

# **UNDERSTANDING THE DISTRIBUTION OF FITNESS EFFECTS (DFE) ACROSS ENVIRONMENTS**

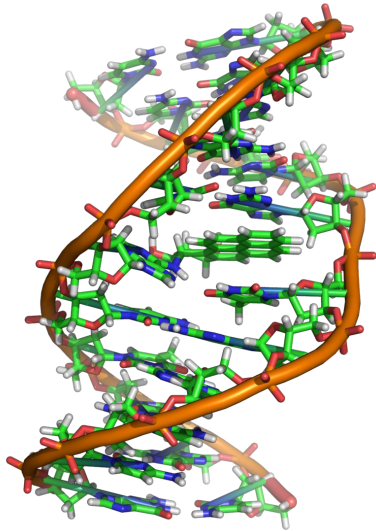
EXPLORING THE STATISTICAL PROPERTIES OF FITNESS LANDSCAPES USING THE  
FISHER'S GEOMETRIC MODEL

Shahnewaz Ahmed

# Fundamental Scales of Living Matter

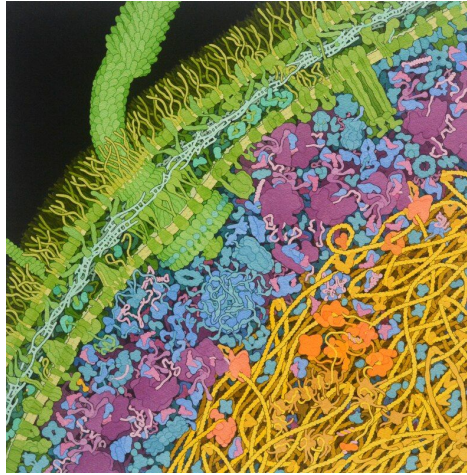
## Genotype

(Molecular/Microscopic scale)



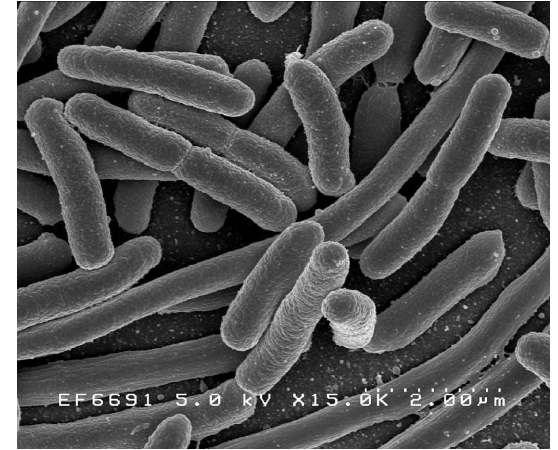
## Phenotype

(Mesoscopic/Cellular scale)



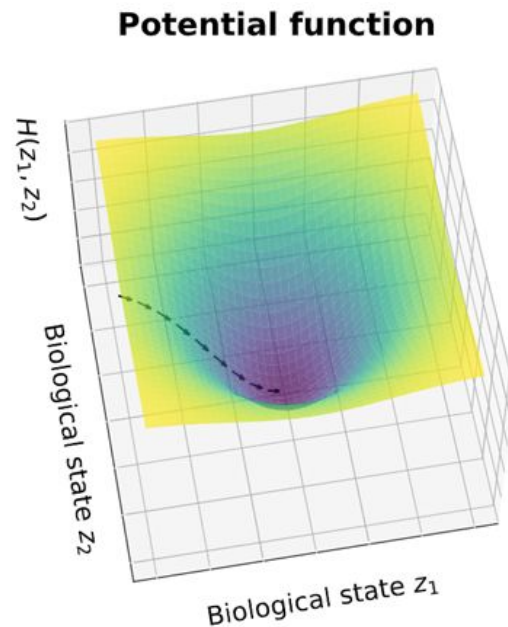
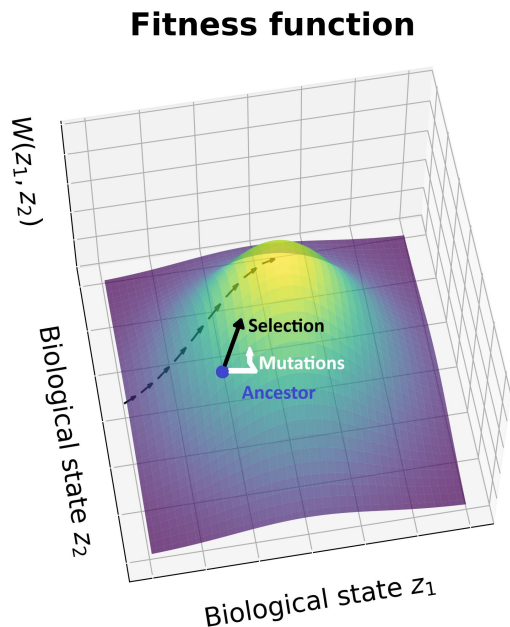
## Fitness

(Macroscopic/Population scale)



