

*TB MAC/WHO Annual meeting
World Bank Offices, Washington DC
September 12th 2018*

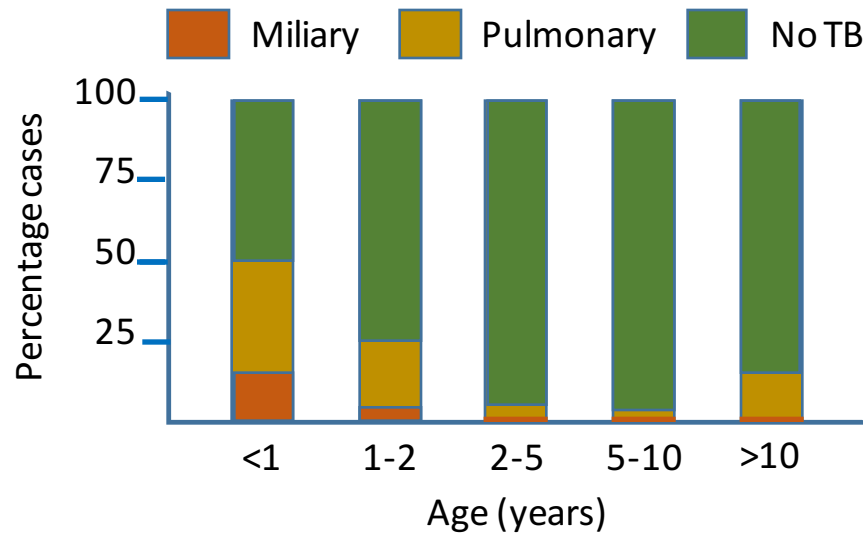
*Modelling TB epidemics in the face of
evolving global demography.*

Joaquín Sanz.

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Université de Montréal & University of Chicago.*

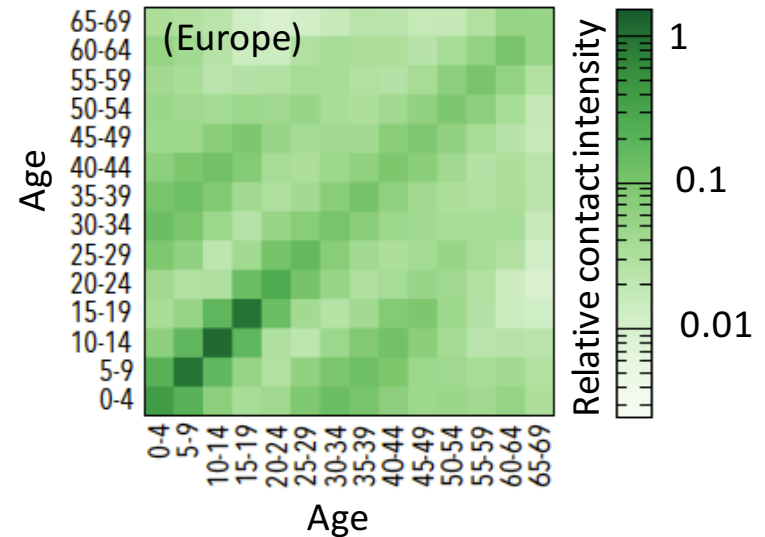
In TB modelling, a proper description of populations' demography, its evolution and coupling to transmission dynamics is key.

Age is not just a major factor shaping the risk for infected individuals to develop active TB disease in its different flavors



