Epiverse TRACE LAC

Pontificia Universidad JAVERIANA Bogotá

Serofoi 0.0.9

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serofoi 0.0.9

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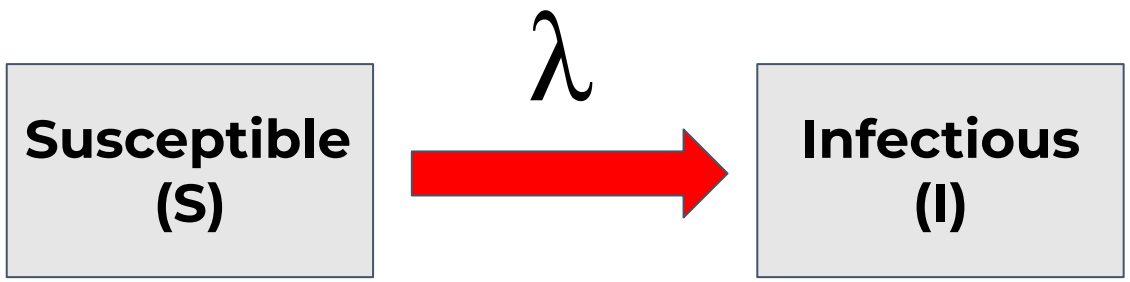
An R package for estimating the **Force-of-Infection (FoI)**



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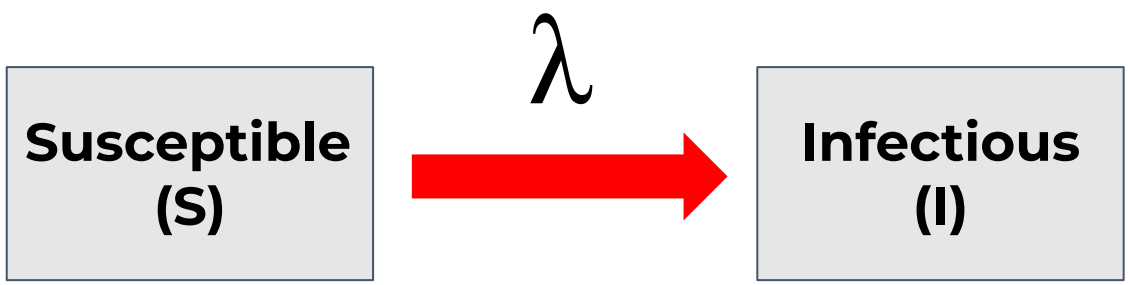
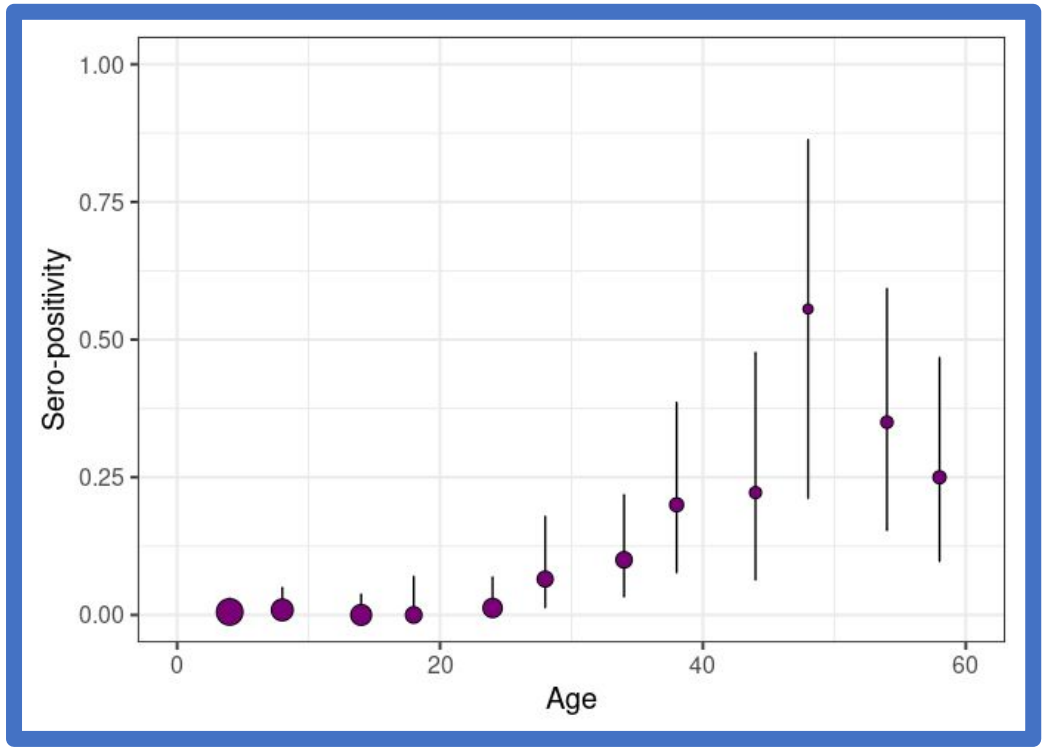
An R package for estimating the **Force-of-Infection (FoI)** from **age-disaggregated** population-based cross-sectional serosurveys.





