

A tentative model for Covid-19 Mortality Age-pattern

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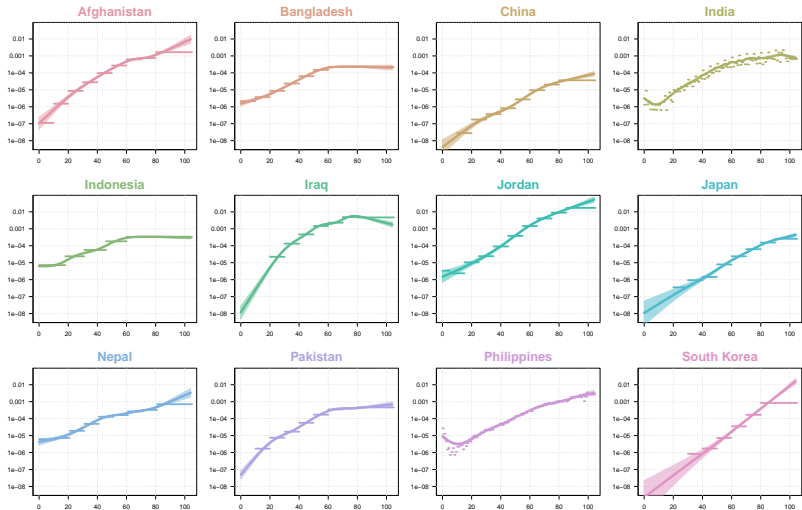
TAG Working Group I, Meeting II

April 16th, 2021

Data and methods

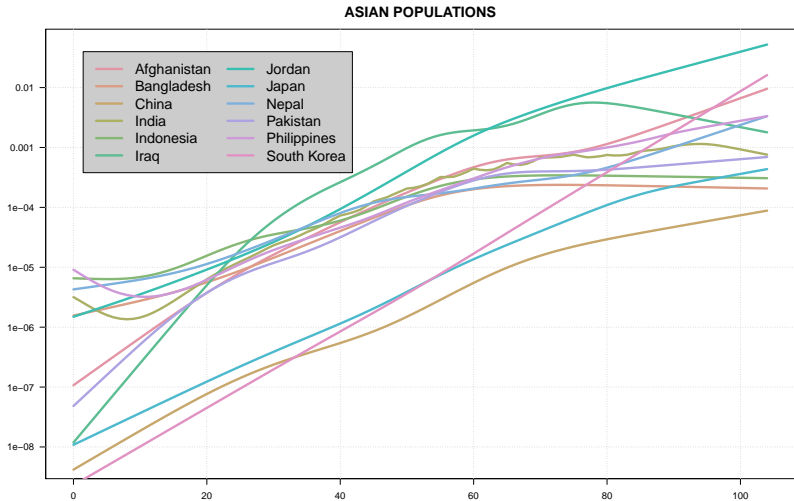
- Data:
 - a subset of COVerAGE-DB with 100+ deaths, both sexes
 - Europe (24), Africa (7), Asia (12), Latin America (13), North-America (3), Oceania (1)
 - scaled to JHU total on Dec 31, 2020
- Modelling options:
 - PCLM*: Population-specific smooth age-pattern
 - + relatively good fit
 - useless for populations with no detailed data
 - PH-PCLM*: Region-specific smooth age-pattern + population-specific scaling factor
 - inevitable mixture of different age-patterns
 - + applicable to populations with no detailed data
- General concerns:
 - Coarse and country-specific age-groups ✓
 - Data quality (coverage issues, age-heaping, ...)

