

GRASSMANN SINGULAR SPECTRUM ANALYSIS FOR BIOACOUSTICS CLASSIFICATION

Lincon S. Souza*, Bernardo B. Gatto†, Kazuhiro Fukui*

lincons@cvlab.cs.tsukuba.ac.jp, bernardo@icomp.ufam.edu.br, kfukui@cs.tsukuba.ac.jp

*University of Tsukuba, Japan

† Federal University of Amazonas, Brazil

ABSTRACT

Bioacoustic signal classification is a powerful tool for biologists, assisting in tasks such as environmental monitoring of biomes in areas of difficult access, and providing clues about the evolution and categorization of animals from the perspective of similarity of their bioacoustic mechanisms. The recently proposed mutual singular spectrum analysis (MSSA) introduced a novel bioacoustic signal representation based on subspaces, which is compact and requires no cost intensive preprocessing techniques (e.g. segmentation, noise reduction or syllable extraction). However, MSSA has no discriminant mechanism to separate classes, and it assumes that a class is composed of linear combinations of the reference signals, which in practice is unlikely, and impairs study of the individuals' signals among the same species. In this paper we propose an extension named Grassmann singular spectrum analysis (GSSA), which preserves the advantages of MSSA in addition to the following contributions: we assume that a class may be composed of a set of subspaces and we simplify bioacoustic signal subspace representation by mapping the subspaces onto a Grassmann manifold; and we offer a discriminant mechanism to separate the species in a classification task. We demonstrate the validity of GSSA through a classification experiment on a publicly available bioacoustic signals dataset.

Index Terms— Bioacoustic signals, subspace method, Grassmann singular spectrum analysis, Grassmann manifold.

1. INTRODUCTION

Bioacoustic signal classification plays an important role in environmental monitoring as it gives experts the means to efficiently acquire information from areas of difficult access. It also assists by providing clues about the evolution and categorization of animals from the perspective of similarity of their bioacoustic mechanisms, which may be useful in new species discovery.

Remote monitoring of areas of difficult access, e.g. dense forests or depths of the sea, allows one to obtain unique information in order to catalog, analyze and infer the habits, interactions and the quality of the wild life contained in that

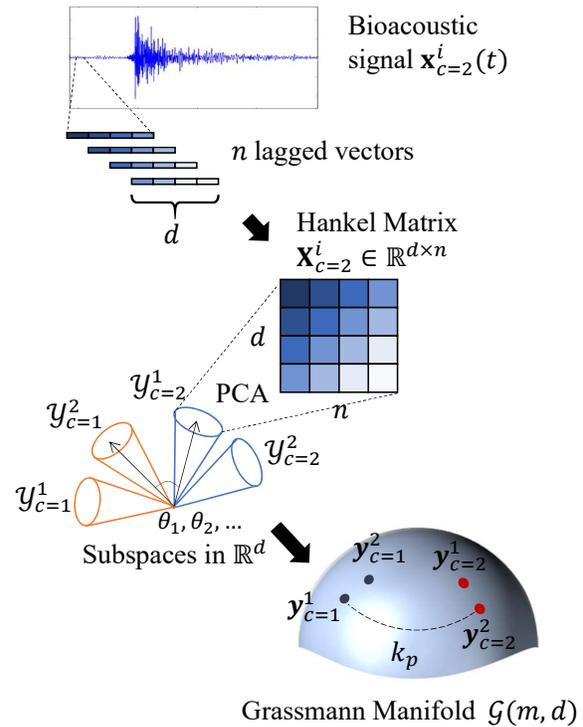


Fig. 1. Conceptual diagram of the proposed GSSA.

specific environment. Therefore, such information is critical in order to predict changes in the population of species and the quality of the sea, air, soil and other natural elements.

An efficient bioacoustic signal classification framework needs to work reliably and within some practical restrictions. Such frameworks need to run on low-cost computational resources, not only to avoid using prohibitively expensive hardware, but to avoid equipments too complex to deploy on the field. That means a classification system should have low computational cost during its acquisition, preprocessing and classification stages. Despite this, several of the bioacoustic signal classification frameworks recently proposed [1, 2] are composed of multiples elements, including noise [3] and dimensionality reduction [4], feature selection [5], model training [6] and, finally, the actual classification [7].

