

Velkscale Modelling Report - 8 October 2026



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Mathematical description of Velkscale's Extended Demographic System

The current system is a constrained demographic reconstruction, with the following order of orchestration as defined by the `NWM` class:

1. **Age–sex reconstruction** produces population stocks, using a logistic transition from sex-specific isotonic graduation over [1750, 1850] to coupled Whittaker–Henderson graduation with Huber loss.
2. **Migration estimation** under a Rogers-Castro scheduler produces preliminary migration and removes its global population-weighted mean.
 1. The exapted Rogers-Castro scheduler was defined by [Husinger \(2022\)](#), with student and retirement schedules dropped due to the pre-1950 domain.
 2. Original Rogers-Castro paper: [Rogers and Castro \(1981\)](#)
3. **Birth/death reconciliation** jointly adjusts migration and vital events within source-aware bounds, imposing local demographic accounting and global migration conservation such that the demographic balancing equation is fulfilled under finite, feasible constraints.

Conversation properties follow from normalisation, centring, and constrained reconciliation, whilst regressions estimate spatial variance. Properties hold under the following constraints:

- All relevant rasters are aligned (WGS84 Equirectangular, 4320x2160) and finite on the stated domain (10000BC-2025AD),
 - The domain is specified in 1000-year steps from 10000BC to 1AD (0 in technical implementation), 100-year steps from 1AD to 1700AD, 10-year steps from 1700AD-1950AD, and 1-year steps since to 2025AD.
- Inputs, parameters as specified, and order of orchestration remain fixed between runs.

In practice, residuals are guaranteed due to floating-point imprecision (ϵ_{32}), therefore demographic balancing cannot converge exactly, but hold only within a reasonable tolerance envelope. 32-bit floats were chosen as the principal format due to their ability to be bit-packed into R, G, B, A channels on transparent rasters (i.e. `.png` , `.bmp`) for easier viewing and calculation.

Definition 1. Age-sex reconstruction via MNL with PAVA-Whittaker constraints

1.1. Notation.

Let:

- $(a \in \mathcal{A} = \{0, \dots, 17\})$ index age bands;
- $(b(i))$ denote the country bin of cell (i) , including an unmapped bin;
- $(i \in \Omega)$ index raster cells;
- $(s \in \{f, m\})$ index sex;
- (t) index processing years;
- (H, U, W) denote HMD, UNWPP, and WorldPop-derived age/sex sources respectively;
- $(P_{i,t} \geq 0)$ denote the population raster for year (t) ;
- $(N_{i,t,a}^s \geq 0)$ denote final age–sex population;
- $(X_{i,t})$ and denote the covariate vector.

The age labels are $(0, 1, 5, 10, \dots, 80)$. Relevant widths and computational midpoints are defined as follows:

$$w_a = \begin{cases} 1, & a = 0, \\ 4, & a = 1, \\ 5, & a \geq 2, \end{cases} \quad x_a = \sum_{c < a} w_c + \frac{w_a}{2}.$$

Thus $x_0 = 0.5$, $x_1 = 3$, $x_2 = 7.5$, and the terminal (80+) band is computationally assigned $w = 5$ due to cohort attrition. Define the covariate year and age–sex clamping population by:

$$\tilde{t} = \min(t, 2023), \quad \tilde{X}_{i,t} = X_{i,\tilde{t}}, \quad P_{i,t}^A = P_{i,\tilde{t}}.$$

In particular, $(P_{i,t}^A)$ need not equal $(P_{i,t})$ after 2023, as such years are covered by UNWPP replacements. For scalars, write:

$$\text{clip}(z; \ell, u) = \min\{u, \max\{\ell, z\}\}.$$

1.2. Training targets and multinomial models

For available training years from 1750 through 2025, select targets

$$T_{i,t,a}^s = \begin{cases} H_{i,t,a}^s, & t < 1950, \\ U_{i,t,a}^s, & 1950 \leq t < 2015, \\ W_{i,t,a}^s, & t \geq 2015, W \text{ available}, \\ U_{i,t,a}^s, & t \geq 2015, W \text{ unavailable}. \end{cases}$$

Under the normalised soft-target training convention,

$$q_{i,t,a}^s = \frac{T_{i,t,a}^s}{\sum_{r,c} T_{i,t,c}^r},$$

on cells with positive target mass.

For anchor year (τ), the intercept-free multinomial model is

$$p_a^{s,(\tau)}(X) = \frac{\exp(X^\top \beta_{\tau,a}^s)}{\sum_{r,c} \exp(X^\top \beta_{\tau,c}^r)}.$$

Its coefficients approximately minimise:

$$- \sum_{i \in \mathcal{I}_\tau} \sum_{s,a} q_{i,\tau,a}^s \log p_a^{s,(\tau)}(\tilde{X}_{i,\tau}),$$

where ($\mathcal{I}_\tau$) is the selected training sample. The visible default parameters are:

$$\lambda_{\text{MNL}} = 0, \quad \eta_{\text{learning}} = 0.1, \quad K_{\text{max}} = 50, \quad \varepsilon_{\text{fit}} = 10^{-4}, \quad \text{sample limit} = 15,000$$

The normalised-target loss is an assumption about the unsupplied training helper. A differently weighted loss changes estimates but not subsequent conservation arguments.

1.3. Coverage-weighted temporal ensemble

Let (n_τ) be the saved sample count, with fallback (1000), and define

$$n_{\text{max}} = \max \left(1, \max_{\tau} n_{\tau} \right),$$

$$c_\tau = \left(\frac{n_\tau}{n_{\text{max}}} \right)^{0.3}, \quad \omega_\tau = \frac{c_\tau}{\sum_{\nu} c_\nu}.$$

Temporal weights for any year t are:

$$v_\tau(t) = \frac{\omega_\tau e^{-|t-\tau|/50}}{\sum_{\nu} \omega_\nu e^{-|t-\nu|/50}}.$$

When a same-year model exists,

$$\alpha_\tau(t) = 0.8v_\tau(t) + 0.2 \mathbf{1}_{\{\tau=t\}};$$

otherwise,

$$\alpha_\tau(t) = v_\tau(t).$$

A same-year model absent from the original ensemble is included with initial ensemble weight zero before adding its (0.2) contribution.

