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Research article

On the criteria for diagnosing depression in bereaved individuals: a self-organizing map approach

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Abstract: Bereavement exclusion (BE) is a criterion for excluding the diagnosis of major depressive disorder (MDD). Simplistically, this criterion states that an individual who reports MDD symptoms should not be diagnosed as suffering from this mental illness, if such an individual is grieving a sorrowful loss. BE was introduced in 1980 to avoid confusing MDD with normal grief, because several cognitive and physical symptoms of grief and depression can look similar. However, in 2013, BE was removed from the MDD diagnosis guidelines. Here, this controversial topic is computationally investigated. A virtual population is generated according to the Brazilian data of death rate and MDD prevalence and its five kinds of individuals are clustered by using a Kohonen's self-organizing map (SOM). In addition, by examining the current guidelines for diagnosing MDD from an analytical perspective, a slight modification is proposed. With this modification, an adequate clustering is achieved by the SOM neural network. Therefore, for mathematical consistency, unbalanced scores should be assigned to the items composing the MDD diagnostic criteria. With the proposed criteria, the co-occurrence of normal grief and MDD can also be satisfactorily clustered.

Keywords: bereavement exclusion; grief; Kohonen network; major depressive disorder; psychometrics; self-organizing map

1. Introduction

Grief is an expected human response to a significant loss, particularly, the death of a loved one. Despite its negative health effects, grief is not considered to be a pathological state; it is viewed as a natural emotional reaction to losing someone that was truly important [1, 2]. Several psychological and physiological symptoms associated with this painful reaction are similar to those found in people suffering from major depressive disorder (MDD), the mental illness commonly known as depression. These symptoms include intense sadness, lowered appetite, sleep disturbance, suicidal thoughts.

Hence, due to this apparent overlap of mental and somatic manifestations, people experiencing normal grief can be misdiagnosed as suffering from MDD [3–9]. In fact, recently bereaved individuals usually exhibit depressive symptoms.

Bereavement exclusion (BE) means that MDD should not be assigned to a bereaved individual in the acute phase. The duration of this phase depends on many factors, such as the relationship to the deceased and the manner of death. Thus, BE would be a criterion for avoiding false positive diagnosis of MDD [3–9].

This rationale behind BE has been a matter of debate [3–9], because BE implies that grief must be considered as a distinctive stressor causing depressive symptoms. However, other life-changing events, such as bankruptcy, job loss, major illness or injury, and marital separation, are well-known stressors that can also adversely and strongly affect the psyche and the wellness.

In the third edition in 1980 of the Diagnostic and Statistical Manual of Mental Disorders (DSM-III) by the American Psychiatric Association, BE was introduced [10]; in the fifth edition (DSM-5) in 2013, BE was deleted [11]. By removing BE, DSM-5 explicitly assumes that grief and MDD can simultaneously occur. Here, we agree with this assumption, but we also consider that grief is an atypical sorrowful circumstance. Financial troubles, health problems, and relationship difficulties can be satisfactorily overcome in some way, but death cannot be undone. The solution to the bereaved individual is try to adapt to the new reality without the deceased. Unfortunately, not everyone can properly cope with this change.

Distinguishing between MDD during bereavement and normal grief can be a challenging task. Here, this issue is examined as a data-clustering problem by using an artificial neural network. Artificial intelligence techniques and statistical analyses have been widely used in studies on MDD [12–18]. Usually, these tools are employed to detect MDD in people; here, the consistency of the criteria for diagnosing MDD is evaluated by a self-organizing map (SOM) [19, 20].

In this work, a population composed of five kinds of individuals considering the MDD prevalence and the mortality rate is created. Then, these individuals are clustered by a SOM network in function of the list of symptoms to diagnose MDD [11]. This list comprises nine items. Obviously, grief is not a symptom, but here it is taken as an extra item. These ten items are represented by binary variables. In the numerical experiments, the two possible values of these binary variables are the same for all items or not. Our experiments revealed that to adequately cluster the data, these values must be suitably chosen, which suggests a modification in the existing criteria for MDD diagnosis. In fact, it is shown here that the current criteria are mathematically inconsistent; hence, they should be modified to improve the data clustering process (by an algorithm or a real-world physician). Such criteria were already criticized in other works [6, 21–24].

