

Evolutionary consequences of the physiological costs of reproduction: An application of Multitrait Population Projection Matrix models

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Introduction : Life History Theory and Evolutionary Demography

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- For a population: **antagonistic pleiotropy** of genes ⇒ **genetic trade-offs**

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- Current reproduction trades off with future fitness (fertility, survival)
- The most prominent of all trade-offs¹.

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- Physiological and genetic costs are related to the main evolutionary theories of aging.
 - Antagonistic Pleiotropy Theory² \Leftrightarrow Genetic costs
 - Disposable Soma Theory³ \Leftrightarrow Physiological costs

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Overview

- ① Introduction
- ② Costs of reproduction: concepts and life history model
- ③ Multitrait Population Projection Models
- ④ Evolutionary and demographic consequences of physiological costs of reproduction
- ⑤ Discussion

The two sides of Williams' physiological costs of reproduction

In 1930, Fisher¹ asks : " ... what circumstances in the life-history and environment would render profitable the diversion of a greater or lesser share of the available resources towards reproduction"

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Williams' 1966 article²

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$$v_i = \underbrace{\quad}_{\text{reproductive value at age } i} +$$

with f_i , s_i , the fertility and survival rates at age i and λ the asymptotic growth rate.

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- **Physiological side** → a **Fluctuating Capital** which is **supplied** by resources acquired from the **environment**
- ⇒ FC is related to acquirable resources e.g. food, energy

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- **Evolutionary side** → a **Ratchet Capital** which is **invested** according to an **evolved** reproductive strategy.
 - ⇒ RC is related to non-acquirable resources e.g. time, DNA maintenance capital

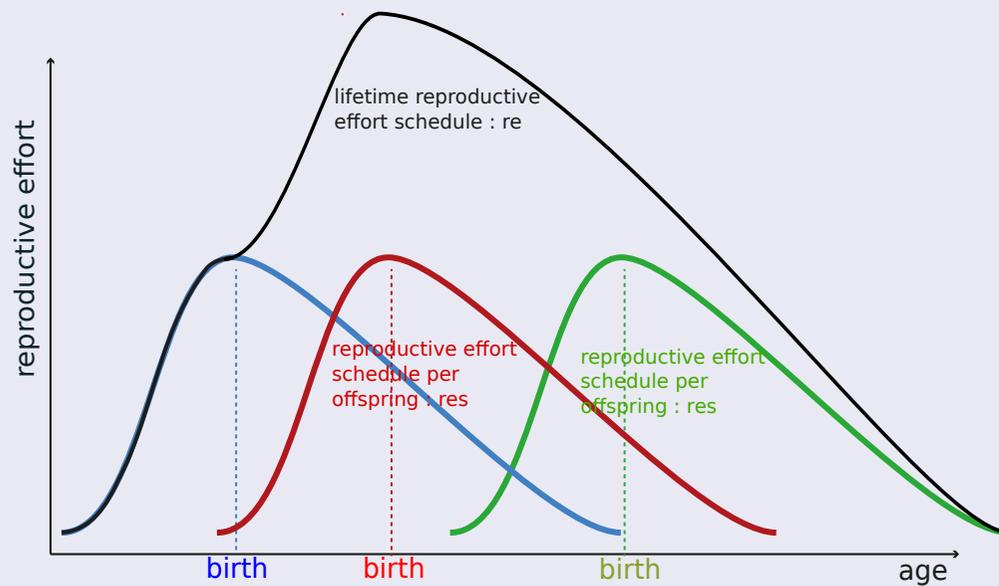
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Fluctuating and Ratchet Capitals

Lifetime reproductive effort schedule re

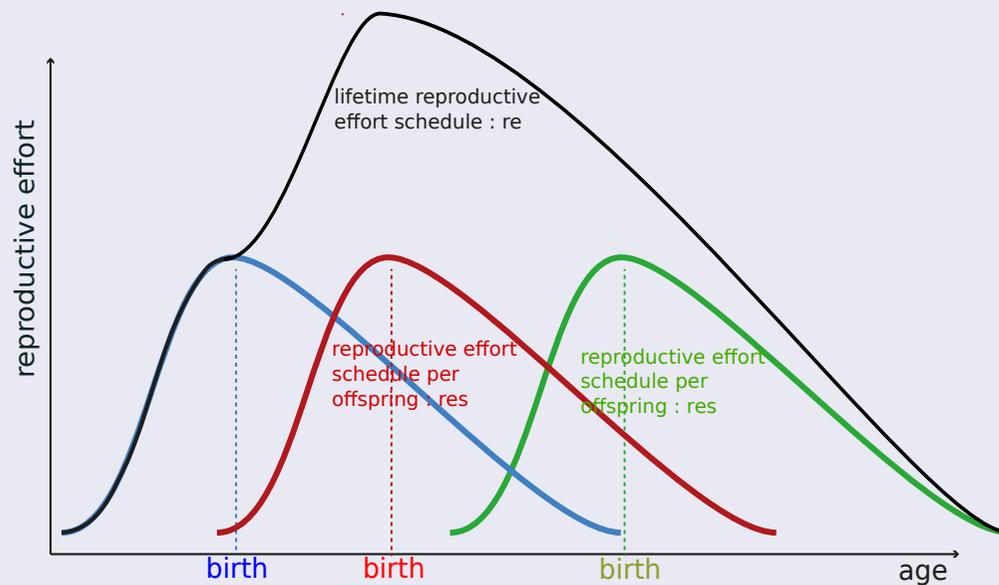


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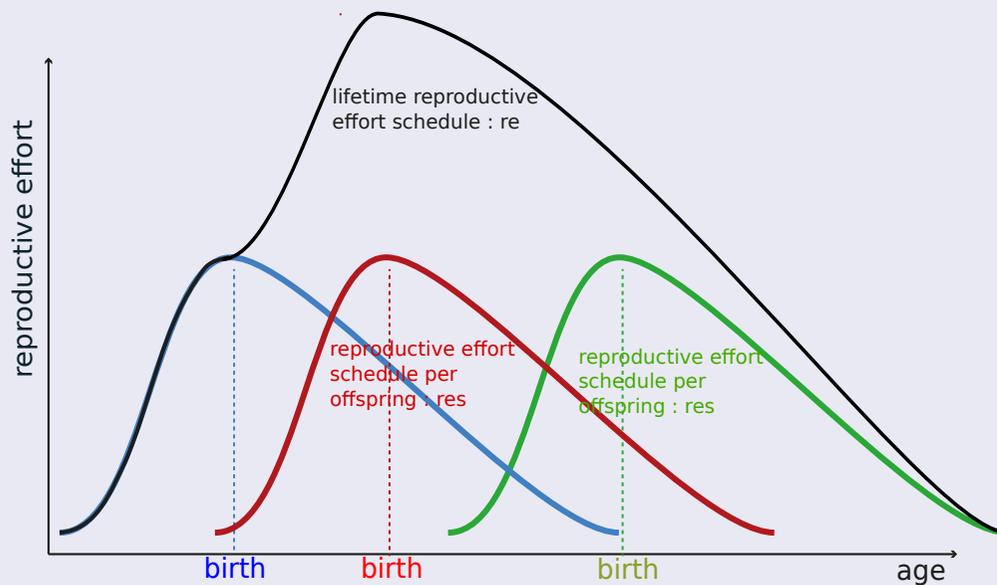
re is the convolution of

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- with fertility schedule f :

$$re(a) = (f * res)(a) = \int_{t=0}^{e(0)} f(t) \cdot res(t - a) \cdot dt$$

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Among the different moments of re :

$$sfc = \frac{\sum i \cdot re(i)}{\sum re(i)}$$

\Rightarrow sfc positions organism on **Slow-Fast continuum**.

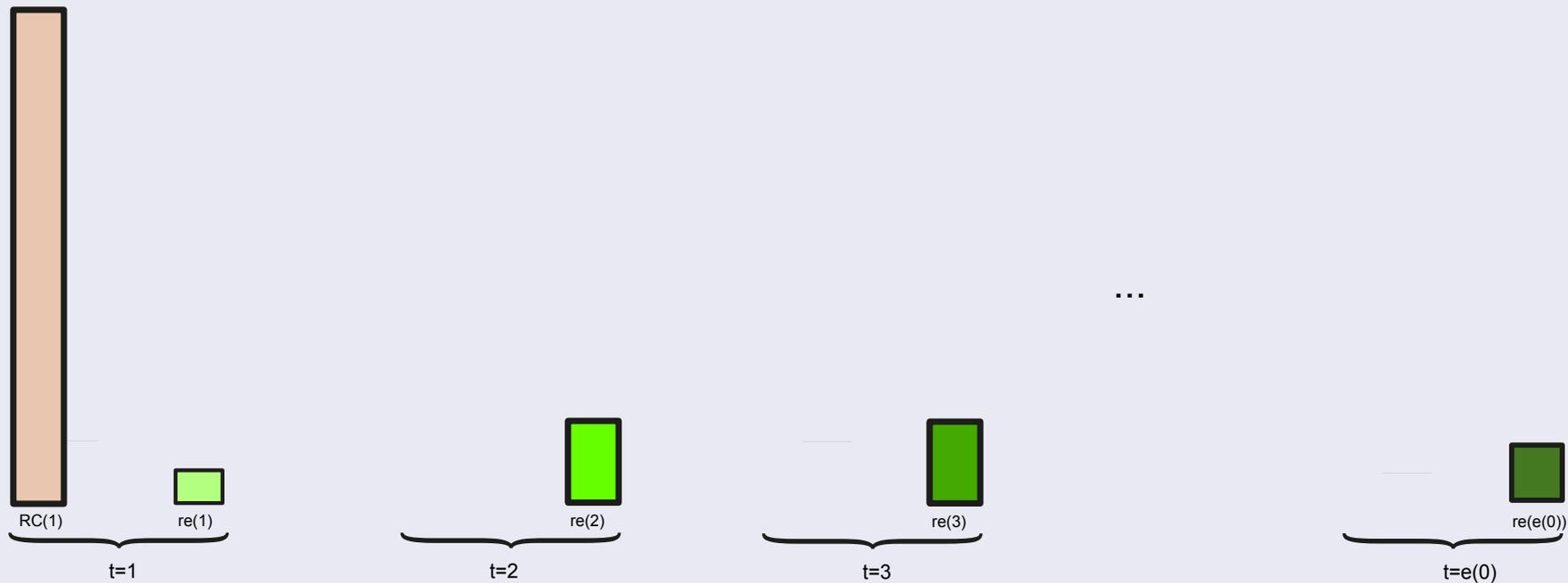
Fluctuating and Ratchet Capitals

Ratchet Capital RC

- Its initial value RC_1 is generated *backwards* from the species *evolved* lifetime reproductive effort schedule re

$$\left\{ \begin{array}{l} RC_1 = \sum_{a=1}^{e(0)} re(a) \end{array} \right.$$

Capital Dynamics



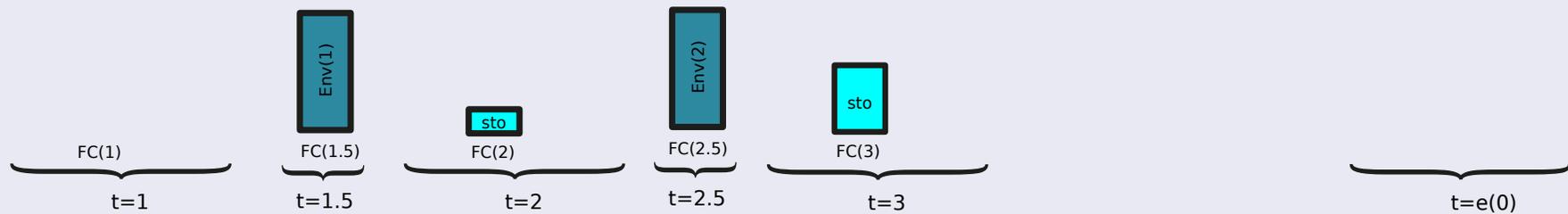
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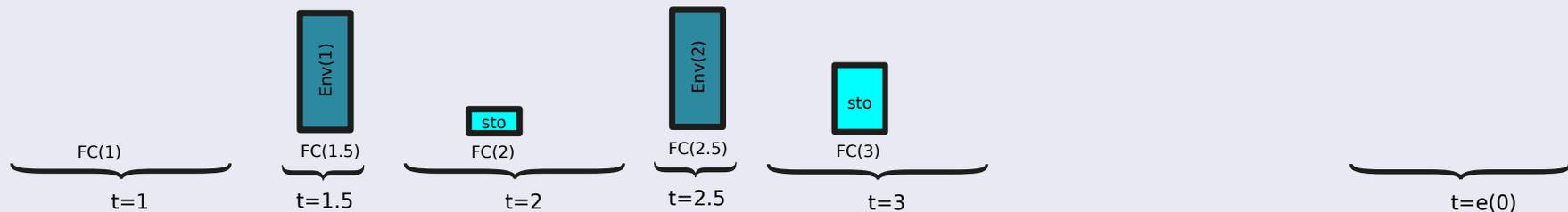
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- FC starts at zero
- Each season, FC resources are acquired from the environment, some can be stored
- stor* positions organism on Income-Capital Breeding spectrum

$$\left\{ \begin{array}{l} FC_{t+1} = stor.(FC_t + Env_t - RE_t) \end{array} \right.$$

Capital Dynamics



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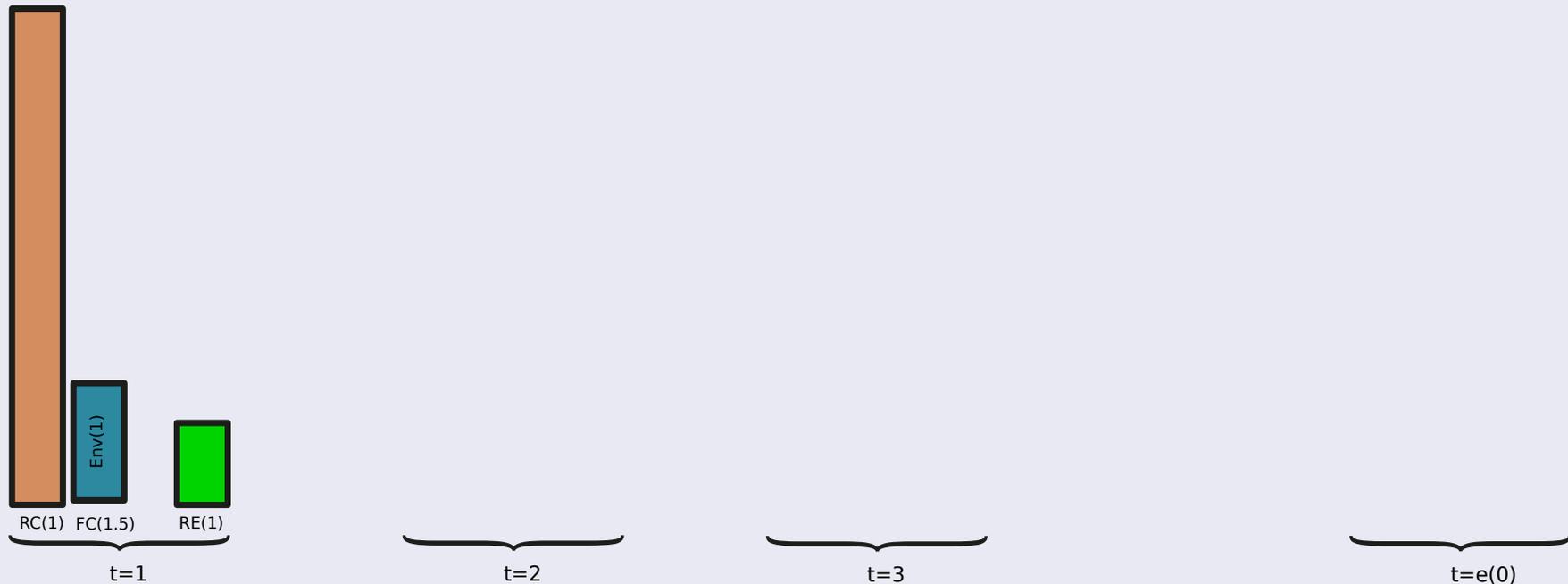
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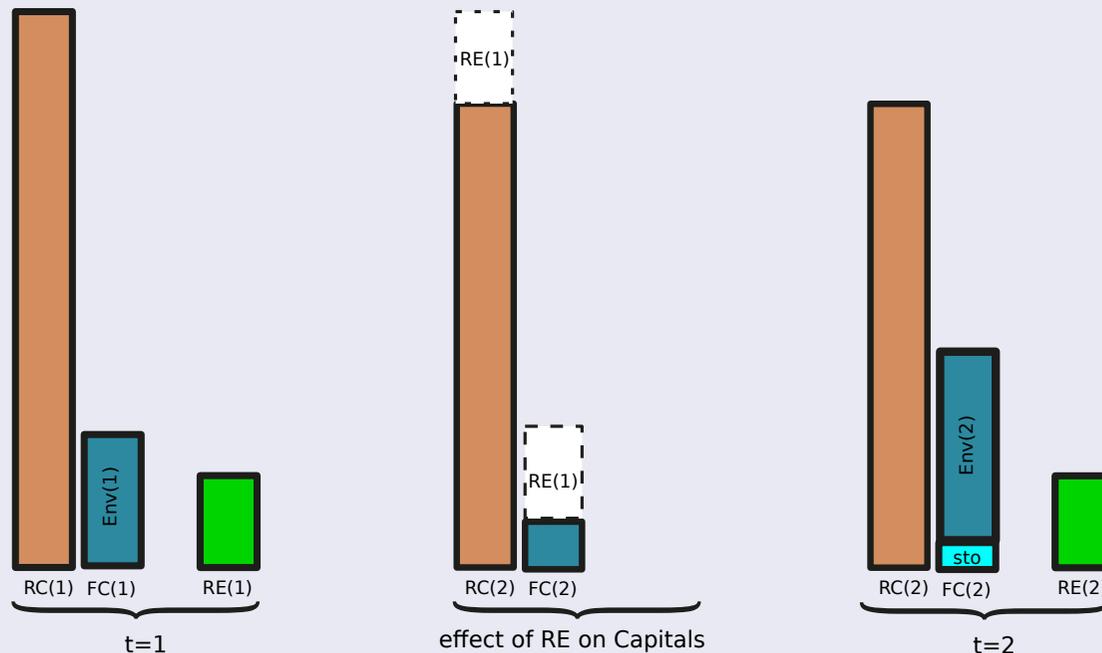
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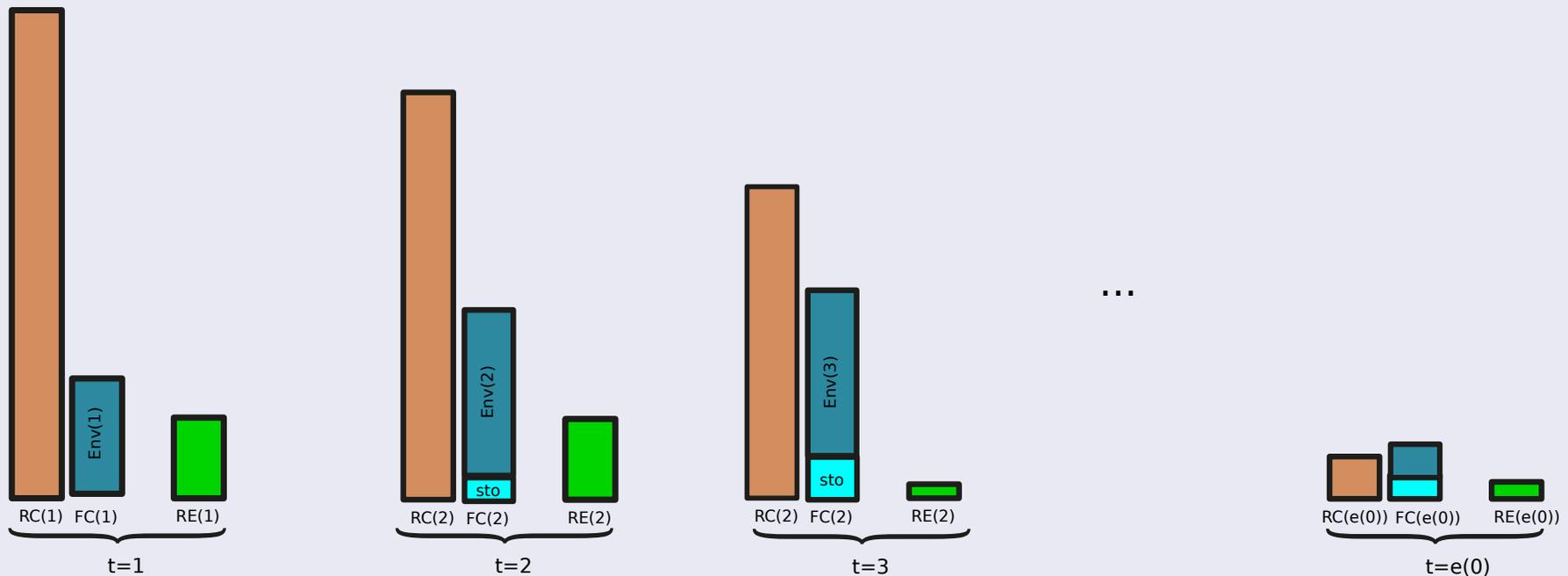
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Capital Dynamics



