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Medical genetics and cancer studies based on next-gen sequencing presented at the bioinformatics conferences and young scientists schools

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Motivation and Aim: Next-Generation Sequencing (NGS)-driven analysis and Systems Biology approaches commonly serve as a backdrop for a study of a tumor genome. This field became extremely important for biomedical studies to be discussed at the series of international events [1, 5]. Thus, recent issue of *BMC Medical Genomics* presents recent works discussed at the 11th Young Scientists School SBB-2019 "Systems Biology and Bioinformatics", held in Novosibirsk, Russia [8, 9]. The SBB school series on bioinformatics proceeds annually since 2008 under the joint steerage of the Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences and Novosibirsk State University. We had publications in special topic issues after the Schools in *BMC Genomics*, *BMC Medical Genomics* and related BioMed Central family journals since 2014 [7].

Methods and Algorithms: Recently we have organized the Research Topic (special journal issue) at *Frontiers in Genetics* to collect the papers focused on the ancestry studies [3]. We have organized special journal issue in *Frontiers in Genetics* considering genetic background and molecular mechanisms of the human diseases [5]. We collated some cancer gene expression studies, some mutation profiling studies as well as some insightful case reports [8]. The SBB Schools in Novosibirsk were initially conceived as satellite event for young scientists held at the same time as BGRS\SB (Bioinformatics of Genome Regulation and Structure\Systems Biology) conference series, since 1998 taking place biannually. The articles comprising the issue *of BMC Medical Genomics* are focused on cancer genomics [8]. Using transcriptomic data, bioinformatic models can be built for patient-oriented ranking of cancer drugs.

Results: We have considered the themes on gene network studies and next-gen sequencing for the special issues [8, 6]. The articles comprising this issue of *BMC Medical Genomics* are focused on cancer genomics [10]. Using transcriptomic data, bioinformatic models can be built for patient-oriented ranking of cancer drugs. Thus, the database for cancer gene expression profiles associated with clinical outcomes of the chemotherapy treatments [8]. Authors mined Gene Expression Omnibus (GEO), The Cancer Genome Atlas (TCGA) and Tumor Alterations Relevant for GEnomics-driven Therapy (TARGET) repositories to pull a database of gene expression profiles

associated with clinical responses on chemotherapy. The cases represented breast cancer, lung cancer, low-grade glioma, endothelial carcinoma, multiple myeloma, adult leukemia, pediatric leukemia and kidney tumors and suitable for machine learning study of these malignancy. A.Lavrov and co-authors reviewed pathogenic variants targetable by single base editing [4]. E.Pudova and colleagues discussed miRNA expression in cancer [10]. The trends in cancer genomics and bioinformatics [1] extend towards ncRNA studies, gene network and associative network models [11, 6].

Conclusion: We hope for continuing international exchange and education via the schools and competitions for young scientists in Russia. We support systems biology meetings and young scientists school looking for new organizational formats (online and offline, hybrid forms). Digital Medicine Forum (Digital Medicine Forum) and MGNGS-2022 (Medical Genetics – Next-Generation Sequencing) (http://ngs.med-gen.ru) events are organized in spring 2022. Importance of Big Data analysis methods based on NGS continue to be challenging biomedical problems [2].

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