Bilateral symmetry aspects in computer-aided Alzheimer’s disease diagnosis by single-photon emission-computed tomography imaging

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ABSTRACT

Objective: This paper explores the importance of the latent symmetry of the brain in computer-aided systems for diagnosing Alzheimer’s disease (AD). Symmetry and asymmetry are studied from two points of view: (i) the development of an effective classifier within the scope of machine learning techniques, and (ii) the assessment of its relevance to the AD diagnosis in the early stages of the disease.

Methods: The proposed methodology is based on eigenimage decomposition of single-photon emission-computed tomography images, using an eigenspace extension to accommodate odd and even eigenvectors separately. This feature extraction technique allows for support-vector-machine classification and image analysis.

Results: Identification of AD patterns is improved when the latent symmetry of the brain is considered, with an estimated 92.78% accuracy (92.86% sensitivity, 92.68% specificity) using a linear kernel and a leave-one-out cross validation strategy. Also, asymmetries may be used to define a test for AD that is very specific (90.24% specificity) but not especially sensitive.

Conclusions: Two main conclusions are derived from the analysis of the eigenimage spectrum. Firstly, the recognition of AD patterns is improved when considering only the symmetric part of the spectrum. Secondly, asymmetries in the hypo-metabolic patterns, when present, are more pronounced in subjects with AD.

1. Introduction

Alzheimer’s disease (AD) is the most common cause of dementia among people over the age of 65. A considerable amount of new information has been gathered over the last 30 years concerning the factors responsible for AD, which has resulted in the development of new treatments. Although extensive clinical studies have characterized the time course of many cognitive and behavioral measures, and clinical data has been correlated with autopsy findings, a final cure remains undiscovered. In order to test and develop medical treatments and cure, early and accurate diagnosis is crucial.

The diagnosis of AD is a field of active research that includes studies of biological markers associated with the disease, and neuropsychological testing or neuroimaging techniques such as functional and structural brain imaging. Single-photon emission-computed tomography (SPECT) imaging offers the opportunity to explore functional brain behavior, as the regional cerebral blood flow. Even though the perfusion pattern and its evolution is not the same for all patients, there do seem to be some typical hypo-perfusion patterns for the disease, such as the tempo-parietal region or the posterior cingulate gyri and precunei. Still, no single perfusion pattern differentiates AD patients from healthy subjects. The value of SPECT as an objective diagnostic tool for AD may depend on the degree to which abnormal metabolic patterns can be detected by quantitative classification methods.

Much of the AD literature suggests that early manifestations of AD occur in a prodromal stage, years before the symptoms of the disease appear and are clinically detectable. This makes it suitable to use non-invasive techniques such as nuclear imaging for detection. The examination of the predictive abilities of nuclear imaging with respect to AD in this early stage has been widely studied, through visual assessments performed by experts[1–4], or by means of voxel-wise statistical analysis such as SPM, NEUROSTAT & 3D-SSP, ANOVA or MANCOVA[5–12]. Recently, a new branch of emerging research has shown that machine-learning techniques may also be powerful analysis tools for brain imaging. As an example, recent works have been published that adapt state-of-the-art computer-vision techniques in magnetic-resonance imaging for...
early AD diagnosis [13,14], support-vector-machine (SVM) classification in SPECT [15–18], or positron-emission-tomography analysis [19,20]. This framework, which is geared towards decision-making, usually considers feature vectors containing a set of voxels, allowing for a regional or global brain-image analysis, which is contrary to voxel-wise statistical tools. On the other hand, the framework suffers from the small-sample-size problem. This significant problem, associated with pattern-recognition systems, occurs when the number of available features for designing the classifier is very large compared with the number of available training examples.

Symmetry has profound and important implications with regard to recognition and pattern representation, and it has also been claimed to have a privileged status in the brain response to complex stimuli, as faces when viewed as a whole [21,22]. A natural emerging question is whether symmetry has the same connected with the disease itself.

2. Materials and methods

The tool for conducting the analysis is based on principal-component analysis (PCA) on an enhanced set of images. This procedure identifies the main deviations from the mean, and attempts to separate them into a set of linear independent images. This new set can be separated into symmetric and asymmetric images, as described in Section 2.1.

