

Ma thèse d'Actuariat en 10 min
Extensions multivariées pour la modélisation de
la mortalité

Antoine Burg, CEREMADE Université Paris Dauphine, SCOR

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Mortality is driven by several major causes of death

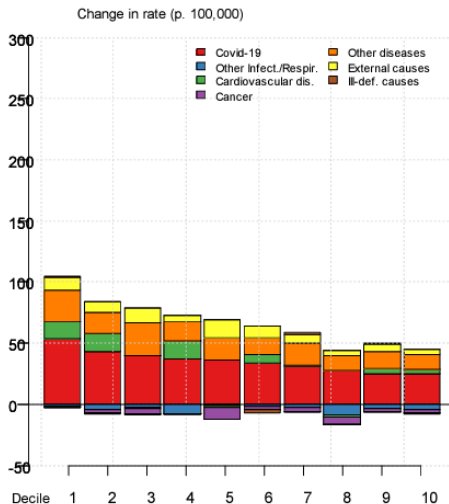


Figure 1: US mortality between 2019 and 2022 by socio-economic groups, Females [Barbieri, 2024].

Outline

- 1 Closed-form estimators for multivariate regressions models - a single categorical variable approach
- 2 Alternative estimation framework based on GLM for mortality models: from single population to Cause-of-Death modelling
- 3 Practical aspects of multivariate LSTM for mortality forecasts

Closed-form estimators for multivariate regressions models - a single categorical variable approach

Motivation: get closed-form formulas for repeated GLM fits for model selection or ensemble methods.

Assumptions:

- Multivariate GLM framework
- Multinomial or Dirichlet distribution for the response variable
- Explanatory variables consist of a single categorical variable with a dummy structure

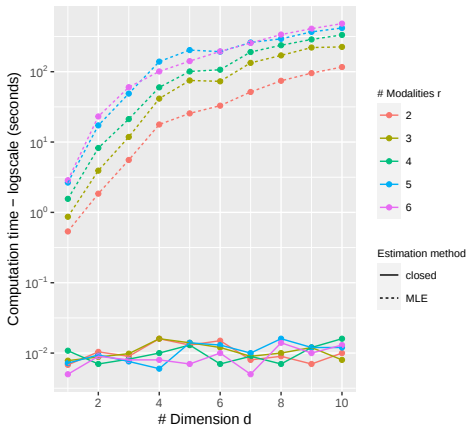
Main results:

- Closed-form formulas for MGLM regression parameters in special case of categorical variables for both Multinomial and Dirichlet distributions
- Faster computation time, especially in high dimensions
- New class of estimators for Dirichlet distribution with asymptotic properties

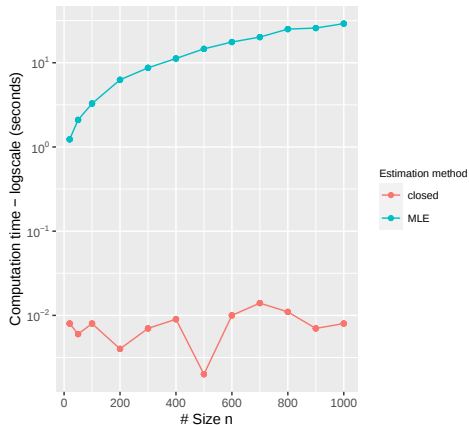


Computation time on Simulated Data for MGLM regression parameters with multinomial distribution

Computation time in function of Dimension d
Size $n = 1000$



Computation time in function of Size n
Dimension $d = 5$, Number of modalities $r = 3$



Alternative estimation framework based on GLM for mortality models: from single population to Cause-of-Death modelling

Motivation: provide a unified framework for single population, multi-population and causes-of-deaths modelling.

Assumptions:

- Death counts $D_{x,t}$ follow a multinomial distribution
- Only mortality models with linear components $\eta_{x,t}^{(j)} = \alpha_x^{(j)} + \sum_i \beta_x^{i,(j)} \kappa_t^{i,(j)} + \beta_x^{(0)} \gamma_{t-x}^{(j)}$

Main results:

- Alternative estimators for mortality models involving single population, multi-population and causes-of-death.
- Explicit estimators
- For multi-populations models: 1-step procedure instead of 2-step Li-Lee calibration, with no convergence issue.
- Better performance for causes-of-death modelling.

