# Dr. Daniel Janies
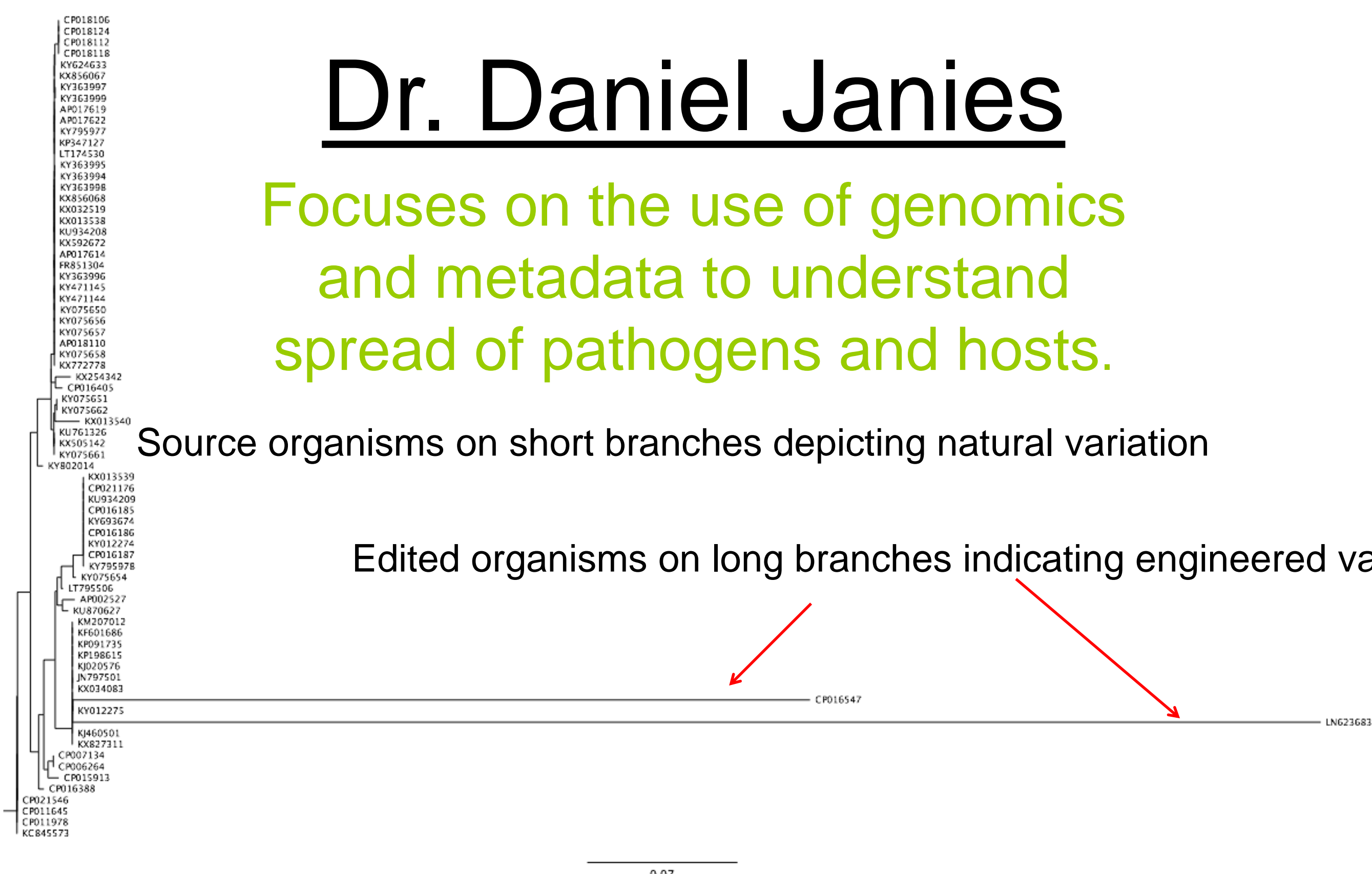
Focuses on the use of genomics and metadata to understand spread of pathogens and hosts.