Source: Wikipedia

# Evolutionary Analog of Statistical Mechanics

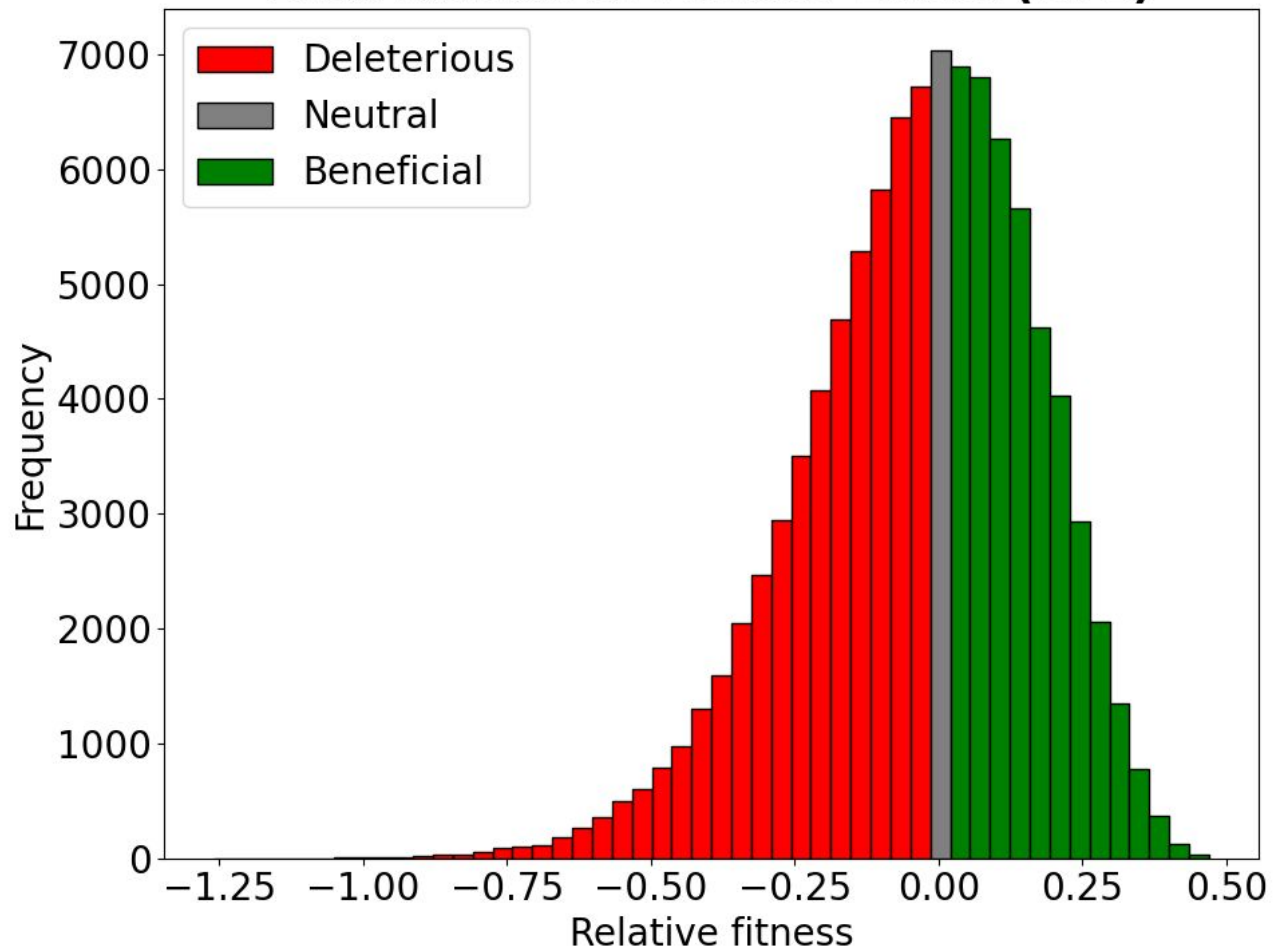


Fitness  $\longleftrightarrow$  Energy

Mutations  $\longleftrightarrow$  Entropic force

Finite size fluctuation  $\longleftrightarrow$  Thermal fluctuation

## Distribution of Fitness Effect (DFE)



# Importance of DFE

- Understanding what kind of effect mutation have on species especially on humans
- Central to questions in evolutionary biology
- Quantitative genetic variation

# Key Questions

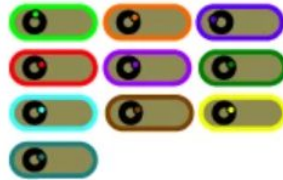
- \* How does the distribution of fitness effects (DFE) change across different environments?
- \* Are the mean and variance of the DFE more sensitive to environmental changes than the overall shape?
- \* What is the correlation of fitness effects for mutations across different environments?

# Experiment

For each  
bacterium:



Transposon  
mutants



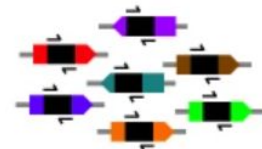
Start

High-throughput  
growth assays



After

Counting by  
sequencing

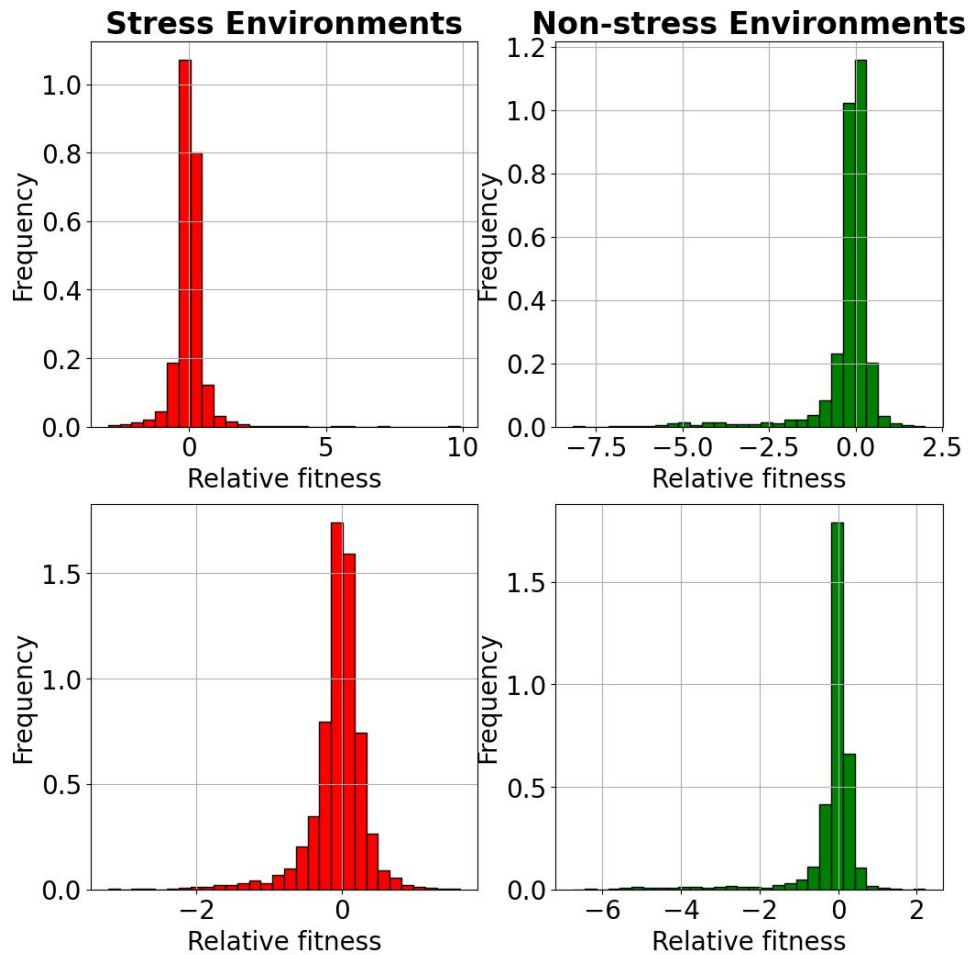


$$\text{Mutant fitness} = \log_2 \left( \frac{\text{abundance after}}{\text{abundance at the start}} \right)$$

