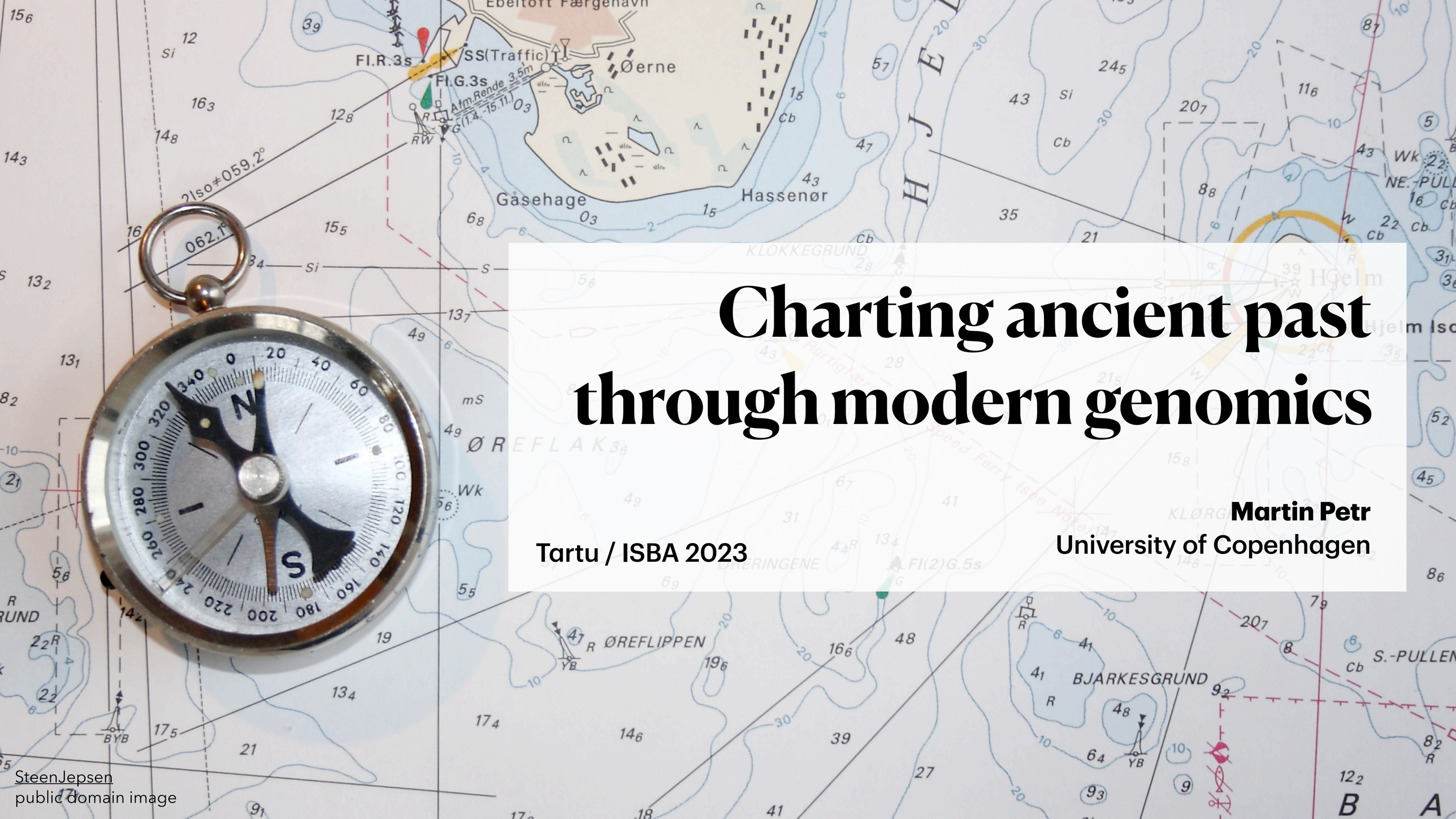
Charting ancient past through modern genomics

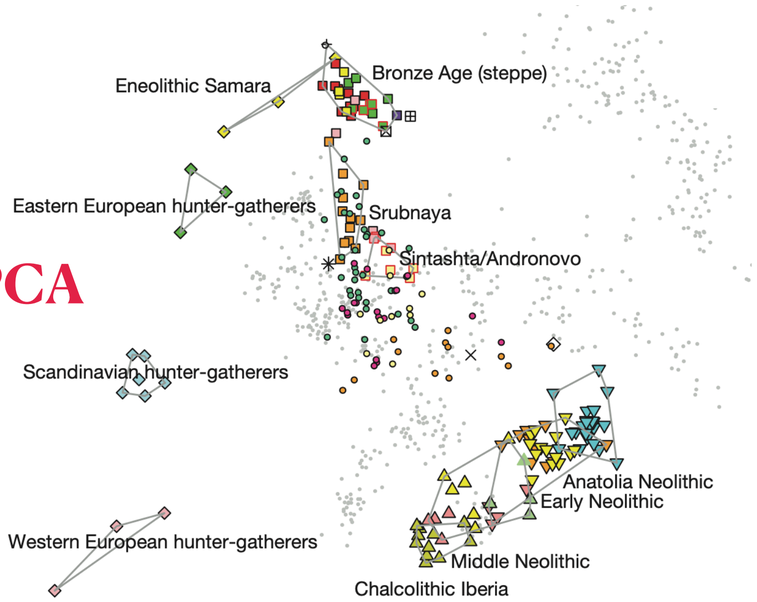
Martin Petr
University of Copenhagen

Tartu / ISBA 2023



SteenJepsen
public domain image

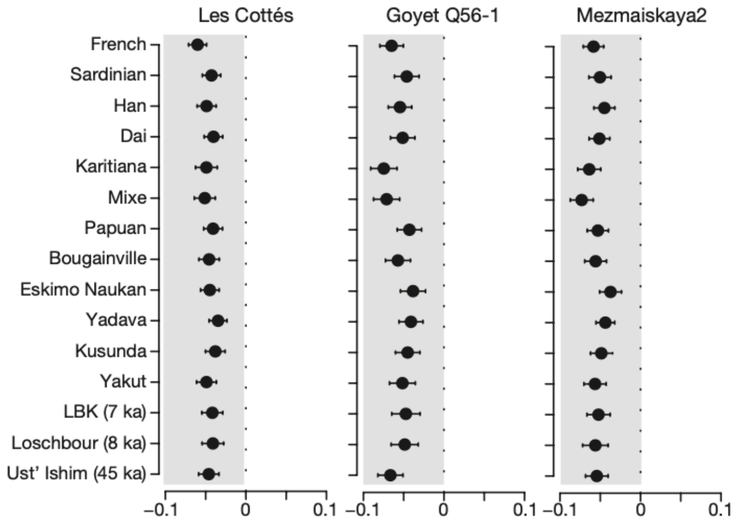
The all-stars of ancient population genomics



PCA

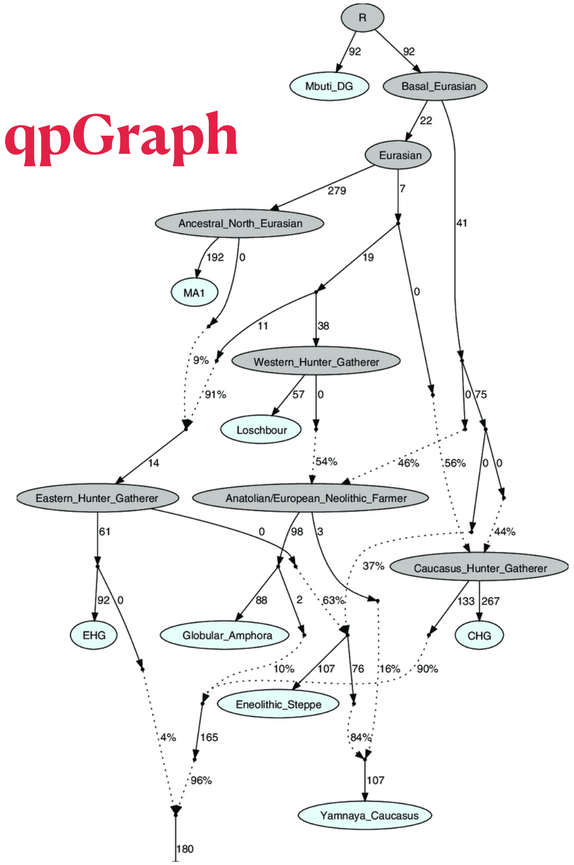
Mathieson *et al*. 2015

f-statistics

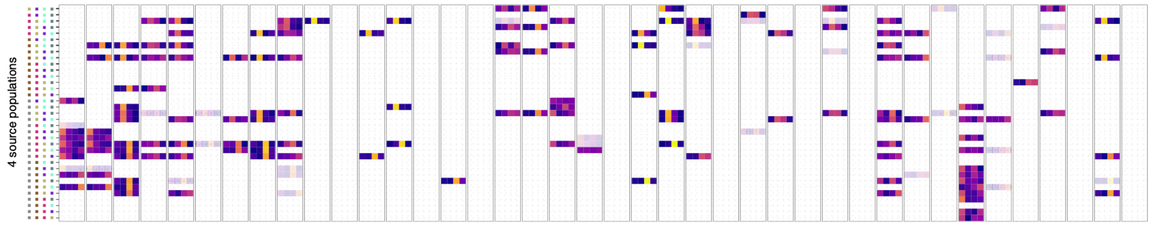


Hajdinjak *et al*. 2018

qpGraph



Wang *et al*. 2019

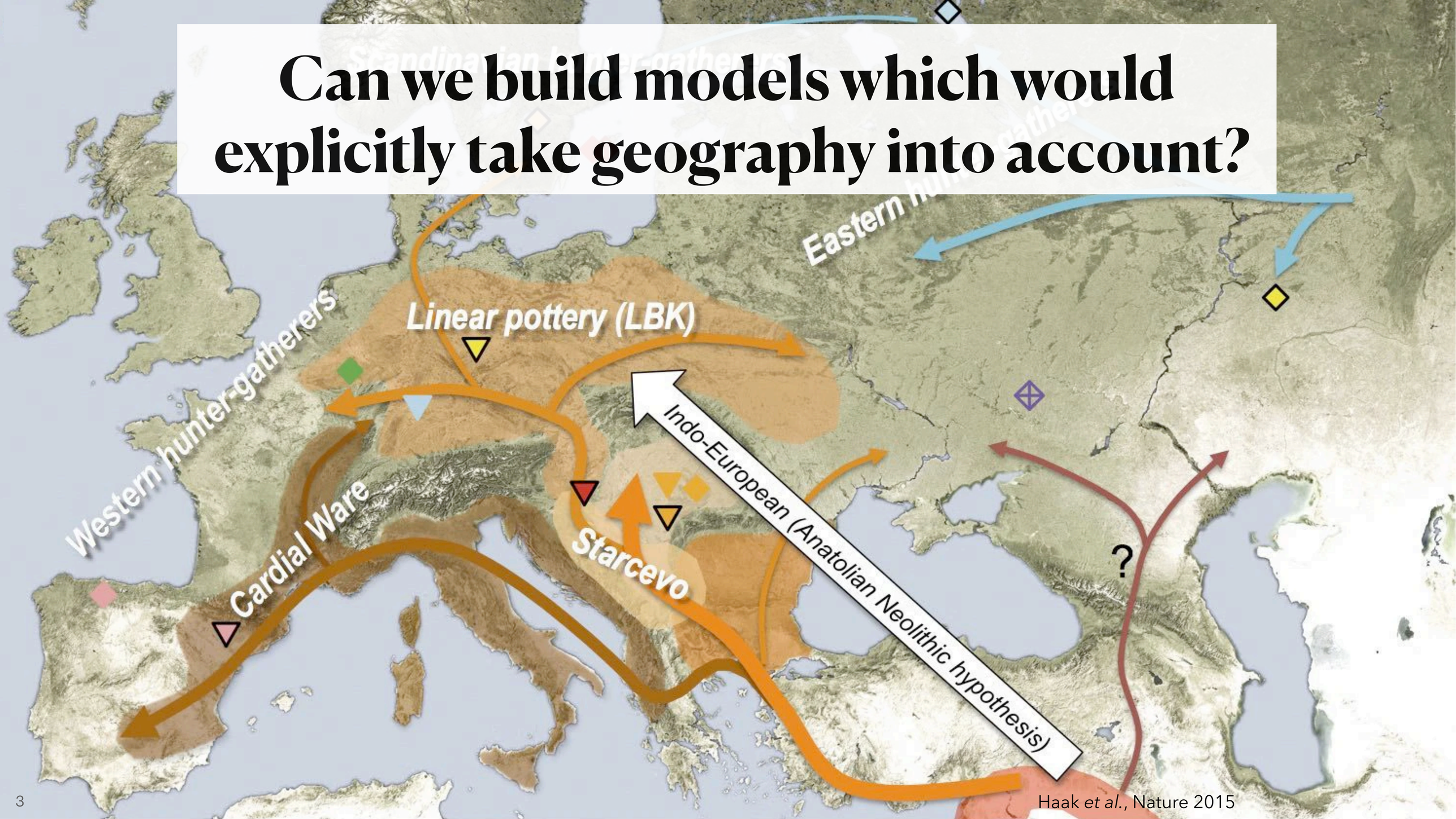


qpAdm

Sikora *et al*. 2019

Haak *et al.*, Nature 2015

Can we build models which would explicitly take geography into account?



Haak *et al.*, Nature 2015

PNAS

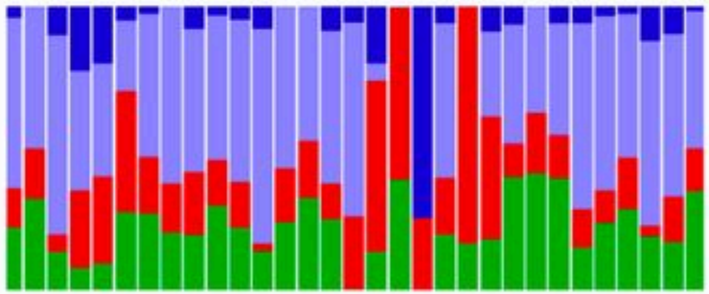
The spatiotemporal spread of human migrations during the European Holocene

Fernando Racimo[a,1], Jessie Woodbridge[b], Ralph M. Fyfe[b], Martin Sikora[a], Karl-Göran Sjögren[c], Kristian Kristiansen[c], and Marc Vander Linden[d]

[a]Lundbeck GeoGenetics Centre, The Globe Institute, University of Copenhagen, 1350 Copenhagen, Denmark; [b]School of Geography, Earth, and Environmental Sciences, University of Plymouth, Plymouth PL4 8AA, United Kingdom; [c]Department of Historical Studies, University of Gothenburg, 405 30 Gothenburg, Sweden; and [d]Department of Archaeology, University of Cambridge, Cambridge CB2 1TN, United Kingdom

Spatio-temporal mapping of genetic ancestry

ADMIXTURE analysis



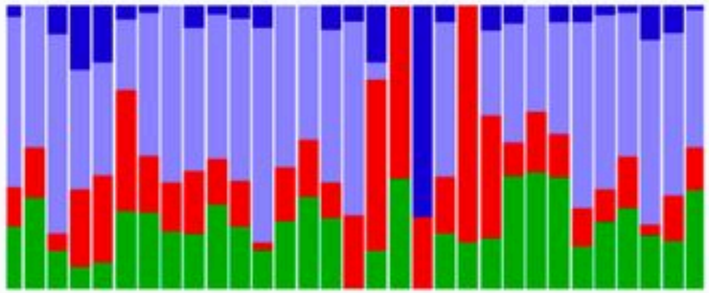
farmer (NEOL) ancestry
Yamnaya (YAM) ancestry
hunter-gatherer ancestry
in each sequenced individual

Racimo *et al.*, PNAS 2020

Spatio-temporal mapping of genetic ancestry

position of each individual
(and their ancestry) on a map

ADMIXTURE analysis



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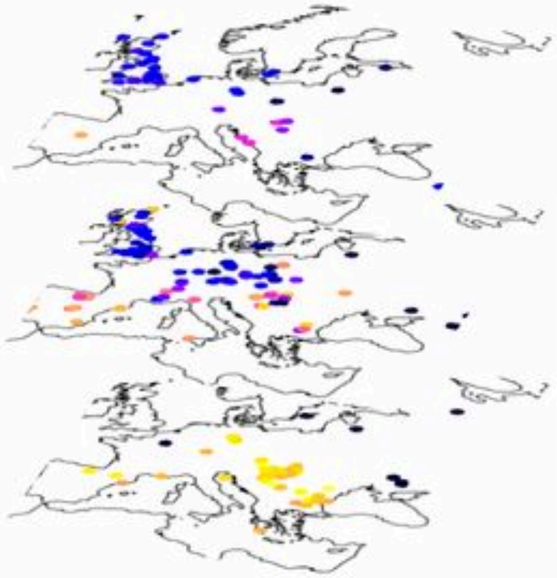

Racimo *et al.*, PNAS 2020

Spatio-temporal mapping of genetic ancestry

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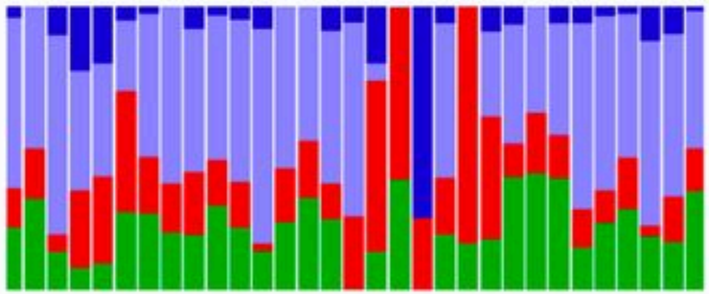
interpolated ancestry maps



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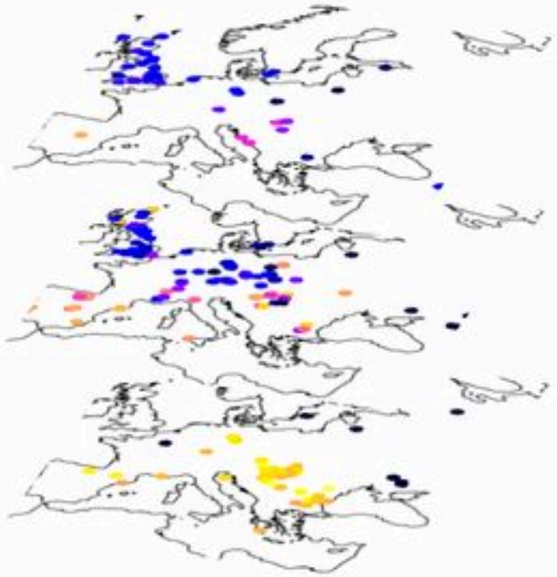


Racimo *et al.*, PNAS 2020

Interpolated ancestry maps

"NEOL" ancestry

-10800

"YAM" ancestry

-10800

2020

Interpolated ancestry maps

"NEOL" ancestry

-10800

"YAM" ancestry

-10800

2020

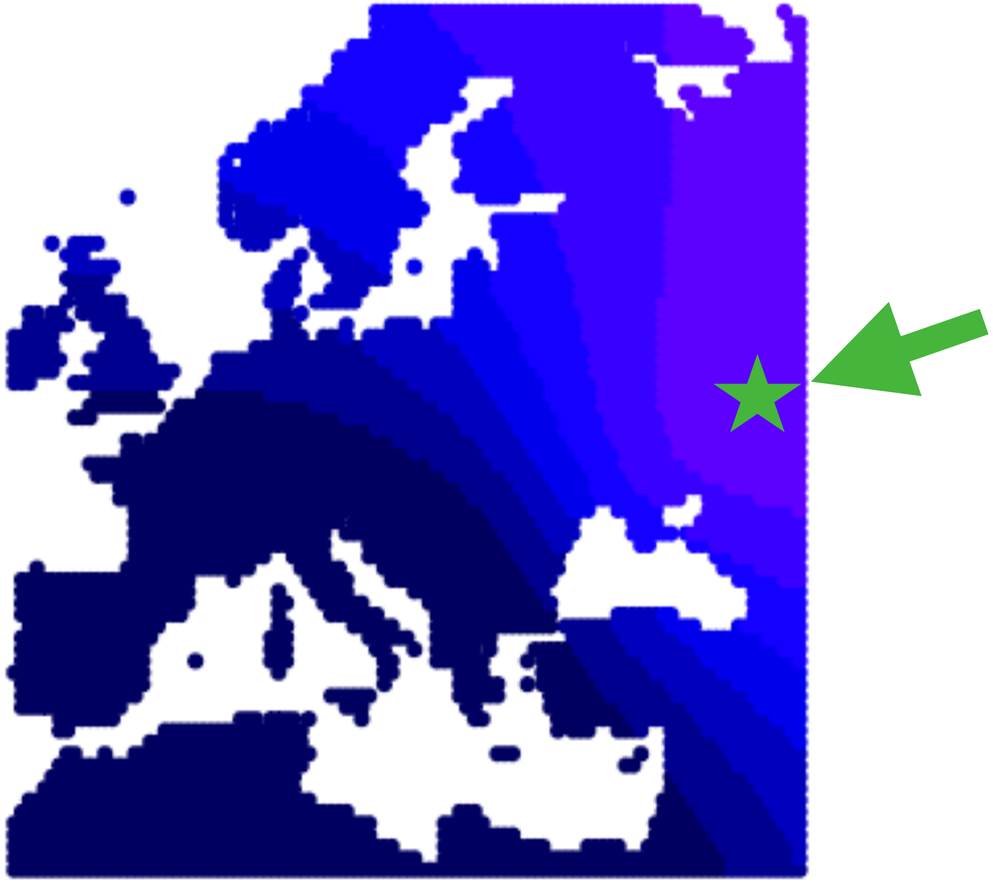
How fast did an "ancestry wave" move from its origin?

"NEOL" ancestry

-10800 BP

"YAM" ancestry

-10800 BP



Racimo *et al.*, PNAS 2020

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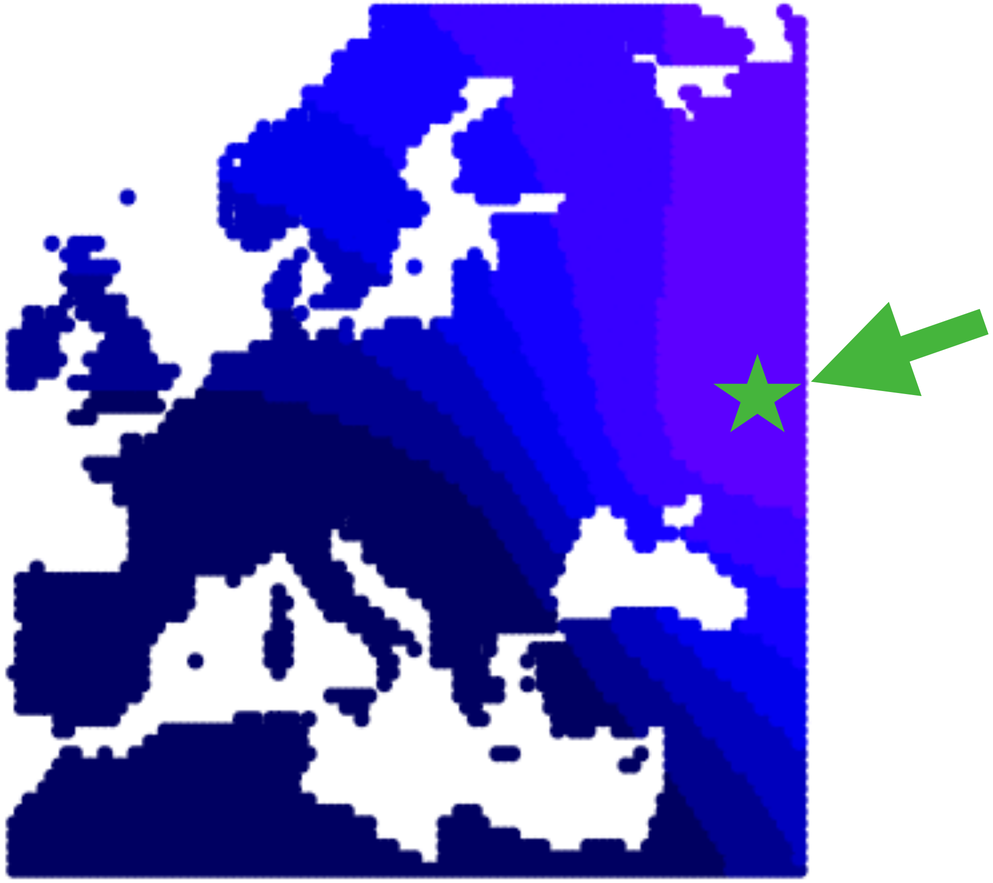

Racimo *et al.*, PNAS 2020

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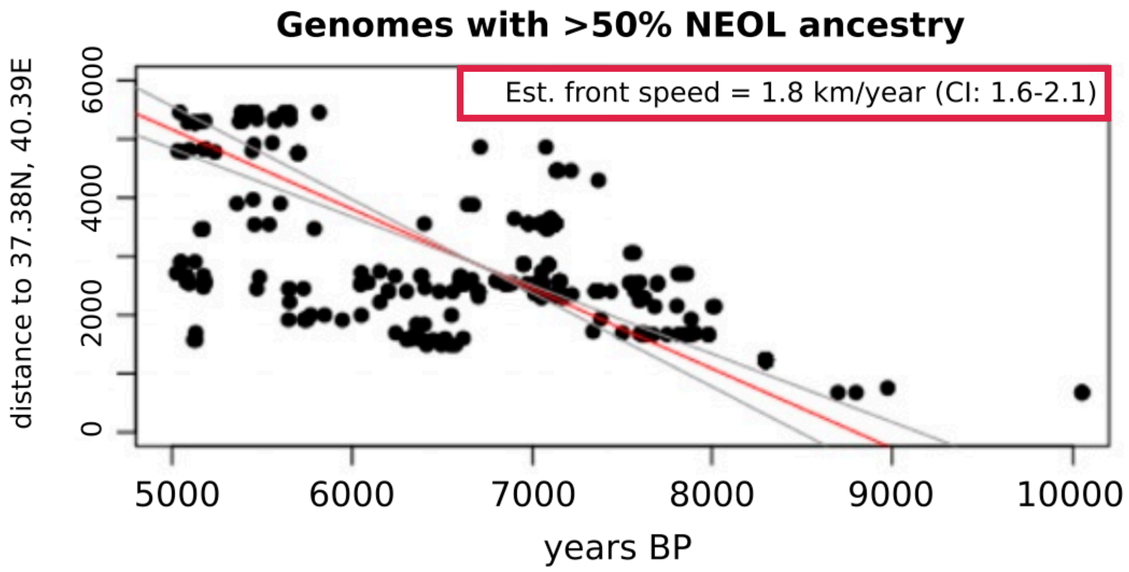
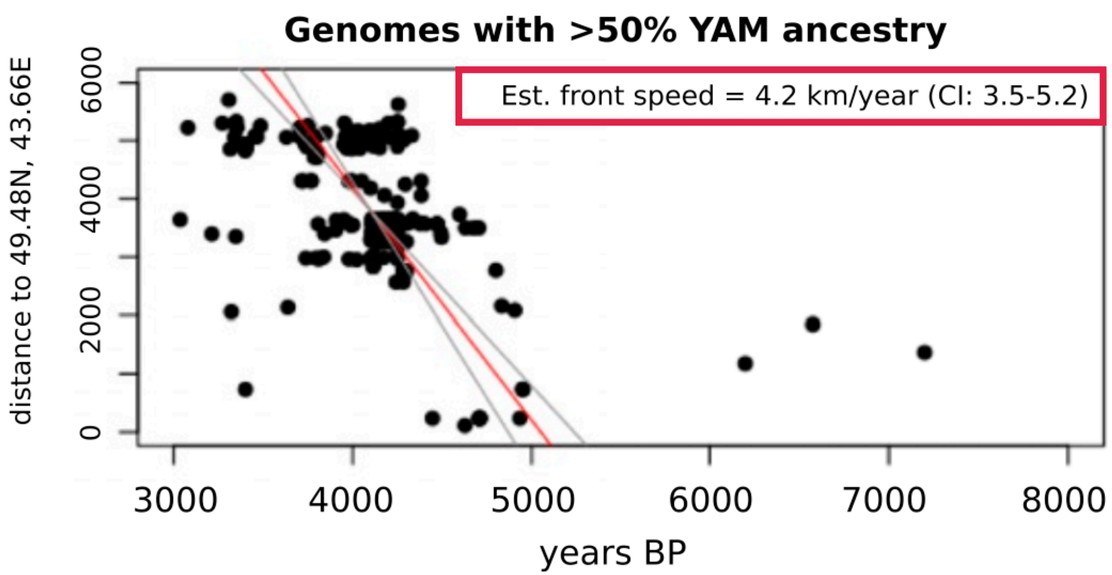


"YAM" ancestry



Racimo *et al.*, PNAS 2020

PNAS

RESEARCH ARTICLE | GENETICS
ANTHROPOLOGY

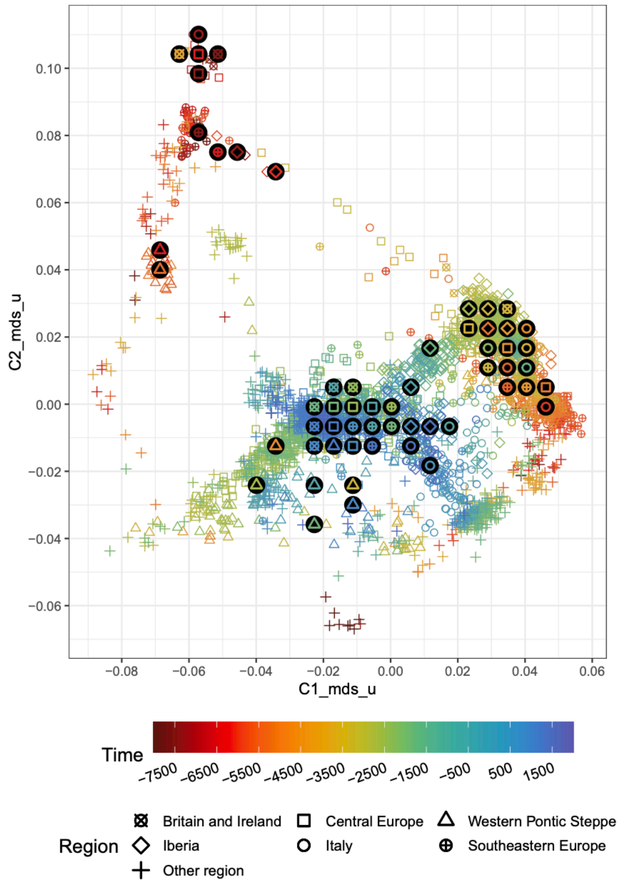
Estimating human mobility in Holocene Western Eurasia with large-scale ancient genomic data

Clemens Schmid[a,b] and Stephan Schiffels[a,1]

Edited by Liisa Loog, University of Oxford, Cambridge, UK; received November 1, 2022; accepted December 5, 2022, by Editorial Board Member Richard G. Klein

Where does a sample trace its ancestral origin?

MDS / PCA



Schmid and Schiffels, PNAS 2023

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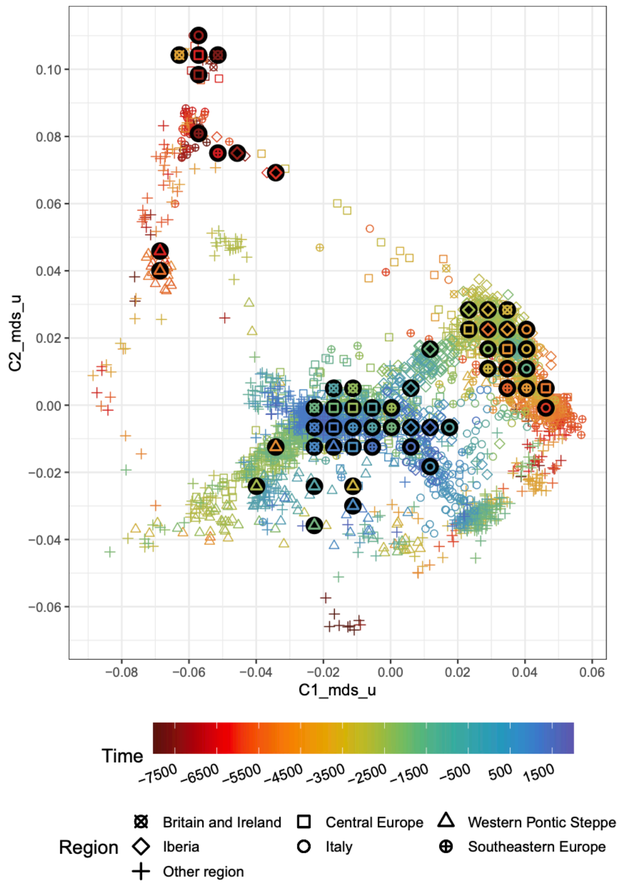
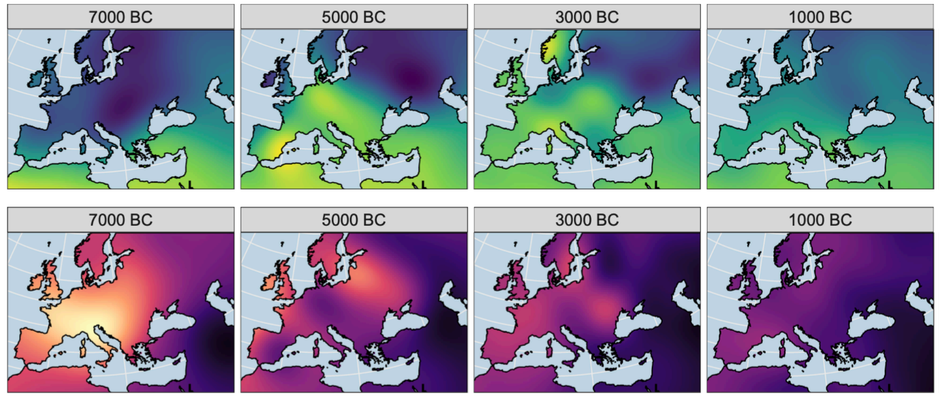


spatio-temporal interpolated "PCA field"



"farmer" component

"Yamnaya" component

Schmid and Schiffels, PNAS 2023

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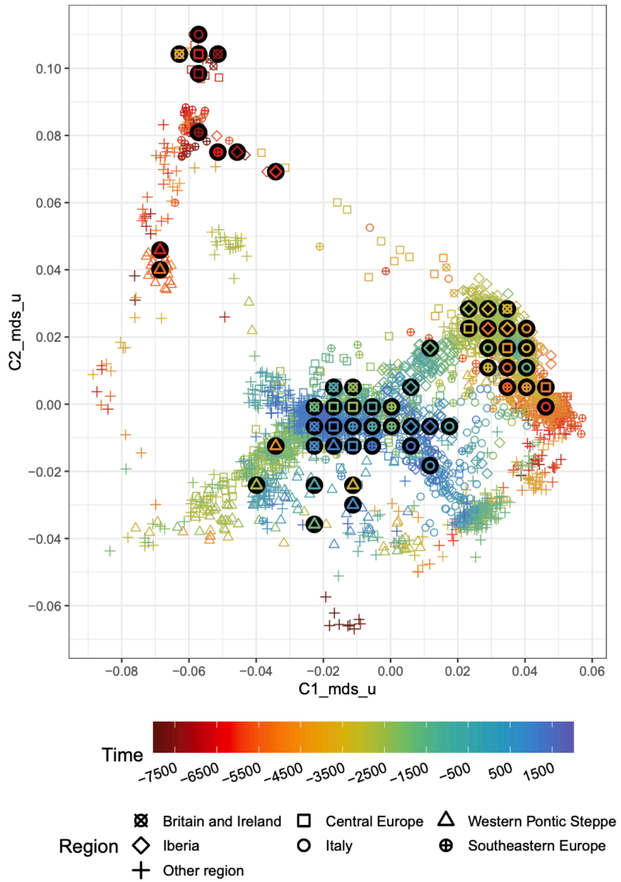

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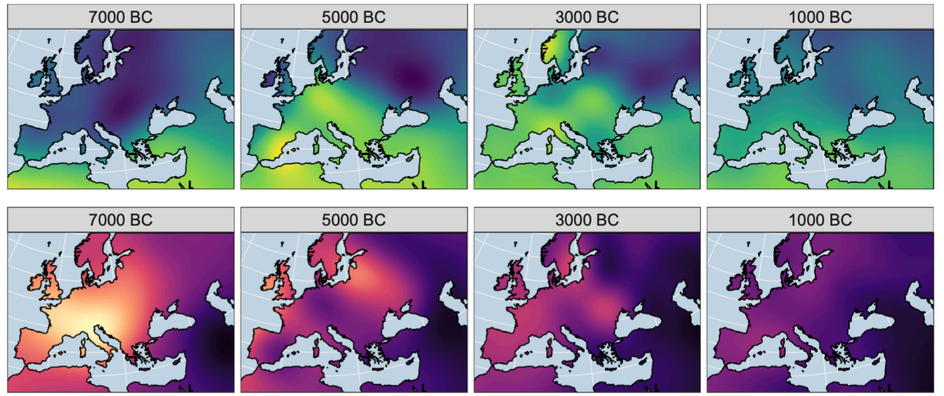

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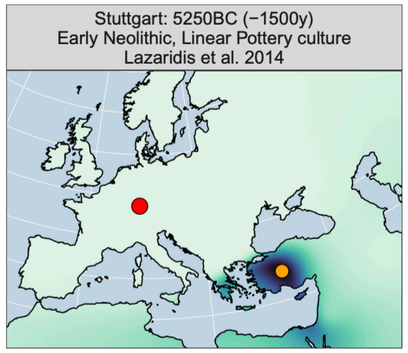

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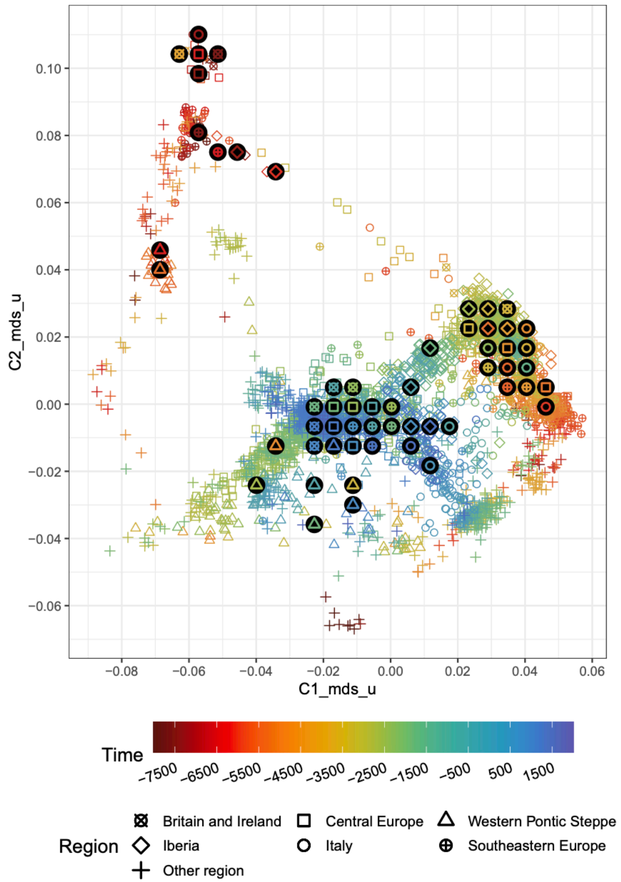

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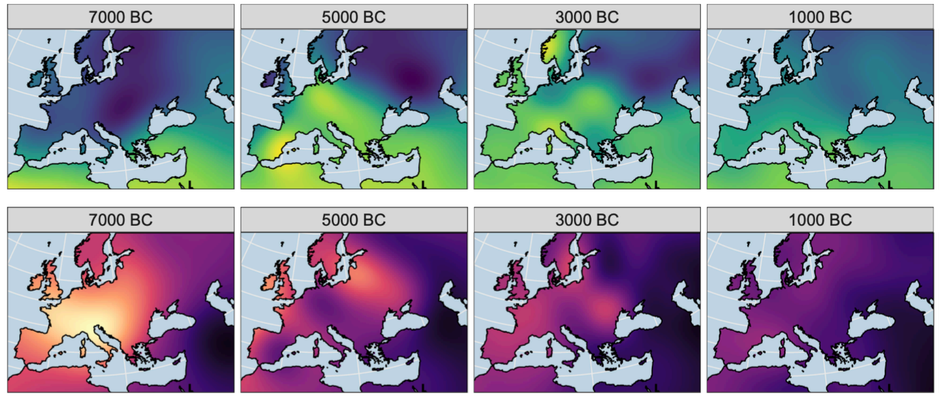

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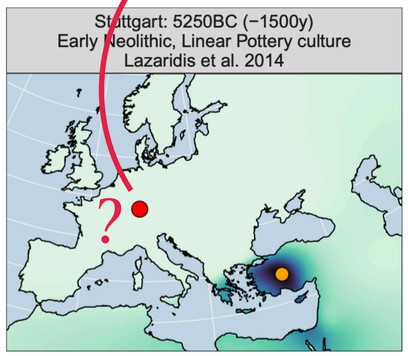

Schmid and Schiffels, PNAS 2023

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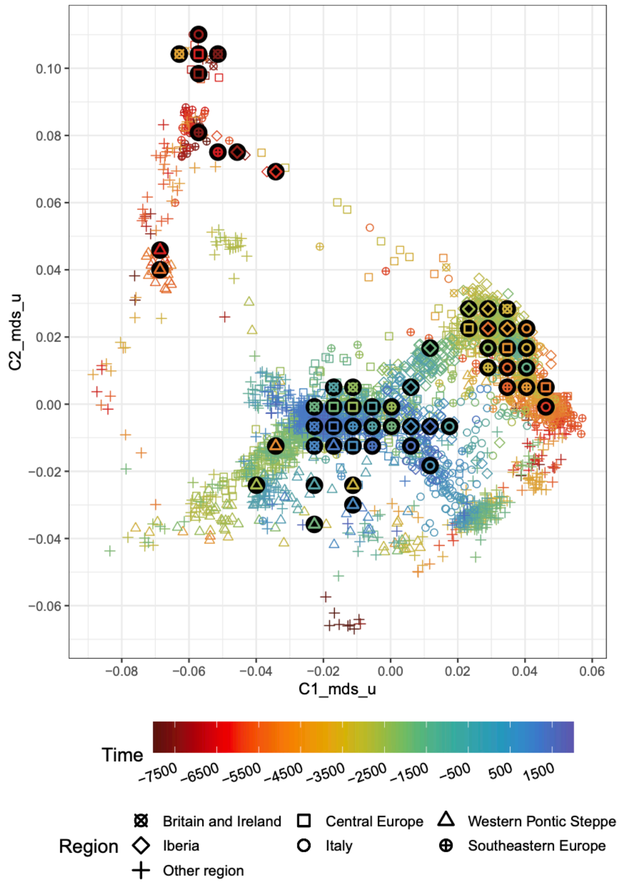

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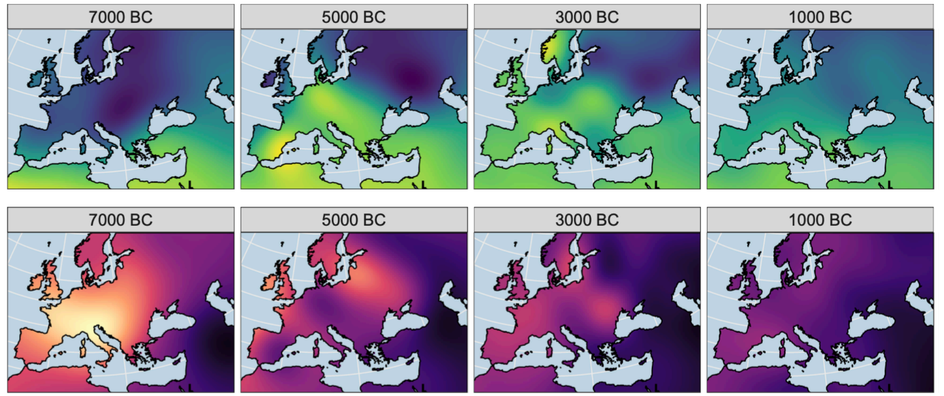

