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# MAFODKM: Mobile Application Framework for the management of Omics Data and Knowledge Mining

O Oluwagbemi<sup>1</sup>, Adewumi<sup>2</sup> and S Misra<sup>3</sup>, Marcelo Leon<sup>4</sup>

<sup>1</sup>Department of Mathematical Sciences, Stellenbosch University, South Africa

<sup>2</sup>School of Advanced Technology, Algonquin College, Ottawa, Canada

<sup>3</sup>Department of Electrical and Information Engineering, Covenant University, Nigeria

<sup>4</sup>Universidad Nacional de Loja, Ecuador

olugbenga.oluwagbemi@fulbrightmail.org, wolejr@gmail.com,  
sanjay.misra@covenantuniversity.edu.ng, marceloleon11@hotmail.com

**Abstract.** There are many infectious diseases still plaguing different nations of the world. Some of these infectious diseases such as HIV, malaria, Ebola, and Lassa fever tend to affect less developed nations including those in Africa. In order to combat these diseases, there is need for ready access to omics data as the knowledge gained from this data can be used to combat infectious diseases globally. This study proposes a Mobile Application Framework for the management of Omics Data and Knowledge Mining (MAFODKM). The proposed framework was designed using a layered architecture. A prototype client application was implemented using JavaScript. In order to make it cross-platform, Apache Cordova framework was leveraged. The proposed framework will among other benefits provide an integrated platform for researchers to collaborate and conduct omics-related research to fight infectious diseases.

## 1. Introduction

There are many infectious diseases still plaguing different nations of the world today. Some of these infectious diseases such as HIV, malaria, Ebola and Lassa fever tend to affect less developed nations including those in Africa. In many developing countries, omics research and data of infectious diseases have not been well explored. These have also not been extensively applied towards the control of infectious diseases. This is evident because computational biology and bioinformatics research is still gradually gaining grounds and has not reached advanced stages in many countries within Africa. In order to bridge this gap, there is need for a framework that allows ready access to omics data.

In recent times, some studies [1-10] have been conducted on the application of mobile devices to biological data, healthcare systems, the application of databases to biological data, the application of modeling and information systems to infectious diseases research, but very few, have been specifically dedicated and targeted towards the application of mobile application to the mining and management of



infectious disease omics data. This study therefore proposes a Mobile Application Framework for the management of Omics Data and Knowledge Mining (MAFODKM).

The rest of this paper is structured as follows: Section 2 explores existing literature. Section 3 describes the methodology adopted in realizing the framework as well as an overview of the various elements of the framework. The results obtained are discussed in Section 4 and Section 5 concludes the paper.

