Inferring whole-genome histories in large population datasets
Kelleher et al. (2019)

Terms and Abbreviations

You define the important terms and abbreviations that are used in your paper.

π	steady-state distribution of nucleotides (frequencies)
P	transition probability matrix
v	evolutionary distance (expected substitutions per site)
S	transitional differences (frequencies)
V	transversional differences (frequencies)
κ	transition transversion rate ratio
Q	substitution rate matrix
q_{ij}	substitution rate from nucleotide i to j
q_{ii}	diagonal element of substitution rate matrix $(i = j)$
μ	rescaling factor
L	likelihood
ℓ	log-likelihood $(\log_e)$
Pr_{site}	probability of observing nucleotide i and j at a given site of the alignment
p_{ij}	probability of substitution of nucleotide i to j

Context

You shortly describe the context of the paper, i.e. the area of topics where it can be of interest.

Main Points

You summarise the main points.

References

Kelleher, J., Wong, Y., Wohns, A.W., Fadil, C., Albers, P.K., McVean, G., 2019. Inferring whole-genome histories in large population datasets. Nature Genetics 51, 1330–1338. https://doi.org/10.1038/s41588-019-0483-y