

# Quantum associative memory with linear and non-linear algorithms for the diagnosis of some tropical diseases

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September 25, 2018

## Abstract

This paper presents the QAMDiagnos, a model of Quantum Associative Memory (QAM) that can be a helpful tool for medical staff without experience or laboratory facilities, for the diagnosis of four tropical diseases (malaria, typhoid fever, yellow fever and dengue) which have several similar signs and symptoms. The memory can distinguish a single infection from a polyinfection. Our model is a combination of the improved versions of the original linear quantum retrieving algorithm proposed by Ventura and the non-linear quantum search algorithm of Abrams and Lloyd. From the given simulation results, it appears that the efficiency of recognition is good when particular signs and symptoms of a disease are inserted given that the linear algorithm is the main algorithm. The non-linear algorithm helps confirm or correct the diagnosis or give some advice to the medical staff for the treatment. So, our QAMDiagnos that has a friendly graphical user interface for desktop and smart-phone is a sensitive and a low-cost diagnostic tool that enables rapid and accurate diagnosis of four tropical diseases.

## 1 Introduction

Diagnosis is the identification of a situation, a difficulty or a phenomenon by interpreting external signs or lesions. In the medical field, it consists of identifying abnormal condition that afflicts a specific patient, based on manifested clinical data. If the final diagnosis matches a disease that afflicts a patient, the diagnostic process is correct; otherwise, a misdiagnosis occurs. Medical diagnosis can also be defined as the process that allows a physician, through information collected from a history and physical examination of a person, to make prediction about features of clinical situations and determine appropriate course of action. It implements a complex decision process that involves a lot of vagueness and uncertainty management, especially when a disease has multiple signs and symptoms or non-specific signs and symptoms.

From the point of view of statistics, the diagnostic procedure involves classification tests. That is, the task is made on the basis of measured features to assign a patient to one of a small set of classes [1]. Then, Artificial Neural Networks (ANN) provide powerful tools that help physicians avoid misdiagnosis by analyzing, modelling and making sense of complex clinical data across a broad-range of medical applications. As ANNs have the ability of prediction, parallel operation and adaptability, they have been widely used as computer-assisted tools among many techniques about automatic disease diagnosis proposed in the literature [2, 3]. ANNs have been used for example for the diagnosis of colorectal cancer, multiple sclerosis lesions, colon cancer, tuberculosis, pancreatic disease, gynecological diseases and early diabetes [2].

Associative Memories (AM) are a class of ANNs specialised in pattern recognition that have drawn the attention of major research groups in the world due to a number of properties such as a rapidity, a compute efficient best-match and an intrinsic noise tolerance. Aldape-Pérez *et al.* gave in the ref. [4] a good summary of the AM evolution, from the first model, the Lernmatrix developed by Karl Steinbuch in 1961, to the recent model proposed between 1982-1984 by Hopfield [5, 6]. The latter is an AM that uses the Hebbian learning rule and it is able to recall patterns from noisy or partial representation.

Some computer-assisted tools in the case of tropical diseases, are already built and some of them use ANNs, but they are mainly specialized for malaria [7, 8, 9, 10, 2]. It is worth noting that malaria is the most parasitic disease spread over the world. 40% of the world's population are concerned, especially those of tropical regions. In Cameroon, as in the most Sub-Saharan countries, it is a public health problem because the whole population is exposed to the disease. To diagnose malaria, the World Health Organisation (WHO) [11] recommends the use of rapid diagnostic tests. However these tools need some conservation facilities that are difficult to find in rural and semi-urban regions in developing countries. So, the most widely used technique for determining the development stage of malaria is through visual microscopical evaluation of Giemsa stained blood smears. However, this is

a routine and time-consuming task and it requires a well-trained operator. In addition, there is frequently a misdiagnosis because of confusion between signs and symptoms of malaria and that of other tropical diseases such as typhoid fever, yellow fever and dengue, or inexperience of medical staff. As malaria, these tropical diseases are also life-threatening.

In order to provide a rapid and accurate tool for the diagnosis of the above mentioned four tropical diseases (malaria, typhoid fever, yellow fever and dengue), we propose the framework QAMDiagnos, Quantum Associative Memory for the Diagnosis, associated with a friendly multi-platform graphical user interface (Android, Linux, MS Windows). It is a combination of improved versions of the original linear quantum retrieving algorithm proposed by Ventura [12] and the non-linear quantum search algorithm of Abrams and Lloyd [13]. The aim of QAMDiagnos is to (i) act as an advisory tool to inexperienced medical staff, especially senior nurses in rural health centres having no or a limited number of physicians; (ii) act as a decision-support tool for medical diagnosis for physicians in under-staffed health centres; (iii) provide an alternative way to reach a reasonable tentative diagnosis, and hence early commencement of clinical management of patients in the absence of laboratory facilities in many rural and semi-urban health centres; (iv) facilitate the treatment and prevent potential pandemics given the fact that today the increase of international air travel/traffic, tourism to tropical regions and human migration led to a rising incidence of tropical diseases (since vaccines are unavailable for most major tropical infections). Our framework, which is more robust than that of Agarkar and Ghathol [14] that uses the FFANN for the diagnosis of malaria, typhoid fever and dengue, can be extended to a wide range of tropical diseases.

The paper is structured as it follows: Section 2 provides a description of foundations of our model of Quantum Associative Memory. In Section 3 a brief description of each disease is given. Signs and symptoms of diseases are given in Appendix A. Section 4 is devoted to simulations results and discussion whereas in Section 5 we explain the use of the multi-platform friendly graphical user interface (GUI) of QAMDiagnos, designed for the medical staff. Finally, we conclude with an outlook of possible future improvements.

## 2 Description of Quantum Associative Memory

Associative Memories are a class of Artificial Neural Networks that can memorise information, field of knowledge or patterns and can retrieve that from partial or noisy data. Quantum Associative Memories (QAM) combine neurocomputing with quantum computations. Therefore, QAM models share main features both of quantum information theory and Associative Memory.