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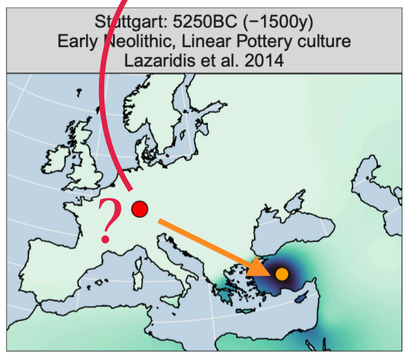

Schmid and Schiffels, PNAS 2023

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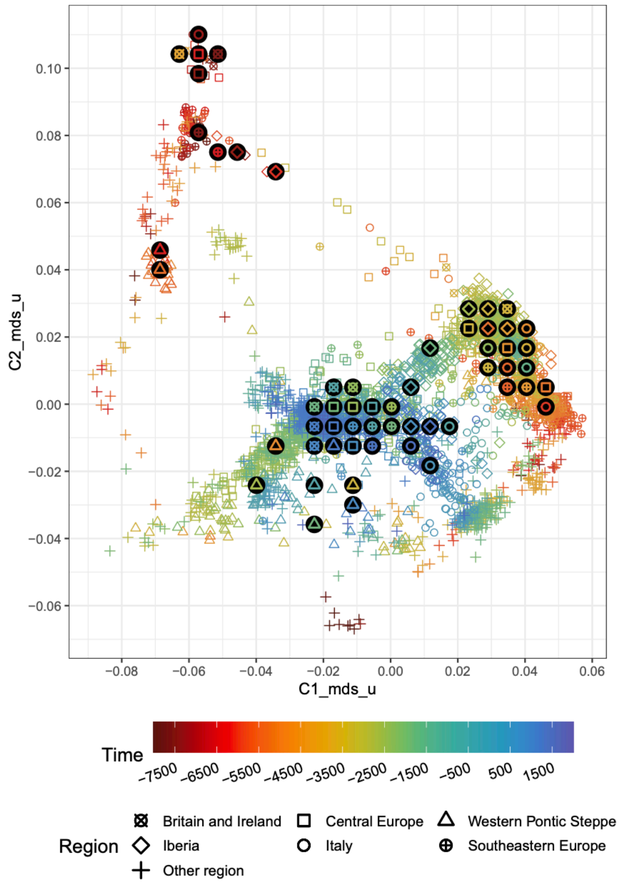

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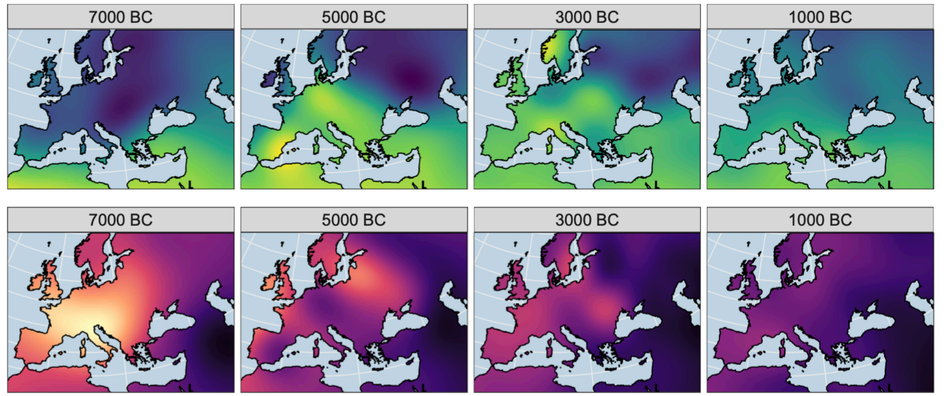

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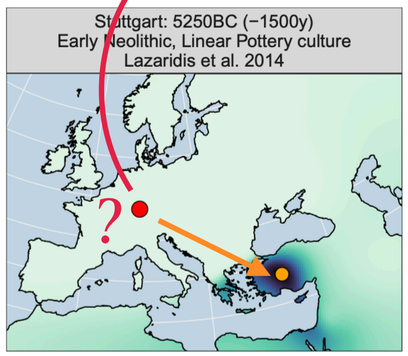
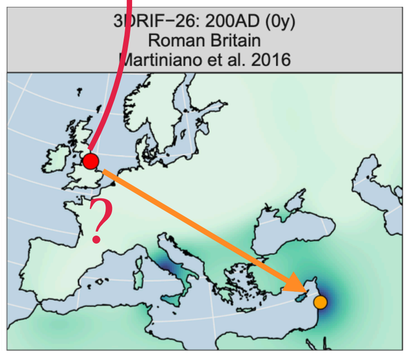
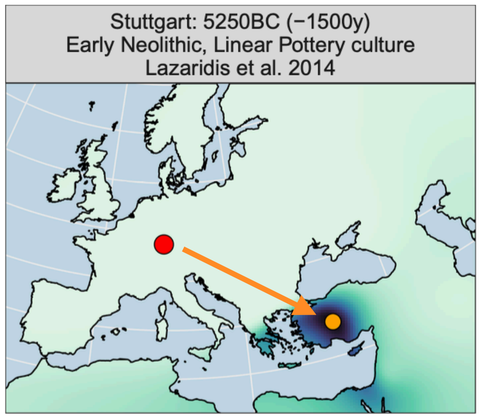




Schmid and Schiffels, PNAS 2023

A "global" summary of individual mobilities across time



aggregation of **lengths** and **directions** of many mobility vectors

Schmid and Schiffels, PNAS 2023

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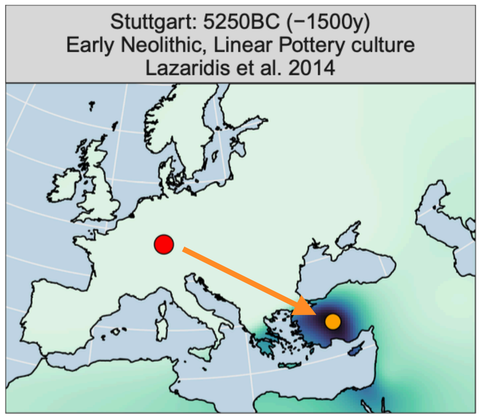

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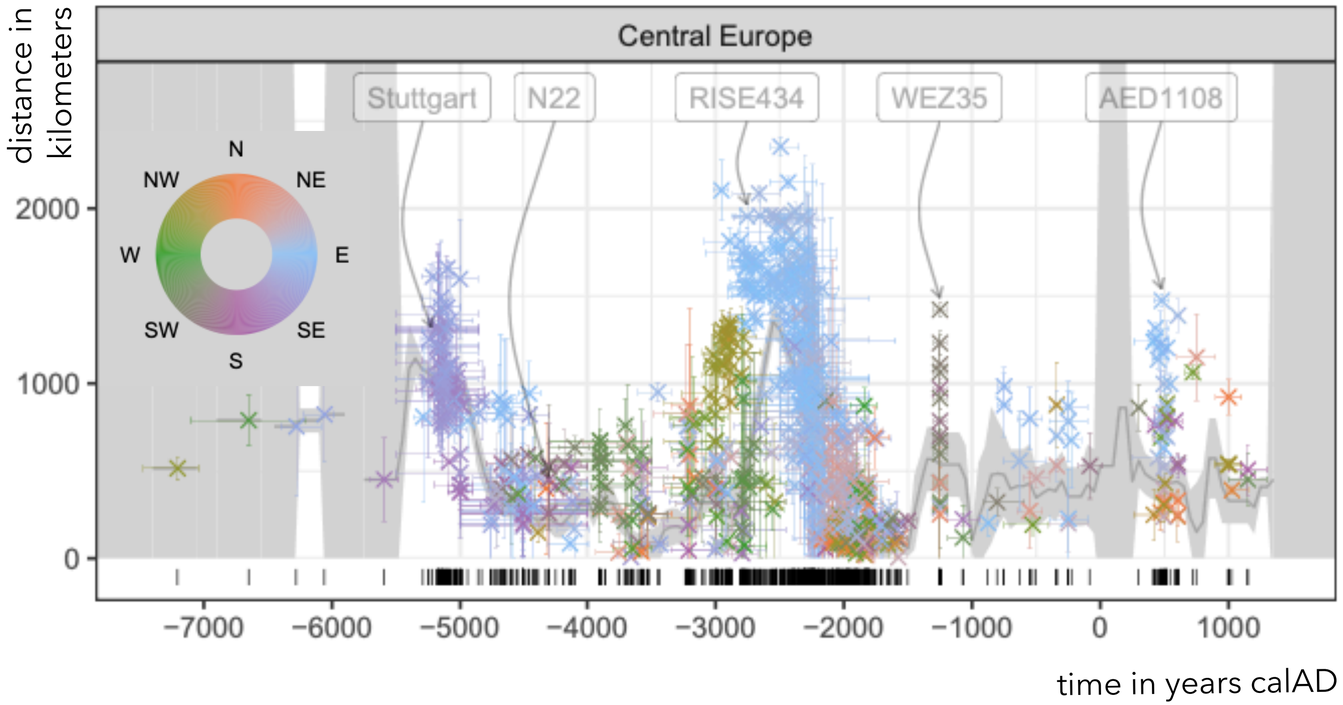

Schmid and Schiffels, PNAS 2023

www.slendr.net

slendr: a framework for spatio-temporal population genomic simulations on geographic landscapes

Martin Petr, Benjamin C. Haller, Peter L. Ralph, Fernando Racimo

(2023), bioRxiv, ver.5, peer-reviewed and recommended by PCI Evol Biol

https://doi.org/10.1101/2022.03.20.485041

PCI Evol Biol

https://peercommunityin.org/

slendr can simulate genomic data from...

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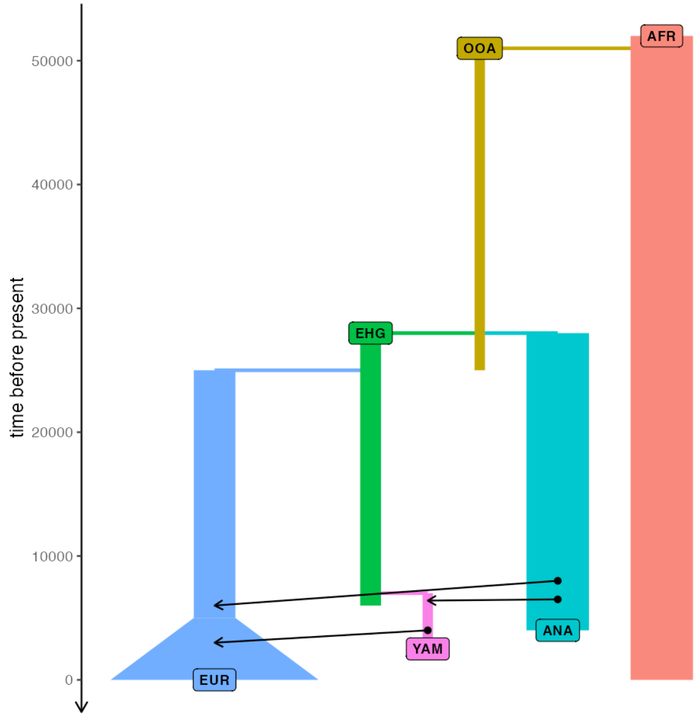
... traditional demographic models...



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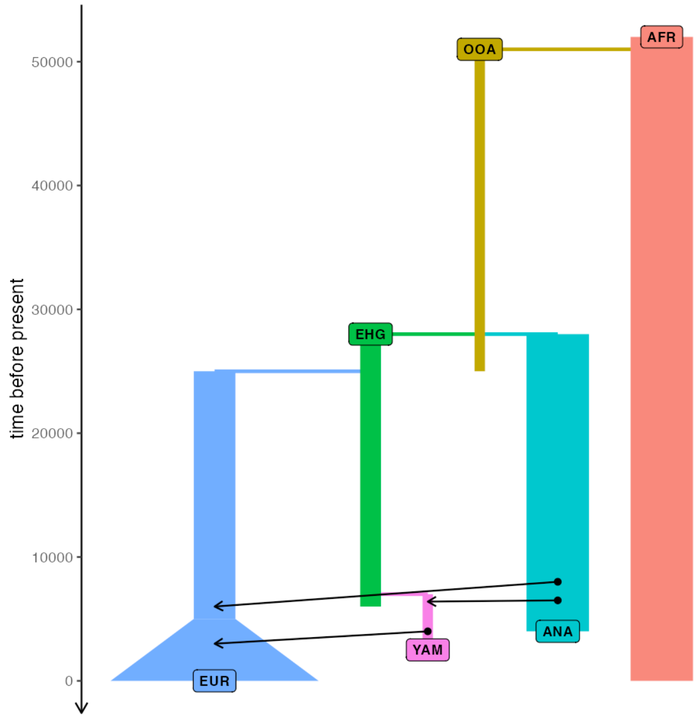
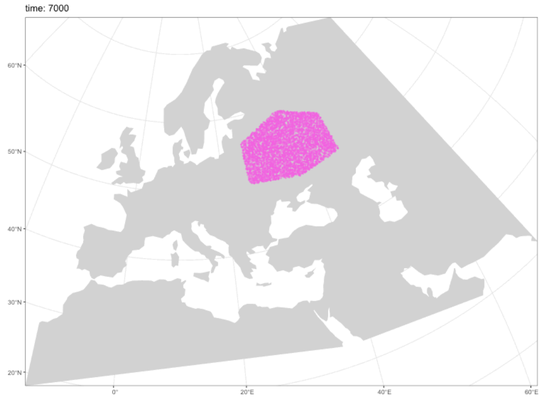
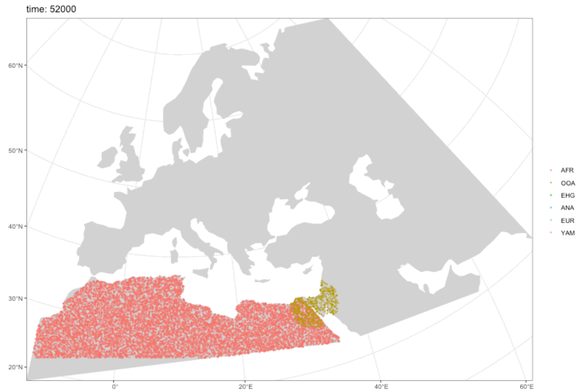


... but also explicitly spatial models!

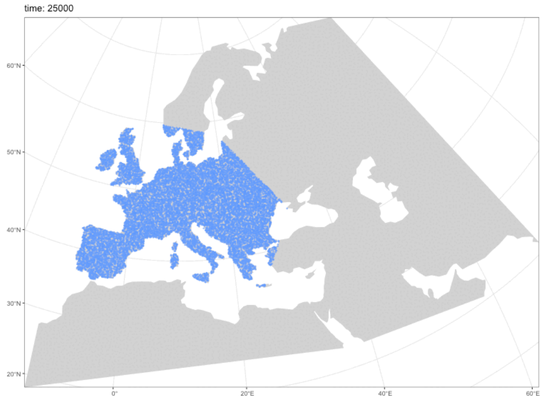
"farmer expansion"



"Yamnaya migration"



"Out-of-Africa migration"



"Europeans"

Tree sequence / Ancestral Recombination Graph (ARG)

tsinfer

Inferring whole-genome histories in large population datasets

Jerome Kelleher*, Yan Wong, Anthony W. Wohns, Chaimaa Fadil, Patrick K. Albers and Gil McVean

2019

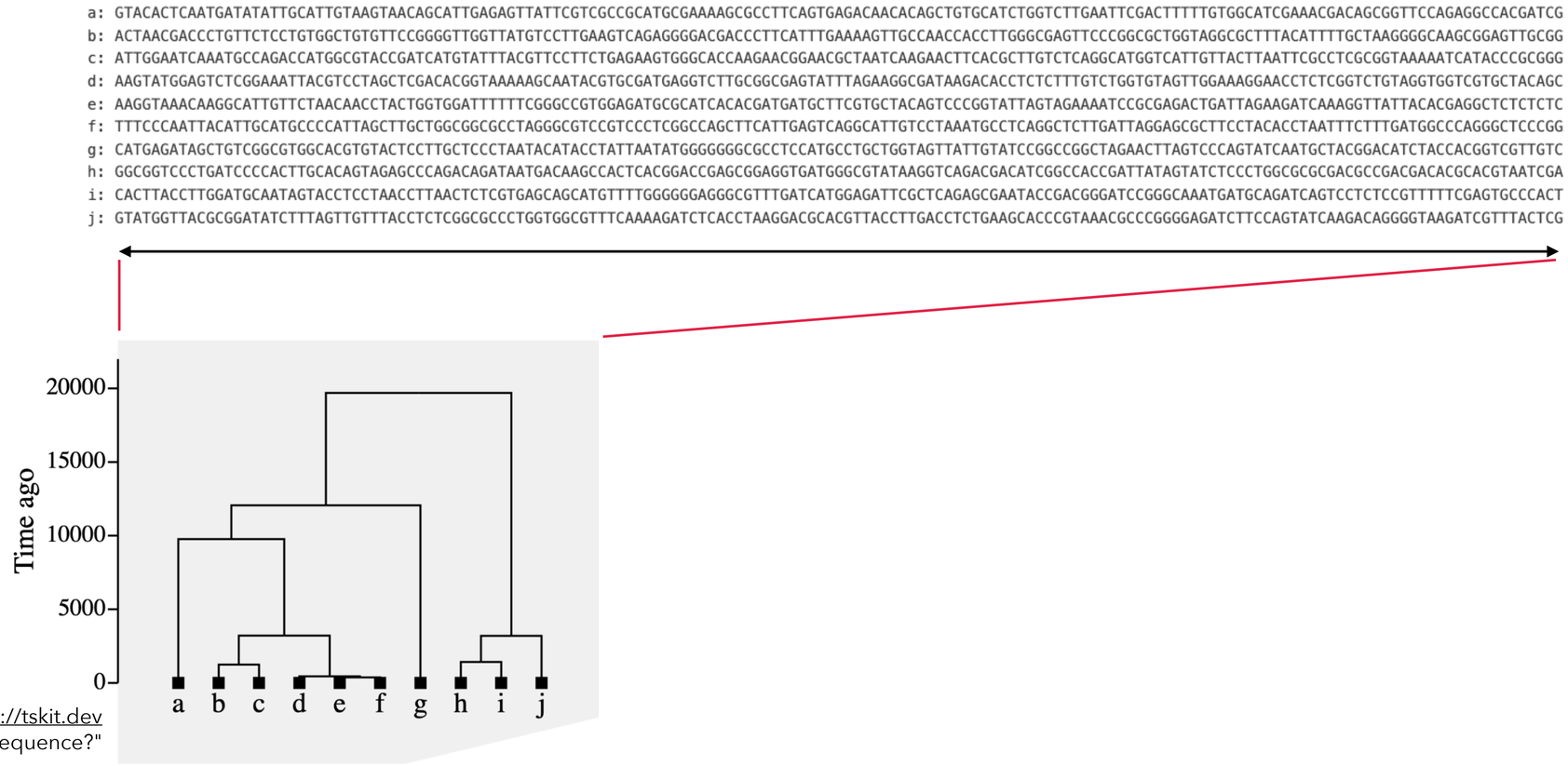
Relate

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

Leo Speidel[1], Marie Forest[2], Sinan Shi[1] and Simon R. Myers[1,3]*

2019

Tree sequence / Ancestral Recombination Graph (ARG)



trees from https://tskit.dev
"What is a tree sequence?"

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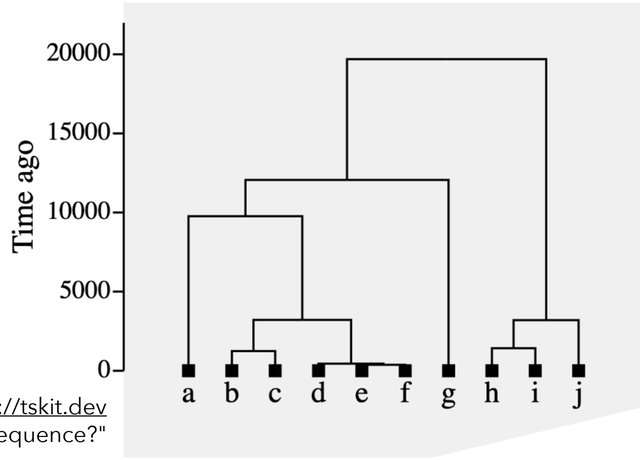

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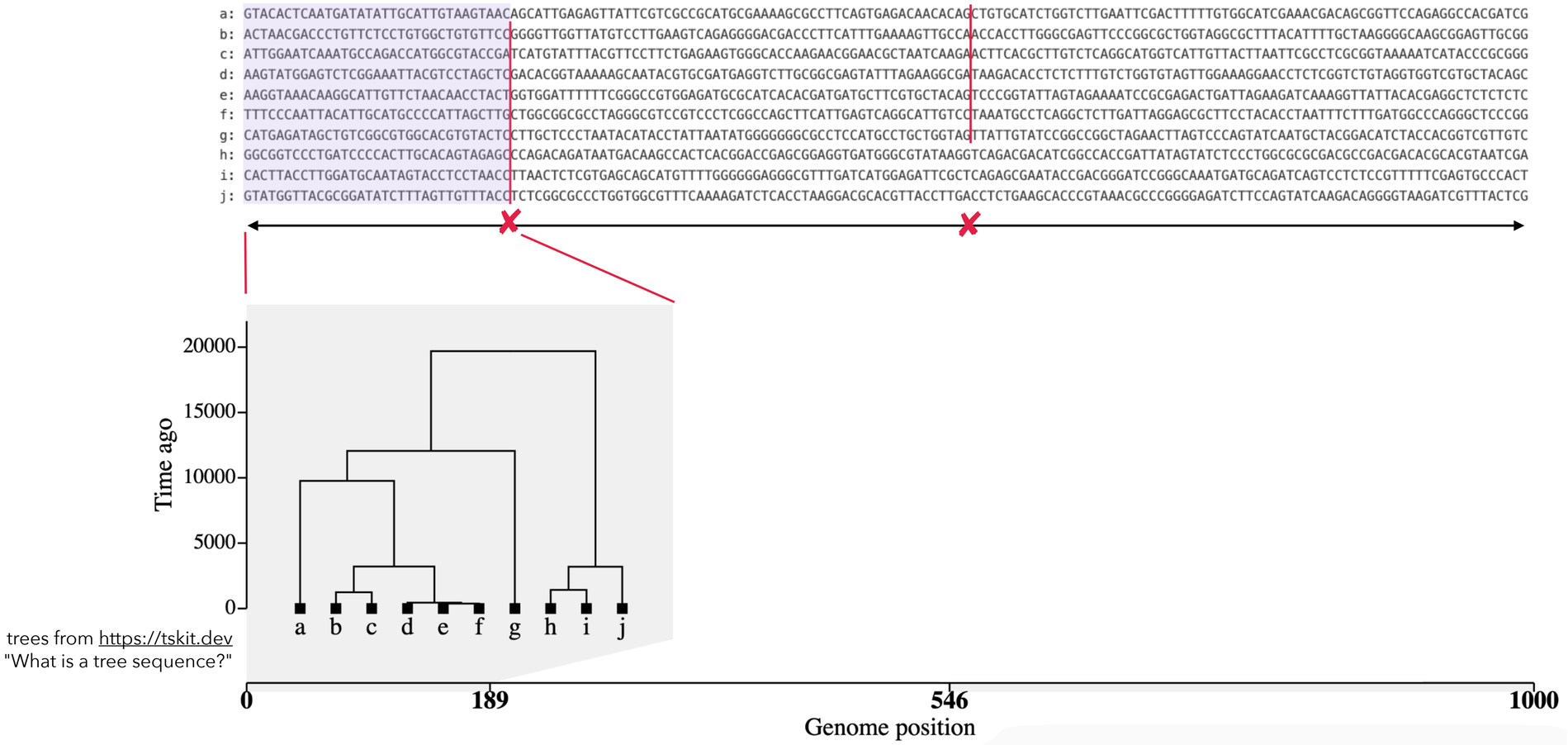

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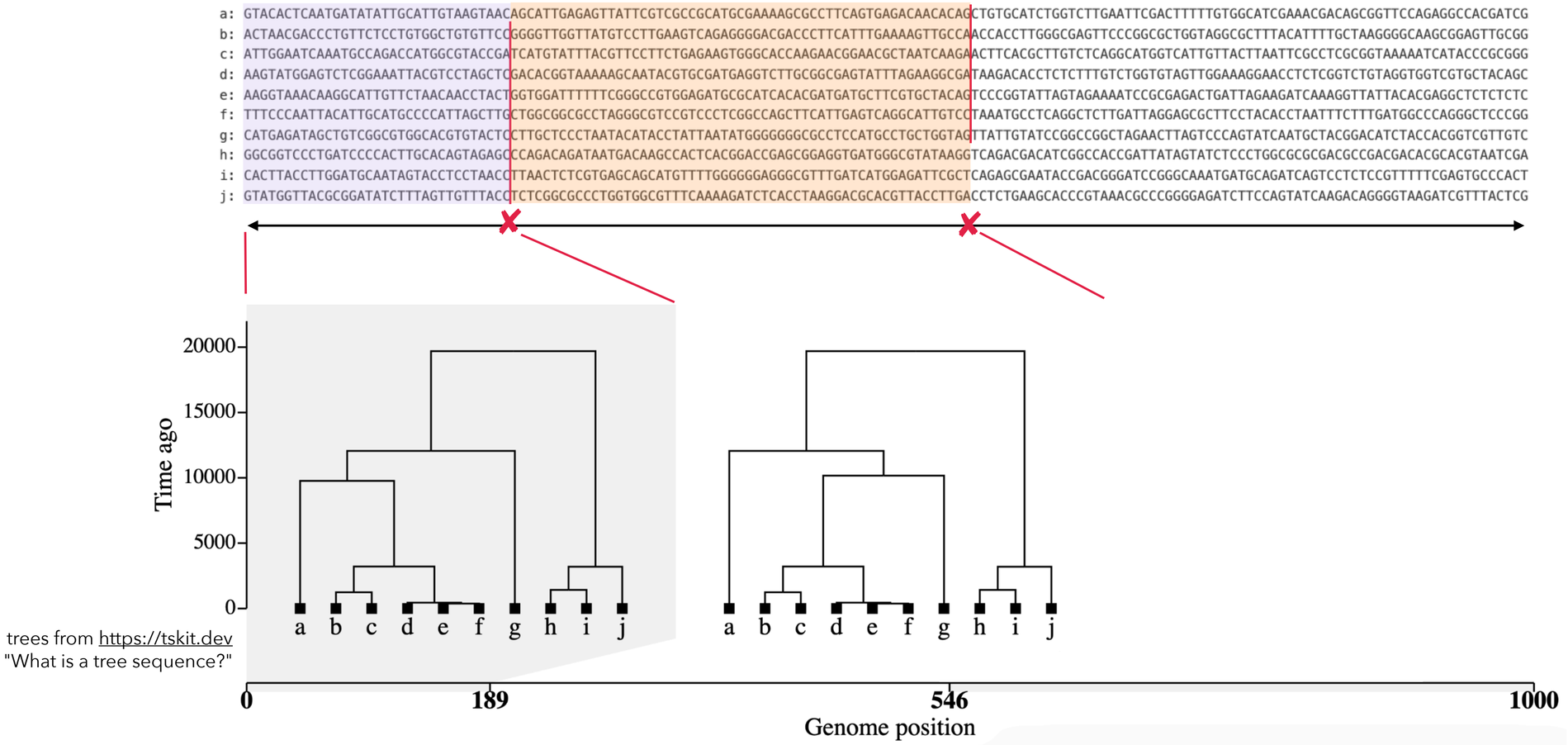
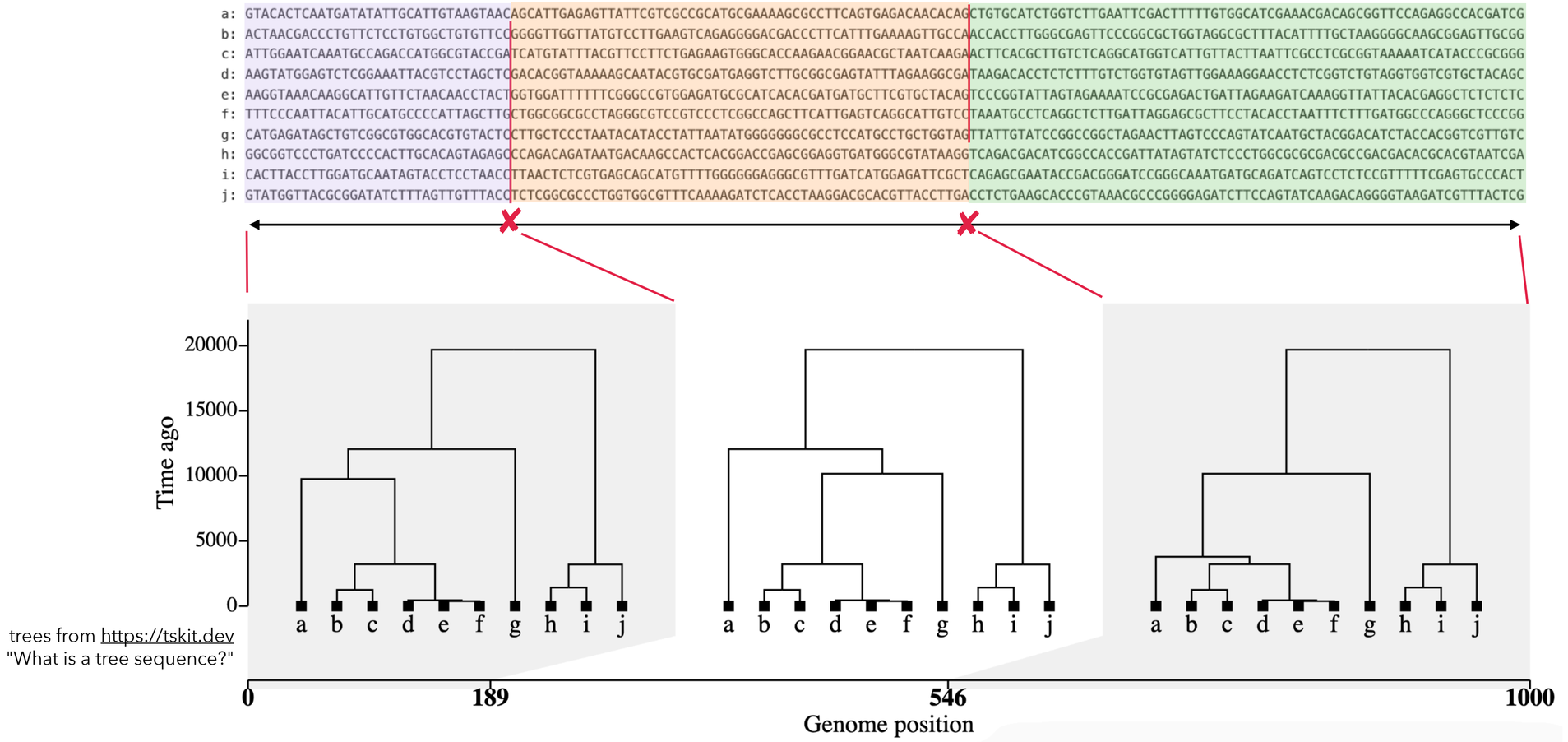


trees from https://tskit.dev
"What is a tree sequence?"

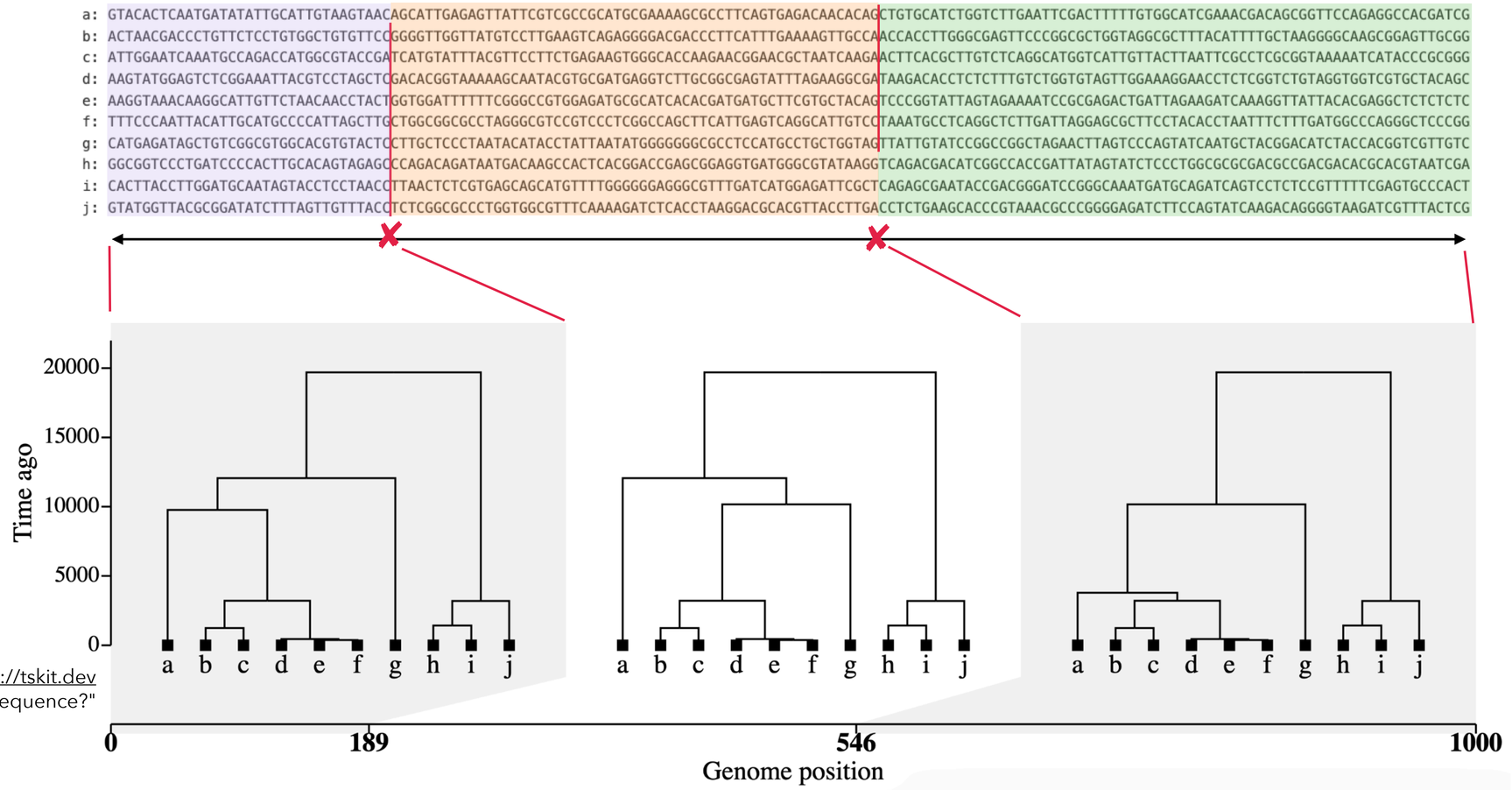
Tree sequence / Ancestral Recombination Graph (ARG)



trees from https://tskit.dev
"What is a tree sequence?"

Recombination produces a sequence of (correlated) trees along the genome

Tree sequence / Ancestral Recombination Graph (ARG)



trees from https://tskit.dev
"What is a tree sequence?"

A tree sequence represents

everything knowable about an evolutionary process.

What we (usually) have

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	HG00096	HG00099	HG00101
12	60076	.	A	C	100	PASS	.	GT	1|0	0|0	0|0
12	60252	.	A	G	100	PASS	.	GT	0|0	0|0	0|1
12	60317	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	60344	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60383	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	60405	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60474	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	60614	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60628	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60654	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61021	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61107	.	G	T	100	PASS	.	GT	0|0	0|0	0|0
12	61172	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61220	.	G	A	100	PASS	.	GT	0|0	0|0	0|1
12	61258	.	C	T	100	PASS	.	GT	0|0	0|0	0|1
12	61272	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	61329	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61341	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	61368	.	C	T	100	PASS	.	GT	0|0	0|1	0|1
12	61392	.	T	A	100	PASS	.	GT	0|0	0|0	0|0
12	61405	.	G	C	100	PASS	.	GT	0|0	0|0	0|0
12	61411	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	61416	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
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12	61516	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61552	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61604	.	T	G	100	PASS	.	GT	0|0	0|0	0|0
12	61687	.	G	A	100	PASS	.	GT	1|0	0|1	0|1
12	61700	.	C	T	100	PASS	.	GT	0|0	0|0	0|0

What we (usually) have

positions along a chromosome

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	HG00096	HG00099	HG00101
12	60076	.	A	C	100	PASS	.	GT	1|0	0|0	0|0
12	60252	.	A	G	100	PASS	.	GT	0|0	0|0	0|1
12	60317	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	60344	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60383	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	60405	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60474	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	60614	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60628	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60654	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61021	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
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12	61172	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
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12	61258	.	C	T	100	PASS	.	GT	0|0	0|0	0|1
12	61272	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	61329	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61341	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	61368	.	C	T	100	PASS	.	GT	0|0	0|1	0|1
12	61392	.	T	A	100	PASS	.	GT	0|0	0|0	0|0
12	61405	.	G	C	100	PASS	.	GT	0|0	0|0	0|0
12	61411	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	61416	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61422	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61476	.	C	G	100	PASS	.	GT	0|0	0|0	0|0
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12	61516	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61552	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61604	.	T	G	100	PASS	.	GT	0|0	0|0	0|0
12	61687	.	G	A	100	PASS	.	GT	1|0	0|1	0|1
12	61700	.	C	T	100	PASS	.	GT	0|0	0|0	0|0

What we (usually) have

positions along a chromosome

									ind. #1	ind. #2	ind. #3	...
#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	HG00096	HG00099	HG00101	
12	60076	.	A	C	100	PASS	.	GT	1|0	0|0	0|0	
12	60252	.	A	G	100	PASS	.	GT	0|0	0|0	0|1	
12	60317	.	C	T	100	PASS	.	GT	0|0	0|0	0|0	
12	60344	.	C	A	100	PASS	.	GT	0|0	0|0	0|0	
12	60383	.	G	A	100	PASS	.	GT	0|0	0|0	0|0	
12	60405	.	T	C	100	PASS	.	GT	0|0	0|0	0|0	
12	60474	.	G	A	100	PASS	.	GT	0|0	0|1	0|1	
12	60614	.	C	A	100	PASS	.	GT	0|0	0|0	0|0	
12	60628	.	T	C	100	PASS	.	GT	0|0	0|0	0|0	
12	60654	.	G	A	100	PASS	.	GT	0|0	0|0	0|0	
12	61021	.	C	T	100	PASS	.	GT	0|0	0|0	0|0	
12	61107	.	G	T	100	PASS	.	GT	0|0	0|0	0|0	
12	61172	.	G	A	100	PASS	.	GT	0|0	0|0	0|0	
12	61220	.	G	A	100	PASS	.	GT	0|0	0|0	0|1	
12	61258	.	C	T	100	PASS	.	GT	0|0	0|0	0|1	
12	61272	.	T	C	100	PASS	.	GT	0|0	0|0	0|0	
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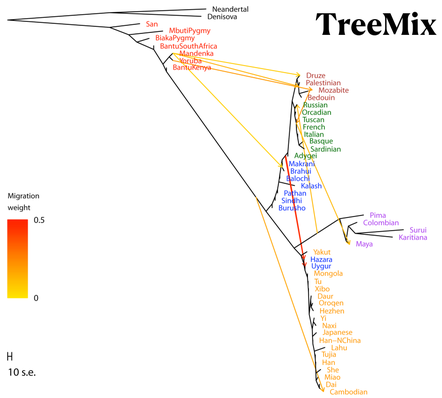
12	61341	.	G	A	100	PASS	.	GT	0|0	0|1	0|1	
12	61368	.	C	T	100	PASS	.	GT	0|0	0|1	0|1	
12	61392	.	T	A	100	PASS	.	GT	0|0	0|0	0|0	
12	61405	.	G	C	100	PASS	.	GT	0|0	0|0	0|0	
12	61411	.	C	A	100	PASS	.	GT	0|0	0|0	0|0	
12	61416	.	G	A	100	PASS	.	GT	0|0	0|0	0|0	
12	61422	.	C	T	100	PASS	.	GT	0|0	0|0	0|0	
12	61476	.	C	G	100	PASS	.	GT	0|0	0|0	0|0	
12	61510	.	G	A	100	PASS	.	GT	0|0	0|0	0|0	
12	61516	.	C	T	100	PASS	.	GT	0|0	0|0	0|0	
12	61552	.	C	T	100	PASS	.	GT	0|0	0|0	0|0	
12	61604	.	T	G	100	PASS	.	GT	0|0	0|0	0|0	
12	61687	.	G	A	100	PASS	.	GT	1|0	0|1	0|1	
12	61700	.	C	T	100	PASS	.	GT	0|0	0|0	0|0	

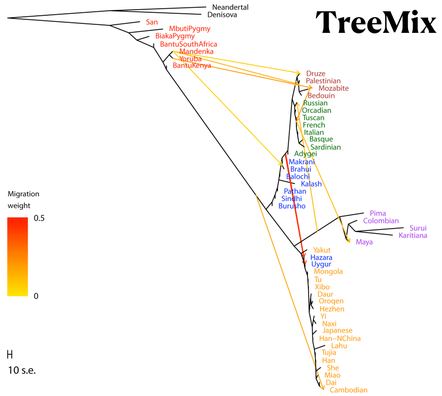
What we (usually) *want*

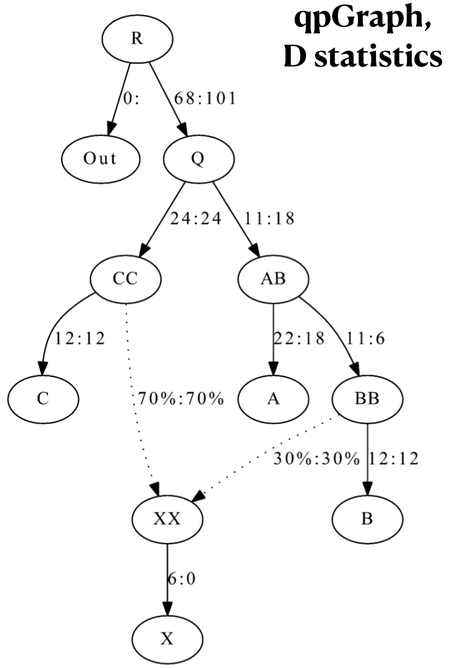
- estimate split times between populations



What we (usually) *want*

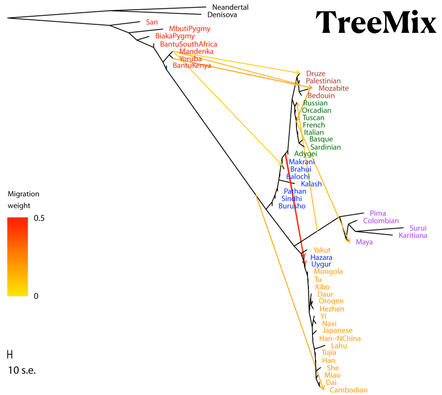
- estimate split times between populations
- investigate admixture hypotheses

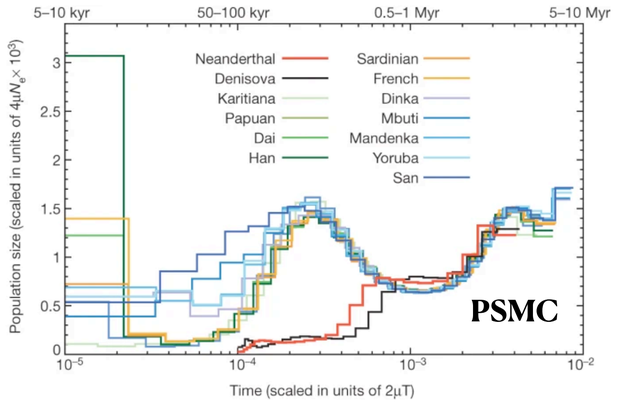


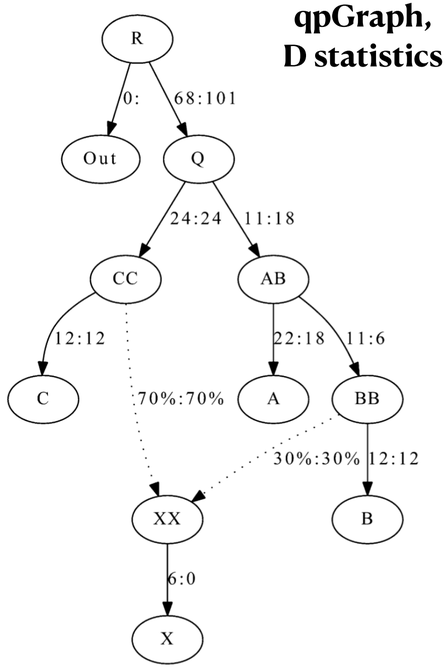


What we (usually) *want*

- estimate split times between populations
- investigate admixture hypotheses
- infer population sizes changes over time







What we (usually) *want*

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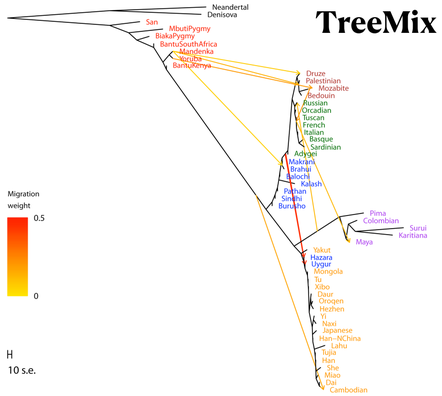
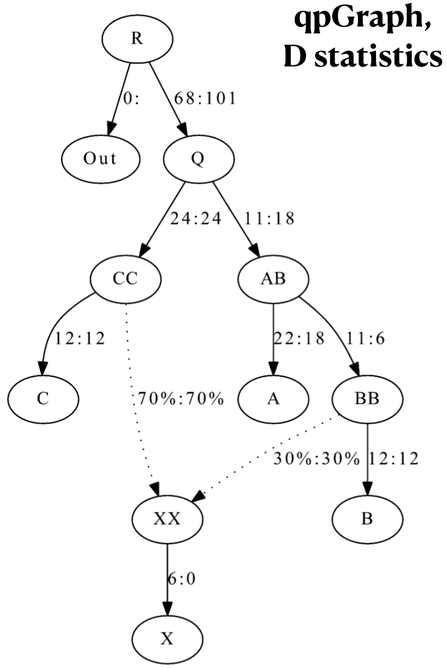
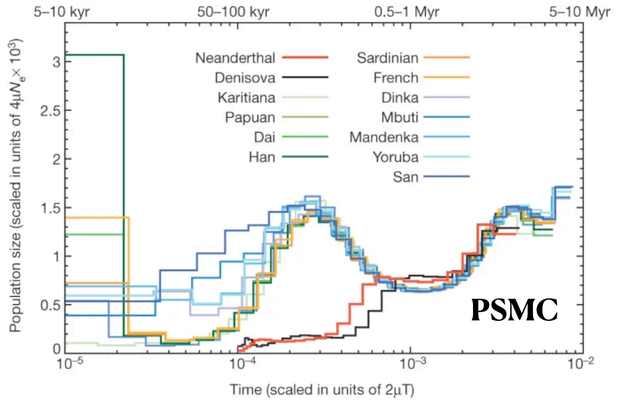
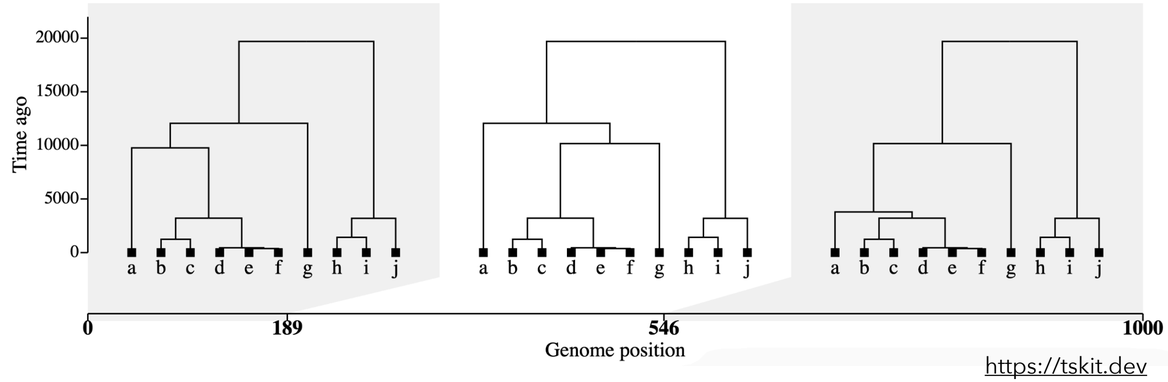
These are all features of a real (but hidden) genealogical process.









https://tskit.dev
"What is a tree sequence?"