Multi-populations example

- Countries: France, Italy, Spain
- Age band: 50-84
- Period: 2001-2020
- Sex: Male
- Source: Human Mortality Database
- Model: Li-Lee structure [Li and Lee, 2005] with M3 models and one common factor K_t

$$\begin{cases} \eta_{x,t,g_1} = \alpha_{x,g_1} + K_t + \kappa_{t,g_1} + \gamma_{t-x,g_1} \\ \eta_{x,t,g_2} = \alpha_{x,g_2} + K_t + \kappa_{t,g_2} + \gamma_{t-x,g_2} \\ \eta_{x,t,g_3} = \alpha_{x,g_3} + K_t + \kappa_{t,g_3} + \gamma_{t-x,g_3} \end{cases}$$

Multi-populations example - trend factors

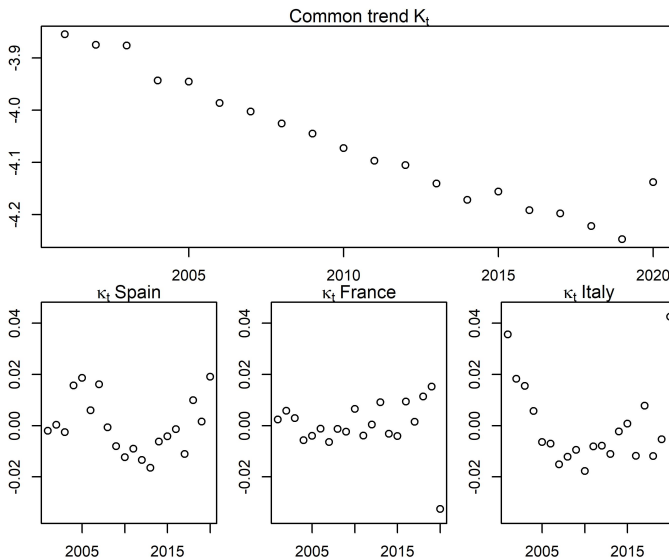


Figure 2: Common and specific trend parameters, Males.

Causes-of-death example

- Country: USA
- Age band: 50-84
- Period: 2001-2020
- Sex: Male
- Source: Human Mortality Database, based on [ICD10](#) classification
- For each of the 16 selected causes, M3 model with cause-specific parameters is assumed

$$\eta_{x,t}^{(j)} = \alpha_x^{(j)} + \kappa_t^{(j)} + \gamma_{t-x}^{(j)}.$$

- Estimators: comparison between univariate independent single population VS multinomial assumption (exact same numbers of parameters).

Table 1: Goodness of fit

Parameters	Deviance	AIC	MSE	MAE	MAPE (%)
Independent univariate	11883	107342	2.55E-07	1.58E-04	7,03%
Multivariate	5149	97172	8.88E-09	2.56E-05	2.14%

State of the art of mortality forecasting

Usual forecasting framework consists in assuming a random walk or another time series model for time-dependent parameters κ_t^i of a GAPC

$$\kappa_t^i = \kappa_{t-1}^i + \nu + \epsilon_t.$$

Deep learning literature provide several architectures to deal with time-series

- Recurrent Neural Networks
- Convolutional Networks
- Generative Adversarial Networks
- Transformers
- Long Short Term Memory (LSTM) Networks

LSTM architecture

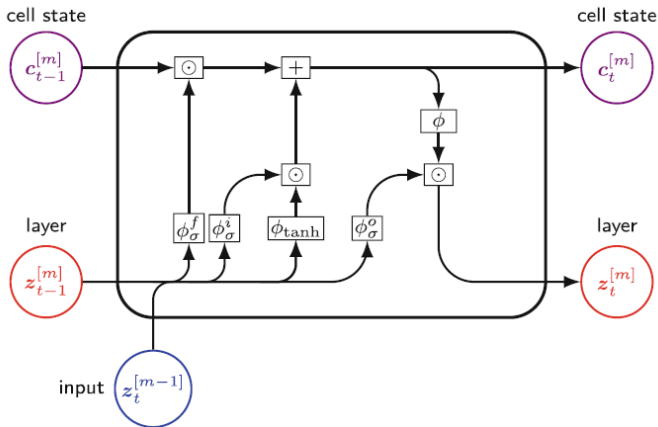


Figure 3: A LSTM cell. Source: [Wüthrich and Merz, 2023].

