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Until about a decade ago, the non-coding part of the genome was considered without function. RNA sequencing studies have shown, however, that a considerable part of the non-coding genome is transcribed and that these non-coding RNAs (nc-RNAs) can regulate gene expression. Almost on weekly basis, new findings reveal the regulatory role of nc-RNAs exert in many biological processes. Overall, these studies are making increasingly clear that, both in model organisms and in humans, complexity is not a function of the number of protein-coding genes, but results from the possibility of using combinations of genetic programs and controlling their spatial and temporal regulation during development, senescence and in disease by regulatory RNAs. This has generated a novel picture of gene regulatory networks where regulatory nc-RNAs represent novel layers of regulation. Particularly well-characterized is the role of microRNAs (miRNAs), small nc-RNAs, that bind to mRNAs and regulate gene expression after transcritpion. This message is particularly clear in the nervous system, where miRNAs have been involved in regulating cellular pathways controlling fundamental functions during development, synaptic plasticity and in neurodegenerative disease. It has also been shown that neuronal miRNAs are tightly regulated by electrical activity at the level of transcription, biogenesis, stability and specifically targeted to dendrites and synapses. Deregulation of expression of miRNAs is proposed not only as potential disease

biomarker, but it has been implicated directly in the pathogenesis of complex neurodegenerative disease. This so-called RNA revolution also lead to the exploitation of RNA interference and the development of related tools as potential treatment of a vast array of CNS disease that could benefit from regulation of disease-associated genes. In spite of these advancements, the relatively young age of this field together with the inherent high molecular complexity of RNA regulation of biological processes have somewhat hindered its communication to the whole of the neuroscience community. This Research Topic aims at improving this aspect by putting around the same virtual table scientists covering aspects ranging from basic molecular mechanisms of regulatory RNAs in the nervous system to the analysis of the role of specific regulatory RNAs in neurobiological processes of development, plasticity and aging. Furthermore, we included papers analyzing the role of regulatory RNAs in disease models from neuromuscular to higher cognitive functions, and more technically oriented papers dealing with new methodologies to study regulatory RNA biology and its translational potential.