ModEDI

An Extendable Software Architecture for Examining the Effects of Developmental Interactions on Evolutionary Trajectories

Elizabeth Brooks
Dept. of Computer Science
Western Washington University

Graham Roberts
Dept. of Computer Science
Western Washington University

Alison Scoville
Dept. of Biology
Central Washington University

Filip Jagodzinski
Dept. of Computer Science
Western Washington University

Background - *Quantitative Genetics*

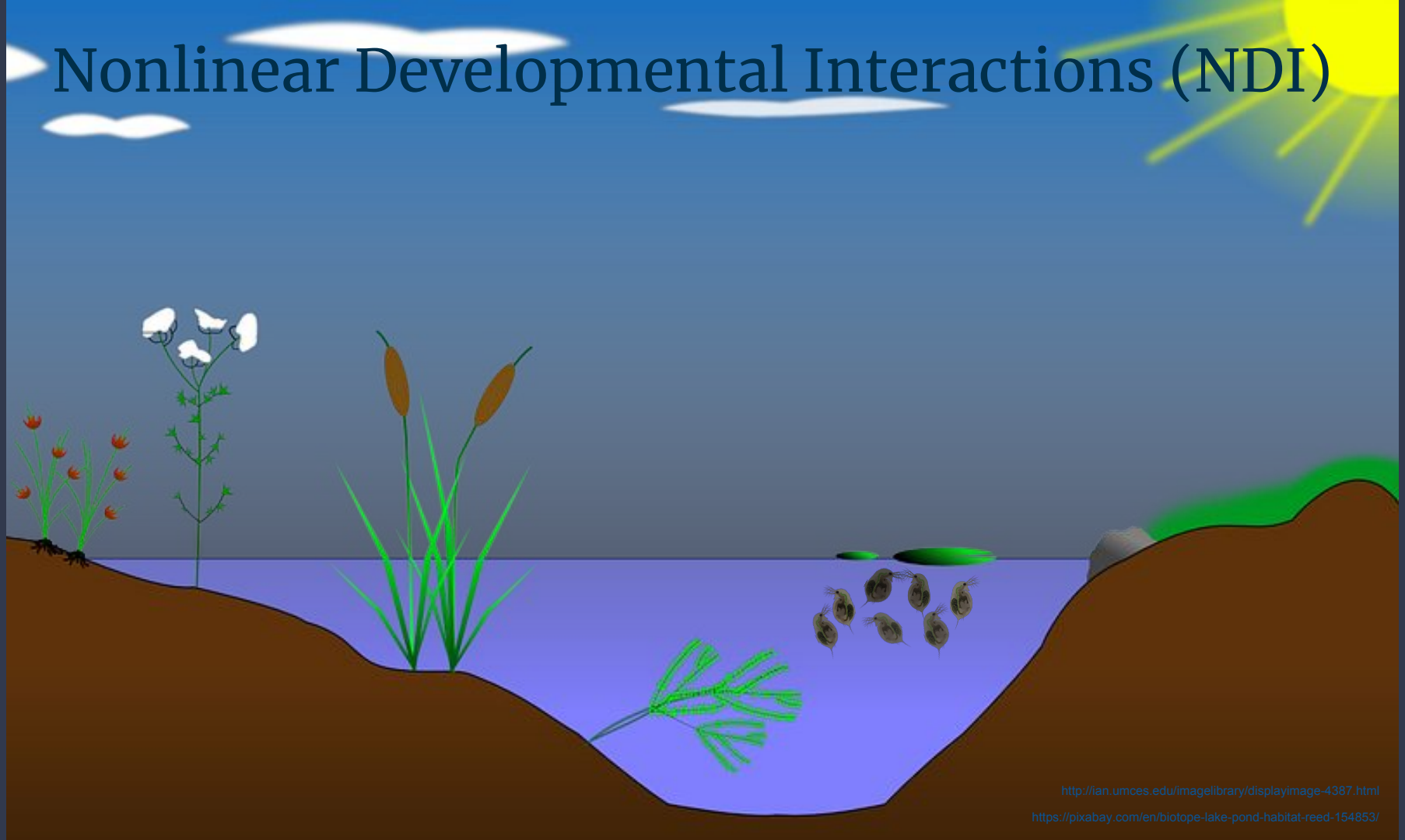
http://www.bio.miami.edu/dana/250/250SS15_2print.html

