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Newsletter Collaborating Platform for Epidemic Modelling and Data Analytics

Year 2026, Edition 4, 28 April 2026

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Funding update

The good news about the structural funding for pandemic preparedness has probably not escaped your attention; see: Kamerbrief over Pakket Pandemische Paraatheid. At the same time, it is not yet clear what this will mean in practice, or whether, and how much, funding will be available for the collaborative platform including research projects focused on capacity building. We expect more clarity in the coming months, and we will keep you updated as soon as we know more.

Annual Meeting on HIV, mpox, and STI Modelling 2026

On Monday, March 9th 2026, the annual meeting on modelling HIV, mpox, and STIs was held at RIVM under the Collaborative Platform for Epidemic Modelling and Data Analytics. Around 35 researchers attended, all involved in or interested in modelling mpox, HIV, and other STIs. With many participants knowing each other for years, the meeting felt much like a yearly reunion. In addition to RIVM colleagues, participants came from a range of institutions across the Netherlands, including GGD Amsterdam, GGD regio Utrecht, Amsterdam UMC, UMC Utrecht, Soa Aids Nederland, Stichting HIV Monitoring, Maastricht University, Erasmus MC, and the University of Groningen.

Eight researchers presented their latest findings, including modelling studies on mpox (Jacob Roberts – UMC Utrecht, Fumi Miura – RIVM), HIV (Alexandra Teslya – UMC Utrecht, Haoyi Wang – Maastricht University), syphilis (Noga Shalev – Amsterdam UMC), and chlamydia (Veronica Malizia – RIVM). The meeting also had an international dimension: Professor Erik Volz from Imperial College London joined online to present research using Dutch data on behavioural and immunological factors in mpox transmission. David de Vijver (Erasmus MC) discussed the impact of rapid HIV testing and self-testing on lenacapavir effectiveness and resistance in Thailand.

Looking forward, the next steps for the field involve not only securing additional funding, but also focusing on bridging the gap between modelling and practical application - translating models into real-world impact.

UNITY project modelling workshop, 10 April 2026

The scientific advice that was provided to policy makers during COVID-19 has been rightly criticized for initially being too biomedically oriented. Especially as the pandemic endured, the need for recognition and advice on more broad societal impacts of the pandemic and pandemic policy became apparent. Although first steps were taken to address this, amongst others via the founding of the MIT ("maatschappelijk" or societal impact team), the process of generating biomedical and societal advice could be further improved.

The UNITY project (UNified Integration of Health and Societal Impact Translation of Yield to policy and practice), which runs from September 2025 to the end of 2026, aims to develop an integrated framework for generation and delivery of scientific advice for pandemic policy. To this end, UNITY brings together a broad range of disciplines ranging from biomedical to mathematical modellers to social scientists. Here, one of the aims of UNITY is to formulate a cohesive modelling framework capable of rapidly delivering predictions to support pandemic decision-making, as part of a modelling workpackage led by Luc Coffeng (Erasmus MC) and Ganna Rozhnova (UMCU).

On April 10th, the UNITY project hosted a modelling workshop in Utrecht. The morning opened with a presentation on the Dutch policy advice cycle and a summary of a catalogue of 32 mathematical modelling papers identified for the Dutch context. This was followed by a discussion on a critical appraisal framework for assessing the suitability of models to provide timely and actionable pandemic predictions, enriched by invited appraisals from Don Klinkenberg (RIVM) and Martijn Schoot Uiterkamp (Tilburg University). In the afternoon, the group focused on synthesis methods for pooling of individual model predictions into a coherent signal that policy makers can act on. Colleagues from SEO Amsterdam

Economics closed the day by presenting mechanisms of translating epidemiological outcomes into socio-economic impacts, which is another critical dimension complementary to health-related outcomes.

Final meeting ZonMw Projects ‘Modelling for Pandemic Preparedness’

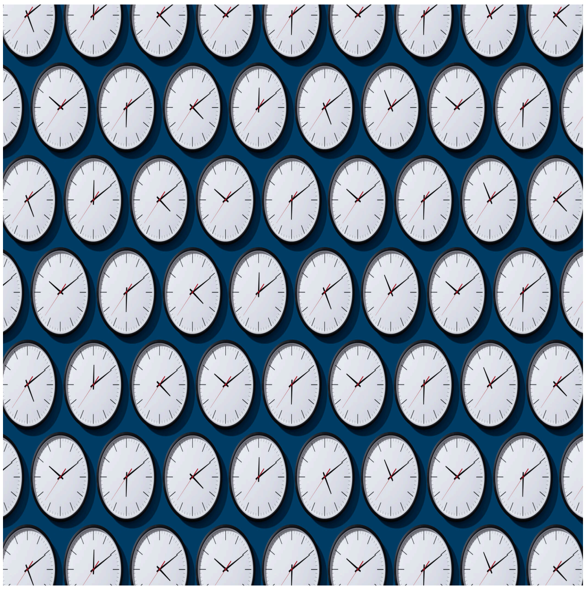
On June 16, a closed meeting will take place for the projects funded under the ZonMw grant round ‘Modelling for Pandemic Preparedness’. As these projects are now nearing completion, project leaders and various stakeholders will meet to discuss the final outcomes.

Background of the grant round

Commissioned by the Ministry of Health, Welfare and Sport (VWS), this ZonMw grant round was set up with a central focus on knowledge development and innovation in modelling for pandemic preparedness and infectious disease control. The main objective was to expand the capabilities of infectious disease modelling, ensuring that the Netherlands can anticipate and respond to future pandemics or large-scale outbreaks more effectively.