The 80/20 weighting is a generalisation of the Pareto principle, and was found in internal testing to yield the highest R^2 fit over sex-stratified curves in country bins evaluated separately and averaged. Assuming probability-mixture evaluation,

$$p_{i,t,a}^s = \sum_{\tau} \alpha_{\tau}(t) p_a^{s,(\tau)}(\tilde{X}_{i,t}).$$

Each valid prediction satisfies:

$$p_{i,t,a}^s \geq 0, \quad \sum_{s,a} p_{i,t,a}^s = 1.$$

1.4. Country-bin aggregation

Let $(\mathcal{E}_{b,t})$ contain cells assigned to bin (b) that are eligible for modeled graduation. Under the preceding description, eligibility requires:

$$P_{i,t}^A \geq 0.01$$

and excludes cells using the pre-1950 HMD bypass. Preliminary country populations are:

$$R_{b,t,a}^s = \sum_{i \in \mathcal{E}_{b,t}} P_{i,t}^A p_{i,t,a}^s.$$

Define:

$$R_{b,t,a} = R_{b,t,a}^f + R_{b,t,a}^m,$$

$$d_{b,t,a}^s = \frac{R_{b,t,a}^s}{w_a}, \quad d_{b,t,a} = \frac{R_{b,t,a}}{w_a}.$$

Below, suppress (b, t) where convenient. Such country bins are defined by non-fractional ISO3-geocode on a WGS84 4320x2160 Equirectangular raster.

1.5. Sex-specific PAVA endpoint

Let the graduated suffix be:

$$\mathcal{A}_+ = \{2, \dots, 17\}.$$

Where each element is the index of the relevant age band. For each sex separately, define the weighted decreasing isotonic projection:

$$\hat{d}^{s,I} = \underset{z_2 \geq z_3 \geq \dots \geq z_{17} \geq 0}{\operatorname{argmin}} \sum_{a=2}^{17} w_a (z_a - d_a^s)^2.$$

The isotonic endpoint is:

$$G_a^{s,I} = \begin{cases} R_a^s, & a < 2, \\ w_a \hat{d}_a^{s,I}, & a \geq 2. \end{cases}$$

This guarantees decreasing annualised density separately for female and male populations over the graduated suffix. For a pooled block ($\mathcal{B}$), PAVA assigns:

$$\bar{d}_{\mathcal{B}}^s = \frac{\sum_{a \in \mathcal{B}} w_a d_a^s}{\sum_{a \in \mathcal{B}} w_a}.$$

Therefore,

$$\sum_{a \in \mathcal{B}} w_a \bar{d}_{\mathcal{B}}^s = \sum_{a \in \mathcal{B}} R_a^s.$$

Summing pooled blocks proves:

$$\boxed{\sum_a G_a^{s,I} = \sum_a R_a^s \quad \text{for each sex } s.}$$

This sex-specific preservation differs from combined-sex PAVA followed by a new sex allocation.

1.6. Coupled Whittaker–Henderson endpoint

The Whittaker endpoint graduates:

1. Combined age density on ($\mathcal{A}_+$);
2. Male shares over all ages.

Male-specific anchoring is chosen for actuarial and consistency reasons. Define the Huber loss function as follows:

$$\rho_{\delta}(e) = \begin{cases} \frac{1}{2}e^2, & |e| \leq \delta, \\ \delta|e| - \frac{1}{2}\delta^2, & |e| > \delta. \end{cases}$$

For a positive combined suffix, define:

$$\bar{d} = \frac{\sum_{a=2}^{17} R_a}{\sum_{a=2}^{17} w_a}, \quad y_a = \frac{d_a}{\bar{d}}.$$

A conventional mathematical representation of the robust Whittaker solver is:

$$\hat{z} \approx \underset{z_a \geq 0}{\operatorname{argmin}} \left\{ \sum_{a=2}^{17} w_a \rho_\delta(z_a - y_a) + \frac{\lambda_d}{2} \sum_{a=2}^{15} (\Delta^2 z_a)^2 + \frac{\mu_d}{2} \sum_{a=2}^{16} [\Delta z_a]_+^2 \right\},$$

where:

$$\Delta z_a = z_{a+1} - z_a, \quad \Delta^2 z_a = z_{a+2} - 2z_{a+1} + z_a, \quad [u]_+ = \max(0, u).$$

The fidelity weights are the integration band widths w_a . The μ_d term operates as a **soft** monotonicity penalty, penalising only positive slopes (increasing density) without enforcing a hard isotonic constraint. The coordinate descent halts when the absolute maximum KKT gradient residual falls below 10^{-5} .

The visible orchestrator passes $\delta = 0.05$, $\lambda_d = 20$, $\mu_d = 5000$ unless parameters are overridden. A direct call to the supplied coupling function instead defaults to ($\mu_d = 0$). Restore combined suffix population using:

$$c_d = \frac{\sum_{a=2}^{17} R_a}{\sum_{a=2}^{17} w_a \bar{d} \hat{z}_a}.$$

Then:

$$G_a^W = \begin{cases} R_a, & a < 2, \\ c_d w_a \bar{d} \hat{z}_a, & a \geq 2. \end{cases}$$

This requires finite positive provisional suffix mass. Empty suffixes remain zero.

For male shares, define:

$$m_a = \begin{cases} R_a^m / R_a, & R_a > 0, \\ \rho_a^{\text{base}} / (1 + \rho_a^{\text{base}}), & R_a = 0 \text{ and a prior exists,} \\ 1/2, & \text{otherwise.} \end{cases}$$

Unless fixed ratios are requested, the share graduation is represented by:

$$\hat{m} \approx \underset{u_a \geq 0}{\operatorname{argmin}} \left\{ \sum_{a=0}^{17} w_a \rho_{0.05}(u_a - m_a) + \frac{20}{2} \sum_{a=0}^{15} (\Delta^2 u_a)^2 \right\}.$$

When ratio bounds ($[\rho_a^-, \rho_a^+]$) are enforced, use

$$m_a^W = \operatorname{clip} \left(\hat{m}_a; \frac{\rho_a^-}{1 + \rho_a^-}, \frac{\rho_a^+}{1 + \rho_a^+} \right).$$

The supplied default bounds are

$$[\rho_a^-, \rho_a^+] = \begin{cases} [1.02, 1.07], & a = 0, \\ [1.01, 1.07], & a = 1, \\ [0.95, 1.10], & a = 2, 3, \\ [0.50, 1.80], & a = 4, \dots, 13, \\ [0.30, 1.05], & a = 14, \dots, 17. \end{cases}$$

Without ratio bounds, the necessary validity condition is $0 \leq \hat{m}_a \leq 1$, because the supplied share-smoothing call explicitly constrains only the lower endpoint. Allocate:

$$G_a^{m,W} = G_a^W m_a^W, \quad G_a^{f,W} = G_a^W (1 - m_a^W).$$

Thus:

$$\boxed{\sum_{s,a} G_a^{s,W} = \sum_{s,a} R_a^s.}$$

Separate male and female totals need not be preserved.