Models for *Daphnia*

http://andynewman.org/html/daphnia_water_flea.html

http://www.archive.org

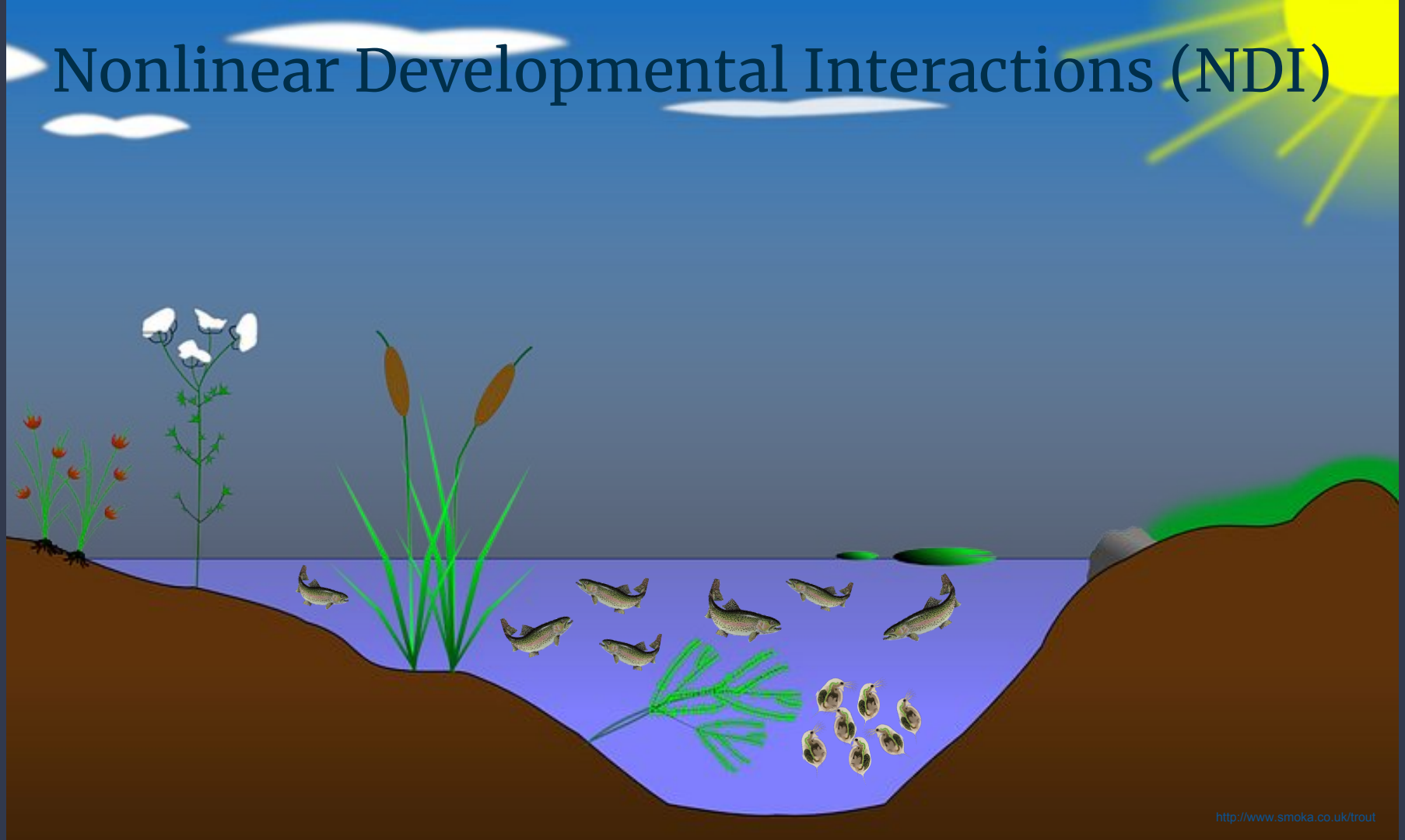
Nonlinear Developmental Interactions (NDI)



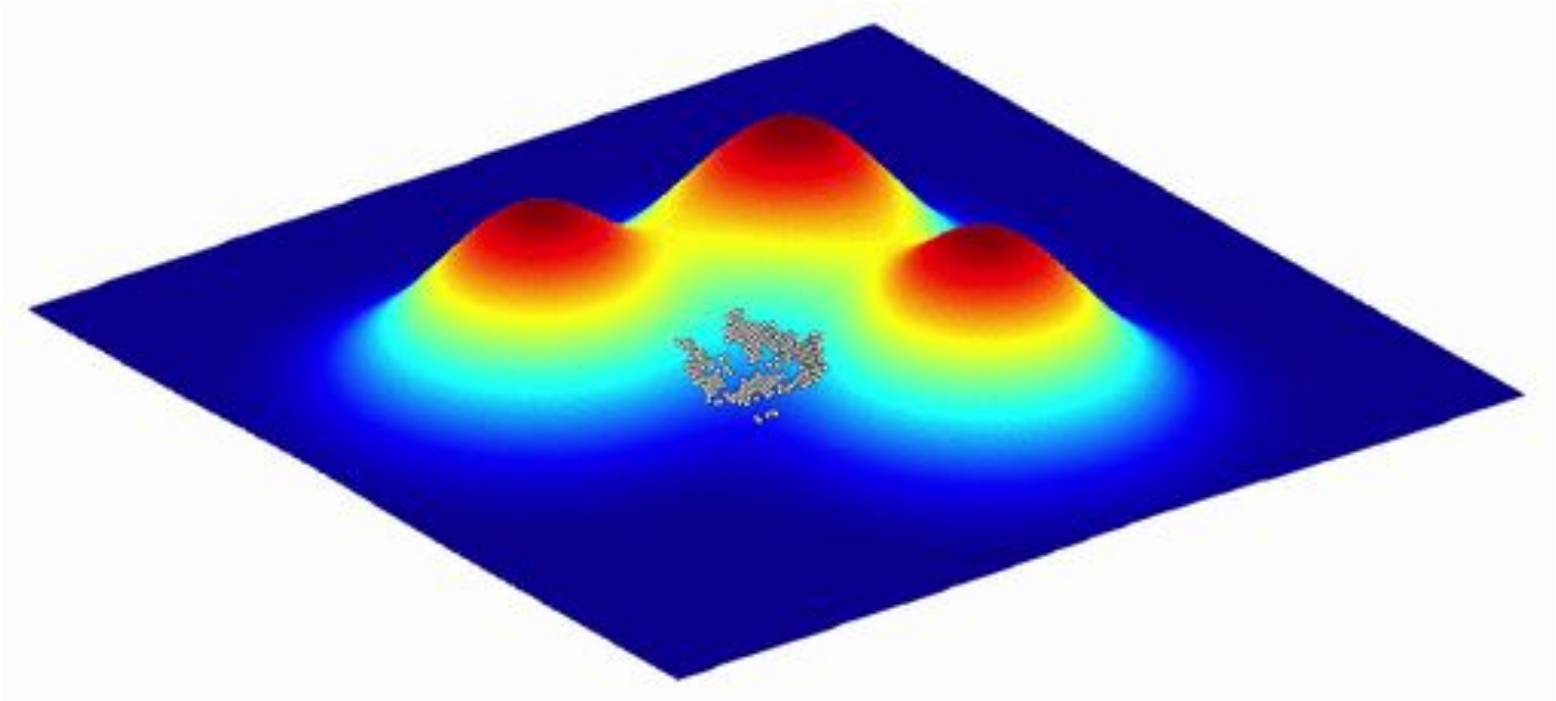
http://ian.umces.edu/imagelibrary/displayimage-4387.html

https://pixabay.com/en/biotope-lake-pond-habitat-reed-154853/

Nonlinear Developmental Interactions (NDI)



