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Computational Methods for High-Throughput Small RNA Analysis in Plants

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Propositions/Stellingen

As part of the thesis

Computational Methods for High-Throughput

Small RNA Analysis in Plants

Lionel Morgado

1. The large number of bioinformatics tools dedicated to small RNA analysis and the fast algorithmic development verified over the last years justifies the development of repositories containing detailed descriptions of these tools to facilitate the selection of the most appropriate software to tackle specific biological problems and to ease further software improvements.
2. More intelligible guidelines are needed to improve small RNA categorization in plants, and that can be achieved by considering functional aspects of the putative sequences.
3. Incorporating information about the capacity of a small RNA to associate with a given Argonaute protein is a procedure that can improve small RNA function prediction.
4. Libraries of experimentally validated heterochromatic small RNAs are urgently needed to improve our knowledge on how small RNAs guide epigenetics. Experimental methodologies derived from popular genome editing tools such as CRISPR-Cas9 can be extremely useful in such endeavor.
5. The automation of bioinformatics pipelines brings great benefits to biologists as it drives attention away from software assembly and allows to focus instead on data analysis and the interpretation of results.
6. Intergenic regions encompass innumerable short-length regulatory elements that urge being studied to grasp a better picture of genomic regulation.
7. The study of intricate epigenetic regulatory networks guided by small RNAs is essential for a better understanding of complex traits and to reduce the “missing heritability”.