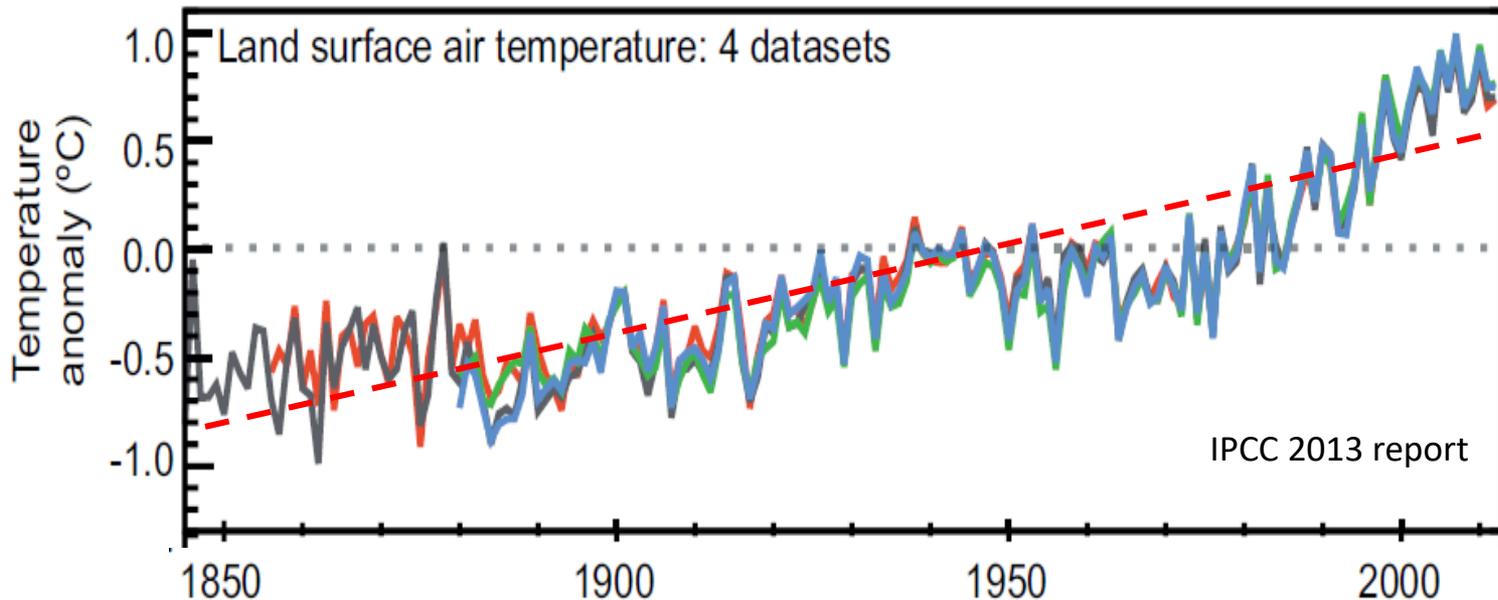# Genetics and ecology of adaptation to stochastic environments

Luis-Miguel Chevin
CEFE – CNRS, Montpellier

Environments vary randomly

- Virtually all natural environments exhibit noisy, random fluctuations.

Land surface air temperature: 4 datasets

IPCC 2013 report

- Faster than trends: major challenge for organisms in the wild

Stocker et al (2013 IPCC report)

Environments vary randomly

- Stochastic fluctuations are **random**, but can be **predicted probabilistically**
- Time scale of predictability depends on **temporal autocorrelation** ρ

$\rho = 0.1$ $\rho = 0.9$
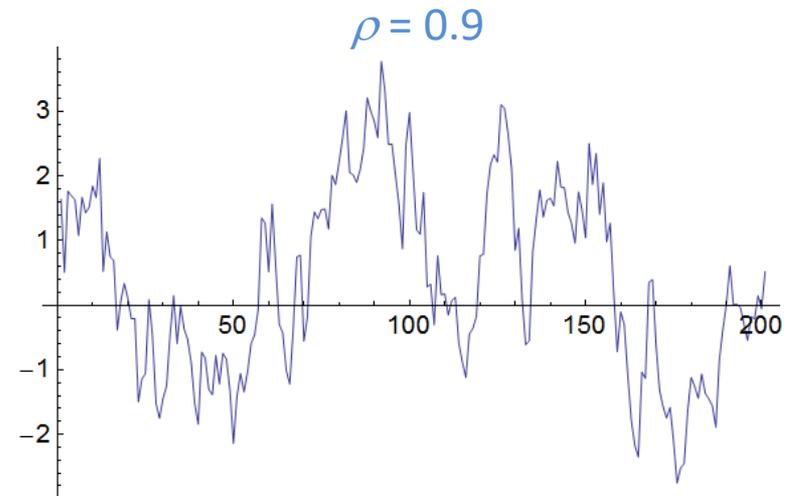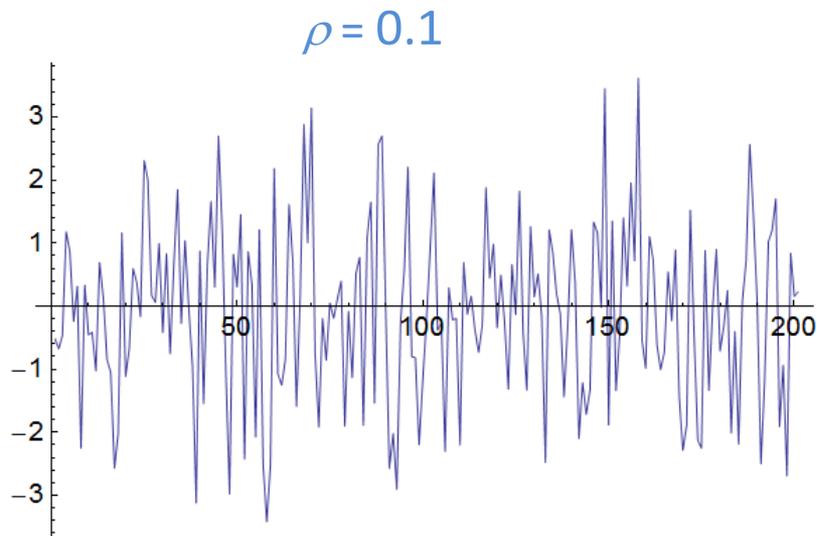
- Climate change is altering not only mean environments (= trend), but also their (auto)correlation structure

Stochastic environments affect ecology and evolution

- Fluctuating demographic vital rates → **Fluctuating population size/density**[1]

Great tits[2]

Cods[3]
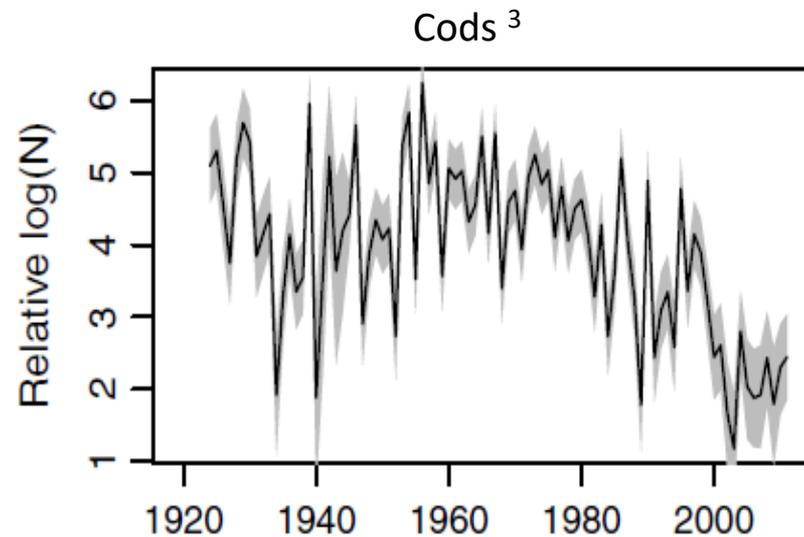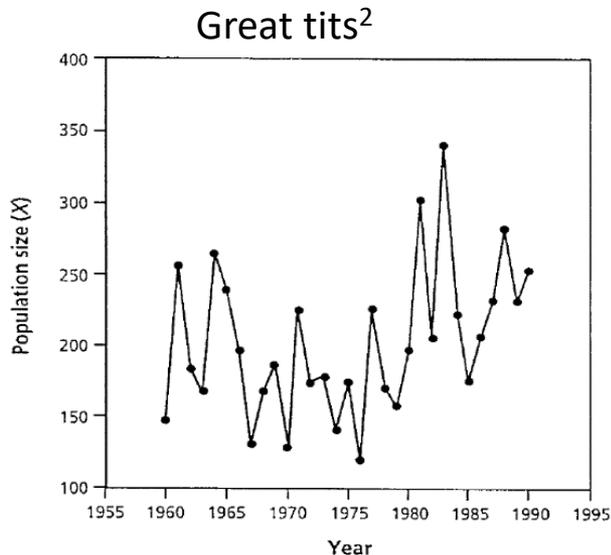
- Affects all individuals at all population sizes[1]
  → Strong source of stochasticity and extinction risk.

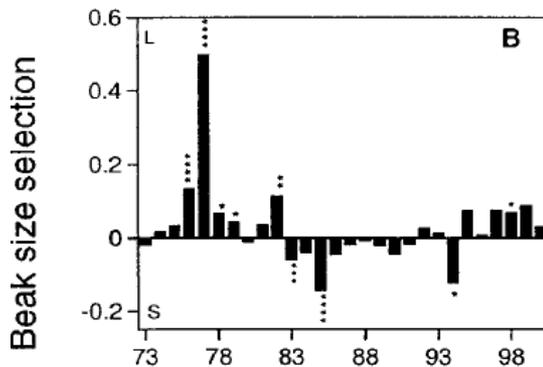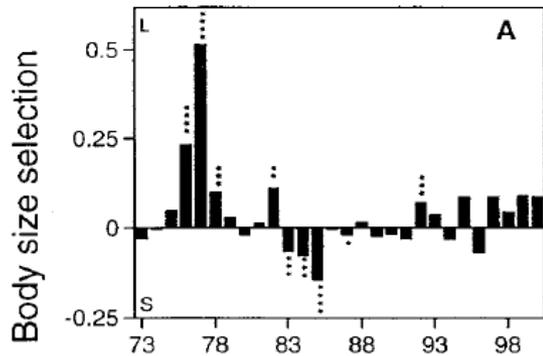1: reviewed by Lande et al (2003 Oxford U. Pr.)   2: Saether et al (1998, Am Nat)   3: Rogers et al (2017 J Anim Ecol)

Stochastic environments affect ecology and evolution
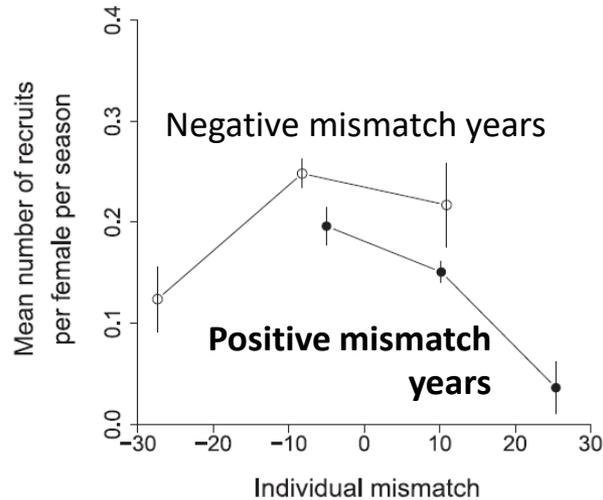
- Source of **fluctuating selection**

Darwin's finches
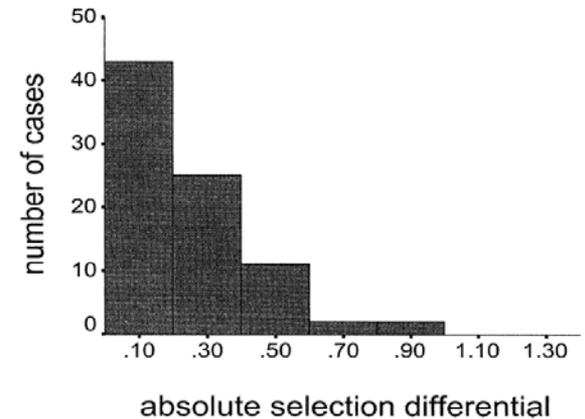Grant & Grant 2002 Science

Great tit (breeding time)
Reed et al 2013 Science

Sticklebacks (spine number)
Reimchen & Nosil 2002 Evolution

Stochastic environments affect ecology and evolution

- Source of **fluctuating selection**

- Can cause the evolution of specific response mechanisms:
  bet hedging, or **phenotypic plasticity**

- Major **source of chance** in evolution:
  Environmental stochasticity increases variance among replicate instances of evolution, similar to drift (causing fixations, etc…)

Predictability of population responses

- How do random fluctuations in the environment translate into fluctuations at all levels of population biology?
  With **what predictability at each level**?