Allocation Process

Allocation depends on both capitals and life history strategies

$$\begin{cases} aRE(t) \approx \min(FC(t) - stor.\overline{RE}, RC(t) - \bar{r}e.K(2.sfc - t)) \\ RE(t) \sim \mathcal{B}(\lfloor \frac{aRE(t)}{\bar{r}e} \cdot \frac{1}{gr} \rfloor, p).bre \end{cases}$$

with $0 < K < 1$ an RC flexibility parameter, *bre* the basic RE and $\mathcal{B}(n, p)$ a *n*-nomial Bernoulli of parameter *p*.

Allocation in detail

Allocation Process

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$$\begin{cases} aRE(t) \approx \min(FC(t) - stor.\overline{RE}, RC(t) - \bar{r}e.K(2.sfc - t)) \\ RE(t) \sim \mathcal{B}(\lfloor \frac{aRE(t)}{\bar{r}e} \cdot \frac{1}{gr} \rfloor, p).bre \end{cases}$$

with $0 < K < 1$ an RC flexibility parameter, *bre* the basic RE and $\mathcal{B}(n, p)$ a *n*-nomial Bernoulli of parameter *p*.

Allocation in detail

- Allocation requires both capitals (reproductive efforts require both types of resources)

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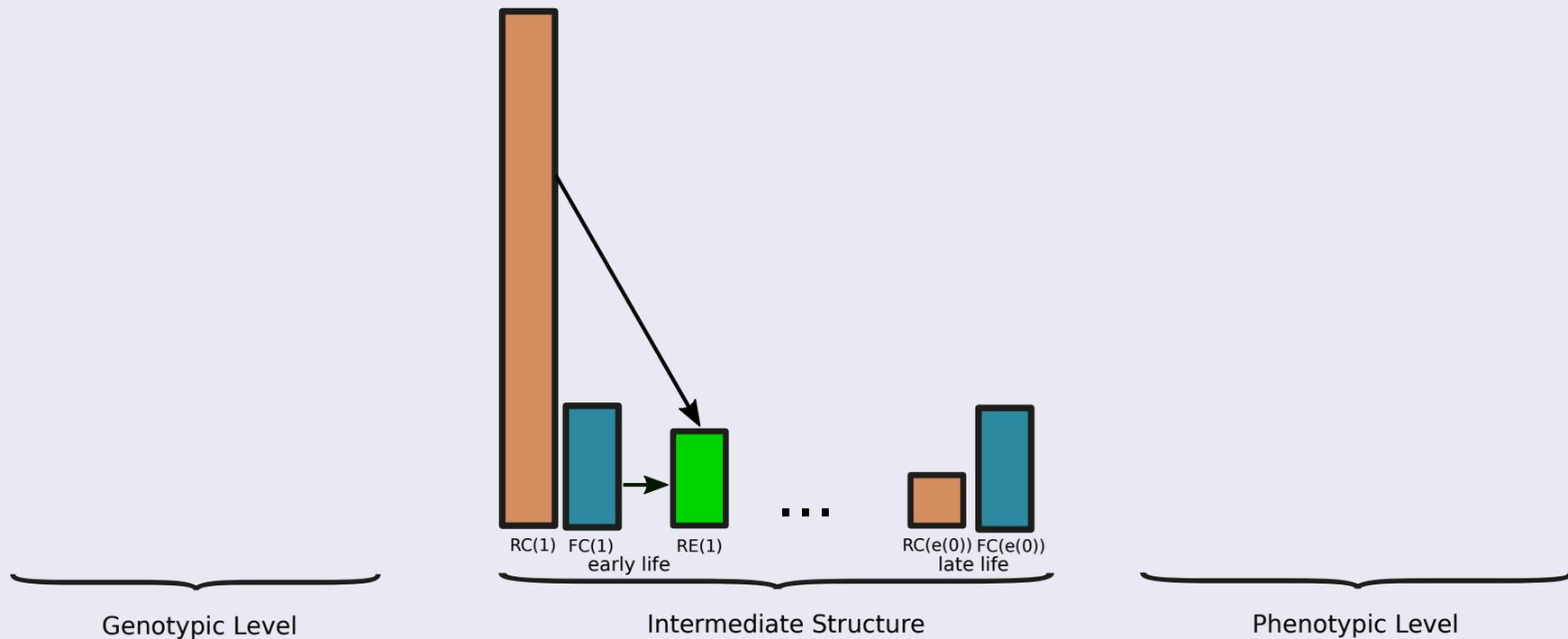
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- ⇒ gr positions an organism on the quantity-quality life history continuum.
- Allocation process is a function of the position of the organism on:
 - The Slow-Fast continuum
 - The Income-Capital Breeding continuum
 - The Quantity-Quality continuum

Genotypic and Phenotypic Levels

Stearns¹ Trade-off Triptych



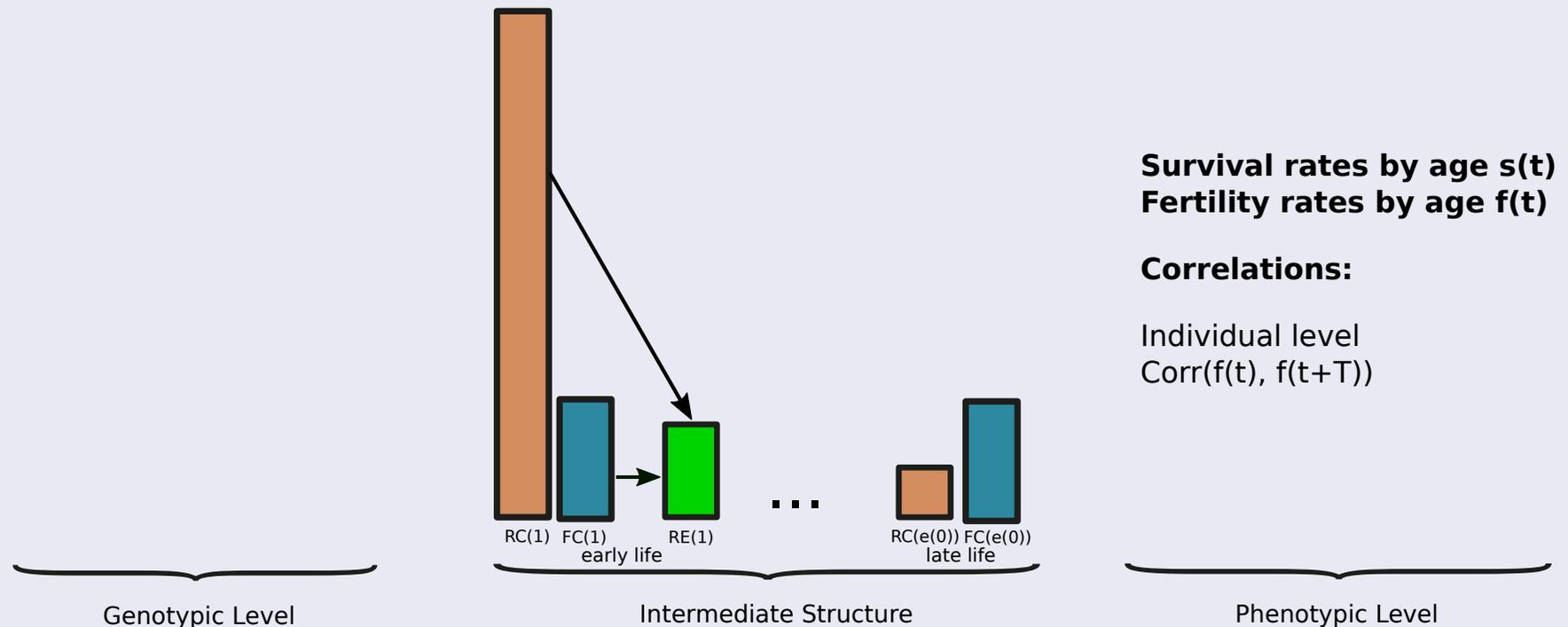
Stearns¹ trade-off architecture

- genotypic level : genetic basis of the trade-off.
- phenotypic level :
 - ⇒ where negative correlations may emerge
 - ⇒ where natural selection acts
- intermediate structure : physiological mechanism in-between.

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Genotypic and Phenotypic Levels

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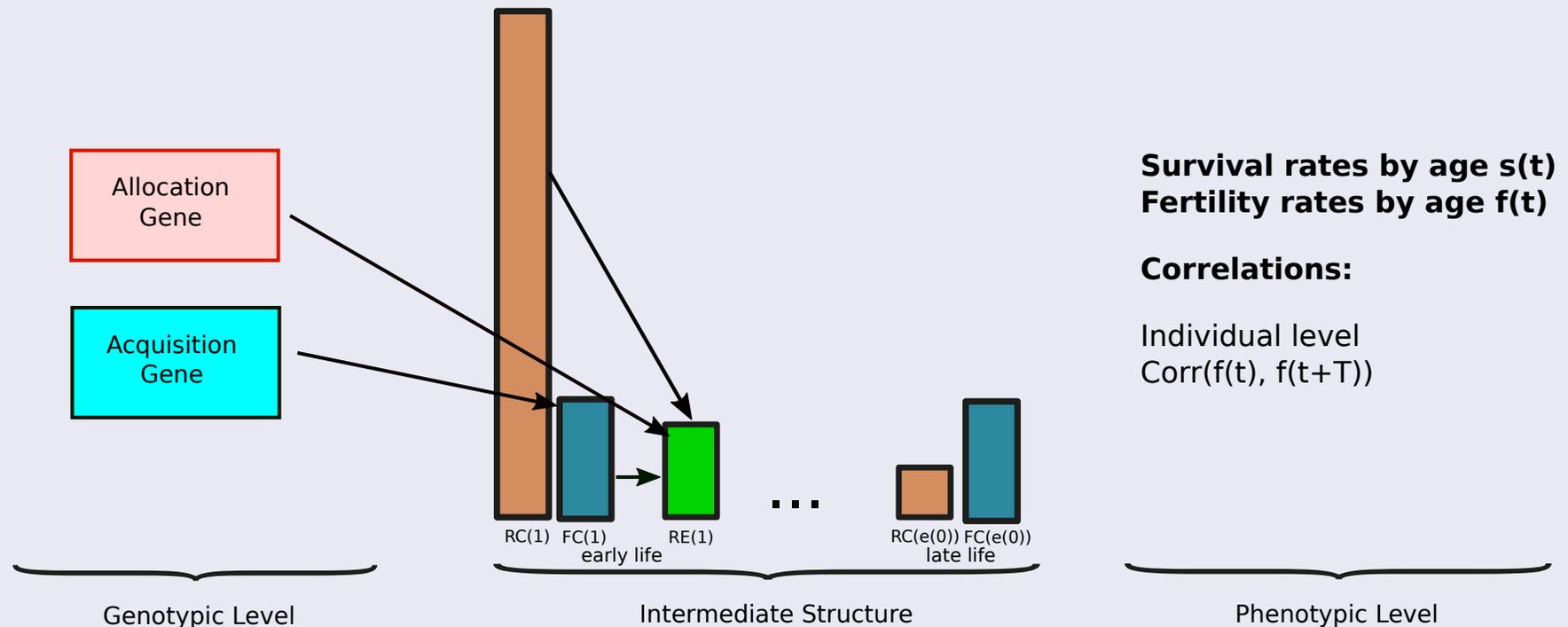
Stearns¹ trade-off architecture for **costs of reproduction**

