

NELSON KIPCHIRCHIR KIBINGE

CONTACT INFORMATION
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Digital Medicine, Orion Pharma
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PROFESSIONAL SUMMARY
A computational biologist interested in data-driven and cutting edge tool development for applications in drug discovery and academic research. I possess extensive experience and set of skills working with multiple teams and in lead roles. My major interest is in the production of applied statistics and software code utilized in clinical trials, epidemiological studies and therapeutic target discovery. As a PhD-trained scientist, I am involved in diverse research projects and in teaching postgraduate courses.

CORE COMPETENCIES

- Drug-Target and Biomarker discovery
- Statistical Genomics
- Clinical trial statistics
- Protein mass spectrometry
- protein microarrays
- Systems Biology
- Machine Learning
- Next generation sequencing (MiSeq and Oxford Nanopore)
- Compartmental Epidemiological Modeling
- Advanced R programming
- Intermediate level perl and basic python programming
- Unix shell scripting,
- Tensorflow

PROFESSIONAL EXPERIENCE
Senior Scientist Feb 2020 to present
Computational Biology, Digital Medicine Department
Orion Pharma

PROFESSIONAL EXPERIENCE
Senior Research Associate June 2019 to present
Genetic Epidemiology Lab, MRC IEU
University of Bristol

Senior Postdoctoral Scientist Nov 2018 to present
Senior postdoctoral scientist leading the biostatistics department
KEMRI-Wellcome Trust Research Programe, Kenya

Visiting Research Fellow Feb 2019 to Mar 2019
Project: *Multi-center malaria antigen discovery project*
University of Heidelberg Germany

Visiting Research Fellow (Mathematical modeling) Feb 2017 to May 2017
Project: *Modeling the genetic diversification in RSV transmission*
University of Warwick, United Kingdom

	Early Career Postdoctoral Research Fellow	Apr 2016 to Dec 2018
	Project: <i>Evaluating local respiratory syncytial virus (RSV) genetic diversity: a statistical perspective</i>	
	Virus Epidemiology and Control Group, KEMRI-Wellcome Trust Research Programme, Kenya	
	Research Assistant	Apr 2013 to March 2016
	Project: <i>Data mining methods for understanding gene expression in high throughput technologies</i>	
	Computational systems biology laboratory, Nara Institute of Science and Technology Supervisor: Kanaya Shigehiko, Ph.D	
	Research Assistant	Jun 2007 to May 2008
	Project: <i>Biosafety; gene flow in wild oryzae sativa in Mwea region</i>	
	School of Biological Sciences, University of Nairobi Supervisor: Samuel Kiboi, Ph.D	
TEACHING EXPERIENCE	Part-time Lecturer	September 2017 to Present
	MSc Course: Biostatistics and Research Methods Courses taught: Biostatistics, databases and data visualization, Research methods and experimental design Department of Biochemistry, Pwani University, Kenya	
	Teaching Assistant	Dec 2012 to Mar 2013
	Bioinformatics II Professor: Kensuke Nakamura Department of Life Science and Informatics, Maebashi Institute of Technology, Japan	
	Teaching Assistant	Oct 2011 to Oct 2014
	Systems Biology Professor: Md Altaf-Ul-Amin Graduate School of Information Science, Nara Institute of Science and Technology, Japan	
OTHER WORK EXPERIENCE	Medical Representative	Sep 2008 to Dec 2009
	Pharmaken Limited Kenya Nairobi office	
EDUCATION	Nara Institute of Science and Technology (NAIST),Japan	
	Ph.D. Bioinformatics, March 2016	
	<ul style="list-style-type: none"> • Thesis title: <i>Transcription regulation network analysis towards integrative big data biology</i> • Advisors: Shigehiko KANAYA, PhD and Naoaki ONO, PhD 	
	M.Sc. Bioinformatics and biostatistics, March 2013	
	<ul style="list-style-type: none"> • Advisors: Shigehiko KANAYA, PhD and Kensuke NAKAMURA, PhD 	
	University of Nairobi, Nairobi Kenya	
	B.Sc. Biology (First Class Honours), October 2008	

- Advisor: Samuel Kiboi, Ph.D

FUNDING AND AWARDS

Funding

- IDeAL postdoctoral funding Apr 2016 to Sep 2018 GBP: 175000
- TDMoNet tropical disease modeling seed fund Jan 2017 to Jun 2017 GBP: 4600
- KEMRI Institutional Research Grant (IRG) June 2018 to Dec 2019 KES: 3967814

Awards

- Japanese Language studentship Osaka University Apr 2010 to Sep 2010
- Research Fellowship Oct 2010 to Mar 2011
- Masters Scholarship Apr 2011 to Mar 2013
- Doctoral Course Scholarship Apr 2013 to Mar 2016
- Gandhi Smarak Nidhi Trustee Fund Prize (Top undergraduate student SBS) May 2011

PROFESSIONAL MEMBERSHIP

Scientific Societies

May 2010 – Present

- Molecular Biology Society of Japan (MBSJ)
- International Society of Computational Biology (ISCB)
- African Society for Bioinformatics and Computational Biology (ASBCB)

Student Societies

July 2004 – Aug 2008

- Biology Association of Nairobi University Students(BANUS) July 2004 to July 2007
- Organising Secretary BANUS Aug 2007 to July 2008

