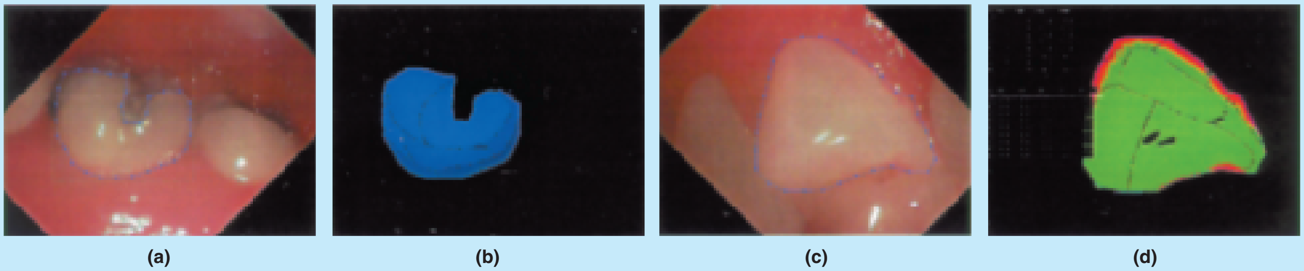

Figure 2. Examples are shown of **Biomedical Image** segmentation, morphing, and classification.

GUI (see Figure 1) that allows users to do an end-to-end run of a patient's record, including tooth segmentation of all teeth, grid morphing of each segmented tooth, and plaque classification of each tooth image.

The automated and accurate processing of the captured images to segment each tooth [see Figure 2(a)] and then detect plaque on a tooth-by-tooth basis is a critical component of the PlaqTrak system to do clinical trials and analysis with minimal human intervention. These features offer distinct advantages over other competing systems that analyze groups of teeth or synthetic teeth. PlaqTrak divides each segmented tooth into eight regions using an advanced graphics morphing procedure [see results on a chipped tooth in Figure 2(b)], and a pattern recognition classifier is then used to locate plaque [red regions in Figure 2(d)] and enamel regions. The morphing allows analysis within regions of teeth, thereby facilitating detailed statistical analysis such as the amount of plaque present on the biting surfaces on teeth.

This software system is applicable to a host of biomedical applications, such as cell analysis and life detection, or robotic applications, such as product inspection or assembly of parts in space and industry.

*This work was done by Ashit Talukder, James Lambert, and Raymond Lam of Caltech for* **NASA's Jet Propulsion Laboratory**. *Further information is contained in a TSP (see page 1).*

*In accordance with Public Law 96-517, the contractor has elected to retain title to this invention. Inquiries concerning rights for its commercial use should be addressed to:*

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*Refer to NPO-30417, volume and number of this* NASA Tech Briefs *issue, and the page number.*

# Rapid Chemometric Filtering of Spectral Data

## Target species would be identified in real time.

*NASA's Jet Propulsion Laboratory, Pasadena, California*

A method of rapid, programmable filtering of spectral transmittance, reflectance, or fluorescence data to measure the concentrations of chemical species has been proposed. By "programmable" is meant that a variety of spectral analyses can readily be performed and modified in software, firmware, and/or electronic hardware, without need to change optical filters or other optical hardware of the associated spectrometers. The method is intended to enable real-time identification of single or multiple target chemical species in applications that involve high-throughput screening of multiple samples. Examples of such applications include (but are not limited to) combinatorial chemistry, flow cytometry, bead assays, testing drugs, remote sensing, and identification of targets.

The basic concept of the proposed method is to perform real-time cross-correlations of a measured spectrum with one or more analytical function(s) of wavelength that could be, for example, the known spectra of target species. Assuming that measured spectral intensities are proportional to concentrations of target species plus background spectral intensities, then after subtraction of background levels, it should be possible to determine target-species concentrations from cross-correlation values. Of course, the problem of determining the concentrations is more complex when spectra of different species overlap, but the problem can be solved by use of multiple analytical functions in combination with computational techniques that have been developed previously for analyses of this type.

The method is applicable to the design and operation of a spectrometer in which spectrally dispersed light is measured by means of an active-pixel sensor (APS) array. The row or column dimension of such an array is generally chosen to be aligned along the spectral-dispersion dimension, so that each pixel intercepts light in a narrow spectral band centered on a wavelength that is a known function of the pixel position. The proposed method admits of two hardware implementations for computing cross-correlations in real time.

