Lossless Compression of Multidimensional Medical Images

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Abstract— We introduce an efficient lossless algorithm that can be used for the compression of multidimensional medical images. We experimentally test our approach on a test set of 3-D computed tomography (CT) and 3-D magnetic resonance (MR) images. The achieved results outperform other state-of-the-art approaches.

***Keywords*—** multidimensional medical images compression; multidimensional medical images coding; multidimensional data compression;

I. Introduction

TODAY medical digital imaging techniques are continuously evolving. The research activities in medical imaging focus primarily on the improvement of the acquisition and transmission algorithms. Thanks to the wide diffusion of inter-connections new services are provided to medical staffs: for examples, exchange of medical data among different entities/structures connected by networks (e.g. trough Internet, Clouds services, P2P networks, etc.), telemedicine, tele-radiology, real-time tele-consultation, PACS (Picture Archiving and Communication Systems), etc..

For all these applications one of the main disadvantages is related to the large amount of storage space needed to save the images and for the time required to transmit the data.

These costs grow proportionally to the size of data. Future expectations in medical applications will further increase the requests for memory space and/or efficient transmission time.

Different medical imaging methodologies produce multidimensional data. For instance, Computed Tomography (*CT*) and Magnetic Resonance (*MR*) imaging technologies produce three-dimensional (N=3) data.

A 3-D CT image is acquired through X-rays. The acquisition process is performed via a computer. By using the computer we are able to obtain different cross-sectional views.

3-D CT images are an important tool for the identification of normal or abnormal structures of the human body. It is important to emphasize that an X-ray scanner allows the generation of different images, by considering different angles around the body part which is undergo analysis. Once processed by the dedicated computer, the output is a collection of the cross-sectional images, often referred as slices.

3-D MR images are an important source of information, in different medical applications and, especially, in medical diagnosis (ranging from neuroimaging to oncology). MR images are often preferred. In fact, in the case in which, both CT and MR images, produce the same information, these latter techniques are preferred, since MR acquisitions do not use any ionizing radiation. From the other hand, in presence of subjects with cardiac pacemakers and/or metallic foreign bodies, MR techniques cannot be applied.

Medical data need to be managed in an efficient and effective manner and data compression techniques are essential in order to solve the transmission and storage problems.

For medical images, lossless compression is often required and, in many situations, indispensable. In fact, these data are precious or often obtained by means of unrepeatable medical exams.

Lossy compression techniques could sometime be considered, but it is necessary take into account that that the information lost might lead to incorrect diagnosis or it could affect the reanalysis of data.

In this paper, we consider lossless predictive techniques. We have focused on multidimensional medical image sequences (3-D computed tomography images, functional resonance magnetic images), which have considerable space memory requirements (many hundreds of megabytes/gigabytes per acquisition).

This paper introduces a multidimensional, configurable, predictive structure that can be used for the compression of multidimensional medical images.

The predictor we propose is scalable, adjustable, and adaptive and we present experimental evidences of its performance on multidimensional medical images: 3-D Computed Tomography (CT) and 3-D Magnetic Resonance (MR).

This paper is organized as follows: Section 2 describes the predictive structure. Section 3 reports our experimental results. Section 4 highlights our conclusions and outlines future research directions.

II. Predictive Coding for Multidimensional Images

The predictive model we propose is based on the least squares optimization technique. In order to perform the prediction of the current sample, a prediction context, composed by the neighboring samples of the current component and one (or more) reference component(s), is used. The reference component(s) can be of different dimension(s), with respect to the current component. Therefore the

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prediction is achieved by using a multidimensional prediction context.

Without loss of generality, for the following definitions, we assume that the multidimensional image which we have to compress, has the following size: $<M_1, M_2, \ldots, M_{N-2}, X, Y>$, where X and Y are respectively the width and the height of the bi-dimensional components and M_f is the size of the f-th dimension ($1 \leq f \leq N-2$). A specific bi-dimensional component can be univocally identified through a vector of $N-2$ elements: $[p_1, p_2, \ldots, p_{N-2}]$, where $p_i \in \{1,2,\ldots,M_i\}$.

