

## CURRICULUM VITAE



Name: Mark Wamalwa (PhD)

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### Research Interests:

My research interests focus on improved food and nutritional security, and environmental sustainability leveraging technology for knowledge exchange. In addition, I have special interest in elucidating host-pathogen interactions where I have been developing high throughput bioinformatics protocols including next generation sequencing data analysis to study diseases such as sleeping sickness and Maize Lethal Necrotic Disease (MLND). Ongoing research is aimed at epidemiological dynamics of SARS-COV-2 using mathematical models. In the recent past, my research involved prediction of cross-species molecular interactions between the tick vector *Rhipicephalus appendiculatus*, the pathogen *Theileria parva* and its bovine host (*Bos taurus*). At the core of this research is the application of simulation models and high throughput technologies to investigate the link between genotype and phenotype and deciphering protein-protein interactions using support vector machines (SVMs). Previously, I was involved in supporting the generation and analysis of “Big Data” for biological/agricultural solutions at the Biosciences eastern and central Africa-International Livestock Research Institute (BecA-ILRI) Hub. The genomics-driven (genotyping, gene expression, and next-generation sequencing data) platforms at the Hub generated Next Generation Sequencing (NGS) data in terms of volume and complexity, which required increased sophistication in data manipulation, storage and integration using the Linux-based High Performance Computing (HPC) cluster. I have developed mobile-based applications for phenotypic data collection and backend database integration. Further, I modelled the evolution of microsatellites using random-walk-without-drift model by fitting negative binomial distributions to dipteran insect and parasite genomic perfect short tandem repeat data.

My current research focuses on the use of (bio)-informatics and (meta)-genomics to understand the functional impact of variation. In addition, I am implementing strategies to tame the curse of the witchweed, *Striga hermonthica*, in tropical maize using high throughput technologies to investigate the link between genotype and phenotype and deciphering protein-protein interaction using artificial intelligence (AI) techniques such as data mining and SVMs.

## PERSONAL DETAILS

Name: Mark Wamalwa

Contact Address: Department of Biochemistry Microbiology & Biotechnology  
Kenyatta University  
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Kenya,  
East Africa.  
[mwamal@gmail.com](mailto:mwamal@gmail.com)

Nationality: Kenyan  
Languages: Fluent in English, and Swahili

## Academic Background

2012-2016 Post-Doctoral Scientist Bioinformatics, Biosciences eastern and central Africa–International Livestock Research Institute (BecA-ILRI) Hub, Nairobi, Kenya.

2008-2011 PhD. Bioinformatics, South African National Bioinformatics Institute (SANBI), University of Western Cape, South Africa.

2002-2004 Master of Bioinformatics (MBF), Wageningen University Research, Netherlands.

1993-1998 Bachelor of Veterinary Medicine (BVM), University of Nairobi.

**Msc. Thesis Title:** Discovery of cis-regulatory elements, for amino acid metabolism, in *Sulfolobus solfataricus*, through a comparative genomics approach.

**PhD. Thesis Title:** Development of a comprehensive annotation and curation framework for analysis of *Glossina morsitans morsitans* Expressed Sequence Tags.

## Specialization/Skills

- ✓ **Programming:** JAVA, Perl, Python, C++, HTML, PHP and R.
- ✓ **Modeling & Simulation** in R, Perl, Swarm and Python.
- ✓ **Database Management:** MySQL, Oracle.
- ✓ **Operating Systems:** Proficient in Linux and Windows.
- ✓ **Next Generation Sequence (NGS)** and metagenomics data analyses.
- ✓ **Artificial intelligence techniques:** Neural Networks and SVMs.
- ✓ **Computational Drug discovery:** – High-throughput and virtual screening.
- ✓ **Mobile application development**

## Work Experience

- 2012-Present Lecturer, Department of Biochemistry & Biotechnology, Kenyatta University, Nairobi, Kenya.
- 2012-2016 Post-Doctoral Scientist - Bioinformatics, Biosciences eastern and central Africa - International Livestock Research Institute (BeCA-ILRI) Hub, Nairobi, Kenya.
- 2008-2011 Post-graduate Student (Ph.D.), University of Western Cape, Capetown, South Africa.
- 2005-2007 Assistant Lecturer, Kenyatta University, Nairobi Kenya.
- 2002-2004 Graduate Student (MSc.), Wageningen University Research, Wageningen, Netherlands.
- 2003-2004 Research Fellow, Solvay Pharmaceuticals BV, Netherlands. Inventory of current proteomics approaches in the discovery of G protein coupled receptors (GPCR's).
- 1999-2002 Veterinary Surgeon, Highlands Vet. Clinic, Nairobi, Kenya.