(A) Phenotypic plasticity
(B) Fluctuating selection
(C) Stochastic demography
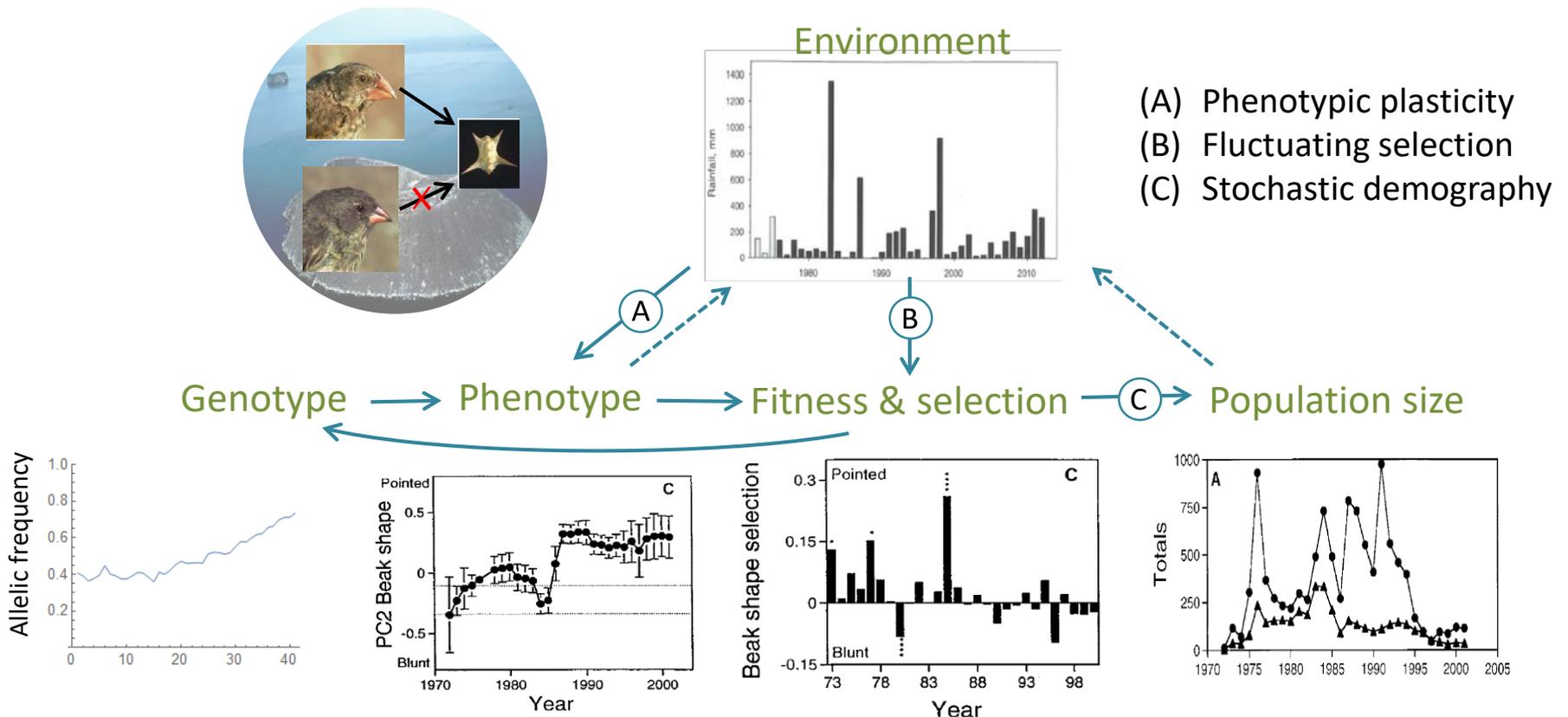
Figures from Grant & Grant (2002 Science, 2014 PUP)

Predictability of population responses

- How do random fluctuations in the environment translate into fluctuations at all levels of population biology?
  With **what predictability at each level**?

- Investigating stochasticity requires a **high level of replication**, to account for randomness in the process

- An approach **combining experimental evolution with theory** can help shed light on patterns from natural populations.

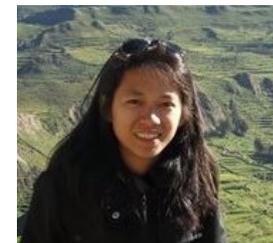# I – Experimental evolution in stochastic environments

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Lab manager

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Postdoc

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Christelle LEUNG
Postdoc FRQNT

Experimental evolution with *Dunaliella salina*

- **Halotolerant micro-algae** (freshwater to NaCl saturation).
  Shallow water (lagoons): **salinity fluctuates** with precipitation, wind, sunlight

- Short generation time ~ 1 day

- Extremophile: few ecological interactions
  → Niche easily mimicked in the lab

- **Physiological traits respond plastically to salinity**: metabolite content.
  Glycerol: osmotic stress
  Carotene: Protection against light, oxidative stress.

Low carotene cell

High carotene cell

http://www.lesalindegruissan.fr/

Experimental evolution
under randomly fluctuating salinity
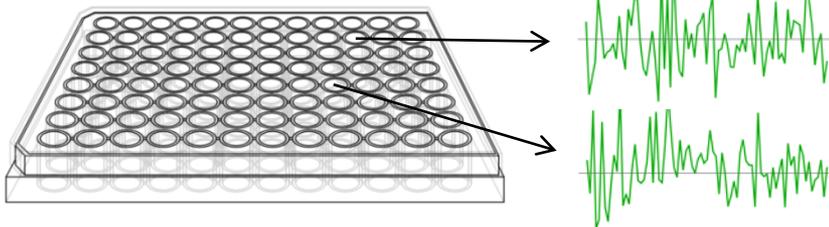
- Salinity changed at each transfer (every 3-4 generations),
  using a liquid-handling robot: - High replication

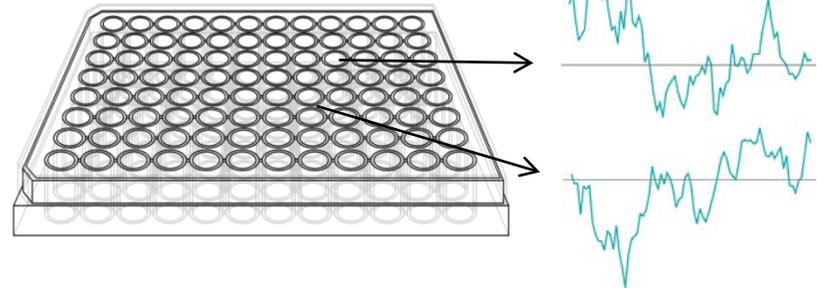   - Complex fluctuation pattern

Experimental evolution
under randomly fluctuating salinity

- Autocorrelation as the treatment: ρ = -0.5, 0, 0.5, 0.9

**Low-predictability treatment**

High-predictability treatment

- >35 independent time series per autocorrelation

- Applied to 3 collection strains, single *vs* pair mixes
  = high *vs* low genetic variance

- Population size at each transfer estimated using flow cytometry + absorbance + fluorescence.
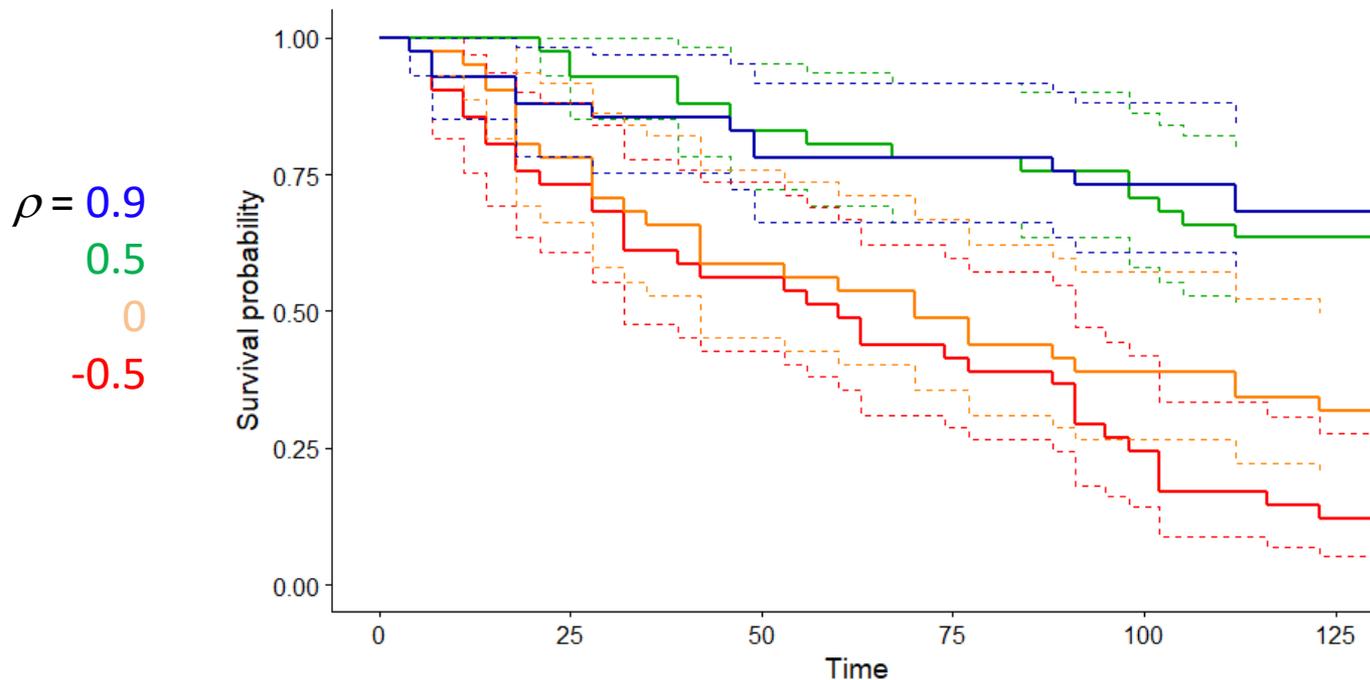
Stochastic population dynamics

- **Combined time series and treatments**
  Population size rapidly reaches **stationary distribution**, at a balance between randomly fluctuating growth and density-dependent regulation