For example, if we consider a three-dimensional image, $<Z, X, Y>$ the dataset is composed of Z components (among the third dimension), where each component has respectively width X and height Y.

As we outlined above, our predictive model uses one or more reference components, which will be specified through the Sets of References or (References Set).

If the current sample has coordinates $(m_1, m_2, \ldots, m_{N-2}, x, y)$ (where $1 \leq x \leq X$ and $1 \leq y \leq Y$), for each of the $N-2$ dimension, we define a *references set*, denoted as:

$R_i = \{r_1^i, r_2^i, \ldots, r_{t_i}^i\}$, for $i \in \{1,2,\ldots,N-2\}$, where $r_j^i \in \{1,2,\ldots,M_i\} \cup \{-1,-2,\ldots,-M_i\}$, $t_i = |R_i|$, $1 \leq j \leq t_i$, and $\left|\bigcup_{i=1}^{N-2} R_i\right| > 0$.

Such references sets are univocally set up at the beginning of the algorithm and are used in the prediction step.

A generic element $r_j^i \in R_i$ ($1 \leq i \leq N-2$), denotes a specific bi-dimensional component. We will use the following notation: if $r_j^i > 0$, then the denoted component is the one identified through the vector $[m_1, m_2, \ldots, m_{i-1}, r_j^i, m_{i+1}, \ldots, m_{N-2}]$, or, if $r_j^i < 0$, then the denoted component is the one identified through the vector $[m_1, m_2, \ldots, m_{i-1}, m_i - |r_j^i|, m_{i+1}, \ldots, m_{N-2}]$.

The proposed predictive model is based on the least squares optimization technique. The prediction is formed by using the current component and all the (valid) components of the references sets.

In order to refer to a sample without the use of its coordinates, we define an *enumeration*. Its main objective is the relative indexing among all the samples (or a subset of them) of the same component. In particular, by fixing a sample, namely the reference sample, all the other samples of the component will be indexed with respect to it. Therefore, in this manner, it is possible to address a sample by using its relative index. The relative indexing of the samples is used for the definition of the multidimensional prediction context involved by our predictive model.

Let E denotes a 2-D enumeration, which has as objective the relative indexing of the samples in a bi-dimensional context, with respect to a specific reference sample. The fundamental requisites that the enumeration E needs to satisfy are that the specified reference sample has 0 as index and that any two samples (with different coordinates) do not have the same index.

Let $x_j^{(e)}(r_s^j)$ (where $r_s^j \in R_j$) denotes the e-th sample in the bi-dimensional context according to the enumeration E with respect to the sample with coordinate $(m_1, m_2, \ldots, m_{j-1}, r_s^j, m_{j+1}, \ldots, m_{N-2}, x, y)$ when $r_s^j > 0$, or $(m_1, m_2, \ldots, m_{j-1}, m_j - |r_s^j|, m_{j+1}, \ldots, m_{N-2}, x, y)$ when $r_s^j < 0$.

Finally, let $x^{(e)}$ denotes the e-th sample, according to the enumeration E, with respect to the current sample. Notice that $x^{(0)}$ denotes precisely the current sample.

The T-order prediction (where $T = \sum_{i=1}^{N-2} t_i = \sum_{i=1}^{N-2} |R_i|$) of the current sample $x^{(0)}$ is obtained by:

$$\hat{x}^{(0)} = \sum_{i=1}^{N-2} \sum_{j=1}^{t_i} \alpha_i^j \cdot x_i^{(0)}(r_j^i). \quad (1)$$

The $\alpha_0 = [\alpha_1^1, \ldots, \alpha_1^{t_1}, \ldots, \alpha_i^1, \ldots, \alpha_i^{t_i}, \ldots, \alpha_{N-2}^1, \ldots, \alpha_{N-2}^{t_{N-2}}]^t$ coefficients are chosen to minimize the energy of the prediction error:

$$P = \sum_{i=1}^{H} \left(x^{(i)} - \hat{x}^{(i)}\right)^2 \quad (2)$$

H indicates the number of samples used, for the current and for each of the components specified in the references sets. Thus, $H \cdot (T+1) + T$ samples are used for the prediction.