## Research Grants, Awards & Honors

- 2016 Co-Principal Investigator - BMGF Funded "Viral metagenomics for exploration of plant virus diversity and evolution using herbaria-preserved plant species from East and West Africa" Research Grant (\$1,193,955). A project in collaboration with Mikocheni Agricultural Research Institute (MARI), Tanzania.
- 2015 Principal Investigator – "Taming *Striga hermonthica* by upgrading lignification of secondary cell walls of maize roots through two biotechnology approaches". Regional Universities Forum for Capacity Building in Agriculture (RUFORUM). Grant ID: RU2014 GRG-093 (\$65,000).
- 2015 Co-Principal Investigator - The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Funded "Transcriptome Analysis and SNP Marker Identification of Finger Millet at Critical Stages of Striga Infestation" Research Grant (\$15,000).
- 2007-2011 National Research Foundation (NRF), South Africa Ph.D. Training Fellowship.
- 2009 National Research Foundation (NRF), South Africa Travel Award to attend and present at the Genome Informatics Conference, Cold Spring Harbor. New York, USA.
- 2009 NRF Travel Award to attend and present at the International Society for Computational Biology Africa ASBCB: Joint Conference on Bioinformatics of Infectious Diseases. Bamako, Mali.
- 2006-2007 WHO/NIH/TDR Travel Award to attend and facilitate at the African Center for Training in Functional genomics of insect vectors of human diseases (AFRO VECTGEN).
- 2002-2004 WOTRO Science for Global Development. Msc. Fellowship.

## Student supervision

- ✓ **Agyirifo, Daniel Sakyi (PhD, completed)**, Kenyatta University, Department of Biochemistry and Biotechnology, School of Pure and Applied Sciences.
- ✓ **Jacinta Kavuluko (PhD, completed)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Francis Chaka Wekesa (PhD candidate)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Anne Ndanu (PhD candidate)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Jacinta, Kavuluko (PhD candidate)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Dickson Bennet Kinyanyi (PhD. candidate)**, College of Biological And Physical Sciences, Centre for Biotechnology and Bioinformatics, University of Nairobi.
- ✓ **Dickson Bennet Kinyanyi (Msc. completed)**, College of Biological And Physical Sciences, Centre for Biotechnology and Bioinformatics, University of Nairobi.
- ✓ **Everlyne Kamau (Msc. completed)**, Jomo Kenyatta University of Agriculture and Technology, P.O. Box 64895, 00620 Nairobi, Kenya.
- ✓ **Milcah Kigoni (completed)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Dorothy mbuvi (Msc. completed)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Mikwa Erick Owuor (Msc. completed)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Duncan Njora Waweru (Msc. completed)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Simon Wandafu (Msc. candidate)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Immaculate Mueni Mwangangi (Msc. completed)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Laban Ahija (Msc. completed)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Tonny Videnyi Yalwala (Msc. candidate)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.
- ✓ **Jonathan Mateba (Msc. candidate)**, Kenyatta University, Dept. of Biochemistry and Biotechnology, Kenya.

## Conferences and Workshops

- ✓ **Mark Wamalwa**, (2019). Alien invasive fruit flies in Southern Africa: Implementation of a sustainable IPM programme to combat their menaces. IDRC/ACIAR fruit fly inception meeting, 24th-26th July 2019, Chilanga, Zambia
- ✓ **Mark Wamalwa**, Francesca Stomeo, Jagger Harvey, Miano Douglas, Neil Boonham, Ian Adams, Dora Kilalo, Appolinaire Djikeng (2014). Pathogen Diversity in African Small Farming Systems for the Assessment of Food Security and the Improvement of African Agricultural Productivity. Plant & Animal Genome conference XXII, San Diego, California, USA.
- ✓ Francesca Stomeo, **Mark Wamalwa**, Jagger Harvey, Miano Douglas, Neil Boonham, Ian Adams, Dora Kilalo, Appolinaire Djikeng (2014). A Computational Framework for High-

throughput Virus Detection and Pathogen Discovery. Plant & Animal Genome conference XXII, San Diego, California, USA.

