

Working with GONE

Introduction to GONE

Genetic Optimization for N_e Estimation

- Originally published in 2020
- New version, GONE2, released last week
- Not to be confused with GONE (Coombs et al., 2011. Molecular Ecology Resources)

JOURNAL ARTICLE

Recent Demographic History Inferred by High-Resolution Analysis of Linkage Disequilibrium

Enrique Santiago  , Irene Novo , Antonio F Pardiñas , María Saura , Jinliang Wang , Armando Caballero

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Accounting for population structure and data quality in demographic inference with linkage disequilibrium methods

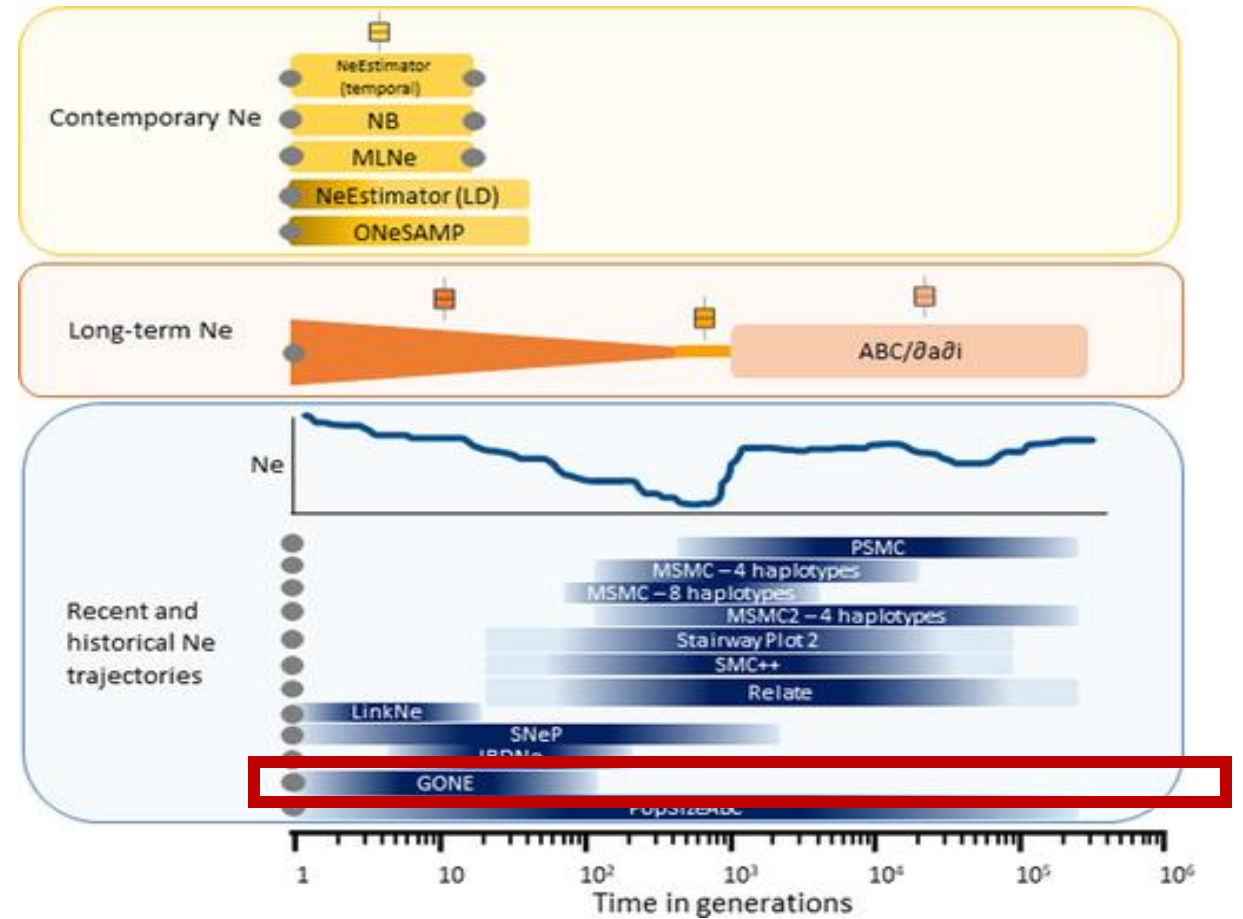
[Enrique Santiago](#) , [Carlos Köpke](#) & [Armando Caballero](#)

[Nature Communications](#) **16**, Article number: 6054 (2025) | [Cite this article](#)

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Introduction to GONE

- Linkage Disequilibrium-based method
- Uses genome-wide data (SNPs) to infer recent demographic history
- Highest resolution within last 100-200 generations