Historical data, USA, 1970-2022

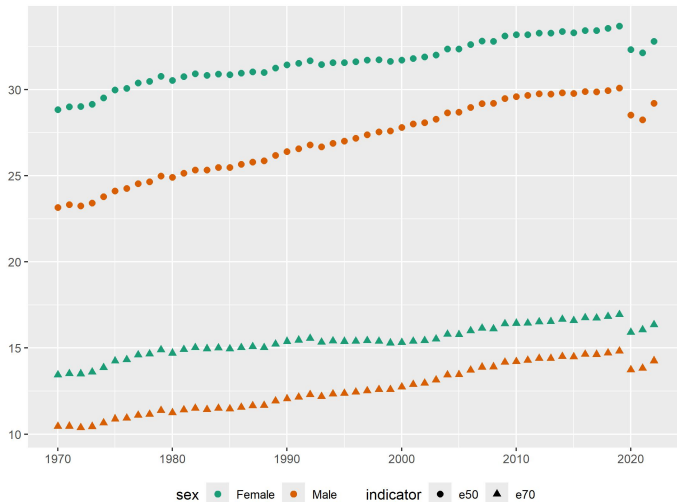


Figure 4: Evolution of residual life expectancy at ages 50 and 70.

Use case: stationary (no mortality shock), USA, Female

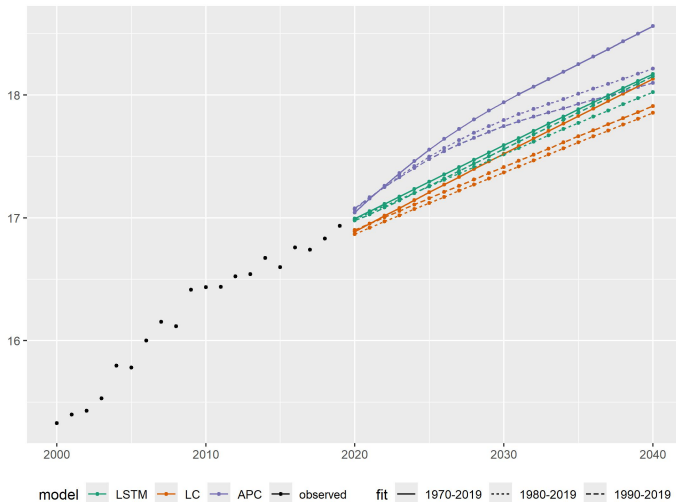


Figure 5: Forecasts of residual life expectancy at age 70 over several calibration periods.

Use case: presence of a mortality shock, USA, Female

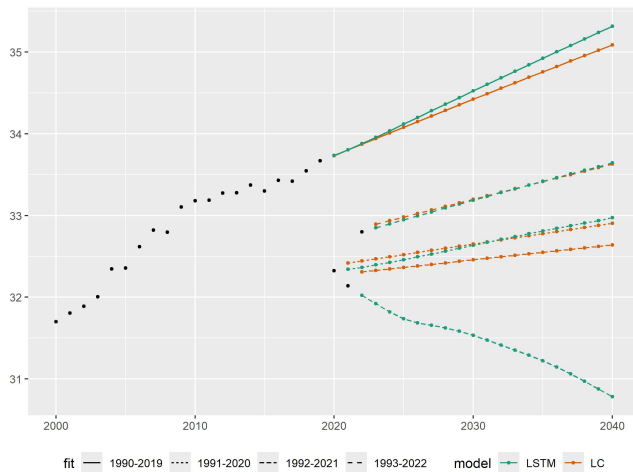


Figure 6: Forecasts of residual life expectancy at age 50 in presence of a pandemic shock.

Main results

- Analysis of Multivariate LSTM in multiple use cases with emphasis on forecasts
- Forecasts appear more influenced by recent data points than with other models
- In particular, very sensitive to short-term fluctuations

Merci pour votre attention !