An illustrative example: Asian populations



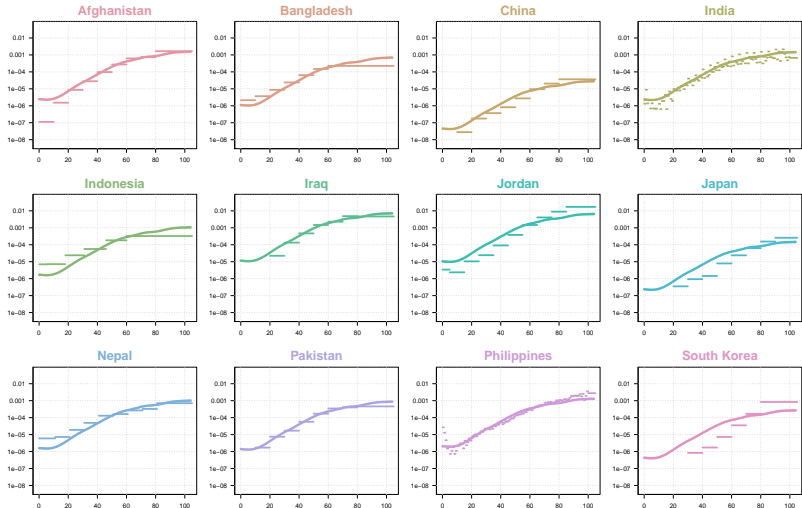
Treating each population independently

An illustrative example: Asian populations



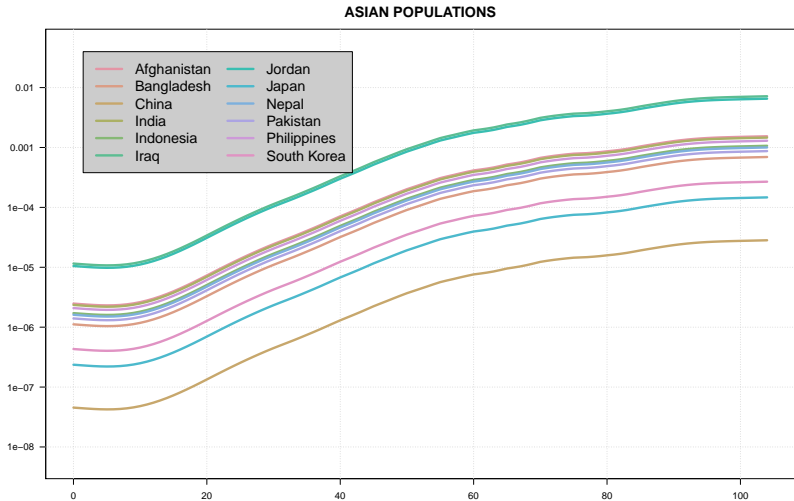
Treating each population independently

An illustrative example: Asian populations



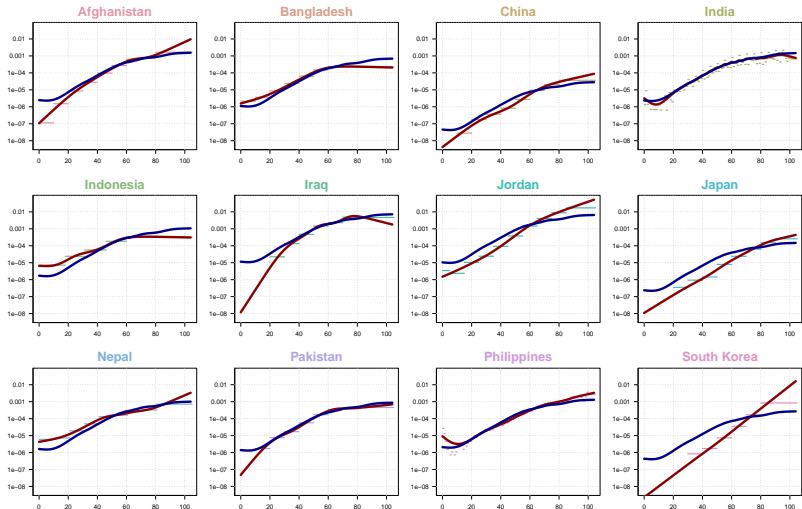
Region-specific pattern + population-specific scaling factor