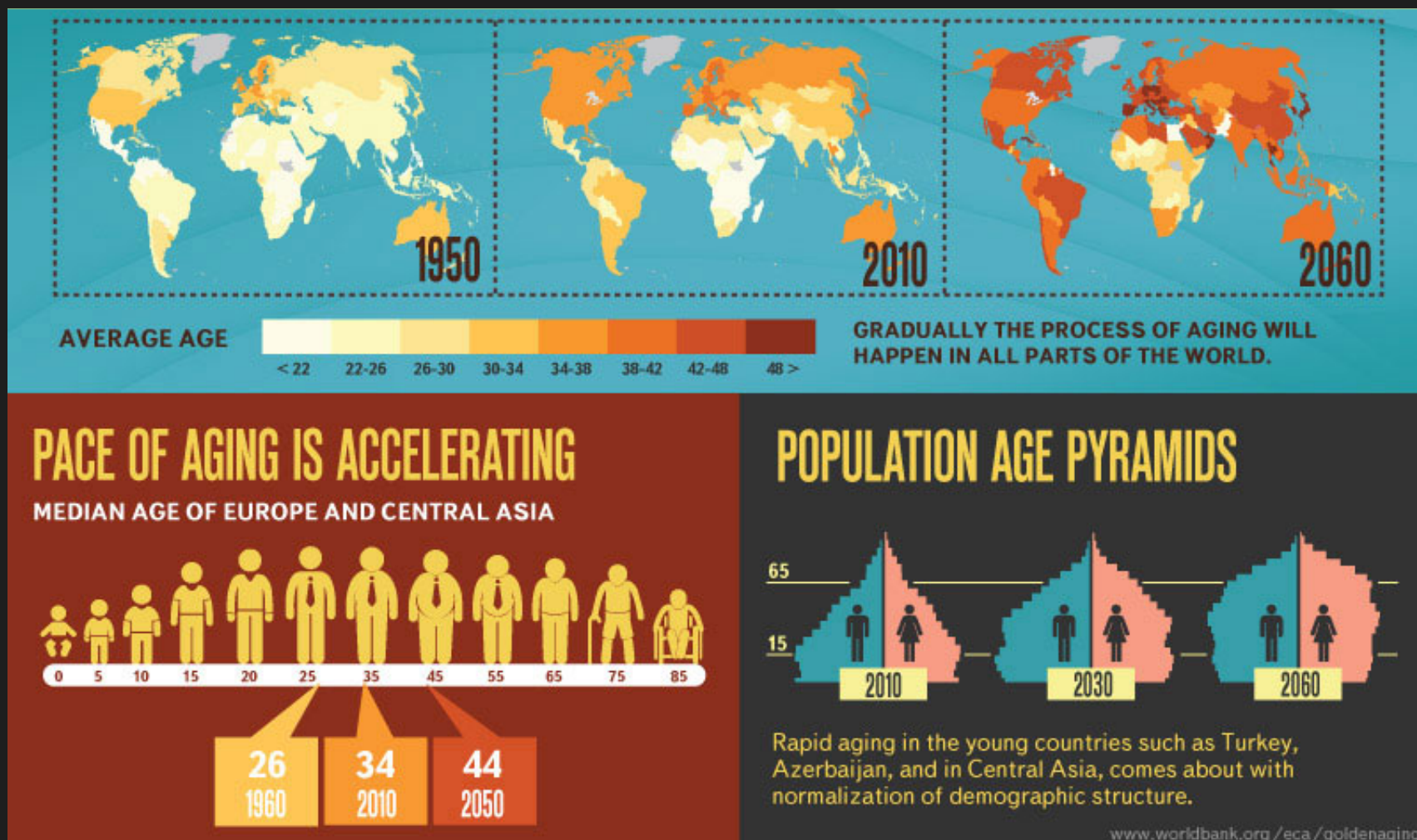
Elaborated from data in Marais et al.
Int. J. Lung Dis. 8(4)392-402 (2004)