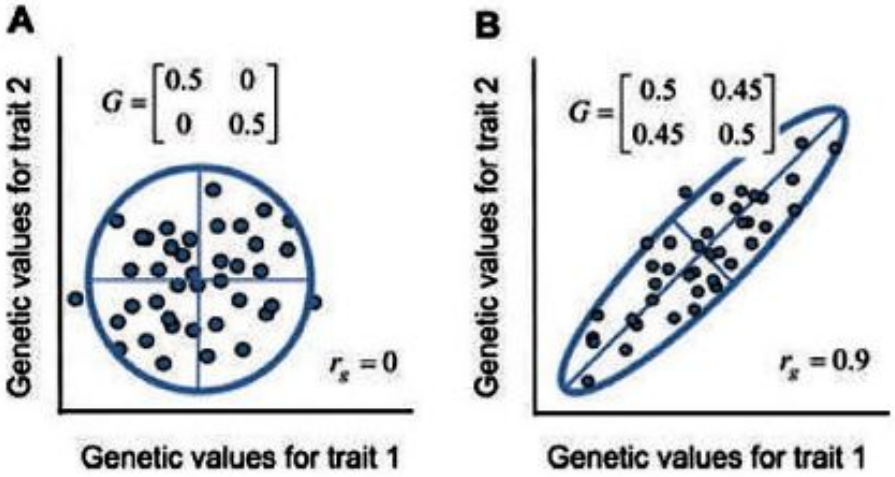
Central Concept – *Fitness Surface*

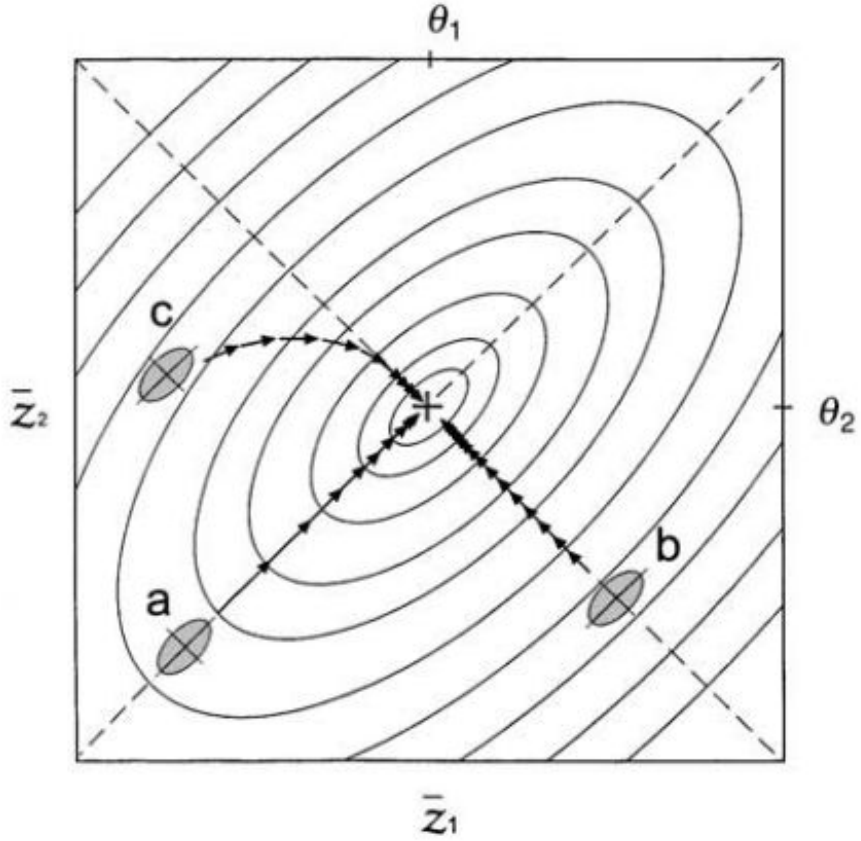


https://commons.wikimedia.org/wiki/File:Visualization_of_a_population_evolving_in_a_static_fitness_landscape.gif

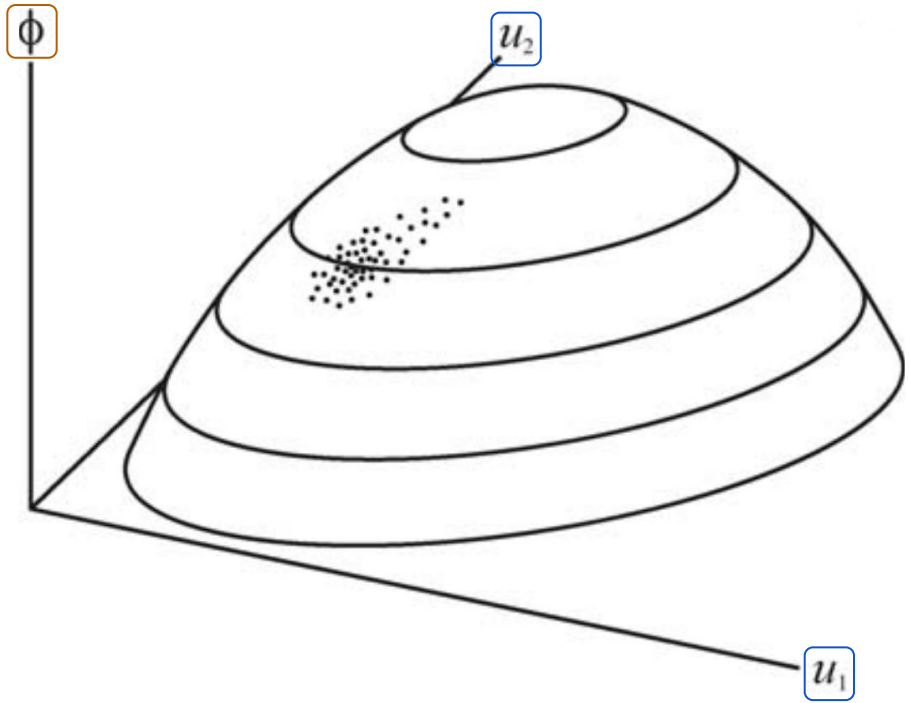
Central Concept - *GMatrix*

$$\Delta z = G\beta \Rightarrow \begin{bmatrix}\Delta z_1 \\ \Delta z_2\end{bmatrix} = \begin{bmatrix}G_{11} & G_{12} \\ G_{12} & G_{22}\end{bmatrix}\begin{bmatrix}\beta_1 \\ \beta_2\end{bmatrix}$$





