

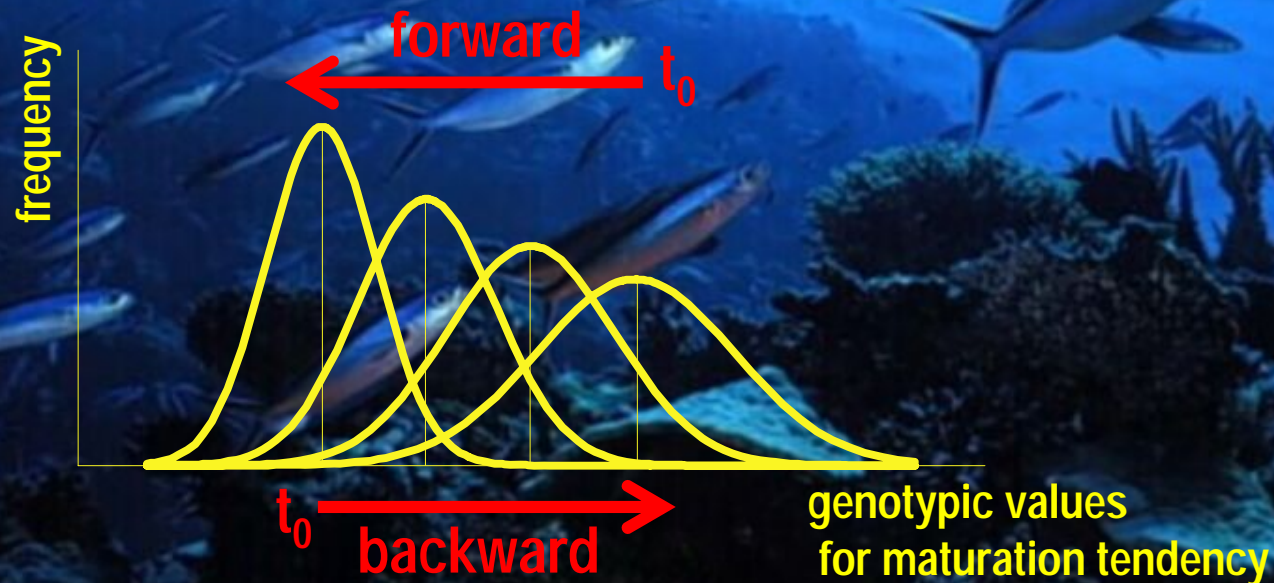


Linking ecological and genetical approaches of maturation reaction norms

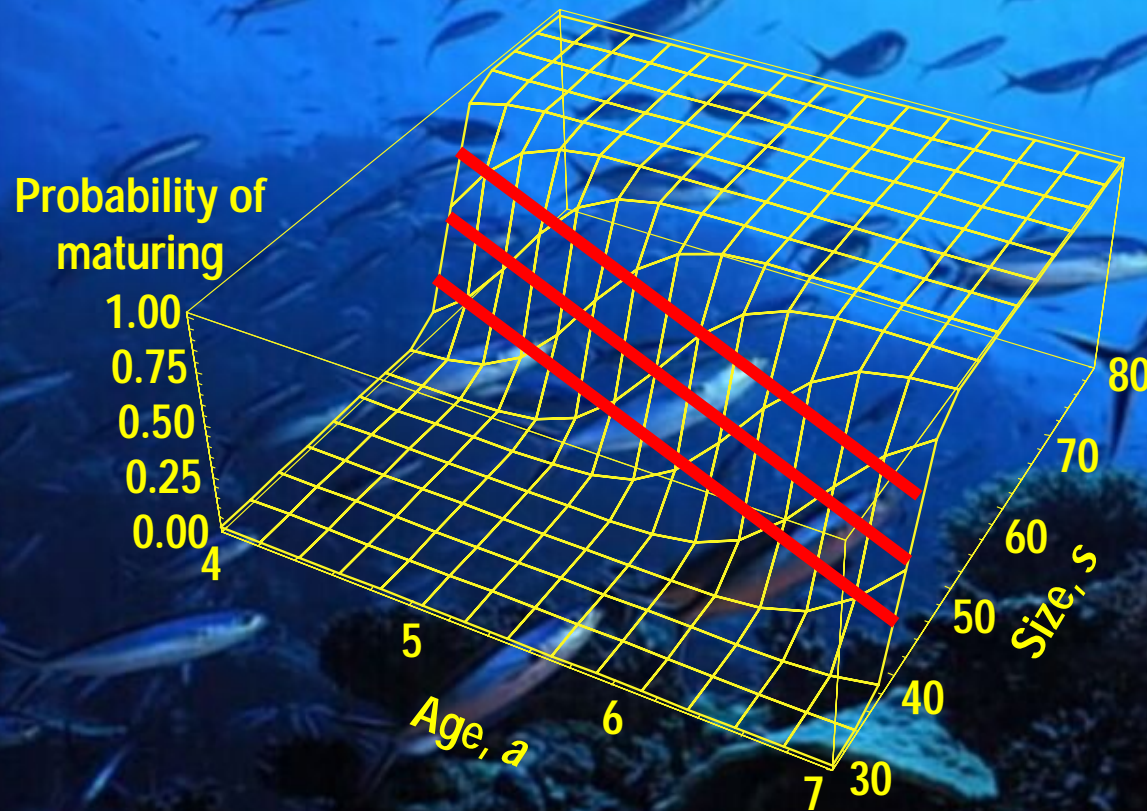
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Objectives

