中央研究院統計科學研究所
學　術　演　講

講　題：Applications of Weighted Correlation Network Analysis (WGCNA) to Huntington's disease, aging and circadian oscillations

演講人：Dr. Peter Langfelder

University of California, Los Angeles

時　間：2019年10月30日（星期三）上午10:30-12:00

地　點：中央研究院統計科學研究所6005會議室(環境變遷研究大樓A棟)

※茶　會：上午 10：10 開始

Abstract

Huntington disease (HD) is a neurodegenerative disorder caused by a CAG tri-nucleotide expansion in the Huntingtin (Htt) gene. The disease is characterized by motor and behavioral symptoms associated with major neuropathology of mainly the caudate nucleus and cerebral cortex. I will briefly introduce weighted co-expression network analysis (WGCNA) and describe its application to analysis of several large sets of RNA-seq data. Specifically, I will start with a brief review of a consensus analysis of 3 striatum data sets that identified 13 modules strongly changed in HD models vs. control mice, revealing expression changes in major functional groups of genes. A separate consensus analysis of striatum and cerebellum data identified modules with similar as well as distinct response to CAG length expansion in these two brain regions. In particular, we identify a module enriched in markers of striatal medium spiny neuron genes that is sharply downregulated in striatum and upregulated in cerebellum in samples with high CAG length, suggesting defects in maintenance of cell identity gene expression programs in HD. I will also describe applications of WGCNA to aging and circadian data and their connection to molecular changes in HD.

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