

SEMINAR

**Mon, 20 Nov 2023 | 2 pm | DBS Conference Room 1**

Hosted by Assoc. Prof Frank Rheindt

# A non-coding approach to animal complexity & systematics



**By Bastian Fromm**

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## **About the Speaker**

*Dr. Bastian Fromm is the leader of the research group for biosystematics and paleotranscriptomics in The Arctic University of Norway. He first got in touch with Ernst Haeckel's "Artforms of Nature" as a high school student and determined to be a zoologist. Then he joined the University of Jena, Germany and the phyletic Museum founded by Haeckel himself.*

*Dr. Fromm did his Masters in Neuropeptidomics and phylogenetics of blattopteran insects. He got his PhD in Evolutionary Parasitology at the Natural History Museum of Oslo, Norway, where he worked with microRNAs in flatworms and found that parasitic flatworms gradually lose gene-regulators which was correlated to a loss of complexity.*

*After PhD study, Dr. Fromm did his postdoc at the Cancer Institute in Oslo reannotating all human microRNAs and erecting MirGeneDB. He started working in the field of paleotranscriptomics as a Senior Researcher in Stockholm before he started his current position in Norway in 2021.*

With more than 16 000 annual publications, microRNAs keep dominating the expanding non-coding RNA field. Despite this uninterrupted and increasing interest in these important gene-regulators, a number of serious issues on the quality of microRNA annotations and reproducibility of microRNA studies have troubled the field. Due to the previous lack of consistently curated microRNA complements across the animal tree of life, missing data was often incorrectly interpreted.

With the establishment of the manually curated microRNA gene database MirGeneDB in 2015, we could show that microRNAs are indeed among the most conserved elements of metazoan genomes and are excellent phylogenetic markers. We find that the evolution of microRNAs is indeed hierarchical, stable and produces increasing microRNA numbers for increasingly complex lifeforms and, thus, might hold the key to understand the evolution of morphological complexity in metazoans.

I will briefly introduce microRNAs, outline their scientific history, including the challenges on defining what is and what is not a microRNA, and present the work of my group on evolution & microRNA curation and bioinformatics methods development. Finally, I will give an update of our MIRevolution project, that aims at sampling all animal phyla and the new field of paleotranscriptomics.