A MULTIPLICATION-FREE FRAMEWORK FOR SIGNAL PROCESSING AND APPLICATIONS IN BIOMEDICAL IMAGE ANALYSIS

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Abstract

A new framework for signal processing is introduced based on a novel vector product definition that permits a multiplier- free implementation. First a new product of two real numbers is defined as the sum of their absolute values, with the sign determined by product of the hard-limited numbers. This new product of real numbers is used to define a similar product of vectors in R^N . The new vector product of two identical vectors reduces to a scaled version of the l_1 norm of the vector. The main advantage of this framework is that it yields multiplication-free computationally efficient algorithms for performing some important tasks in signal processing. An application to the problem of cancer cell line image classification is presented that uses the notion of a co-difference matrix that is analogous to a covariance matrix except that the vector products are based on our new proposed framework. Results show the effectiveness of this approach when the proposed co-difference matrix is compared with a covariance matrix.

Index terms: Inner-product space, image classification, region covariance, co-difference

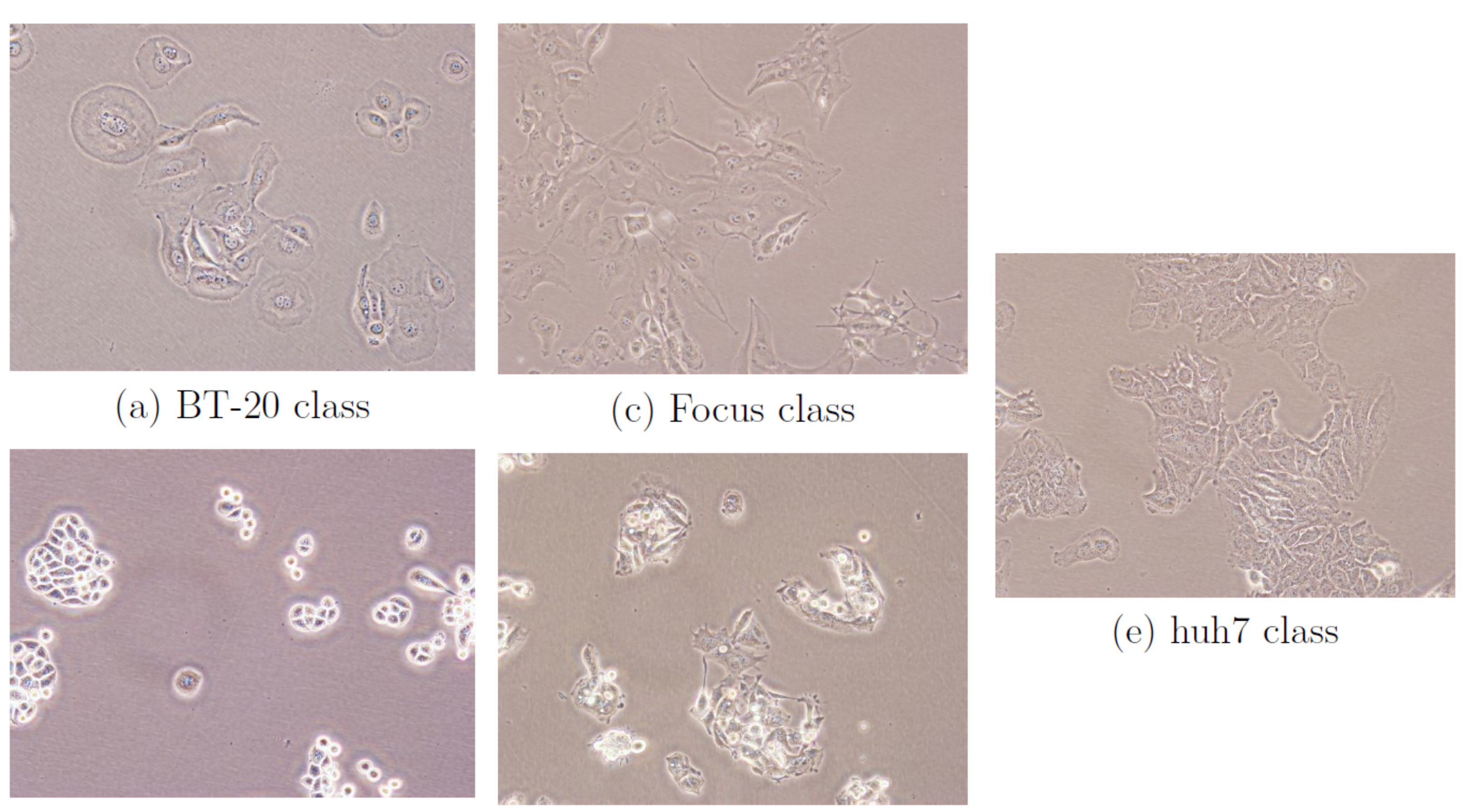
Problem Statement

Cancer cell lines are grown in tissue culture, usually in a lab environment. They represent generations of a primary culture. Identification of carcinoma cells has to be done at several stages of an experiment in molecular biology.