Mathematical approaches have been developed to study MDD [25–27] and grief [28–30]. This manuscript about the possible co-occurrence of MDD and normal grief is organized as follows. In Section 2, the characteristics of the sample population are described. In Section 3, the algorithm of the SOM neural network is detailed. In Section 4, analytical and numerical results about data clustering by using a SOM network are presented. In Section 5, the possible implications of our work on the psychometric properties of the MDD criteria are discussed.

2. The sample population

There are five kinds of individuals in the considered population: depressed individuals (D), grieving individuals (G), grieving individuals with MDD (GD), non-grieving individuals without MDD symptoms (NGW), non-grieving individuals having some MDD symptoms (NGS). The numbers of D, G, GD, NGW and NGS-individuals are n_D, n_G, n_{GD}, n_{NGW} and n_{NGS}, respectively. The total number of individuals is n; therefore, $n_D + n_G + n_{GD} + n_{NGW} + n_{NGS} = n$.

A fictitious population with $n = 1000$ individuals based on Brazilian statistics was created. Since the MDD prevalence in Brazil was 5.8% in 2015 [31], then $n_D = 58$, by considering the BE-criterion (similar numbers can found, for instance, in Germany [25]). The mortality rate was taken as 6 individuals per 1000 individuals per year [32]. Assume that each deceased person leaves two individuals in mourning; therefore, $n_G + n_{GD} = 12$. Assume also that $n_{GD} = 4$ (1/3 of 12). With these choices, $n_G = 8$ and $n_{NGW} + n_{NGS} = 930$. Suppose that 620 individuals (2/3 of 930) do not have any symptom of MDD and 310 individuals have at least one symptom of MDD, but they are not diagnosed as having MDD. Thus, $n_{NGW} = 620$ and $n_{NGS} = 310$.

Here, each individual of this population is represented by a vector $\vec{y}$. The components of $\vec{y}$ are the values y_j of the items listed in Table 1. In order to reduce its dimension, a vector $\vec{x}$ is built from a vector $\vec{y}$ by taking:

$$x_1 = \sum_{j=1}^{2} y_j \tag{2.1}$$

$$x_2 = \sum_{j=3}^{9} y_j \tag{2.2}$$

$$x_3 = y_{10} \tag{2.3}$$

If BE is considered, $\vec{y} = \{y_1, y_2, ..., y_9\}$ and $\vec{x} = \{x_1, x_2\}$; if BE is discarded, $\vec{y} = \{y_1, y_2, ..., y_{10}\}$ and $\vec{x} = \{x_1, x_2, x_3\}$. Hence, the dimension d of $\vec{x}$ is 2 or 3.

Table 1. Items 1 to 9 compose the symptom checklist for MDD found in DSM-5 [11]. Grief is taken into account in item 10. Absence of symptom/grief corresponds to $y_j = 0$; presence, to $y_j \neq 0$ (for $j = 1, 2, ..., 10$). The constants a, b and c are positive numbers.

#	item	binary variable
1	depressed mood	$y_1 = \{0, a\}$
2	loss of interest or pleasure	$y_2 = \{0, a\}$
3	weight loss or gain	$y_3 = \{0, b\}$
4	insomnia or hypersomnia	$y_4 = \{0, b\}$
5	psychomotor agitation or retardation	$y_5 = \{0, b\}$
6	fatigue or loss of energy	$y_6 = \{0, b\}$
7	feelings of worthlessness or guilt	$y_7 = \{0, b\}$
8	decreased concentration	$y_8 = \{0, b\}$
9	recurrent thoughts of death	$y_9 = \{0, b\}$
10	grief	$y_{10} = \{0, c\}$

According to DSM-5 [11], the diagnosis of MDD is based on the presence over at least two weeks of five or more symptoms from the nine-item checklist presented in Table 1. The two first symptoms of this checklist are depressed mood and loss of interest or pleasure, and the MDD diagnostic criteria also require that at least one of these two symptoms must be present. In consonance with Table 1 and DSM-5, D-individuals have $y_1 \neq 0$ and/or $y_2 \neq 0$, and $y_j \neq 0$ for at least five items for $j = 1, 2, ..., 9$.

