JOINT LIFETIME MODELLING WITH MATRIX DISTRIBUTIONS

HANSJÖRG ALBRECHER, MARTIN BLADT, AND ALARIC J.A. MÜLLER

ABSTRACT. Acyclic phase-type (PH) distributions have been a popular tool in survival analysis, thanks to their natural interpretation in terms of ageing towards its inevitable absorption. In this paper, we consider an extension to the bivariate setting for the modelling of joint lifetimes. In contrast to previous models in the literature that were based on a separate estimation of the marginal behavior and the dependence structure through a copula, we propose a new time-inhomogeneous version of a multivariate PH class (mIPh) that leads to a model for joint lifetimes without that separation. We study properties of mIPh class members and provide an adapted estimation procedure that allows for right-censoring and covariate information. We show that initial distribution vectors in our construction can be tailored to reflect the dependence of the random variables, and use multinomial regression to determine the influence of covariates on starting probabilities. Moreover, we highlight the flexibility and parsimony, in terms of needed phases, introduced by the time-inhomogeneity. Numerical illustrations are given for the data set of joint lifetimes of Frees et al. [15], where 10 phases turn out to be sufficient for a reasonable fitting performance. As a by-product, the proposed approach enables a natural causal interpretation of the association in the ageing mechanism of joint lifetimes that goes beyond a statistical fit.

1. Introduction

When studying insurance products on multiple lives, it is natural to assume that individuals who are exposed to very similar life conditions may have somewhat correlated lifetimes. This is especially true for married couples, since, once married, the spouses typically share to a large extent a similar lifestyle. Indeed, the simplistic assumption of independence of lifetimes of partners has been shown to be inappropriate in various papers. For example, Frees et al. [15] used a bivariate Frank copula model to assess the effect of dependency between husband and wife on insurance annuities, illustrating their approach on a by now classical data set of a large insurer. The same data was used in Carriere [10], where multiple bivariate copula models were studied. The Linear-Mixing Frailty copula was found to be the best suited model to describe the data. Shemyakin & Youn [22] introduce a general conditional Bayesian copula for joint last survivor analysis. They allow entry ages of spouses to have a selection effect on his/her mortality, as well as on the other spouse’s mortality. For that same data set, Luciano et al. [19] captured the dependence between survival times of spouses by an Archimedean copula, whose marginals were estimated according to a stochastic intensity approach. In a similar spirit, Dufresne et al. [13] allow for the Archimedean copula parameter to depend on the age difference of partners at issue of the policy, in order to describe the dependence of the remaining lifetime of a couple. In Gobbi et al. [16], extended Marshall-Olkin models were employed for that same data set, where the continuous copula approach is extended by allowing for fatal events that affect

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both marginal lives.

In this paper we propose an alternative to copula-based methods for the modelling of joint remaining lifetimes in a couple based on multivariate phase-type distributions. Phase-type (PH) distributions are interesting candidates since they broaden favourable properties of exponential random variables to scenarios where the latter alone would not be appropriate. In particular, the denseness of PH distributions among all distributions on the positive half-line in the sense of weak convergence, which extends to the multivariate setup, is a major advantage when one wants to approximate a distribution. For more details on PH distributions we refer readers to Bladt & Nielsen [8]. As opposed to copula-based methods, a PH distribution can give rise to a natural interpretation when used to approximate lifetime distributions. One can view the path of a Markov jump process as the life of an individual, which goes through several different states (for instance biological markers) before reaching the inevitable absorption (death) state. Along this interpretation, acyclic PH distributions have been the first choice for modelling the ageing process of a human life, since they only allow forward transitions or direct exits to the absorption state. This characteristic makes them an appropriate tool for describing lifetimes ended by natural ageing or accidents. In Lin & Liu [18], a PH distribution with Coxian structure was used to explain the physical ageing process of marginal lifetimes. This approach was extended in Asmussen et al. [5] to generalised Coxian distributions for the purpose of pricing equity-linked products. The first contribution to lift the PH approach to bivariate lifetime models was Ji et al. [17], where a Markovian multi-state model and a semi-Markov model are used to describe the dependence between the lifetimes of husbands and wives. Spreeuw & Owadally [23] also use a Markovian multi-state model, with more attention given on how to tie the bereavement effect to forces of mortality. Moutanabbir & Abdelrahman [20] then used a bivariate Sarmanov distribution with PH marginals to model joint lifetimes. Both papers focused on the pricing of multiple-life insurance contracts. Recently, Albrecher et al. [2] introduced time-inhomogeneous PH (IPH) distributions for the purpose of lifetime modelling, which leads to a considerable reduction of necessary phases for a satisfactory fit of given data, since the introduced inhomogeneity can more efficiently accommodate non-exponential shapes than an augmentation of the phase dimension. In particular, [2] applied regression on the intensity functions of the IPH distributions to associate lifetimes of different cohorts and populations.

In this paper, we propose a different route for using available information in the data set, namely to incorporate multinomial logistic regressions in the estimation procedure of multivariate PH distributions. In particular, the regression is applied to the initial distribution vectors of each IPH component, which adapts an approach presented in Bladt & Yslas [9] to the multivariate case. The resulting dependence structure allows for explicit formulas alongside an intuitive ‘ageing’ interpretation and, beyond the theoretical contribution, for a satisfactory fit to the bivariate spouses’ lifetime data.

The remainder of the paper is structured as follows. Section 2 introduces the class of multivariate PH distributions that we will use to describe joint lifetimes of couples; we also provide some additional properties. In Section 3 an estimation method for this multivariate PH distribution is introduced, which allows for right censoring and covariate information.
Section 4 then applies and illustrates the procedure on the classical spouses’ lifetime data set from [15] and interprets the results. Section 5 concludes.

2. Multivariate phase-type distributions

We first recall the mPH class, which was introduced in Bladt [7].

2.1. mPH distributions. Let \( \{J_t^{(i)}\}_{t \geq 0}, i = 1, \ldots, d \), denote separate homogeneous Markov pure-jump processes on the common state space \( E = \{1, \ldots, p, p + 1\} \), with states \( 1, \ldots, p \) being transient and \( p + 1 \) absorbing. Defining transition probabilities as

\[
p_{ji}(s, t) = \mathbb{P}(J_t^{(i)} = l | J_s^{(i)} = j), \quad 0 \leq j, l \leq p + 1, \quad 0 < i \leq d,
\]

we may write

\[
P_i(s, t) = \exp(\Lambda_i(t - s)) = \begin{pmatrix} \exp(T_i(t - s)) - \exp(T_i(t - s))e \\ e_1 \end{pmatrix} \in \mathbb{R}^{(p+1) \times (p+1)},
\]

for \( s < t, \ 0 \leq i \leq d \), where \( \Lambda_i(t) \) are intensity matrices. In the following we write \( e_k \) for the \( k \)-th canonical basis vector in \( \mathbb{R}^p \), \( e = \sum_{j=1}^p e_j \), and

\[
T_i = \{t_{ks}^{(i)}\}_{k,s=1,\ldots,p}, \quad t_i = -T_i e = (t_{1i}^{(i)}, \ldots, t_{pi}^{(i)})^\top, \quad k = 1, \ldots, p.
\]

The crucial property of this class of PH distributions is now its dependence structure. Concretely, the assumption is that all jump processes start in the same state at time \( t = 0 \), but proceed independently thereafter until absorption. That is, dependence is introduced solely through the shared initial state, which leads to a particularly tractable yet flexible model class. More formally,

\[
J_0^{(i)} = J_0^{(l)}, \quad \{J_t^{(i)}\}_{t \geq 0} \overset{d}{=} J_0^{(i)} \{J_t^{(l)}\}_{t \geq 0, t \neq i}, \quad \forall i, l \in \{1, \ldots, d\}.
\]

