Biomedical and Health Informatics (BHI)

Problem-Based Learning to Peer-Reviewed Publications

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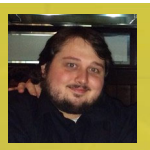


Hybrid Spatiotemporal Modeling of Ebola Propagation in West Africa Between 2014-16

Abstract—The Ebola virus disease epidemic that occurred in West Africa between 2014-16 was one of the deadliest to date. A literature analysis of existing mathematical models reveal that there is a great disconnect for which parameters are most significant in modeling the progression of EVD. There are two central issues related to parameter sensitivity. (1) Regarding temporal progression, deterministic models are very limited in modeling the beginning of an epidemic, whereas stochastic models are very limited in modeling large-scale epidemics. (2) Due to the lack of data and the severe under-reporting of data, there are no existing spatial progression models that are specifically designed for EVD in Liberia, Guinea, and Sierra Leone. To solve these issues, we performed a thorough literature analysis to identify the most appropriate models. Based on the literature analysis, we designed a hybrid agent-based and compartmental model that tracks the spatiotemporal progression of EVD. We managed to model disease progression very accurately by validating with CDC datasets. We concluded that the most important parameter for curbing disease progression is limiting community contact by introducing isolation barriers and quarantine zones.

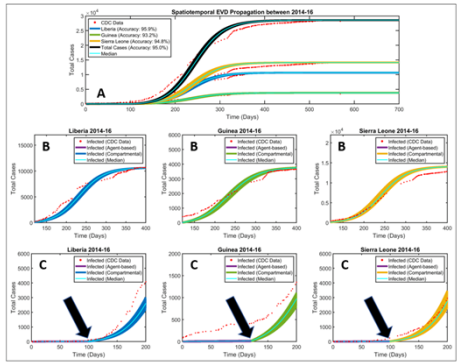
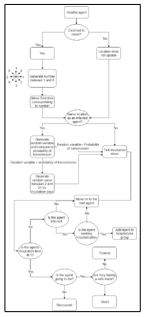


Figure 7. Monte Carlo simulations (1000 runs) of the hybrid model. **A.** Spatiotemporal propagation of EVD in Liberia, Guinea, and Sierra Leone. The curve representing the total number of cases in all three countries is also presented. The accuracy for each model was determined by comparing the median simulation outputs to CDC data. **B.** The classical 'S' shape of an epidemic's progression. Only the compartmental model is depicted here. **C.** Both the agent-based and compartmental models are depicted here with the point at which the model transitions from an agent-based to a compartmental model (black arrow).



C. Tanade, N. Pate, E. Paljug, R. A. Hoffman and M. D. Wang, "Hybrid Modeling of Ebola Propagation," *2019 IEEE 19th International Conference on Bioinformatics and Bioengineering (BIBE)*, Athens, Greece, 2019, pp. 204-210. doi: 10.1109/BIBE.2019.00044


Cyrus Tanade


Elianna Paljug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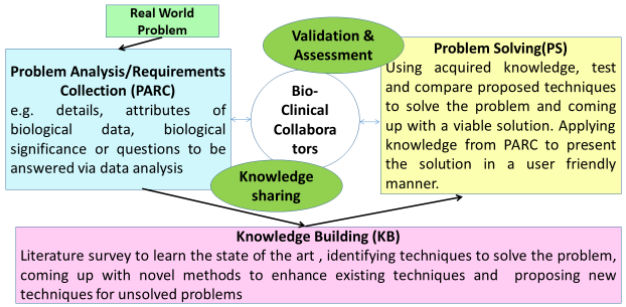
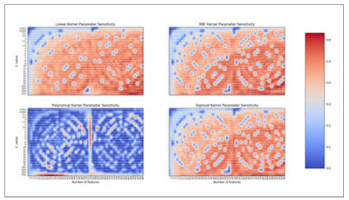
Problem Based Learning of
Biomedical and Health Informatics Problem.



Predicting Breast Cancer Patient Survival Using Multimodal Omics Data

Abstract—Using multimodal genomics data consisting of copy number variation (CNV), gene expression, methylation intensities, and miRNA expression, an ensemble machine learning model was developed that predicted 5-year breast cancer survival with an accuracy of 85% and area under the curve of 87%. The model performed best selectively using the methylation, miRNA, and gene expression modalities, indicating that CNV data is not useful for such predictions. This model recapitulated several previously reported biomarkers of breast cancer survival and yielded many novel biomarkers. Further analysis of these biomarkers could lend insight into the molecular mechanisms that determine patient survival.



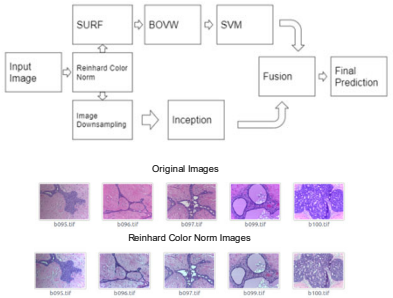
Mitchel J, Chatlin K, Tong Li and Wang MD. "A Translational Pipeline for Overall Survival Prediction of Breast Cancer Patients by Decision-Level Integration of Multi-Omics Data". 2019 IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM 2019)

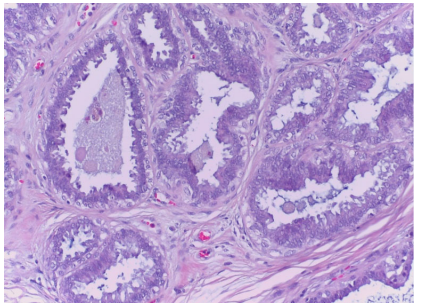

Kevin Chatlin

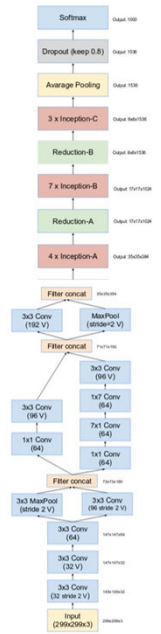

Jonathan Mitchel

ICIAR Challenge: Application of Fusion for Breast Cancer Classification

Abstract—Breast cancer is a deadly disease that affects millions of women worldwide. The ICIAR BACH challenge was created to develop tools to aid pathologists and doctors in the classification of breast cancer histopathology images. Using the challenge dataset, we developed a pipeline that uses the fusion of both a support vector machine (SVM) and a convolutional neural network (CNN). This pipeline was able to achieve 86.25% accuracy with just the CNN with the fusion algorithms performing just under that. This pipeline and implementation of different fusion algorithms demonstrates that this is a prosperous area for further study.



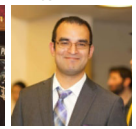




Vizcarra J, Place R, Tong L, Gutman D and Wang MD. "Fusion in Breast Cancer Histology Classification". The 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2019). Niagara Falls, NY, Sept 7-10, 2019.

Ryan Place

JC Vizcarra



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