Bayesian multi-state models and software for intermittently-observed individual data, motivated by estimating infection duration distributions.

Chris Jackson





Outline

Brief introduction to multi-state models for intermittently-observed data

Introducing a new R package msmbayes, which makes these models Bayesian

Work in progress using these models, made easier with this software:

- using Bayesian methods to facilitate relaxing the Markov assumption
- estimating the duration of infection from intermittent testing data

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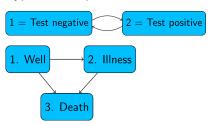
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Multi-state process

Multi-state models represent how an individual can move between different states over time.

Typical examples:



They have been applied to many different kinds of data structures

b diverse modelling frameworks and literature

Intermittently observed, individual data

For a set of individuals, a state is observed, at a set of arbitrary times.

Person	Time	State
1	0	1
1	1.2	1
1	5	2
1 2 2	0.1	1
2	8	3

State in between the times is **not necessarily known** at any other times

[&]quot;Intermittently-observed", "panel", "interval-censored" data.

Continuous-time multi-state models

Parameters: transition intensities $q_{rs}(t)$: rate of moving to s for people in r at time t.

With covariates x, typically $q_{rs}(t;\mathbf{x})=q_{rs}^{(0)}(t)\exp(\beta_{rs}^{'}\mathbf{x})$

Given these, determine the transition probabilities

$$p_{rs}(u,t) = P(S(t+u) = s \quad | \quad S(t) = r, \quad \ldots)$$

for a state S(t) over any time interval t, t+u

hence compute the likelihood for intermittently-observed individual data

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Transition probabilities can be calculated easily in practice (via solving Kolmogorov differential equation)

- if the intensities $q_{rs}(t)$ don't depend on previous states visited and transition times: Markov assumption
- lackbox however they can easily depend on the time t since the start of the process

Solution particularly simple if $q_{rs}(t)$ is constant with t

lacksquare Sojourn time (one period in state r) is \sim Exponential($\sum_s q_{rs}$)

(Simple generalisation if $q_{rs}(t)$ is piecewise-constant, different in different time periods)

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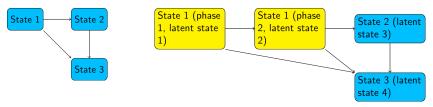
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Phase-type models: relaxing the Markov assumption

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Replace an observable state (state 1 in this picture) with a set of latent states ("phases"). Latent states follow a Markov model.

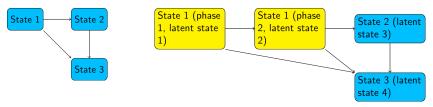
Hidden Markov model: hence likelihood calculation tractable

Semi-Markov model:

- Risk of transition out of state depends on time spent in it
- Observable state has a "phase-type" sojourn distribution, instead of the exponential.
- More latent phases and transitions → more flexible sojourn distribution (... more estimation challenges).

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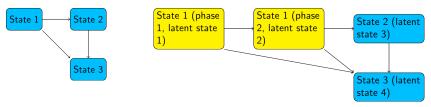
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Fits multi-state models for intermittently-observed data, and variants, using maximum likelihood

► Stock R optimisation algorithms ("BFGS" by default)

- Convergence failed, or unreliable ("non positive-definite Hessian").
- ... Evidence of weak identifiability, irregular likelihoods.
- Often due to users specifying over-parameterised models
 - Hard to relate the meaning of the "transition intensity" parameters to the (intermittently-observed) data
 - Confusion with discrete-time, where transition probabilities easily estimated by proportions transitioning in data
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Aim: Develop a Bayesian equivalent to the msm package

Constrain parameters using prior information

Emphasise posterior and prior distributions, to communicate uncertainty

making any weakness of information clearer to users

Exploit modern computational algorithms

both correctness and speed desirable

A motivating application: infection positivity duration

Determining the length of an infection (defined as testing positive) based on individual, longitudinal, testing data

Times in infection (and non-infection) states typically not exponentially-distributed

Simulate data roughly inspired by respiratory infections (SIREN study of healthcare workers, COVID-19 Infection Survey)

➤ 3600 observations (36 monthly tests from 100 people), though will be more in practice...

msmbayes R package

https://chjackson.github.io/msmbayes.

- Uses Stan for Bayesian estimation, via the cmdstanr package.
- ► MCMC, variational inference or posterior mode optimisation / Laplace approximation
- posterior package and rvar data type were helpful

To fit a model, supply the data, a matrix indicating the allowed transitions, and the priors. Example syntax:

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Specify judgements for $1/q_{rs}$: the mean time from state r to s (given no competing risks)

Supply prior median and upper (or lower) 95% quantile, e.g

- \blacktriangleright 10 months (up to 30 months) for mean time until next infection $1/q_{12}$
- lacksquare 2 weeks (up to 1 month) for mean length of infection $1/q_{21}$
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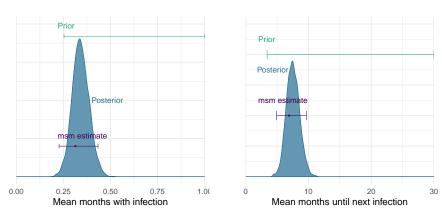
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Outputs: two transition rates, no covariates.

