Advanced Medical Imaging Project

TO THE EDITOR: With great interest we read the recent articles on Java-based remote viewing and processing of nuclear medicine images by Slomka et al. (*1*) and on Java and teleradioloy by Wallis (*2*), both published in the January issue of the *Journal of Nuclear Medicine*. In these articles the authors nicely show how nuclear medicine images can be viewed and processed using Java applets. We would like to add some information to this topic and clarify some issues discussed in these articles.

Performance

Slomka et al. (*1*) mentioned that performance problems might occur if computationally intensive tasks written in Java are performed. Recently, we developed an iterative algorithm (*3*) to reconstruct SPECT data written entirely in Java using the freely available Java Development Kit (JDK) 1.3 β (*4*), which already applies the HotSpot technology. The HotSpot performance engine uses advanced adaptive optimization techniques by identifying the "hot spots," i.e., the parts of the application where the most time is spent, and by executing byte code and accelerating the rate of execution for this performance-critical code. The application of HotSpot should accelerate applications by ~30%. We are able to reconstruct a patient study (360° SPECT, 64 × 64 matrix, 6° steps/frame) using standard personal computer equipment within ~120 s, which is reasonable even for routine daily clinical studies.

Security

With the installation of JDK 1.2, the applied Java security model has been significantly improved and is now totally different from its JDK 1.1 predecessor. The Java 1.2 platform provides specific permission (with policy files) to individual resources. This allows applets to interact with objects outside their own virtual machine, including the local file system.

Implementation of New Software Design Models

Use of a new programming language, as compared with merely porting an already existing software code, should influence the way software is designed. The goal to develop medical image processing software using the Jini software design model (*5*), as well as the Java2D, Java Advanced Imaging, and Java3D application programming interfaces (APIs), has recently been achieved by the "advanced medical imaging" (AMI) project (*6*).

Jini

Jini technology is built on top of Java and extends the availability of Java to safely move codes around by providing a homogenous view of the network. It allows communication between plugged-in hardware devices and services through interfaces, without installing drivers or additional software on client machines. Furthermore, it does not require any centralized administration of available services, which is the basis for a truly distributed system (5). To apply Jini, it is necessary to run:

- A simple hypertext transfer protocol (HTTP) server
- The Remote Method Invocation Daemon (RMID)
- A lookup service
- A transaction manager

The HTTP server is used for downloading software code. The RMID uses a log file to keep track of the on-demand activation and persistent service registration, so that once a service has already been registered, it does not have to be reregistered after each reboot. Instead, RMID will restart it on start-up (*4*). The lookup service is used by Jini services to announce their availability and to store their proxy objects. The Jini leasing concept allows registering a service only for a chosen period of time. Afterwards, the service is automatically removed from the network. Therefore, a distributed system using Jini prevents the accretion of persistent state in long-lived systems by allocating resources only for a fixed period of time. The lookup service also supplies the Jini client with a proxy object reference. Transaction managers are used by Jini services to ensure either that multiple operations across components or systems are performed together as a whole or that components and systems will be the starting point.

We have already used this technology to develop a Jini reconstruction service. In this application, the physician simply has to select a patient SPECT study from a database, and a Jini reconstruction client automatically searches in the local area network (LAN) for lookup services. If successful, the Jini client automatically receives the information to get into contact with the Jini reconstruction service and starts to reconstruct the patient study. Applying this Jini reconstruction service, auxiliary files can be loaded in advance, and the whole object is reconstructed and visualized after only 10–15 s, using a Java applet and the Java2D API.

Java Image Processing

Despite the fact that the use of Java will change the way software is designed, Java also provides us with lots of APIs that are extremely useful for medical image processing:

- Java2D
- Java Advanced Imaging (JAI)
- Java3D

Java2D provides some extremely helpful routines, such as pixel interpolation, elementary transformation (scale, rotation, etc.), and text manipulation. The JAI API is a toolkit for more advanced image processing, such as frequency domain processing (Fourier or cosine transform), image manipulation (perspective transformation, warping, etc.), and image analysis (histogram generation and statistical operations). Furthermore, JAI allows the exporting of image files with different file formats (jpeg, tiff, bmp, and png). Java3D is used to write three-dimensional graphics applications and applets and provides reasonable rendering rates on most modern PCs, especially those with three-dimensional graphics accelerator cards.

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Hemodialysis in a Patient Being Treated with ^{153}Sm

TO THE EDITOR: We recently treated a 79-y-old, 53.6-kg woman with 1,558 MBq (42.1 mCi) ^{153}Sm for bone pain palliation secondary to breast metastases. In consultation with Burlex Laboratories, Inc., the supplier of ^{153}Sm, the dose was lowered to 27.75 MBq/kg (0.75 mCi/kg) to take into account the lack of renal excretion. The package insert indicates 34.5% ± 15.5% excretion in the urine in the first 6 h. The patient was having dialysis at an outpatient clinic. We were unable to find any information from the supplier or in the literature on the amount of radioactivity to expect in the blood and dialysate at the time of the next treatment, which was scheduled to be 44 h after administration of the ^{153}Sm. On learning that the patient's blood and dialysate might be radioactive, the clinic did not wish to provide subsequent dialysis treatment. The patient therefore was referred back to the hospital. This provided the opportunity to measure the blood and dialysate radioactivity concentrations. Fifteen minutes after the administration of the radiopharmaceutical, a blood sample was obtained for the initial blood concentration. When the patient returned 44 h later, a blood sample and a sample of the dialysate were obtained. Samples were counted in a well counter with a pulse height analyzer window encompassing the 100-keV photopeak. The decay-corrected blood concentration at 44 h was 0.23% and that of the dialysate was 0.05% of the initial blood concentration. The slightly contaminated disposable portions of the dialysis equipment were stored for decay.

