Statistical technique helps cancer researchers understand tumor makeup, personalize care

August 9 2015

A new statistical method for analyzing next-generation sequencing (NGS) data that helps researchers study the genome of various organisms such as human tumors and could help bring about personalized cancer treatments was presented today at a session of the 2015 Joint Statistical Meetings (JSM 2015) in Seattle.

Yuan Ji, director of the Program for Computational Genomics and Medicine Research Institute at NorthShore University HealthSystem and associate professor of biostatistics at The University of Chicago, described the new technique—called Bayesian feature allocation models—during a presentation titled "Bayesian Models for Heterogeneity in Human Cancers."

Ji collaborated on development of the models with Peter Mueller, professor of mathematics at The University of Texas at Austin; Juhee Lee, assistant professor of applied mathematics and statistics at the University of California, Santa Cruz; Yanxun Xu, assistant professor of statistics at The Johns Hopkins University; Subhajit Sengupta, postdoctoral fellow at NorthShore University HealthSystem; and Kamalakar Gulukota, director of the Center for Molecular Medicine at NorthShore University HealthSystem.

The successful development of personalized cancer treatments will be driven by the accurate description of the genetic composition of a patient's cancerous tumor. Recent breakthroughs in cancer genomics research reveals cells within each malignant tumor are genetically

heterogeneous, possessing new and evolving DNA mutations.

Traditional one-size-fit-all approaches for treating cancer cannot eliminate all the subclones—the next generation of a mutant cell arising in a clone—within a tumor. After treatment, residual cells become resistant and repopulate a new tumor that becomes more challenging to treat. Consequently, it is important for cancer researchers to fully understand the subclonal genetics in a tumor so the disease can be attacked more effectively using combinations of drugs that target all the subclones.

To do so, the first step is to determine which subclones are present and the various types of mutations the subclones possess. Using NGS data, Ji and his collaborators developed Bayesian feature allocation models to extrapolate the number and population frequencies of subclones in a tumor sample. They also established subclonal sequence and structural mutations as part of the inference results, both of which help physicians select targeted drugs based on the models' findings.

"By applying the powerful Bayesian feature allocation models to analyze NGS data, we believe we can understand the genetic and cellular heterogeneity within each tumor and thus facilitate precision cancer treatment decisions by a patient's attending physician," said Ji, concluding his presentation.

JSM 2015 is being held August 8-13 at the Washington State Convention Center in Seattle. More than 6,000 statisticians—representing academia, business and industry, as well as national, state and local governments—from numerous countries are attending North America's largest statistical science gathering.

More information: www.amstat.org/meetings/jsm/20 … fm?abstractid=314448