$\rho =$ 0.9
0.5
0
-0.5
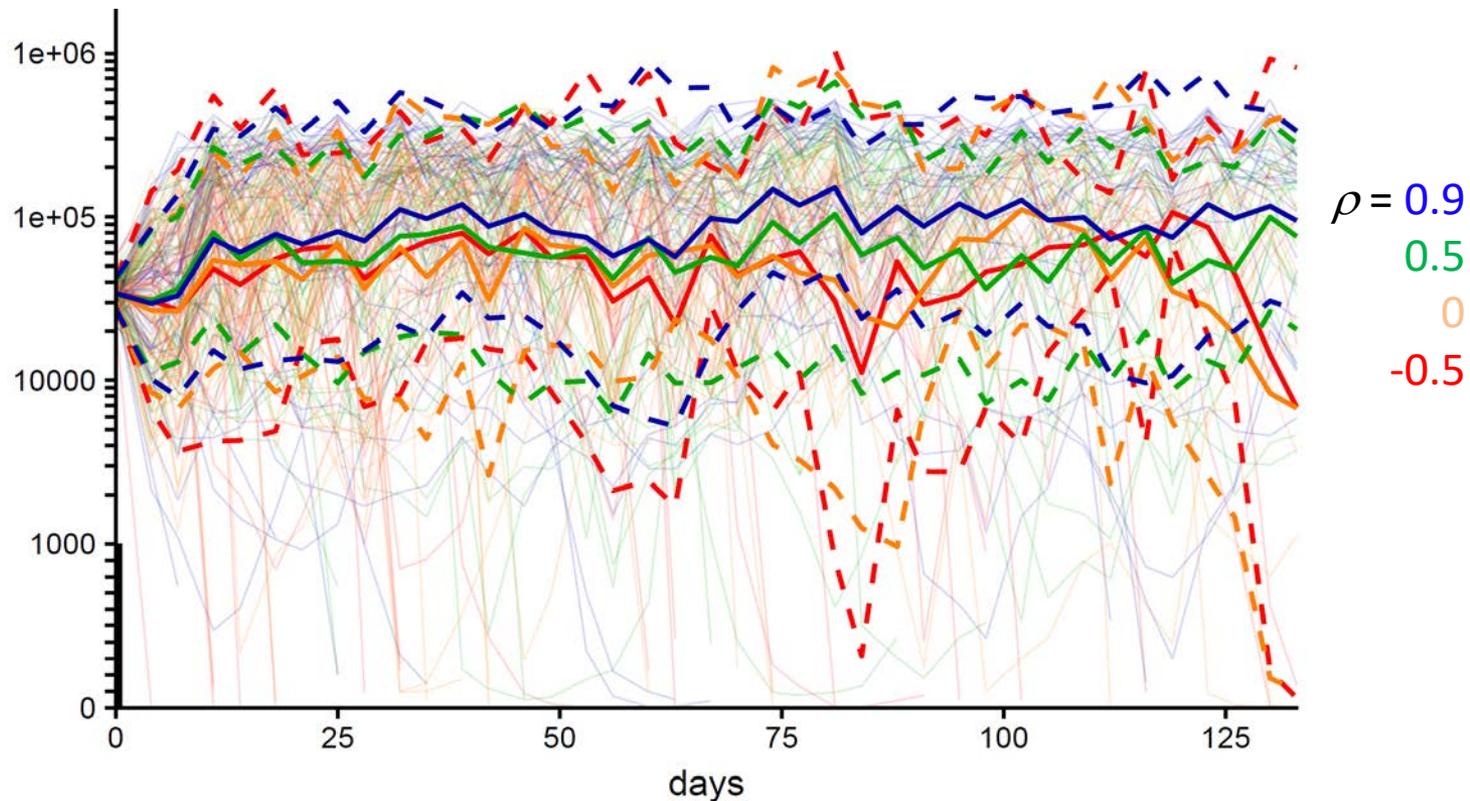
Extinction rate

- Population survival curve: fraction of populations persist up to t days

$\rho =$ 0.9   0.5   0   -0.5

- **Faster extinction under smaller environmental autocorrelation**
- No clear effect of genetic variance (mixtures vs single strains) overall

Distribution of population size

- Stationary distribution of ln*N* well described by a reverse gamma, more skewed in more autocorrelated environments …
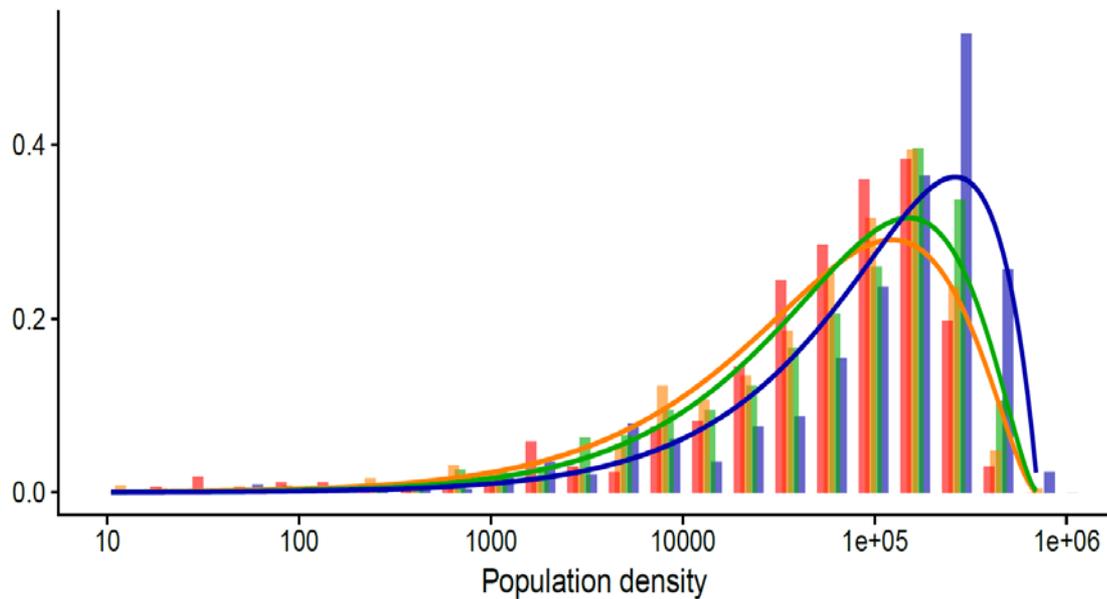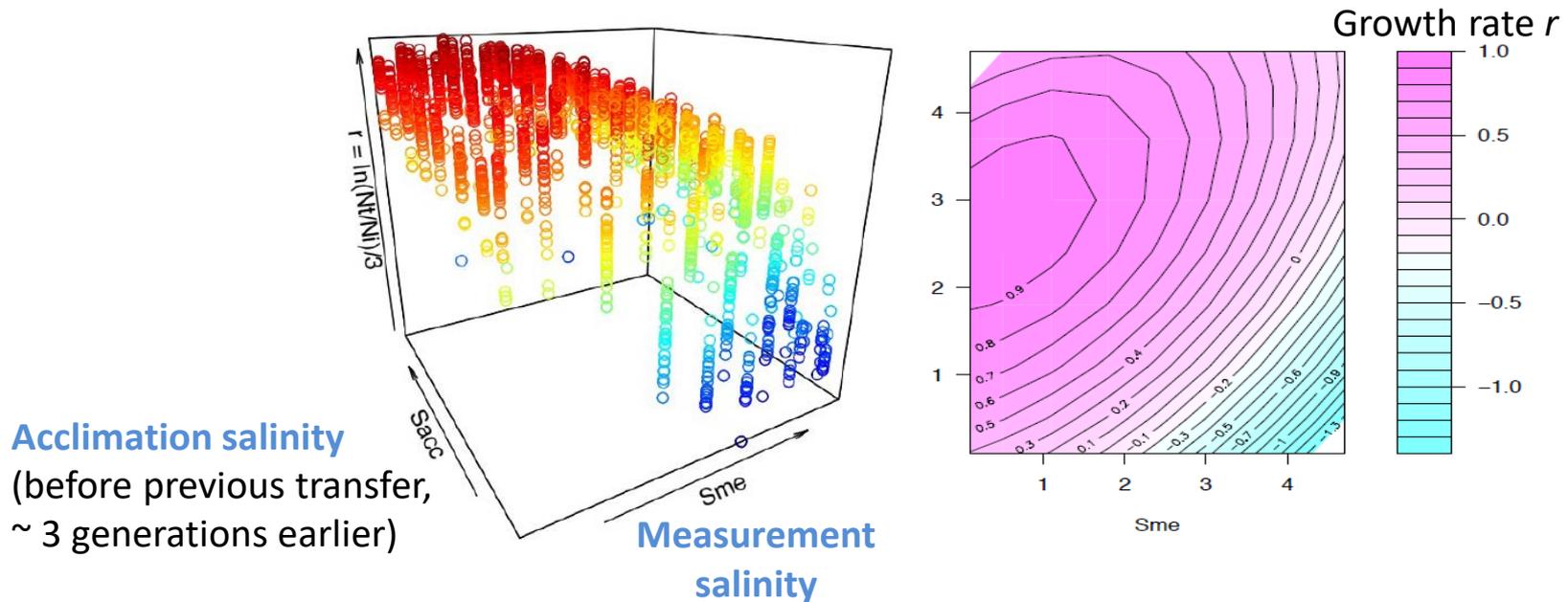
… as predicted by theory of fluctuating optimum[1]

1: Chevin, Cotto & Ashander (2017 Am Nat)
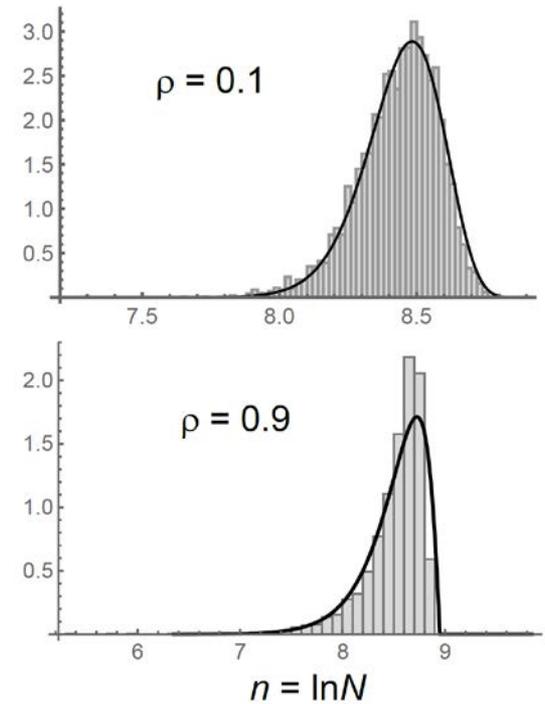
Trans-generational tolerance curves

- Measure **tolerance curve with environmental memory, mediated by transgenerational plasticity**