1.7. Logistic demographic-transition kernel

Let $t_0 = 1750$, $t_1 = 1850$, $k = 8$, and define the logistic function:

$$\sigma(u) = \frac{1}{1 + e^{-u}}.$$

The transition weight is:

$$\gamma(t) = \begin{cases} 0, & t \leq t_0, \\ \frac{\sigma\left(k\left(\frac{t-t_0}{t_1-t_0} - \frac{1}{2}\right)\right) - \sigma(-k/2)}{\sigma(k/2) - \sigma(-k/2)}, & t_0 < t < t_1, \\ 1, & t \geq t_1. \end{cases}$$

Consequently,

$$0 \leq \gamma(t) \leq 1, \quad \gamma(1800) = \frac{1}{2}.$$

Blend cohort populations, rather than objective-function coefficients:

$$\boxed{G_{b,t,a}^s = [1 - \gamma(t)]G_{b,t,a}^{s,I} + \gamma(t)G_{b,t,a}^{s,W}.}$$

Therefore:

- Before or at 1750, the endpoint is sex-specific PAVA;
- After or at 1850, the endpoint is coupled Whittaker graduation;

- During the transition, the output is a convex mixture.

Because both endpoints conserve combined mass,

$$\sum_{s,a} G_{b,t,a}^s = \sum_{s,a} R_{b,t,a}^s.$$

The blend is non-negative when both endpoints are non-negative.

Sex-specific decreasing density is guaranteed at the PAVA endpoint, but not generally throughout the transition. Likewise, bounds applied only to the Whittaker endpoint do not automatically hold for the blended state. Additional ratio clipping would be an additional operation and could alter the PAVA monotonicity property.

1.8. Cell redistribution and source compositing

Define country scaling factors:

$$k_{b,t,a}^s = \begin{cases} G_{b,t,a}^s / R_{b,t,a}^s, & R_{b,t,a}^s > 0, \\ 1, & R_{b,t,a}^s = 0. \end{cases}$$

For a modeled cell,

$$N_{i,t,a}^{s,\text{model}} = P_{i,t}^A \frac{p_{i,t,a}^s k_{b(i),t,a}^s}{\sum_{r,c} p_{i,t,c}^r k_{b(i),t,c}^r}.$$

If the denominator is zero, use:

$$N_{i,t,a}^{s,\text{model}} = \frac{P_{i,t}^A}{36}.$$

For an eligible pre-1950 HMD-bypass cell,

$$N_{i,t,a}^{s,\text{clamp}} = P_{i,t}^A \frac{H_{i,t,a}^s}{\sum_{r,c} H_{i,t,c}^r}.$$

Otherwise,

$$N_{i,t,a}^{s,\text{clamp}} = N_{i,t,a}^{s,\text{model}}.$$

The final compositor selects, by available cohort/year raster,

$$N_{i,t,a}^s = \begin{cases} U_{i,t,a}^s, & 1950 \leq t < 2015, U \text{ available,} \\ W_{i,t,a}^s, & 2015 \leq t \leq 2025, W \text{ available,} \\ U_{i,t,a}^s, & 2015 \leq t \leq 2025, W \text{ absent, } U \text{ available,} \\ N_{i,t,a}^{s,\text{clamp}}, & \text{otherwise.} \end{cases}$$

Cell normalisation does not generally preserve the target country cohort totals ($G_{b,t,a}^s$), and multiplicative scaling cannot create support in a category whose predictions are identically zero.

1.9. Stock-reconciliation theorem

For each valid normalized clamped cell,

$$\sum_{s,a} N_{i,t,a}^{s,\text{clamp}} = P_{i,t}^A,$$

because the numerator terms sum to the denominator. For the final composited state, assume:

$$\sum_{s,a} N_{i,t,a}^s = P_{i,t}$$

for the selected source combination, including compatibility between (P^A) and (P) wherever modelled outputs are selected. Then:

$$\boxed{\sum_{s,a} N_{i,t,a}^s = P_{i,t}, \quad \sum_i \sum_{s,a} N_{i,t,a}^s = \sum_i P_{i,t}.$$

This compatibility is only guaranteed for proxy rasters and HMD coverage (pre-1950), as opposed to empirical data from UNWPP. Years after 2023 currently utilise proxy extrapolations from the 2023 population. If injected modern data or subsequent extrapolations violate aggregate population constraints, a final normalisation against ($P_{i,t}$) is necessary for compatibility to hold.

Definition 2. Migration estimation, calibration, and global conservation

2.1. Notation

For a fixed year (t), let:

- (A^B, A^{D_f}, A^{D_m}) be source birth and death counts;
- ($g_{i,t} = \Delta P_{i,t}/h_t$) be annualised population change;
- ($h_t = t - t^- > 0$), with ($h_t = 1$) when no predecessor exists;

- (M^{pred}) be modelled migration;
- $(\widetilde{M})$ be preliminary migration before global centring;
- (M^0) be centred migration passed to final reconciliation;
- $(M^{s,0})$ be its sex-specific allocation.
- (t^-) be the preceding HYDE time point;
- $(\Omega_+(t) = \{i : P_{i,t} > 0\})$ be the active population domain;
- $(\Delta P_{i,t})$ be the supplied population-change raster;

Let $(v \in \{M, B, D_f, D_m\})$ index modelled variables. For the shared regression/calibration machinery, let:

- $(f_{i,t}^v)$ denote calibrated factors or rates.
- $(u_{i,t}^v \in [0, 1])$ denote normalized predictions;
- $(z_{i,t}^v)$ denote raw predictions;
- (Y^v) denote training targets;
- $(Z_{i,\tilde{t}})$ denote the linear-model design vector;
- (θ_τ^v) denote year-specific coefficients;

The covariates are the supplied land-use, population, economic, and change rasters, evaluated at $(\tilde{t} = \min(t, 2023))$.

2.2. Migration targets

For target construction, choose valid Niva et al. birth and death data where available; otherwise use UNWPP:

$$(A_{i,t}^B, A_{i,t}^D) = \begin{cases} (A_{i,t}^{B,K}, A_{i,t}^{D,K}), & \text{valid Niva et al. pair available,} \\ (A_{i,t}^{B,U}, A_{i,t}^{D_f,U} + A_{i,t}^{D_m,U}), & \text{otherwise, with valid UNWPP births.} \end{cases}$$

Negative vital counts are replaced by zero. The supplied UNWPP fallback also replaces missing sex-specific deaths by zero. Define residual migration:

$$A_{i,t}^M = g_{i,t} - A_{i,t}^B + A_{i,t}^D.$$

For target years $(t \geq 1950)$ and cells with $(P_{i,t} \geq 1)$,

$$Y_{i,t}^M = \text{clip} \left(\frac{A_{i,t}^M}{P_{i,t}}; -1, 1 \right).$$

These are residual targets, not independently observed migration.

2.3. Ridge Regression

For each variable (v) and training year (τ),

$$\hat{\theta}_\tau^v = \underset{\theta}{\operatorname{argmin}} \left\{ \sum_{i \in \mathcal{I}_\tau^v} \left(Y_{i,\tau}^v - Z_{i,\tau}^\top \theta \right)^2 + \lambda_v \theta^\top J \theta \right\}, \quad \lambda_v = 1.$$

Here (J) specifies which coefficients are penalized. Intercept treatment and loss normalization depend on the unsupplied fitting helper.

