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SEMINAR ANNOUNCEMENT

Gaining insight into whole-genome biology: large sequencing experiments and fast algorithms

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3:00 pm - 4:00 pm
Whistler Agricultural Research Building, Rm. 116

High-throughput, low-cost DNA sequencing technologies have profoundly changed the landscape of research in biology. For the first time it is possible to investigate biological processes that happen on whole-genome and whole-population scales. Examples of biological questions that can be addressed using this technology are the analysis of transcriptional networks, the control of gene expression at the epigenetic level, and the mechanisms of phenomena such as heterosis. More importantly, as read lengths increase and the cost of data falls, larger and more complex genomes become easier to investigate. Rather than being restricted to model animals and plants with small, relatively non-repetitive genomes, biologists can now begin to investigate complex, repetitive genes and structures in large, polyploid crop plant genomes, aneuploid systems such as human cancer, and the genomes of communities of organisms living in symbiosis. The Hudson lab is focused on developing scientific approaches that combine sequencing with computational analysis to address the most pressing questions of genome science. Results will be presented showing that combinations of different sequencing techniques (such as whole genome, transcriptome, exome, small RNA and degraded mRNA) can reveal new phenomena in a range of complex organisms including crop plants (soybean, maize and perennial grasses), root-fungus symbiosis and honeybee disease.