The coefficients α_0 are obtained by using the optimal linear prediction method, as in [25].
We can rewrite the equation (2) in the form:

$P = (\boldsymbol{C}\alpha - \boldsymbol{X})^t \cdot (\boldsymbol{C}\alpha - \boldsymbol{X})$,

by using matrix notation.

The linear system is obtained, as in [25], by taking the derivate of the equation (2) with respect to α, and by setting it to zero.

$$(\boldsymbol{C}^t\boldsymbol{C})\ \alpha_0 = (\boldsymbol{C}^t\boldsymbol{X}). \quad (3)$$

Thus, by computing the coefficients α_0, which solve the linear system (3), it is possible to determinate the prediction of the current sample, $\hat{x}^{(0)}$, by using equation (1).

The prediction error

$$e = \left\lfloor x^{(0)} - \hat{x}^{(0)} \right\rfloor \quad (4)$$

can then be sent to an entropy encoder.

It is important to outline that H x $(T+1)$ + H samples are used to achieve the prediction. Our predictive structure involves only by past information: there is no need to send any side information to the decompression algorithm.

The computational complexity of the prediction is related to the two configurable parameters: H and the Sets of

References. It is possible to model the multidimensional prediction context by specifying its wideness and the number of the reference components. By doing this it is possible either to define a prediction context which can minimize the use of the computational resources or to refine the accurateness of the prediction by using more computational resources.

In some situations, our predictive structure can be ineffective. In particular, when the linear system of equations (3) cannot be solved because it has no solutions or infinitely many solutions. In such scenarios, which we referred as *exceptions*, the predictive structure is not able to perform the prediction.

In presence of a sample that cannot be predicted through the proposed predictive structure (because an exception is verified), an alternative predictive structure (as for instance Median Predictor, etc.) shall be used.

III. Experimental Results

We have tested our prediction model by implementing a predictive-based compression scheme, and then we have experimented this algorithm on two different types of multidimensional medical images: 3-D computed tomography images and 3-D magnetic resonance images.

The algorithm predicts the current sample by using the previously coded samples. In this way, it is possible to have a consistent prediction for both the compression and the decompression algorithm.

After the prediction step, the prediction error is obtained by the encoder as a difference between the current sample and its prediction.

Finally, the prediction error can be encoded by using an entropy or a statistical coder. In our tests, we have used as error encoder: PAQ8 [10], Prediction by Partial Matching with Information Inheritance (PPMd or PPMII) [26].

The algorithm uses the 2-D Linearized Median Predictor (2D-LMP) [21], for all the components which have no component references, and our multidimensional predictive structure, for all the other components.

In order to define the prediction context, we need to enumerate the neighboring pixels of X in the current and in the previous bands.

For these reasons, we define an enumeration that depends on a distance d, defined as:

$$d((z,u,v),(z,w,z)) = \sqrt{(u-w)^2 + (v-z)^2}$$

When more pixels have the same indices, it is possible to reassign the indices of these pixels in clockwise order with respect to X.

To improve the readability, we used the mnemonic name of the dimension instead of its index for the references sets. For example, R_Z indicates the reference set for the Z dimension.

3.1. 3-D Computed Tomography Images

We have performed experiments on a the test set described in [21], composed by four 3-D CT images, in which each sample is stored by using 8 bits. For the coding of prediction errors, which we have mapped similarly to [15], then we have used PAQ8 and we have managed the exceptions with the 3-D Differences-based Linearized Median Predictor (3D-DLMP) [21].

The following tables summarize the results we have obtained on the four CT images in terms of bits-per-sample (BPS) by using different configurations for the H parameter and the references set. The results are compared with other state-of-the-art techniques.

Our approach outperforms, in average, all the other state-of-the-art techniques, as it is possible to see from Table 5.

