Ancient genomics activity

Mick Westbury

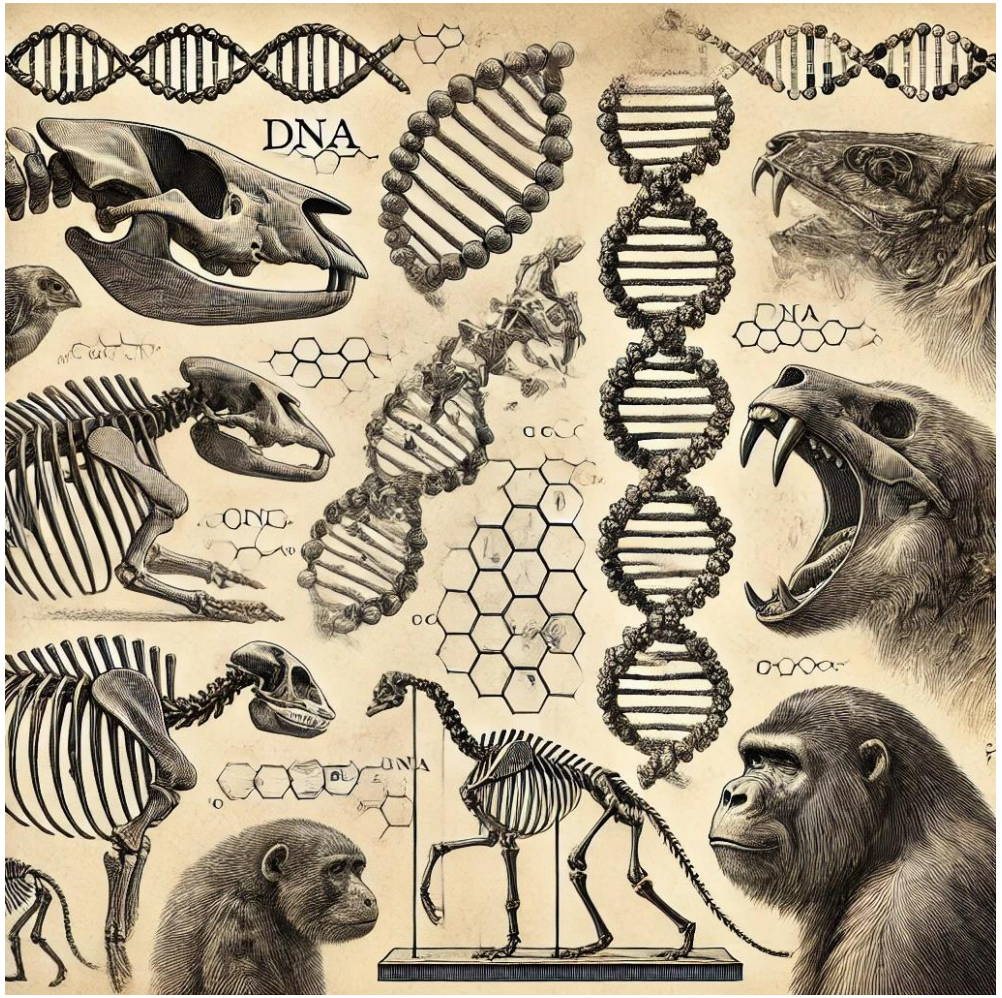
KØBENHAVNS UNIVERSITET

Ancient DNA

- Palaeontological
- Museum specimens
- Forensics

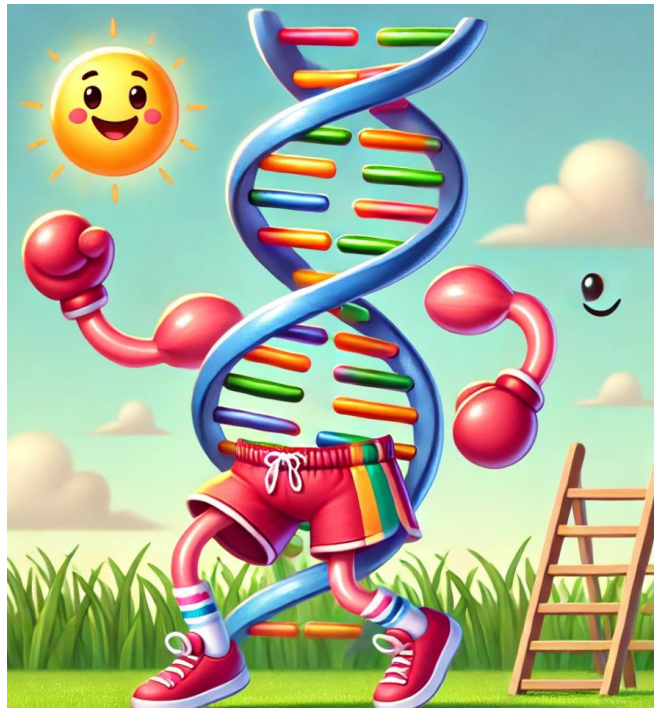
Ancient DNA - problems

- Short fragment lengths
- DNA damage
- Contamination



