

Ancient genomics activity

Mick Westbury

KØBENHAVNS UNIVERSITET



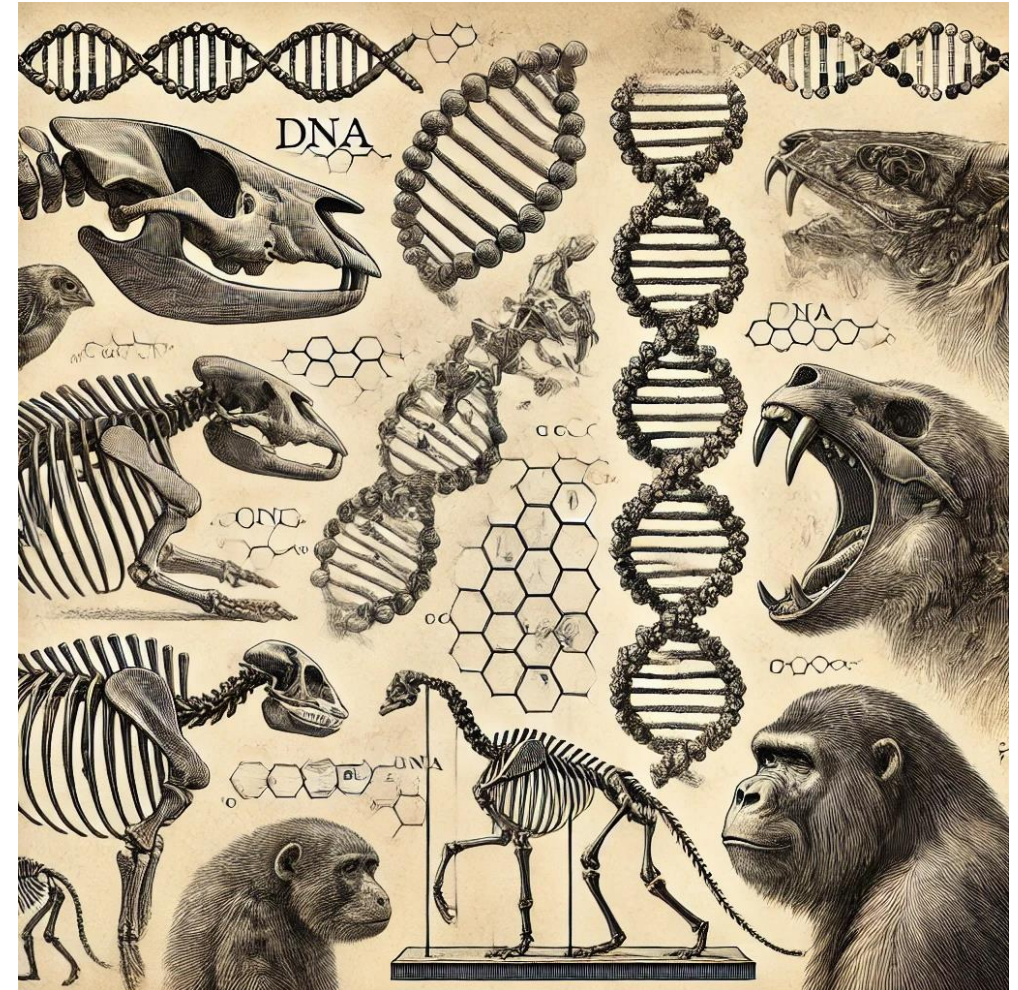
Ancient DNA

- Palaeontological
- Museum specimens
- Forensics



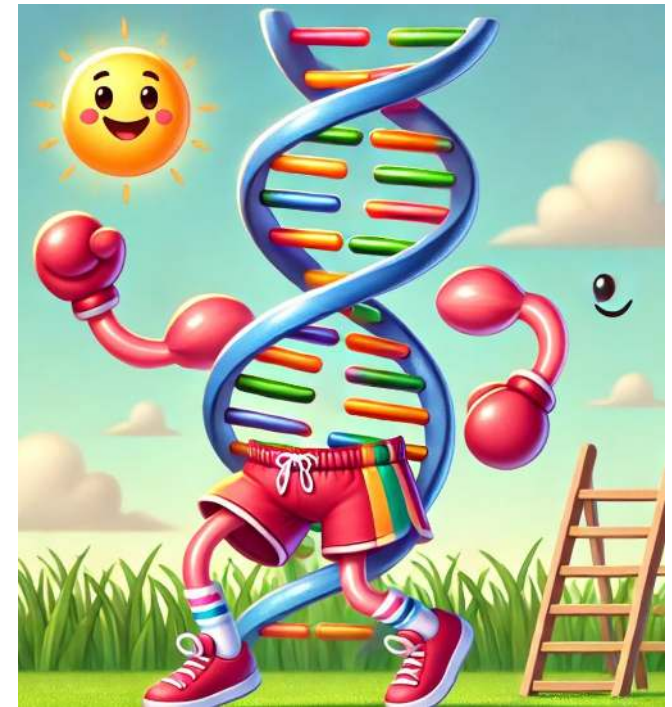
Ancient DNA - problems

- Short fragment lengths
- DNA damage
- Contamination



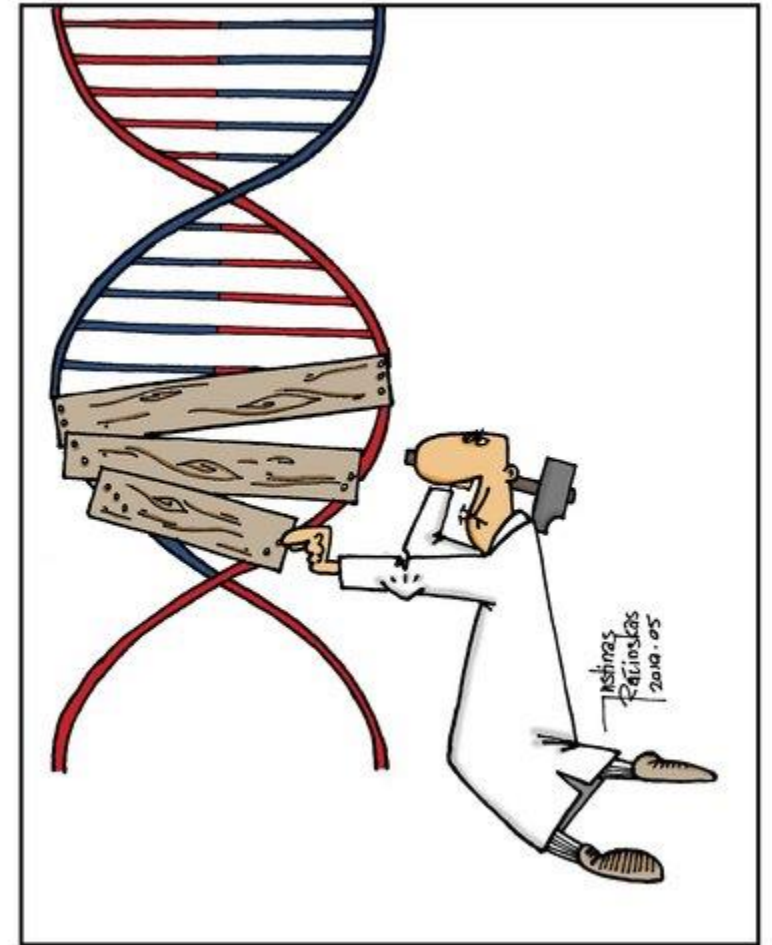
Ancient DNA - problems

- **Short fragment lengths**
 - <100bp
- DNA damage
- Contamination



