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Longevity R&D Centre

Mortality forecasting by Cause of Death and Basis Risk modelling with Compositional Data

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Introduction

- National demographic data are frequently used to predict future mortality improvements due to the homogeneity and robustness of the data.
- Inherent differences in the risk profile of an insured population from the general population create a basis risk.
- In the following, distribution and dynamic of cause-specific mortality differ between the general and insured/subpopulation.
- Using the framework of the compositional data, Aitchison (1986), we obtain projections by cause of death based on two components :
  - The density of mortality for a cause given the death by this cause,
  - and the vector of the proportions of deaths related to each cause.
- A deterministic relationship between the insured and the general population is established and experts judgements on future potentials changes in the two components are integrated to capture the basis risk.

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Compositional data framework

- Compositional data (CoDA) consist of vectors whose components are the proportions or percentage of some whole.
- Their sum is constrained to be some constant, equal to 1 for proportions or possibly some other constant for other situations.
- Use the framework of the CoDa and map the original data from a simplex space to a non constrained space.
- In a forecasting mortality context, it has been used by Bergeron-Bouchet *et al.* (2017) and Kjærgaard *et al.* (2018) in studying subpopulations and by Oeppen (2008) in modeling causes of death.
- Compositional data framework automatically deals with the competing risks.

Summary of the approach

1. Model and forecast all causes mortality of the general population with traditional mortality models, e.g. Poisson log-likelihood developed by Brouhns *et al.* (2002).
2. Breakdown the forecasted mortality of the general population by cause of death using compositional Lee-carter.
3. Complete the mortality table at high age by cause of death using compositional linear model.
4. Derived the projected proportions of deaths related to each cause and the density of mortality for a cause given the death by this cause.
5. Applied the trends derived in step 4. to subpopulation estimates of the two components.
6. Applied experts judgements to adjust the trends observed on a few causes of death.

Notation and assumptions

In the following, we denote by

- X_t, the residual life expectancy of an individual in calendar year t.
- $q_{x,t} = \mathbb{P}\Big[x \leq X_t < x+1 | x > X_t\Big]$, the probability of death all causes, and $q_{x,t,i}$ for the cause i, i.e, $\sum_i q_{x,t,i} = q_{x,t}$.
- $\mu_{x,t}$, the forces of mortality at attained age x for calendar year t.
- $d_{x,t} = \mathbb{P}\Big[x \leq X_t < x+1\Big]$, the density of mortality all causes, and $d_{x,t,i} = \mathbb{P}\Big[x \leq X_t < x+1, CoD = i\Big]$ the density of mortality for the cause i, i.e ; $\sum_i d_{x,t,i} = d_{x,t}$.
- $\delta_{x,t,i} = \mathbb{P}\Big[x < X_t < x+1 | CoD = i\Big]$, hence $\sum_x \delta_{x,t,i} = 1$.
- $\pi_{t,i} = \mathbb{P}\Big[CoD = i | T = t\Big]$, and $\sum_i \pi_{t,i} = 1$

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Step 1 | Forecast all cause mortality of the general population

- We estimate and forecast the mortality dynamics on the general population due to the homogeneity and robustness of the data.
- We aim at constraining the dynamics to avoid the structural increase when extrapolating the mortality improvements by cause in an compositional data framework.
- The number of deaths, $D_{x,t}$, for $x \in \left[x_1, x_n\right]$ and $t = 1, \ldots, m$, are modeled using traditional mortality models, e.g. Poisson log-likelihood developed by Brouhns *et al.* (2002)

$$D_{x,t} \sim \text{ Poisson}\left(E_{x,t}\, \mu_{x,t}\right) \quad \text{with } \mu_{x,t} = \exp\Big(\alpha_x + \beta_x\, \kappa_t\Big)$$

- Arima model is fitted to the time varying parameter and we extrapolate the coefficient κ_t for $t = m+1, \ldots, m+h$ using the fitted time series models.