We will use \( J_0 := J_0^{(i)} \) to simplify notation. Let \( \mathbb{P}(J_0 = j) = \pi_j, j = 1, \ldots, p \) and \( \pi = (\pi_1, \ldots, \pi_p) \) denote the distribution vector of the shared initial state. The random variables

\[
X_i = \inf \{t > 0 : J_t^{(i)} = p + 1\}, \quad i = 1, \ldots, d,
\]

are then all univariate PH distributed. We say that the random vector \( X = (X_1, \ldots, X_d) \in \mathbb{R}_+^d \) has a multivariate phase-type distribution (mPH) if each marginal variable \( X_i, i = 1, 2, \ldots, d \) is given by (2.2) and pairwise dependence is defined by (2.1). We use the notation

\[
X \sim \text{mPH}(\pi, \mathcal{T}), \quad \text{with} \quad \mathcal{T} = \{T_1, \ldots, T_d\}.
\]

The joint cumulative distribution function of \( X \) is given by

\[
F_X(x) = \mathbb{P}(X_1 \leq x_1, X_2 \leq x_2, \ldots, X_d \leq x_d) = \sum_{j=1}^p \mathbb{P}(X_1 \leq x_1, X_2 \leq x_2, \ldots, X_d \leq x_d | J_0 = j) \mathbb{P}(J_0 = j) = \sum_{j=1}^p \pi_j \prod_{i=1}^d (1 - e_j^T \exp(T_i x_i)) e, \quad x \in \mathbb{R}_+^d.
\]
Furthermore, the survival function is
\[ S_X(x) = \mathbb{P}(X_1 > x_1, X_2 > x_2, \ldots, X_d > x_d) \]
\[ = \sum_{j=1}^{p} \pi_j \prod_{i=1}^{d} e_i^T \exp(T_i x_i) e, \]
and the probability density function is given by
\[ f_X(x) = \sum_{j=1}^{p} \pi_j \prod_{i=1}^{d} e_i^T \exp(T_i x_i) t_i. \]

For more details, cf. [7].

2.2. mIPH distributions. The particular focus in this paper will now be on an inhomogeneous extension of the mPH distribution (briefly mentioned in [7, Sec. 6.1]). When considering time-inhomogeneous Markov pure jump processes on the common state-space \( E \), it follows from Albrecher & Bladt [1] that the transition matrices are modified to
\[ P(s, t) = \prod_{s}^t (I + \Lambda(u) du) := I + \sum_{k=1}^{\infty} \int_s^t \int_s^u \cdots \int_s^u \Lambda(u_1) \cdots \Lambda(u_k) du_1 \cdots du_k, \]
with sub-intensity matrix
\[ \Lambda(t) = \begin{pmatrix} T(t) & t(t) \\ 0 & 0 \end{pmatrix} \in \mathbb{R}^{(p+1) \times (p+1)}, \quad t \geq 0. \]

The random variables \( Y_i = \inf\{ t > 0 : J_t^{(i)} = p + 1 \}, \; i = 1, \ldots, d \), then follow univariate inhomogeneous phase-type (IPH) distributions, cf. [1] for more details.

Here we focus on the particularly tractable case \( T_i(t) = \lambda_i(t) T \). A random vector \( Y = (X_1, \ldots, X_d) \) is said to have an inhomogeneous multivariate PH (mIPH) distribution if all marginals follow IPH distributions and the dependence structure is defined by (2.1). We write
\[ Y \sim \text{mIPH} (\pi, \mathcal{T}, \mathcal{L}), \quad \text{where} \quad \mathcal{T} = \{T_1, \ldots, T_d\}, \quad \mathcal{L} = \{\lambda_1, \ldots, \lambda_d\}. \]

With
\[ g_i^{-1}(y) := \int_0^y \lambda_i(u) du, \quad i = 1, \ldots, d, \]
the cumulative distribution function, survival function and density of \( X \) are given by
\[ F_Y(y) = \sum_{j=1}^{p} \pi_j \prod_{i=1}^{d} (1 - e_i^T \exp(T_i g_i^{-1}(y_i)) e), \quad y \in \mathbb{R}_+^d, \]
\[ S_Y(y) = \sum_{j=1}^{p} \pi_j \prod_{i=1}^{d} e_i^T \exp(T_i g_i^{-1}(y_i)) e, \quad y \in \mathbb{R}_+^d, \]
and
\[ f_Y(y) = \sum_{j=1}^{p} \pi_j \prod_{i=1}^{d} e_i^T \exp(T_i g_i^{-1}(y_i)) t_i \lambda_i(y_i), \quad y \in \mathbb{R}_+^d, \]
respectively. Note that one can view each IPH random variable as a transformation of a PH random variable (and correspondingly the absorption time of a time-transformed formerly time-homogenous Markov jump process), with \( X \sim \text{PH}(\pi, T) \) and \( g(X) \sim \text{IPH}(\pi, T, \lambda) \).

The construction of mIPH(\( \pi, T, L \)) allows different sub-intensity matrices and inhomogeneity functions for each marginal, as long as they share the same state-space. This leads to a considerable model flexibility. In particular, when compared to the homogeneous case, time-inhomogeneity allows for substantially smaller state-spaces for appropriate fits of data with potentially non-exponential tails (cf. [1]), and the mIPH class inherits this feature.

When we condition a mIPH distribution on one or more marginals, we obtain another mIPH distribution with a new initial distribution vector and smaller dimension: Let \( Y \sim \text{mIPH}(\pi, T, L) \) and condition on the value of \( Y_i, l \leq d \). The conditional density is

\[
f_{Y|Y_l}(y | y_l) = \sum_{j=1}^{p} \frac{\pi_j e_j^T \exp(T_l g_l^{-1}(y_l)) t_l \lambda_l(y_l)}{\pi \exp(T_l g_l^{-1}(y_l)) t_l \lambda_l(y_l)} \prod_{i \neq l} e_i^T \exp(T_i g_i^{-1}(y_i)) t_i \lambda_i(y_i).
\]

That is,

(2.3) \[
Y \mid Y_i = y_l \sim \text{mIPH}(\alpha, T \setminus T_l, L \setminus \lambda_l),
\]

with initial distribution vector

\[
\alpha = \left\{ \frac{\pi_j e_j^T \exp(T_l g_l^{-1}(y_l)) t_l \lambda_l(y_l)}{\pi \exp(T_l g_l^{-1}(y_l)) t_l \lambda_l(y_l)} \right\}_{j=1,\ldots,p}.
\]

The same reasoning can be applied to obtain

(2.4) \[
Y \mid Y_i \geq y_l \sim \text{mIPH}(\nu, T \setminus T_l, L \setminus \lambda_l),
\]

with

\[
\nu = \left\{ \frac{\pi_j e_j^T \exp(T_l g_l^{-1}(y_l)) e}{\pi \exp(T_l g_l^{-1}(y_l)) e} \right\}_{j=1,\ldots,p}.
\]

**Remark 2.1.** One might be tempted to argue that Assumption (2.1) necessarily leads to positive dependence of the resulting random variables (in our case lifetimes). However, sharing the initial state is not sufficient to obtain positive dependence, as the different intensity matrices may introduce counter-effects. For instance, after starting in the same state we could have a very small expected holding time and direct absorption for one marginal, while the second has to pass through the entire state space before absorption happens, leading to a very large survival time. This behaviour could very well be reversed when starting in another (but common) state. Consequently, certain combinations of individual intensity matrices may give rise to negative dependence as well.