### 2.1 Few basic concepts of quantum information theory

#### 2.1.1 Quantum bit

Quantum information use a *quantum bit* or a *qubit* instead of an ordinary bit as the fundamental unit of information. The qubit can be an atom, a molecule or a photon that can be in a superposed state (energy or spin for example). As the classical bit, the qubit can take two particular states noted  $|0\rangle$  and  $|1\rangle$  that are the basis states of a Hilbert space  $\mathcal{H}$  of 2 dimensions. The fundamental difference between the qubit and the classical bit is that the qubit can take simultaneously both values. So, the state of the qubit can be represented by the following *superposed state*:

$$|\psi\rangle = \alpha |0\rangle + \beta |1\rangle, \quad (1a)$$

with at any time

$$|\alpha|^2 + |\beta|^2 = 1, \quad \alpha, \beta \in \mathbb{C}. \quad (1b)$$

$|\alpha|^2$  and  $|\beta|^2$  are the probabilities of the qubit to be found in the states  $|0\rangle$  and  $|1\rangle$  respectively after a measurement.  $(|0\rangle, |1\rangle)$  is the most used computational basis that is a pair of orthonormal vectors defined as

$$|0\rangle = \begin{pmatrix} 1 \\ 0 \end{pmatrix}, \quad |1\rangle = \begin{pmatrix} 0 \\ 1 \end{pmatrix}. \quad (2)$$

Therefore, quantum superposition suggest that an  $n$ -qubits register can exist in all its possible  $2^n$  states at the same time.

#### 2.1.2 Quantum entanglement

The use of only one qubit does not highlight the power of quantum information. A purely quantum phenomenon that has non classical analogue is a *quantum entanglement*. We are talking about the quantum entanglement when at least a pair of qubits has quantum correlation. It means that any interaction with one of the qubits affects instantaneously the other despite the separation distance, highlighting the non-local features of quantum theory. In this case, we should see the whole qubits as one unique physical system instead of many separated

subsystems. So, no classical consideration can allow to know the state of each qubit. A well-known entangled states are the following EPR states:

$$|\Psi^+\rangle = \frac{1}{\sqrt{2}}(|00\rangle + |11\rangle), |\Psi^-\rangle = \frac{1}{\sqrt{2}}(|00\rangle - |11\rangle), |\Phi^+\rangle = \frac{1}{\sqrt{2}}(|01\rangle + |10\rangle), |\Phi^-\rangle = \frac{1}{\sqrt{2}}(|01\rangle - |10\rangle), \quad (3)$$

that cannot be written as the products of independent states of two separate subsystems.

### 2.1.3 Quantum parallelism and decoherence

Due to the quantum superposition and the quantum entanglement it is possible to perform multiple computations simultaneously or *quantum parallelism* on a system. But a measurement on the system destroys the quantum superposition and the system collapses to one of its possible states. This phenomenon is the *quantum decoherence* that can be seen as an interaction between a qubit and its environment. One of the challenges of quantum processing consists of increasing the probability to observe a needed state before the quantum decoherence occurs.

### 2.1.4 Elementary quantum gate

Quantum computing (that is changing the state of a qubit to another) is carried out through *unitary operators* or *quantum logic gates* when they are used in quantum circuit. Unlike many classical logic gates, the quantum logic gates are reversible, and therefore allow to avoid energy dissipation. Let us recall that the operator  $U$  is an unitary operator if

$$UU^\dagger = U^\dagger U = \mathbb{I}, \quad (4)$$

where  $\mathbb{I}$  is the identity operator, and  $U^\dagger$  the complex conjugate transpose of  $U$ . Any unitary operator can be written as

$$U = \exp(-iG), \quad (5)$$

where  $G$  is an hermitian operator, that is  $G = G^\dagger$ .

In the present work, the NOT gate  $X = |1-x\rangle\langle x|$  and the Walsh-Hadamard gate  $W = \frac{1}{\sqrt{2}}((-1)^x|x\rangle\langle x| + |1-x\rangle\langle x|)$  will be the most using single-qubit quantum logic gates:

$$|x\rangle \xrightarrow{X} |1-x\rangle \quad X = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix} \quad (6)$$

$$|x\rangle \xrightarrow{W} \frac{1}{\sqrt{2}}((-1)^x|x\rangle + |1-x\rangle) \quad W = \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix}, \quad (7)$$

where  $x \in \{0, 1\}$ .

The two-qubit quantum logic gate mostly used in this work will be the controlled NOT gate  $CX = (|0\rangle\langle 0| \otimes \mathbb{I} + |1\rangle\langle 1| \otimes X)$ :

$$\begin{array}{c} |x\rangle \text{---} \bullet \text{---} |x\rangle \\ |y\rangle \text{---} \boxed{X} \text{---} |1-y\rangle \end{array} \quad CX = \begin{pmatrix} \mathbb{I} & \mathbb{O} \\ \mathbb{O} & X \end{pmatrix} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{pmatrix}, \quad (8)$$

where  $x, y \in \{0, 1\}$ . The  $CX$  gate acts on two-qubits and performs the  $X$  operation on the second qubit only when the first qubit is in the state  $|1\rangle$ , and otherwise leaves it unchanged.

## 2.2 Few basic concepts of Associative Memories

A Neural Network, more properly referred to as an *Artificial Neural Network* (ANN), is a computing system made up of several important basic elements, which include the concept of a processing element (neuron), the transformation performed by this element (in general, input summation and non-linear mapping of the result into an output value), the interconnection structure between neurons, the network dynamics, and the learning rules that govern the modification of interconnection strengths [15]. A major dichotomisation of Neural Networks can be realised by considering whether they are trained in a supervised or unsupervised manner. An example of the latter is the Hopfield model of content-addressable memory, or Associative Memory, using the concept of attractor states. This model has an apparent similarity to human episodic memory: it can recall patterns after a single exposure using a Hebbian learning rule, and it is capable to retrieve the above mentioned patterns from partial information, partial and noisy information or noisy ones.