Source organisms on short branches depicting natural variation

Edited organisms on long branches indicating engineered variation



**NODE CATEGORY**

☑ Author (green) ☑ Cloning Vector (cyan)
☑ Location (yellow) ☑ Products (blue)
☑ Title (purple) ☑ CRISPR/Cas9 (red)

● a crispr-based gene drive system targeting female reproduction in the malaria mosquito

**Genome sequencing, phylogenetics, and network analysis of metadata** on genomes can be used to understand the sources and methods that produced the edited organisms. Phylogenetics can be used to link edited organisms (red arrows) to their natural sources to reveal evidence of the editing process. Edited organisms have long branches in a phylogeny that illustrate the quality and quantity of engineering.
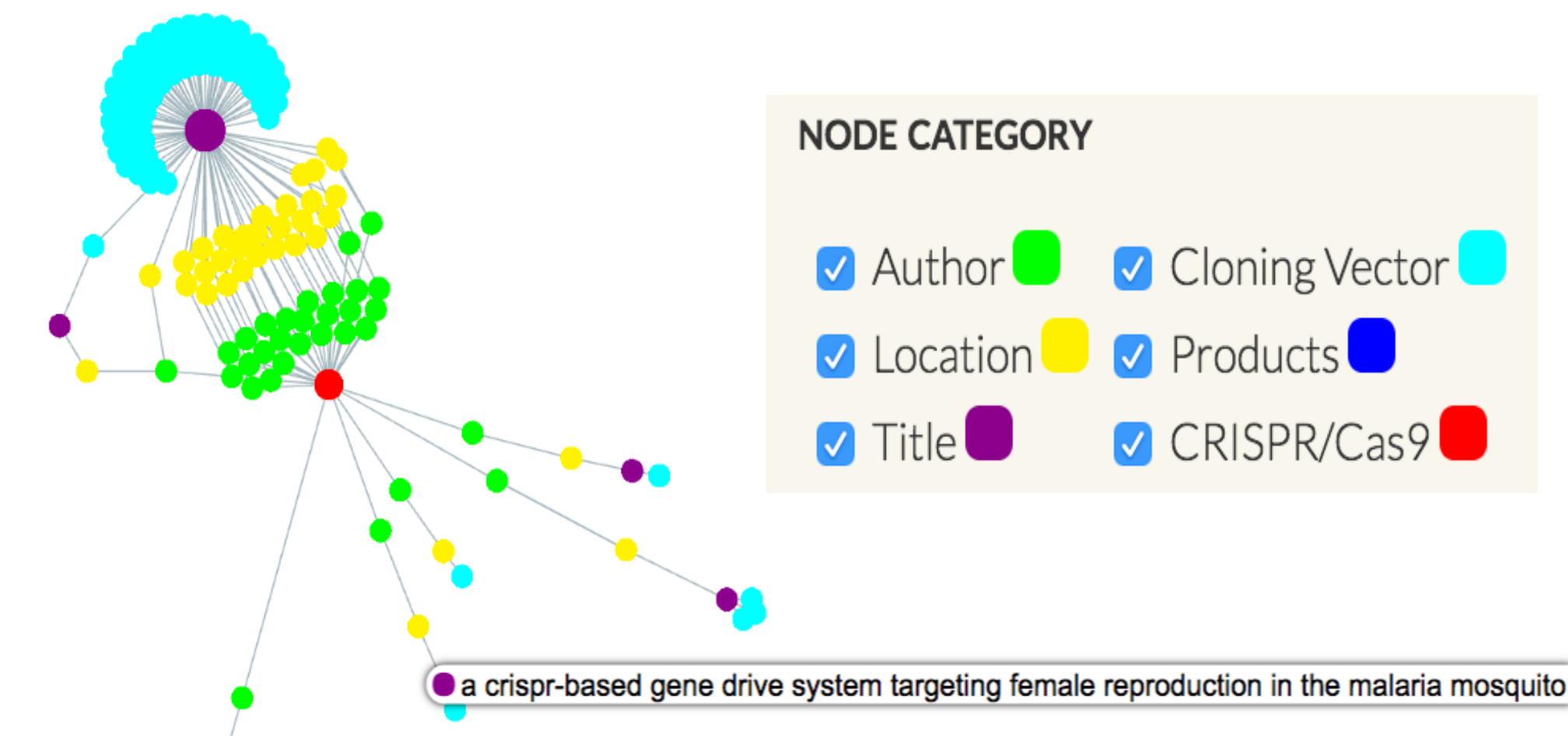
**A network of labs using CRISPR/Cas9.** Nodes represent labs, experiments, and the cloning vectors used. Edges represent shared use of vectors in various labs. Newly discovered edited organisms will be integrated into this network to attribute the newly discovered edited organisms to researchers, locations, and methods.

# Dr. Way Sung

Focuses on the mutation process, the evolution of mutation rate, and detecting signatures of variation using experimental approaches.