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#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	HG00096	HG00099	HG00101
12	60076	.	A	C	100	PASS	.	GT	1|0	0|0	0|0
12	60252	.	A	G	100	PASS	.	GT	0|0	0|0	0|1
12	60317	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	60344	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60383	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	60405	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60474	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	60614	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60628	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60654	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61021	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61107	.	G	T	100	PASS	.	GT	0|0	0|0	0|0
12	61172	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61220	.	G	A	100	PASS	.	GT	0|0	0|0	0|1
12	61258	.	C	T	100	PASS	.	GT	0|0	0|0	0|1
12	61272	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	61329	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61341	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	61368	.	C	T	100	PASS	.	GT	0|0	0|1	0|1
12	61392	.	T	A	100	PASS	.	GT	0|0	0|0	0|0
12	61405	.	G	C	100	PASS	.	GT	0|0	0|0	0|0
12	61411	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	61416	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61422	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
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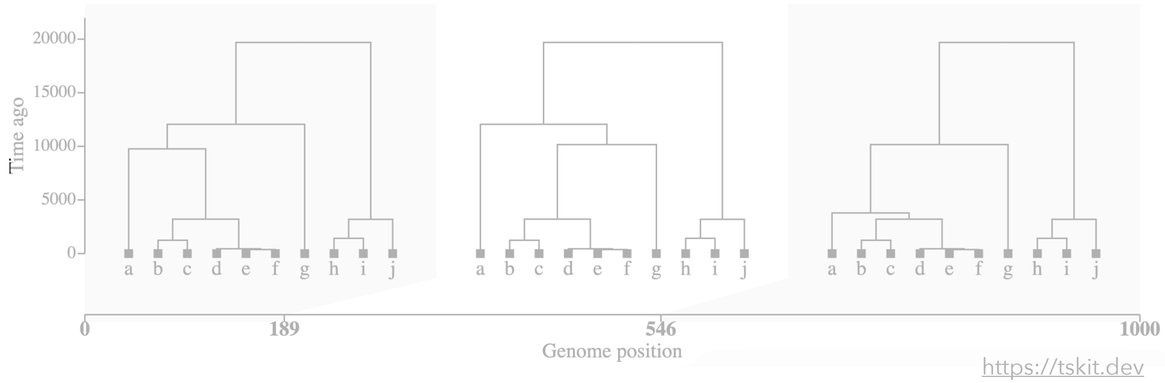
12	61510	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61516	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61552	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61604	.	T	G	100	PASS	.	GT	0|0	0|0	0|0
12	61687	.	G	A	100	PASS	.	GT	1|0	0|1	0|1
12	61700	.	C	T	100	PASS	.	GT	0|0	0|0	0|0



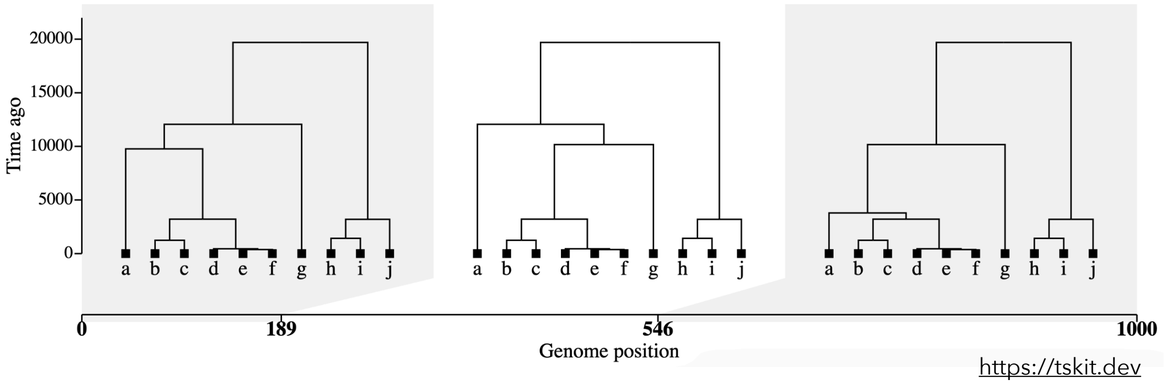
https://tskit.dev
"What is a tree sequence?"

What we (usually) *want*

- estimate split times between populations
- investigate admixture hypotheses
- infer population sizes changes over time

These are all features of a real (but hidden) genealogical process.

If we have a tree sequence, we get direct answers almost "for free".



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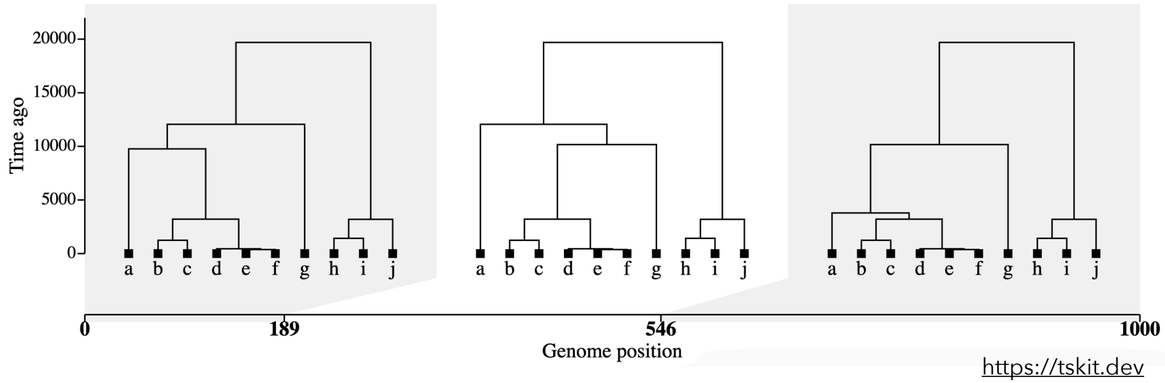
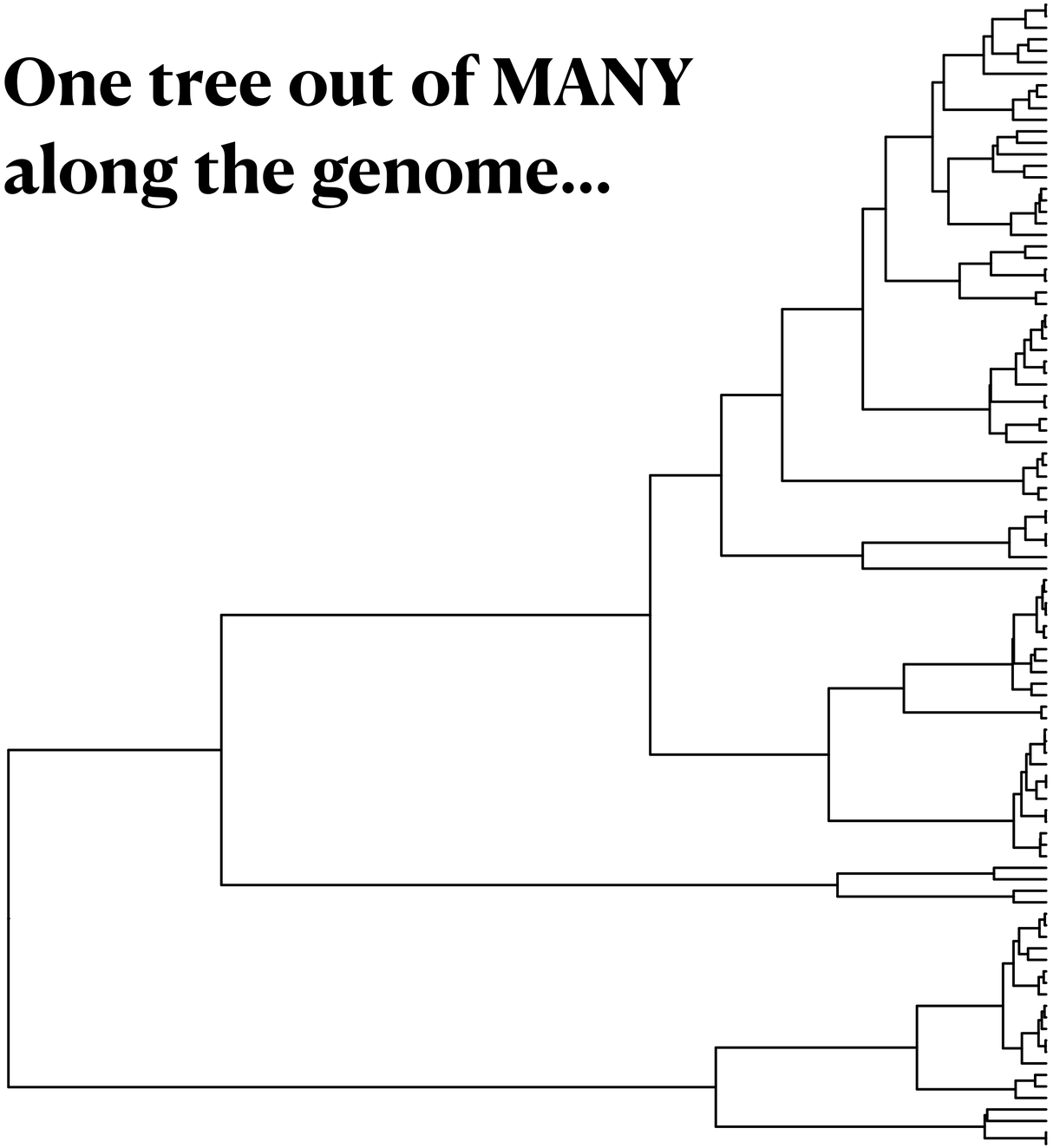


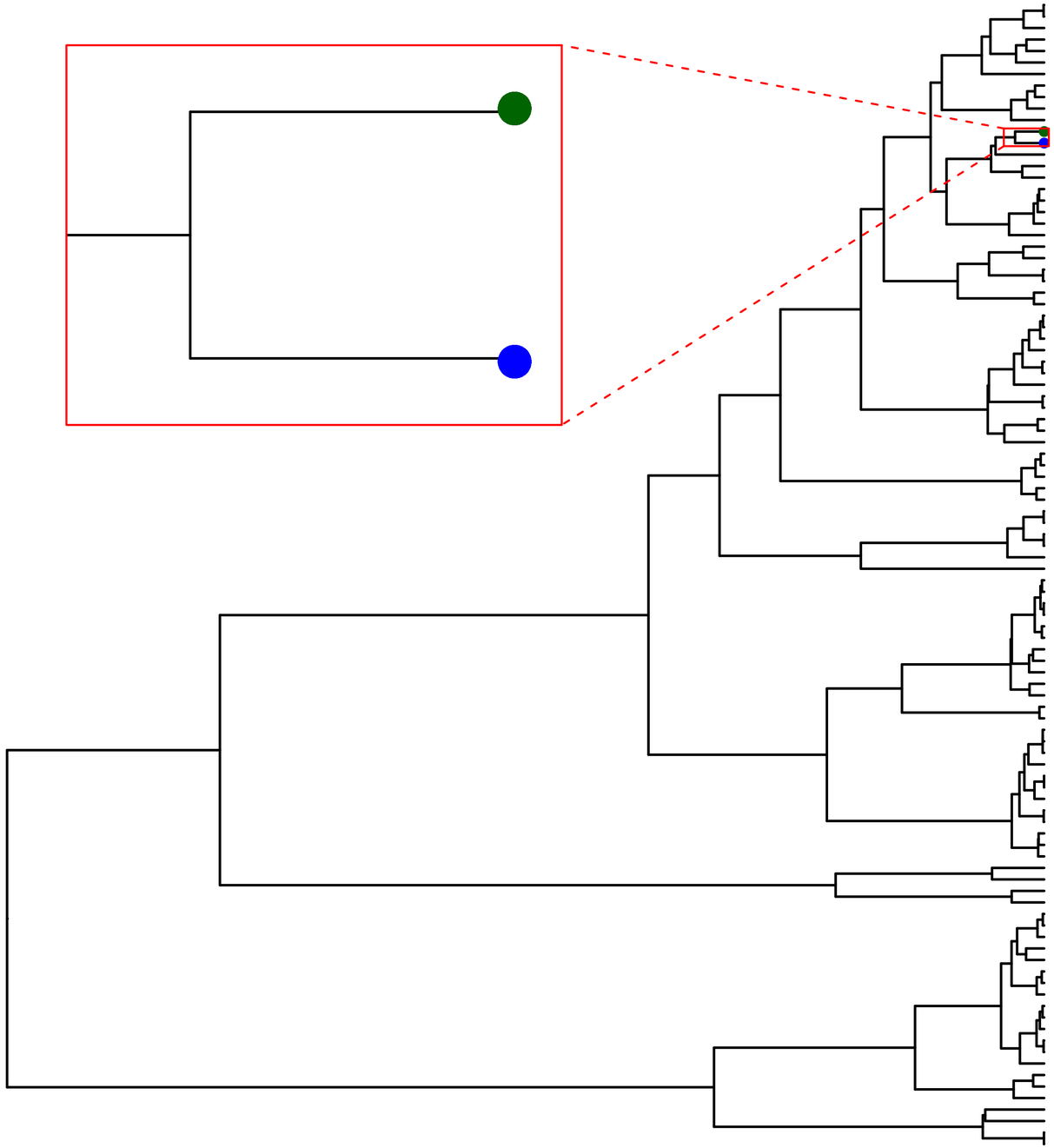
https://tskit.dev
"What is a tree sequence?"

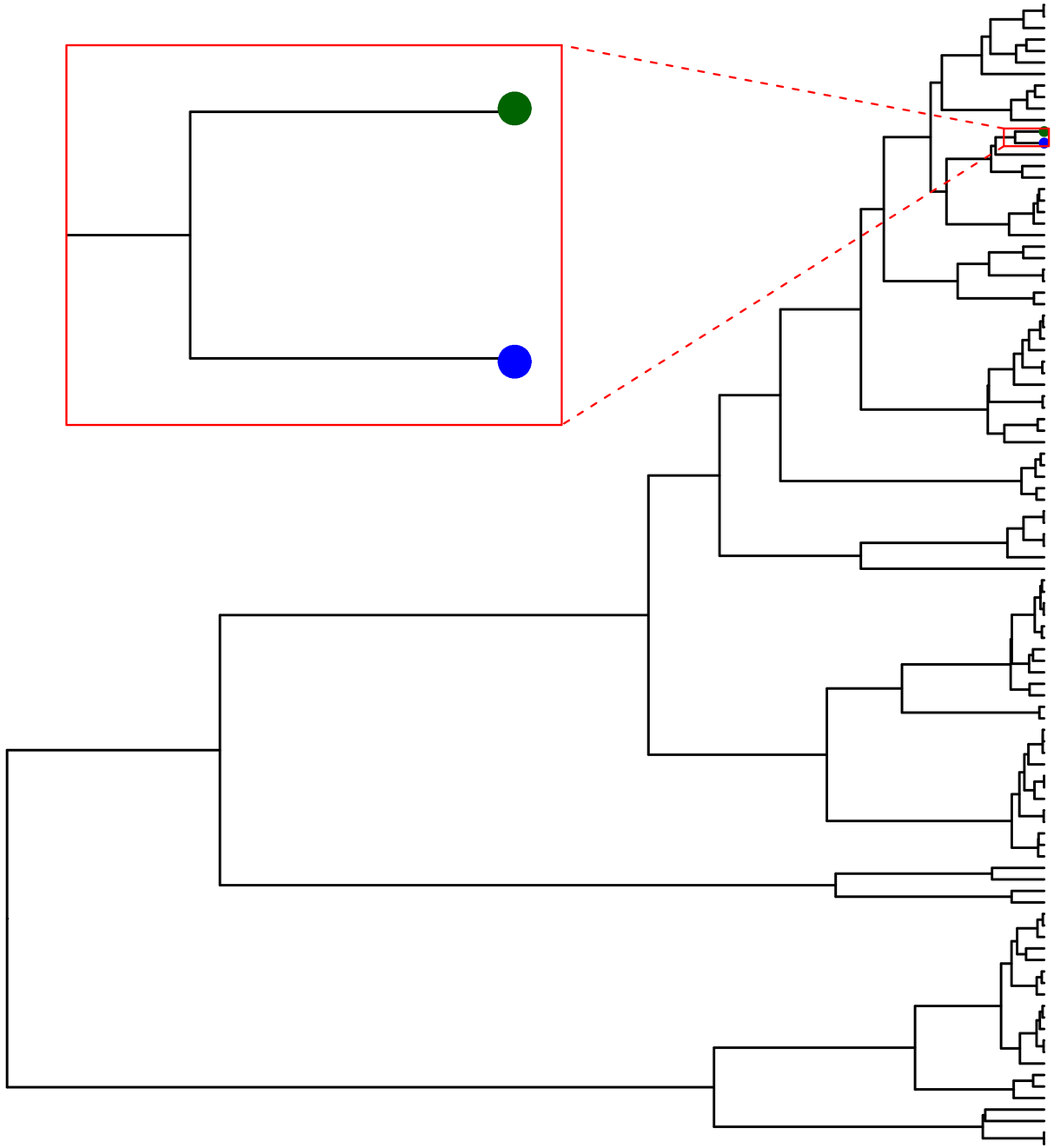
[... although the tree sequence must first be inferred from real data.]

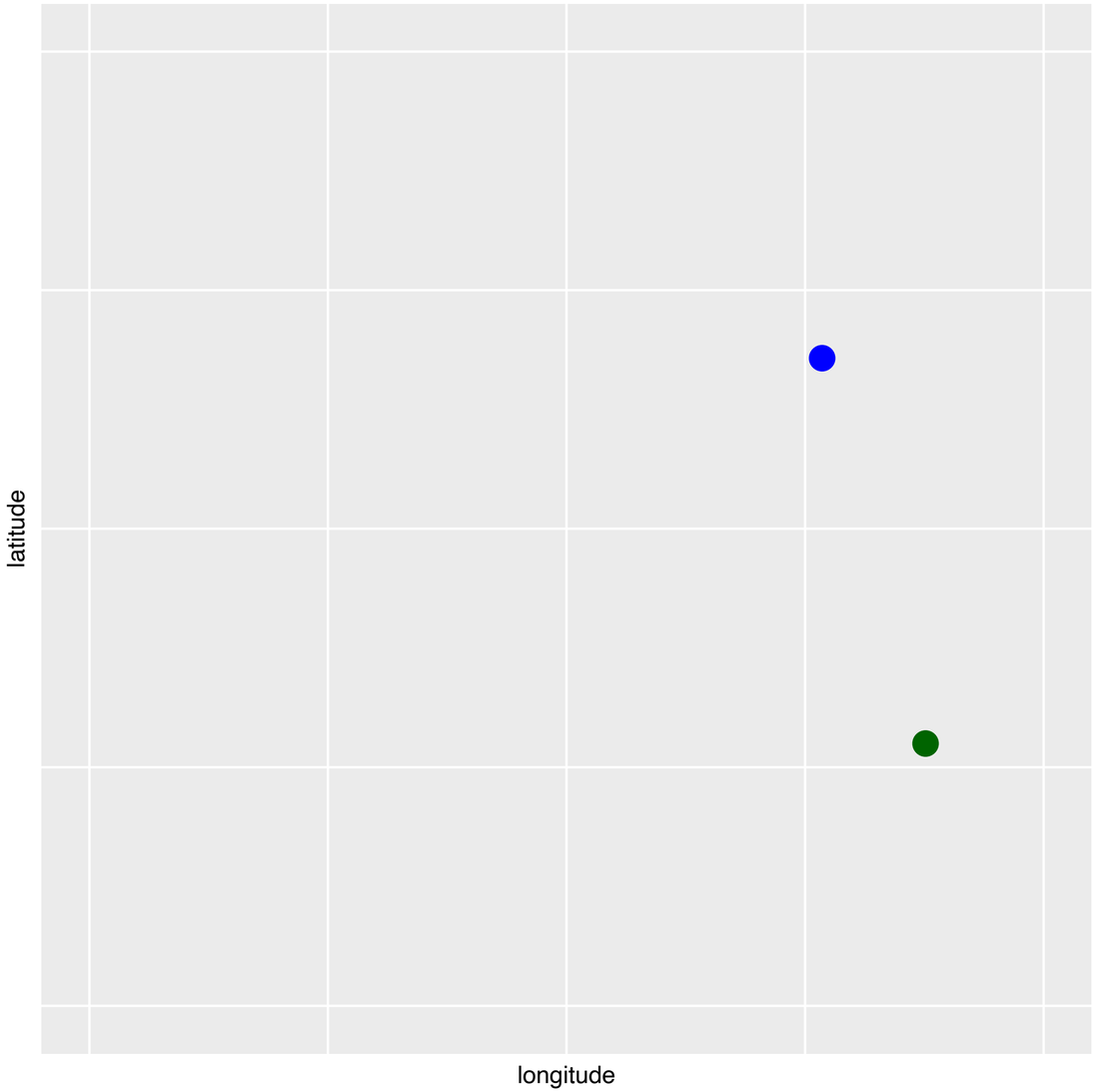

Tree sequences will
push spatial inference
to the next level.

One tree out of MANY along the genome...





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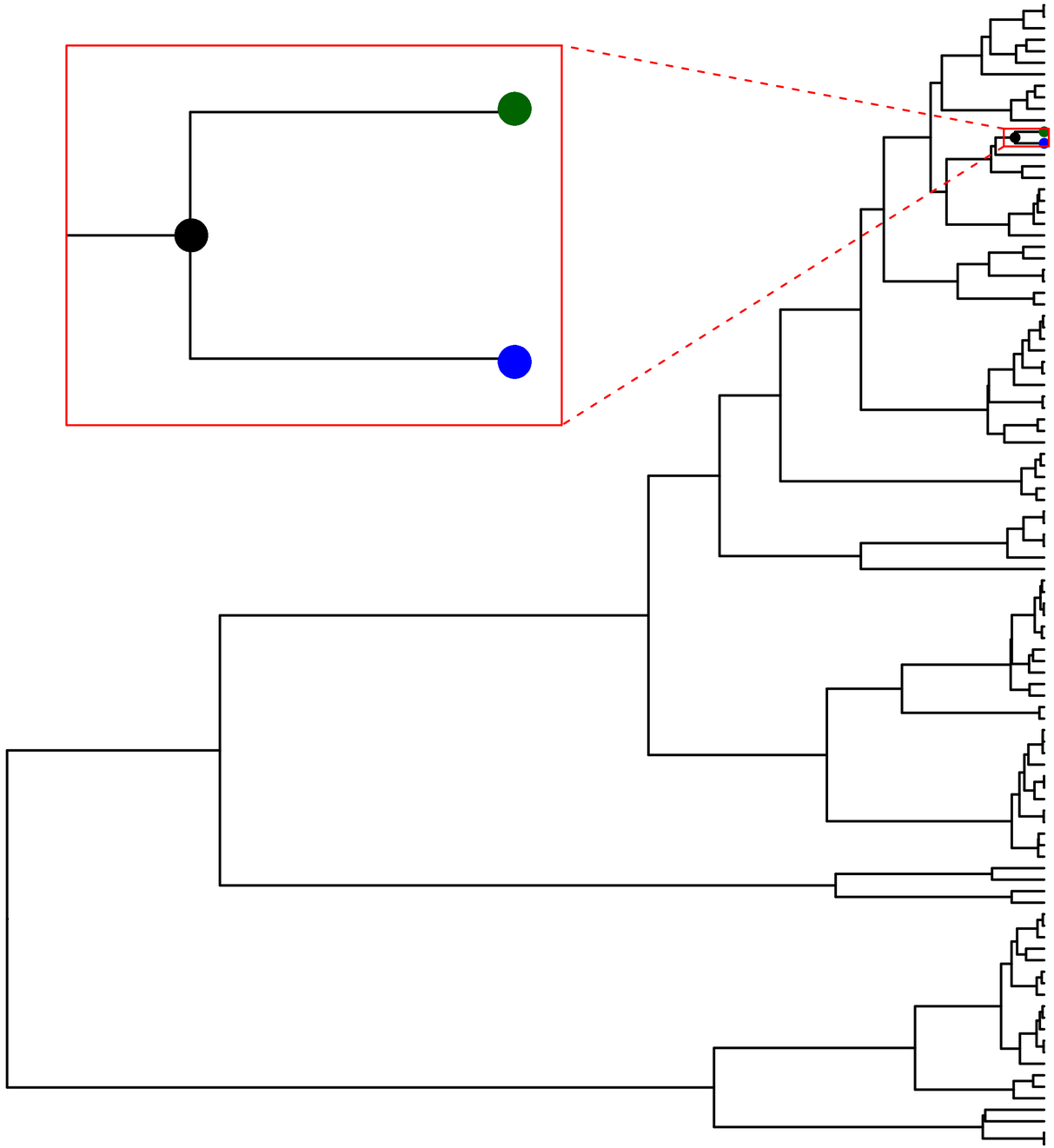
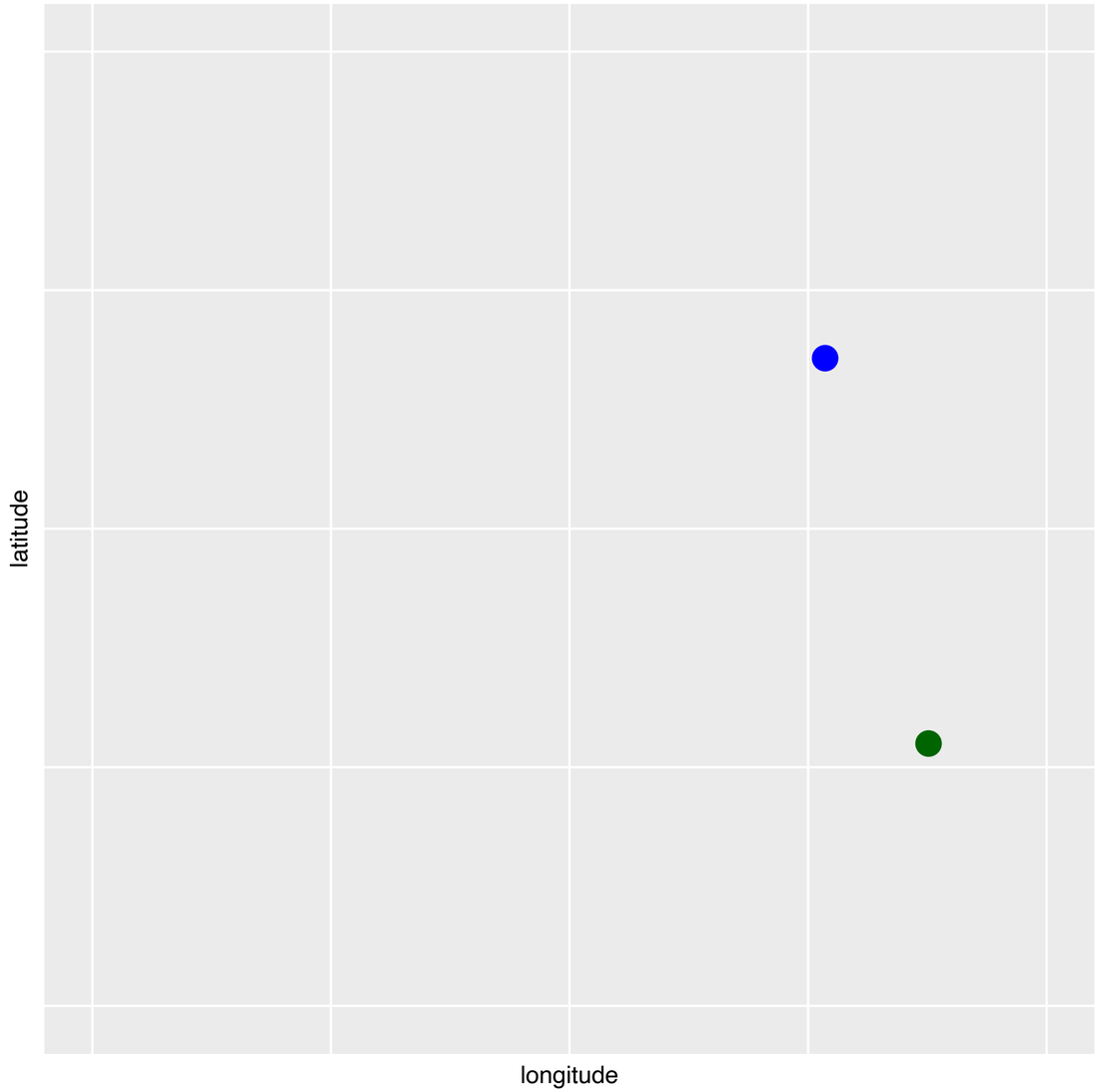
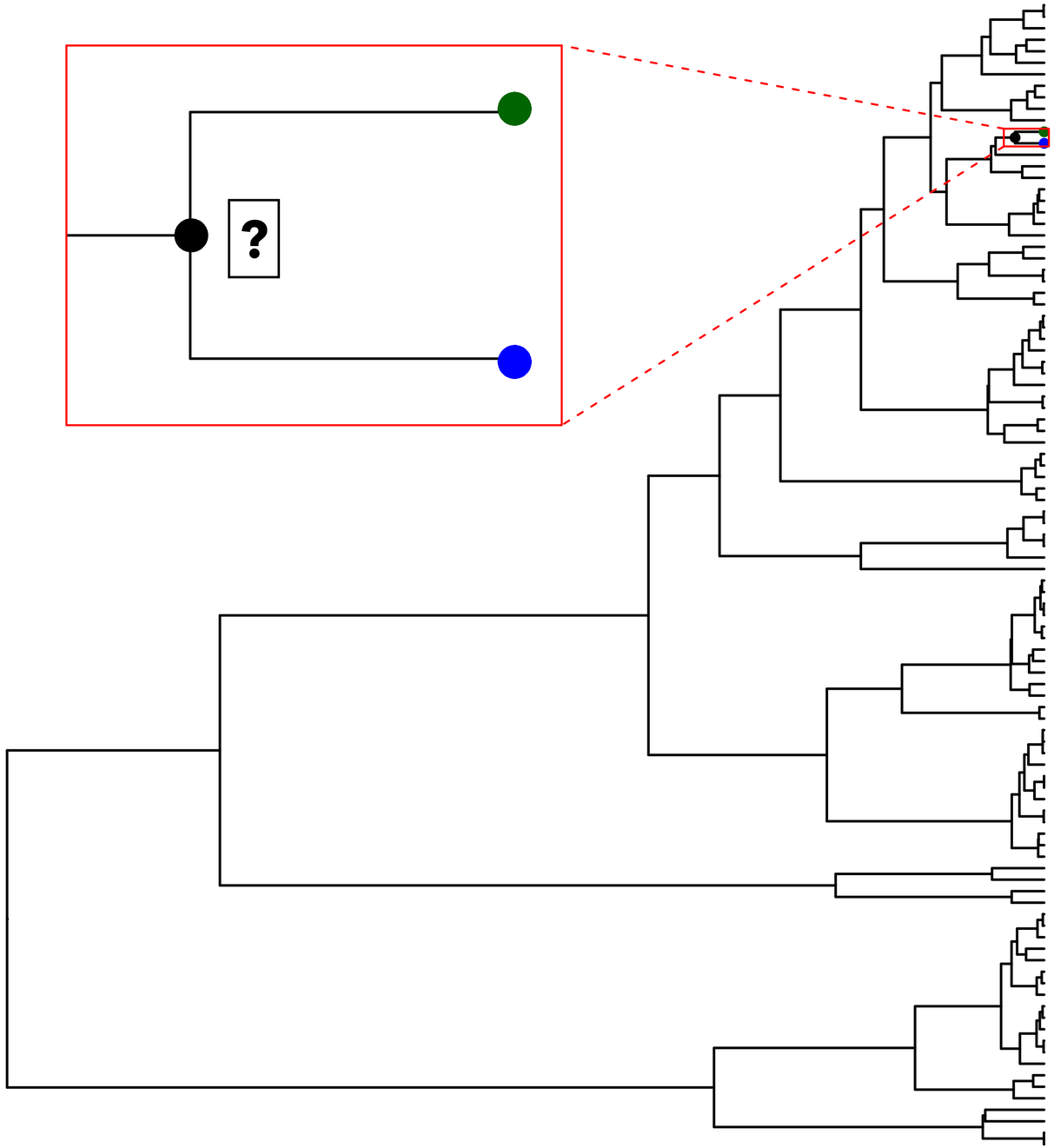
longitude