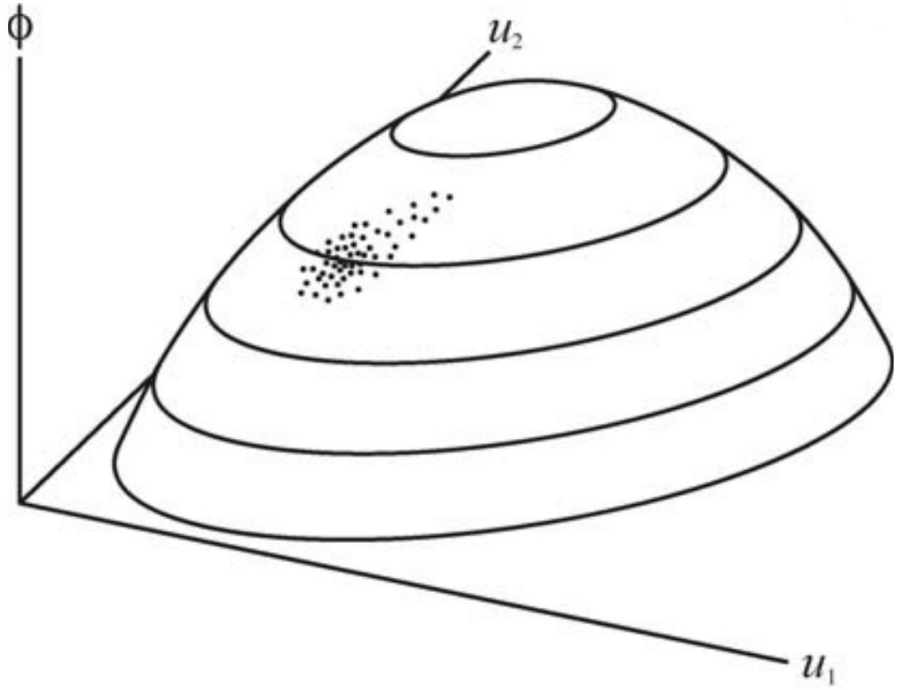
Central Concept – *Phenotype Surface*



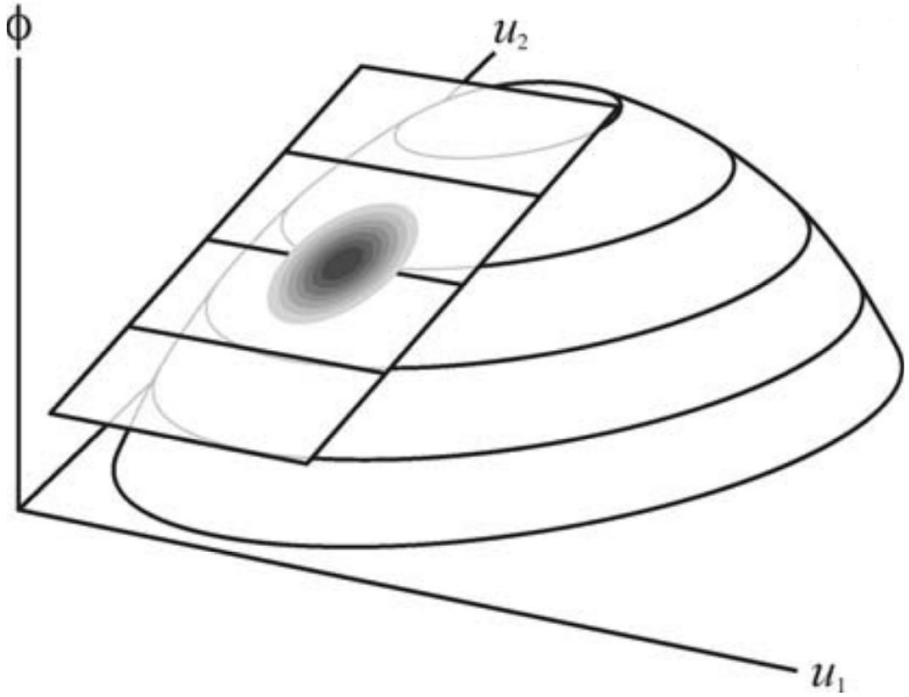
- **ϕ** represents a physical trait
- ***u*$_1$** and ***u*$_2$** represent underlying genetic factors
- Measures genetic variances
  - Additive
  - Dominance
  - Epistasis
  - Environmental

http://www.faculty.biol.ttu.edu/rice/rice08b.pdf

Phenotype Surface vs GMatrix



Phenotype Surface

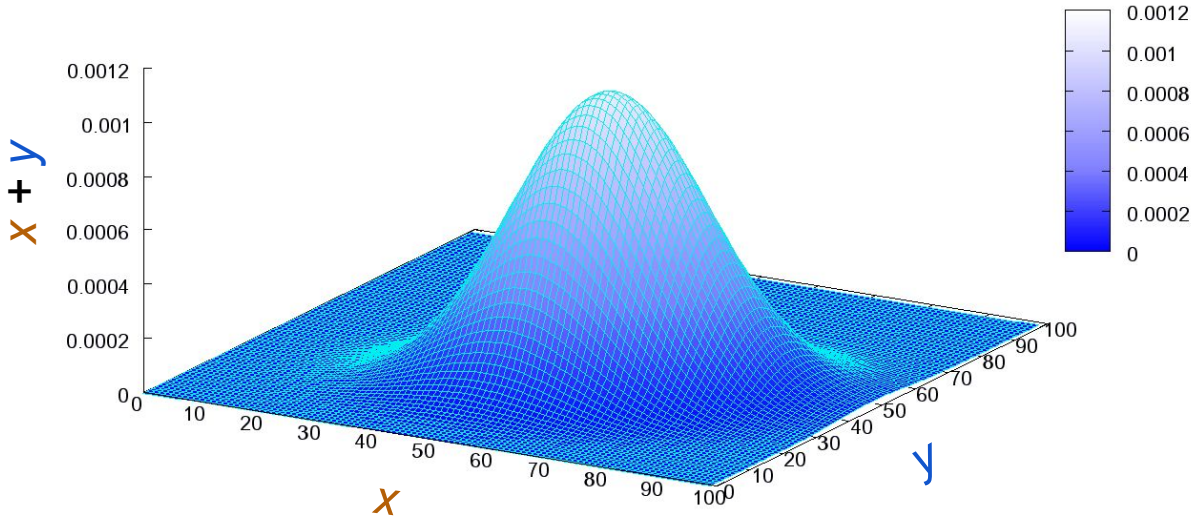


G-matrix Approximation

Surface Distribution – *Bivariate Normal*

- *x* and *y* are normally distributed values
- The sum of *x* and *y* form the bivariate normal distribution

