caBIG™ cancer Biomedical Informatics Grid™

“Entering the Era of Personalized Medicine”

caBIG™ in Action at Baylor College of Medicine

Dr. Traber: We are at a point in history where there are two juxtaposed things going on. One, we have challenges in our healthcare system. The delivery is expensive; the outcomes aren't as good as they should be. On the other hand, we are in a point in history where scientific discovery is moving at light speed.

Dr. Steffan: We’re on the cusp of a major significant change in the way research is done and in particular in the way biomedical research is done.

Dr. Osborn: We're entering the era of personalized medicine. There is an enormous amount of data now coming out of these studies and we need to have the tools to be able to put all that data together.

Dr. Itmann: caBIG™ is a set of tools which allows people to handle data, many different kinds of data, from tissue to clinical, expression data. It provides standard operating framework for handling data.

Dr. Steffan: We’ve given the question of which tools we should adopt in what order from caBIG™ a great deal of thought. The Breast Center is supplying a lot of personnel for the caBIG project at Baylor and so we all sat down and got together and it turns out their pain point is managing microarray data and so we looked at the tools that were available and perhaps the most mature of all the caBIG™ tools is caArray.

Dr. Ayala: caArray is designed to look at gene profiling or gene-array studies, and we all know that usually, you’re getting between 30,000 and 50,000 data points per patient. When you’re doing this across a spectrum of 5,000 patients, the amount of data is really, really very large.

Dr. Ittmann: caBIG™ may be useful in accelerating inter-institutional collaborations in particular. There are many, many bio-marker studies in prostate cancer, for example, that have been carried out in a single institution. A very important road block in terms of adopting these bio-markers has been the lack of replication prospectively across multiple institutions.

Dr. Osborn: When you're dealing with multiple institutions, multiple hospitals, multiple physicians, each with a different need and a different data that they're collecting, it becomes very difficult. Each hospital or investigator wants to do it their own way.

Dr. Traber: Science and medicine is now about interactions, collaboration and big science, big numbers of information across multiple sources.

Dr. Ayala: In two to five years, I envision that tools like caBIG™ will permit a biomarker that I've developed in my laboratory to be validated within one year. And if you say that to anyone right now, they're going to laugh, because it is virtually impossible to do it. The real impact of caBIG™ is going to be when large groups of institutions start using these tools to acquire tissues, standardize tissue, and data-acquisition. When that happens, we will be able to do research much quicker, and have results that are clinically valid and transferable to the patient, with individualized, personalized care.

Dr. Traber: We found over the last several decades that providing the technology and the interactions and large data sets to creative scientists can lead to spectacular and unimagined findings. At Baylor College of Medicine we think that's essential to the future of healthcare research and progress, so we are committed to any effort like caBIG™ that will help to make that common language and connection across multiple institutions.

Interviewees

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For more information, please visit http://cabig.cancer.gov