- ✓ **Mark Wamalwa** and Appolinaire Djikeng (2013). Enhancing Capacity of National Cassava Research Programs to Manage Viruses Effectively. Fourth Annual Meeting, Nampula, Mozambique, 23-25 October 2013.
- ✓ Francesca Stomeo, **Mark Wamalwa**, Jagger Harvey, Douglas W. Miano, Neil Boonham, Dora Kilalo, Ian Adams, Appolinaire Djikeng (2013). Plant virome ecology in African farming systems: A genomics and bioinformatics framework for high-throughput Virus detection and Pathogen Discovery. Regional workshop to develop a strategy for Maize lethal Necrosis Disease (MLND) in Eastern and Central Africa. 21-23 August 2013, Nairobi, Kenya.
- ✓ **Mark Wamalwa** and Alan Christoffels, (2010). The transcriptome profile of *Glossina morsitans morsitans*: a vector for sleeping sickness. 22nd International CODATA Conference on Scientific Data and Sustainable Development. 24-27 October 2010, Cape Town, South Africa.
- ✓ **Mark Wamalwa** and Alan Christoffels (2009). Comparative genome analysis of *Glossina morsitans* transcriptome: a vector for sleeping sickness. Genome Informatics. Cold Spring Harbor. New York, USA
- ✓ **Mark Wamalwa** and Alan Christoffels. Comparative genomics analysis of *Glossina morsitans* transcriptome: vector for sleeping sickness. International Society for Computational Biology Africa ASBCB: Joint Conference on Bioinformatics of Infectious Diseases. 30 Nov – 05 Dec 2009, Bamako, Mali.

**Resource person and presenter in the following Bioinformatics conferences & workshops:**

- ✓ Mark Wamalwa *et al.*, (2020). The Eastern Africa Network of Bioinformatics Training (EANBiT) - Implementing genomics workflows using Docker. July 8<sup>th</sup> 2020, International Centre for Insect Physiology and Ecology (ICIPE), Nairobi, Kenya.
- ✓ Mark Wamalwa *et al.*, (2015). H3BioNet - Pan African Bioinformatics Network for H3Africa training workshop. November 30<sup>th</sup> – December 5<sup>th</sup>, 2015, International Centre for Insect Physiology and Ecology (ICIPE), Nairobi, Kenya.
- ✓ Mark Wamalwa *et al.*, (2015). Next generation sequencing Advanced Bioinformatics Workshop. September 7<sup>th</sup> - 18<sup>th</sup>, 2015, International Livestock Research Institute (ILRI), Nairobi, Kenya.
- ✓ Mark Wamalwa *et al.*, (2015). Introduction to molecular Biology and Bioinformatics Training Workshop BecA-ILRI Hub, Nairobi, Kenya May 11-22, 2015.
- ✓ Mark Wamalwa *et al.*, (2014). The eBioKit Bioinformatics Workshop, Commission for Biotechnology & Genetic Engineering, National Center for Research, Sudan, December 1 - 6, 2014
- ✓ Mark Wamalwa *et al.*, (2014). The eBioKit Bioinformatics Workshop University of Buea; Cameroon, October 27 - 31, 2014.
- ✓ Mark Wamalwa *et al.*, (2014). Next generation sequencing Advanced Bioinformatics Workshop. August 18<sup>th</sup>-29<sup>th</sup>, 2014, International Livestock Research Institute (ILRI), Nairobi, Kenya.
- ✓ Mark Wamalwa *et al.*, (2014). Introduction to molecular Biology and Bioinformatics Training Workshop BecA-ILRI Hub, Nairobi, Kenya May 5-16, 2014.