In short, Associative Memories are Neural Networks centralised around two algorithms. The first is to memorise information or patterns and known as *learning algorithm*. The second is for the restitution of learned information or patterns from partial or noisy data. It is known as *retrieving algorithm*.

Related to quantum theory, Associative Memories are called Quantum Associative Memories (QAM) where the learning and retrieving algorithms are quantum algorithms. The QAM is one of the most promising approaches to quantum neurocomputing. The linear part of the QAM design here is an improved version of the one built by Ventura and Martinez where the stored patterns are considered as the basis states of the memory quantum state [16].

It should be noted that in the classical Hopfield network the existence of symmetric, Hebbian connections, guarantees the stability of a unique stored pattern; similarly, in a quantum analogue of the Hopfield network the quantum entanglement ensures the integrity of a stored pattern (basis state).

The Tab. 1 summarises the analogies used in developing a QAM [15].

Classical Neural Networks	Quantum Associative Memory
Neuronal state $x_i \in \{0, 1\}$	Qubit $ x\rangle = \alpha 0\rangle + \beta 1\rangle$
Connections $\{w_{ij}\}_{ij=1}^{p-1}$	Quantum entanglement $ x_0x_1 \dots x_{p-1}\rangle$
Learning rule $\sum_{s=1}^p x_i^s x_j^s$	Superposition of entangled states $\sum_{s=1}^p \alpha_s  x_0x_1 \dots x_{p-1}\rangle$
Winner search $n = \max_i \arg(f_i)$	Unitary transformation $\mathbf{U} \psi\rangle =  \psi'\rangle$
Output result $n$	Decoherence $\sum_{s=1}^p \alpha_s  x^s\rangle \Rightarrow  x^k\rangle$

Table 1: Corresponding concepts from the domains of classical Neural Networks and Quantum Associative Memory.

It is worth noting that there are some other interesting models of quantum inspired neural networks and quantum inspired evolutionary optimization algorithms [17, 18, 19, 20].

In Subsections 2.3 and 2.4 we will briefly describe the quantum learning and quantum retrieving algorithms used on our QAM model. The full details can be found in refs. [12] and [13].

### 2.3 Quantum learning algorithm

For our QAM an operator name BDD is used as the learning algorithm. The BDD operator is obtained by using the Binary Superposed Quantum Decision Diagram (BSQDD) proposed by Rosenbaum [21]. Contrarily to other quantum learning algorithms such as the one of Ventura [22], which needs the initial state to be  $|00\dots 0\rangle$ , the BSQDD is computed by using any basis states  $|z\rangle$  of the Hilbert space of  $2^n$  dimensions. The idea behind the BSQDD is to represent a quantum superposition as a decision diagram where each node corresponds to a gate. The gate that corresponds to the node on each branch of the BSQDD is controlled by the path used to reach it from the root of the decision diagram. Thereby three steps, given by Algorithm 1, are needed to construct one BSQDD.

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#### Algorithm 1 Linear QAM retrieving algorithm with distributed query for diagnosis

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- 1: **Finding the unsimplified BSQDD by using the Hadamard gates, Feymann gates, and inverters;** {The number of nodes of this unsimplified BSQDD represents the upper bound on the number of the gates that the quantum array generated by the BSQDD needs for being constructed.}
  - 2: **Reducing the BSQDD to obtain the final BSQDD;** {The goal is to have the lower bound on the number of quantum gates. To achieve this goal, we need to merge some nodes (gates) according to the links that can occur between qubits (like control qubit and target qubit). Two rules are used to obtain the final BSQDD. The first rule states that in two different branches of different nodes that correspond to the same next node, that same nodes merge. The second rule states that in different branches of different nodes that generate the same branch, that same branches merge.}
  - 3: **Converting the BSQDD to a quantum array that generates the desired quantum state.** {The array is obtained by adding the gates that correspond to the nodes in each layer of the final BSQDD. The starting point is the last layer and we always place the new gates to the right of the previously placed gates in the quantum array.}
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**Example 1** Fig. 1 gives the three steps allowing to construct the state  $\sqrt{\frac{1}{5}}(|000\rangle + |010\rangle + |110\rangle + |001\rangle + |101\rangle)$  from the starting state  $|000\rangle$ . The elementary gates used are respectively the rotation gates

$$\mathbf{R}(\theta) = \begin{pmatrix} \sqrt{\frac{3}{5}} & \sqrt{\frac{2}{5}} \\ \sqrt{\frac{2}{5}} & -\sqrt{\frac{3}{5}} \end{pmatrix}, \mathbf{R}(\alpha) = \begin{pmatrix} \sqrt{\frac{2}{3}} & \frac{1}{\sqrt{3}} \\ \frac{1}{\sqrt{3}} & -\sqrt{\frac{2}{3}} \end{pmatrix}, \quad (9)$$

the Hadamard gate  $W$ , and the NOT gate  $X$ . Then  $|\psi_3\rangle = \sqrt{\frac{3}{5}}|000\rangle + \sqrt{\frac{2}{5}}|100\rangle$  and  $|\psi_2\rangle = \sqrt{\frac{2}{5}}|000\rangle + \frac{1}{\sqrt{5}}|010\rangle + \frac{1}{\sqrt{5}}|100\rangle + \frac{1}{\sqrt{5}}|110\rangle$ .

