Demographic Projections in the Colombian Context with the PyCCM Library

Juliana Echeverri Jaramillo, Charlie Rahal, and Jiani Yan

Banco de la República and the University of Oxford

Populorum, April 15th, 2026

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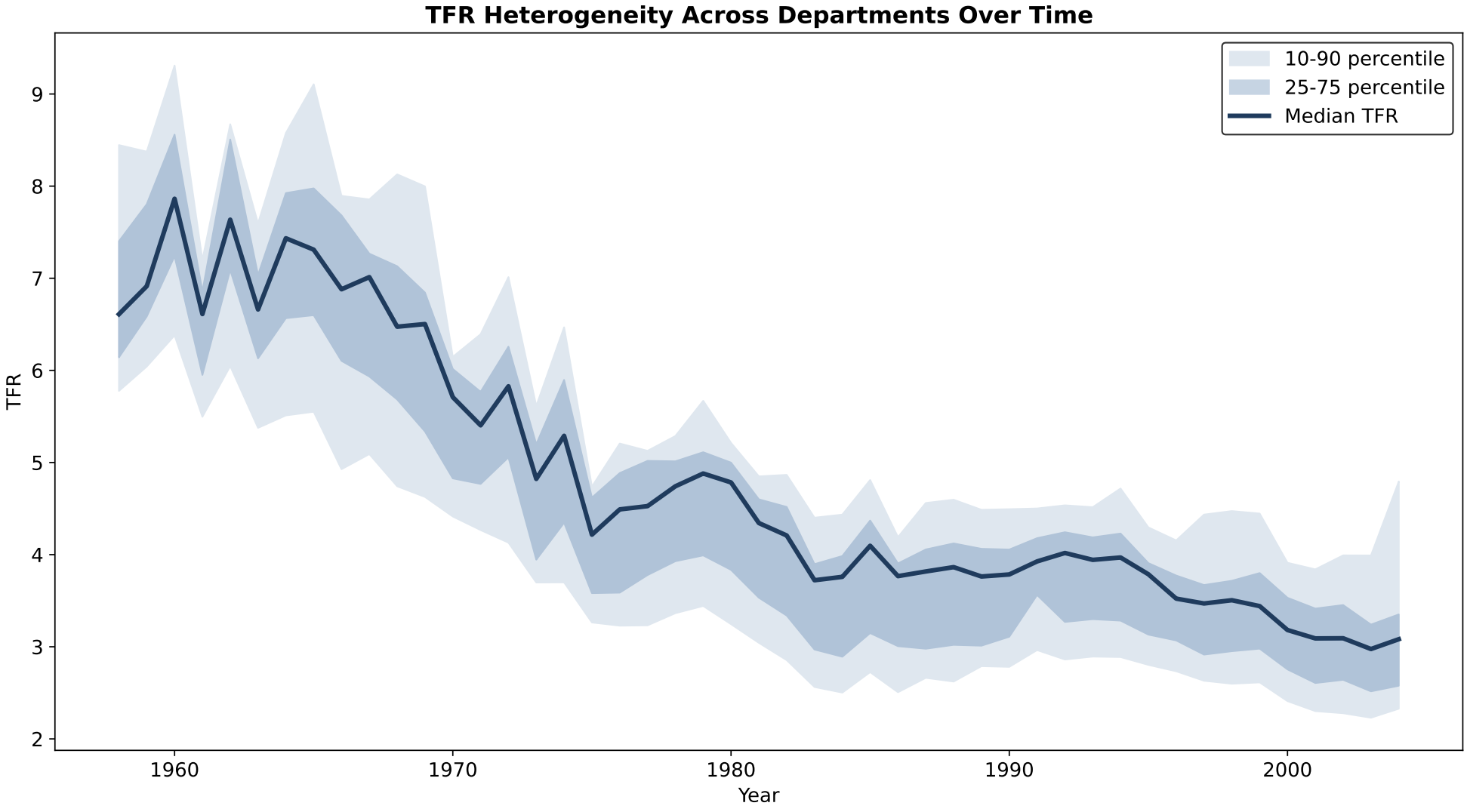

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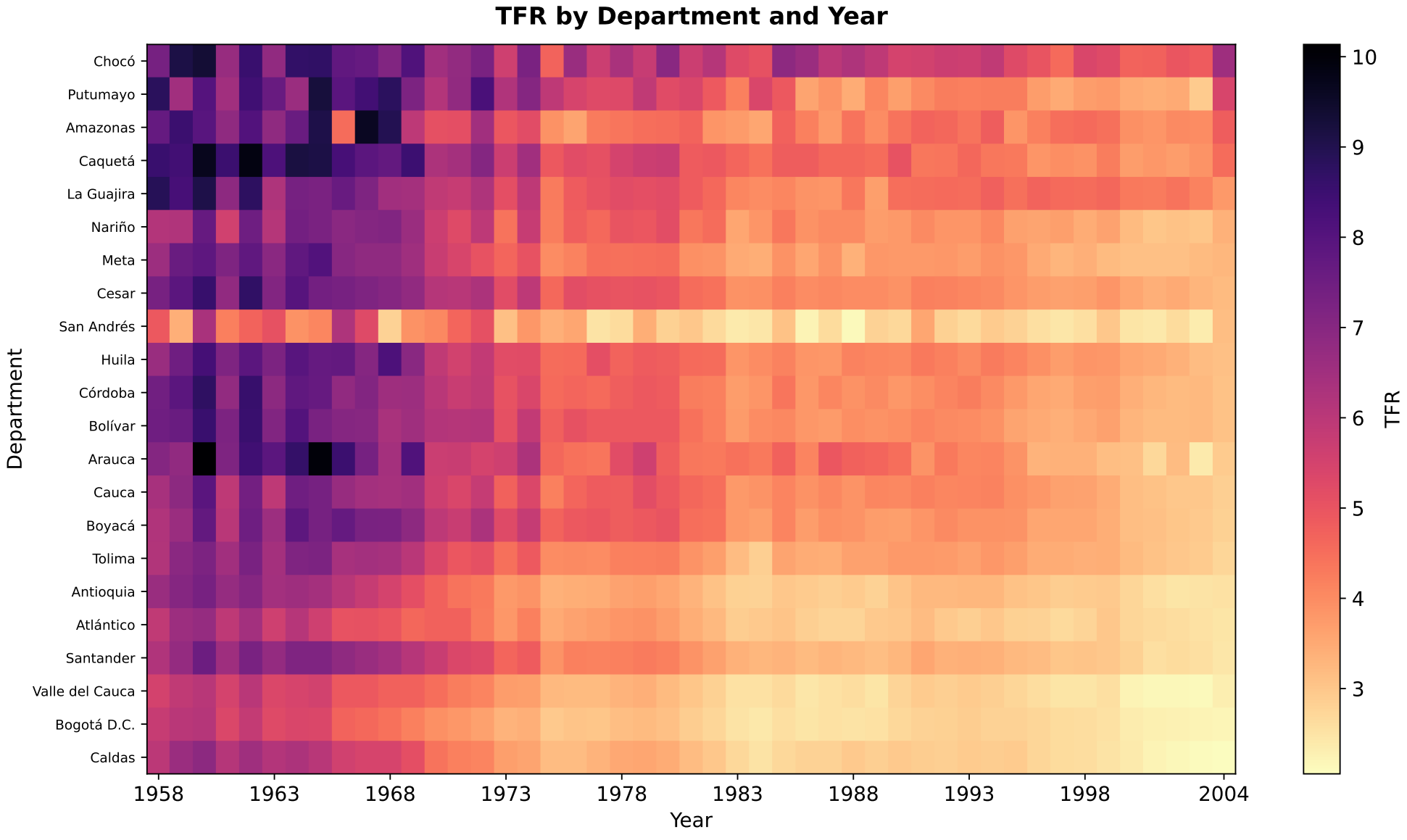

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- Is *similar* to DANE's apprach, but gives user control.

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(Including all data inputs: thanks to Juliana, incredible work!)

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- Has (reasonable?) defaults, but allows user-specified choices.
- Actively developed, documented, and tracked on GitHub.
- Can be publicly released under a GNU GPL 3.0 license.

crahal Some attempted updates for better parralisation (not enough to close ... cbb8bf1 · 4 months ago 69 Commits

course	remove redundant files	6 months ago
data	Add mortality_improvements_example.csv	5 months ago
docs	remove redundant files	6 months ago
src	Some attempted updates for better parralisation (not en...	4 months ago
tests	update the documents to include projections and correct ...	6 months ago
.gitignore	Reorganize documentation structure and update all test s...	6 months ago
LICENSE	Initial commit	10 months ago
README.md	Adding Jiani to the citation! Maybe we could do a .CFT in t...	6 months ago
config.yaml	Fix #24; about age bins being overridden (taken out of ya...	4 months ago
pyproject.toml	source file changes from code reviewing	6 months ago

README GPL-3.0 license

PyCCM

License GNUGPL3.0 | Python 3.7 | 3.8 | 3.9 | 3.10 | 3.11 | Tests 211 passing | Quality 4.7/5 stars | OS Linux | Windows | macOS

Population projection pipeline with single-year ages ("unabridged") and joint parameter sweeps for fertility & mortality assumptions. Supports parallelized scenario runs and consolidated outputs (life tables, ASFR, Leslie matrices, projections).

> **Repo name:** `PyCCM`
> **Entry point:** `src/main_compute.py`
> **Config:** `config.yaml` (root)
> **Data dir:** `data/` (CSV inputs)
> **Outputs:** `results_unabridged/` (default)
> **Status:** Production Ready (211/211 tests passing)

A Python library for making cohort component based projections.

Readme
GPL-3.0 license
Activity
5 stars
0 watching
2 forks

Releases

No releases published
Create a new release

Packages

No packages published
Publish your first package

Contributors 2

crahal
vallerrr J Yan

Languages

Jupyter Notebook 73.1%
Python 26.9%

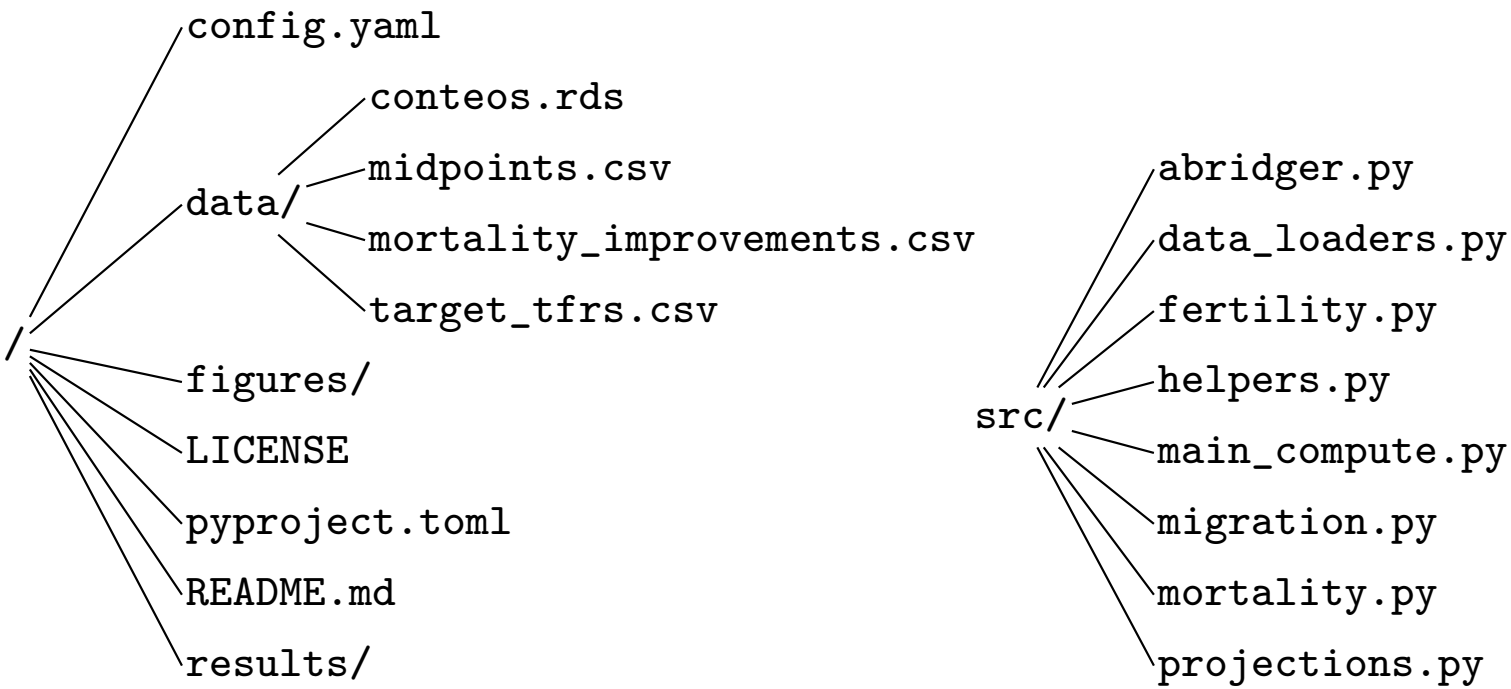
Suggested workflows

Based on your tech stack

Python package Configure

Create and test a Python package on multiple Python versions.

Project Structure



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- Migration data collected through 2024.
- Data is 'semi-abridged':
    - It has 0-1, 2-4, and then 5 year intervals through 90+.

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Immense thanks to Juliana for curating a brilliant `conteos.rds`!

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  2. From a Uniform distribution;
  3. From a Beta distribution.

YAML configuration file

Key sections control paths, behavior, horizon, and assumptions.

- **paths** – input/output file locations.
- **housekeeping** – clean run, diagnostics toggles.
- **projections** – start/end years, death data choices.
- **fertility** – TFR target, convergence, smoother.
- **mortality** – MA smoothing, improvement targets.
- **age_bins** – expected input bins.
- **runs & parallel** – scenarios, number of processes.

Role. A single declarative record of inputs & parameterse.

Abridger: parsing and infant adjustment

Inputs. Counts with `EDADs` (e.g. `0-1`, `2--4`, ..., `90+`) and totals.

Step 1. Parse ages.

- Intervals: a–$b \mapsto [a, b]$.
- Open-ended: $a+ \mapsto [a, \infty)$ (passed through).
- Convention: a–$(a+1)$ collapsed to point a.

Step 2. Infant adjustment (`poblacion_total`).

- If 0–4 present: distribute into 0,1,2,3,4.
- If 1–4 present: distribute into 1,2,3,4.
- Weights w_a proportional to $nL_a(l_0, \ldots, l_5, a_0)$ (from survivorship).

Abridger: smoothing and tails

Step 3. Constraint system.

- Variables x_a = single-year counts.
- For each input bin B: enforce $\sum_{a \in B} x_a = y_B$ (total abridged count).

Step 4. Smooth solution.

$$\min_{x \geq 0} \ \|D_2 x\|^2 + \rho \|x\|^2 \quad \text{s.t. } Ax = b,$$

with D_2 = 2nd-difference, $\rho \approx 10^{-6}$ (ridge). Negatives clipped to 0.

Step 5. Tail harmonization (to 90+).

- Migration: split 70+, 80+ using population shares.
- Population/deaths: geometric splits, different for pop vs. deaths.

Outputs. Single-year `EDAD`, totals preserved on all input bins.

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These go into a Leslie Matrix which is multiplied by:

- A population vector

Midpoint deaths (EEVV–Censo blend)

For the `death_choice = "midpoint"` option, baseline deaths are a convex combination of the two sources.

For each department d, sex s, age a at $t_0 =$ `START_YEAR`: deaths from EEVV, D^{EEVV}_{dsa}, and from Censo, D^{censo}_{dsa}.

Per–department $w_d \in [0,1]$ from `midpoints.csv`; fallback to YAML `midpoints.default_eevv_weight`. We clip w_d to $[0,1]$.

Blend (deaths only):

$$D^{\text{mid}}_{dsa} \;=\; w_d\, D^{\text{EEVV}}_{dsa} \;+\; (1 - w_d)\, D^{\text{censo}}_{dsa}.$$

Ages are aligned/grouped before blending; the result D^{mid}_{dsa} is used to build the life table for the midpoint run. The blend is fixed at t_0 and reused for all projection years for this option.

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We also allow the user to specify custom targets per DPTO.

Smoothing

Setup. Single-year ages $x \in \mathbb{Z}_{\geq 0}$ with exposures E_x and deaths D_x. Crude rates: $m_x = D_x/E_x$ (with numerical floor on E_x).

Centered log–moving average (window W).

$$\tilde{m}_x \;=\; \exp\!\left(\frac{1}{|\mathcal{N}_W(x)|}\sum_{r\in\mathcal{N}_W(x)} \log m_r\right), \quad \mathcal{N}_W(x) = \{x-\lfloor W/2\rfloor, \ldots, x+\lfloor W/2\rfloor\}$$

(edge windows shrink). Use $\tilde{m}_x$ downstream.

Life table (abridged formulas, $n_x = 1$ except open end).

$$q_x \;=\; \frac{\tilde{m}_x}{1+(1-a_x)\tilde{m}_x}, \quad p_x = 1-q_x, \quad \ell_0 = R, \;\; \ell_{x+1} = \ell_x p_x.$$

Final open interval handled in the usual way via $L_\omega = \ell_\omega/\tilde{m}_\omega$.

Life table detail: a_x for age 0–1

General rule. For most ages,

$$a_x \approx \tfrac{1}{2} n_x,$$

i.e. deaths are assumed uniformly distributed within the interval.

