## 7<sup>th</sup> International Conference on **Proteomics & Bioinformatics** October 24-26, 2016 Rome, Italy

## Of men and not mice: Comparative genomic analysis of human diseases and mouse models

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A cornerstone of modern biomedical research is the use of mouse models to explore basic disease mechanisms, evaluate new therapeutic approaches and make decisions to carry new drug candidates forward into clinical trials. However, few of these human trials have shown success. Here, we systematically compared the genomic response from publically available datasets of patients of different acute inflammatory diseases and corresponding murine models; and showed that, although inflammation from different etiologies resulted in highly similar genomic responses in humans, the responses in mouse models correlated poorly with the human disease and also with one another. Among genes changed significantly in humans, the murine orthologs are close to random in matching their human counterparts. Our findings suggest that a disease model shall be carefully (re) examined to see how well it reproduces the human disease at the molecular level because virtually every drug and drug candidate target gene product(s). In addition, our comparisons of trauma patients reveal genomic signature between complicated outcomes, and specific mediators which serve as predictive biomarkers for the development of targeted treatments at the bedside.

## **Biography**

Wenzhong Xiao directs the Computational Genomics lab at Stanford Genome Technology Center, Stanford Medical School and is responsible for solving computational problems in the development of new genomic and proteomic techniques and their applications. He is also the Director of the Immuno-Metabolic Computational Center at Massachusetts General Hospital. At the interface of computation, genomics and medicine, he focuses on "Computational challenges in development and application of omics for diagnosis, prevention and therapy, especially of human immune and metabolic diseases".

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