DR. GEORGE VASMATZIS: We've applied the BIMA3 We started applying it for T-cell lymphoma first. We moved to prostate cancer and lung cancer. We also worked with clinicians in endometrial cancer and ovarian cancer. And we've been finding biomarkers in all these diseases. And we plan to expand it to other cancers as well.

The problem is that technology gives you hundreds of millions of sequences, billions of bits of information that you need to handle. So you need algorithms to be able to handle this kind of information. You need computer programs. The only way that much information can be interpreted is using computers.

What we're seeing in the future is that the patient will come to the clinic. We will capture some of the tumor cells, either by biopsy and maybe use laser capture microdissection and reach for tumor cells.

We will extract the DNA. We will sequence that DNA. Then we will use this algorithm to map that tumor DNA back to the reference genome. And then we will be able to find the alterations for that particular patient. Then contrast this alterations with the biomarkers we have already developed through doing the same process for many other patients. And then be able to guide the treatment of that patient.

The future for this, for BIMA3, would be to be able to disseminate it beyond research, but to clinical labs. To get it to a point which is so robust so that it can be used into practice.

What we have done a lot with this algorithm is that we've run thousands of tumor samples already. And what that allows us to do is to be able to find recurrent genes that they actually are altered frequently into some particular cancer. Those genes will eventually become tests that those cancer patients can be immutested for their disease.