### 3. Parameter estimation for right-censored data and covariate information

In the following we firstly introduce the components needed to estimate the parameters of mIPH distributions, when right-censored data is present. Secondly, we present how to estimate initial distribution vectors considering covariate information. Finally, we propose an adapted Expectation Maximisation algorithm, which we name ERMI algorithm.
3.1. EM algorithm for right-censored data. Taking inspiration from Asmussen et al. [6] and Olsson [21], we now derive conditional expectations needed in the EM algorithm for mPH distributions, where absorption times are allowed to be right-censored. Since the eventually targeted mPH distributions are transformed mPH distributions, after transformation of the data the E-Step and M-Step of the algorithm are the same as for the time-homogeneous case.

Let \( X = (X_1, \ldots, X_d) \) be the collection of random variables we are interested in. Let \( \mathbf{x} = (x_1^{(m)}, \ldots, x_d^{(m)}) \) be the observations of absorption times assumed to be generated from \( X \sim \text{mPH}(\pi, T) \), where \( x_i^{(m)} \in \mathbb{R}_+^n \) for \( i = 1, \ldots, d \). We assume that the censoring mechanism is independent of the size of the random variables. The marginals \( X_i^{(m)} = \min(x_i^{(m)}, R_i^{(m)}) \) follow \( \text{PH}(\pi, T_i) \) distributions, where \( R_i^{(m)} \) is a random censoring point for the \( m \)-th observation. The realisation of random right-censoring indicators can be found in \( \Delta = (\delta_1^{(m)}, \ldots, \delta_d^{(m)}) \), where elements \( \delta_i^{(m)} \in \mathbb{R}_+^n, i = 1, \ldots, d \), are equal to 1 if the absorption time \( x_i^{(m)} \) is fully observed and 0 if \( x_i^{(m)} \geq R_i^{(m)} \) is right-censored.

The sample \( X \) is associated to the latent sample paths \( \{J_t^{(i,m)}\}_{t \geq 0}, i = 1, \ldots, d, m = 1, \ldots, n \), which are not observed. To face this issue, we make the following definitions. Let

\[
B_k = \sum_{i=1}^d \sum_{m=1}^n 1\{J_0^{(i,m)} = k\}, \quad k = 1, \ldots, p,
\]

\[
N_{ks}^{(i)} = \sum_{m=1}^n \sum_{t \geq 0} 1\{J_s^{(i,m)} = k, J_t^{(i,m)} = s\}, \quad k, s = 1, \ldots, p, \quad i = 1, \ldots, d,
\]

\[
N_k^{(i)} = \sum_{m=1}^n \sum_{t \geq 0} 1\{J_t^{(i,m)} = k, J_t^{(i,m)} = p + 1\}, \quad k = 1, \ldots, p, \quad i = 1, \ldots, d,
\]

\[
Z_k^{(i)} = \sum_{m=1}^n \int_0^\infty 1\{J_t^{(i,m)} = k\} dt, \quad k = 1, \ldots, p, \quad i = 1, \ldots, d.
\]

\( B_k \) is the number of times marginal jump processes start in State \( k \), \( N_{ks}^{(i)} \) is the number of transitions from State \( k \) to \( s \) for jump process \( i \) and \( N_k^{(i)} \) is the number of absorptions from State \( k \) for jump process \( i \). Finally, \( Z_k^{(i)} \) is the time spent in state \( k \) prior to absorption of jump process \( i \). These statistics are not observable, but are sufficient to describe the dynamics of the underlying Markov process. Moreover, they are essential to construct an effective EM-like algorithm. Then, the completely observed likelihood can be expressed using the sufficient statistics defined above, as

\[
\mathcal{L}_c(\pi, T; \mathbf{x}) = \left( \prod_{k=1}^p \tau_k^{B_k} \right) \left( \prod_{i=1}^d \prod_{k=1}^p \prod_{s \neq k} t_{ks}^{N_{ks}^{(i)}} e^{-t_{ks}^{N_{ks}^{(i)}}} Z_k^{(i)} \right) \left( \prod_{k=1}^p t_k^{N_k^{(i)}} e^{-t_k^{N_k^{(i)}}} Z_k^{(i)} \right),
\]

which is seen to conveniently fall into the exponential family of distributions, and thus has explicit maximum likelihood estimators.

With these assumptions, the derivation of \( B_k, Z_k^{(i)}, N_{ks}^{(i)} \) and \( N_k^{(i)} \), for \( k, s = 1, \ldots, p \) and \( i = 1, \ldots, d \), is analogous to the fully uncensored case (see [7]). The only difference from
the fully observed case is that marginals may have right-censored absorption times. To see how this affects the expectation step of the EM algorithm, we give a detailed derivation of

\[ \mathbb{E}(B_k \mid X = x) = \sum_{i=1}^{d} \sum_{m=1}^{n} \mathbb{E}(1\{J_0^{(i,m)} = k\} \mid X = x) \]

\[ = d \times \sum_{m=1}^{n} \mathbb{P}(J_0^{(m)} = k \mid X = x) \]

\[ = d \times \sum_{m=1}^{n} \frac{\mathbb{P}(J_0^{(m)} = k) \mathbb{P}(X_j \in dx_j^{(m)} \mid X \geq x_i^{(m)} ; j \in i_{un}^{(m)}, l \in i_{rc}^{(m)} \mid J_0^{(m)} = k)}{\mathbb{P}(X_j \in dx_j^{(m)} \mid X \geq x_i^{(m)} ; j \in i_{un}^{(m)}, l \in i_{rc}^{(m)})} \]

\[ = d \times \sum_{m=1}^{n} \frac{\pi_k^{(m)} \prod_{j \in i_{un}^{(m)}} e_k^\top \exp(T_j x_j^{(m)}) t_j \prod_{l \in i_{rc}^{(m)}} e_l^\top \exp(T_l x_l^{(m)}) e_l}{\sum_{s=1}^{p} \sum_{j \in i_{un}^{(m)}} e_s^\top \exp(T_j x_j^{(m)}) t_j \prod_{l \in i_{rc}^{(m)}} e_s^\top \exp(T_l x_l^{(m)}) e_s}, \]

where we see a mix of marginal densities and survival functions appearing in both the numerator and denominator. This expectation can also be expressed, using the \( \Delta \) notation, as

\[ \mathbb{E}(B_k \mid X = x) = d \times \sum_{m=1}^{n} \frac{\pi_k^{(m)} \prod_{i=1}^{d} e_i^\top \exp(T_j x_j^{(m)}) t_j \prod_{l} e_l^\top \exp(T_l x_l^{(m)}) e_l}{\sum_{i=1}^{p} \prod_{j \neq i} e_j^\top \exp(T_j x_j^{(m)}) t_j \prod_{l} e_l^\top \exp(T_l x_l^{(m)}) e_l} \]

and we shall use this style in the following. The other needed conditional expectations are obtained in a similar way, reading

\[ \mathbb{E}(Z_k^{(i)} \mid X = x) = \sum_{m=1}^{n} \sum_{j=1}^{p} \pi_j^{(m)} \prod_{l \neq i} e_l^\top \exp(T_j x_j^{(m)}) t_j \prod_{l} e_l^\top \exp(T_l x_l^{(m)}) e_l \times \bigg[ e_k^\top \int_0^{x_i^{(m)}} \exp(T_i x_i^{(m)} - t) t_i e_j^\top \exp(T_j t) dt \bigg]^{\delta_i^{(m)}} \bigg[ e_k^\top \int_0^{x_i^{(m)} - t} \exp(T_i x_i^{(m)} - t) e_j^\top \exp(T_j t) dt \bigg]^{1 - \delta_i^{(m)}} \]