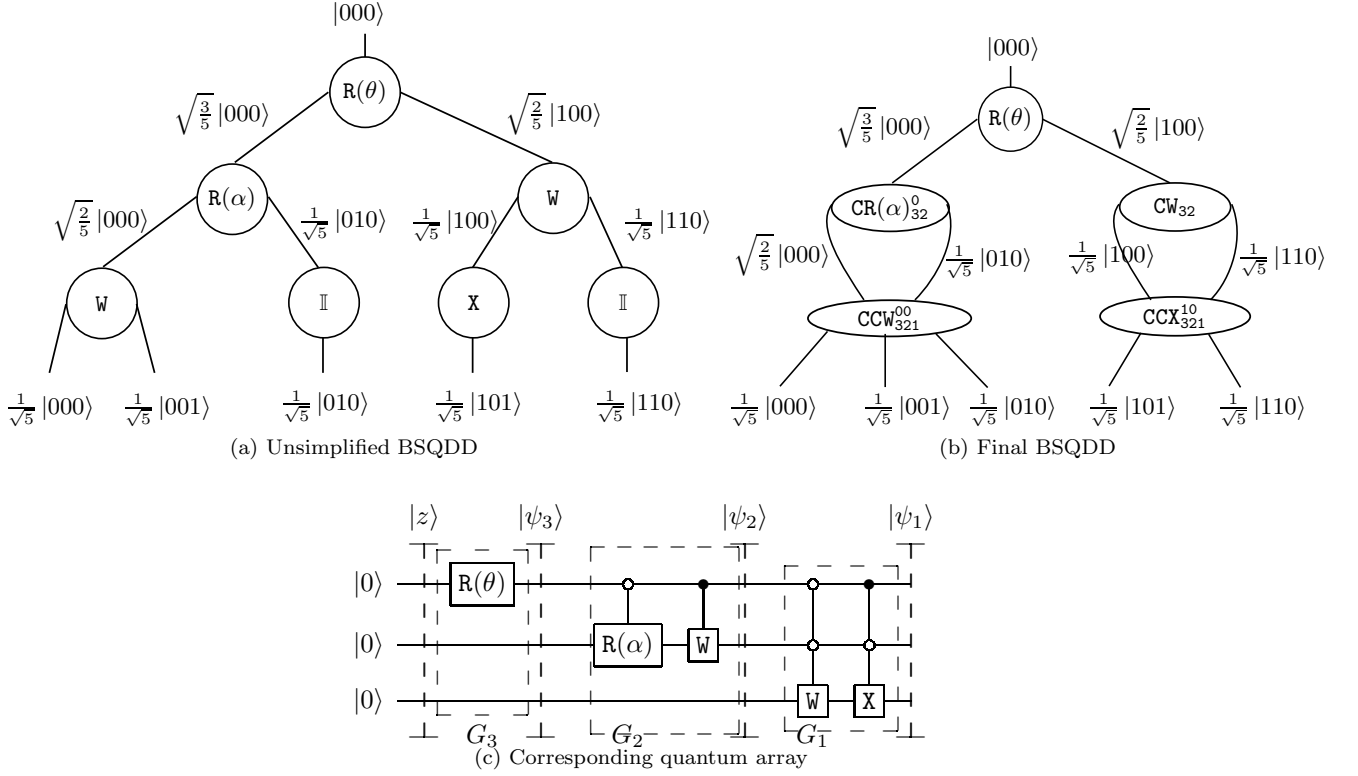


Figure 1: BSQDD to obtain the state  $|\psi_1\rangle = \sqrt{\frac{1}{5}}(|000\rangle + |010\rangle + |110\rangle + |001\rangle + |101\rangle)$ . The two BSQDDs of the Fig. are equivalent.

## 2.4 Quantum retrieving algorithms

We use two quantum retrieving algorithms that work together but with different learning approaches.

### 2.4.1 Linear QAM algorithm

The linear QAM retrieving algorithm given by Algorithm 2 is a slightly modified version of **QAM-C1** that we have proposed in ref. [12]. It uses an *exclusion learning approach*. That approach states that the system must be in the superposition of all the possible states, except the pattern states. Let us consider  $M$  as a set of patterns and  $m$  the number of patterns of length  $n$ , then

$$|\Psi\rangle = \frac{1}{\sqrt{N-m}} \sum_{x \notin M}^{N-1} |x\rangle, \quad N = 2^n. \quad (10)$$

In the Algorithm 2,

- $\mathcal{O}$  is the oracle operator that inverts the phase of the query state  $|Req^p\rangle$ ,

$$\mathcal{O} = \mathbb{I} - (1 - e^{i\pi}) |Req^p\rangle \langle Req^p|, \quad (11)$$

$$\mathcal{O} : a_x \mapsto a_x - 2Req_x^p \left( \sum_{x=0}^{2^n-1} (Req_x^p)^* a_x \right), \quad (12)$$

where  $a_x$  is the probability amplitude of the state  $|x\rangle$ . The distributed query  $|Req^p\rangle$  is in the following superposed states

$$|Req^p\rangle = \sum_{x=0}^{N-1} Req_x^p |x\rangle, \quad (13)$$

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**Algorithm 2** Linear QAM retrieving algorithm with distributed query for diagnosis
 

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1: Apply the oracle operator  $\mathcal{O}$  to the register;
2: Apply the diffusion operator  $\mathcal{D}$  to the register;
3: if  $\Lambda > 1$  then
4:   Apply the operator  $\mathcal{I}_M$  to the register;
5:   Apply the diffusion operator  $\mathcal{D}$  to the register;
6:   for  $1 \leq i \leq \Lambda - 1$  do
7:     Apply the oracle operator  $\mathcal{O}$  to the register;
8:     Apply the diffusion operator  $\mathcal{D}$  to the register;
9:      $i = i + 1$ ;
10:  end for
11: end if
12: Observe the system.

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where  $Req_x^p$  obey to binomial distribution

$$\|Req_x^p\|^2 = a^{d_H(p,x)}(1-a)^{n-d_H(p,x)}. \quad (14)$$

In equation (14),

- $p$  marks the state  $|p\rangle$  that is referred as the query centre;
- $a \in ]0, \frac{1}{2}[$  is an arbitrary value that tunes the width of the distribution;
- the **Hamming distance**  $d_H(p, x) = |p - x|$  between binary strings  $p$  and  $x$  is an important tool that gives the correlation between input and output;
- the amplitudes are such that  $\sum_x \|Req_x^p\|^2 = 1$ .