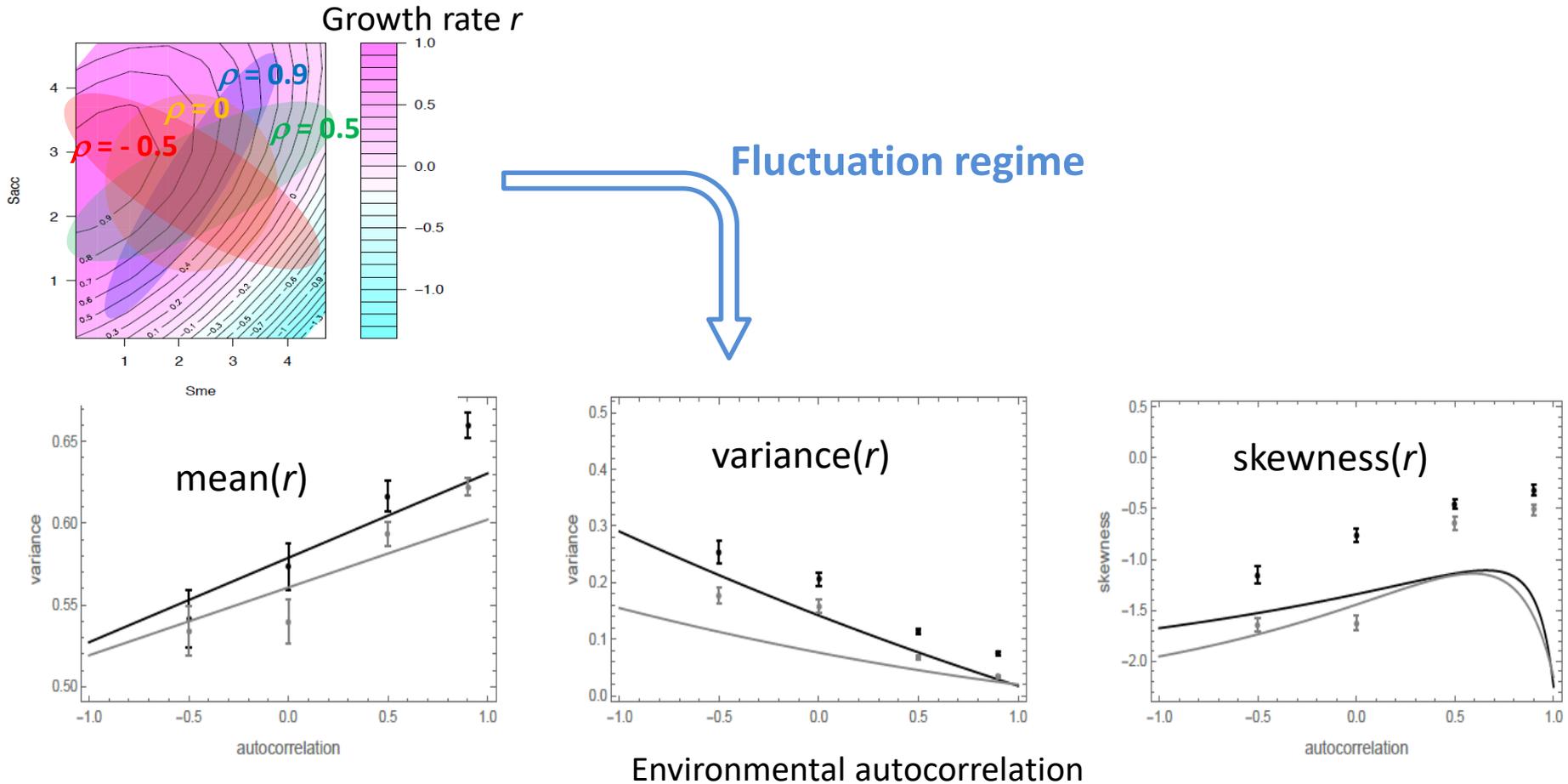**Acclimation salinity**
(before previous transfer,
~ 3 generations earlier)

Measurement salinity

Growth rate *r*

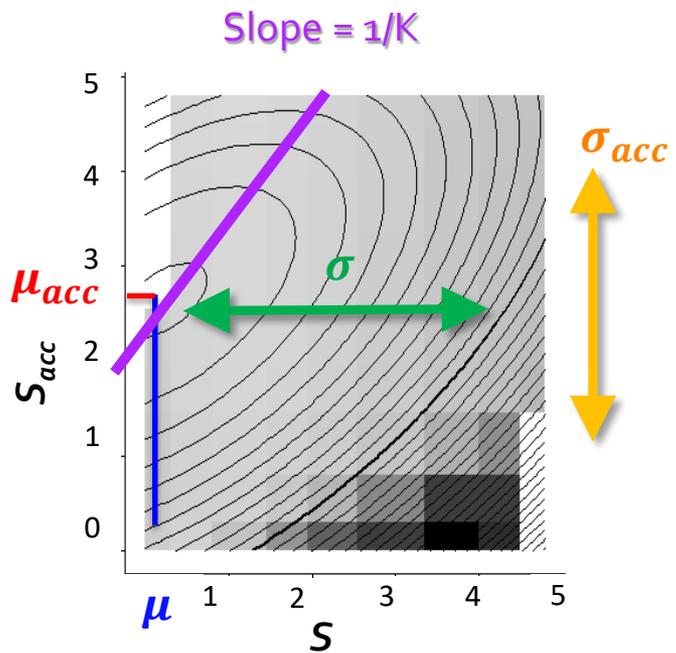- Lowest *r* in shifts from low to high salinity.

Trans-generational tolerance curves

- Combined with pattern of experimental fluctuations, this predicts well the effects of salinity on population growth

Growth rate *r*

$\rho = 0.9$

$\rho = 0$

$\rho = 0.5$

$\rho = -0.5$

Fluctuation regime

mean(*r*)

variance(*r*)

skewness(*r*)

Environmental autocorrelation

Evolutionary responses

- These tolerance curves have evolved in response to our stochastic treatments
- Little to no effect on current tolerance breadth σ,
  but effect on interaction K between past and current environment.

	Mean	Variance	Autocorrelation ρ	Predictability ρ^2
Rmax	-		+	-
K			-	+
μ_{acc}		-		-
μ		-	+	-
σ_{acc}				
σ	-			

Evolutionary responses

- Currently investigating **salinity reaction norms of underlying traits**:
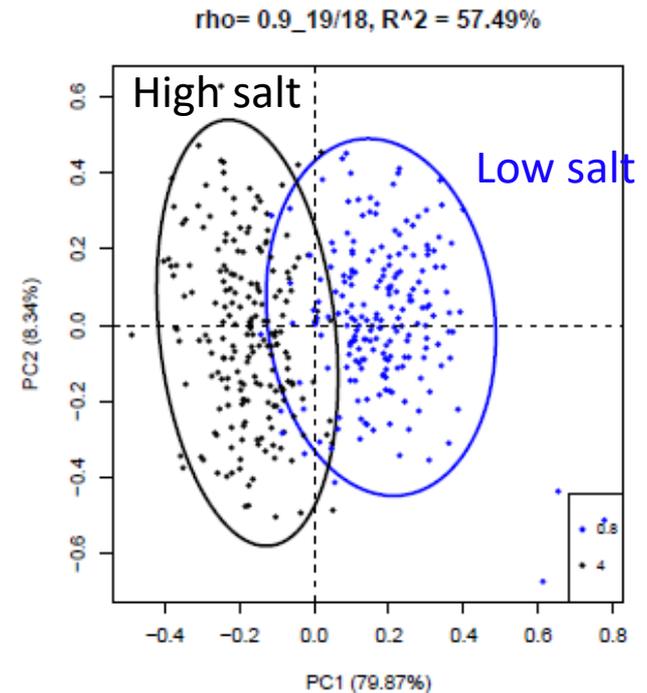
  - Cell morphology and content (Glycerol, carotene…)

  - Gene expression

  - Epigenetic marks

  - Recombination rate

  - …

rho= 0.9_19/18, R^2 = 57.49%

High salt

Low salt

PC2 (8.34%)

PC1 (79.87%)

Tracking genetic change

- Populations were stored at multiple time points in all surviving replicates, and DNA extracted.

- Sequencing markers (ITS) and candidate genes to track population genetic change in this experiment

→ Measure mean and variance of allele frequency change
- over unit time step (~infinitesimal diffusion parameters)
- on longer run.

Fluctuating selection:
from phenotype to genotype

- In such experiments with randomly changing environments, what kind of genetic change do we expect to observe?

- How does this depend on the genetic basis of adaptation to environmental stress:
  - Polygenic vs oligogenic response?
  - Gene affecting the trait or its plasticity?

II – Theory:
Genetic basis of adaptation to stochastic environment

Selection at QTL

- Covered here:
  What are the properties of **selective sweeps in randomly fluctuating environment**, for genes affecting phenotypic trait,
  possibly with background polygenic variation?
  How does this depend on pattern of environmental fluctuations
  (variance, autocorrelation…)?

- Not covered here:
  Adaptive maintenance of genetic/phenotypic variance for a trait[1]
  Maintenance of polymorphism in models with no explicit phenotype[2]
  Distribution of fitness effects in fluctuating environment[3]
  …

1: Bull (1987); Svardal et al (2015)
2: Dempster (1955), Gillespie (1991),…
3: Connallon & Clark (2015):

Moving optimum model

- Changing environment assumed to cause **moving optimum phenotype** for an ecologically important trait

- Optimum follows Gaussian autoregressive process, with mean $\bar{\theta}$, variance σ_θ^2 and autocorrelation ρ (over 1 generation).

Classic evolutionary assumption[1]...   ... with some empirical support[2]

$$W(z) = W_{\max} \exp\left(-\frac{(z-\theta_t)^2}{2\omega^2}\right)$$

Mean phenotype

Optimum phenotype (with CI)
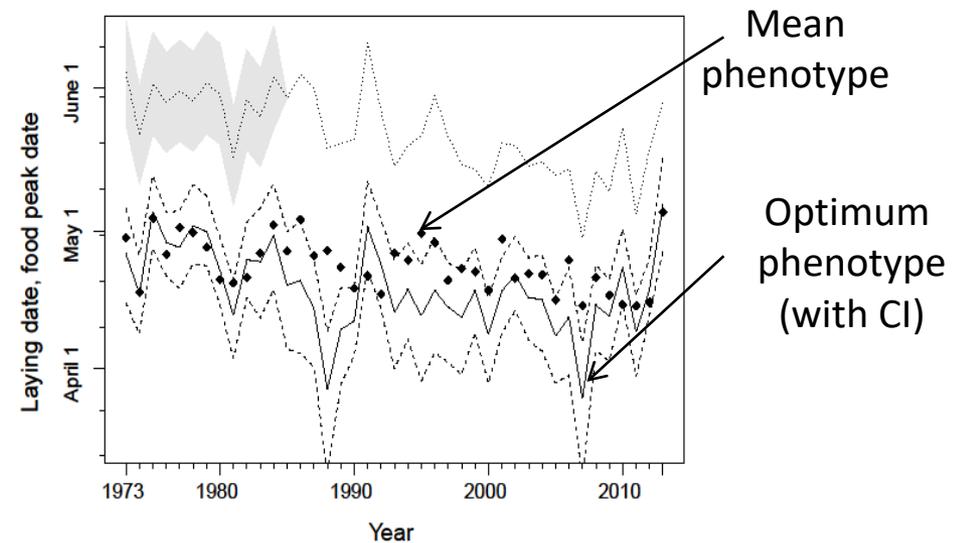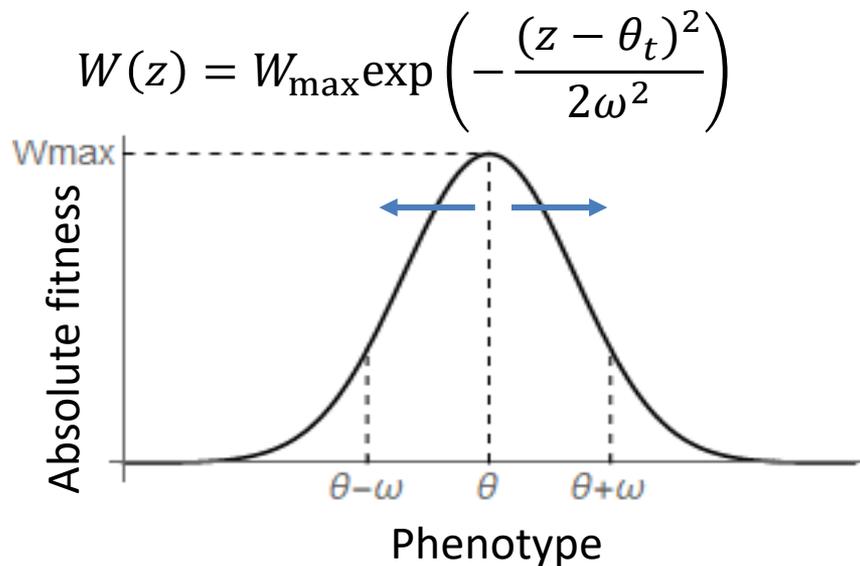
1 : Reviewed by Kopp & Matuszewski (2014 Evol Appl)
2: Chevin, Visser & Tufto (2015 Evolution)

"Major" QTL and polygenes

- Genetic model[1]

- **Haploid sexual** population (easily extended to diploid)

- **Major quantitative trait locus**: Bi-allelic A|a, frequencies $p|q$

  Additive effect a on mean trait

- **Polygenic background**: Unlinked variation at many unlinked loci causes normally distributed breeding values in background.