An illustrative example: Asian populations



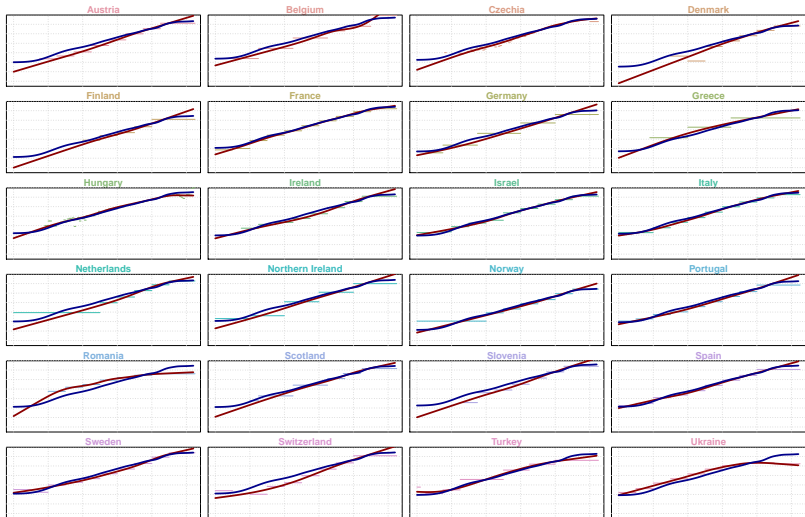
Region-specific pattern + population-specific scaling factor