Note that, in this population, there are 620 individuals with $y_j = 0$ for all j and 310 individuals with $y_{10} = 0$ and $y_j \neq 0$ for some values of $j = 1, 2, ..., 9$ without meeting the MDD criteria. Also, there are 58 individuals meeting the MDD criteria and with $y_{10} = 0$, 4 individuals meeting the MDD criteria and with $y_{10} \neq 0$, and 8 individuals who do not meet the MDD criteria and with $y_{10} \neq 0$. For instance, if the absence of symptom/grieving is represented by 0 and the presence by 1, then the vector $\vec{y} = \{1, 1, 1, 1, 0, 0, 0, 1, 1, 0\}$ (which corresponds to $\vec{x} = \{2, 4, 0\}$) describes a D-individual; the vector $\vec{y} = \{0, 0, 0, 1, 0, 0, 1, 0, 0, 0\}$ (which corresponds to $\vec{x} = \{0, 2, 0\}$) describes a NGS-individual. To cluster these individuals, the neural network detailed in the next section is used. The inputs of this network are the vectors $\vec{x}$ of the $n = 1000$ individuals.

3. The Kohonen neural network

Kohonen developed the first model of neural network known as self-organizing map (SOM) [19, 20]. In his network, the neurons of an one-dimensional input layer, represented by the vector $\vec{x}$ with dimension d, are connected to the neurons composing a two-dimensional output layer $\ell \times \ell$. The weights of these connections are represented by the vector $\vec{w}_k$, in which the index k labels the output neurons. Observe that there are $d\ell^2$ connections between the two layers. The boundary condition of the output layer is here assumed to be periodic; that is, the top edge contacts the bottom edge and the left edge contacts the right edge (in order to eliminate edge effects). By employing an unsupervised learning algorithm, Kohonen showed that similarities of the input array can be translated into distance relations in the output grid.

At each time step t of the learning phase of the Kohonen network, a vector $\vec{x}$ from the training data set is used as input and such an input actives one neuron in the output layer. The activated neuron is the one for which the Euclidian distance between $\vec{x}$ and $\vec{w}_k$ is minimum. This winning neuron, denoted by k^*, defines a neighborhood $V(k^*)$ centered around it. Then, the weights of the k-th neuron are modified by following this update rule [19, 20]:

$$w_{kj}(t+1) = w_{kj}(t) + \Delta(t) \quad \text{if} \quad k \in V(k^*) \tag{3.1}$$

$$w_{kj}(t+1) = w_{kj}(t) \quad \text{if} \quad k \notin V(k^*) \tag{3.2}$$

The adjustment $\Delta(t)$ is calculated from:

$$\Delta(t) = \eta(t)\theta(t)[x_j(t) - w_{kj}(t)] \tag{3.3}$$

Note that $x_j(t)$ is the j-th component of the input $\vec{x}(t)$; that is, the value of the j-th neuron in the input array at the time step t; and $w_{kj}(t)$ is the weight of the connection between the j-th neuron in the input array and the k-th neuron in the output grid at the time step t. The $d\ell^2$ weights w_{kj} are randomly initialized between the minimum and the maximum values of x_j. In Eq (3.3), $\eta(t)$ is the learning rate and $\theta(t)$ is a function that has its maximum for $k = k^*$ and it decays as the distance from k^* increases. Both these functions are assumed to be decreasing with t.

Here, the learning rate $\eta(t)$ decays exponentially according to:

$$\eta(t) = \exp(-t/10^4) \tag{3.4}$$

The neighborhood of each output neuron is considered to be the whole grid $\ell \times \ell$ and the neighborhood function $\theta(t)$ is taken as a Gaussian written as:

$$\theta(t) = \exp(-\delta(t)^2/(2\sigma(t)^2)) \tag{3.5}$$

In Eq (3.5), $\delta(t)$ is the Euclidian distance between the winning neuron k^* and the k-th neuron belonging to its neighborhood $V(k^*)$ at the time step t. Observe that $\theta = 1$ for $k = k^*$ (because $\delta = 0$) and $\theta < 1$ for $k \neq k^*$. In addition, $\sigma(t)$ is given by:

$$\sigma(t) = \exp(-t/10^3) \tag{3.6}$$

Note that $\sigma(t)$ decreases exponentially as the time t passes by and, consequently, $\theta(t)$ also decreases (for $k \neq k^*$).

