



## This Week in Genome Biology

Aug 12, 2015

The J. Craig Venter Institute's Derrick Fouts and colleagues describe the method they used to [peek at the pan-genome](#) of the genetically variable bacteria *Acinetobacter baumannii*. With the pan-genome orthology clustering tool PanOCT, the researchers assessed draft genome sequences for 50 newly sequenced *A. baumannii* isolates collected from the US military healthcare system, coupled with existing sequence data for nearly 200 previously sequenced isolates. The approach made it possible to characterize core genes and flexible portions of the pan-genome, including gene clusters that are lost or gained in strains with variable fitness features, drug resistance patterns, and so on.

Researchers from the University of Leipzig and elsewhere describe efforts to sequence, assemble, and start analyzing the [genome of the brown kiwi bird](#), one of five nocturnal species in the *Apteryx* genus. The team put together an almost 1.6 billion base genome assembly for the bird, using tens of billions of reads generated from several *A. mantelli* DNA libraries. From *de novo* gene predictions, transcript-aided annotation, and comparisons with other well-characterized bird genomes, the study's authors detected almost 28,000 predicted protein-coding genes as well as genes that appear to have been inactivated in the kiwi, such as opsin genes involved in color vision in other birds. GenomeWeb has more on this study [here](#).

A Brown University group [introduces a statistical strategy](#) for identifying mutually exclusive mutations in sequenced tumor samples. The method, known as the "combinations of mutually exclusive alterations" (CoMEt) algorithm, is designed to statistically uncover multiple combinations of mutually exclusive mutations based on features such as the frequency with which various alterations occur. In their proof-of-principle analyses, for example, the researchers applied CoMEt for finding new and known cancer genes and pathways from simulated tumor sequence data as well as authentic data representing five different cancer types.

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