One hardware implementation would exploit programmable circuitry within each pixel of an APS array. The analog spectral-intensity reading of the photodetector in each pixel would be multiplied by a gain proportional to value of the analytical function for the wavelength that corresponds to the pixel position. As a result, the output from each pixel would be proportional to contribution of the pixel to the cross-correlation (plus background). The outputs of all the pixels along the spectral-dispersion dimension would be summed to obtain the value of the cross-correlation (plus background).

Such on-chip cross-correlation could be performed rapidly because the analytical function could be statically programmed into the APS array and the multiplications could be done simultaneously or nearly so. All of the additions could be done simultaneously by means of a single binning instruction. The charge wells of all the pixels could be connected simultaneously, collecting all the charge outputs from multiplication operations into one "superpixel," the single readout value of which would constitute the cross-correlation value for the given analytical function. For an instrument in which the APS rows were aligned along the spectral-dispersion dimension and in which the image of a spectrograph slit was aligned along the pixel columns and spanned multiple pixel rows, it would be possible to perform simultaneous cross-correlations for multiple target species by applying, to each pixel row, the analytical function corresponding to one of the target species. A separate readout would be needed for each target species.

In the other hardware implementation, cross-correlations would be computed externally to the APS array. The multiplications and additions would be performed in pipeline fashion. If the APS-array outputs were analog, then programmable analog signals representing the analytical functions would be synthesized in phase with the corresponding stream of analog APS-array outputs and the multiplications and additions would be performed by relatively inexpensive, commercially available analog mixing and filtering circuits, respectively. If the APS-array outputs were digital, the cross-correlations could be computed by a digital signal processor. Ordinarily, the analog approach would be preferable because the analog operations can be performed much more rapidly than can the corresponding digital multiplications and additions.

*This work was done by Gregory Bearman, Michael Pelletier, and Suresh Seshadri of Caltech for* **NASA's Jet Propulsion Laboratory**. *Further information is contained in a TSP (see page 1).*

*In accordance with Public Law 96-517, the contractor has elected to retain title to this invention. Inquiries concerning rights for its commercial use should be addressed to:*

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*Refer to NPO-30912, volume and number of this* NASA Tech Briefs *issue, and the page number.*

# Prioritizing Scientific Data for Transmission

*NASA's Jet Propulsion Laboratory, Pasadena, California*

A software system has been developed for prioritizing newly acquired geological data onboard a planetary rover. The system has been designed to enable efficient use of limited communication resources by transmitting the data likely to have the most scientific value. This software operates onboard a rover by analyzing collected data, identifying potential scientific targets, and then using that information to prioritize data for transmission to Earth. Currently, the system is focused on the analysis of acquired images, although the general techniques are applicable to a wide range of data modalities. Image prioritization is performed using two main steps. In the first step, the software detects features of interest from each image. In its current application, the system is focused on visual properties of rocks. Thus, rocks are located in each image and rock properties, such as shape, texture, and albedo, are extracted from the identified rocks. In the second step, the features extracted from a group of images are used to prioritize the images using three different methods: (1) identification of key target signature (finding specific rock features the scientist has identified as important), (2) novelty detection (finding rocks we haven't seen before), and (3) representative rock sampling (finding the most average sample of each rock type). These methods use techniques such as K-means unsupervised clustering and a discrimination-based kernel classifier to rank images based on their interest level.

*This program was written by Rebecca Castano, Robert Anderson, Tara Estlin, Dennis DeCoste, Daniel Gaines, Dominic Mazzoni, Forest Fisher, and Michele Judd of Caltech for* **NASA's Jet Propulsion Laboratory**. *Further information is contained in a TSP (see page 1).*

*This software is available for commercial licensing. Please contact Don Hart of the California Institute of Technology at (818) 393-3425. Refer to NPO-40265.*

# Determining Sizes of Particles in a Flow From DPIV Data

## The same equipment would be used to measure sizes as well as velocities.

*John H. Glenn Research Center, Cleveland, Ohio*

A proposed method of measuring the size of particles entrained in a flow of a liquid or gas would involve utilization of data from digital particle-image velocimetry (DPIV) of the flow. That is to say, with proper design and operation of a DPIV system, the DPIV data could be processed according to the proposed method to obtain particle sizes in addition to particle velocities. As an additional benefit, one could then compute the mass flux of the entrained particles from the particle sizes and velocities.

As in DPIV as practiced heretofore, a pulsed laser beam would be formed into a thin sheet to illuminate a plane of interest in a flow field and the illuminated plane would be observed by means of a