Tutorial title: RNA-seq and single-cell data analysis

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Abstract:
Contemporary life sciences and medicine are moving towards the era of large data as represented by high-throughput sequencing. How to model, analyze and interpret genomic data will determine whether we can quickly and accurately discover new biological phenomena and rules, and provide accurate medical care for patients. This tutorial will introduce RNA-seq and single-cell sequencing data types in genomics, and statistical analysis and plotting methods commonly used in data analysis, including exploratory data analysis, normalization and clustering. The tutorial will discuss related literature and data examples, and use the R programming environment for data analysis and plotting exercises.

Related course material:
http://202.205.131.32/forum/upload/forum.php?mod=viewthread&tid=323

Cheng Li's biography:

Dr. Cheng Li studied computer science at Beijing Normal University (BS, 1995) and statistics at University of California, Los Angeles (PhD, 2001). He has worked at Harvard School of Public Health and Dana-Farber Cancer Institute as an Assistant Professor since 2002 and Associate Professor since 2008. Dr. Cheng Li's group has developed many novel gene expression and SNP microarray analysis and visualization methods, and implemented and maintained highly-cited genomics analysis software such as dChip and batch effect adjustment software ComBat (2600 citations). He has worked at Peking University, School of Life Sciences since 2013 and now focuses on 3D genomics experiments, analysis and applications to cancer.