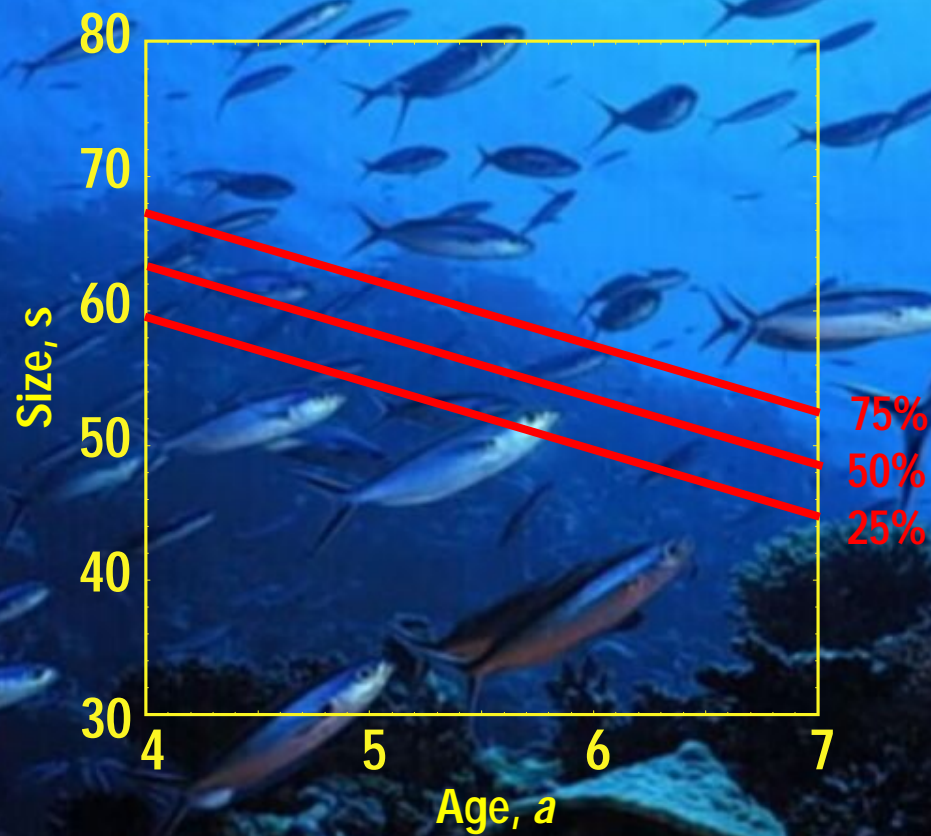
- Evaluate/disentangle genetic and environmental variation in maturation tendency of exploited fish stocks
- Backward estimation of genetic variance erosion and/or shift of genetic mean in maturation tendency
- Forward prediction of future evolution of maturation tendency