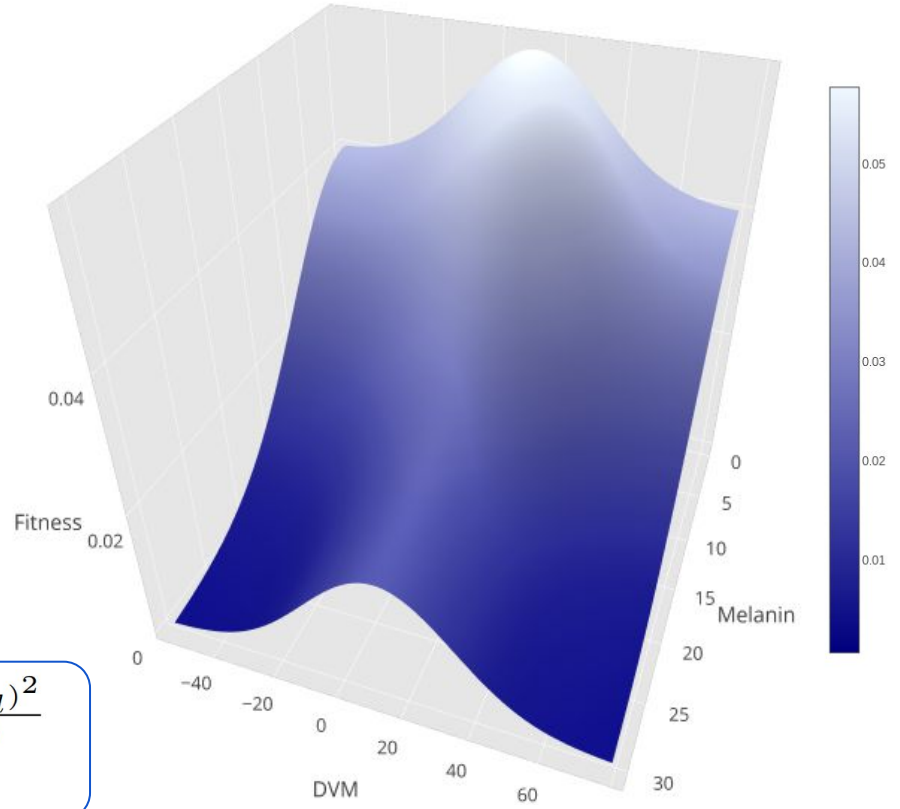
$w = N(\langle x \rangle, \sigma_x) + N(\langle y \rangle, \sigma_y)$



https://commons.wikimedia.org/wiki/File:Multivariate_Gaussian.png

Surface Distribution – *Bivariate Normal*

- Melanin and DVM are normally distributed trait values
- The sum of Melanin and DVM form the bivariate normal distribution



$$w = \frac{1}{\sqrt{v_m 2\pi}} e^{-\frac{(m-\omega_m)^2}{2v_m}} + \frac{1}{\sqrt{v_d 2\pi}} e^{-\frac{(d-\omega_d)^2}{2v_d}}$$

Classic Model – *G-matrix*

- h^2 is the diagonal values of the heritability matrix
- $\bar{w}$ is the mean population fitness
- σ_d and σ_m are the DVM ($\bar{d}$) and Melanin ($\bar{m}$) phenotypic variances

$$\Delta \mathbf{z} = \mathbf{G}\boldsymbol{\beta} \Longrightarrow \begin{bmatrix} \Delta z_1 \\ \Delta z_2 \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} \\ G_{12} & G_{22} \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix}$$

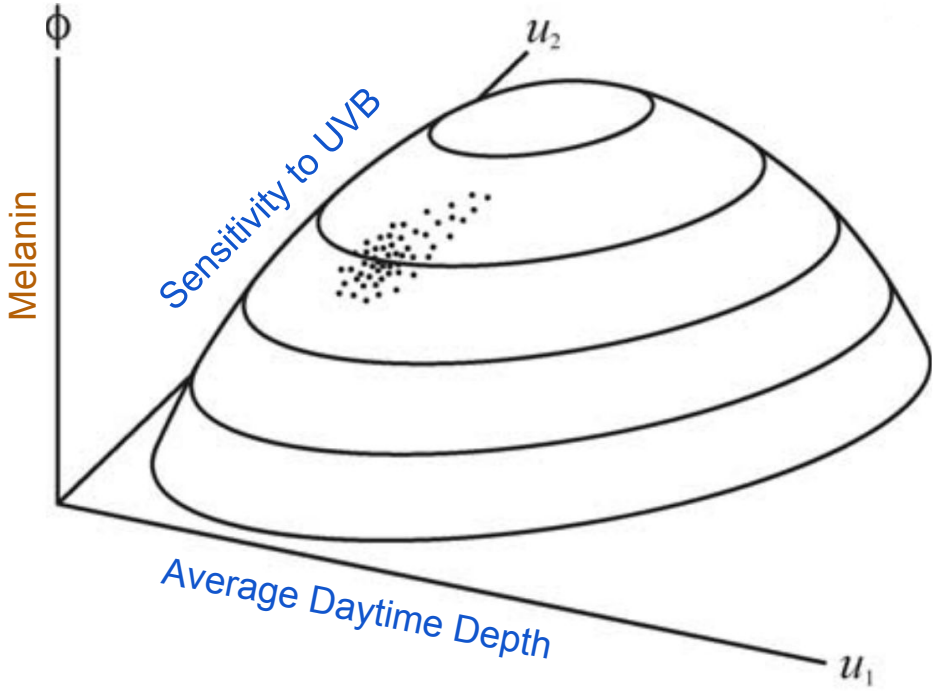
Melanin development:

$$\bar{m}_{t+1} = \bar{m}_t + h^2 \frac{1}{\bar{w}} \frac{\partial w}{\partial m} \sigma_m$$