\[ \mathbb{E}(N_k^{(i)} \mid X = x) = t_{ks}^{(i)} \times \sum_{m=1}^{n} \sum_{j=1}^{p} \pi_j^{(m)} \prod_{l \neq i} e_l^\top \exp(T_j x_j^{(m)}) t_j \prod_{l} e_l^\top \exp(T_l x_l^{(m)}) e_l \times \bigg[ e_k^\top \int_0^{x_i^{(m)} - t} \exp(T_i x_i^{(m)} - t) e_j^\top \exp(T_j t) dt \bigg]^{\delta_i^{(m)}} \bigg[ e_k^\top \int_0^{x_i^{(m)} - t} \exp(T_i x_i^{(m)} - t) e_j^\top \exp(T_j t) dt \bigg]^{1 - \delta_i^{(m)}} \]
\[
\begin{align*}
&= \left[e_s \int_0^{x_i^{(m)}} \exp\left(T_i(x_i^{(m)} - t)\right) t_i e_j^T \exp(T_i t) dt e_k\right] \delta_i^{(m)} \\
&\times \left[e_s \int_0^{x_i^{(m)}} \exp\left(T_i(x_i^{(m)} - t)\right) e e_j^T \exp(T_i t) dt e_k\right]^{1-\delta_i^{(m)}},
\end{align*}
\]
and finally
\[
E(N_k^{(i)} \mid X = x) = t_k^{(i)} \times \sum_{m=1}^n \sum_{j=1}^p \pi_j^{(m)} e_j^T \exp(T_i x_i^{(m)}) e_k \delta_i^{(m)} \times \\
\times \frac{\prod_{l \neq i} \left(e_j^T \exp\left(T_i x_i^{(m)}\right) t_l\right) \delta_i^{(m)} \left(e_j^T \exp\left(T_i x_i^{(m)}\right) e\right)^{1-\delta_i^{(m)}}}{\sum_{j=1}^p \pi_j^{(m)} \prod_{i=1}^d \left(e_j^T \exp\left(T_i x_i^{(m)}\right) t_i\right) \delta_i^{(m)} \left(e_j^T \exp\left(T_i x_i^{(m)}\right) e\right)^{1-\delta_i^{(m)}}}.
\]

3.2. Initial distribution vectors. Adapting an idea developed in [9], we apply the regression component to the initial distribution, i.e. we estimate a ‘personalised’ initial distribution vector as a function of covariates, which increases the flexibility of the model. To that end, we use multinomial logistic regressions, where we consider the initial probabilities as response variables that depend on covariate information found in \(A^{(m)^T} \in \mathbb{R}^q\), with \(g\) being the number of explanatory variables, \(m = 1, \ldots, n\), and regression coefficients in \(\gamma \in \mathbb{R}^{p \times g}\). Concretely, the initial distribution probabilities are then given as

\[
\pi_k^{(m)} = \frac{\exp\left(A^{(m)^T} \gamma_k\right)}{\sum_{j=1}^p \exp\left(A^{(m)^T} \gamma_j\right)},
\]

with \(\gamma_k \in \mathbb{R}^g\) for \(k = 1, \ldots, p\).

In every iteration of the expectation-maximisation (EM) algorithm to be described later, we use the conditional expectation of the number of times that the underlying process starts in a specific state as weights for the regression coefficients in \(\gamma\). Let us consider the information carried by \(E(B_k^{(m)} \mid X = x)\) separately. For a row of observations \(m\), the expected number of times that the marginal jump processes start in state \(k\) is

\[
E(B_k^{(m)} \mid X = x) = d \times \frac{\pi_k^{(m)} \prod_{i=1}^d \left(e_k^T \exp\left(T_i x_i^{(m)}\right) t_i\right) \delta_i^{(m)} \left(e_k^T \exp\left(T_i x_i^{(m)}\right) e\right)^{1-\delta_i^{(m)}}}{\sum_{j=1}^p \pi_j^{(m)} \prod_{i=1}^d \left(e_j^T \exp\left(T_i x_i^{(m)}\right) t_i\right) \delta_i^{(m)} \left(e_j^T \exp\left(T_i x_i^{(m)}\right) e\right)^{1-\delta_i^{(m)}}},
\]

for \(k = 1, \ldots, p\). We then solve the optimisation problem

\[
\hat{\gamma} = \arg\max_{\gamma} \sum_{m=1}^n \sum_{k=1}^p E(B_k^{(m)} \mid X = x) \log(\pi_k^{(m)} (A^{(m)}; \gamma))
\]

and set

\[
\hat{\pi}_k^{(m)} = \pi_k^{(m)} (A^{(m)}; \hat{\gamma}) = \frac{\exp\left(A^{(m)^T} \gamma_k\right)}{\sum_{j=1}^p \exp\left(A^{(m)^T} \gamma_j\right)}
\]

(3.2)
in every iteration. The initial distribution hence depends on covariate information. Recall that all marginal processes \( \{ J_t^{(i)} \}_{t \geq 0} \) are assumed to start in the same state (drawn from the initial distribution with probabilities \( (3.2) \)), but afterwards transit independently to other states according to their specific sub-intensity matrices (and the latter do not depend on covariate information).

3.3. ERMI algorithm. Consider now a multivariate sample of right-censored absorption times \( \mathbf{y} = (y_{1}^{(m)}, \ldots, y_{d}^{(m)}) \), which we assume to originate from \( Y^{(m)} \sim \text{mIPH}(\pi^{(m)}, \mathcal{T}, \mathcal{L}) \). The associated inhomogeneity functions depend on parameters \( \beta_{i}, \ i = 1, \ldots, d \), and the right-censoring indicators are collected in \( \Delta \). The resulting EM algorithm with covariate information is depicted in Algorithm 1. As in Albrecher et al. [4], we firstly take care of time-inhomogeneity. Using the relation \( g_{i}^{-1}(y_{i}^{(m)}) = \int_{0}^{y_{i}^{(m)}} \lambda_{i}(u; \beta_{i}) du, \ i = 1, \ldots, d \), we obtain a time-homogeneous random sample \( \left( x_{1}^{(m)}, \ldots, x_{d}^{(m)} \right) \), for which we know how to evaluate conditional expectations of sufficient statistics (E step). Using these expectations (as given above), we estimate the marginal sub-intensity matrices (M step), while the initial distribution vectors are predicted by multinomial logistic regressions (R step). Once we have estimated both, we need to find optimal inhomogeneity parameters \( \beta_{i}, \ i = 1, \ldots, d \), that maximise the joint likelihood of the time-inhomogeneous sample (I step). Concretely, we solve

\[
\hat{\beta} = \arg \max_{\beta} \sum_{m=1}^{n} \log \left( \sum_{j=1}^{p} \pi_{j}^{(m)} \prod_{i=1}^{d} \left( \mathbf{e}_{j}^{T} \exp(\mathbf{T}_i x_{i}^{(m)}) \mathbf{i}_i \lambda_{i}(y_{i}^{(m)}, \beta_{i}) \right)^{\delta_{i}^{(m)}} \left( \mathbf{e}_{j}^{T} \exp(\mathbf{T}_i x_{i}^{(m)}) \mathbf{e} \right)^{1-\delta_{i}^{(m)}} \right),
\]

where \( x_{i}^{(m)} = g_{i}^{-1}(y_{i}^{(m)}) \). We repeat the procedure until a stopping rule is satisfied, and finally obtain the estimated distribution \( \text{mIPH}(\hat{\pi}, \hat{\mathcal{T}}, \hat{\mathcal{L}}) \). Here \( \hat{\pi} \) is a matrix, where each row is a distribution vector \( \hat{\pi}^{(m)} \), which is shared by marginals with the same covariates.