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Usage:

Infectious diseases for which IgG antibodies can be measured.

Serosurvey Criteria for serofoi

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- Are population-based cross-sectional surveys (not hospital-based).

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- Indicate diagnostic test(s) used. The current version of ***serofoi*** only applies to IgG antibodies.

Serosurvey Criteria for serofoi

- Are population-based cross-sectional surveys (not hospital-based)
- Specify individuals' age or age group
- Indicate diagnostic test(s) used. The current version of ***serofoi*** only applies to IgG antibodies
- Identify the date (year) and place of sample collection

Biological Assumptions of serofoi

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- No sero-reversion.

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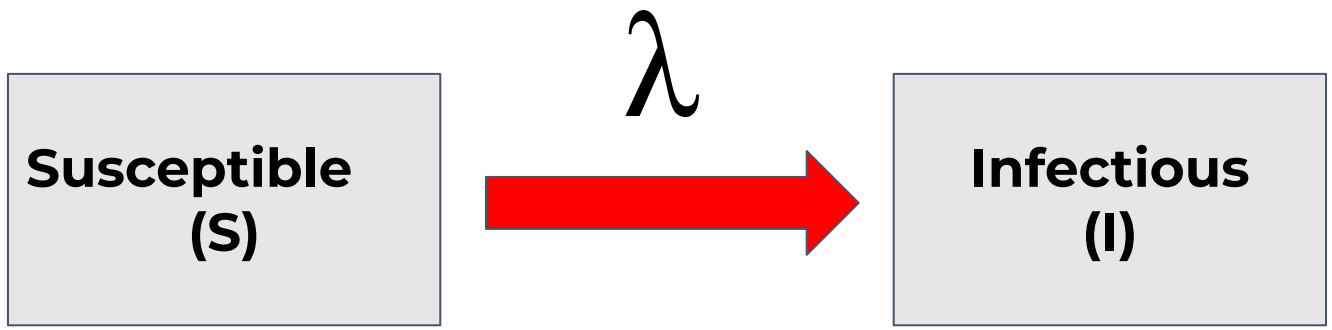
- No sero-reversion.
- No age-dependency.
- No impact from migration processes.
- No differences in the mortality rate of infected versus susceptible individuals.

Force of Infection (FoI)

Rate at which susceptible individuals exposed to a pathogen become infected.



Constant vs Time-varying FoI:

- The FoI is often incorrectly assumed to be constant over time.