## 2. Literature Review

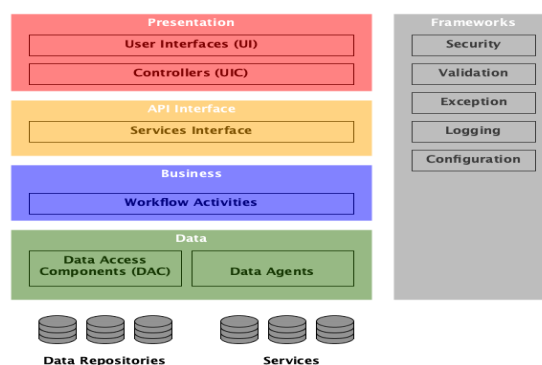
Previous works have discussed and conducted experiments on the management of omics data towards infectious disease control. A recent review highlighted modern strategies for gene expression analysis and provided the best transcriptomics approaches available in the field of functional cure in HIV paediatric infection [11]. Multi-omics approaches have been applied to the disturbance caused by gut microbiota during antibiotic therapy, in providing solutions to the challenge [12]. The multi-omics approaches included metagenomics, metametabolomics, metatranscriptomics and metaproteomics. There are challenges associated with data integration, especially in this omics era. In the work discussed by Gomez-Cabrero et al. [13], these challenges were highlighted. In biotechnology, Yugi et al. [14] proposed and discussed the application of trans-omics analysis for the reconstruction of global biochemical networks. They also proposed a trans-Ome-Wide Association Study (OWAS), which helped to provide appropriate links between phenotypes and trans omics networks. This can help in characterizing many complex diseases. In another work, it was revealed that genomic medicine, gene editing, lipidome, proteomics and pharmacogenetics, and big data, hold great promise for personalized medicine. Personalized medicine can help proffer solutions to many infectious diseases [15]. Some omics researches have been very useful at providing insight to the discovery of novel molecular drug targets for the control of infectious diseases. For instance, the conducted by Ray et al. [16] provides insight to the discovery of new diagnostics targets for dengue fever. Metabolomics can help provide insight into the underlying mechanisms of different physiological processes, including infectious diseases [17]. Tuberculosis is one of the infectious diseases affecting many in different regions of the world. The knowledge of omics (transcriptomics, proteomics and metabolomics), can be applied in the rapid diagnosis of active tuberculosis [18]. Interactive online tools have also been developed to analyze omics related data [19]. Portals have also been developed specifically to access immunological related data [20]. Some authors in previous studies have also developed tools for analyzing genomes such as the GWAS Analyzer [21]. The tool can be used to analyze infectious disease data and thus, useful for providing insight on the control of infectious diseases [21]. Another study discussed the significance of providing biobanks for infectious diseases, towards managing tuberculosis related data, in order to proffer solution to the infectious disease [22]. The knowledge can also be linked to personalized medicine. Another study discussed the characteristics and challenges associated with omic and HER data, associated and the data analytics [23]. Hasin et al. [24] discussed multi-omics approaches to diseases. Omics approaches can be used to address challenges associated with antibacterial resistance [25]. This can be applied to different infectious diseases, towards proffering solutions to them. Omics and multi-omics approaches can be applied solving problems of infectious diseases [26] [27] [28].

Some years ago, mobile application frameworks were developed. Some of the relevant works in this domain include the one developed by Mirelli et al. [29]. They adopted Java programming to develop a simple mobile agent system for bio scientists. Riikonen et al. [1] [30] developed a bioinformatics wireless application protocol (BioWAP), to provide scientists, easy ways of accessing bioinformatics applications and biological databases on the internet. They implemented this by using a Wireless Markup Language (WML). Some of the limitations of BioWAP include inability to perform some tasks like multiple sequence alignments and other tasks. Furthermore, with 4G, 5G and possibly 6G systems of mobile communication, BioWAP may have to undergo major upgrades. Other useful forms of mobile tools have been developed by other scientists. Breslauer et al. [31], built a mobile-phone - mounted light microscope for efficient screening and diagnosis of infectious diseases. Krejcar

et al. [32] conducted research on a platform that can help track and locate users/objects accurately and efficiently. Such technology can be applied to public health, by extending the tracking and location efforts, to vectors responsible for the transmission of infectious diseases. Oluwagbemi et al. [4] also developed a mobile tool or mobile dictionary, for searching keyterms in bioinformatics and computational biology. The mobile tool had some limitations in that it could not assess infectious disease data. Kovachev et al. [33] presented a mobile augmented cloud service which could assist in offloading resources from mobile devices to the cloud. It could also help to manage applications. Istepanian et al. [34] designed a mobile telemedical system by using the channels of cellular phones. It showed the relevance of mobile systems to the provision of good health. Corradini and Merelli [35] presented a research on agent-based middleware for mobile computing. In another research, Matthiessen developed a biocomputing tool, the BioWareDB search engine. This tool can provide assistance or grant researchers and bioinformaticians working on HIV and other infectious diseases, access to useful resources in their fields [36].

### 3. Proposed Architecture

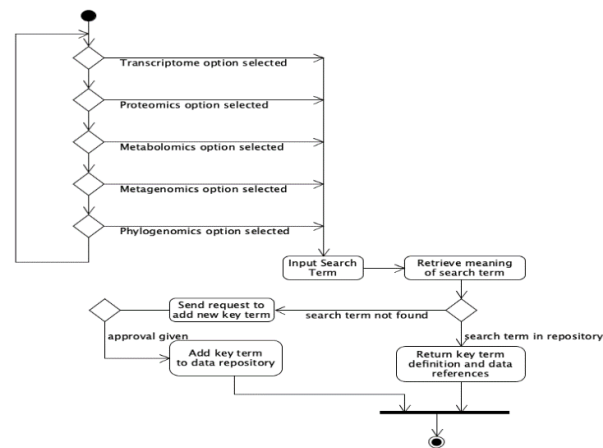
In order to design MAFODKM, a layered architectural pattern was used and the various components that make up the framework are discussed in the following subsections. The proposed framework is depicted in Figure 1.