- $\mathcal{D}$  is the diffusion operator that inverts the probability amplitude of the states of  $|\Psi\rangle$  over their average amplitude and for the others over the value 0:

$$\mathcal{D} = (1 - e^{i\pi}) |\Psi\rangle \langle \Psi| - \mathbb{I}, \quad (15)$$

$$\mathcal{D} : a_x \mapsto 2m_x \left( \sum_{x=0}^{N-1} m_x^* a_x \right) - a_x, \quad (16)$$

where  $m_x$  is the probability amplitude of a state of  $|\Psi\rangle$ .

- $\Lambda$  is the number of iterations that yields the maximal value of amplitudes, which must be as far as possible nearest to an integer,

$$\Lambda = T\left(\frac{1}{4} + \alpha\right), \quad T = \frac{2\pi}{\omega}, \quad \alpha \in \mathbb{N}, \quad (17)$$

with the frequency of Grover

$$\omega = 2 \arcsin B, \quad B = \frac{1}{\sqrt{N-m}} \sum_{x=0, x \notin M}^{N-1} Req_x^p. \quad (18)$$

- According to the approach **QAM-C1** of the ref. [12]  $\mathcal{I}_M$  inverts only the phase of the memory pattern states as in the model of Ventura,

$$\mathcal{I}_M = \mathbb{I} - (1 - e^{i\pi}) |\varphi\rangle \langle \varphi|, \quad |\varphi\rangle \langle \varphi| = \sum_{x \in M} |x\rangle \langle x|, \quad (19a)$$

$$\mathcal{I}_M : a_x \mapsto \begin{cases} -a_x & \text{if } |x\rangle \in M \\ a_x & \text{if not.} \end{cases} \quad (19b)$$

The linear QAM algorithm is used here as main algorithm given that it increases the probability amplitude of the searched disease.

### 2.4.2 Non-linear QAM algorithm

The non-linear QAM retrieving algorithm given by Algorithm 3 is formally the same with the one we have proposed in ref. [13] (see that ref. for more details) that is an improved version of the one given by [23]. It uses *inclusion learning approach*.

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**Algorithm 3** Non-linear QAM retrieving algorithm for diagnosis

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- 1: Apply the oracle operator  $U_f$ , with  $f$  a function
  - 2: **repeat**  $(c - r)$  times step (3) to step (5) (i.e., one time per qubit of the first register starting from  $(r + 1)^{th}$  qubit with the flag qubit)
  - 3:   Apply the unitary operator  $U$
  - 4:
    1. Apply the non-linear operator  $NL^-$
    2. Apply the non-linear operator  $NL^+$
  - 5:   Apply the Hadamard operator  $W$  on the qubit of the first register and the NOT operator  $X$  on the flag qubit
  - 6: Observe the flag qubit
- 

Algorithm 3 is used on the subspace of signs and symptoms and allows to know if signs and symptoms related to a particular disease exist in the database. In the Algorithm 3,

- $n$  is the number of qubits of the first register.
- $p \leq 2^n$  is the number of stored patterns.
- $q \leq p$  is the number of stored patterns if the values of  $t$  qubits are known (i.e.  $t$  qubits have been measured or are already disentangled to others or the oracle acts on a subspace of  $(n - t)$  qubits).
- $c = \text{ceil}(\log_2 q)$ , that is the least integer greater or equal to  $\log_2 q$ .
- $m \leq q$  is the number of values  $x$  for which  $f(x) = 1$ .
- $r = \text{int}(\log_2 m)$  is the integer part of  $\log_2 m$ .

## 3 Database: signs and symptoms of the four tropical diseases

### 3.1 Short description of the four diseases

Based on [24, 25, 26, 27] we are going to give a briefly description of the four tropical diseases of our study. Appendix A gives their signs and symptoms.

**Malaria** is a life-threatening disease caused by protozoan parasites of the genus *Plasmodium*. The parasite is generally transmitted from one human to another through the bite of infected females Anopheles mosquitoes. Five species infect humans by entering the bloodstream: *P. knowlesi*, *P. ovale*, *P. malariae*, *P. vivax* and *P. falciparum*. The last two ones, *P. vivax* and *P. falciparum*, are the greatest threat because they affect a greater proportion of the red blood cells than the others. *P. falciparum* is the most prevalent malaria parasite on the African continent. It is generally responsible for most malaria-related deaths. *P. vivax* has a wider distribution than *P. falciparum*, and predominates in many countries outside Africa. About 3.2 billion people, almost half of the world population, are exposed to malaria. Sub-saharan Africa carries a disproportionately high share of the global malaria burden. In 2015, the region was home of 89% of malaria cases and 91% of malaria deaths.

**Typhoid fever**, also known as salmonellosis, is a life-threatening illness caused by the bacterium *Salmonella typhi*, also known as *Salmonella enterica* serotype typhi, growing in the intestines and blood. Dirt (poor sanitation and poor hygiene) is the main cause of transmission of the disease. Contaminated food and unsafe water are the main vectors. Typhoid fever remains a serious worldwide threat, especially in developing countries. The estimated cases of this disease are nearby 16-33 millions each year; this leads to more than half million death cases. The disease is endemic in India, Southeast Asia, Africa, South America and many other areas.

**Yellow fever** is an acute viral hemorrhagic disease caused by a *Flavivirus*. The virus is transmitted through the bite of an infected female mosquito (*Aedes aegypti*). The virus causes deterioration of the liver. There are an estimated 200,000 cases of yellow fever, causing 30,000 worldwide deaths each year, with 90% occurring in Africa. Forty-four endemic countries in Africa and Latin America, with a combined population of over



900 millions, are at risk. In Africa, an estimated 508 millions people live in 31 countries exposed to the disease. The remaining population at risk are in 13 countries in Latin America. Bolivia, Brazil, Colombia, Ecuador and Peru are at greatest risk.