latitude
longitude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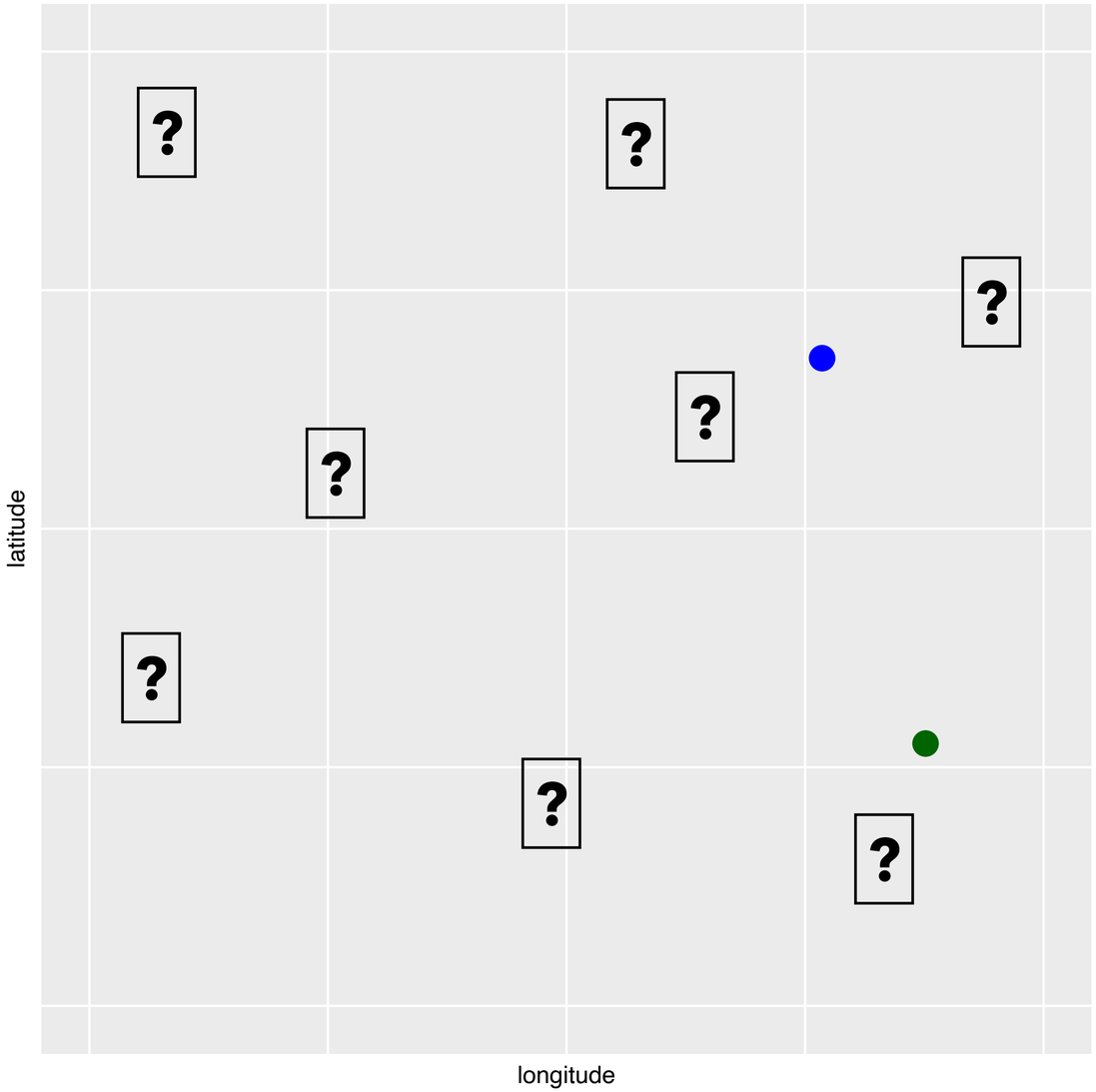
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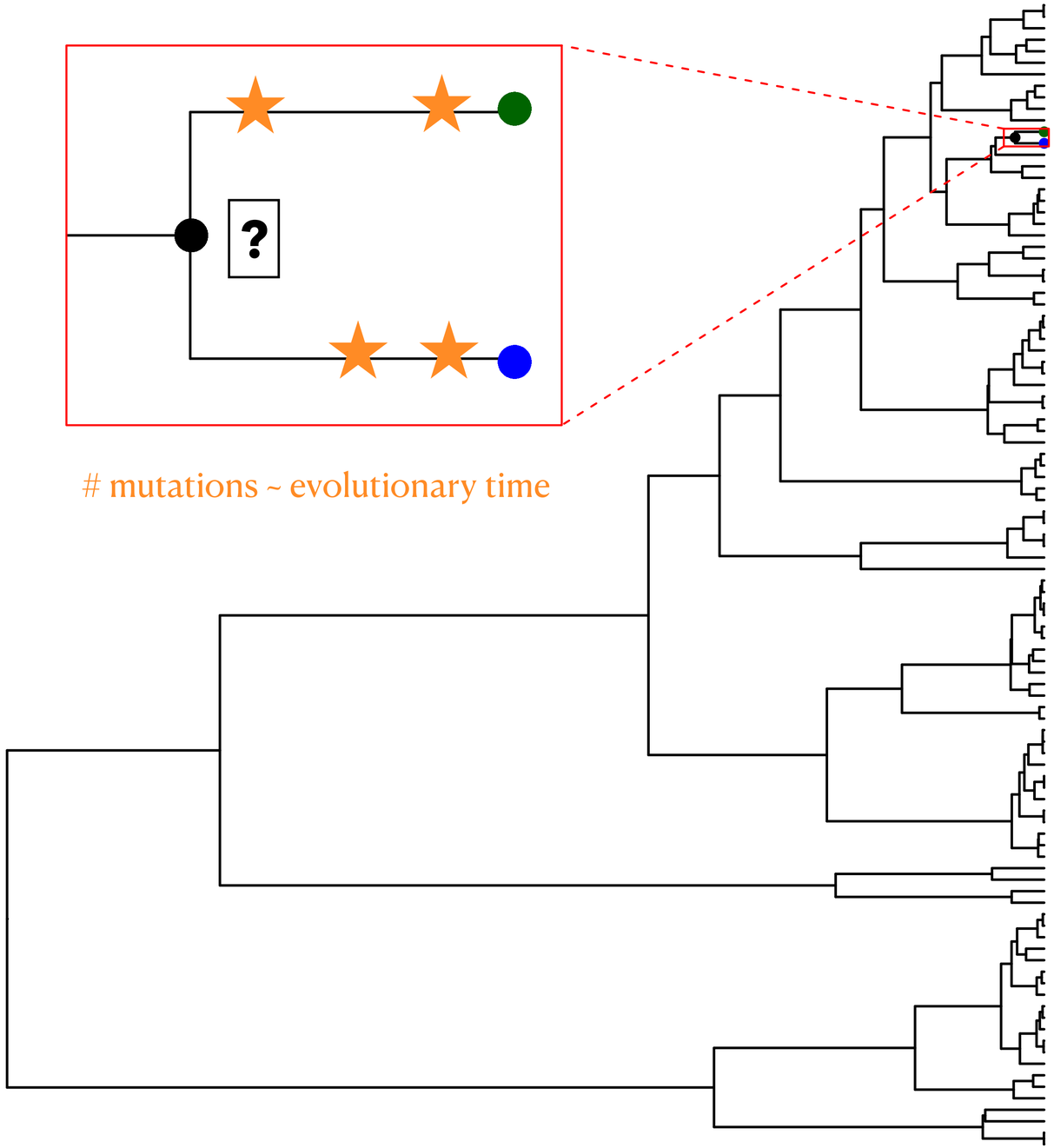
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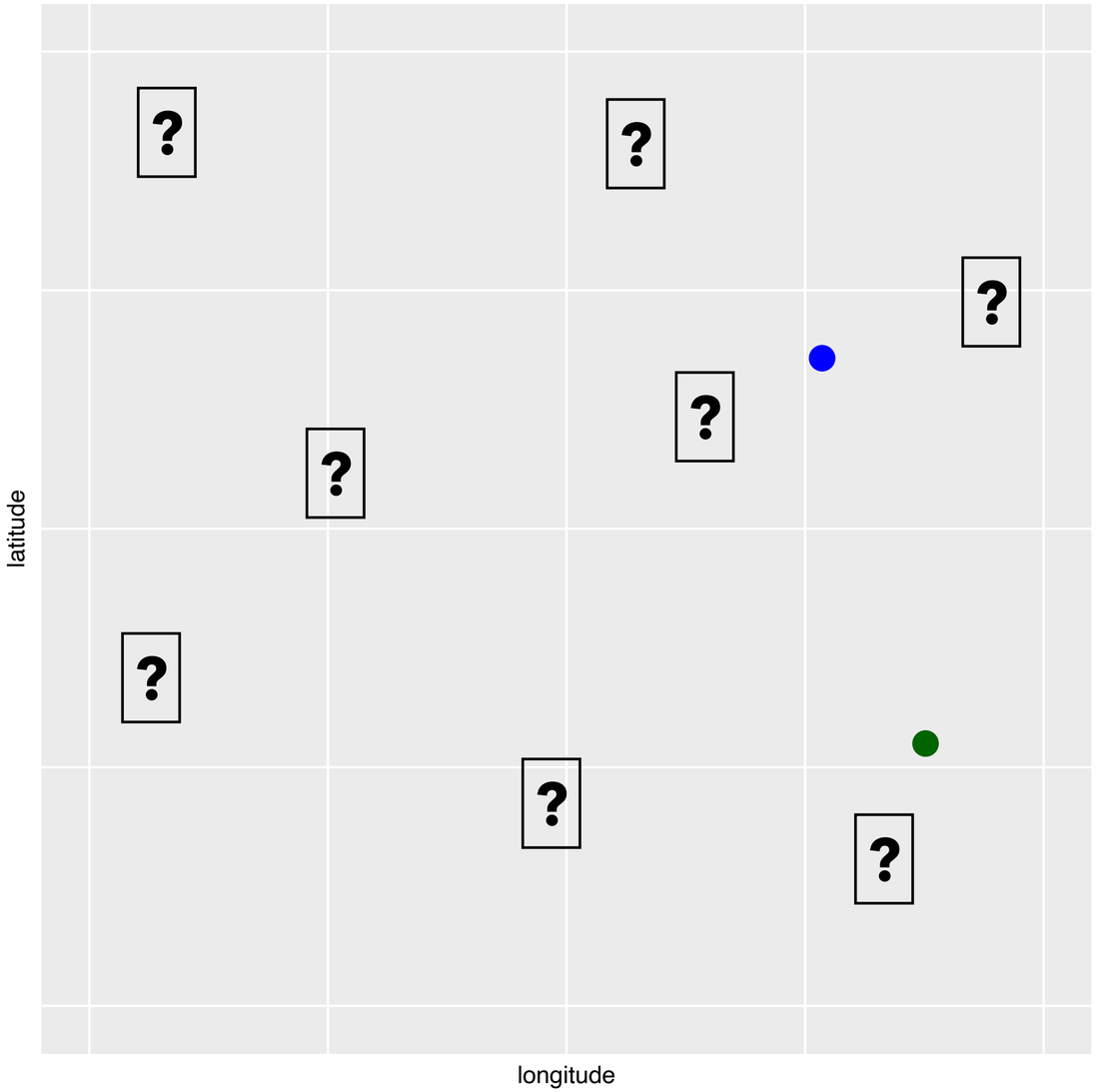
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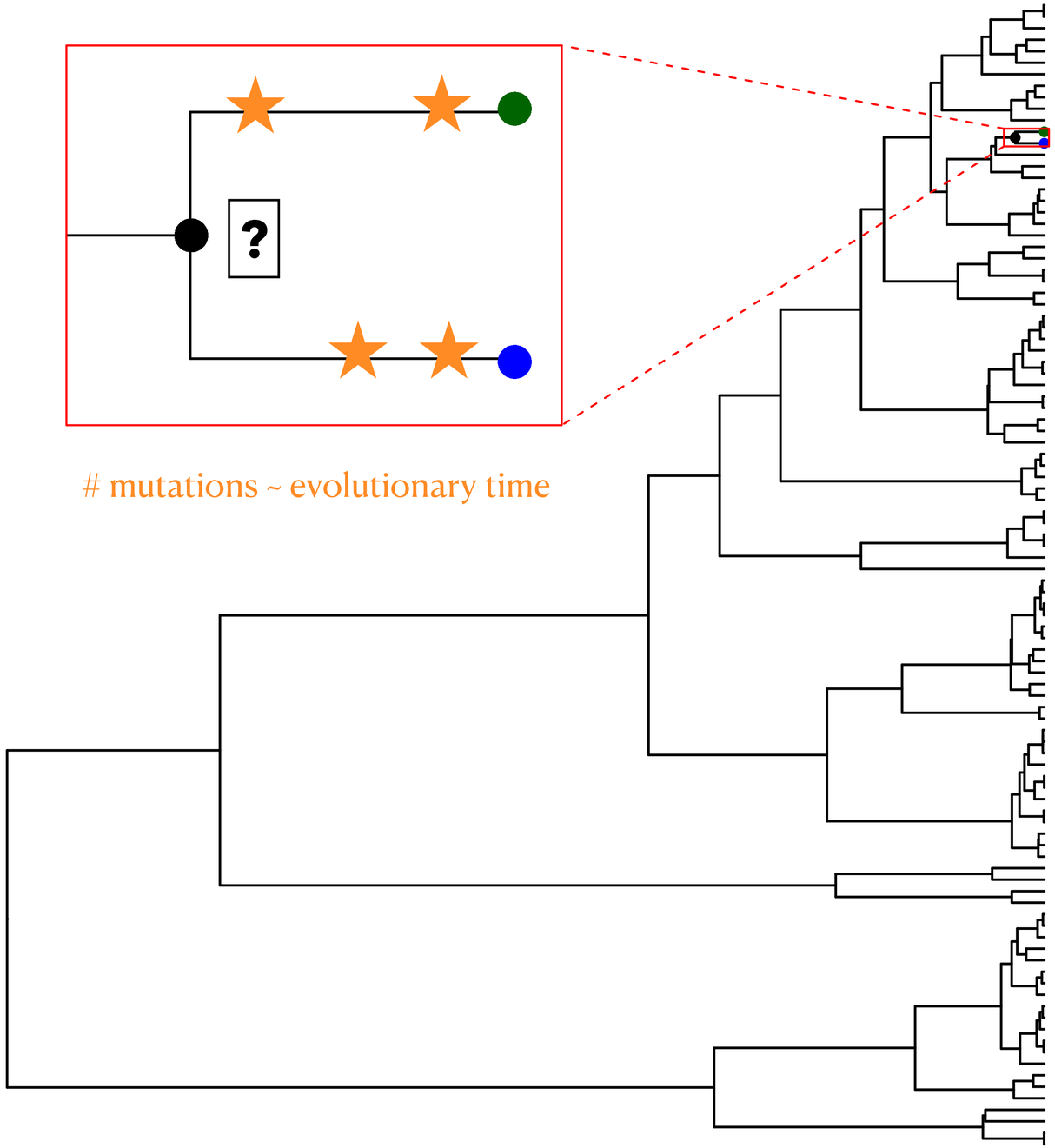
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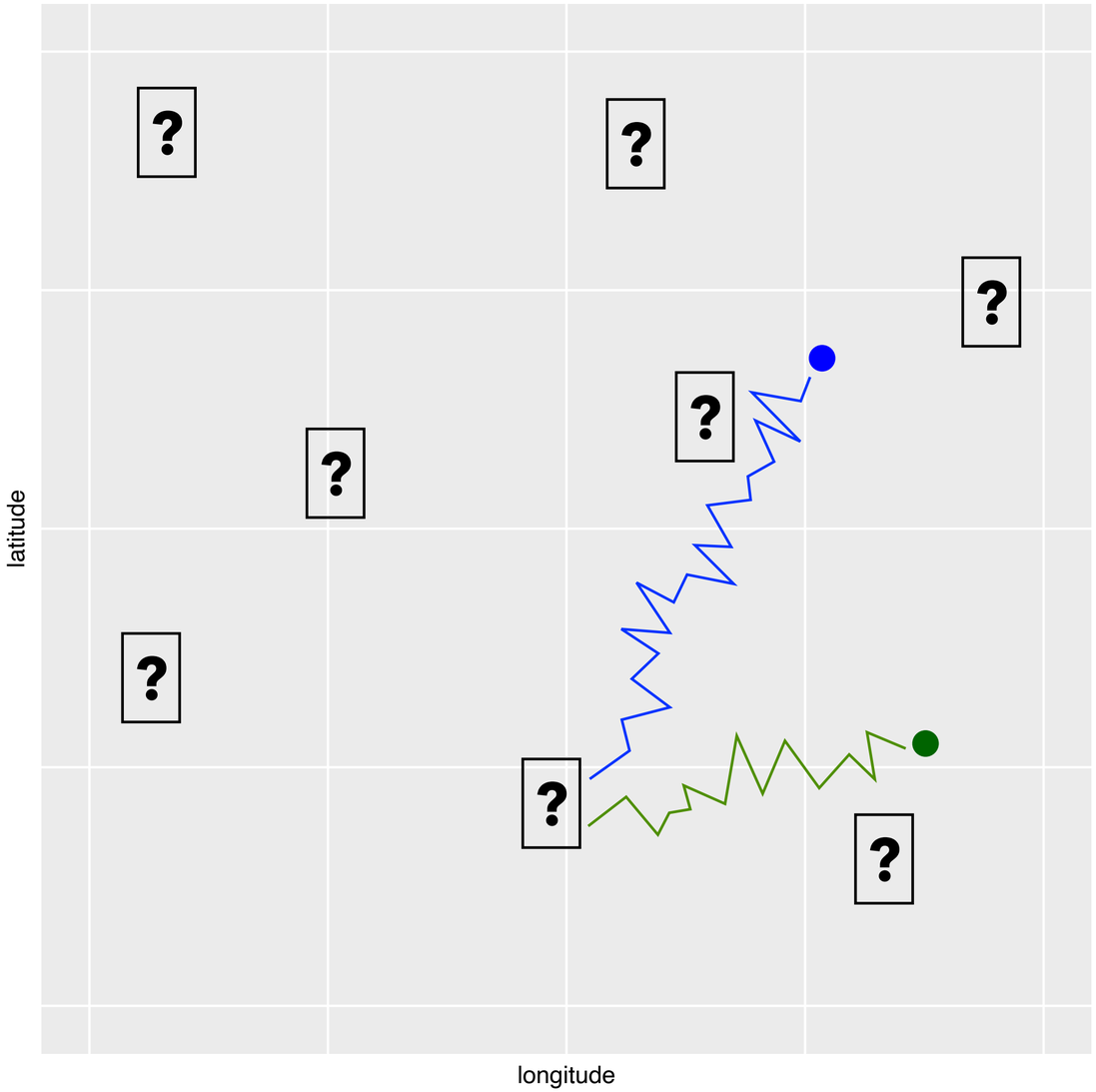
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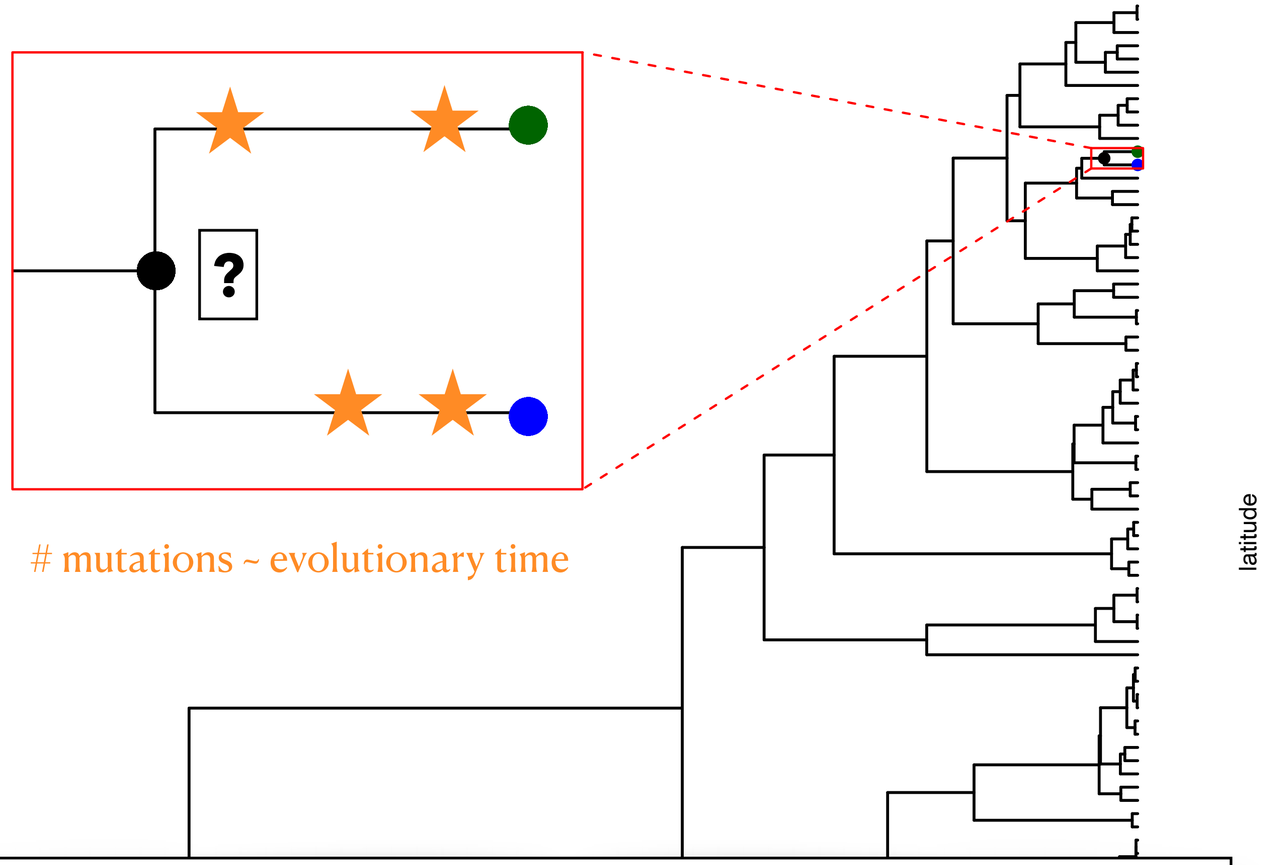

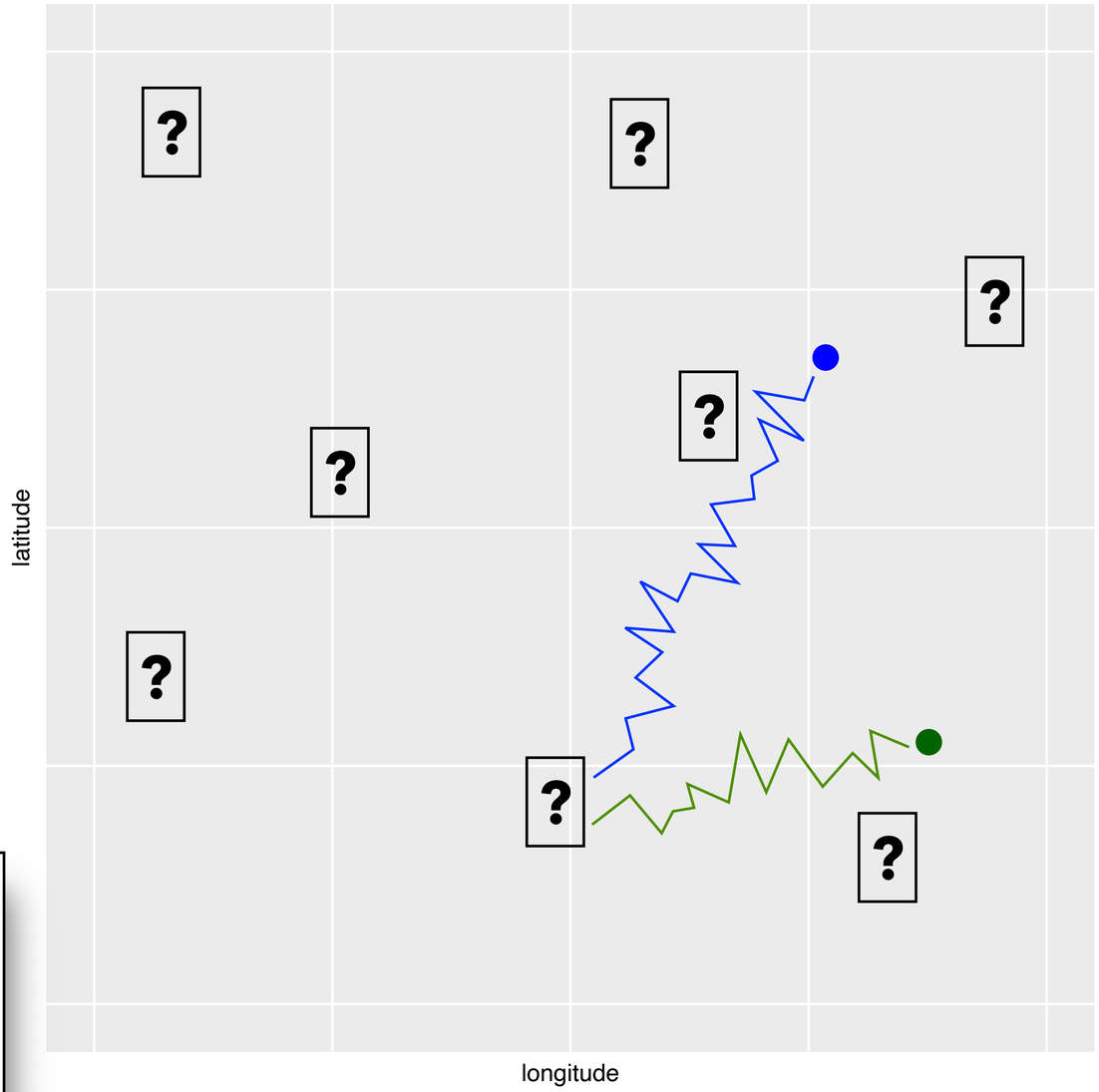

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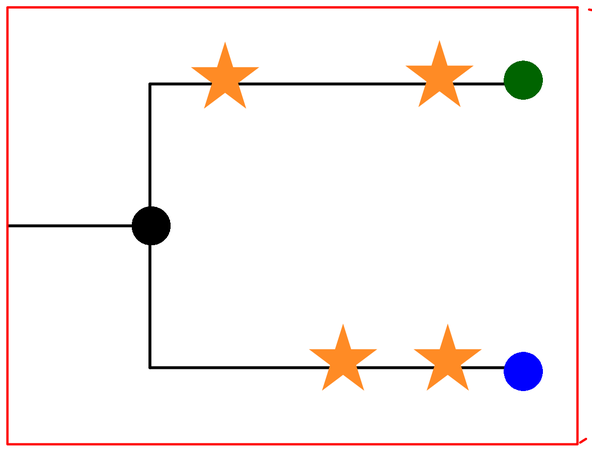
MCMC using NumPyro



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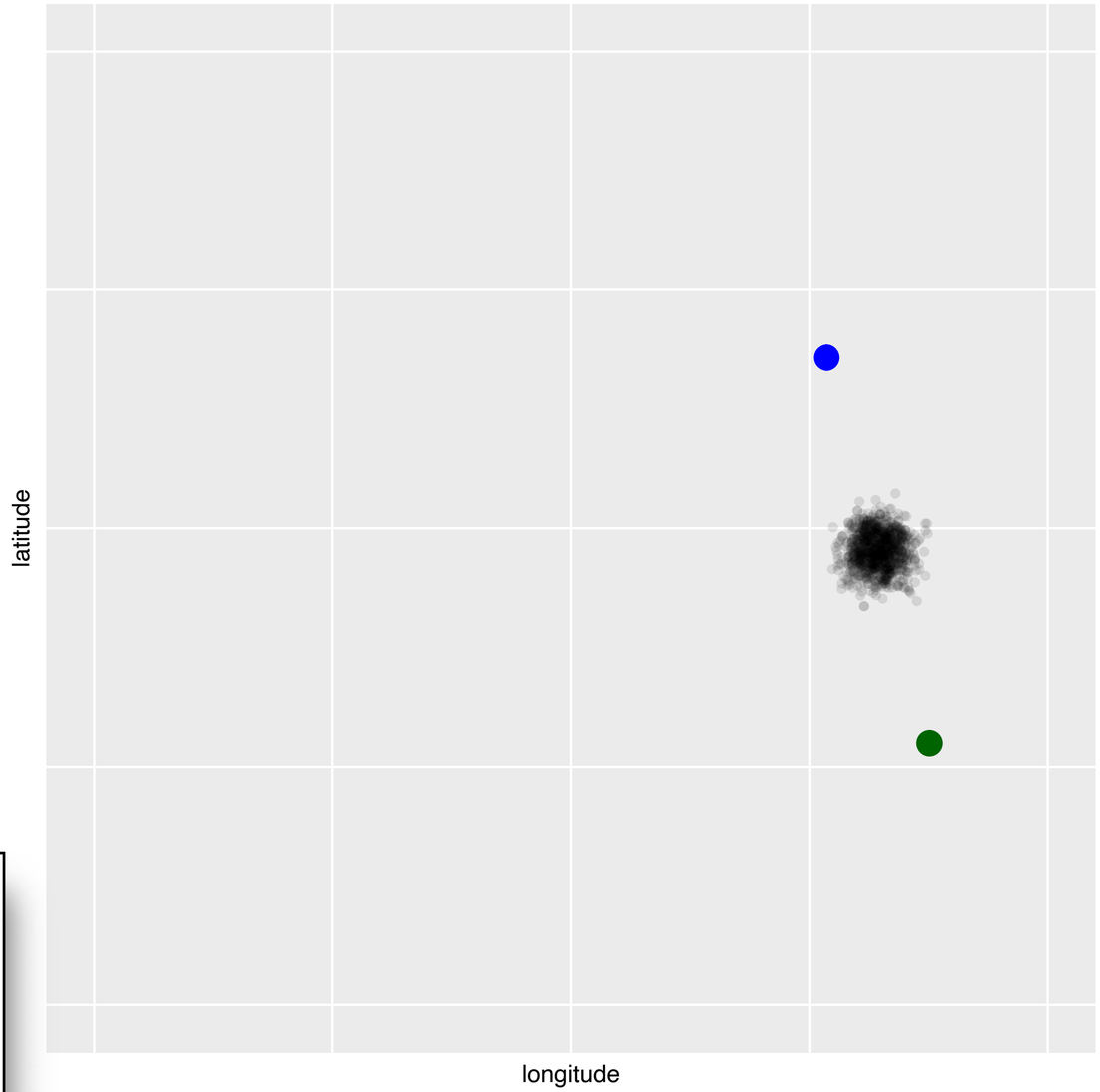

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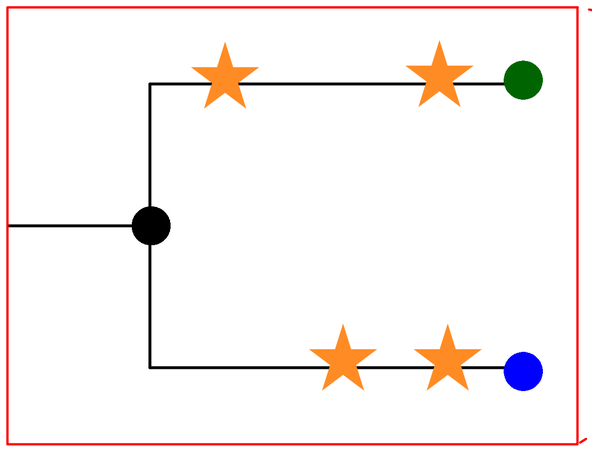

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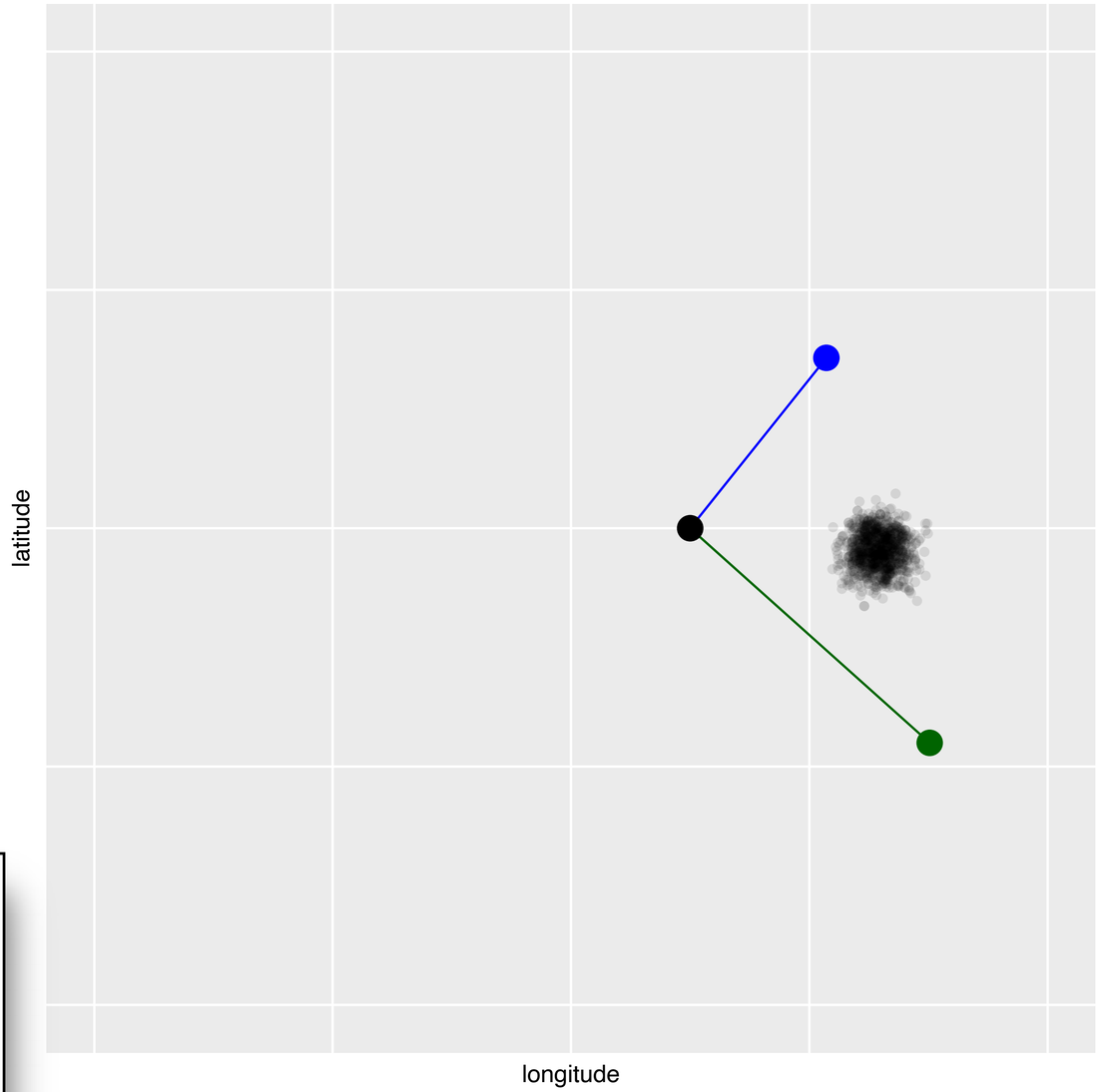

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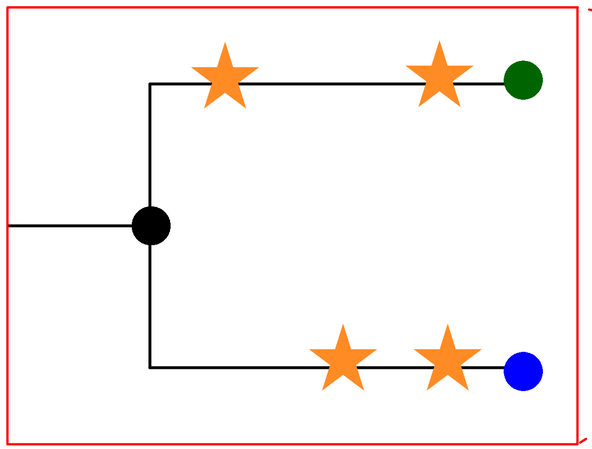

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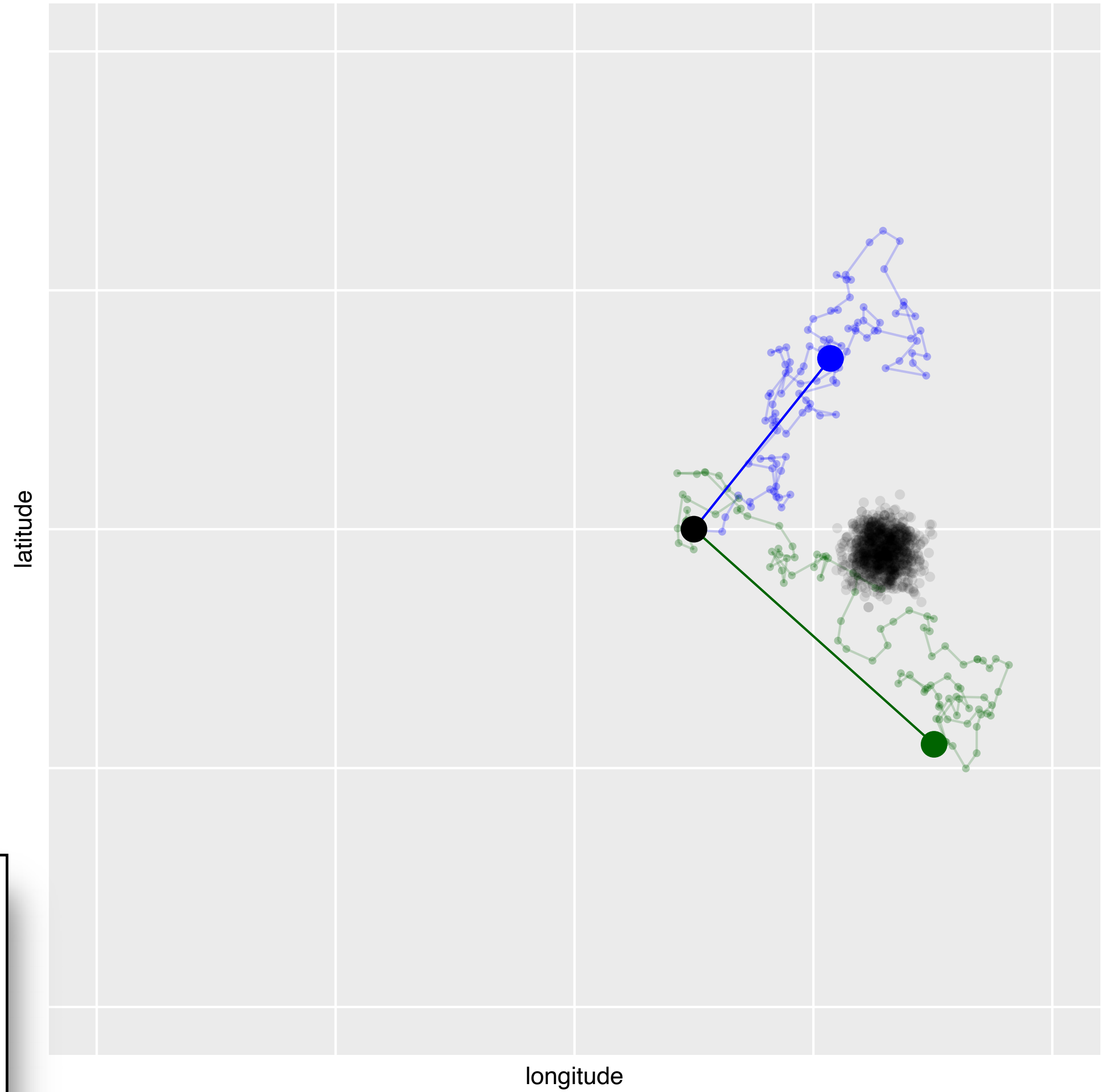

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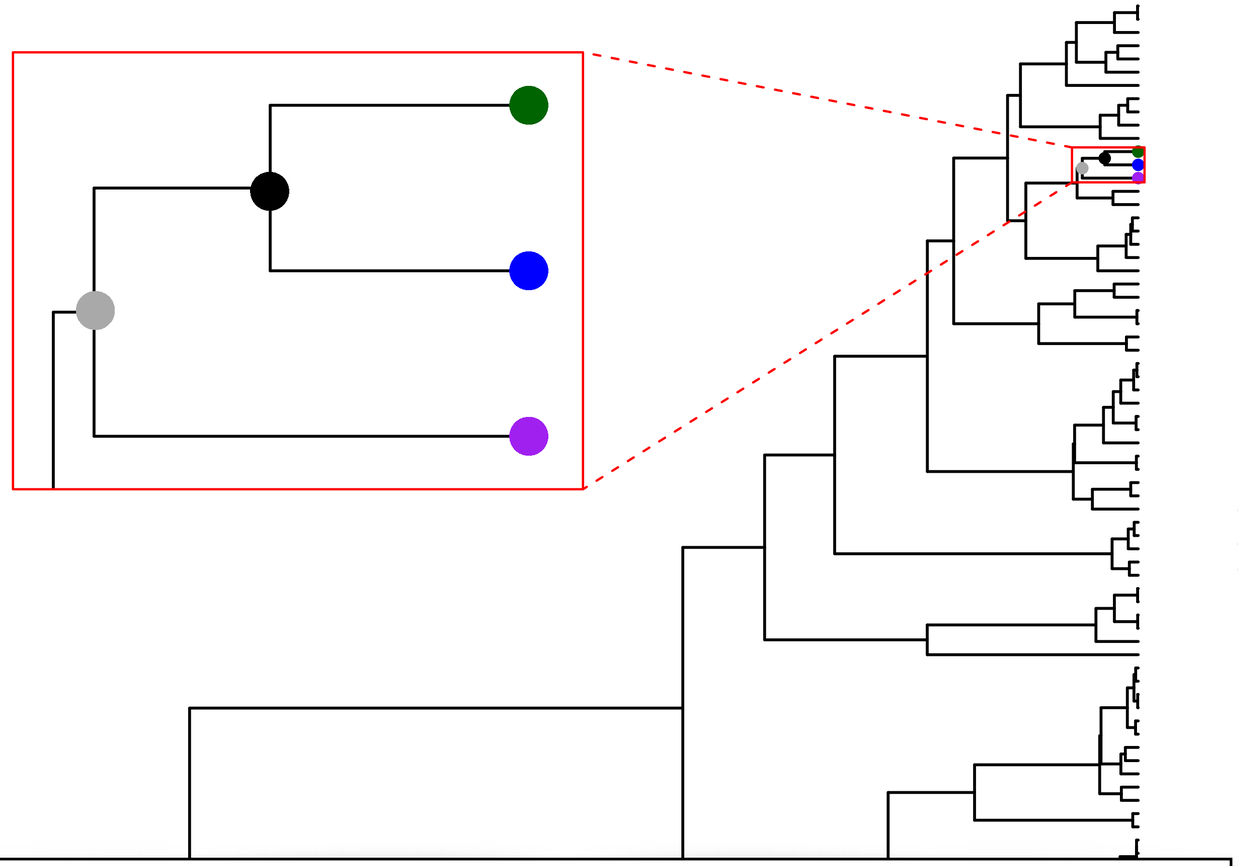

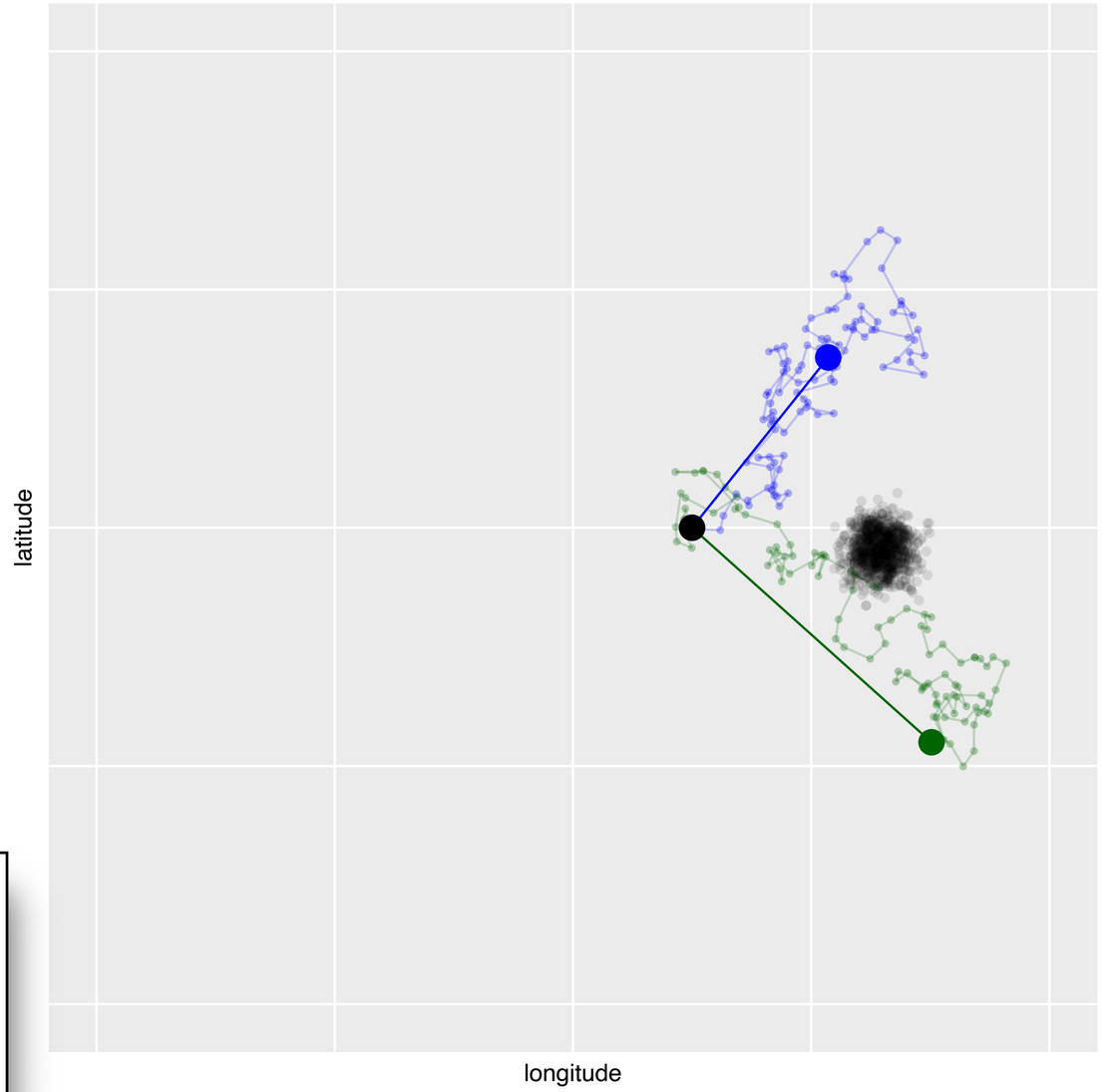

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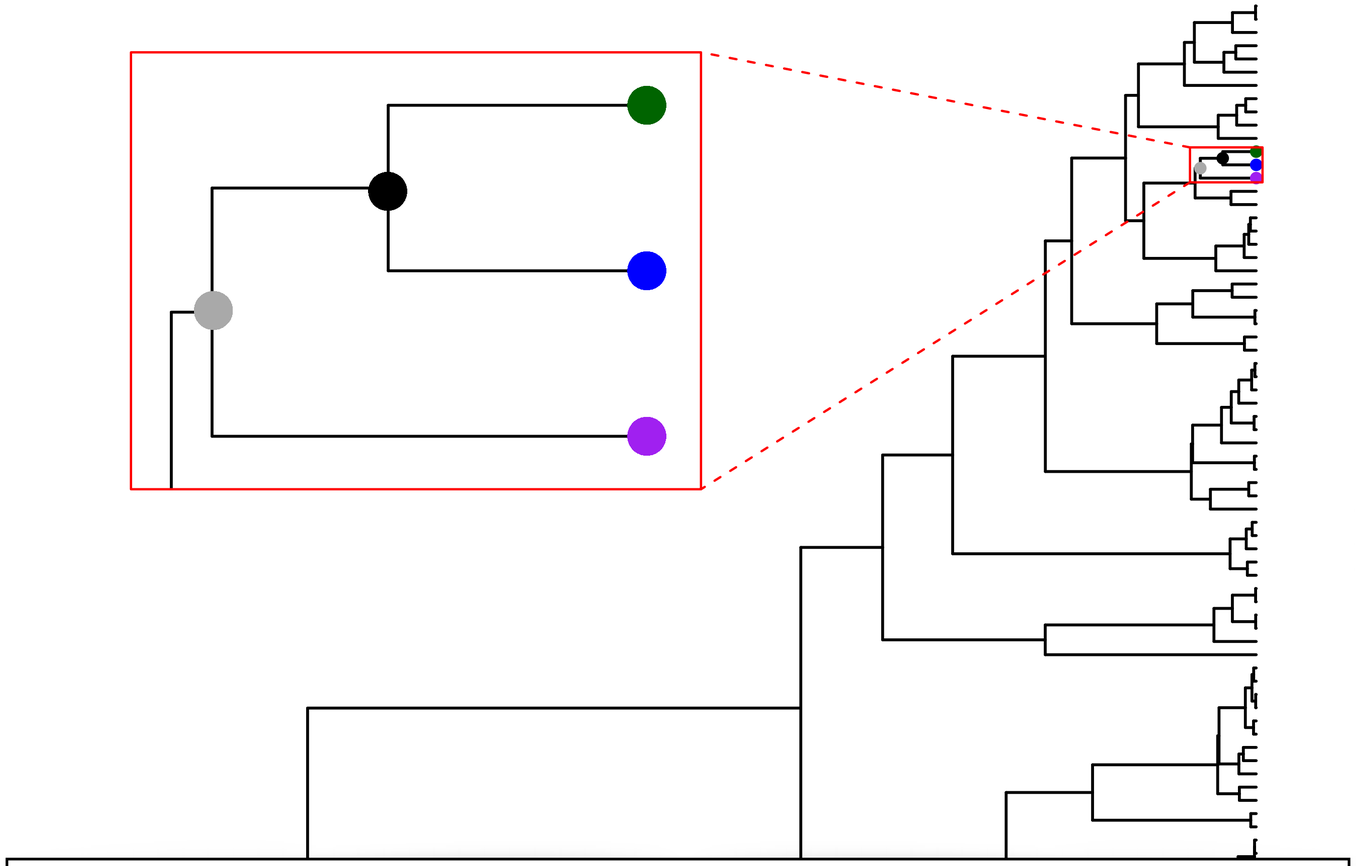