**Figure 1.** Proposed architecture of MAFODKM

In order to realize MAFODKM, a variety of web frameworks can be leveraged such as Ruby on Rails, Laravel or Spring Model View Controller (MVC) framework. These frameworks implement some form of security, validation, exception handling, logging and configuration that can be leveraged.

The presentation module gives users access to the application which can be accessed across multiple devices especially mobile devices. The presentation module interfaces with the API interface which acts as the intermediary between a user's query and the corresponding service being queried. Based on a user's query, the business module handles the processing of requests between the presentation and data module. The details of the workflow are depicted in Figure 2. There are quite a number of data repositories from which omics data can be gleaned among which is VectorBase (<https://www.vectorbase.org/navigation/data>). For the Ebola virus (<https://www.ncbi.nlm.nih.gov/genome/viruses/variation/ebola>) and for HIV (<https://www.ncbi.nlm.nih.gov/genome/10319>). These data repositories contain omics data for organisms, humans, animals and plants.



**Figure 2.** Workflow activity of MAFODKM

From Figure 2, the workflow begins by selecting the possible Omics option to interact with (Transcriptomics, Proteomics, Metabolomics, Metagenomics, and Phylogenomics). In order to search items within the Omics repository, the input term is entered. If the Omics term exists, the corresponding meanings are displayed. Furthermore, references or links to infectious diseases sample Omics data for the displayed Omics term are provided and users are allowed to download such data for research purpose. If the Omics term does not exist in the Omics repository, the application makes provision for the user to send request to add new Omics terms to the repository. This can either be approved or disapproved by an administrator. If approved, the data is added to the Omics repository.

#### 4. Implementation and Discussion

The user interface of MAFODKM was implemented as a cross-platform mobile app using JavaScript. These types of applications load HTML page and dynamically update that page as the user interacts with the app. AJAX and HTML5 were used to create a fluid and responsive mobile Web app, without constant page reloads. Ratchet is the CSS toolkit that allowed for styling the user interface. The app as a whole achieves cross-platform capability by leveraging the Apache Cordova framework. Data storage and retrieval was accomplished using the Web SQL Database API of Apache Cordova. For the purpose of this study, the mobile app was compiled as an APK and deployed to <https://apkpure.com/mafodkm/com.wole.bengawolex>

Some of the benefits of the proposed framework are: (i) It will help provide scientists with easy access to necessary tools required to conduct quality research on HIV and other infectious diseases (ii) It will provide a comprehensively integrated platform for researchers globally, to conduct omics-related research (iii) It is also expected that this proposed generic framework, if fully implemented, will grant researchers from developing and developed countries, easy access to open access research articles, omics data and other research articles that would have been difficult to access. In summary, the proposed generic framework will be useful for reference and information gathering.

#### 5. Conclusion

Currently, MAFODKM has been developed as a stand-alone mobile application with corresponding web interface connectivity especially to omics-related online databases. We are making effort to extend the development of MAFODKM into a generic multi agent-based mobile application for Omics data and extensive Omics data management by introducing mobile agents. The proposed generic framework, if fully implemented real-life, will be of immense benefit to scientists globally.

#### References

- [1] Olayinka A O, Misra S, Mikail O O, Aliyu A. Towards an iterative maintainability Web service