In contrast to copula-based methods, this approach does not separate the estimation of marginals and multivariate parameters. This may be considered preferable as the implied multivariate distribution has a natural and causal interpretation and is intimately connected to the marginal behaviour of the risks, whereas choosing a concrete copula family on given (and possibly already fitted) marginal risks is often a somewhat more arbitrary choice for the modelling of multivariate phenomena.

4. Modelling joint excess lifetimes of couples

In this section we present an application of Algorithm 1 to the well-known data set of joint lives used in [15]. In addition to survival times, this data set provides information on individuals’ ages at issue of an insurance policy. This leads to left-truncated data in this particular case, and one might indeed consider the different entry ages with a left-truncated likelihood in the estimation process, which is, however, quite inefficient. Instead, we propose here to use entry age as a covariate information and use multinomial logistic regression to deal with the different ages at issue. Entry ages were also considered as relevant factors for the dependence modelling in [22]. Initial distribution vectors obtained via regression will then incorporate the fact that an old couple is expected to survive less long than a
young one, and that the bereavement effect may be different for different age dynamics in a couple. In PH terms, when using an acyclical distribution, the older the couple the larger the starting probabilities should be for states closer to the absorbing state, so that fewer states will be visited until absorption. Passing through fewer states translates into less time spent in the state-space before exiting, which results in smaller remaining lifetimes.

**Algorithm 1** Adapted expectation maximisation (ERMI) algorithm for mIPH distributions

**Input:** Observed absorption times $y \in \mathbb{R}_+^{n \times d}$, right-censoring indicators $\Delta \in \mathbb{R}^{n \times d}$ and arbitrary initial parameters for $(\pi, T, L)$.

1) For each marginal, transform the data in $x_i^{(m)} = g_i^{-1}(y_i^{(m)}; \beta_i)$, $i = 1, 2, \ldots, d$ and $m = 1, 2, \ldots, n$

2) **E-step:** Calculate

$$
\mathbb{E}(B_k^{(m)} \mid Y = y) \quad k = 1, \ldots, p, \quad m = 1, \ldots, n
$$

$$
\mathbb{E}(Z_k^{(i)} \mid Y = y) \quad k = 1, \ldots, p, \quad i = 1, \ldots, d
$$

$$
\mathbb{E}(N_{ks}^{(i)} \mid Y = y) \quad k, s = 1, \ldots, p, \quad i = 1, \ldots, d
$$

$$
\mathbb{E}(N_k^{(i)} \mid Y = y) \quad k = 1, \ldots, p, \quad i = 1, \ldots, d
$$

3) **R-step:** Perform a multinomial regression with weights given by $\mathbb{E}(B_k^{(m)} \mid Y = y)$ and predict $\hat{z}^{(m)}_k$ for $k = 1, \ldots, p$ and $m = 1, \ldots, n$. 

4) **M-step:** Let

$$
\hat{t}^{(i)}_{ks} = \frac{\mathbb{E}(N_{ks}^{(i)} \mid Y = y)}{\mathbb{E}(Z_k^{(i)} \mid Y = y)}, \quad k, s = 1, \ldots, p, \quad i = 1, \ldots, d
$$

$$
\hat{t}^{(i)}_k = \frac{\mathbb{E}(N_k^{(i)} \mid Y = y)}{\mathbb{E}(Z_k^{(i)} \mid Y = y)} \quad k = 1, \ldots, p, \quad i = 1, \ldots, d
$$

$$
\hat{t}^{(i)}_{kk} = - \sum_{s \neq k} \hat{t}^{(i)}_{ks} - \hat{t}^{(i)}_k \quad k, s = 1, \ldots, p, \quad i = 1, \ldots, d
$$

Let $\hat{\pi} = (\hat{\pi}_1^{(m)}, \ldots, \hat{\pi}_p^{(m)})$, $\hat{T}_i = (\hat{t}^{(i)}_{ks})_{k, s = 1, \ldots, p}$, and $\hat{t}_i = \begin{pmatrix} \hat{t}^{(i)}_1 \\ \vdots \\ \hat{t}^{(i)}_p \end{pmatrix}$.

5) **I-step:** Compute

$$
\hat{\beta} = \arg \max_{\beta} \sum_{m=1}^n \log \left( f_Y(y^{(m)}; \hat{\pi}, \hat{T}, \beta, \Delta) \right)
$$

$$
= \arg \max_{\beta} \sum_{m=1}^n \log \left( \sum_{j=1}^p \hat{\pi}_j^{(m)} \prod_{i=1}^d \left( e_j^T \exp(\hat{T}_i x_i^{(m)} \hat{t}_i) \lambda_i(y_i^{(m)}; \beta_i) \right) \right)
$$

6) **Assign** $\pi = \hat{\pi}$, $T_i = \hat{T}_i$ and $\beta_i = \hat{\beta}_i$ then repeat from Step 1 until a stopping rule is satisfied.

**Output:** Fitted representations $(\hat{\pi}, \hat{T}, \hat{L})$, for $m = 1, \ldots, n$.  


4.1. Description of the data set. The data set at hand provides information about
14947 insurance products on joint lives, which were observed from December 29, 1988 until
December 31, 1993. We consider January 1, 1994 as the right censoring limit. For the
purpose of this paper, we only consider birthdays, sexes (and potential death dates) of
policyholders, given that we are only interested in mortality, i.e. we do not make use of the
monetary details of each contract.

After removing same-sex couples and multiple entries (due to several contracts of the same
couple), we compute the remaining lifetime that any person lived from the start of the
observation period until the right-censoring date 01.01.1994, given that they are at least
40 years old at the issue of the policy. Note that the terms “remaining” and “excess” are
used interchangeably in the following. Doing so leads to 8834 different joint excess survival
times, with 155 cases where both individuals died, 1057 where only one individual died and
7622 where neither died. Consequently, less than 2% of joint remaining survival times are
fully observed. Among the couples where only one person died, in 820 of them this was
the man, and in the complementary 237 cases the woman died. Hereafter, we refer to the
start of the observation period as the “issue of the policy”, although the actual issue date
may be later than 29.12.1988.

To prepare the data for the multinomial regression, we construct the covariate matrix
\[ A = \begin{pmatrix} 1 & \text{age}_{y_1} & \text{age}_{y_2} & \text{interact} \end{pmatrix}, \quad A \in \mathbb{R}^{n \times 4} \]

The column vector \( \text{age}_{y_1} \) is the collection of all ages of men, at issue of a policy, while \( \text{age}_{y_2} \) contains all ages of women. We also
consider an interaction term in \( \text{interact} \), which gathers element-wise multiplication of ages
in a couple. Finally, to perform multinomial regressions via neural networks (R package
\textit{nnet}), we divide the data by 100, such that an absorption time of 0.01 given by estimated
distributions actually corresponds to 1 year.

4.2. Fitting the mIPH distribution: Marginal behaviour. We assume that the re-
maining lifetimes in a couple, after issue of an insurance policy, follow mIPH distributions.
We use information previously discussed as covariates to link starting probabilities to ages
of individuals in couples, in order to reflect different ageing dynamics in our model.