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serofoi allows both

- Constant FoI
- Time-varying FoI

Constant vs Time-varying FoI:

Model Option	Description and usage
`constant`	Constant FoI
`tv_normal`	Time-varying normal FoI: slow change in FoI
`tv_normal_log`	Time-varying normal-log FoI: fast epidemic change in FoI

https://epiverse-trace.github.io/serofoi/articles/foi_models.html

Getting started with *serofoi*

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Case study 1:
Chikungunya (fast-spreading epidemic)

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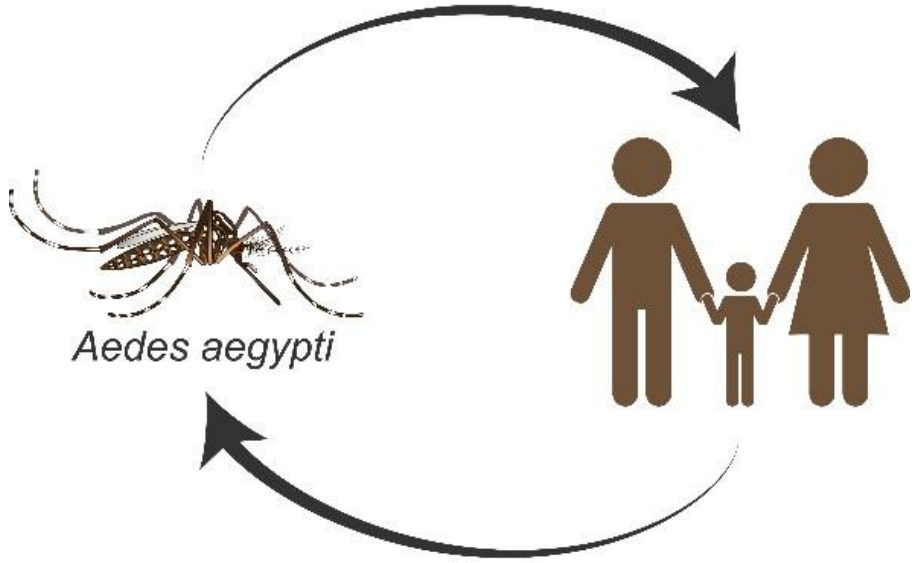
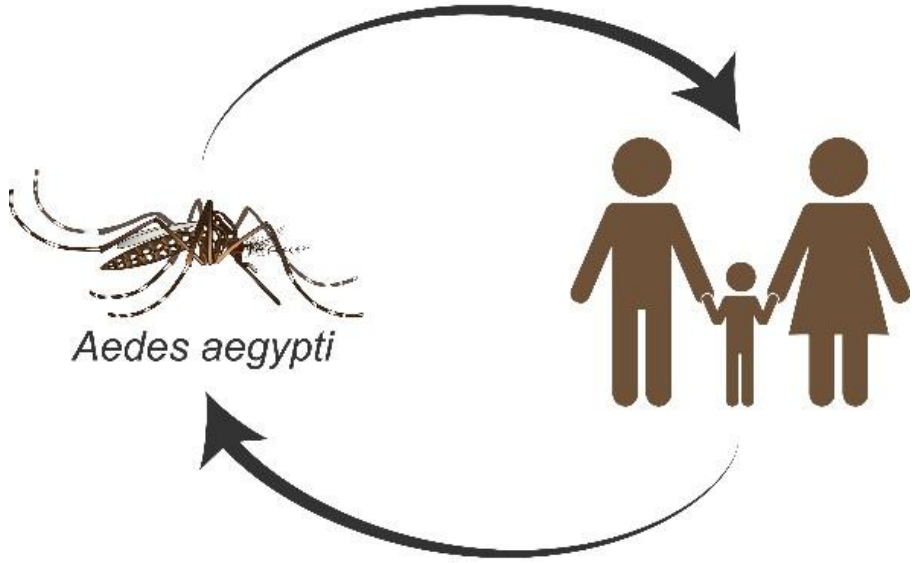
- Transmitted mainly by the *Aedes aegypti* mosquito



Case study 1: Chikungunya (fast-spreading epidemic)

- Transmitted mainly by the *Aedes aegypti* mosquito
- Originally endemic to Africa and Asia
- Arrives to the Americas on 2013 with no prior immunity in the population



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Case study 1:
Chikungunya (fast-spreading epidemic)

Methodological challenge:

How is it best to untangle the endemic and epidemic patterns of Chikungunya?