Introduction to GONE

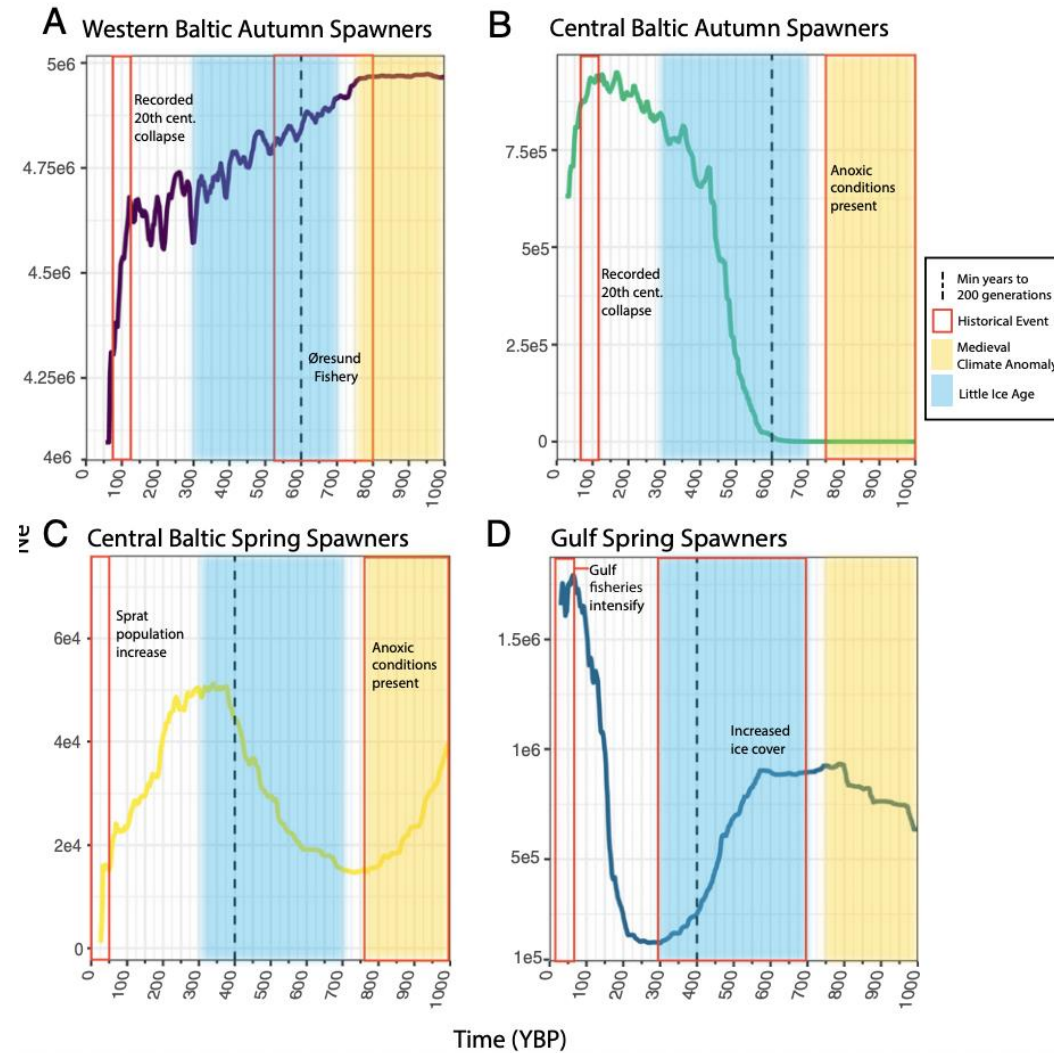


Figure from Atmore et al., 2022. *PNAS*

Linkage Disequilibrium

- Non-random association between alleles at two or more loci
- Function of both **population size** and **physical distance** between loci