Let \( Y_i^{(m)} = g_i(X_i^{(m)}) = \log(\beta_i X_i^{(m)} + 1)/\beta_i \), be the IPH distributed marginal remaining
lifetimes, with \( X_i^{(m)} = (\exp(\beta_i Y_i^{(m)}) - 1) / \beta_i \sim \text{PH}(\pi^{(m)}, T_i) \) and \( \beta_i > 0 \), where \( i = 1 \) corresponds to men and \( i = 2 \) to women. Then, the distribution with covariate information
we work with is given by marginal Matrix-Gompertz distributions, and we consider general
Coxian sub-intensity matrices \( T_i \) of dimension \( p = 10 \) (cf. [2]). The order \( p \) was found
by fitting models with various respective choices, until a satisfactory approximation of
marginals was reached. Finding the optimal dimension \( p \) is still an open problem, and the
literature on solving the identifiability issue of PH distributions is quite narrow (see for
instance [14] and [3]).

According to the dependence structure defined in (2.1), after both underlying processes
\( \{ J_t^{(1)} \}_{t \geq 0} \) and \( \{ J_t^{(2)} \}_{t \geq 0} \) start in the same state they evolve independently until absorption.
With a general Coxian sub-intensity matrix, each marginal jump process is only allowed
to transit to the next state or directly to the absorption state. This stochastic structure
has a nice interpretation in terms of ageing. Indeed, we can think of forward transitions
as natural ageing steps, given that each time the process jumps to a certain state, the
time of absorption gets closer. Moreover, premature exits can be interpreted as deaths due to causes not related to ageing. Indeed, given that exit rates are positive in each state, the absorption of a process may be caused by a transition to State $p + 1$ from a state smaller than $p$. Finally, granting the underlying processes to start in different states allows heterogeneity of health statuses for individuals of the same age (this philosophy was already underlying the construction in [18], but with the present inhomogeneity, much fewer states are needed to describe the data satisfactorily).

Algorithm 1 is now applied for 1000 iterations. In principle, this estimation procedure provides $n = 8834$ different initial distribution vectors, one for each couple depending on the ages at issue. Figure 4.1 depicts the age combinations in the data, with a majority of couples having a small age difference at policy issue. For illustration purposes, we depict below the estimated initial distributions for four different age combinations (age man, age woman): (63,63), (68,63), (63,68) and (73,63), which were chosen arbitrarily, but to represent different ageing dynamics at issue of the policy. Let $Y^c = (Y_1^c, Y_2^c) \sim \text{mIPH}(\hat{\pi}^c, \hat{T}, \hat{L})$ denote the bivariate distribution of excess lifetimes for these four couples, where $c = 1, 2, 3, 4$, $\mathcal{T} = \{T_1, T_2\}$ and $\mathcal{L} = \{\lambda_1(\cdot, \hat{\beta}_1), \lambda_2(\cdot, \hat{\beta}_2)\}$. The common estimated

![Ages of couples](image.png)

**Figure 4.1.** Ages at issue of policies, for all couples. $x$ and $y$ correspond to age$_{y_1}$ and age$_{y_2}$, respectively.
sex-specific sub-intensity matrices are

\( \hat{T}_1 = \begin{pmatrix}
-0.049 & 1.7 \times 10^7 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & -3.662 & 2.877 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & -1.8 \times 10^7 & 1.8 \times 10^7 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -1.9 \times 10^4 & 1.9 \times 10^4 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & -0.611 & 0.611 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -0.002 & 0.002 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -1.852 & 1.099 \\
\end{pmatrix} \) 

(4.1)

for men and

\( \hat{T}_2 = \begin{pmatrix}
-0.196 & 0.196 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & -0.291 & 0.291 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & -0.763 & 0.763 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -2.8 \times 10^8 & 2.8 \times 10^8 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & -0.001 & 0.001 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & -0.003 & 0.003 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -3.182 & 1.165 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -0.008 & 2.3 \times 10^{10} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -3 \times 10^6 \\
\end{pmatrix} \) 

(4.2)

for women. The optimal inhomogeneity parameters are \( \hat{\beta}_1 = 43.101 \) and \( \hat{\beta}_2 = 47.474 \), and Table 4.1 presents the estimated coefficients of the last multinomial regression performed in Algorithm 1. Except for States 8 and 9, all coefficients in \( \hat{\gamma} \) are significant. Note that having non-significant coefficients for States 8 and 9 does not necessarily indicate that the state space is too large. One has to separate the PH interpretation of the state space from the regression framework. Table 4.1 is claiming that the covariates used in the regression are not significant in explaining starting probabilities of States 8 and 9. Nevertheless, both states have their role in the description of random variables we are interested in.

Initial distribution vector estimates for these four couples are

\( \hat{\pi}_1 = \begin{pmatrix}
0.0526 & 0.0734 & 0.0448 & 0.0886 & 0.4065 & 0.0330 & 0.0326 & 0.0569 & 0.1077 & 0.1039 \\
\end{pmatrix} \),

\( \hat{\pi}_2 = \begin{pmatrix}
0.0356 & 0.0313 & 0.0297 & 0.0398 & 0.2805 & 0.0476 & 0.0396 & 0.0384 & 0.2472 & 0.2102 \\
\end{pmatrix} \),

\( \hat{\pi}_3 = \begin{pmatrix}
0.0285 & 0.0242 & 0.0114 & 0.1625 & 0.4399 & 0.0419 & 0.0304 & 0.1282 & 0.0819 & 0.0510 \\
\end{pmatrix} \),

\( \hat{\pi}_4 = \begin{pmatrix}
0.0172 & 0.0095 & 0.0140 & 0.0127 & 0.1378 & 0.0489 & 0.0343 & 0.0184 & 0.4041 & 0.3030 \\
\end{pmatrix} \).

At first glance, it might seem odd that survival times of spouses with large age difference start in the same state of the distribution, but personalised starting probabilities and sex-specific transition intensities account for this. For example, consider Couple 4. If both excess survival times start in State 1, we see that the man’s underlying jump process is much more likely to reach the absorbing state directly from State 1, while the woman’s will
Table 4.1. Coefficients of multinomial regression with associated standard errors in brackets. For a two sided statistical test symbols *** , ** and * correspond to significance levels of 1%, 5% and 10% respectively.

| p  | Intercept   | age\_y1 | age\_y2 | age\_y1 \cdot age\_y2 |
|----|-------------|---------|---------|------------------------|
| 2  | -20.963***  | 43.733*** | 43.021*** | -84.049***             |
|    | (7.157)     | (11.238) | (12.400) | (19.311)               |
| 3  | 24.826***   | -24.630** | -39.256*** | 38.453**               |
|    | (6.677)     | (10.476) | (11.639) | (18.073)               |
| 4  | -51.036***  | 57.442*** | 90.062*** | -104.233***            |
|    | (9.894)     | (15.348) | (15.820) | (24.374)               |
| 5  | -42.469***  | 56.804*** | 70.273*** | -89.556***             |
|    | (6.873)     | (10.638) | (11.443) | (17.559)               |
| 6  | 14.850*     | -41.377*** | -39.438*** | 89.687***             |
|    | (8.004)     | (12.150) | (12.824) | (19.317)               |
| 7  | 54.157***   | -97.618*** | -98.445*** | 173.553***            |
|    | (6.617)     | (10.263) | (11.010) | (16.817)               |
| 8  | -14.363     | -5.608   | 22.990   | 8.794                  |
|    | (9.419)     | (14.387) | (14.885) | (22.584)               |
| 9  | -11.589     | 12.732   | -4.892   | 18.559                 |
|    | (7.224)     | (11.046) | (11.889) | (18.050)               |
| 10 | 21.474***   | -31.068*** | -54.907*** | 84.080***             |
|    | (6.504)     | (10.054) | (10.892) | (16.670)               |

at least advance to State 7 before absorption becomes possible. Thus, marginal intensities mixed with age-dependent initial distribution vectors compensate the initialisation in a shared state. In Figure 4.2 we depict the resulting marginal densities of the fitted remaining lifetime distributions for each of the four couples. As expected, the densities for women (solid black lines) allocate more mass to larger values than the male counterpart, and for older individuals there is more probability mass for shorter survival times. Comparing Couples 1 and 4, we see that the density of the 63-year-old man has a major mode at \( y_1 = 22 \), while for the 73-year-old man, the major mode is at \( y_1 = 17 \). Note that despite the fact that the women in Couples 1 and 4 are of comparable age, their densities have substantially different modes. This is due to the fact that the estimation of the marginal distributions is not separated from the estimation of the joint distributions, and the age of their spouse at the time of policy issue evidently plays an important role for the distribution of the remaining lifetime, seen at the time of policy issue.
Figure 4.2. Marginal densities of remaining life times (in years).