The recently proposed mutual singular spectrum analysis (MSSA) [8] introduced a novel bioacoustic signal representation based on subspaces, which is compact and requires no cost intensive preprocessing techniques (e.g. segmentation, noise reduction or syllable extraction). The input signals are represented within the singular spectrum analysis (SSA) paradigm, by a set of leftmost eigenvectors extracted based on the signals' accumulated energy. This set forms a basis for a subspace in the vector space, since the vectors are orthonormal [9, 10]. Then, canonical angles [11, 12] between the different bioacoustic subspaces are used to measure their similarity, and 1-NN classification is performed. This algorithm is known as mutual subspace method (MSM) [9, 13].

Although MSSA has efficiently addressed these bioacoustics challenges, its representation has some issues that decrease its reliability as a monitoring instrument: it has no discriminant mechanism to separate classes (e.g. species of animals); and it assumes that a class is composed of linear combinations of the reference signals, which in practice is unlikely, and impairs study of the individuals' signals among the same species.

To tackle these issues, we propose a new algorithm of Grassmann singular spectrum analysis (GSSA), which is depicted as a conceptual illustration in the Figure 1. We introduce a Grassmann manifold formulation, which simplifies the complicated procedure of the subspace based method using canonical angles. The Grassmann manifold, symbolized as $\mathcal{G}(m, d)$, is defined as a set of m -dimensional linear subspaces of \mathbb{R}^d [14]. In this framework, a subspace-based method is regarded as a simple classification method on a Grassmann manifold, where each single subspace is treated as a point, and thereby, each bioacoustic signal is represented by a point in the manifold. Various types of classification methods have been constructed on a Grassmann manifold [15, 16, 17, 18]. In particular, discriminant analysis on a Grassmann manifold (GDA) has been one of the popular tools for image set classification. GDA can be conducted as a kernel discriminant analysis through the kernel trick with a Grassmann kernel. Thus, we are introducing a discriminatory mechanism to the bioacoustic signal classification by utilizing GDA.

We summarize our contributions as follows: (1) We propose a bioacoustics classification algorithm assuming that a class may be composed of a set of subspaces, and we simplify bioacoustic signal subspace representation by mapping the subspaces onto a Grassmann manifold; (2) We introduce a discriminant mechanism to separate classes by the use of GDA; (3) As an extension of MSSA, our method preserves various of its advantages, namely: It requires less storage than most conventional methods; has a solid formulation to select compactness ratio; can handle arbitrary signal lengths; and does not need any preprocessing techniques, such as segmentation, or syllable extraction.

2. PROPOSED METHOD

In this section, we formulate the classification problem based on the bioacoustic signals. Then, we describe the representation by SSA subspaces, and the concept of canonical angles and Grassmann manifold, and how to use it to perform GDA.

2.1. Problem Formulation

Consider N_c reference bioacoustic signals $\mathbf{x}_c^i(t)$ for each c -th class ($c = 1, \dots, C$), where $i = 1, \dots, N_c$, and N_c can be different for each class. The index $t = 1, \dots, L_c^i$ indicates the ordering of the signal in time up to its length L_c^i .

This framework assumes that each signal $\mathbf{x}_c^i(t)$ can be represented by a linear mapping in terms of its autocorrelation. Note that this differs from MSSA in that the assumption has been reduced to the autocorrelation of each single signal, rather than the original assumption of a linear mapping in terms of the average correlation of a whole class of signals. As such, each signal can be represented by the first m orthonormal vectors ordered by the signal's accumulated energy, where $m \ll L_c^i$. These vectors span a subspace \mathcal{Y}_c^i ; thus a class of signals is effectively represented by a set of subspaces $\{\mathcal{Y}_c\}$, a relaxation similar to a Gaussian mixture rather than a single Gaussian distribution.