- ✓ Mark Wamalwa *et al.*, (2013). Metagenomics and Next generation sequencing Advanced Bioinformatics Workshop. 7<sup>th</sup>-18<sup>th</sup> October, 2013, International Livestock Research Institute (ILRI), Nairobi, Kenya.
- ✓ Mark Wamalwa *et al.*, (2013). Genotyping by Sequencing (GBS) workshop. A collaboration between Cornell University's Institute for Genomic Diversity and ICRISAT
- ✓ Funded by BREAD (Basic Research to Enable Agriculture Development). 6<sup>th</sup>-9<sup>th</sup> August, 2013. BecA-ILRI Hub, Nairobi, Kenya
- ✓ Mark Wamalwa *et al.*, (2013). Next Generation Sequencing Technologies and Application to Infectious Diseases, BecA-ILRI Hub/JCVI/NIAID Training Workshop. 22<sup>nd</sup>-28<sup>th</sup> August 2013, International Livestock Research Institute (ILRI), Nairobi, Kenya.
- ✓ Mark Wamalwa *et al.*, (2013). Introduction to Molecular Biology and Bioinformatics Workshop. 6<sup>th</sup>-17<sup>th</sup> May 2013, International Livestock Research Institute (ILRI), Nairobi, Kenya.
- ✓ Mark Wamalwa *et al.*, (2005). The second WHO/NIH/TDR training course on Functional Genomics of Insect Vectors of Human Diseases. October 26 - November 10, 2005, the African Center for Training in Functional genomics of insect vectors of human diseases (AFRO VECTGEN), Bamako, Mali.
- ✓ Mark Wamalwa *et al.*, (2004). Facilitator for the Bioinformatics workshop held under the Biochemical Society of Kenya (BSK) umbrella and sponsored by the Third World Academy of Sciences (TWAS) held at the Computer Science Department, Egerton University, Njoro Campus, Nakuru Kenya from 6-8 September 2004.

### Peer-reviewed Publications

- Watanabe J, Hattori M, Berriman M, Lehane MJ, Hall N, Solano P, Aksoy S, Hide W, Touré Y, Attardo GM, Darby AC, Toyoda A, Hertz-Fowler C, Larkin DM, Cotton JA, Watanabe J, Sanders MJ, Swain MT, Hattori M, Berriman M, Quail MA, Inoue N, Ravel S, Taylor TD, Srivastava TP, Sharma V, Warren W, Wilson RK, Suzuki Y, Lawson D, Hughes DS, Megy K, Masiga DK, Mireji PO, Attardo GM, Hansen IA, Van Den Abbeele J, Mireji PO, Nyanjom SR, Telleria EL, Caljon G, Van Den Abbeele J, Ribeiro JM, Acosta-Serrano A, Benoit JB, Ooi CP, Rose C, Price DP, Haines LR, Lehane MJ, Christoffels A, Sim C, Zhang Q, **Wamalwa M.**, et al., (2014). Genome sequence of the tsetse fly (*Glossina morsitans*): vector of African trypanosomiasis. *Science*. 2014 Apr 25; 344(6182): 380-6.
- Kilonzo, C. M., Wamalwa, M., Whegang, S. Y., & Tonnang, H. E. Z. (2022). Assessing the impact of non-pharmaceutical interventions (NPIs) and BCG vaccine cross-protection in the transmission dynamics of SARS-CoV-2 in eastern Africa. *BMC Research Notes* 2022 15:1, 15(1), 1–7. <https://doi.org/10.1186/S13104-022-06171-4>
- Wamalwa, M., & Tonnang, H. E. Z. (2022). Using outbreak data to estimate the dynamic COVID-19 landscape in Eastern Africa. *BMC Infectious Diseases* 2022 22:1, 22(1), 1–19. <https://doi.org/10.1186/S12879-022-07510-3>
- Wekesa, F. C., Wamalwa, M., & Oduor, R. (2022). Serological evidence of inter-epidemic circulation of Rift valley fever virus in livestock in Kenya. *East African Agricultural and Forestry Journal*, 85(1-4 SE-Articles), 13–13. Retrieved from <https://www.kalro.org/www.eaafj.or.ke/index.php/path/article/view/509>
- Mohamed, S. A., Wamalwa, M., Obala, F., Tonnang, H. E. Z., Tefera, T., Calatayud, P. A., Subramanian, S., et al. (2021). A deadly encounter: Alien invasive Spodoptera