2.1. Enhanced dataset: parity study

The three-dimensional volume of a brain image is represented by a scalar function \( f(x) \) of position \( x = (x, y, z) \) (in the following, an image), with the image centered on the dividing plane of both hemispheres \( x = 0 \). We consider the possibility of extending the database to an ensemble of images:

\[
t_n(x, y, z) \cup t_n(-x, y, z)
\]

with \( n = 1, 2, \ldots, N \), where \( N \) is the number of images. The symmetrized and averaged brain image of the dataset is defined as:

\[
f(x, y, z) = \frac{1}{2N} \sum_{n=1}^{N} \{ t_n(x, y, z) + t_n(-x, y, z) \}
\]

Following the approach in [17], each brain image is represented by its eigenbrain expansion. Firstly, PCA requires that the average of the image set is subtracted from each brain image, producing a new set \( \hat{t}_n = t_n - \bar{t} \). Here, an image \( \bar{t} \) is even (in the mid-plane) if:

\[
\hat{t}_n(x, y, z) = \hat{t}_n(-x, y, z)
\]

and odd if

\[
\hat{t}_n(x, y, z) = -\hat{t}_n(-x, y, z)
\]

In practice, the function \( \hat{t}_n \) takes only discrete values at voxels. The intensity values of \( \hat{t}_n(x, y, z) \) are concatenated to form the \( M \)-dimensional column vector \( \hat{t}_n \), and the mirrored counterpart \( \hat{t}_n(-x, y, z) \) forms the column vector \( \hat{t}_n \), where \( M \) is the total number of voxels in the image. On the set \( \{ \hat{t}_n \cup \bar{t}_n \} \), a PCA transformation is composed of \( M \)-dimensional orthogonal vectors \( u_i \), such that

\[
\lambda_i = \frac{1}{2N} \sum_{n=1}^{N} (u_i^T (t_n + \bar{t}_n))^2
\]

is maximum, subject to the constraint:

\[
u_i^T u_j = \delta_{ij}
\]

where \( \delta_{ij} \) is the Kronecker delta. The resulting \( u_i \) and \( \lambda_i \) are the eigenvectors and eigenvalues respectively of the covariance matrix:

\[
C = \frac{1}{2N} \sum_{n=1}^{N} [\hat{t}_n \hat{t}_n^T + \bar{t}_n \bar{t}_n^T]
\]

The orthogonal eigenvector basis \( \{ u_i \} : i = 1, \ldots, 2N \) forms the so-called eigenbrains. Within this framework, the coefficients in the eigenbrain expansion are uncorrelated, and each eigenvalue represents the statistical variance of the corresponding coefficient in the expansion. As is directly verified, we can rewrite \( C \) as the sum of an even part \( C^e \) and an odd one \( C^o \):

\[
C^e = \frac{1}{4N} \sum_{n=1}^{N} [\hat{t}_n + \bar{t}_n][\hat{t}_n + \bar{t}_n]^T
\]

\[
C^o = \frac{1}{4N} \sum_{n=1}^{N} [\hat{t}_n - \bar{t}_n][\hat{t}_n - \bar{t}_n]^T
\]

that which are orthogonal and have eigenvectors that are even and odd, respectively. In other words, the eigenspace of \( C, E(C) \) can be expressed as the direct sum of \( E(C^e) \) and \( E(C^o) \) (see [25]), that is:

\[
E(C) = E(C^e) \oplus E(C^o)
\]

If we define the symmetric image \( t^e_n \) as:

\[
t^e_n = t_n + \bar{t}_n
\]

and the asymmetric image \( t^o_n \) as:

\[
t^o_n = t_n - \bar{t}_n
\]

it follows that we should consider the following two decoupled problems:

\[
C^e u^e_i = \lambda^e_i u^e_i
\]

\[
C^o u^o_i = \lambda^o_i u^o_i
\]

where:

\[
C^e = \frac{1}{4N} \sum_{n=1}^{N} t^e_n(t^e_n)^T
\]

\[
C^o = \frac{1}{4N} \sum_{n=1}^{N} t^o_n(t^o_n)^T
\]

These two problems can be viewed as equivalent to starting out with two separated ensembles \( t^e_n \) and \( t^o_n \), \( n = 1, 2, \ldots, N \) consisting of even and odd images, and then proceed with the two cases independently. To solve them, it is necessary to diagonalize two \( M \times M \) covariance matrices, which for brain images would be approximately a \( 5 \times 10^3 \times 5 \times 10^3 \) matrix. There are alternatives to deal with these problems, for instance based on the diagonalization of the