Prediction uses:

$$\theta^v(t) = \begin{cases} \hat{\theta}_t^v, & \text{same-year model exists,} \\ \bar{\theta}^v, & \text{otherwise,} \end{cases}$$

$$z_{i,t}^v = Z_{i,t}^\top \theta^v(t).$$

The fallback is produced by `geomeanOLSMoDeLs` with an absolute-value weighting function. Its precise algebra is not identified by that call alone.

If the sign-group convention from the preceding description is retained as an explicit assumption, then, for coefficient (j),

$$\bar{\theta}_j^v = \frac{|\mathcal{P}_j|}{K} \exp \left(\frac{\sum_{\tau \in \mathcal{P}_j} \log \hat{\theta}_{\tau,j}^v}{|\mathcal{P}_j|} \right) - \frac{|\mathcal{N}_j|}{K} \exp \left(\frac{\sum_{\tau \in \mathcal{N}_j} \log |\hat{\theta}_{\tau,j}^v|}{|\mathcal{N}_j|} \right),$$

where $(\mathcal{P}_j, \mathcal{N}_j)$ are the positive and negative coefficient groups, (K) is the number of contributing models, and empty groups contribute zero. Results do not depend on which finite fallback aggregation is used.

2.4. Shared target-bound calibration

For a sorted sample $(y_{(0)}, \dots, y_{(n-1)})$, define:

$$Q_p(y) = y_{(\lfloor np \rfloor)}$$

for the quantiles used below. For years with sampled targets,

$$\ell_t^v = Q_{0.01}(Y_t^v), \quad u_t^{v,\text{bound}} = Q_{0.99}(Y_t^v).$$

Across selected processing years,

$$\ell_*^v = \min_t \ell_t^v, \quad u_*^{v,\text{bound}} = \max_t u_t^{v,\text{bound}}.$$

The sampling conventions are:

- Migration: every seventeenth pixel, retaining ($P > 10000$) and ($|Y^M| > 10^{-10}$);
- Births/deaths: every seventh pixel, retaining positive targets.

Let (n_t^M) be the retained migration sample count and (n_t^v) for vital events be seven times their retained sample count. Define:

$$\varepsilon_t^v = e^{-n_t^v/15}.$$

Then:

$$L_t^v = (1 - \varepsilon_t^v)\ell_t^v + \varepsilon_t^v\ell_*^v,$$

$$U_t^v = (1 - \varepsilon_t^v)u_t^{v,\text{bound}} + \varepsilon_t^v u_*^{v,\text{bound}}.$$

Without same-year target statistics, use the global bounds. Vital-event lower bounds are additionally clipped below at zero. For raw predictions on valid inhabited land, let

$$q_1 = Q_{0.25}(z_t^v), \quad q_3 = Q_{0.75}(z_t^v), \quad I = q_3 - q_1,$$

and let (σ_z) denote their population standard deviation. Set:

$$a = \begin{cases} I, & I > 10^{-5}, \\ \sigma_z, & I \leq 10^{-5}, \sigma_z > 10^{-5}, \\ 0.01, & \text{otherwise.} \end{cases}$$

With

$$T^- = q_1 - 1.5a, \quad T^+ = q_3 + 1.5a,$$

define:

$$R(z) = \begin{cases} T^+ + a \log \left(1 + \frac{z - T^+}{a} \right), & z > T^+, \\ T^- - a \log \left(1 + \frac{T^- - z}{a} \right), & z < T^-, \\ z, & \text{otherwise.} \end{cases}$$

Writing $(R_{\min} = \min_i R(z_i))$ and $(R_{\max} = \max_i R(z_i))$,

$$u_{i,t}^v = \begin{cases} \text{clip} \left(\frac{R(z_{i,t}^v) - R_{\min}}{R_{\max} - R_{\min}}; 0, 1 \right), & R_{\max} > R_{\min}, \\ 1/2, & R_{\max} = R_{\min}. \end{cases}$$

Finally,

$$\boxed{f_{i,t}^v = L_t^v + u_{i,t}^v (U_t^v - L_t^v).}$$

Thus:

$$L_t^v \leq f_{i,t}^v \leq U_t^v.$$

Denote this complete calibration operator by $(\mathcal{C}_{v,t})$. Thus concludes the given implementation of Tukey's fences (log-tail normalisation).

2.5. Preliminary migration and global centering

Modelled migration is:

$$M_{i,t}^{\text{pred}} = P_{i,t} f_{i,t}^M.$$

When all required UNWPP vital-event files and the delta raster exist, the final migration generator uses:

$$\widetilde{M}_{i,t} = g_{i,t} - A_{i,t}^{B,U} + A_{i,t}^{D_f,U} + A_{i,t}^{D_m,U}.$$

Otherwise,

$$\widetilde{M}_{i,t} = M_{i,t}^{\text{pred}}.$$

The current final-generation branch uses UNWPP, even though training targets may prefer Niva et al. For positive total population, define:

$$P_{\Sigma,t} = \sum_{i \in \Omega_+(t)} P_{i,t},$$

$$\kappa_t = - \frac{\sum_{i \in \Omega_+(t)} \widetilde{M}_{i,t}}{P_{\Sigma,t}}.$$

The supplied current code centres all active cells:

$$M_{i,t}^0 = \widetilde{M}_{i,t} + P_{i,t} \kappa_t.$$

Therefore,

$$\sum_i M_{i,t}^0 = \sum_i \widetilde{M}_{i,t} + \kappa_t P_{\Sigma,t} = 0.$$

Hence:

$$\sum_i M_{i,t}^0 = 0.$$

This result does not require an adjustable, unanchored subpopulation because this version does not exempt empirical residuals from centring.

2.6. Sex allocation

For the empirical branch,

$$M_{i,t}^{f,0} = 0.488M_{i,t}^0, \quad M_{i,t}^{m,0} = 0.512M_{i,t}^0.$$

Where 0.488 and 0.512 is the sex ratio at birth (SRB). For the modelled branch, define the Rogers-Castro schedule:

$$W_s(x) = 0.02e^{-0.1x} + 0.06 \exp \left[-0.1(x - \mu_s) - e^{-0.3(x-\mu_s)} \right] + 0.003,$$

with parameters $\mu_f = 20$, $\mu_m = 22.5$. Sex potentials are:

$$V_{i,t}^s = \sum_a N_{i,t,a}^s W_s(x_a).$$

Set:

$$\pi_{f,i,t}^M = \begin{cases} \frac{V_{i,t}^f}{V_{i,t}^f + V_{i,t}^m}, & V_{i,t}^f + V_{i,t}^m > 0, \\ 0.488, & \text{otherwise,} \end{cases}$$

$$\pi_{m,i,t}^M = 1 - \pi_{f,i,t}^M, \quad M_{i,t}^{s,0} = \pi_{s,i,t}^M M_{i,t}^0.$$

Consequently,

$$M_{i,t}^{f,0} + M_{i,t}^{m,0} = M_{i,t}^0.$$

These schedules allocate signed net migration; they do not separately identify immigration and emigration. The contract thereby guarantees that global net migration holds to 0, as every emigrant must immigrate somewhere.

