

Computational Non-coding RNA Biology

Yun Zheng, Kunming University of Science and Technology, Yunnan, China

Computational Non-coding RNA Biology explains the computational methods for the identification and quantification of non-coding RNAs including miRNAs, tasiRNAs, phasiRNAs, lariat originated circRNAs, and back-spliced circRNAs, for the identification of miRNA/siRNA targets, and for the identification of mutations and editing sites in miRNAs. The computational steps of the methods are also introduced, allowing the readers to repeat the same methods using their own datasets. This book serves as a good resource for complete answers to many computational tasks of non-coding RNAs.

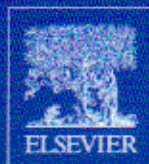
Computational Non-coding RNA Biology allows biologists, computer scientists, medical doctors, and researchers alike to understand the computational methods for the identification and quantification of non-coding RNAs.

Key Features

- Presents a comprehensive list of computational methods for the identification and quantification of non-coding RNAs
- Introduces 23 practical computational pipelines for various topics of non-coding RNAs
- Provides a guide to assist biologists and other researchers dealing with complex datasets
- Introduces basic computational methods and provides guidelines for their replication by researchers
- Offers a solution to researchers approaching large and complex sequencing datasets

About the Author

Dr. Zheng is currently an Associate Professor in bioinformatics at Kunming University of Science and Technology in Kunming, China, and has been serving as an Academic Editor of PLOS ONE since 2014. Yun Zheng holds a PhD from the Nanyang Technological University in Singapore. Dr. Zheng was an Associate Professor in bioinformatics at Fudan University in Shanghai, China. Dr. Zheng has been working in the field of bioinformatics, focusing on topics of non-coding RNAs for more than 10 years. He has published more than 30 papers on non-coding RNAs, covering a wide range of topics within the field. His work is highly respected and has often been cited in works that advance the field of non-coding RNAs. Dr. Zheng has independently developed many novel tools for a wide range of computational topics in non-coding RNAs that have been validated by some of the seminal works in the field.



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