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Dear colleagues,

We introduce the current issue of the *Vavilov Journal of Genetics and Breeding*, dedicated to computational biology.

Methods for genome sequencing have been rapidly developed over the past two decades. Sequencing has become cheaper by almost five orders of magnitude: for instance, from $100,000 to $500 for a personal human genome. Great progress has been made in transcriptomics, proteomics, metabolomics, and other omics technologies. We witness a new generation of techniques for biological object visualization on the genome, cellular, tissue, and organismal levels of living system organization. This informational explosion makes genetics the main source of huge bodies of data. Genetics outruns not only other fields of knowledge but global social media in the rate of information accumulation. Indeed, up to 40 exabytes of data are produced in life sciences annually, whereas the largest social platform YouTube produces only 2 exabytes, 20 times less.

Analysis of big genetic data has given rise to a new paradigm of modern genetics. It is focused on gene networks: groups of orchestrated genes that interact via their products: RNA, proteins, and metabolites. Gene networks are responsible for the formation of molecular, biochemical, cellular, physiological, morphological, behavioral, and other traits of the body on the base of information encoded in the genome. The regulation of gene networks is enormously complicated. The complexity is evident from the fact that the operation of a particular gene network element can be controlled by tens and hundreds of elementary regulatory processes. This is true for gene transcription regulation, mediated by tens of transcription factors, which interact with binding sites in gene promoters, and for proteins, whose activity is modulated by interaction with numerous ligands, acting as allosteric regulators. The same is true for metabolic pathways, where the number of elementary regulatory processes sometimes exceeds the number of biochemical reactions by an order of magnitude. Another fundamental property of living systems found in big data analysis is the extremely high level of genetic variability in populations of humans, animals, plants, and microorganisms.

Analysis of big genetic data requires the development of a new generation of methods to process very large bodies of information. This generation includes bioinformatics methods for the reconstruction, analysis, and modeling of structural organization and molecular mechanisms of the functioning of genomes, genes, and genetic macromolecules encoded by them: RNA and proteins. It also includes novel methods of computational systems biology for the reconstruction, analysis, and modeling of genetics systems operating on the levels of cells, tissues, organs, and entire organisms.

The new epoch of big genetic data, including life sciences, demands transformation of key approaches in bioinformatics and computational systems biology. What are fundamental trends in this field? First, it is the integration of conventional

methods in bioinformatics and computational systems biology with artificial intelligence and deep machine learning. Second, employment of the results as grounds for the development of a new generation of software and data support for interpreting big genetic data, and, most importantly, for planning experiments to verify the results of computer-aided predictions from big data analysis. Progress in this direction would mark a fundamental transformation of the basic paradigm in modern research: Science directed by hypotheses is complemented by new science directed by big data analysis.

This progress occurs in all sciences, but just bioinformatics and computational systems biology are at the forefront.

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