  Background mean m and genetic variance G

Assume linkage equilibrium, and background variance at equilibrium between stabilizing selection and mutation + recombination.

- Residual component of phenotypic variation with variance V_e.
  Total phenotypic variance $P = G + V_e$

1: modified from Lande (1983 Heredity)

"Major" QTL and polygenes

- Response to selection[1]:

Frequency at major gene: $\Delta p = pq \dfrac{\partial ln\bar{W}}{\partial p}$

Mean phenotype in the background: $\Delta m = G \dfrac{\partial ln\bar{W}}{\partial m}$

Genetic variance

x

Selection gradient

- Mean fitness is mixture of Gaussians

$$\bar{W} = W_{\max}\sqrt{S\omega^2}\left[p\exp\left(-\frac{S}{2}(m+a-\theta)^2\right) + q\exp\left(-\frac{S}{2}(m-\theta)^2\right)\right]$$

$S = \dfrac{1}{\omega^2+P}$ is the strength of stabilizing selection

1: modified from Lande (1983 Heredity)

"Major" QTL and polygenes

- Alternative description of selection:

$$\frac{p'}{q'} = \frac{p}{q} \frac{W_A}{W_a} = \frac{p}{q} \exp\left\{ -\frac{S}{2} [a^2 + 2a(m - \theta)] \right\}$$

→ **Genomic fitness epistasis** : selection at focal locus depends on background mean phenotype m, which may evolve in time because of all other polymorphic loci.

- Mutation favored if allows approaching optimum,
$0 < a < -2(m - \theta)$ (for $m \le \theta$)
→ Necessarily deleterious when background at optimum ($m = \theta$)

- In the long run:
$$\frac{p_t}{q_t} = \frac{p_0}{q_0} \exp\left\{ -\frac{S}{2} [a^2 t + 2a \sum_{i=0}^{t-1}(m_i - \theta_i)] \right\}$$
→ Cumulative influence of epistasis depends on summed background mismatch with optimum

Single locus dynamics
(no background genetic variance)

- First assume background m cannot evolve

- Then $\ln(p/q)$ is Gaussian, with mean:

$$\mathrm{E}\left\{\ln\left(\frac{p}{q}\right)\right\} = \ln\left(\frac{p_0}{q_0}\right) - \frac{S}{2}[a^2 + 2a\left(m - \bar{\theta}\right)]t = \ln\left(\frac{p_0}{q_0}\right) + \mathrm{E}(s)t$$

→ **Expected selection coefficient $\mathrm{E}(s)$ is constant, and unaffected by environmental fluctuations**
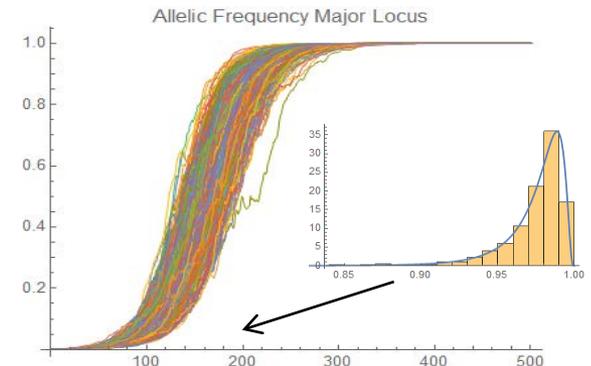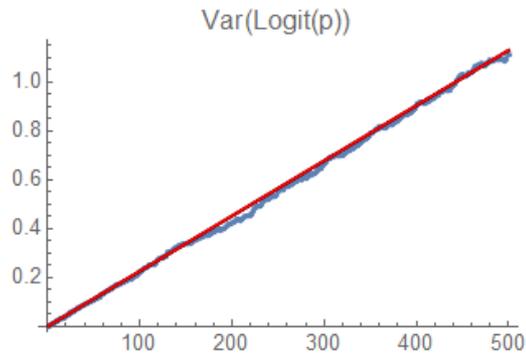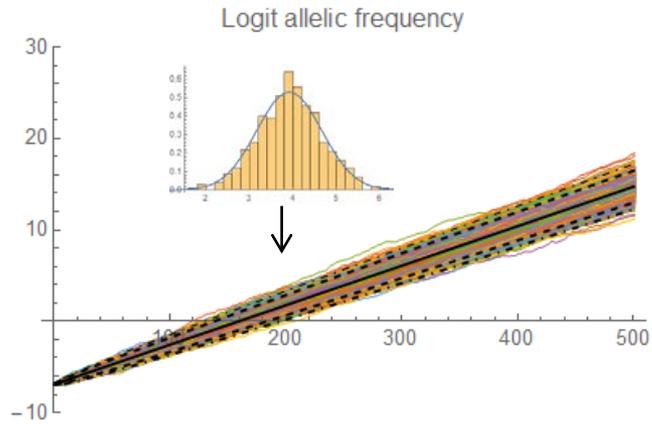
- The variance of $\ln(p/q)$ is:

$$\mathrm{var}\left(\ln\left(\frac{p}{q}\right)\right) = (Sa)^2\mathrm{var}(\sum_{i=0}^{t}\theta_i) \approx (Sa\sigma_\theta)^2\left[\frac{1+\rho}{1-\rho}t - 2\left(\frac{\rho}{1-\rho}\right)^2\right]$$

→ Variance increases close to linearly with time,
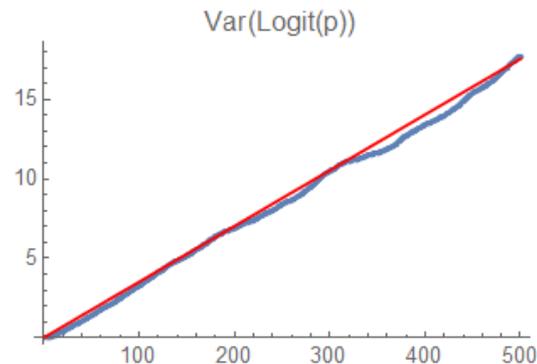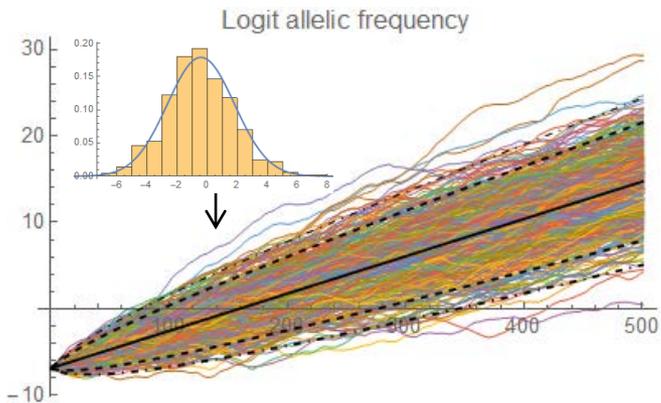**more rapidly with larger environmental aucotocorrelation**

Single locus dynamics
(no background genetic variance)

- Small autocorrelation of optimum ($\rho = 0.1$)

- Large autocorrelation of optimum ($\rho = 0.9$)
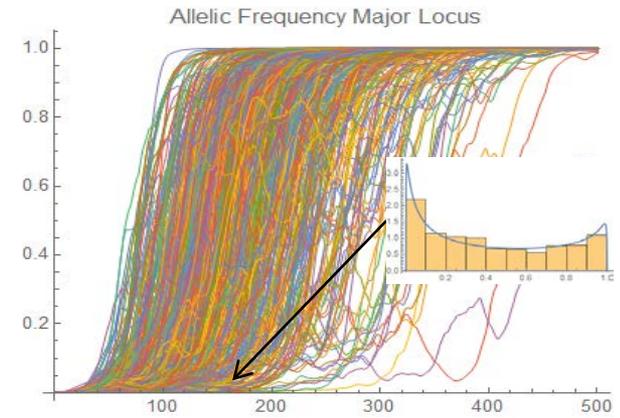
Evolving mean background trait

- Selection gradient on mean phenotype:

$$\beta = \frac{\partial ln\overline{W}}{\partial m} = -S(m + p'a - \theta) \;\; \rightarrow \text{mismatch of overall mean trait}$$

Dynamics of mean background m and frequency p at major locus are coupled.

- **In constant environment**:

One **unstable polymorphic equilibrium**:

$$p = \frac{1}{2}, m = \theta - \frac{a}{2}$$

Two **stable monomorphic equilibria**:

$p = 0, m = \theta$ $\qquad \rightarrow$ Loss of mutation

$p = 1, m = \theta - a$ $\qquad \rightarrow$ Fixation of mutation

Evolving mean background trait

- Close to unstable equilibrium, a slight change in initial conditions or parameter values affects which stable equilibrium is reached:
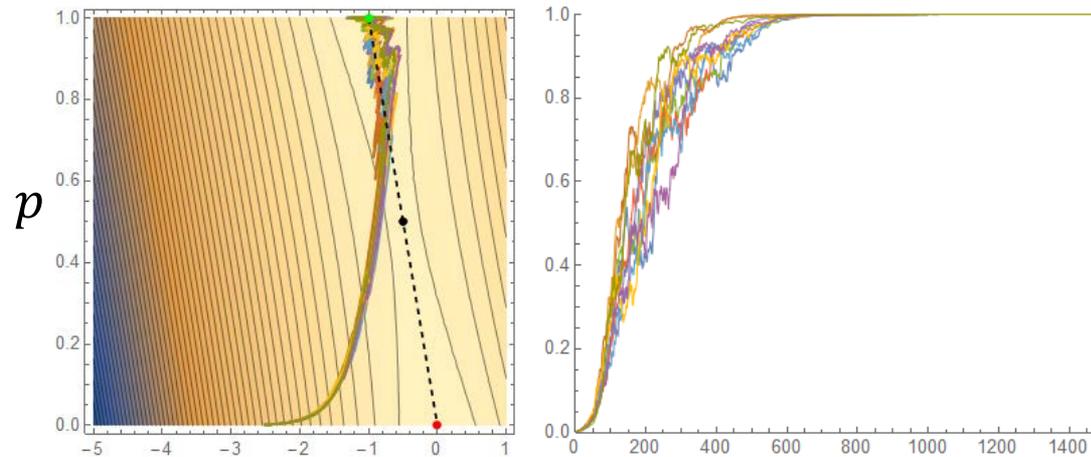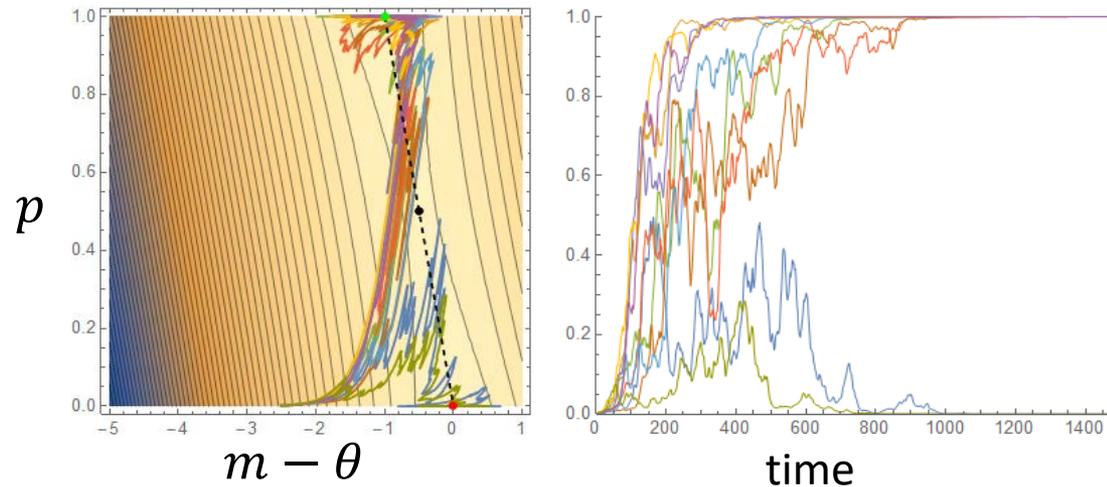