From results to policy and practice

The meeting on June 16 is primarily focused on how the delivered results can be translated into concrete use within policy and practice. In addition



19 June 2026: 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 Juni, 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 to sharing final results among the projects, participants and stakeholders will explore how these modelling insights can effectively support pandemic preparedness.

The following projects will participate in the meeting: Met kennis werken aan een goede gezondheid voor iedereen

Reporting
Although this is a closed event, a report of the meeting will be compiled afterwards. This report will be shared via this newsletter at a later date.

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

We warmly invite you to join!
Please register here: Lorentz Symposium

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.

Figure 1. CD8 T cell antigenic map of historical influenza A viruses, visualising the virus-virus and virus-epitope distances. Note that the map contains all three major human subtypes. Also note that the recent H5N1 avian influenza viruses are antigenically close to recent human H1N1 viruses. Similar visualisations are available for human coronaviruses.

Collaborating ZonMw-funded project: Predicting pre-existing immunity to novel pandemic viruses

Project lead: Michiel van Boven (University Medical Center Utrecht)

Partners: Farzaneh Meimandi Parizi, Johannes Textor (Radboud University), Oscar Jordan, Can Kesmir, Rob de Boer (Utrecht University)

Programme: ZonMw Pandemic Preparedness Knowledge Program

Abstract and aims: Human pandemics caused by novel viruses have emerged many times throughout human history. The public health impact of such viruses can vary dramatically, depending on pre-existing immunity in the human population. Immunity to pathogens varies between different people, resulting from differences in genes involved in presenting antigens to the immune system. In our project we aim to computationally predict the presence of pre-existing immunity against potential pandemic viruses. We focus on T cell mediated immune memory by identifying MHC class I epitopes (short peptides of the viral proteome that are recognised by the immune system) in novel viruses. These epitopes are then compared to a pool of previously encountered reference epitopes, and potential cross-reactive matches are identified. Using this approach, we predict pre-existing immunity to be present in a subset of the population representing specific HLA and age groups. The main output of these analyses is a table of epitope predictions for novel viruses, and their predicted cross-reactive matches against reference epitopes. This information can be used as an advisory resource in the event of an emerging pandemic. In a parallel track, we build and analyse a new class of transmission models that can take historical and genetic variations into account, to forecast immune histories in groups stratified by age and genetics.

Lessons learned: First, a one-and-a-half-year project is short for a multidisciplinary effort that combines immunology, computational modelling, and infectious-disease epidemiology. Nevertheless, the project has led to progress in various directions. For instance, a lesson has been that modern protein language models can capture biologically meaningful information about peptide sequences that is relevant for T-cell recognition.

Publications: We are currently drafting two manuscripts describing the computational prediction framework and its application to emerging influenza A viruses and coronaviruses (see the figure for a sample), and we plan to further develop the modelling in follow-up work. We have submitted a manuscript on the time-age-genetics stratified transmission model (van Boven et al (2026) Optimal vaccination in aging populations under age-dependent infection fatality risks).

Seminar Series: Mathematical Epidemiology at Utrecht University

Next semester (September 2026 -January 2027), there will be a seminar series on mathematical epidemiology at Utrecht University (course code WISM436). The seminar will be on Mondays, from 9.00-10.45 and the location will be somewhere at the Uithof.

The seminar series is intended for mathematics students, but participants from other institutes and with other backgrounds are welcome as well. The first part of the seminar will be based on the book “Mathematical Tools for Understanding Infectious Disease Dynamics” by Odo Diekmann, Hans Heesterbeek and Tom Britton. In the second part we will discuss (recent) articles.

The aim is that the participants, in turns, will study a part of the book and give a (constructive critical) presentation for the other participants who should have read that part as well. After each presentation there will be a discussion about the material.

More information on the course can be obtained from Martin Bootsma. The participants will be awarded 7.5 ECTS credits after successful participation. If you are interested in participating, please contact Martin Bootsma (M.C.J.Bootsma@uu.nl).

Recent Publications

- **Baas, S., Dijkstra, S., Boucherie, R. J., & Zander, A.** (2026). A stochastic programming approach for dynamic allocation of bed capacity and assignment of patients to collaborating hospitals during pandemic outbreaks. Health Care Management Science, 29(2), 18. https://doi.org/10.1007/s10729-025-09747-1
- **Otten, T., Knol, M., Montessori, L. M., de Boer, P., & Steens, A.** (2026). Clinical impact and cost-effectiveness of vaccinating infants and adolescents against invasive meningococcal B disease in the Netherlands. BMC medicine. https://doi.org/10.1186/s12916-026-04651-z
- **Romeijnders, M., van Boven, M., & Panja, D.** (2026). Risk mapping novel respiratory pathogens with large-scale dynamic contact networks. Communications Medicine. https://doi.org/10.1038/s43856-026-01446-4
- **de Wit, M. M., Beaunée, G., Dellar, M., Münger, E., Krol, L., Atama, N., ... & Ten Bosch, Q. A.** (2026). Silent reservoir species are shaping the emergence of Usutu virus. Nature Ecology & Evolution, 1-12. https://doi.org/10.1038/s41559-025-02973-4

Upcoming Events

- **May 29, 2026:** Workshop on Pandemic Strategies in Schools, *Utrecht*
- **June 19, 2026:** Symposium Connecting Survival Analysis and Infectious Disease Modelling, *Gorlaeus Building in the Leiden Bio Science Park*

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