

October 8th - 9th, 2015, 13:30-16:00 Dept. Drosophila Genomics and Genetic Resources at Saga campus

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Introduction of Bioinformatics for Sequence Analyses

DNA sequencing has become increasingly common and is currently important for a series of genomic experiments: genome sequencing, annotation, transcriptome and phylogenetic analyses. Therefore, having knowledge of the available bioinformatic resources and the informatic skills to analyze such data is critical. This workshop will provide an introduction to DNA sequence data analyses using simple bioinformatics tools in Unix commands such as *awk* and *grep* followed by integrated tutorial demonstrating the use of popular sequence local/multiple alignment and phylogenetic packages. The tutorial is designed as a self-contained unit that includes example data and detailed instruction for the use of several bioinformatics tools (e.g. Blast, ClustalW).

For more infomation, contact: Takano, Toshiyuki Dept. Drosophila Genomics and Genetic Resources; Tel. 075-873-2660; E-mail. fruitfly@kit.ac.jp このセミナーは平成27年度国際化モデル研究室に採択された「国際交流を起爆剤に推進する精子ゲノム学」事業の 一環として実施するものです