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New Algorithm for Quantification of Myocardial Perfusion SPECT

TO THE EDITOR: We read with interest two back-to-back companion articles written in *The Journal of Nuclear Medicine* (*JNM*) by Germano et al. (*1*) and Sharir et al. (*2*). In these articles the authors describe and validate a new algorithm for quantification of myocardial perfusion. Although this algorithm has many similarities to the CEqual program developed by us (use of normal databases, criteria for abnormality, polar maps, 3fX maps, etc.), those authors have incorporated some differences (e.g., ellipsoid fitting and sampling). They conclude that, "compared to previous methods," these differences resulted in "substantially higher specificity for the detection and localization of CAD [coronary artery disease], with comparably high sensitivity" (*2*).

Their conclusion is not substantiated by the data presented in either of these two articles. They arrived at their conclusion by comparing their results to those obtained by Van Train et al. (*3*). It is incorrect to make their claim based on this comparison for three reasons. First, Bayes theorem tells us that the accuracy of a test is dependent on the prevalence of disease in the population. Only by comparing the two tests in the same population and obtaining significantly better results for one than the other can one test be demonstrated to be superior. Second, the population used by Sharir et al. (*2*) was made up of patients acquired from and processed at their institution, whereas the population used by Van Train et al. (*3*) was from a multicenter trial. Results from in-house validations of data from the same center that used the same population to develop its techniques are expected to have higher accuracy than results from multicenter trials. Third, the claim that a new test has a higher specificity than an old test goes against the expectation that, as a result of post-test referral bias, specificity will continue to drop as referring physicians gain trust in a new test and stop sending patients with normal scans to catheterization. If the "normal" patients are sent for a nuclear perfusion study after catheterization, it must be because some borderline lesions were found. It would be informative to know if the 94 patients in this prospective validation were selected consecutively or whether a different selection scheme was used.

Just like many of the authors of these two articles, we also receive royalties from the sale of our quantitative software. The *JNM* editors should be aware that claims of superiority of one test over another have significant financial implications for both parties. These claims should be allowed only when comparisons are made between two tests using the same patient population (preferably patients from outside the center that developed the technique) and in which investigators have no financial interest.

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REPLY: Thank you for the opportunity to clarify some points made in our original articles (*1*,*2*). First, we would like to stress that CEqual was jointly developed at Cedars-Sinai Medical Center

and Emory University by the authors of the original letter to the editor (Van Train and Garcia), two of the authors of this reply, and other investigators currently at other institutions. All of these individuals have a financial interest in CEqual and no incentive to unfairly present its limitations.

As a consequence of pioneering quantitative efforts like CEqual and the concurrent growth in computing power of the workstations used in nuclear medicine, the 1990s saw the development of more computationally demanding algorithms, operating in three-dimensional space and based on sampling schemes not directly related to circumferential profiles and short-axis slices. Although some of the results are still displayed as polar maps, the maps are now conceived as a collection of a constant number of myocardial samples, not several circumferential profiles dependent on heart size. As a result of this approach, comparison with normal limits is now easier and more straightforward. Quantitative gated perfusion SPECT (QPS) represents Cedars-Sinai's contribution to this new generation of algorithms, which includes techniques developed by several other groups (*3*).

Van Train and Garcia are correct in stating that direct comparison of different algorithms applied to the same patient population is highly desirable. As we reported previously (*4*), we performed exactly such a comparison between QPS and CEqual, studying 62 SPECT patients who also underwent coronary angiography. By analysis of receiver operating characteristics, it was found that the basic difference in the performance of the two algorithms lies in the optimal threshold for abnormality, which is the minimal extent of perfusion abnormality required to call a study abnormal. The specificity of QPS and CEqual in those same patients was 73% and 55%, respectively. Another three-dimensional perfusion quantification algorithm has also been reported to result in a higher normalcy rate (58% vs. 34%) than that of CEqual (*5*). For clarification, the 94 patients referred to in the letter were a consecutive group undergoing perfusion SPECT and angiography.

How is the improved specificity explained? Balancing the decreasing specificity of nuclear techniques resulting from post-test referral bias is an improvement in specificity achieved by more complete tests, better algorithms, and more accurate quantification. For example, both attenuation correction and gating of a perfusion SPECT study have been clearly reported to result in higher specificity for the detection of coronary artery disease. Studies evaluating the diagnostic accuracy of visual interpretation of stress ^{99m}Tc sestamibi have consistently demonstrated specificity of ~80%, which is comparable with the results we reported for the QPS algorithm (*2*). Thus, one might argue that it is entirely reasonable to expect algorithms based in the three-dimensional space to better measure perfusion in the three-dimensional myocardium compared with slice-based techniques.

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