- intermediate structure : location of the allocation process.
- phenotypic level:
 - ⇒ fitness components : fertility and survival rates impacted directly by allocation process
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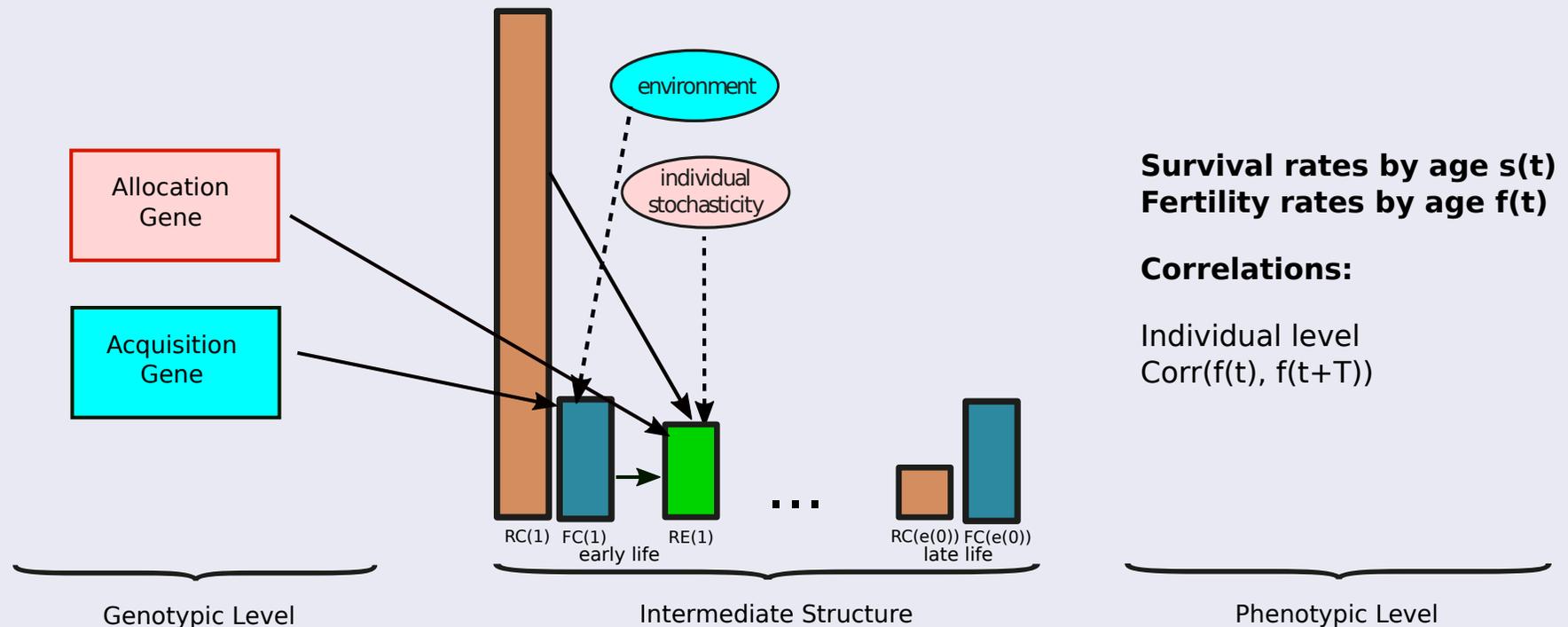
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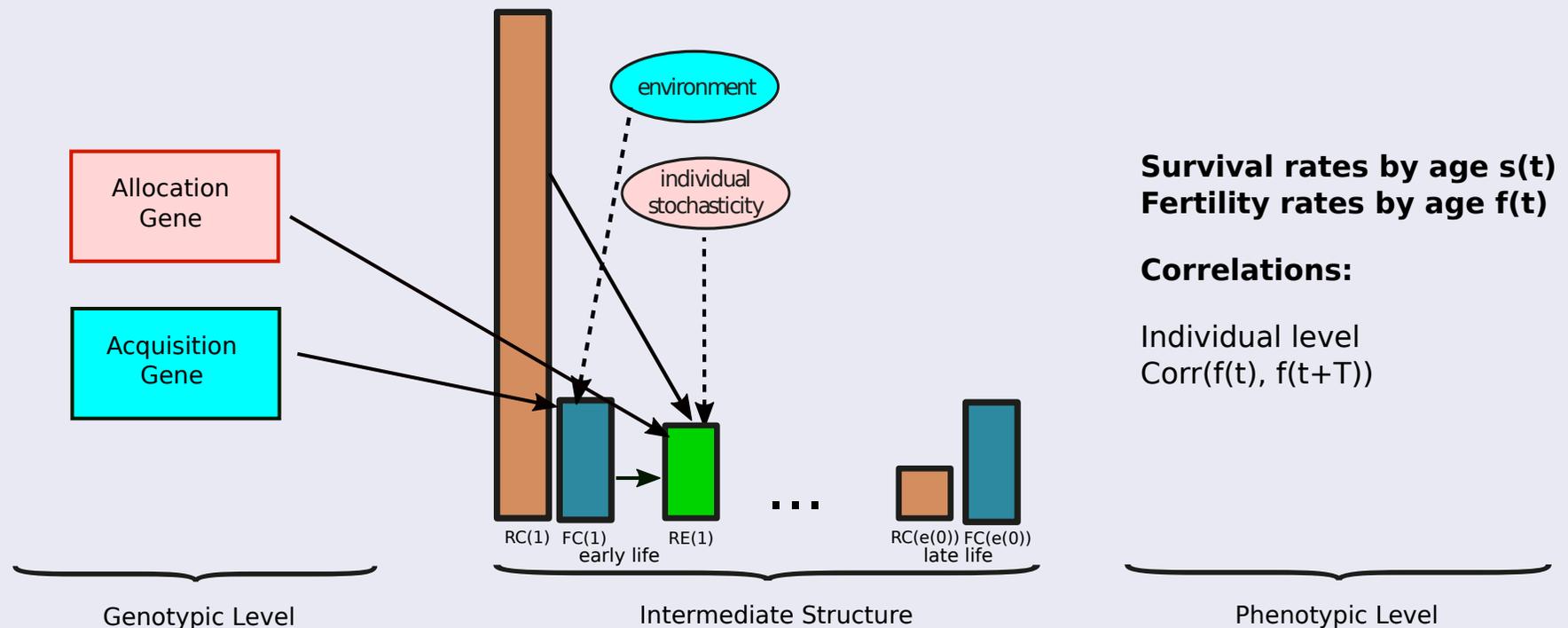
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- phenotypic trade-off = constraint + variance
 - ⇒ environmental and individual stochasticities also located at the intermediate level

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Genotypic and Phenotypic Levels

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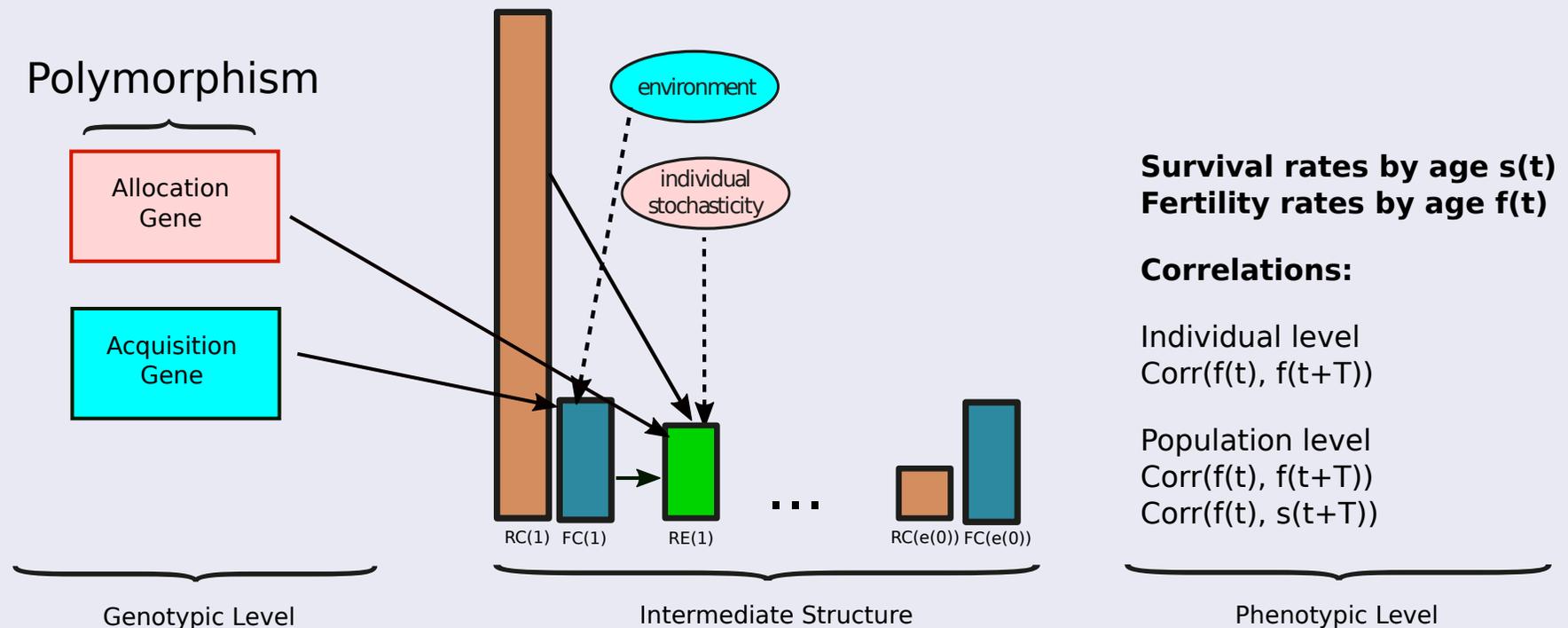
Predictions of Detectability of Physiological Costs of Reproduction

- Early-Mid life costs are function of position on Income-Capital Breeding spectrum.
- Long-term and Late-life costs are function of position on Slow-Fast Continuum.
- Low Environment increases detectability
- Individual Stochasticity fuels detectability
- Environmental Variance hinders detectability

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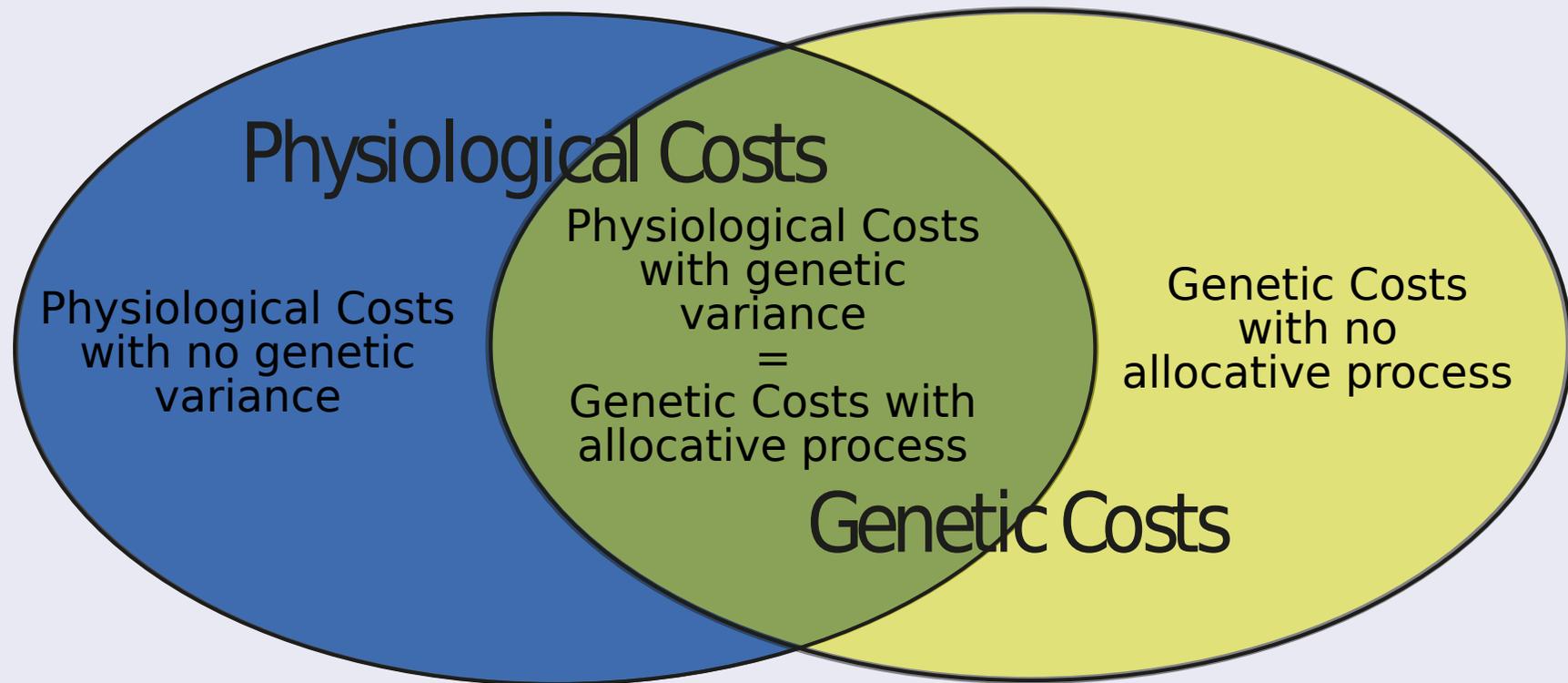
Variance at the genotypic level

- Allocation gene has antagonistic pleiotropic effects on early fertility rates and later vital rates
 - variance in allocation gene \Rightarrow genetic costs of reproduction
 - positions an organism on the slow-fast continuum
- However genetic costs \nRightarrow physiological costs

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Genetic and Physiological Costs of reproduction

Genetic and Physiological Costs



Genetic Costs as variance in 2 orthogonal genes

allocation and acquisition

We extend Genetic Costs

⇒ include **genetic variance** in both **allocation** and **acquisition** genes

We consider **two "orthogonal" genes**:

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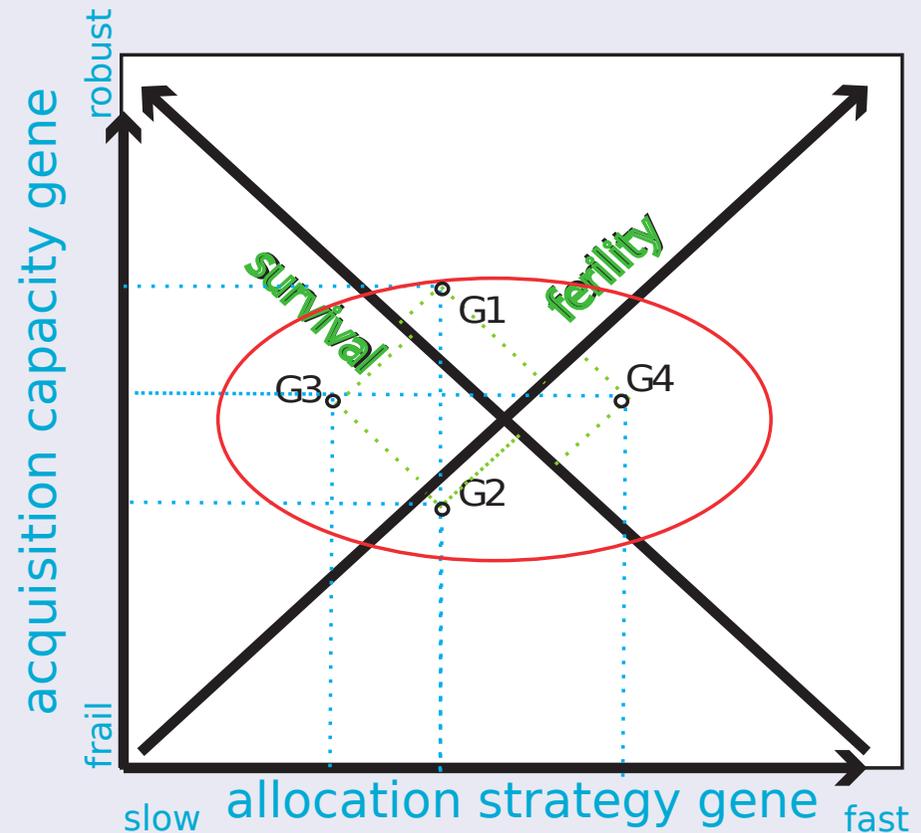
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⇒ buffers populations against environmental changes
- G1 and G2 cohabit because of environmental variance
⇒ In other/recent environments G2 is fitter than G1

Genotypic map



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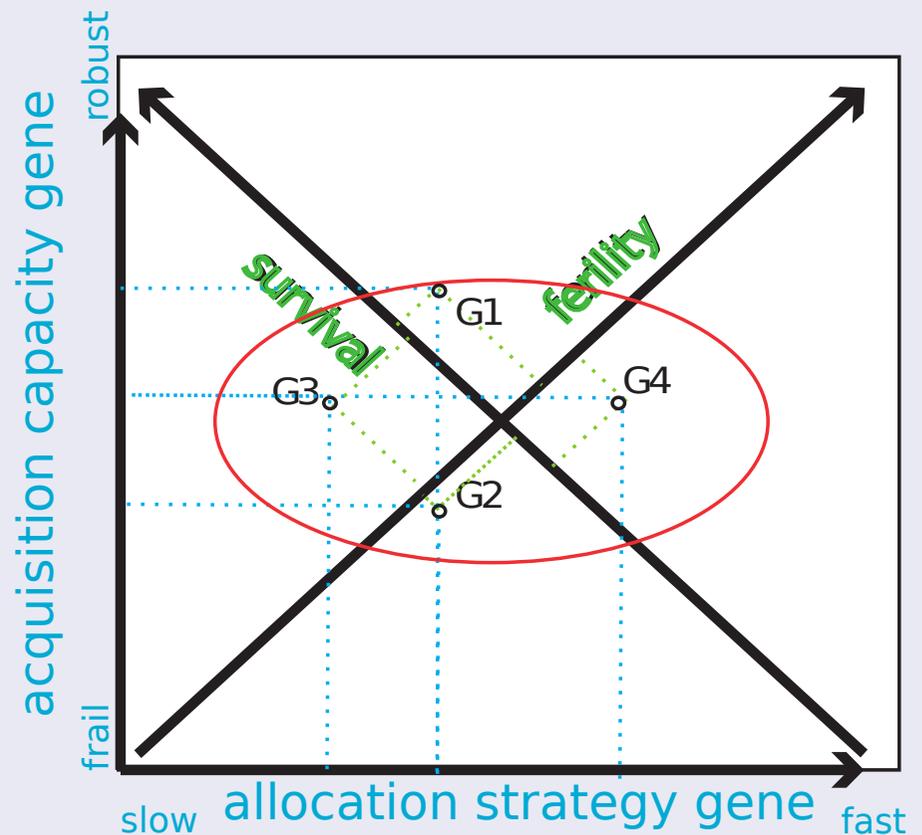
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Detectability of Genetic Costs depends on ratio¹

- allocation gene variance vs
- acquisition gene variance

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Questions

Summary and Questions

- **Physiological costs** are **evolutionary mechanisms**, but this does not make them genetic costs.
- **Physiological and genetic costs** both **buffer the environment** and **generate negative correlations** between early fertility and late fitness
- But they are **different** and **operate on different scales**
 - ⇒ Physiological costs work at the individual level, within life history trajectories
 - ⇒ Genetic costs work at the population level, and on an evolutionary timescale

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- To answer such questions requires to be able to **implement physiological trade-offs in an evolutionary demography model**.
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 - ⇒ Individual dynamics such as physiological costs are classically modeled by Agent-Based Models.
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- **How to implement a multivariate constraint such as the physiological costs of reproduction into a matrix model ?**

Overview

① Introduction

② Costs of reproduction: concepts and life history model

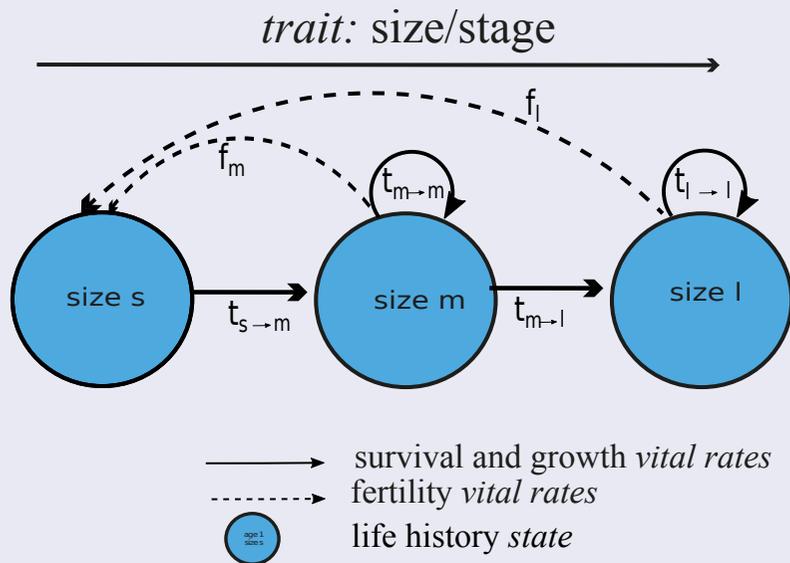
③ **Multitrait Population Projection Models**

④ Evolutionary and demographic consequences of physiological costs of reproduction

⑤ Discussion

One-trait structured life-cycle in matrix form

From a life history structured by size/stage ...