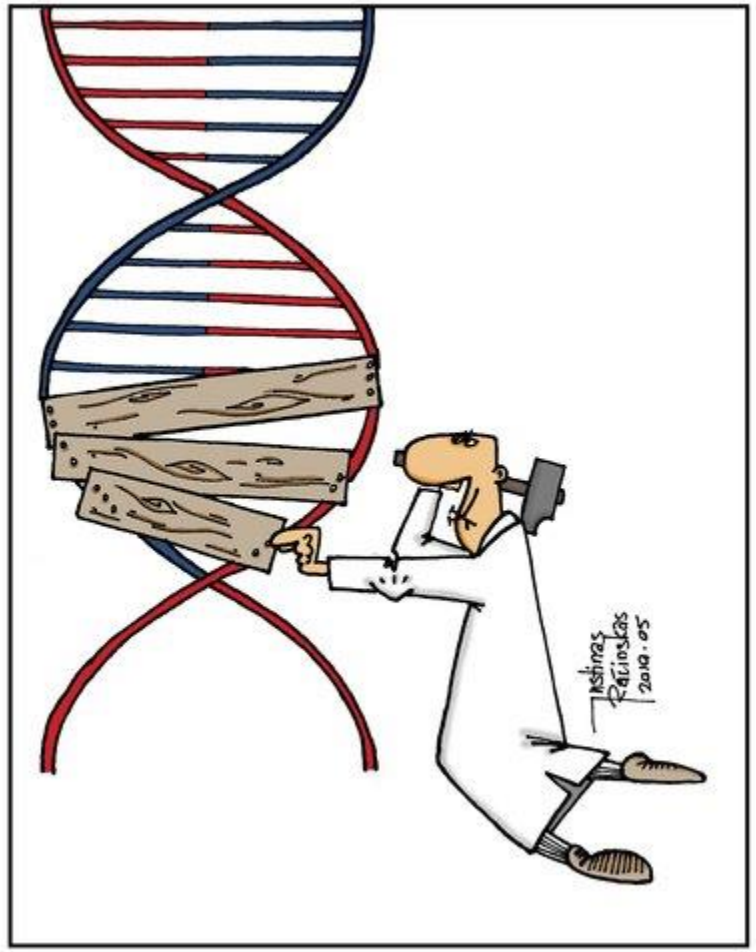
Ancient DNA - problems

- **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

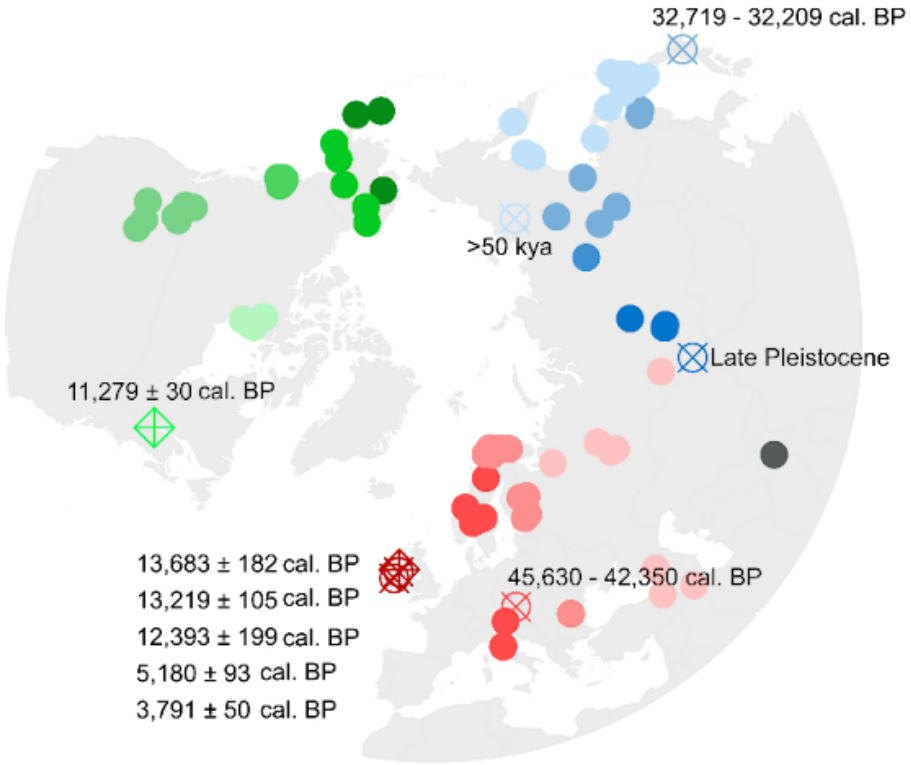
- Simulate data with aDNA properties
  - “Damage” modern genomic data
  - Gargammel
    - Renaud et al 2017
  - TAPAS
    - Taron et al 2018

