MIRNA-MEDIATED REGULATORY CIRCUITS IN PEACH: COMPUTATIONAL IDENTIFICATION AND DYNAMIC SIMULATION WITH A SYNTHETIC BIOLOGY APPROACH

COLAIACOVO M.*, MARCHISIO M.A.**, STELLING J.**, CASELLE M.***, FACCIOLI P.*

*) CRA - Genomics Research Centre, Via S Protaso 302, 29017 Fiorenzuola d’Arda (Italy)
**) Department of Biosystems Science and Engineering and Swiss Institute of Bioinformatics, ETH Zurich, Basel (Switzerland)
***) Department of Physics and INFN, University of Turin, Turin (Italy)

microRNA, peach, feedforward loops, synthetic circuits, network motifs

Most biological processes are performed through complex interactions which can be decomposed into simpler regulatory patterns called "network motifs". One of the most interesting motifs in living organisms is the microRNA-mediated feedforward loop (FFL), a regulatory circuit where a transcription factor controls a microRNA and regulates, together with it, the expression of one or more target genes. Because of its peculiar dynamical properties, this motif has been extensively studied especially in humans. However, similar studies are lacking in plant species. In this work, we show a computational pipeline for the identification of FFLs in a plant species of agronomical interest, namely Prunus persica, whose genome has been recently sequenced. Moreover, we show a method for the design and the dynamic simulation of a regulatory circuit with composable parts, reproducing a FFL in a eukaryotic context. The different parts were built with MDL language and implemented in ProMoT, a software for the object-oriented and modular composition of models for dynamic processes.