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Step 2 | Breakdown by cause of death

- We decompose the forecasted mortality of the general population by cause of death using a compositional Lee-Carter model applied to the mortality ratio $q_{x,t,i}/q_{x,t}$ for $x \in \left[x_1, x_n\right]$, $t = 1, \ldots, m$ and $i = 1, \ldots, I$:

$$\text{clr}\left(\frac{q_{x,t,i}}{q_{x,t} \cdot \alpha_{x,i}}\right) = \sum_{k=1}^{K} \beta_{x,i,k}\, \kappa_{t,i,k}; \;\; \text{clr}(Z) = \left[\ln\left(\frac{z_1}{g}\right), \ln\left(\frac{z_2}{g}\right), \ldots, \ln\left(\frac{z_c}{g}\right)\right]$$

$$\text{and } g = \left(z_1 \cdot z_2 \cdot \ldots \cdot z_c\right)^{1/c}.$$

- Arima models are fitted to each of the $\left\{\kappa_{t,i,k}\right\}$, $k = 1, \ldots, K$. and the coefficients $\left\{\kappa_{t,i,k}\right\}$, $k = 1, \ldots, K$. for $t = m+1, \ldots, m+h$ are extrapolated using the fitted time series models.
- The extrapolated mortality for the cause i for $t = m+1, \ldots, m+h$ is :

$$\text{clr}^{-1}\left(\sum_{k=1}^{K} \beta_{x,k,i}\, \kappa_{t,k,i}\right) \cdot \alpha_{x,i} \cdot q_{x,t}; \;\; \text{clr}^{-1}(Z) = \text{C}\left[\exp(z_1), \exp(z_2), \ldots, \exp(z_c)\right]$$

$$\text{and } \text{C}\left[Z\right] = \left[\frac{z_1}{\sum z}, \frac{z_2}{\sum z}, \ldots, \frac{z_c}{\sum z}\right].$$

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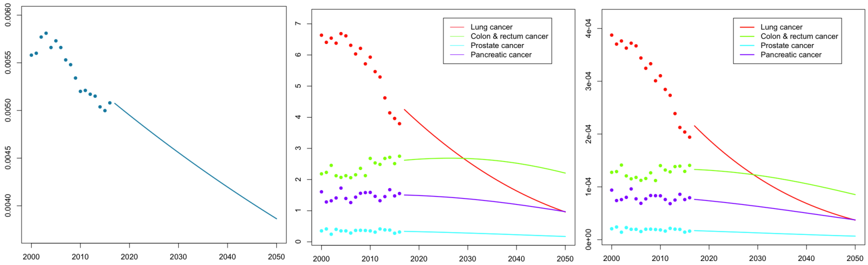
Step 2 | Breakdown by cause of death - illustration



(a) $q_{x,t}$ (b) $q_{x,t,i}/q_{x,t}$ (c) $q_{x,t,i}$

FIGURE: Breakdown by cause, neoplasms, Age 50, US male population.

Step 3 | Complete the mortality by cause at high ages

- Close the mortality tables by cause until an age limit x_ω :
  - to enable transfers of deaths at high ages allowing mortality improvements and avoiding a concentration of the deaths at x_n,
  - to apply possible experts judgements beyond x_n.
- In a similar manner than steps 1 and 2,

1. Close the all cause mortality table by a completion method, e.g. Denuit and Goderniaux (2005).
2. Extrapolate the mortality $\frac{q_{x,t,i}}{q_{x,t}}$, using compositional linear model,

$$\text{clr}\left(\frac{q_{x,t,i}}{q_{x,t}}\right) = a + b \cdot x.$$

3. Obtain the extrapolated mortality by cause at high ages : $\text{clr}^{-1}(a + b \cdot x) \cdot q_{x,t}$, for $x = x_n, \ldots, x_\omega$.

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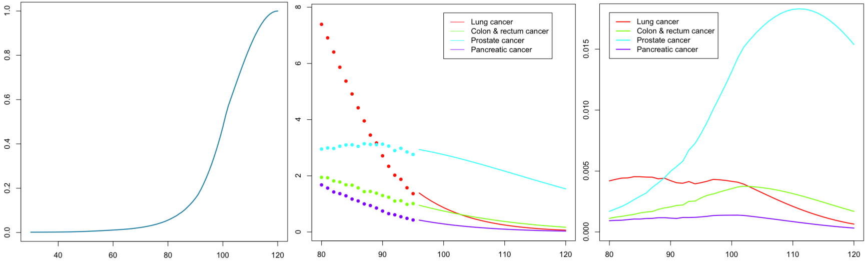
Step 3 | Complete the mortality by cause at high ages - illustration



(a) $q_{x,t}$ (b) $q_{x,t,i}/q_{x,t}$ (c) $q_{x,t,i}$

FIGURE: Completion by cause, 2014, neoplasms, US male population.