The multimodality we observe in all marginal densities may be due to having different cohorts in the data. We decided not to manipulate the data set further, in order to avoid restricting our analysis to specific couples. Although spouses with small age difference can be thought of as belonging to the same cohort, we would also need to restrain the ages at issue to instances where enough data points are available for a meaningful estimation procedure (in particular uncensored data points). Doing so would lead to analysing only couples where both spouses are aged around 65 years old.

To assess the precision of our estimated marginals $Y_{ic} \sim \text{IPH}(\hat{\pi}, \hat{T}, \hat{\beta})$, $i = 1, 2$ and $c = 1, 2, 3, 4$, we use the conditional Kaplan-Meier (K-M in the following) estimator, also known as Beran estimator. For a sample $X_1, X_2, \ldots, X_n$ and covariate matrix $A$, the conditional K-M estimator we use is

$$
\hat{P}(X \leq t \mid A = a) = \hat{F}_X(t \mid a) = 1 - \prod_{i: X_{ic} \leq t} \left( 1 - \frac{\delta_{i:n} K \frac{a - A_{i:n}}{b_n}}{\sum_{j=1}^n K \frac{a - A_{j:n}}{b_n}} \right),
$$

(4.3)
where \( X_{i:n} \) are order statistics of the sample, \( \delta_{i:n} \) the respective right-censoring indicators, \( K(\cdot) \) is a kernel function and \( b_n \) is a band sequence. In our instance, the kernel function is a multivariate Gaussian density and \( b_n = 0.001 \). For more details on the conditional K-M estimator we refer the reader to Dabrowska [12]. Figures 4.3 and 4.4 compare the survival probabilities obtained by the conditional K-M estimators with the one of the fitted distributions. One sees that in all cases the fit is in fact quite satisfactory.

4.3. Joint behaviour. Let us now consider the resulting bivariate densities. In Figure 4.5 we find the bivariate densities for the four specified couples. The joint density of Couple 1 shows that large differences in their survival times are quite unlikely (the vast majority of the joint mass being located close the identity line). Also, the most likely survival times are close to 23 years. There is also a considerable probability mass above the identity line, where the woman survives longer than the man. For instance, we have \( \bar{F}_{Y_1}(12, 30) = 32\% \) while \( \bar{F}_{Y_1}(30, 12) = 11.79\% \). For Couple 2 the situation is different (top right panel of Figure 4.5): with the man being already 68 years and the woman being 63 years old, the remaining lifetimes are shorter, with the major mode of the joint distribution being located near \((y_1, y_2) = (23, 24)\), the second largest close to \((y_1, y_2) = (17, 35)\) and the next ones in the neighbourhood of \((y_1, y_2) = (17, 19)\) and \((y_1, y_2) = (9, 19)\), respectively. There is now a much higher probability for the husband to die sooner.

The joint density for Couple 3 resembles the one of Couple 1, with survival times beyond 40 years being more unlikely. Despite the man being the same age as the man in Couple 1, there is a larger probability for the couple to have survival times close to \((y_1, y_2) = (29, 45)\) than for Couple 1. Finally, the joint density of Couple 4 is close to the one of Couple 2. The spike around \((y_1, y_2) = (17, 35)\) is more pronounced than the analogue of Couple 2, while the spike close to \((y_1, y_2) = (23, 24)\) is less important than its counterpart in Couple 2.

One may be tempted to conclude from these four distributions that for the same age, having a younger partner leads to longer survival times, which would signal that the bereavement effect is weaker when spouses have larger differences in age at issue of a policy.

4.4. Dependence measures. Let us now explore some dependence measures for these four exemplary couples. In addition to Kendall’s tau and Spearman’s rho, we also consider three measures of time-dependent association, which were analysed in Luciano et al. [19]. The mIPH distributions we consider all have the same copula as the corresponding mPH distributions with equal representation, since matrix-Gompertz distributions are monotone increasing transformations of PH distributions. At the same time, for the mPH class we have explicit expressions for Kendall’s tau and Spearman’s rho. The pairwise Kendall’s tau of marginals \( X_k \) and \( X_l \) is

\[
\tau_{X_k, X_l} = 4 \sum_{i=1}^{p} \sum_{j=1}^{p} \pi_i \pi_j (e_i^T \otimes e_j^T)[-T_k \oplus T_k]^{-1}(e \otimes t_k)(e_i^T \otimes e_j^T)[-T_l \oplus T_l]^{-1}(e \otimes t_l) - 1,
\]

while Spearman’s rank correlation is given as

\[
\rho^S_{X_k, X_l} = 12 \sum_{j=1}^{p} \pi_j \left(1 - (\pi \otimes e_j^T)[-T_k \oplus T_k]^{-1}(e \otimes t_k)\right) \left(1 - (\pi \otimes e_j^T)[-T_l \oplus T_l]^{-1}(e \otimes T_l)\right) - 3,
\]
Figure 4.3. Conditional K-M estimators vs the fitted distribution, Couples 1 and 2.

cf. [7]. Calculating these quantities for the four specified couples, one obtains

\[ \tau_{Y_1^1,Y_2^1} = 0.3104, \quad \tau_{Y_1^2,Y_2^2} = 0.2562, \quad \tau_{Y_1^3,Y_2^3} = 0.4367, \quad \tau_{Y_1^4,Y_2^4} = 0.2139, \]
\[ \rho_{S,Y_1^1,Y_2^1} = 0.4526, \quad \rho_{S,Y_1^2,Y_2^2} = 0.3938, \quad \rho_{S,Y_1^3,Y_2^3} = 0.6144, \quad \rho_{S,Y_1^4,Y_2^4} = 0.3381. \]
All couples manifest positive concordance, which on top of Figure 4.5 is additional evidence that the lifetimes of individuals in a couple are correlated. We find the strongest concordance in couples where women are older than their husbands. Concretely, Couple 3 has the highest Kendall’s tau and Spearman’s rho values, followed by Couple 1. Couple 2 and
Figure 4.5. Contour plots of the bivariate lifetime densities for the four couples

Couple 4 have lower, and similar, corresponding values.

As a first measure of time-dependent association, we consider in Figure 4.6

\[ \Psi_1(y_1, y_2) = \frac{S(y_1, y_2)}{S_{Y_1}(y_1)S_{Y_2}(y_2)}. \]

Most of the resulting values are greater than 1, indicating positive dependence. However, for values of \( y_2 \) close to 30, Couples 1, 2 and 3 exhibit \( \Psi_1(y_1, y_2) < 1 \). This suggests negative dependence for remaining lifetimes when women survive at least 30 years and men at least
20 years. One can see that, roughly, after values \( y_1 = 29 \) and \( y_2 = 39 \), the ratios \( \Psi_1(y_1, y_2) \) remain constant. This happens since for very large survival times \( y_1, y_2 \), marginal survival probabilities change very little, and this change is absorbed by \( S(y_1, y_2) \).