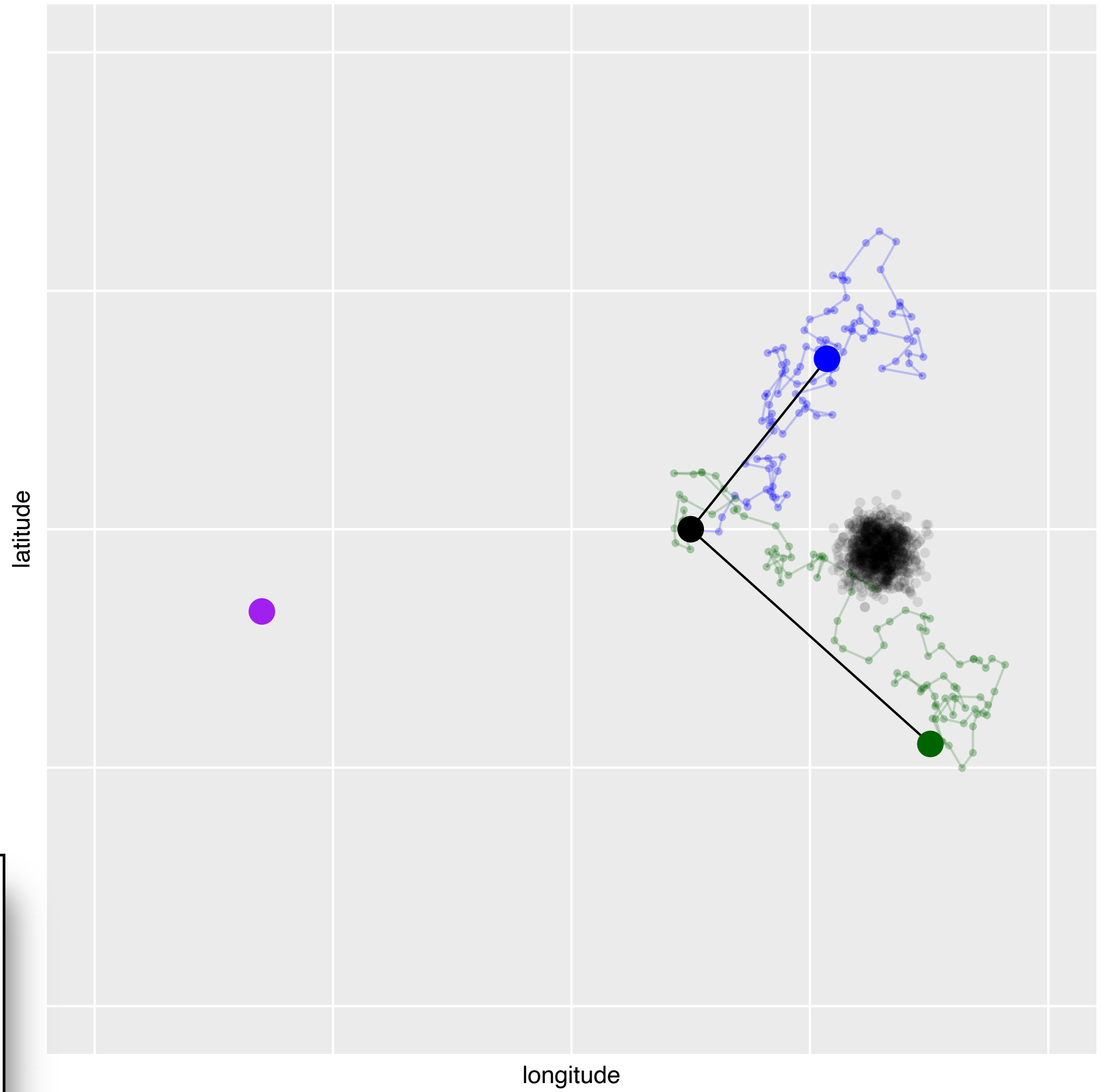

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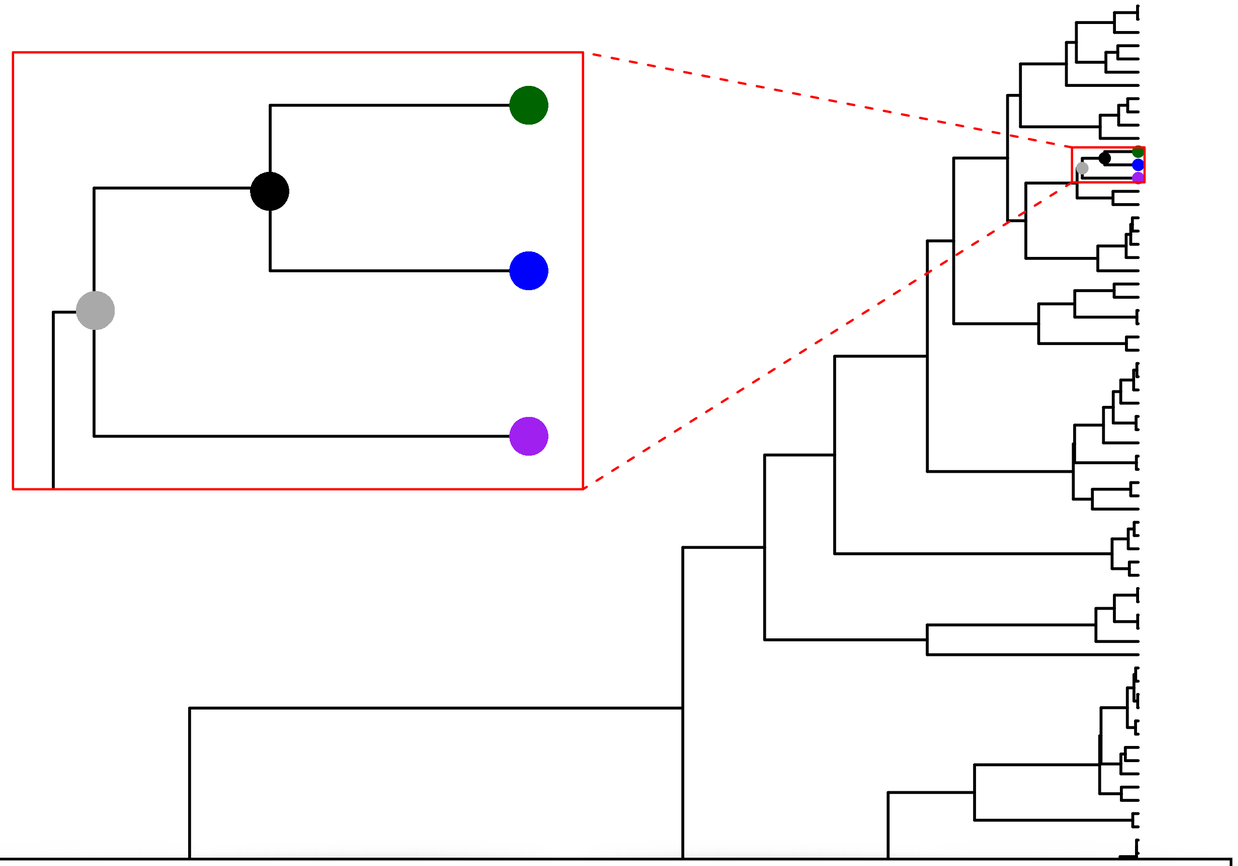

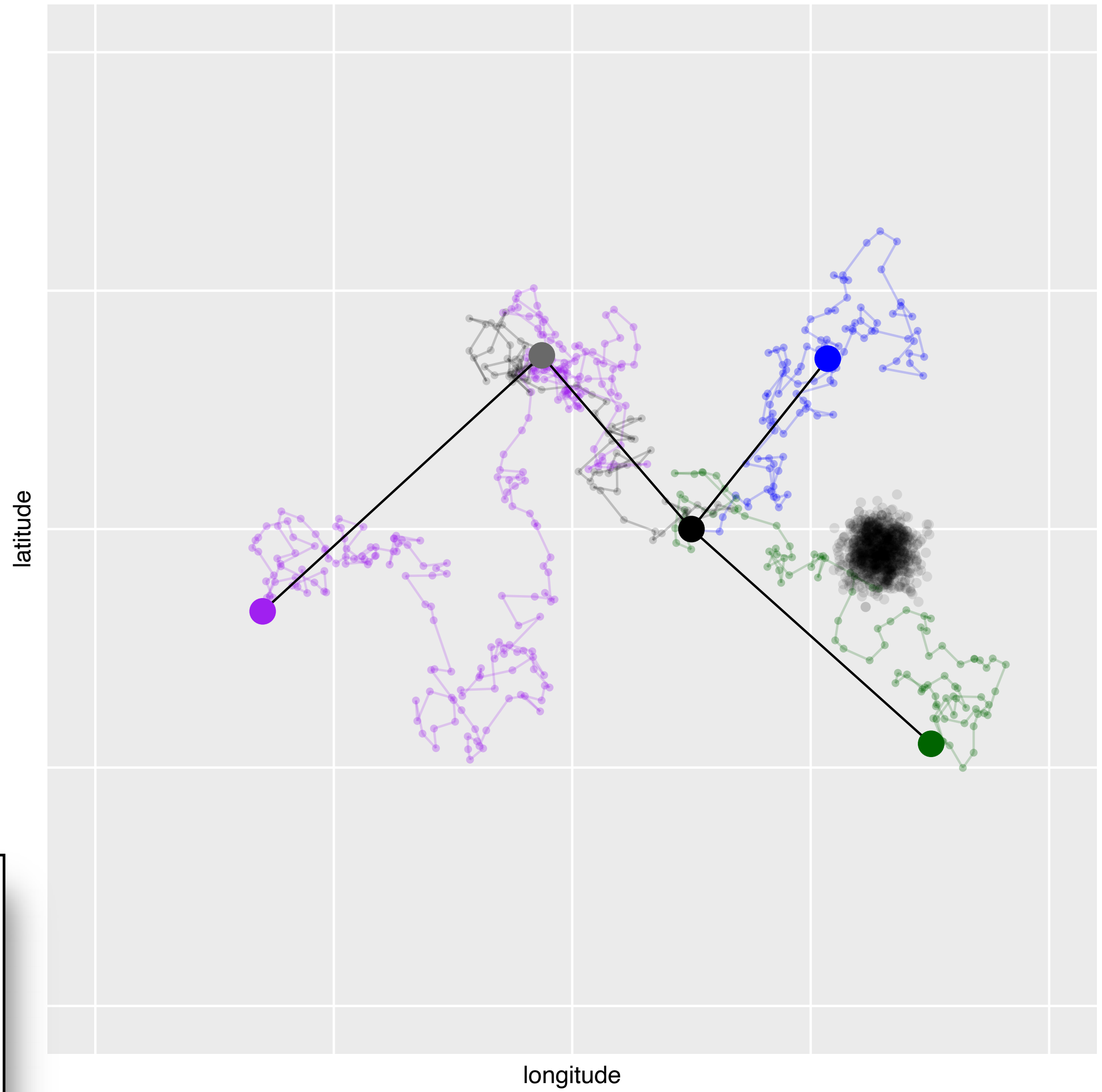

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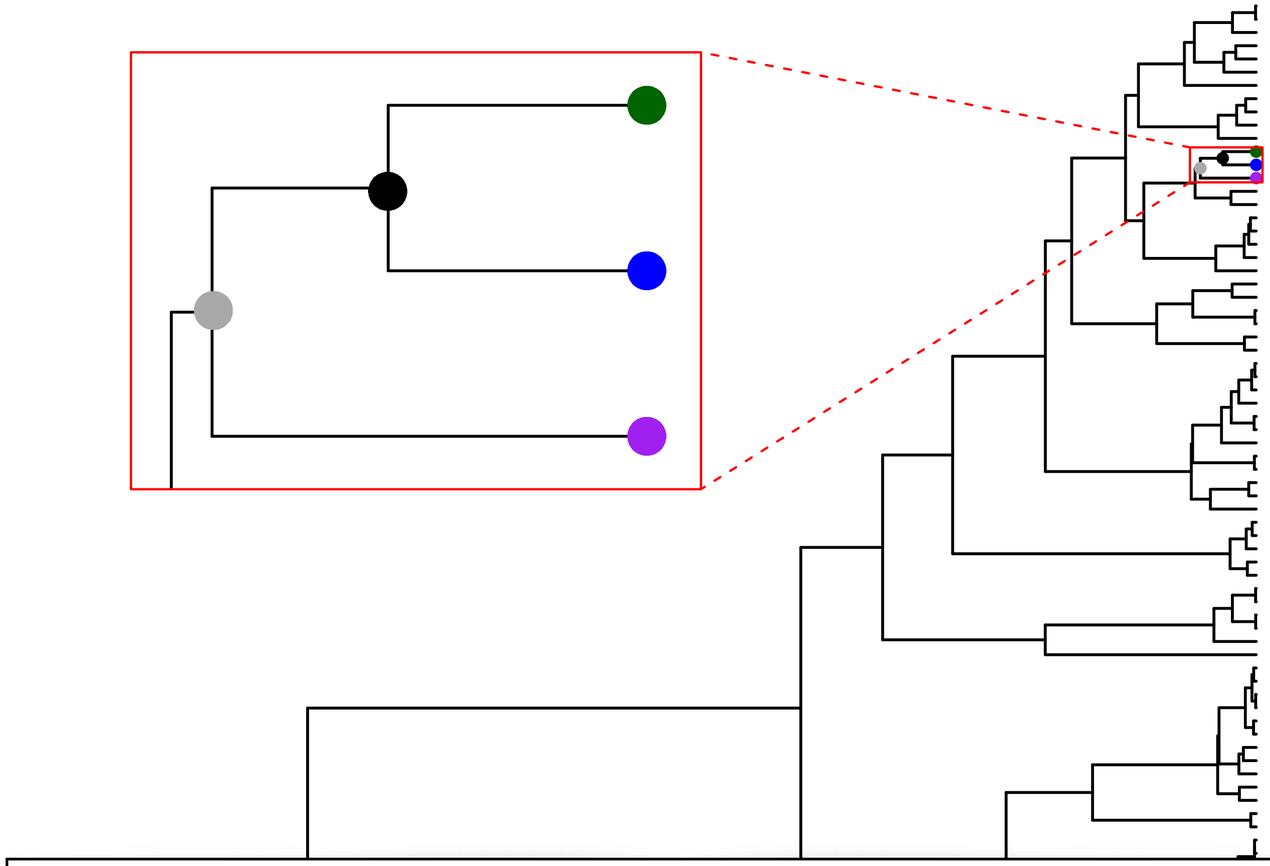

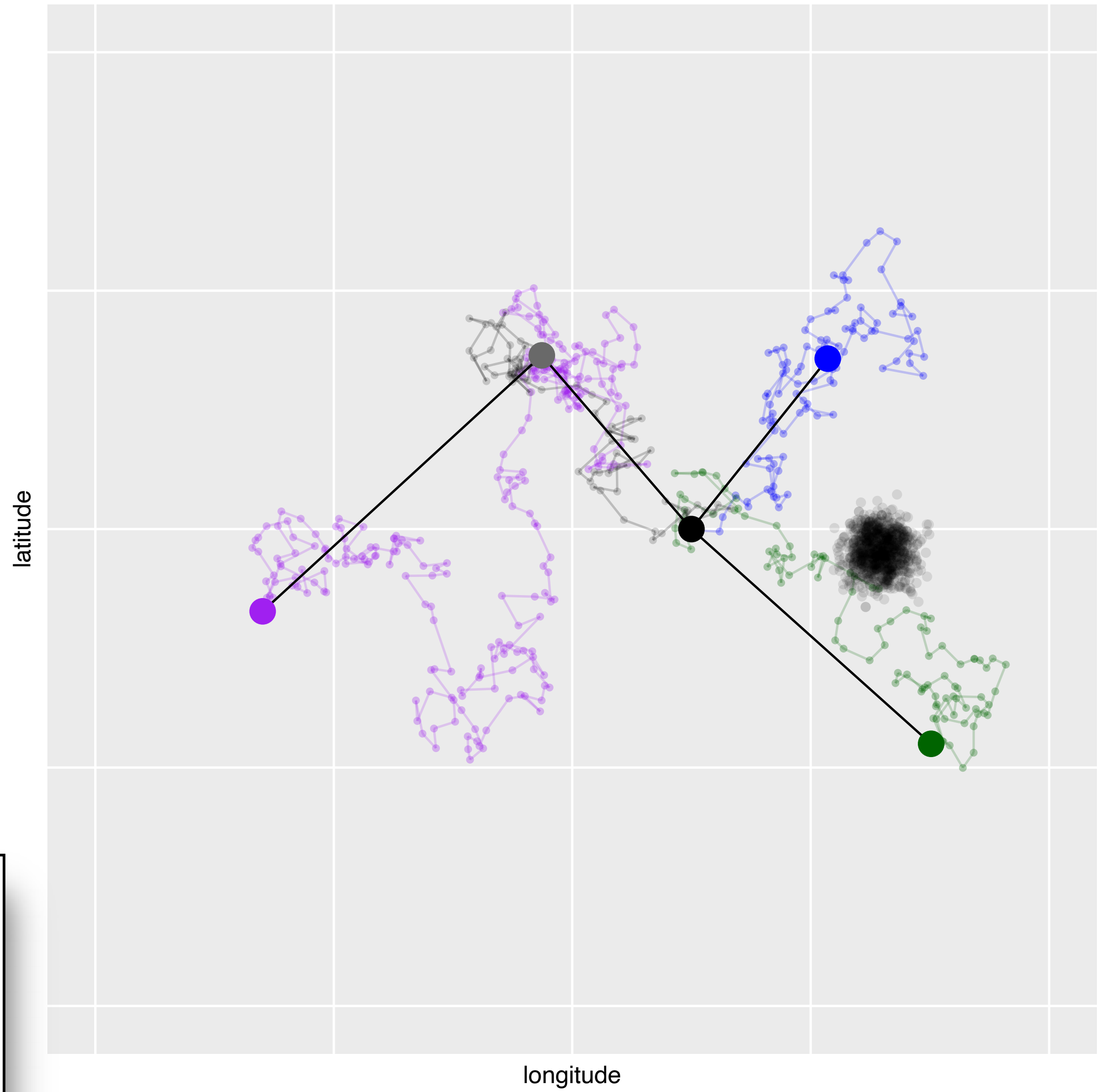

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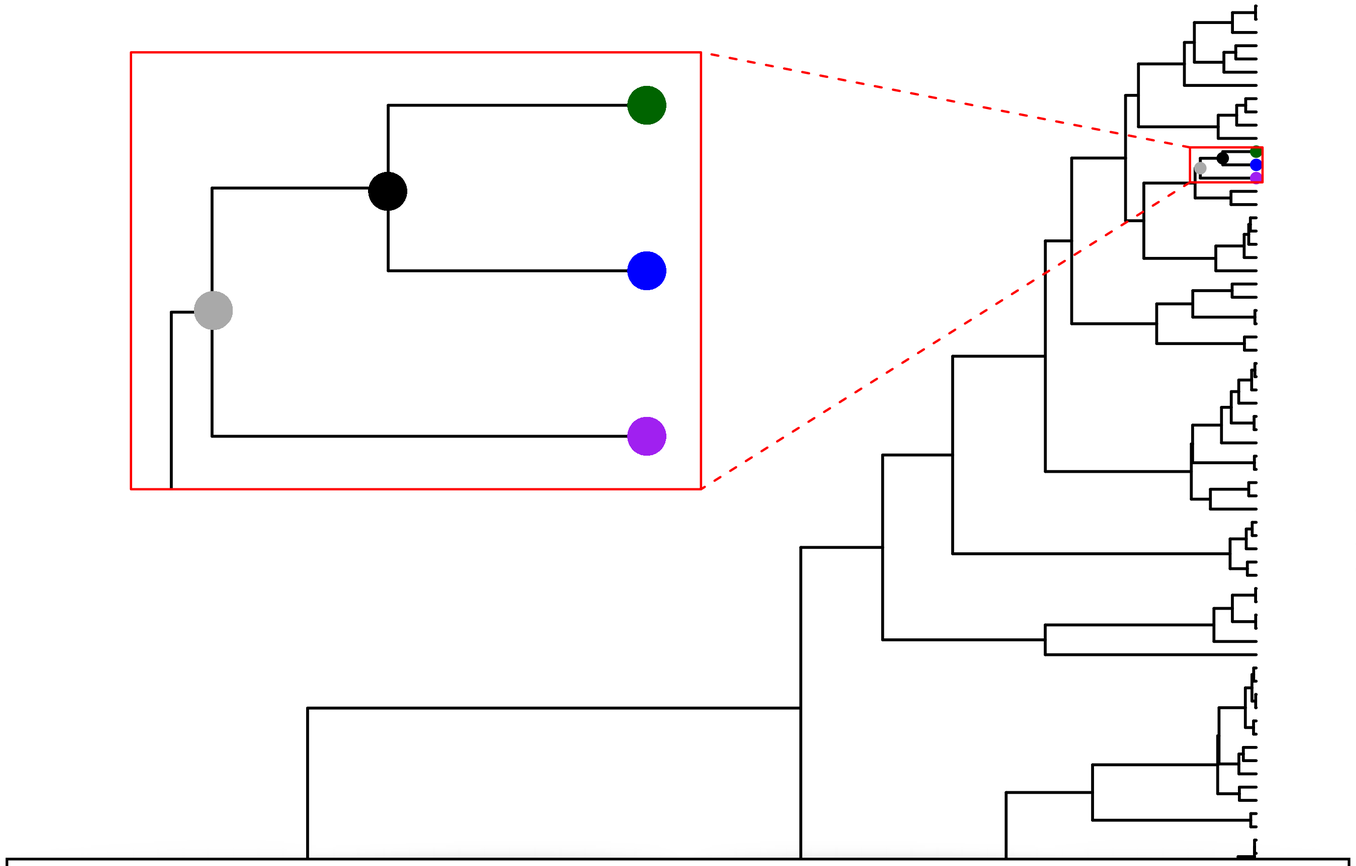

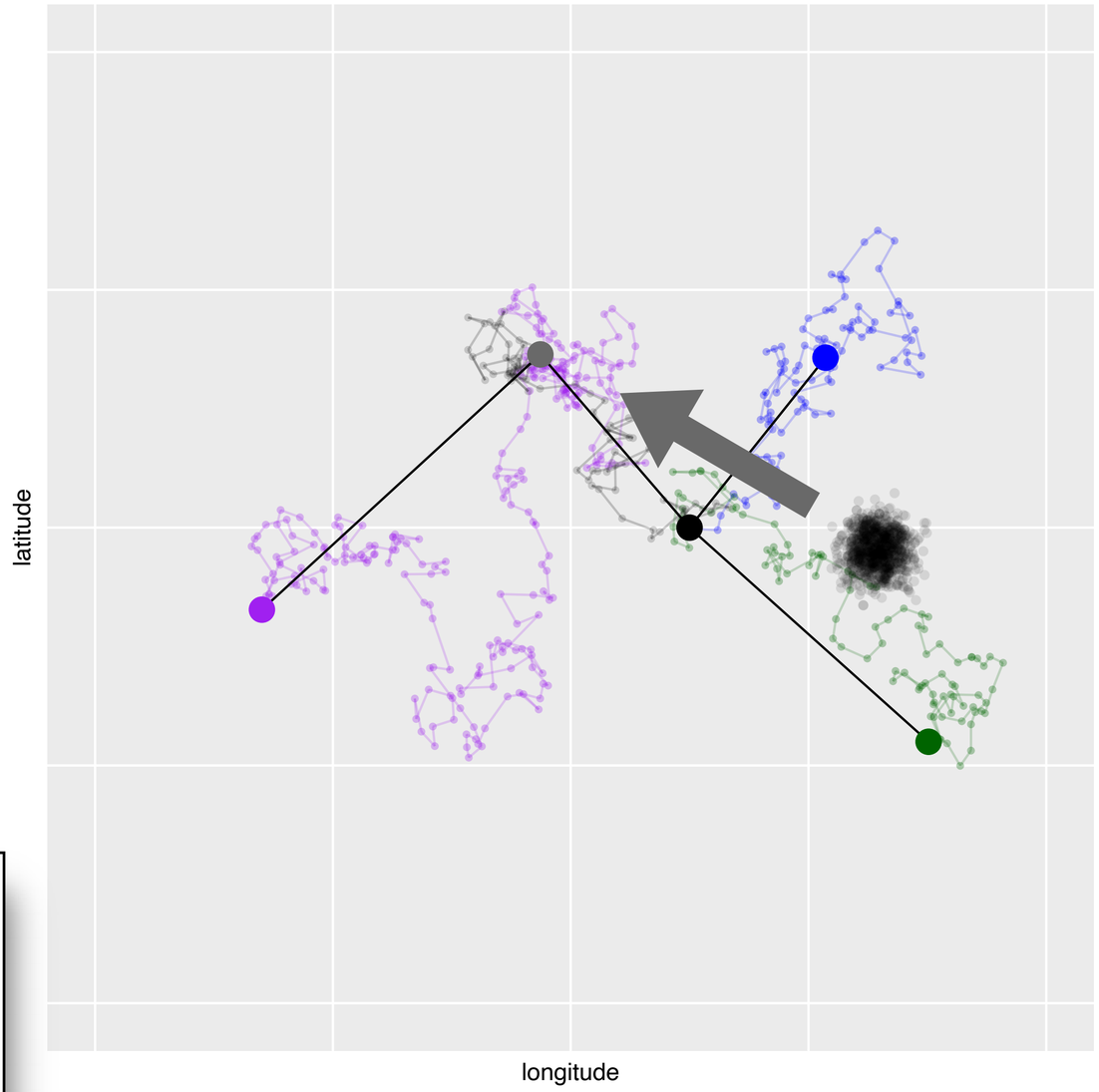

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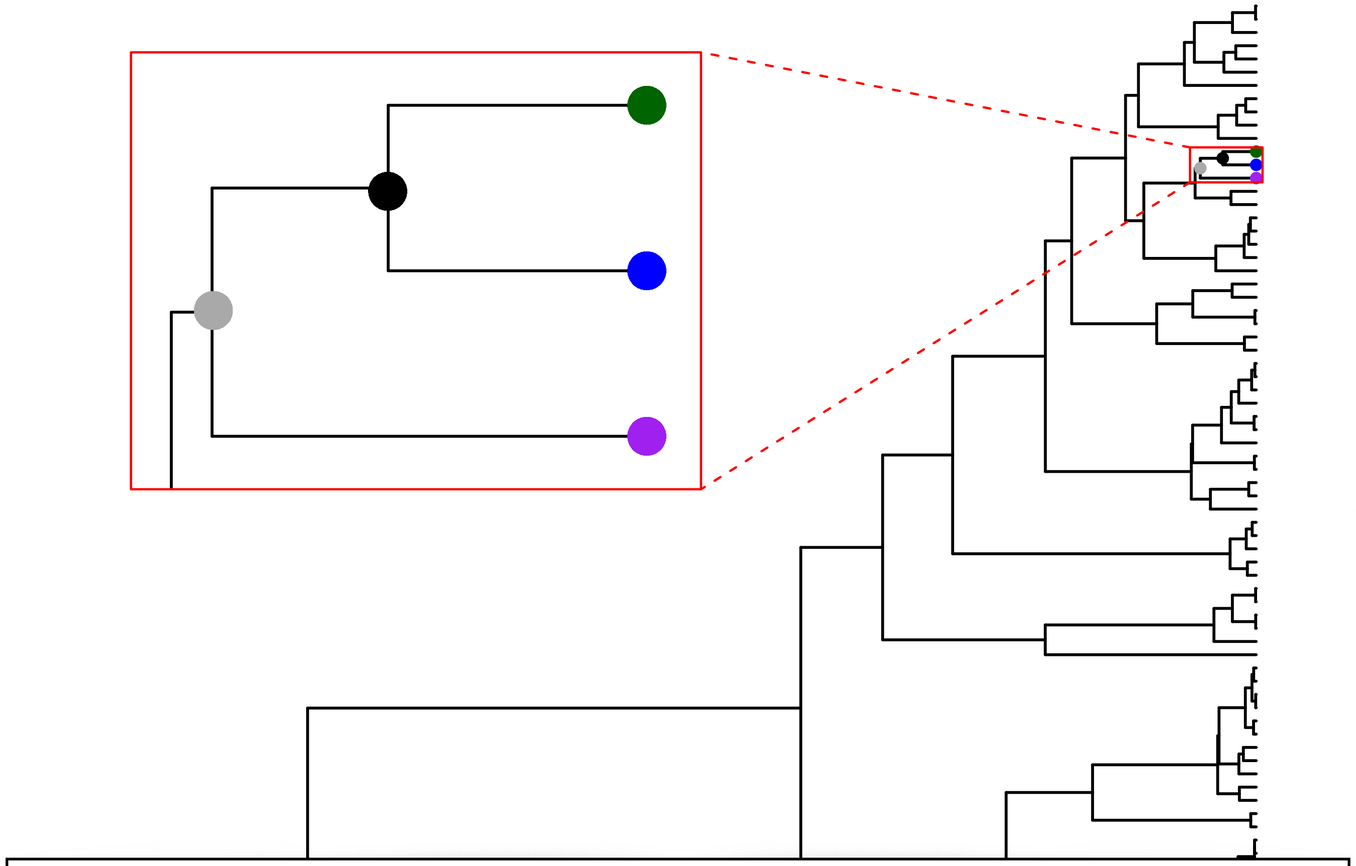

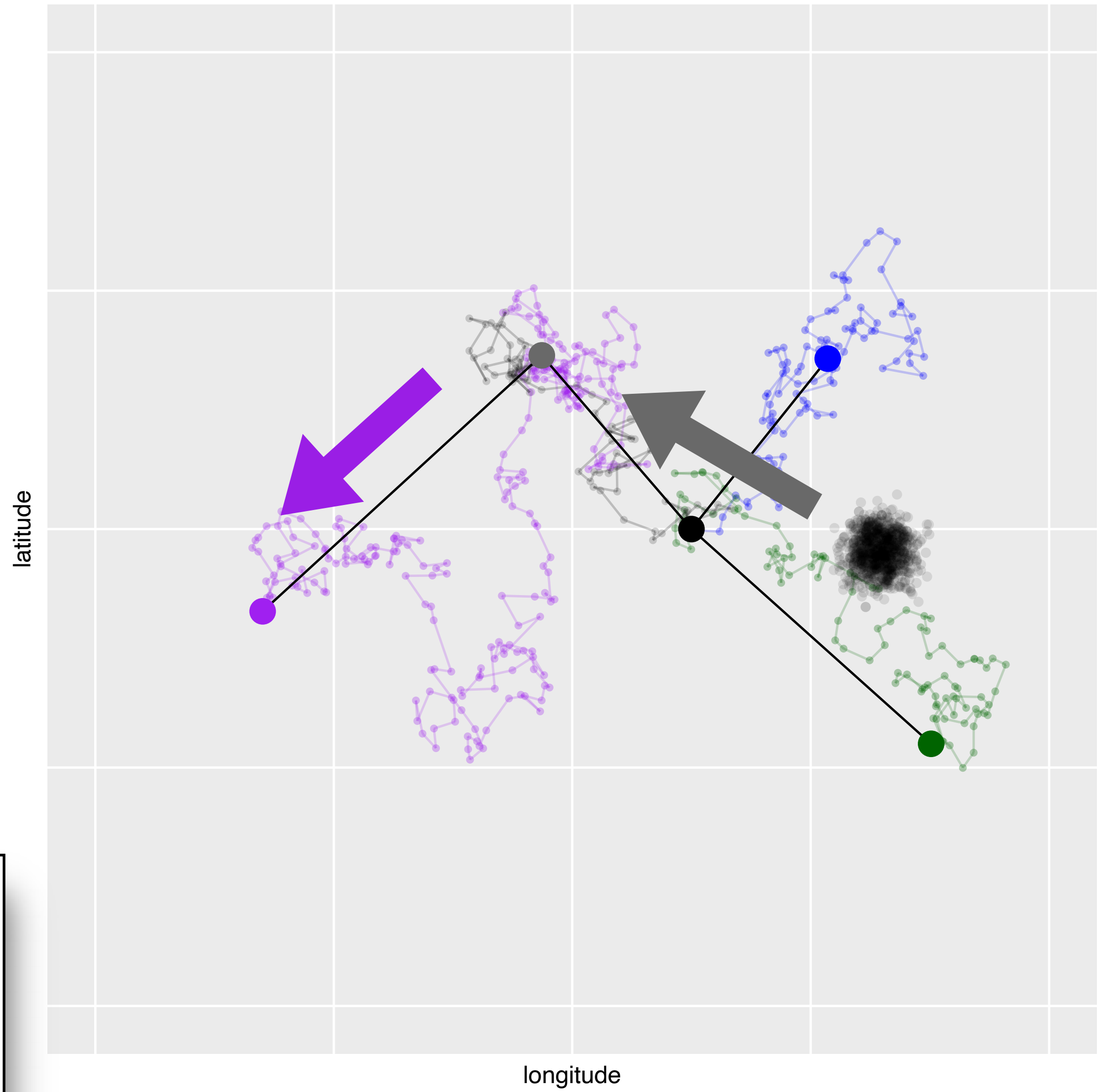

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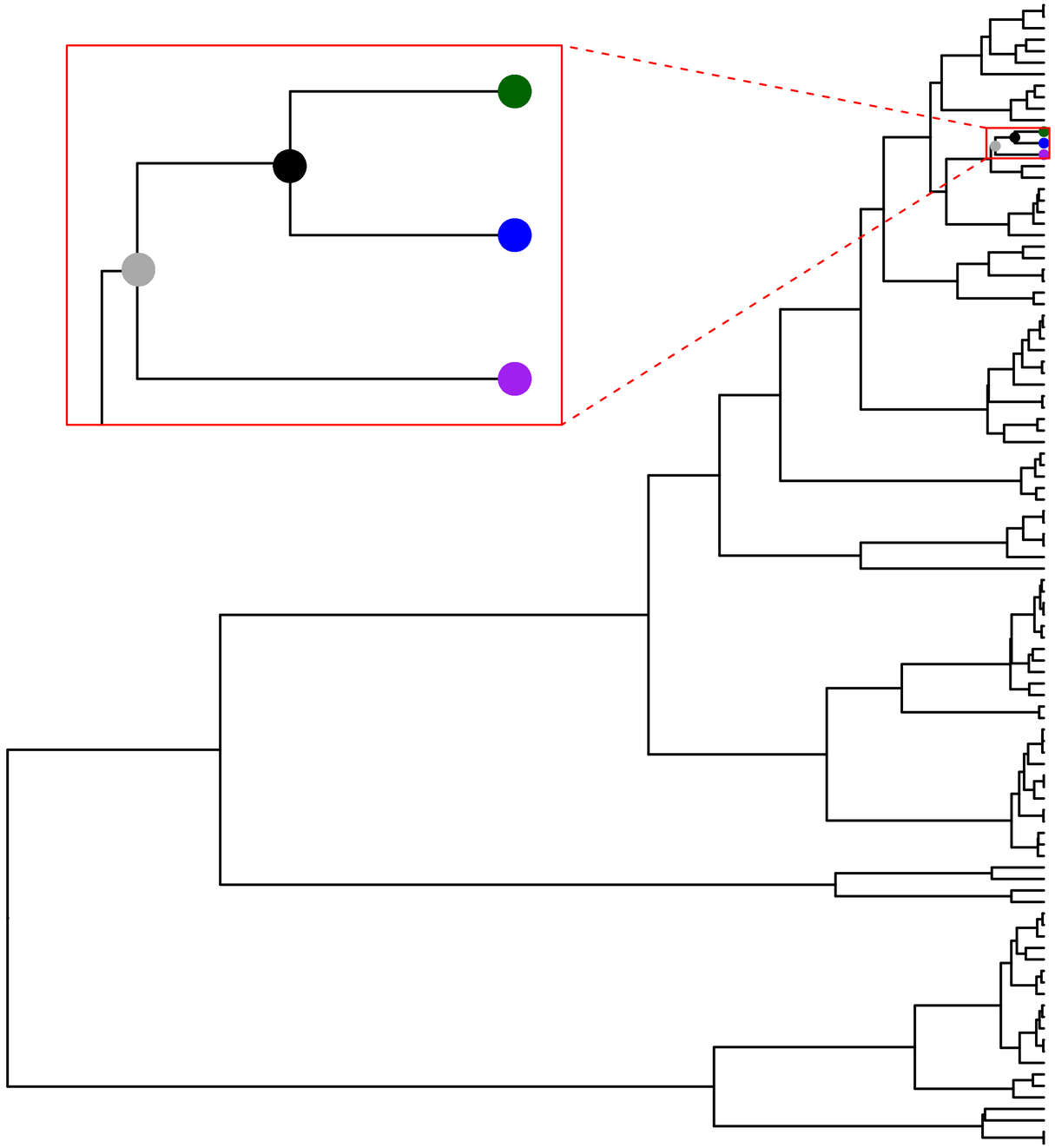

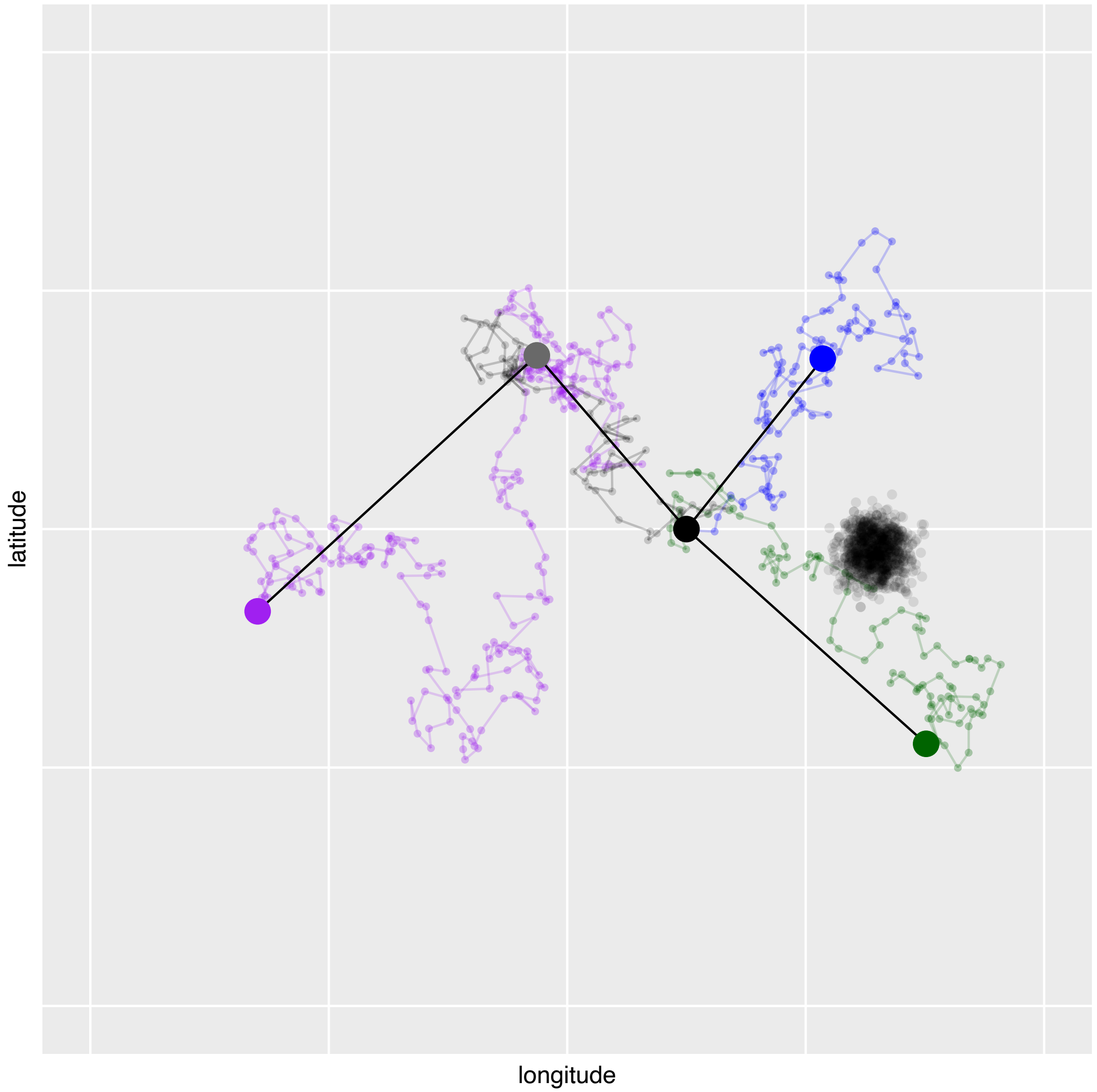

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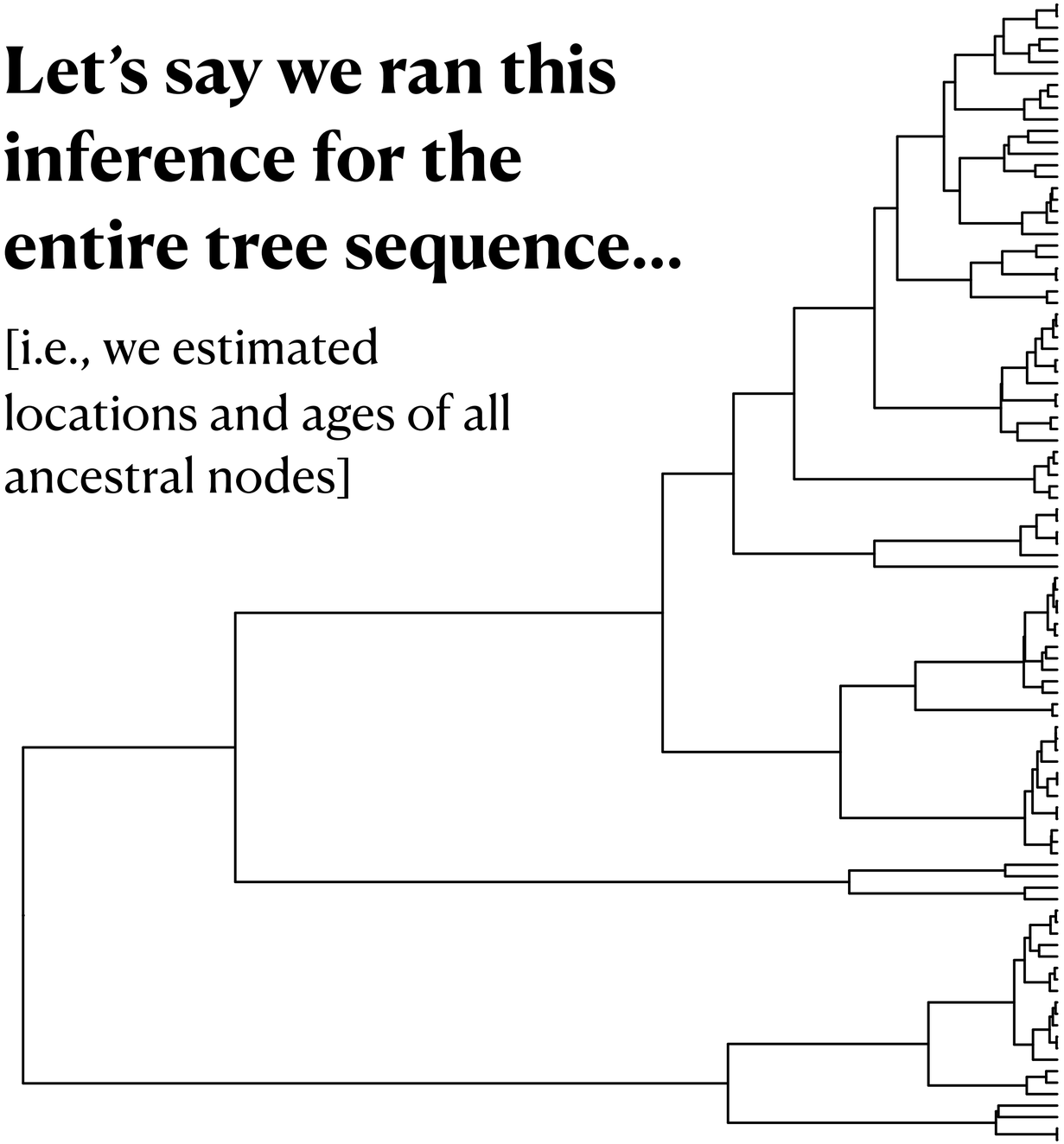