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1 It is to be understood that the vectors \( t_n \) and \( \bar{t}_n \) are centered as \( \bar{t}_n \), but explicit reference has been removed in order to simplify the notation.
The training data is obtained from the raw data as:
\[
(x_i)_t = u_i^T t_n, \quad n = 1, \ldots, N \quad i = 1, 2, \ldots, L
\]  
where \( L \) is the total number of eigenbrains. These coefficients \((x_i)_t\) are the coordinates of the \( n \)-th brain image \( t_n \) in the subspace spanned by the \( L \) eigenbrain images (for \( u_i \) being the full set \([u_1^T] \cup [u_2^T] \)). These coordinate values \( x_i \) are used as \( N \times L \)-dimensional training vectors:
\[
x_n = [x_1, x_2, \ldots, x_L]_n, \quad n = 1, 2, \ldots, N
\]  
each of which has its corresponding class label \( y_n \in \{ \pm 1 \} \).

SVM separates a given set of binary labeled training data with a hyperplane that is maximally distant from the two classes (known as the maximal margin hyper-plane). The objective is to build a function \( f : R^L \rightarrow \{ \pm 1 \} \) using training data that is, \( L \)-dimensional patterns \( x_n \) and class labels \( y_n \):
\[
(x_1, y_1), (x_2, y_2), \ldots, (x_N, y_N) \in R^L \times \{ \pm 1 \},
\]  
so that \( f \) will correctly classify new examples \((x, y)\).

Linear discriminant functions define decision hyper-surfaces or hyperplanes in a multidimensional feature space; that is:
\[
g(x) = w^T x + w_0 = 0,
\]  
where \( w \) is known as the weight vector and \( w_0 \) as the bias. The weight vector \( w \) is orthogonal to the decision hyperplane and the optimization task consists of finding the unknown parameters \( w_i, i = 1, \ldots, L \), thereby defining the decision hyperplane.

When no linear separation of the training data is possible, SVM can work effectively in combination with kernel techniques so that the hyperplane defining the SVM corresponds to a non-linear decision boundary in the input space. If the data is mapped to some other (possibly infinite dimensional) euclidean space using a mapping \( \Phi(x) \), the training algorithm only depends on the data through dot products in such a space; that is, on functions of the form \( \Phi(x) \cdot \Phi(x_i) \). If a “kernel function” \( K \) is defined such that \( K(x, x_i) = \Phi(x) \cdot \Phi(x_i) \), it is not necessary to know the \( \Phi \) function. In the test phase, a SVM is used by computing the dot products of a given test point \( x \) with \( w \), or more specifically by computing the sign of
\[
f(x) = \sum_{i=1}^{N} \alpha_i y_i \Phi(s_i) \cdot \Phi(x) + w_0 = \sum_{i=1}^{N} \alpha_i y_i K(s_i, x) + w_0,
\]  
where \( s_i \) are the support vectors. Common kernels that are used by SVM practitioners for the nonlinear feature mapping are:

- **Polynomial**
  \[
  K(x, y) = [\gamma (x \cdot y) + c]^d.
  \]  

- **Radial basis function (RBF)**
  \[
  K(x, y) = \exp( -\gamma ||x - y||^2).
  \]  
as well as the linear kernel, in which \( K(.,.) \) is simply a scalar product.

The SVM ‘learns’ from the labeled training data obtaining a hyperplane that separates the data into the two classes, which maximizes the margin between them. Once the hyperplane has been obtained, new samples with unknown labels can be categorized. A feature vector is obtained from the test image using Eqs. (17) and (18), and the vector is classified according to its sign in Eq. (21) once the hyperplane has been determined. Also, samples with known labels may be used to test the reliability of the method, with some cross-validation strategy.

