

Hong Kong Branch-Guangzhou Marine Laboratory Joint Postdoctoral Seminar

A multi-omics data analysis platform for advancing functional genomics



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Highlights: Tomato (*Solanum lycopersicum*), belonging to the Solanaceae family, is the model plant for studying fruit ripening and disease resistance. Here, we integrated 343 transcriptome and 136 epigenomic data sets to construct co-expression network and defined 35 chromatin states, respectively. Through supplying the annotation of relatively complete gene sets, comparative between two networks, high-efficiency analysis tools and visualization, we constructed Tomato multi-omics data Analysis Platform (TomAP, <http://bioinformatics.cau.edu.cn/TomAP/>). Our aspiration is that the platform can enable the identification of functional genes or modules that underpin critical tomato agronomic traits for advancing functional genomic research.



28 Feb 2024 (Wednesday)

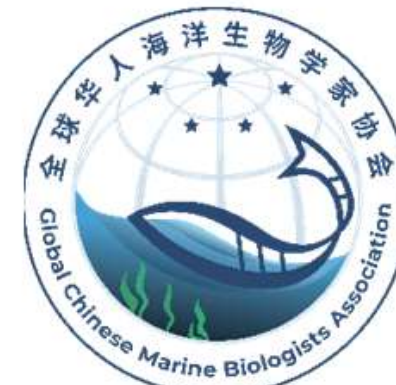
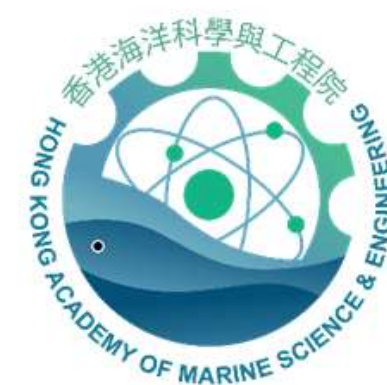
2:30 pm - 3:30 pm (GMT +8, HKT)

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