This training algorithm can be summarized as follows [19, 20]. At each time step t, an input vector $\vec{x}$ is chosen from the training data set and presented to the network. This data set consists of n vectors $\vec{x}$ randomly ordered. Recall that here n is the total number of individuals in the sample population. Then, k^* is determined, the weights of neurons within $V(k^*)$ are adjusted by following Eq (3.1), and the next vector $\vec{x}$ is used as input to the network. Here, the learning phase finishes when the sum of the adjustments Δ (given by Eq (3.3)) for all n inputs is below to $\epsilon = 10^{-3}d\ell^2$; that is, when the adjustment per connection is below to 10^{-3} considering all n inputs. At the end, nearby inputs activate (are mapped into) neighboring output neurons. Thus, the output layer exhibits a spatially organized representation of features of the inputs [19, 20]. Notice that the process of self-organization (which gives the network its name) occurs during the learning phase.

In order to quantitatively evaluate the results through internal measures after the learning phase, an average information entropy H was computed. For each activated neuron in the output layer, its information entropy h is determined by [33]:

$$h = -\sum_{\beta} p_\beta \log_2(p_\beta) \tag{3.7}$$

in which p_β is the relative frequency of occurrence of the β-th kind of individual in such a neuron, with $\beta \in \{D, G, GD, NGW, NGS\}$. For instance, assume that a neuron in the output layer is the winning neuron for five inputs $\vec{x}$, in which one input belongs to the G-group and four inputs belong to the GD-group. For this neuron, $h = -(1/5)\log_2(1/5) - (4/5)\log_2(4/5) \simeq 0.72$. Notice that if this neuron is activated only by inputs belonging to a single group, then $h = 0$ (because $p_\beta = 1$ for this group and $p_\beta = 0$ for the four remaining groups). The average information entropy H is the average value of h by considering all the output neurons that are activated by at least one input. This average entropy is shown in the caption of each figure of the next section. It is a measure of the heterogeneity of the output layer. The less heterogeneous the winning neurons, the lower the value of H.

The SOM network can assist physicians in clinical decision making [34]. In the context of this work, this assistance can be about treating some grieving individuals. The results obtained with the SOM network are presented in the next section.

4. Analytical and numerical results

The main goal of this work is to investigate if the SOM neural network can correctly cluster the sample population. Recall that each individual corresponds to a vector $\vec{y}$, which is transformed into a vector $\vec{x}$ with $d = 2$ or 3 components. The D, G, GD, NGW and NGS-individuals were randomly generated by following the features and restrictions described in Section 2. Recall also that the sample population is composed of $n_D = 58$, $n_G = 8$, $n_{GD} = 4$, $n_{NGW} = 620$ and $n_{NGS} = 310$. The size of the output layer of the SOM network is taken as $\ell = 7$.

The results of six numerical experiments are here presented. In the figures showing self-organized maps, a D-individual is represented by a red dot, a G-individual by a black dot, a GD-individual by a cyan dot, a NGW-individual by a blue dot, and a NGS-individual by a yellow dot.

In the first experiment, $d = 2$ and $a = b = 1$; that is, BE is considered (because x_3 does not compose the vector $\vec{x}$) and all binary variables y_j are in the same range. The result is shown in Figure 1. Observe that all NGW-individuals (blue) active a single neuron in the output layer. This was expected, because all these individuals are represented by a null vector. The other four groups are distributed over the output layer. Observe that there is an overlap in their representations. For instance, the neuron at the second line and second column is activated by D-individuals (red) and GD-individuals (cyan); the neuron at the sixth line and third column is activated by G-individuals (black) and NGS-individuals (yellow); the neuron at the fifth line and second column is activated by D-individuals (red) and NGS-individuals (yellow). In this figure, $H \simeq 0.16 \pm 0.29$. Notice that this result was obtained by strictly following the DSM-5 guidelines.

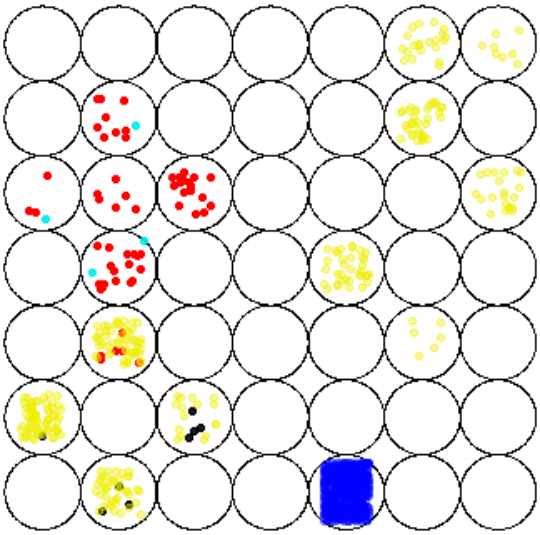

Figure 1. The self-organized map of the sample population with $n = 1000$ individuals, in which a D-individual is represented by a red dot, a G-individual by a black dot, a GD-individual by a cyan dot, a NGW-individual by a blue dot, and a NGS-individual by a yellow dot. Recall that $n_D = 58$, $n_G = 8$, $n_{GD} = 4$, $n_{NGW} = 620$ and $n_{NGS} = 310$. In this case, $d = 2$ and $a = b = 1$. In this figure, $H \simeq 0.16 \pm 0.29$.

