"Trends" Expert Overview Sessions Revived at ICASSP 2011: Part 2

INTRODUCTION

This is the second in a series of three columns summarizing the "Trends" expert sessions organized by the Signal Processing Society Technical Committees during ICASSP 2011 in Prague, Czech Republic. Readers have an opportunity to access these Trends session summaries authored by the Technical Committees.

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—Note: Additional multimedia resources for these sessions can be found at http://www.signalprocessingsociety.org/publications/periodicals/spm/columns-resources/. Alternatively, the Tag to the left can be scanned using your smart phone (with a free reader download) to access this Web site.

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Trends in Bioimaging and Signal Processing

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The area of bioimaging and signal processing (BISP) is concerned with the development of dedicated tools for biomedical and bioinformatics applications and with fostering interdisciplinary and integrative approaches of biomedical topics by bridging the biology, medicine, and SP communities [1]. Increasingly sophisticated imaging devices and protocols are now being developed for biological and medical imaging. Understanding functional and pathological mechanisms in patients or model organisms indeed requires being able to visualize and measure in vivo and in situ at scales ranging from subcellular to whole body. A similar trend occurs in the area of genomics and proteomics, where sophisticated bioinformatics methods are required to assemble, decipher, and compare data from large-scale sequencing data [2]. This article focuses on the latest developments in biomedical imaging that has sparked a full array of challenging topics for the signal and image processing community.

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IMAGE PROCESSING CHALLENGES IN BIOIMAGING

With the recent development of fluorescent probes and of new high-resolution microscopes [e.g., confocal, two-photon, stimulated emission depletion (STED), photo activated light microscopy (PALM), stochastic optical reconstruction microscopy (STORM)], biological imaging has grown quite sophisticated and is presently having a profound impact on the way research is being conducted in cell biology [3]. Biomedical scientists can visualize subcellular components and processes, both structurally and functionally, in two or three dimensions, at different wavelengths (spectroscopy), and they can perform time-lapse imaging to investigate cellular dynamics. Researchers are faced with an ever-increasing volume of data to visualize, analyze, and process; in particular, in the context of high throughput screening that requires the engineering of fast, robust algorithms with minimal user interaction. We have grouped the related SP challenges in three broad categories:

- *Image reconstruction and mathematical imaging*: While there have been tremendous advances in the instrumentation, it is very likely that the capabilities of modern microscopes can be further enhanced with the help of sophisticated SP for denoising, three-dimensional (3-D) deconvolution, and/or tomographic reconstruction. The problems that are specific to this kind of imaging are high levels of noise (photon-counting statistics), photo-bleaching, and the presence of aberrations (in particular, the depth dependence of the point spread function). In addition, the challenge is to design true 3-D (or 3-D + time) reconstruction algorithms that are fast enough to be used in practice. The foundation of such methods is a

(continued on page 191)

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physically accurate model of image formation with a reasonably small number of parameters. Regularized inverse methods must not only preserve, but also precisely reconstruct biological structures in their shapes and intensity level. This appears to be an area where nonlinear techniques (e.g., ℓ1-norm minimization) hold great promises.

- *Quantitative image analysis (3-D + time)*: Biologists are in great need of quantitative data that can be collected, stored, and subjected to statistical analyses. Concretely, this requires the detection of fluorescent probes, segmentation, particle tracking, shape and motility analysis of cells, and the extraction of gene expression profiles. The challenge there is to develop global algorithms that can address the detection and tracking problems simultaneously, and also handle huge amounts of data, including very crowed image scenes, both in two-dimensional (2-D) and 3-D.
- *Novel methods for the extraction and characterization of 3-D features and structure of networks*: Biological structures are inherently 3-D. They can also be rather complex; for example, the dense networks of neurons, microvascularization, or cellular scaffolds. This calls for the development of a novel panoply of 3-D detectors for finding filaments, sheets, open curves defining singularities without jump in the intensity function, and more generally, key points that are specific to biology. One possible venue is the design of optimized templates using 3-D steerable filters and wavelets or the design of new variational functionals involving appropriate differential operators. It is necessary to develop graph-based models or other mathematical tools to link such structures (missing data managing) and to compose the underlying networks. One also needs to define new dedicated metrics that allow the comparison, classification and assessment of such higher-level entities.

These challenges involve a multidisciplinary context: biologists (preparation, imaging protocol, and interpretation of results), biochemists (staining, fluorescent markers), imaging scientists (design of cutting-edge instrumentation), and finally, image processing. A last aspect that should not be overlooked by signal processors is the design of user-friendly imaging software (e.g., in the form of a plug-in for ImageJ or Icy [4]) that can be readily used by biologists with minimal knowledge of computer science. Ultimately, the best impact that we can hope for is that biologists and microscopists rely on our algorithms to perform their work.

MEDICAL IMAGING

Advances in image acquisition have sparked a steady expansion of the dimensionality of data sets, especially when data sets include local directional information on fiber orientation or four-dimensional (4-D) blood flow. Such high-dimensional data sets cannot be interpreted visually without adequate image analysis and, as such, there is a major ongoing effort toward developing analysis techniques for such complexly structured data.

A second recent trend is the advent of in-vivo molecular imaging modalities such as fluorescence and bioluminescence imaging, which enable the live imaging of gene expression and protein interactions. Combined with detailed structural imaging modalities such as magnetic resonance (MR), the biochemical onset of disease and therapy can be monitored in combination with structural and functional consequences over time. Main analysis challenges are the fusion of heterogeneous data (e.g., registration of photographs to 3-D data of animals with highly variable posture), and linking in-vivo imaging to existing genomics databases, such as the Allen brain database [5].

A third important trend is longitudinal image analysis. Increasingly, imaging data is acquired in a follow-up manner, where the subtle changes over time reflect the information of interest. Longitudinal imaging studies are typically performed to characterize diseases in single patients or patient cohorts. However, large follow-up population imaging studies are also being performed on cohorts of 6,000–20,000 healthy subjects to image the process of healthy aging, and to identify early disease biomarkers upon the onset of disease in individual study subjects [6]. Analysis challenges lie in the sheer data volume that necessitates full automation, and in feature extraction and data mining in such large image databases

Finally, there is a strong trend toward objective quantitative benchmarking of analysis methods, where data sets with expert annotations are made publicly available, and standardized evaluation pipelines can be applied for algorithm benchmarking. Since the initial MICCAI Segmentation Challenge in 2007, competitive challenge events have been organized on, among others, liver, coronary, brain, and carotid segmentation as well as on image registration. Their importance is underscored by the fact that novel analysis techniques for these problems should today often be benchmarked against these public evaluation frameworks to qualify for publication acceptance.

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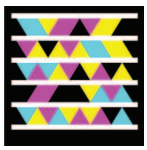
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