Next, we depict in Figure 4.7 the measures

\[
\Psi_1^1(0, y_2) = \frac{\mathbb{E}(Y_1 | Y_2 \geq y_2)}{\mathbb{E}(Y_1)}, \\
\Psi_2^2(y_1, 0) = \frac{\mathbb{E}(Y_2 | Y_1 \geq y_1)}{\mathbb{E}(Y_2)}
\]

for all four couples, which give the relative change of conditional expectations of spouses’ excess lifetimes, given that the partner survives at least \( y_2(y_1) \) years. We see that the latter increase throughout with \( y_2(y_1) \). In general, the ratios \( \Psi_i^*(\cdot, \cdot), \ i = 1, 2, \) are close in value when \( y_1, y_2 \leq 20 \), meaning that the survival of a spouse has a similar effect on the remaining lifetime of the partner for the first 20 years. After that, the relative lifetime improvement increases much faster for women, i.e. their expected lifetime improvement is
then more sensitive to the survival of the partner than vice versa. Like in Figure 4.6, both ratios remain constant after spouses’ survival times of $y_1 = 29$ for women and $y_2 = 39$ for men.

The last measure of time-dependent association we consider here is the cross-ratio

$$CR(y_1, y_2) = S(y_1, y_2) \frac{\frac{d^2}{dy_1 dy_2}S(y_1, y_2)}{\frac{d}{dy_1}S_{Y_1}(y_1) \frac{d}{dy_2}S_{Y_2}(y_2)}$$

originally introduced by Clayton [11], which gives the relative increase of the force of mortality of an individual immediately after death of the partner. The quantity relevant in our model is $CR(u, u)$, and Figure 4.8 depicts the resulting figures for our model. In Luciano et al. [19], the resulting curves were monotone increasing in $u$, as a result of the imposed copula assumption on the joint lifetimes. In contrast, in the present setup these curves are not monotone increasing in $u$. One may interpret that in the present approach the a priori dependence assumptions are less specified, and the data have a stronger impact on the resulting shape of $CR(u, u)$ than in a specified copula model, where the data merely influence the value of the dependence parameter. One can see from Figure 4.8 that the cross-ratios exceed 1 for $u \leq 29$, so the survivor’s force of mortality is increased immediately after the death of the spouse, showing a bereavement effect (or broken-heart syndrome), but not a monotone one (with the magnitude varying across age combinations of the couple).
This bereavement effect somewhat seems to disappear for survival times beyond 29 years, and for this reason we do not plot values \( u > 29 \), but in that range survival probabilities are very low anyway, and there are very few data points in that range to draw strong conclusions.

Eventually, like in many other situations, it may depend on the number of available data points whether one prefers to have a flexible dependence structure in the fitting or a pre-specified copula family with possibly attractive stylized features, especially for extrapolated conclusions in regions with few data points. In this discussion, one may still appreciate the immediate causal interpretation of the mIPH model in terms of a common ageing mechanism.

4.5. **Life expectancies.** Let us finally also use the model fit to get some insight into expected remaining lifetimes in the couple. Using Property (2.4), we are able to derive expected survival times for an individual, conditional on the survival time of their partner. Moreover, using optimal regression coefficients found by Algorithm 1 (Table 4.1) we can study how marginal expectations vary with ages in a couple. Letting the man’s and woman’s age vary from age 60 to 100, we get for each age combination a distinct mIPH distribution for the random vector \( \mathbf{Y} \). Given these distributions, we summarise in Figure 4.9 how the expected remaining lifetime at issue changes as a function of the male’s and female’s age.
at that point in time. For both man and woman, the marginal expected survival times
decrease when both individuals in the couple grow older. For any specific age, both men
and women have larger marginal expectations as their spouses become younger. That
marginal expectation varies more for women, as one can see from the steepness and range
of the women’s curve in Figure 4.9. Another way to interpret this is that men’s expected
survival times are affected less by the age of their partner, compared to women.

![Figure 4.9](image-url)

**Figure 4.9.** Marginal expected excess survival times as a function of men’s
age $y_1$ and women’s $y_2$ at issue.

![Figure 4.10](image-url)

**Figure 4.10.** Marginal expected excess survival times, conditional on
spouse survival during 10 years.
Besides age, conditioning also on the survival time of the spouse affects the initial distribution vector, leading to different expected values. Figures 4.10 and 4.11 present marginal expected survival times, conditional on a spouse survival of at least 10 and 15 years counted from issue of the policy, respectively. The respective change in the men’s remaining life expectation is notable by mere visual comparison, whereas for women it is less pronounced. From Figure 4.10 we see that the expectation increases for almost all ages, compared with Figure 4.9. For men, one notices that the shape of the curve is changed for ages $65 \leq y_1 \leq 75$. Moreover, for older ages $y_1$ and $y_2$ the curve is now slightly steeper than before. In the women’s case, marginal expectations for a woman aged 60 or 100 with husband aged 60 are now equivalent, and no other major change can be easily observed. The marginal expectation for men whose spouses survive at least 15 years are very much different from their unconditional counterparts. Inspecting Figure 4.11, one can see a sizeable change of the curve. Men with spouses of age $y_2 \in (80, 100)$ are now expected to survive much longer than before, while once again for women we only have a rather minor twist of the curve. In all figures we see that the women’s curves do not show major change. Still, they suggest that women are more sensitive to both age and survival of their partner.

5. Conclusion

In this paper, we introduce the mIPH class, study some of its properties and develop an estimation procedure that allows for right-censored observations and covariate information. In particular, we use this framework to propose a bivariate Matrix-Gompertz distribution for the modelling of excess joint lifetimes of couples. Adapting a respective Expectation-Maximisation algorithm, we estimate sub-intensity matrices, inhomogeneity functions and different initial distribution vectors without separating joint features from marginals. Initial probabilities are assumed to be linked to spouses’ ages at the issue of an insurance
policy. Employing multinomial logistic regressions to predict the latter, tailor-made bivariate distributions are produced that reflect distinct ageing dynamics and dependence structures. The resulting mIPH distributions showcase strong positive concordance for remaining lifetimes of spouses, particularly when the difference in age at the issue of the policy is small.

The results and illustrations given in this paper demonstrate the accuracy and flexibility of the mIPH class, which may also be employed in areas beyond the present lifetime setup, including applications in non-life insurance. The mIPH class may be considered a valid alternative to copula-based methods, particularly when one wants to estimate marginal and multivariate properties at the same time, and has sufficiently many data points available to keep the pre-imposed dependence assumptions (and structure) minimal. In addition, modelling with members of the mIPH class allows for an immediate causal interpretation of the resulting model in terms of common ageing through stages.

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Department of Actuarial Science, Faculty of Business and Economics, University of Lausanne, UNIL-Dorigny, 1015 Lausanne and Swiss Finance Institute, 1015 Lausanne

*Email address: hansjoerg.albrecher@unil.ch*

Department of Actuarial Science, Faculty of Business and Economics, University of Lausanne, UNIL-Dorigny, 1015 Lausanne

*Email address: martin.bladt@unil.ch*

Department of Actuarial Science, Faculty of Business and Economics, University of Lausanne, UNIL-Dorigny, 1015 Lausanne

*Email address: alaric.mueller@unil.ch*