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Perspectives

- Study more asymptotic properties of the regression estimators, e.g. comparison to MLE, speed of convergence
- Leverage closed-form formulas within ensemble methods, especially GLM-trees and GLM-forests
- Study the forecasts based on the alternative estimator
- Perform studies assuming a Dirichlet distribution instead of multinomial
- Apply multivariate LSTM for multi-populations or cause-of-death forecasts

Multivariate Poisson extensions

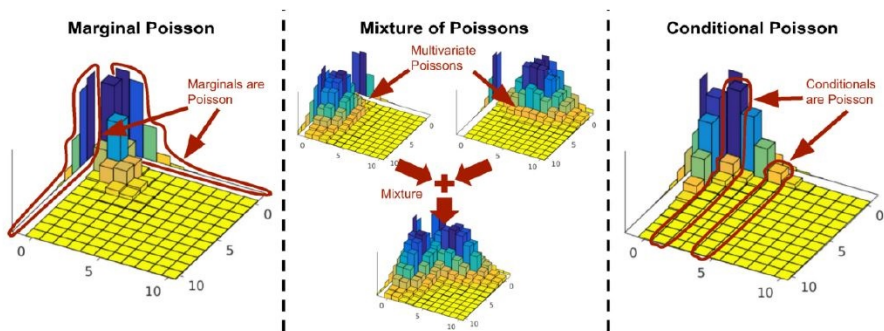
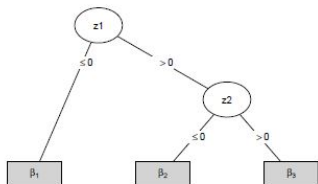


Figure 7: Source: [Inouye et al., 2017].

Motivation - Use of Generalized Linear Models (GLM)-trees

The GLM-based tree algorithm [Rusch and Zeileis, 2013] is a recursive split of the dataset based on partitioning variables, similar to other tree algorithm, e.g. CART.

A GLM is fitted at each node on a set of explanatory variables.



Main steps are:

- 1 Fit the GLM on the current sample
- 2 Asses parameter stability for each partition variable
- 3 Choose the best splitting point

Example from [Seibold et al., 2019]: GLM tree with 2 partition variables

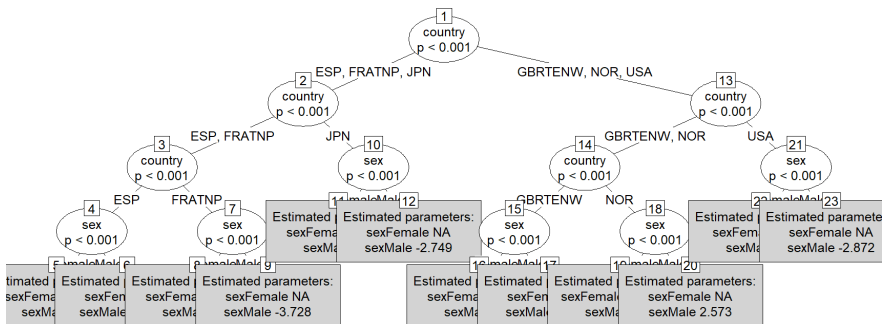
$$g(E(Y_i)) = \begin{cases} \beta_1 & \text{if } z_1 \leq 0 \\ \beta_2 & \text{if } z_1 > 0 \text{ and } z_2 \leq 0 \\ \beta_3 & \text{if } z_1 > 0 \text{ and } z_2 > 0 \end{cases}$$

Advantages: Automatic partitioning → enables classification + increased accuracy.

Drawbacks: Numerical optimization of the MLE → high computational time.

Use case - classification based on all-cause mortality

- Data source: Human Mortality Database
- Explicative variables: age (50-84) and year (1990-2019)
- Partitioning variables: country (France, Japan, Norway, Spain, UK, US) and sex (Male or Female)
- Computation time: 39s
- Convergence: numerical optimization may fail to converge to a solution
→ known issue with glm.fit in R when data are already well partitioned.



ICD10 classification

	Disease	ICD10
1	Certain infectious diseases	A00-B99
2	Neoplasms	C00-D48
3	Diseases of the blood and blood-forming organs	D50-D89
4	Endocrine, nutritional and metabolic diseases	E00-E88
5	Mental and behavioural disorders	F01-F99
6	Diseases of the nervous system and the sense organs	G00-G44, G47-H93
7	Heart diseases	I00-I51
8	Cerebrovascular diseases	G45, I60-I69
9	Other and unspecified disorders of the circulatory system	I70-I99, K64
10	Acute respiratory diseases	J00-J22, U04, U07
11	Other respiratory diseases	J30-J98
12	Diseases of the digestive system	K00-K63, K65-K92
13	Diseases of the skin	L00-M99
14	Diseases of the genitourinary system	N00-O99
15	Certain conditions originating in the perinatal period	P00-Q99, R95
16	External causes	V01-Y89

Back to [MGAPC](#).