Exception: infants (0–1). Mortality is concentrated near birth, so special Coale–Demeny style formulas are used:

$$a_0 = \begin{cases} 0.14903 - 2.05527\, m_0, & m_0 < 0.01724, \\ 0.04667 + 3.88089\, m_0, & 0.01724 \le m_0 < 0.06891, \\ 0.31411, & m_0 \ge 0.06891, \end{cases}$$

where m_0 is the central death rate in the 0–1 interval.

Rationale. These piecewise linear adjustments better reflect observed timing of infant deaths, avoiding bias in q_0 and survivorship.

Target mortality improvements

Parameters (per unit).

- Total improvement fraction: $\theta \in (0, 1)$ (e.g. $0.10 = 10\%$ reduction).
- Convergence horizon: C years.
- Smoother type: exponential (default) or logistic.

Exponential smoother.

$$G = -\ln(1-\theta), \qquad S_t = 1 - \exp\left(-\frac{-\ln(1-\rho)}{C}\, t\right), \qquad \phi_t = e^{-GS_t},$$

with $\rho \approx 0.99$ target convergence fraction.

For year t after baseline, multiply each mortality rate by factor

$$m_x(t) \;\leftarrow\; \phi_t \cdot m_x(t).$$

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- F: 78.47 (censo_2018), 78.15 (EEV), 78.36 ($\frac{1}{2}$ midpoint)
- M: 72.80 (censo_2018), 71.35 (EEV), 71.70 ($\frac{1}{2}$ midpoint)
- T: 75.23 (censo_2018), 74.41 (EEV), 74.83 ($\frac{1}{2}$ midpoint)

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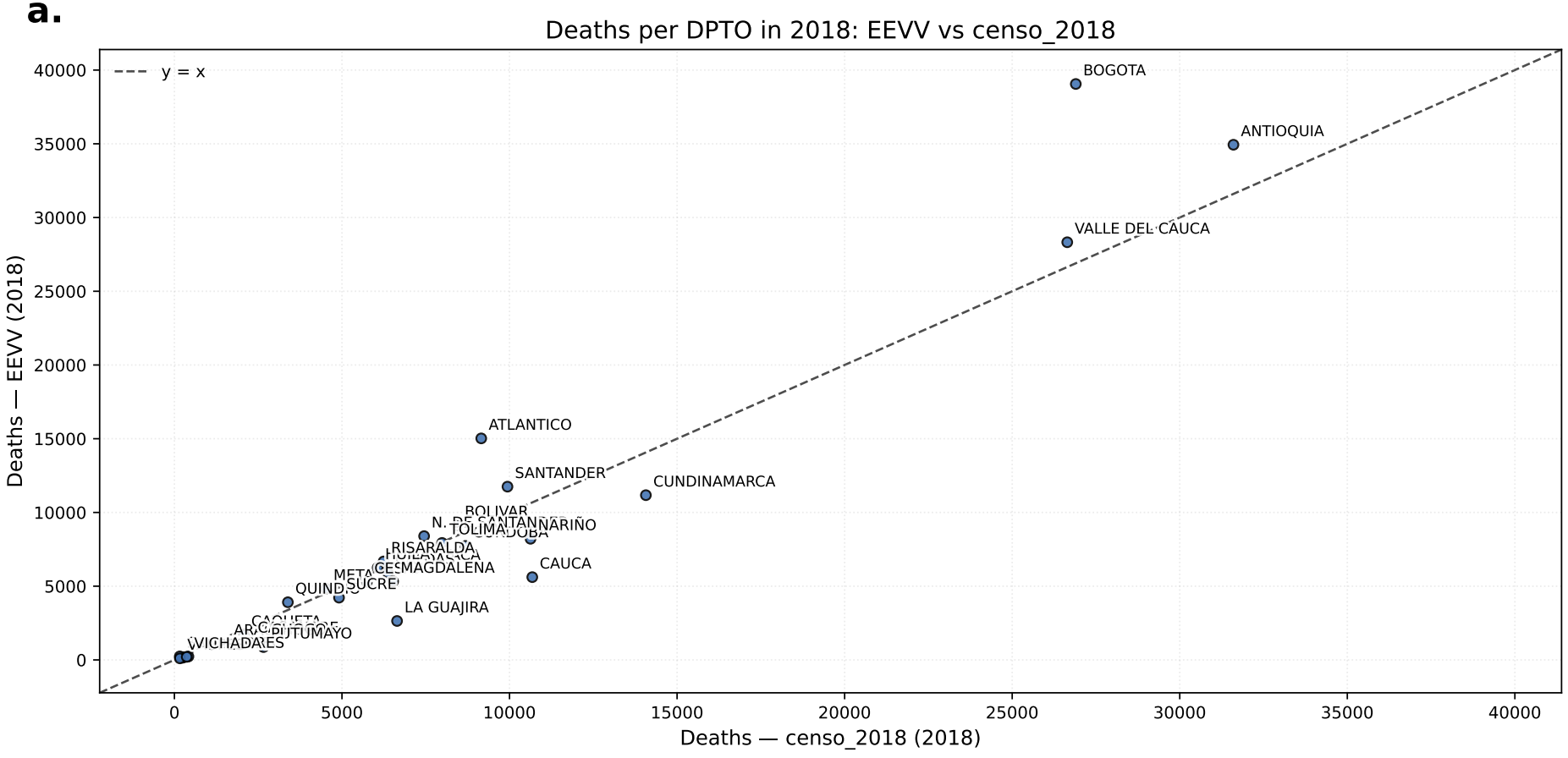
OMISSIONs relatively little impact as typically same for deaths/population: an invariant transformation unless the values differ.

Life Table Extract (2018, Female, total_nacional)

DPTO	death	impr	ma	year	Sex	EDAD	n	mx	ax	qx	px	lx	dx	Lx	Tx	ex
total	mid	0.25	3	2018	F	0	1	0.0183	0.498	0.0181	0.982	100000	1808	99093	7798074	78.36
total	mid	0.25	3	2018	F	1	1	0.0121	0.500	0.0121	0.988	98192	1184	97599	7698981	78.41
total	mid	0.25	3	2018	F	2	1	0.00173	0.500	0.00173	0.99827	97008	168	96924	7601381	78.36
total	mid	0.25	3	2018	F	3	1	0.0000521	0.500	0.0000521	0.99995	96840	5	96837	7504457	77.49
total	mid	0.25	3	2018	F	4	1	0.000000885	0.500	0.000000885	0.999999	96835	0	96835	7407620	76.50
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
total	mid	0.25	3	2018	F	85	1	0.0704	0.500	0.0680	0.932	49770	3384	48078	235871	4.74
total	mid	0.25	3	2018	F	86	1	0.0785	0.500	0.0755	0.924	46386	3504	44634	187793	4.05
total	mid	0.25	3	2018	F	87	1	0.0886	0.500	0.0848	0.915	42882	3637	41064	143159	3.34
total	mid	0.25	3	2018	F	88	1	0.102	0.500	0.0969	0.903	39246	3802	37345	102095	2.60
total	mid	0.25	3	2018	F	89	1	0.190	0.500	0.173	0.827	35443	6136	32375	64750	1.83
total	mid	0.25	3	2018	F	90+	5	0.905	2.500	1.000	0.000	29307	29307	32375	32375	1.10

a.


Deaths per DPTO in 2018: EEVV vs censo_2018
y = x
Deaths — EEVV (2018)
Deaths — censo_2018 (2018)
BOGOTA
ANTIOQUIA
VALLE DEL CAUCA
ATLANTICO
SANTANDER
CUNDINAMARCA
BOLIVAR
TOLIMA
RISARALDA
CAUCA
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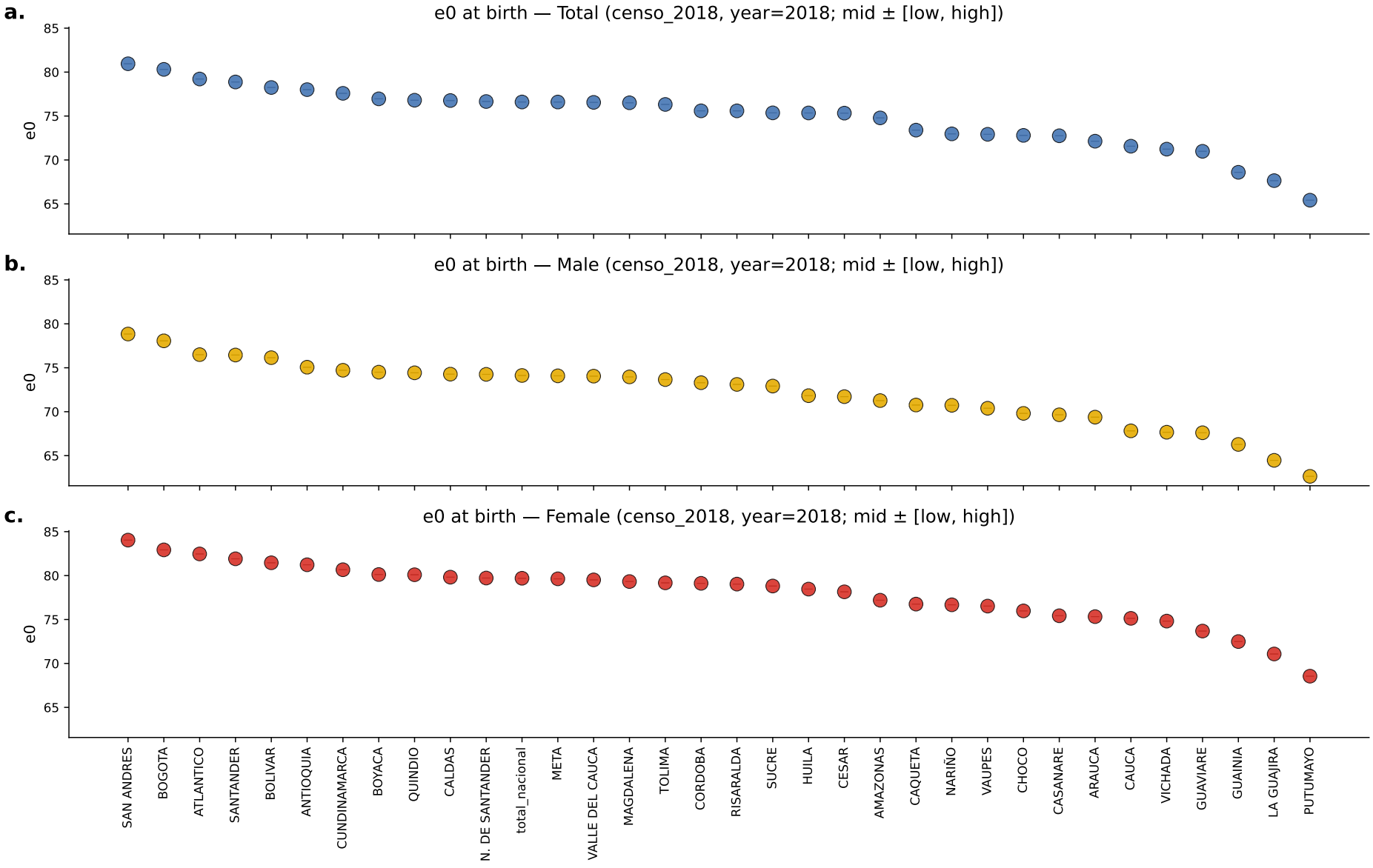
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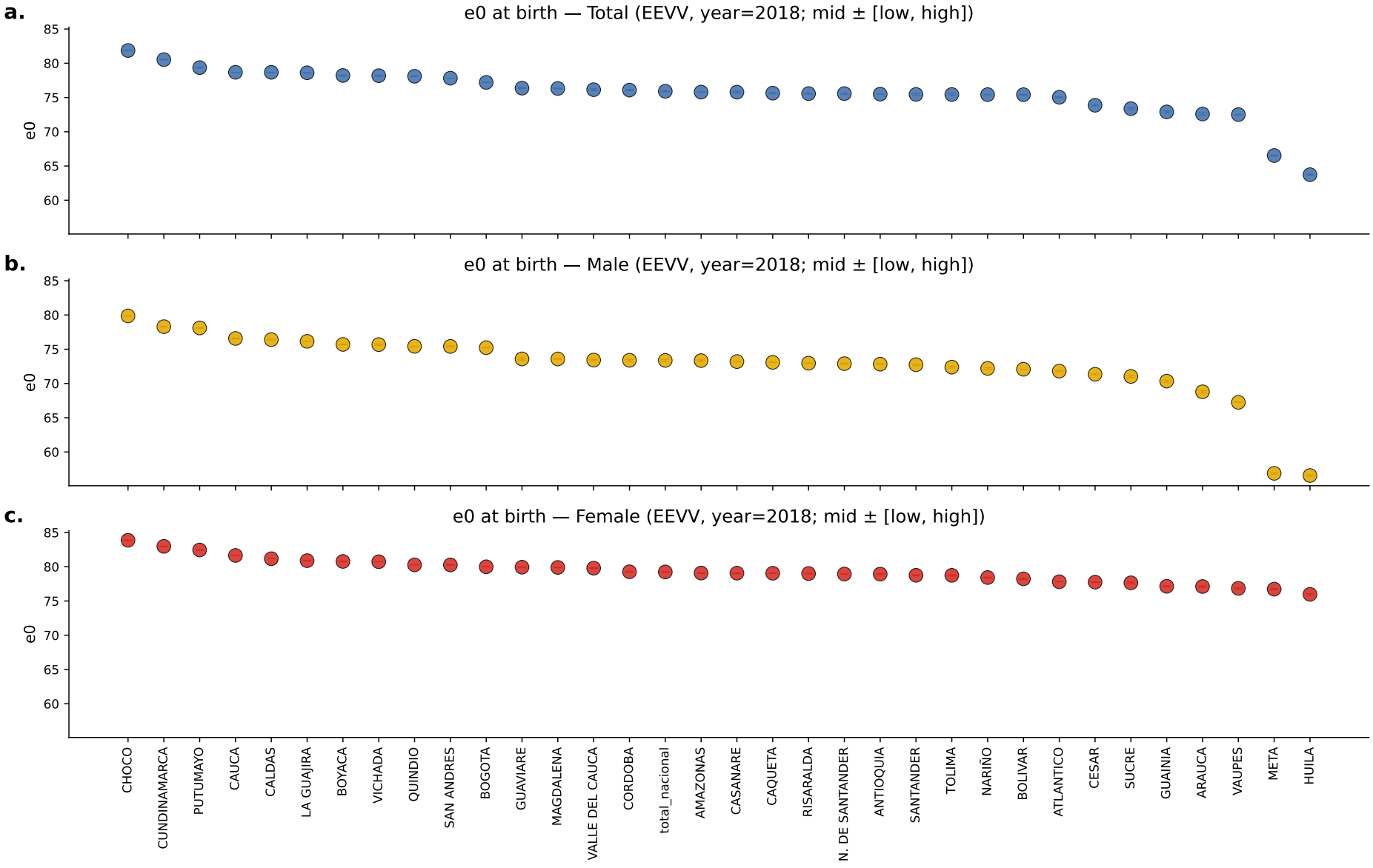
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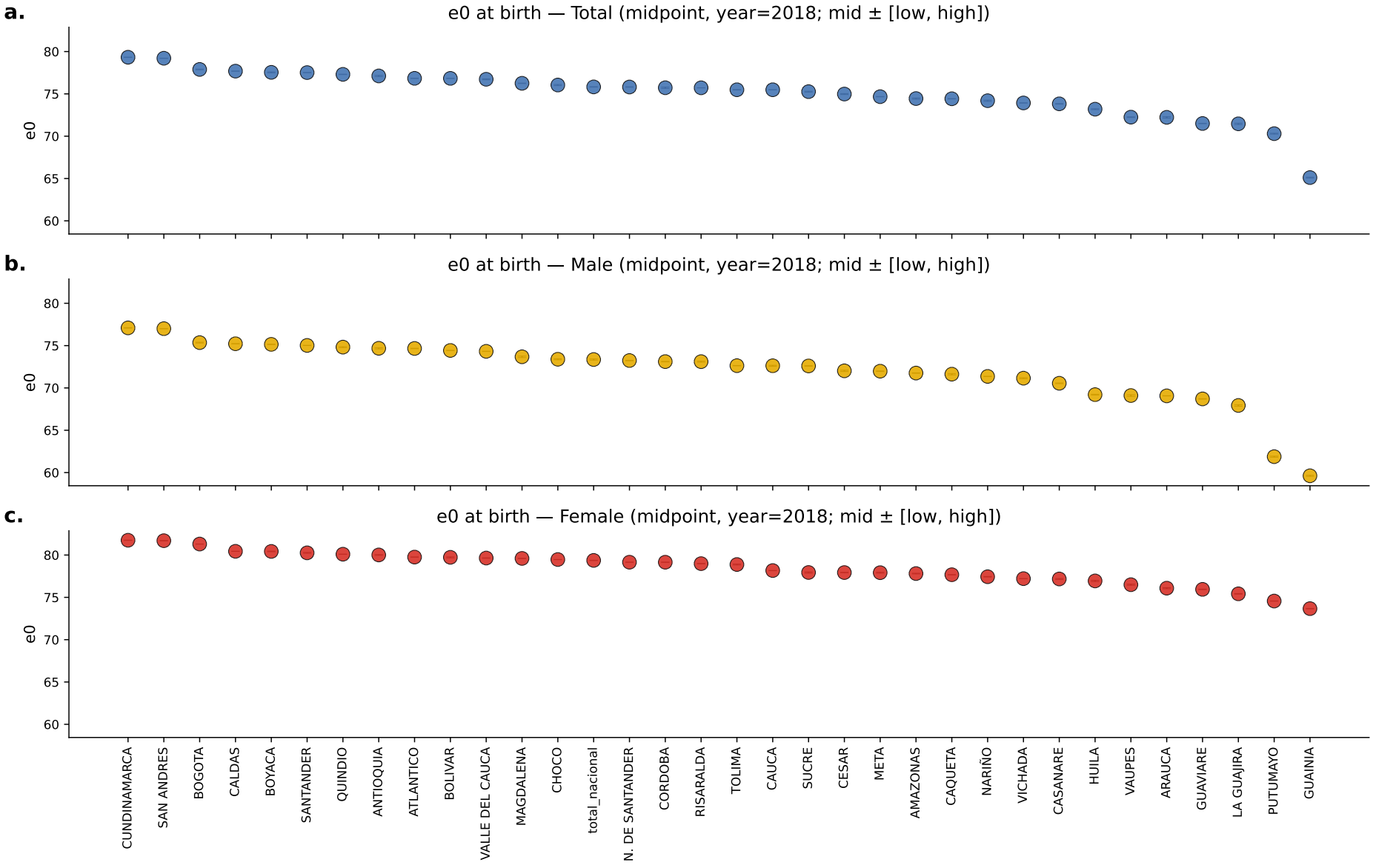
VICHADA
QUINDIO
SAN ANDRES
BOGOTA
GUAVIARE
MAGDALENA
VALLE DEL CAUCA
CORDOBA
total_nacional
AMAZONAS
CASANARE
CAQUETA
RISARALDA
N. DE SANTANDER
ANTIOQUIA
SANTANDER
TOLIMA
NARIÑO
BOLIVAR
ATLANTICO
CESAR
SUCRE
GUAINIA
ARAUCA
VAUPES
META
HUILA


a.
e0 at birth — Total (midpoint, year=2018; mid ± [low, high])
b.
e0 at birth — Male (midpoint, year=2018; mid ± [low, high])
c.
e0 at birth — Female (midpoint, year=2018; mid ± [low, high])
e0
80
75
70
65
60
CUNDINAMARCA
SAN ANDRES
BOGOTA
CALDAS
BOYACA
SANTANDER
QUINDIO
ANTIOQUIA
ATLANTICO
BOLIVAR
VALLE DEL CAUCA
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N. DE SANTANDER
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VAUPES
ARAUCA
GUAVIARE
LA GUAJIRA
PUTUMAYO
GUAINIA

Target TFR: inputs, identification, and baseline

Files and configuration.