Gene Name	D-Glucose (C)	Spectinomycin 0.0125 mg/ml
talB	-0.001	-2.712
yaaJ	-0.127	0.275
polB	-0.055	-0.328

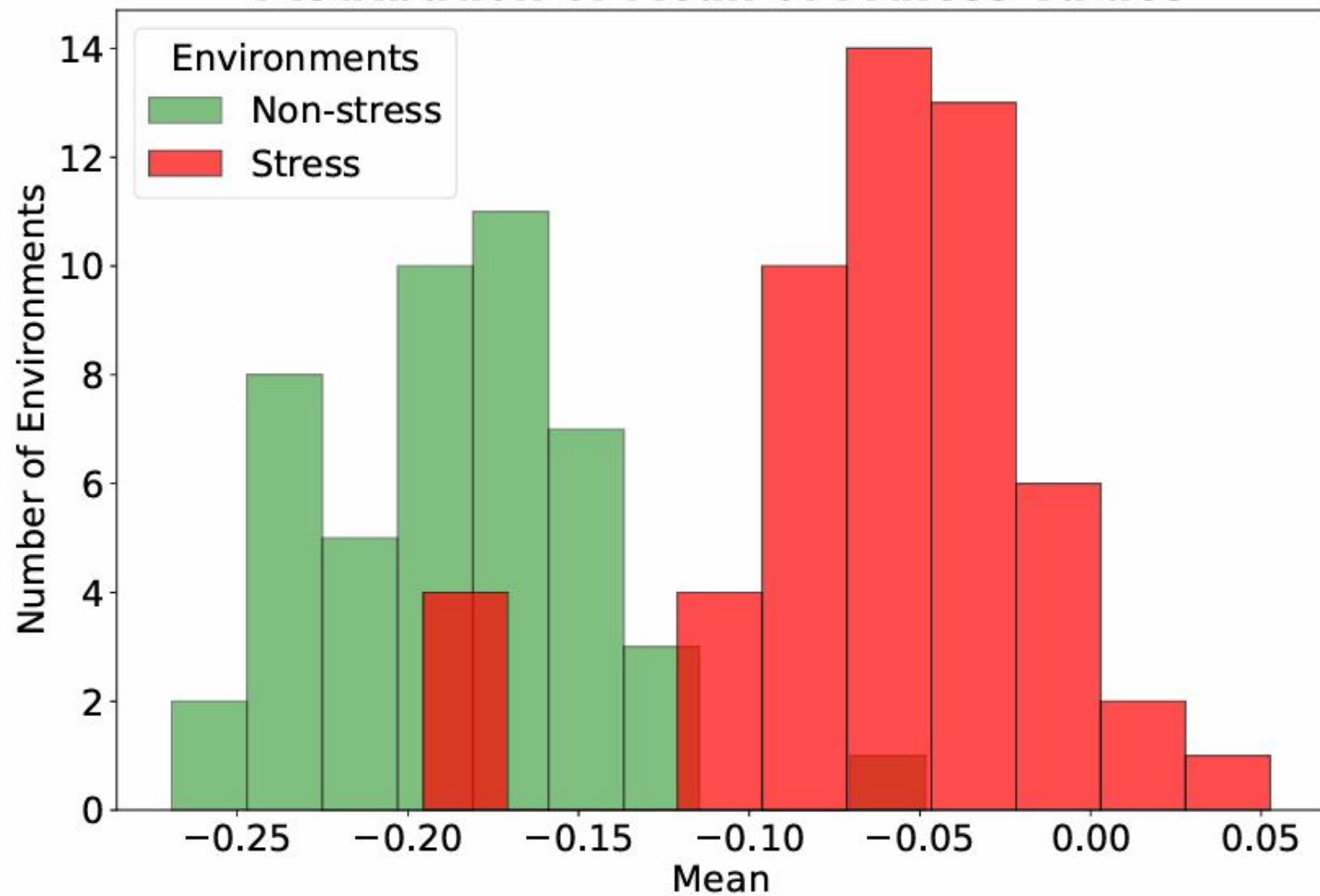
Source: [Price et. al. 2018](#)