2.7. Relation to local demographic accounting

The local identity is:

$$g_{i,t} = B_{i,t} - D_{i,t} + M_{i,t}.$$

In the empirical branch, residual migration satisfies it before centring. After centring,

$$A_{i,t}^B - A_{i,t}^D + M_{i,t}^0 - g_{i,t} = P_{i,t}\kappa_t.$$

Therefore global migration centring generally creates a local residual. The next definition eliminates that residual while retaining global balance.

Definition 3. Birth/death estimation; feasible demographic reconciliation

3.1. Notation

For a fixed year, suppress (t) where convenient. Let:

- $(g_i = \Delta P_i / h_t)$ reflect annualised population change;
- $(\ell_{B,i}, \ell_{f,i}, \ell_{m,i} \in \{0, 1\})$ indicate effective hard source locks.
- $(B_i^0, D_{f,i}^0, D_{m,i}^0)$ be preliminary vital counts;
- $(B_i^\pm, D_i^\pm, M_i^\pm)$ be lower and upper feasible bounds;
- (B_i^*, D_i^*, M_i^*) be final reconciled totals;
- $(D_i^0 = D_{f,i}^0 + D_{m,i}^0)$; i.e. female plus male deaths;
- (M_i^0) be globally centred migration from Definition 2;
- $(N_{i,a}^s)$ be the finalised age–sex state;
- (P_i) be population;
- $(Q_i^B, Q_i^{D_s})$ be birth and death predictors;

The operators $(\mathcal{C}_{v,t})$, variables (u^v, f^v) , and Ridge estimates are those defined in Definition 2. All reconciliation sums below are over the complete active domain with positive population and valid migration and population-change values.

3.2. Birth predictor

The infant population is given by:

$$Q_{i,t}^B = N_{i,t,0}^f + N_{i,t,0}^m.$$

Under age–sex stock reconciliation,

$$0 \leq Q_{i,t}^B \leq P_{i,t}.$$

3.3. Death predictors

Define recent local growth:

$$r_{i,t} = \begin{cases} \frac{\log(P_{i,t}/P_{i,t^-})}{h_t}, & P_{i,t^-} > 0, \\ 0, & \text{otherwise.} \end{cases}$$

If the previous population raster is unavailable, current population is substituted, giving ($r = 0$).
Construct sex-specific growth-adjusted density:

$$S_{i,t,a}^s = \frac{N_{i,t,a}^s}{w_a} e^{r_{i,t} x_a}.$$

Where $S_{i,t,a}^s$ is the Euler-Lotka survivorship proxy. Apply weighted decreasing isotonic regression over all ages:

$$\hat{S}_{i,t}^s = \underset{z_0 \geq \dots \geq z_{17} \geq 0}{\operatorname{argmin}} \sum_{a=0}^{17} w_a (z_a - S_{i,t,a}^s)^2.$$

This mortality-proxy PAVA is distinct from the age-sex transition kernel. In the supplied birth/death code it is applied in every year.

For ($a < 17$),

$$\hat{\mu}_{i,t,a}^s = \begin{cases} \frac{\hat{S}_{i,t,a}^s - \hat{S}_{i,t,a+1}^s}{\hat{S}_{i,t,a}^s (x_{a+1} - x_a)}, & \hat{S}_{i,t,a}^s > 0, \\ 0, & \text{otherwise.} \end{cases}$$

For the terminal band,

$$\hat{\mu}_{i,t,17}^s = \begin{cases} 1/5, & \hat{S}_{i,t,17}^s > 0, \\ 0, & \text{otherwise.} \end{cases}$$

Then:

$$\boxed{Q_{i,t}^{D_s} = \sum_a N_{i,t,a}^s \hat{\mu}_{i,t,a}^s.}$$

Monotonicity implies:

$$0 \leq \hat{\mu}_{i,t,a}^s \leq \frac{1}{x_{a+1} - x_a} \quad (a < 17).$$

The midpoint gaps are (2.5, 4.5, 5, ..., 5), so:

$$0 \leq Q_{i,t}^{D_s} \leq 0.4 \sum_a N_{i,t,a}^s.$$

This is a structural age-profile predictor. PAVA does not independently identify mortality or exactly remove migration effects.

3.4. Vital-event targets and preliminary counts

Choose HMD sources before 1950 and UNWPP thereafter. On valid target cells,

$$Y_{i,t}^B = \min \left(1.5, \frac{A_{i,t}^B}{Q_{i,t}^B} \right),$$

$$Y_{i,t}^{D_s} = \min \left(3, \frac{A_{i,t}^{D_s}}{Q_{i,t}^{D_s}} \right).$$

The target filters require:

$$A_{i,t}^v > 0, \quad Q_{i,t}^v \geq 1,$$

and, when the population raster exists,

$$P_{i,t} \geq 10000.$$

Fit, predict, and calibrate using Definition 2:

$$f_{i,t}^v = C_{v,t} \left(Z_{i,t}^\top \theta^v(t) \right).$$

On the ordinary modelled/source-override branch, positive source values replace modelled counts. Otherwise,

$$B_i^0 = \min(f_i^B Q_i^B, 1.5 Q_i^B),$$

$$\tilde{D}_i^s = \min(f_i^{D_s} Q_i^{D_s}, P_i).$$

If neither death component has a positive source override, define:

$$\pi_{m,i}^D = \begin{cases} \frac{u_i^{D_m}}{u_i^{D_m} + u_i^{D_f}}, & u_i^{D_m} + u_i^{D_f} > 0, \\ 1/2, & \text{otherwise.} \end{cases}$$

Then:

$$D_{m,i}^0 = \pi_{m,i}^D (\tilde{D}_i^m + \tilde{D}_i^f),$$

$$D_{f,i}^0 = (1 - \pi_{m,i}^D) (\tilde{D}_i^m + \tilde{D}_i^f).$$

If either component is overridden, this redistribution is skipped. When all three UNWPP vital files exist, the special empirical branch instead initialises:

$$(B_i^0, D_{f,i}^0, D_{m,i}^0) = (A_i^{B,U}, A_i^{D_f,U}, A_i^{D_m,U}),$$

after the code's non-negative sanitation, and skips this preliminary sex redistribution.

