Bio-imaging Toolkit for Indexing, Searching, Navigation, Discovery and Annotation

Afzal Godil[1], Benny Cheung[1], Asim Wagan[1], and Xiaolan Li[1,2]

[1] National Institute of Standards and Technology, USA
[2] Zhejiang Gongshang University, P.R. China
{godil,bcheung,wagan,lixlan}@nist.gov

Abstract. Bio-imaging toolkit is an application for biological imaging community that will bring in the latest efforts in indexing, searching, navigation, discovery, analysis and annotation for both biological image and video collections. This paper discusses both metadata-based and content-based representation, indexing, querying, navigation, discovery, and retrieval, as well as video segmentation and image/video annotations. It also discusses image retrieval by texture similarity, shape similarity, color similarity, and spatio-temporal relationships for the bio-imaging database. A highly interactive multimedia information retrieval system has been developed which is based on Service Oriented Architecture (SOA) that relies on the REST based web-service model to create efficient web components. Application designed is a light weight container application that can be deployed easily without any expertise and easy to understand for novice users.

1 Introduction

A web based application has been developed for storage of bio-images and interface for indexing, searching, discovery and annotation. These tools and the framework can be very valuable for retrieval, exploration, annotation and analysis from 2D cellular imaging databases. For instance, one may use the shape descriptors based on texture, shape and temporal signal, which have been developed to identify cell images and classify them. The similarity matrix used in a web browser that displays and facilitates query on cellular images and on the features derived based on shape, texture and temporal signal for live cells.

Previous generic image and video management systems for bio-imaging community were mainly devised to help scientists store their biological image and video databases without any overt emphasis on indexing, searching, navigation, usability and other complexity issues.

This application has the advantage of easy to deploy and use, for people with no expertise. Historically there are many systems proposed for biological multimedia management. One of the main applications which is widely known is Open Microscopy Environment (OME) [3, 4]. The system is designed as a web based system with modules to manage media. Although OME is very similar to our system, but our system differs from it in the use of SOA based design with emphasis on ease of installation and management of the application itself. Another system which is known as Cell Centered Database (CCD) [5, 6, 7, 8] provides the similar facility but is only limited to images.

G. Bebis et al. (Eds.): ISVC 2008, Part II, LNCS 5359, pp. 915–923, 2008.
© Springer-Verlag Berlin Heidelberg 2008

Another system which was designed by Godil [1] has the facility for video segmentation [15] and annotation. The information content based tracking of the videos is similar to video tracking in our system, but our system provides much wider selection of features on which tracking can be performed. Video annotation has also been explored [2]. For videos MPEG [11, 12, 13] provides a very large and comprehensive standard for describing video content, but due to complexity we have relied on using external or automated video content descriptors. Application of Dublin Core in Multimedia searching interfaces has been used earlier by [10].

2 Exploration

2.1 Interface

The interface for web-based video review is shown in Figure 3. The panel on the left is for searching. It has two tabs, one for basic searching and the other for advanced searching. The basic searching is based on filtering based on the cell area and based on the Dublin core and other metadata. The advanced tab provides capability for content based searching based on retrieval by texture similarity, shape similarity, color similarity, and spatial-temporal relationships similarity. The second panel on the left side shows all the experiments that are the results of the basic search and are available for further exploration. There are three areas on the right side. The top area shows one of the images in focus from all the images in the image-set. In case of a video it embeds the video plug-in to show, play, pause and stop the video. Below that is a compact pictorial summarization/thumbnail of all the images in the image-set. In case of a video it shows the key-frames which is a pictorial summarization of the original video based on segmentation. The bottom area has tabs to show basic statistics of each image or the whole image-set, and graphs of the basic statistics quantities such as area of cells, etc. There is also a tab to post and view annotations for both images and videos.

To calculate the number of cells or entropy we use the following algorithm.

1. For the complete experiment OTSU [15] based thresholding is used to get the global threshold values. According to OTSU's method the optimum threshold maximizes the between class variance. So maximization of the eq.1 gives the optimum threshold value at.

$$\sigma^2_{BET}(T) = n_B(T)n_O(T)[\mu_B(T) - \mu_O(T)]^2 \quad .....(1)$$

2. The watershed algorithm is used to separate the connected cells while cells at boundaries are ignored.
3. After initial processing we have a set of non connected regions, which are then catalogued in the database with unique IDs and their relationship to the experiments and image in the database. The Figure 2 shows the experiments cell counter created using this method.
4. For the content based searching we also store the additional features calculated for each cell and image such as Gabor [17] and Zernike [12].