Ancient DNA - problems

- Short fragment lengths
- **DNA damage**
 - ↑ C-T transitions
- Contamination



How can this effect your analyses?

- Biases?
 - Modern vs ancient DNA
 - Reference biases?

Evaluating biases

- Simulate data with aDNA properties
 - “Damage” modern genomic data
 - Gargammel
 - Renaud et al 2017
 - TAPAS
 - Taron et al 2018

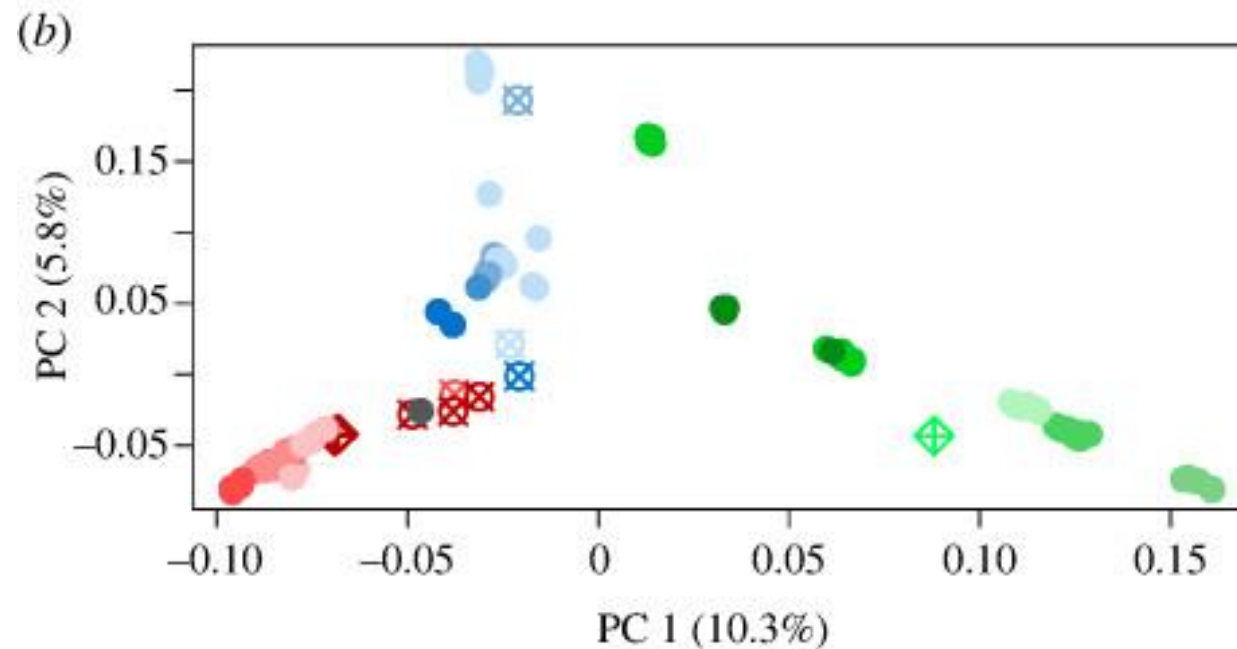
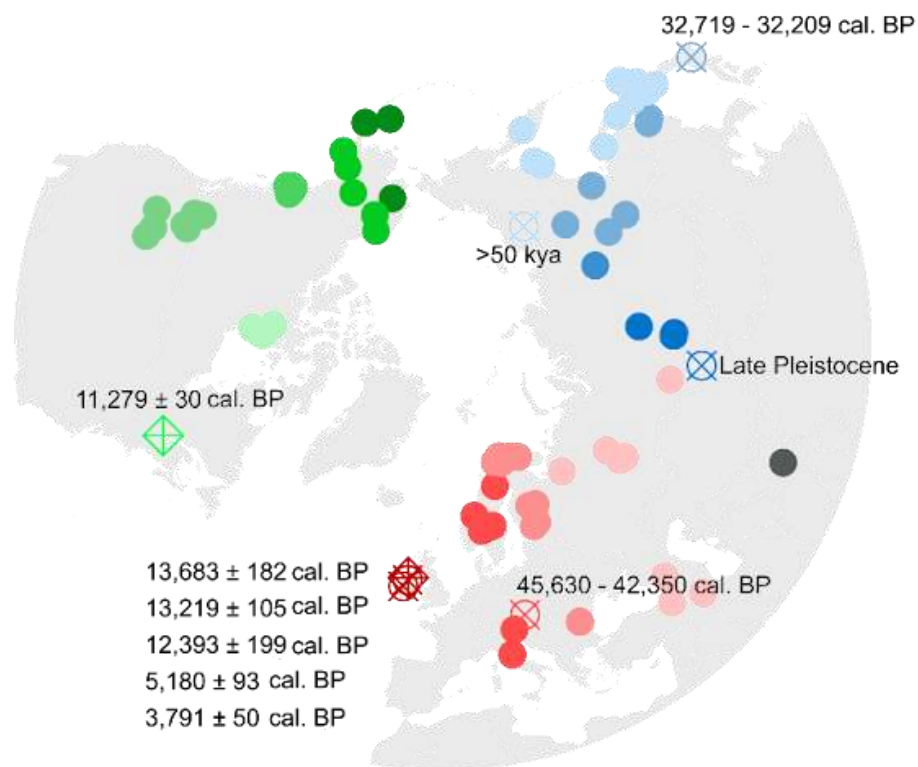