3.5. Effective locks and vital-event bounds

Retain the notation introduced at the start of Definition 3. In particular, $(B_i^0, D_{f,i}^0, D_{m,i}^0)$ are preliminary vital counts, $(D_i^0 = D_{f,i}^0 + D_{m,i}^0)$, and $(\ell_{B,i}, \ell_{f,i}, \ell_{m,i})$ are effective source-lock indicators.

The total-death bounds completing the preceding expression are:

$$(D_i^-, D_i^+) = \begin{cases} (D_i^0, D_i^0), & \ell_{f,i} = \ell_{m,i} = 1, \\ (D_{f,i}^0, \max\{D_{f,i}^0, P_i\}), & \ell_{f,i} = 1, \ell_{m,i} = 0, \\ (D_{m,i}^0, \max\{D_{m,i}^0, P_i\}), & \ell_{f,i} = 0, \ell_{m,i} = 1, \\ (0, P_i), & \ell_{f,i} = \ell_{m,i} = 0. \end{cases}$$

Thus the admissible vital-event rectangle is:

$$\mathcal{V}_i = [B_i^-, B_i^+] \times [D_i^-, D_i^+].$$

Its bounds satisfy:

$$0 \leq B_i^- \leq B_i^+, \quad 0 \leq D_i^- \leq D_i^+.$$

A locked death component can exceed the population cap: the code explicitly prioritises preserving that source value by using the maximum above. Therefore, $(D_i \leq P_i)$ is guaranteed only where the applicable bounds impose it.

3.6. Exact local feasible domain

The demographic balancing equation is given by:

$$g_i = B_i - D_i + M_i,$$

where $(g_i = \Delta P_i / h_t)$ is annualized annualised change. Rearranging:

$$M_i = g_i - B_i + D_i.$$

Over $(\mathcal{V}_i)$, the smallest migration occurs at the largest births and smallest deaths; the largest migration occurs at the smallest births and largest deaths. Consequently:

$$\boxed{M_i^- = g_i - B_i^+ + D_i^-, \quad M_i^+ = g_i - B_i^- + D_i^+}.$$

These bounds are ordered because:

$$M_i^+ - M_i^- = (B_i^+ - B_i^-) + (D_i^+ - D_i^-) \geq 0.$$

Moreover, every value between the endpoints is attainable: the continuous affine map $(B_i, D_i) \mapsto g_i - B_i + D_i$ maps the rectangle $(\mathcal{V}_i)$ onto the interval $\mathcal{M}_i = [M_i^-, M_i^+]$.

Equivalently, for a specified migration value (M_i) , natural increase must satisfy:

$$\boxed{B_i^- - D_i^+ \leq g_i - M_i \leq B_i^+ - D_i^-}.$$

This condition is both necessary and sufficient for local demographic closure within the vital-event bounds.

For a positive-population cell, the corresponding feasible per-capita migration interval is:

$$\boxed{\frac{g_i - B_i^+ + D_i^-}{P_i} \leq \frac{M_i}{P_i} \leq \frac{g_i - B_i^- + D_i^+}{P_i}}.$$

These are accounting-feasibility bounds. They need not coincide with the initial migration model's calibrated rate bounds, which are not imposed again during final reconciliation.

3.7. Exact global feasible domain

Let $(\mathcal{R}_t)$ denote the reconciled domain. Under the complete-coverage premise, it contains every positive-population cell contributing migration, with finite (g_i) and (M_i^0) .

Define the globally feasible migration set:

$$\mathcal{F}_t = \left\{ \mathbf{M} : M_i^- \leq M_i \leq M_i^+ \text{ for all } i \in \mathcal{R}_t, \quad \sum_{i \in \mathcal{R}_t} M_i = 0 \right\}.$$

Then:

$$\boxed{\mathcal{F}_t \neq \emptyset \iff \sum_i M_i^- \leq 0 \leq \sum_i M_i^+}.$$

Proof. Necessity follows by summing the component-wise bounds. For sufficiency, the attainable sums of independently selected interval values form the interval:

$$\left[\sum_i M_i^-, \sum_i M_i^+ \right].$$

The stated inequalities put zero in this interval. Hence there is an admissible migration vector with zero sum.

Substituting the definitions of $(M_i^\pm)$ gives the equivalent range for aggregate annualized population change:

$$\boxed{\sum_i (B_i^- - D_i^+) \leq \sum_i g_i \leq \sum_i (B_i^+ - D_i^-)}.$$

This is the necessary and sufficient global feasibility condition for the specified vital-event bounds. If every vital count is locked, each migration interval collapses to:

$$M_i^- = M_i^+ = g_i - B_i^0 + D_i^0.$$

Global feasibility then requires:

$$\sum_i (g_i - B_i^0 + D_i^0) = 0.$$

No adjustment of migration can otherwise preserve every locked vital count, satisfy every local identity, and conserve migration globally.

3.8. Globally balanced migration projection

Let:

$$\text{clip}(z; \ell, u) = \min\{u, \max\{\ell, z\}\}.$$

For a scalar shift (λ) , define:

$$M_i(\lambda) = \text{clip}(M_i^0 + P_i \lambda; M_i^-, M_i^+),$$

and

$$F_t(\lambda) = \sum_{i \in \mathcal{R}_t} M_i(\lambda).$$

The reconciled migration is:

$$\boxed{M_i^* = M_i(\lambda^*), \quad F_t(\lambda^*) = 0.}$$

Each summand is continuous and nondecreasing. Since $(P_i > 0)$ on $(\mathcal{R}_t)$,

$$\lim_{\lambda \rightarrow -\infty} F_t(\lambda) = \sum_i M_i^-, \quad \lim_{\lambda \rightarrow +\infty} F_t(\lambda) = \sum_i M_i^+.$$

Thus global feasibility guarantees a balancing root. A finite bracket guaranteed to contain a root is:

$$\lambda_L = \min_i \frac{M_i^- - M_i^0}{P_i}, \quad \lambda_U = \max_i \frac{M_i^+ - M_i^0}{P_i}.$$

At (λ_L) , every component is at its lower bound; at (λ_U) , every component is at its upper bound. Hence:

$$F_t(\lambda_L) \leq 0 \leq F_t(\lambda_U).$$

The scalar (λ^*) need not be unique because clipping may create a zero-valued plateau. Nevertheless, the resulting migration vector is unique. Specifically, $(\mathbf{M}^*)$ solves:

$$\underset{\mathbf{M} \in \mathcal{F}_t}{\text{minimise}} \quad \frac{1}{2} \sum_i \frac{(M_i - M_i^0)^2}{P_i}.$$

The objective is strictly convex because every $(P_i > 0)$, and $(\mathcal{F}_t)$ is convex. The minimiser is therefore unique. Its multiplier equations yield precisely the clipped common-shift construction.