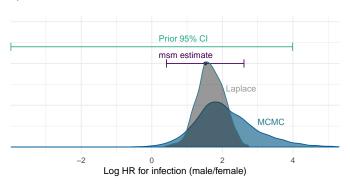


Posterior distribution from msmbayes agrees with maximum likelihood estimates from msm

Influence of prior apparent from moved posterior mode

Outputs: two transition rates, two covariates on each.

8 parameters, 3600 observations. Example parameter estimate:



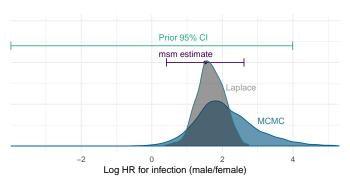
Speed / accuracy trade-off

1 hour for MCMC, which reveals skewed posterior

A few seconds to estimate posterior mode by optimisation (similar speed to msm). 1 min for Laplace approx around mode, which underestimates uncertainty

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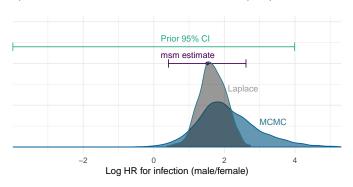
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Fitting phase-type models



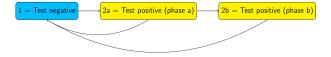
Simulate data with phase-type model for infection state:

... Sojourn distribution is a 50/50 mixture of latent "short stayers" (exponential mean 4 days) and "long stayers" (sum of exponentials mean 4+30)

Maximum likelihood estimation of this model in msm does not converge!

Instead, fit model in msmbayes. Simply specify nphase: number of hidden phases per state.

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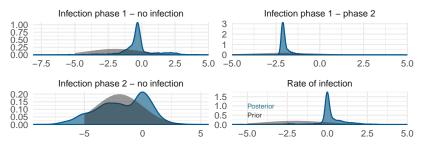
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Priors + posteriors from fitted phase-type models

Log transition rates

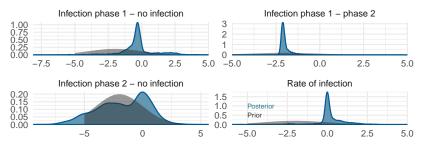


Transition rate from latent phase 2 is not identifiable

Mean sojourn time in infection state is identifiable, and more uncertain than under a basic Markov model

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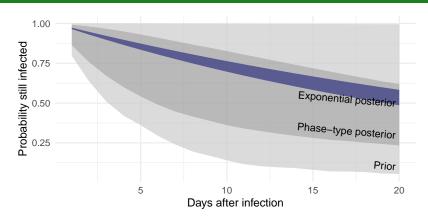


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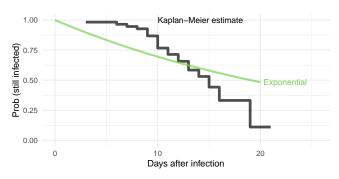
Phase-type model	Markov model
30 days (12, 37)	31 (27, 37)
Phase 1 21 (2, 34), Phase 2 43 (4, 254)	

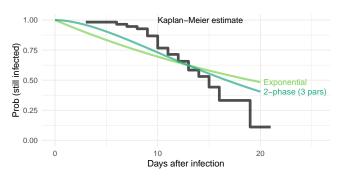
Posterior of sojourn distribution from phase-type model

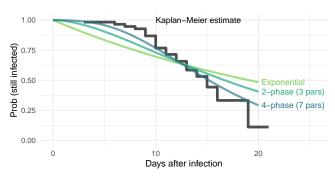


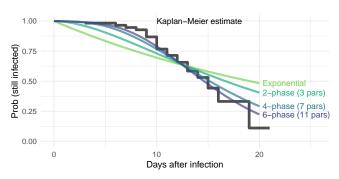
Very uncertain, but influenced by the weak prior for the unidentifiable transition rate

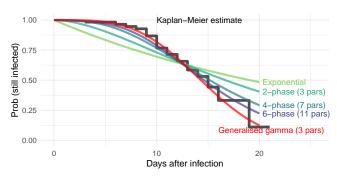
Further research needed on constructing meaningful priors in phase-type models



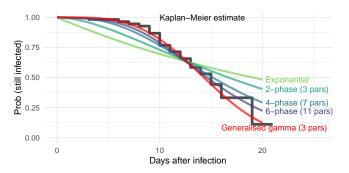








From ATACCC "Assessment of Transmission and Contagiousness of COVID-19 in Contacts" study, via daily PCR tests from 57 people



Phase-type model can be made to fit arbitrarily well, but may not be "parameter-efficient".

However its structure as a latent Markov model allows easy computation for intermittently-observed data, where generic time-to-event models (e.g. Weibull, gamma...) are difficult

Discussion

msmbayes package allows the multi-state models from msm to be enhanced with priors

▶ advantages: use of background knowledge and judgement, stabler computation, clearer uncertainty presentation

Facilitates phase-type models which relax the (strong) Markov assumption

Open questions about choice of structure / priors for optimal fit to data and plausible uncertainty

Application to infection duration distribution estimation?

- Compare with other assumption-light approaches (Joshua Blake's thesis: integrating over latent event times)
- More complex problem than suggested here (more predictors of incidence and duration, states representing immunity... scalability issues)

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