- Read `target_tfr_csv` with columns: DPTO_NOMBRE, Target_TFR, and (optionally) convergence years.
- If absent, use global defaults from YAML:
  $\tau_{\text{glob}} = \texttt{fertility.default\_tfr\_target}$,
  $C_{\text{glob}} = \texttt{fertility.convergence\_years}$.

Departmental targets and convergence.

$$\tau_d = \begin{cases} \text{CSV value} & \text{if present} \\ \tau_{\text{glob}} & \text{otherwise,} \end{cases} \qquad C_d = \begin{cases} \text{CSV value} & \text{if present,} \\ C_{\text{glob}} & \text{otherwise.} \end{cases}$$

National target if not given

If $\tau_{\texttt{total\_nacional}}$ is missing, compute it as an exposure–weighted mean over departments (exposures restricted to ASFR ages):

$$\tau_{\text{nat}}\big(t,\ \texttt{death\_choice}\big) \;=\; \sum_{d \neq \text{nat}} w_d(t)\, \tau_d\big(t,\ \texttt{death\_choice}\big)$$

and

$$w_d(t) \;=\; \frac{E_d(t)}{\displaystyle\sum_{j \neq \text{nat}} E_j(t)}$$

where $E_d(t)$ is female exposure by department at $t = \texttt{START\_YEAR}$.

Baseline ASFR and weights

For each unit $u \in \{d, \text{nat}\}$ and a cutoff year $t_0(u)$ (last observed for the chosen death series):

$$\text{ASFR}_a^{(0)}(u) \;=\; \frac{B_a(u)}{P_a(u)}, \qquad \text{TFR}_0(u) \;=\; \sum_a \text{ASFR}_a^{(0)}(u)\, n_a,$$

$$w_a(u) \;=\; \frac{\text{ASFR}_a^{(0)}(u)}{\text{TFR}_0(u)} \quad \text{(stored and reused as the shape over ages).}$$

If $\text{TFR}_0(u)$ is not finite, code falls back to previously stored weights for u, or to national weights if departmental ones unavailable.

Target TFR: smoothing path/ASFR reconstruction

For year $t \geq t_0(u)$, let the fractional progress to target be $S_t \in [0, 1]$.

Exponential parameters:
C_u and $\phi \in (0, 1) =$ `smoother.converge_frac`:

$$\kappa \;=\; -\frac{\ln(1-\phi)}{C_u}, \qquad S_t \;=\; 1 - e^{-\kappa(t-t_0)}.$$

Logistic parametres:
C_u, mid-fraction $m \in (0, 1)$, steepness $s > 0$:

$$x \;=\; \frac{t - t_0}{C_u} - m, \qquad S_t \;=\; \frac{1}{1 + e^{-sx}},$$

with a default s chosen so that $S_{t_0+C_u} \approx 0.99$ if not provided.

TFR trajectory and ASFRs. Let τ_u be the (departmental or national) target TFR and $\mathrm{TFR}_0(u)$ the baseline:

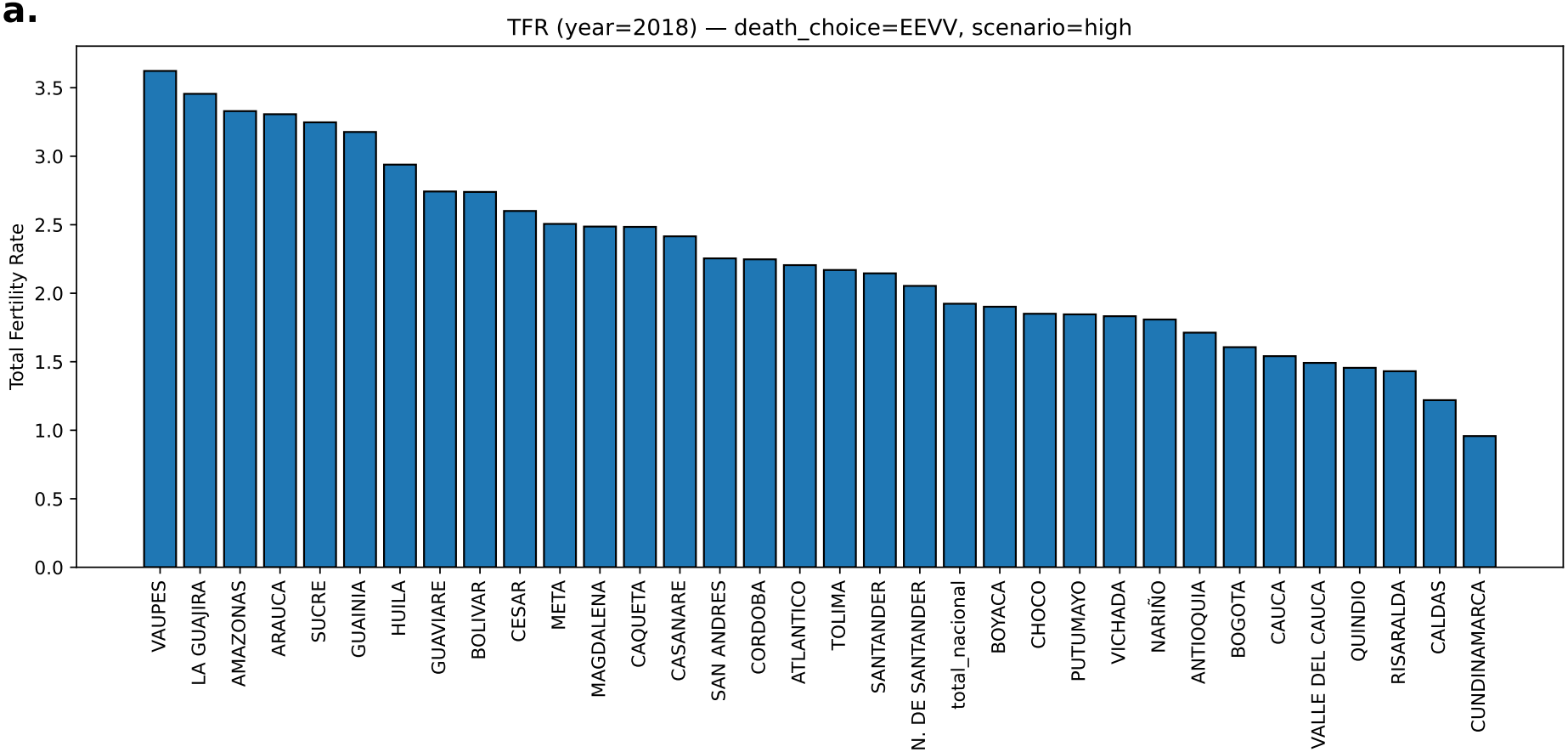
$$\mathrm{TFR}_t(u) \;=\; (1 - S_t)\,\mathrm{TFR}_0(u) \;+\; S_t\,\tau_u.$$

ASFRs annually rebuilt, rescaling fixed $w_a(u)$ to $\mathrm{TFR}_t(u)$:

$$\widehat{\mathrm{ASFR}}_a(u,t) \;=\; \widetilde{w}_a(u;\{n_a\})\,\mathrm{TFR}_t(u), \quad \text{with } \sum_a \widetilde{w}_a(u)\,n_a = 1.$$

The implementation normalizes w_a to the age index. It also checks $\sum_a \widehat{\mathrm{ASFR}}_a n_a = \mathrm{TFR}_t$ to 10^{-6} tolerance, clipping non-finite values.

a.


TFR (year=2018) — death_choice=EEVV, scenario=high
Total Fertility Rate
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
VAUPES
LA GUAJIRA
AMAZONAS
ARAUCA
SUCRE
GUAINIA
HUILA
GUAVIARE
BOLIVAR
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META
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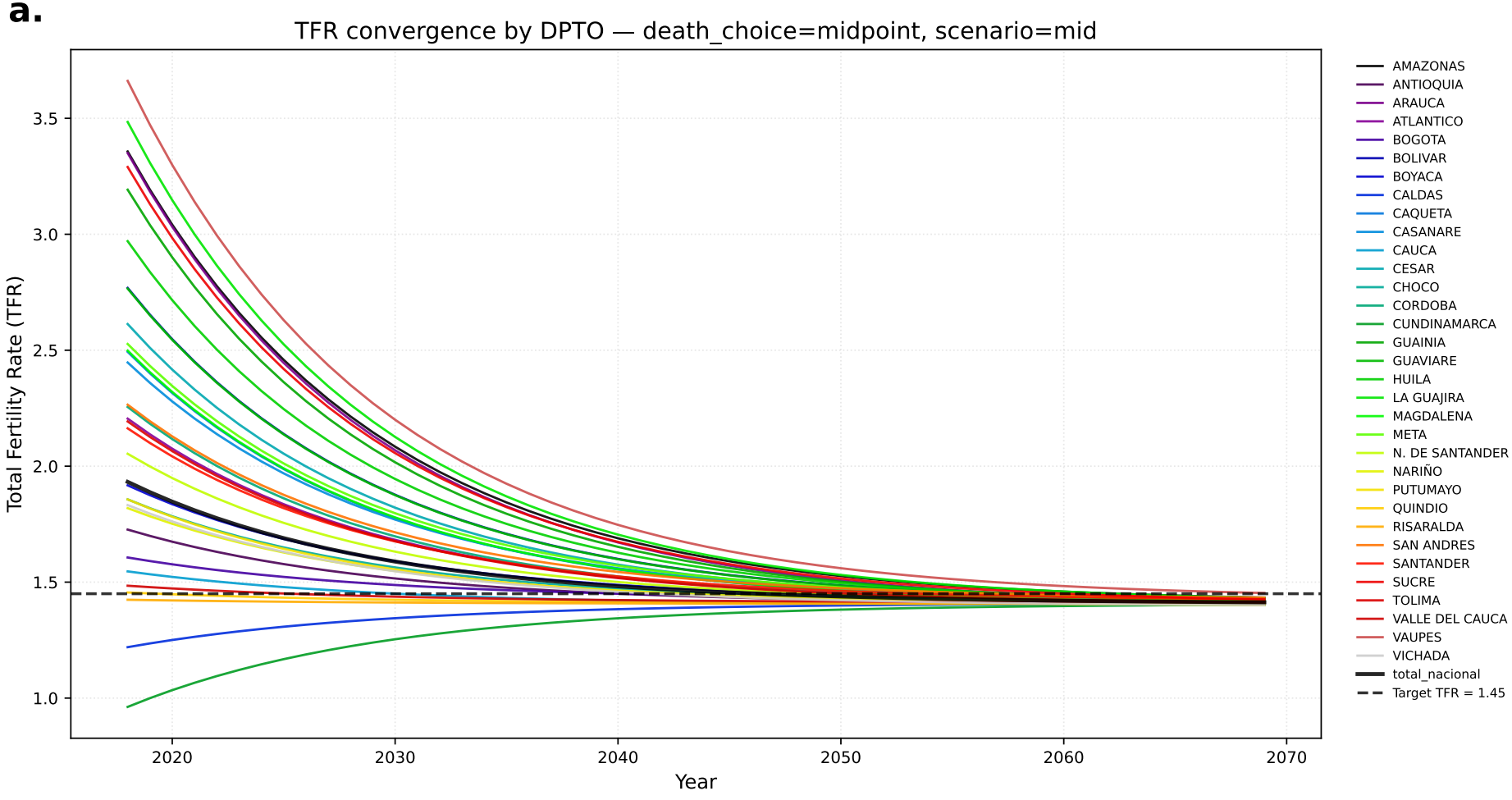
a.


TFR convergence by DPTO — death_choice=midpoint, scenario=mid
Total Fertility Rate (TFR)
Year
3.5
3.0
2.5
2.0
1.5
1.0
2020
2030
2040
2050
2060
2070
AMAZONAS
ANTIOQUIA
ARAUCA
ATLANTICO
BOGOTA
BOLIVAR
BOYACA
CALDAS
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QUINDIO
RISARALDA
SAN ANDRES
SANTANDER
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TOLIMA
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VAUPES
VICHADA
total_nacional
Target TFR = 1.45

Migration module: goal and inputs

Objective: Construct age–sex migration panels for projection.

Inputs from `conteos`:

- `poblacion_total` $\longrightarrow P_{a,s}(y)$.
- `flujo_inmigracion` (IN), `flujo_emigracion` (OUT).
- Ages in 5-year bins, 0–$4, \ldots, 80+$; sex $\in \{1, 2\}$.

Preprocessing:

- Coerce counts ≥ 0; ensure ordered categories for age, sex, year.

Constructing migration measures (2018 slice)

Population aggregation:

$$P_{a,s}(y) = \sum_{(\text{ANO}=y,\ \text{EDAD}=a,\ \text{SEXO}=s)} \text{VALOR}.$$

Flows:

$$I_{a,s}(y) = \sum \mathbf{1}_{\text{IN}}\text{VALOR}, \qquad E_{a,s}(y) = \sum \mathbf{1}_{\text{OUT}}\text{VALOR}.$$

Derived:

$$\text{Net}_{a,s}(y) = I_{a,s}(y) - E_{a,s}(y), \quad r^{\text{net}}_{a,s}(y) = \frac{\text{Net}_{a,s}(y)}{P_{a,s}(y)}.$$

Return panel for $y = 2018$: $\{a, s, I, E, \text{Net}, P, r^{\text{net}}\}$.

National flows and departmental scaling

Recency rule. For projection year t:

$$y^{\text{flows}} = \min(t,\ \texttt{FLOWS\_LATEST\_YEAR}),$$

so migration profiles are frozen at the most recent observed year.

National totals:

$$I^{\text{nat}}_{a,s} = \sum_d I_{a,s}(d, y^{\text{flows}}), \quad E^{\text{nat}}_{a,s} = \sum_d E_{a,s}(d, y^{\text{flows}}).$$

Department shares:

$$\rho_{a,s}(d,t) = \frac{P_{a,s}(d,t)}{P^{\text{nat}}_{a,s}(t)}.$$

Scaled flows:

$$\Delta_{a,s}(d,t) = \texttt{PERIOD\_YEARS} \cdot \rho_{a,s}(d,t) \left(I^{\text{nat}}_{a,s} - E^{\text{nat}}_{a,s}\right).$$

Half-flow convention and state update

Mid-interval exposure:

$$P^*_{a,s}(d,t) = P_{a,s}(d,t) + \tfrac{1}{2}\Delta_{a,s}(d,t),$$

used only as denominator for ASFRs and mortality rates.

End-of-period stock:

$$P_{a,s}(d,t+\Delta) = \mathcal{L}_{a,s}\big(P^*(d,t)\big) + \Delta_{a,s}(d,t).$$

Thus: half of Δ enters via exposures (rates), the full Δ updates the stock. No double-counting.

Leslie construction for 1-year ages (female block)

Setup. Ages $a = 0, 1, \ldots, A$ (e.g. up to $90+$).
Let $\mathcal{F} = \{a_{\min}, \ldots, a_{\max}\}$ be fertile ages (e.g. $12:49$). With 1-year steps, widths $n_a \equiv 1$.

Ingredients at year t:

- ASFR shape $\widehat{f}_a(t)$ for $a \in \mathcal{F}$ (else 0), normalized to TFR_t.
- Survival $p_a^F(t) = 1 - q_a^F(t)$ from life table (female).
- Sex-at-birth fraction κ_F (female share of births).