**Genomic modifications** can leave residual signatures in DNA. In this figure, modification to mismatch-repair enzymes in *Bacillis subtilis* yields signatures of context-dependent mutations, whereby the mutation rate at the same nucleotide can very depending on the two adjacent nucleotides. As the heatmap shows, these patterns are nearly identical on both sides of the origin of replication, with certain contexts altering site-specific mutation rate by as much as 75-fold. An understanding of these signatures of mutation can provide historical insight on the types of genomic modification that have occurred in an organism.



*Bacillus subtilis* (MMR-)
Base-substitution Mutation Rate per Site per Generation ($\mu_x$)
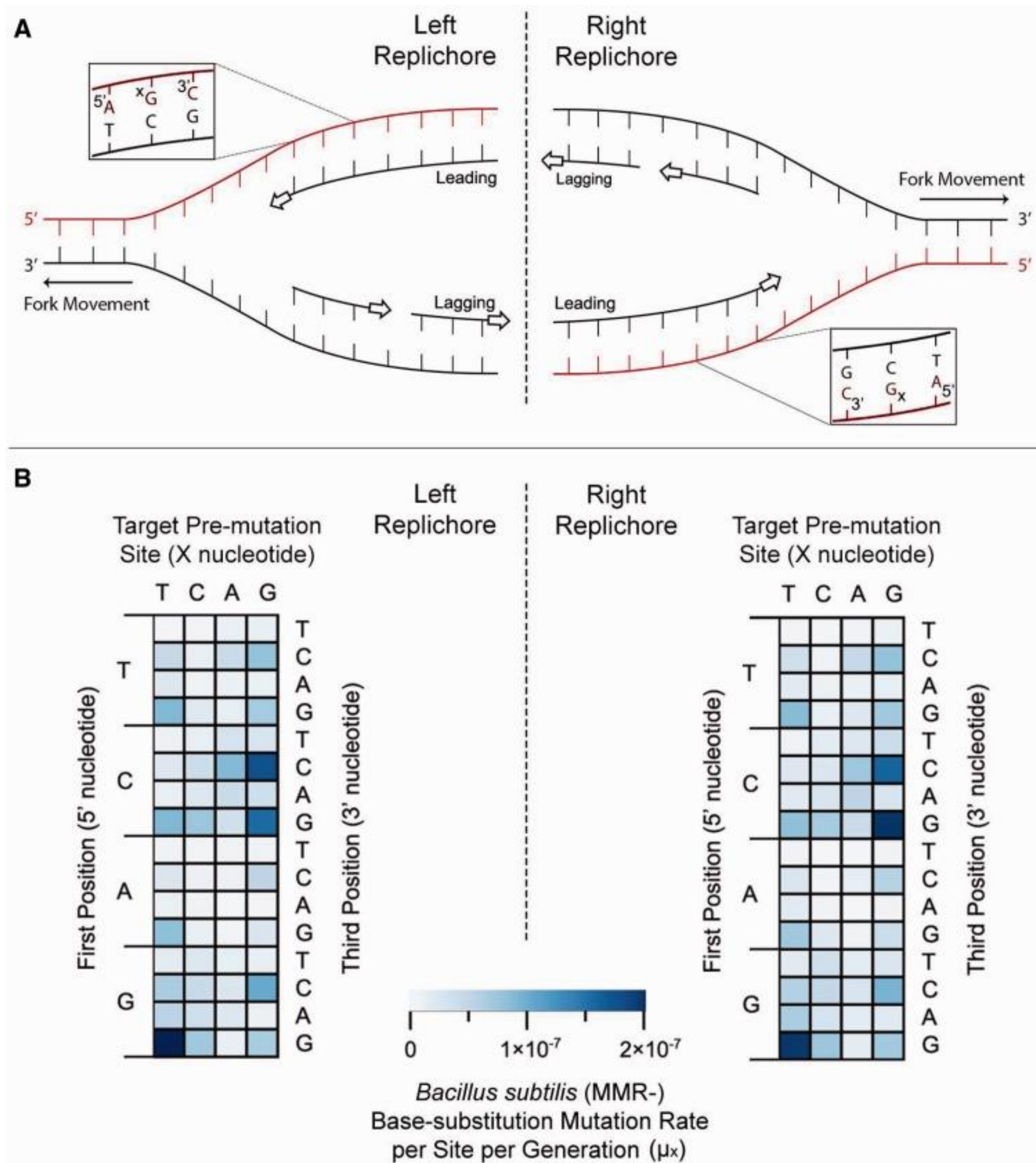
Specific capabilities our group is seeking: mathematical modelers, structural biologists, and or proteomics experts.

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