ) |> pfilter(Np=1000) |>
  replicate(n=20) |> concat() -> pf
pf |> logLik() |> logmeanexp(se=TRUE)
```

est	se
-168.856637	1.265223

License, acknowledgments, and links

- ▶ This lesson is prepared for the Simulation-based Inference for Epidemiological Dynamics module at the Summer Institute in Statistics and Modeling in Infectious Diseases, SISIMID.
- ▶ The materials build on previous versions of this course and related courses.
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- ▶ Produced with R version 4.4.2 and pomp version 6.3.
- ▶ Compiled on 2025-07-23.

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