... to the related Lefkovich/Usher matrix

Matrix form of life cycle, projection, eigen-analysis and sensibility

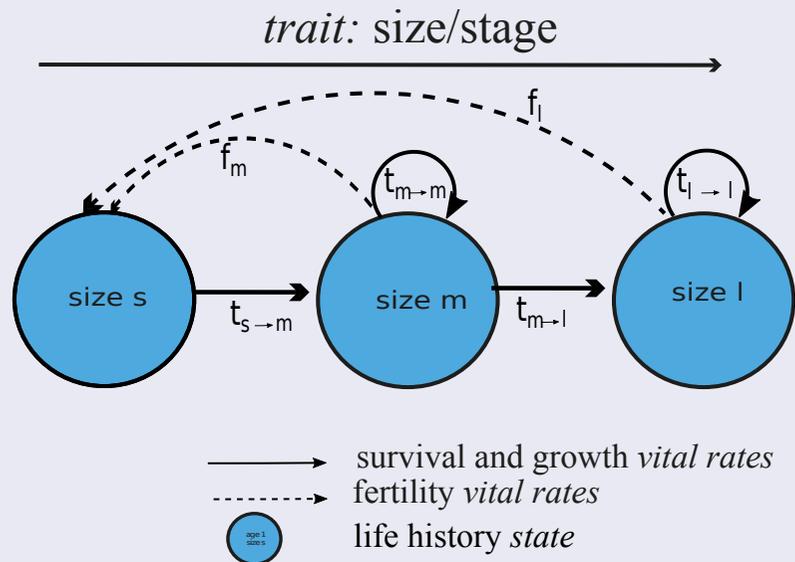
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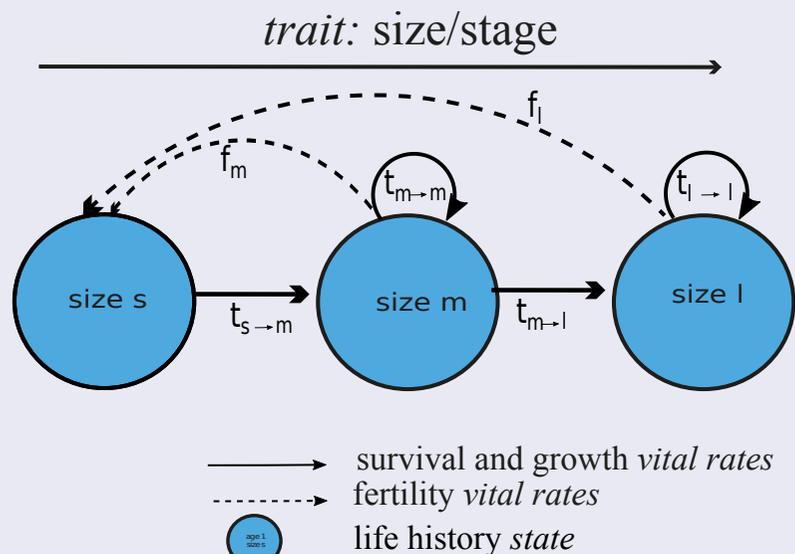
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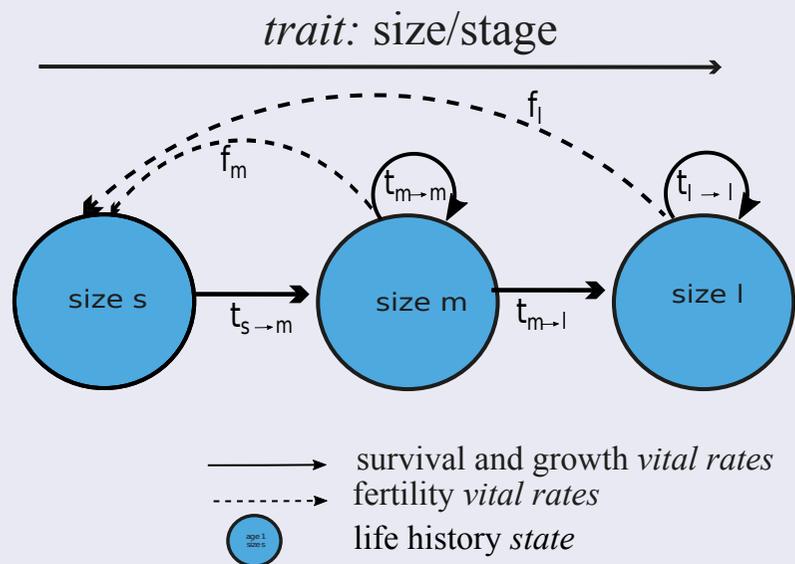
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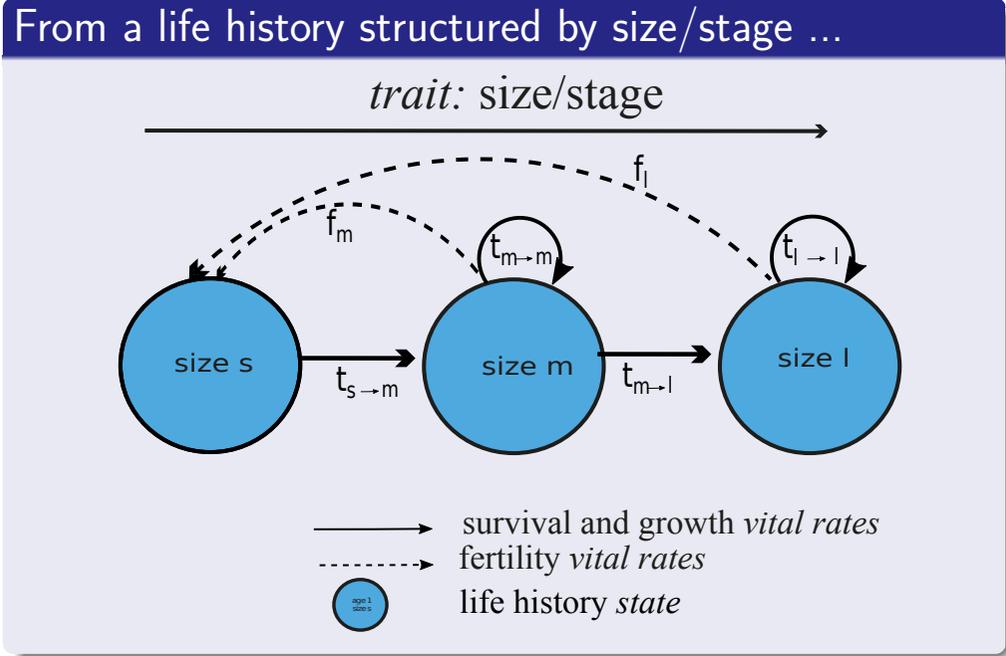
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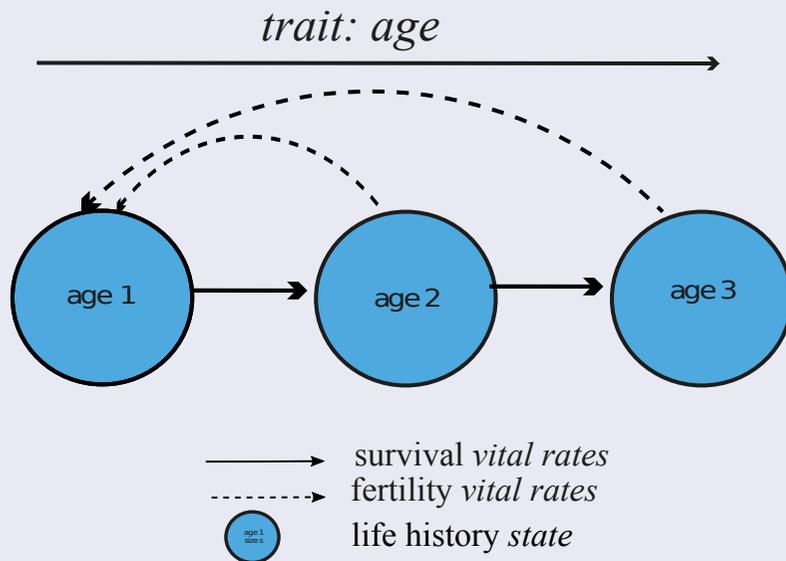
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 - But for any vector of features, e.g. $\mathbf{y} = \begin{bmatrix} f_1 \\ f_3 \end{bmatrix}$, we have² $\frac{d\mathbf{y}}{dt} = \mathbf{G} \cdot \nabla \lambda$ where $\nabla \lambda = \begin{bmatrix} \frac{\partial \lambda}{\partial f_1} \\ \frac{\partial \lambda}{\partial f_3} \end{bmatrix}$.
- \Rightarrow If strategy is optimal (ESS) i.e. $\frac{d\mathbf{y}}{dt} = 0 \Rightarrow$ we have genetic constraints \mathbf{G} from sensitivities $\nabla \lambda = \frac{\partial \lambda}{\partial \mathbf{M}}$.

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Special case of age-structured life-cycle in matrix form

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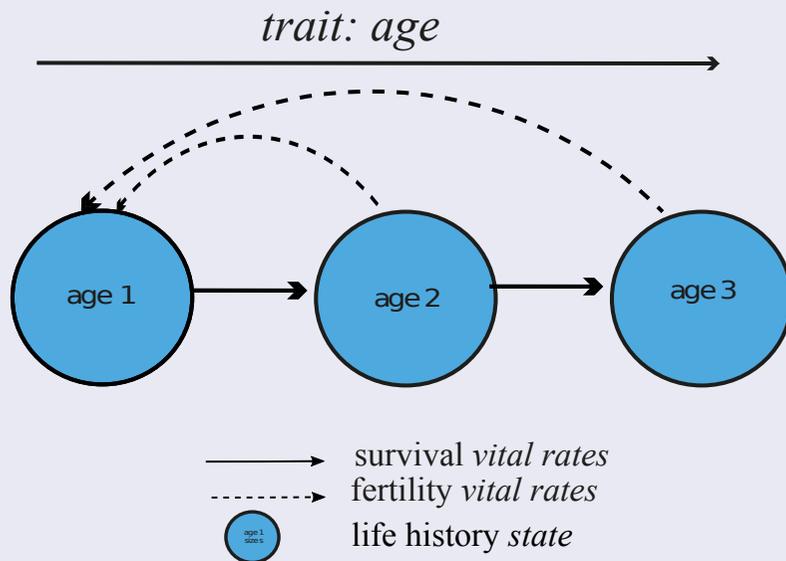
Matrix form of life cycle, projection, eigen-analysis and sensibility: familiar results from Leslie matrices

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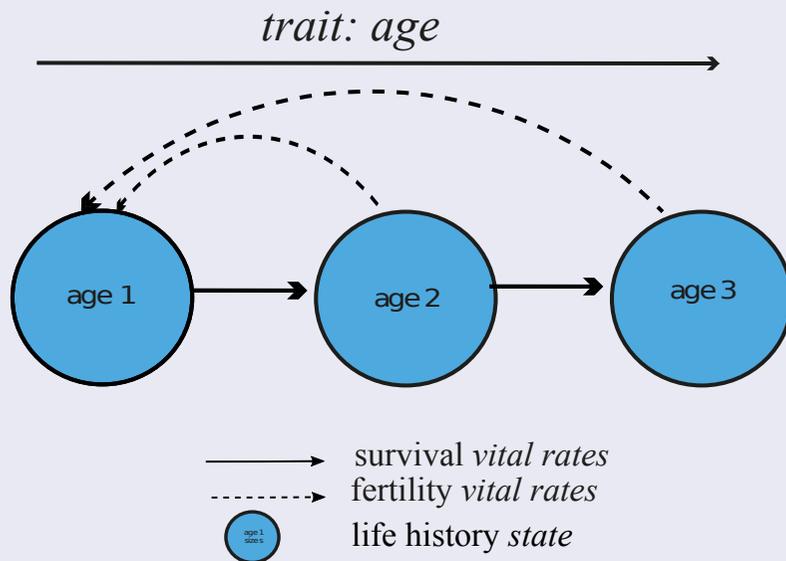
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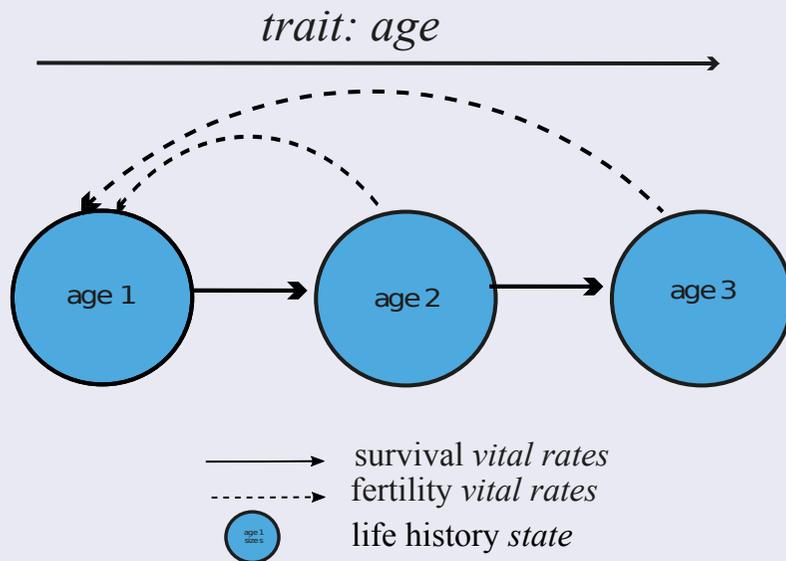
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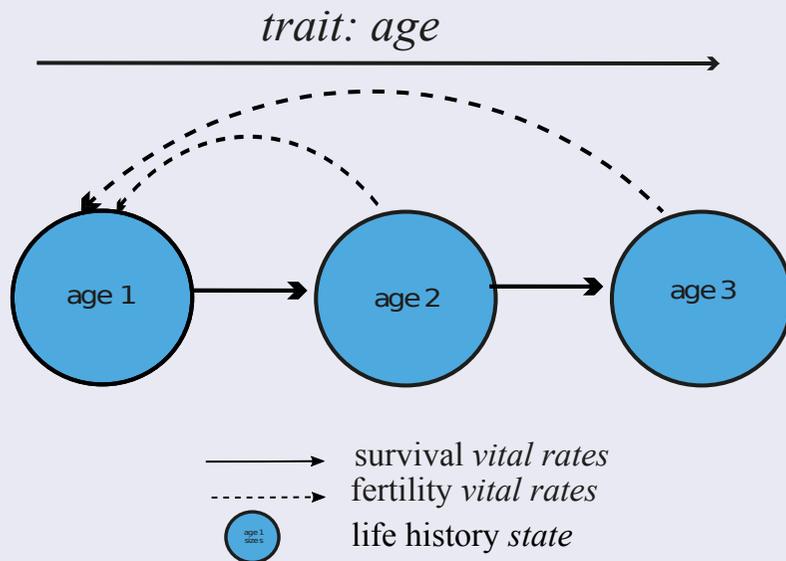
$$\mathbf{w} = \frac{1}{1 + s_1 \cdot \lambda^{-1} + s_1 \cdot s_2 \cdot \lambda^{-2}} \left[1 \quad \frac{s_1}{\lambda} \quad \frac{s_1 \cdot s_2}{\lambda^2} \right]$$

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Special case of age-structured life-cycle in matrix form

From a life history structured by age ...



... to the related Leslie matrix

$$\mathbf{M} = \begin{bmatrix} f_1 & f_2 & f_3 \\ s_1 & 0 & 0 \\ 0 & s_2 & 0 \end{bmatrix}$$

Matrix form of life cycle, projection, eigen-analysis and sensibility: familiar results from Leslie matrices

The matrix form yields the same result than the classical age-structure (discrete and continuous times) analyses¹:

- The age-structured characteristic equation **is** the Euler-Lotka equation :
 $\det(\mathbf{M} - x \cdot \mathbf{I}) = 0 \Leftrightarrow f_1 \cdot \lambda^{-1} + f_2 \cdot s_1 \cdot \lambda^{-2} + f_3 \cdot s_1 \cdot s_2 \cdot \lambda^{-3} = 0$
- The associated left-eigenvector (scaled so its first element is 1) **is** Fisher's reproductive value²:
 $\mathbf{v} = \left[1 \quad \frac{f_2}{\lambda} + \frac{f_3 \cdot s_2}{\lambda^2} \quad \frac{f_3}{\lambda} \right]$
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- Denoting $d_i = f_i \cdot \lambda^{-i} \cdot \prod_{j=1}^{i-1} s_j$ the distribution of parental age, and $c_i = v_i \cdot w_i$ the age-class reproductive value, selection gradients **correspond to** Hamilton's elasticity formulae⁴ : $\frac{\partial \log \lambda}{\partial \log f_i} = v_1 \cdot w_1 \cdot d_i$ and $\frac{\partial \log \lambda}{\partial \log s_i} = c_{i+1}$

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Basic traits correspond to the **best determinants of life-history**

- age (inherent to any projection model)
- other basic traits can be added: e.g. stage, size, sex, location ..