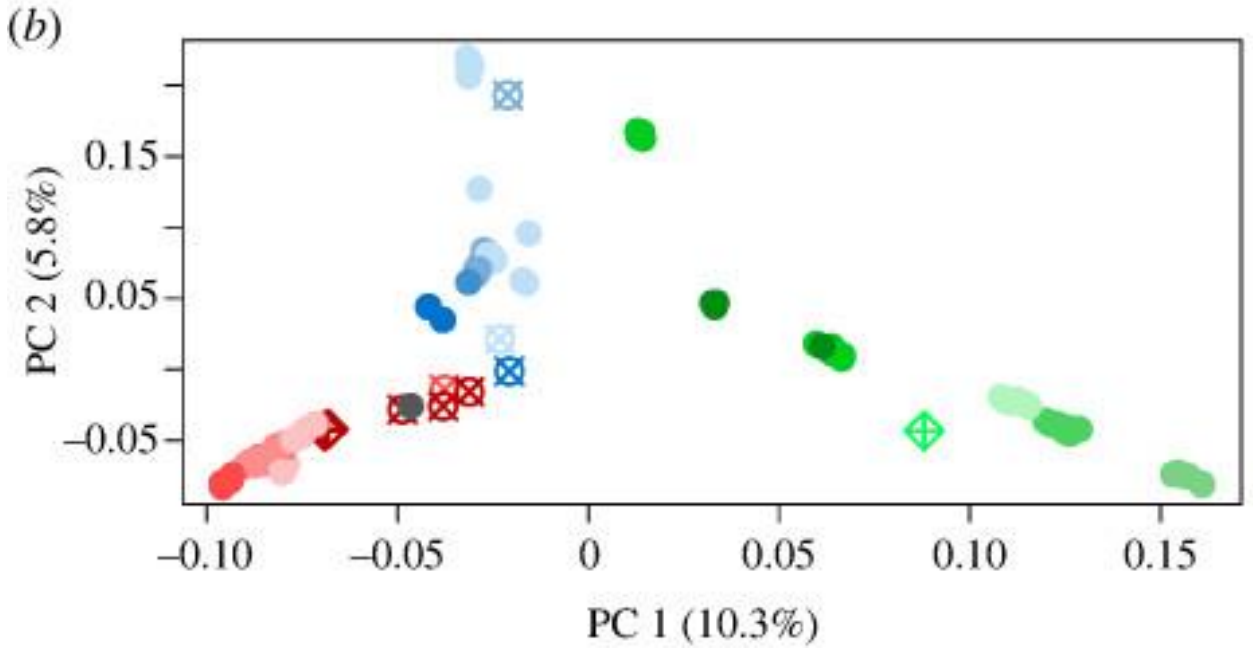
Goals for today

- **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

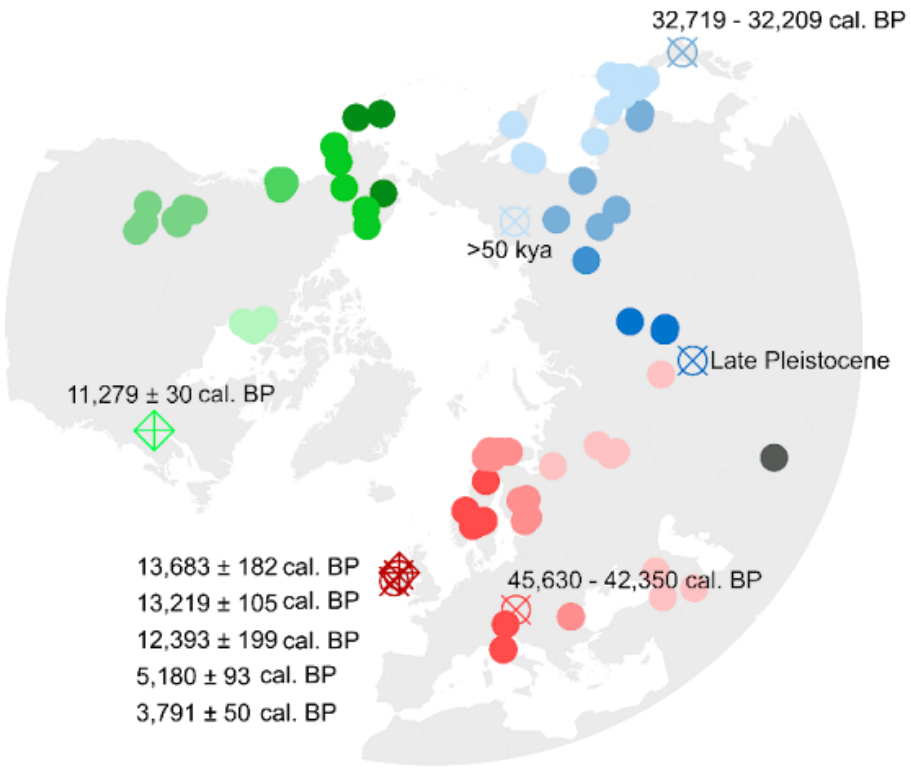


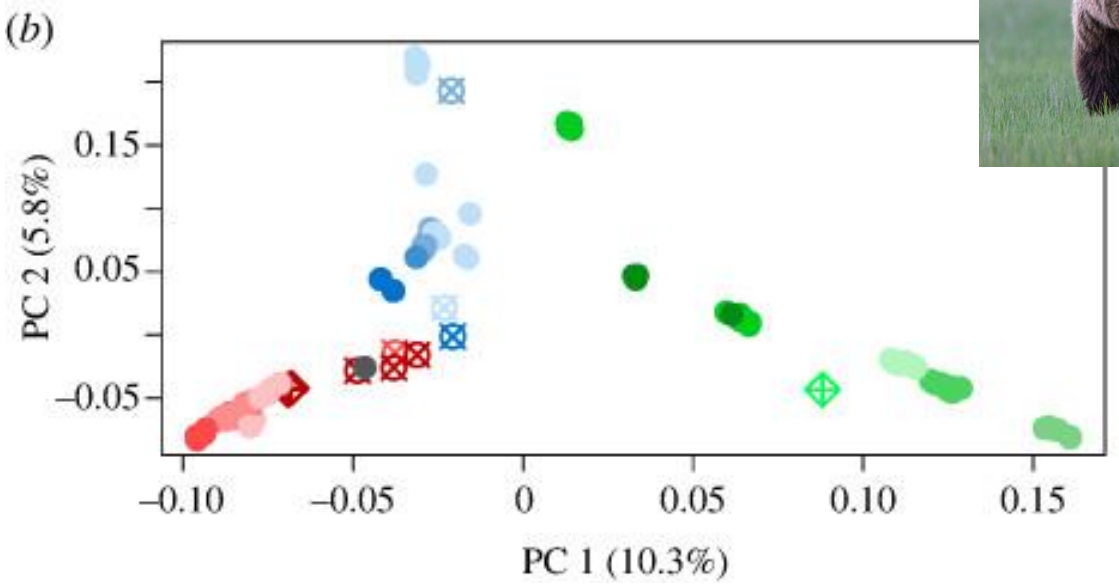


