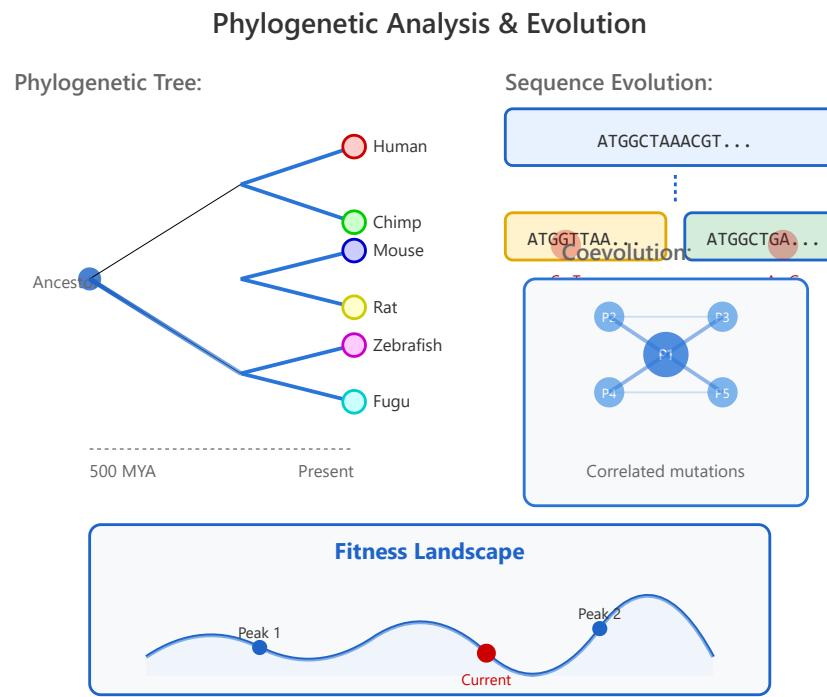


Evolution Modeling

Computational Approaches to Understanding Biological Evolution



Sequence Evolution

Substitution models & rates

Phylogenetic Inference

Tree reconstruction methods

Ancestral Reconstruction

Ancient sequence prediction

Coevolution

Correlated mutations analysis

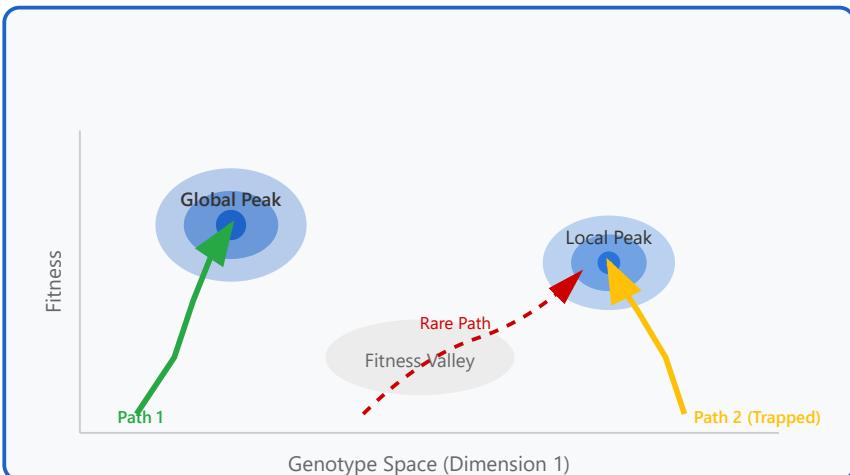
Fitness Landscapes

Adaptive evolution mapping

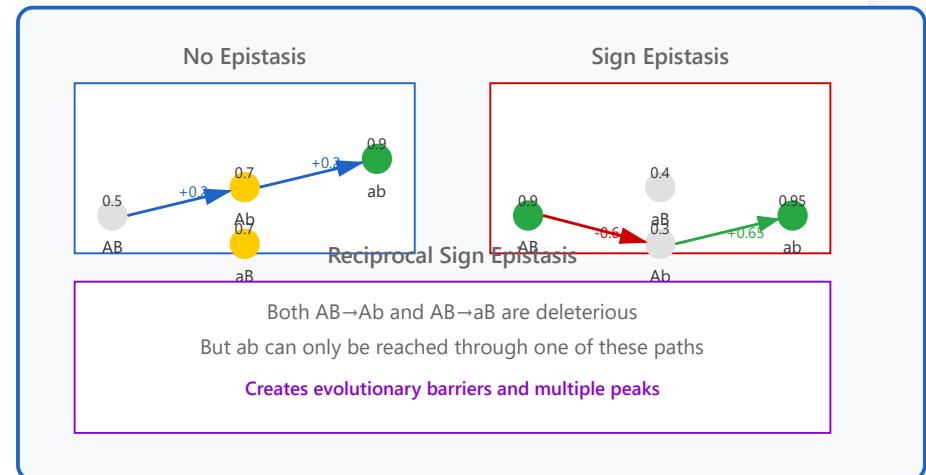
Fitness landscapes represent the relationship between genotypes or phenotypes and their reproductive success. These multidimensional spaces help us understand evolutionary trajectories, constraints on adaptation, and the accessibility of beneficial mutations through the complex topology of sequence space.

Fitness Landscape Topology and Evolutionary Paths

3D Fitness Landscape (2D Projection)

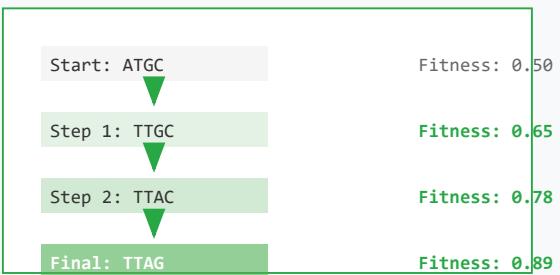


Epistatic Interactions



Adaptive Walks and Evolutionary Dynamics

Greedy Adaptive Walk



Population Dynamics



Key Factors

- Population size (N)
Large N → selection dominates
- Mutation rate (μ)
High μ → more exploration
- Selection strength (s)
Strong s → fast adaptation
- Recombination (r)
 $r > 0$ → breaks linkage

Key Concepts:

- **Fitness Peaks:** Genotypes with maximum fitness in their local neighborhood; populations tend to evolve toward peaks
- **Fitness Valleys:** Low-fitness regions between peaks that can trap populations and prevent access to higher peaks