- model for effective mobile healthcare delivery. In 2013 IEEE International Conference on Emerging & Sustainable Technologies for Power & ICT in a Developing Society (NIGERCON) 2013 Nov 14, pp. 177-181. IEEE.
- [2] Feldt J, Mata R A, and Dieterich J M 2012 Atomdroid: A Computational Chemistry Tool for Mobile Platforms, *Journal of Chemical Information and Modeling* 52 (4) pp. 1072–1078
- [3] Cheng C, Stokes, T H, Hang S, Wang M D 2010. TissueWikiMobile : An integrative protein expression image browser for pathological knowledge sharing and annotation on a mobile device, *IEEE International Conference on Bioinformatics and Biomedicine Workshop (BIBMW)*, pp. 473-480
- [4] Oluwabgemi O O, Adewumi A and Esuruoso A 2012 MACBenAbim: A Multi-platform Mobile Application for searching keyterms in Computational Biology and Bioinformatics, *Bioinformatics* 8(16) pp. 1-2
- [5] Misra S, Banubakode SM, Dhawale CA. Novel user interface for text entry on touch screen mobile device for visually impaired users. In 2014 Global Summit on Computer & Information Technology (GSCIT) 2014 Jun 14 ,pp. 1-5. IEEE.
- [6] Itheme P, Omoregbe N A, Misra S, Adeloye D, and Adewumi, A. 2017. Mobile-Bayesian Diagnostic System for Childhood Infectious Diseases. In ICADIWT , pp. 109-118.
- [7] Yao J, Zhang J, Chen S, Wang C, Levy D and Liu Q 2013 A mobile cloud with trusted data provenance services for bioinformatics research. In *Data Provenance and Data Management in eScience* (pp. 109-128). Springer, Berlin, Heidelberg
- [8] Oluwabgemi O O 2008 Development and implementation of a bioinformatics online distance education learning tool for Africa, *International Journal of Natural and Applied Sciences* 4 (3), pp. 256-262
- [9] Oluwabgemi O O, Fornadel C M, Adebisi E F, Norris D E and Rasgon J L, 2013. ANOSPEX: a stochastic, spatially explicit model for studying Anopheles metapopulation dynamics. *PLoS one*, 8(7)
- [10] Oluwabgemi O O, Adeoye E and Fatumo S 2009 Building a computer-based expert system for malaria environmental diagnosis: An alternative malaria control strategy. *Egyptian Computer Science Journal*, 33(1), pp. 55-69
- [11] Cotugno N, De Armas L, Pallikkuth S, Rossi P, Palma P and Pahwa S 2015 Paediatric HIV infection in the ‘omics era: defining transcriptional signatures of viral control and vaccine responses, *Journal of Virus Eradication* 2015 Jul; 1(3): 153–158
- [12] Pérez-Cobas A E, Gosalbes M J, Friedrichs A, Knecht H, Artacho A, Eismann K, Otto W, Rojo D, Bargiela R, von Bergen, M and Neuling S C, 2013 Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. *Gut*, 62(11), pp.1591-1601
- [13] Gomez-Cabrero D, Abugessaisa I, Maier D, Teschendorff A, Merckenschlager M, Gisel A, Ballestar E, Bongcam-Rudloff E, Conesa A and Tegnér J, 2014 Data integration in the era of omics: current and future challenges
- [14] Yugi K, Kubota H, Hatano A and Kuroda S, 2016 Trans-omics: how to reconstruct biochemical networks across multiple ‘omic’ layers. *Trends in biotechnology*, 34(4), pp.276-290
- [15] Auffray C, Caulfield T, Griffin J L, Khoury M J, Lupski J R and Schwab M 2016 From genomic medicine to precision medicine: highlights of 2015. <https://doi.org/10.1186/s13073-016-0265-4>
- [16] Ray S, Srivastava R, Tripathi K, Vaibhav V, Patankar S and Srivastava S, 2012 Serum proteome changes in dengue virus-infected patients from a dengue-endemic area of India: towards new molecular targets?. *Omics: a journal of integrative biology*, 16(10), pp. 527-536
- [17] Johnson C H, Ivanisevic J and Siuzdak G 2016 Metabolomics: beyond biomarkers and towards mechanisms. *Nature reviews Molecular cell biology*, 17(7), pp. 451-459
- [18] Haas C T, Roe J K, Pollara G, Mehta M and Noursadeghi M 2016 Diagnostic ‘omics’ for active tuberculosis. *BMC medicine*, 14(1), p.37
- [19] Gowda H, Ivanisevic J, Johnson C H, Kurczy M E, Benton H P, Rinehart D, Nguyen T, Ray J,