- frugiperda in Africa and indigenous natural enemy, *Cotesia icipe* (Hymenoptera, Braconidae). *PLoS ONE*, 16(7 July). Public Library of Science.
- Timilsena, B. P., Niassy, S., Kimathi, E., Abdel-Rahman, E. M., Seidl-Adams, I., Wamalwa, M., Tonnang, H. E. Z., et al. (2022). Potential Distribution of Fall Armyworm in Africa and Beyond , Considering Climate Change and Irrigation Patterns. *Sci Rep* 12, 539. <https://doi.org/10.1038/s41598-021-04369-3>.
- Kavuluko, J., Kibe, M., Sugut, I., Kibet, W., Masanga, J., Mutinda, S., Wamalwa, M., et al. (2021). GWAS provides biological insights into mechanisms of the parasitic plant (Striga) resistance in sorghum. *BMC Plant Biology*, 21(1), 392.
- Masanga, J., Mwangi, B. N., Kibet, W., Sagero, P., Wamalwa, M., Oduor, R., Ngugi, M., et al. (2021). Physiological and ecological warnings that dodders pose an exigent threat to farmlands in Eastern Africa. *Plant Physiology*, 185(4), 1457–1467. Oxford University Press (OUP).
- Kinyanyi D., Amwayi P., **Wamalwa M.**, Obiero G., (2019). Comparative *in silico* study of congocidine congeners as potential inhibitors of African swine fever virus. *PLoS ONE* 14(8):e0221175. <https://doi.org/10.1371/journal.pone.0221175>
- Agyirifo, D. S., **Wamalwa, M.**, Otwe, E. P., Galyuon, I., Runo, S., Takrama, J., & Ngeranwa, J. (2019). Metagenomics analysis of cocoa bean fermentation microbiome identifying species diversity and putative functional capabilities. *Heliyon*, 5(7), e02170. <https://doi.org/10.1016/j.heliyon.2019.e02170>.
- Mutuku, J. M., Wamonje, F. O., Mukeshimana, G., Njuguna, J., **Wamalwa, M.**, Choi, S. K., Tungadi T., Djikeng A., Kelly K., Domelevo Entfellner J.B., Ghimire S.R., Mignouna H.D., Carr J.P., Harvey, J. (2018). Metagenomic Analysis of Plant Virus Occurrence in Common Bean (*Phaseolus vulgaris*) in Central Kenya. *Frontiers in microbiology*, 9, 2939.
- Wamaitha, M. J., Nigam, D., Maina, S., Stomeo, F., Wangai, A., Njuguna, J. N., Holton T.A., Wanjala B.W., **Wamalwa M.**, Lucas T., Djikeng A., Garcia-Ruiz, H. (2018). Metagenomic analysis of viruses associated with maize lethal necrosis in Kenya. *Virology Journal*, 15(1), 90.
- Kinyanyi, D., Obiero, G., Obiero, G. F. O., Amwayi, P., Mwaniki, S., & **Wamalwa, M.**, (2018). *In silico* structural and functional prediction of African swine fever virus protein-B263R reveals features of a TATA-binding protein. *PeerJ*, 6, e4396.
- Mbuvi, D. A., Masiga, C. W., Kuria, E. K., Masanga, J., **Wamalwa, M.**, Mohamed, A., Runo, S.M. (2017). Novel Sources of Witchweed (Striga) Resistance from Wild Sorghum Accessions. *Frontiers in Plant Science*, 8, 116.
- Maritim T., Kamunya S., Mwendia C., Mireji P., Muoki R., **Wamalwa M.**, Francesca Stomeo F., Schaack S., Kyalo M., and Wachira F. (2016). Transcriptome-Based Identification of Water-Deficit Stress Responsive Genes in the Tea Plant, *Camellia Sinensis*. *Journal of Plant Biotechnology*, 43 (2016), 302–10.
- Kamau E., Nyanjom, S.G., **Wamalwa M.**, & Ng'ang'a, J. (2016). Prediction of protein–protein interactions between *Theileria parva* and *Bos taurus* based on sequence homology. *Bioscience Horizons* 9: hzw006.

