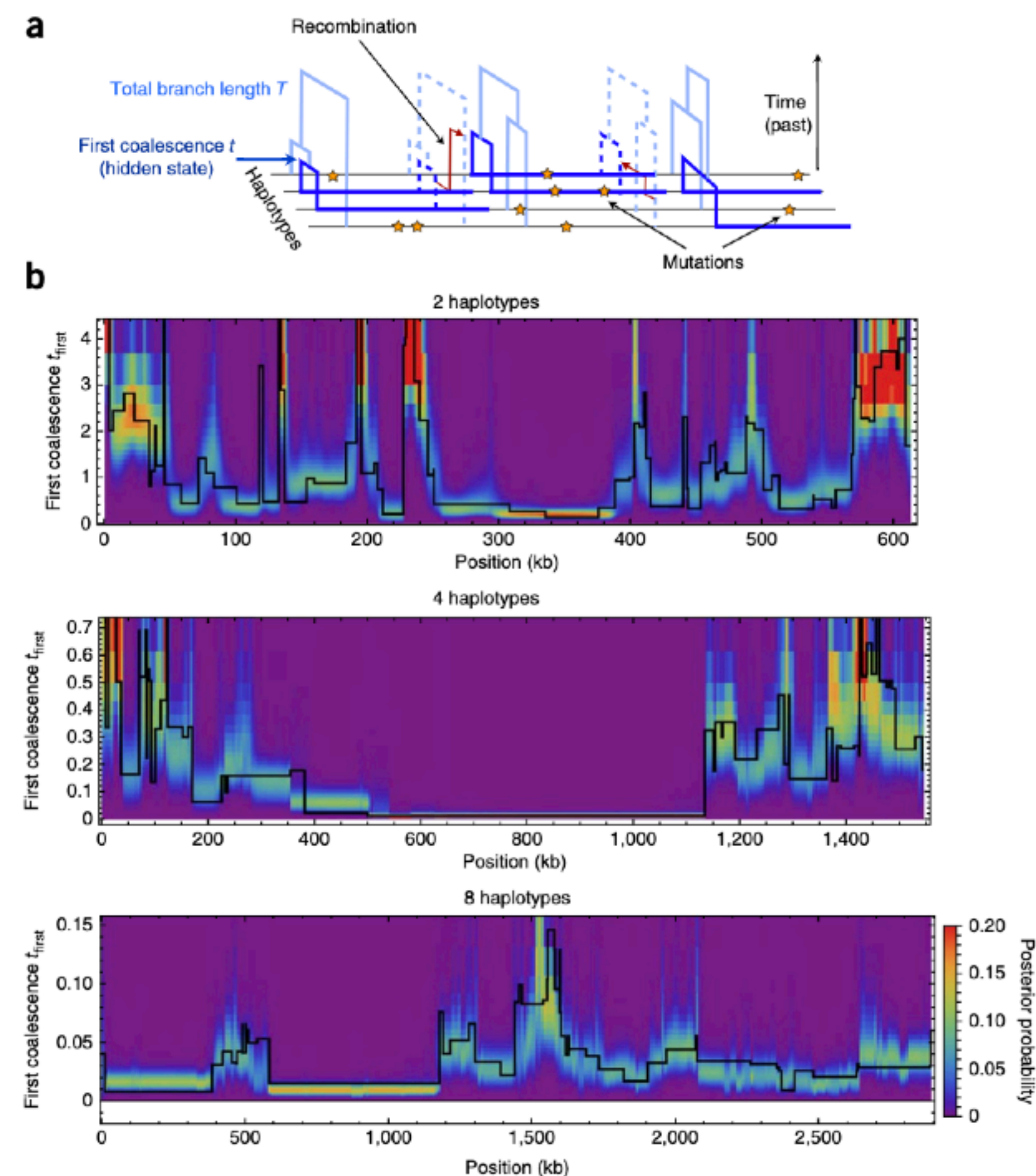


Generalizing beyond diploids

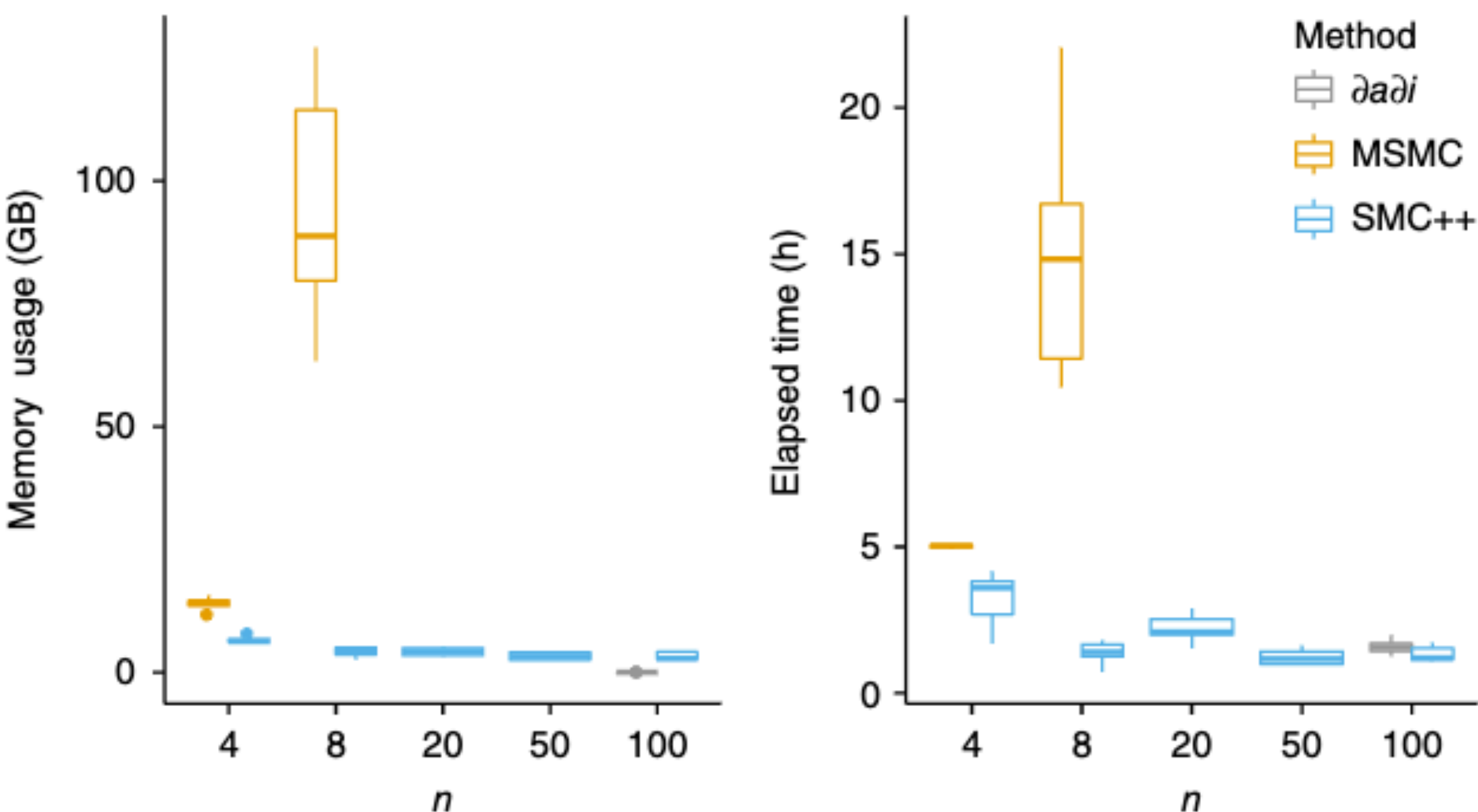
Inferring human population size and separation history from multiple genome sequences

Stephan Schiffels & Richard Durbin



Robust and scalable inference of population history from hundreds of unphased whole genomes