But it also impacts individuals' contribution to transmission

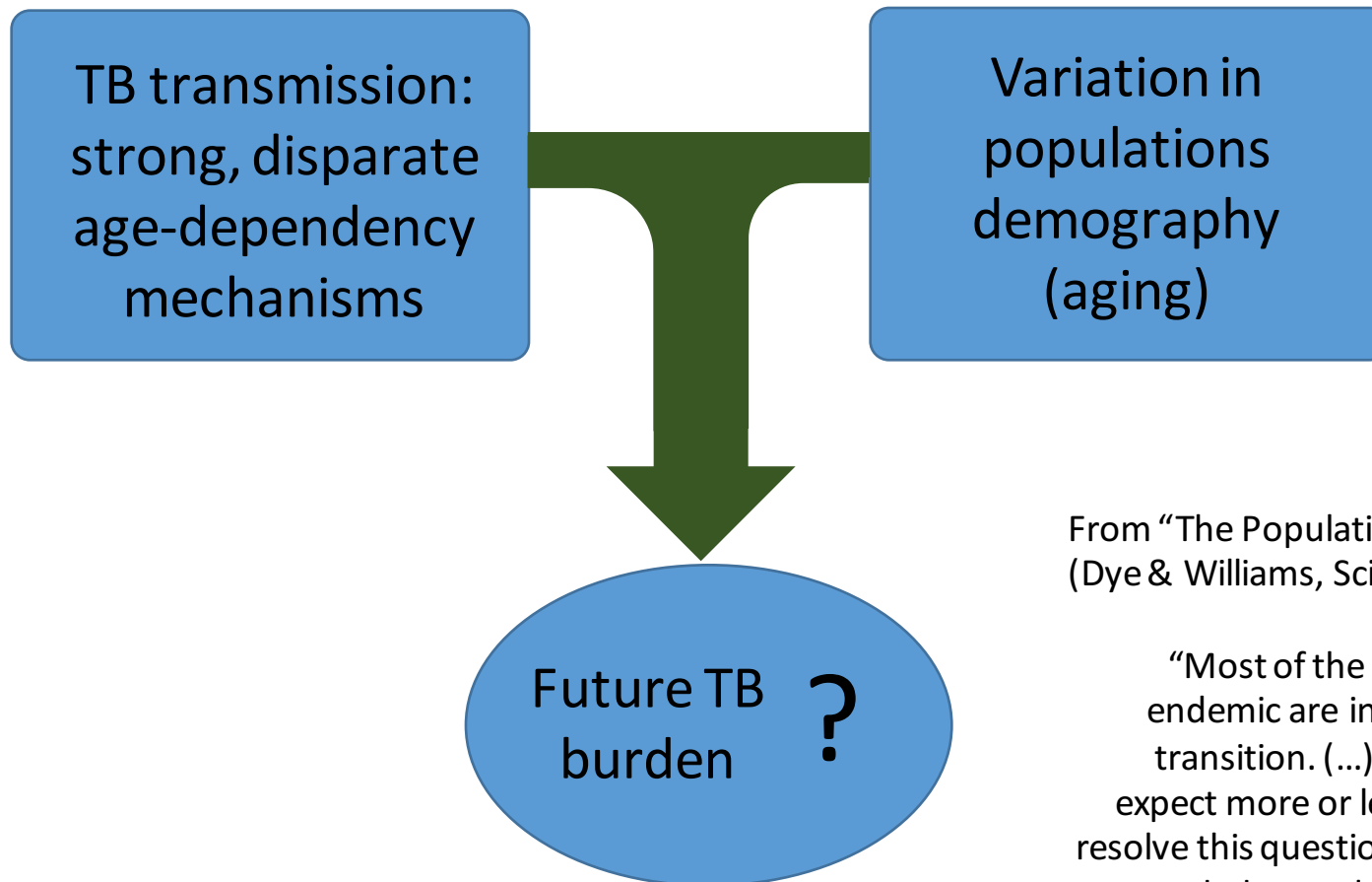


Elaborated from data in Mossong et al.
PLoS Medicine (2008)

In TB modelling, a proper description of populations' demography, its evolution and coupling to transmission dynamics is key.



...Also, age distributions are changing all around the globe



From "The Population Dynamics and Control of TB (Dye & Williams, Science, 2010):

"Most of the countries where TB remains highly endemic are in demographic and epidemiological transition. (...). But it is not clear whether we can expect more or less TB in aging populations. (...) To resolve this question, the standard model needs to be extended to explore the interplay between survival, fertility, and the risk of TB with age".