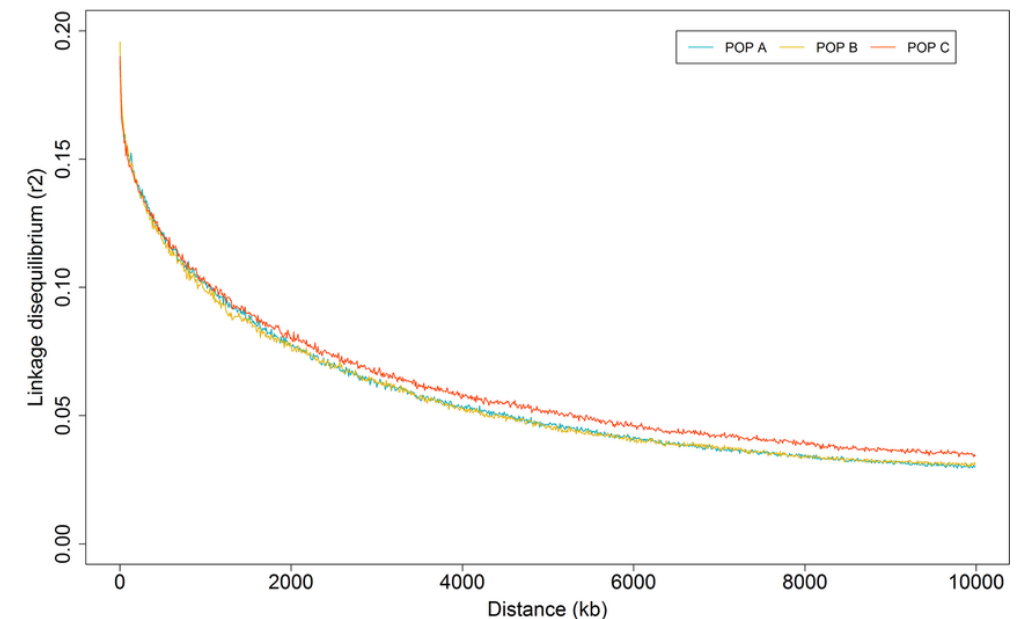
Population size

- Small population → strong drift → more LD
- Large population → weak drift → less LD

Physical distance

- Closely linked loci → LD decays slowly
- Loosely linked loci → LD decays quickly

LD decay in three Nile tilapia populations



Linkage disequilibrium patterns reflect population history

Loosely linked loci

- Few generations to be shuffled → recent past

Closely linked loci: distant past

- Many generations to be shuffled → distant past

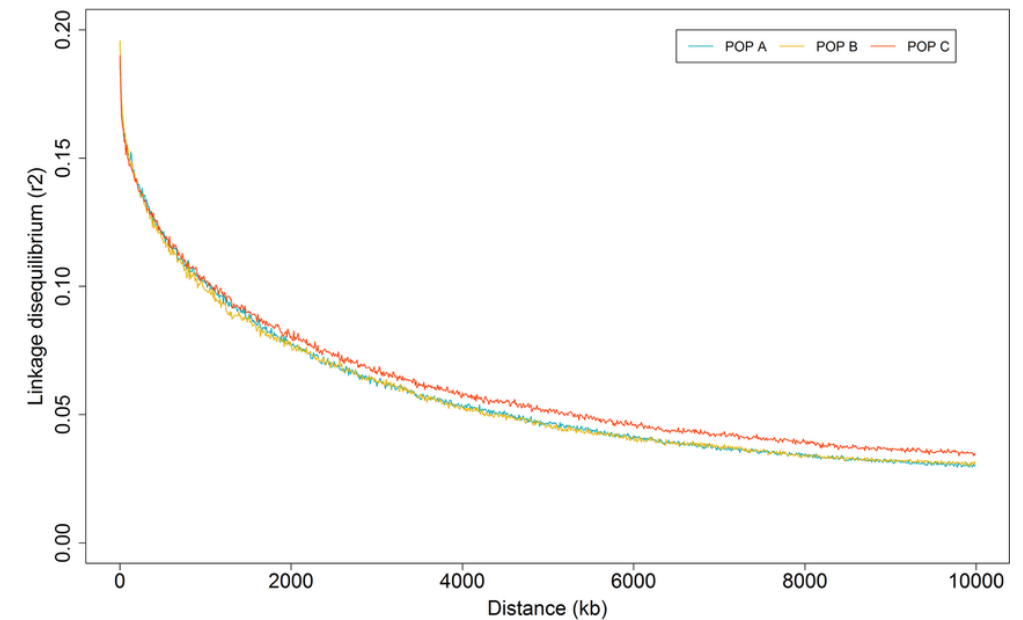
GONE: linked loci

→ Population size through time

NeEstimator: unlinked loci

→ Contemporary population size

LD decay in three Nile tilapia populations



Distant past

Recent past

Working with GONE

INPUT

- SNP data from a population (ideally more than 10 individuals, number depends on population size)
- Map information
 - Physical distance: absolute distance between SNPs
 - Genetic distance: relative distance between SNPs (if available)
- Input parameters
 - Average recombination rate (if genetic map unavailable)
 - Phase
 - MAF
 - Maximum value of recombination rate
 - ...

Working with GONE

ANALYSIS

1. LD measurement between many loci
2. Estimation of N_e using genetic optimization algorithm

OUTPUT

File containing generations and geometric means

Pitfalls and considerations

- Requires a contiguous reference genome
- Developed for an *ideal* population (no gene-flow, randomly mating, discrete generations)
 - Usually not the case in wild populations
- Number of sampled individuals depends on population size
 - Small population size → strong LD patterns → less individuals required for accurate estimates
- Increasing number of SNPs does not automatically increase accuracy

Improvements in GONE2

- Population structure (big issue in original GONE)
- Low-coverage sequencing data
- Genotyping errors
- Faster and more user-friendly