Goals for today

- **Task 1**
 - Assess DNA damage
- **Task 2**
 - PCA, NJ tree, D-statistics
- **Task 3**
 - Simulated damaged data
- **Task 4**
 - Assess base call, damage, and reference biases

Examples

Modern vs Ancient PCA

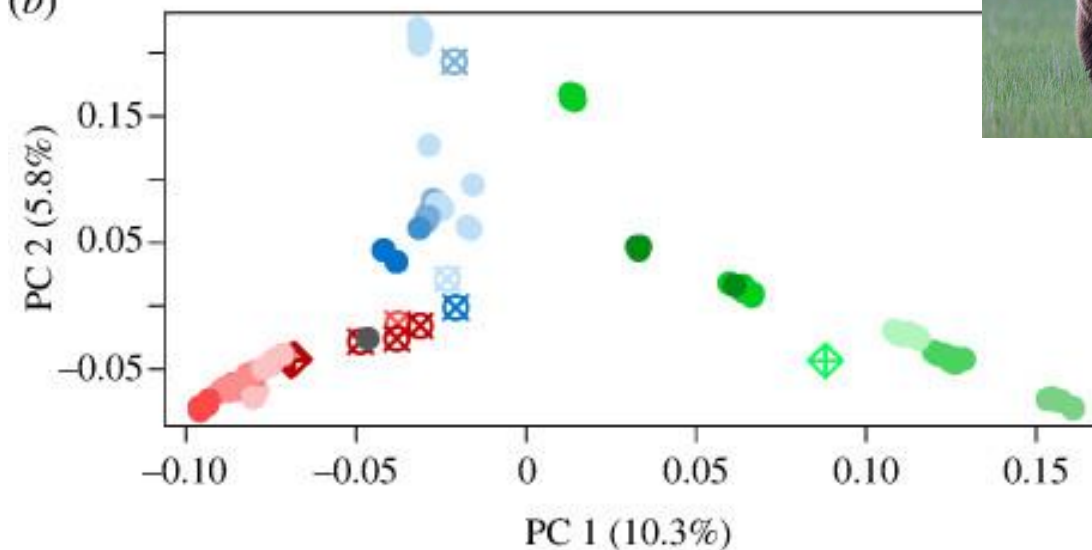


0.01x – 1.46x

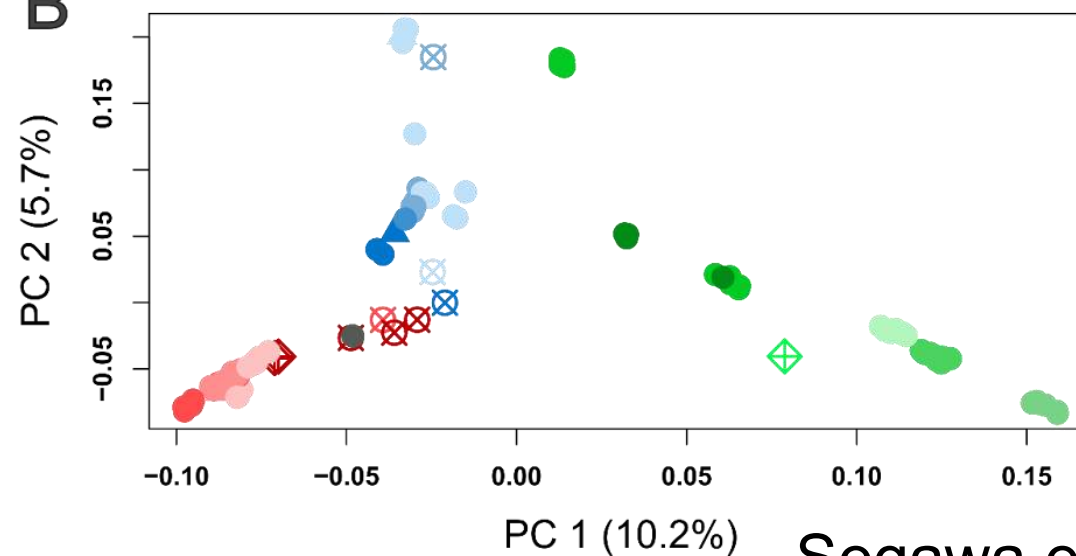
Segawa et al 2024

Modern vs Ancient

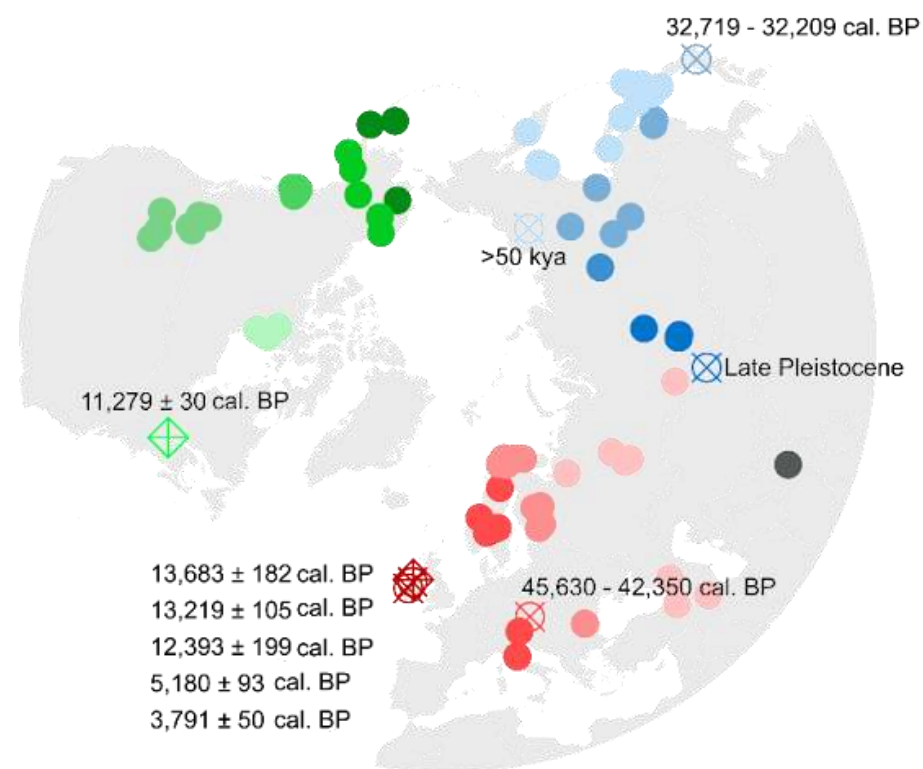
(b)