*Methods: a novel model to describe TB transmission
on evolving demographics*

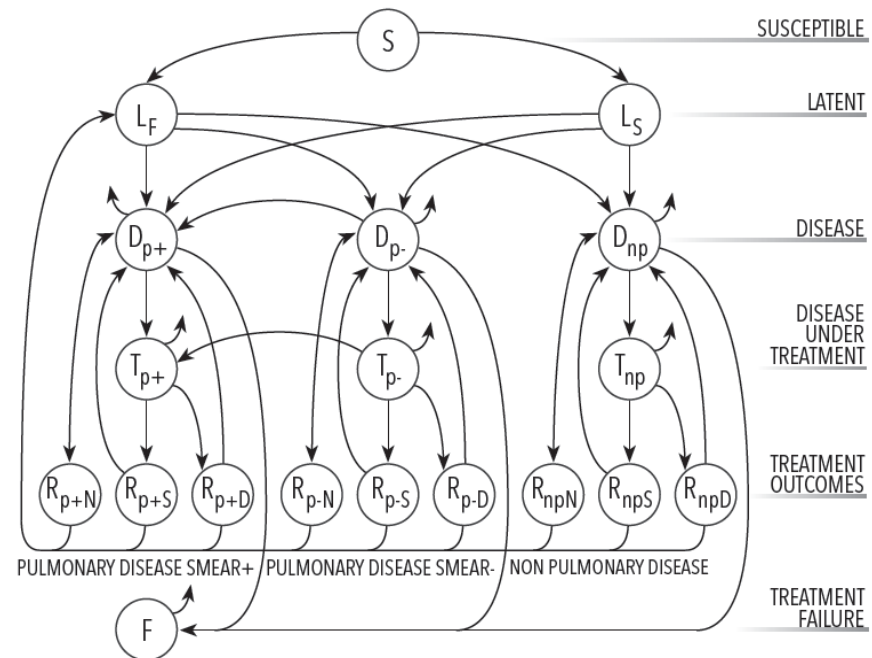
Goal: build a model where coupling between age structure and TB is made compatible with the observed/projected demographic evolution of nowadays' human populations.

Data-driven model for the assessment of *Mycobacterium tuberculosis* transmission in evolving demographic structures

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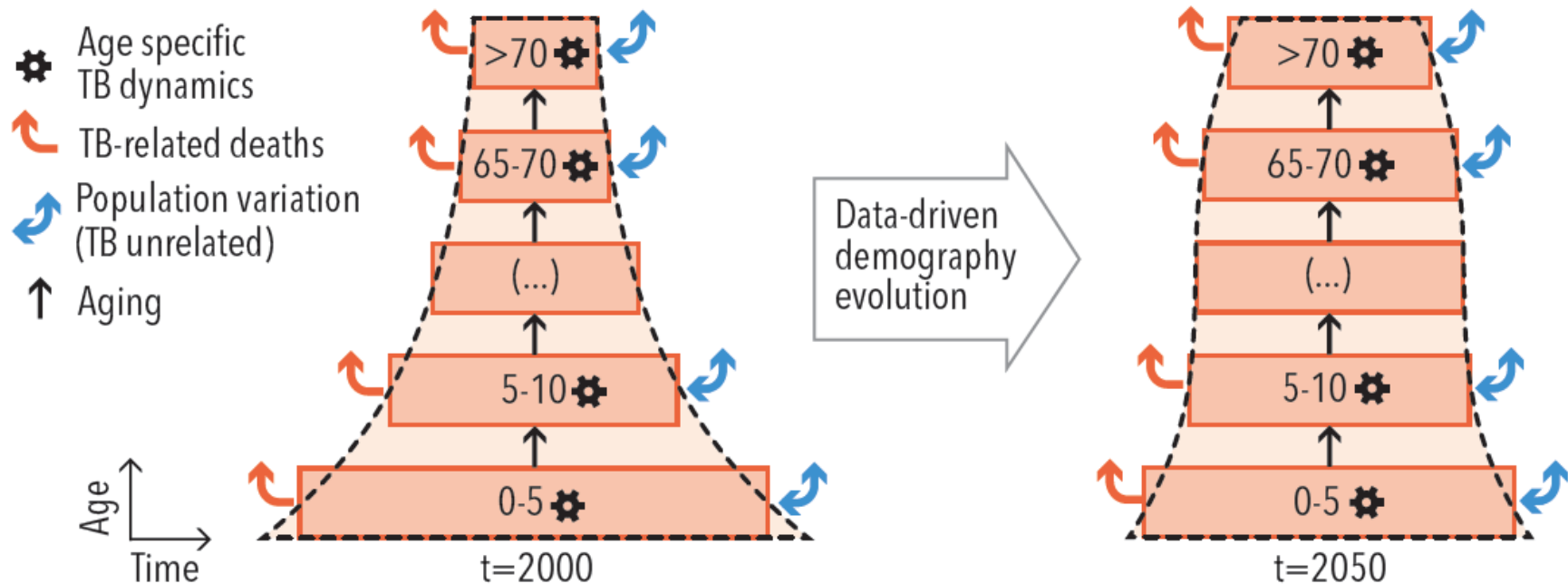
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Model basic architecture:
Natural History scheme
broadly compatible with
the standard model.