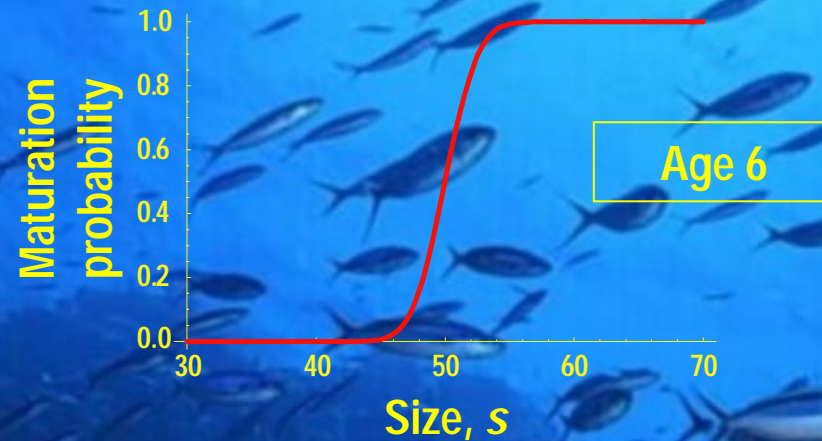
The concept of probabilistic reaction norm



The concept of probabilistic reaction norm

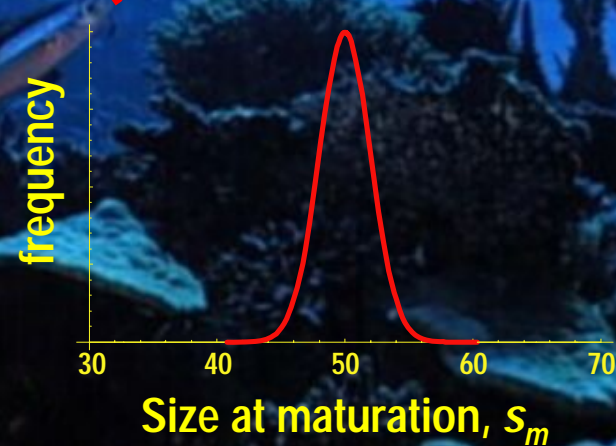
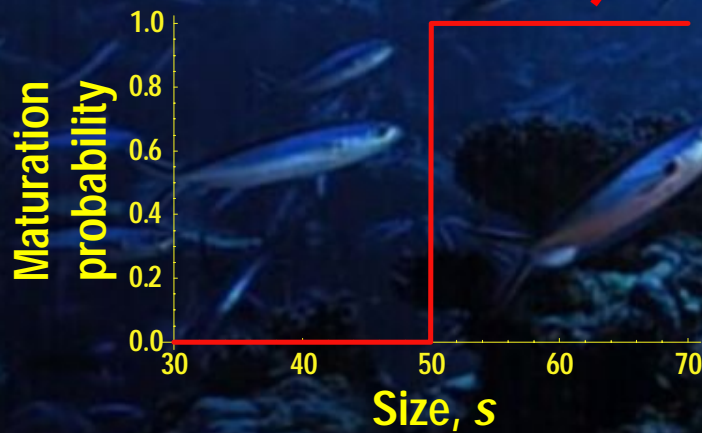


Turning probabilistic maturation reaction norms into classical quantitative traits



Individual level

Population level

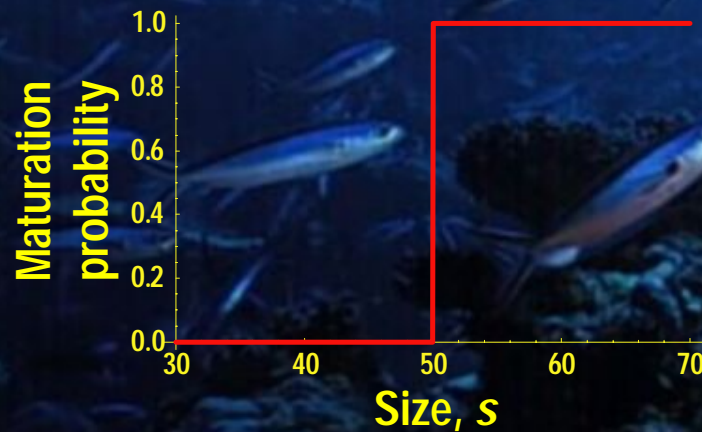


Turning probabilistic maturation reaction norms into classical quantitative traits

