The University of Hong Kong

HKU Med

LKS Faculty of Medicine
Department of Pharmacology & Pharmacy
香港大學藥理及藥劑學系

*Seminar*

# "Modelling P450 Bioactivation: the Metabolism and Subsequent Toxicity of Drugs"

will be delivered by


## Dr Joshua Swamidass, MD, PhD

**Associate Professor**
**Laboratory and Genomic Medicine Division**
**Washington University**
**St Louis , USA**


**on Wednesday, October 31, 2018**
**at 4:00pm**

**Seminar Room 4, Ground Floor, Laboratory Block**
**LKS Faculty of Medicine Building**
**21 Sassoon Road, Hong Kong**

**All are welcome**


Many medicines become toxic only after bioactivation by metabolizing enzymes. Often, metabolic enzymes transform them into chemically reactive species, which subsequently conjugate to proteins and cause adverse events. For example, carbamazepine is metabolized by P450 enzymes in the liver, but then conjugates to proteins, causing Steven Johnsons Syndrome in some patients. The most difficult-to-predict drug reactions, idiosyncratic adverse drug reactions (IADRs), often depend on bioactivation. Our group has been using deep learning to model the metabolism of diverse chemicals, and the subsequent reactivity of their metabolites. Deep learning systematically summarizes the information from thousands of publications into quantitative models of bioactivation, modelling precisely how medicines are modified by metabolic enzymes. These models are giving a deeper understanding of why some drugs become toxic, and others do not. At the same time, deep learning can be used to understand drug toxicity as it arises in clinical data, and why some patients are affected, but not others. A conversation between the basic and clinical sciences is now possible, where patient outcomes can be understood in light of bioactivation mechanisms, and these mechanisms can explain why some patients are susceptible to drug toxicity, and others are not.