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Dating The Hematoma Of Haemorrhagic Stroke By Analysis Of The Disintegration Of Oxyhemoglobin Nuclei

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Abstract - Hemorrhagic stroke is caused by the rupture of cerebral blood vessels discharging blood onto the surrounding tissues causing the hematoma. The knowledge of the evolutionary profile of the hematoma is essential at the end of the stroke, because it allows specialists to direct the treatment. The present work aims to develop a method to characterize the four stages of evolution of the hematoma. The material consists of haemorrhagic CT scan images collected at the Cotonou CNHU CT scan unit and processed in MATLAB R2015a environment. The proposed method made it possible to determine a mathematical function that can model the density distribution of oxyhemoglobins in the hematoma. The results obtained made it possible to characterize the different evolutionary stages of the hemorrhagic stroke with a success rate of 97,09% on a database of 103 images. This method of dating the hematoma will certainly be a decision-making tool in the diagnosis and management of haemorrhagic stroke.

Key words: Evolutionary profile, hemorrhagic stroke, oxyhemoglobin

1. INTRODUCTION

The stroke is a neurological deficit suddenly caused by an infarction or hemorrhage. The hemorrhagic stroke, is caused by the rupture of cerebral blood vessels spilling blood into the surrounding tissues. The hematoma is the blood clot resulting from cerebral hemorrhage [2]. According to the 2015 WHO report on the causes of death worldwide, ischemia and hemorrhagic stroke are largely ahead of respiratory diseases, cancer and AIDS. According to a report published by WHO [6], WHO does not hesitate to talk about Pandemic and expects a progressive increase in the incidence of stroke worldwide from 16 million cases in 2005 to nearly of 23 million in 2030. The strokes are nowadays a major public health problem.In general, in case of stroke, when the life threatening is engaged, it is the cerebral CT scan without injection which is the examination most often carried out urgently for the diagnosis of hematoma [3]. The goal of imaging is to make the diagnosis of hematoma, is to know the evolutionary profile, and to recognize the

underlying causes because of the risk of bleeding recurrence and treatment possibilities.

Table 1 : WHO statistics and forecasts (Source : [7])

YEAR	Number of Victims	Number de Deaths
1990	10 100 000	4 700 000
2010	16 800 000	5 900 000
2030	23 000 000	12 000 000

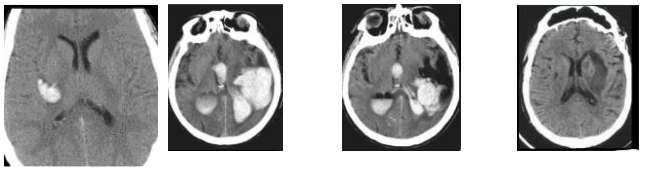
The precision in the diagnosis and the promptness in the care are essential at the stroke outcome. This is why the establishment of a method for dating the hematoma is certainly a decision-making tool that can provide more precision and speed in the diagnosis of hemorrhagic stroke. Four evolutionary profiles of the hematoma are classically distinguished: the hyperacute, acute, subacute and chronic stages. For example, we have:

- In the hyperaigu stage (3 to 6 hours)

The clot consists of a heterogeneous mass composed of red blood cells filled with oxyhemoglobins. In CT scan, the hematoma is hyperdense compared to the cerebral parenchyma but it can be heterogeneous and contain hypodense areas [5], [2].

- At the sub-acute stage (3 days-4 weeks)

The oxidative denaturation of hemoglobin progresses and deoxyhemoglobin is transformed into methemoglobin. On CT scan, the density of the hematoma decreases further, the edges become blurred, isodense and hypodense [5], [2].



Hyperacute stage Acute stage Sub-acute stage Chronic stage

Fig. 1 : differents stages or evolutionary

2. MATERIAL AND METHODS

2.1 Material

The material consists of brain CT scan images collected at the CT scan unit of the Hubert MAGA University Hospital Center (CNHU-HKM) located at the Faculty of Health Sciences of Cotonou and supplemented by images for free download on the Net. This image database was processed in a Matlab version 8.5 environment (R2015a)

2.2 Methods

2.2.1 Disintegration of oxyhemoglobin nuclei

The hematoma dating method used here is based on the knowledge of the anatomical transformations of the hematoma [1]. The global analysis of the hematoma transformations shows a continuous decrease of the oxyhemoglobin level in the hematoma. In fact, the density of oxyhemoglobins, generally represented in the image of the CT scan, by blocks of white pixels, gradually decreases from the edges of the hematoma towards the center following the evolutionary stages of the hemorrhagic stroke to cancel at the chronic phase [2]. This decrease in oxyhemoglobin level can be modeled by the radioactive decay function.