Two main technical difficulties / differences to previous approaches.

First: our model makes demographic pyramids to evolve according to external data (UN Population Division prospects)

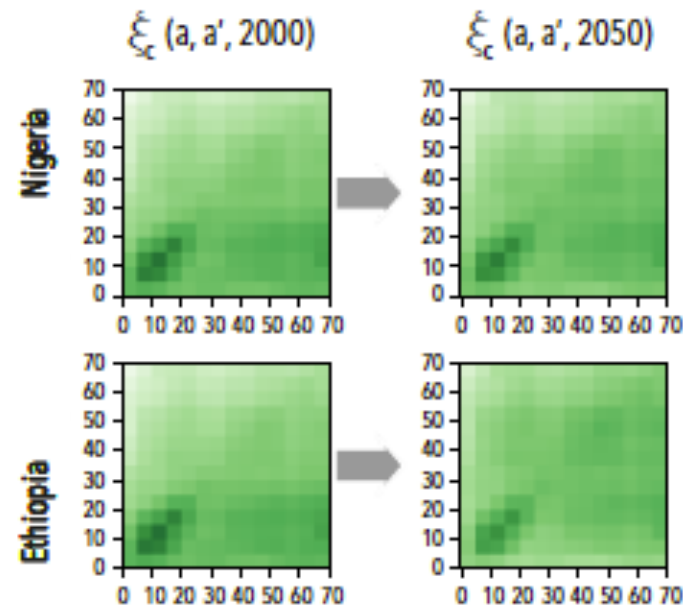


(Key hypothesis: TB-unrelated population variation terms do not modify relative prevalence of individuals in each disease-related-class)

Two main technical difficulties / differences to previous approaches.

Second: our model abandons the hypothesis of homogeneous mixing among age strata in favor of heterogeneous, empiric contact structures.