This representation provides more flexibility for a class with non-gaussian noise, and also scales well with an increasing number of signals per class. That implies mainly two points: a signal can be modeled independently and added to the class as another subspace, without needing to recalculate a single model for the whole class; and the trade-off problem of compactness ratio and representativity is slightly alleviated. The dimension of subspaces m , corresponding to the signal's compactness ratio, is selected empirically during the training. For a given unknown input bioacoustic signal $\mathbf{x}_{in}(t)$ of length L_{in} , the task is to compute a subspace \mathcal{Y}_{in} and predict its corresponding bioacoustic class (e.g. species) based on the nearest subspace.

2.2. Representation by SSA subspaces

Here we review the representation by a SSA subspace; for that, consider a single signal $\mathbf{x}(t)$. First, we apply a sliding window over $\mathbf{x}(t)$ to turn the 1-dimensional signal of length L in a sequence of n lagged vectors of length d arranged in a Hankel matrix $\mathbf{X} \in \mathbb{R}^{d \times n}$ as:

$$\mathbf{X} = \begin{bmatrix} \mathbf{x}_1 & \mathbf{x}_2 & \cdots & \mathbf{x}_n \\ \mathbf{x}_2 & \mathbf{x}_3 & \cdots & \mathbf{x}_{n+1} \\ \vdots & & \ddots & \vdots \\ \mathbf{x}_d & \mathbf{x}_{d+1} & \cdots & \mathbf{x}_{d+n-1} \end{bmatrix}, \quad (1)$$

where the number of columns n is the number of desired oscillatory components (or principal components), which has a

direct correspondence with the maximum delay of the autocorrelation. Therefore, the total number of columns in matrix \mathbf{X} is given by relationship $n = L - d + 1$. Note that the anti-diagonal elements in \mathbf{X} are equal.

The singular value decomposition (SVD) of the autocorrelation matrix $\mathbf{X}^\top \mathbf{X}$ is performed to find the directions of maximum variance of the Hankel matrix \mathbf{X} ; that is, for this case: $\mathbf{U}\mathbf{\Lambda}\mathbf{U}^\top = \mathbf{X}^\top \mathbf{X}$, where the columns of $\mathbf{U} \in \mathbb{R}^{n \times n}$ corresponds to the eigenvectors of \mathbf{X} and the diagonal of $\mathbf{\Lambda}$ corresponds to the singular values λ_j ($j = 1, \dots, n$), i.e. $\text{diag}(\mathbf{\Lambda}) = \lambda_1, \lambda_2, \dots, \lambda_n$ in decreasing order. Given the compactness ratio m , the leftmost matrix $\mathbf{U}^* \in \mathbb{R}^{n \times m}$ from \mathbf{U} is selected, containing the first m eigenvectors corresponding to the highest eigenvalues. The Hankel matrix \mathbf{X} is projected onto the subspace spanned by \mathbf{U}^* to obtain $\mathbf{Y} = \mathbf{X}\mathbf{U}^* \in \mathbb{R}^{d \times n}$, which is the best m -rank approximation of \mathbf{X} and spans the subspace \mathcal{Y} that characterizes our signal.

In our classification framework, we utilize the previous procedure to compute basis matrices $\mathbf{Y}_c^i \in \mathbb{R}^{d \times m}$ for a SSA subspace \mathcal{Y}_c^i corresponding to each reference signal $\mathbf{x}_c^i(t)$.

2.3. Canonical Angles

After modeling each signal as a SSA subspace by computing the set of basis vectors which maximizes variance, we need to compute the distance between the subspaces to perform classification. The natural metric for subspaces is the similarity, obtained from the canonical angles [19]. Accordingly, in our framework, canonical angles are used as the distance measure between two bioacoustic signals.

The standard approach to measure the canonical angles between subspaces \mathcal{Y}_1 and \mathcal{Y}_2 is to calculate the singular values $\{\lambda_j\}_{j=1}^m$ of the correlation matrix between their basis matrices $\mathbf{Y}_1, \mathbf{Y}_2 \in \mathbb{R}^{d \times m}$, i.e. solving the SVD of $\mathbf{V}\mathbf{\Lambda}\mathbf{V}^\top = \mathbf{Y}_1^\top \mathbf{Y}_2$. This corresponds to finding the rotation of each basis that is closest to the opposing subspace. From solving this problem, the canonical angles can be obtained by $\theta_j = \cos^{-1}(\lambda_j)$, where $j = 1, \dots, m$.