Fertile ages $\mathcal{F} = \{a_{\min}, \ldots, a_{\max}\}$. Define

$$b_a(t) = \begin{cases} \kappa_F \widehat{f}_a(t)\, p_0^F(t), & a \in \mathcal{F}, \\ 0, & \text{otherwise.} \end{cases}$$

$$L^{(F)}(t) = \begin{pmatrix} b_0 & b_1 & b_2 & \cdots & b_{A-1} & b_A \\ p_0^F & 0 & 0 & \cdots & 0 & 0 \\ 0 & p_1^F & 0 & \cdots & 0 & 0 \\ \vdots & \ddots & \ddots & \ddots & \vdots & \vdots \\ 0 & \cdots & 0 & p_{A-2}^F & 0 & 0 \\ 0 & \cdots & 0 & 0 & p_{A-1}^F & r_A^F \end{pmatrix}$$

Notes: (i) $b_0 = 0$, so newborns are not fertile; (ii) sub-diagonal entries are one-year survivals $p_a^F(t)$; (iii) the open age uses a diagonal retention $r_A^F(t) \in [0, 1]$.

Blocks. With male survival $p_a^M(t)$ and male share $\kappa_M = 1 - \kappa_F$,

$$L_{MF}(t) = \Big[\text{first row } b_a^{(M)}(t) = \kappa_M \widehat{f}_a(t)\, p_0^M(t);\ \text{subdiag } 0\Big],$$

$L_{MM}(t) =$ male survival sub-diagonal like L_{FF} but no fertility row.

Projection with additive migration. For departmental vectors $N^F(t), N^M(t)$ (by single year),

$$\begin{bmatrix} N^F(t{+}1) \\ N^M(t{+}1) \end{bmatrix} = \begin{bmatrix} L_{FF}(t) & 0 \\ L_{MF}(t) & L_{MM}(t) \end{bmatrix} \begin{bmatrix} N^F(t) \\ N^M(t) \end{bmatrix} + \begin{bmatrix} \Delta^F(t) \\ \Delta^M(t) \end{bmatrix}.$$

Here $\Delta^{\cdot}(t)$ are the *full-period* net migration vectors (age–sex specific). The "half-flow" $\frac{1}{2}\Delta$ is used only to adjust exposures for rate computation; it is *not* inserted into L.

Running the Code:

- Running the code is as simple as:

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cd src; python main_compute.py
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     ```
     cd src; python main_compute.py
     ```
- Concatenated outputs: Produces `all_lifetables`, `all_asfr`, `all_leslie_matrices`, and `all_projections` in CSV/Parquet.

Unit Testing in PyCCM:

- PyCCM currently has **211 automated tests** across the core modules.
- Coverage spans mortality, fertility, migration, abridging, helpers, and pipeline orchestration.
- All tests are run with `pytest` and include unit, integration, and edge-case checks.
- Current module-level test counts are:
  1. `test_mortality.py`: 37 tests
  2. `test_fertility.py`: 40 tests
  3. `test_migration.py`: 24 tests
  4. `test_abridger.py`: 46 tests
  5. `test_main_compute.py`: 24 tests
  6. `test_helpers.py`: 40 tests
- Latest documented run: **100% passing** (211/211).

Documentation in PyCCM:

- PyCCM is supported by **extensive technical documentation** across code, tests, and methods.
- Current docs include roughly **110,000 words** spanning module explainers, assessments, and reports.
- Each core module has dedicated material covering:
  1. algorithmic logic and implementation details,
  2. demographic assumptions and methodological choices,
  3. test summaries, known limitations, and recommended improvements.
- Consolidated reports provide both executive summaries and deep-dive validation notes.
- This documentation supports reproducibility, onboarding, and transparent review of the full pipeline.

Root `config.yaml` Defaults (1/7):

- Exact defaults currently in the root YAML:
  1. **Theme: Paths**
     - 1.1 `paths.data_dir = "./data"`
     - 1.2 `paths.results_dir = "./results"`
     - 1.3 `paths.target_tfr_csv = "./data/target_tfrs.csv"`
     - 1.4 `paths.midpoints_csv = "./data/midpoints.csv"`
     - 1.5 `paths.mortality_improvements_csv = "./data/mortality_improvements_in_class.csv"`

Root `config.yaml` Defaults (2/7):

- Exact defaults currently in the root YAML:
  2. **Theme: Diagnostics and Maintenance**
     - 2.1 `diagnostics.print_target_csv = true`
     - 2.2 `diagnostics.mortality_improvements_debug = true`
     - 2.3 `maintenance.clean_run = true`
     - 2.4 `unabridging.enabled = true`

Root `config.yaml` Defaults (3/7):

- Exact defaults currently in the root YAML:

3. **Theme: Projection Horizon and Inputs**

3.1 `projections.start_year = 2018`
3.2 `projections.end_year = 2069`
3.3 `projections.step_years = 1`
3.4 `projections.death_choices = ["EEVV"]`
3.5 `projections.period_years = 1`
3.6 `projections.flows_latest_year = 2024`
3.7 `last_observed_year_by_death.EEVV = 2023`
3.8 `last_observed_year_by_death.censo_2018 = 2018`
3.9 `last_observed_year_by_death.midpoint = 2018`

Root `config.yaml` Defaults (4/7):

- Exact defaults currently in the root YAML:

4. **Theme: Fertility Settings**

4.1 `fertility.default_tfr_target = 1.45`
4.2 `fertility.convergence_years = 52`
4.3 `fertility.smoother.kind = "exp"`
4.4 `fertility.smoother.converge_frac = 0.99`
4.5 `fertility.smoother.logistic.mid_frac = 0.5`
4.6 `fertility.smoother.logistic.steepness = null`
4.7 `fertility.default_tfr_target_range.start = 1.45`
4.8 `fertility.default_tfr_target_range.stop = 1.45`
4.9 `fertility.default_tfr_target_range.step = 0.05`

Root `config.yaml` Defaults (5/7):

- Exact defaults currently in the root YAML:
  5. **Theme: Midpoint Settings**
     5.1 `midpoints.default_eevv_weight = 0.5`

Root `config.yaml` Defaults (6/7):

- Exact defaults currently in the root YAML:

6. **Theme: Mortality Settings**

6.1 `mortality.use_ma = true`
6.2 `mortality.ma_window = 5`
6.3 `mortality.improvement_total = 0.2`
6.4 `mortality.convergence_years = 52`
6.5 `mortality.smoother.kind = "exp"`
6.6 `mortality.smoother.converge_frac = 0.99`
6.7 `mortality.smoother.logistic.mid_frac = 0.5`
6.8 `mortality.smoother.logistic.steepness = null`
6.9 `mortality.improvement_total_range.start = 0.25`
6.10 `mortality.improvement_total_range.stop = 0.25`
6.11 `mortality.improvement_total_range.step = 0.05`
6.12 `mortality.ma_window_range.start = 5`
6.13 `mortality.ma_window_range.stop = 5`
6.14 `mortality.ma_window_range.step = 1`

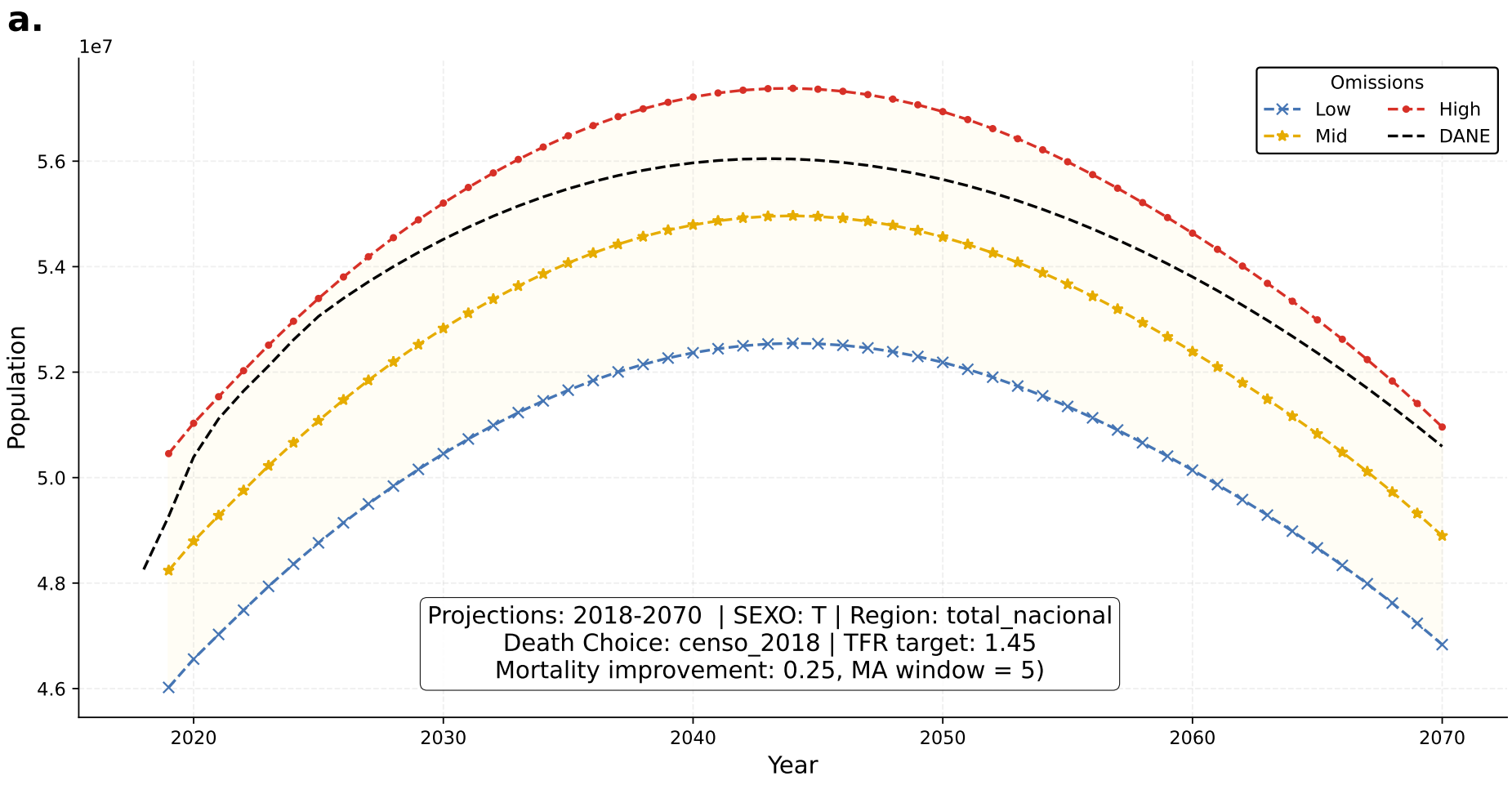
Root `config.yaml` Defaults (7/7):

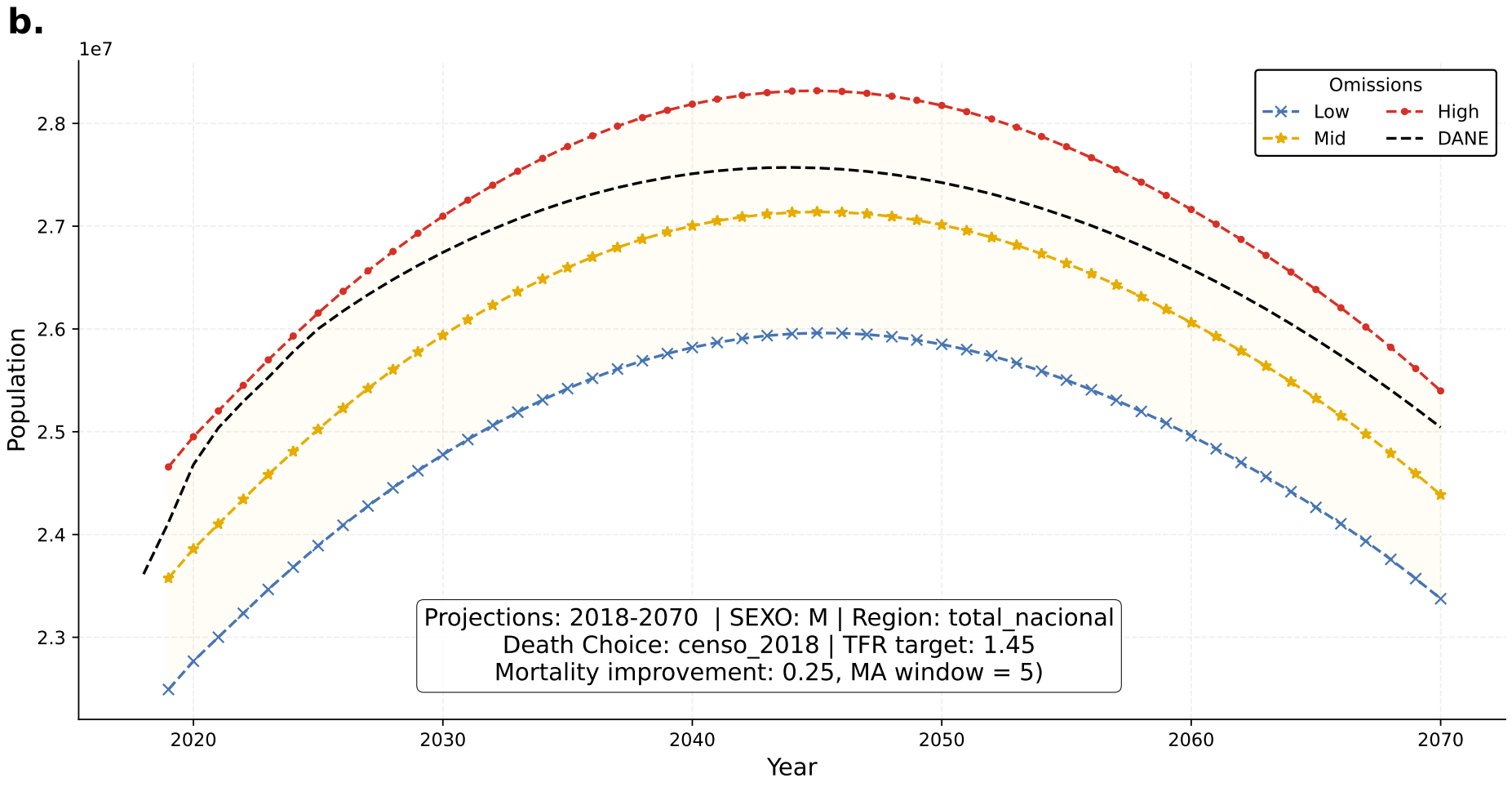
- Exact defaults currently in the root YAML:

7. **Theme: Runs, Parallel, and Filenames**

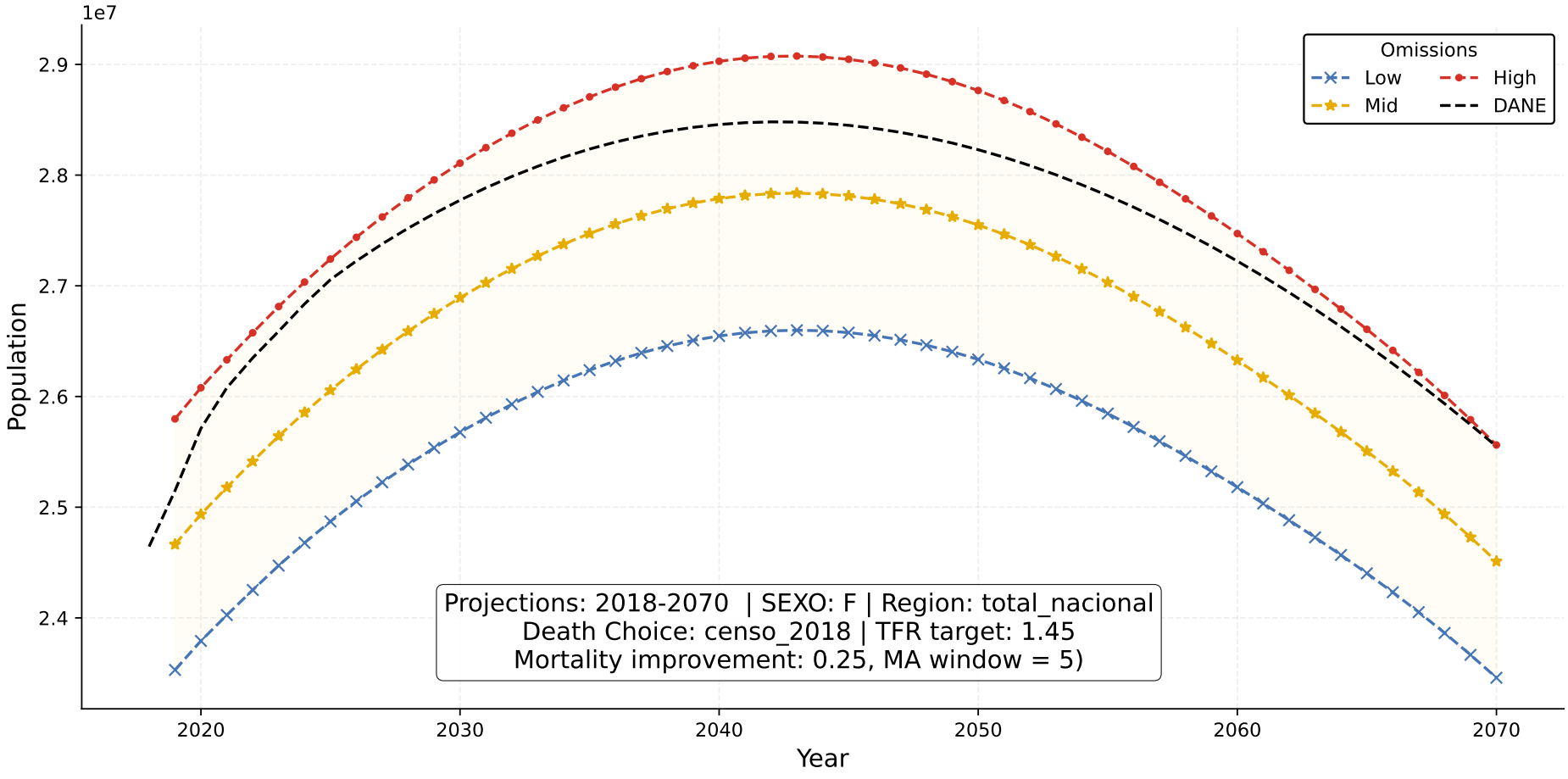
7.1 `runs.mode = "no_draws"`
7.2 `runs.no_draws_tasks = [mid_omissions, low_omissions, high_omissions]`
7.3 `runs.draws.num_draws = 1000`
7.4 `runs.draws.dist_types = ["uniform"]`
7.5 `runs.draws.label_pattern = "{dist}_draw_{i}"`
7.6 `parallel.processes = 20`
7.7 `filenames.asfr = "asfr.csv"`
7.8 `filenames.lt_M = "lt_M_t.csv"`
7.9 `filenames.lt_F = "lt_F_t.csv"`
7.10 `filenames.lt_T = "lt_T_t.csv"`

Lets finally see what these (very conservative) defaults look like...!