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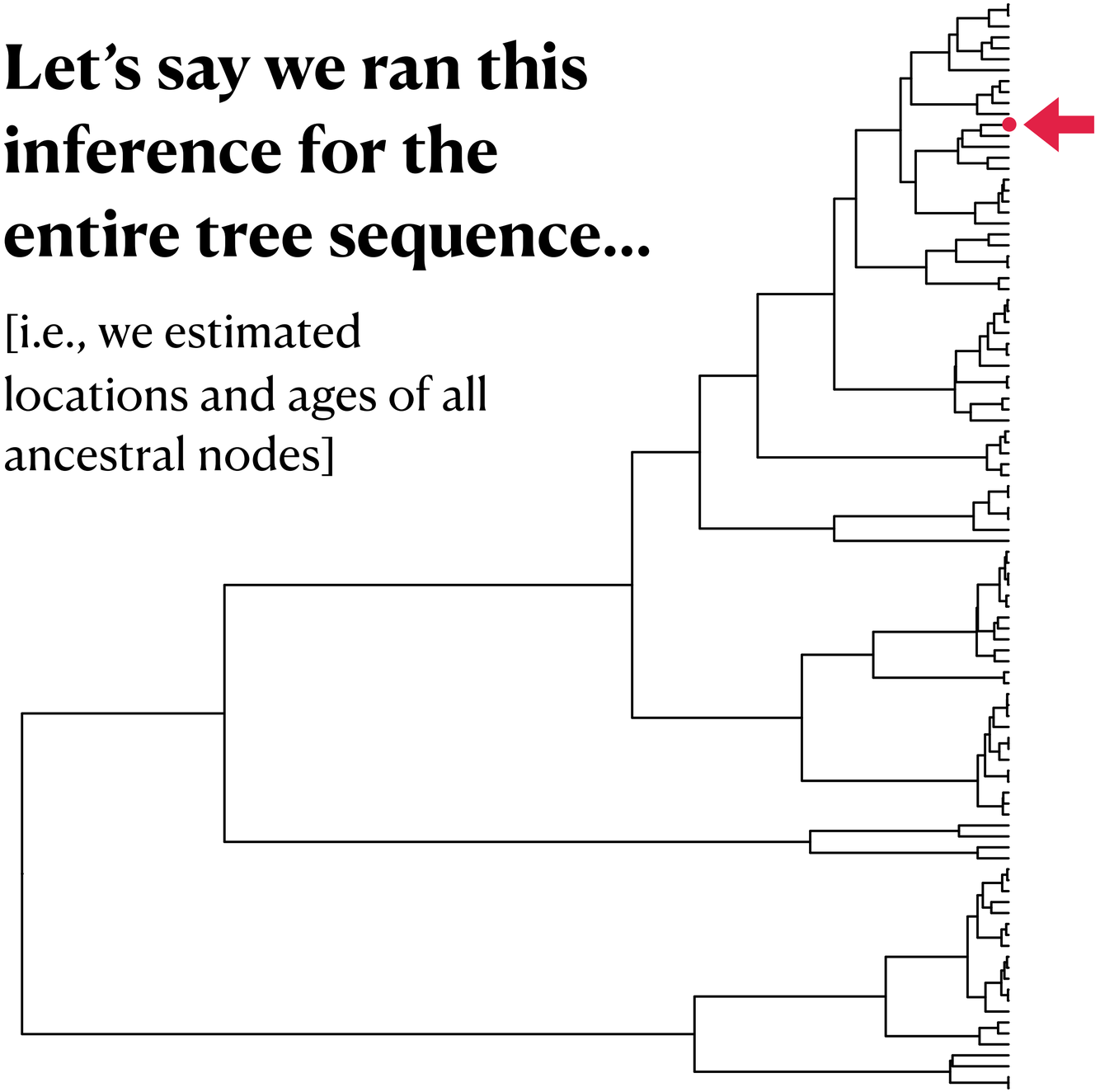

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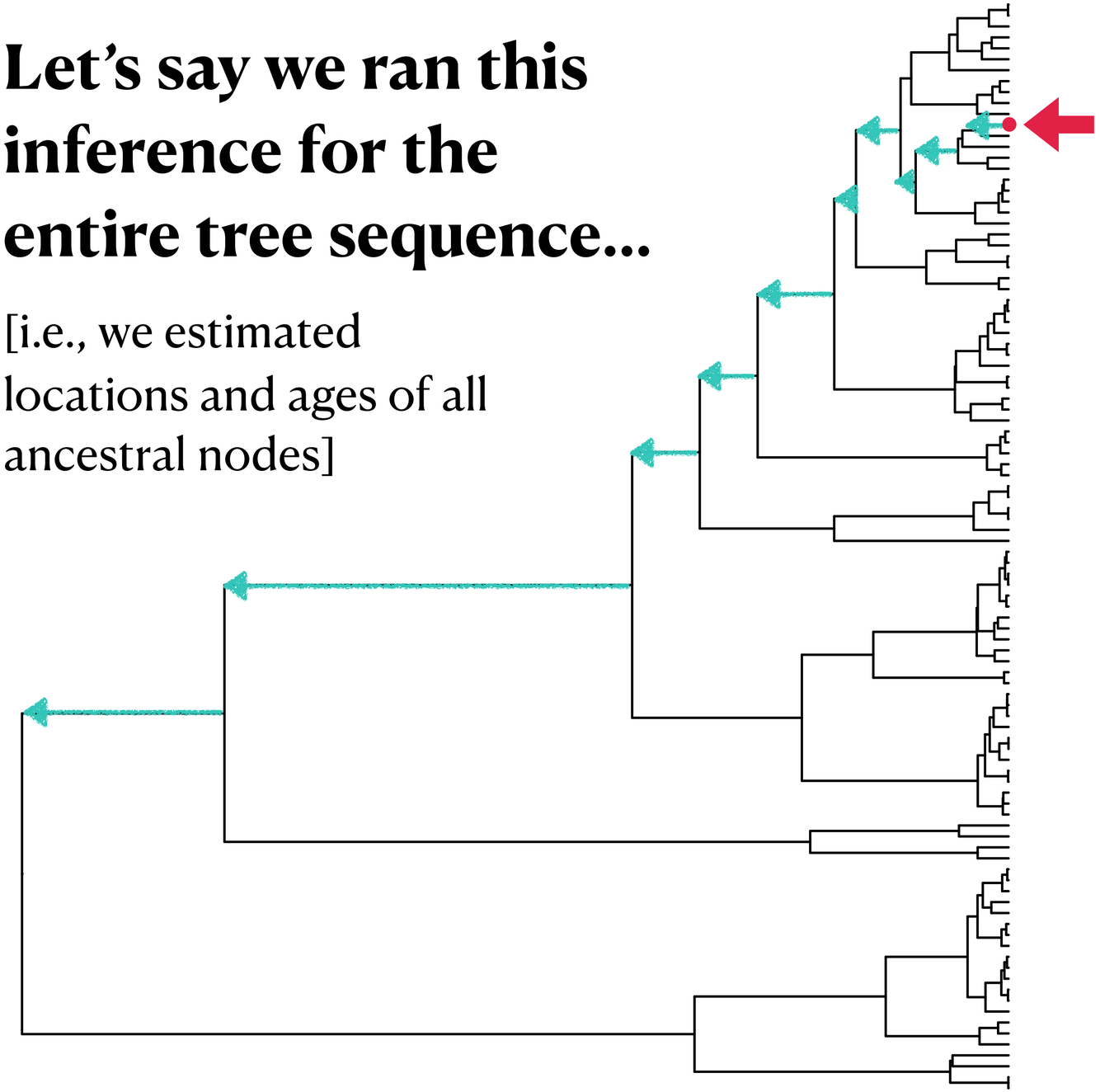

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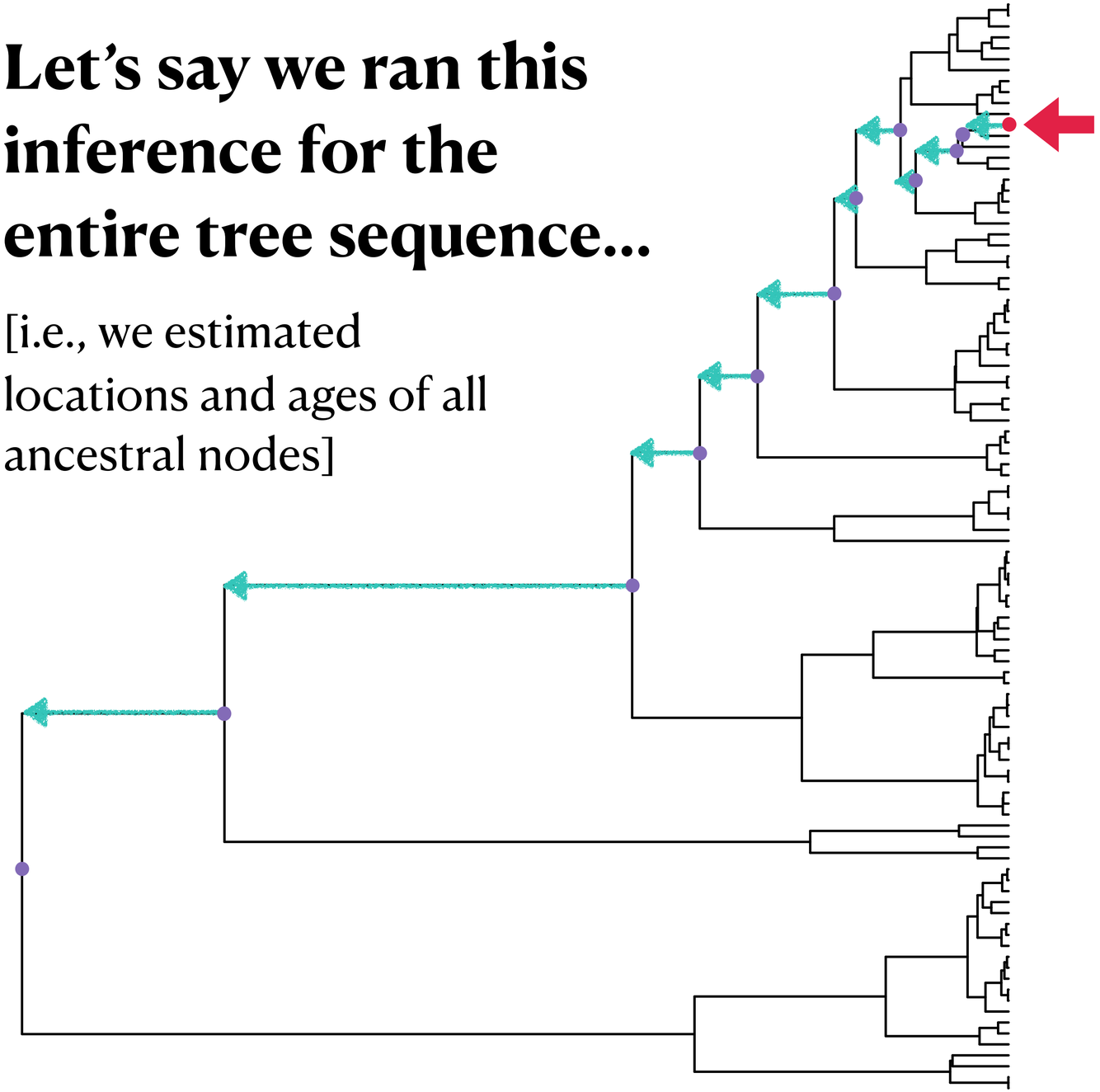
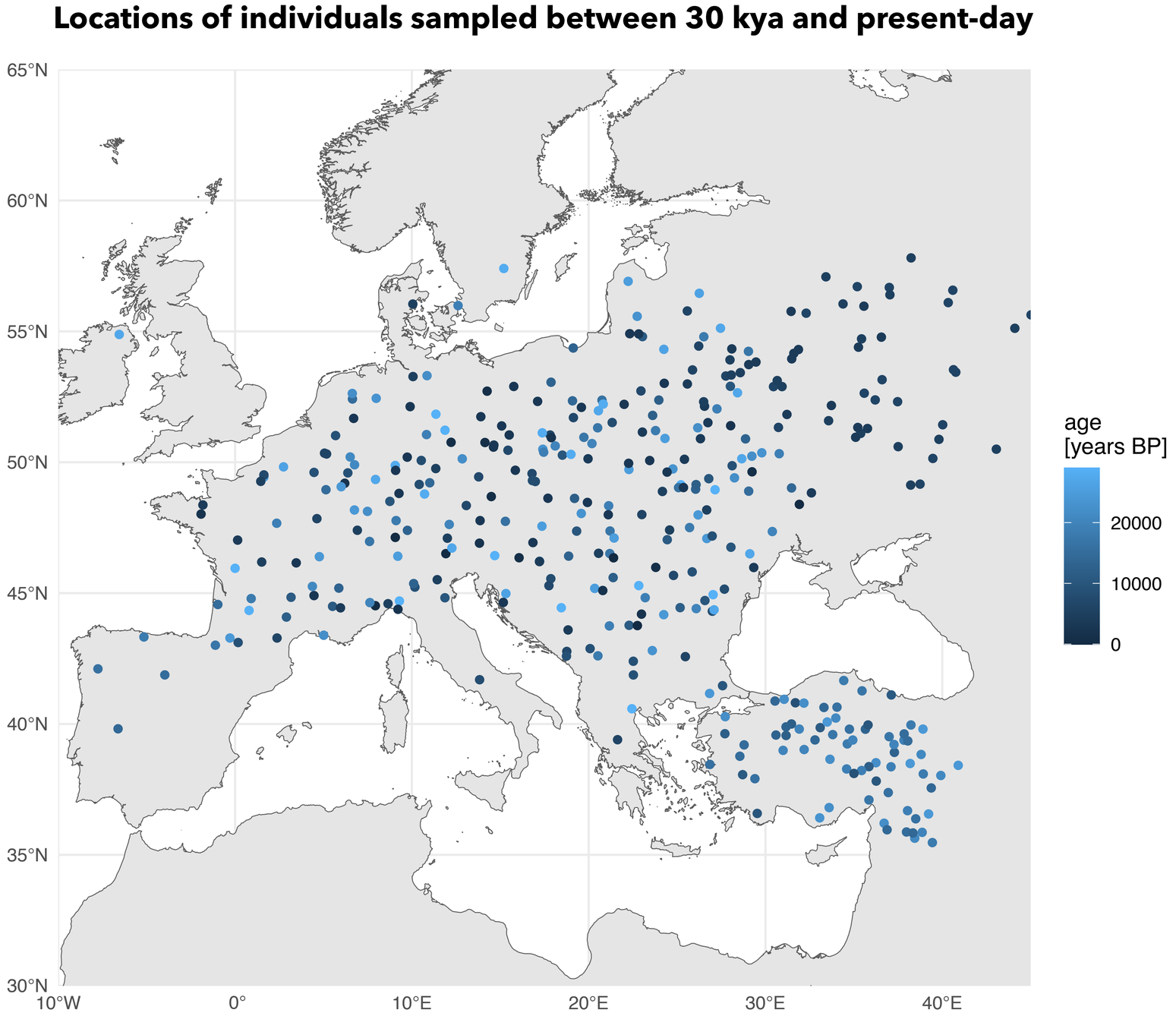


For a **given individual** we can **"climb up"** each tree and collect "paths" through inferred **ancestral locations**.

The Holy Grail?



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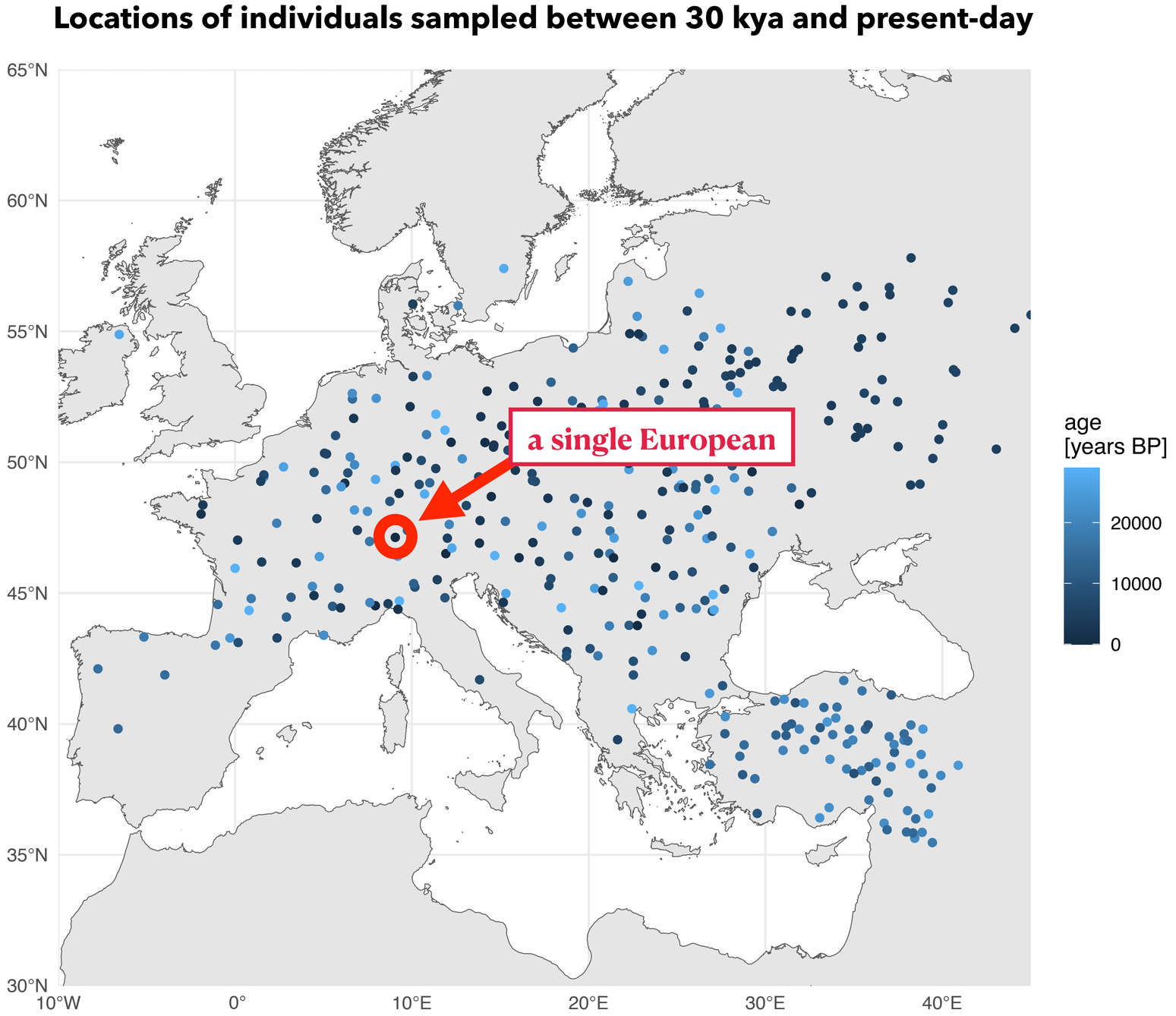

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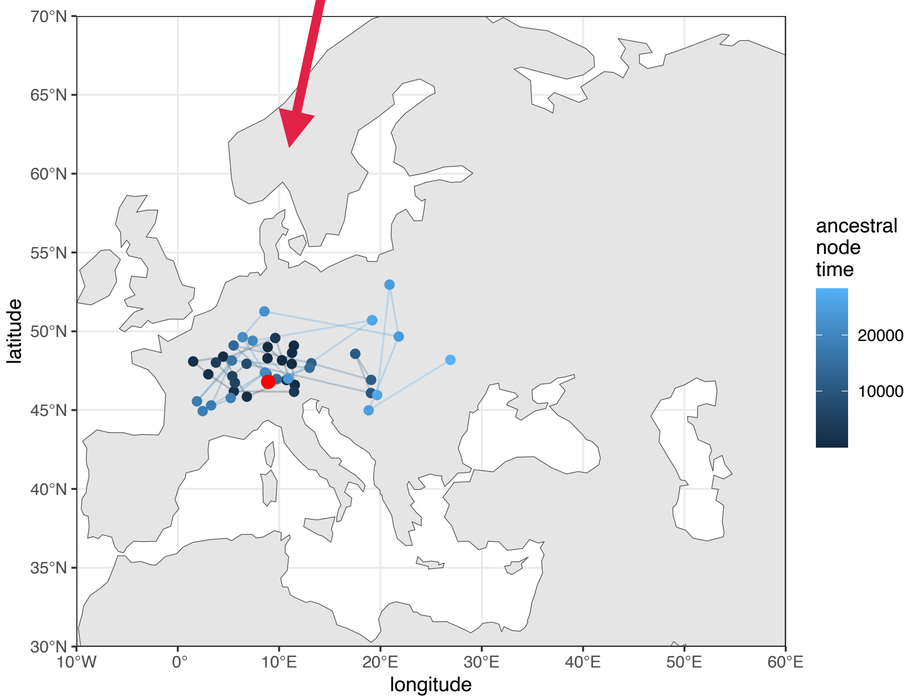

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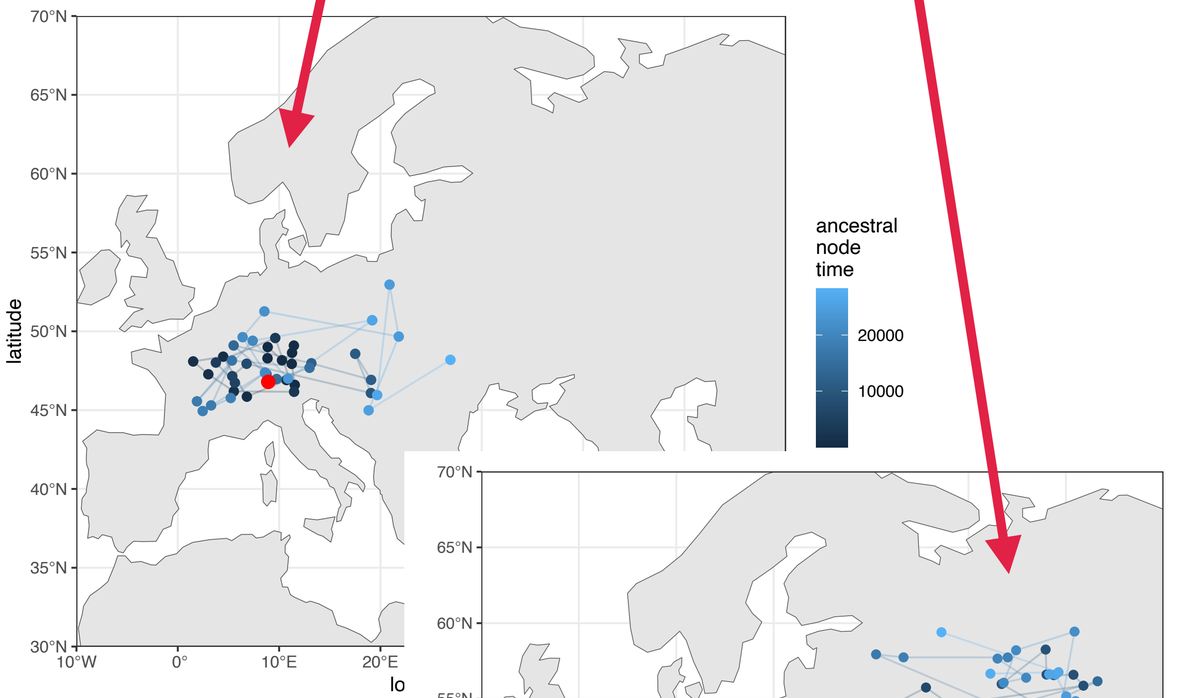

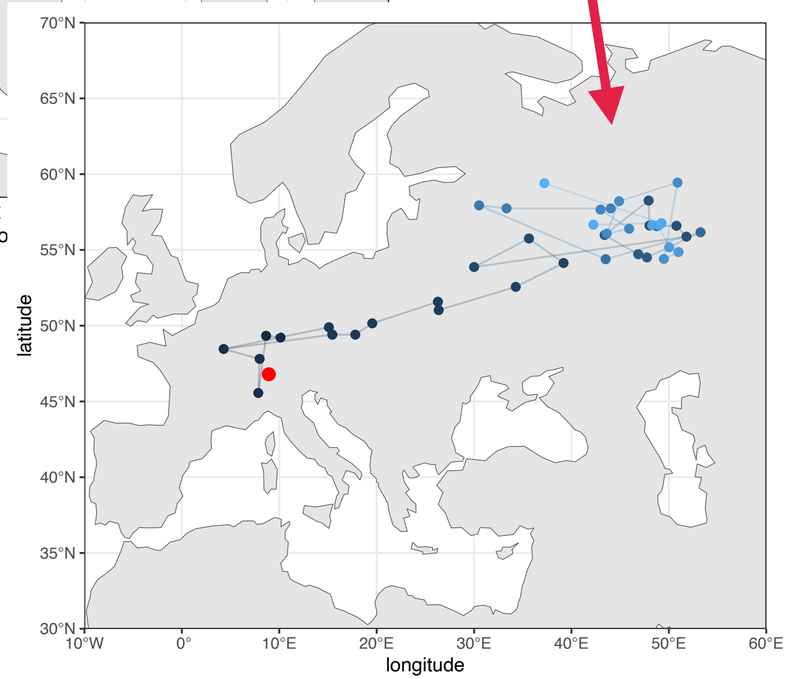

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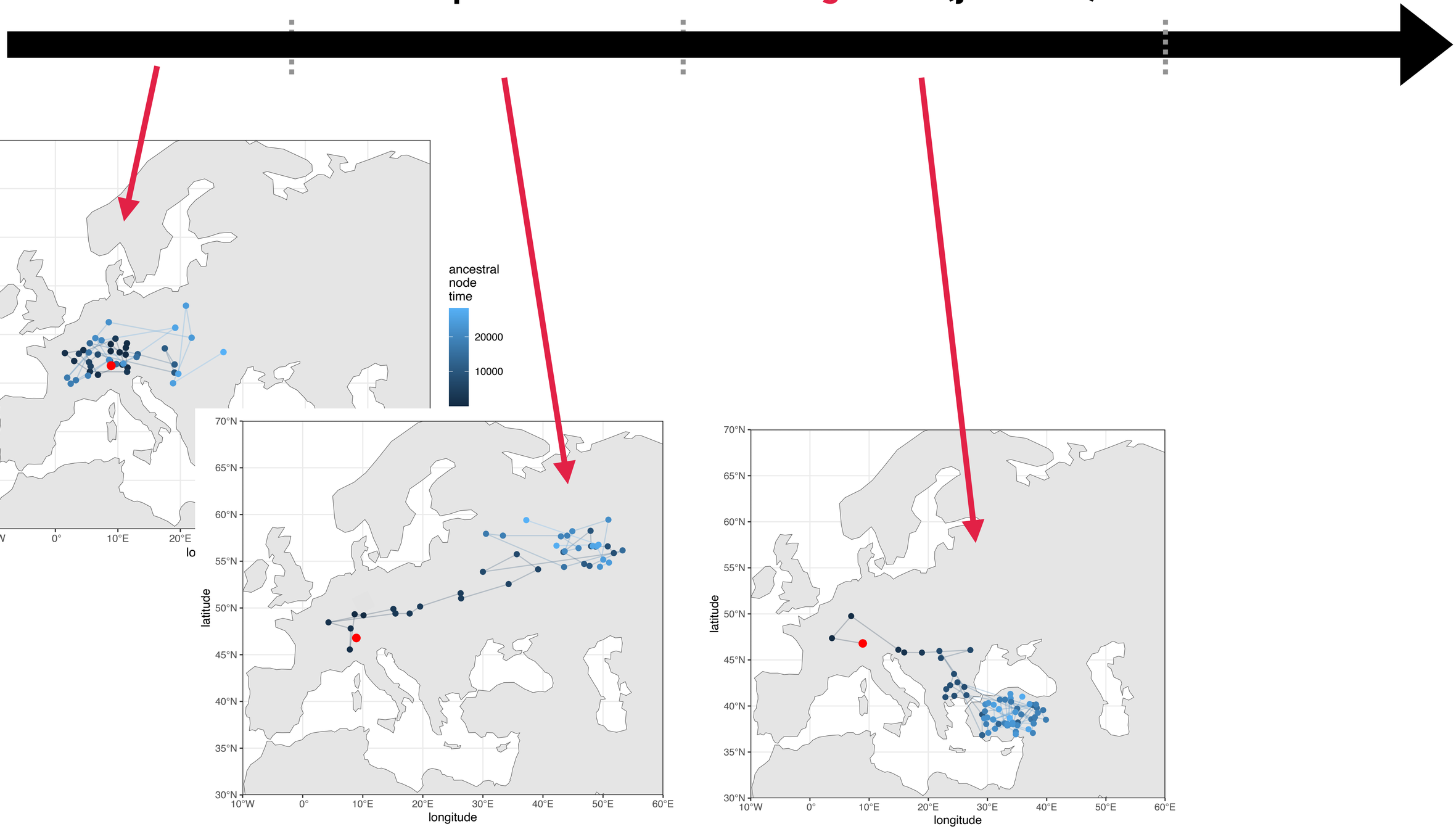

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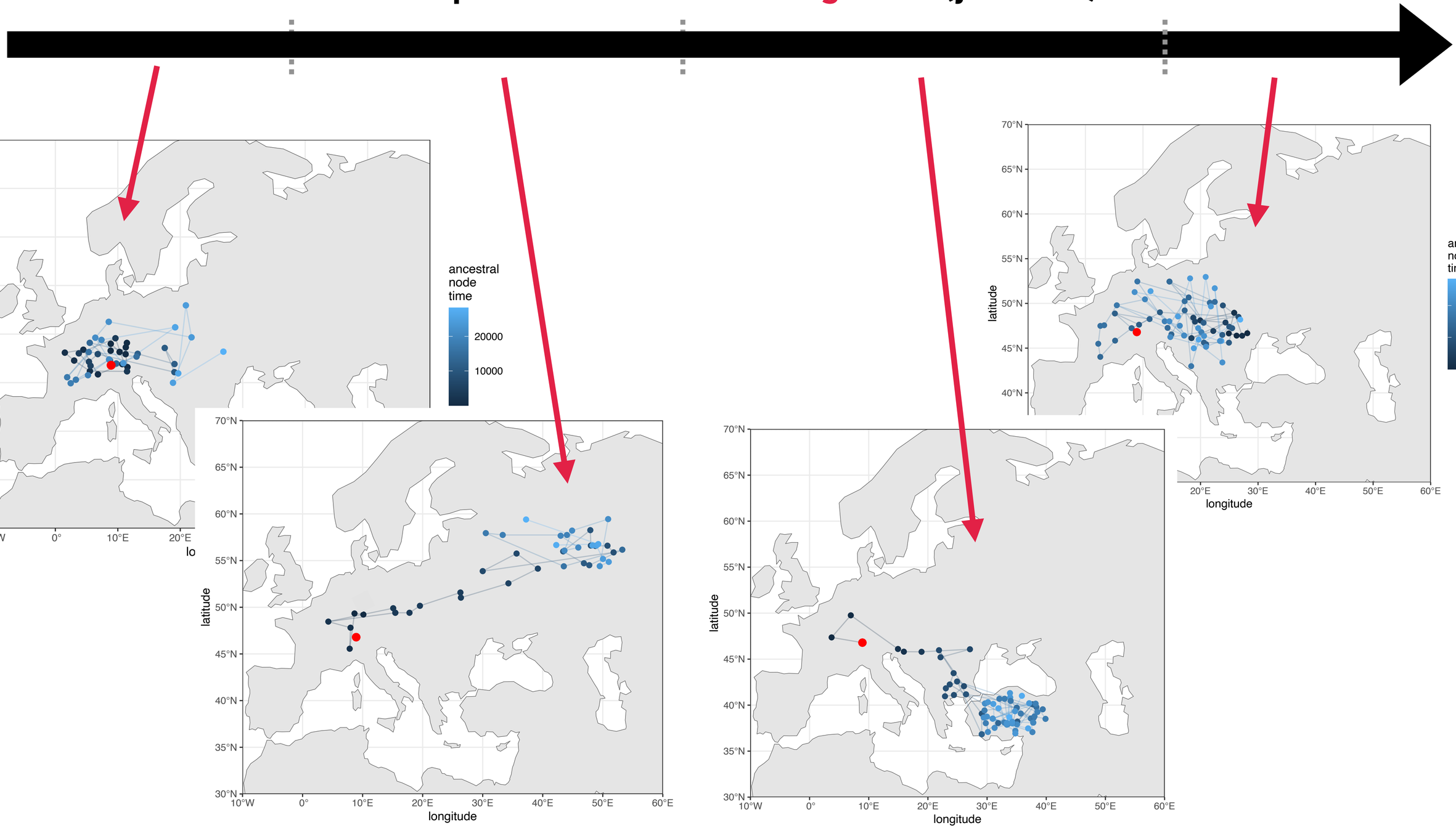

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2. **Tree sequence** is a true game-changer in population genetic simulation and facilitates novel approaches for analysis of large-scale data sets.

3. We are close to entirely **new kinds of geographically-explicit studies** of the history of genetic ancestry across space and time.

Thanks!

Fernando Racimo

& the whole Racimo group

Ben Haller, Peter L. Ralph

UNIVERSITY OF COPENHAGEN

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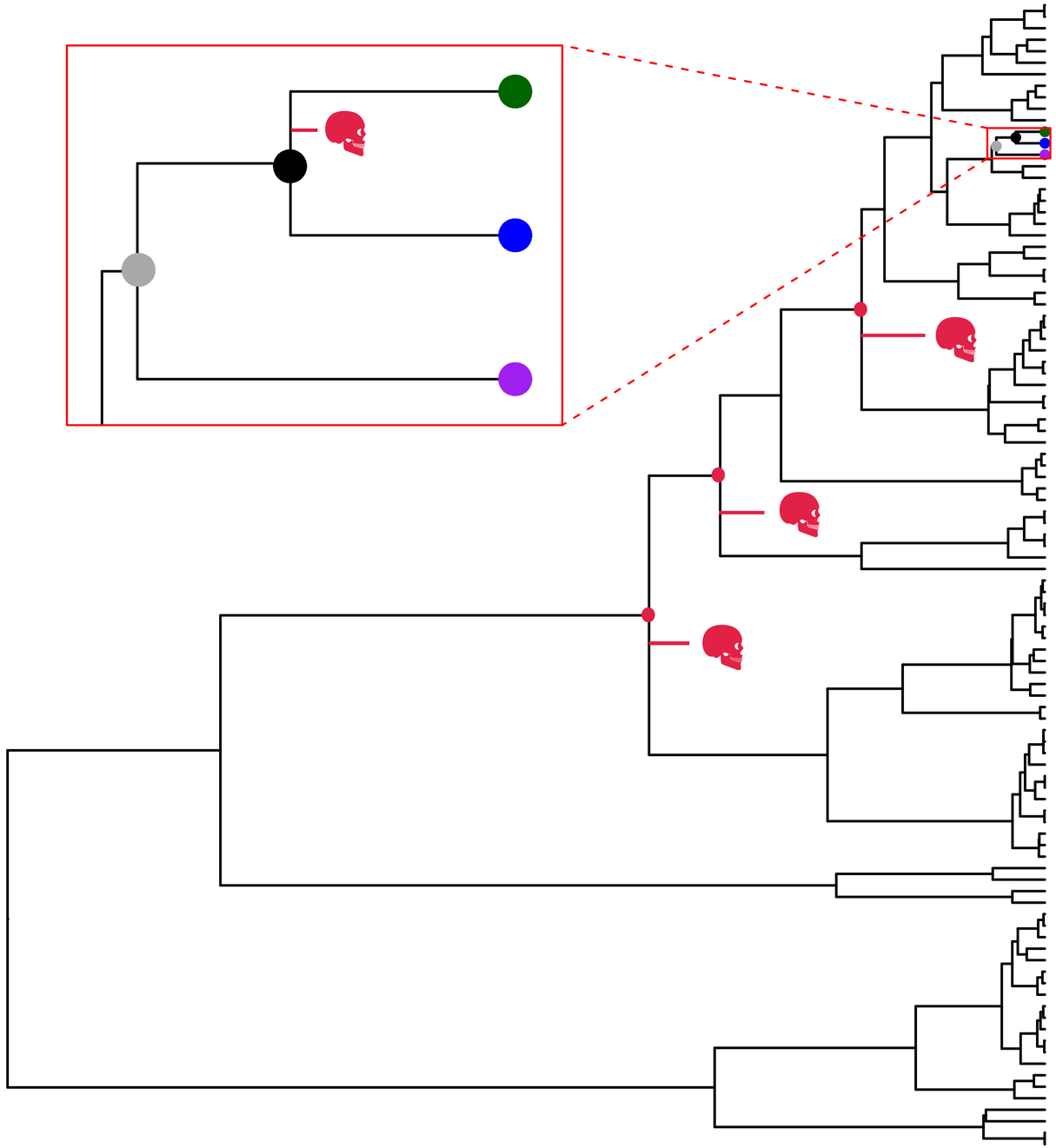
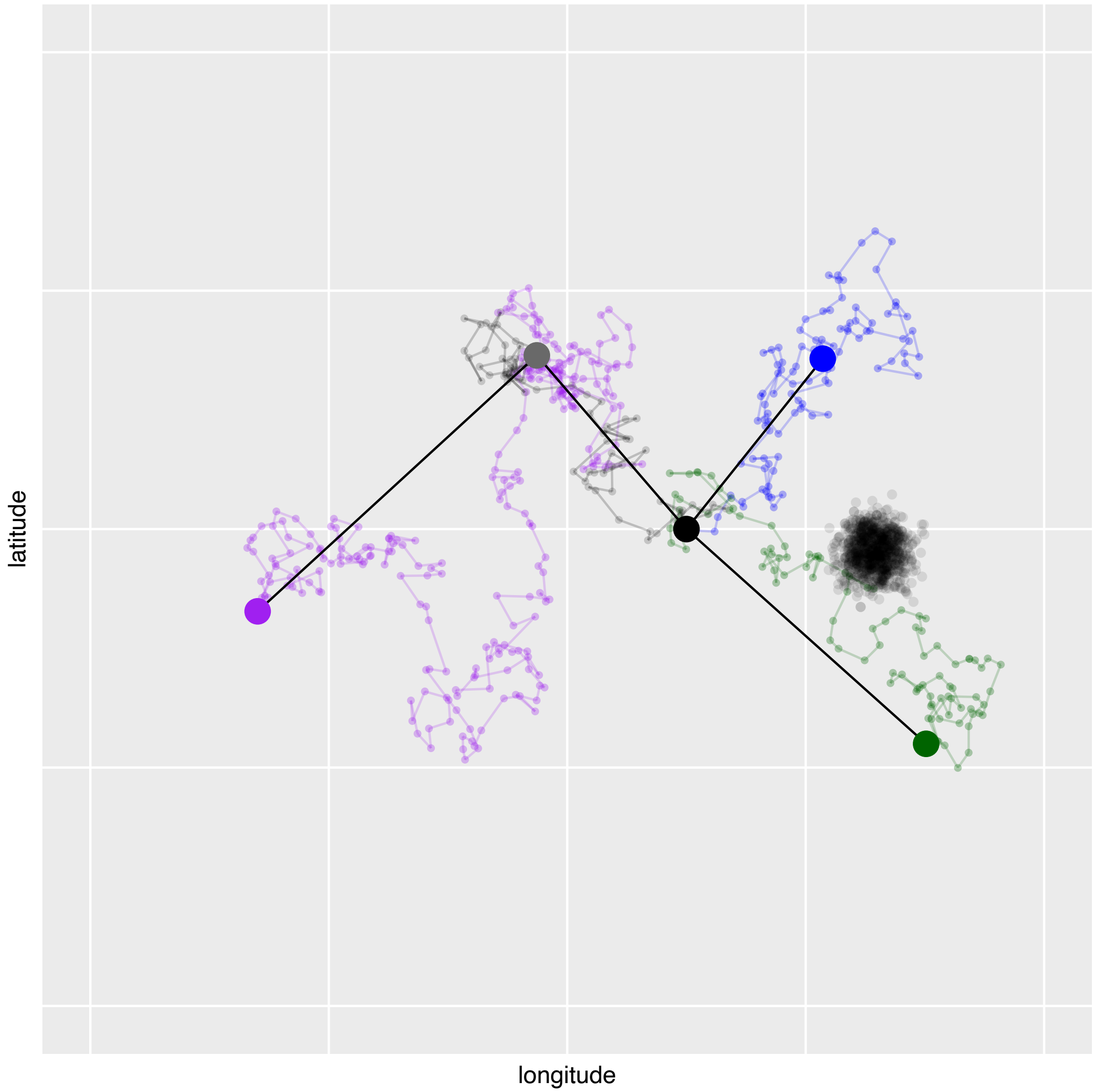
novo nordisk fonden

email: mp@bodkan.net

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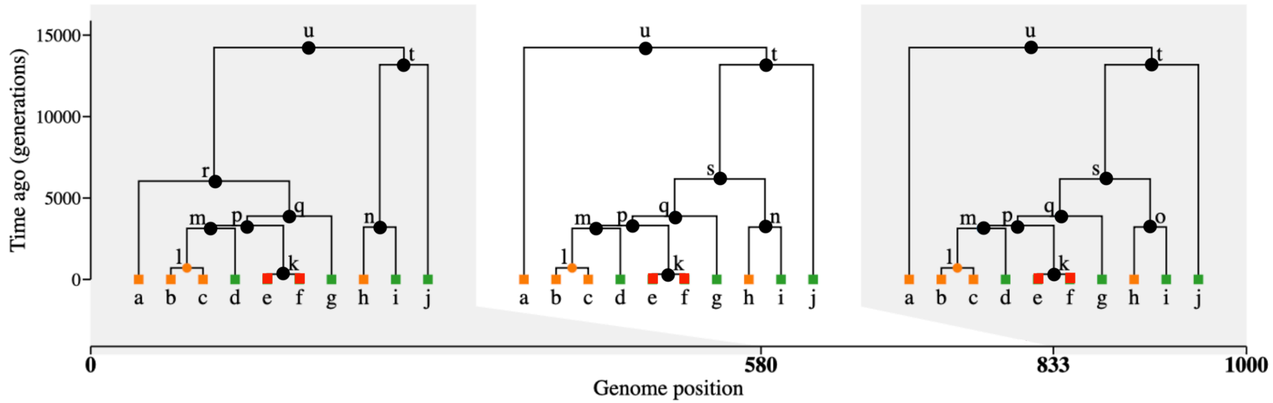
Genealogical nearest neighbours (GNN)



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Kelleher *et al.*, Nat Genetics 2019

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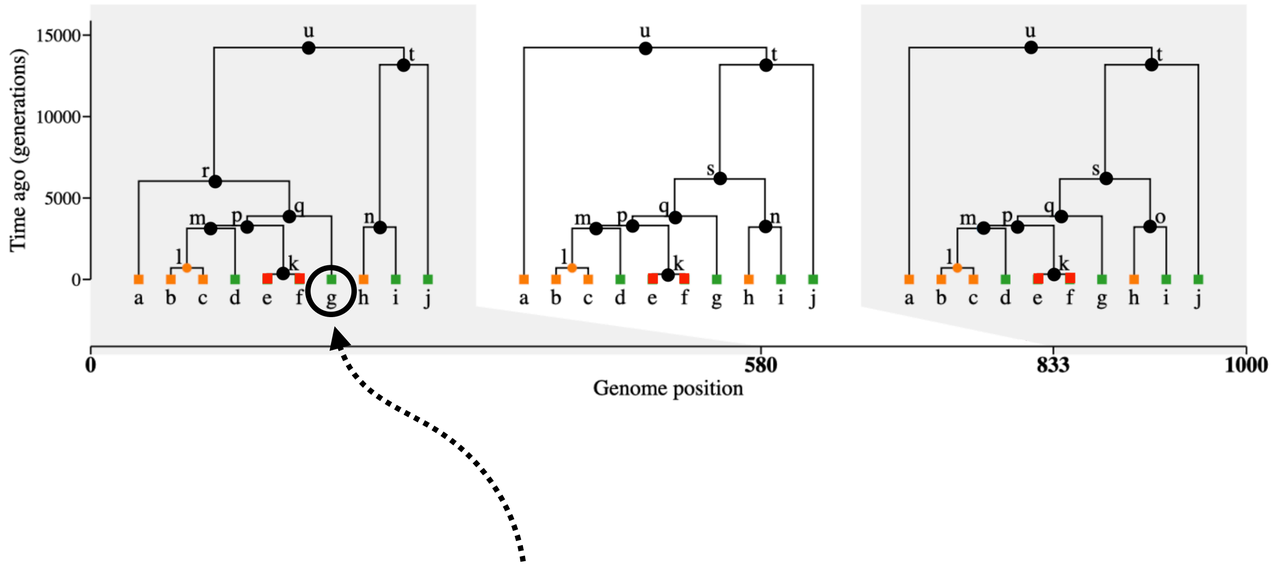

