

Title : Transcriptome data analysis

Lecturers: Hyun Goo Woo, Ji-Hye Choi, Yeun-Jun Chung, Jiyeon Park

Day: 13-14th of Jan, 2020

Affiliation: Ajou University School of Medicine, Catholic University College of Medicine

Outline: Recent advances in genome sequencing (e.g., RNA-Seq) and microarray technology enabled us to profile genome-wide transcriptome from tissues. More recently, single cell sequencing technology has been developed, which can profile single cell level transcriptomes. Compared to the bulk RNA-Seq profile, these profiles are useful resources to understand cell level heterogeneity. In this course, attendees learn basic knowledge for data processing and analyses of the transcriptome data from different platforms of microarrays, RNA-SEQ, and single-cell RNA-SEQ. Attendees can learn the analytical skills for data processing procedures including quality control, normalization, annotation, and etc. Functional analyses for differential expression, gene set, and network analyses will also be covered. Also, basic programming language skills for R programming using Bioconductor under the Windows platform will be provided.

	Time	Lecture	Lecturer
Day1	Session 1 (09:00-10:30)	Introduction to transcriptome data	Hyun Goo Woo
	(10:30-10:45)	Break	
	Session 2 (10:45-12:15)	Lab: R/ Rstudio	Ji-Hye Choi
		Lunch	
	Session 3 (13:30-15:00)	RNA-SEQ data analysis (QC/Normalization/Differential expression)	Hyun Goo Woo
	(15:00-15:15)	Break	
	Session 4 (15:15-16:45)	Lab: Bioconductor	Ji-Hye Choi

Day2	Session 5 (09:00-10:30)	Functional analysis (Gene Ontology/Pathway analysis)	Yeun-Jun Chung/Jiyeon Park
	(10:30-10:45)	Break	
	Session 6 (10:45-12:15)	Single Cell Transcriptome	Hyun Goo Woo
		Lunch	
	Session 7 (13:30-15:00)	Lab: DEG/ GO analysis	Ji-Hye Choi
	(15:00-15:15)	Break	
	Session 8 (15:15-16:45)	Lab: Single-Cell RNA-Seq	Ji-Hye Choi