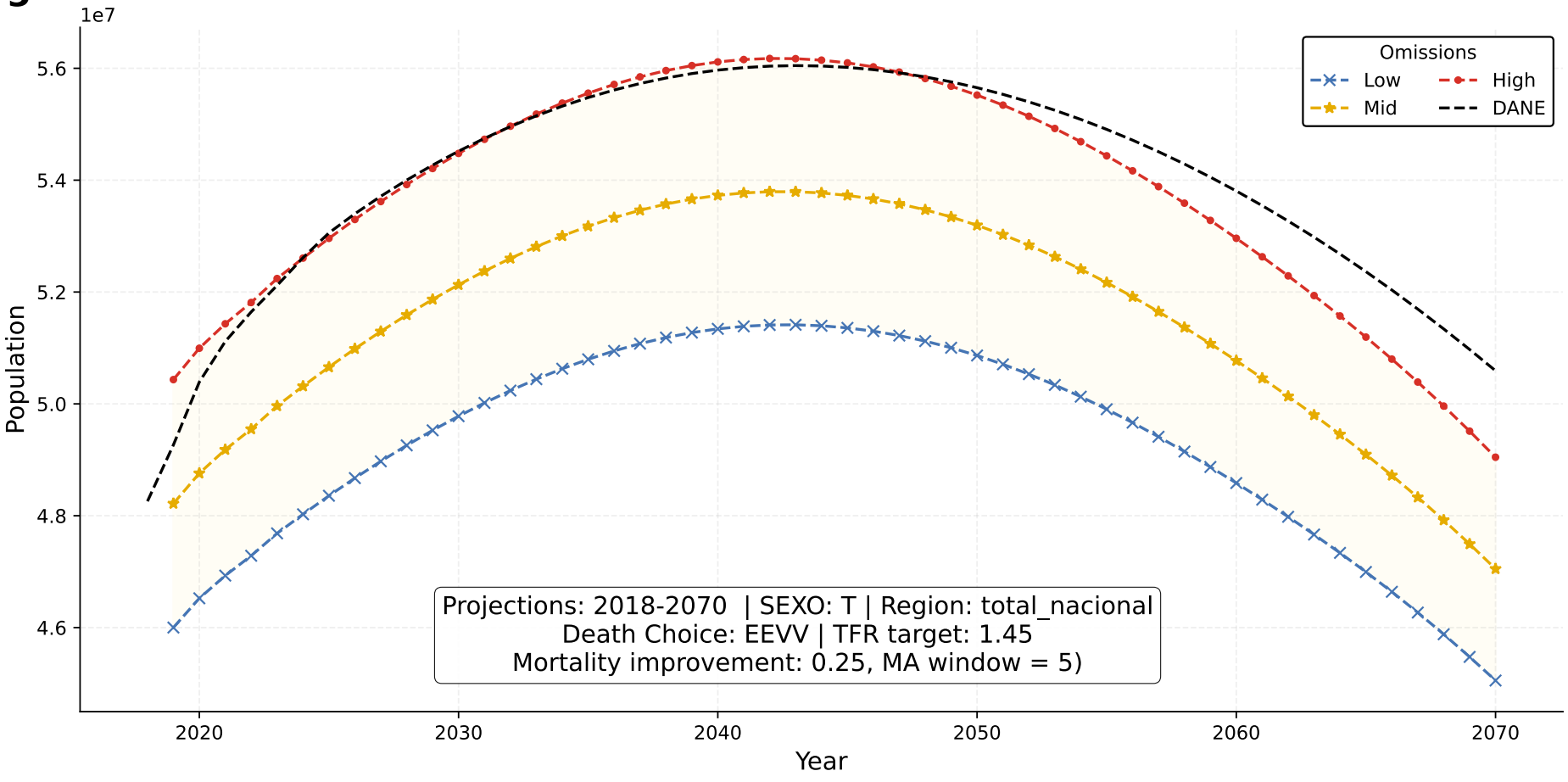

a.
1e7
5.6
5.4
5.2
5.0
4.8
4.6
Population
2020
2030
2040
2050
2060
2070
Year
Omissions
Low
High
Mid
DANE
Projections: 2018-2070 | SEXO: T | Region: total_nacional
Death Choice: censo_2018 | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)


b.
1e7
2.8
2.7
2.6
2.5
2.4
2.3
Population
2020
2030
2040
2050
2060
2070
Year
Omissions
Low
High
Mid
DANE
Projections: 2018-2070 | SEXO: M | Region: total_nacional
Death Choice: censo_2018 | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)

c.


1e7
2.9
2.8
2.7
2.6
2.5
2.4
Population
2020
2030
2040
2050
2060
2070
Year
Omissions
Low
High
Mid
DANE
Projections: 2018-2070 | SEXO: F | Region: total_nacional
Death Choice: censo_2018 | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)

g.


1e7
5.6
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Population
2020
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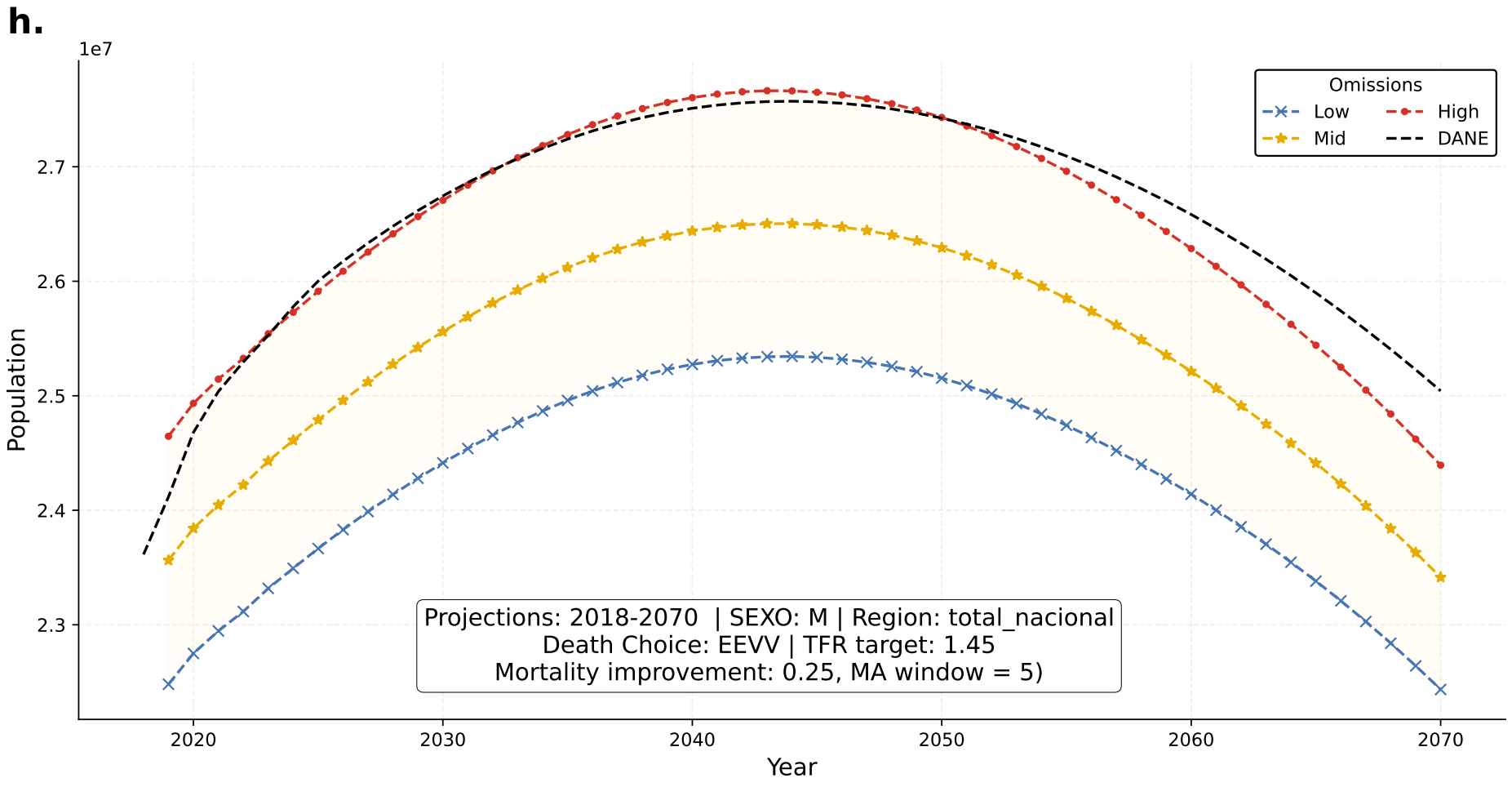
2070
Year
Omissions
Low
High
Mid
DANE
Projections: 2018-2070 | SEXO: T | Region: total_nacional
Death Choice: EEVV | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)