### 2.3. Image pre-processing and labeling

The database consists of a set of 3D SPECT brain images produced with an injected gamma emitting 99mTc-ECD radiopharmaceutical and acquired by a three-head gamma camera Picker Prism 3000. Images of the brain cross sections are reconstructed from the projection data using the filtered back-projection algorithm combined with a Butterworth noise-removal filter. To allow for comparisons between groups of images, the reconstructed images must satisfy the condition that the same position in the coordinate system within different images corresponds to the same anatomical position. Moreover, for this particular study of the natural symmetry of the brain, it is crucial that the vertical alignment of the dividing plane be set equally through the dataset. To accomplish these requirements, the SPECT images are spatially normalized using the SPM5 software [5]. The normalization method assumes a general affine model with 12 parameters [27] and a Bayesian framework that maximizes the product of the prior function (based on the probability of obtaining a particular set of zooms and shears) and the likelihood function (derived from the residual squared difference between the template and the source image):
\[
CF = \sum_i [f_i(Ax_i) - f_0(x_i)]^2,
\]  
where \( f \) denotes the source image and \( f_0 \) the template. For each voxel \( x = (x, y, z) \) in an image, the affine transformation into the coordinates \( x’ = Ax \), where \( A \) is a \( 4 \times 4 \) matrix, encoding 9 rotation-free parameters together with 3 translation-free parameters, and \( x = (x, y, z, 1) \) has an additional dimension to allow for a compact matrix notation. The standard Montreal Neurological Institute template (www.mni.mcgill.ca) is used, with the additional requirement of having the symmetry plane perfectly aligned with the vertical line, to ensure that the normalized images satisfy the parity definition of Eqs. (3) and (4). Therefore, the template \( f_0 \) is symmetrized to \( f_0^T \) as:
\[
f_0^T = \frac{1}{2} [f_0(x, y, z) + f_0(-x, y, z)]
\]  
minimizing the possible effects of deviations from aligned orientations, as is discussed in the next section.

After the affine normalization, the resulting image is registered using a non-rigid spatial transformation. The deformations are parameterized by a linear combination of the lowest-frequency components of the three-dimensional cosine-transform bases [28].

A small-deformation approach is used and bending the energy of the displacement field achieves regularization. SPECT images consist of functional information. Therefore, direct comparison of the voxel intensities is not possible without normalizing the intensities, even for different acquisitions of the same subject. The intensity level of the images is normalized to the maximum intensity, which is computed for each image individually by averaging over the 0.1% of the highest voxel intensities. This normalization does not modify the histogram of the images and reduces the effect of possible intensity outliers.

The database is comprised of imaging studies of subjects following the protocol of a hospital-based service. Firstly, the neurologist evaluated the cognitive function. Those patients with findings of memory loss or dementia were referred to the nuclear medicine department in the “Virgen de las Nieves” hospital (Granada, Spain), in order to acquire complementary screening information for...
The first test is to verify the working assumptions, paying particular attention to the registration step. AD patterns are usually subtle deviations from typical perfusion patterns and are easily disturbed by noisy instances. This fact requires the sources of variability coming from the preprocessing of the images to be minimized. A failure in the symmetry plane identification would produce an enhanced dataset that does not fulfill the conditions of Eq. (1).

When Eq. (25) is not applied and eigenimage analysis is performed, a typical ‘movement artifact’ image – represented in Fig. 1 – appears in the spectrum. The eigenbrains represent deviations from the mean. Fig. 1 shows that the deviation is asymmetric and most prominent in regions with high intensity gradient, such as borders and thalamus. This means that reflected images by the $x=0$ plane $t_n(-x, y, z)$ are shifted in this direction when compared with the original ones $t_n(x, y, z)$. The aforementioned source of variation is the second eigenimage sorted by variance, explaining 7% of the total variance, compared to 14% explained by the first eigenbrain.

Table 1
Demographic details of the dataset. CTRL = Control, AD1 = mild perfusion deficit, AD2 = moderate deficit, AD3 = severe deficit. $\mu$ and $\sigma$ stand for population mean and standard deviation respectively.

<table>
<thead>
<tr>
<th>Sex (%)</th>
<th>Age</th>
<th>#</th>
<th>M</th>
<th>F</th>
<th>$\mu$</th>
<th>$\sigma$</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTRL</td>
<td></td>
<td>41</td>
<td>73.17</td>
<td>26.83</td>
<td>71.51</td>
<td>7.99</td>
<td>46–85</td>
</tr>
<tr>
<td>AD1</td>
<td></td>
<td>30</td>
<td>36.67</td>
<td>63.33</td>
<td>65.86</td>
<td>13.36</td>
<td>23–81</td>
</tr>
<tr>
<td>AD2</td>
<td></td>
<td>22</td>
<td>54.55</td>
<td>45.45</td>
<td>67.22</td>
<td>8.25</td>
<td>46–86</td>
</tr>
<tr>
<td>AD3</td>
<td></td>
<td>4</td>
<td>100.00</td>
<td>0</td>
<td>76</td>
<td>9.90</td>
<td>69–83</td>
</tr>
</tbody>
</table>

2 Unfortunately, clinical information is not available for privacy reasons; only demographic information is available.
and 6% explained by the third. The spatial position of the images is controlled by the registration step, which transforms the raw data to a common space, defined by the alignment of the template. The template re-orientation cannot be tackled with a manual fine-tuning, since small deviations from centering are not only present in the $x=0$ plane, but also exist in the $y=0$ and $z=0$ planes. However, the problem may be solved by using a symmetric template $f_s$ for registration, as defined in Eq. (25), which eliminates the source of variability that is not related to the disease.