This is a population-weighted projection of migration. It is the first step of a sequential reconciliation, not a simultaneous least-squares minimisation over all three flows.

3.9. Closed-form local birth/death projection

Once (M_i^*) is fixed, define required natural increase:

$$H_i = g_i - M_i^*.$$

Local closure requires:

$$B_i - D_i = H_i.$$

Substituting $(D_i = B_i - H_i)$, the feasible birth interval becomes:

$$L_i = \max\{B_i^-, H_i + D_i^-\},$$

$$U_i = \min\{B_i^+, H_i + D_i^+\}.$$

The migration bounds imply:

$$B_i^- - D_i^+ \leq H_i \leq B_i^+ - D_i^-,$$

which guarantees:

$$L_i \leq U_i.$$

The code's equal-weight local projection is:

$$B_i^* = \text{clip} \left(\frac{B_i^0 + D_i^0 + H_i}{2}; L_i, U_i \right), \quad D_i^* = B_i^* - H_i.$$

It minimises $(B_i - B_i^0)^2 + (D_i - D_i^0)^2$ subject to $(B_i, D_i) \in \mathcal{V}_i$, $B_i - D_i = H_i$.

Indeed, substituting $(D_i = B_i - H_i)$ gives the unconstrained minimiser:

$$B_i = \frac{B_i^0 + D_i^0 + H_i}{2}.$$

Clipping to $([L_i, U_i])$ gives the constrained minimiser. By construction,

$$B_i^- \leq B_i^* \leq B_i^+, \quad D_i^- \leq D_i^* \leq D_i^+,$$

and

$$B_i^* - D_i^* + M_i^* = H_i + M_i^* = g_i.$$

When all vital counts are locked, this reduces as follows:

$$B_i^* = B_i^0, \quad D_i^* = D_i^0, \quad M_i^* = g_i - B_i^0 + D_i^0.$$

Thus the code's fully locked special case is already included in the mathematical projection.

3.10. Sex-specific death and migration allocation

The reconciled death total is allocated as follows:

$$(D_{f,i}^*, D_{m,i}^*) = \begin{cases} (D_{f,i}^0, D_{m,i}^0), & \ell_{f,i} = \ell_{m,i} = 1, \\ (D_{f,i}^0, D_i^* - D_{f,i}^0), & \ell_{f,i} = 1, \ell_{m,i} = 0, \\ (D_i^* - D_{m,i}^0, D_{m,i}^0), & \ell_{f,i} = 0, \ell_{m,i} = 1, \\ ((1 - \rho_i)D_i^*, \rho_i D_i^*), & \ell_{f,i} = \ell_{m,i} = 0, \end{cases}$$

where:

$$\rho_i = \begin{cases} D_{m,i}^0 / D_i^0, & D_i^0 > 0, \\ 0.512, & D_i^0 = 0. \end{cases}$$

The death lower bounds guarantee nonnegative remainders in the singly locked cases.

Therefore,

$$D_{f,i}^* \geq 0, \quad D_{m,i}^* \geq 0, \quad D_{f,i}^* + D_{m,i}^* = D_i^*.$$

For migration, let the initial allocations satisfy:

$$M_{f,i}^0 + M_{m,i}^0 = M_i^0.$$

Define:

$$\eta_{f,i} = \begin{cases} M_{f,i}^0 / M_i^0, & M_i^0 \neq 0, \\ 0.488, & M_i^0 = 0, \end{cases} \quad \eta_{m,i} = 1 - \eta_{f,i}.$$

Under Definition 2's common-sign allocations, both shares lie in $([0, 1])$. The reconciliation updates:

$$M_{s,i}^* = M_{s,i}^0 + \eta_{s,i}(M_i^* - M_i^0), \quad s \in \{f, m\}.$$

Consequently,

$$M_{f,i}^* + M_{m,i}^* = M_i^*.$$

These allocations do not impose separate global female and male migration balances or separate sex-specific demographic identities.

3.11. Closure theorem and numerical implementation

On the complete feasible reconciled domain, in exact arithmetic with an exact balancing root and consistent final writes,

$$\begin{aligned} g_i &= B_i^* - D_{f,i}^* - D_{m,i}^* + M_{f,i}^* + M_{m,i}^*, \\ \sum_i (M_{f,i}^* + M_{m,i}^*) &= 0. \end{aligned}$$

Summing local closure gives:

$$\sum_i g_i = \sum_i B_i^* - \sum_i (D_{f,i}^* + D_{m,i}^*).$$

The supplied implementation approximates this mathematical construction:

- its initial balancing bracket is $([-10, 10])$, with at most five expansions per endpoint;
- it performs at most 45 bisection iterations;
- its early stopping condition is $(|F_t(\lambda)| < 10^{-5})$;
- migration changes of magnitude at most (10^{-7}) are not written;
- intermediate and final arrays use floating-point storage.

Accordingly, finite iteration and conditional writes can introduce residuals even apart from floating-point rounding. If a migration update is skipped, the exact-arithmetic local residual using the saved migration is:

$$g_i - (B_i^* - D_i^* + M_i^{\text{saved}}) = M_i^* - M_i^{\text{saved}},$$

whose magnitude is at most (10^{-7}) for that skipped update.

If the global feasibility inequalities fail, no method can satisfy all stated constraints without relaxing at least one bound, lock, or conservation requirement. The current implementation logs a warning but does not thereby restore feasibility.

Definition 4. Compact Form

4.1. Notation

For each year (t) , let:

- $(a \in \mathcal{A} = \{0, \dots, 17\})$ index age bands;
- $(i \in \Omega)$ index the complete raster domain;
- $(s \in \{f, m\})$ index sex;
- $(g_{i,t} = (P_{i,t} - P_{i,t^-})/h_t)$, assuming the delta raster represents that difference;
- $(p_{i,t,a}^s)$ be multinomial cohort probabilities;
- (t^-) be the preceding population observation and $(h_t = t - t^- > 0)$;
- $(\mathcal{A}_t)$ be the cell redistribution and source-compositing operator of Definition 1;
- $(\mathcal{I})$ be the sex-specific, suffix PAVA operator;
- $(\widetilde{M}_{i,t})$ be preliminary empirical-residual or modelled migration;
- $(M_{i,t}^0)$ be its globally centred value;
- $(N_{i,t,a}^s)$ be the finalised age–sex population;
- $(P_{i,t} \geq 0)$ be total population;
- $(R_{b,t,a}^s)$ be preliminary country-bin cohort populations;
- $(\mathcal{W})$ be the coupled, population-preserving Whittaker operator;
- $(\mathcal{V}_t)$ be the predictor, regression, calibration, source-selection, and preliminary-allocation construction of Definition 3;
 - $(B_{i,t}^0, D_{f,i,t}^0, D_{m,i,t}^0)$ be its preliminary vital counts;
 - $(B_{i,t}^\pm, D_{i,t}^\pm)$ be source-aware feasible bounds;
- $(\gamma(t) \in [0, 1])$ be the logistic transition weight;
- a superscript $(*)$ identify final reconciled flows.