In a sample of radioactive material consisting of radioactive nuclei of a given species, the number of nuclei will decrease over time, and will be noted N (t). If we call N_0 the number of nuclei initially present, we have the relation :

$$N(t) = N_0 e^{-\lambda t} \quad (1)$$

With λ the probability that a kernel disintegrates per unit of time.

From the relation Eq. (1) we can determine λ

$$\lambda = \frac{1}{t} log \frac{N_0}{N(t)} \quad (2)$$

The analysis of a database of brain CT scan images of the same individual over several days made it possible to draw an empirical curve of the decay of oxyhemoglobins.

2.2.2 Determination of a reference threshold T_0

The threshold T_0 sought here corresponds to the threshold of the distributions of the oxyhemoglobins at the date T_0 corresponding to the day 1 of the beginning of the stroke. To do this, the Otsu threshold determination method was applied to all day 1 images. The average of the calculated thresholds made it possible to obtain a reference threshold T_0.

Otsu's [8] method automatically detects the threshold by seeking to minimize the variance within each region, which amounts to maximizing the variance between the two regions. This Otsu thresholding algorithm can be summed up to [4] :

$$T_{otsu} = argmin_T \left\{ \sum_{k<T} h(k)(\mu_0 - \mu)^2 + \sum_{K \geq T} h(k)(\mu_1 - \mu)^2 \right\} \quad (3)$$

With : μ = moy{I(x)} , μ_0 = moy{I(x) for I(x) < T} and μ_1= moy{I(x) for I(x) ≥ T}. h being the histogram function.

2.2.3 Correlation between the empirical curve and the modeling function

- Kolmogorov-Smirnov test

In order to determine the value of the parameter λ which makes it possible to obtain a correlation between the empirical curve and the theoretical function modeling this distribution, the Komogorov-smirnov test is used.

Indeed, the Kolmogorov-Smirnov (KS) bilateral D_n test statistic is widely used to measure the quality of fit between the empirical distribution of a set of n observations and a continuous probability distribution. It is defined by :

$$D_n = \sup_x \left| G(x) - \hat{G}_n(x) \right| \quad (4)$$

Where n is the number of (independent) observations, G_n is the function of the empirical cumulative distribution and G is a fully specified continuous theoretical cumulative distribution function. Let F_n be the cumulative distribution function of D_n responding to the null hypothesis H_0 for which the n observations are independent and whose function is of cumulative distribution G, we have :

$$F_{n(x)} = P[D_n \leq x | H_0] \quad \text{for } x \in [0,1] \quad (5)$$

The value λ corresponding to the hypothesis $H_0 = 0$ is then the correlation value of the empirical curve and the theoretical curve.

The general algorithm of the method is :

VARIABLES InputImage, SizeofImage, N0, landa, Dn, N(t), n

PREDEFINED FUNCTIONS SmirnovTest

ASSIGNMENT H0=1, landa = 0,009

BEGING

//Détermination of N_O per size of image

READ InputImage

IF(SizeofImage =114x106) THEN

```
N0=9303
WHILE (Dn !=0)
n++
DO
Landa=landa-0.001
N(t) = N0*exp(-landa*t)
END WHILE
ELSE IF (SizeofImage = 75x96) THEN
N0=2650
WHILE (Dn !=0)
n++
DO
Landa=landa-0.001
N(t) = N0*exp (-landa*t)
END WHILE
ELSE IF (SizeofImage=34x34) THEN
N0=907
WHILE(Dn !=0)
n++
DO
Landa=landa-0.001
N(t) = N0*exp(-landa*t)
END WHILE
END IF
END
// Détermination  of reference threshold
VARIABLES refInputImage, n, T0
PREDEFINED FUNCTIONS OtsuThreshold
BEGING
READ RefInputImage
T= OtsuThreshold(refInputImage)
FOR (1 to n)
DO
T0 =∑(T)/n
END FOR
END
```