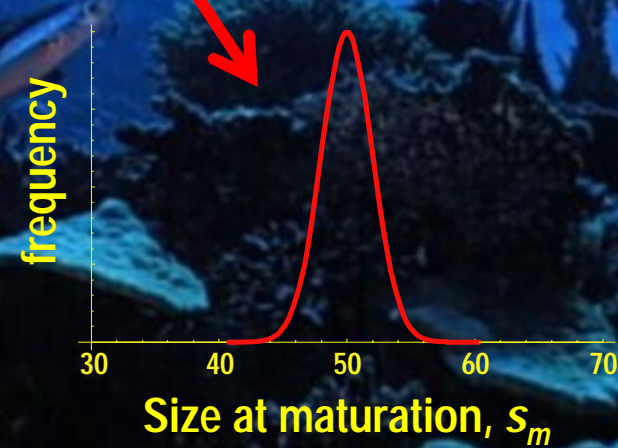


The distribution of age and size at maturation can be inferred from the probabilistic reaction norm

Individual level

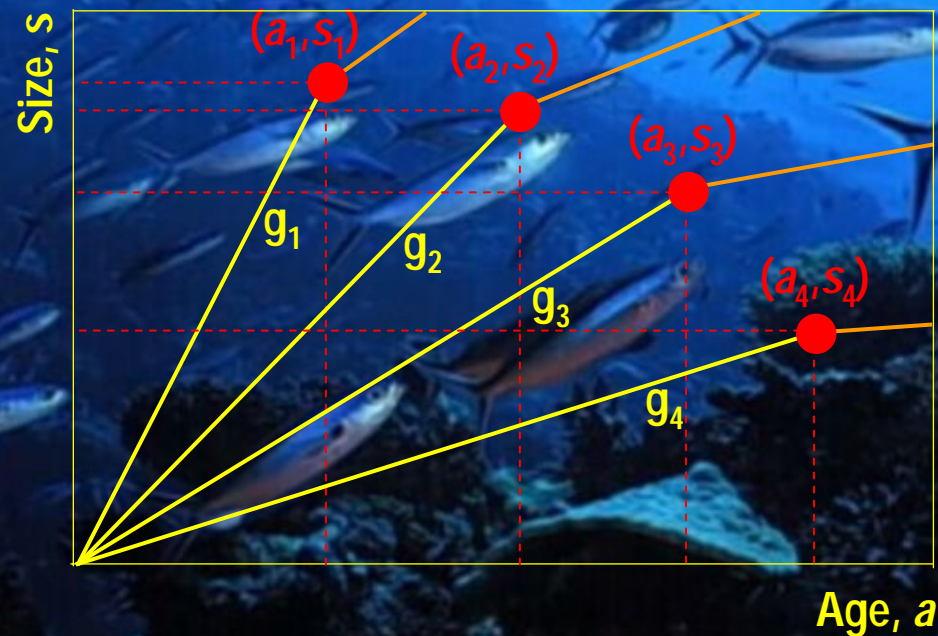


Population level



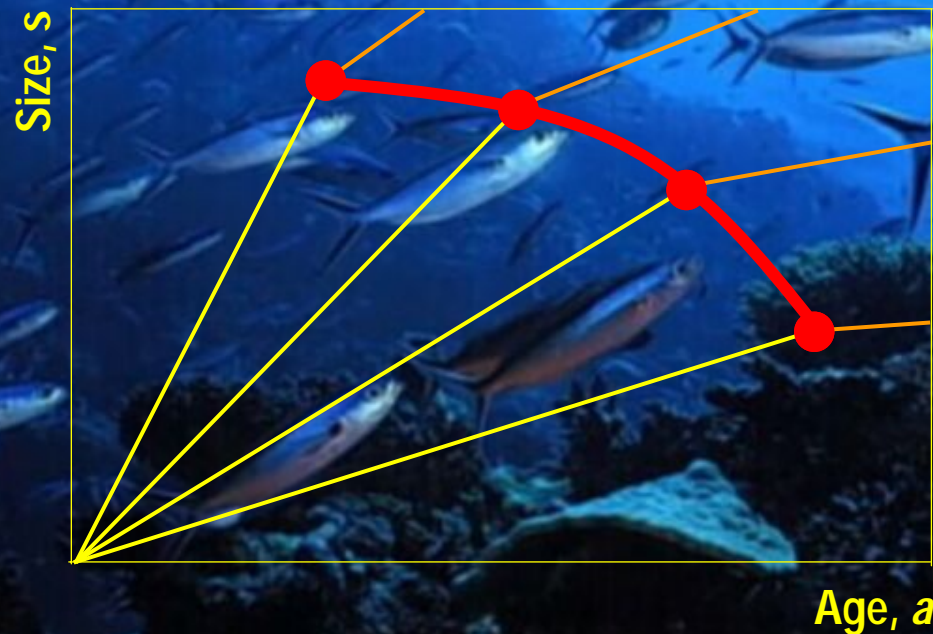
Two quantitative approaches

- A **bivariate approach** with age and size at maturation as two correlated quantitative traits (a_m, s_m)
- An **infinite-dimensional approach** with the reaction norm in itself being a quantitative trait $s_m(a)$



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Bivariate phenotype : the basic model

Individual phenotype

genotype

growth

environment beyond growth

$$\begin{pmatrix} a_m \\ s_m \end{pmatrix}_{igkl} = G_i + E_g + E_k +$$
$$I_{G_i \times E_g} + I_{G_i \times E_k} + I_{E_g \times E_k} + I_{G_i \times E_g \times E_k} +$$

