NELSON KIPCHIRCHIR KIBINGE

CONTACT INFORMATION	Room OS1, OakField House Oakfield Grove// MRC IEU, University of Bristol Tel: +447379009237 nelson.kibinge@bristol.ac.uk

PROFESSIONAL SUMMARY

A researcher, educator, and data scientist using data to understand problems in molecular biology, human health and education. I am a self-driven and motivated with extensive experience working with diverse teams and in lead roles involving the production of applied statistics and informatics data tools and code that have been utilized in clinical trials, epidemiological studies and academic purposes. As a PhD-trained computational biologist and statistician, I am involved in large-scale health research and also in teaching postgraduate courses at the university.

CORE COMPETENCIES

- Biomarker discovery pipeline development
- Mendelian Randomization
- Clinical trial statistics
- Bayesian statistics
- Protein mass spectrometry
- protein microarrays
- Systems Biology
- Machine learning for biology
- Next generation sequencing (MiSeq and Oxford Nanopore)
- Compartmental Epidemiological Modeling
- Biostatistical programming: R and MATLAB
- Scripting languages: perl and python
- Unix shell scripting,
- Other applications: Machine learning tools such as support vector machines and decision tree modelling, LaTeX,database, spreadsheet, and presentation software
- Capacity building
- Operating Systems: Unix/Linux, MacOSX.

PROFESSIONAL EXPERIENCE

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

Senior Postdoctoral Scientist-Statistics and bioinformatics   Nov 2018 to present
Senior postdoctoral scientist leading the biostatistics and bioinformatics department at the KEMRI-Wellcome Kilifi unit
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: *Evaluating local respiratory syncytial virus (RSV) genetic diversity: a statistical perspective*

Virus Epidemiology and Control Group,

KEMRI-Wellcome Trust Research Programe, Kenya

Research Assistant   Apr 2013 to March 2016
Project: *Data mining methods for understanding gene expression in high througphut technologies*
Computational systems biology laboratory,
Nara Institute of Science and Technology
Supervisor: Kanaya Shigehiko, Ph.D

Research Assistant   Jun 2007 to May 2008
Project: *Biosafety; gene flow in wild oryzae sativa in Mwea region*
School of Biological Sciences,
University of Nairobi
Supervisor: Samuel Kiboi, Ph.D

TEACHING   **Part-time Lecturer**   September 2017 to Present
EXPERIENCE   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   **Medical Representative**   Sep 2008 to Dec 2009
EXPERIENCE   Pharmaken Limited Kenya
                  Nairobi office

EDUCATION   **Nara Institute of Science and Technology (NAIST)**,Japan

                  Ph.D. Bioinformatics, March 2016
                  - Thesis title: *Transcription regulation network analysis towards integrative big data biology*
                  - Advisors: Shigehiko KANAYA, PhD and Naoaki ONO, PhD

                  M.Sc. Bioinformatics and biostatistics, March 2013
                  - 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

Funding
- IDeAL postdoctoral funding   Apr 2016 to Sep 2018   GBP: 175000
- TDModNet 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. 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.

2. 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.

3. 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.*

4. 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.*

5. **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.

6. **Kibinge, N.**, and Kiboi, S. (2016). Increasing the role of systems biology towards leveraging ecology research in Kenya. *CICSJ Bulletin Japan*, 34(2), 59.

7. 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.

8. **Kibinge, N.**, Ikeda, S., Ono, N., Altaf-Ul-Amin, M., and Kanaya, S. (2014). Integration of Residue Attributes for Sequence Diversity Characterization of Terpenoid Enzymes. *BioMed Research International*, 2014.

9. Ohtana, Y., Abdullah, A. A., Altaf-Ul-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

10. 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.

11. 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.

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MANUSCRIPTS IN
PREPARATION/
SUBMITTED

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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.*

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CONFERENCE AND
POSTER
PRESENTATIONS

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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 Surveilance *Epidemics 6 2017*, SItges, Spain, November 28-December 2, 2017

2. **Nelson Kibinge**, Naoaki Ono, Masafumi Horie, Ming Huang, Tetsuo Sato, Tadao Sugiura, Md. Altaf-Ul-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-Ul-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 moleculars biology society of Japan Fukuoka*, December, 11–14, 2012

4. **Nelson Kibinge**, Shun Ikeda, Farit Afendi, Naoaki Ono, Nakamura Kensuke, MD Altaf-Ul-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

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REFEREES   Professor Philip Bejon
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