

Category : **Cardiovascular: cardiac arrest\CPR**

A272 - Aicr 1, artificial intelligency in cardiac arrest 1: automatized extraction tool by text mining in cardiac arrest.

R Lombardi¹ ; T Le Blévenec² ; A Mazeraud³ ; D Duhautbout⁴ ; G Bernardin¹ ; P Deswardt⁵ ; PM Bertrand⁶ ; J Dellamonica⁷ ; T Sharshar³

¹CHU L'Archet-Nice, Médecine intensive-réanimation, Nice, France, ²Talan solutions, Talan solutions, Paris, France, ³GHU Paris Psychiatrie et Neurosciences, Neurointensive Care and Neuroanesthesia Department, Paris, France, ⁴Aiintense, Aiintense, Evry, France, ⁵Centre hospitalisation d'Antibes-Juan les Pins, Service de réanimation polyvalente, Antibes, France, ⁶Centre hospitalier de Cannes, service de médecine-intensive réanimation, Cannes, France, ⁷CHU L'Archet-Nice, service de médecine-intensive réanimation, Nice, France

Introduction:

Cardiac arrest is a public health key, with 10.985 patient/year, with an extremely high death rate (overall survival rate at hospital discharge is 10%) [1, 2]. In the literature, there are many examples of the artificial intelligence (AI) efficiency, specially, in intensive care unit (ICU), in the prediction, in database creation, in the therapeutic help [3–5]. In some case, it could be fastidious to create a database, so we developed an automatized extraction tool, based on a text mining approach.

Methods:

We used unstructured data, including computerized hospital report (CHR), from two centres. Successive samples of CHR have been drawn randomly and annotated, to reach a total of 143 annotated CHR. We incrementally increased the size of samples. If the concordance rate exceeded or if it was equal to 90%, for every interest variable, we considered the sample validated. Once the data are extracted, we performed a clustering, to identify patterns in the CHR, a missing value and a miss extraction value analysis.

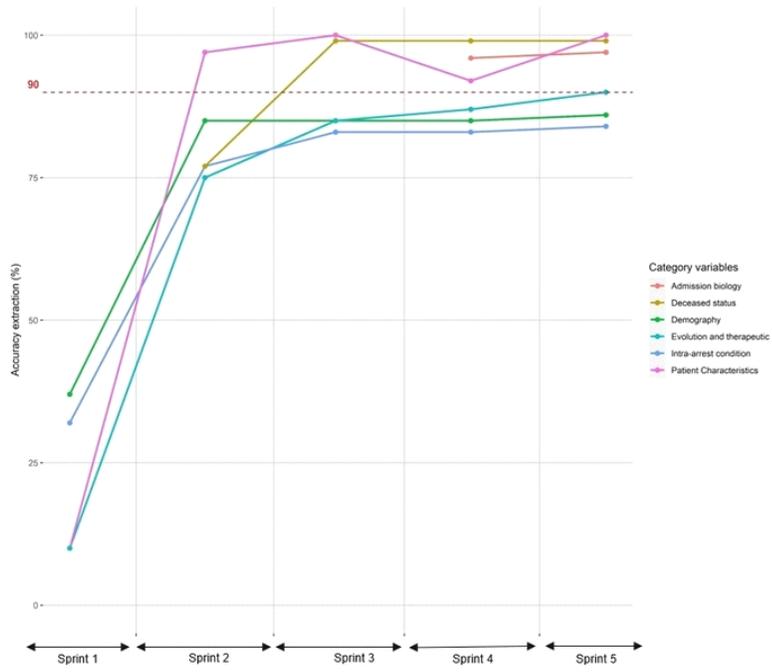
Results:

After the full development and the training of our tool, we can extract 51 variables, with a mean accuracy of 92.75%, with the better performance in admission biology, patient characteristics, and the deceased status, **figure 1**. An analysis on algorithms errors showed that the main extractions errors were attributable to the complexity context and to the complexity variables (36% both). The most missing values were found in the biology variables (59.27%). The clustering results showed two group of CHR, differing for death, witness presence, multi-organ failure, status epilepticus and Glasgow scale.

Conclusion:

We developed a reliable extraction tool, fully automated and adaptative, able to extract hundreds of data in seconds (0.27 seconds for one CHR and 137.6 seconds for 504 CHR). It is useful for data base creation, by its simplicity and its quick use.

Image :



Accuracy extraction, by category, in the training sample (143 CHR), sprint corresponding to two months