Case study 1:
Chikungunya (fast-spreading epidemic)

```
# Load and prepare data
data("chik2015")
chik2015p <- prepare_serodata(chik2015)
```

population-based study conducted in Bahia, Brazil in October-December 2015.

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Case study 1: Chikungunya (fast-spreading epidemic)

```r
# Implementation of the models
m1_chik <- run_seromodel(serodata = chik2015p,
                         foi_model = "constant",
                         n_iters = 1000,
                         n_thin = 2)

m2_chik <- run_seromodel(serodata = chik2015p,
                         foi_model = "tv_normal",
                         n_iters = 1500,
                         n_thin = 2)

m3_chik <- run_seromodel(serodata = chik2015p,
                         foi_model = "tv_normal_log",
                         n_iters = 1500,
                         n_thin = 2)
```

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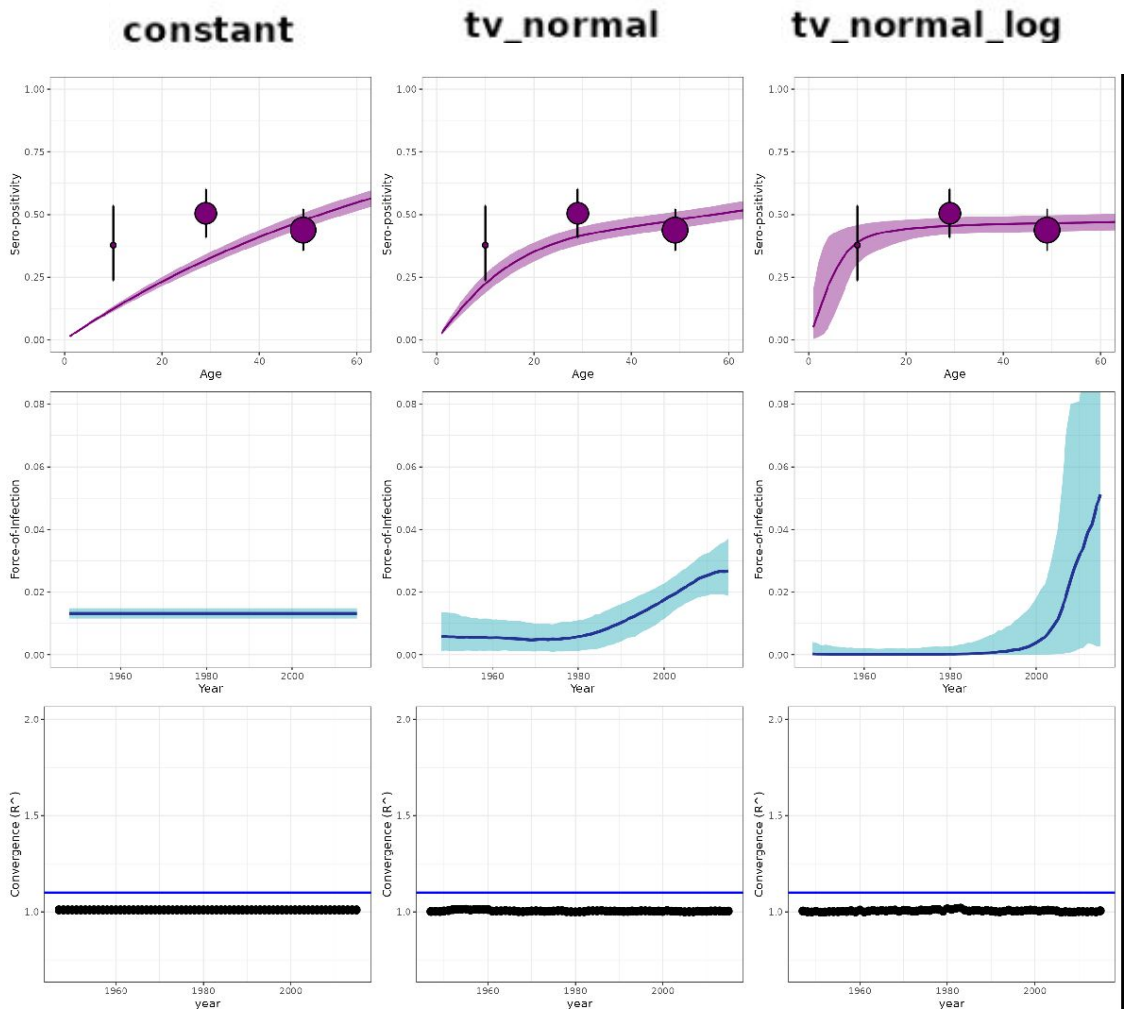
Case study 1: Chikungunya (fast-spreading epidemic)