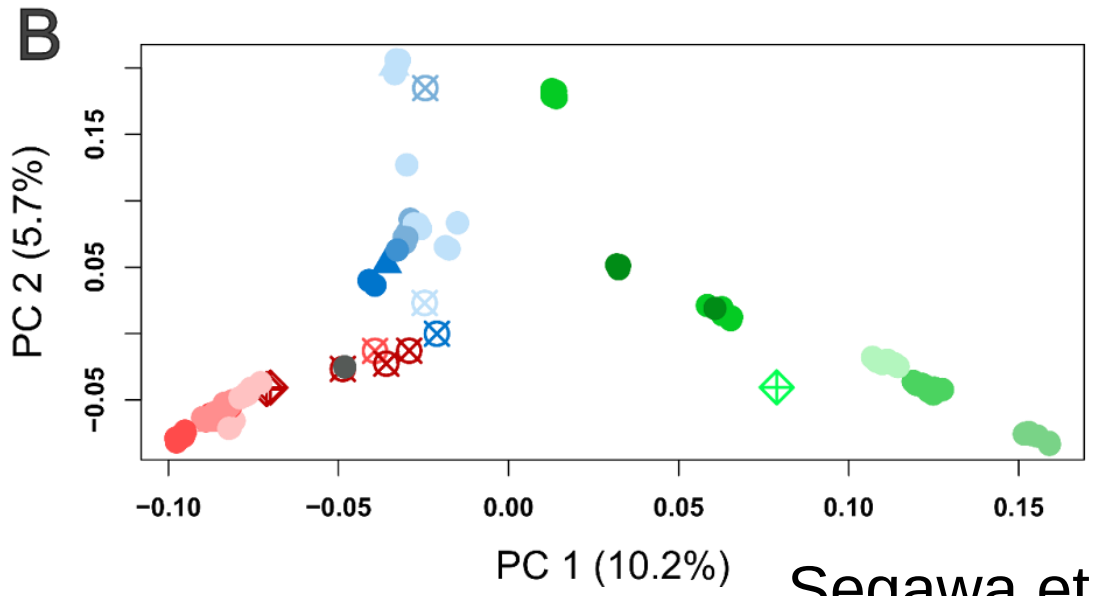
0.01x – 1.46x

Segawa et al 2024

Modern vs Ancient







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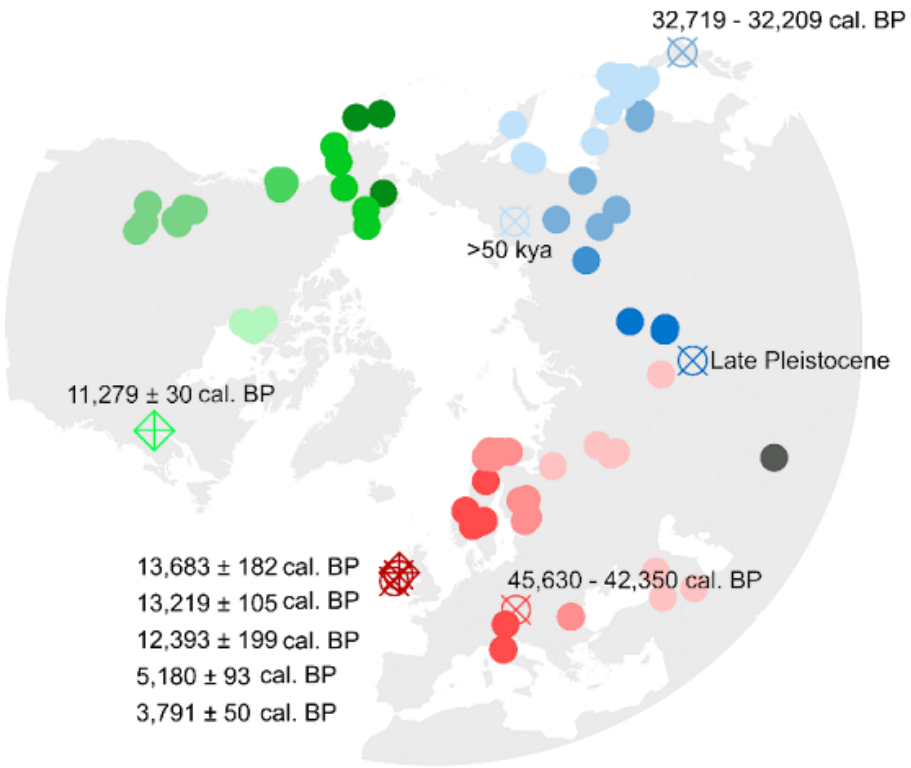