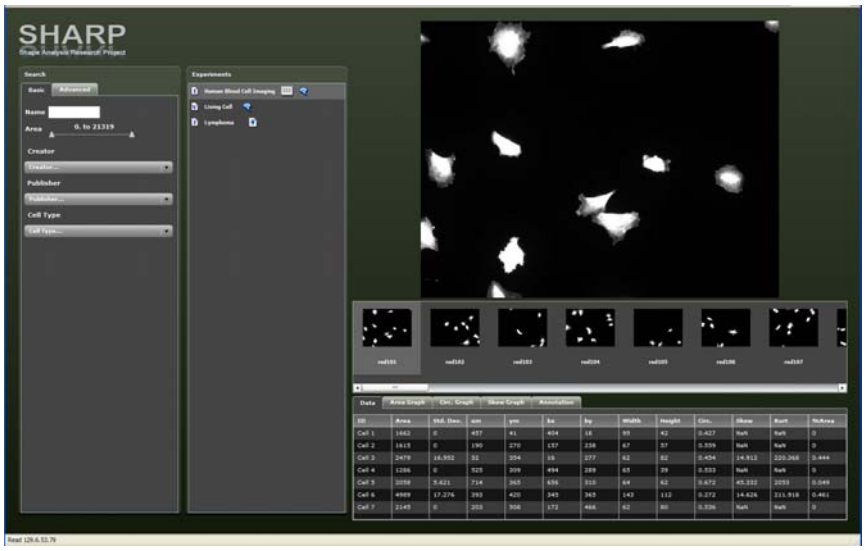

Fig. 1. Main Interface of the Bio-imaging toolkit

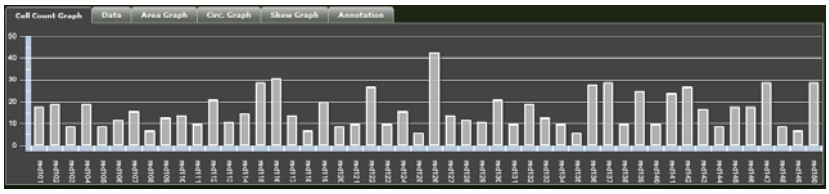

Fig. 2. Experiment measure based explorer of the Bio-imaging toolkit

2.2 Video Review and Navigation

In different bio-imaging experiments large amount of time dependent images are captured and are usually stored as video. This has created an impetus for creating tools to help viewing and analyzing the video more efficiently [1][15]. A tool for video review and summarization for the video has been implemented. Automatic summarization based on video analysis and segmentation is one such method. It creates a subset of keyframes which contain information about some abrupt changes in the original video. From the summaries provided the biologist can quickly find parts of the video which are interesting. The segmentation tool finds the keyframes based on the difference in the image entropy, percentage of cell area, or number of cells, etc, between two successive frames and a threshold level to create a filmstrip of keyframes images. The generated keyframes are a compact pictorial summarization of the video. The keyframes images are also hyperlinked back to the video -- clicking the keyframes starts the video playing from that point in time.

