A general approach for identifying profile shifts in functional genomics data

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Functional genomics assays using high-throughput sequencing (e.g. ATAC-seq, or ChIP-seq) provide unparalleled opportunities for investigating cellular processes at unprecedented detail. Commonly these assays are used to compare a perturbation (e.g. infection, knockdown or inhibition of specific genes or proteins) against a control and identify changes between these conditions. While standard differential approaches focus on changes in read counts for specific genomic regions, we and others showed that such perturbations can result in more complex shifts in read distributions, such as RNA Polymerase occupancy changes due to alterations in pausing and termination. To identify such profile shifts, we developed a general approach, RegCFinder, based on a linear-time solution for a well-known computational problem, the “all maximum scoring subsequences” problem. This talk will provide an overview on the biological motivation and theoretical foundations of RegCFinder and illustrate its applicability on examples.

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