e_{igkl}

interactions

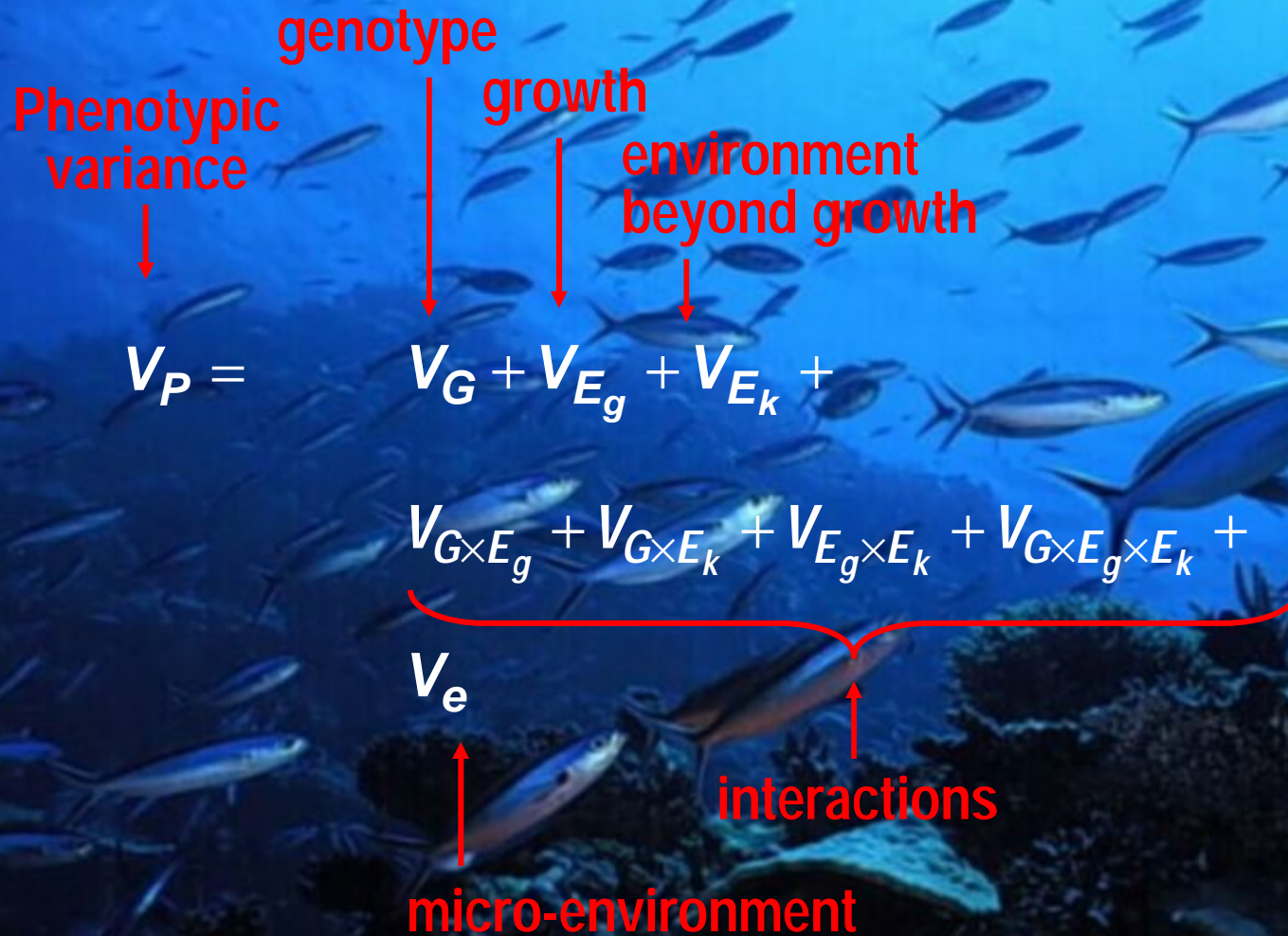
micro-environment

The diagram illustrates the bivariate phenotype model. It shows the relationship between genotype, growth, environment, and interactions. The model is represented by the equation:
$$\begin{pmatrix} a_m \\ s_m \end{pmatrix}_{igkl} = G_i + E_g + E_k + I_{G_i \times E_g} + I_{G_i \times E_k} + I_{E_g \times E_k} + I_{G_i \times E_g \times E_k} + e_{igkl}$$
 The terms are defined as follows:

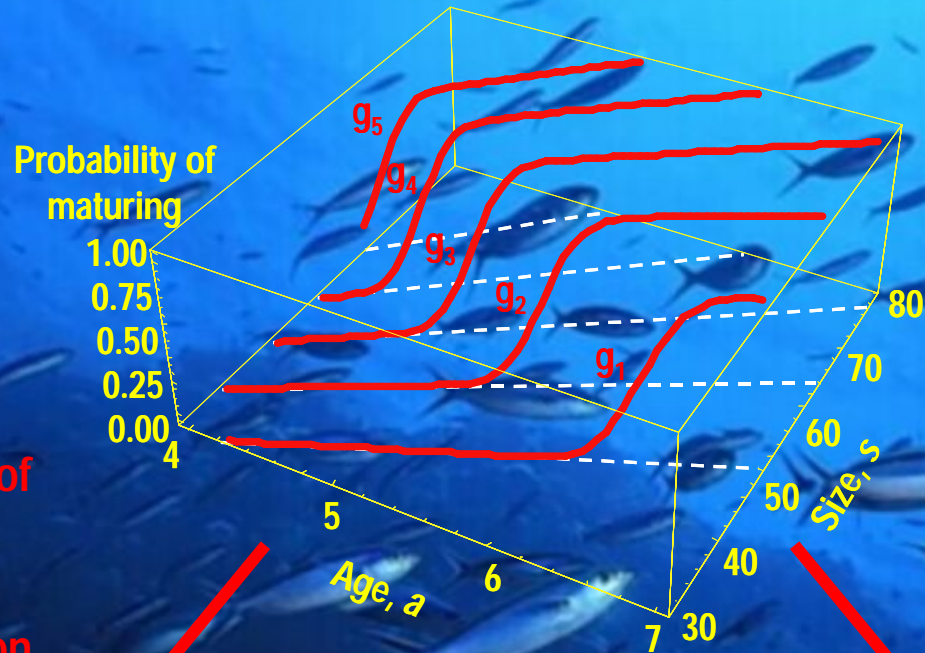
- G_i : genotype
- E_g : growth
- E_k : environment beyond growth
- $I_{G_i \times E_g}$, $I_{G_i \times E_k}$, $I_{E_g \times E_k}$, and $I_{G_i \times E_g \times E_k}$: interactions
- e_{igkl} : micro-environment

 The individual phenotype is represented by the vector $\begin{pmatrix} a_m \\ s_m \end{pmatrix}_{igkl}$.

Bivariate phenotype : (co)variance components



What can we extract using the bivariate approach?



Distribution of age at maturation conditional on growth

Distribution of size at maturation conditional on growth



$$\bar{a}_m(g_1) \quad \bar{a}_m(g_2) \quad \bar{a}_m(g_3)$$

$$\bar{s}_m(g_1) \quad \bar{s}_m(g_2) \quad \bar{s}_m(g_3)$$

What can we extract using the bivariate approach?

