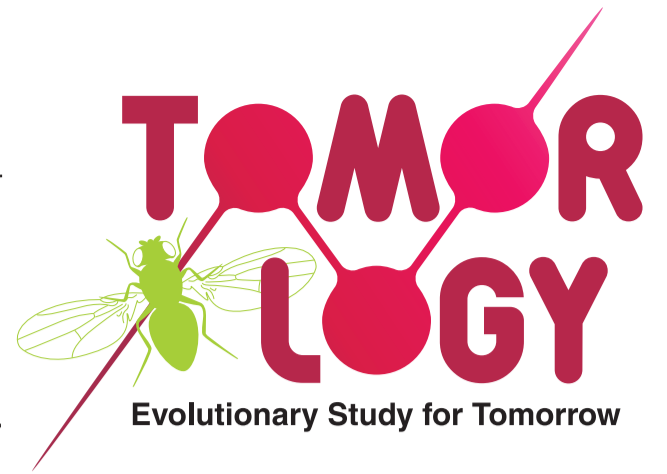


TOP GLOBAL
UNIVERSITY JAPAN

SGU - DGGR



Workshop

October 15th - 16th, 2015, 13:30-16:00

Dept. Drosophila Genomics and Genetic Resources at Saga campus

Dr. Brian Oliver

Laboratory of Cellular and Developmental Biology

NIDDK, NIH

Functional Genomics

We have learned a great deal about the logic of development and disease by studying transcription over the last several decades. The techniques have evolved from analysis of expression of single genes to rapidly evolving genome-wide techniques. We will focus on next generation sequencing and discuss elements of experimental design, the use of exogenous RNAs of known concentration as internal standards, and computational null models using simulations. There are many applications for expression analysis. These include the use of expression data for genome annotation to identify UTR extensions, novel exons, and novel genes, especially in the male transcriptome. Not every segment of transcribed DNA is functional. Operating under the assumption that functional elements will show conserved expression in the genus, we will illustrate the value of comparative gene expression profiling used to determine if novel transcribed segments in *D. melanogaster* were functional. Gene expression profiles are a molecular phenotype. We will discuss using expression phenotypes to address genome-wide questions, particularly about the nature and evolution of gene content and dosage compensation due to sexual selection, and as a valuable tool for building genetic pathways.

For more information, contact: Takano, Toshiyuki

Dept. Drosophila Genomics and Genetic Resources; Tel. 075-873-2660; E-mail. fruitfly@kit.ac.jp

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