DVM development:

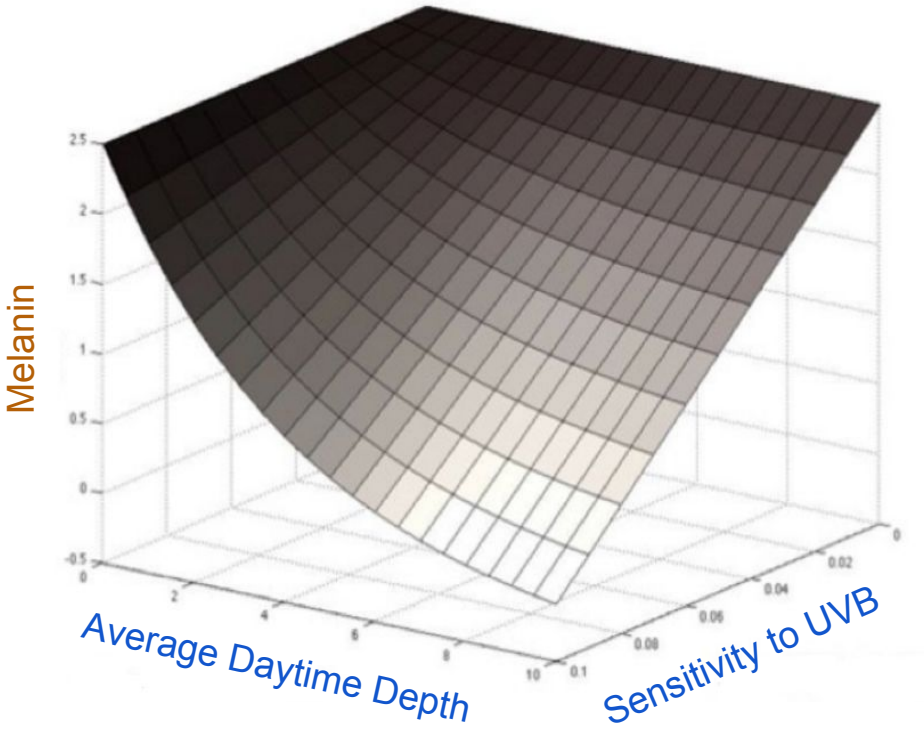
$$\bar{d}_{t+1} = \bar{d}_t + h^2 \frac{1}{\bar{w}} \frac{\partial w}{\partial d} \sigma_d$$

Tanning Model – *Phenotype Surface*



- **ϕ** represents a physical trait, Melanin
- $\boldsymbol{u_1}$ and $\boldsymbol{u_2}$ represent underlying genetic factors, Average Daytime Depth and Sensitivity to UVB

Tanning Model – *Phenotype Surface*



$$m = z + pa$$

- *z* is the concentration of melanin produced in response to UV light
- *p* is the slope of the reaction norm indicating sensitivity to UVB
- *a* is the change in UVB exposure

Tanning Model - *NDI*

- ***d*** is DVM, treated as a quantitative genetic trait
- ***H*** is the heritability matrix
- ***U*** represents the change in DVM, simplified
- ***V*** represents the change in Melanin, simplified

$$\Delta \mathbf{z} = \mathbf{G}\boldsymbol{\beta} \Longrightarrow \begin{bmatrix} \Delta z_1 \\ \Delta z_2 \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} \\ G_{12} & G_{22} \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix}$$

Melanin production:

$$m = z + pa$$

Development of genetic factors:

$$\begin{pmatrix} \bar{z} \\ \bar{p} \\ \bar{d} \end{pmatrix}_{t+1} = \begin{pmatrix} \bar{z} \\ \bar{p} \\ \bar{d} \end{pmatrix}_{t} + H \frac{1}{\bar{w}} \boxed{U} \boxed{V}$$

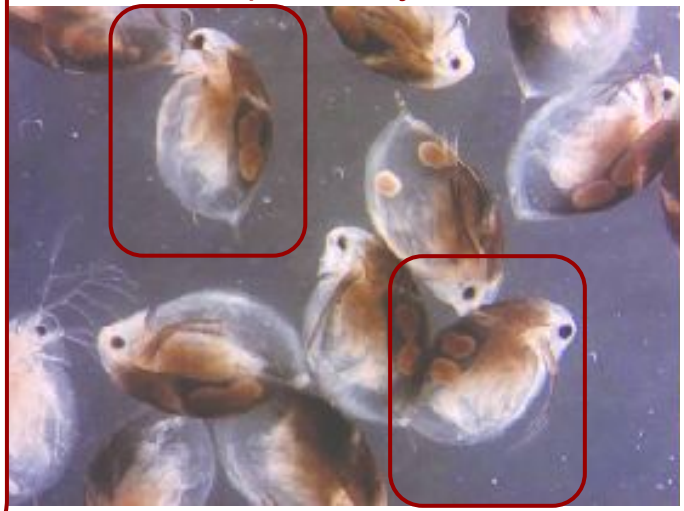
Daphnia Species Objects

- States represent phenotypic traits, DVM and Melanin
- Behaviours represent the phenotypic functions of the **Classic** and **Tanning** *Daphnia* models