- The **growth-related environmental (co)variance** can be estimated as the (co)variance of the mean age and size at maturation conditional to growth

$$\rightarrow V_{E_g}$$

- The distribution of age and size at maturation can be averaged over growth rates, which gives access to **an upward biased estimate of genetic (co)variance**,

$$\rightarrow V_G + V_{E_k} + V_{G \times E_k}$$

- An upward biased estimate of **the variance related to the genotype-growth interaction** can be obtained by subtracting the two previous estimates from total phenotypic variance,

$$\rightarrow V_{G \times E_g} + V_{E_g \times E_k} + V_{G \times E_g \times E_k}$$

Infinite-dimensional phenotype: the basic model

Individual phenotype

genotype

environment beyond growth

micro-environment

$$s_m(\mathbf{a})_{ikl} = \text{hand}_i(\mathbf{a}) + \text{hand}_k(\mathbf{a}) + m_{ikl}(\mathbf{a})$$

The diagram illustrates the basic model for an infinite-dimensional phenotype. It features a school of fish swimming over a coral reef. Four red arrows point downwards from text labels to a mathematical equation. The labels are 'Individual phenotype', 'genotype', 'environment beyond growth', and 'micro-environment'. The equation is $s_m(\mathbf{a})_{ikl} = \text{hand}_i(\mathbf{a}) + \text{hand}_k(\mathbf{a}) + m_{ikl}(\mathbf{a})$. The terms $\text{hand}_i(\mathbf{a})$ and $\text{hand}_k(\mathbf{a})$ are accompanied by hand icons pointing to the i and k subscripts respectively.