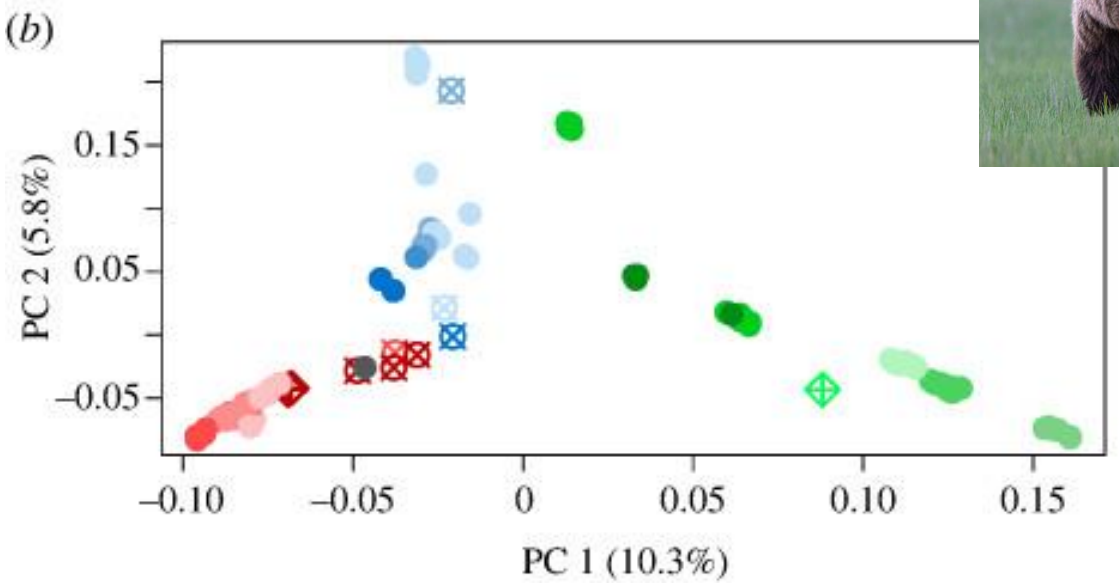

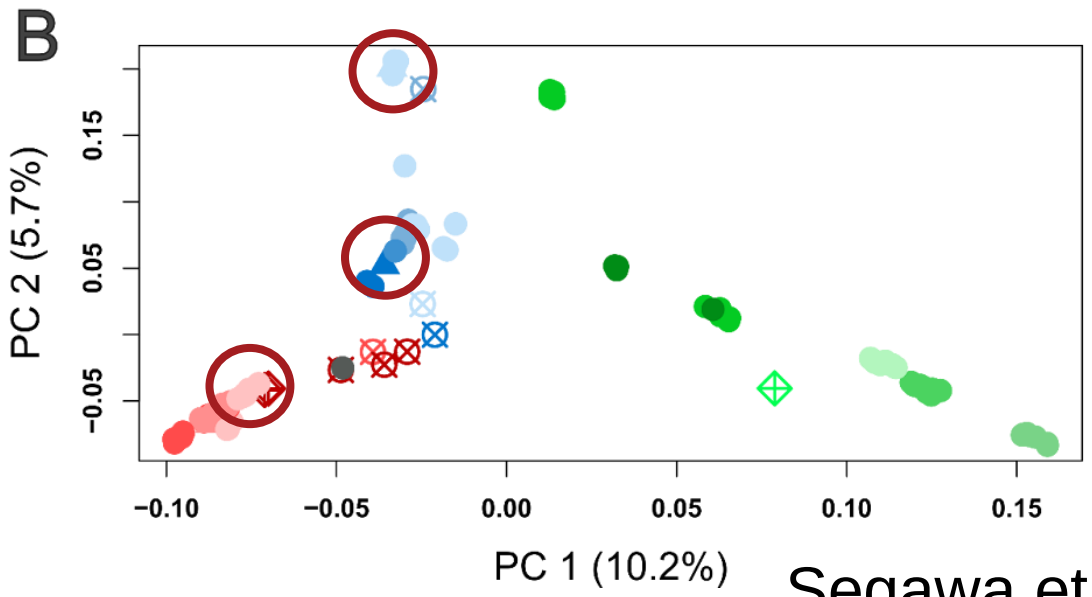

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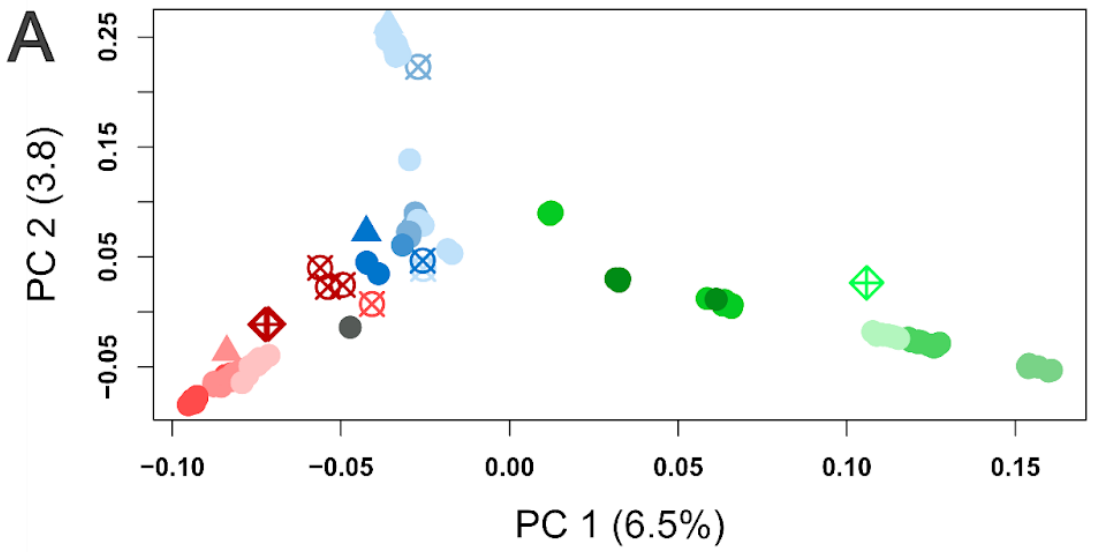
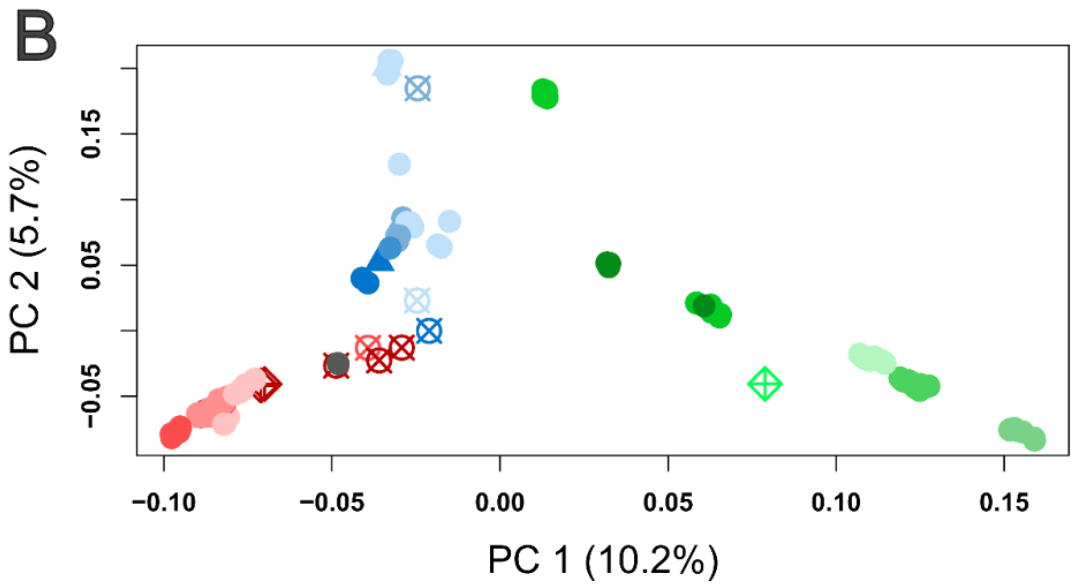
Base call approach?