Step 4 | Derive $\pi_{t,i}$ and $\delta_{x,t,i}$

- Having extrapolated the mortality by cause in steps 2 and 3, we derive the resulting projections of the following two components :
  - With $d_{x,t,i} = S_{x,t} \cdot q_{x,t,i}$
  - $\delta_{x,t,i} = d_{x,t,i} / \sum_x d_{x,t,i}$, the density of mortality for a cause given the death by this cause,
  - and $\pi_{t,i} = \sum_x d_{x,t,i}$, the vector of the proportions of deaths related to each cause.
- Hence $d_{x,t,i} = \pi_{t,i} \cdot \delta_{x,t,i}$.
- By doing so, we modeled explicitly that mortality improvements are originating from :
  - a delay of the age at death from the cause (for example due to the effectiveness of a treatment)
  - a reduction in the number of deaths from this cause (due to the appearance of a vaccine or screening programs) .

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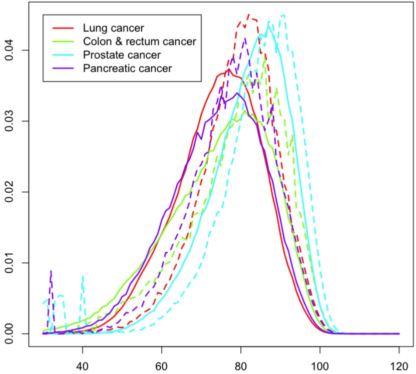
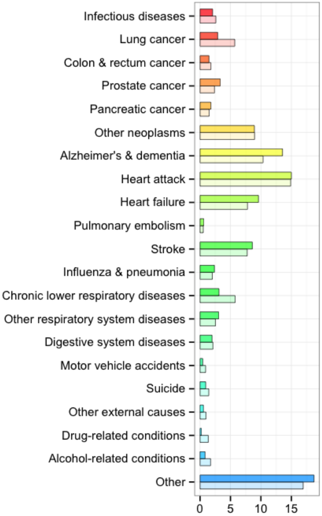
Step 4 | $\pi_{t,i}$ and $\delta_{x,t,i}$ - illustration



(a) $\delta_{x,t,i}$, full : general, dashed : subpopulation



(b) $\pi_{t,i}$, light : general, dark : subpopulation

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Step 5 | Apply the general population trends to subpopulation estimates

- We decompose the $\pi_{t,i}$ and $\delta_{x,t,i}$ by fitting a compositional Lee and Carter (1992) :
  - $\text{clr}\left(\frac{\pi_{t,i}}{\alpha_i}\right) = \sum_{k=1}^{K_\pi} \beta^{\pi}_{i,k}\ \kappa^{\pi}_{t,k}$, and
  - $\text{clr}\left(\frac{\delta_{x,t,i}}{\alpha_x}\right) = \sum_{k=1}^{K_\delta} \beta^{\delta}_{x,t,i,p}\ \kappa^{\delta}_{t,i,p}$
- The projected subpopulation estimates are obtained by plugging-in the level of $\pi^{\text{sub}}_{t^0}$ and $\delta^{\text{sub}}_{x,t^0,i}$ with the trends derived on the general population for $t = t^0 + 1, \ldots, m + h$,

$$\pi^{\text{sub}}_{t,i} = \pi^{\text{sub}}_{t^0,i} \cdot \mathcal{C}\left[\exp\left(\sum_{k=1}^{K^\pi} \beta^{\pi}_{i,k}\ \Delta\kappa^{\pi}_{t,k}\right)\right],$$

$$\text{and } \delta^{\text{sub}}_{x,t,i} = \delta^{\text{sub}}_{x,t^0,i} \cdot \mathcal{C}\left[\exp\left(\sum_{k=1}^{K^\delta} \beta^{\delta}_{x,p}\ \Delta\kappa^{\delta}_{t,i,p}\right)\right].$$