In the second experiment, $d = 3$ and $a = b = c = 1$; thus, grief is considered an extra item and the corresponding variable (y_{10}) is in the same range of the other nine variables (y_1 to y_9). The result is shown in Figure 2. The overlap among the representations persists; however, $H \simeq 0.10 \pm 0.27$, which is lower than the value of H of Figure 1.

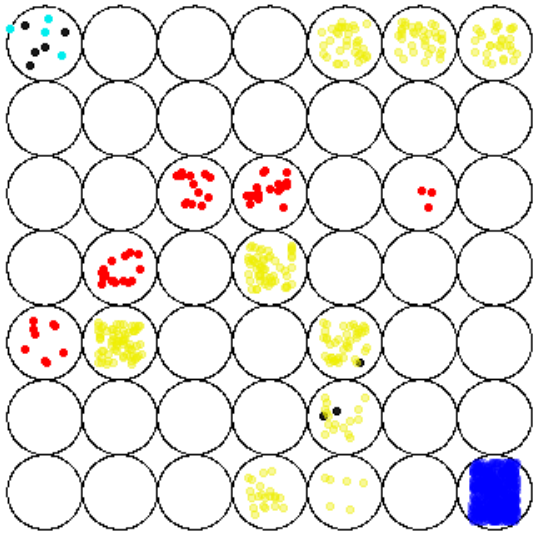

Figure 2. The self-organized map for $d = 3$ and $a = b = c = 1$. Here, $H \simeq 0.10 \pm 0.27$.

In the third experiment, presented in Figure 3, $c = x_1 + x_2$ (recall that $x_1 + x_2 = \sum_{j=1}^{9} y_j$). This choice of c does not eliminate the overlap for $d = 3$ and $a = b = 1$. In this case, $H \simeq 0.16 \pm 0.28$.

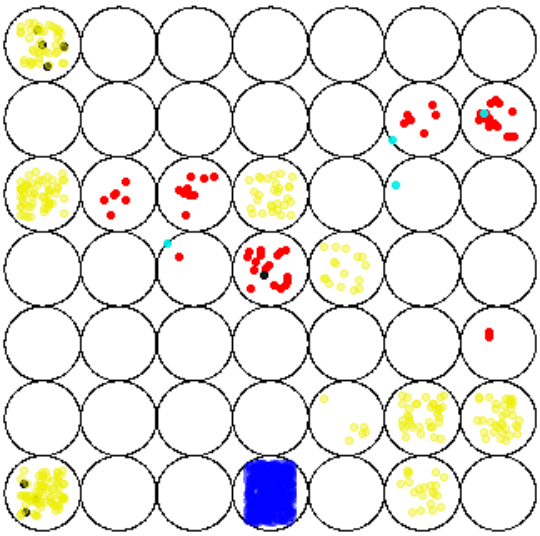

Figure 3. The self-organized map for $d = 3$, $a = b = 1$, and $c = Y = x_1 + x_2$. Here, $H \simeq 0.16 \pm 0.28$.

Therefore, in these three experiments, the employed SOM network was not able to successfully cluster the data. This conclusion may not be surprising, because the importance of the items 1 and 2 for diagnosing MDD is not highlighted by taking $a = b$ in Table 1. In fact, in agreement with DSM-5 [11], it would be consistent to assume that $a > b$.