# Distribution of Fitness Effect from Experimental Data

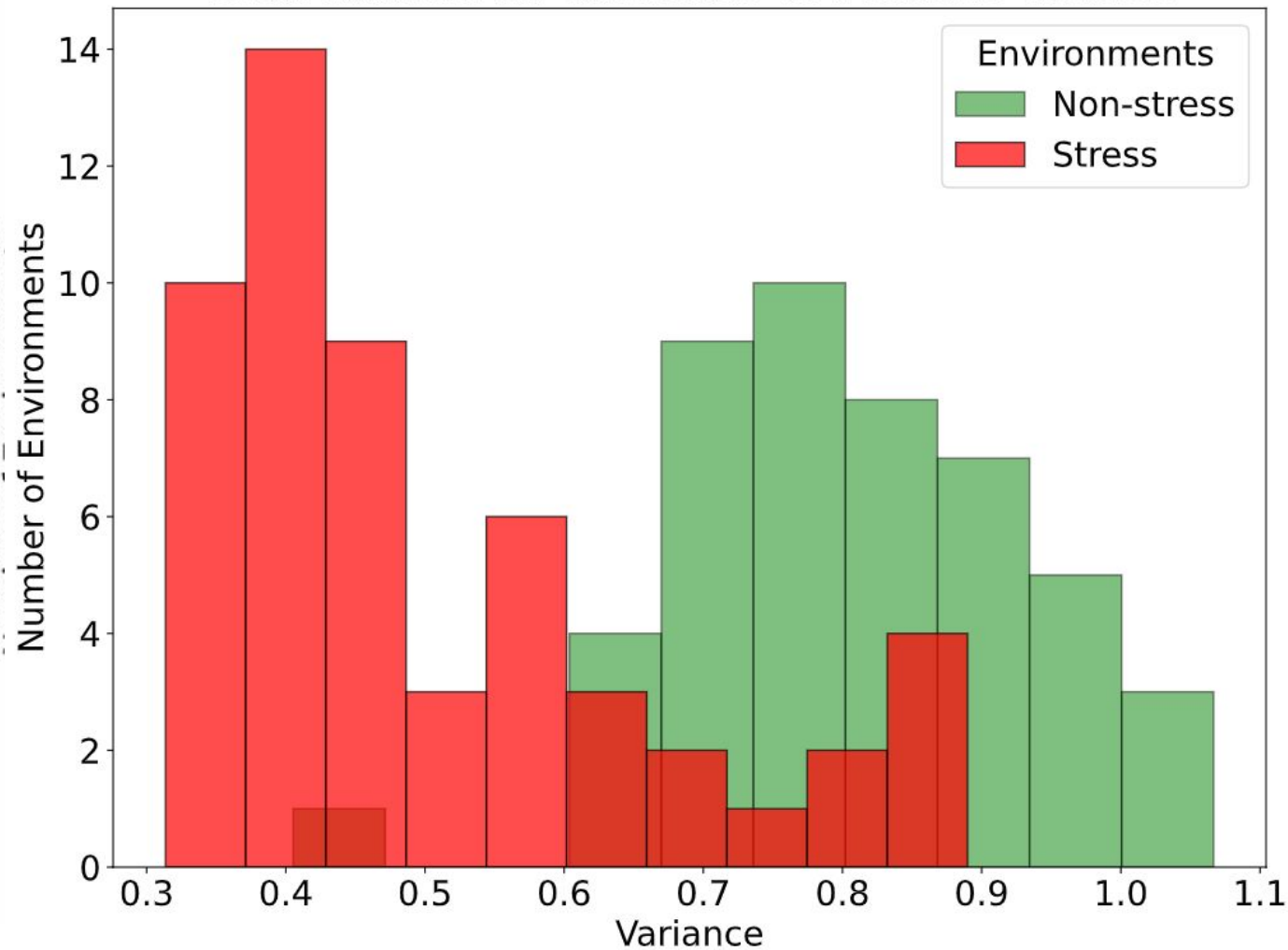




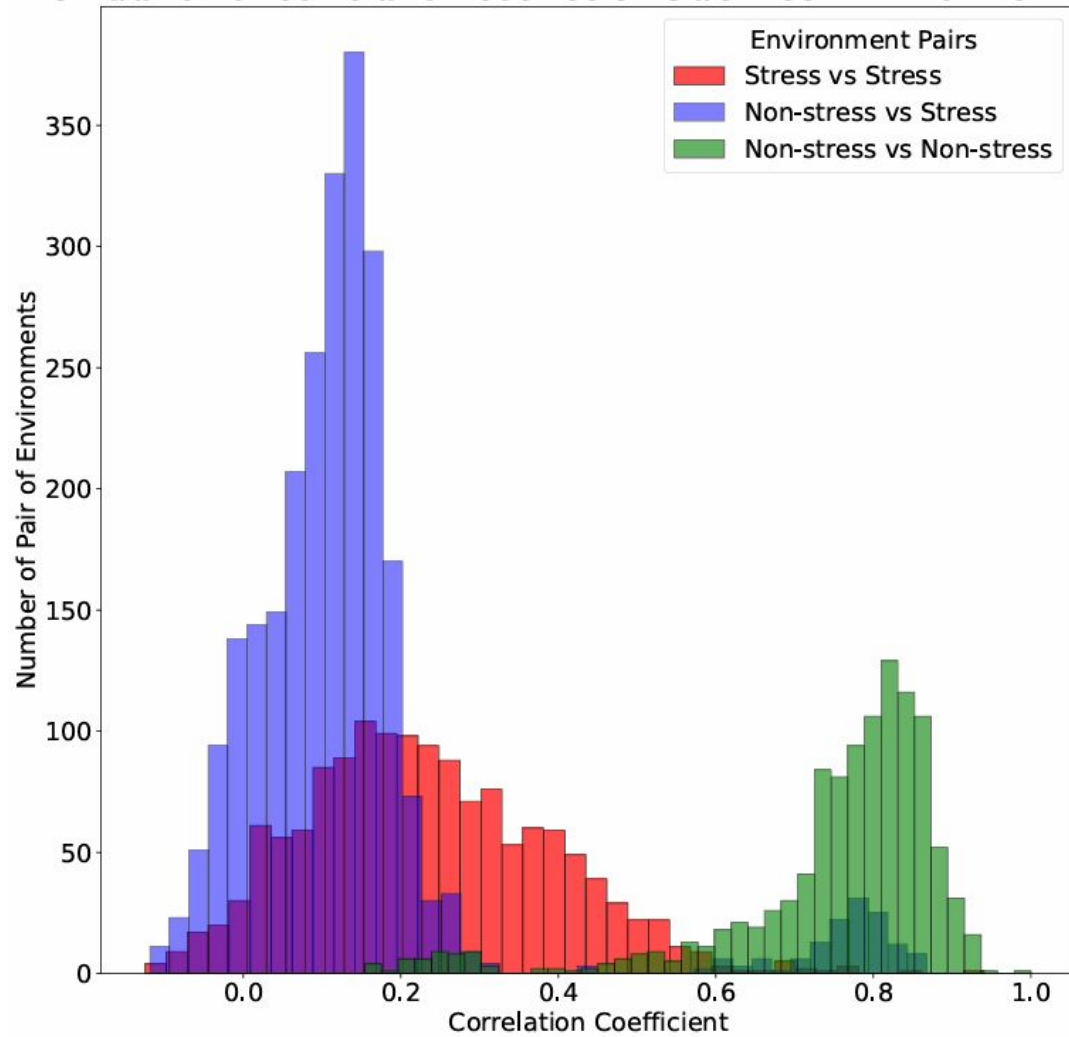
# Distribution of Mean of Fitness Values



