syngo.via for Molecular Imaging Reduces Labor, Speeds Interpretations

Increasing the volume of patients at a PET facility may come with many challenges. The need for greater efficiency is fundamental as physicians interpret more images each day. At the Sand Lake Imaging Center in Orlando, Florida, USA, Siemens' new reading solution, *syngo*.via for Molecular Imaging, paved the way for this transition.

By **John Hayes**

With capabilities in both clinical practice and academic research, Sand Lake Imaging Center was primed to move from a mobile PET/CT service to a fixed operation. Demand for PET/CT in oncology and potentially neurology was growing. Installing a Biograph mCT PET•CT system on-site would handle patient volume. But that was only part of the challenge facing the Orlando, Florida, center.

PET/CT scans were taking 45 to 50 minutes to read. This was fast enough when handling the low patient volume of a mobile service. But not the increased rate possible with a high-performance, fixed PET/CT, which demanded greater efficiency.

The staff at Sand Lake Imaging met the challenge in November 2012 with the installation of Siemens' *syngo*®.via. This early-version software assisted in the collection, presentation, analysis and reporting of imaging studies. An upgrade to Siemens latest reading solution *syngo*.via for Molecular Imaging, promised to markedly boost the center's productivity, automating the technical aspects of collecting and presenting scan data and speeding interpretations.

"We sought a software solution that would enable us to be more efficient and accurate in delivering information to our referring doctors," said Stephen Bravo, MD, medical director of Sand Lake Imaging Center.

Now in commercial form, *syngo*.via for Molecular Imaging easily handles routine and time-consuming tasks, allowing reading physicians to concentrate on making interpretations, just as it helps analyze quantitative data. The software also helps produce a report that referring physicians can easily understand and trust to accurately guide therapy decisions.

syngo.via for Molecular Imaging does this by leveraging three functions. The first involves image alignment. The software aligns images from past and current studies performed with CT, MR or PET/CT, using organ-based, anatomical reference points. Second, algorithms compute normalized quantifications of SUVs (standard uptake values) obtained from current and prior studies. With this, SUV calculations are scanner independent and comparable for longitudinal trending, for example, as part of therapy assessment. Third, special reporting tools supplement the narrative report with automatically generated tabular information related to the images.

Cutting the Labor

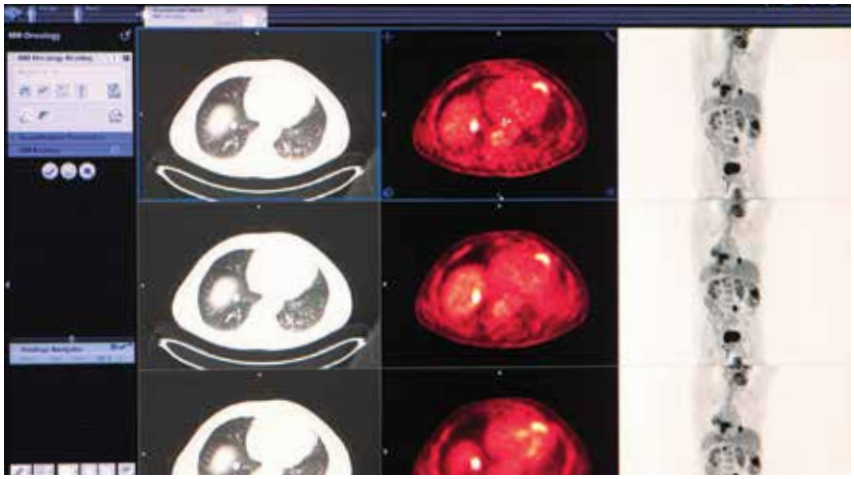
Before *syngo*.via for Molecular Imaging, physicians who read PET/CT scans had to spend substantial time preparing the case for interpretation. This preparation was particularly fatiguing when reading cases with two or more time points, Bravo said.

"*syngo*.via software takes out the pre-processing and allows us to set up organ-specific protocols that ensure we make a very thorough evaluation," Bravo said.

Two features are key. One is SMART Layout, which automatically loads physician-specific organ-based reading protocols. The other is automated image registration based on ALPHA technology, which registers images from prior studies even when they have been done with other PET/CT scanners or over different scan ranges.

"SMART Layout allows us to automatically translate the raw data of the PET/CT into a physician-specific layout that is constant and reproducible," Bravo said. "Doing so allows physicians to start reading immediately with their own process."

SMART Layout makes it so radiologists can click on the most recent study and compare it to prior ones. *syngo*.via tools allow them to see the anatomic CT information, along with the PET information, Bravo said. Images from the two studies appear next to each other.



ALPHA Landmark Registration and SMART layout enable organ-based reading.

The ALPHA technology handles registration, between current and prior studies. This takes manual pre-processing out of the equation. Bravo describes ALPHA-based Anatomical Registration as "transformative."

"Independent of the alignment or source, you have immediate registration," he said. "The pre-process work drops from minutes to instantaneous."

Anatomy-based Registration

With *syngo*.via for Molecular Imaging, reading physicians no longer have to go through the laborious process of bringing up an image, scrolling to the region of interest, reviewing it, repeating the process for the comparison image and then clicking back and forth between them. Even with images obtained over multiple time points, it is possible to click on one study and see images from studies taken at other time points exactly aligned, so that comparisons can be easily made.

"As you scroll through one study, you scroll through the images for the other studies as well," Bravo said.