A simple strategy to solve this problem is to choose values of a and b so that the sum $\sum_{j=1}^{9} y_j = Y$ can help differentiate depressed from non-depressed individuals. Thus, for depressed individuals, $Y \geq T$; for non-depressed individuals, $Y < T$, in which T is a threshold. According to the criteria for diagnosing MMD found in DSM-5, this threshold exists if $\min\{2a + 3b, a + 4b\} \geq \max\{2a + 2b, a + 3b, 7b\}$. It is very interesting to conclude that this system of inequations has no solution, because it implies $a \geq 3b$, $a \geq 2b$, and $a \leq 2b$, which is impossible. Thus, from this standpoint, the current diagnostic criteria lack of mathematical consistency. This finding motivates us to propose the following change in the criteria: if the symptoms 1 and 2 are both present, then the presence of just one more symptom (instead of three additional symptoms) is enough to diagnose MDD. Analytically, this statement can be written as $\min\{2a + b, a + 4b\} \geq \max\{2a, a + 3b, 7b\}$, whose solution is $3b \leq a \leq 4b$. By taking $b = 1$, then $a = 3.5$ is a convenient number. With these choices, $T = 7.5$.

In the fourth experiment reported here, $d = 2$, $a = 3.5$, and $b = 1$. In this case, the first and the second symptoms presented in Table 1 have greater scores than the other seven symptoms. Also, the criteria for diagnosing MDD were modified and BE was taken into consideration. The result, presented in Figure 4, has a significant difference when compared to Figure 1: the overlap between D and NGS-individuals was removed. The overlaps between D and GD (red and cyan) and between G and NGS (black and yellow) still occur because $x_3 = y_{10}$ was not taken into account. However, despite this qualitative difference, the value of H is similar to that of Figure 1. In Figure 4, $H \simeq 0.16 \pm 0.29$.

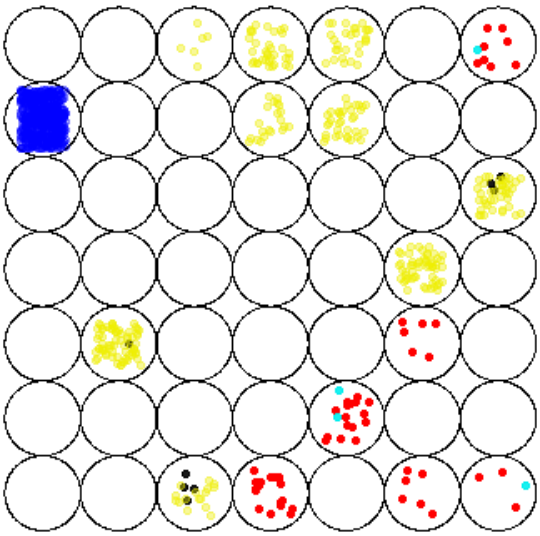

Figure 4. The self-organized map for $d = 2$, $a = 3.5$, and $b = 1$. Here, $H \simeq 0.16 \pm 0.29$.

Figure 5 shows a better clustering. In this figure, obtained by taking $d = 3$, $a = 3.5$, and $b = c = 1$, the overlap occurs only for G and GD (black and cyan). Also, $H \simeq 0.06 \pm 0.23$, which is lower than the value of H found in Figure 4.

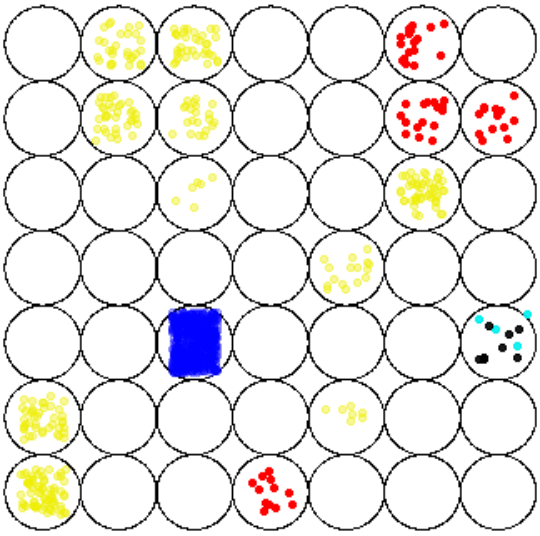

Figure 5. The self-organized map for $d = 3$, $a = 3.5$, and $b = c = 1$. Here, $H \simeq 0.06 \pm 0.23$.

In the sixth experiment, $d = 3$, $a = 3.5$, $b = 1$, and $c = Y$; thus, the value of c (for grieving people) is the sum of the scores of the usual nine items (as in Figure 3). With this choice, G and GD-individuals are mapped into specific output neurons, as shown in Figure 6. In fact, there is no overlap in this figure; therefore, $H = 0$.