- **Ruggedness:** The complexity of the landscape; rugged landscapes have many local optima
- **Epistasis:** Interactions between mutations where the effect of one depends on genetic background
- **Sign Epistasis:** When a mutation is beneficial in one background but deleterious in another
- **Evolutionary Accessibility:** Which genotypes can be reached through single mutational steps
- **Adaptive Walks:** Trajectories through sequence space following fitness gradients

Wright-Fisher Model for Fixation Probability:

$$P(\text{fixation}) \approx (1 - e^{(-2Ns)}) / (1 - e^{(-4Ns)})$$

where N = population size, s = selection coefficient

Example: Antibiotic Resistance Evolution

Studies of beta-lactamase evolution revealed a rugged fitness landscape where the path to high-level antibiotic resistance requires crossing fitness valleys. Some highly resistant variants can only be accessed through specific mutational paths involving 5+ mutations, explaining why certain resistance mechanisms emerge more frequently than others in clinical settings. Sign epistasis between mutations means that intermediate genotypes have lower fitness, creating evolutionary constraints.

Protein Engineering

Navigate sequence space to design proteins with desired properties

Drug Resistance

Predict evolutionary trajectories of pathogens under drug pressure

Crop Improvement

Guide breeding strategies to optimize multiple traits simultaneously

 **Synthetic Biology**

Design genetic circuits with predictable
evolutionary stability