Key aspect: dynamic demography implies dynamic contact structures

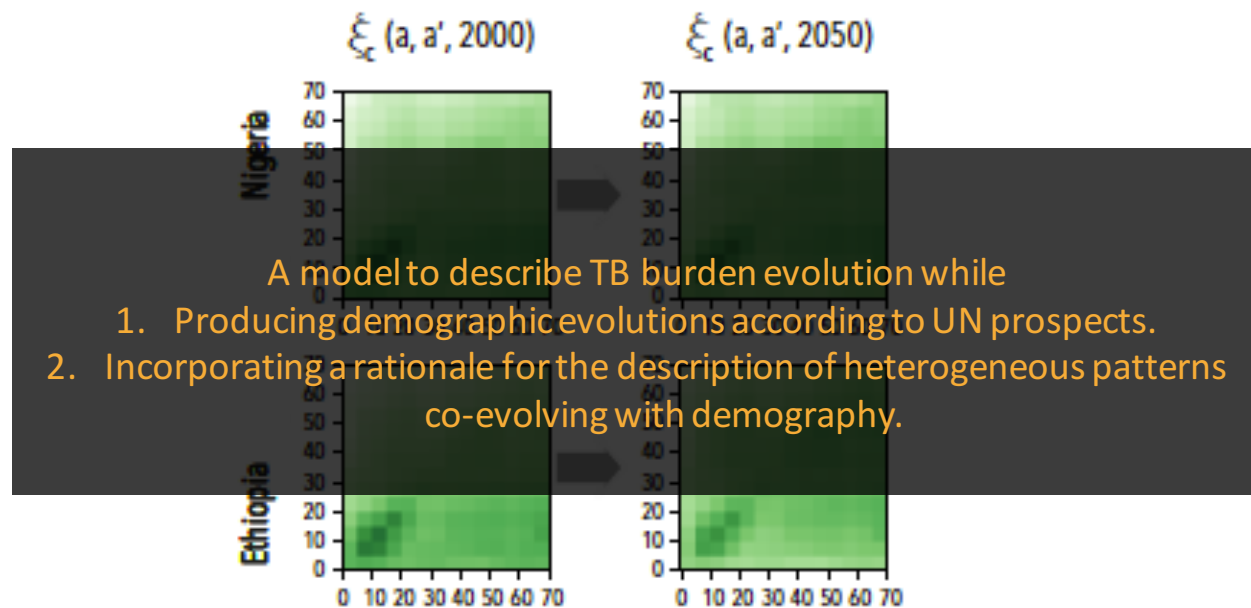


More information at: Arregui, Aleta, Sanz & Moreno: "Projecting social contact matrices to different demographic structures" Bioarxiv
doi: <https://doi.org/10.1101/343491>

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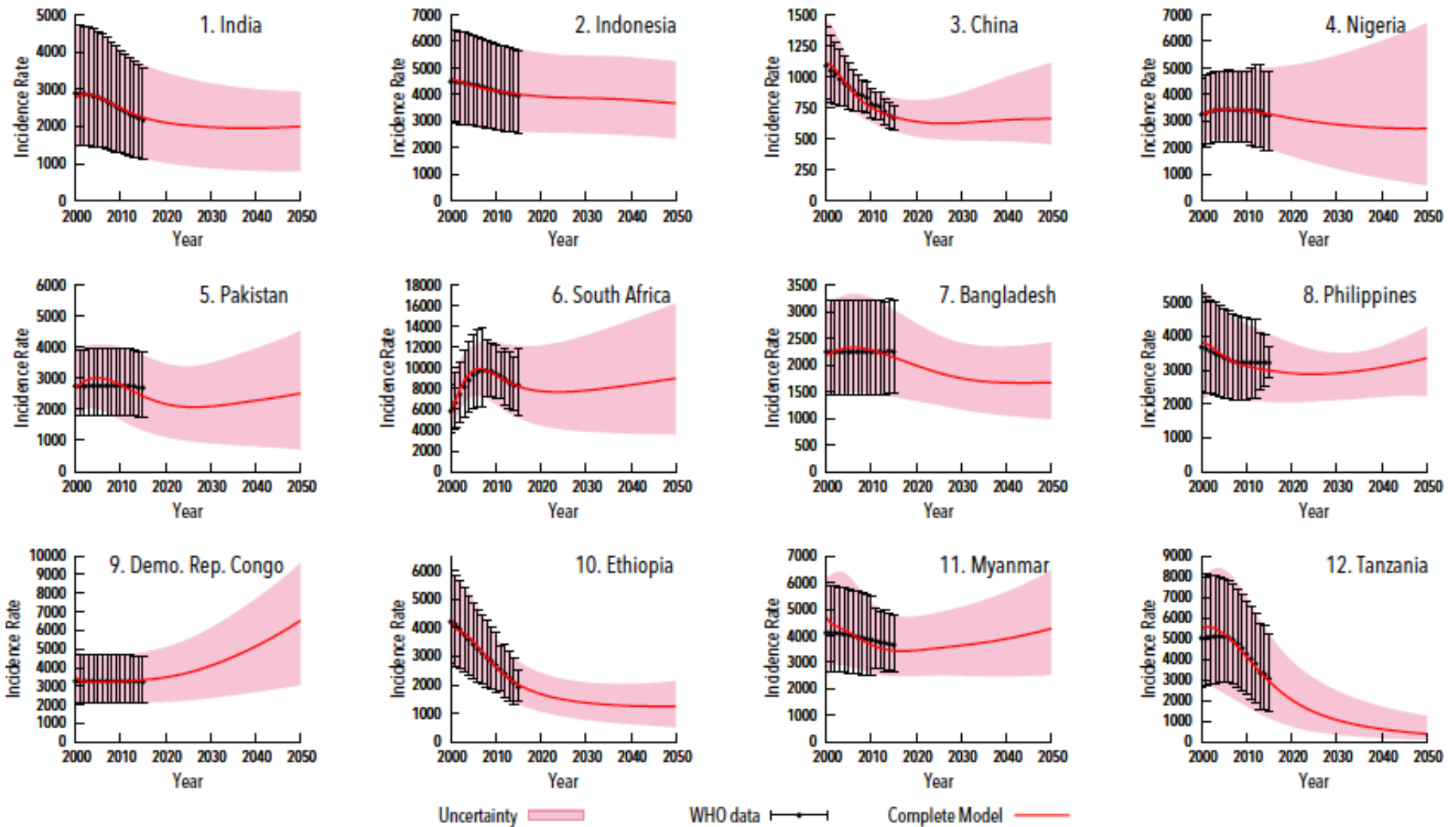
Key aspect: dynamic demography implies dynamic contact structures