The ALPHA Anatomical Registration technology, which is proprietary to Siemens, automatically lines up the images using a set of up to 28 landmarks. A sophisticated algorithm then performs an integrity check between the landmarks.

Unlike traditional registration systems, which focus on low-level information such as grayscale, edges, patterns or regions of an image, ALPHA operates like a human interpreter, recognizing high-level struc-

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tures using a process its inventor, Xiang "Sean" Zhou, PhD, calls "recognition before registration." In essence, the system "understands" what is in the image before it tries to determine which part of one image can be matched up with another image.

Zhou, head of technology and research at Siemens Healthcare, explains that traditional registration algorithms work well if two whole-body PET/CT images are comparable in coverage (e.g., image field of view) or patient posture. They fail, however, if one image was acquired with the patient's hands up and the other with hands down, or if the shared body coverage was relatively small. The reason? Comparable image regions are "contaminated" with non-comparable regions. This can often throw the conventional algorithm off. But not the one developed by Zhou and his team.

ALPHA "recognizes" the neck, for example, or the base of the spine regardless of hand position. It achieves this "understanding" of human anatomy by learning from hundreds of annotated training images, specific to the modality. These images are acquired using systems from a variety of vendors.

Because ALPHA dependably registers images, reading physicians don't have to click back and forth between images to reorient themselves when comparing current and prior studies. This is a huge time saver. And it reduces error.

"Any system that takes 30 to 45 minutes to generate a report is prone to user error," Bravo said. "It's very difficult to maintain concentration for that long a time. Inevitably, if you are interrupted in the flow of the case by busy work processes, there will be a time when you say, 'Oh, there was a lung lesion I forgot to look at because I was too busy processing something else'."

Apples to Apples Quantitation

Molecular imaging is an inherently quantitative modality. But, until now, using quantitative measurements obtained over multiple studies has been a challenge. One problem is that different PET scanners use different methods to calculate SUVs. To interpret them accurately, reading physicians had to know how to compensate for these differences. Doing so was especially important when assessing patient response to therapy, as changes in SUVs may indicate response —or lack of response—to therapy.

Siemens tackled this problem by developing two techniques and integrating them into *syngo*.via for Molecular Imaging. One, called PERCIST (PET response criteria in solid tumors), references SUV_{peak} with SUVs associated with liver and blood pool background. Together, these SUVs establish a baseline for follow-up studies. As well, to speed up the quantitation, ALPHA offers automatic placement of the reference regions of interest (ROI) in the liver and the descending aorta.

The second, called EQ•PET, harmonizes SUVs to a NEMA reference independently of scanner make, model or reconstruction algorithms. This harmonization provides confidence that the quantitative values obtained through multiple studies are comparable at different time points and across different equipment.

"It makes sure that the reading physician is actually comparing apples to apples," Bravo said.

EQ•PET, which is a new technology and currently applicable only in oncology, was particularly useful when calculating tumor growth rates over the period of time two or more studies were performed. The technique is useful in drawing conclusions regarding routine cases as well as those conducted during clinical trials. Sites in a multi-center trial typically use different PET/CTs.

ALPHA operates like a human interpreter, recognizing high-level structures using a process called "recognition before registration."

Xiang "Sean" Zhou, Head of Technology and Research at Siemens Healthcare, ALPHA Inventor

About three-fourths of the PET/CT scans performed at Sand Lake Imaging Center relate to oncology. One quarter are in neurology.

Patients suspected of having Alzheimer's disease, for example, are evaluated according to the prevalence and location of neurofibrillary tangles in the brain. These tangles are comprised of amyloid plaque to which radiotracers specifically attach.

Qualitative assessments are susceptible to inter-reader variation. One physician may evaluate a PET scan as normal. Another, looking at the same images, may judge the scan to be abnormal.

Siemens has pioneered the implementation of SUV ratio analysis and further integrated into *syngo*.via for Molecular Imaging databases that define the distribution of amyloid binding radiotracers in a "normal" brain. These data were drawn from images acquired during clinical trials using FDA approved amyloid radiotracers for the assessment of patients suspected of Alzheimer's disease and other causes of cognitive decline. Users of *syngo*.via for Molecular Imaging also have the option to add their own data indicating normal results.

When evaluating patient scans, the software compares the distribution of isotope in the patient scan to those in the databases, then calculates a standard deviation for the patient scan data above or below the norm.

"Instead of saying this is consistent with high quantities of beta amyloid plaque pathophysiologically, with *syngo*.via for Molecular Imaging I can say the deposition in the frontal lobe is 6.5 standard deviations above the norm," Bravo said. "With this comparison, I can feel more confident concluding that the scan is abnormal."

Pulling the Report Together

Molecular imaging reports can be long, complex and difficult for time-pressed referring physicians to digest. Here, *syngo*.via for Molecular Imaging also helps.

"The software allows us to create objective quantification charts, graphs and other data that auto-populate the report and summarize all the wordy text in a form that is quickly and easily assimilated by the referring doctor," Bravo said.

This is done through a Findings Navigator, which tracks the results obtained during the interpretation, places them into the report, then relates them to the image. Referring physicians reading the report can see the findings in context by clicking on the Findings Navigator, which relates them to the images. Using this navigator, they can also retrieve and toggle among findings regarding a lesion appearing, for example, in multiple images taken over a series of time points.

"This evidence-based report allows us to contribute data points that are reproducible, objective and scientific," Bravo said. "It has helped us in our relationships with referring doctors, facilitating their acceptance of the data that we present to them. And that has generated more business for us."