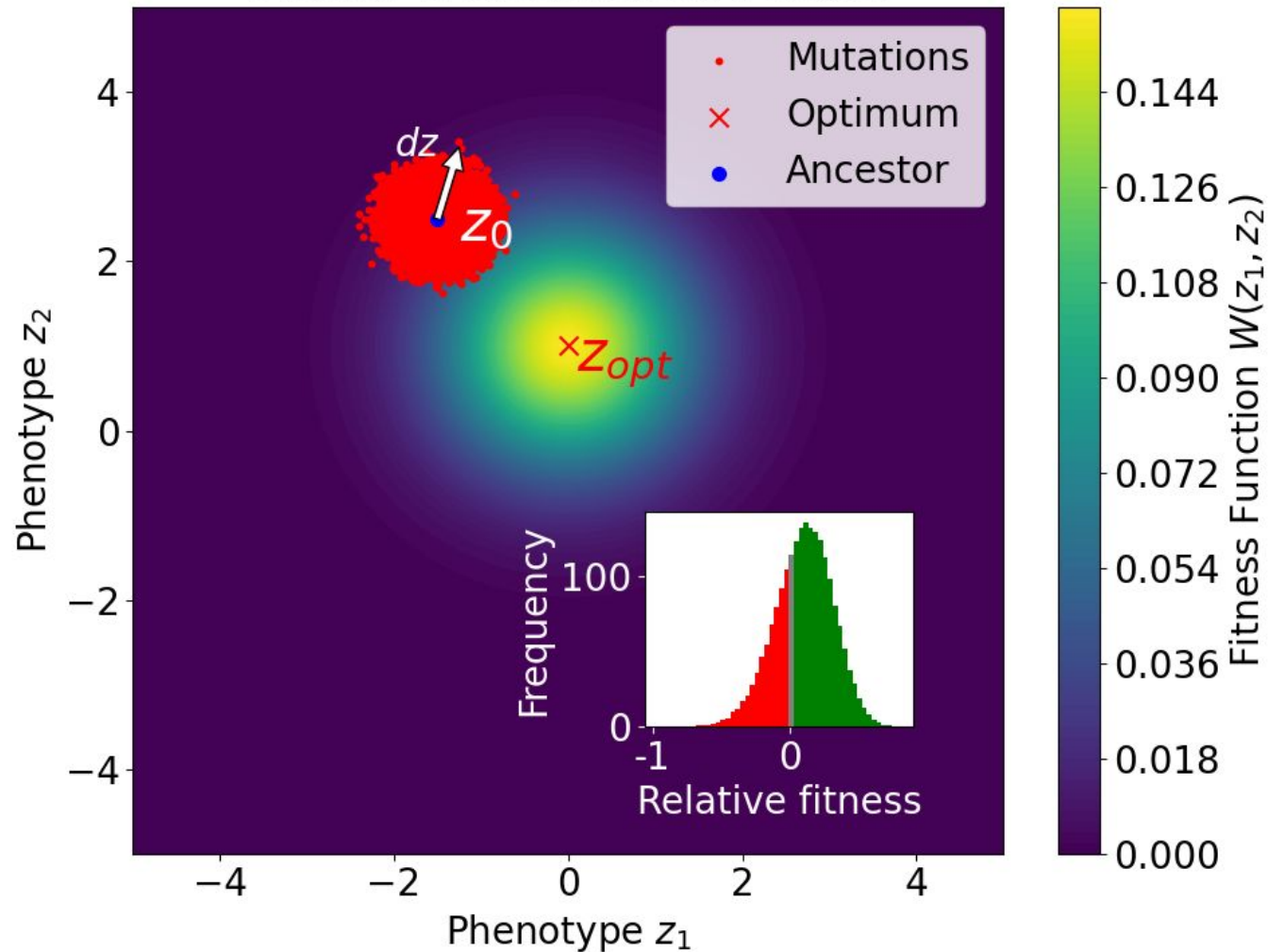
**Distribution of Variance of Fitness Values**