REFEREED JOURNAL PUBLICATIONS

1. **Kibinge, N. K.**, Relton, C. L., Gaunt, T. R., and Richardson, T. G. (2020). Characterizing the Causal Pathway for Genetic Variants Associated with Neurological Phenotypes Using Human Brain-Derived Proteome Data. *The American Journal of Human Genetics*, 106(6), 885-892.
2. Kamuyu, G., Tuju, J., Kimathi, R., Mwai, K., Mburu, J., **Kibinge, N.**, ... and Njunge, J. M. (2018). KILchip v1. 0: a novel Plasmodium falciparum merozoite protein microarray to facilitate malaria vaccine candidate prioritization. *Frontiers in immunology*, 9.
3. Githinji, G., Agoti, C. **N.**, **Kibinge, N.**, Henson, S., Munywoki, P., Brand, S., ... and Worby, C. J. (2018). Assessing the utility of minority variant composition in elucidating RSV transmission pathways. *bioRxiv*, 411512.
4. Mohammed, K. S., **Kibinge, N.**, Prins, P., Agoti, C. N., Cotten, M., Nokes, D. J., and Githinji, G. (2018). Evaluating the performance of tools used to call minority variants from whole genome short-read data. *Wellcome Open Research*, 3.
5. Njunge, J. M., Oyaro, I. N., **Kibinge, N. K.**, Rono, M. K., Kariuki, S. M., Newton, C. R., and Gitau, E. N. (2017). Cerebrospinal fluid markers to distinguish bacterial meningitis from cerebral malaria in children. *Wellcome Open Research*, 2.
6. **Kibinge, N.**, Ono, N., Horie, M., Sato, T., Sugiura, T., Altaf-Ul-Amin, M. and Kanaya, S. (2016). Integrated pathway-based transcription regulation network mining and visualization based on gene expression profiles. *Journal of biomedical informatics*, 61, 194-202.
7. **Kibinge, N.**, and Kiboi, S. (2016). Increasing the role of systems biology towards leveraging ecology research in Kenya. *CICSJ Bulletin Japan*, 34(2), 59.

8. Tanaka, N., Zakaria, N. A., **Kibinge, N. K.**, Kanaya, S., Tamura, T., and Yoshida, M. (2014). Fall-risk classification of the timed up-and-go test with principal component analysis. *International journal of neurorehabilitation*, 1, e106-e106.
9. **Kibinge, N.**, Ikeda, S., Ono, N., Altaf-UI-Amin, M., and Kanaya, S. (2014). Integration of Residue Attributes for Sequence Diversity Characterization of Terpenoid Enzymes. *BioMed Research International*, 2014.
10. Ohtana, Y., Abdullah, A. A., Altaf-UI-Amin, M., Huang, M., Ono, N., Sato, T. and **Kibinge, N. K.** (2014). Clustering of 3D Structure Similarity Based Network of Secondary Metabolites Reveals Their Relationships with Biological Activities. *Molecular Informatics*, 33(11-12), 790-801
11. Afendi, F. M., Ono, N., Nakamura, Y., Nakamura, K., Darusman, L. K., **Kibinge, N.**, and Kanaya, S. (2013). Data mining methods for omics and knowledge of crude medicinal plants toward big data biology. *Computational and structural biotechnology journal*, 4.
12. Ikeda, S., Abe, T., Nakamura, Y., **Kibinge, N.**, Morita, A. H., Nakatani, A., ... and Kanaya, S. (2013). Systematization of the protein sequence diversity in enzymes related to secondary metabolic pathways in plants, in the context of big data biology inspired by the KNAPSAcK Motorcycle database. *Plant and Cell Physiology*, pct041.

MANUSCRIPTS IN
PREPARATION/
SUBMITTED

1. **Nelson Kibinge**, Charles Sande, Ken Mwai, George Githinji, Abdirahman Abdi, James Nokes and James Njunge, TransProt: An analysis pipeline for proteomic and transcriptomic data.
2. **Nelson Kibinge**, Samuel Brand, George Githinji, Charles Agoti, Lister Mirarwa, Everlyn Kamau, James Otieno and James Nokes, Sampling coverage and variant diversity capture in RSV surveillance *Manuscript in prep.*

CONFERENCE AND
POSTER
PRESENTATIONS

1. **Nelson Kibinge**, Samuel Brand, George Githinji, Charles Agoti, James Otieno, Moses Kiti, Matthew Keeling and James Nokes (2017), Sampling considerations for optimizing genetic diversity capture in Respiratory Syncytial virus Surveillance *Epidemics 6 2017*, SIItges, Spain, November 28-December 2, 2017
2. **Nelson Kibinge**, Naoaki Ono, Masafumi Horie, Ming Huang, Tetsuo Sato, Tadao Sugiura, Md. Altaf-UI-Amin, Saito Akira and Shigehiko Kanaya (2014), A systems mapping of transcription regulation in genes and modules of genes in lung cancer pathways, *GIW-ISCB 2014*, Odaiba, Tokyo, December 14-17, 2014.
3. **Nelson Kibinge**, Shun Ikeda, Naoaki Ono, Nakamura Kensuke, MD Altaf-UI-Amin and Shigehiko Kanaya (2012). Utilizing metric properties of amino acids in distance matrix methods for protein sequence analysis BMB2012 *The 35th annual meeting of the molecular biology society of Japan Fukuoka*, December, 11-14, 2012
4. **Nelson Kibinge**, Shun Ikeda, Farit Afendi, Naoaki Ono, Nakamura Kensuke, MD Altaf-UI-Amin and Shigehiko Kanaya (2012). Phylogenetic analyses suggest influence of parasitism on the genomes of malaria parasite. *Genomics of Common Diseases 2012*, Potomac MD, September 19-22, 2012
5. Shun Ikeda, Manabu Ohi, Atsushi Nakatani, **Nelson Kibinge**, Naoaki Ono, Md. Altaf-UI-Amin, Shigehiko Kanaya (2012). Codon usage patterns of pathogenic bacteria. *Genomics of Common Diseases 2012, Potomac MD*, September 19-22, 2012

REFEREES

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