B



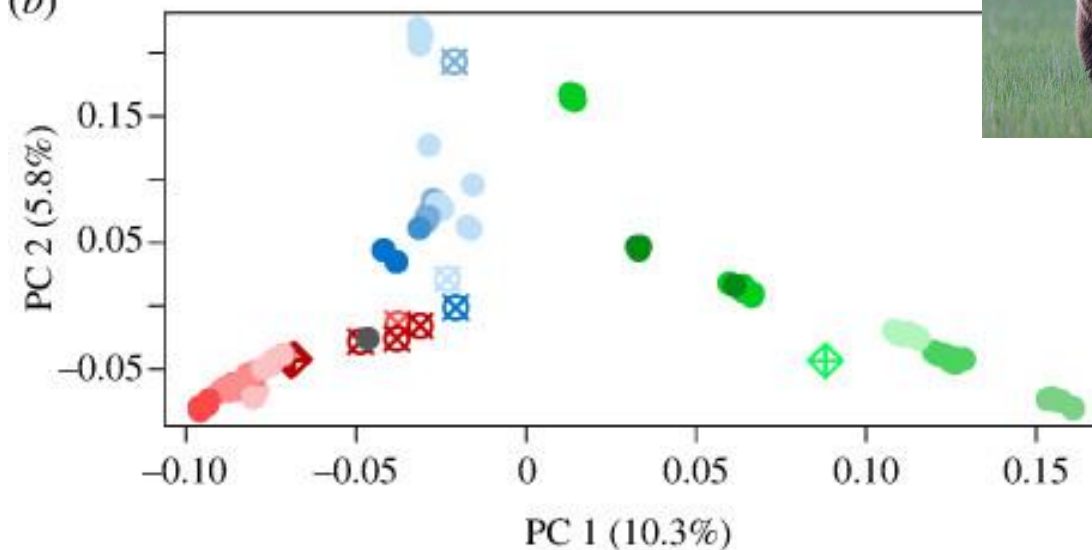
Segawa et al 2024



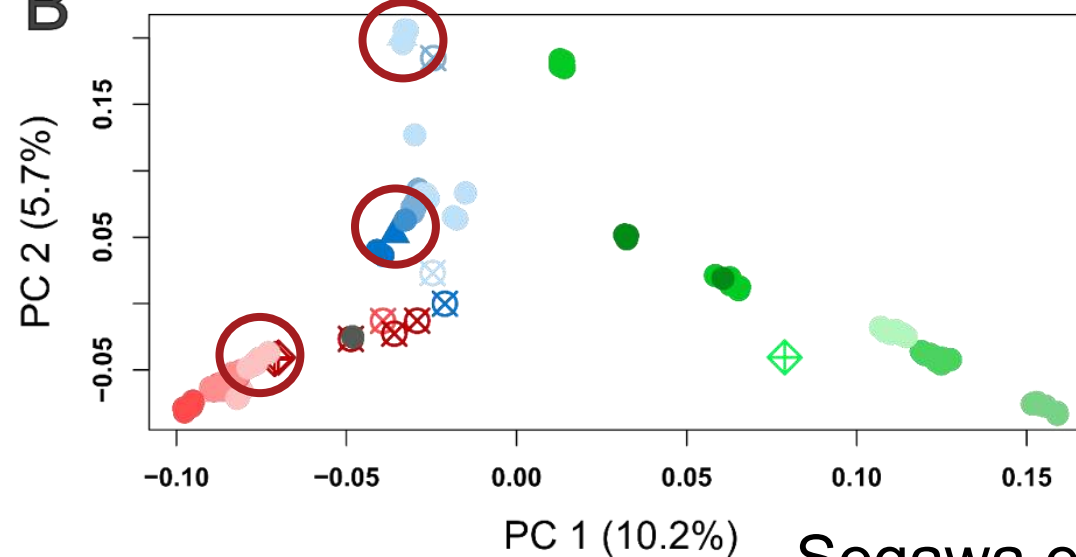
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Modern vs Ancient

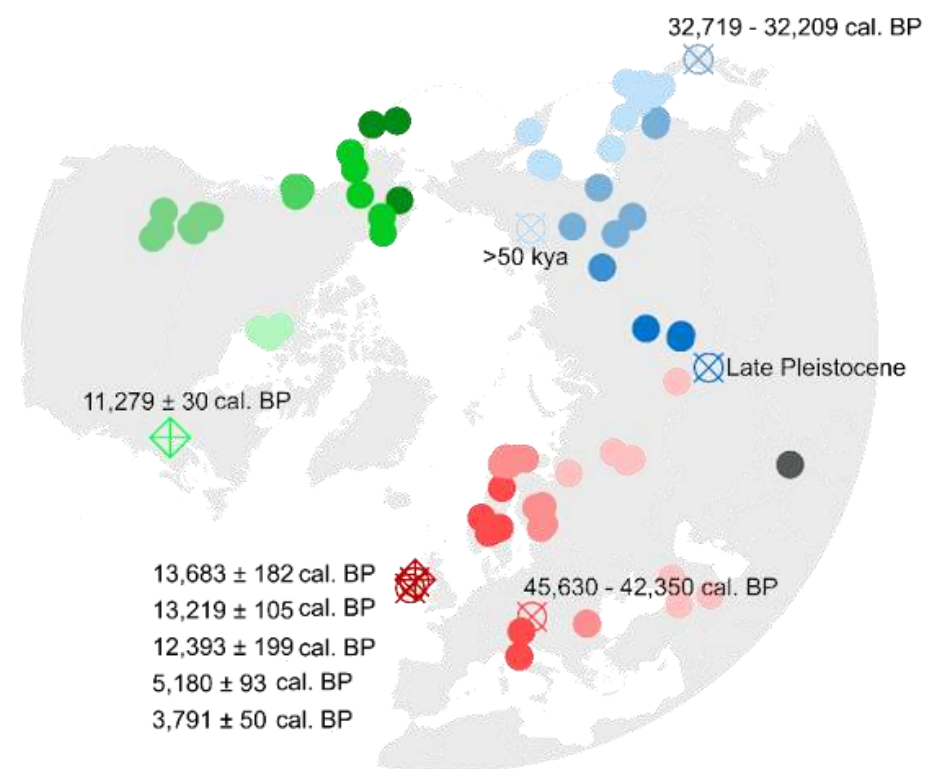
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B