2.4. Grassmann Manifold

Now, we introduce here the concept of Grassmann manifold and how it is useful to correspond subspaces to vectors. The essence is to make a one-to-one mapping such that the similarities between subspaces is preserved, simplifying the representation and allowing general methods to be applicable.

Grassmann manifold $\mathcal{G}(m, d)$ is defined as the set of m -dimensional linear subspaces of \mathbb{R}^d . It is an $m(d - m)$ -dimensional compact Riemannian manifold and can be derived as a quotient space of orthogonal groups $\mathcal{G}(m, d) = \mathcal{O}(d)/\mathcal{O}(m) \times \mathcal{O}(d - m)$, where $\mathcal{O}(m)$ is the group of $m \times m$ orthonormal matrices.

A Grassmann manifold can be embedded in a reproducing kernel Hilbert space by the use of a Grassmann kernel.

In this case, the most popular kernel is the projection kernel k_p , which can be defined as $k_p(\mathcal{Y}_1, \mathcal{Y}_2) = \sum_{j=1}^m \cos^2 \theta_j$, which is homologous to the subspace similarity. We can measure the distance between two points on a Grassmann manifold by using this projection kernel [20], and a subspace \mathcal{Y} can be represented by a vector with regards to a reference subspace dictionary $\{\mathcal{Y}_q\}_{q=1}^N$ as $\mathbf{y} = k_p(\mathcal{Y}, \mathcal{Y}_q) = [k_p(\mathcal{Y}, \mathcal{Y}_1), k_p(\mathcal{Y}, \mathcal{Y}_2), \dots, k_p(\mathcal{Y}, \mathcal{Y}_N)] \in \mathbb{R}^N$.

2.5. Grassmann Discriminant Analysis

We introduce a discriminatory mechanism to separate the classes of signals, which is the Grassmann discriminant analysis (GDA). Basically, GDA is conducted as kernel LDA with the Grassmann kernels. We first outline the algorithm of linear discriminant analysis (LDA) [21]. Let $\mathbf{x}_1, \dots, \mathbf{x}_N$ be the data vectors and y_1, \dots, y_N ($y_i \in 1, \dots, C$) be the class labels. Each class c has N_c number of samples. Let $\boldsymbol{\mu}_c = \frac{1}{N_c} \sum_{i|y_i=c} \mathbf{x}_i$ be the mean of class c , and $\boldsymbol{\mu} = \frac{1}{N} \sum_i \mathbf{x}_i$ be the overall mean. LDA searches for the discriminant direction \mathbf{w} which maximizes the Rayleigh quotient $Ra(\mathbf{w}) = \mathbf{w}^\top \mathbf{S}_b \mathbf{w} / \mathbf{w}^\top \mathbf{S}_w \mathbf{w}$ where \mathbf{S}_b and \mathbf{S}_w are the between-class and within-class covariance matrices respectively:

$$\mathbf{S}_b = \frac{1}{N} \sum_{c=1}^C N_c (\boldsymbol{\mu}_c - \boldsymbol{\mu})(\boldsymbol{\mu}_c - \boldsymbol{\mu})^\top, \quad (2)$$

$$\mathbf{S}_w = \frac{1}{N} \sum_{c=1}^C \sum_{i|y_i=c} (\mathbf{x}_i - \boldsymbol{\mu}_c)(\mathbf{x}_i - \boldsymbol{\mu}_c)^\top. \quad (3)$$

The optimal \mathbf{w} is obtained from the largest eigenvector of $\mathbf{S}_w^{-1} \mathbf{S}_b$. Since $\mathbf{S}_w^{-1} \mathbf{S}_b$ has rank $C - 1$, there are $C - 1$ optima $\mathbf{W} = [\mathbf{w}_1, \dots, \mathbf{w}_{C-1}]$. By projecting data onto the space spanned by \mathbf{W} , we achieve dimensionality reduction and feature extraction of data onto the most discriminant subspace.