**Distribution of Correlation Coefficients between Environment Pairs**



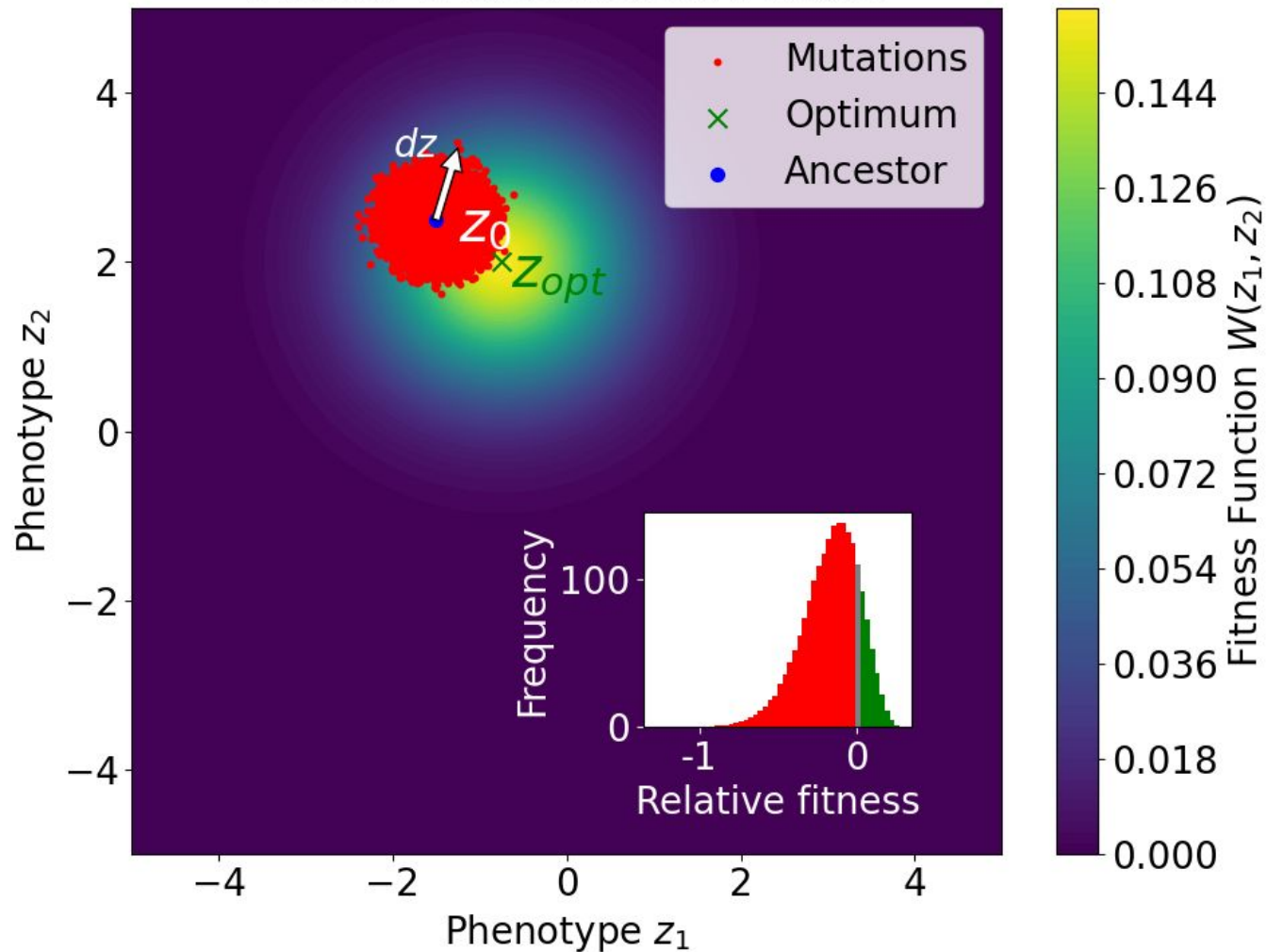
# Fisher's Geometric Model



## Relative Fitness

$$H(\mathbf{z}) = \ln \left( \frac{W(\mathbf{z})}{W(\mathbf{z}_0)} \right)$$

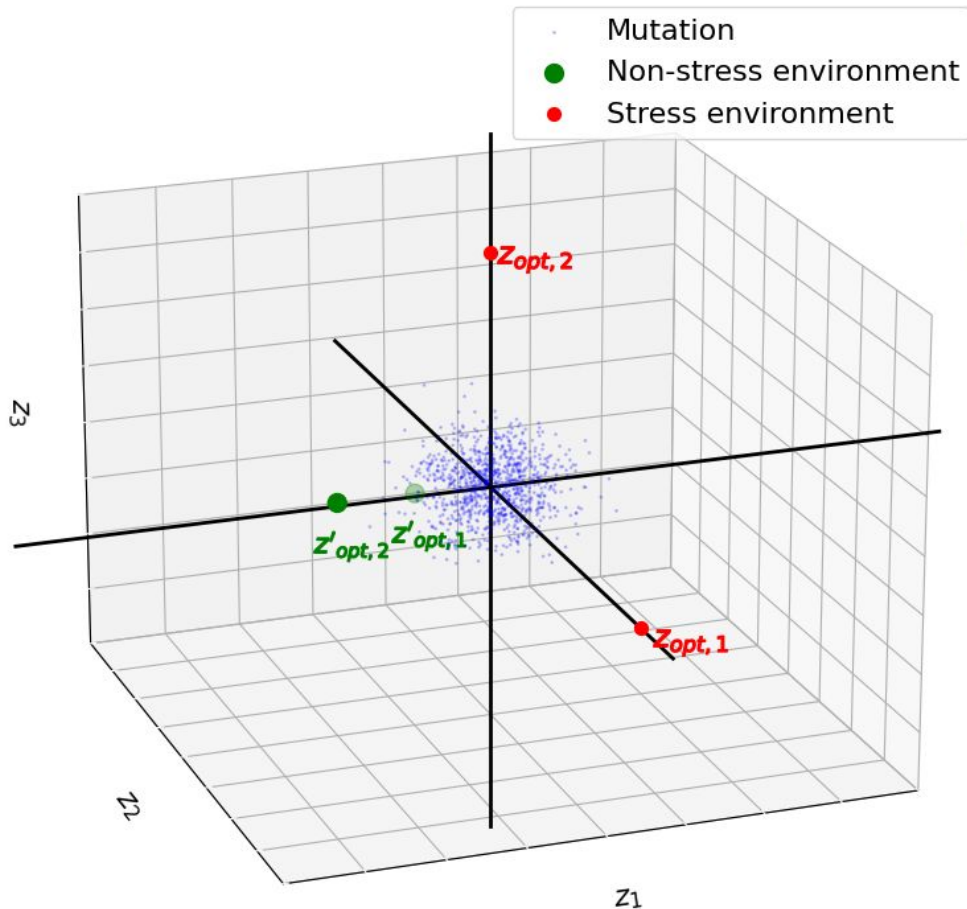
# Fisher's Geometric Model



## Relative Fitness

$$H(\mathbf{z}) = \ln \left( \frac{W(\mathbf{z})}{W(\mathbf{z}_0)} \right)$$

## Environment configurations



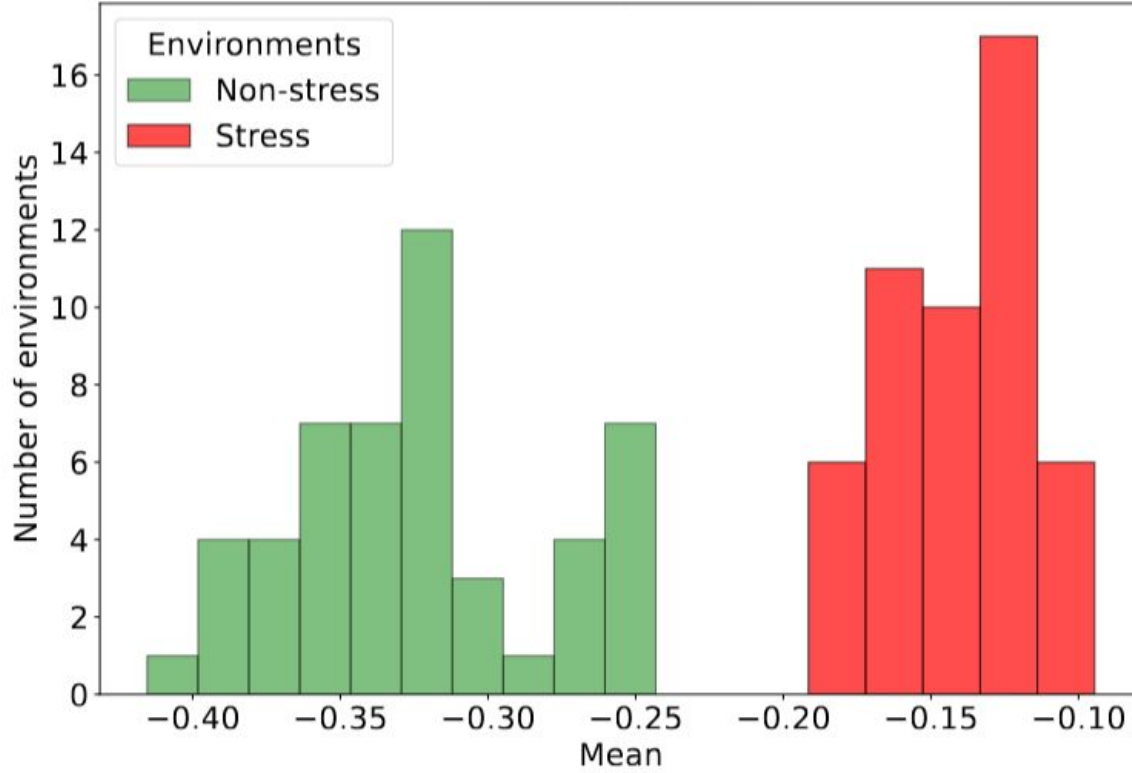
## Fitness Function

$$W(||\mathbf{z} - \mathbf{z}_{opt}||) = e^{\alpha ||\mathbf{z} - \mathbf{z}_{opt}||^Q}$$