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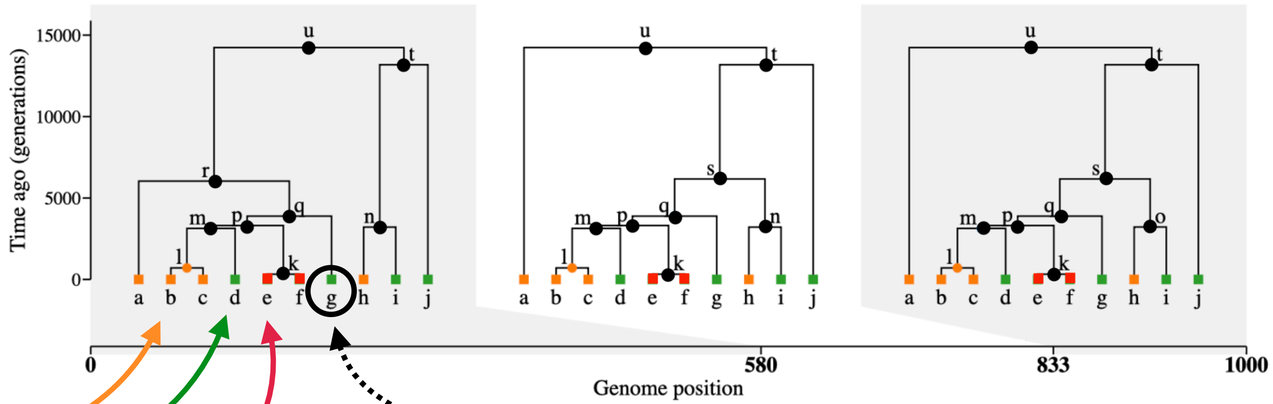

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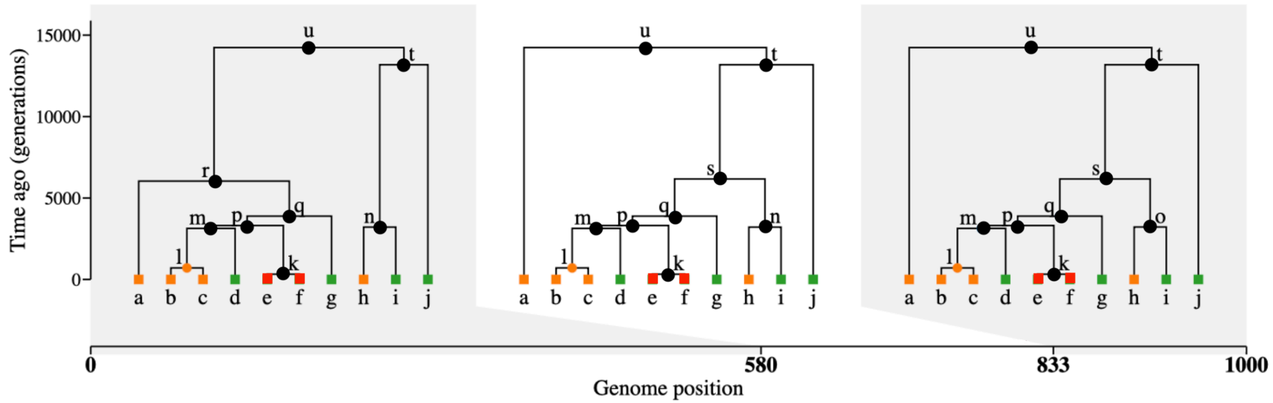

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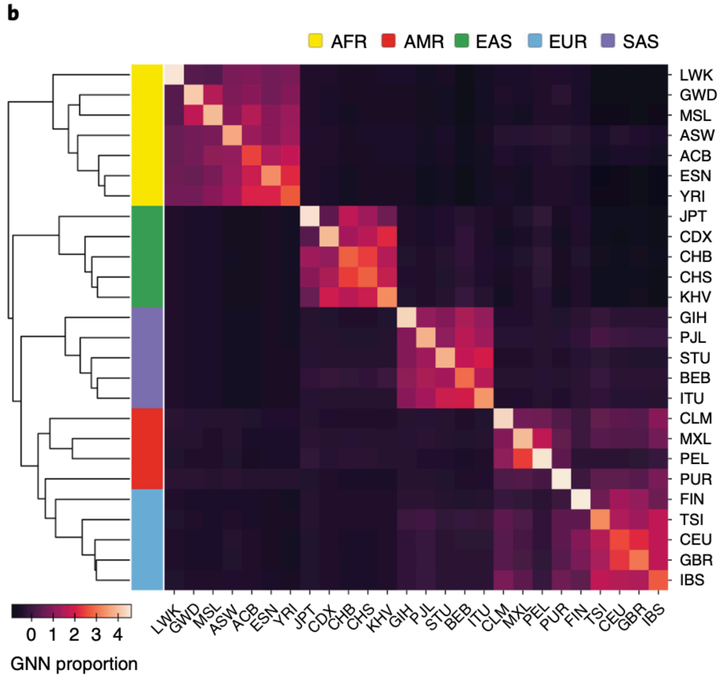
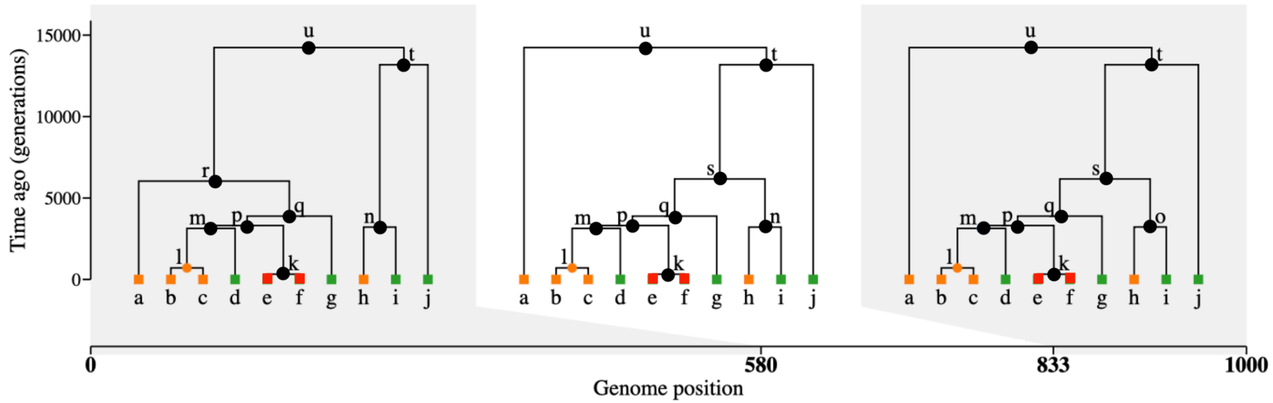


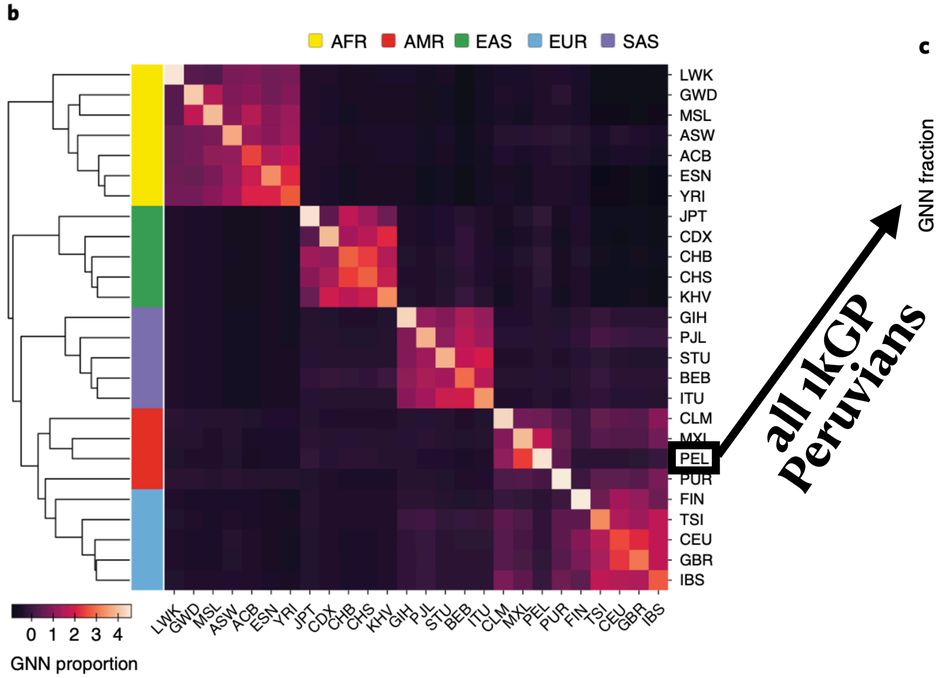
GNN clustering for all 2504 1000 Genomes Project individuals

Kelleher *et al.*, Nat Genetics 2019

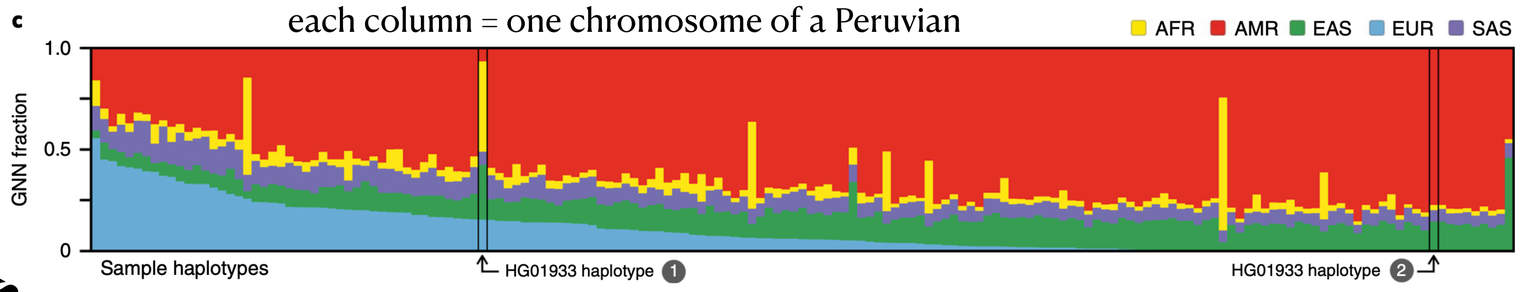
Genealogical nearest neighbours (GNN)



population 1
population 1
population 1



all 1kGP Peruvians



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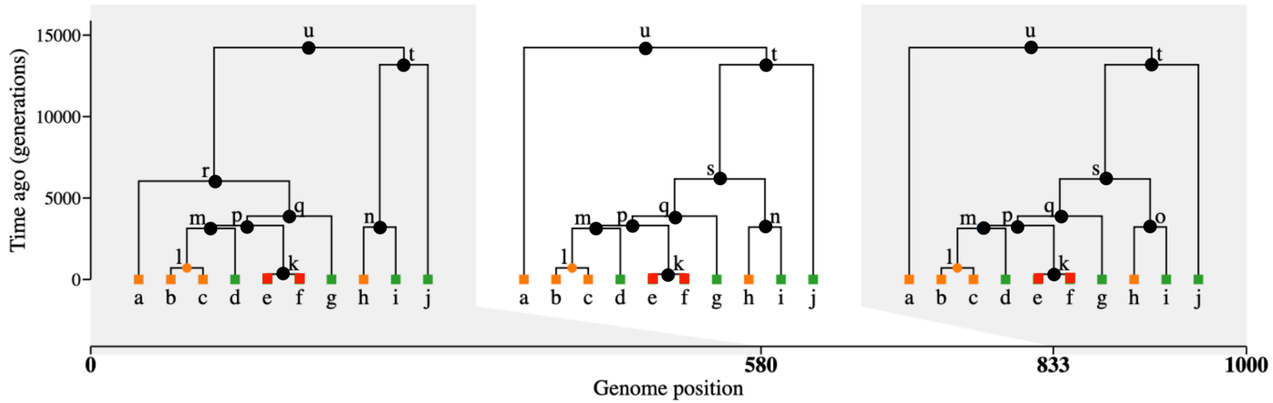
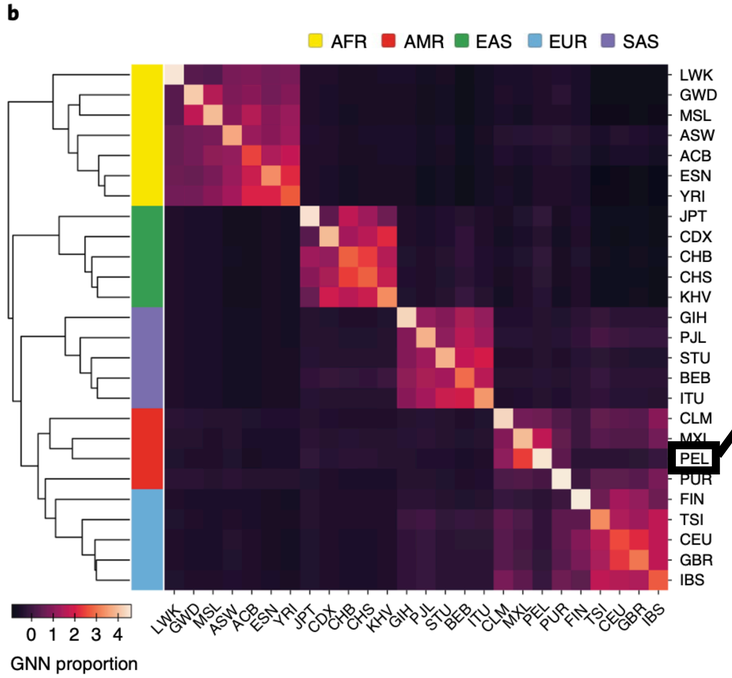


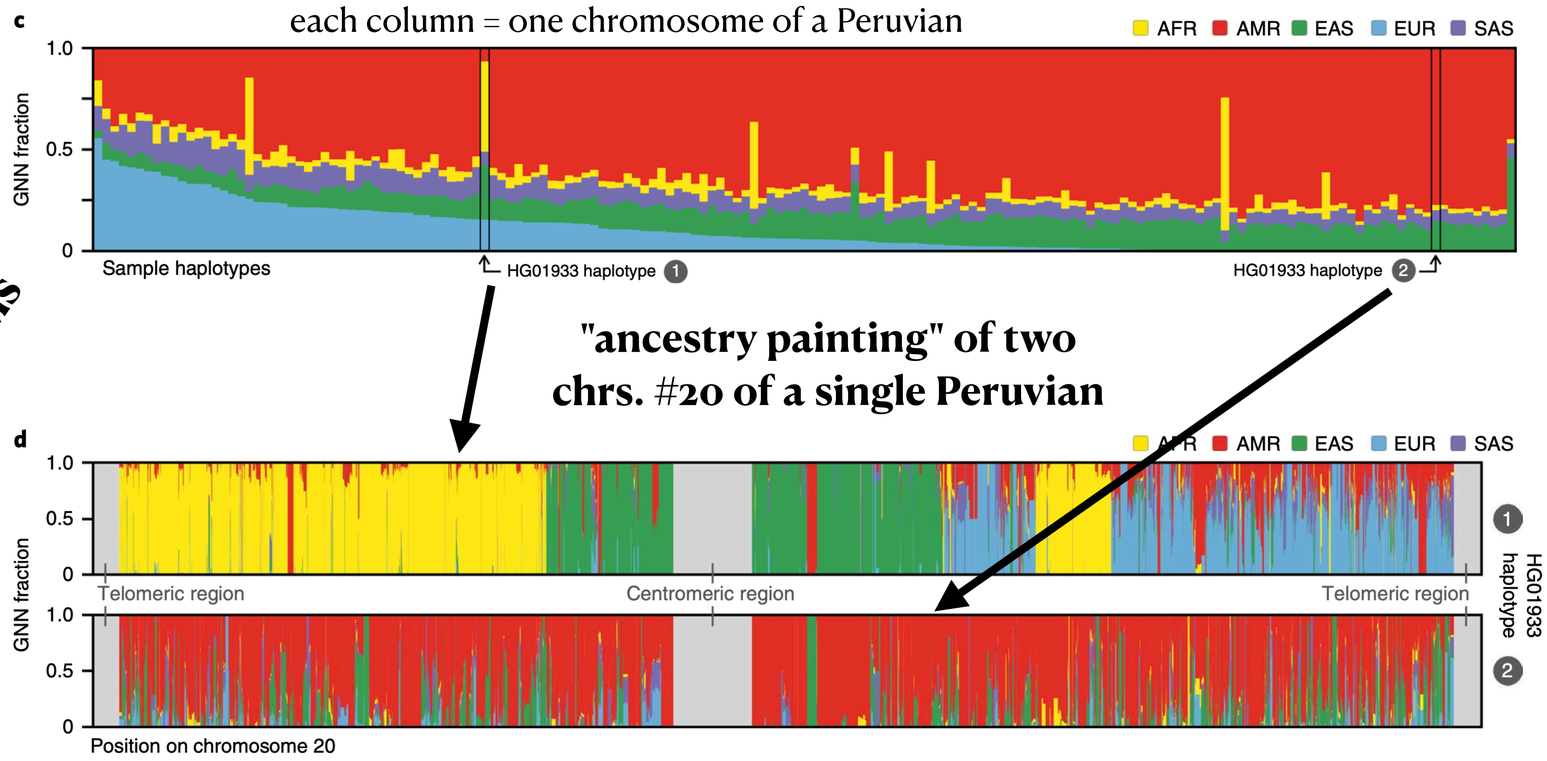
population 1

population 1

population 1



all 1kGP Peruvians



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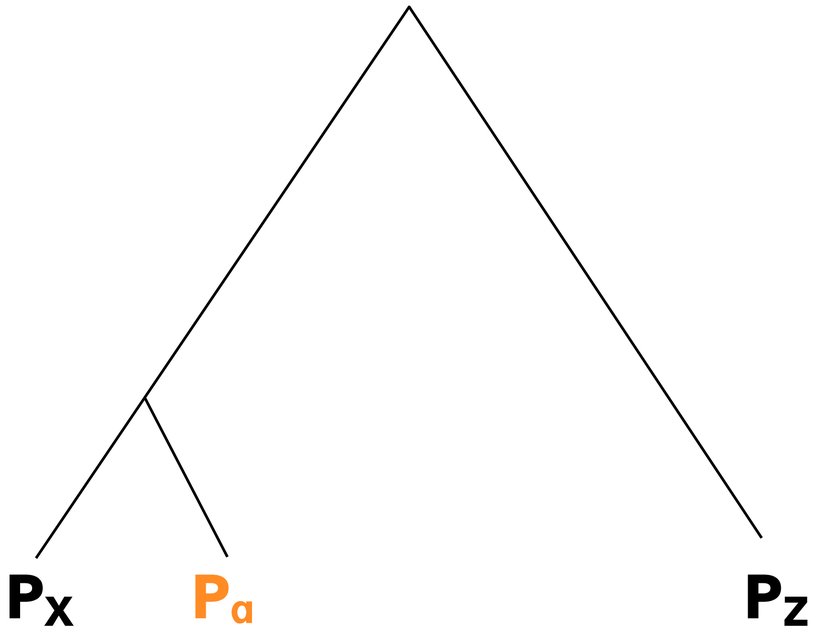
How do traditional popgen statistics work? — *f*-statistics



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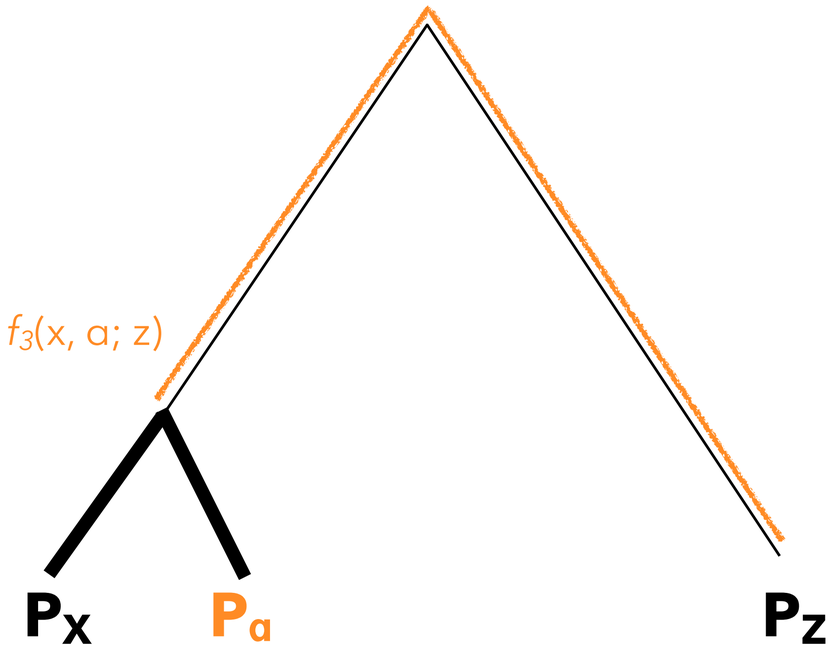

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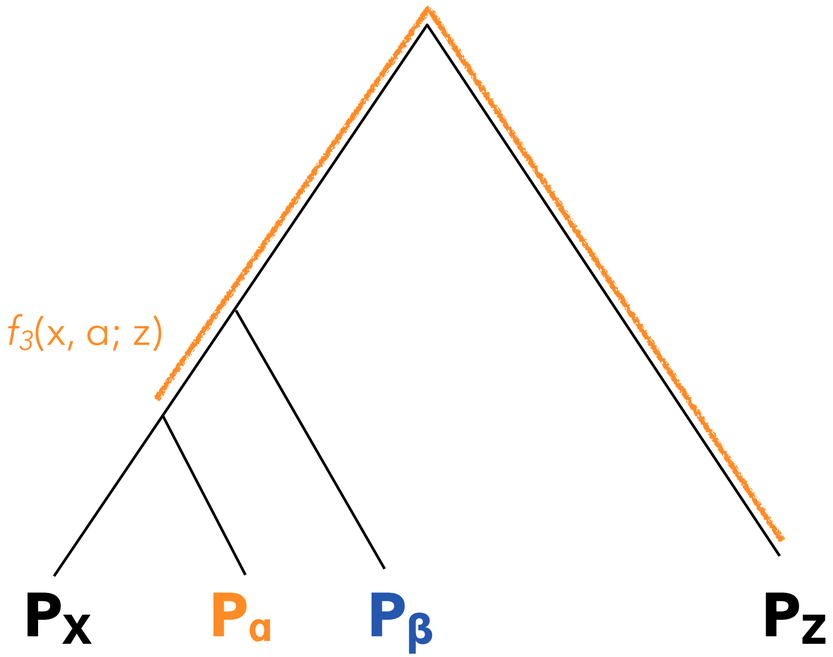

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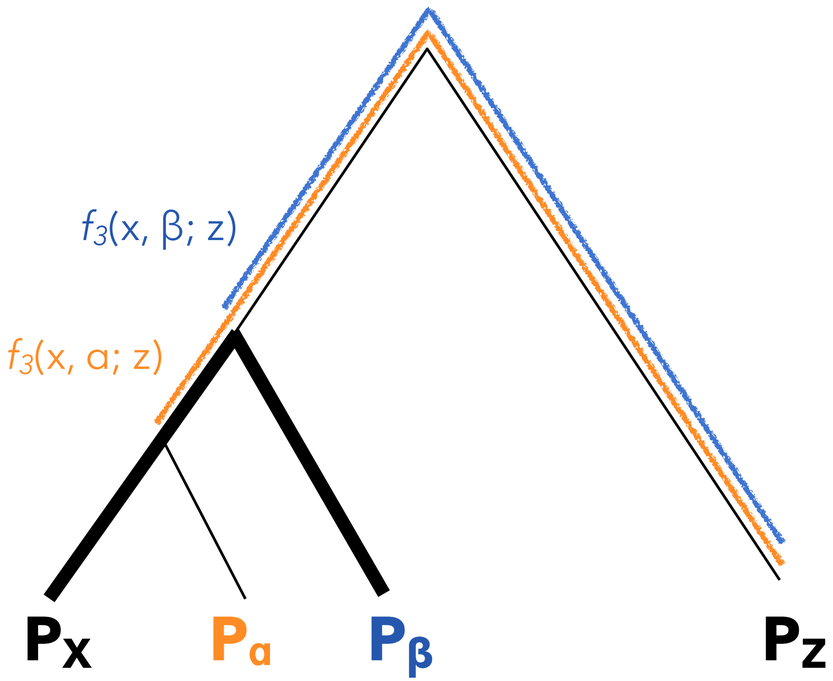

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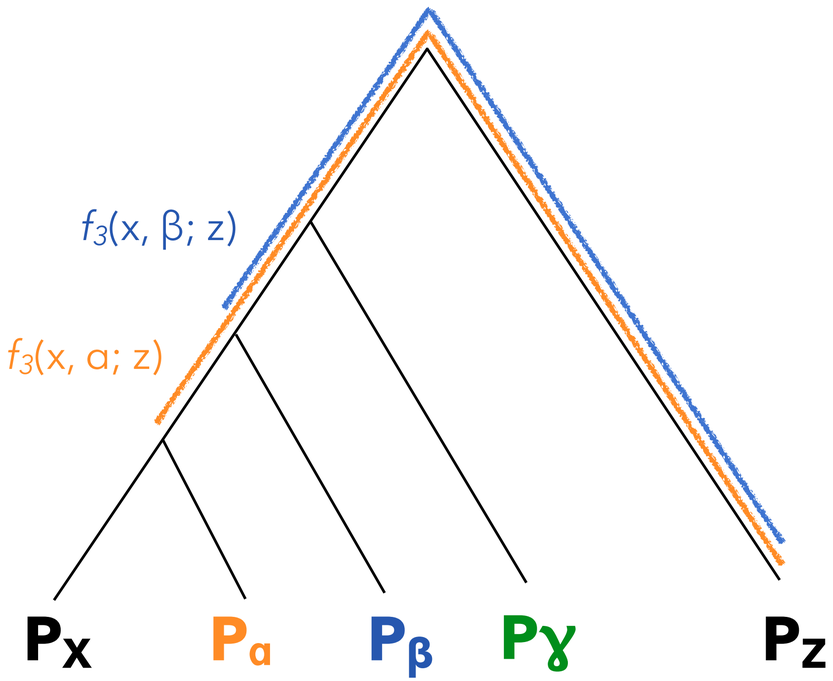

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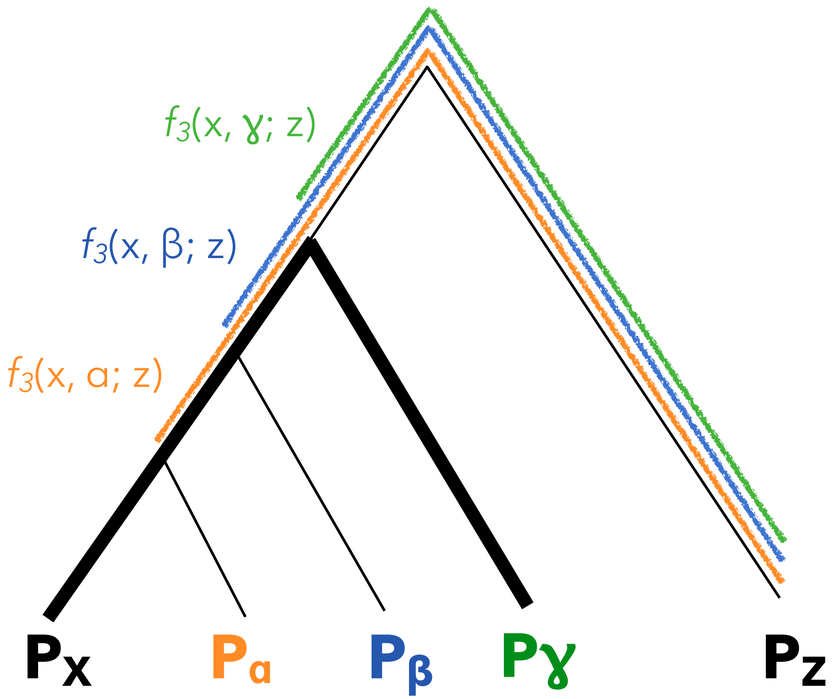

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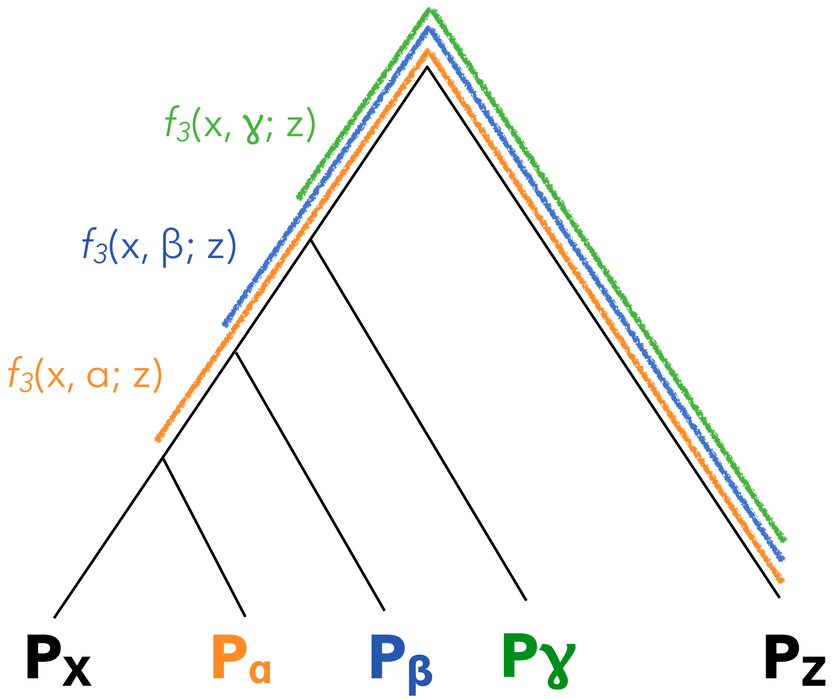

f_3(x, α; z) > f_3(x, β; z) > f_3(x, ɣ; z)

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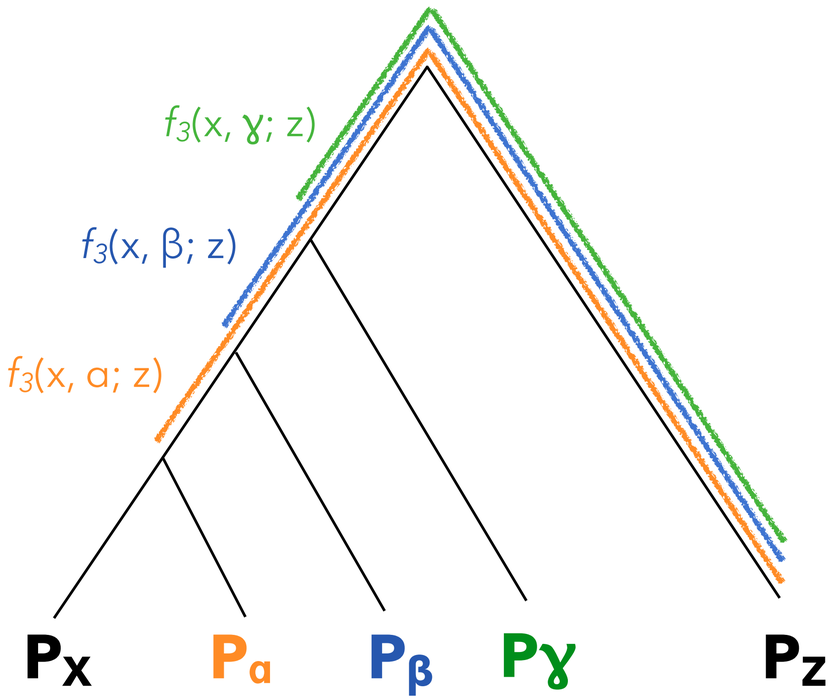
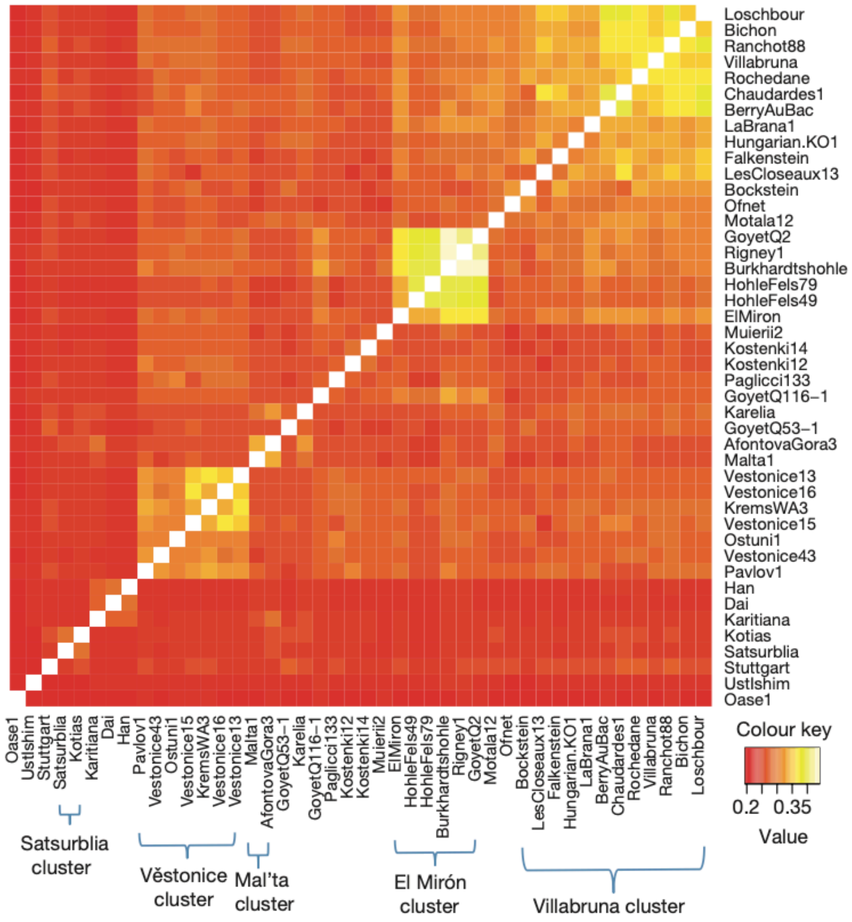


f_3(x, α; z) > f_3(x, β; z) > f_3(x, ɣ; z)

pairwise f_3 heatmap matrix



Fu *et al.*, Nature 2016

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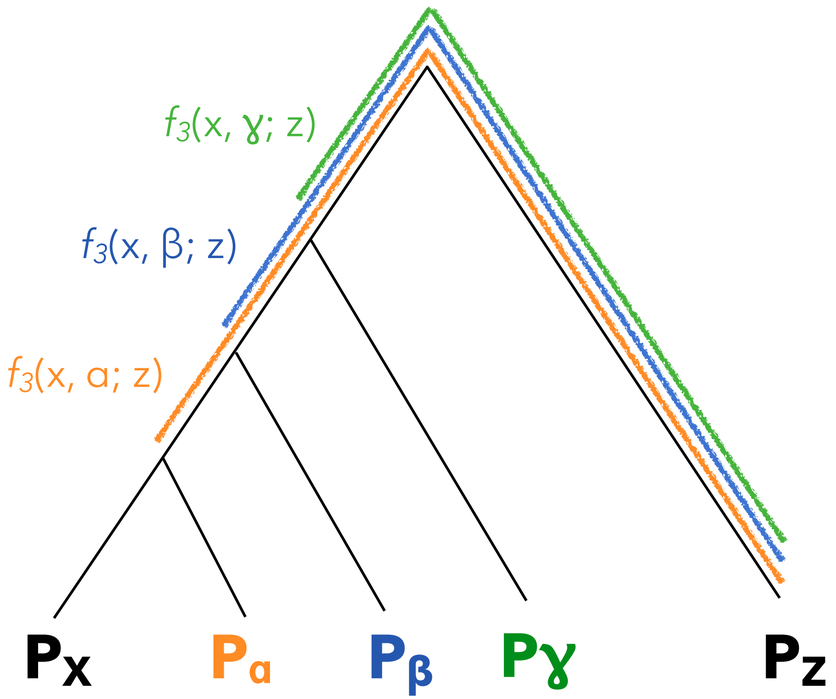
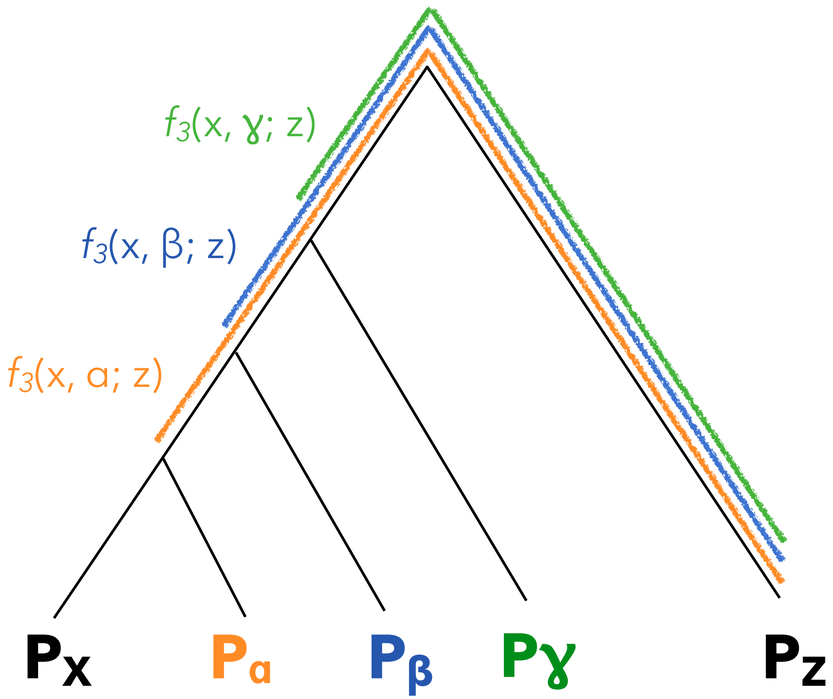


$f_3(x, \alpha; z) > f_3(x, \beta; z) > f_3(x, \gamma; z)$

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	HG00096	HG00099	HG00101
12	60076	.	A	C	100	PASS	.	GT	1|0	0|0	0|0
12	60252	.	A	G	100	PASS	.	GT	0|0	0|0	0|1
12	60317	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	60344	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60383	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	60405	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60474	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	60614	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	60628	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	60654	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61021	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61107	.	G	T	100	PASS	.	GT	0|0	0|0	0|0
12	61172	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61220	.	G	A	100	PASS	.	GT	0|0	0|0	0|1
12	61258	.	C	T	100	PASS	.	GT	0|0	0|0	0|1
12	61272	.	T	C	100	PASS	.	GT	0|0	0|0	0|0
12	61329	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61341	.	G	A	100	PASS	.	GT	0|0	0|1	0|1
12	61368	.	C	T	100	PASS	.	GT	0|0	0|1	0|1
12	61392	.	T	A	100	PASS	.	GT	0|0	0|0	0|0
12	61405	.	G	C	100	PASS	.	GT	0|0	0|0	0|0
12	61411	.	C	A	100	PASS	.	GT	0|0	0|0	0|0
12	61416	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61422	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61476	.	C	G	100	PASS	.	GT	0|0	0|0	0|0
12	61510	.	G	A	100	PASS	.	GT	0|0	0|0	0|0
12	61516	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61552	.	C	T	100	PASS	.	GT	0|0	0|0	0|0
12	61604	.	T	G	100	PASS	.	GT	0|0	0|0	0|0
12	61687	.	G	A	100	PASS	.	GT	1|0	0|1	0|1
12	61700	.	C	T	100	PASS	.	GT	0|0	0|0	0|0

This evaluation of "tree-ness" requires lots of time, disk space, and memory.