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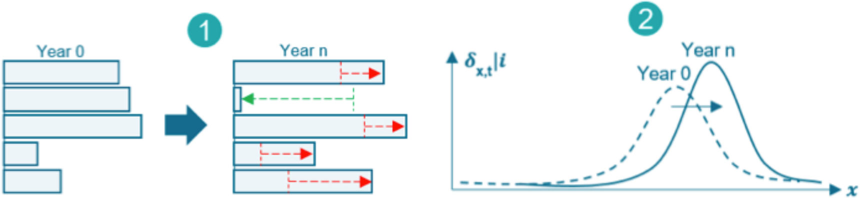
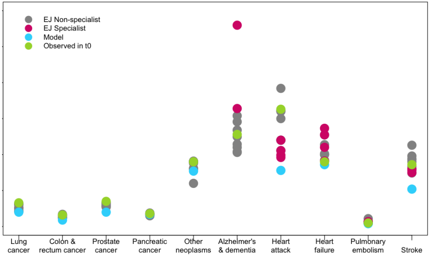
Step 6 | Adjust the trends by applying experts judgements

Working with proportions and mortality densities provides high flexibility for experts judgements inclusion on CoD mortality dynamics :

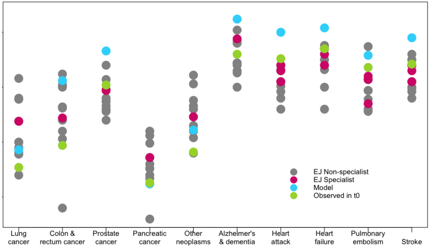
1. Include impacts of an invention of a vaccine or of a screening program by adding a constraint to the CoD proportions.
2. Include the impact of new medical treatments delaying the age at death for a CoD by shifting the density towards the right.



Step 6 | Experts Judgements - illustration



(a) EJ on $\pi_{t^\star,i}$



(b) EJ on $\delta_{x,t^\star,i}$

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Step 6a | Adjusting the proportions of deaths, $\pi_{t,i}$

Assume $j = j_1, \dots, j_{l-1}$ causes with EJ in $t^\star$, and denote $\theta_j = \exp\left(\beta_j \kappa_{t^\star}\right) \cdot \alpha_j$,

$$\pi_{t^\star,j} = \frac{\theta_j}{\sum_j \theta_j + \sum_{i \neq j} \theta_i} \quad \text{then} \quad \theta_j = \pi_{t^\star,j} \left(\sum_j \theta_j + \sum_{i \neq j} \theta_i \right).$$

For j_1, we have $\theta_{j_1}(1 - \pi_{t^\star,j_1}) - \pi_{t^\star,j_1} \sum_{j \neq j_1} \theta_j - \pi_{t^\star,j_1} \sum_{i \neq j} \theta_i = 0$ And the following system :

$$\begin{pmatrix} \widehat{\theta}_{j_1} \\ \widehat{\theta}_{j_2} \\ \vdots \\ \widehat{\theta}_{j_{l-1}} \end{pmatrix} = \begin{pmatrix} 1 - \pi_{\star,j_1} & -\pi_{t^\star,j_1} & \cdots & -\pi_{t^\star,j_1} \\ -\pi_{\star,j_2} & 1 - \pi_{t^\star,j_2} & \cdots & -\pi_{t^\star,j_2} \\ \vdots & \vdots & \ddots & \vdots \\ -\pi_{t^\star,j_{l-1}} & -\pi_{t^\star,j_{l-1}} & \cdots & 1 - \pi_{t^\star,j_{l-1}} \end{pmatrix}^{-1} \begin{pmatrix} \pi_{t^\star,j_1} \sum_{i \neq j} \theta_i \\ \pi_{t^\star,j_2} \sum_{i \neq j} \theta_i \\ \vdots \\ \pi_{t^\star,j_{l-1}} \sum_{i \neq j} \theta_i \end{pmatrix}$$

Then $\widehat{\beta}_j = \ln \left(\frac{\widehat{\theta}_j}{\alpha_j} \right) \frac{1}{\kappa_{t^\star}}$.

