

A Novel Methodological Framework for the Analysis of Health Trajectories and Survival Outcomes in Heart Failure Patients Juliette Murris¹, Tristan Amadei², Tristan Kirscher², Antoine Klein², Anne-Isabelle Tropeano³ & Sandrine Katsahian^{1,3}

¹ HeKA, Inserm, Inria, Université Paris Cité, Pierre Fabre R&D² ENSAE, IP de Paris, ³ CIC-1418, HEGP, AP-HP, Paris, France

CONTEXT & OBJECTIVES

Motivating example

- Heart failure (HF) is common amongst **elderly** patients and associated with a high mortality rate [Farré 2017]
- Chronic HF is often accompanied with repeated hospitalizations and is the • condition with highest 30-days re-hospitalization rate [Constantinou 2021]

Figure 1. ICD-10 architecture

Available data

- The EGB (Echantillon Généraliste des Bénéficiaires) is a random sample representative of the French health insurance databases and provides inhospital electronic health records
- International Classification of Disease (10th edition (ICD-10)) is used to establish primary and associated diagnoses of hospitalizations (Figure 1)









Study objectives

- Identify frequent care sequences in HF patients in France
- > Investigate associations with mortality

METHODOLOGICAL FRAMEWORK

Identify similarities from care pathways using clustering

Input – Care pathways (examples in Table 1), excluding factors like gender and age Methodology

Defining the appropriate distance metric to quantify the distance between two patients' care pathways, based on Levenshtein distance with weighted components of the ICD-10 codes. For two ICD-10 codes A and B:

Table 1. Three patients and their care pathways	
Patient	hospit_course
P0	05K051,05M042,05M16T,05M09T,05M092,05C191,
P6	02C05J,02C05J,05M093,04M132,05C222,23M103
P8	11M041,06C194

$$D_{ICD10}(A,B) = \omega_1 * lev(A_{0:2}, B_{0:2}) + \omega_2 * lev(A[2], B[2]) + \omega_3 * lev(A_{3:5}, B_{3:5}) + \omega_4 * lev(A[5], B[5])$$

 \rightarrow We then compare the *i*th ICD-10 code of a patient with the (i - 1)th i CD-10 codes of another patient, compute the distances and keep the minimum to get the distance between two patient sequences.

- K-medoids algorithm used to group data points into k clusters. Two hyperparameters require settings and are under constraint:
- Ω the weights of the distance metric, with $0 \le \omega_4 \le \omega_3 \le \omega_2 \le \omega_1 \le 100$,
 - $k \in [2,20]$ the number of clusters.

Extract frequent care pathway patterns using sequential pattern mining *Input* – Subset of items (ICD-10 code), event sequence (ordered list of ICD-10) codes)

Methodology – PrefixSpan algorithm was retained and uses the concept of "prefixes" to efficiently search for frequent patterns in a sequence database [Pei 2001]

Clinicians' interest in survival analysis to predict the survival probability of a specific HF patient

Input – Survival time and status (dead or alive), adjusted covariates

Methodology – Random survival forests and survival gradient boosting algorithm (hyperparameter tuning conducted) [Ishwaran 2008, Hothorn 2006], and evaluation using AIC and concordance index [Harrell 1982]

Outputs

- The ten most frequent ICD-10 codes collectively accounted for approximately 50% of trajectories, indicating significant similarity in the care sequences (Figure 2)
- Common sequences leading to death are '05M09' for HF hospitalization, '04M05' for pleurisy, and '04M13' for pulmonary edema and respiratory distress
- Different survival trajectories from the 5 cluster s obtained (Figure 3)
- Aging and prolonged hospital stays are also impactful risk factors







DISCUSSION & CONCLUSION

- Our approach is simple and easily accessible
- While our focus has been on the HF patients, our approach is **adaptable** and can be extended to other clinical problematics and populations

Perspectives

- Include up-to-date methodologies with NLP and embedding techniques to extract event more relevant information from ICD-10 codes
- Include **risky patterns** identified as covariates in survival models

BIBLIOGRAPHY

Constantinou P, Pelletier-Fleury N, Olié V, Gastaldi-Ménager C, Juillère Y, and Tuppin P. Patient stratification for risk of readmission due to heart failure by using nationwide administrative data. Journal of Cardiac Failure, 27(3):266-276, 2021.

Farré N, Vela E, Clèries M, Bustins M, Cainzos-Achirica M, Enjuanes C, Moliner P, Ruiz S, Verdu-Rotellar JM, and Comin-Colet J. Real-world heart failure epidemiology and outcome: A population-based analysis of 88,195 patients. PLOS ONE, 12(2):e0172745, February 2017. ISSN 1932-6203. doi: 10.1371/journal.pone. 0172745. URL https://dx.plos.org/10.1371/journal.pone.0172745.

Harrell F, Califf R, Pryor D, Lee K, and Rosati R. Evaluating the yield of medical tests. Jama, 247(18):2543–2546, 1982.

Hothorn T, Buhlmann P, Dudoit S, Molinaro A, and Van Der Laan M. Survival ensembles. Biostatistics, 7(3):355–373, 2006

Ishwaran H, Kogalur U, Blackstone E, and Lauer M. Random survival forests. The Annals of Applied Statistics, 2(3):841–860, September 2008. ISSN 1932-6157, 1941-7330. doi: 10.1214/08-AOAS169. URL https://projecteuclid.org/journals/annals-of-applied-statistics/volume-2/issue-3/Random-survival-forests/10.1214/08-AOAS169.full.

Pei J, Han J, Mortazavi-Asl B, Pinto H, Chen Q, Dayal U, and Hsu m. PrefixSpan,:mining sequential patterns efficiently by prefix-projected pattern growth. In Proceedings 17th International Conference on Data Engineering, pp. 215–224, Heidelberg, Germany, 2001. IEEE Comput. Soc. ISBN 978-0-7695-1001-9. doi: 10.1109/ICDE.2001.914830. URL http://ieeexplore.ieee.org/document/914830/

Pinaire J, Azé J, Bringay S, and Landais P. Patient healthcare trajectory, an essential monitoring tool: a systematic review. Health information science and systems, 5:1–18, 2017.

https://github.com/Kirscher/TextMining_Parcours_de_soin