



MICRO-SCHOOL

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LncLOOM - an alignment-free approach for detecting functional conserved motifs in rapidly evolving sequences

Dr Caroline Ross (University of Cape Town)

Friday, 25 October 2024 | 12h00-12h30 SAST

Attend online

ABSTRACT

This micro-school introduces participants to LncLOOM, a novel graph-based framework for detecting ultra conserved functional motifs in rapidly evolving sequences. LncLOOM was originally developed for comparative analysis of long noncoding RNAs (lncRNAs) sequences but has broader applications to other less-conserved sequences such as UTRs and enhancers. We will present an overview of the algorithm and demonstrate how to install and run LncLOOM. We will go through examples of output and explain how the findings can be interpreted. By the end of session, attendees will be familiar with the types of datasets LncLOOM can handle and understand when this approach is advantageous over traditional alignment-based tools for comparative sequence analysis.

BIOGRAPHY



Dr Caroline Ross is an RNA biologist specialising in the integration of computational and experimental approaches to explore the complexities of gene regulation. She is a lecturer in the Department of Molecular and Cell Biology at the University of Cape Town.

Caroline earned her PhD in structural bioinformatics from Rhodes University, under the guidance of Prof Özlem Tantan Bishop. Her doctoral research focused on modeling the structural dynamics and protein interactions of enterovirus capsids to elucidate hotspots that mediate the conformational changes underlying viral uncoating and genome release.

Following her PhD, Caroline pursued a postdoctoral position at the Weizmann Institute of Science, where she investigated the functions and evolution of long noncoding RNAs (lncRNAs) in Igor Ulitsky's lab.

Her current research continues to delve into the complexities of the noncoding genome and its implications for gene regulation across a diverse array of organisms, from mammals to fungal pathogens. Her primary objective is to elucidate the regulatory roles of lncRNAs in key cellular processes and to unravel the intricate mechanisms governing their functions. Her work addresses the pressing question of how the functionalities of lncRNAs are encoded in their rapidly evolving sequences, with the ultimate goal of developing targeted RNA-based therapies to disrupt lncRNA activity in disease-relevant contexts.

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