Short tandem repeat (STR) analysis is being used as a standard for the authentication of human cell lines. This is a costly and non-automated process.

Automated analysis will provide a fast and easy-to-use tool that can be used in laboratories to verify cell line identity.

Problem: Classify images from 14 different cell lines.



(a) BT-20 class (c) Focus class (e) huh7 class (b) Cama-1 class (d) HepG2 class

Figure 1: Example images of the cell lines used in our experiments.

Proposed Method

We propose to use region co-difference matrices [2] for feature extraction.
Co-difference computation is about 100-times faster than covariance [1] computation for a given image.

Covariance

$$\mathbf{C}_v = \frac{1}{N-1}\sum_{k=1}^{N}(\mathbf{f_k}-\mu)\cdot(\mathbf{f_k}-\mu)^T$$

Co-difference

$$\mathbf{C}_d = \frac{1}{N-1}\sum_{k=1}^{N}(\mathbf{f_k}-\mu)\oplus(\mathbf{f_k}-\mu)^T$$

where

$$a \oplus b = sgn(a\cdot b)\cdot(|a|+|b|)$$

The co-difference operator has some interesting properties.
One can define a "vector product" as follows:

$$< \mathbf{x}_1, \mathbf{x}_2 >= \sum_{i=1}^{N} x_1(i)\oplus x_2(i)$$

"Multiplication" of a vector with a scalar

$$a\oplus\mathbf{x} = \begin{bmatrix} a\oplus x(1) \\ a\oplus x(2) \\ \vdots \\ a\oplus x(N) \end{bmatrix}$$

Vector product of a vector with itself is a scaled version of the l_1 norm

$$< \mathbf{x}, \mathbf{x} >= \sum_{i=1}^{N} x(i)\oplus x(i) = 2\sum_{i=1}^{N}|x(i)| = 2||x||_1$$

Since our images show a lot of junctions and corners, we use dual-tree complex wavelet (DTCWT) [3] M_{θ}(x,y) and directional co-difference s_{α}(x,y) features.

$$I_\alpha(i) = I(x + i\cdot\tfrac{R}{A}cos(\alpha), y + i\cdot\tfrac{R}{A}sin(\alpha))$$

$$\mathbf{I}_\alpha = [I_\alpha(1), I_\alpha(2), ..., I_\alpha(A)]$$

$$\mathbf{s}_\alpha = I(x,y)\oplus(\mathbf{I}_\alpha - \mu_\alpha)$$

We use the following feature vector:

$$\phi(I,x,y) = [I_a(x,y)\,|I_x|\,|I_y|\,|I_{xx}|\,|I_{yy}|\,\mathbf{M}_\theta(\mathbf{x},\mathbf{y})\,\mathbf{s}_\alpha(\mathbf{x},\mathbf{y})]^T$$

We investigate the effect of normalization of the covariance and co-difference matrices.

$$\hat{\mathbf{C}}(\mathbf{i},\mathbf{j}) = \begin{cases} \sqrt{\mathbf{C}(\mathbf{i},\mathbf{j})}, & \text{if } i=j \\ \frac{\mathbf{C}(\mathbf{i},\mathbf{j})}{\sqrt{\mathbf{C}(\mathbf{i},\mathbf{i})\mathbf{C}(\mathbf{j},\mathbf{j})}}, & \text{otherwise} \end{cases}$$

Background subtraction was carried out by using an EM algorithm, followed by morphological closing and median filtering.

Experimental Results

Our dataset consisted of 14 different cancer cell lines recorded at 20x with 20 images per class. For classification we used an SVM [5] with an RBF kernel and parameters C=1000 and γ=0.5 after cross-validation.

Co-difference features yield comparable performances than covariance features.

Unnormalised Covariance classification	Normalised Covariance classification	Unnormalised Codifference classification	Normalised Codifference classification
96.4	97.5	95.7	98.2

Table 1: Classification accuracies (%) using different feature extraction methods.

Conclusion

In this paper, a new framework for signal processing based on a novel vector product definition that permits a multiplier-free implementation was introduced. The main advantage of this framework is that it yields multiplication-free computationally efficient algorithms for performing some important tasks in signal processing. This operator can be used to construct a so-called region co-difference matrix that has very similar properties to the established region covariance matrix. The co-difference matrix was successfully applied to the problem of classifiying cancer cell line images. The co-difference matrix-based approach produces slightly better results than the covariance matrix without performing any multiplications.

References

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