Assume the transition to $\pi_{t^\star,j}$ starts in t^0, then, for $t = t^0, \dots, t^\star$,

$$\pi_{t,j} = \mathrm{C}\left[\exp(\psi) \cdot \alpha_j\right] \text{ where } \psi = \left(\widehat{\beta} + \frac{\left(\widehat{\beta} - \beta\right)\kappa_{t^0}}{\kappa_{t^\star} - \kappa_{t^0}} \right) \Delta\kappa_t + \widehat{\beta}\kappa_{t^\star}.$$

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Step 6b | Shifting the mortality densities $\delta_{x,t,i}$

- Assessing a distribution can be done by various indicators. Here we consider the modal age at death.
- One way to shift a distribution is to apply the Wang transform, such that

$$d_{x,t,i} = \Delta\Big(\Phi\Big(\Phi^{-1}(F) + w \cdot \lambda\Big)\Big)$$

where w is an asymmetric weighting function assigning the weight 1 to the mode and decreasing to zero at the borders.

1. The density is smoothed by local polynomials and interpolated between entire ages.
2. Find λ corresponding to difference between $\text{mode}_{t^\star,i}$ and the expert judgement by optimization.

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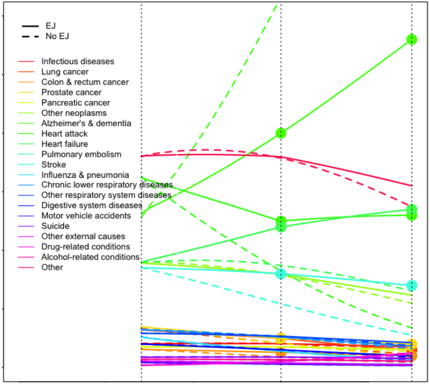
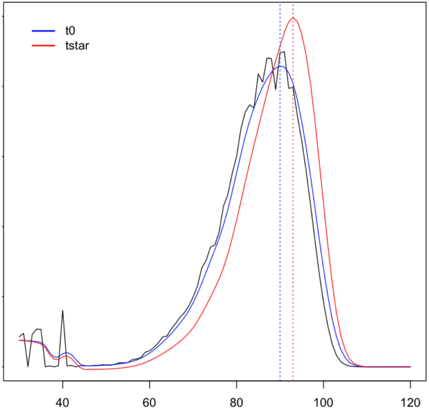
Step 6 | Adjusting $\pi_{t,i}$ and $\delta_{x,t,i}$ - illustration

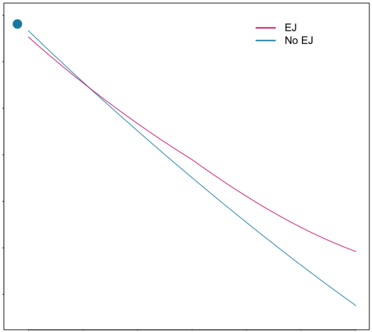


(a) $\pi_{t,i}$ with several EJ.

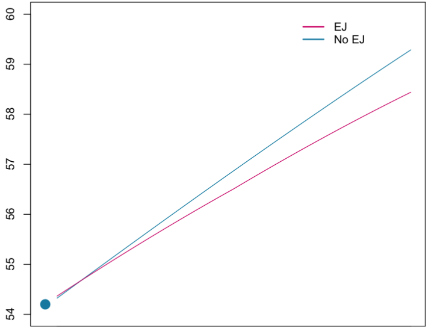


(b) $\delta_{x,t,i}$, pancreatic cancer.

Illustration of the forecasts for the subpopulation



(a) $q_{x,t}$ with several EJ, $t = t^0, \ldots, t^\star$.



(b) Residual life expectancy at age 30.

Conclusion and perspectives

- Compositional data framework has a lot to offer to the competing risks problem.
- The methodology can be used to test scenarios on apparition of a vaccine, screening programs, effectiveness of treatment, etc.
- We aim at
  - including dependances between the $\pi_{t,i}$ and $\delta_{x,t,i}$,
  - using mortality laws to shift mortality densities.

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