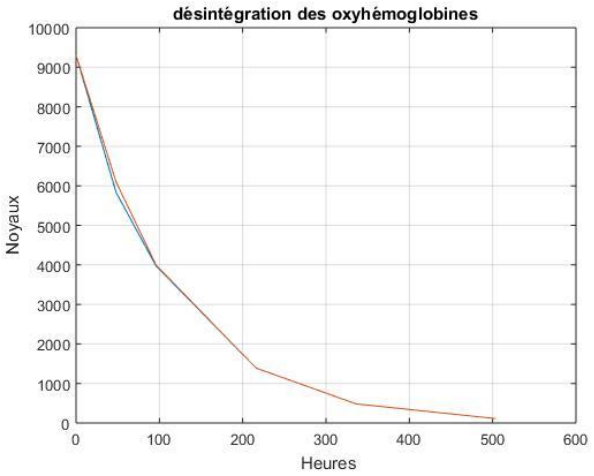
3. RESULTS

3.1 Disintegration equation of oxyhemoglobin nuclei

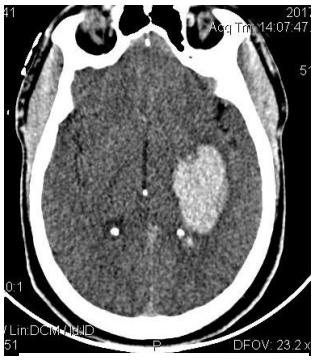
Table 2 **:** Decay equation of oxyhemoglobins as a function of hematoma size

hematoma size	**Threshold T_0**	**λ equivalent to H_0**	**N_0**	**Equation of decay**
114x106	190	$8{,}8x10^{-3}$	9303	$N(t) = 9303\, e^{-0}$
75x96	190	$8{,}8x10^{-3}$	2650	$N(t) = 2650\, e^{-0}$
34x34	190	$8{,}8x10^{-3}$	907	$N(t) = 907\, e^{-0,0}$

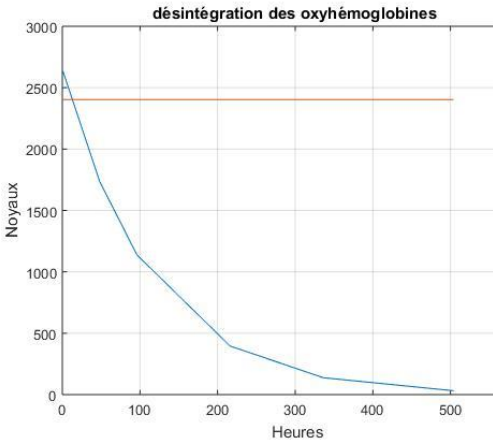
3.2 Correlation curve $H_0 = 0$

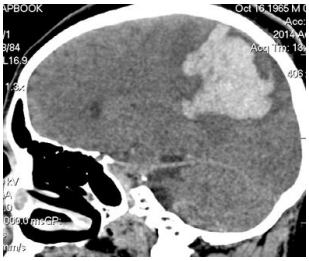


3.1 Hematoma dating result



CT1





CT2

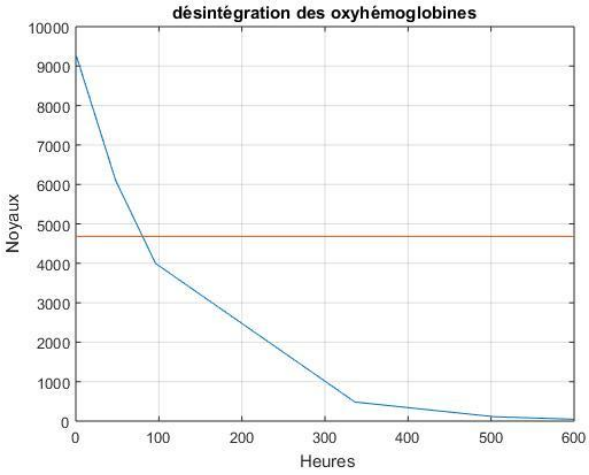


Fig. 4 : CT2 hematoma dating curve

<u>Datation CT 2</u> t = 80,35 hours, day 8.

<u>Evolutionary profile</u> : Subacute stage

3.2 Summary of the application of the method on the images of the database

Table 3 : Percentages of the application of the method

	Numbers	**Percentage**
Hyperacute	4	3,88%
Acute	46	44,46%
Subacute	40	38,83%
Chronic	10	9,71%
Success	100	97,03%
Failure	3	2,91%
Total	103	100%

The relatively low failure rate demonstrates the effectiveness of the method in dating hematomas. Indeed

this rate is related to the poor quality of some images including those download on the net.

4. CONCLUSION

In this study we proceeded to the characterization of hemorrhagic stroke by dating the evolutionary profile of the hematoma. Otsu's inter-mean algorithm allowed us to make a judicious choice of the reference threshold in order to determine the empirical decay curve. The Kolmogorov test made it possible to adjust the parameter λ to obtain a perfect correlation ($H_0 = 0$) between the empirical curve and the theoretical curve. The results obtained made it possible to characterize the different evolutionary stages of the hemorrhagic stroke with a success rate of 97,09% on a database of 103 images. We can conclude that globally the atomic decay function has made it possible to model the distribution of the density of oxyhemoglobins in the hematoma and consequently to characterize the four evolutionary stages of the hemorrhagic stroke.

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