**Dengue fever** is a painful, debilitating mosquito-borne tropical disease caused by *dengue virus*. The virus is transmitted by several species of mosquito within the genus *Aedes*, principally *Aedes aegypti*. WHO has classified dengue as one of the neglected tropical diseases and reported the resurgence of the disease [28]. Dengue is common in more than 110 countries. It infects 50 to 528 millions people worldwide a year, leading to half million hospitalisations, and approximately 25,000 deaths. Cases of the disease have been reported at least in 22 countries in Africa; but it is likely present in all of them with 20% of the population at risk. This makes it one of the most common vector-borne diseases worldwide.

### 3.2 Description of the database

Our database contains signs and symptoms of four tropical diseases: malaria, typhoid fever, dengue fever and yellow fever (see Appendix A). There are seventeen signs and symptoms specific to malaria, eighteen to typhoid fever, twenty-three to dengue and seventeen to yellow fever. Some signs and symptoms are common to different diseases, not only the four, such as fever and headache for example, thereby our database contains ninety-five signs and symptoms. We need six qubits for the computation because each symptom is labelled with a number in its binary form. Therefore we can compute  $2^6$  signs and symptoms per disease. In the subspace of disease we label the signs and symptoms in decimal form by starting with 0. Furthermore, we need four qubits to label the ten groups of diseases presented by the Tab. 2 that are used in the linear QAM algorithm. There is one group per individual disease (N° 1-4); two groups corresponding to common signs and symptoms to malaria and typhoid fever or yellow fever (N° 5-6); two groups corresponding to common signs and symptoms to yellow fever and typhoid fever or dengue (N° 7- 8); one group corresponding to common signs and symptoms to malaria, yellow fever and dengue (N° 9); and finally one group corresponding to common signs and symptoms to each of the four diseases. The last can be found in other diseases such as headache, fever and abdominal pain (N°10). For the non-linear QAM algorithm we need four flag qubits, one for each disease. It appears that we need a register that contains  $n = 14$  qubits, six for signs and symptoms, four for diseases for each QAM algorithm. So, there are two output registers. The labels of the output qubits for the linear QAM algorithm are mentioned above. The other possibilities are pointed to be other diseases and signs and symptoms in our model. Two sets of four qubits for output are needed due to the fact that the learning process of the linear QAM algorithm is different from the one used for the non-linear QAM algorithm. For the non-linear QAM algorithm each flag qubit is associated to one disease. That qubit allows to know if a symptom specific to a particular disease is present. Therefore value 0 means that this particular disease is not present, whereas value 1 means that it is present. Nevertheless, if the values of that four qubits are 0, it means that none specific symptom is introduced.

N°	Group of diseases by signs and symptoms	Label
1	Malaria	0001>
2	Typhoid fever	0010>
3	Yellow fever	0100>
4	Dengue	1000>
5	Malaria + Typhoid fever	0011>
6	Malaria + Yellow fever	0101>
7	Yellow fever + Typhoid fever	0110>
8	Yellow fever + Dengue	1100>
9	Malaria + Yellow fever + Dengue	1101>
10	Other diseases	1111>

Table 2: Groups of diseases by signs and symptoms and their labels in binary form for the linear algorithm. The hamming distance between the label of two groups of diseases is equal to 1 when the signs and symptoms are common to these two groups of diseases and is equal to 2 otherwise. The group N° 10 or *Other diseases* is devoted to signs and symptoms that are common to each 4 diseases and that can also occur in other groups of diseases not mentioned here. We point out the fact that other labels are also consider to be *Other diseases*.

For the linear QAM retrieving algorithm, the determination of the number of iterations is mentioned above. Labelling all the fourteen qubits from  $|q_1\rangle$  to  $|q_{14}\rangle$ , the entire QAM looks as illustrated in Fig. 2.



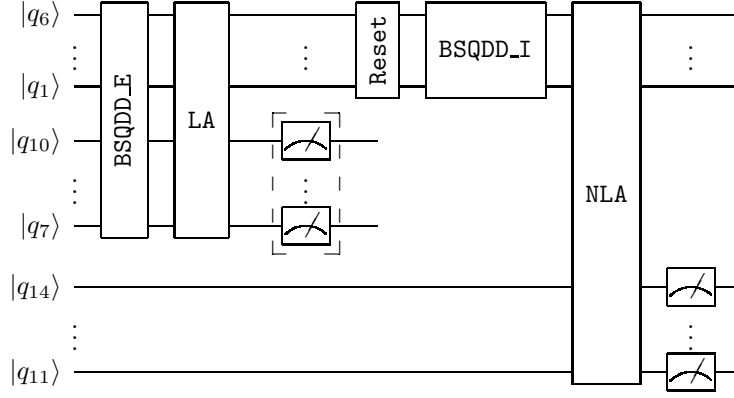


Figure 2: Schematic structure of the QAMDiagnos. BSQDD\_E is the learning part of the linear QAM algorithm, whereas, after reinitialisation, BSQDD\_I is the learning part of the non-linear QAM algorithm. LA is the set of gates simulating the linear QAM algorithm. NLA is a repeated non-linear QAM algorithm, once for each disease. Each flag qubit from  $|q_{11}\rangle$  to  $|q_{14}\rangle$  is devoted to one disease.

## 4 Simulations results and discussion

To design the linear part of the QAMDiagnos, we take into account the four following facts:

1. The arbitrary value that regulates the width distribution around the chosen centre is  $a = 0.4999$  ;
2. The centre of the query is  $|0000\rangle$  because we assume that there is no indication about disease;
3. The difference between the number of iterations  $\Lambda$  and the nearest integer must be less than 0.1;
4. Not more than six signs and symptoms can be chosen.

