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Analysis and integration of large-scale molecular and clinical data in cancers

With the advance of novel measurement technologies, such as microarrays, quantitative mass spectrometry, deep-sequencing and automated microscopes, computational methods have become a vital part of modern medical research. Accordingly, it is possible to obtain billions of data points from an individual patient, and translation of such large amounts of data into medical benefits is impossible without computational methods. In addition to introducing novel computational methods that have been applied to cancer research, we have developed a computational ecosystem that enables efficient analysis of wide spectrum of biomedical data, facilitates integration of existing computational methods and allows the research team to seamlessly interpret the results.

In this lecture, I present recent studies on application of computational methods to biomedical and clinical data in cancers. The computational methods discussed here allow identifying 1) patients who are resistant or sensitive to first line cancer therapy by using molecular data, 2) genes that are activated or silenced as a response to administrating an anti-cancer drug and thus may play a role in drug resistance, and 3) progression markers and druggable targets in cancer. The clinical significance of these findings will be discussed.