An illustrative example: Asian populations



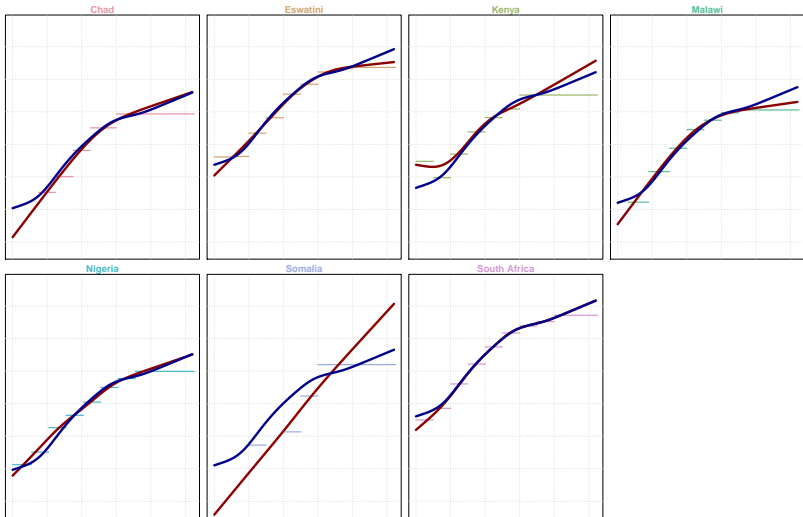
Both approaches: *PCLM* vs. *PH-PCLM*

Other regions: Europe



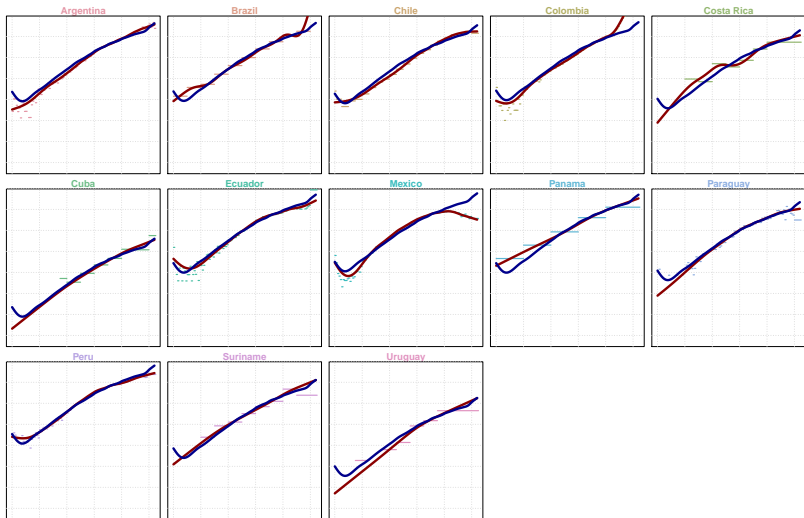
Both approaches: *PCLM* vs. *PH-PCLM*

Other regions: Africa



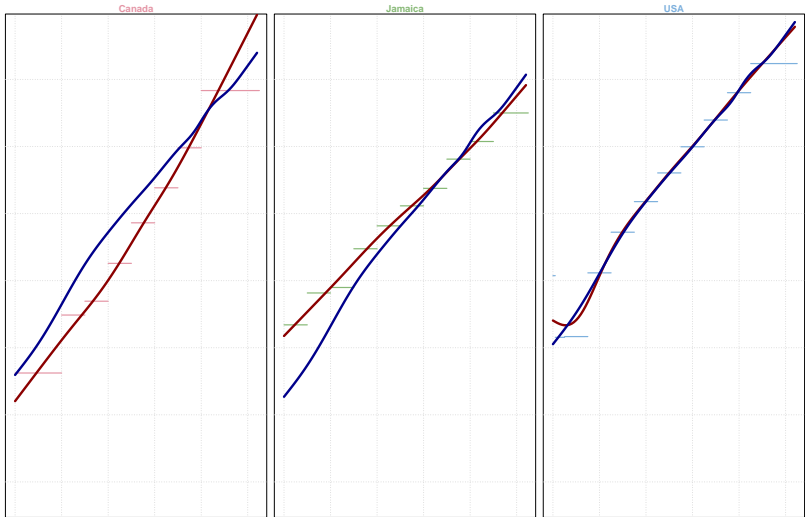
Both approaches: *PCLM* vs. *PH-PCLM*

Other regions: Latin America



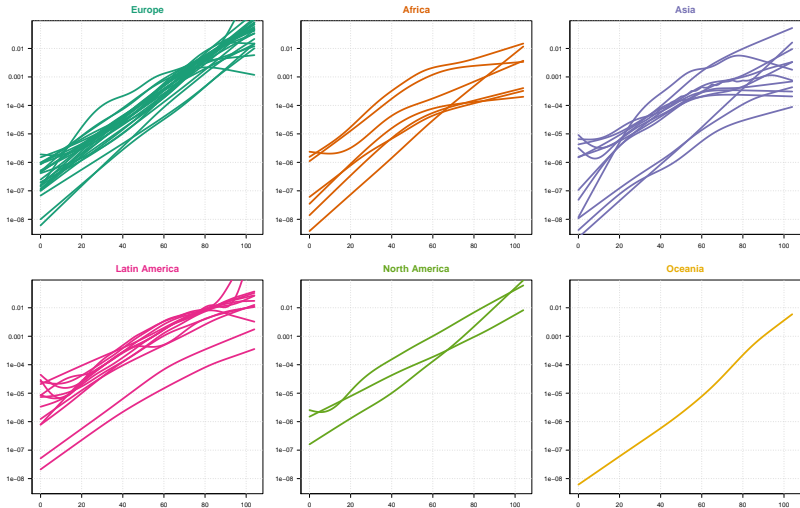
Both approaches: *PCLM* vs. *PH-PCLM*

Other regions: North America



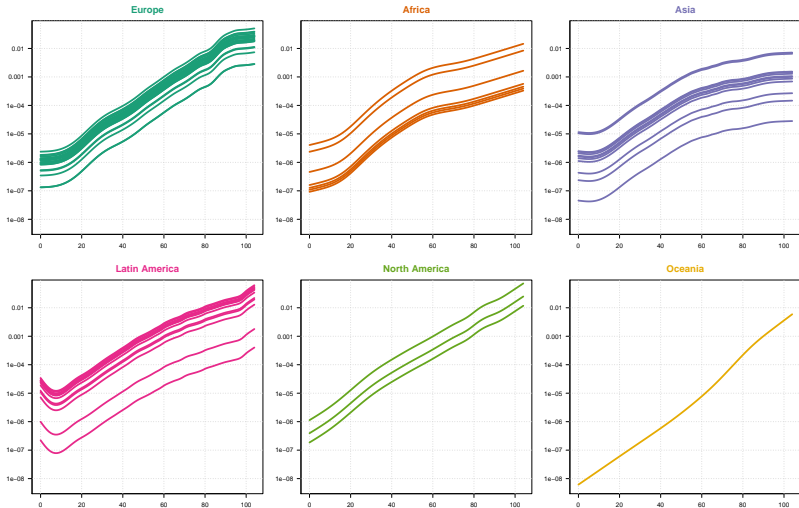
Both approaches: *PCLM* vs. *PH-PCLM*

All data



PCLM

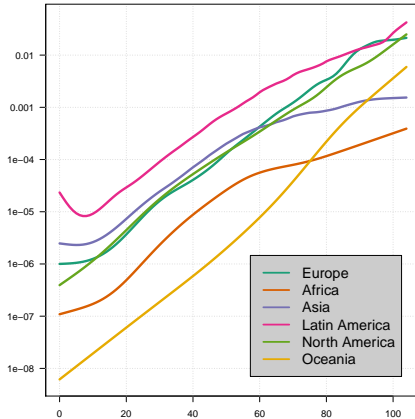
All data



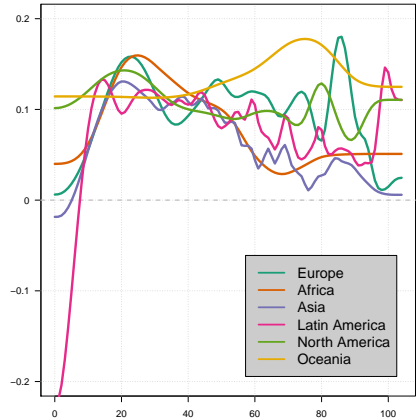
PH-PCLM

All data

Reference age-pattern