h.
1e7
Population
2.7
2.6
2.5
2.4
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2020
2030
2040
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Year
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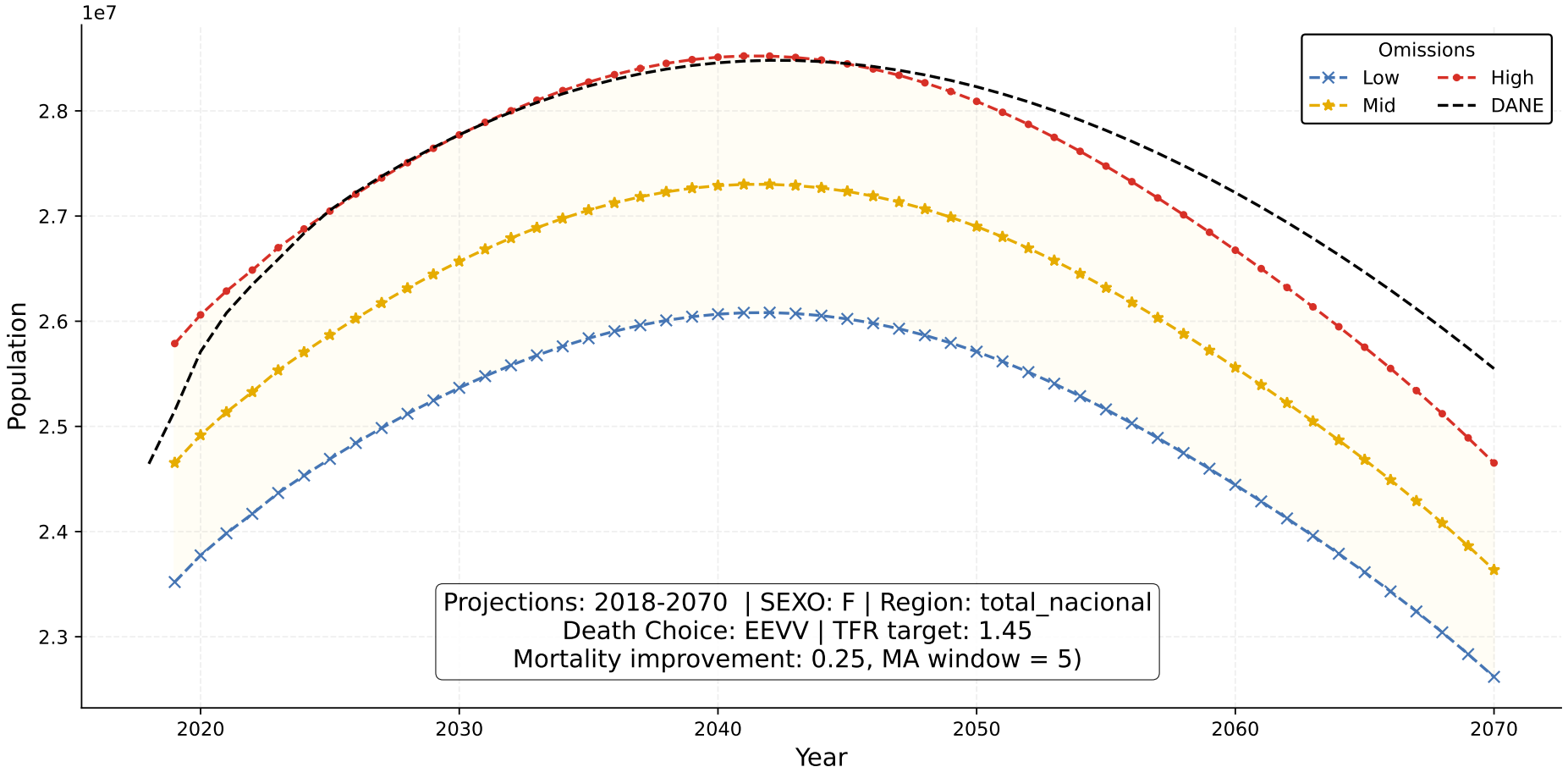
i.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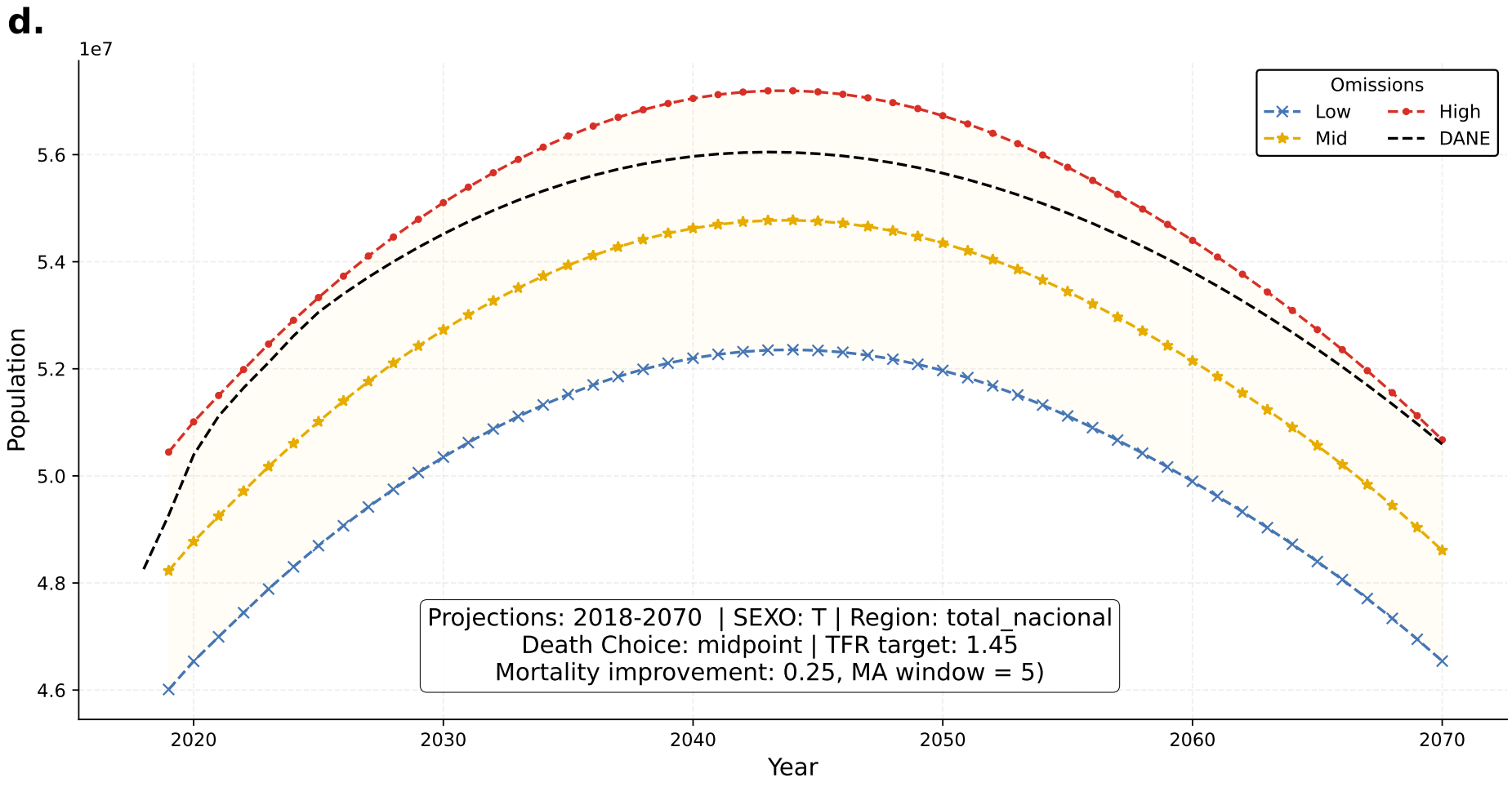
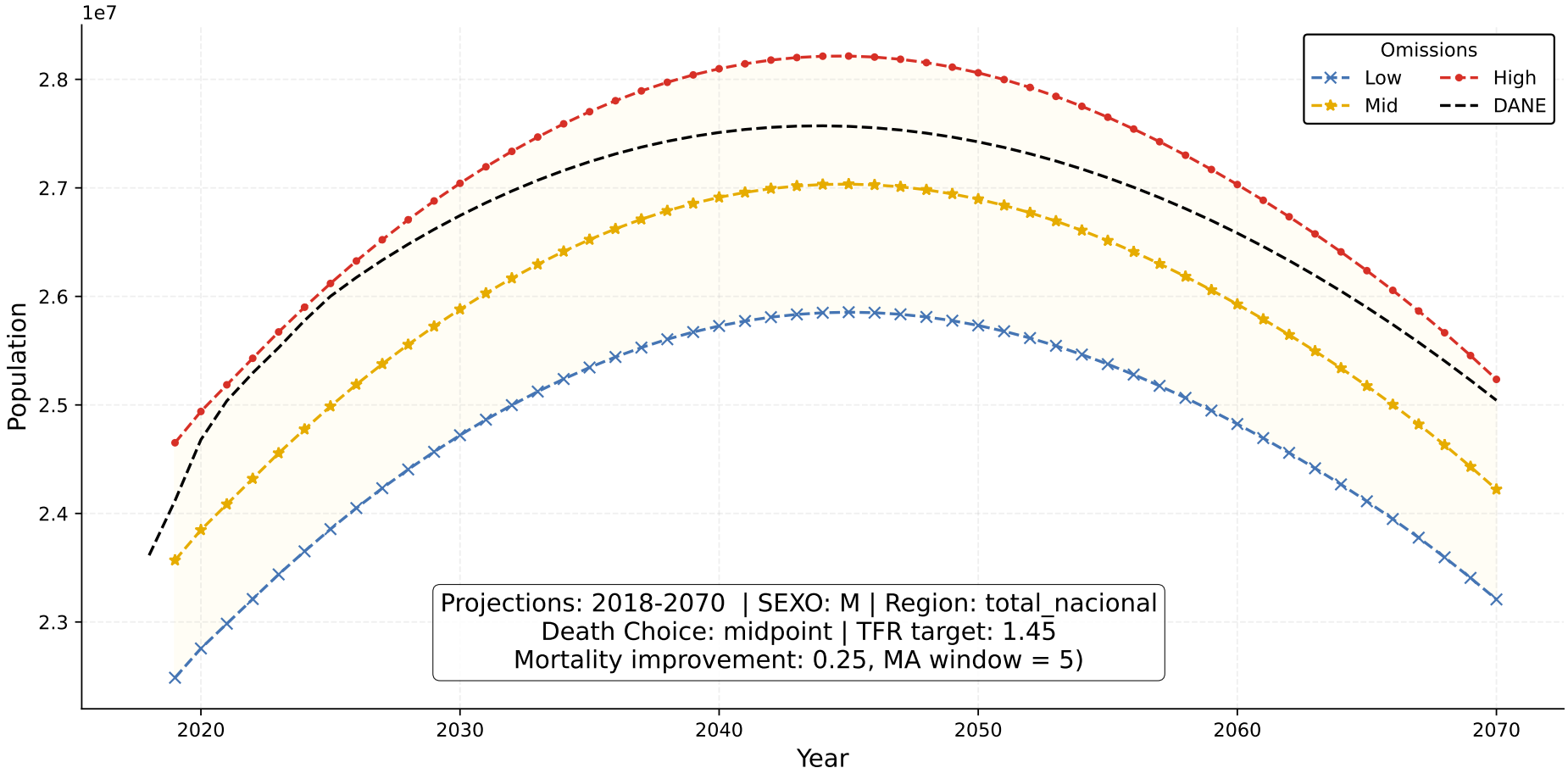
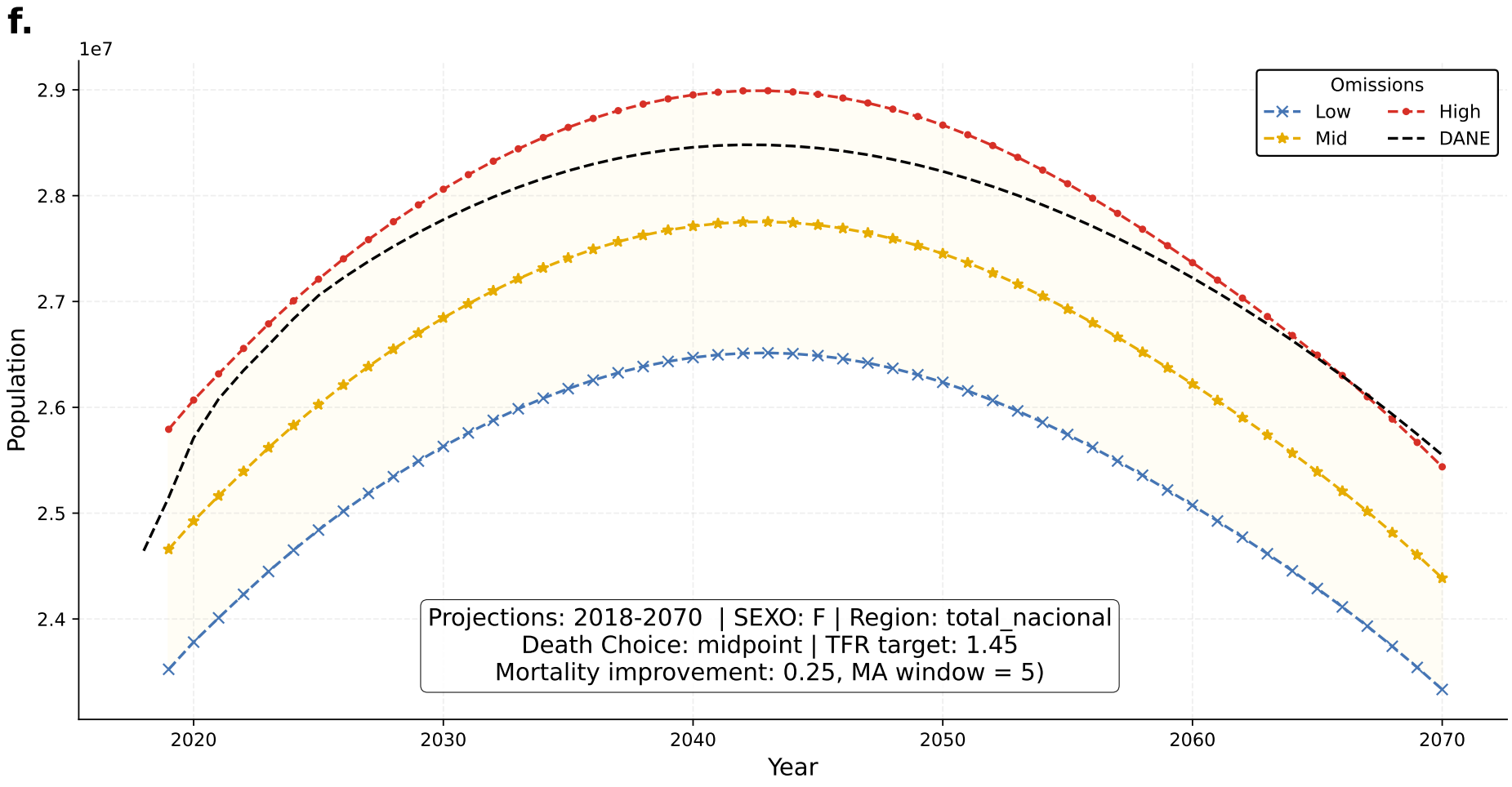
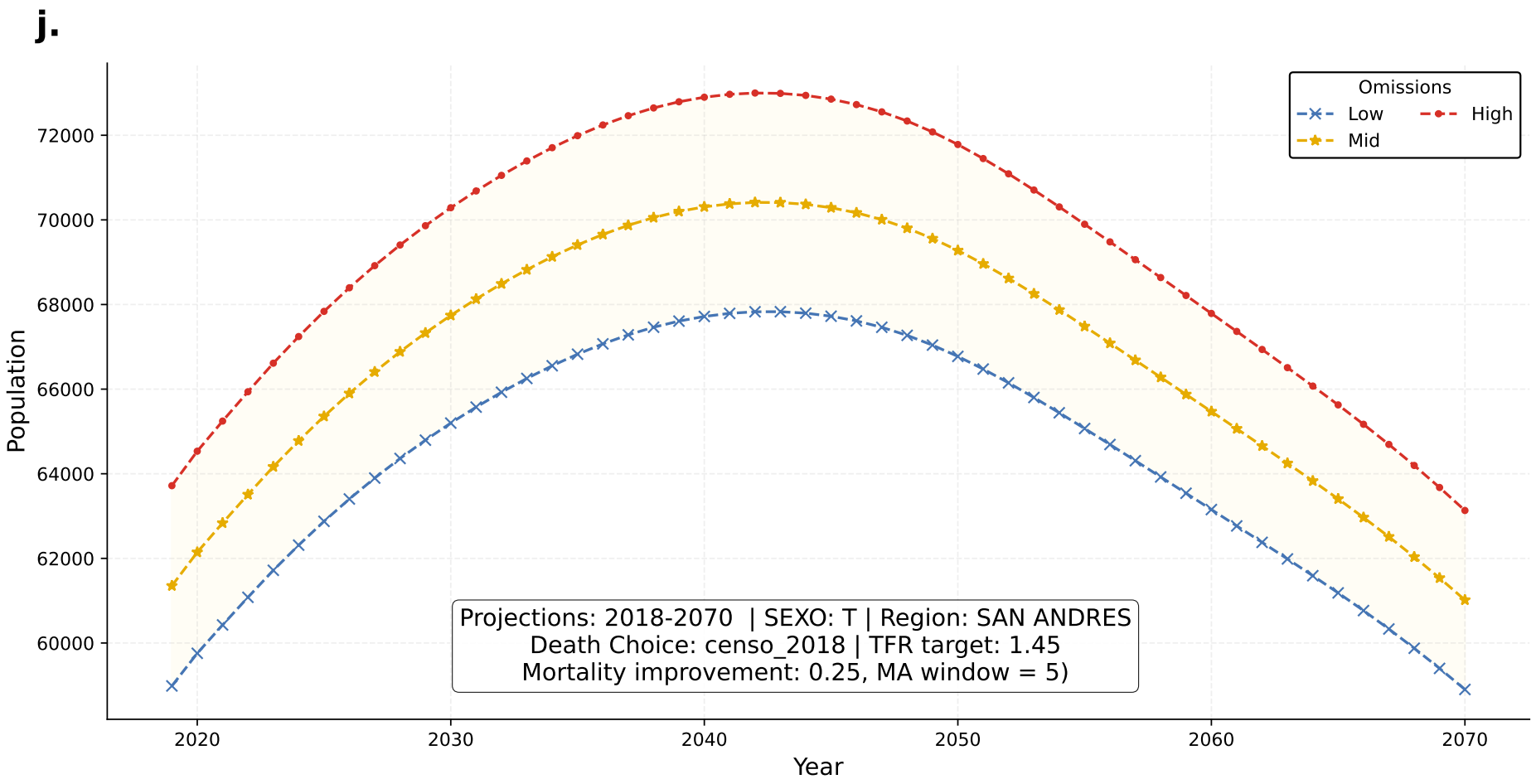

d.
1e7
5.6
5.4
5.2
5.0
4.8
4.6
Population
2020
2030
2040
2050
2060
2070
Year
Omissions
Low
High
Mid
DANE
Projections: 2018-2070 | SEXO: T | Region: total_nacional
Death Choice: midpoint | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)

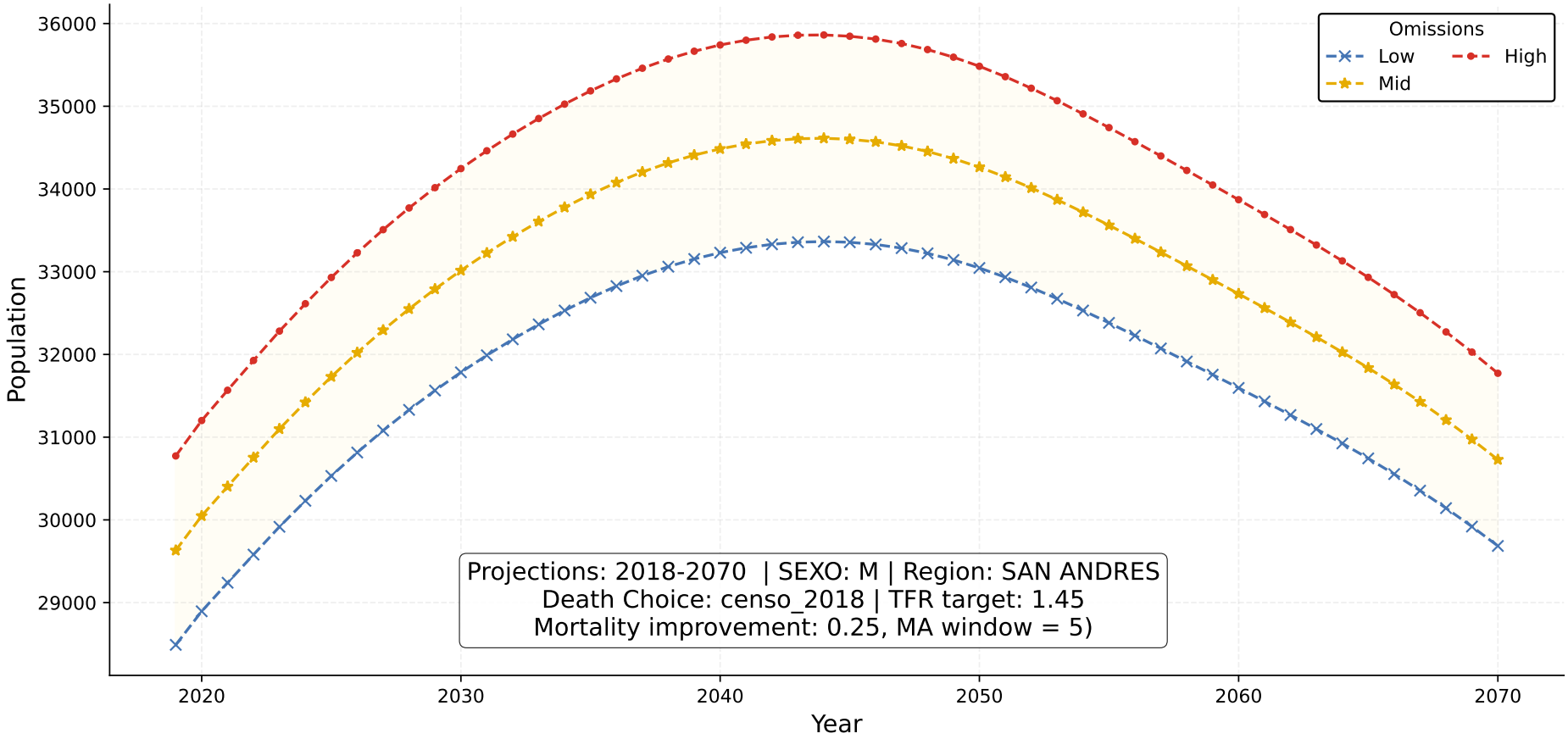
e.