Dynamics of p

$p_0 = 2 * 10^{-3}$

$p_0 = 10^{-3}$

$m - \theta$

p

Adapted from Lande (1983 Heredity),
Chevin & Hospital (2008 Genetics)
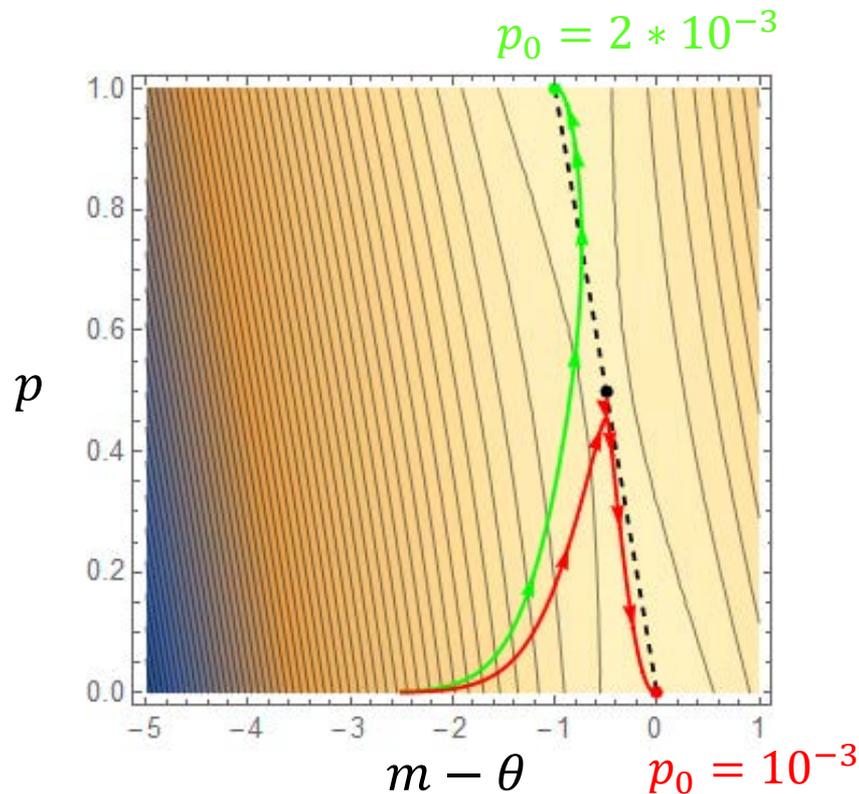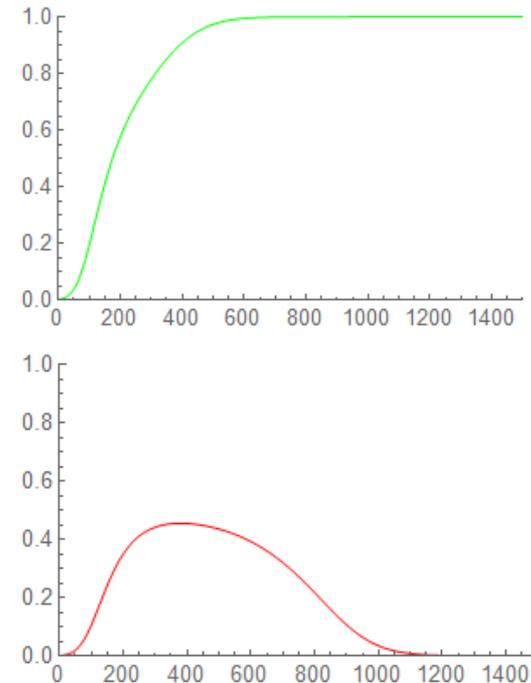
Bistability in stochastic environment

- If optimum fluctuates randomly, then higher environmental autocorrelation causes larger $\mathrm{var}(p)$, and more bistable genetic basis of adaptation.
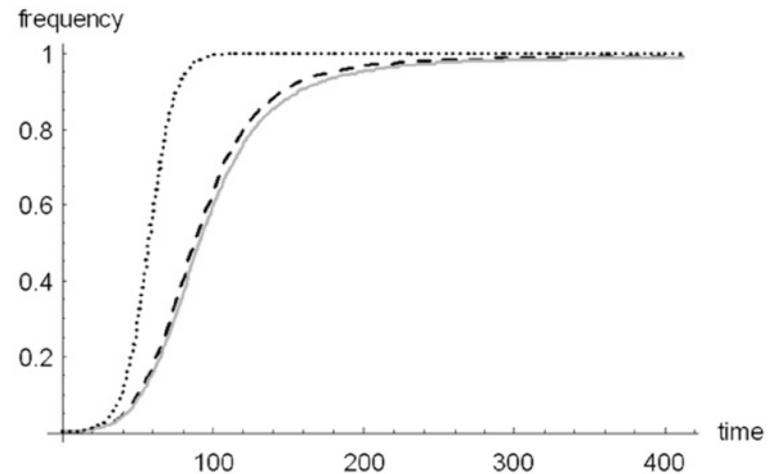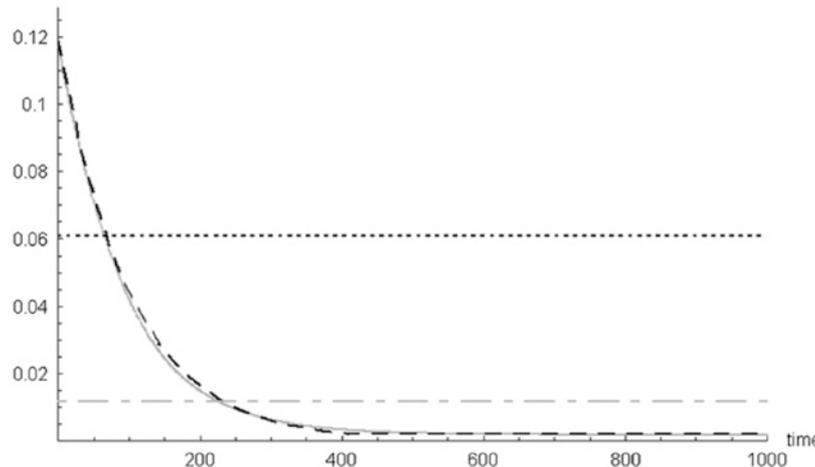
$\rho = 0{,}2$

$\rho = 0{,}8$

p

$m - \theta$

time

Weak effect approximation

- **Weak mutation effect:** $\beta = -S(m + p'a - \theta) \approx -S(m - \theta)$
  → Evolution of mean background can be analyzed first, then plugged into dynamics of QTL.

- In a constant environment, approach of mean background to optimum produces geometric decline of selection coefficient at major gene[1]

Selection coefficient

- This also applies to expected trajectory in fluctuating environment.

1: Chevin & Hospital (2008 Genetics)

Weak effect approximation

- **Applied to stochastic component of selection**:
  Neglect influence of frequency fluctuations at QTL on fluctuating selection on mean background trait.

- Stochastic distribution of mismatch x with optimum known from previous theory[1]:

$$\text{var}(m + p'a - \theta) \approx \sigma_x^2 = \frac{\sigma_\theta^2}{1 - SG/\ln(\rho)}$$

→ Smaller mismatch with higher genetic variance and autocorrelation, because better adaptive tracking of optimum

$$\text{Autocorr}(m + p'a - \theta) \approx \rho_x \approx \rho(1 - SG)$$

1: Lande & Shannon (1996 Evolution);
Chevin & Haller (2014 Evolution)

Weak effect approximation

- With background genetic variance, the variance of $\ln(p/q)$ becomes

$$\text{var}\left(\ln\left(\frac{p}{q}\right)\right) = \frac{(Sa\sigma_x)^2}{SG}\frac{1+\rho_x}{1-\rho_x}[1-\exp(-SGt)]$$

- Variance does not increase indefinitely, it plateaus at:

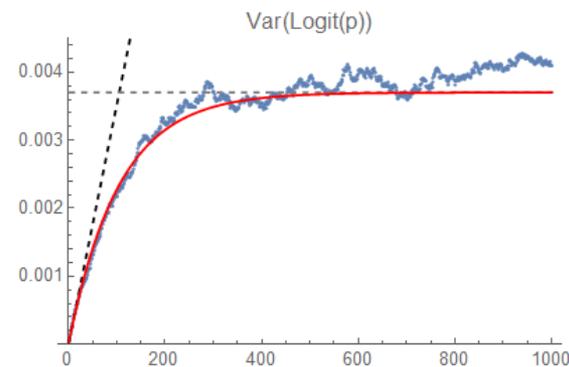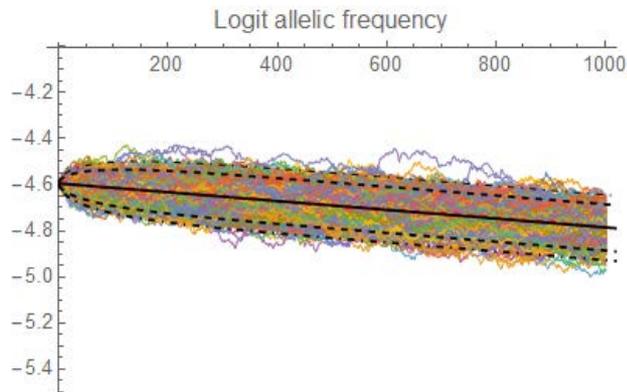$$\text{var}_{\text{max}}\left(\ln\left(\frac{p}{q}\right)\right) = \frac{(Sa\sigma_\theta)^2}{SG}\frac{1+\rho_x}{1-\rho_x}$$
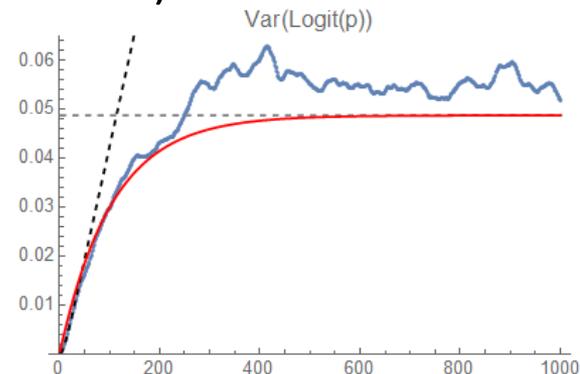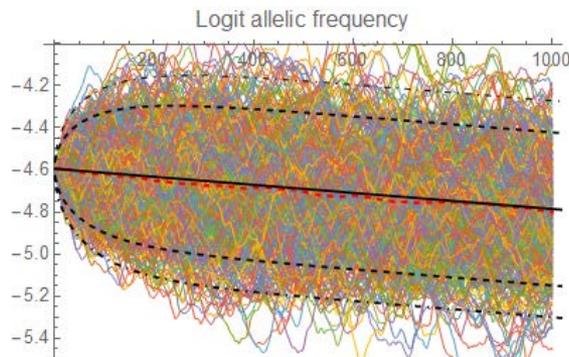
→ Higher background genetic variance G causes:
  - Smaller maximum variance of allelic frequencies
  - Faster approach to this maximum variance.