Pseudohaploid



Genotype likelihoods



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Segawa et al 2024

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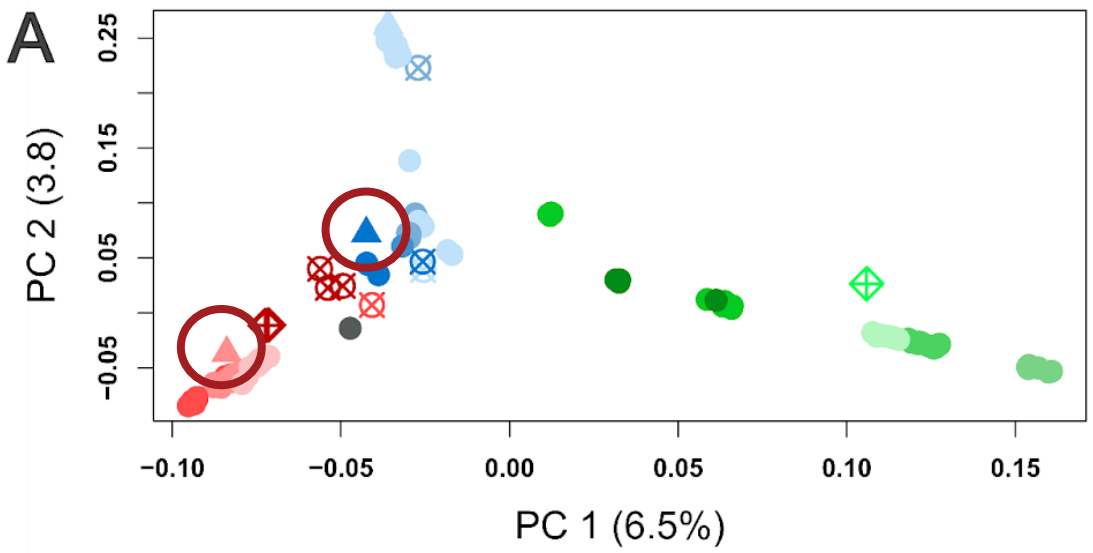

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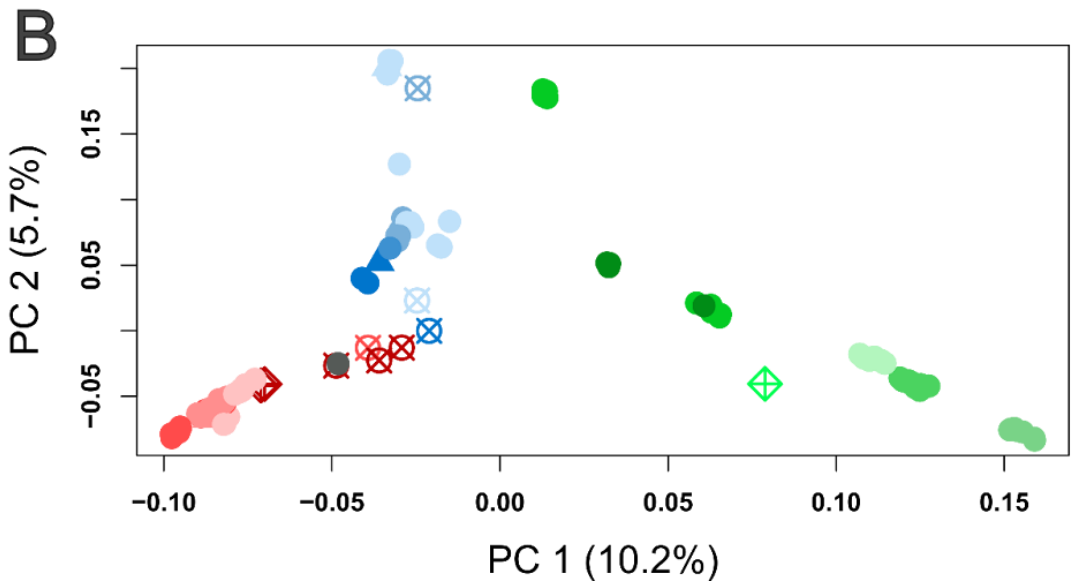