Kernel LDA [22, 23, 24] can be formulated by using the kernel trick as follows. Let $\Gamma : \mathbb{R}^d \rightarrow \mathcal{F}$ be a non-linear map from the input space \mathbb{R}^d to a feature space \mathcal{F} , and $\Gamma = [\boldsymbol{\gamma}_1, \dots, \boldsymbol{\gamma}_N]$ be the feature matrix of the mapped training points $\boldsymbol{\gamma}_i$. Assuming \mathbf{w} is a linear combination of those feature vectors, $\mathbf{w} = \Gamma \boldsymbol{\alpha}$, we can use the kernel trick and rewrite the Rayleigh quotient in terms of $\boldsymbol{\alpha}$ as:

$$\begin{aligned} Ra(\boldsymbol{\alpha}) &= \frac{\boldsymbol{\alpha}^\top \Gamma^\top \mathbf{S}_b \Gamma \boldsymbol{\alpha}}{\boldsymbol{\alpha}^\top \Gamma^\top \mathbf{S}_w \Gamma \boldsymbol{\alpha}} = \\ &= \frac{\boldsymbol{\alpha}^\top \mathbf{K} (\mathbf{V} - \mathbf{e}_N \mathbf{e}_N^\top / N) \mathbf{K} \boldsymbol{\alpha}}{\boldsymbol{\alpha}^\top (\mathbf{K} (\mathbf{I}_N - \mathbf{V}) \mathbf{K} + \sigma^2 \mathbf{I}_N) \boldsymbol{\alpha}} = \\ &= \frac{\boldsymbol{\alpha}^\top \mathbf{S}_b \boldsymbol{\alpha}}{\boldsymbol{\alpha}^\top (\mathbf{S}_w + \sigma^2 \mathbf{I}_N) \boldsymbol{\alpha}}, \end{aligned} \quad (4)$$

where \mathbf{K} is the kernel matrix, \mathbf{e}_N is a vector of ones that has length N , \mathbf{V} is a block-diagonal matrix whose c -th block is

the matrix $e_{N_c} e_{N_c}^\top / N_c$, and $\Sigma_b = \mathbf{K}(\mathbf{V} - e_N e_N^\top / N) \mathbf{K}$. For example, the kernel matrix, \mathbf{K} , is calculated as the similarity matrix between subspaces \mathbf{Y}_q and \mathbf{Y}_w . The term $\sigma^2 \mathbf{I}_N$ is used for regularizing the covariance matrix $\Sigma_w = \mathbf{K}(\mathbf{I}_N - \mathbf{V}) \mathbf{K}$. It is composed of the covariance shrinkage factor $\sigma^2 > 0$, and the identity matrix \mathbf{I}_N of size N . The set of optimal vectors α are computed from the eigenvectors of $(\Sigma_w + \sigma^2 \mathbf{I}_N)^{-1} \Sigma_b$.

We apply the GDA algorithm to the reference subspaces \mathbf{Y}_i^c to generate reference vectors \mathbf{y}_i^c . When given an unknown bioacoustic signal $\mathbf{x}_{in}(t)$, we compute its SSA subspace \mathcal{Y}_{in} and map it onto the manifold to generate a vector \mathbf{y}_{in} ; then we predict its corresponding bioacoustic class (e.g. species) based on the nearest reference vector (1-NN).

3. EXPERIMENTAL RESULTS

In this section, we evaluate the validity of the proposed GSSA through an experiment using the Anuran records dataset, that was also used in [8]. This dataset is described in detail in Table 1. It consists of 60 bioacoustic signals with different duration recorded in Amazon rainforest containing anuran’s croaks and ribbits and various real background noises from the surrounding nature. Anura is the name of an order of animals in the class Amphibia that includes frogs and toads, so the diversity of signal is complex. The classes of this dataset consists of 10 species of anurans.

We evaluate GSSA against 2 variants of MSSA. The variant MSSA-I refers to the conventional method, where the class of signals is assumed to be modeled as a linear mapping in terms of the average correlation of its signals. That means that 1 reference subspace is computed to represent each species, regardless of the amount of records the class contains. The variant MSSA-II computes 1 subspace for each bioacoustic signal. for example, the specie *Rhinella g.* has 5 records, then we produce 5 subspaces. In this scheme we achieve 60 subspaces. However, MSSA-II does not have a discriminant mechanism.

