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Researchers develop software tool for cancer genomics

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Researchers at the Medical College of Wisconsin (MCW) have developed a new bioinformatics software tool designed to more easily identify genetic mutations responsible for cancers. The tool, called DrGaP, is the subject of a new paper published in the *American Journal of Human Genetics*.

Xing Hua, Ph.D., postdoctoral fellow in biostatistics at the National Cancer Institute, and a former visiting scholar at MCW, is the first author of the paper. Yan Lu, Ph.D., assistant professor of physiology, is corresponding author; and Pengyuan Liu, Ph.D., associate professor of physiology at MCW, is the co-corresponding author.

Cancers are caused by the accumulation of genomic alterations, or mutations. Genomic sequencing identifies two specific types of mutations: driver mutations, which are responsible for cancer, and passenger mutations, which are irrelevant to tumor development. A major challenge in cancer genome sequencing is discriminating between the two types of mutations.

The authors incorporated statistical methods and bioinformatics tools into the computational tool DrGaP, which stands for "Driver Genes and Pathways."

"DrGaP is immediately applicable to cancer genome sequencing studies and will lead a more complete identification of altered driver genes and driver signaling pathways in cancer," said Dr. Liu. "Biological

knowledge of the mutation process is fully integrated into the models, and provides several significant improvements and increased power over current methods."

The researchers note that DrGaP not only recaptured a large majority of driver genes previously reported in other studies, but also identified much longer list of additional candidate genes whose mutations may be linked to cancer. This data demonstrates the extreme complexity of tumor cells and has important implications in targeted cancer therapy.

Provided by Medical College of Wisconsin