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Augmented Reality for Bioinformatics

Augmented Reality is a key technology that will facilitate a major paradigm shift in the way users interact with data and has only just recently been recognized as a viable solution for solving many critical needs. Enter augmented reality (AR) technology, which can be used to visualize data from hundreds of sensors simultaneously, overlaying relevant and actionable information over your environment through a headset. With the rapid development of 5G, which makes AR technology much faster, with much more data flow. With easier and more accessible use, for a variety of different functions (besides video gaming), widespread adoption seems likely.

Bioinformatics-related research produces huge heterogeneous amounts of data. This wealth of information includes data describing metabolic mechanisms and pathways, proteomics, transcriptomics, and metabolomics. Often, the visualization and exploration of related structural - usually molecular - data plays an important role in the Bioinformatics. For decades, AR-related technologies were developed and applied to Bioinformatics problems. Often, these approaches provide "just" visual support of the analysis, e.g. in the case of exploring and interacting with a protein on a 3D monitor and compatible interaction hardware. Moreover, in the past, these approaches were limited to cost-intensive professional visualization facilities. The advent of new affordable, and often mobile technologies provides high potential for using similar approaches regularly for daily research. Visual Analytics is successfully being used for several years to analyze complex and heterogeneous datasets. Immersive Analytics combines these approaches now with new immersive and interactive technologies. here is a growing interest in the broad use of Augmented Reality (AR) and Virtual Reality (VR) in the fields of bioinformatics and cheminformatics to visualize complex biological and chemical structures. AR and VR technologies allow for stunning and immersive experiences, offering untapped opportunities for both research and education purposes.

In summary, AR/VR is a cool upcoming wave that will be associated with Bioinformatics, where the vast repositories of data will enable an AR/VR lens into the scenarios in ways that provide near-immediate insight at a level of depth unimaginable previously. As a result, this special session aims to bring the latest results over Bioinformatics and Augmented Reality technologies for both academia and industry. It can help technicians to exchange the latest technical progress.

Zhaoyang Liu et al [1] propose a novel biclustering algorithm based on the beta distribution (BDBB), which realizes the mining of LCPs of m6A epi-transcriptome data. BDBB employs the Gibbs sampling method to complete

parameter estimation. Simulation study showed BDBB can extract all the three actual LCPs implanted in the background data and the overlap conditions between them with considerable accuracy (almost close to 100%). The GOE_Score scoring indicated that the biclustering results of BDBB in the m6A epi-transcriptome data are more biologically meaningful than the results of other biclustering algorithms.

Augmented reality is currently a great interest in biomedical health informatics. "Secure Collaborative Augmented Reality Framework for Biomedical Informatics" [2] introduces a novel secure collaborative augmented reality framework for biomedical health informatics-based applications. In this research work, a system of multiple agents is created for the simulation of the collective behaviors of the smart components of biomedical health informatics. Strong experimental analysis reveals the strength of the proposed framework when directly compared to state-of-the-art biomedical health informatics solutions.

In the work of Xin-chi Shi and others [3], xylose-metabolic genes of *Pichia stipitis* and *Candida tropicalis*, under the control of different promoters, were introduced into *S. cerevisiae*. RNAseq analysis was used to examine the response of *S. cerevisiae* metabolism to the introduction of xylose-metabolic genes. Overexpression of xylulokinase and XR/XDH from *P. stipitis* remarkably decreased xylitol accumulation and increased ethanol production. The results obtained in this work provide new insights on the potential utilization of xylose using bioengineered *S. cerevisiae* strains.

Lu Sun et al. proposed an Electro-CardioGram(ECG)-based Identity Recognition (EIR) technique called Personalized AutoEncoder(PerAE) [4]. Compared with traditional Biometric methods like face recognition, EIR may be less vulnerable to attack. PerAE maintains a small autoencoder model (called Attention-MemAE) for each registered user of a system. The Attention-MemAE enhances the autoencoder by using a memory module and two attention mechanisms. Experiment results show that to train an Attention-MemAE with 90% identification accuracy for a user.

The paper by Li Feng et al [5] addresses challenges of the ambiguous definition of the cavity boundaries in most cavity detection methods for the analysis of molecular cavities, where ligands interact with protein structures. The author proposes a novel method for the interactive exploration of cavity calculation and visualization. Experiments show that our work can effectively identify and calculate cavities.

References

- [1] Liu, Z., Xiao, Y., Hongsheng, Y., Li, X., Chen, S., Xia, K., & Zhang, L.. BDBB: A Novel Beta-distribution-based Biclustering Algorithm for

- Revealing Local Co-methylation Patterns in Epi-transcriptome Profiling Data. *IEEE Journal of Biomedical and Health Informatics*, 2021.
- [2] Djenouri, Y., Belhadi, A., Srivastava, G., & Lin, J. C. W.. Secure Collaborative Augmented Reality Framework for Biomedical Informatics. *IEEE Journal of Biomedical and Health Informatics*, 2021.
- [3] Shi, X., Zhang, Y., Wang, T., Wang, X., Lv, H., Laborda, P., & Duan, T.. Metabolic and transcriptional analysis of recombinant *Saccharomyces cerevisiae* for xylose fermentation: a feasible and efficient approach. *IEEE Journal of Biomedical and Health Informatics*, 2021.
- [4] Sun, L., Zhong, Z., Qu, Z., & Xiong, N.. PerAE: An Effective Personalized AutoEncoder for ECG-based Biometric in Augmented Reality System. *IEEE Journal of Biomedical and Health Informatics*, 2022.
- [5] Feng, L., Wang, F., Zhang, J., Tang, Y., Zhao, J., Zhou, L. J., Wang, D., Guo & Singh, A. K.. Particle-based calculation and visualization of protein cavities using SES models. *IEEE Journal of Biomedical and Health Informatics*, 2021.

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