Segawa et al 2024

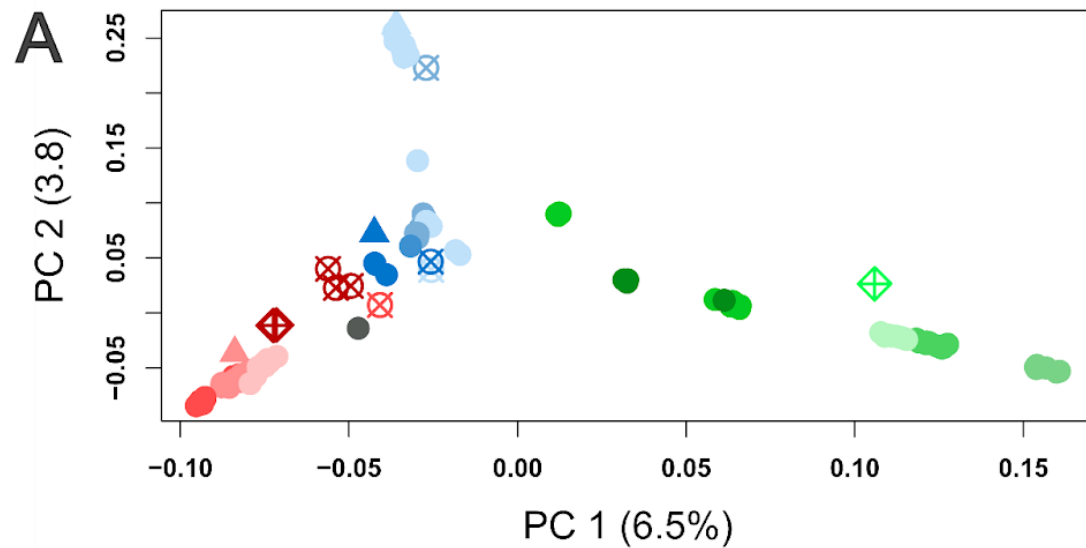


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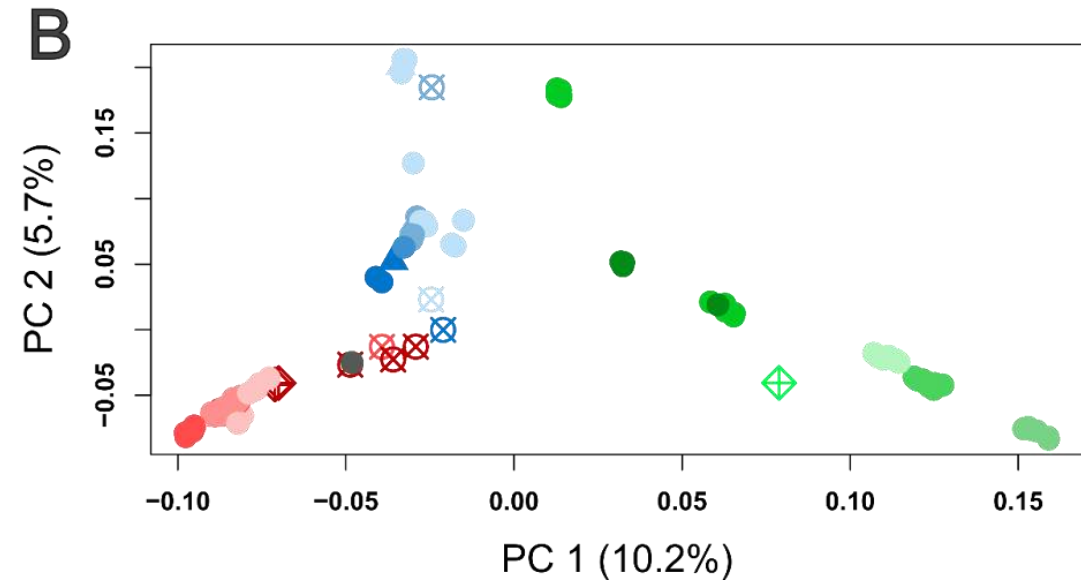
Base call approach?



