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Virtual Workshop on Spatial Genomic Data in R 16th to 20th November 2020

Workshop aim

Genetic sequence data is increasingly becoming available. This combined with ecological information provide new ways to study causes of genetic diversity. Understanding, analyzing and visualizing these data require effective tools. In this workshop, we will learn to integrate genomics, digital maps and ecology data sets using R tools. We will then use that knowledge to demonstrate how pathogens evolve to colonize new locations and hosts.

Program

Steven Runo
Mark Wamalwa

Monday, November 16th 2020 3.00 to 5.00 pm EAT
Background to the workshop and opening remarks

Session 1: • Unix/linux

Getting around
Downloading, viewing, editing files
Local machines vs. remote server

Emily Bellis

Tuesday, November 17th 2020 3.00 to 5.00 pm EAT

Session 2: • Genomics Techniques

Variant (SNP) calling
Wednesday, November 18th 2020 3.00 to 5.00 pm EAT

Emily Bellis
10.30-11.00

Session 3: • R/graphics

Import & visualize SNPs
Thursday, November 18th 2020 3.00 to 5.00 pm EAT

Emily Bellis

Session 4: • Spatial data in R

Vector-plot-shapefiles
Friday, November 18th 2020 3.00 to 5.00 pm EAT

8.30-9.30
A-State Teaching
Assistants

Session 5: • Genomics/genetics of adaptation to ecology

Map pathogens/pathotypes to ecologies

Q and A session

Biographies of facilitators



Steven Runo is an Associate Professor of Molecular Biology at Kenyatta University in the Department of Biochemistry, Microbiology and Biotechnology. His research group uses modern tools in plant sciences – such as genomics, bioinformatics and RNA sequencing to identify sources of resistance to the parasitic plants..



Emily Bellis is an Assistant Professor of Bioinformatics at Arkansas State University in the US. Some of her work involve developing machine learning approaches for improved understanding and prediction of gene-environment interactions, leveraging the extensive genomic and phenotypic resources available for crop systems. Much of our past and ongoing work seeks to understand dynamics of interactions between hosts and their parasite or mutualist partners including Striga-host interactions.



Mark Wamalwa is a Lecturer in the Department of Biochemistry, Microbiology and Biotechnology. He holds a PhD in Bioinformatics from the University of Western Cape, South Africa; an MSc in Bioinformatics from Wageningen University & Research, the Netherlands, and a BSc in Veterinary Medicine from the University of Nairobi.