Symposium *Connecting Survival Analysis and Infectious Disease Modelling*

Time is a central element in both survival analysis and infectious disease dynamics, yet the two disciplines in general evolve in parallel rather than in synergy. During this symposium we will explore how advanced tools from survival analysis — such as multi-state and frailty models — can help infectious disease modelling and how infectious disease models incorporating biological knowledge— such as the SIR model — can inform survival analysis practices. The symposium is organised to share the results of the Workshop '*Connecting Survival Analysis and Infectious Disease Modelling*', organised by the Lorentz Center, with a wider audience. We invited some excellent international speakers to bridge the two disciplines. The symposium will take place on

Friday 19 June, 14:00 – 18:00 in the Gorlaeus Building in the Leiden Bio Science Park.

This symposium is intended for a wider audience of biostatisticians, infectious disease modellers and everybody interested in models applied to inform infectious disease policy.

Programme
14:00 Opening and Welcome
Steven Abrams (UHasselt, Belgium)
14:05 Workshop synthesis
Liesbeth de Wreede (LUMC) and Don Klinkenberg (RIVM)
14:20 Monitoring an epidemic in real time: Can we rely solely on randomly-sampled prevalence studies to nowcast incidence and transmission?
Daniela De Angelis (University of Cambridge, UK)
14:50 Break

15:20 On Heterogeneity in Infection Dynamics: Bridging Compartmental Models and Frailty Models
Niel Hens (UHasselt, Belgium)
15:50 Survival Models for Nosocomial Infection Data
Martin Wolkewitz (University of Freiburg, Germany)
16:20 Panel discussion
Chair Steven Abrams, panel: speakers and organising committee
16:50 Wrap-up
17:00 Drinks (location to be announced)

We warmly invite you to join!
For registration SymposiumLorentz
For information about the programme, please contact Liesbeth de Wreede: l.c.de_wreede@lumc.nl.

The organising committee: Liesbeth de Wreede (LUMC), Don Klinkenberg (RIVM/Wageningen University and Research), Steven Abrams (UHasselt/University of Antwerp), Kylie Ainslie (University of Melbourne/ University of Hongkong), Hein Putter (LUMC), Jacco Wallinga (RIVM/LUMC)

This symposium is sponsored by the Lorentz Center, RIVM, Collaborative Platform for Epidemic Modelling and Data Analytics, ZonMw, LUMC Biomedical Data Sciences and BMS-ANed.

Abstracts

Daniela De Angelis

Monitoring an epidemic in real time: can we rely solely on randomly-sampled prevalence studies to nowcast incidence and transmission?

Nowcasting the risk of infection in real time as an epidemic evolves is challenging. Infections are not observed and estimation is typically carried out using indirect and biased data (e.g. on severe outcomes) from multiple sources, integrated within complex mechanistic models. Appropriately designed prevalence studies could provide an invaluable source of information for nowcasting.
In this talk I will present current work that explores the value of the UK Coronovirus Infection Survey (CIS), a longitudinal study that randomly selected 500,000 households and PCR tested household members on a predetermined schedule over 2020-2023. Data from CIS do not suffer from biases from individuals' changing propensity to test and/or infection status. I will discuss models used to estimate incidence and transmission, reflect on the timeliness of such estimates and discuss further/ongoing work to optimise the design of prevalence surveys to enable the more efficient estimation of both the incidence and the duration of infection.

Niel Hens

On Heterogeneity in Infection Dynamics: Bridging Compartmental Models and Frailty Models

Heterogeneity in infection risk is a key driver of infectious disease dynamics, yet it is handled differently across modelling frameworks. Mechanistic epidemic models incorporate heterogeneity through structured populations, while survival analysis represents it via latent random effects, or frailties. In this talk, we connect these perspectives.

Using a two-pathogen SIR model with heterogeneous risk groups, we generate serological data and assess how well frailty models recover epidemiological parameters such as the force of infection. Ignoring heterogeneity leads to biased inference, whereas shared frailty models provide accurate and robust estimates. We further show how discrete frailty distributions, including the Addams family, allow heterogeneity to be interpreted as latent risk categories, enabling intuitive comparisons across subpopulations.

This unified framework strengthens the link between survival analysis and infectious disease modelling, with practical implications for inference from cross-sectional serological data.

Martin Wolkewitz

Survival Models for Nosocomial Infection Data

In this talk, I will present the application of extended survival models, including competing risks and multistate models, in clinical research settings. Using practical examples, I will highlight common sources of bias, such as immortal time bias and bias arising from competing risks, which can substantially distort clinical decision-making if not properly addressed. Furthermore, I will demonstrate how the framework of target trial emulation can be applied to estimate treatment effects in patients with nosocomial infections.