## Mutant Distribution

$$d\mathbf{z} = \{dz_i\}_{i \in [1,n]} \quad MVN(0, \sigma_m^2 \mathbf{I}_n)$$

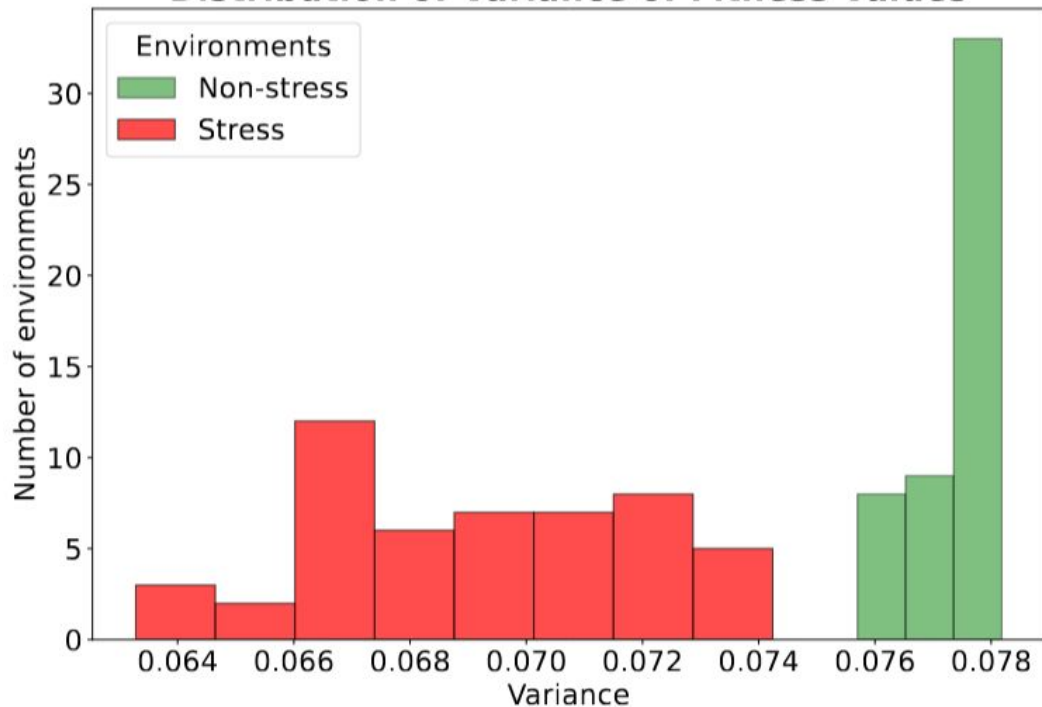
**Distribution of Mean of Fitness Values**



## Mean of DFE

$$M \approx \frac{\alpha \sigma_{\text{mut}}^2}{2} Q(Q + n - 2) \times ||\mathbf{z}_0 - \mathbf{z}_{\text{opt}}||^{Q-2} + o[E[dz^3]]$$

**Distribution of Variance of Fitness Values**

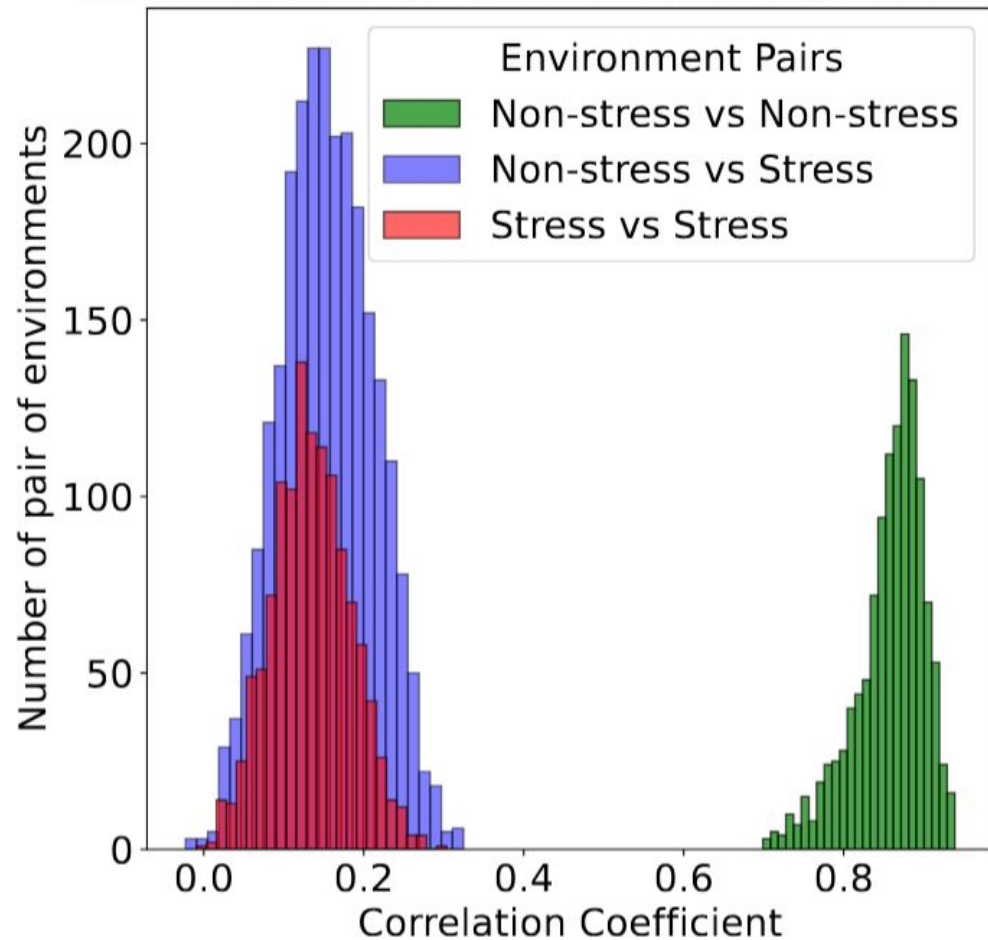


## Variance of DFE

$$V \approx \alpha^2 \sigma_{\text{mut}}^2 Q^2 \times ||\mathbf{z}_0 - \mathbf{z}_{\text{opt}}||^{2Q-2} + o[E[dz^3]]$$