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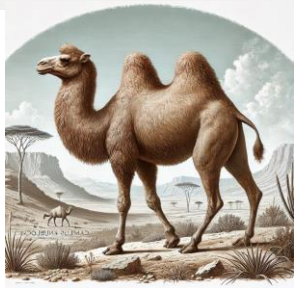
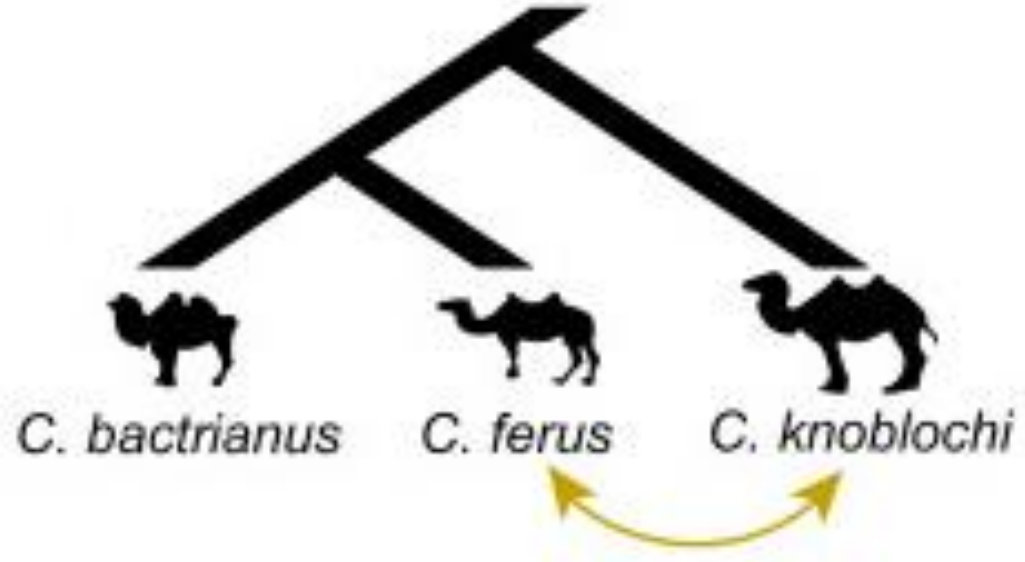
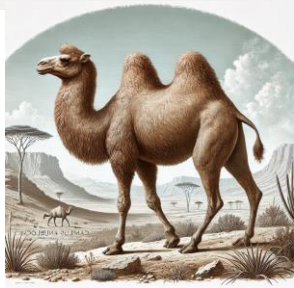
Segawa et al 2024