Pseudohaploid



Genotype likelihoods



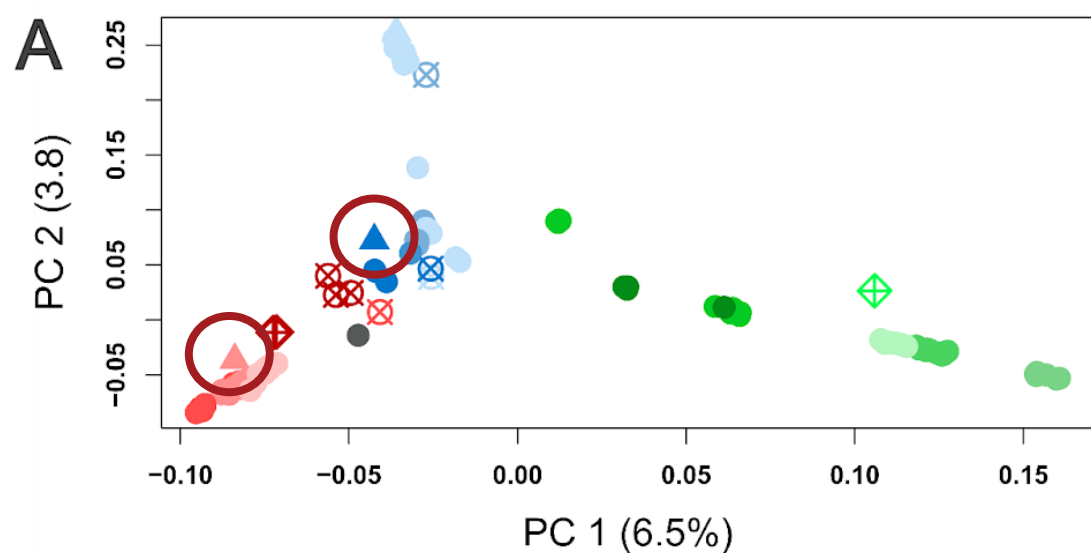
0.01x – 1.46x

Segawa et al 2024

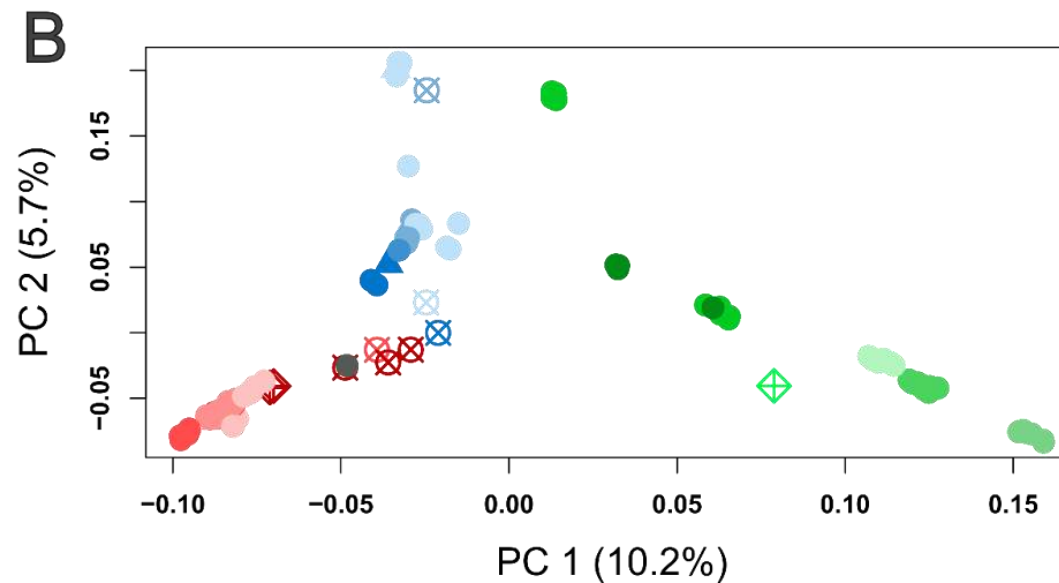
Base call approach?