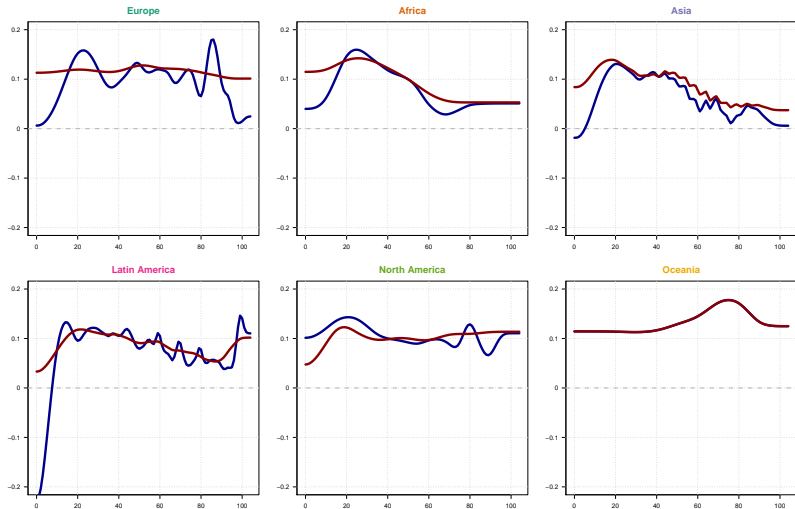


Rate of aging



PH-PCLM

All data



Rate of aging: *PCLM* (from regional mean) vs. *PH-PCLM*

Still to discuss/solve

- **Main question:** can we really characterize regional C-19 mortality age-patterns? Should we think about clustering?
- Other “minor” questions:
 - Some population have clear data issues. To be simply delete?
 - Should we add external variables? If so, how?
 - Should we treat sexes separately? Or an additional layer with region in the hierarchical framework?
 - Smoothing parameter is not optimized
 - Data show clear overdispersion: likely a quasi-Poisson approach would be more suitable
 - Something else from the discussion