1: Lande & Shannon (1996 Evolution);
Chevin & Haller (2014 Evolution)

Background variance buffers fluctuations at major gene

- Small autocorrelation of optimum ($\rho = 0.1$)

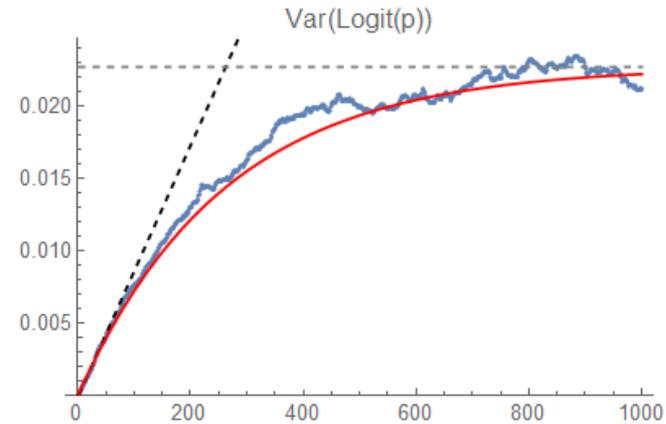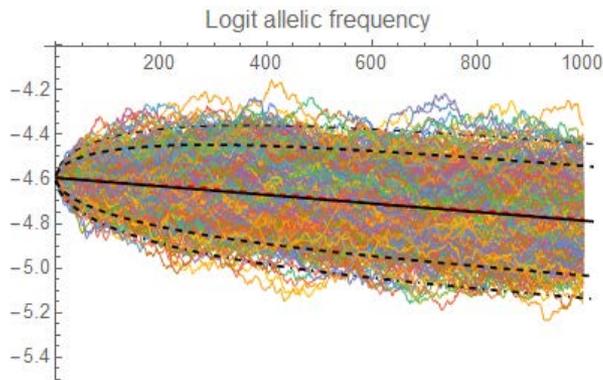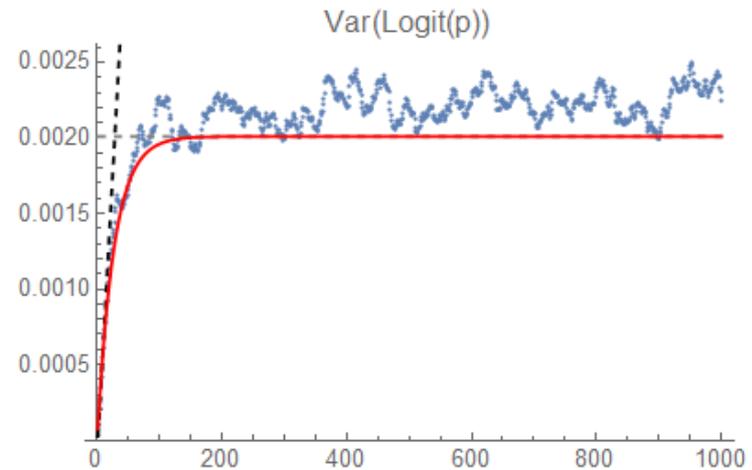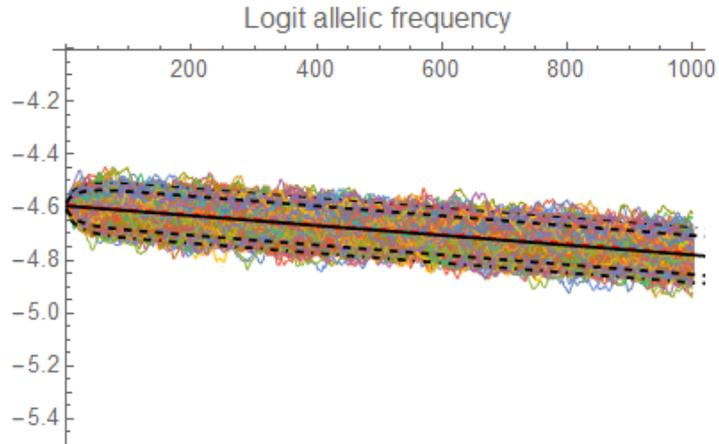- Large autocorrelation of optimum ($\rho = 0.9$)

Background variance buffers fluctuations at major gene

- Small genetic variance ($G = 0.1$)

- Large genetic variance ($G = 1$)

Plasticity QTL

QTL for phenotypic plasticity

- Allelic effect with environment-dependent component: $a + b\,\varepsilon_d$
  Slope b quantifies effect on phenotypic plasticity.

- Environment of development ε_d partially predicts environment of selection ε_s affecting optimum: $\theta = B\varepsilon_s$ (with $\mathrm{E}(\theta) = \mathrm{E}(\varepsilon_d) = \mathrm{E}(\varepsilon_s) = 0$)
  Regression of ε_s on ε_d has slope κ = **predictability of selection**

- Focus on stationary fluctuations, no major shift in optimum.
  → Plasticity only selected through its influence on the stochastic variance of phenotypic mismatch.

Pure plasticity gene
- No background variation -

- Assume mutation at QTL has no net phenotypic effect when averaged across environments: $a = 0, b \neq 0$.
  Also no background genetic variance for the trait.

- **Expected frequency change:**
$$\mathrm{E}\left\{\ln\left(\frac{p'q}{q'p}\right)\right\} = -\frac{S\sigma_\tilde{\varepsilon}^2}{2}\, b(b - 2B\kappa)$$
The expected selection coefficient depends on **predictability κ between development and selection**

  → Plasticity with slope $0 \leq b \leq 2B\kappa$ is favored.
  Selection is maximal for $b = \tilde{b} = B\kappa$.

- Autocorrelation ρ of environment across generations has no effect *per se* on mean selection coefficient, only predictability of selection κ matters

Pure plasticity gene
- No background variation -

- **Variance of allelic frequency**

$$\mathrm{var}\left\{\ln\left(\frac{p'q}{q'p}\right)\right\} = \frac{S^2 b^2 \sigma_\varepsilon^4}{4}\left[4B^2\left(1+\kappa^2\right) + 2b(b - 4B\kappa)\right]$$

- Among values of plasticity that are adaptive on average ($0 \leq b \leq 2B\kappa$), **larger ones cause larger variance of frequency change**, even if same effect on expected selection coefficient.
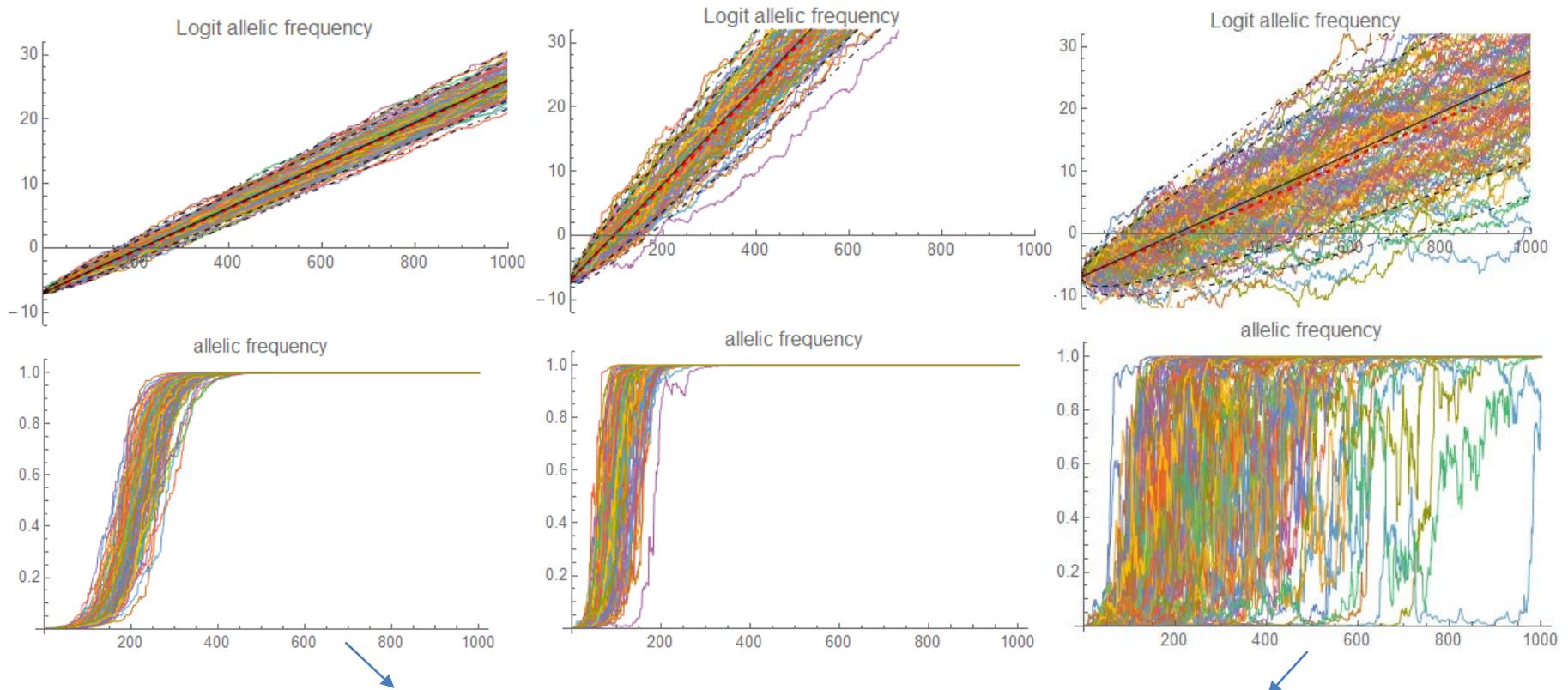
Pure plasticity gene
- No background variation -

- Example with predictability of selection $\kappa = 0.7$

$b = 0{,}25\tilde{b}$ (undershoot) $\qquad\qquad b = \tilde{b} \qquad\qquad b = 1{,}75\tilde{b}$ (overshoot)

**Same expected trajectory, different stochastic variances**

Pure plasticity gene
- WITH background genetic variation -

- Adaptive tracking of the optimum by the mean background phenotype reduces strength of selection on plasticity[1]:

New optimum plasticity $\tilde{b} \approx B \left(\kappa - \dfrac{SG}{SG - \ln(\rho)} \right)$ → Regression slope of mean background on environment of development