Seroprevalence Fitting

FoI estimate

Convergence criteria



Case study 1:
Chikungunya (fast-spreading epidemic)

foi_model: constant
dataset: BRA 2015(S019)
elpd: -39.57
se: 8.48
converged: Yes

foi_model: tv_normal
dataset: BRA 2015(S019)
elpd: -20.76
se: 1.98
converged: Yes

foi_model: tv_normal_log
dataset: BRA 2015(S019)
elpd: -12.58
se: 0.81
converged: Yes

Case study 1:
Chikungunya (fast-spreading epidemic)

foi_model: constant
dataset: BRA 2015(S019)
elpd: -39.57
se: 8.48
converged: Yes

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dataset: BRA 2015(S019)
elpd: -20.76
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dataset: BRA 2015(S019)
elpd: -12.58
se: 0.81
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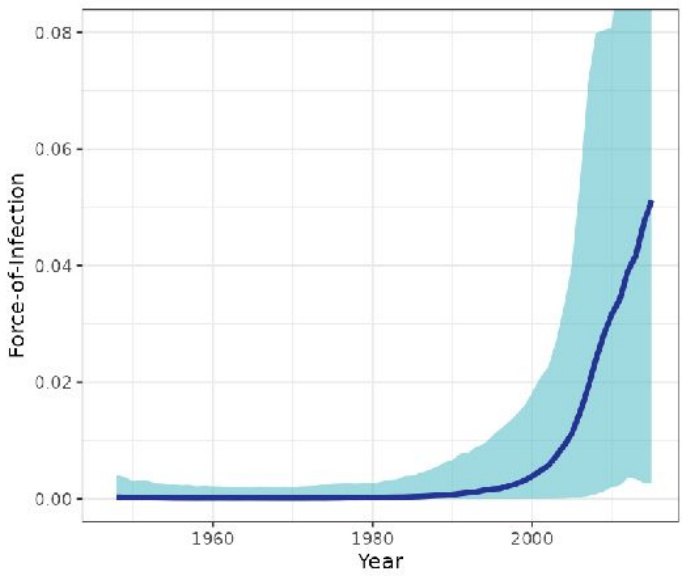