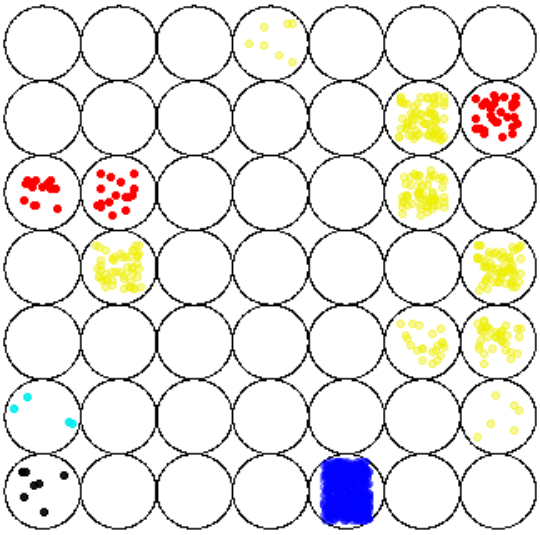

Figure 6. The self-organized map for $d = 3$, $a = 3.5$, $b = 1$, and $c = Y = x_1 + x_2$. In this case, $H = 0$.

A remark: the fictitious population was randomly generated so that the group to which the individual belongs does not change in function of the diagnostic criteria. For instance, there is no $\vec{y} = \{1, 1, 1, 1, 0, 0, 0, 0, 0, 0\}$ (or $\vec{x} = \{2, 2, 0\}$) in the sample, because this vector corresponds to a

NGS-individual according to DSM-5 criteria and to *D*-individual according to our criteria. Hence, the sizes of the five groups are not affected by the criteria considered in the numerical experiments.

5. Discussion and conclusions

This work is based the following assumption: a SOM network clustering data of people with grief and/or MDD can mimic a physician diagnosing these people. If this task is difficult for the SOM network with the current criteria, so it can also be difficult for the physician. In other words, the difficulty faced by this neural network (or any other clustering technique) may reflect the difficulty faced by the physician. In fact, as already pointed out by other authors [6], the DSM-5 criteria for MDD may not be adequate for distinguishing between *G*-individuals and *GD*-individuals.

Here, a set of n vectors $\vec{y}$, representing individuals who may or may not be depressed and/or grieving, were transformed into vectors $\vec{x}$ and used as inputs in a SOM network. Figures 1–6 exhibit the influence of the parameters a, b, and c (related to the binary variables y_j) and the dimension d (of $\vec{x}$) on the self-organized maps. Numerical and analytical results lead us to propose suitable numbers for a, b and c and a modification on the MDD criteria. With such a modification, the sum $Y = \sum_{j=1}^{9} y_j = x_1 + x_2$ is equal to or surpasses a threshold T in depressive individuals and the items in the checklist have distinct values. Suitable choices are $a = 3.5$, $b = 1$, and $c = Y$. Recall that Figure 1 (with overlaps) was obtained from the DSM-5 guidelines; Figure 6 (without overlaps) was obtained from the modified criteria with these values for a, b and c. By comparing the average entropy, it was reduced from $H \simeq 0.26 \pm 0.29$ in Figure 1 to $H = 0$ in Figure 6.

Self-organized maps, as those shown in this work, can be obtained by training the network with data from real-world populations. In these maps, the severity of the symptoms could be taken into account by considering y_j as continuous variables (instead of binary variables).

It is relevant to stress that there may be qualitative differences between the checklist symptoms reported by *G*-individuals and by *D* and *GD*-individuals [3, 5]. Therefore, our score-based approach should be viewed as a support (not a replacement) for the clinical judgment. A preliminary diagnosis could be performed by the SOM network, by identifying the output neuron of the vector $\vec{y}$ describing the new patient (that is, a vector that does not belong to the training set).

The *GD*-individuals should not be confused with individuals suffering from persistent complex bereavement disorder (PCBD). According to DSM-5 [11], PCBD is a complicated grief disorder, which occurs when the acute phase of grief persists for at least one year post-loss.

The relevance of the issue addressed in this work has been fostered by the current COVID-19 pandemic [35,36]. This pandemic, which is a unique significant stressor for triggering MDD, increased the death rate in virtually all countries. As a consequence, the proportions of the *D*, *G*, and *DG*-groups have increased due to the spread of this contagious disease [35, 36]. Diagnosing accurately is even more crucial nowadays, because there are more bereaved people needing pharmacological and/or psychological treatment.

Data Availability

The data used to support the findings of this study are available from the first author upon request.

Conflicts of interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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