1e7
2.8
2.7
2.6
2.5
2.4
2.3
Population
2020
2030
2040
2050
2060
2070
Year
Omissions
Low
High
Mid
DANE
Projections: 2018-2070 | SEXO: M | Region: total_nacional
Death Choice: midpoint | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)

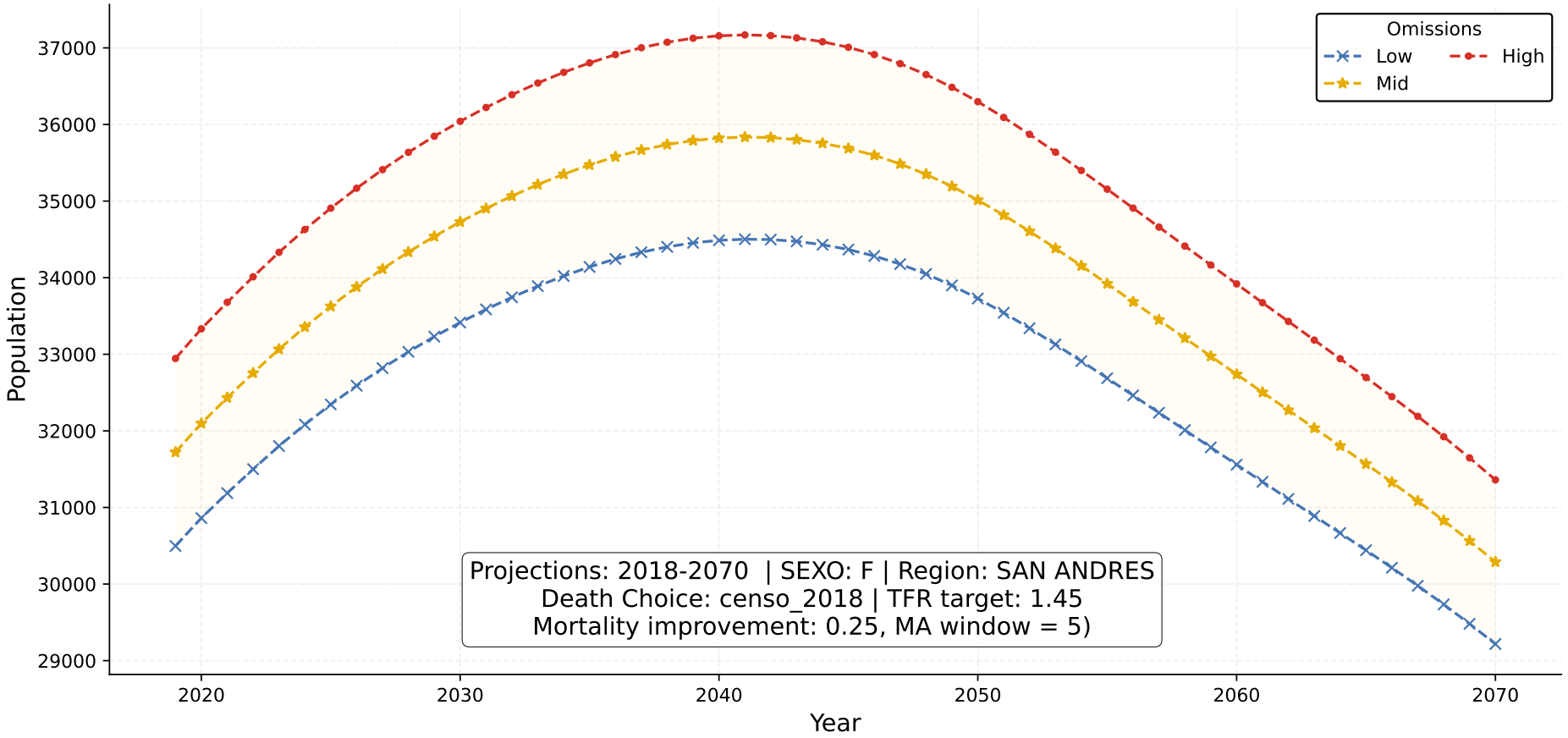

f.
1e7
2.9
2.8
2.7
2.6
2.5
2.4
Population
2020
2030
2040
2050
2060
2070
Year
Omissions
Low
High
Mid
DANE
Projections: 2018-2070 | SEXO: F | Region: total_nacional
Death Choice: midpoint | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)

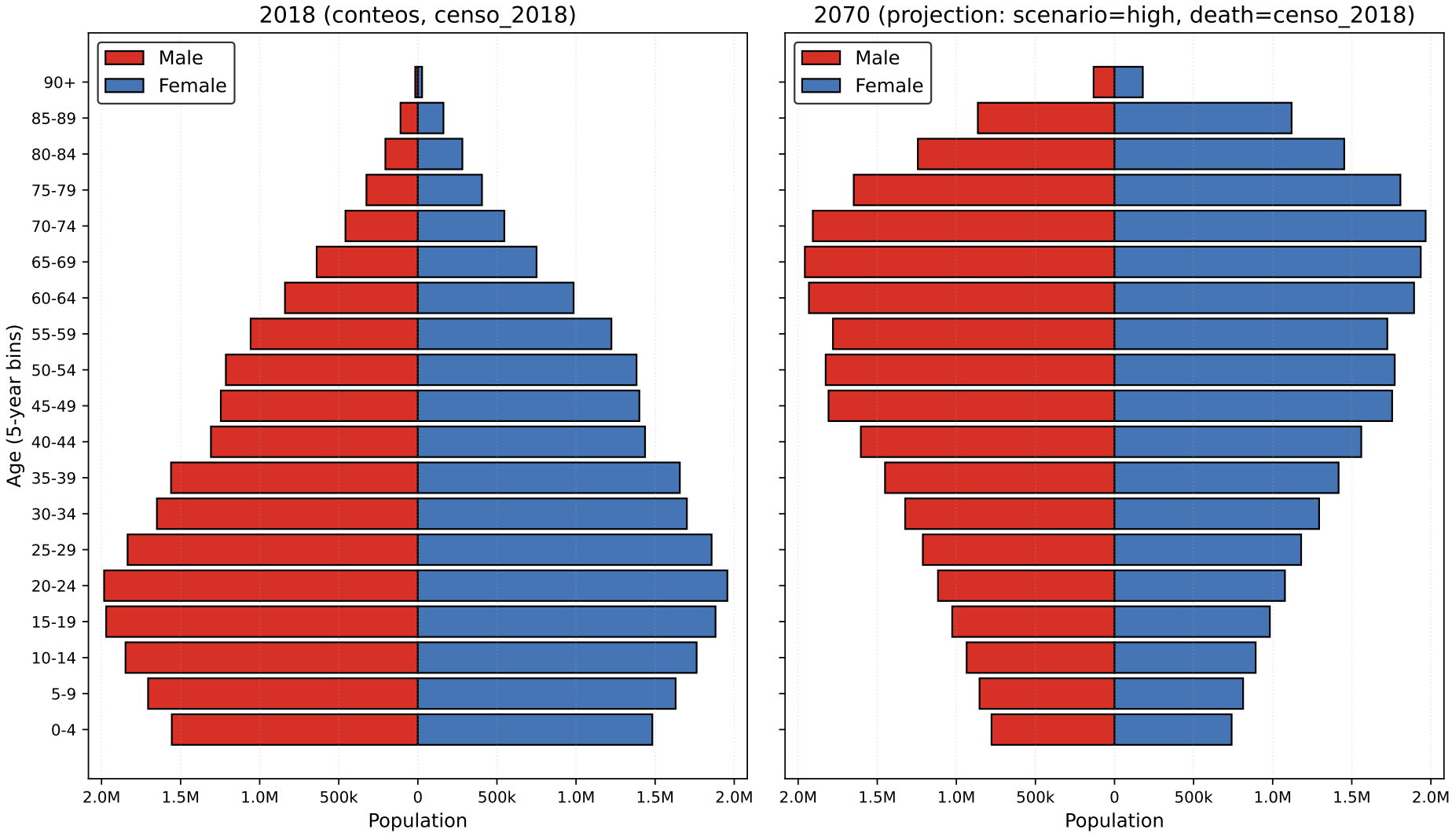

j.
Omissions
Low
Mid
High
Population
72000
70000
68000
66000
64000
62000
60000
2020
2030
2040
2050
2060
2070
Year
Projections: 2018-2070 | SEXO: T | Region: SAN ANDRES
Death Choice: censo_2018 | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)

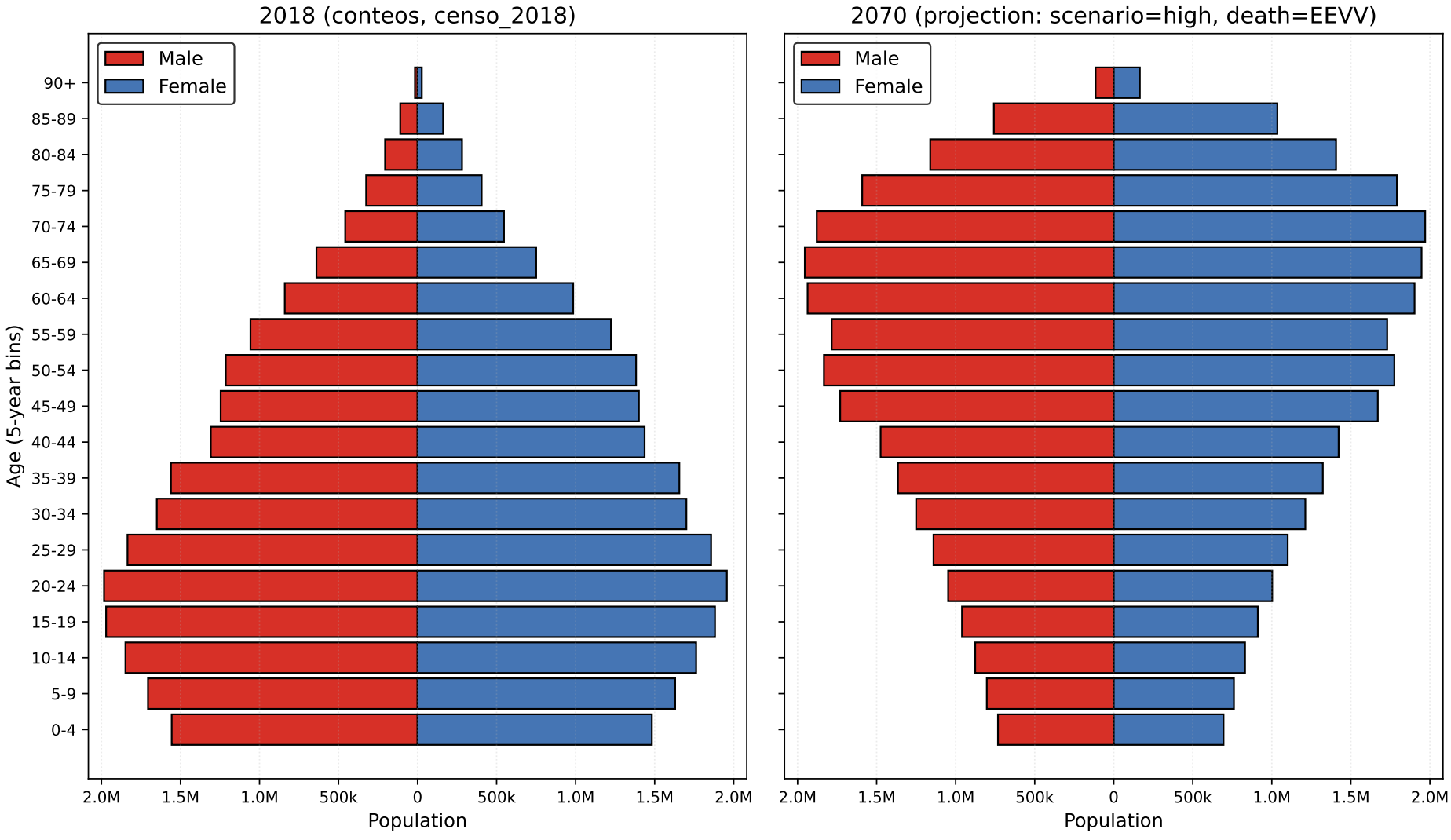
k.

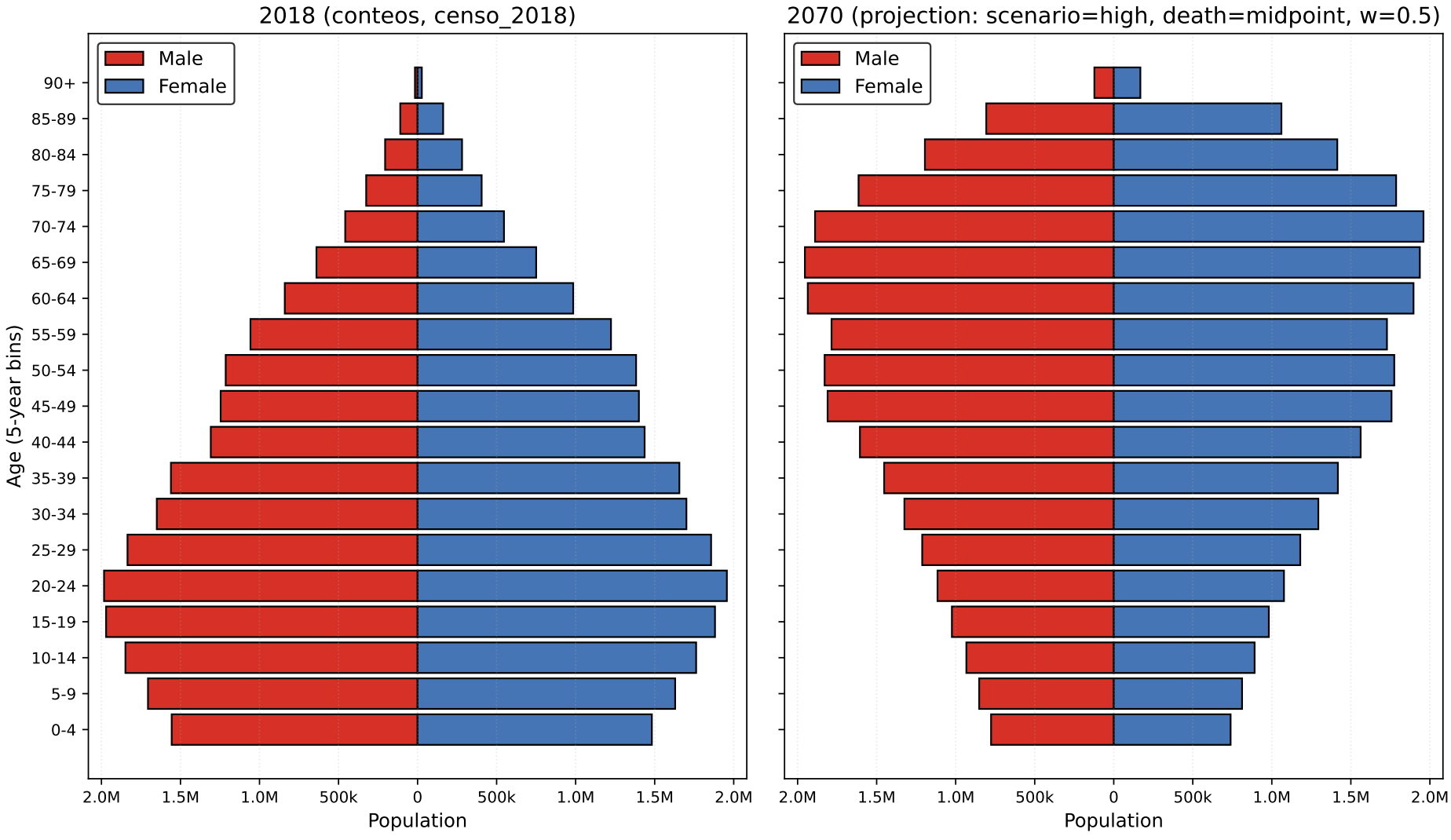

Omissions
Low
Mid
High
Population
Year
36000
35000
34000
33000
32000
31000
30000
29000
2020
2030
2040
2050
2060
2070
Projections: 2018-2070 | SEXO: M | Region: SAN ANDRES
Death Choice: censo_2018 | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)

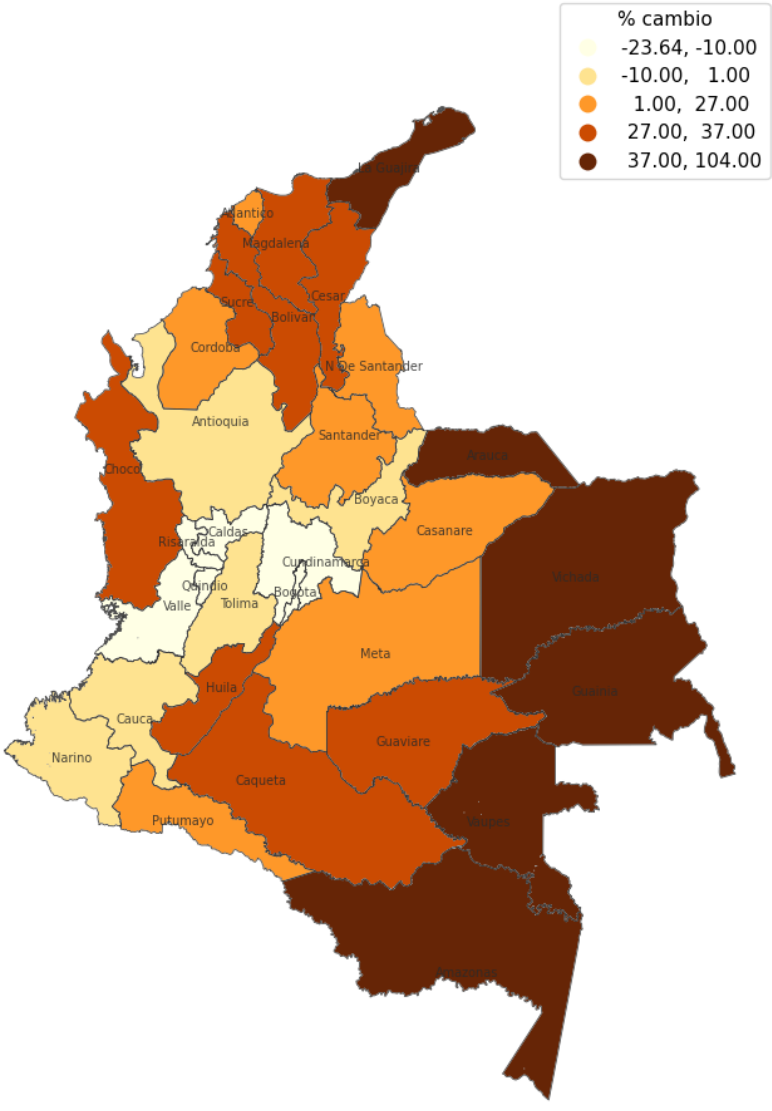
I.

