國立中山大學應用數學系
學術演講

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講　　題：Opportunities and Challenges of Meaningful Use
　　　　　of Electronic Health Record in Precision
　　　　　Medicine
時　　間：2018/03/22（星期四）15:30～16:20
地　　點：理學院四樓理 SC 4009-1 室
茶　　會：15:00 於理 SC 4010 室 (系辦公室)

摘 要

With the advances of high throughput sequencing, our understanding of the molecular changes occurring in diseases has been increasingly comprehensive. In parallel to this extraordinary wealth of molecular information, major progress has been made in understanding their significance for disease management and targeted therapies in general, leading to the development of precision medicine that tailors personalized intervention to a patient based on her genotypes and interactions to the environment. While the presence of a mutation is not always required, several clinical trials have demonstrated that the patients benefiting from the therapy usually have molecular alteration of a gene in the targeted pathway. However, the advance of high throughput sequencing is also making this paradigm more complex. Matching a drug with a particular mutation critically depends on how much is known about the mutation in question, its association with drug response, and at which level it has been demonstrated. To achieve truly personalized precision medicine, it is critical to use advanced data science to link health status, interventions, and genomic sequence alterations in order to improve biomarker applications, drug development, and treatment selection, and thus ultimately reduce morbidity and mortality. One of the major data sources to explore is the electronic health records (EHR), which are now essential in every medical center. Reusing EHR data for research and clinical support is considered promising. The passage of the Health Information Exchange (HIE) Initiatives and the American Recovery and Reinvestment Act (ARRA) of 2009 established the Meaningful Use incentive program aimed at creating EHRs for every American by 2014 in order to allow for improved care quality and safety, more efficient use of health resources, and patient empowerment. This talk will present emerging opportunities and current challenges of using EHR in precision medicine.

Bio: Chun-Nan Hsu, PhD, Associate Professor at the department of Biomedical Informatics, University of California, San Diego. Dr. Hsu has published more than 100 highly cited peer-reviewed research articles in the fields of machine learning, data mining, and biomedical informatics. His team developed widely used software tools for biomedical sciences, leading to commercialized products. He was awarded Senior Member of Association of Computing Machinery (ACM) in 2011 and the IBM Faculty Award for his distinguished contributions to biomedical text mining in 2012.

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