With a tree sequence, computing statistics is trivial...



f_3(x, α; z) > f_3(x, β; z) > f_3(x, ɣ; z)

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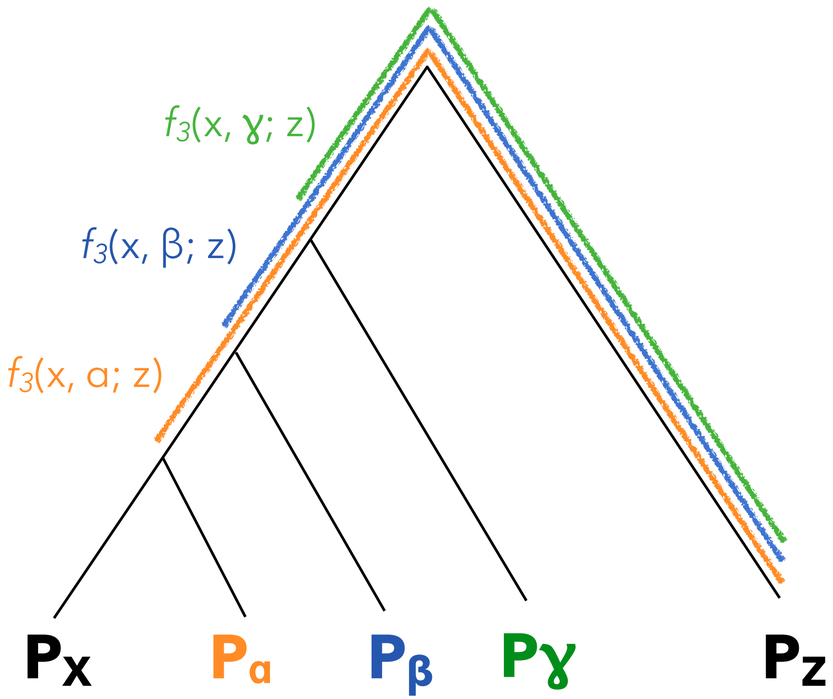

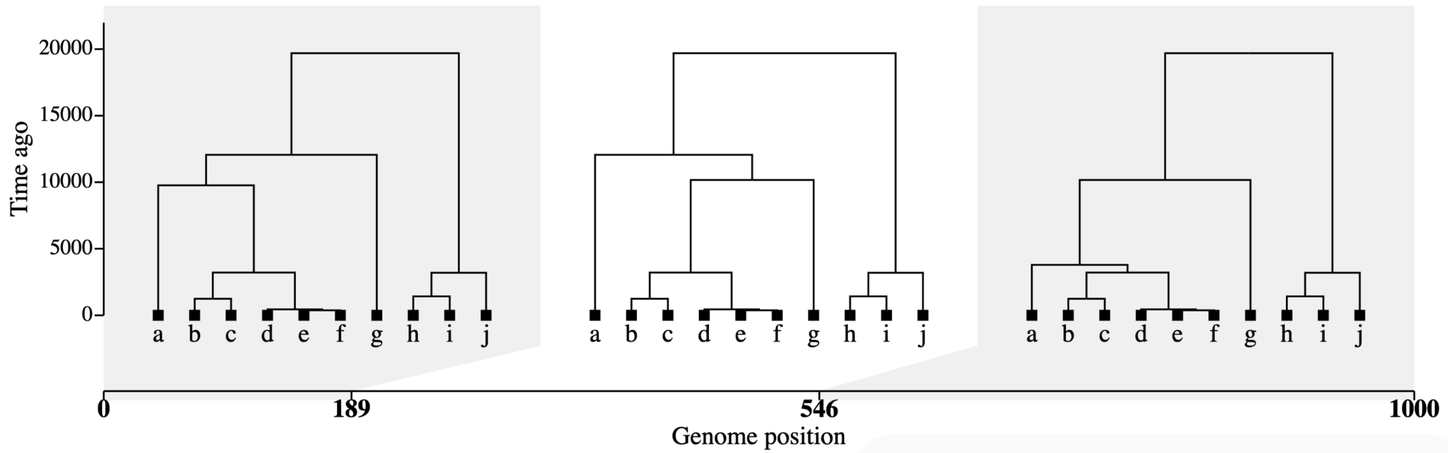

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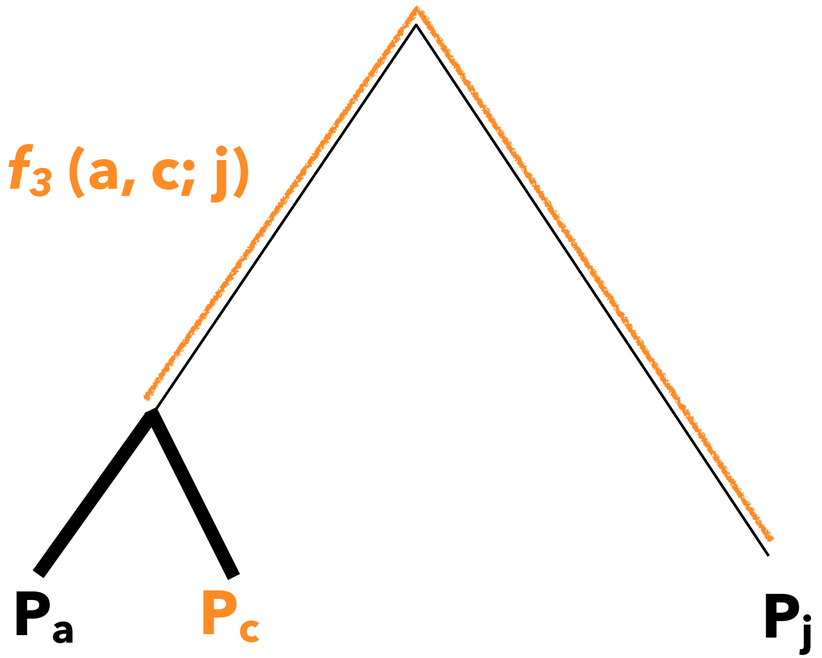

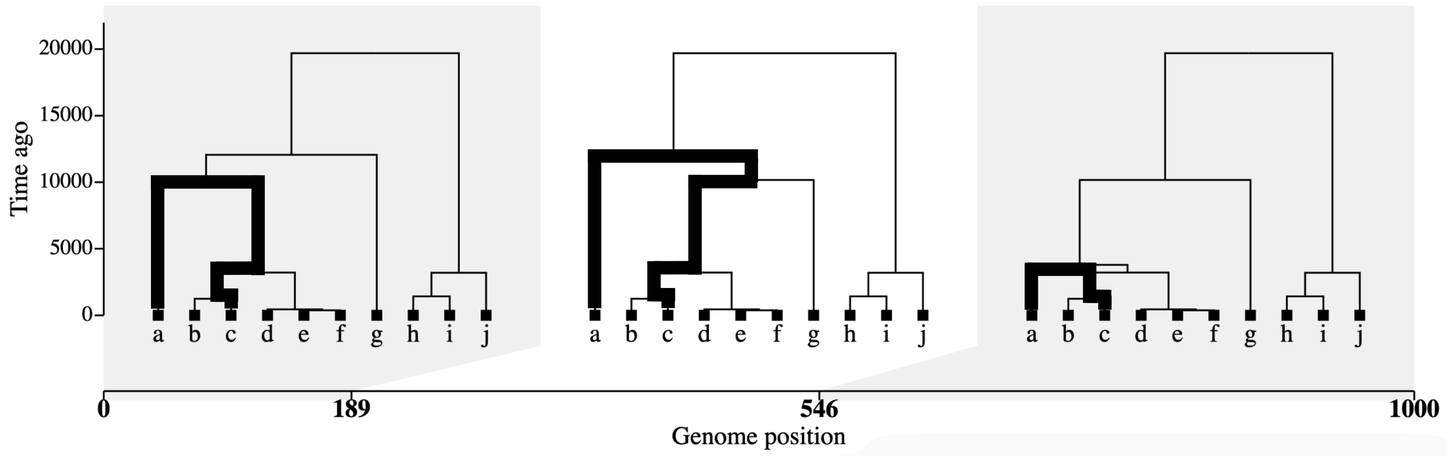

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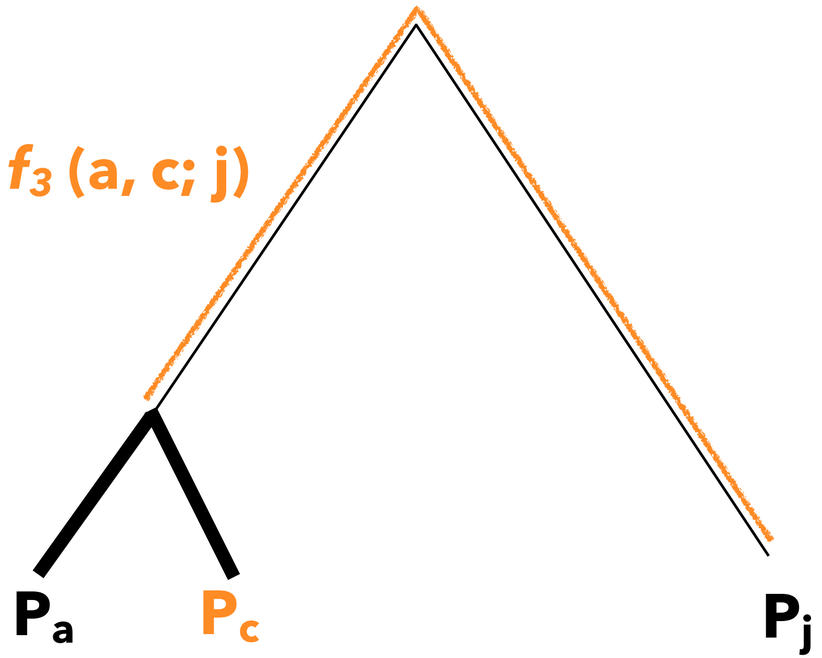

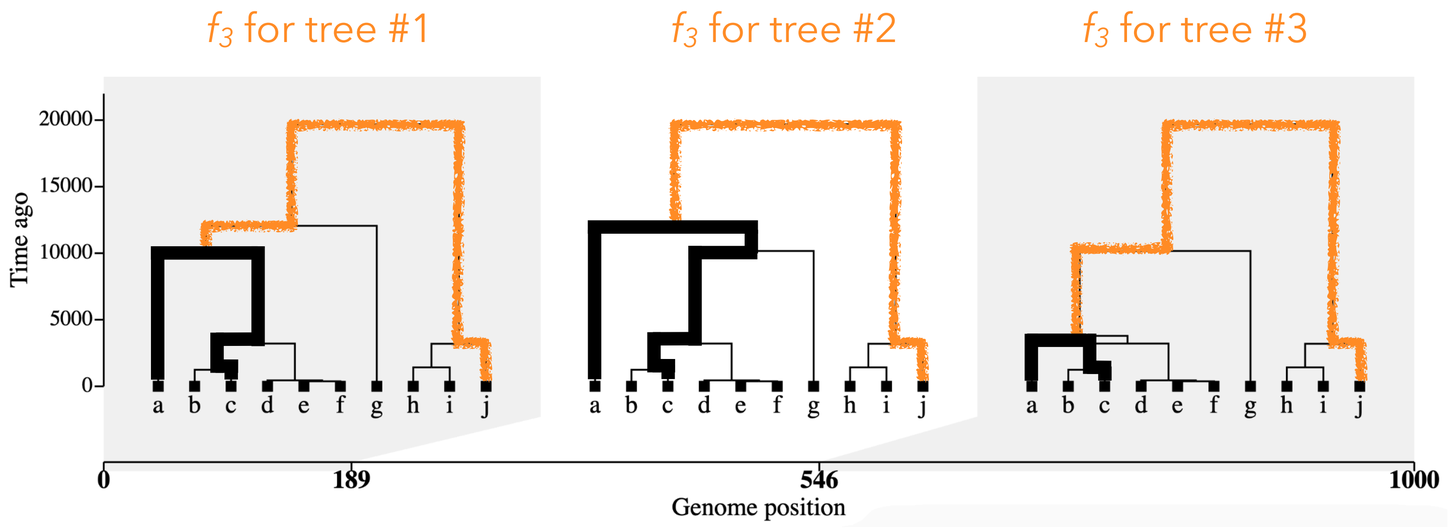

Then aggregate f_3 values across all trees.

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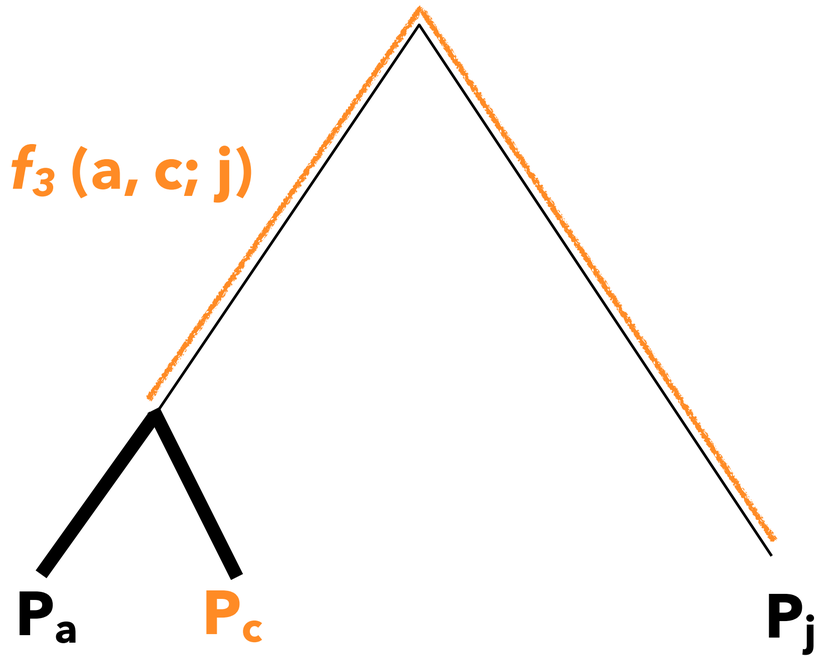

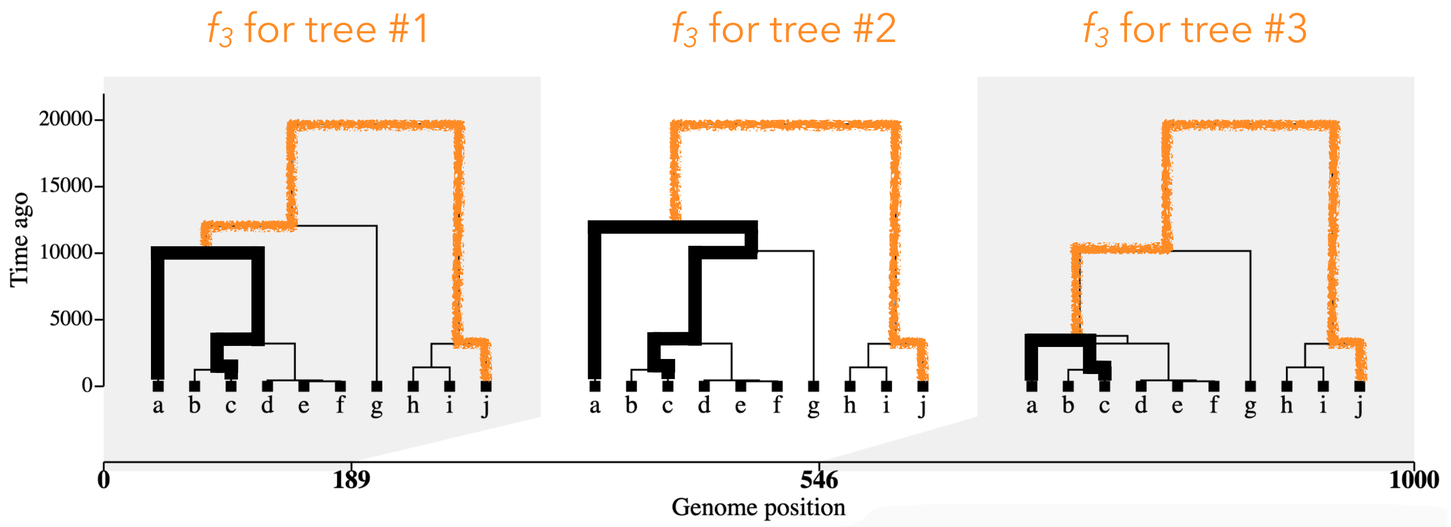

Then aggregate f_3 values across all trees.

This is implemented in *tskit* (tskit.dev) & the R package *slendr* (slendr.net).

Were human migrations associated with changes in landscape?

Racimo *et al.*, PNAS 2020

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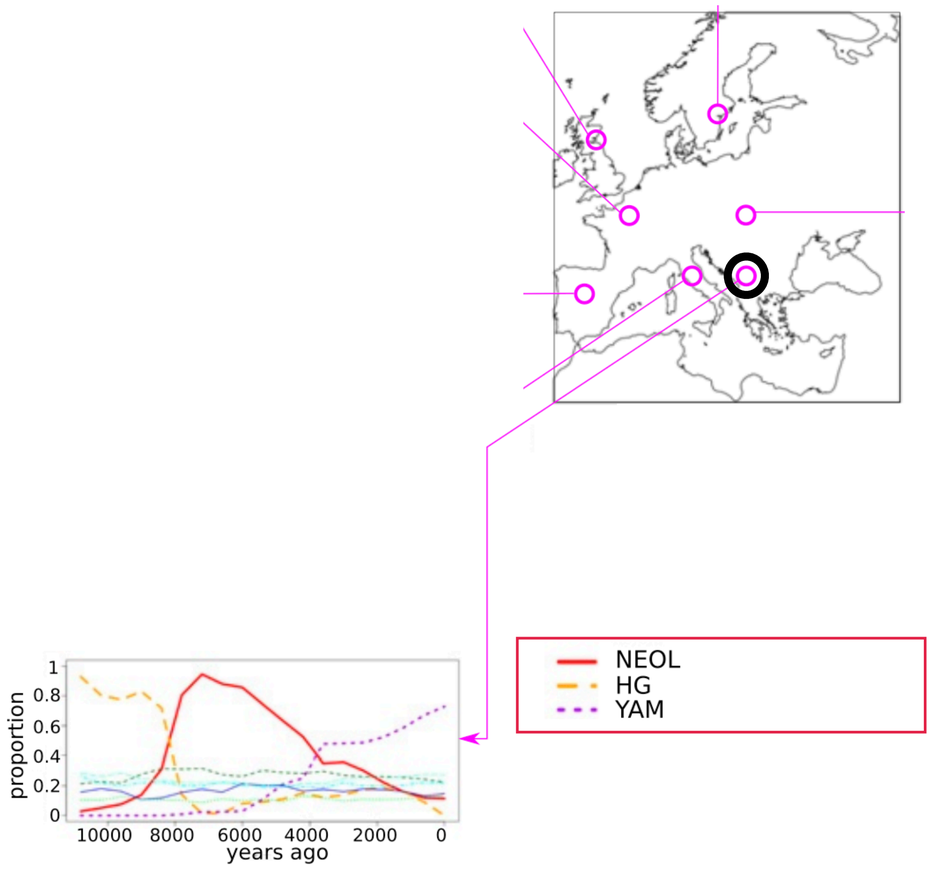

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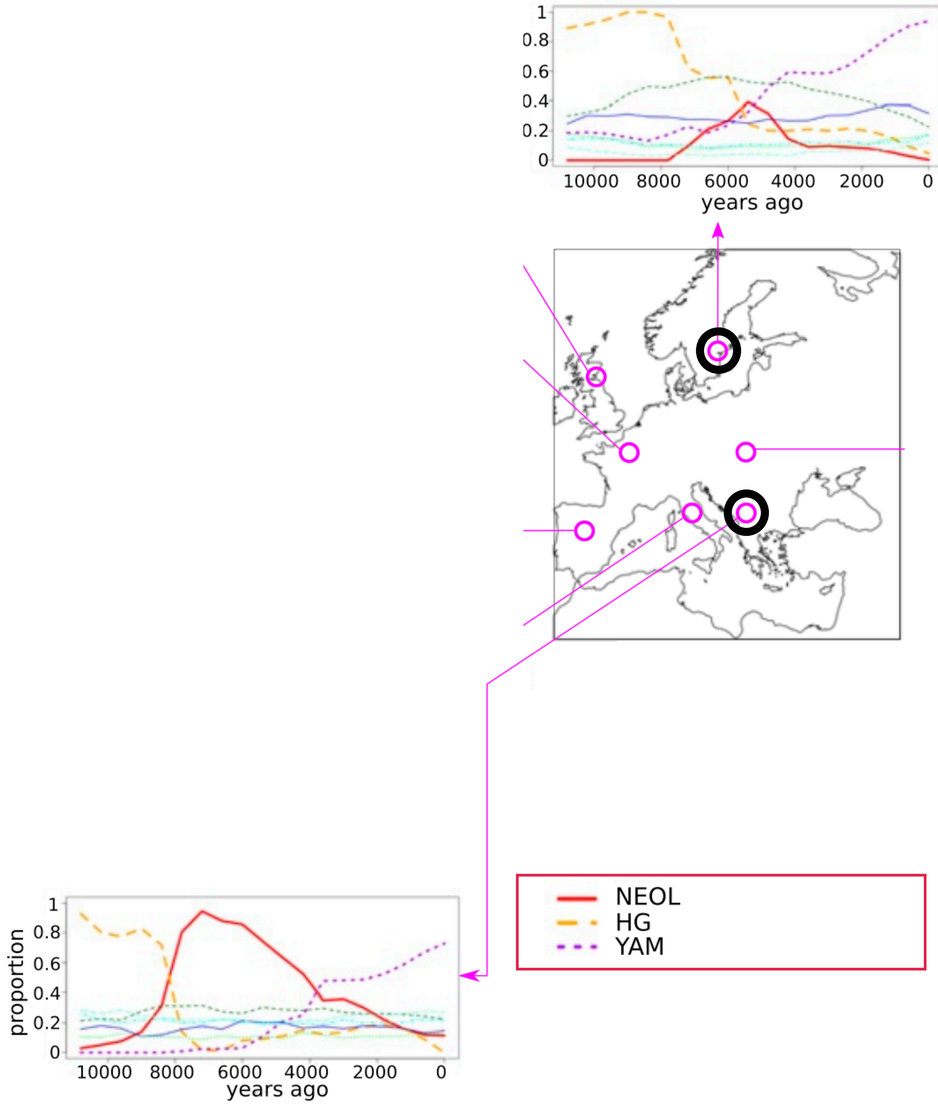

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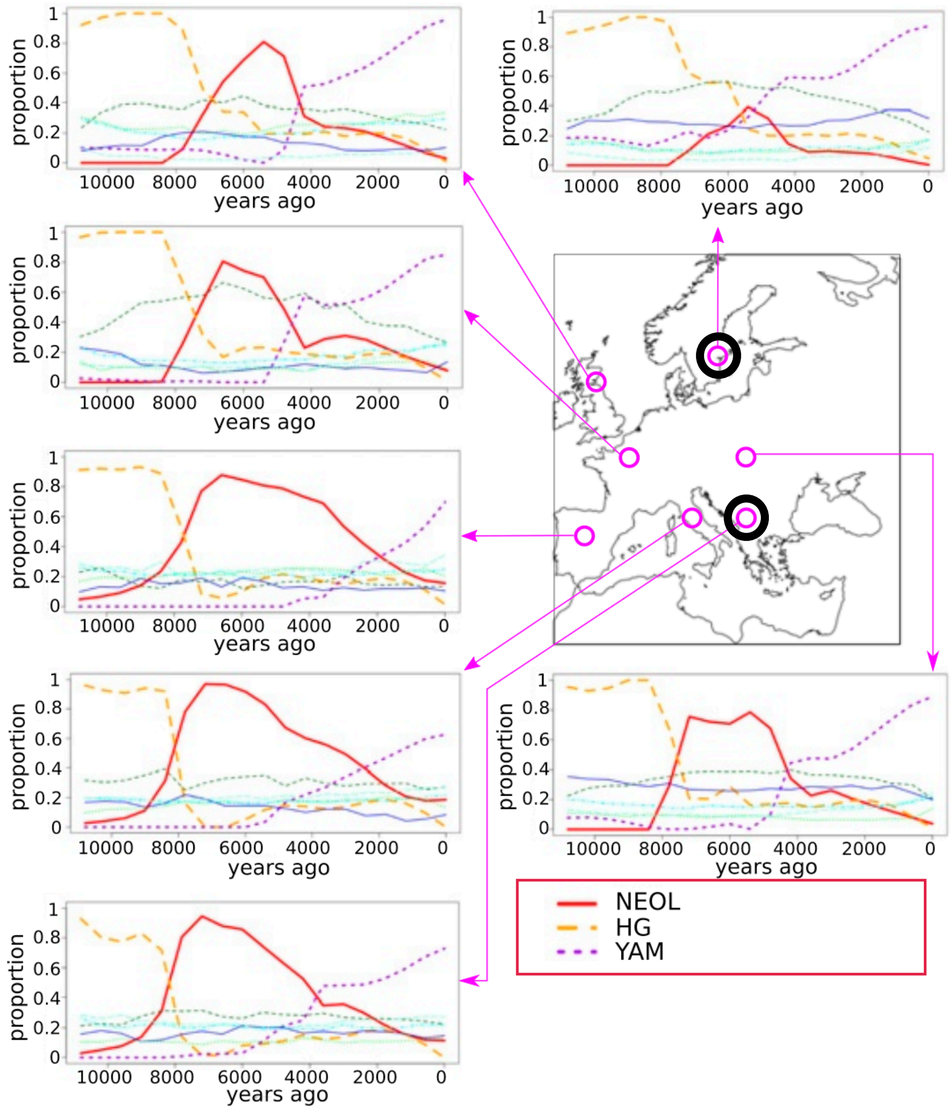

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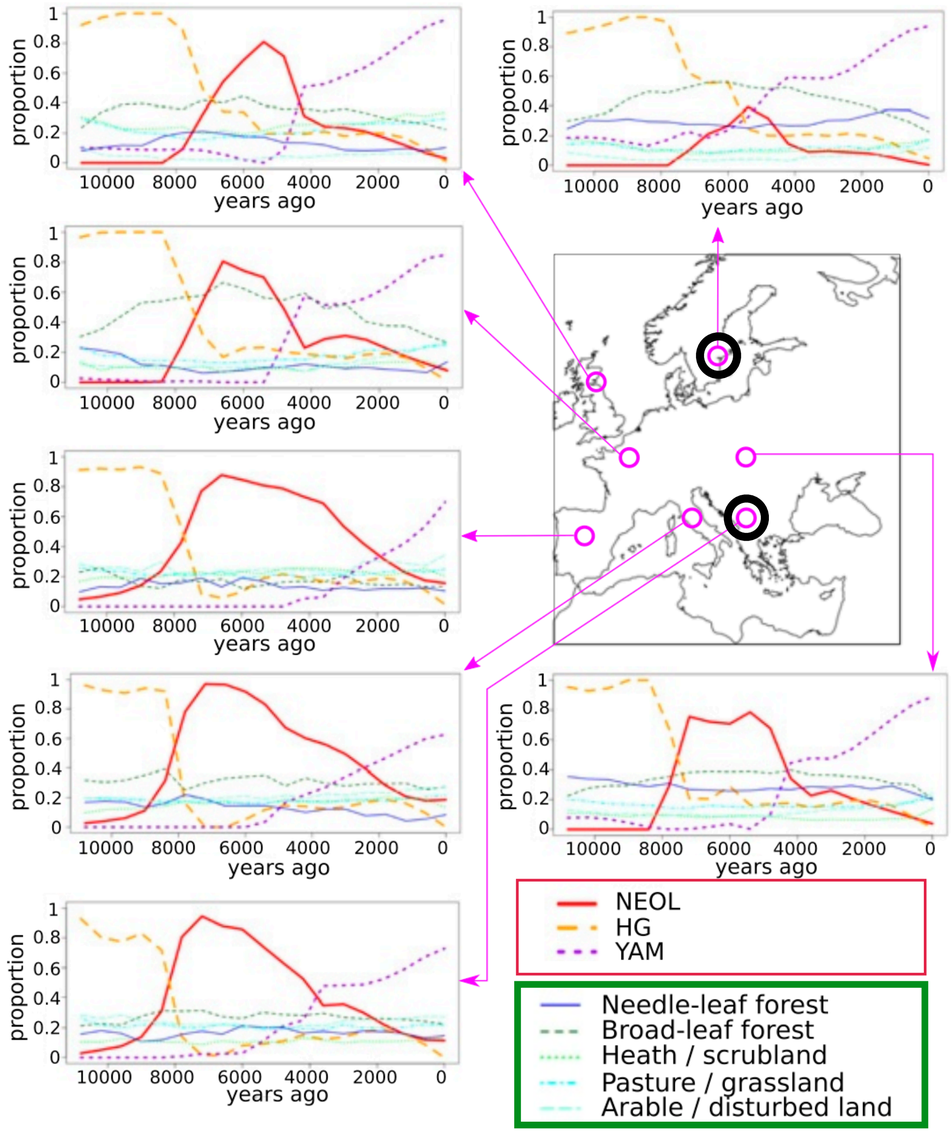

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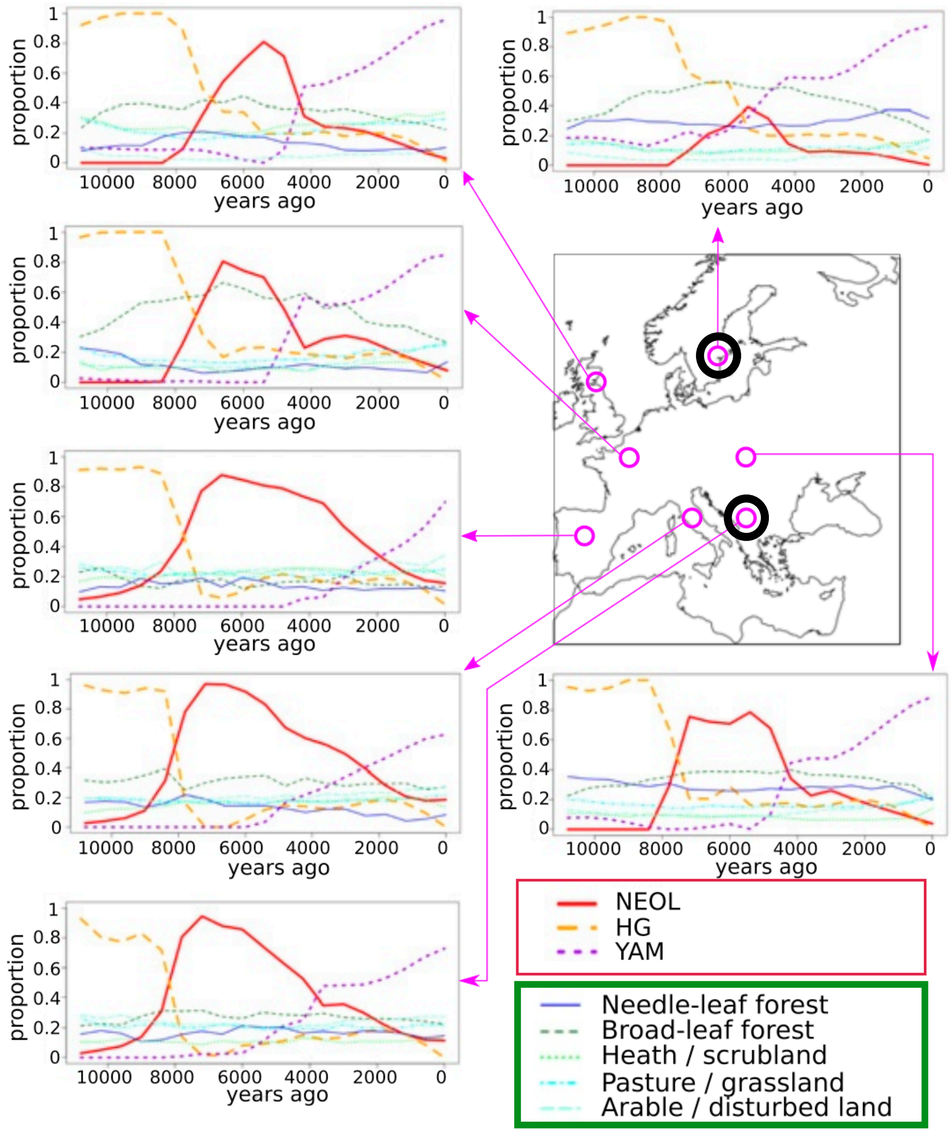
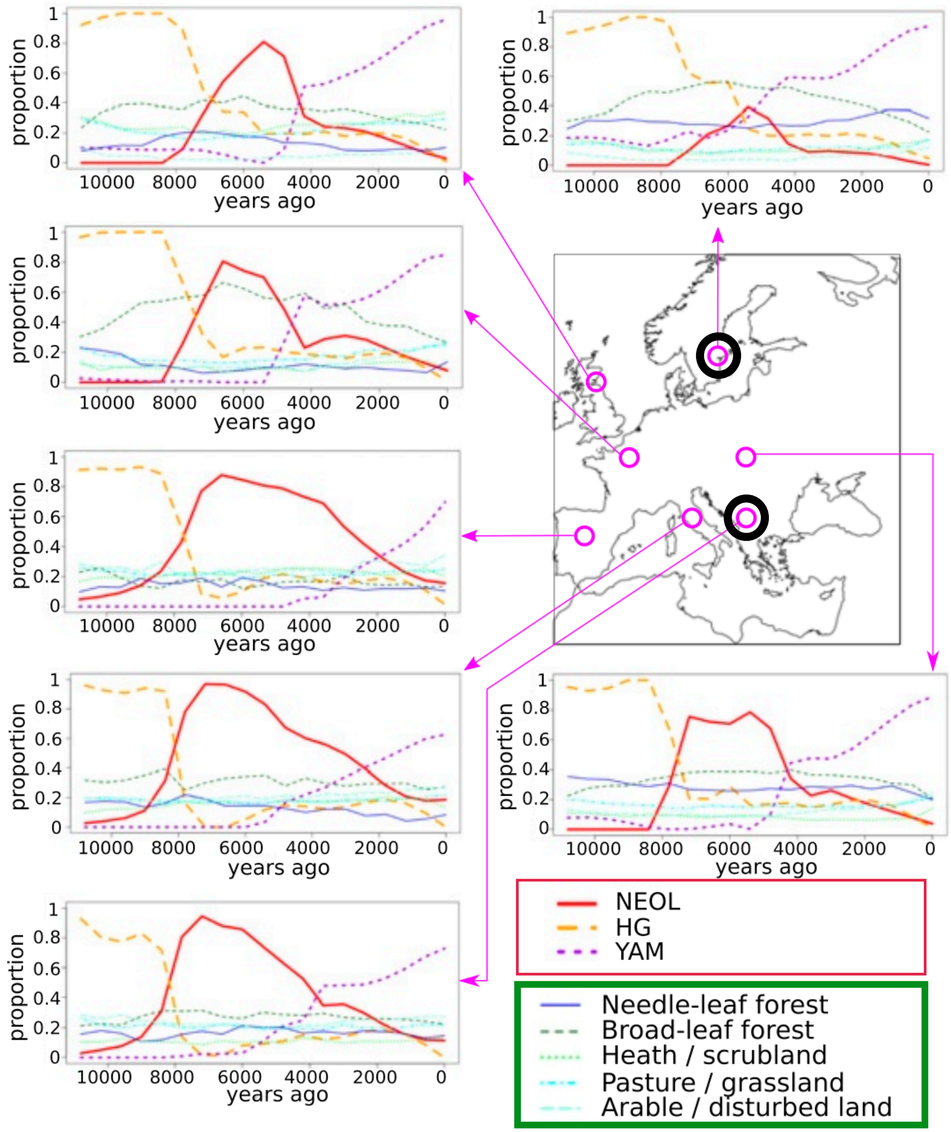


genetic and environmental metrics aggregated over each location of the entire map

Racimo *et al.*, PNAS 2020

Yamnaya coincided with strong vegetation changes



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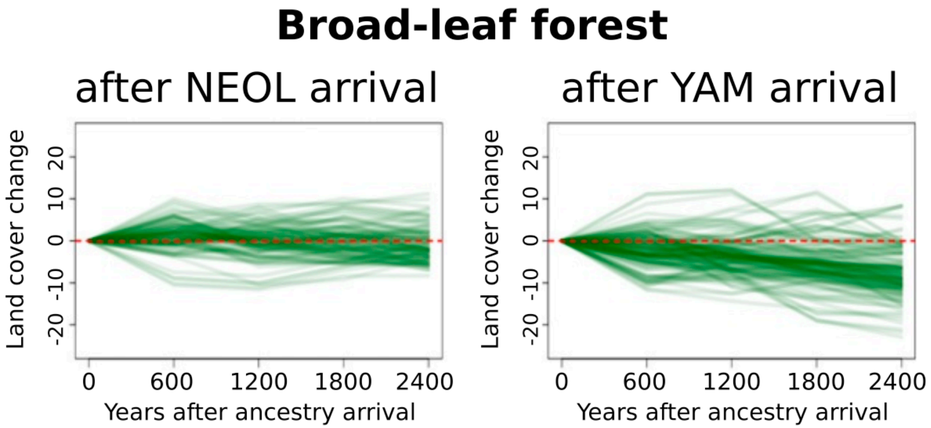

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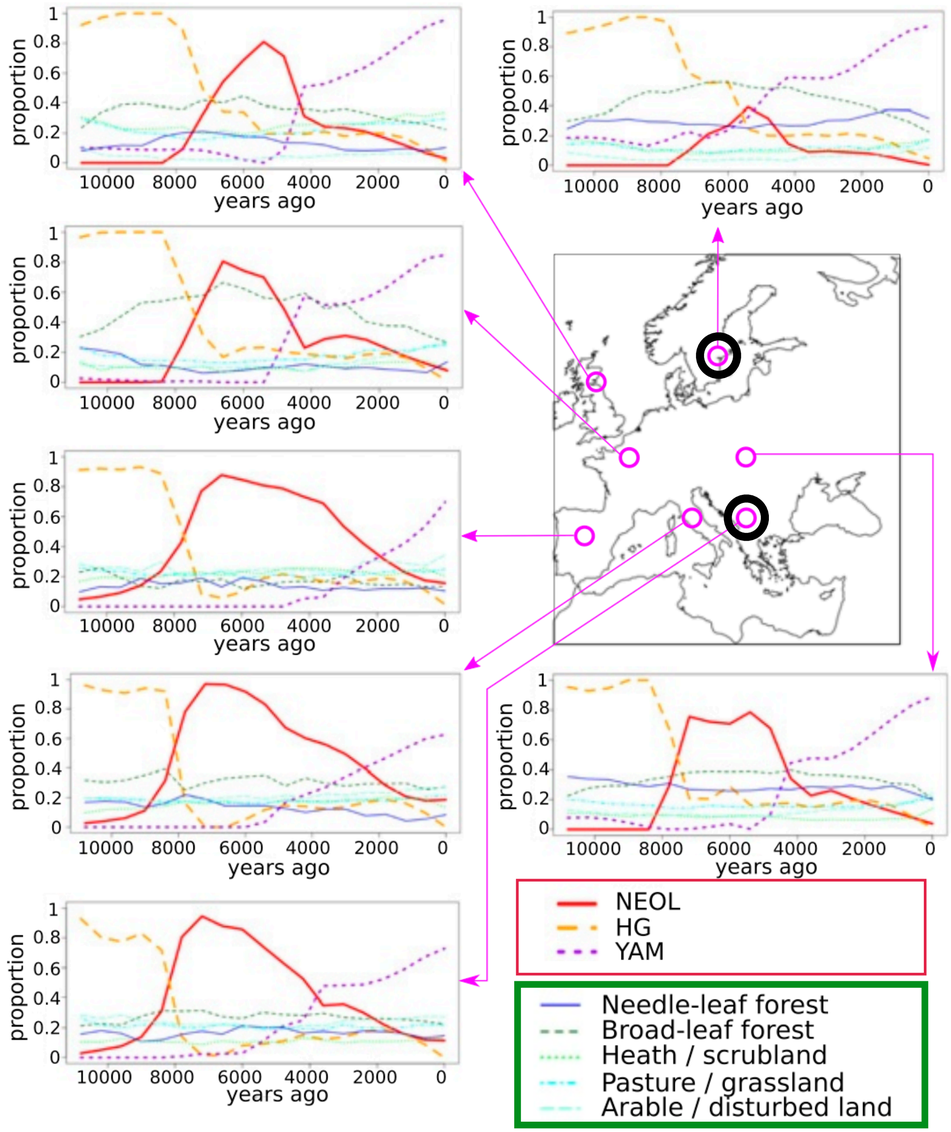

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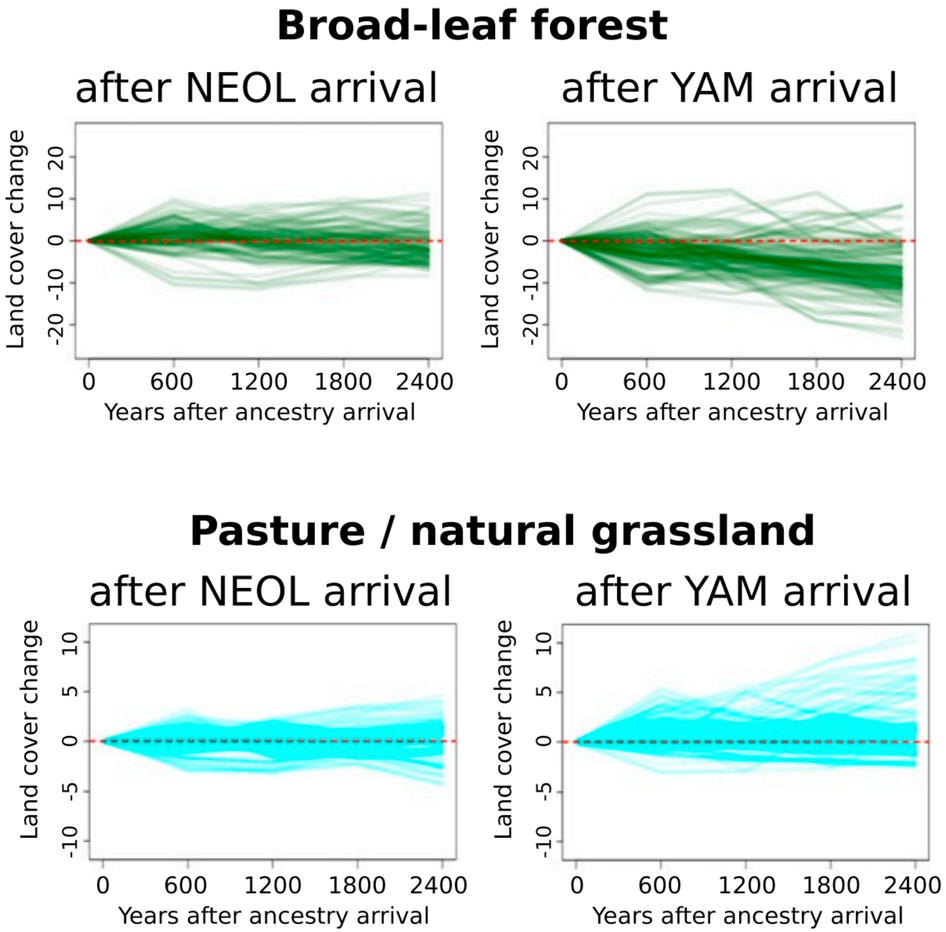

Racimo *et al.*, PNAS 2020

Every other statistic

— nucleotide diversity, IBD, split times, N_e, D statistic, ...—

works in the same way.

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Inferring whole-genome histories in large population datasets

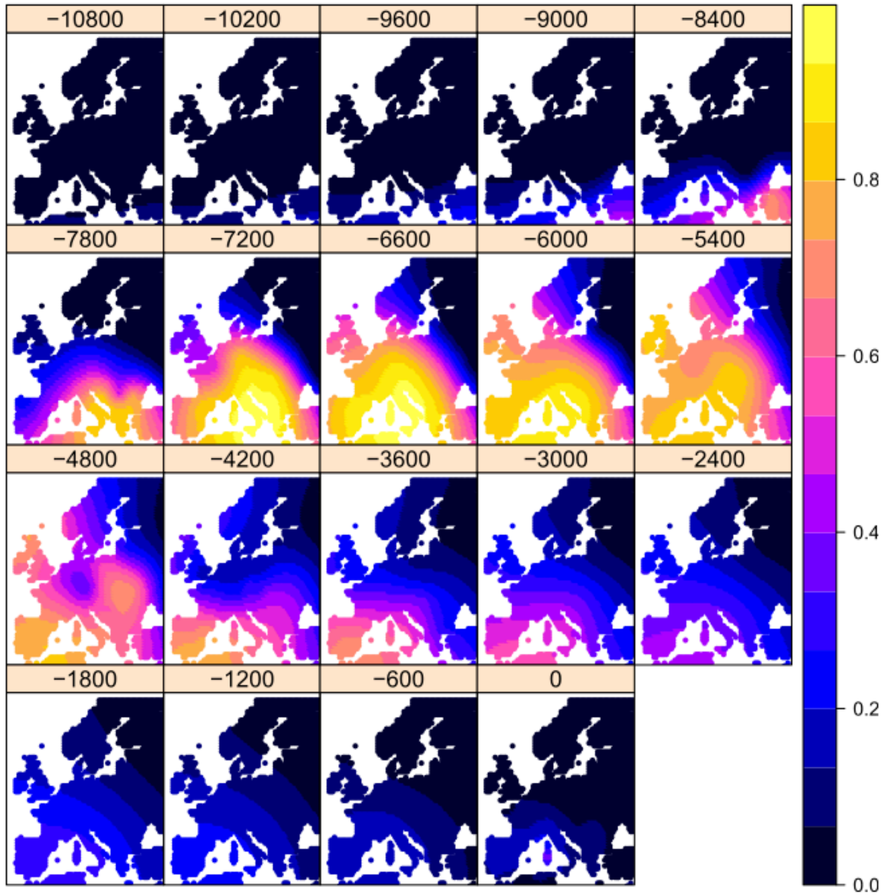
Jerome Kelleher*, Yan Wong, Anthony W. Wohns, Chaimaa Fadil, Patrick K. Albers and Gil McVean

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

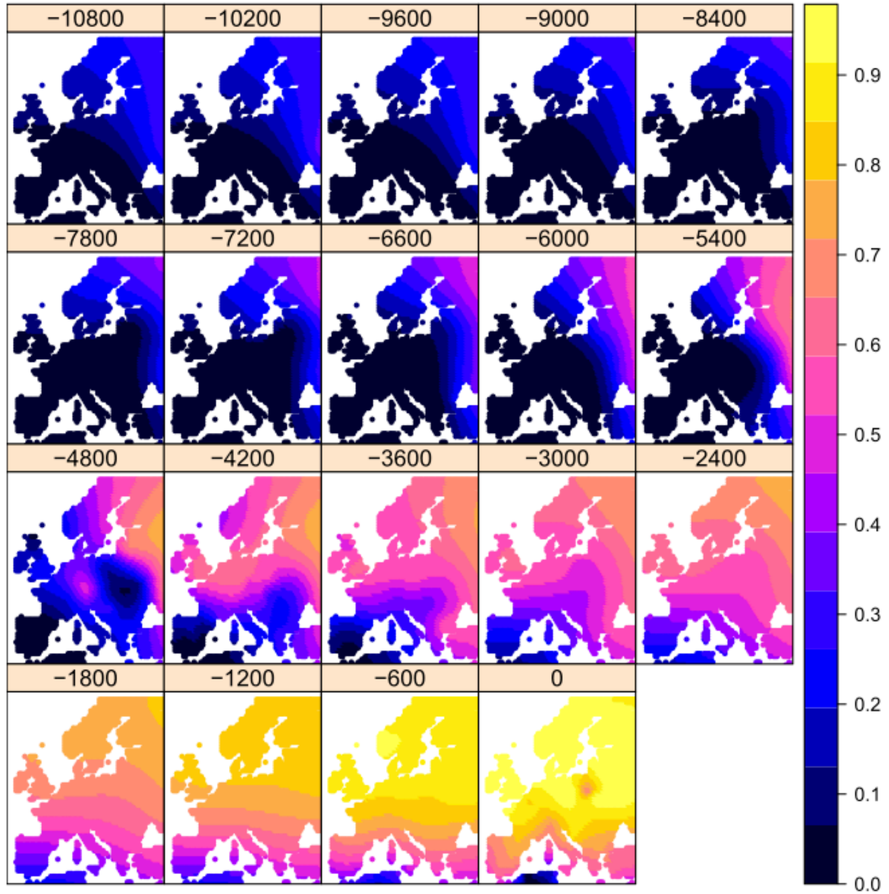
Leo Speidel[1], Marie Forest[2], Sinan Shi[1] and Simon R. Myers[1,3]*

Interpolated ancestry maps

"NEOL" ancestry



"YAM" ancestry



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