Methods / Images Dimensions		**CT_skull** <192, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	1.4836
	H=16, R_Z={-1, -2, -3}	1.5309
	H=8, R_Z={-1, -2, -3}	1.6258
	H=32, R_Z={-1, -2}	1.5393
	H=16, R_Z={-1, -2}	1.5688
	H=8, R_Z={-1, -2}	1.6196
3D-ESCOT [28]		1.8350
MILC [21]		2.0306
AT-SPIHT [6]		1.9180
3D-CB-EZW [3]		2.0095
DPCM+PPMd [1]		2.1190
3D-SPIHT [28]		1.9750
3D-EZW [3]		2.2251
JPEG-LS [4]		2.8460

Table 1: Experimental results obtained on CT skull

Methods / Images Dimensions		**CT_wrist** <176, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	0.8979
	H=16, R_Z={-1, -2, -3}	0.9290
	H=8, R_Z={-1, -2, -3}	1.0042
	H=32, R_Z={-1, -2}	0.9527
	H=16, R_Z={-1, -2}	0.9737
	H=8, R_Z={-1, -2}	1.0110
3D-ESCOT [28]		1.0570
MILC [21]		1.0666
AT-SPIHT [6]		1.1150
3D-CB-EZW [3]		1.1393
DPCM+PPMd [1]		1.0290
3D-SPIHT [28]		1.1720
3D-EZW [3]		1.2828
JPEG-LS [4]		1.6531

Table 2: Experimental results obtained on CT wrist

ISBN: 978-1-61804-286-6

Methods / Images Dimensions		CT_carotid <64, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	1.2783
	H=16, R_Z={-1, -2, -3}	1.2976
	H=8, R_Z={-1, -2, -3}	1.3421
	H=32, R_Z={-1, -2}	1.3363
	H=16, R_Z={-1, -2}	1.3448
	H=8, R_Z={-1, -2}	1.3496
3D-ESCOT [28]		1.3470
MILC [21]		1.3584
AT-SPIHT [6]		1.4790
3D-CB-EZW [3]		1.3930
DPCM+PPMd [1]		1.4710
3D-SPIHT [28]		1.4340
3D-EZW [3]		1.5069
JPEG-LS [4]		1.7388

Table 3: Experimental results obtained on CT carotid

Methods / Images Dimensions		CT_aperts <96, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	0.7283
	H=16, R_Z={-1, -2, -3}	0.7350
	H=8, R_Z={-1, -2, -3}	0.7587
	H=32, R_Z={-1, -2}	0.7265
	H=16, R_Z={-1, -2}	0.7271
	H=8, R_Z={-1, -2}	0.7349
3D-ESCOT [28]		0.8580
MILC [21]		0.8190
AT-SPIHT [6]		0.9090
3D-CB-EZW [3]		0.8923
DPCM+PPMd [1]		0.8670
3D-SPIHT [28]		0.9980
3D-EZW [3]		1.0024
JPEG-LS [4]		1.0637

Table 4: Experimental results obtained on CT aperts

Methods / Images Dimensions		*Average*
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	*1.0970*
	H=16, R_Z={-1, -2, -3}	*1.1231*
	H=8, R_Z={-1, -2, -3}	*1.1827*
	H=32, R_Z={-1, -2}	*1.1387*
	H=16, R_Z={-1, -2}	*1.1536*
	H=8, R_Z={-1, -2}	*1.1788*
3D-ESCOT [28]		*1.2743*
MILC [21]		*1.3187*
AT-SPIHT [6]		*1.3553*
3D-CB-EZW [3]		*1.3585*
DPCM+PPMd [1]		*1.3715*
3D-SPIHT [28]		*1.3948*
3D-EZW [3]		*1.5043*
JPEG-LS [4]		*1.8254*

Table 5: Average experimental results obtained on the four CT images.

3.2 3-D Magnetic Resonance Images

We have performed similar experiments also for the four MR images commonly used for testing in the literature.

As for the CT images the following tables show that our approach outperform the current state of the art algorithms.