- Kuehl J, Arevalo B and Westenskow P D 2014 Interactive XCMS Online: simplifying advanced metabolomic data processing and subsequent statistical analyses. *Analytical chemistry*, 86(14), pp. 6931-6939
- [20] Bhattacharya S, Andorf S, Gomes L, Dunn P, Schaefer H, Pontius J, Berger P, Desborough V, Smith T, Campbell J and Thomson E 2014 ImmPort: disseminating data to the public for the future of immunology. *Immunologic research*, 58(2-3), pp. 234-239
- [21] Fong C, Ko D C, Wasnick M, Radey M, Miller S I and Brittnacher M 2010 GWAS analyzer: integrating genotype, phenotype and public annotation data for genome-wide association study analysis. *Bioinformatics*, 26(4), pp. 560-564
- [22] Betsou F, Parida S K and Guillerme M 2011 Infectious diseases biobanking as a catalyst towards personalized medicine: Mycobacterium tuberculosis paradigm. *Tuberculosis*, 91(6), pp.524-532
- [23] Wu P Y, Cheng C W, Kaddi C D, Venugopalan J, Hoffman R and Wang M D, 2016. –Omic and electronic health record big data analytics for precision medicine. *IEEE Transactions on Biomedical Engineering*, 64(2), pp. 263-273
- [24] Hasin Y, Seldin M and Lusis A 2017 Multi-omics approaches to disease. *Genome biology*, 18(1), p. 83
- [25] Cohen A, Bont L, Engelhard D, Moore E, Fernández D, Kreisberg-Greenblatt R, Oved K, Eden E and Hays J P 2015 A multifaceted ‘omics’ approach for addressing the challenge of antimicrobial resistance. *Future microbiology*, 10(3), pp. 365-376
- [26] Rebollar E A, Antwis R E, Becker M H, Belden L K, Bletz M C, Brucker R M, Harrison X A, Hughey M C, Kueneman J G, Loudon A H and McKenzie V 2016 Using “omics” and integrated multi-omics approaches to guide probiotic selection to mitigate chytridiomycosis and other emerging infectious diseases. *Frontiers in microbiology*, 7, p.68
- [27] Kaiser B L D, Li J, Sanford J A, Kim Y M, Kronewitter S R, Jones M B, Peterson C T, Peterson S N, Frank B C, Purvine S O and Brown J N 2013 A multi-omic view of host-pathogen-commensal interplay in Salmonella-mediated intestinal infection. *PloS one*, 8(6)
- [28] Wheelock C E, Goss V M, Balgoma D, Nicholas B, Brandsma J, Skipp P J, Snowden S, Burg D, D'Amico A, Horvath I and Chaiboonchoe A 2013 Application of omics technologies to biomarker discovery in inflammatory lung diseases. *European Respiratory Journal*, 42(3), pp.802-825
- [29] Merelli E, Culmone R and Mariani L 2002 Bioagent: A mobile agent system for bioscientists. In *Proceedings of the Network Tools and Applications in Biology Workshop Agents in Bioinformatics*
- [30] Riikonen P, Boberg J, Salakoski T and Vihinen M 2002 Mobile access to biological databases on the Internet. *IEEE transactions on biomedical engineering*, 49(12), pp. 1477-1479
- [31] Breslauer D N, Maamari R N, Switz N A, Lam W A and Fletcher D A 2009 Mobile phone based clinical microscopy for global health applications. *PloS one*, 4(7)
- [32] Krejcar O and Cernohorsky J 2008 Database prebuffering as a way to create a mobile control and information system with better response time. In *International Conference on Computational Science* (pp. 489-498). Springer, Berlin, Heidelberg
- [33] Kovachev D, Yu T and Klamma R 2012 Adaptive computation offloading from mobile devices into the cloud. In *2012 IEEE 10th International Symposium on Parallel and Distributed Processing with Applications* (pp. 784-791). IEEE
- [34] Istepanian R H, Woodward B, Gorilas E and Balos P A 1998 Design of mobile telemedicine systems using GSM and IS-54 cellular telephone standards. *Journal of Telemedicine and Telecare*, 4(1\_suppl), pp. 80-82
- [35] Corradini F and Merelli E 2005 Hermes: agent-based middleware for mobile computing. In *School on Formal Methods-Moby* (pp. 234-270). Springer, Berlin, Heidelberg
- [36] Matthiessen M W 2003 BioWareDB: the biomedical software and database search engine. *Bioinformatics*, 19(17), pp. 2319-2320