We give in the next Tabs. 3 and 4 the average probabilities of correct recognition ( $P_c$ ). We take the average due to the convention we chose to label signs and symptoms, and diseases. Therefore, *sensibility* is the conditional probability to have a correct recognition if the disease is present. So, as we can obtain from our QAM probabilities of good recognition, we can see that they look like sensibilities.

### • For single infection

We obtain sensibilities according to the definition.

Disease	Number of signs and symptoms							$q_{11}$	$q_{12}$	$q_{13}$	$q_{14}$
	1	2	3	4	5	6					
Malaria	93.8911	94.5059	97.5402	96.4843	99.9043	96.5960	Without other	1	0	0	0
Typhoid fever	93.8911	94.5059	97.5402	96.4843	99.9043	96.5960		0	1	0	0
Yellow fever	93.8911	94.5059	97.5402	96.4843	99.9043	96.5960	signs and symptoms	0	0	1	0
Dengue	93.8904	94.5052	97.5397	96.4837	99.9041	96.5954		0	0	0	1
Malaria	47.4418	65.0912	72.4296	79.9350	80.5407	-	With 1 other	1	0	0	0
Typhoid fever	47.4418	65.0912	72.4296	79.9350	80.5407	-		0	1	0	0
Yellow fever	47.4418	65.0912	72.4296	79.9350	80.5407	-	sign or symptom	0	0	1	0
Dengue	47.4411	65.0905	72.4289	79.9346	80.5400	-		0	0	0	1
Malaria	32.6307	48.3689	59.9605	64.4826	-	-	With 2 other	1	0	0	0
Typhoid fever	32.6307	48.3689	59.9605	64.4826	-	-		0	1	0	0
Yellow fever	32.6307	48.3689	59.9605	64.4826	-	-	signs and symptoms	0	0	1	0
Dengue	32.6302	48.3683	59.9600	64.4819	-	-		0	0	0	1
Malaria	24.3022	39.9808	48.4219	-	-	-	With 3 other	1	0	0	0
Typhoid fever	24.3022	39.9808	48.4219	-	-	-		0	1	0	0
Yellow fever	24.3022	39.9808	48.4219	-	-	-	signs and symptoms	0	0	1	0
Dengue	24.3018	39.9803	48.4213	-	-	-		0	0	0	1

Table 3: Average probabilities  $P_c$  according to the number of signs and symptoms related to a disease in case of a single infection for the linear part of the QAM. For the non-linear part, each corresponding flag qubit has its value equal to 1. Here “other signs and symptoms” are fever, headache and abdominal pain.

- For polyinfection

We also obtain sensibilities according to the definition.

Disease	Number of symptom of malaria				
	0	1	2	3	
Malaria	0.1577	24.2913	39.9633	48.4079	With 1 sign or symptom of Typhoid f.
Typhoid fever	32.6167	24.2913	19.9844	16.2842	
Malaria + Typhoid f.	65.0886	48.3653	39.9685	32.3538	
Malaria	0.2283	19.9844	32.3460	-	With 2 signs and symptoms of Typhoid f.
Typhoid fever	48.3543	39.9633	32.3460	-	
Malaria + Typhoid f.	48.3653	39.9685	32.3538	-	
Malaria	0.0055	16.2842	-	-	With 3 signs and symptoms of Typhoid f.
Typhoid fever	59.9422	48.4079	-	-	
Malaria + Typhoid f.	39.9685	32.3538	-	-	
Malaria	0.2224	-	-	-	With 4 signs and symptoms of Typhoid f.
Typhoid fever	64.4697	-	-	-	
Malaria + Typhoid f.	32.3538	-	-	-	
$q_{11}$	0	1	1	1	
$q_{12}$	1	1	1	1	
$q_{13}$	0	0	0	0	
$q_{14}$	0	0	0	0	

Table 4: Probabilities  $P_c$  according to the number of signs and symptoms related to diseases in case of a polyinfection for the linear part of the QAM. For the non-linear part, each corresponding flag qubit has its value equal to 1. Here “common sign or symptom“ is the one that is common to the two diseases. Here we have chosen two common signs and symptoms.

As we can see on the Tabs. 3 and 4 the QAM can collapse to a state representing single infection or polyinfection. That is the QAM can distinguish single from polyinfection. That distinction is possible with the lowest (one) or the highest (six) number of particular signs and symptoms of a disease, but it is better in the last case. When the “other signs and symptoms” are inserted, the QAM can also do the distinction. As we observe on the Tab. 5 the “other signs and symptoms” are not related to a particular disease. Therefore, the non-linear part of the QAM completes or corrects the results of the linear part.

Disease	Number of signs and symptoms		
	1	2	3
Other diseases	96.38	96.73	98.53

Table 5: Probabilities  $P_c$  according to the number of “other signs and symptoms” for linear part of the QAM. For the non-linear part, each flag qubit has its value equal to 0. The QAM does not associate these signs and symptoms to one of the four diseases.

We also evaluate the specificity of the QAM. *Specificity* is the conditional probability to have a correct recognition if the disease is not present. In other words it is the ability of the memory to distinguish healthy people from non-healthy ones. For our QAM, to acquire it we use the 448 signs and symptoms without any relation with the four diseases and take the average of probabilities to obtain “Other diseases” as a result. We obtain the Tab. 5 and assume that the specificity is **96.38%**.

## 5 QAMDiagnos: desktop and smart-phone GUI

All the simulations and results were made by encoding the algorithms in C++ language. A multi-platform friendly graphical user interface (GUI) of our QAMDiagnos is designed for the medical staff. (see figures of supplementay material for more details). It is developed with the open source version of the C++ library Qt5.

To use the software, after observing or discussing with a patient, and according to what he observes and the answers of the patient, the physician introduces signs and symptoms in the QAMDiagnos (at least one sign or symptom and a maximum of six signs and symptoms). The result and a proposal of treatment are given in the text box “Treatment proposal“ for the desktop GUI or in the only one text box for the smart-phone GUI. Although weight and age can be important for accurate diagnosis, the QAMDiagnos does not use these data because it can occur that the physician forgets to take them or not. Therefore, in the text box “Treatment proposal“ the

QAMDiagnos shows a treatment proposal which is not bound to the weight or age. We made the simulations on a *classical computer*, so we can obtain each probability (recognition efficiency).