- Amimo J.O., El Zowalaty M.E., Githae D., **Wamalwa M.**, Djikeng A., Nasrallah G.K., (2016). Metagenomic analysis demonstrates the diversity of the fecal virome in asymptomatic pigs in East Africa. *Arch Virol.* 2016 Apr;161(4):887-97. PMID: 26965436
- Dinga J.N., **Wamalwa M.**, Njimoh D.L., Njahira M.N., Djikeng A., Skilton R., Titanji V.P., Pellé R., (2015). TpUB05, a Homologue of the Immunodominant Plasmodium falciparum Protein UB05, Is a Marker of Protective Immune Responses in Cattle Experimentally Vaccinated against East Coast Fever. *PLoS One.* 2015 Jun 8; 10(6): e0128040.
- Hawkins E., Kock R., McKeever D., Gakuya F., Musyoki C., Chege S.M., Mutinda M., Kariuki E., Davidson Z., Low B., Skilton R.A., Njahira M.N., **Wamalwa M.**, Maina E., (2015). Prevalence of *Theileria Equi* and *Babesia Caballi* as well as the identification of associated Ticks in Sympatric Grevy's Zebras (*Equus Grevyi*) and Donkeys (*Equus Africanus Asiaticus*) in Northern Kenya. *J Wildl Dis.* 2015 Jan; 51(1): 137-47. PMID: 25380362.
- Desta A.F., Assefa F., Leta S., Stomeo F., **Wamalwa M.**, Njahira M., Appolinaire D. (2014) Microbial Community Structure and Diversity in an Integrated System of Anaerobic-Aerobic Reactors and a Constructed Wetland for the Treatment of Tannery Wastewater in Modjo, Ethiopia. *PLoS ONE* 9(12): e115576. PMID: 25541981.
- Otieno O.D., Onguso J.M., Matazyoh L.G., Onyango C., **Wamalwa M.**, Wanjala B.W., Jagger H., (2014). Genetic diversity of Kenyan native oyster mushroom (*Pleurotus*). *Mycologia* 2014 13-186. PMID: 25344263.
- Keambou, T. C., Hako, T. B. A., Ommeh, S., Bembide, C., Manjeli, Y., Wamonje, F., Nzuki, I., Wanjala B., **Wamalwa M.**, Njahira M., Kyalo M., Cho C. Y., Skilton R. A. and Djikeng A., (2015). Diversity of genetic types of local chickens and introgression with commercial exotic strains in Cameroon. *Bulletin of Animal Health and Production in Africa.*, Special Ed(May), 147–163.
- Keambou T.C., Hako B.A., Ommeh S., Bembide C., Ngono E.P., Manjeli Y., Wamonje F., Nzuki I., Wanjala B., **Wamalwa M.**, Cho C.Y., Skilton R.A. and Djikeng A., (2014). Genetic Diversity of the Cameroon Indigenous Chicken Ecotypes. *International Journal of Poultry Science*, 13: 279-291.
- Pretorius A., Mandeep K., **Wamalwa M.**, Moegamat F. F., Magbubah E., Vladimir B. and Jasper R. (2013). Functional analysis and characterization of the human RBBP6 promoters using molecular biology and *in silico* approaches. *J. Biosci.* 2013;1:2251–3159.
- Semegni, J.Y., **Wamalwa M.**, Gaujoux, R., Harkins, G.W., Gray, A., & Martin, D. P. (2011). NASP: a parallel program for identifying evolutionarily conserved nucleic acid secondary structures from nucleotide sequence alignments. *Bioinformatics*, 27(17), 2443-2445.
- Koen C., Harkins G.W., **Wamalwa M.**, Gaunt M.W., (2010). Modeling Short Tandem Repeat Length Data – Some Important Statistical Considerations, Illustrated by Negative Binomial Distribution Fitting. *Unpublished*.



**Objectives:**

- ✓ To use my skills so far gained in Bioinformatics and Veterinary Medicine towards achieving the organization's goals.
- ✓ To further my career in Bioinformatics through participation in on-going research.

**Professional affiliations:**

- ✓ International Society for Computational Biology (ISCB) International Society for Computational Biology Africa (ASBCB).
- ✓ The International Glossina Genome Initiative (IGGI)
- ✓ Biochemical Society of Kenya (BSK).
- ✓ Kenya Veterinary Association (KVA).

**Interests:**

- ✓ Technology oriented ventures.
- ✓ Communal Health.
- ✓ Working with the less fortunate in society.

**Referees:**

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