Daphnia Blueprint

Daphnia melanica
- DVM: int - Melanin: int
+ setDVM + setMelanin

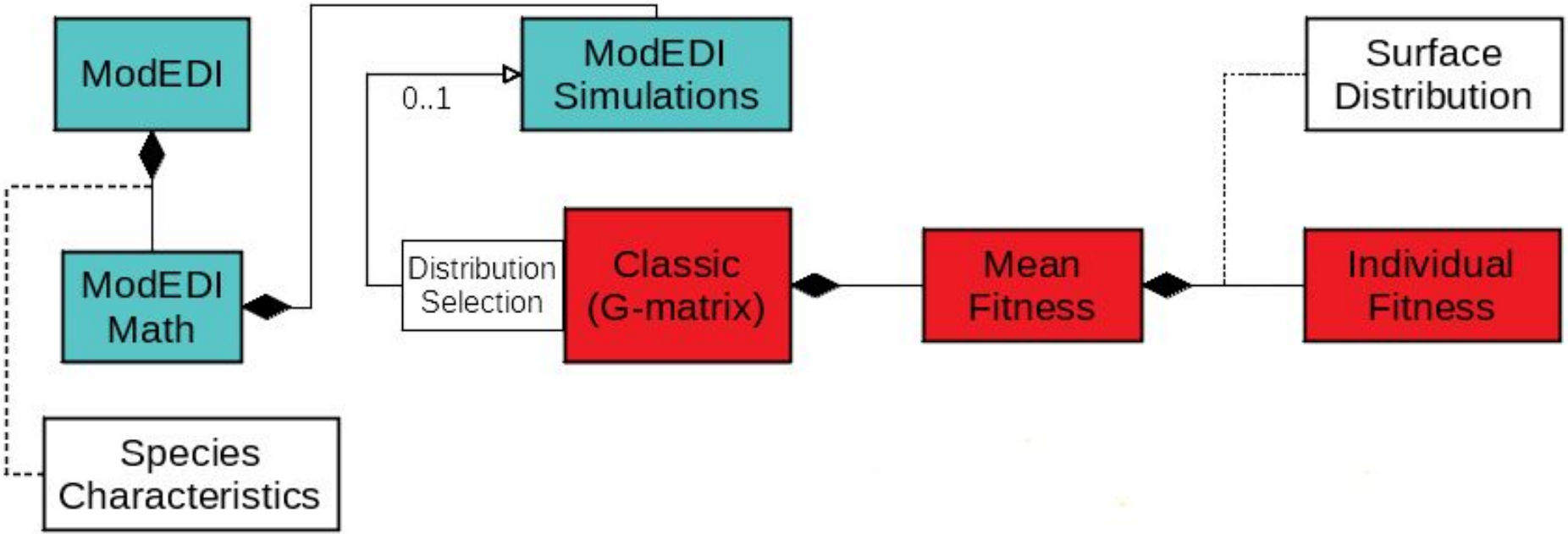
Daphnia Objects



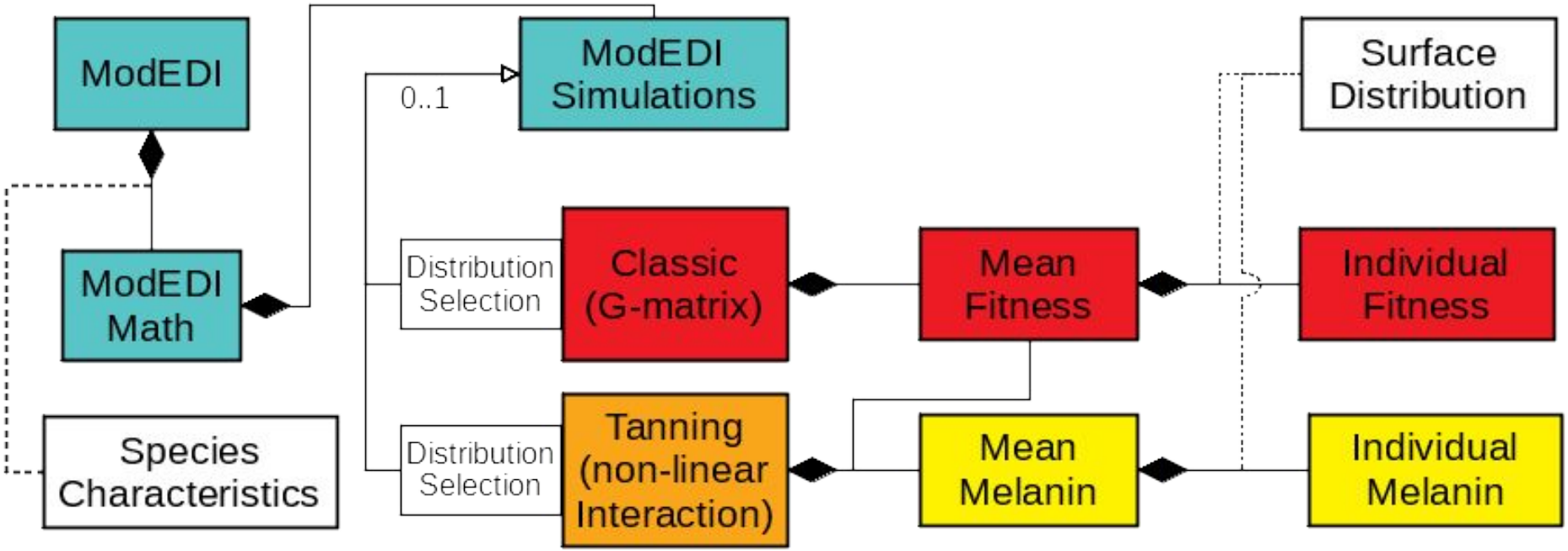
https://t3.ftcdn.net/jpg/00/47/53/14/240_F_47531414_8Vj6iYmdowUNtgFrxmmtgPdT8gRTzCdy.jpg

https://www.researchgate.net/figure/51073279_fig5_Fig-5-Pigmented-zooplankton-Melanised-Daphnia-umbra-left-and-Eudiaptomus-graciloides

