TB Modelling and Analysis Consortium

Dear <<First Name>>,

Welcome to the latest TB Modelling and Analysis Consortium (TB MAC) newsletter, with information for TB modellers, epidemiologists, and decision-makers. This newsletter contains details on the next TB MAC seminar and papers from our community.

A reminder that the seminar ***Limited impacts of spatially-targeted tuberculosis screening in Lima, Peru: A model-based analysis*** given by Joshua Havumaki has been postponed to **Thursday, 2 May from 1600-1700 BST.**

**Join our next TB MAC seminar: Andrew Iskaukas on Calibrating complex TB models using emulation and history matching [23rd May 1500-1600 BST]**

TB MAC would like to invite you to join us for a seminar on Calibrating complex disease models using emulation and history matching, given by a member of the TB MAC community, Andrew Iskaukas on the 23rd May 1500-1600 BST. See below for more details on the seminar, presenters and how to join.

Seminar summary:

Complex models of disease transmission and dynamics are paramount in investigating the impact of interventions or making predictions of future outcomes. However, their complexity can be a barrier to an exhaustive exploration of parameter space, whether as a result of stochasticity, high-dimensional input space, or computational expense of simulator runs. To surmount this problem one may use the twin methodologies of emulation (a means by which a potentially slow simulator can be represented by a fast statistical surrogate) coupled with history matching (an exploration method that finds acceptable matches to observational data in the presence of uncertainty). Even where these techniques are well-defined, it may be difficult to implement such methods into a standard calibration workflow: I will demonstrate how the R package hmer enabled their application to a complex deterministic TB model across multiple countries, and discuss built-in extensions for stochastic simulators.

Presenter bio:

Andy Iskauskas is an Assistant Professor in Statistics and Willmore Fellow at Durham University, with particular focus on Bayesian calibration. He has worked with epidemiologists across the world modelling a number of different diseases, as well as non-epidemiological applications in physics, biology, and industry, and developed and maintains the history matching and emulation package hmer.

Joining details:

The seminar will take place online on the 23rd May 1500-1600 BST, dial-in details:

https://lshtm.zoom.us/j/93164733602?pwd=UXNoYXBxWU02NlVDOGx6K0IyQkpFUT09

Meeting ID: 931 6473 3602

Password: 454657

Click below to add the event to your calendar and ensure you don't miss out!

Apple Google Office 365 Outlook Outlook.com Yahoo

A reminder that recordings of previous seminars can be found in the TB MAC video library:

https://tb-mac.org/tb-mac-resource/tb-modelling-video-library/

**Papers:**

Fuller et al review models of DR-TB for bacterial heterogeneity

Starshinova et al model the effect of reduced screening due to COVID-19 on TB in Russia

Clark et al estimate the potential public health value of BCG revaccination

Emani et al use modelling to quantify gaps in the TB care cascade in Brazil

Ricks et al estimate the potential impact of expanding private sector engagement in India

Inayaturohmat et al review models of TB, malaria and HIV/AIDS for coinfections

Lan et al use a spatial model to identify local foci of M.tb transmission in Moldova

Jing et al model reduced diagnostic delay and vaccination in Jiangsu, China

Fromsa et al model the effect of BCG vaccination on bovine tuberculosis transmission

For more information on TB MAC, or to get involved, please contact any of the TB MAC Committee, visit www.tb-mac.org or email us directly at tb-mac@lshtm.ac.uk.

Best wishes,
Richard, Finn, Christina and the TB MAC Committee
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