## Distribution of Correlation Coefficients



## Correlation Coefficient

$$\rho_{H,H'} \approx \cos\left(\theta_{\mathbf{z}_{\text{opt}}, \mathbf{z}'_{\text{opt}}}\right) + o[E[dz^3]]$$

# Conclusion

1. Mechanistic Models: Link DFEs to molecular mechanisms (e.g., protein stability, metabolic fluxes) to move beyond phenomenological descriptions.
2. Environment Dimensionality: Develop scalable methods to handle high-dimensional environmental spaces (e.g., multi-nutrient gradients, biotic interactions).
3. Epistasis and Dynamics: Explore how DFEs change as populations evolve (i.e., epistasis) and incorporate temporal environmental fluctuations.
4. Cross-Species Frameworks: Test whether DFE patterns generalize across bacteria, eukaryotes, or viruses, revealing universal evolutionary constraints.

**Thank You**

# Key Assumptions

## 7. Fitness potential:

$$H(\mathbf{z}) = \log \left( \frac{W(\mathbf{z}_0 + d\mathbf{z})}{W(\mathbf{z}_0)} \right)$$

## Relative fitness:

$$dw = \frac{W(\mathbf{z}_0 + d\mathbf{z}) - W(\mathbf{z}_0)}{W(\mathbf{z}_0)}$$

$$dw \approx \ln(1 + dw) = \ln W(\mathbf{z}_0 + d\mathbf{z}) - \ln W(\mathbf{z}_0)$$

# Key Assumptions

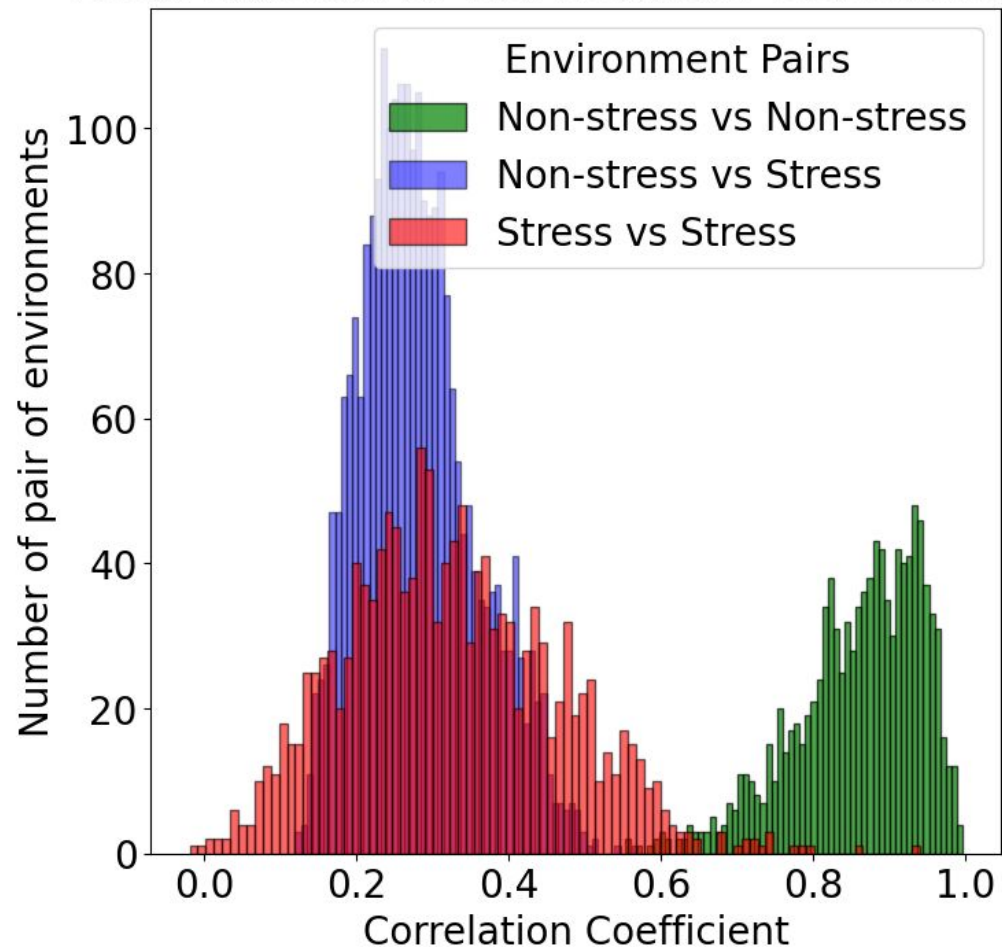
1. **Phenotype Space:**  $\mathbf{z} = \{z_i\}_{i \in [1, n]}$
2. **Genotype to Phenotype Relationship:**  $d\mathbf{z} = \{dz_i\}_{i \in [1, n]} \sim MVN(0, \sigma_m^2 \mathbf{I}_n)$
3. **Phenotypic Fitness Landscape:**  $W(\mathbf{z}_0)$
4. **Monotonicity of Fitness Function**
5. **Environmental Change**
6. **Stress and Non-stress Environment**

# Dataset

Gene Name	Description	D-Glucose (C)	L-Arginine (N)	Bacitracin 0.5 mg/ml	Spectinomycin 0.0125 mg/ml	Aluminum chloride 5 mM
talB	transaldolase B (NCBI)	-0.001	-0.027	-0.812	-2.712	-0.429
yaaJ	predicted transporter (NCBI)	-0.127	0.123	0.200	0.275	0.008
polB	DNA polymerase II (NCBI)	-0.055	-0.079	-0.169	-0.328	-0.113
ddlB	D-alanylanine synthetase (NCBI)	-0.509	-0.018	-1.366	-0.670	0.198
yacG	zinc-binding protein (NCBI)	-0.909	-0.525	0.309	0.546	0.750

Source: [Price et. al. 2018](#)

## Distribution of Correlation Coefficients



# Distribution of the number of fitness maxima in Fisher's geometric model

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