Research area:

Pathogen evolution & genomics

Key interest:

Genome evolution & pangenomics

- Making pangenome graphs allows better mutation detection

- New insights at hypervariable & complex genomic regions (see image)

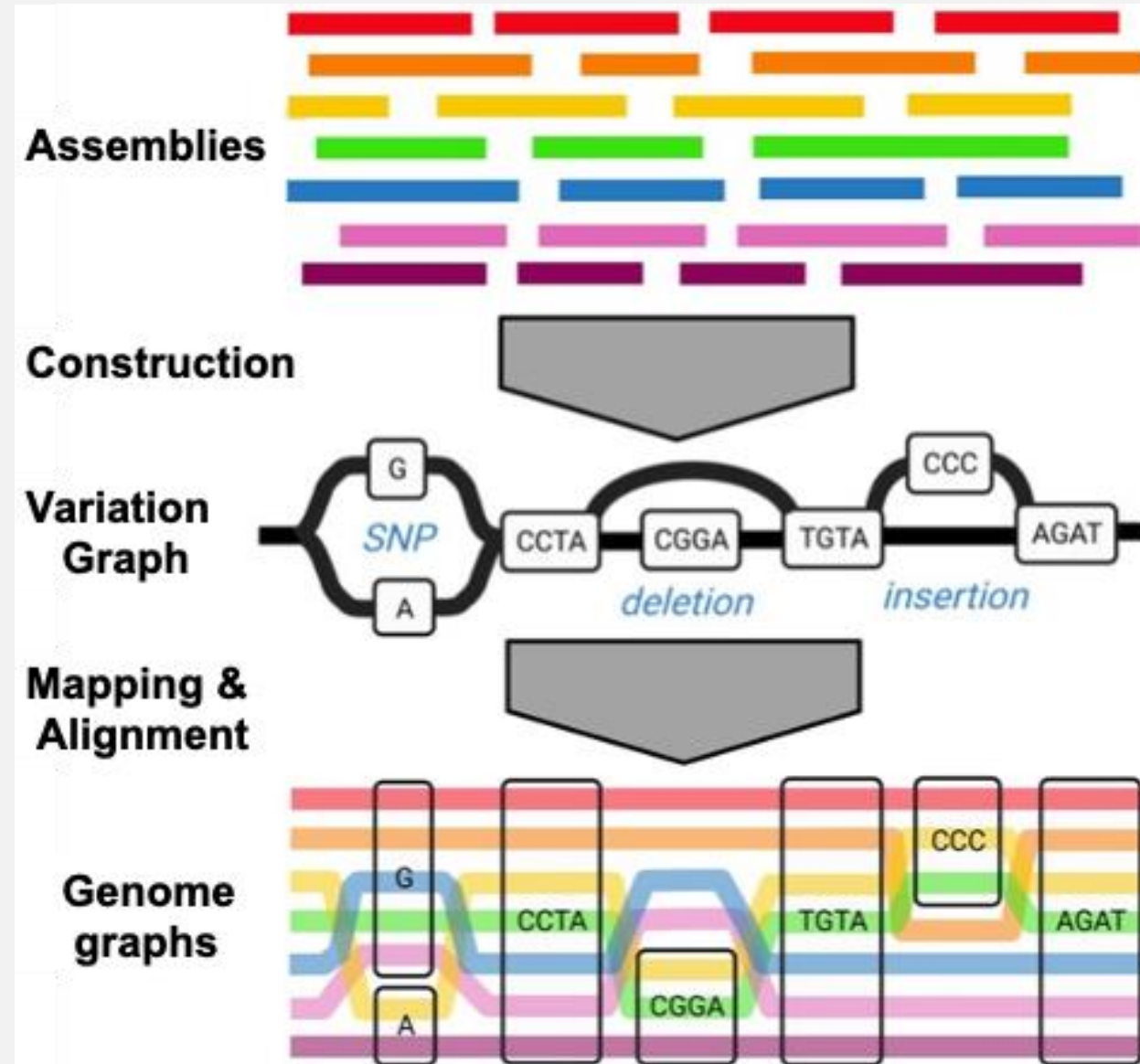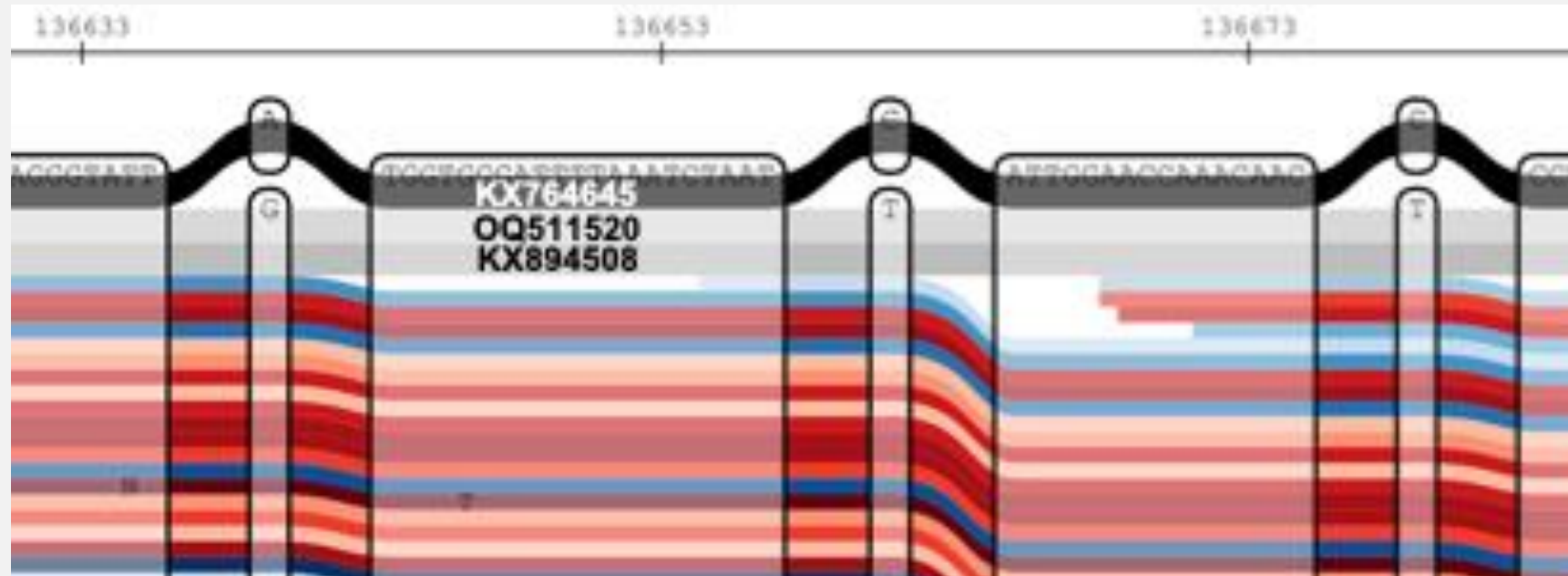# Mutation discovery using pangenome graphs

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Example: segment of 3-reference poxvirus pangenome graph

3 adjacent SNPs with differing alleles in one reference

- Mapping reads to a single reference leads to bias

- De novo assembly can ineffective

So use pangenome graphs to track diversity more accurately

see https://arxiv.org/abs/2412.05096
https://www.biorxiv.org/content/10.1101/2025.04.10.646565v2
https://www.pirbright.ac.uk/our-science/scientists/dr-tim-downing

www.pirbright.ac.uk