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- **Fixed-heterogeneity traits** correspond to fixed-at-birth heterogeneity/genotypes.
 - ⇒ Fixed-heterogeneity traits can implement **genetic trade-offs**
- Structured Population Genetics Model:
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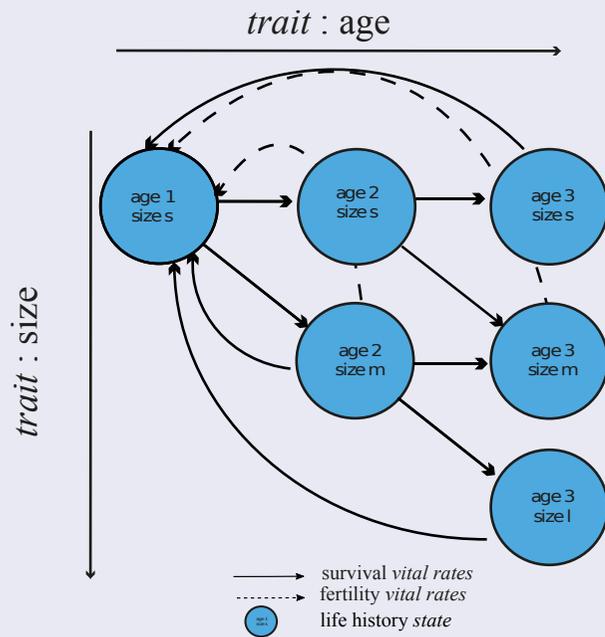
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Dynamic Heterogeneity for physiological costs

- **Dynamic-heterogeneity traits** track variations in life trajectories between individuals with the same genotype.
 - ⇒ Dynamic-heterogeneity traits can implement **physiological trade-offs**

Multitrait structured life-cycle in matrix form

A multitrait life history in matrix form, how ?



multidimensional population vectors have to be vectorized

$$\mathbb{N} = \begin{bmatrix} n_{1,1} & n_{2,1} & n_{3,1} \\ n_{1,2} & n_{2,2} & n_{3,2} \\ n_{1,3} & n_{2,3} & n_{3,3} \end{bmatrix} \mapsto \mathbf{n} = \text{vec}(\mathbb{N}) = \begin{bmatrix} n_{1,1} \\ n_{2,1} \\ n_{3,1} \\ n_{1,2} \\ n_{2,2} \\ n_{3,2} \\ n_{1,3} \\ n_{2,3} \\ n_{3,3} \end{bmatrix}$$

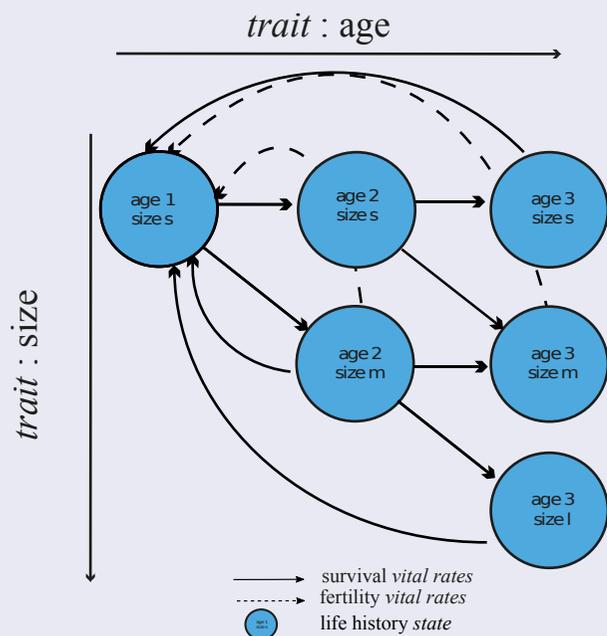
Matrix form of life cycle, projection, eigen-analysis and sensibility

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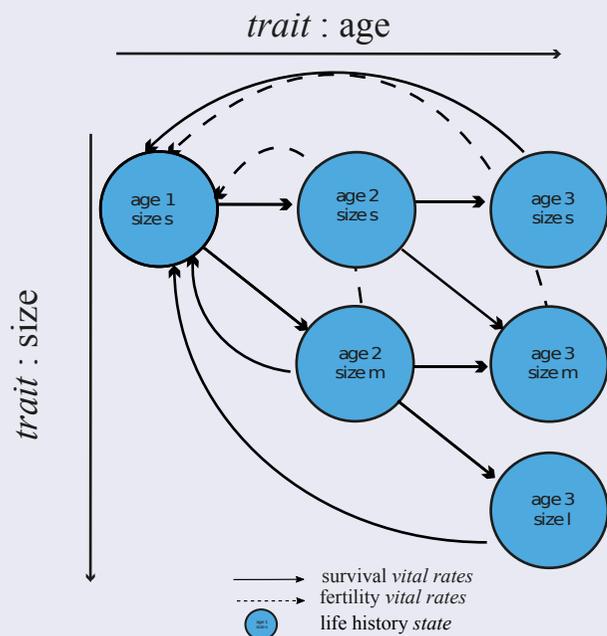
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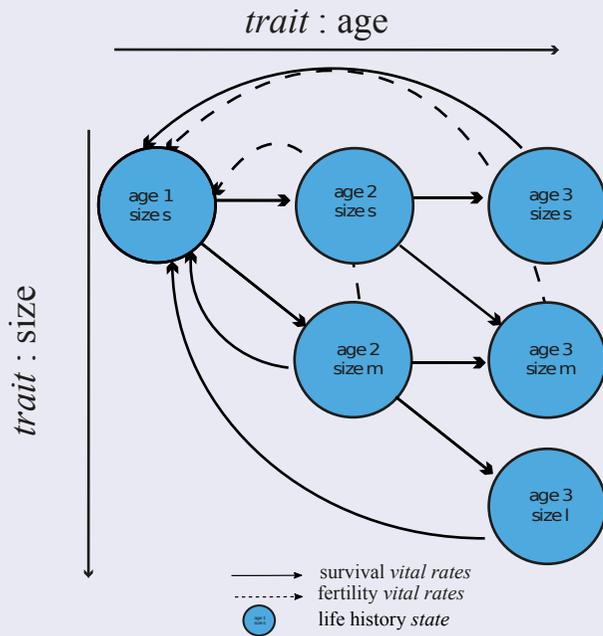
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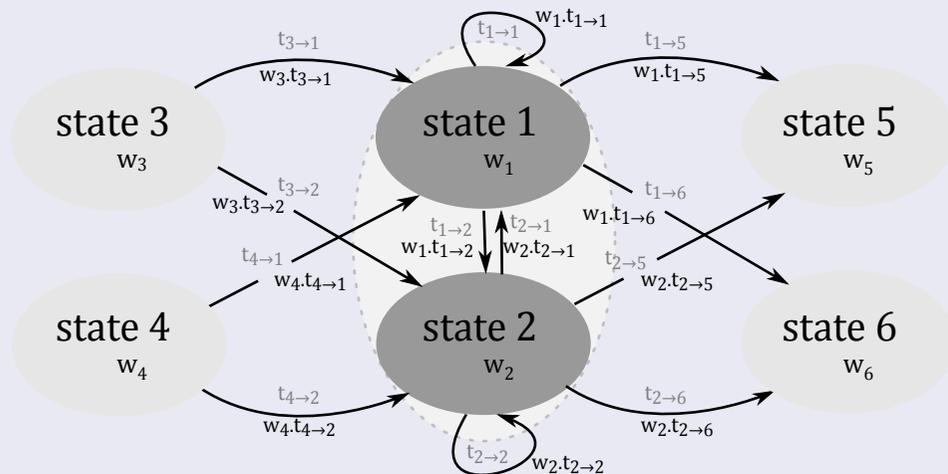
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- From \mathbb{S} the parameter sensitivity matrix, we can calculate sensitivities: $\mathbb{S} \circ \mathbf{S}$

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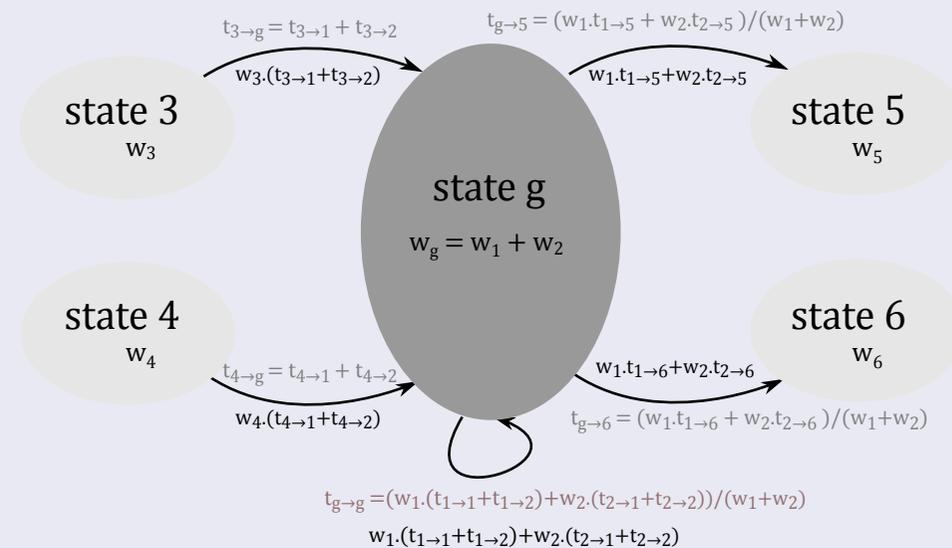
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Ergodic Flow Preserving - Merging

Ergodic-Flow Preserving Merging (before)



Ergodic-Flow Preserving Merging (after)



Two states are grouped, via EFP-merging, by ...

- summing, for each state, transition rates **towards** the group
- summing, for each state, the ergodic-abundances-weighted transition rates **from** the group

From EFP-Merging to folding

- EFP-Merging preserves ergodic flows, λ and w .
- at the cost of other properties $\Rightarrow v$ and therefore $S = [w \cdot v']$ are not preserved.

w_i : relative ergodic abundance of state i
 $t_{i \rightarrow j}$: edge/ transition value
 $w_i \cdot t_{i \rightarrow j}$: relative ergodic flow

Folding and Trait Level Analysis

EFP-merging can be extended from states to traits:

- **M** MPPM with trait vector $\mathbf{s} = (t_1, t_2)$ can be *folded* over trait t_2 -yielding $\mathbf{M}_{t_1}^{\text{fold}}$ - by EFP-merging all states sharing the same values for trait t_1 .

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2 traits, each of size 2

$$\mathbf{M}_{t_1, t_2} = \begin{bmatrix} M_{(1,1) \rightarrow (1,1)} & M_{(2,1) \rightarrow (1,1)} & M_{(1,2) \rightarrow (1,1)} & M_{(2,2) \rightarrow (1,1)} \\ M_{(1,1) \rightarrow (2,1)} & M_{(2,1) \rightarrow (2,1)} & M_{(1,2) \rightarrow (2,1)} & M_{(2,2) \rightarrow (2,1)} \\ M_{(1,1) \rightarrow (1,2)} & M_{(2,1) \rightarrow (1,2)} & M_{(1,2) \rightarrow (1,2)} & M_{(2,2) \rightarrow (1,2)} \\ M_{(1,1) \rightarrow (2,2)} & M_{(2,1) \rightarrow (2,2)} & M_{(1,2) \rightarrow (2,2)} & M_{(2,2) \rightarrow (2,2)} \end{bmatrix}$$

$$\mathbf{M}_{t_1}^{\text{fold}} = \begin{bmatrix} \frac{w_{(1,1)} \cdot (M_{(1,1) \rightarrow (1,1)} + M_{(1,1) \rightarrow (1,2)}) + w_{(1,2)} \cdot (M_{(1,2) \rightarrow (1,1)} + M_{(1,2) \rightarrow (1,2)})}{w_{(1,1)} + w_{(1,2)}} & \frac{w_{(2,1)} \cdot (M_{(2,1) \rightarrow (1,1)} + M_{(2,1) \rightarrow (1,2)}) + w_{(2,2)} \cdot (M_{(2,2) \rightarrow (1,1)} + M_{(2,2) \rightarrow (1,2)})}{w_{(2,1)} + w_{(2,2)}} \\ \frac{w_{(1,1)} \cdot (M_{(1,1) \rightarrow (2,1)} + M_{(1,1) \rightarrow (2,2)}) + w_{(1,2)} \cdot (M_{(1,2) \rightarrow (2,1)} + M_{(1,2) \rightarrow (2,2)})}{w_{(1,1)} + w_{(1,2)}} & \frac{w_{(2,1)} \cdot (M_{(2,1) \rightarrow (1,1)} + M_{(2,1) \rightarrow (1,2)}) + w_{(2,2)} \cdot (M_{(2,2) \rightarrow (1,1)} + M_{(2,2) \rightarrow (1,2)})}{w_{(2,1)} + w_{(2,2)}} \end{bmatrix}$$

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General Case

From the permutation of traits σ , we have multidimensional matrix operator $perm_\sigma$,

$$\forall \mathbb{A} \in \mathcal{M}_s(\mathbb{R}) \quad perm_\sigma(\mathbb{A})_{i_1, i_2, \dots, i_n} = \mathbb{A}_{\sigma(i_1, i_2, \dots, i_n)}$$

$$\Rightarrow \text{corresponding permutation of states } \sigma^*, \quad \sigma^*(1, \dots, q) = vec(perm_\sigma(vec_s^{-1}(1, \dots, q)))$$

This allows to generate $\mathbf{M}_{t \setminus st}^{\text{fold}} = \underbrace{\mathbf{P}^{\text{BF}}}_{\text{Block-Folding "permutation" matrix}} \cdot (\mathbf{M} \circ \underbrace{\mathbf{W}}_{\text{Ergodic abundance weights}}) \cdot \mathbf{P}^{\text{BF}'}$

\Rightarrow **Folding, the mechanism constituting Trait Level Analysis, is an asymptotically neutral framework that allows to measure the evolutionary and demographic importance of traits**

Overview

- ① Introduction
- ② Costs of reproduction: concepts and life history model
- ③ Multitrait Population Projection Models
- ④ Evolutionary and demographic consequences of physiological costs of reproduction
- ⑤ Discussion

The Model

a 3-trait MPPM

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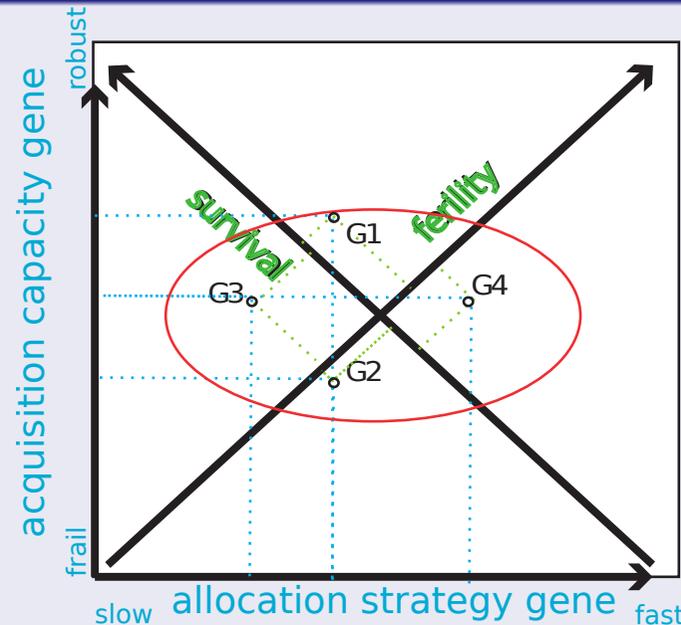
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- To distinguish physiological and genetic costs of reproduction, we set vital rates as the product of:

$$vr_{a,p,h}^e = \underbrace{vr_{x,0,h}^e}_{\text{zero-parity vital rates} \rightarrow \text{genetic costs}} \times \underbrace{\left(1 - \frac{p}{\beta - \alpha + 1}\right)}_{\text{parity effect} \rightarrow \text{physiological costs}}$$

The Model

Genotypic map



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- ⇒ slow genotypes (like G3) have higher zero-parity survival rate and lower zero-parity fertility rate than fast genotypes (like G4)
- ⇒ robust genotypes (like G1) have higher zero-parity vital rates than frailer genotypes (like G2)

The Model: MPPM and stochastic model

deterministic structure

- age structure : $\omega = 3$ age-classes, with $\alpha = 2$ and $\beta = 3$

stochastic structure

MPPM M^e

Zero-parity Leslie matrix for fast genotype g_f , with fertility F and survival s independent from age :

$$M^e_{g_f, p=0} = \begin{bmatrix} 0 & F & F \\ s & \cdot & \cdot \\ \cdot & s & \cdot \end{bmatrix}$$

The Model: MPPM and stochastic model

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- *age* structure : $\omega = 3$ *age*-classes, with $\alpha = 2$ and $\beta = 3$
- *age* and *parity* structure : there are $\beta - \alpha + 1 = 2$ *parity* classes.

stochastic structure

MPPM M^e

matrix implementing physiological costs for fast genotype g_f (zero-parity rates F and s) :

$$M^e_{g_f} = \begin{bmatrix} 0 & F & F & \cdot & \cdot & \frac{F}{2} \\ s & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & s.(1-F) & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & s.F & \cdot & \cdot & \cdot & \cdot \end{bmatrix}$$

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MPPM M^e

$$M^e = \begin{bmatrix} 0 & (1-\mu).F & (1-\mu).F & \dots & (1-\mu).\frac{F}{2} & 0 & \mu.f & \mu.f & \dots & \mu.\frac{f}{2} \\ s & \cdot \\ \cdot & s.(1-F) & \cdot \\ \cdot & \cdot \\ \cdot & s.F & \cdot \\ 0 & \mu.F & \mu.F & \dots & \mu.\frac{F}{2} & \cdot & (1-\mu).f & (1-\mu).f & \dots & (1-\mu).\frac{f}{2} \\ \cdot & \cdot & \cdot & \cdot & \cdot & S & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & S.(1-f) & \cdot & \cdot & \cdot \\ \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & S.f & \cdot & \cdot & \cdot \end{bmatrix}$$