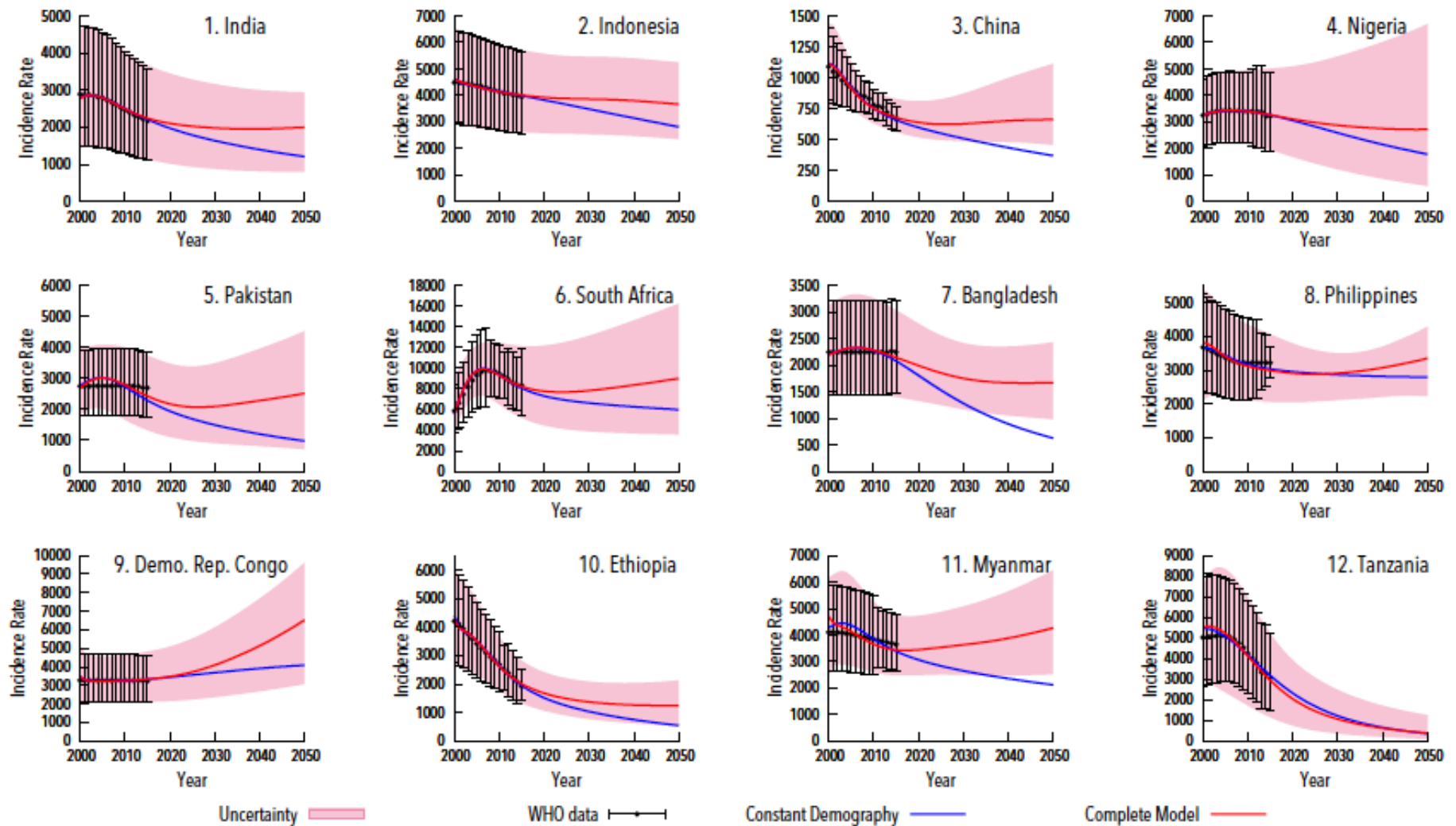
More information at: Arregui, Aleta, Sanz & Moreno: "Projecting social contact matrices to different demographic structures" Bioarxiv
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*Results: quantifying the effects of
populations' aging on future TB trends.*

