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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Rehovot, Israel

Unique features of transcription termination and initiation at closely spaced tandem human genes

The synthesis of RNA Polymerase II (Pol2) products, which include messenger RNAs or long noncoding RNAs, culminates in transcription termination. How the transcriptional termination of a gene impacts the activity of promoters found immediately downstream of it, and which can be subject to potential transcriptional interference, remains largely unknown. We examined in an unbiased manner features of the intergenic region of pairs of 'tandem genes' – closely spaced (<2kb) human genes found on the same strand. Intergenic regions separating tandem genes are enriched with Guanines and are characterized by binding of several proteins, including AGO1 and AGO2 of the RNA interference pathway. Additionally, we found that Pol2 is particularly enriched in this region, and it is lost upon perturbations affecting splicing or transcriptional elongation. Perturbations of genes involved in Pol2 pausing and R loop biology preferentially affect expression of downstream genes in tandem gene pairs. Overall, we find that features associated with potential Pol2 recycling rather than those associated with avoidance of transcriptional interference are the predominant driving force shaping short tandem intergenic regions.

Date: Monday, February 21st, 2022

Time: 16:15 h – 17:30h

Location: Online via Zoom:

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