Thus, the physician can also compare the recognition efficiency of the linear part of the QAMDiagnos for each disease given in the "Results" area. So, the disease with the greatest recognition efficiency can be viewed as the corresponding disease of the patient. To achieve this goal, that is to simulate the probabilistic nature of the quantum theory, we use the `qrand()` function of `Qt5` that allows us to choose arbitrarily one of the diseases according to its probability. As the linear QAM algorithm is the main algorithm, the disease with the highest probability is given as result with the associated treatment proposal. Before that, the non-linear QAM algorithm identifies if a sign or symptom specific to a particular disease is present. The results of the linear QAM algorithm and the non-linear QAM algorithm are given together to help the physician in his decision.

The complementary of the two algorithms is more highlighted in the case of polyinfection. For example, if common signs and symptoms to malaria, yellow fever and dengue are inserted and symptom particular to malaria and another to yellow fever are also inserted, the linear QAM algorithm will identify this combination as a polyinfection. But, the non-linear QAM algorithm will identify the signs and symptoms of malaria and yellow fever. This gives to the physician the possibility to focus only on two diseases (malaria and yellow fever) instead of the three.

Some snapshots of the QAMDiagnos allowing better understanding are available as supplementary material associated to this paper.

## 6 Conclusion

We have presented in this paper the QAMDiagnos, a Quantum Associative Memory framework that can be helpful to diagnose four tropical diseases (malaria, typhoid fever, yellow fever and dengue) with several common signs and symptoms. The framework that has a friendly multi-platform GUI, is a combination of the improved versions of original quantum linear retrieving algorithm proposed by Ventura and the non-linear quantum search algorithm of Abrams and Lloyd. While the phase-inversion introduced in the original linear QAM algorithm increases the capacity of the memory to make a good diagnosis, the non-linear QAM algorithm helps to confirm or to correct the diagnosis and to make some suggestions to the medical staff for the treatment. In addition, the QAMDiagnos can distinguish a single infection from a co-infection and needs only few specific signs and symptoms of disease and common signs and symptoms. Therefore, the QAMDiagnos framework can be a good tool to help inexperienced medical staff or medical staff without laboratory facilities to rapidly and accurately diagnose malaria, typhoid fever, yellow fever and dengue, four tropical diseases that are often confused. Due to its highly automated nature, health centres personnel can be trained to operate the QAMDiagnos in just one day.

For future works, it is planned to build up a device that can help acquire physiological parameters on a patient and transfer them to the QAMDiagnos.

## Acknowledgements

We thank Pr. Paul WOAFO for his helpful discussions and remarks. We also thank Dr. OKALA, Dr. DOUALLA and Pr. LUMA of the Hopital Général de Douala (Cameroon) for their remarks and their help on the classification of signs and symptoms. We also thank Moise SOH, the Senior Translator, for proofreading our work.

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## A Symptoms of each group of diseases

<b>Malaria</b>	<b>Typhoid fever</b>	<b>Yellow fever</b>	<b>Dengue</b>
Headache	Headache	Headache	Headache
Abdominal pain	Abdominal pain	Abdominal pain	Abdominal pain
Fever	Fever	Fever	Fever
Myalgia		Myalgie	Myalgia
Renal failure		Renal failure	Renal failure
Nausea		Nausea	Nausea
Vomiting		Vomiting	Vomiting
Shiver or cold sensation		Shiver or cold sensation	
Hemorrhage		Hemorrhage	
Icterus		Icterus	
Oliguria		Oliguria	
Anorexia	Anorexia		
Coma	Coma		
Prostration	Prostration		
	Epistaxis	Epistaxis	
	Myocarditis	Myocarditis	
		Rachiodynia	Rachiodynia
		Heart failure	Heart failure
		Hepatic failure	Hepatic failure
		Conjunctival injection	Conjunctival injection
		Somnolence	Somnolence
Anemia	Asthenia	Acidosis	Accumulation of fluid and respiratory distress
Shock	Bouveret's ulcer	Bradycardia related to temperature	Generalized adenopathy
Generalized or focal convulsion	Relative bradycardia	Infectious shock	Agitation or Lethargy
Multiple convulsion	Constipation	Terminal coma	Arthralgia
Stiffness	Yellowy diarrhea	Excessive dryness	Asthma prolonge
Delirium	Encephalitis	Back pain	Elevation of the hematocrit and fast drop of platelets
Respiratory distress	Lenticular exanthem of limbless man	Limb pain	Corrected shock
Diarrhea	Rumble in the right iliac cavity	Renal pain	Uncorrected shock
Hemoglobinuria	Digestive hemorrhage or digestive perforation	Epigastric pain	Tensor fall
Hepatosplenomegaly	Insomnia	Fatigue	Desquamation of macular eruption
Hypoglycemia	Sabural tongue	Foul breath	Retro-orbital pain
Malaise	Abdominal heaviness	Hypotension	Encephalopathy
Pulmonary edema	Peritonitis	Lumbago	Macular eruption
Palenes	Dissociate pulse	Prolongation of the PR and QT intervals on electrocardiography	Maculopapular exanthem
Sub-icterus	Septicemia	Light proteinuria	Hepatomegaly (>2cm)
Profuse sweat	Splenomegaly	Purpura	Sudden hypothermia
Conscience trouble	Moderate splenomegaly	Vomito negro	Leukopenia
	Typhoid state		Obnubilation
			Vascular purpura
			Benign cutaneous or mucous bleeding
			Severe cutaneous or mucous bleeding
			Persistent vomiting

Table 6: signs and symptoms of the database [24, 25, 26, 27].