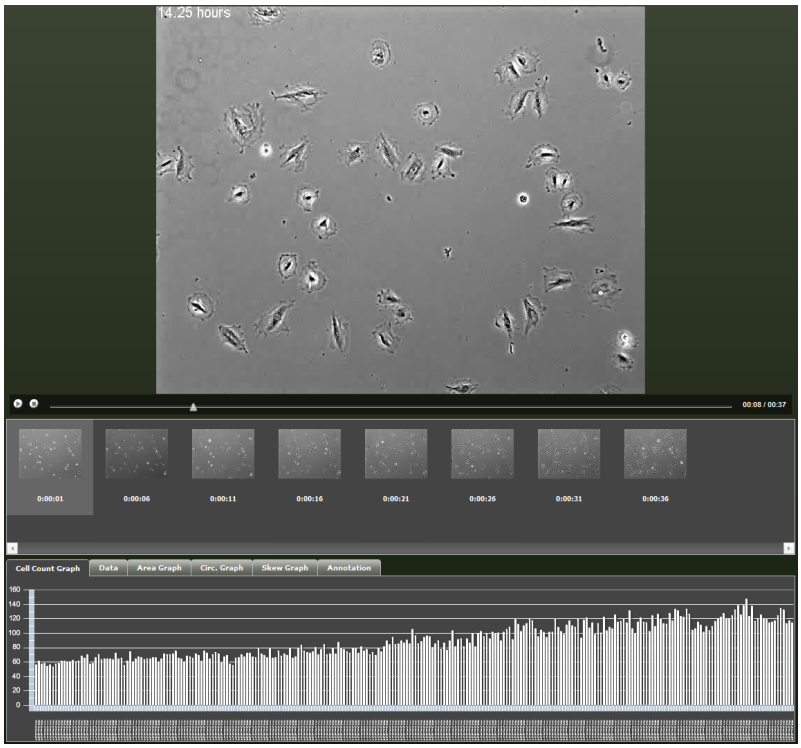

Fig. 3. Video exploration with film strip and cell counter enabled

Using the tool graphs of entropy or number of cells, or percentage of cell area vs. time have been created. The graph created is linked to the video so that clicking on the graph causes the video to play at the selected time point as shown in Figure 3. Hence the application can also index the video based on the graphs and the filmstrip of keyframes.

To calculate the content information for generating exploration graph the similar algorithm as used in the experiment based analysis has been utilized. The only difference is the initial addition of some noise removal methods are used to smooth out the noise so that further processing can be easily done. The noise removal method have been used is based on the nonlinear anisotropic diffusion equations as propose by Perona and Malik [18]. The diffusion based on this model helps to keep the edges intact while smoothing out the noise. This model smoothes out the images in nonlinear fashion so that edges remain stable while other regions are smoothes out gradually over time.

$$I_i = div\ (C\ (x, y, t)\nabla I)\ldots\ldots(2)$$

In the eq.2 the *div* is the divergence operator while ∇ is the gradient operator. The C basically enables the eq.2 to do nonlinear smoothing of the image.

The results obtained from the method described are segmented and details about cell area and numbers are stored for further processing, such as generation of the graphs or exploration interfaces.

3 Annotation

A web-based annotation system has been created for the reviewer to post comments or annotate the image set or the video to indicate "interesting things" happened in the image or video as shown in Figure 4. Annotations can be reviewed later and can be used to cue image set or the video by clicking on the time stamp (Figure 4).

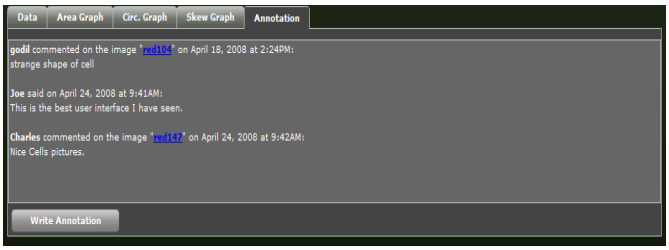

Fig. 4. (a) Review of annotation

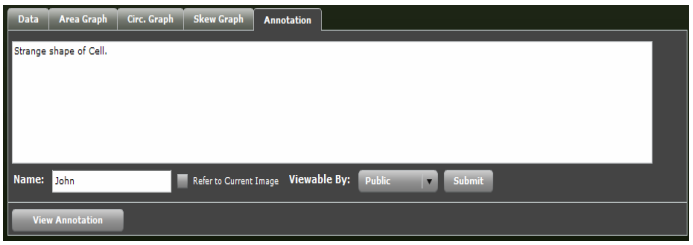

Fig. 4. (b) Posting of Annotation

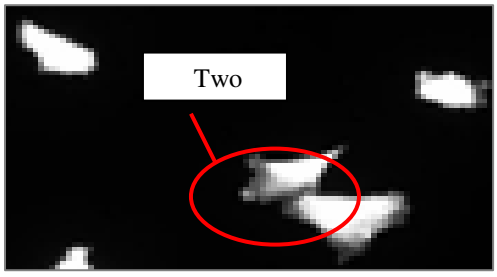

Fig. 4. (c) Annotation of an image

It is also possible to annotate part of images as shown in Figure 4c, by drawing a basic shape (such as: circle, rectangle, etc) around an area of interest to highlight it and then to have textual comments associated with it.