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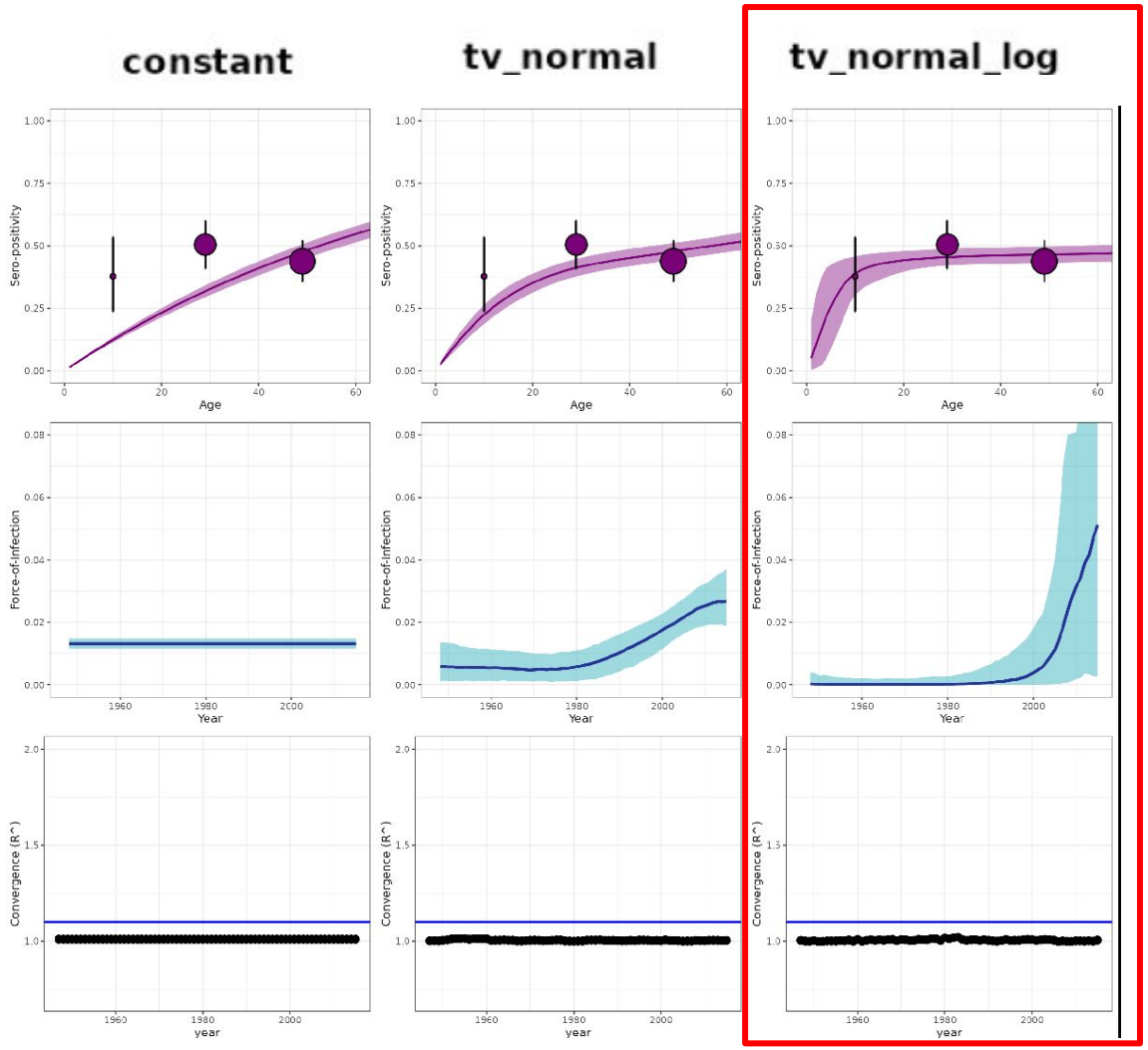

Case study 2: Chagas Disease

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Case study 2: Chagas Disease

- *Trypanosoma cruzi*
- Endemic to Latin America
- Transmitted by triatomine bugs

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Case study 2: Chagas Disease

Control: Insecticide spraying has been extensively implemented in Latin America since the 1970s-80s.

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Case study 2: Chagas Disease

Methodological challenge:

Estimate the historical effectiveness of the control strategies across endemic areas?

Case study 2: Chagas Disesase

```
# Load and prepare data
data("chagas2012")
chagas2012p <- prepare_serodata(chagas2012)

# Implementation of the models
m1_cha <- run_seromodel(serodata = chagas2012p,
                        foi_model = "constant",
                        n_iters = 800)
m2_cha <- run_seromodel(serodata = chagas2012p,
                        foi_model = "tv_normal",
                        n_iters = 800)
```