We performed a 10-fold cross-validation by dividing the signals randomly, with 30 for training and 30 for test, and always ensuring that at least one signal of each anuran species is present in both groups. The parameters were varied in the following manner: the number of lagged vectors n was varied from 10 to 50 and the dimension of SSA subspaces were varied from 3 to 9.

The experimental results can be seen in Table 2. The accuracy refers to the average among all folds, and the standard deviation is calculated from the folds assuming a Gaussian distribution. First, we can see that MSSA-II outperforms MSSA-I by approximately 3%, which shows that relaxing the linearity assumption is effective to improve performance. But the main point in this experiment is that although MSSA-I has recently been shown to be the state-of-art in bioacoustics classification [8], we can note that GSSA outperforms MSSA

Table 1. Anuran records dataset. The columns min and max stand for the minimum and maximum time duration in seconds of each record in the set. This parameter gives an idea on how different the length of the signals can be.

ID	Species	n° Records	Time length (s)	
			min	max
(a)	<i>Adenomera a.</i>	8	12	360
(b)	<i>Adenomera h.</i>	11	40	187
(c)	<i>Ameerega t.</i>	5	11	52
(d)	<i>Hyla m.</i>	11	8	56
(e)	<i>Hypsiboas cin.</i>	4	6	238
(f)	<i>Hypsiboas cor.</i>	4	67	346
(g)	<i>Leptodactylus f.</i>	4	13	118
(h)	<i>Osteocephalus o.</i>	3	3	72
(i)	<i>Rhinella g.</i>	5	13	210
(j)	<i>Scinax ruber</i>	5	7	62
Summary		60	$94 \pm 113.26(s)$	

by more than 11%. This result is a compelling evidence that the discriminant mechanism of the proposed method is able to enhance the performance of bioacoustic classification in this subspace representation paradigm.

Table 2. Results for the experiment with the Anuran data. The accuracy refers to the average among all folds.

Method	Accuracy (%)	Std. Deviation
GSSA	71.33	3.91
MSSA-I	60.17	4.11
MSSA-II	62.88	4.08

4. CONCLUSIONS

In this paper we have proposed Grassmann singular spectrum analysis (GSSA), an extension to MSSA, to address more effectively the classification of bioacoustic signals. The key idea of our proposed method is twofold: relaxing the assumption that a class is composed of linear combinations of the reference signals to that it consists of a set of subspaces; and simplifying bioacoustic signal subspace representation by mapping the subspaces onto a Grassmann manifold, to then introduce a discriminatory mechanism for class separation by using Grassmann discriminant analysis (GDA). Our method also inherits various advantages of MSSA, such as low storage, consistent compactness ratio selection, signal length free formulation, and no need preprocessing techniques. The validity of GSSA was demonstrated through a classification experiment with the Anuran data where it outperformed the state-of-the-art method MSSA.