Reference biases - Dstatistics

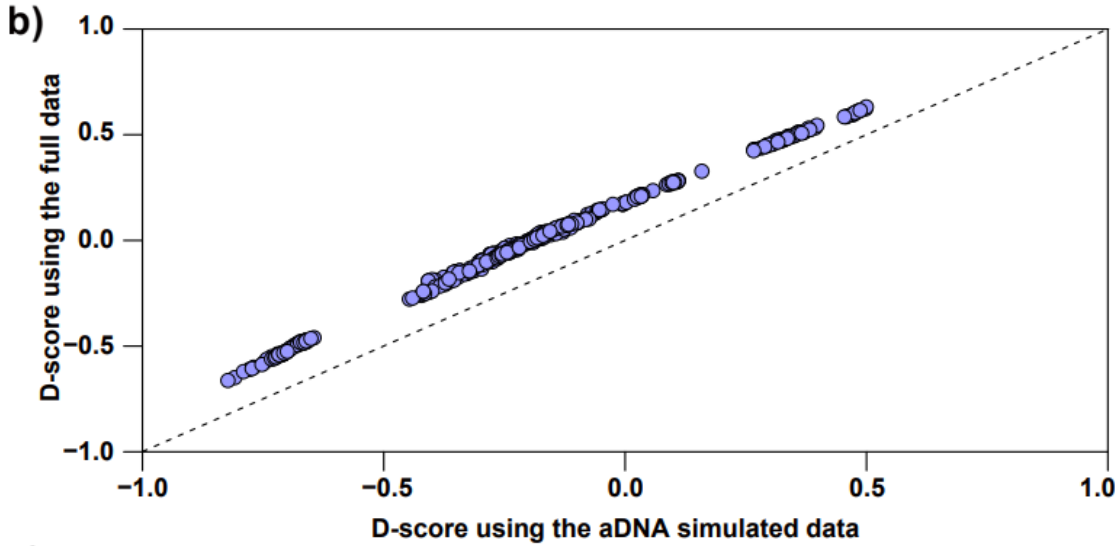


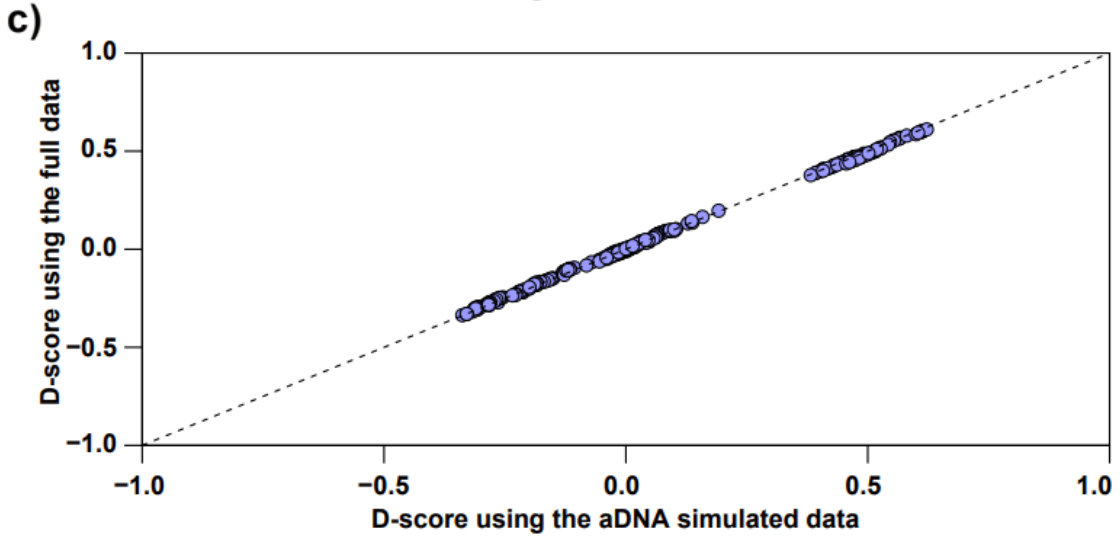
Yuan et al 2024



Reference biases

Outgroup mapping





P3 aDNA

~0.06x

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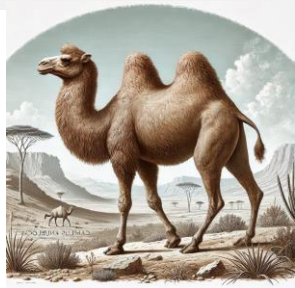

Reference biases

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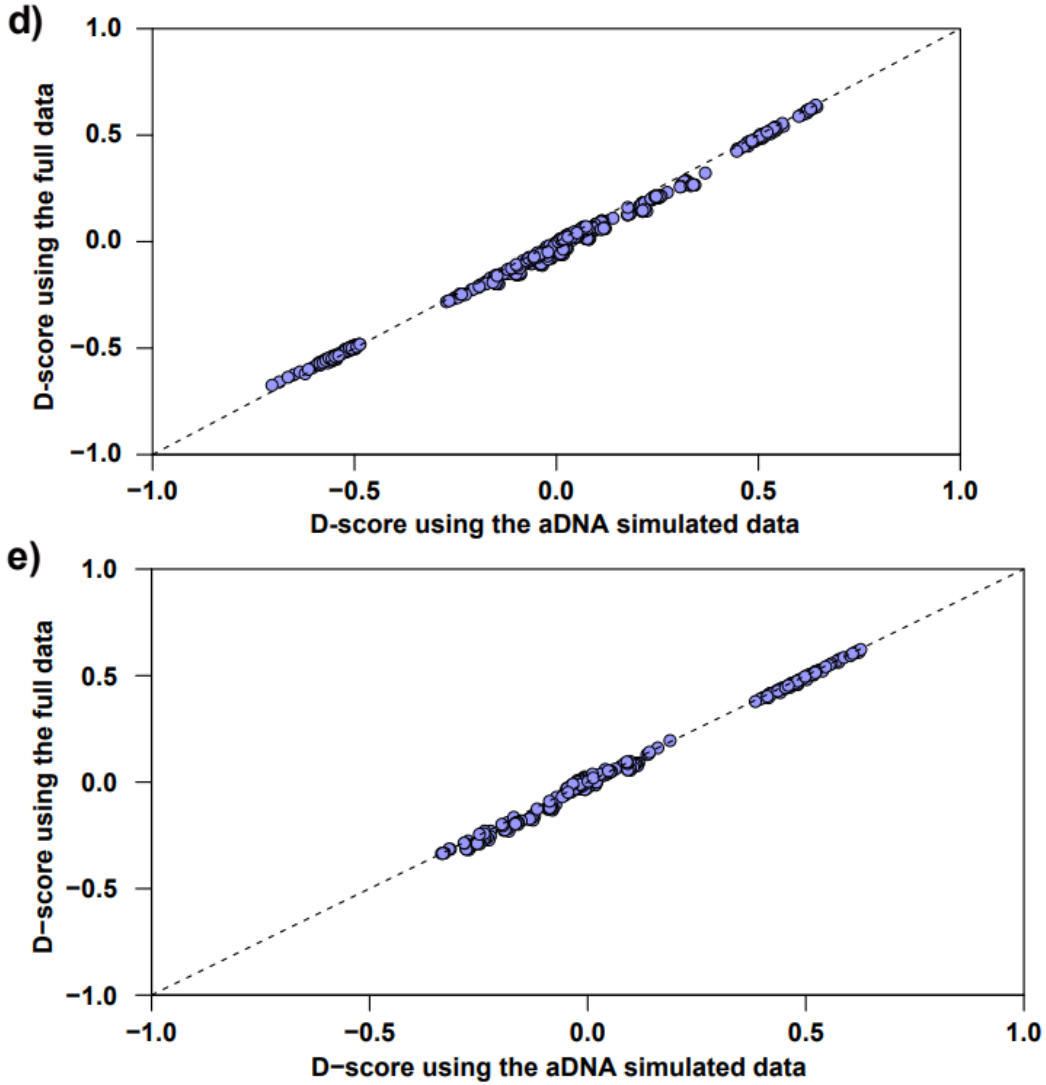

P2 aDNA

P3 aDNA

~0.06x

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