Jonathan Terhorst¹, John A Kamm^{1,2} & Yun S Song¹⁻⁴



The future: tree sequence inference

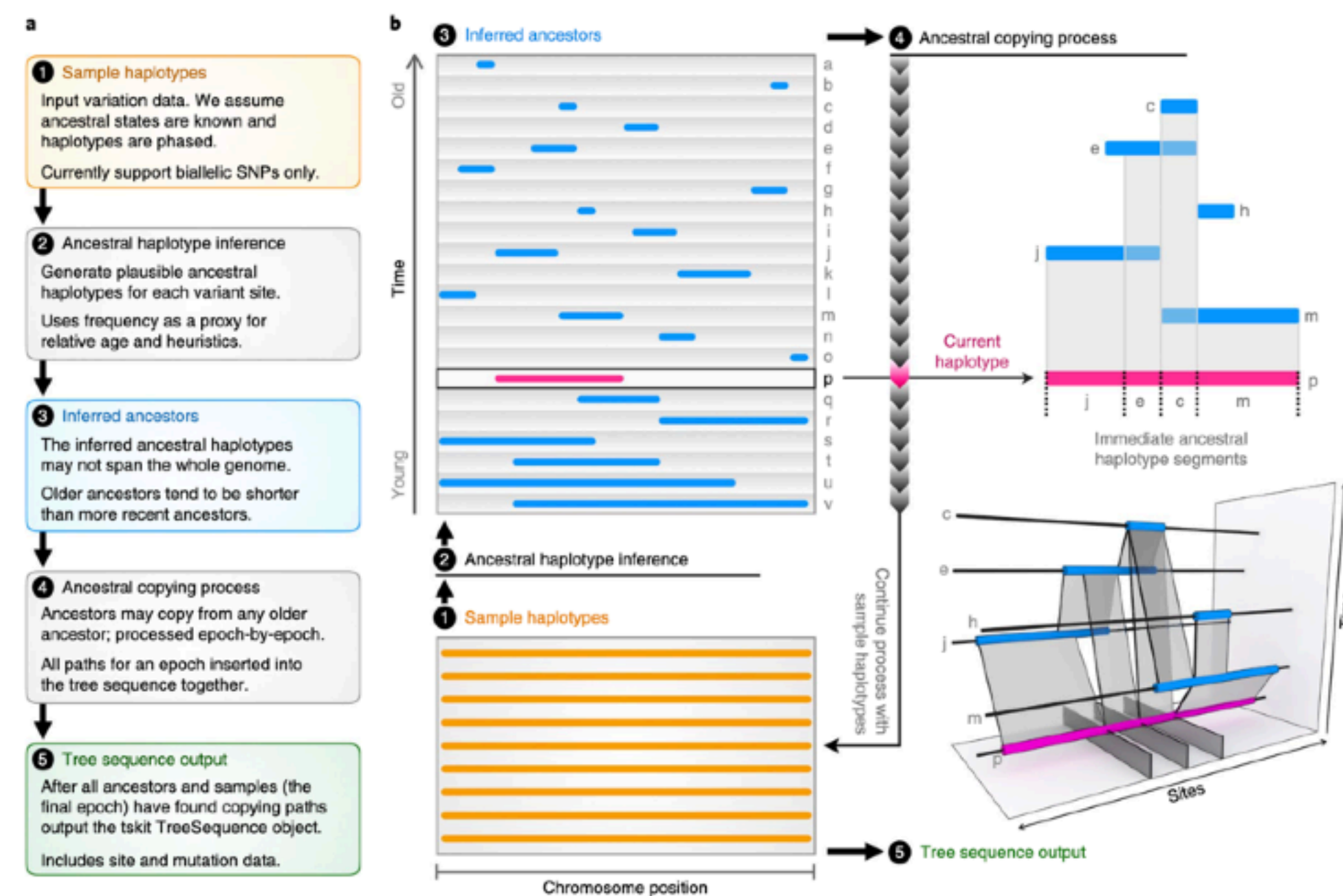
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<https://doi.org/10.1038/s41588-019-0483-y>

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Inferring whole-genome histories in large population datasets

Jerome Kelleher¹*, Yan Wong, Anthony W. Wohns², Chaimaa Fadil³, Patrick K. Albers⁴ and Gil McVean¹



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A method for genome-wide genealogy estimation for thousands of samples

Leo Speidel¹, Marie Forest², Sinan Shi¹ and Simon R. Myers^{1,3}*