Software Architecture – *Classic Model*



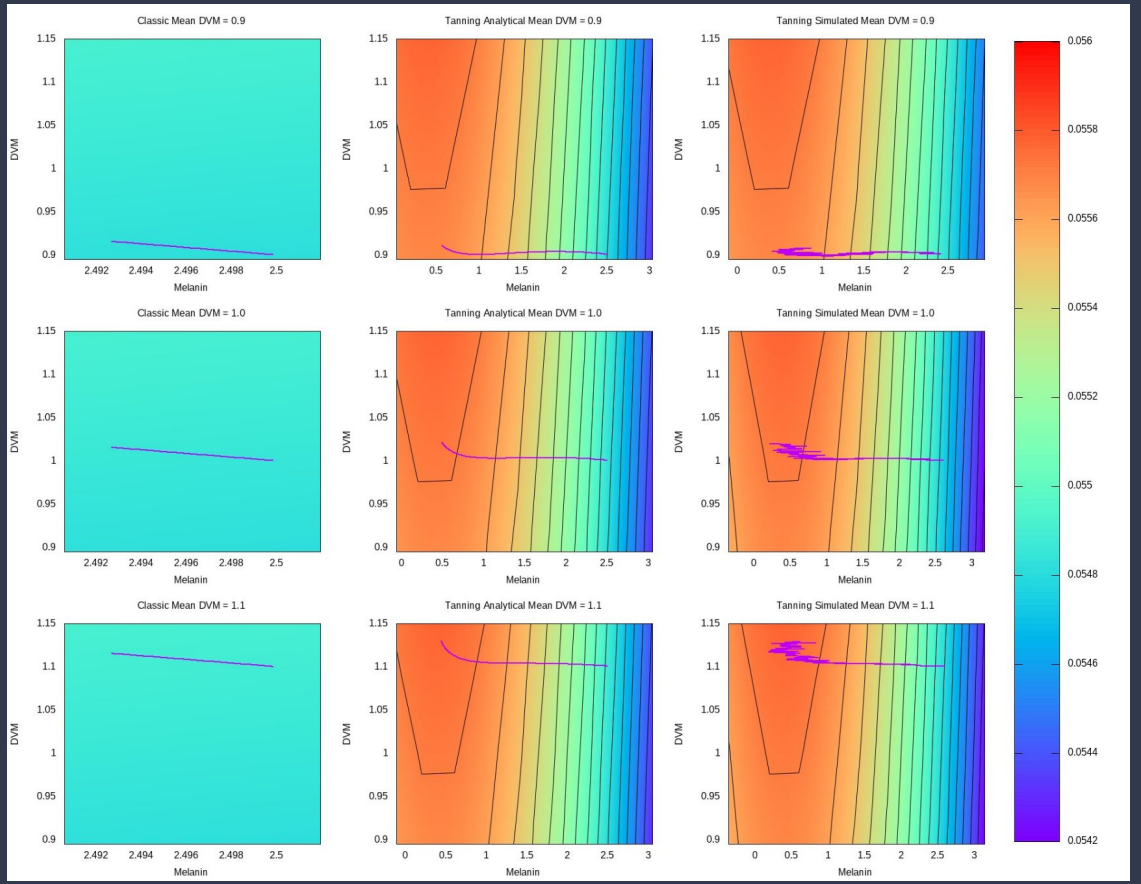
Software Architecture – *Tanning Model*



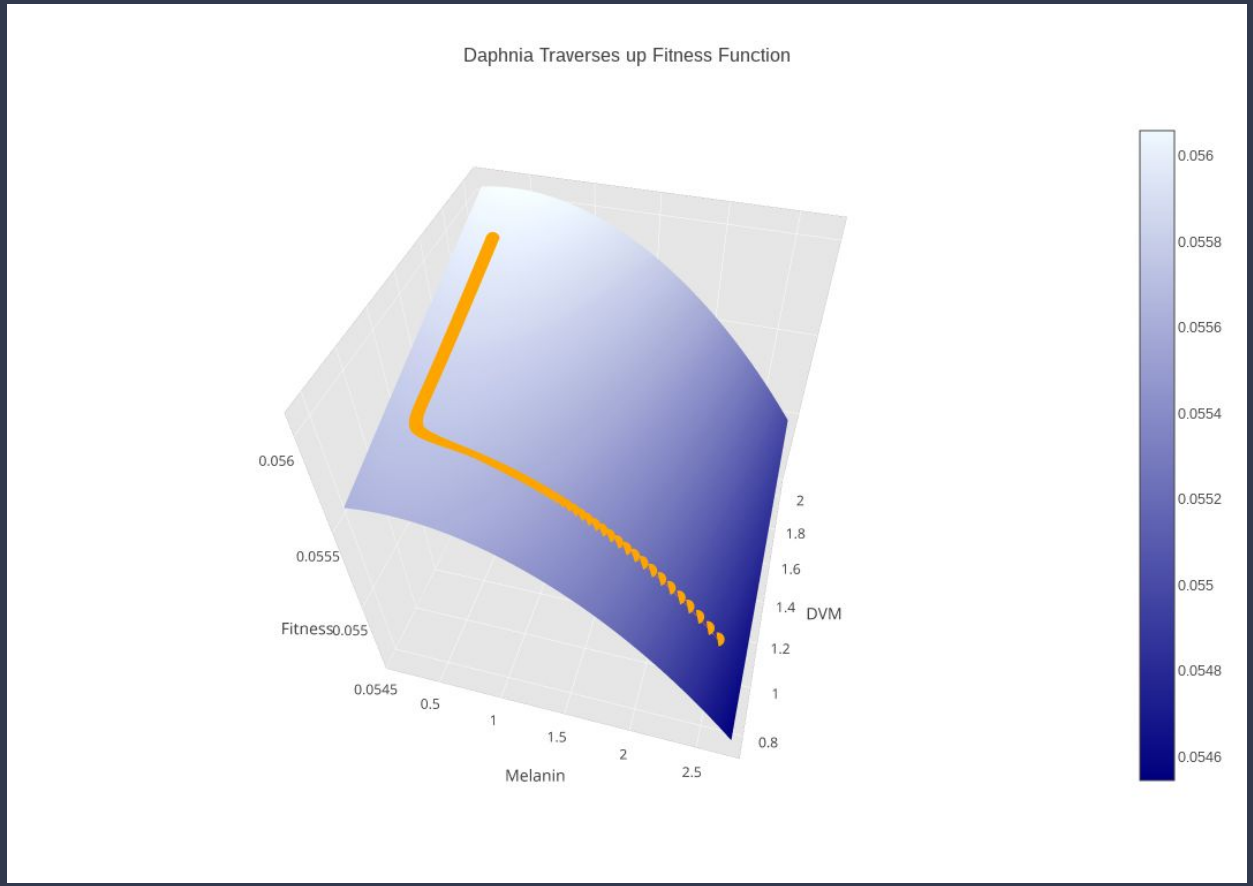
Mean DVM Parameter Sweep

Conclusions:

- Less fluctuation in trajectories
- Higher overall fitness
- Quicker to reach trait optima
- *Classic* model evolves more slowly than *Tanning*



Daphnia Case Study – *Results*



Future Work

- Increased generalization
  - Support any number of physical traits
  - Support any number of developmental factors for each trait
- Add support for other fitness and phenotype distributions
- Make available as a R package
- Update online user interface

Acknowledgements

- CWU Science Honors Research Program
- WWU College of the Sciences and Engineering