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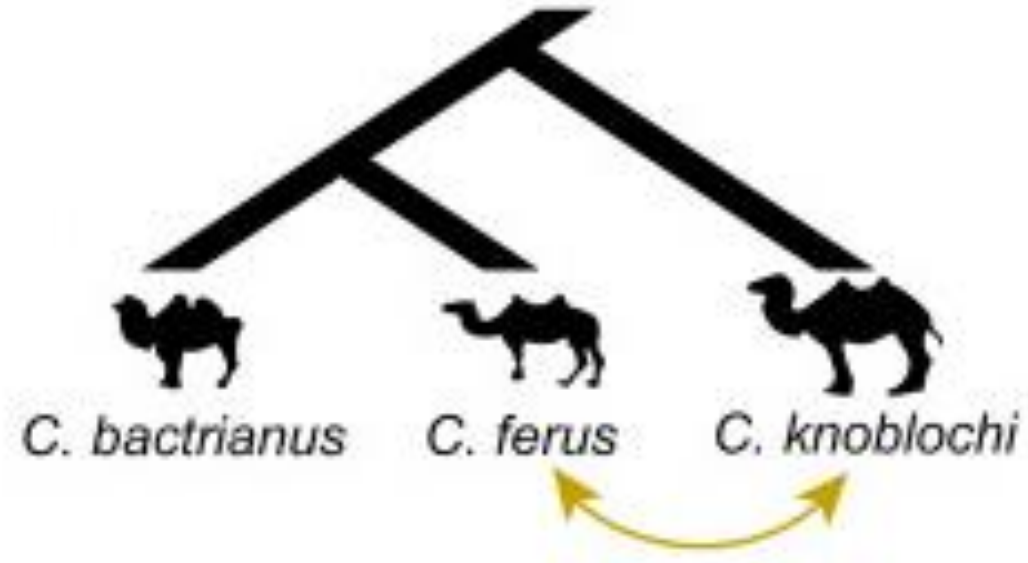
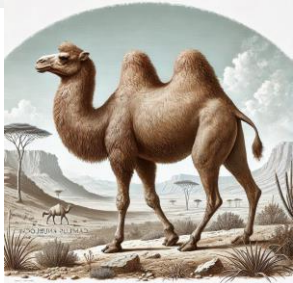
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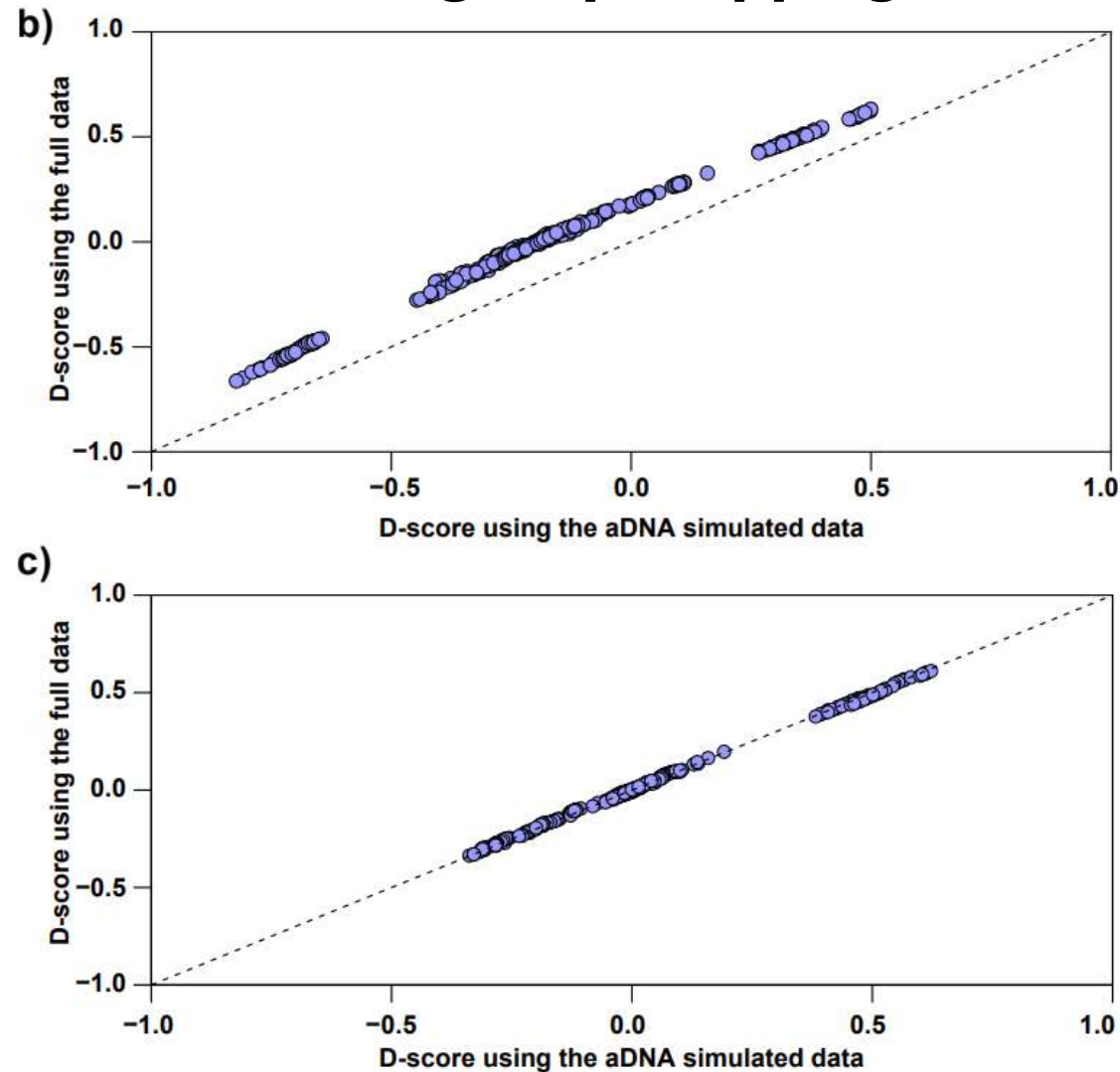
Segawa et al 2024