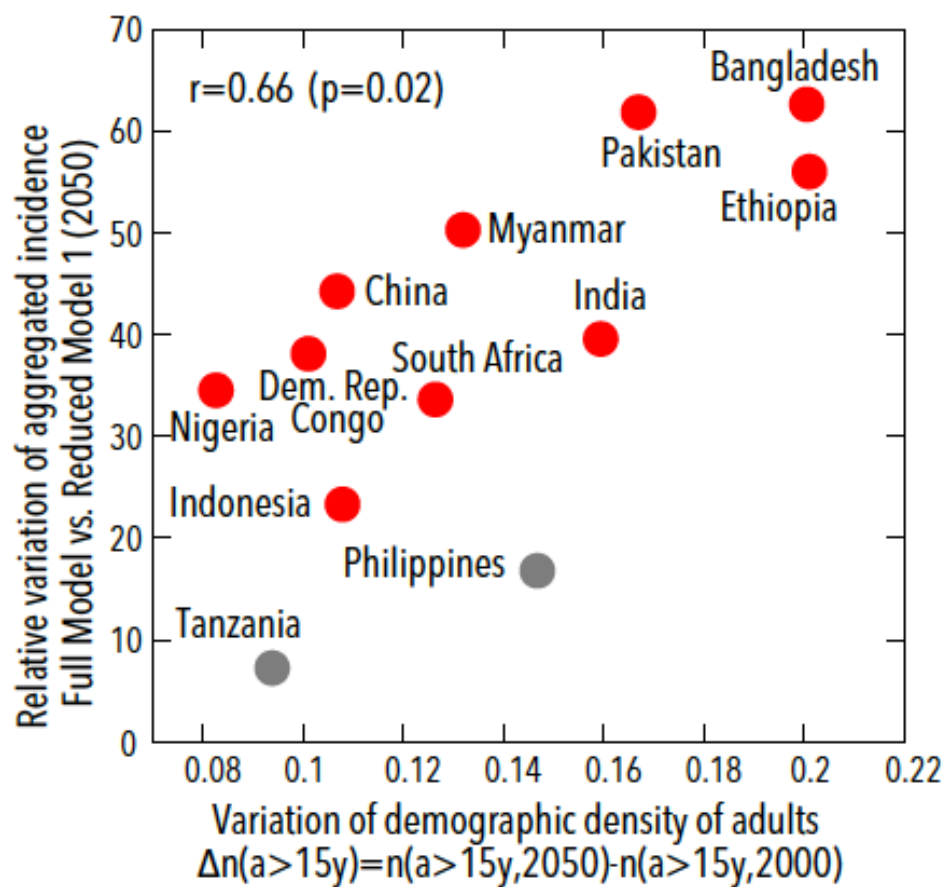
The model is useful to capture current TB trends in the countries most affected by the disease nowadays...



And in the forecasts it produces for the decades to come, populations aging appears linked to higher TB incidence



Relationship between the strength of the demographic change (i.e. aging) and differences in forecasted TB levels.



Increase in incidence correlates with intensity of aging across countries

Prospects, limitations, next steps...

We have provided a comprehensive methodology to integrate demographic dynamics and contact heterogeneities in TB transmission models, and quantified the effects derived from doing that. Incorporate these ingredients will be of utmost importance to remove biases from model-based evaluation of novel epidemiological interventions. Our results indicate that future TB burden levels might be higher than anticipated, which emphasizes the need of an improved new vaccine, which in this scenario is expected to be more impactful.

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Thanks for your attention !!

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