The ability to annotate bio-images and video can provide an added value to the bio-imaging toolkit and the comments provides personal notes and facilitate asynchronous collaboration. The number of comments also provides a clue to the users on how interesting an experiment or study is. A usability evaluation of the annotation part of the application is planned to be performed to see how useful this part is to the users.

4 Searching

The search interface provides two ways of searching, one for content based multimedia searching and the other for searching based on metadata. Both of these interfaces enable the users to easily navigate the system where there might be thousands or even millions of images.

4.1 Meta Information

The meta-data is based on Dublin Core elements [9] and additional meta-data for instruments, environmental conditions and experimental setup for the biological image database. The application at the backend is composed of web services which display the images and the Dublin core elements. Textual searching is based on these meta-data contents. The advantage of using standards based metadata is that the application can easily interoperate and collaborate with other communities in bio-imaging and with other applications.

4.2 Content Based Searching

Content based searching is a term used for describing the searching based on the visual information present in the image or video such as shape, texture, color and event. Figure 5 shows the interface for content based searching.

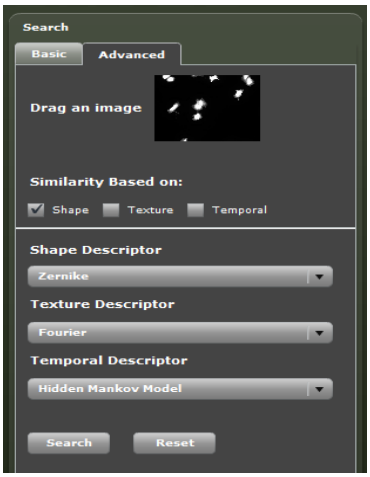

Fig. 5. The advance content based searching interface

Content based searching provides on the basis of some well known features such as Gabor, Fourier and Wavelet Features. Content based searching is performed by using many set of feature vectors. Each feature vector is calculated at many scales, where each scale corresponds to cell, image and experiment or videos level. These are categorized as following.

Cell Level: These features are composed of some texture and shape features such as Zernike moments and Haralick textures [16].

Image Level: These features are composed of the feature vectors generated mainly from texture and color information. These contain features like Wavelet, Gabor and Fourier.

Video or experiment Level: These features correspond to the features captured from as Cell and Image level. But these are stored as temporal models to be used by Markovian models to detect particular events in the collection of videos or experiments.

5 Zoomable Interface

For image exploration a zoomable interface is provided that helps in exploring large datasets as shown in figure 6. This zoomable interface gives a unique insight into the image collection, This view is reconfigurable so that clustering can be performed, which enables the users to see the clusters of the images according to some similarity criteria.

Zoomable interface is composed of a series of collection of images at multiple levels that enables the users to view the collection at multi-scales.

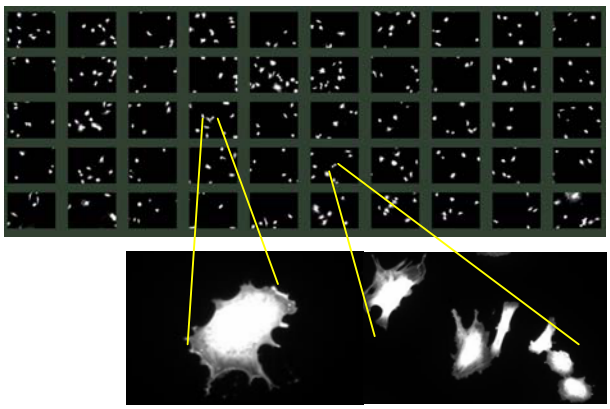

Fig. 6. Shows the zoom-able interface

6 Conclusion

This paper presents an overview of an integrated visualization and exploration interface for biological images. This interface facilitates the biological community in

keeping and exploring the video and image collection of biological data. The interface provided is web based and light weight. It provides lots of different facilities for searching based on both metadata and content. The main goal is to create an easily deployable application without lots of complex configuration and installation issues.

