Preface

Mammalian central and peripheral nervous systems are highly complex at the structural, genetic and molecular levels, composed of multiple cell types and tissue structures. Thousands of genes, regulated at the genomic level via sequence variation or epigenetic regulation, are expressed at the RNA level and translated into proteins required to develop and maintain these cells and tissues, and along with small regulatory RNA molecules, lipids, and small molecule neurotransmitters, these gene products constitute the physical substrate for learning, memory, emotion, sensory perception, and consciousness itself. The potential for malfunction of this large number of complex biological systems is great, leading to the many behavioral and cognitive deficits observed in human psychiatric and neurological disorders, such as schizophrenia, autism and Alzheimer's disease.

This Volume of Advances of Neurobiology discusses research designed to increase our understanding of the nervous system and its structures and activities, through the utilization of genomic and proteomic technologies, addressing facets including development and epigenetic regulation, functions in learning and memory, and changes associated with neurological and psychiatric disorders. Specifically, the development of high-throughput genomic and proteomic analysis technologies, including microarray and high-throughput DNA sequencing technology, as well as integrated protein separation and mass spectrometry analysis systems, have created the opportunity for researchers to collect datasets that include measurements for all or most of the RNA species or the complement of proteins, within a particular biological sample. These high dimensional datasets are being generated for different nervous system cells and tissues, such as laser-capture microdissected neurons, or samples of postmortem pre-frontal cortical tissue. Different approaches have then been utilized to extract pertinent information, and these range from comparisons of postmortem cells and/or tissues using samples collected from subjects with and without disease states, for example patients with Alzheimer's disease compared to control subjects, in order to discover differences between the samples that reflect aspects of the disease pathology, and that can then be investigated further to determine their role(s) in disease development. In addition, and in disorders such as autism, genome-wide expression analysis can provide data that allows for more focused investigations to test hypotheses regarding disease etiology, such as immune system dysfunction. Other experimental approaches include the utilization

of tissue or animal models to determine the effects of external stimuli on for example, investigation of prenatal viral infection as a model of schizophrenia.

Although studies that utilize genomic and proteomic approaches differ widely, they can provide both data to support pre-existing hypotheses, plus they can implicate previously unconsidered biological networks and pathways in mammalian development, in nervous system functioning, and in the etiologies of diseases. A further important aspect in the development of genomic and proteomic approaches to nervous system research is the use of computational interrogation methods, that can be used to extract relevant information from the high dimensional data-sets. These techniques include cluster analysis and group classification algorithms, and the development of software tools allows the bench researcher to perform useful analyses of the multivariate datasets produced in genomics and proteomics experiments. The future ability to collect, store and analyze large-scale datasets will be central to the growing area of personalized medicine, whereby treatment choices and monitoring of individual's responses to medications will be performed through the utilization of genomic and proteomic methods.

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