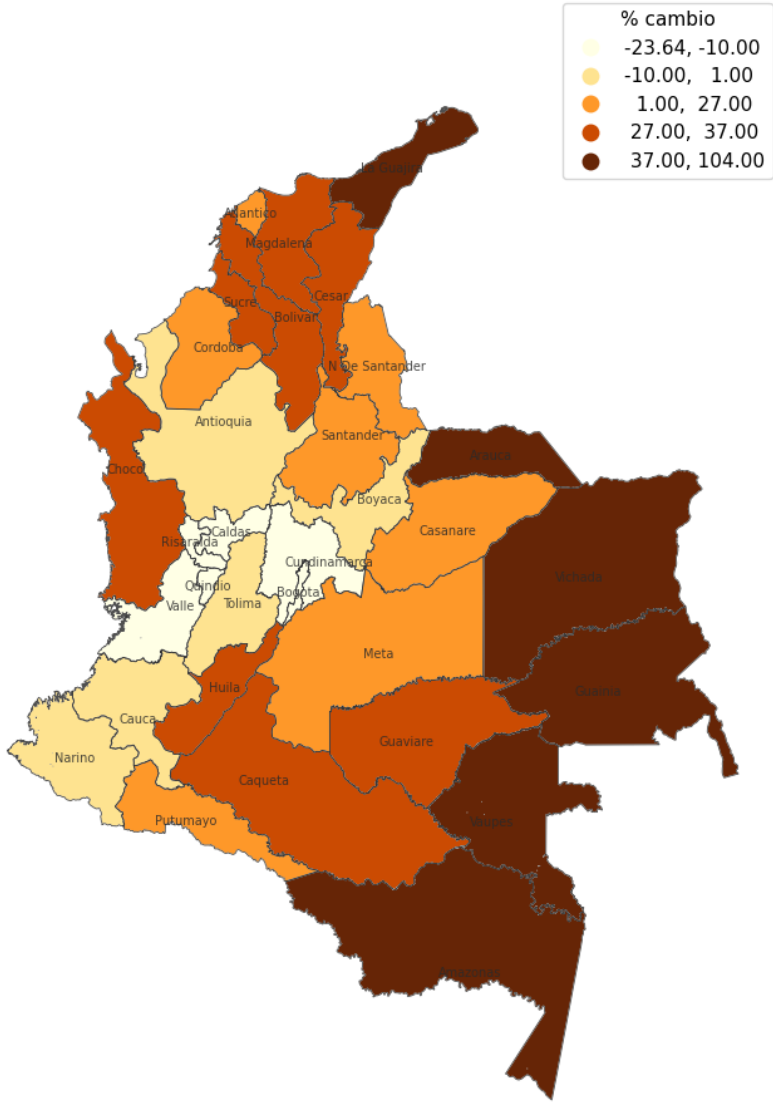

Omissions
Low
Mid
High
Population
Year
37000
36000
35000
34000
33000
32000
31000
30000
29000
2020
2030
2040
2050
2060
2070
Projections: 2018-2070 | SEXO: F | Region: SAN ANDRES
Death Choice: censo_2018 | TFR target: 1.45
Mortality improvement: 0.25, MA window = 5)


2018 (conteos, censo_2018)
2070 (projection: scenario=high, death=censo_2018)
Male
Female
Age (5-year bins)
90+
85-89
80-84
75-79
70-74
65-69
60-64
55-59
50-54
45-49
40-44
35-39
30-34
25-29
20-24
15-19
10-14
5-9
0-4
2.0M
1.5M
1.0M
500k
0
500k
1.0M
1.5M
2.0M
Population


2018 (conteos, censo_2018)
2070 (projection: scenario=high, death=EEVV)
Male
Female
Age (5-year bins)
90+
85-89
80-84
75-79
70-74
65-69
60-64
55-59
50-54
45-49
40-44
35-39
30-34
25-29
20-24
15-19
10-14
5-9
0-4
2.0M
1.5M
1.0M
500k
0
Population


2018 (conteos, censo_2018)
2070 (projection: scenario=high, death=midpoint, w=0.5)
Male
Female
Age (5-year bins)
90+
85-89
80-84
75-79
70-74
65-69
60-64
55-59
50-54
45-49
40-44
35-39
30-34
25-29
20-24
15-19
10-14
5-9
0-4
2.0M
1.5M
1.0M
500k
0
Population


% cambio
-23.64, -10.00
-10.00, 1.00
1.00, 27.00
27.00, 37.00
37.00, 104.00
Atlantico
Magdalena
Cesar
Sucre
Bolivar
Cordoba
N de Santander
Antioquia
Santander
Choco
Boyaca
Caldas
Risaralda
Cundinamarca
Casanare
Arauca
Vichada
Quindio
Valle
Tolima
Bogota
Meta
Huila
Guainia
Cauca
Guaviare
Narino
Caqueta
Putumayo
Vaupes


% cambio
-23.64, -10.00
-10.00, 1.00
1.00, 27.00
27.00, 37.00
37.00, 104.00
Atlantico
Magdalena
Cesar
Sucre
Bolivar
Cordoba
N de Santander
Antioquia
Santander
Choco
Boyaca
Caldas
Risaralda
Cundinamarca
Casanare
Arauca
Vichada
Quindio
Valle
Tolima
Bogota
Meta
Huila
Guainia
Cauca
Guaviare
Narino
Caqueta
Putumayo
Vaupes

Lets now see a way by which PyCCM can be used to do scenario analysis

Lets now see a way by which PyCCM can be used to do scenario analysis

(Thanks again to Juliana... incredible work as always!)

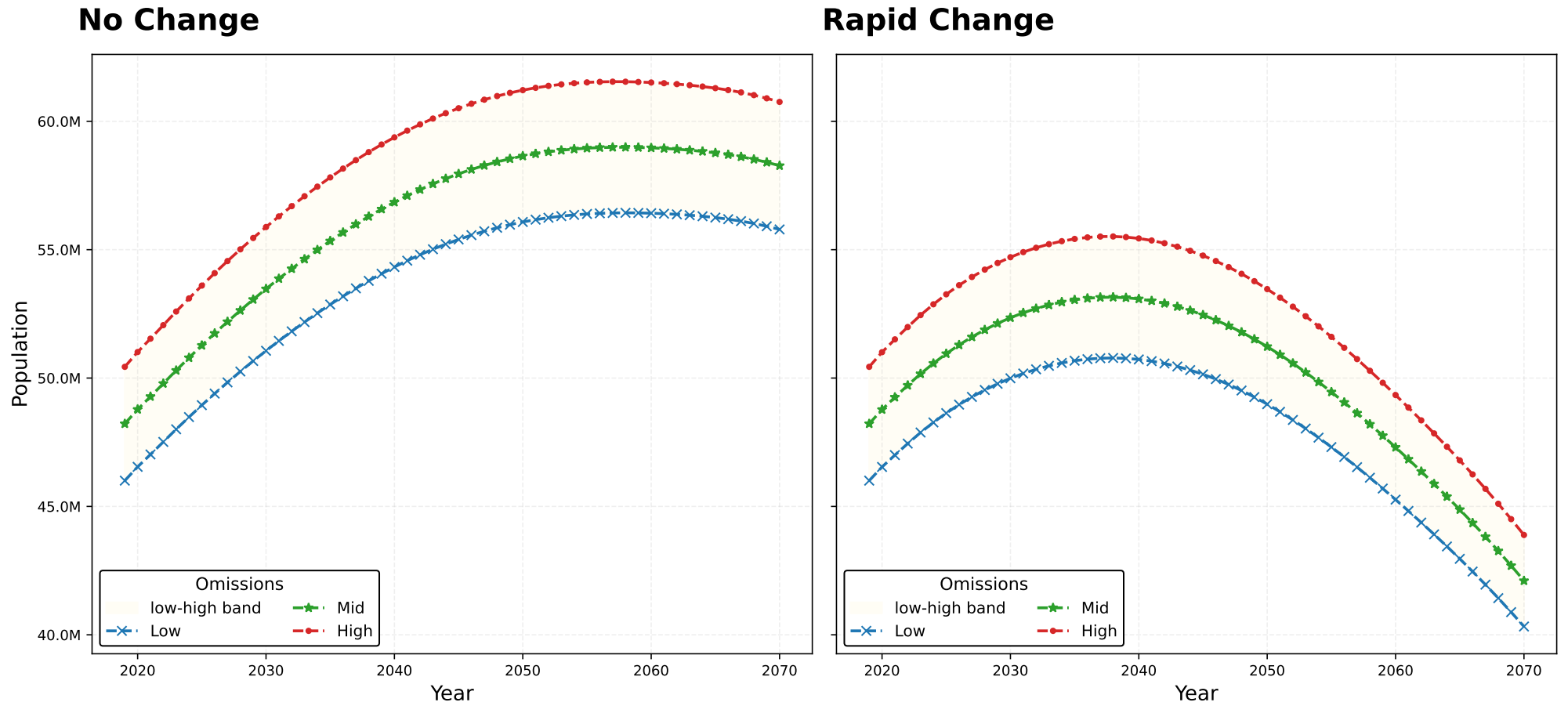
Scenario Design Summary:

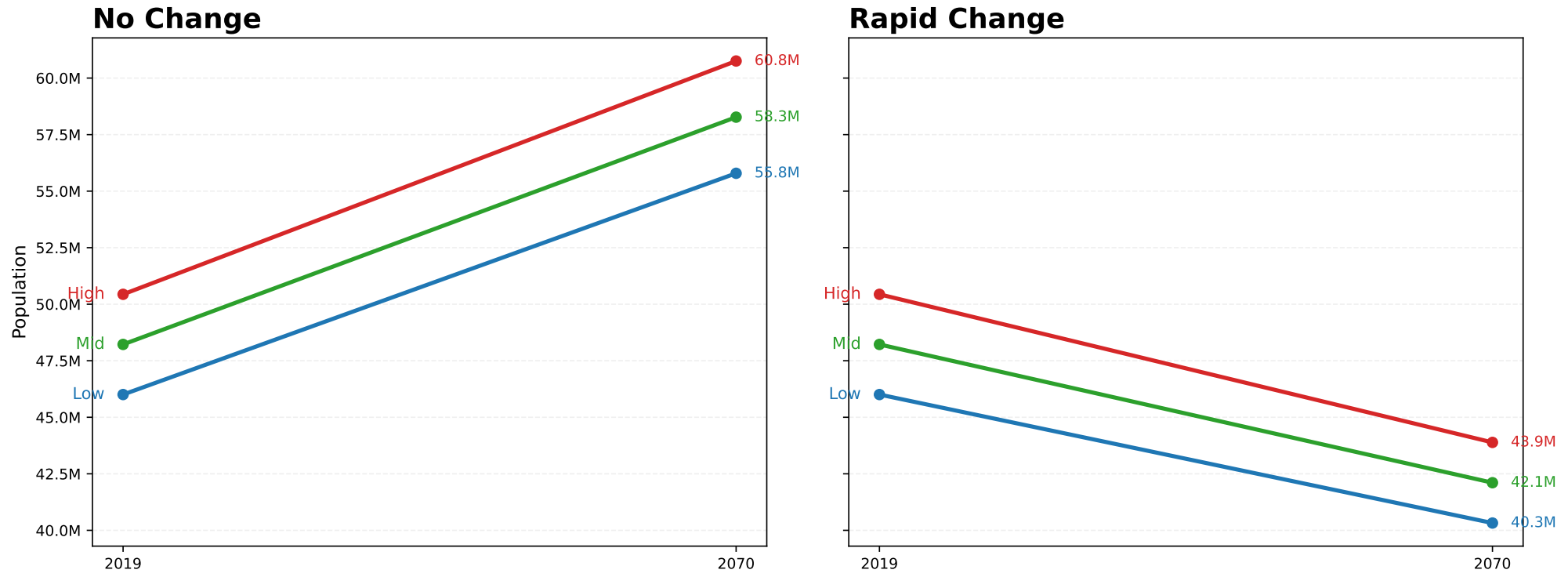
1. No Demographic Change Scenario

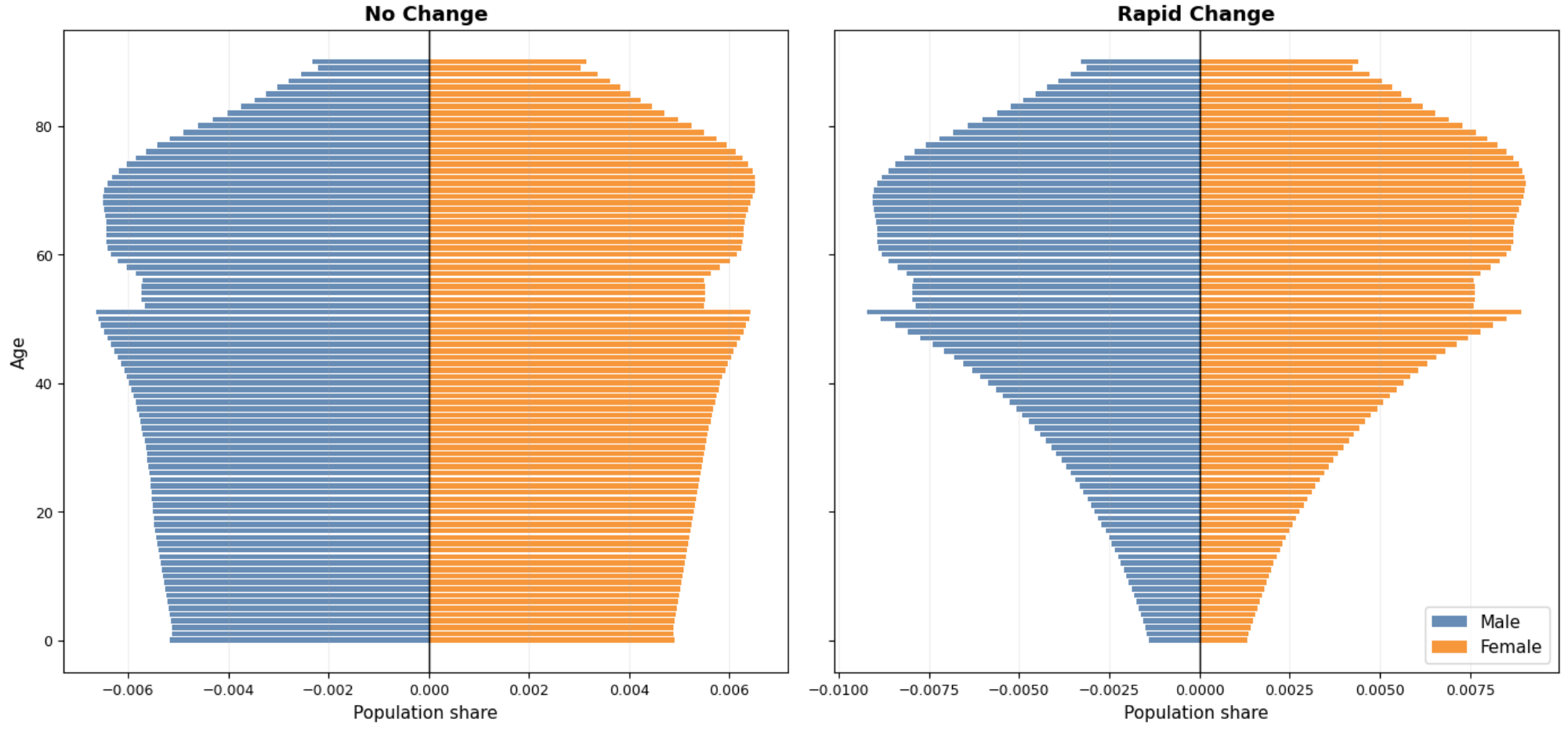
- **Mortality:** No long-run mortality improvement.
- `improvement_total = 0` for all departments in `mortality_improvements_no_change.csv`.
- **Fertility:** Department TFR fixed at observed 2018 DANE level.
- In `target_tfrs_no_change.csv`, `Target_TFR` is the department-specific TFR from the DANE 2005–2018 report.

2. Accelerated Demographic Change Scenario

- **Mortality:** Heterogeneous improvements by department.
- `improvement_total` ranges from 0.3 to 0.8; 10-year convergence.
- **Fertility:** Department TFR converges over 5 years to projected 2024 TFR minus 0.2 children/woman.
- `Target_TFR` is set from department-specific DANE 2024 projected TFR minus 0.2.


No Change
Rapid Change
Population
60.0M
55.0M
50.0M
45.0M
40.0M
2020
2030
2040
2050
2060
2070
Year
Omissions
low-high band
Low
Mid
High


Start vs End Population by Omission Scenario
No Change
Rapid Change
Population
60.0M
57.5M
55.0M
52.5M
50.0M
47.5M
45.0M
42.5M
40.0M
High
Mid
Low
60.8M
58.3M
55.8M
43.9M
42.1M
40.3M
2019
2070


Population Pyramid, total_nacional, Year 2070 (mid scenario)
No Change
Rapid Change
Age
0
20
40
60
80
−0.006
−0.004
−0.002
0.000
0.002
0.004
0.006
−0.0100
−0.0075
−0.0050
−0.0025
0.0000
0.0025
0.0050
0.0075
Population share
Population share
Male
Female

Still TODO....:

A few things we are still working on:

Still TODO....:

A few things we are still working on:

1. Fixing a small issue with graduating 0-1 infants who've survived

Still TODO....:

A few things we are still working on:

1. Fixing a small issue with graduating 0-1 infants who've survived
2. Precomputing all feasible grids of parameterisations

Still TODO....:

A few things we are still working on:

1. Fixing a small issue with graduating 0-1 infants who've survived
2. Precomputing all feasible grids of parameterisations
3. Turning this grid into a live, interactive dashboard and accompanying academic paper

ICSC
INTERNATIONAL CONFERENCE ON SOCIAL COMPUTING

THE 2026 EDITION OF THE

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SCAN TO SUBMIT BEFORE MAY 25TH

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- **Notification Date:** June 15th, 2026
- **Camera Ready:** August 17th, 2026
- **Taught workshop:** September 2nd, 2026
- **Conference Dates:** September 3rd-4th, 2026

CONFERENCE HIGHLIGHTS

Proceedings: Papers will be considered for optional publication in our Conference Proceedings. A selection of outstanding papers will be fast-tracked to ACM Transactions on Social Computing or the Journal of Social Computing. If publication in the proceedings is not sought, papers - or extended abstracts - can be submitted in any format.

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Points for discussion:

1. Are our defaults reasonable?
2. How can we include ‘tempo’ in our analysis, given data constraints?
3. Are our analytical choices – in terms of how to build the CCM – reasonable?
4. What other functionality should PyCCM include?