Acknowledgements

This work was supported by SIMA and IDUS program.

References

[1] Godil, A.: ViSA: Video Segmentation and Annotation. In: UPA 2004 conference, Minneapolis, MN, June 6-11 (2004)
[2] Bargeron, D., Gupta, A., Sanocki, E., Grudin, J.: Annotations for streaming video on the web: System Design and Usage Studies. In: Proceeding of WWW8, pp. 61–75 (1999)
[3] Swedlow, J.R., Goldberg, I., Brauner, E., Sorger, P.K.: Informatics and Quantitative Analysis in Biological Imaging. Science 300 (April 4, 2003)
[4] Sorger, P., Rines, D., Goldberg, I., Swedlow, J., Hughes, B.: The Open Microscopy Environment
[5] Martone, M.E., Tran, J., Wong, W.W., Sargis, J., Fong, L., Larson, S., Lamont, S.P., Gupta, A., Ellisman, M.H.: Cell Centered Database, The National Center for Microscopy and Imaging Research (NCMIR) at the University of California San Diego
[6] Martone, M.E., Tran, J., Wong, W.W., Sargis, J., Fong, L., Larson, S., Lamont, S.P., Gupta, A., Ellisman, M.H.: The Cell Centered Database project: An update on building community resources for managing and sharing 3D imaging data. J. Struct. Biol. (October 16, 2007)
[7] Martone, M.E., Sargis, J., Tran, J., Wong, W.W., Jiles, H., Mangir, C.: Database resources for cellular electron microscopy. Methods Cell Biol. 79, 799–822 (2007); PMID: 17327184
[8] Martone, M.E., Gupta, A., Wong, M., Qian, X., Sosinsky, G., Ludaescher, B., Ellisman, M.H.: A cell centered database for electron tomographic data. J. Struct. Biol. 138, 145–155 (2002)
[9] DCMI 1998. Dublin Core Metadata Element Set, version 1.0: Reference description. Retrieved January 10 (2007)
[10] Hunter, J., Newmarch, J.: An Indexing, Browsing, Search and Retrieval System for Audiovisual Libraries. In: Third European Conference on Research and Advanced Technology for Digital Libraries, ECDL 1999, Paris, September, pp. 22–24 (1999)
[11] Hunter, J.: Adding Multimedia to the Semantic Web: Building an MPEG-7 Ontology. In: Proc. Int'l Semantic Web Working Symp. (SWWS 2001), pp. 261–283 (2001)
[12] Martinez, J.: Overview of the MPEG-7 Standard, MPEG Document: ISO/IEC JTC1/SC29/WG11 N4509 Pattaya (December 2001)
[13] ISO/IEC 15938-5 FDIS Information Technology - Multimedia Content Description Interface - Part 5: Multimedia Description Schemes, MPEG Document: ISO/IEC JTC1/SC29/WG11 Document W4242, Sydney (July 2001)
[14] Prata Jr., A., Rusch, W.V.T.: Algorithm for computation of Zernike polynomials expansion coefficients. Appl. Opt. 28(4), 749–754 (1989)

[15] Chiu, P., Girgensohn, A., Polak, W., Rieffel, E., Wilcox, L.: A Genetic Algorithm for Video Segmentation and Summarization. In: Proceedings of IEEE International Conference on Multimedia and Expo, vol. III, pp. 1329–1332 (2000)
[16] Haralick, R.M., Shanmugam, K., Dinstein, I.: Textural Features for Image Classification. IEEE Transactions on Systems, Man, and Cybernetics (1979)
[17] Manjunath, B.S., Ma, W.Y.: Texture features for browsing and retrieval of large image data. IEEE Transactions on Pattern Analysis and Machine Intelligence (Special Issue on Digital Libraries) 18(8), 837–842 (1996)
[18] Perona, P., Malik, J.: Scale-Space and Edge Detection Using Anisotropic Diffusion. IEEE Transactions on Pattern Analysis and Machine Intelligence 12(7), 629–639 (1990)
[19] Otsu, N.: A Threshold Selection Method from Gray-Level Histograms. IEEE Transactions on Systems, Man and Cybernetics 9(1), 62–66 (January 19)