Once basics assumptions have been assured, PCA decomposition in the enhanced dataset provide a spectrum of eigenimages, as represented in Fig. 3. The above-mentioned dichotomy of even or odd images in the mid-plane is evident in this figure, where odd eigenbrains appear first in the sixth and ninth places. An expected result is that the first eigenbrain in terms of variance (see Fig. 2) is responsible for hypo-perfusion in the parietal-temporal regions, as has been found previously in the literature [17,19]. Also unsurprisingly, only two of the first 10 eigenbrains are odd, while the largest eigenvalues correspond to the even ones, in the light of the latent symmetry of the brain. This evidence becomes clearer by Fig. 4. Only 23.9% of the total variance of the data is explained by odd eigenbrains, while the remaining 76.1% is explained by even ones.

Classification is achieved through a SVM. The SVM is trained using three different kernels: linear, quadratic (setting $\gamma = 1$, $c = 0$ and $d = 2$ in Eq. (22)) and RBF, and is tested using a leave-one-out cross-validation strategy. Two classifiers are built in order to separately study the asymmetric/symmetric-related issues by considering only the scores related to odd/even eigenbrains:

\begin{align}
(x_{in}^e)_{n} &= (u_i^e)_{n}^T \mathbf{t}_n, \quad n = 1, \ldots, N \quad i = 1, 2, \ldots, L \quad (26) \\
(x_{in}^o)_{n} &= (u_i^o)_{n}^T \mathbf{t}_n, \quad n = 1, \ldots, N \quad i = 1, 2, \ldots, L \quad (27)
\end{align}

and follow Eq. (18) to form the feature vectors for classification.
Fig. 5. Asymmetry/symmetry related classification. (a) Linear kernel with even eigenbrains; (b) linear kernel with odd eigenbrains; (c) quadratic kernel with even eigenbrains; (d) quadratic kernel with odd eigenbrains; (e) RBF kernel with even eigenbrains; (f) RBF kernel with odd eigenbrains.

The results are summarized in Fig. 5, where performance parameters are studied while varying the number of eigenbrains $L$ used to grow the feature vectors. In the left column, symmetry-related scores are used by means of Eq. (26), while in the right column only odd eigenbrains are used to form the feature vectors by means of Eq. (27). Concerning the symmetric part of the images, the optimal dimension of the feature vectors $L$ is below 10 for SVM classification. This reproduces a known result [17,19], together with a manifestation of the well-known peaking phenomenon, as an increase in the complexity of the kernel used reduces the performance of the classifier to random classification when the dimensionality of the feature space is enhanced (see Fig. 5(c) and (e)).

The results in Table 2 are the most compelling when all of the possible combinations of the first 10 eigenbrains are used, and the table also refers to the performance values obtained using the other published methods. The performance of the classifier is compared to a feature extraction using PCA without symmetry-related issues [17,19], and the results obtained by a parsing-based approach that
Table 2
Statistical performance measures of PCA, PCA in presence of symmetry and spatial component analysis (SCA) for L=10.

<table>
<thead>
<tr>
<th>Parameter (%)</th>
<th>Linear</th>
<th>RBF</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCA Sensitivity</td>
<td>87.50</td>
<td>85.37</td>
</tr>
<tr>
<td>Specificity</td>
<td>90.24</td>
<td>91.07</td>
</tr>
<tr>
<td>Accuracy</td>
<td>86.67</td>
<td>88.67</td>
</tr>
<tr>
<td>PCA symmetric Sensitivity</td>
<td>92.86</td>
<td>85.37</td>
</tr>
<tr>
<td>Specificity</td>
<td>92.68</td>
<td>92.86</td>
</tr>
<tr>
<td>Accuracy</td>
<td>92.78</td>
<td>89.69</td>
</tr>
<tr>
<td>SCA Sensitivity</td>
<td>84.54</td>
<td>-</td>
</tr>
<tr>
<td>Specificity</td>
<td>87.73</td>
<td>-</td>
</tr>
<tr>
<td>Accuracy</td>
<td>89.03</td>
<td>-</td>
</tr>
</tbody>
</table>

considers fractions or components of the whole image individually (spatial component analysis (SCA) [24]). Recognition rates using both linear and RBF kernels are improved when those eigenbrains responsible for asymmetries are removed, benefiting from the presence of latent symmetry. This result supports the hypothesis that considering the symmetry of the brain globally plays an essential role in the identification and classification of AD-related patterns, in the sense that it increases the capability of identifying AD-affected subjects.