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- Environmental stochasticity: \mathbf{M}^e is the deterministic structure for env. \mathbf{e} . (distribution \mathcal{D}_e)

MPPM \mathbf{M}^e

$$\mathbf{M}^e = \begin{bmatrix} 0 & (1-\mu).F & (1-\mu).F & \dots & (1-\mu).\frac{F}{2} & 0 & \mu.f & \mu.f & \dots & \mu.\frac{f}{2} \\ s & \cdot \\ \cdot & s.(1-F) & \cdot \\ \cdot & \cdot \\ \cdot & \cdot \\ \cdot & s.F & \cdot \\ 0 & \mu.F & \mu.F & \dots & \mu.\frac{F}{2} & \cdot & (1-\mu).f & (1-\mu).f & \dots & (1-\mu).\frac{f}{2} \\ \cdot & \cdot & \cdot & \cdot & \cdot & S & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & S.(1-f) & \cdot & \cdot & \cdot \\ \cdot & \cdot \\ \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & S.f & \cdot & \cdot & \cdot \end{bmatrix}$$

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stochastic structure

- Environmental stochasticity: \mathbf{M}^e is the deterministic structure for env. \mathbf{e} . (distribution \mathcal{D}_e)
- Individual stochasticity: Random variable of fertility events is a Bernoulli $\mathcal{F}_{a,p,h} = \mathcal{B}(f_{a,p,h})$,
 - \Rightarrow full stochastic model : $\{\mathbf{M}^e, \mathcal{D}_e, \mathcal{F}_{a,p,h}^e\}$

MPPM \mathbf{M}^e

$$\mathbf{M}^e = \begin{bmatrix}
 0 & (1-\mu).F & (1-\mu).F & \dots & (1-\mu).\frac{F}{2} & 0 & \mu.f & \mu.f & \dots & \mu.\frac{f}{2} \\
 s & \cdot \\
 \cdot & s.(1-F) & \cdot \\
 \cdot & \cdot \\
 \cdot & s.F & \cdot \\
 0 & \mu.F & \mu.F & \dots & \mu.\frac{F}{2} & \cdot & (1-\mu).f & (1-\mu).f & \dots & (1-\mu).\frac{f}{2} \\
 \cdot & \cdot & \cdot & \cdot & \cdot & S & \cdot & \cdot & \cdot & \cdot \\
 \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & S.(1-f) & \cdot & \cdot & \cdot \\
 \cdot & \cdot \\
 \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & S.f & \cdot & \cdot & \cdot
 \end{bmatrix}$$

The Methods

Trait Level Analysis

To measure the evolutionary effects of the costs of reproduction, we use Trait Level Analysis to compare:

- **M** the (*age-parity-heterogeneity*)-MPPM implementing physiological and genetic costs of reproduction.
- **M_{age}^{fold}** the reference Leslie matrix, an *age-only* model without any cost of reproduction.

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$$\ln \lambda_s \approx \ln \lambda - \left(\frac{1}{2} \cdot \underbrace{\sigma_e^2}_{\text{environmental variance}} \right) - \left(\frac{1}{2 \cdot N} \cdot \underbrace{\sigma_d^2}_{\text{demographic variance}} \right)$$

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- **lifetime individual** fitness measure \mathcal{LRO} the **reproductive success**.
 - ⇒ $E(\mathcal{LRO}) = \mathbf{R}_0$ preserved *in this model* by folding
 - ⇒ The effect of the costs on reproductive success will be measurable by their effects on **variance in reproductive success** $\sigma_{\mathcal{LRO}}^2$

$$\sigma_{\mathcal{LRO}}^2 = \underbrace{\sigma_{\mathcal{LRO}}^2}_{\text{sto}} + \underbrace{\sigma_{\mathcal{LRO}}^2}_{\text{het}}$$

$E_h(\sigma_{h\mathcal{LRO}}^2) = \text{mean variance across genotypes} \leftarrow \text{physiological costs}$ $Var_h(\mathbf{R}_{h0}) = \text{difference in } \mathbf{R}_0 \text{ between genotypes} \leftarrow \text{genetic costs}$

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$$\sigma_{\mathcal{LRO}}^2 = \underbrace{\sigma_{\mathcal{LRO}}^2}_{sto} + \underbrace{\sigma_{\mathcal{LRO}}^2}_{het}$$

$E_h(\sigma_h^2_{\mathcal{LRO}})$ =mean variance across genotypes←**physiological costs** $Var_h(\mathbf{R}_{h0})$ =difference in \mathbf{R}_0 between genotypes←**genetic costs**

⇒ $\sigma_{\mathcal{LRO}}^2$ computed via closed form formula for **M_a^{fold}**, using **new** formulas for matrix models with **several offspring classes** for **M_{a,h}^{fold}**, and with **Markov chains with rewards** for **M**.

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Computation of variance in reproductive success I

Leslie matrix : age-structured population

$$\sigma_{\mathcal{LRO}}^2 = \alpha_1 = \sum_{i=1}^n P_i \left[\text{Var}(\mathcal{F}_i) + y_{i+1}^2 s_i (1 - s_i) \right],$$

- \mathcal{F}_i is the fertility process at age i of expectation f_i
- s_i the survival rate at age i , $P_i = \prod_{k=1}^{i-1} s_k$ the probability to survive to age i
- $y(i) = \frac{1}{P_i} \sum_{j=i}^n f_j P_j$ the expectation of \mathcal{LRO}_i (remaining reproductive output for an individual aged i)

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Populations with hidden-heterogeneity trait (several classes of offspring) : age-heterogeneity matrix

From

- survival-fertility decomposition of $\mathbf{M} = \mathbf{T} + \mathbf{F}$
- Next-Generation Matrix $\mathbf{R} = \mathbf{F} \cdot (\mathbf{I} - \mathbf{T})^{-1}$ and the sum of its lines $\mathbf{e}_{\mathcal{LRO}}$
- \mathbf{w}^\diamond the vector of relative ergodic abundances of offspring states

We get,

$$E(\mathcal{LRO}) = \sum_{h=1}^{het} e_h^{\mathcal{LRO}} \cdot w_h^\diamond$$

$$\sigma_{\mathcal{LRO}}^2 = \underbrace{w_1^\diamond \cdot \sigma_{\mathcal{LRO}_1}^2 + w_2^\diamond \cdot \sigma_{\mathcal{LRO}_2}^2}_{\sigma_{\mathcal{LRO}}^{\text{sto}}{}^2} + \underbrace{w_1^\diamond \cdot e_{\mathcal{LRO}_1}^2 + w_2^\diamond \cdot e_{\mathcal{LRO}_2}^2 - e_{\mathcal{LRO}}^2}_{\sigma_{\mathcal{LRO}}^{\text{het}}{}^2}$$

Computation of variance in reproductive success II

Populations with dynamic heterogeneity trait: *age-parity-heterogeneity* matrix

Stochastic fertility processes may become dependent on the *output* state

⇒ **Markov Chain with Rewards**¹

$$\tilde{\mathbf{T}} = \left[\begin{array}{c|c} \mathbf{T} & 0 \\ \hline \mathbf{1}' - \mathbf{1}' \cdot \mathbf{T} & 1 \end{array} \right] \quad \mathbf{Rw}^k = \left[\begin{array}{ccc} \dots & \dots & \dots \\ \dots & R w_{i,j}^k = \mathcal{F}_{T:j \rightarrow i}^k & \dots \\ \dots & \dots & \dots \end{array} \right] = \left[\begin{array}{cccccc|c} \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & 0 \\ 0 & \cdot & \cdot & \cdot & \cdot & \cdot & 0 \\ \cdot & 0 & \cdot & \cdot & \cdot & \cdot & 0 \\ 1 & \cdot & 0 & \cdot & \cdot & \cdot & 0 \\ \cdot & 1 & \cdot & 0 & \cdot & \cdot & 0 \\ \cdot & \cdot & 1 & \cdot & 0 & \cdot & 0 \\ \hline f_1 & f_2 & \dots & f_i & \cdot & f_q & 1 \end{array} \right]$$

Bernoulli fertility for *age-parity* MPPM

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$\rho_k = k^{th}$ moment of \mathcal{LRO} , indexed on "starting" states, obtained by convergence.

$$\rho_1 = \lim_{t \rightarrow +\infty} \rho_1(t) \text{ with } \rho_1(t+1) = (\tilde{\mathbf{T}} \circ \mathbf{Rw}^1)' \cdot \mathbf{1} + \tilde{\mathbf{T}} \cdot \rho_1(t)$$

$$\rho_2 = \lim_{t \rightarrow +\infty} \rho_2(t) \text{ with } \rho_2(t+1) = (\tilde{\mathbf{T}} \circ \mathbf{Rw}^2)' \cdot \mathbf{1} + 2 \cdot (\tilde{\mathbf{T}} \circ \mathbf{Rw}^1)' \cdot \rho_1(t) + \tilde{\mathbf{T}} \cdot \rho_2(t)$$

with initial conditions $\rho_1(0) = \rho_2(0) = \mathbf{0}$ (\circ is the Hadamard, termwise, product)

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Result I: Effects of costs on vital rates

Age-independent organism with physiological costs and genotypic polymorphism...

full (*age,parity,heterogeneity*)-MPPM \mathbf{M} with

- physiological costs
- two *heterogeneity* classes: a robust genotype and a frail genotype
- **age-independent vital rates**

We extract vital rates from $\mathbf{M}_{\text{age}}^{\text{fold}}$, the Reference Leslie Matrix

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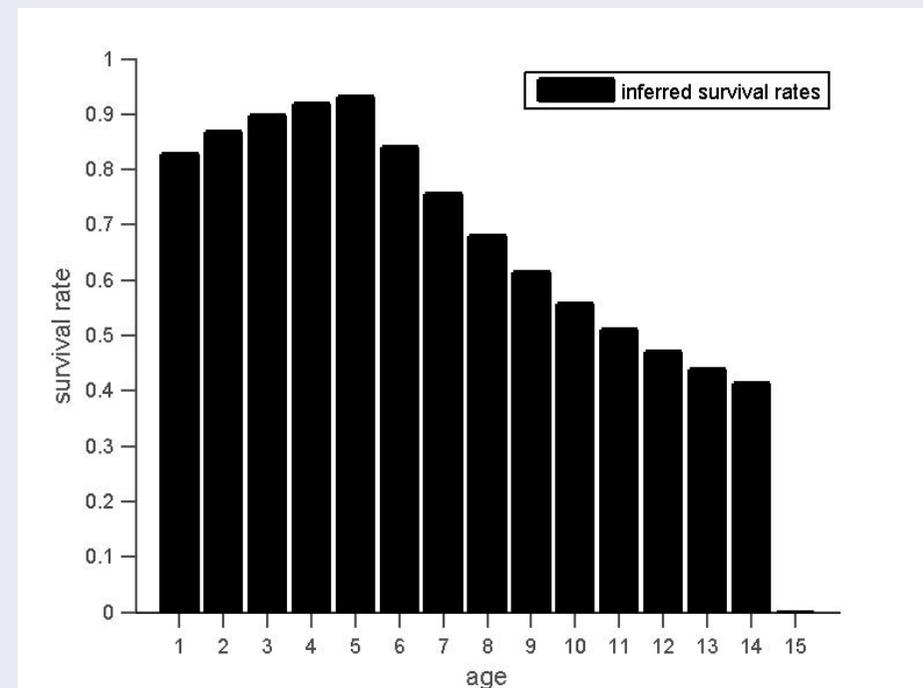
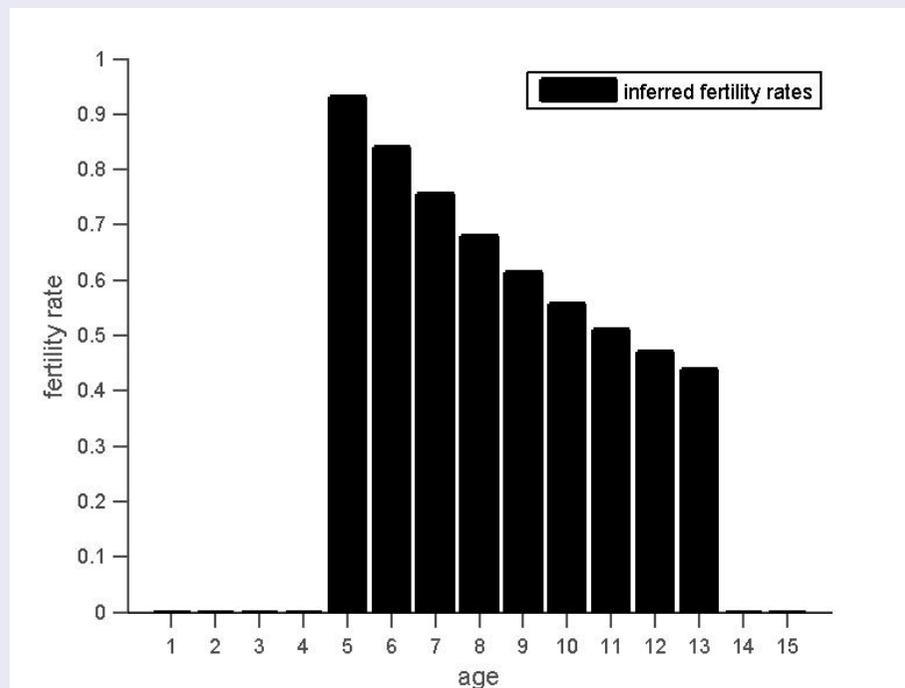
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⇒ when population considered by **age only**, vital rates **now vary with age** ← transfers of costs

... exhibits familiar vital rates curves when studied by *age only*



Result IIa: Effects of physiological costs of reproduction on selection gradients

Physiological costs reduce selection gradients

- Model is homogeneous age-parity \mathbf{M}^1 implementing physiological costs.
- We compare fertility selection gradients - $\frac{\partial \ln \lambda}{\partial \ln f_a}$ - for \mathbf{M} and $\mathbf{M}_{\text{age}}^{\text{fold}}$

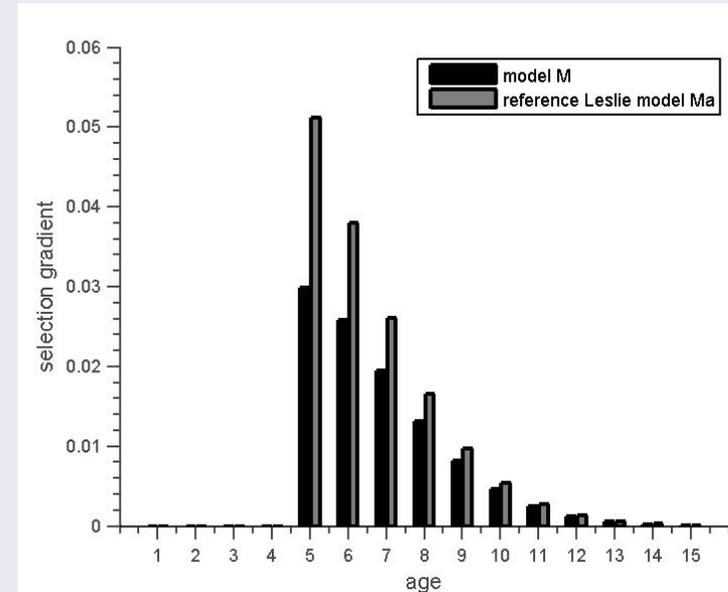
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Fertility selection gradients by age



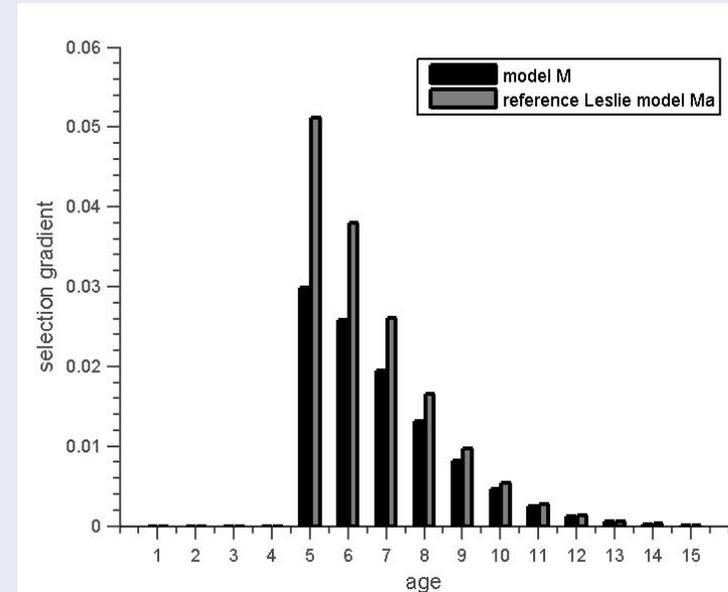
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- "unrealized" fertility events are postponed rather than forfeited.