Reference biases - Dstatistics



Reference biases

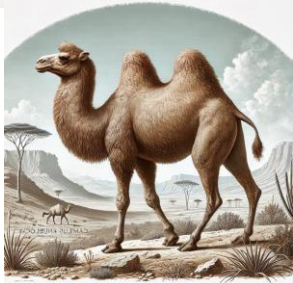
Outgroup mapping



~0.06x

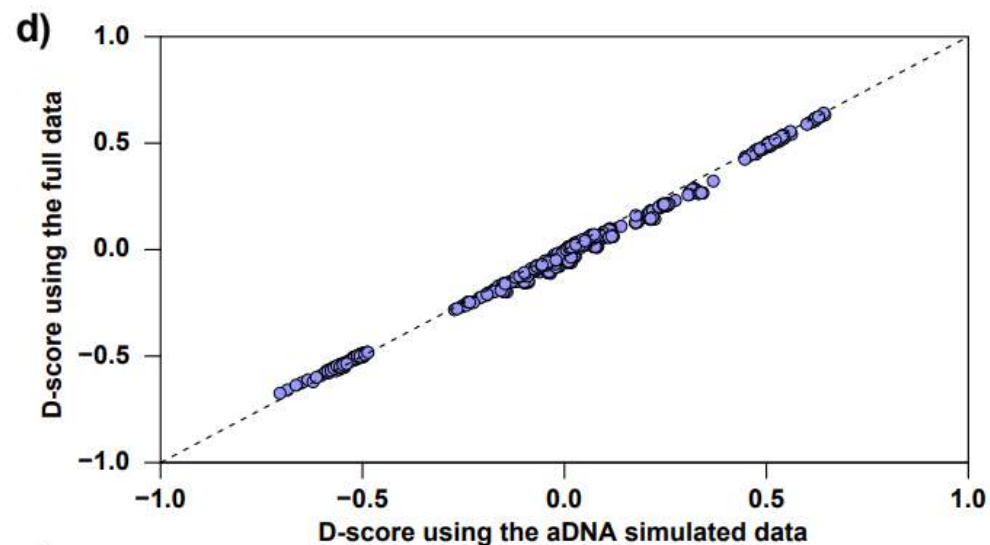
P3 aDNA

Yuan et al 2024

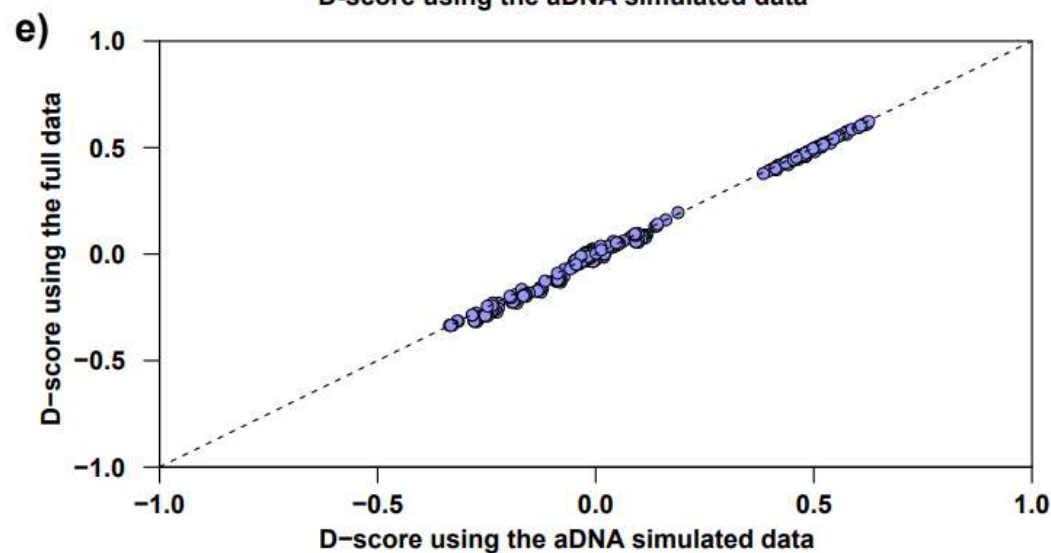


Reference biases

Ingroup mapping



P2 aDNA



P3 aDNA

~0.06x

Yuan et al 2024

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