University of Basel
Department Biozentrum

SIB Swiss Institute of Bioinformatics

BIOZENTRUM
The Center for Molecular Life Sciences

Basel Computational Biology Seminar

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New methods and insights into the condensation-driven RNP assembly and function

Crosslinking and Immunoprecipitation (CLIP) can be used to obtain transcriptome-wide maps of in vivo protein-RNA interactions for specific RNA binding proteins (RBP). We recently developed software that identifies enriched motifs from CLIP (positionally-enriched k-mer analysis, PEKA) in a way that is particularly suitable for discovery and visualisation of multivalent RNA regions. I will report on insights we gained into such regions by analyses of public CLIP data, showing that RBP domain arrangement has a major impact on the extent of motif enrichment and multivalency of binding regions. Moreover, we developed an improved individual nucleotide resolution CLIP protocol (iiCLIP), which produces highly sensitive and specific data, and thus enables quantitative comparisons of interactions across conditions (Lee et al., 2021). By comparing with public data for various CLIP protocols, we show that these improvements help in the study of multivalent RNA regions composed of clustered motifs. I will demonstrate how these methods were used in our recent study of the role of condensation in the specificity and functions of TDP-43 (Hallegger et al., 2021). Taken together, I'll discuss the experimental and computational approaches that enable study of RBP condensation on specific RNA binding-regions, and how this could help understand their capacity to selectively remodel of RNA networks in the context of signalling, disease, and evolution.

Date: Monday, October 11, 2021

Time: 16:15 h

Location: online via zoom

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