5. REFERENCES

- [1] Ana Alves, Ricardo Antunes, Anna Bird, Peter L Tyack, Patrick JO Miller, Frans-Peter A Lam, and Petter H Kvadsheim, "Vocal matching of naval sonar signals by long-finned pilot whales (*globicephala melas*)," *Marine Mammal Science*, vol. 30, no. 3, pp. 1248–1257, 2014.
- [2] Juan Gabriel Colonna, Marco Cristo, Mario Salvatierra, and Eduardo Freire Nakamura, "An incremental technique for real-time bioacoustic signal segmentation," *Expert Systems with Applications*, vol. 42, no. 21, pp. 7367–7374, 2015.
- [3] Jesús B Alonso, Josué Cabrera, Rohit Shyamnani, Carlos M Travieso, Federico Bolaños, Adrián García, Alexander Villegas, and Mark Wainwright, "Automatic anuran identification using noise removal and audio activity detection," *Expert Systems with Applications*, vol. 72, pp. 83–92, 2017.
- [4] JF Ruiz-Muñoz, Zeyu You, Raviv Raich, and Xiaoli Z Fern, "Dictionary learning for bioacoustics monitoring with applications to species classification," *Journal of Signal Processing Systems*, pp. 1–15, 2016.
- [5] Farook Sattar, Sarika Cullis-Suzuki, and Feng Jin, "Identification of fish vocalizations from ocean acoustic data," *Applied Acoustics*, vol. 110, pp. 248–255, 2016.
- [6] Ilyas Potamitis, Stavros Ntalampiras, Olaf Jahn, and Klaus Riede, "Automatic bird sound detection in long real-field recordings: Applications and tools," *Applied Acoustics*, vol. 80, pp. 1–9, 2014.
- [7] Mohammad Pourhomayoun, Peter Dugan, Marian Popescu, and Christopher Clark, "Bioacoustic signal classification based on continuous region processing, grid masking and artificial neural network," *arXiv preprint arXiv:1305.3635*, 2013.
- [8] Bernardo Bentes Gatto, Juan Gabriel Colonna, Eulanda Miranda dos Santos, and Eduardo Freire Nakamura, "Mutual singular spectrum analysis for bioacoustics classification," in *Machine Learning for Signal Processing, 2017 IEEE International Workshop on*. IEEE, 2017.
- [9] Kazuhiro Fukui and Atsuto Maki, "Difference subspace and its generalization for subspace-based methods," *IEEE transactions on pattern analysis and machine intelligence*, vol. 37, no. 11, pp. 2164–2177, 2015.
- [10] Bernardo Bentes Gatto, Lincon S. Souza, and Eulanda M dos Santos, "A deep network model based on subspaces: A novel approach for image classification," in *Machine Vision Applications (MVA), 2017 Fifteenth IAPR International Conference on*. IEEE, 2017, pp. 436–439.
- [11] H. Hotelling, "Relation between two sets of variables," *Biometrika*, vol. 28, pp. 322–377, 1936.
- [12] SN Afriat, "Orthogonal and oblique projectors and the characteristics of pairs of vector spaces," *Proc. Cambridge Philos. Soc.*, vol. 53, pp. 800–816, 1957.
- [13] O. Yamaguchi, K. Fukui, and K. Maeda, "Face recognition using temporal image sequence," *Proc. International Conference on Automatic Face and Gesture Recognition*, pp. 318–323, 1998.
- [14] Yasuko Chikuse, "Statistics on special manifolds," *Springer, Lecture. Notes in Statistics*, vol. 174, 2013.
- [15] Jihun Hamm and Daniel D Lee, "Grassmann discriminant analysis: a unifying view on subspace-based learning," in *Proceedings of the 25th international conference on Machine learning*. ACM, 2008, pp. 376–383.
- [16] Pavan Turaga, Ashok Veeraraghavan, Anuj Srivastava, and Rama Chellappa, "Statistical computations on grassmann and stiefel manifolds for image and video-based recognition," *IEEE Trans. Pattern Analysis and Machine Intelligence*, vol. 33, no. 11, pp. 2273–2286, 2011.
- [17] Lincon Souza, Hideitsu Hino, and Kazuhiro Fukui, "3d object recognition with enhanced grassmann discriminant analysis," in *ACCV 2016 Workshop (HIS 2016)*, 2016.
- [18] Lincon S. Souza, Bernardo Bentes Gatto, and Kazuhiro Fukui, "Enhancing discriminability of randomized time warping for motion recognition," in *Machine Vision Applications (MVA), 2017 Fifteenth IAPR International Conference on*. IEEE, 2017, pp. 77–80.
- [19] Françoise Chatelin, *Eigenvalues of Matrices: Revised Edition*, vol. 71, SIAM, 2012.
- [20] Jihun Hamm, "Subspace-based learning with grassmann kernels," 2008.
- [21] Reinosuke Fukunaga, "Statistical pattern recognition," 1990.
- [22] Bernhard Scholkopf and Klaus-Robert Mullert, "Fisher discriminant analysis with kernels," *Neural networks for signal processing IX*, vol. 1, no. 1, pp. 1, 1999.
- [23] Gaston Baudat and Fatiha Anouar, "Generalized discriminant analysis using a kernel approach," *Neural computation*, vol. 12, no. 10, pp. 2385–2404, 2000.
- [24] Y Li, S Gong, and H Liddell, "Constructing structures of facial identities using kernel discriminant analysis," in *The 2nd International Workshop on Statistical and Computational Theories of Vision*, 2001.