### Innovations in formal and mathematical demography

#### Wednesday 3 September, 5.45pm

### Beyond Age Patterns: A Multidimensional Bayesian Extension of the Rogers-Castro Model for Harmonizing Migration Data

#### Aysha Basheer, Arkadiusz Wiśniowski - The University of Manchester

Accurate estimation of international migration flows remains challenging due to inconsistent reporting and lack of standardized data collection methods. Migration patterns are often understood through the lens of age distributions, with the Rogers-Castro multi-exponential model serving as the standard framework. While effective, this approach lacks integration of additional demographic variables and fails to address discrepancies between reporting sources. Our research extends the Rogers-Castro model by incorporating sex, origin, destination, and time dimensions within a Bayesian framework.

Using European migration data from the Eurostat database spanning 31 countries from 2008-2022, disaggregated by five-year age intervals and sex, we develop a methodology that harmonizes migration counts reported from two different sources. We implement a Bayesian hierarchical model in JAGS that structurally modifies the migration schedule to estimate age-specific bilateral flows across origin-destination pairs, sexes and time periods. The model retains the flexible five-component exponential structure of the original model while introducing country- and sex-specific parameters to accommodate demographic heterogeneity. Model estimation is performed using Markov Chain Monte Carlo (MCMC) sampling, allowing us to incorporate prior information and fully propagate uncertainty. In addition to estimating counts, the model also yields age- and sex-specific proportions, enabling insights into the demographic composition of migrant flows.

Our model successfully captures temporal trends, bilateral migration flows and sex-specific patterns of migration while preserving the age-specific characteristics. This extension improves accuracy by harmonizing inconsistent and incomplete data sources, integrated modelling of demographic variables, and uncertainty quantification through probabilistic estimation. The resulting harmonized estimates provide policymakers and researchers with a more comprehensive understanding of European migration dynamics. They can inform inclusive migration and integration policies, help forecast population change, and support the planning and allocation of education, health, employment and housing infrastructure, enabling evidence-based decision-making in an era of increasing population mobility.

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# New Approach to Understanding Population Change in Central and Eastern Europe Csaba G. Tóth - HUN-REN Centre for Economic and Regional Studies (Hungary)

This research introduces a novel approach to decomposing population change by isolating the contributions of fertility, mortality, net migration, and initial age structure. This method relies on scenario analyses conducted using the cohort-component model, with counterfactual scenarios grounded in stable population theory. Its strength lies in the additivity of the results: the contributions of these factors, along with the interaction effect, sum to equal the total population change. In addition, identifying the direct impact of initial age structure on population change offers new insights into the drivers of population dynamics.

The population of Central and Eastern Europe, which includes the 11 countries that joined the EU after 2000, declined by 8% between 1990 and 2020, with significant country-level variation ranging from -29% to +5%. Our preliminary results indicate that the population loss in the whole CEE region was driven by a 14% decline due to below-replacement fertility and a 6% decline due to negative net migration. However, these effects were partially offset by a 5% improvement in mortality and a 6% contribution from initial age structure relative to the population in 1990. One of our main findings is that initial age structure played a crucial role in population change across the region. Applying our new decomposition method, we demonstrated that the heterogeneity across the CEE region is more complex than previously assumed. While migration is a key factor explaining differences in population change, the initial age structure also plays a crucial role and must be considered for a comprehensive understanding.

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## Probabilistic projections of distributions of kin over the life course Joe W B Butterick, Jason Hilton, Jakub Bijak, Peter W F Smith, Erengul Dodd - University of Southampton

#### Background:

Mathematical kinship demography is an expanding area of research. Recent papers have explored the expected number of kin a reference individual should experience. Despite the uncertainty in future numbers and distributions of kin, only one paper attempts to quantify this analytically.

#### Aims:

To estimate probabilities that a reference population member experiences one or more of some kin at any age through its life course. We seek a discrete probability distribution which characterises the integer number -- or "kin-number" -- of some kin type the individual experiences over any age of the individual, any age of kin, and over all possible ages of kin.

#### Methods:

Combinatorics and matrix algebra are used to construct the kin-number probability distribution. Convolution theory is applied to project the distribution. Our model requires age-specific mortality and fertility as inputs.

#### Results:

Over all ages of the reference individual, we present kin-number probabilities for fixed age, and over all possible ages, of kin. Naturally emerging from these probabilities are expectations, variances, and higher order moments for kin-number. We demonstrate how the probabilities of experiencing specific kin-types are conditional on familial events involving other kin-types; an example being the relationship between birth-order probability and age of mother.

#### Contribution:

This research contributes to the literature by extending recent advances in mathematical kinship demography to account for demographic stochasticity. We present the first analytic approach allowing the projection of a full probability distribution of the number of kin of arbitrary type that a population member has over the life course.

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