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SPECIAL ISSUE

**Exploring the Frontier of Data-driven Biology:
Advances in Bioinformatics Research**

Guest Editor:

Prof. Dr. Gökhan **KARAKÜLAH**



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ABSTRACTED AND INDEXED

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Exploring the Frontier of Data-driven Biology: Advances in Bioinformatics Research

In the rapidly advancing realm of biological sciences, the discipline of bioinformatics has not only emerged as a complementary field but has become a cornerstone of modern research. The Turkish Journal of Biology is pleased to announce a special issue titled “Exploring the Frontier of Data-driven Biology: Advances in Bioinformatics Research” as a testament to our commitment to advancing this critical area of study. The convergence of biology with computational technology, embodied in bioinformatics, is revolutionizing our approach to understanding the complexities of life and enabling the analysis of massive biological datasets, from genomic sequences to proteomic patterns. This, in turn, facilitates breakthroughs in areas such as disease modeling, evolutionary studies, and environmental biology. By embracing the power of data-driven analysis, this issue aims to highlight the transformative impact of bioinformatics in unraveling the mysteries of life at both molecular and systemic levels.

The array of articles in this issue summarizes the dynamic and multifaceted nature of bioinformatics research. Covering a wide spectrum of topics, these manuscripts explore various domains such as genomic sequence analysis, providing foundational insights into genetic blueprints, and protein structure prediction, a field critical to understanding biological mechanisms and developing new therapeutics. The scope also extends to transcriptomics, revealing the complex patterns of gene expression and their implications in various biological contexts. Each piece of research offers a unique perspective, whether through novel approaches in systems biology that decipher the intricate networks of life or through advanced data mining techniques that extract profound insights from vast datasets. This collection of articles, rigorously peer-reviewed, exemplifies the diverse applications of bioinformatics, highlighting its indispensable role in contemporary biological research and its capacity to address some of the challenging questions in science today.

The collection of papers in this issue collectively pushes the boundaries of our biological understanding, each providing unique insights into the complex world of bioinformatics. For instance, “SVM-DO: identification of tumor-discriminating mRNA signatures via support vector machines supported by Disease Ontology” offers a novel approach to cancer research, utilizing machine learning to distinguish tumor-specific mRNA profiles. A review article, “Deep learning in bioinformatics,” introduces the integration of advanced AI techniques within bioinformatics, showcasing their application in analyzing biological data. Another study, “StemnesScoRe: An R package to estimate the stemness of glioma cancer cells at single-cell resolution,” presents an innovative tool for cancer research, focusing on the crucial aspect of cell stemness in glioma. Each of these studies exemplifies the transformative potential of bioinformatics in various realms, from disease modeling to data interpretation, reinforcing the central role of the field in the era of big data.

The versatility and necessity of bioinformatics in areas like health and environmental sciences are further highlighted by the remaining studies in this issue. For example, “CompCorona: A web application for comparative transcriptome analyses of coronaviruses reveals SARS-Cov2 specific host response” provides crucial insights into the host response to different coronaviruses, a topic of immense relevance in current healthcare research. Additionally, “Classification of colon cancer patients into consensus molecular subtypes using support vector machines” and “SUMA: a lightweight machine learning model powered shared nearest neighbour based clustering application of scRNA-Seq” both contribute significantly to personalized medicine and cancer classification, demonstrating the practical applications of bioinformatics in health sciences. Lastly, “Physicochemical differences between camelid single-domain antibodies and mammalian antibodies” offers valuable insights into antibody engineering, a field with far-reaching implications in therapeutics and diagnostics. These studies underscore the interdisciplinary nature of bioinformatics and its potential to catalyze advancements across various fields.

In conclusion, this special issue serves as a vibrant showcase of the transformative impact of bioinformatics in contemporary scientific research. The diverse range of studies presented here not only demonstrates the robust versatility of the field but also its critical role in fostering interdisciplinary collaboration and innovation. As the editor, I am honored to bring together these pioneering works, each contributing to the rich tapestry of knowledge in bioinformatics. We hope that this collection inspires continued exploration and discovery, encouraging researchers and scientists to further push the boundaries of what is possible in bioinformatics. Ultimately, the contributions in this issue represent not just scientific progress but a step forward in our collective quest to understand and harness the complexity of biological systems for a better future.

Prof. Dr. Gökhan KARAKÜLAH
Guest Editor

CONTENTS

SVM-DO: identification of tumor-discriminating mRNA signatures via support vector machines supported by Disease Ontology	349
Mustafa Erhan ÖZER, Pemra ÖZBEK SARICA, Kazım Yalçın ARĞA	
Deep learning in bioinformatics	366
Malik YOUSEF, Jens ALLMER	
StemnesScore: an R package to estimate the stemness of glioma cancer cells at single-cell resolution	383
Necla KOÇHAN, Yavuz OKTAY, Gökhan KARAKÜLAH	
CompCorona: A web application for comparative transcriptome analyses of coronaviruses reveals SARS-CoV-2-specific host response	393
Rana SALİHOĞLU, Fatih SARAÇOĞLU, Mustafa SİBAİ, Talip ZENGİN, Başak ABAK MASUD, Onur KARASOY, Tuğba SÜZEK	
Classification of colon cancer patients into consensus molecular subtypes using support vector machines	406
Necla KOÇHAN, Barış Emre DAYANÇ	
SUMA: a lightweight machine learning model-powered shared nearest neighbour-based clustering application interface for scRNA-Seq data	413
Hamza Umut KARAKURT, Pınar PİR	
Physicochemical differences between camelid single-domain antibodies and mammalian antibodies	423
Nazlı Eda ESKİER, Doğa ESKİER, Esin FİRUZAN, Sibel KALYONCU UZUNLAR	