A natural question that arises is whether the asymmetric patterns can be matched to represent the affection or, in other words, if AD affects brain functions asymmetrically. In view of Fig. 5(b) and (f), this question can not be answered definitively, as the classifier performance is not superior to its counterpart using symmetry-related issues. A partial answer can be given in light of Fig. 5(b), since the impossibility of a linear separation of the asymmetric information reveals that AD does not affect one preferred hemisphere. However, an interesting result is obtained when using a quadratic kernel (Fig. 5(d)). High specificity values with nonzero sensitivity are obtained when an important proportion of asymmetric information is collected. This fact reveals that a high number of controls (37 out of 41 in the maximum) are correctly identified, while substantial proportion of AD patients are also detected (17 out of 56 in the maximum). One interpretation for this could be that marked deviations from symmetry only comprise AD subjects. Also, these deviations affect randomly both hemispheres, as a non-linear kernel is required in order to detect them. The decay of the performance values when using all the available information can be understood as a peaking phenomenon. The same reason would explain why this asymmetry identification is not present in Fig. 5(f), when a more complex kernel is used.

This information may be useful for developing an independent test based on growing a specific classifier for this task. Therefore, testing for the presence of asymmetries may be a very specific test for AD, with 90.24% specificity. Despite being far from sensitive, this test can rule out some possibilities. Asymmetries are proven to be specific to AD, but they are not enough to characterize the hypo-perfusion pattern of AD and are only present in a limited number of cases. This result is consistent with previous findings in the literature about asymmetry in AD [31–34].

If AD started to affect brain functions asymmetrically, the asymmetry in the perfusion pattern could be an important indicator for early diagnosis of AD. Centering the analysis in the CTRL vs. AD1 SVM classification using a quadratic kernel reproduces specific results of Fig. 5(d), with 37 of 41 controls correctly identified, together with 9 of 30 AD patients. The sample size and the balance between classes limit the study, requiring further verification in an independent dataset. An independent test is also required in order to check the generalization capabilities of the method, and could serve to verify whether it has potential to be used in clinical practice. In other words, the test would check whether the method becomes relevant in the study of mild cognitive impairment and its relations to AD, or if it could also be extended to characterize other illnesses in which asymmetry plays an essential role, as epilepsy [35], constituting work in progress.

Most imaging studies of AD are analyzed based on a voxel-wise or regions of interest (ROI) technique, focusing on a single domain of the brain perfusion pattern and discarding the irrelevant part of the brain image. The ROI selection depends on an observer’s a priori choice and involves some visual inspection and recognition, which is dependent upon the observer’s experience and expertise. These approaches have proven to be remarkably successful [29,30]. However, other pattern-recognition problems solved accurately by humans, as face recognition, provide compelling evidence for the holistic character of recognition [36,22]. In the debate regarding whether a brain image should be parsed or viewed holistically for CAD, one important consequence of using symmetries for pattern characterization has an impact on recognition, in support of the approach taken here. Although some parsing approaches have proven to be very robust, viewing the images as a whole can be considered beneficial in the light of the results presented here.

4. Conclusions

The notion of data extension using the natural symmetry of the brain makes it possible to represent patterns in terms of an eigenbrain basis that possesses more structure. Adopting this approach in brain imaging of AD provides further characterization of the disease, separating the spectrum of eigenbrains into even and odd parts. Recognition rates are increased when all of the asymmetric information of the spectrum is discarded by means of a linear SVM classification of the symmetric patterns. Furthermore, a non-linear kernel makes it possible to separate hypo-metabolic patterns with asymmetry, which are present mainly in AD cases, from non-asymmetric cases, which are comprised of both normal and AD patterns. The proposed work is not limited to AD diagnosis on SPECT images, but provides an automated methodology with which to study the importance of bilateral symmetry in brain imaging.

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