Fertility selection gradients by age



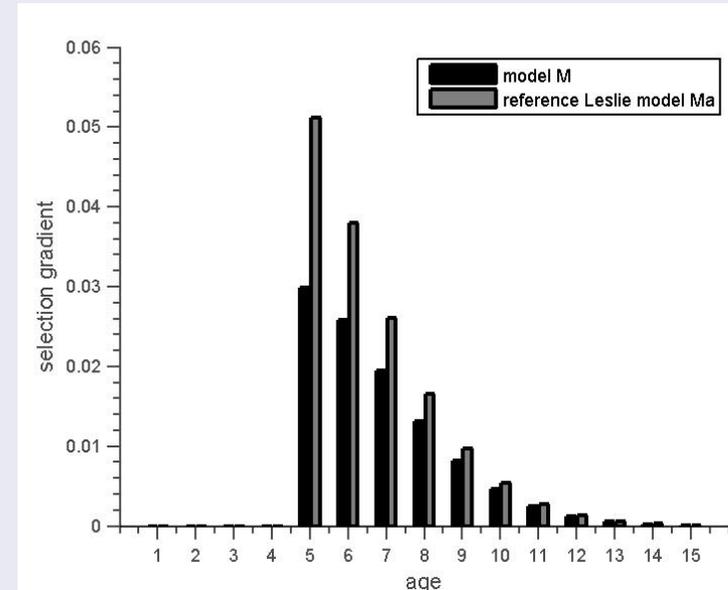
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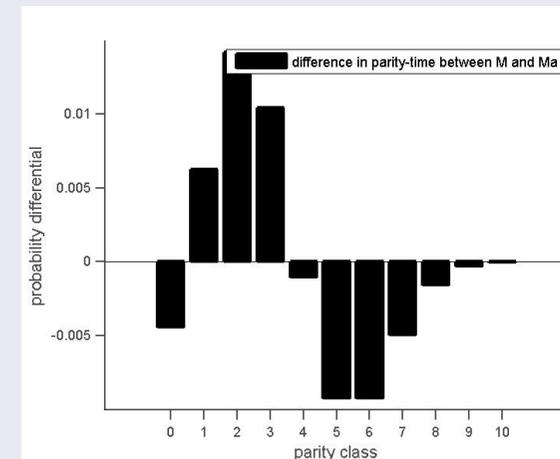
Fertility selection gradients by age



Physiological costs concentrate parity classes

- We compare the stable state abundances of parity classes for \mathbf{M} and $\mathbf{M}_{\text{age}}^{\text{fold}}$
- ⇒ Costs of reproduction concentrate parities in the population

Stable state parity abundances distribution



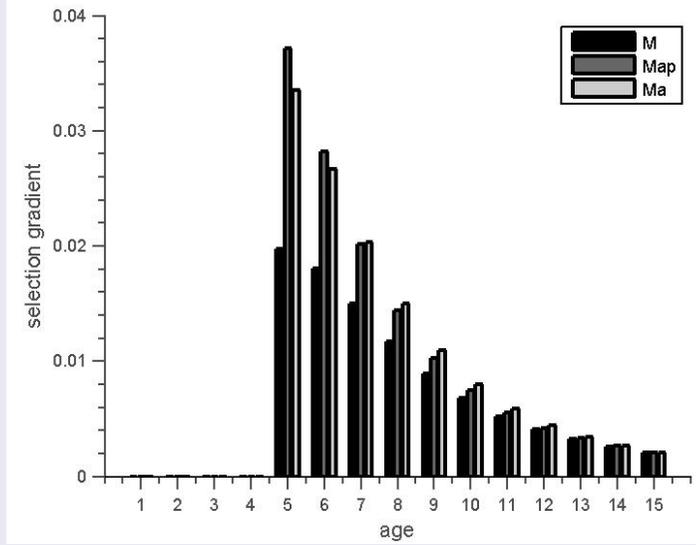
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Result IIb: selection gradients and detectability

New detectability result

- We add variance in allocation (but no variance in robustness)
 - ⇒ physiological and genetic costs are implemented in **M**
 - ⇒ genotypes have the same fitness

Fertility selection gradients by age



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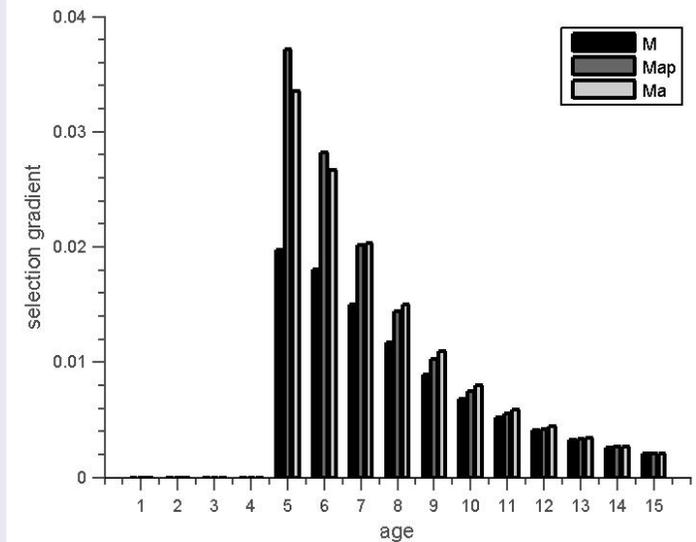
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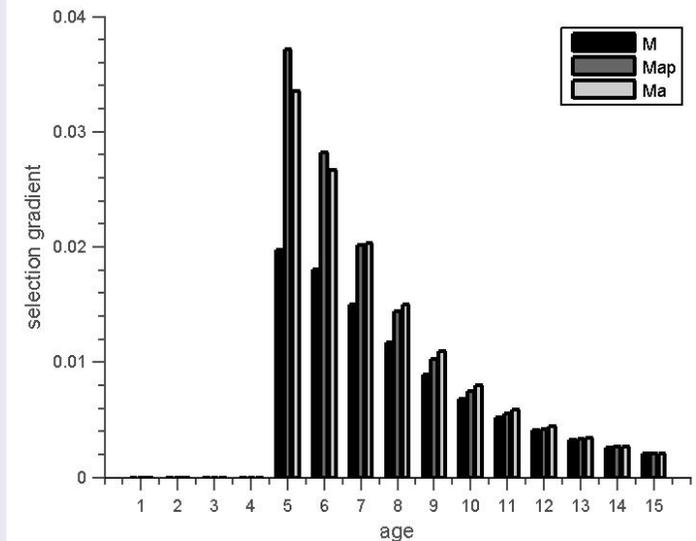
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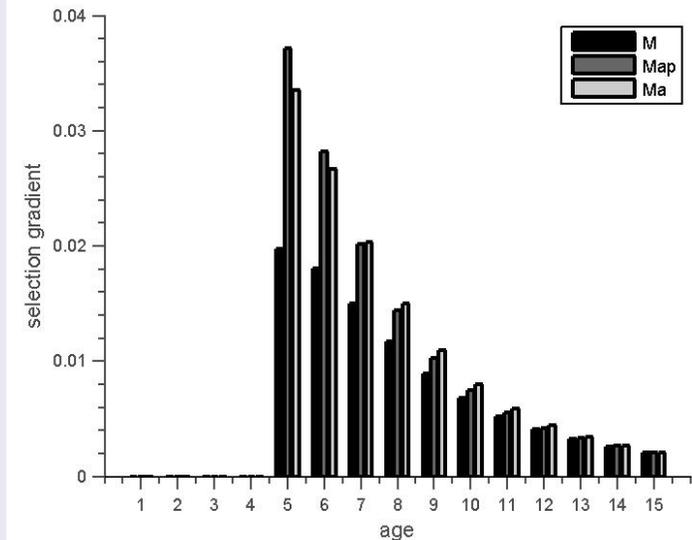
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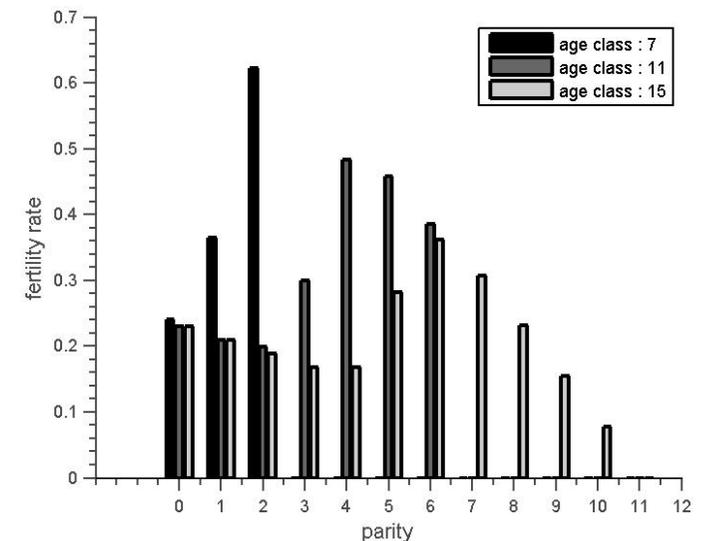
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Fertility selection gradients by age



Inferred fertility rates by parity for $\mathbf{M}_{\text{age,parity}}^{\text{fold}}$



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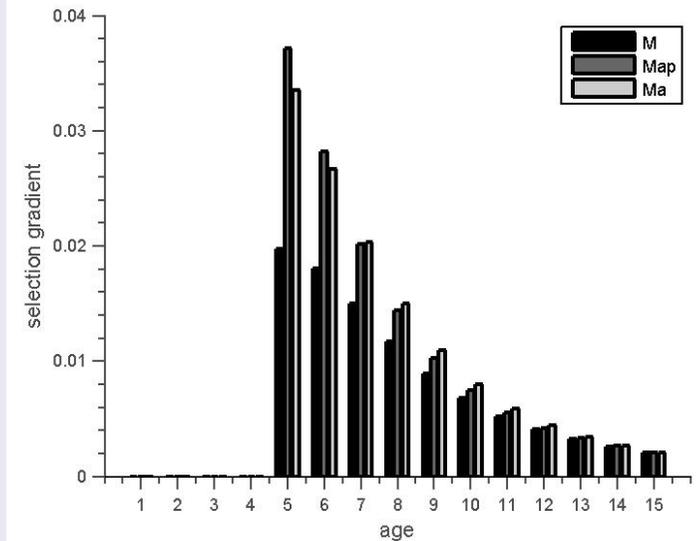
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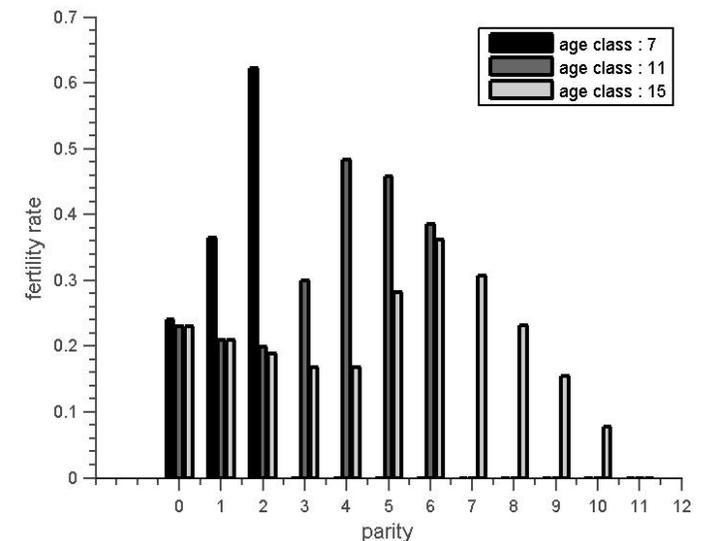
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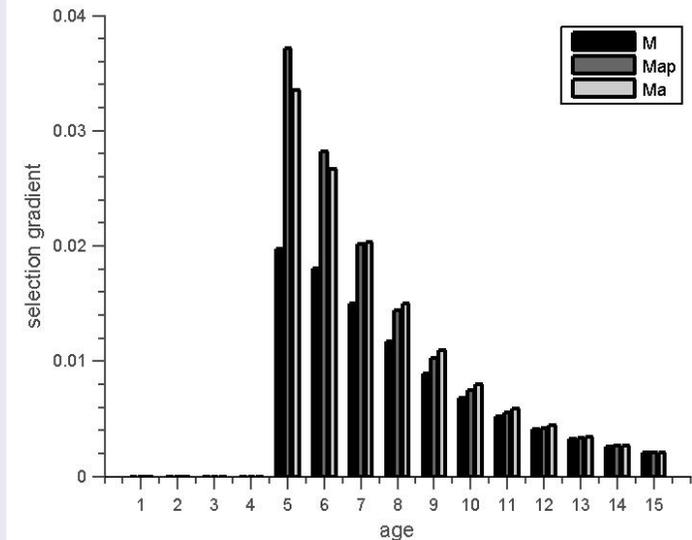
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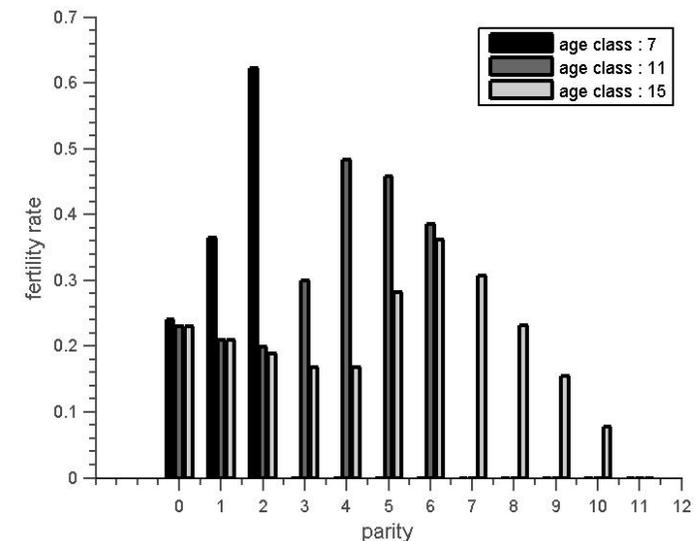
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 - In 1986, van Noordwijk and de Jong¹ ⇒ **physiological costs** hidden by allocation variance

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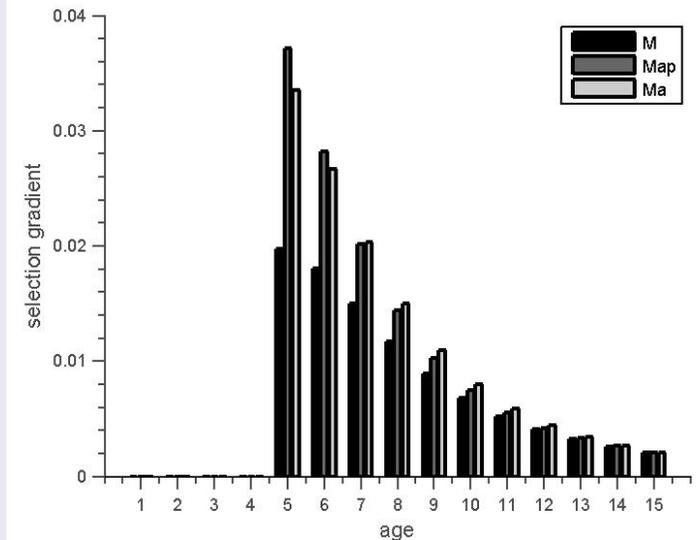
Result IIb: selection gradients and detectability

New detectability result

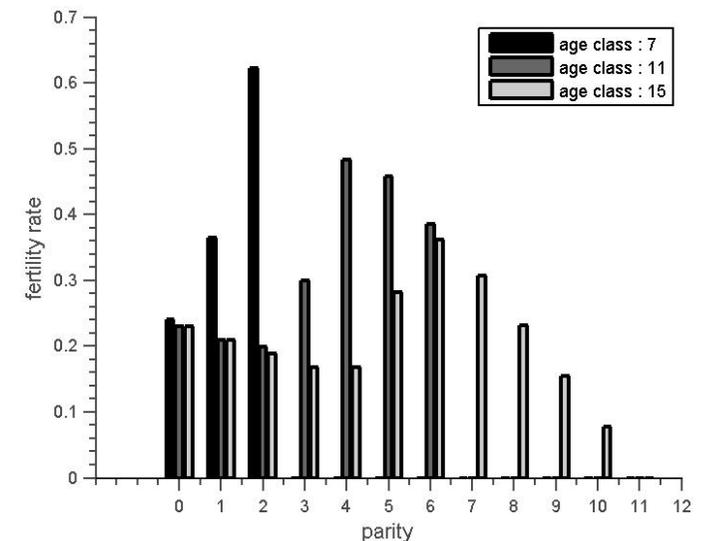
- We add variance in allocation (but no variance in robustness)
 - ⇒ physiological and genetic costs are implemented in \mathbf{M}
 - ⇒ genotypes have the same fitness
- Reference Leslie matrix $\mathbf{M}_{\text{age}}^{\text{fold}}$ has still higher selection gradients than \mathbf{M}
- But gradients of $\mathbf{M}_{\text{age,parity}}^{\text{fold}}$ are higher still.
- ⇒ When genetic costs are not accounted for, **benefits of reproduction** may emerge instead of **costs**.