New approach with Multivariate LSTM

Several strategies are available with LSTM depending on input/output dimension

- "one-to-one", e.g. univariate forecasts of (κ_t)
[Nigri et al., 2021, Marino et al., 2021, Lindholm and Palmborg, 2022]
- "many-to-one", e.g. forecasts of mortality rate by age
[Richman and Wuthrich, 2019, Euthum et al., 2024]
- "many-to-many": proposed model

Table 2: Dataset characteristics

Model	Input size τ_0	Output size
• [Nigri et al., 2021, Marino et al., 2021, Lindholm and Palmborg, 2022]	1	1
[Richman and Wuthrich, 2019, Euthum et al., 2024]	5	1
Proposed model	71	71

- Data transformation: log-ratio transform and normalization,
- Hyperparameters tuned using Bayesian Optimization: number of cells, number of layers, learning rate and lookback period.

Parameters and Hyper-parameters

Model	population	$\mathcal{X}_0$	$\mathcal{T}_0$	T	τ_0	$\#\mathcal{X}_0$	$\#\mathcal{T}_0$	$ T $
[Richman and Wuthrich, 2019]	Switzerland	0-99	1950-1999	10	5	100	40	4000
[Euthum et al., 2024]	Italy	50-95	1982-2014	10	5	45	23	9522
Proposed model	USA	30-100	1970-2019	$\{3, \dots, 7\}$	71	71	$\{30;40;50\}$	$\#\mathcal{T}_0 - 7$

Table 3: Summary of dataset characteristics

Hyperparameter	Calibration period			
	1990-2019	1991-2020	1992 - 2021	1993 - 2022
Learning rate	1.75E-03	6.27E-04	4.93E-03	1E-05
Number of neurons	20	15	6	40
Number of layers	1	1	2	2
Lookback period	3	3	7	5
Number of parameters	7440	5280	2232	31200

Table 4: Selected hyperparameters.

LSTM and confidence intervals

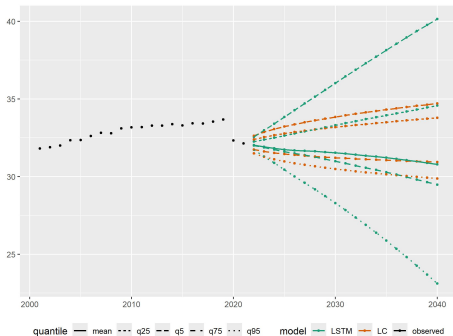


Figure 8: Forecasts of residual life expectancy at age 50 with confidence intervals, Female, 1992-2021.

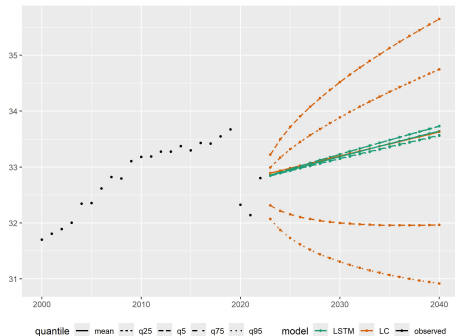


Figure 9: Forecasts of residual life expectancy at age 50 with confidence intervals, Female, 1993-2022.

LSTM for cause-of-death mortality forecasts

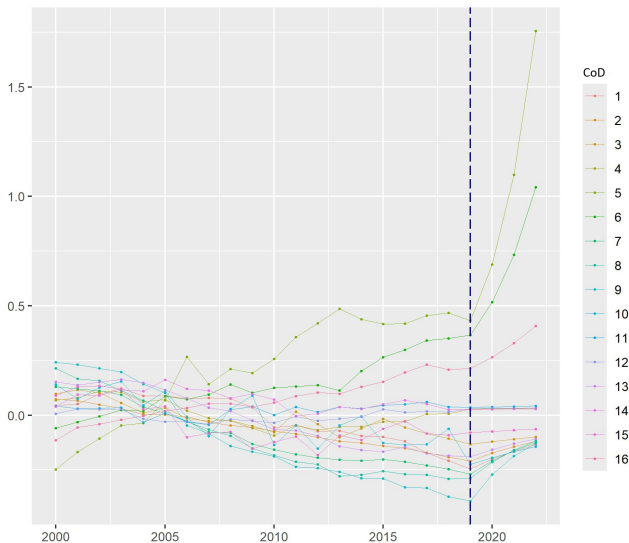


Figure 10: Forecasts of trend parameters, M3 assumed for each cause, Females, 1990-2019.