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The mutational interference mapping experiment (MIME) for studying RNA structure and function

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RNA has long been believed to mainly serve as a blueprint for proteins. However, a large diversity of so called non coding RNAs has been discovered lately to regulate virtually all cellular processes. Characterizing functional domains and structure-function-relationships in RNA is a major challenge as classical experimental approaches are time-consuming and require substantial investigator expertise. To overcome these obstacles we recently developed MIME which coupled to a bioinformatics analysis pipeline implemented in the cross-platform software MIMEAnTo allows to identify domains and structures in RNA that are important for its function. In MIME, target RNAs are randomly mutated, selected by function, physically separated and sequenced using next-generation sequencing (NGS). Consequently, quantitative effects of mutations at every nucleotide position are recovered. While the location of function-disrupting mutations in the RNA allows identifying binding domains, permitted patterns of mutations reveal the functional role of each nucleotide. Moreover, through co-variation analysis it is possible to de novo model the structure of the RNA that is associated with the analyzed function.

Biography

Max Von Kleist has an undergraduate background in Bioinformatics and holds a PhD in Mathematics, which he has completed in 2009 at the Hamilton Institute, National University of Ireland. After a short Postdoctoral phase at the Freie Universität Berlin (2010-2011), he gradually built up an own research group. He has published over 30 papers to date.

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