The active reconciliation domain is:

$$\Omega_+(t) = \{i : P_{i,t} > 0\}.$$

It is assumed to contain all relevant flows. A zero-current-population cell with nonzero population change would require separate treatment because the supplied reconciliation excludes it. As before:

$$\text{clip}(z; \ell, u) = \min\{u, \max\{\ell, z\}\}.$$

4.2. Ordered construction

The execution order is orchestrated as follows:

1. Age-sex stocks
2. Globally-centred migration
3. Final vital-event and migration reconciliation

A. Age–sex stocks

Let $(\sigma(z) = (1 + e^{-z})^{-1})$. With the supplied transition defaults,

$$\gamma(t) = \begin{cases} 0, & t \leq 1750, \\ \frac{\sigma\left(8\left(\frac{t-1750}{100} - \frac{1}{2}\right)\right) - \sigma(-4)}{\sigma(4) - \sigma(-4)}, & 1750 < t < 1850, \\ 1, & t \geq 1850. \end{cases}$$

Construct country-bin graduation targets.

$$G_{b,t,a}^s = [1 - \gamma(t)] \mathcal{I}(R)_{b,t,a}^s + \gamma(t) \mathcal{W}(R)_{b,t,a}^s.$$

Redistribute and composite:

$$\boxed{\mathbf{N}_t = \mathcal{A}_t(\mathbf{p}_t, \mathbf{G}_t; \text{population and sources}).}$$

Under the population-compatibility premise of Definition 1:

$$N_{i,t,a}^s \geq 0, \quad \sum_{s,a} N_{i,t,a}^s = P_{i,t}.$$

B. Preliminary migration and global centering

Construct preliminary migration by the applicable branch:

$$\widetilde{M}_{i,t} = \begin{cases} g_{i,t} - A_{i,t}^{B,U} + A_{i,t}^{D_f,U} + A_{i,t}^{D_m,U}, & \text{empirical branch,} \\ P_{i,t} f_{i,t}^M, & \text{modeled branch.} \end{cases}$$

Then:

$$M_{i,t}^0 = \widetilde{M}_{i,t} - P_{i,t} \frac{\sum_{j \in \Omega_+(t)} \widetilde{M}_{j,t}}{\sum_{j \in \Omega_+(t)} P_{j,t}}.$$

Therefore,

$$\sum_i M_{i,t}^0 = 0.$$

C. Preliminary vital events and admissible bounds

Construct:

$$(B_{i,t}^0, D_{f,i,t}^0, D_{m,i,t}^0) = \mathcal{V}_t(\mathbf{N}, \mathbf{P}, \mathbf{X}; \text{sources}),$$

and set:

$$D_{i,t}^0 = D_{f,i,t}^0 + D_{m,i,t}^0.$$

Establish the source-aware bounds of Definition 3, then define:

$$M_{i,t}^- = g_{i,t} - B_{i,t}^+ + D_{i,t}^-,$$

$$M_{i,t}^+ = g_{i,t} - B_{i,t}^- + D_{i,t}^+.$$

The construction is globally feasible precisely when:

$$\sum_i M_{i,t}^- \leq 0 \leq \sum_i M_{i,t}^+.$$

D. Final migration and vital-event reconciliation

Choose a balancing root (λ_t^*) satisfying:

$$\sum_i \text{clip} \left(M_{i,t}^0 + P_{i,t} \lambda_t^*; M_{i,t}^-, M_{i,t}^+ \right) = 0.$$

Set:

$$M_{i,t}^* = \text{clip} \left(M_{i,t}^0 + P_{i,t} \lambda_t^*; M_{i,t}^-, M_{i,t}^+ \right),$$

$$H_{i,t} = g_{i,t} - M_{i,t}^*,$$

$$L_{i,t} = \max\{B_{i,t}^-, H_{i,t} + D_{i,t}^-\},$$

$$U_{i,t} = \min\{B_{i,t}^+, H_{i,t} + D_{i,t}^+\}.$$

The final vital totals are:

$$\boxed{\begin{aligned} B_{i,t}^* &= \text{clip}\left(\frac{B_{i,t}^0 + D_{i,t}^0 + H_{i,t}}{2}; L_{i,t}, U_{i,t}\right), \\ D_{i,t}^* &= B_{i,t}^* - H_{i,t}. \end{aligned}}$$

Allocate deaths and migration between sexes using Definition 3.10, preserving:

$$D_{f,i,t}^* + D_{m,i,t}^* = D_{i,t}^*, \quad M_{f,i,t}^* + M_{m,i,t}^* = M_{i,t}^*.$$

4.3. The three simultaneous constraints

On the complete feasible domain with exact reconciliation, the final state satisfies:

Age-sex stock reconciliation:	$\sum_{s,a} N_{i,t,a}^s = P_{i,t},$
Global migration conservation:	$\sum_i M_{i,t}^* = 0,$
Local demographic closure:	$\frac{P_{i,t} - P_{i,t^-}}{h_t} = B_{i,t}^* - D_{f,i,t}^* - D_{m,i,t}^* + M_{f,i,t}^* + M_{m,i,t}^*.$

The local identity is equivalently the interval stock equation

$$\boxed{P_{i,t} = P_{i,t^-} + h_t (B_{i,t}^* - D_{i,t}^* + M_{i,t}^*)}.$$

Summing over the complete domain eliminates migration:

$$\boxed{\sum_i P_{i,t} - \sum_i P_{i,t^-} = h_t \left(\sum_i B_{i,t}^* - \sum_i D_{i,t}^* \right)}.$$

Under fixed inputs and execution conventions, this defines a deterministic reconstruction. Due to irregular time intervals between HYDE rasters, such reconstructions are not cohort-dependent, and thus Leslie Matrices with added migration does not temporally hold.

Footnotes.

1. From 1750-1850 is the main period of the First Industrial Revolution. This is not actually the reason for why this domain was chosen, it was because HMD starts in 1750, and it is not until 1850 that we log the first non-isotonic population pyramids. A steepness of 8 is used, since the period in question is decadal, therefore there are 8 interceding rasters excluding the start and ends.
2. Whittaker-Henderson parameters chosen due to compute and convergence constraints.
3. Hardcoded sex ratios from sex ratio at birth (SRB) and maximum estimated envelopes from 20th century HMD/UNWPP.
4. Pareto Ensemble from 80/20 rule. 0.3 is used as it is the scaling used for Word2Vec, but that is a matter of convention.
5. Magic numbers from implementation by Husinger for Rogers-Castro; UC Berkeley, Applied Demography.
6. Log-tail normalisation with Tukey's fences used to preserve intra-country spatial variance.