- This is a new trade-off detectability theorem:
 - In 1986, van Noordwijk and de Jong¹ ⇒ **physiological costs** hidden by allocation variance
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Fertility selection gradients by age



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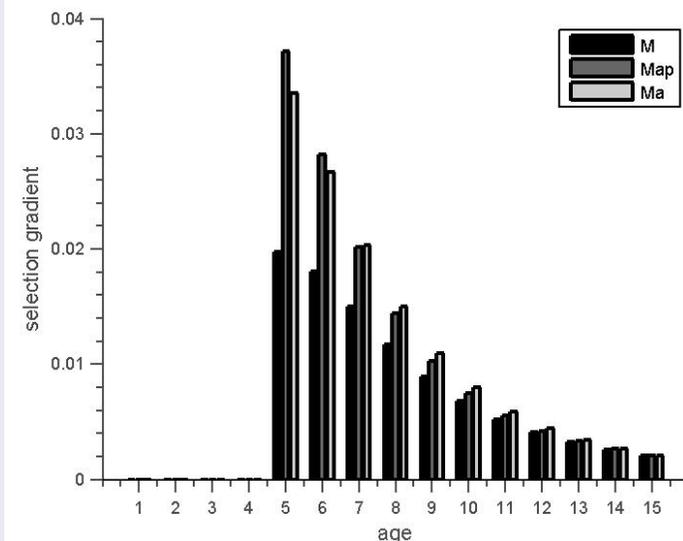
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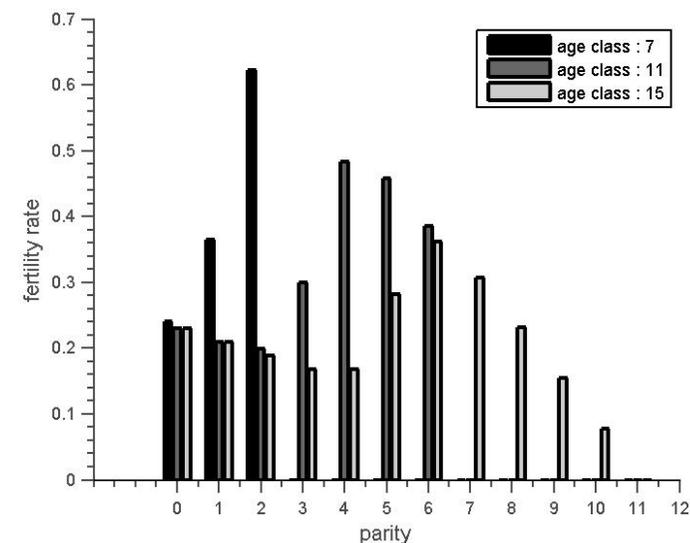
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 - Our result ⇒ **detection of physiological costs can be blurred by the genetic costs**

Fertility selection gradients by age



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Result IIIa: Physiological costs of reproduction reduce σ_{LRO}^2

Effects of life history strategy on $\sigma_{LRO}^2[\mathbf{M}] - \sigma_{LRO}^2[\mathbf{M}_{age}^{fold}]$

- For \mathbf{M} implementing physiological costs ,

$$\sigma_{LRO}^2[\mathbf{M}] < \sigma_{LRO}^2[\mathbf{M}_{age}^{fold}]$$

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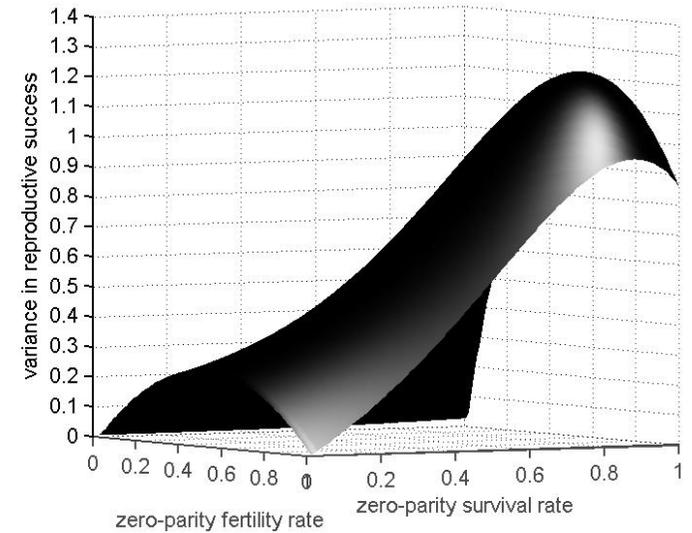
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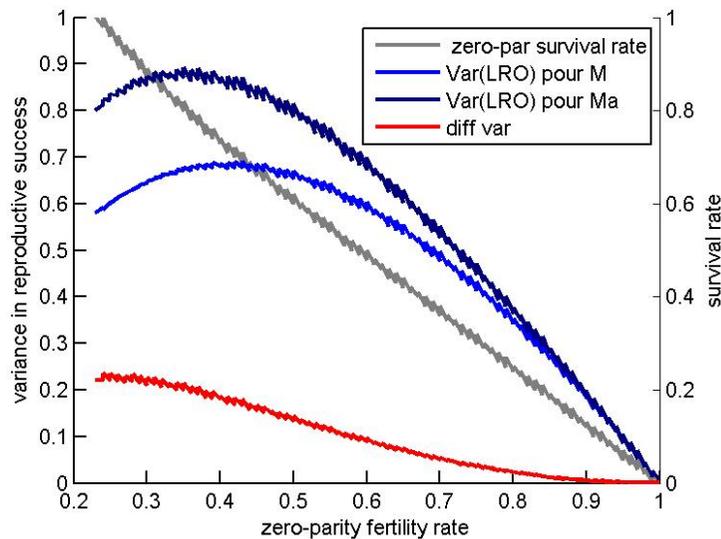
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- σ_{LRO}^2 is a function of *allocation* \times *acquisition* genotypes :
 $\Rightarrow \sigma_{LRO}^2$ maximum for central fertility and central/high survival

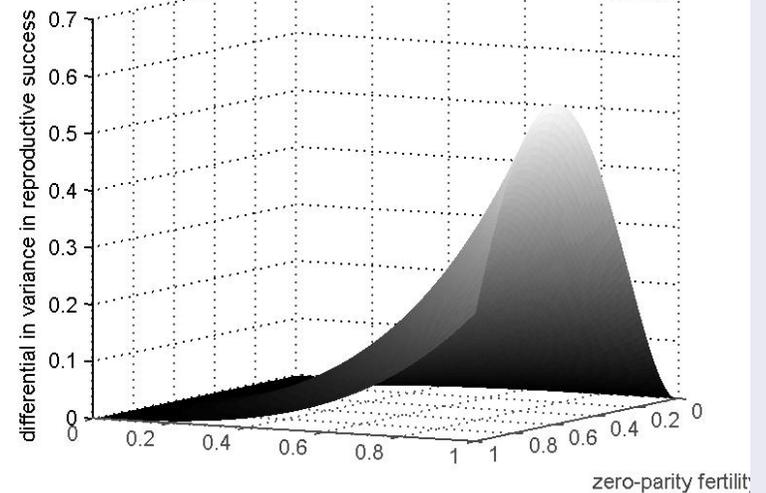
σ_{LRO}^2 for Reference Leslie matrix¹



$\lambda = R_0 = 1$ -isoclines¹



Effects of costs¹ on σ_{LRO}^2



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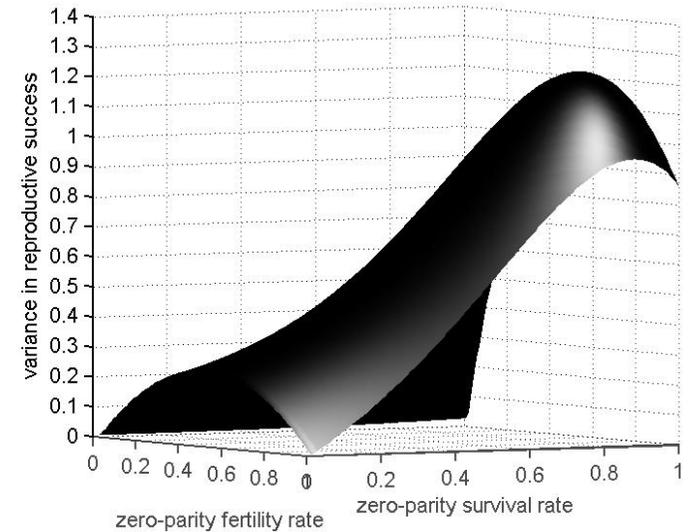
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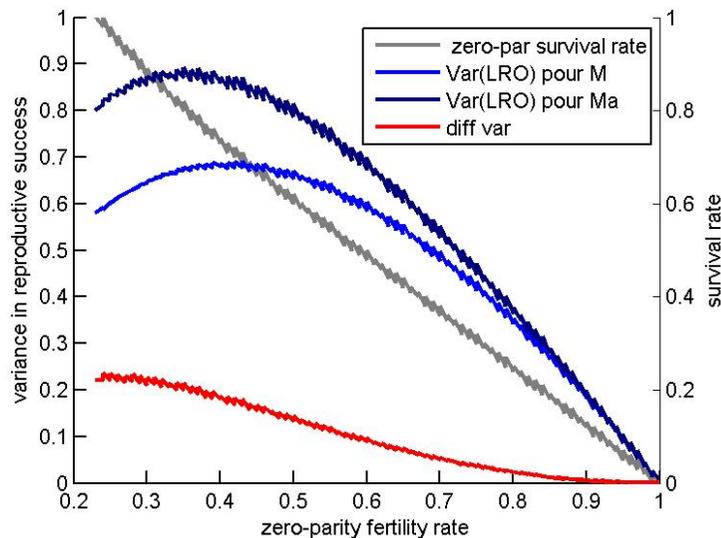
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- $\Delta\sigma_{LRO}^2$ also a function of the genotypic map but
 \Rightarrow no buffering effects of the costs for fast/semelparous organisms
 \Rightarrow the effect keeps increasing as organisms are slower.

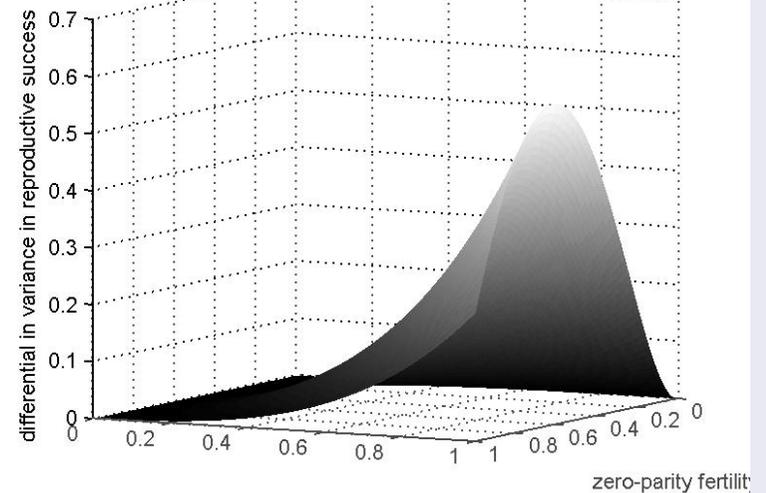
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Result IIIb: Effects of physiological costs of reproduction on effective size

Demographic variance and effective size

- N_e the size of an "ideal" population with same rate of genetic drift¹ \Rightarrow same selection effectiveness

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- This is one possible answer for the antagonistic pleiotropy riddle of populations structured by age only
- \Rightarrow fast organisms have high gradients are therefore invaded by ever faster alleles
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- \Rightarrow Physiological and Genetic costs buffer stochasticity with different time horizons
- \Rightarrow **slow individuals** are mainly buffered by **physiological** costs, and **fast populations** by **genetic** costs

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Result IV: Effects of physiological costs on stochastic growth rate

Costs buffer both stochasticities

We introduce environmental variations.

We can demonstrate formally **physiological costs reduce environmental stochasticity** .

Here we show a simulation:

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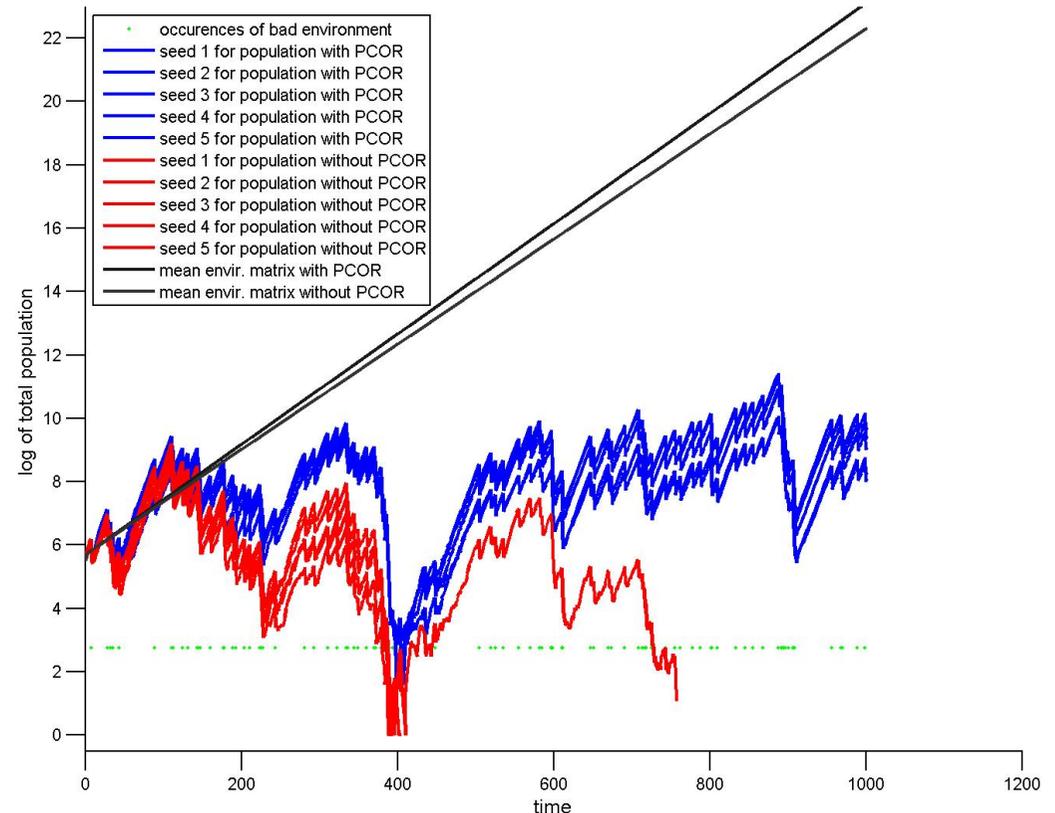
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- M_g implements physiological costs
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Projection



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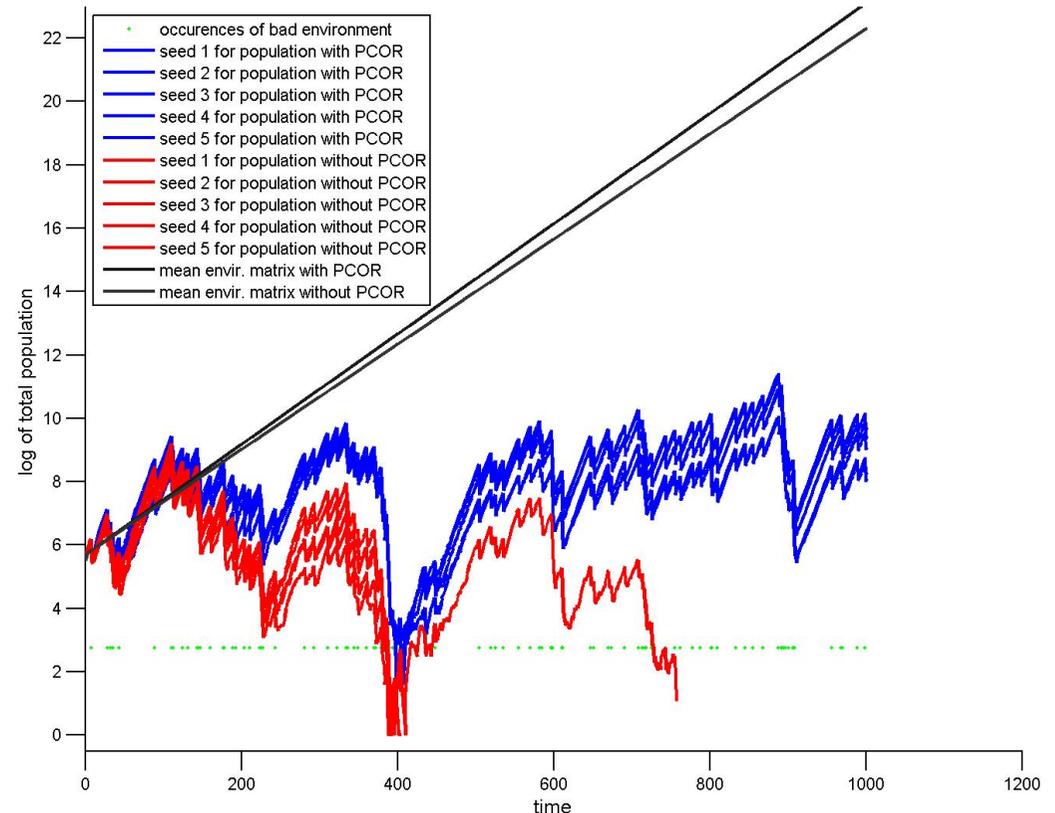
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- all plotted populations share the same environmental series
- ⇒ differences between time-steps caused by environmental stochasticity
- ⇒ differences between populations caused by individual stochasticity

Projection



Overview

- ① Introduction
- ② Costs of reproduction: concepts and life history model
- ③ Multitrait Population Projection Models
- ④ Evolutionary and demographic consequences of physiological costs of reproduction
- ⑤ Discussion

Discussion

main results

MPPM methodology and in particular *Trait Level Analysis* has allowed to confirm that:

- Physiological and genetic costs can cohabit. Conjointly they are partly responsible for shaping vital rates curves by age
- Genetic costs hinder detectability of physiological costs
- Forsaking physiological costs leads to overestimation (resp. underestimation) of strength of antagonistic pleiotropy for fast (resp. slow) organisms
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Zooming out

- These results hint at the necessity of factoring two traits to model trade-offs ⇒ danger of using one trait only to model life history.
 - ⇒ Using only the best predictor of vital rates may yield appropriate demographic results but evolutionary measures are off.
 - ⇒ In particular, this hints at an important difference between properties of age-structured populations and populations structured by *age only* that should not be confused.
- Multitrait structured demography can develop in many directions: demographic measures, alternative folding methods, development of transient demographic tools

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Other applications of MPPMs/ *Trait Level Analysis*

One key extension concerns kinship demography. This new field aims at studying the coevolution of kinship structures and demographic traits. From a modeling perspective this asks :

- how does the demography of a population affects the distribution of kin
- how to implement effects of kin (cooperation/competition) in a demography model

The End

Acknowledgments

I wish to thank my supervisors **Frederic Austerlitz** and **Samuel Pavard** as well as **Evelyne Heyer** heading the lab of Eco-anthropology et Ethnobiology of MNHN/Musée de l'Homme

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And to **Emmanuelle Porcher** for presiding the jury of my PHD defence