Infinite-dimensional phenotype: variance components

Phenotypic
variance

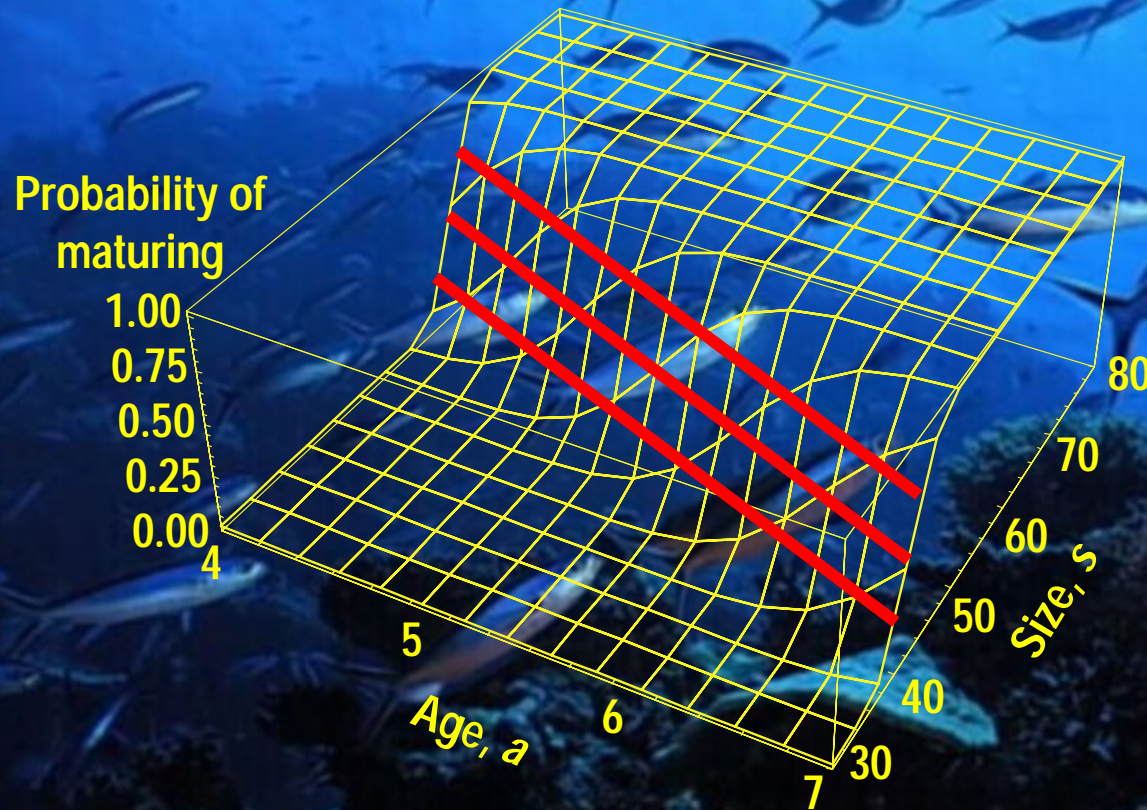
genotype

environment
beyond growth

micro-environment

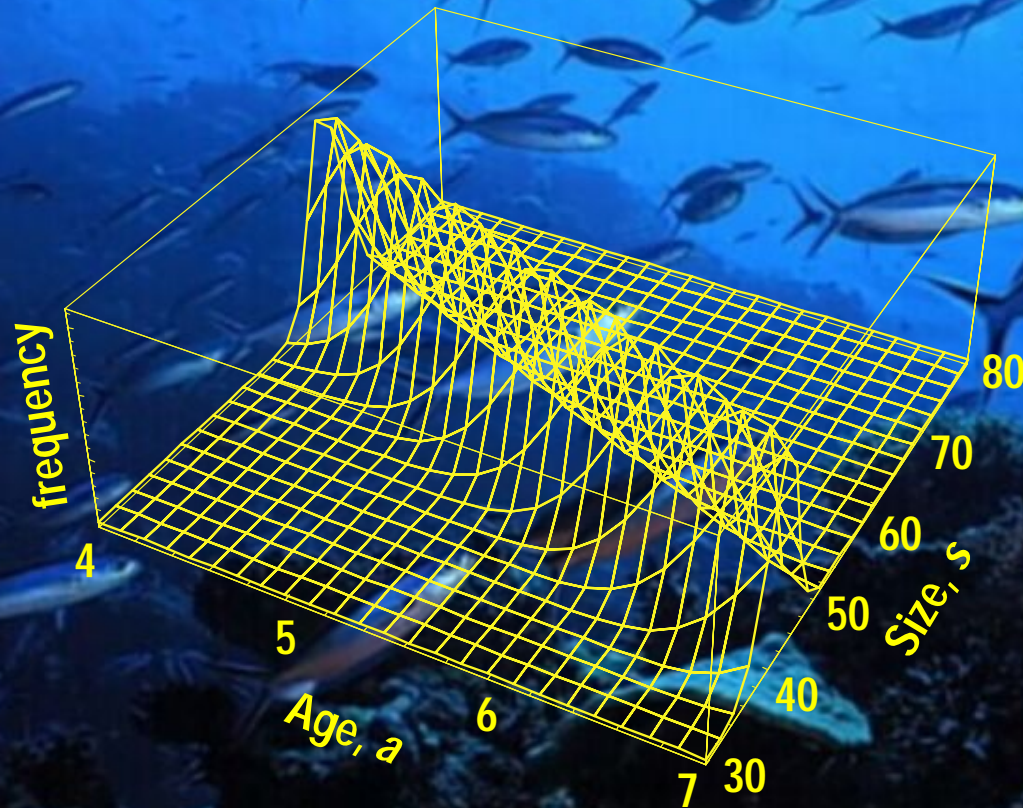
$$\dagger \mu(a) = \dagger g(a) + \dagger k(a) + \dagger m(a)$$

What can we extract using the infinite-dimensional approach?



What can we extract using the infinite-dimensional approach?

The whole distribution of age and size at maturation can be inferred from the probabilistic maturation reaction norm



What can we extract using the infinite-dimensional approach?

- Since the effect of growth is already removed in the infinite-dimensional approach, the phenotypic variance of the infinite-dimensional approach is already an upward biased estimate of genetic variance

$$\rightarrow \sigma^2_{P(a)} = \sigma^2_{\mu(a)} + \sigma^2_{\sigma_k(a)} + \sigma^2_{m(a)}$$

What are future needs of research?

- The **coefficient of relatedness** between individuals is needed to obtain unbiased estimates of

- $V_G, V_{G \times E_g}$

- $\pm (a)$

- **Classical quantitative genetics experiments** with controlled mating design

- ✓ Advantage: high statistical power

- ✓ Disadvantages:

- long experiments (maturity of most commercially exploited fish occurs late in life),

- experimental environmental variation might be not representative of natural environmental variation

What are future needs of research?

- **Using micro-satellites** to determine the coefficient of relatedness between individuals in the wild
 - ✓ Advantage:
 - representative of natural environmental variation
 - information available immediately
 - ✓ Disadvantages:
 - is it possible?,
 - low statistical power