Methods / Images Dimensions		MR_liver_t1 <48, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	1.8511
	H=16, R_Z={-1, -2, -3}	1.8850
	H=8, R_Z={-1, -2, -3}	1.9894
	H=32, R_Z={-1, -2}	1.8996
	H=16, R_Z={-1, -2}	1.9089
	H=8, R_Z={-1, -2}	1.9471
3D-ESCOT		2.0760
MILC		2.1968
3D-SPIHT		2.2480
3D-CB-EZW		2.2076
DPCM+PPMd		2.3900
3D-EZW		2.3743
JPEG-LS		3.1582

Table 6: Experimental results obtained on MR liver_t1

Methods / Images Dimensions		MR_liver_t2e1 <48, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	1.2539
	H=16, R_Z={-1, -2, -3}	1.2783
	H=8, R_Z={-1, -2, -3}	1.3360
	H=32, R_Z={-1, -2}	1.3101
	H=16, R_Z={-1, -2}	1.3232
	H=8, R_Z={-1, -2}	1.3482
3D-ESCOT		1.5100
MILC		1.7590
3D-SPIHT		1.6700
3D-CB-EZW		1.6591
DPCM+PPMd		2.0250
3D-EZW		1.8085
JPEG-LS		2.3692

Table 7: Experimental results obtained on MR liver_t2e1

Methods / Images Dimensions		MR_sag_head <48, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	1.4890
	H=16, R_Z={-1, -2, -3}	1.5311
	H=8, R_Z={-1, -2, -3}	1.6020
	H=32, R_Z={-1, -2}	1.5477
	H=16, R_Z={-1, -2}	1.5737
	H=8, R_Z={-1, -2}	1.6094
3D-ESCOT		1.9370
MILC		2.0975
3D-SPIHT		2.0710
3D-CB-EZW		2.2846
DPCM+PPMd		2.1270
3D-EZW		2.3883
JPEG-LS		2.5567

Table 8: Experimental results obtained on MR sag_head

ISBN: 978-1-61804-286-6

Methods / Images Dimensions		MR_ped_chest <64, 256, 256>
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	1.2920
	H=16, R_Z={-1, -2, -3}	1.3498
	H=8, R_Z={-1, -2, -3}	1.4669
	H=32, R_Z={-1, -2}	1.3740
	H=16, R_Z={-1, -2}	1.4053
	H=8, R_Z={-1, -2}	1.4694
3D-ESCOT		1.6180
MILC		1.6556
3D-SPIHT		1.7420
3D-CB-EZW		1.8705
DPCM+PPMd		1.6890
3D-EZW		2.0499
JPEG-LS		2.9282

Table 9: Experimental results obtained on MR ped_chest

Methods / Images Dimensions		*Average*
Proposed \\ Parameters	H=32, R_Z={-1, -2, -3}	*1.4715*
	H=16, R_Z={-1, -2, -3}	*1.5111*
	H=8, R_Z={-1, -2, -3}	*1.5986*
	H=32, R_Z={-1, -2}	*1.5329*
	H=16, R_Z={-1, -2}	*1.5528*
	H=8, R_Z={-1, -2}	*1.5935*
3D-ESCOT		*1.7853*
MILC		*1.9272*
3D-SPIHT		*1.9328*
3D-CB-EZW		*2.0055*
DPCM+PPMd		*2.0578*
3D-EZW		*2.1553*
JPEG-LS		*2.7531*

Table 10: Average experimental results obtained on the four MR images.

IV. Conclusions and Future Work

In this paper, we have proposed a Multidimensional Predictive Model that can be used for lossless compression of multidimensional medical image. We have experimentally tested our method on 3-D magnetic resonance (MR) and 3-D computed tomography (CT) images.

Future work will include the testing of our approach on 4-D and 5-D functional Magnetic Resonance Imaging (fMRI) data, the usage of the model in a lossy codec, and deeper experimentation on lossless compression by using other N-D data (eg. 4-D ultrasound images, etc.).

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