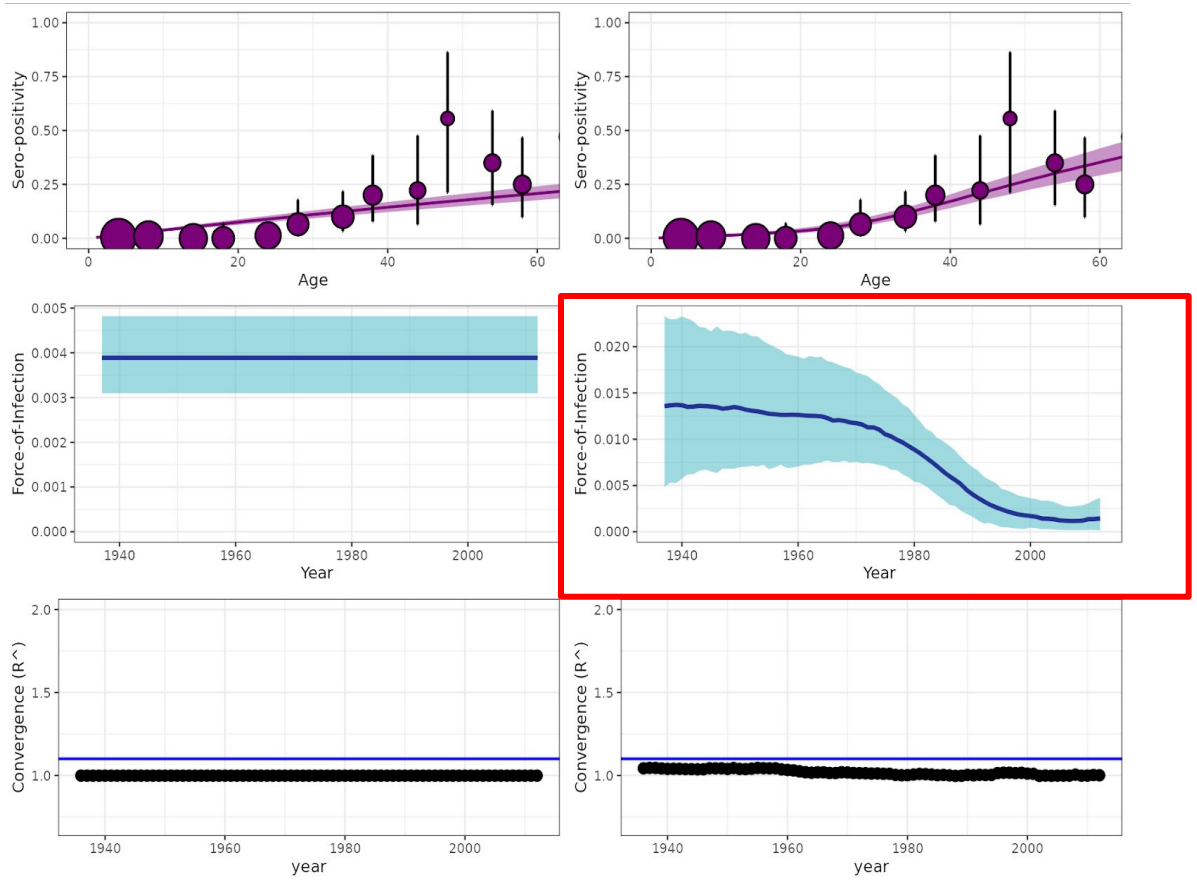
Case study 2: Chagas Disesase

```
# Load and prepare data
data("chagas2012")
chagas2012p <- prepare_serodata(chagas2012)

# Implementation of the models
m1_cha <- run_seromodel(serodata = chagas2012p,
                        foi_model = "constant",
                        n_iters = 800)
m2_cha <- run_seromodel(serodata = chagas2012p,
                        foi_model = "tv_normal",
                        n_iters = 800)
```

foi_model: constant
elpd: -92.64
se: 6.41
converged: Yes

foi_model: tv_normal
elpd: -74.52
se: 5.92
converged: Yes



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Conclusions

- **serofoi** FoI estimations in different real case scenarios
- **serofoi** is able to recover the endemic or epidemic trends of different diseases
- Bayesian comparison criteria can be used to identify trends on the FoI
- Future versions of **serofoi** might include additional models, visualization tools and further model comparison criteria

Contribute in serofoi:

Contributions are welcome via pull requests, taking into account the code of conduct.

GitHub: https://github.com/epiverse-trace/serofoi

Website: https://epiverse-trace.github.io/serofoi/

Get in touch:

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Thanks!