Logit allelic frequency

$$b = \tilde{b}$$

Expected *s* without background variance

Expected *s* with background variance
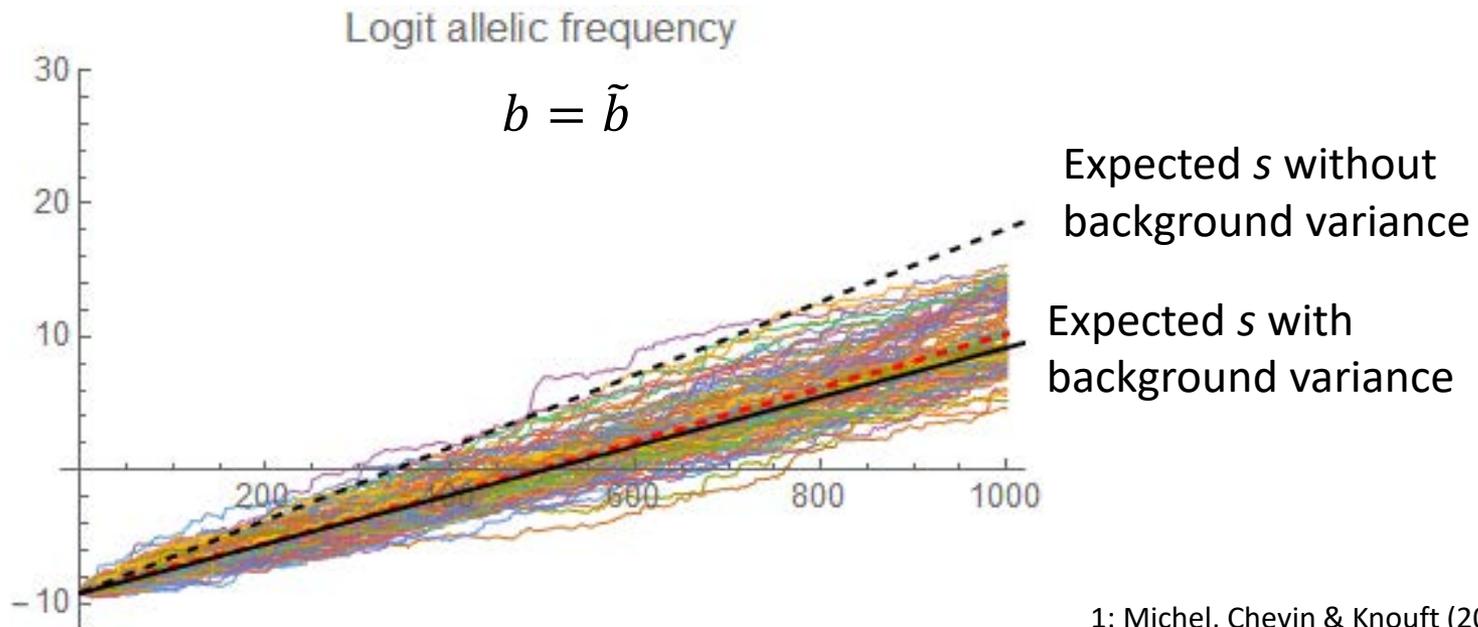
1: Michel, Chevin & Knouft (2014 Evolution)
Tufto (2015 Evolution)

Plasticity gene with pleiotropic effect

- Mutation at QTL biases the phenotype in all environments: $a \neq 0, b \neq 0$

- Expected selection coefficient has an additional term, which is deleterious in stationary environment, as it displaces mean phenotype from average optimum .

- Still spreads if advantage of plasticity overcomes pleiotropic cost , $c = -\frac{S}{2}a^2$.
  Expected background compensates by evolving away from average optimum

allelic frequency

Background mean phenotype

$-a$
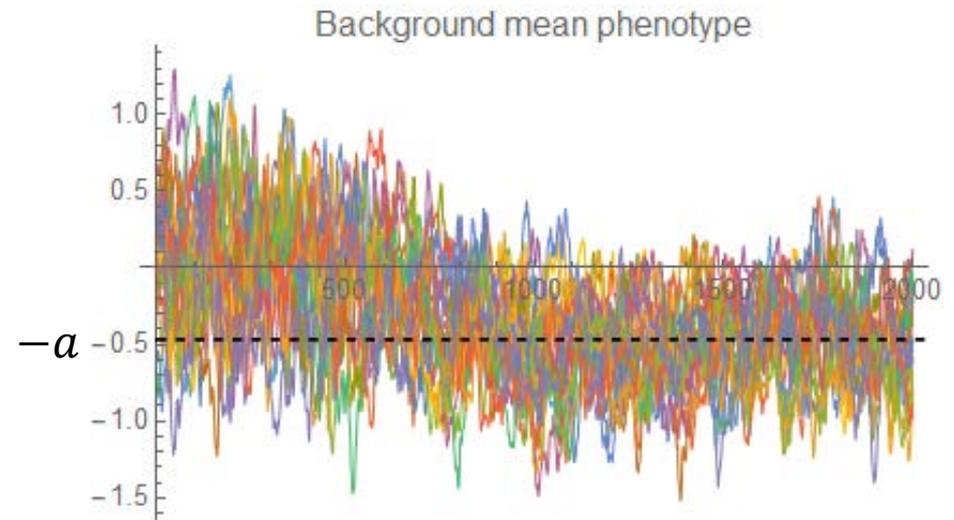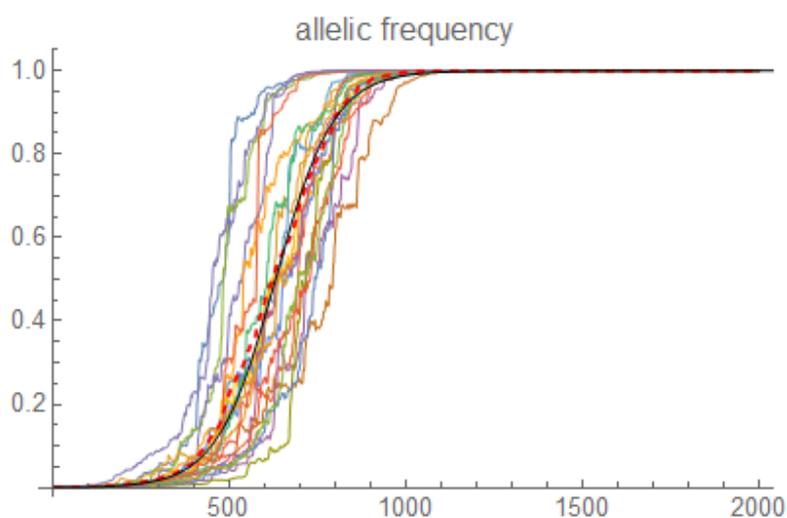
Ongoing/future extensions

- Evolving plasticity in the background
  → Competition between major and minor genes towards optimal plasticity

- Include genetic drift: additional source of stochasticity

- Contrast to individual-based simulations, notably for genetic variance in autocorrelated env[1]

- More explicit model relating selection to tolerance curves to match our experiment

1: Burger & Gimelfarb (2002 Genet Res)

Summary

Experiments

- Models with moving optimum phenotype/environment **correctly predict population fluctuations** in stochastic environment

- Experimental evolution of **transgenerational acclimation**, but **not tolerance breadth to current environment**

Theory

- Temporal autocorrelation **increases variance of allelic frequency**

- **Background genetic variance limits fluctuations** at focal QTL

- **QTL for plasticity can sweep despite pleiotropic cost** in average environment.

Thanks!

StG FluctEvol

Realized environmental time series

Autocorrelation
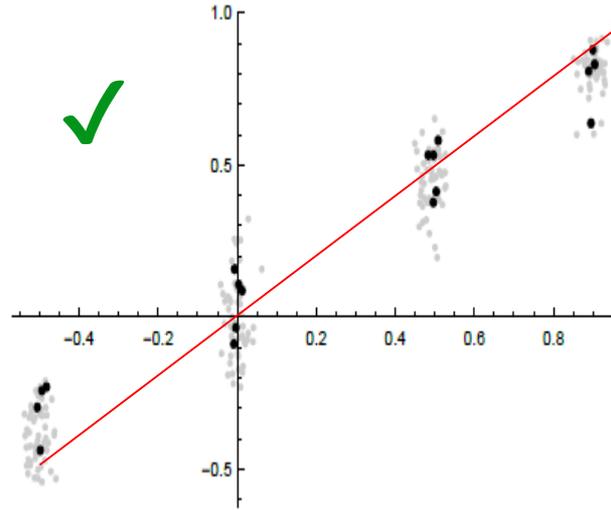
Variance
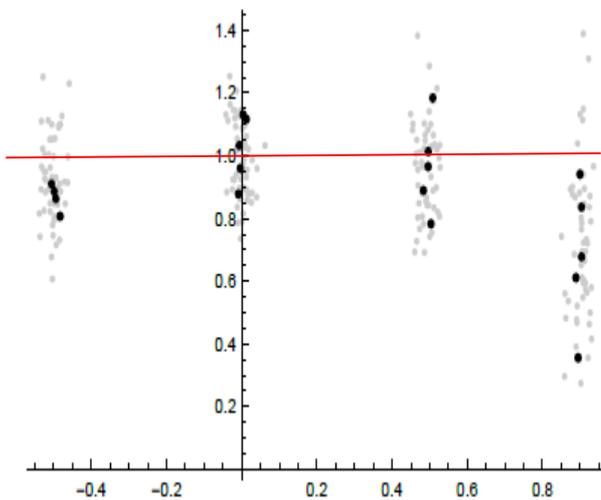
} Truncation reduces variance in highly correlated environment

Mean
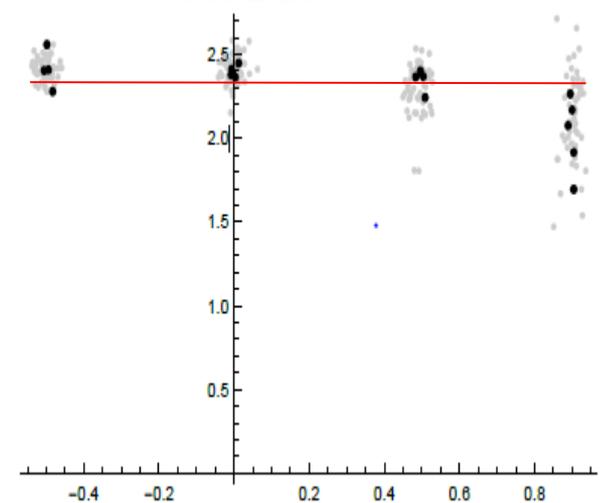
Stochastic population dynamics

- **Individual time series**
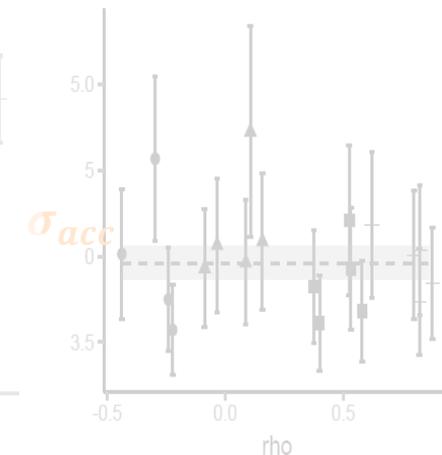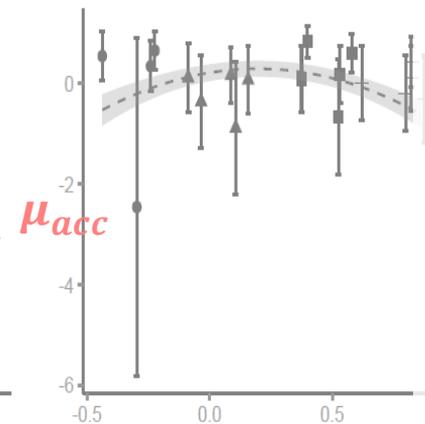 Combination of 3 measurement types allows precise estimates of N

Strain C, $\rho = 0.9$

Strain B, $\rho = 0$
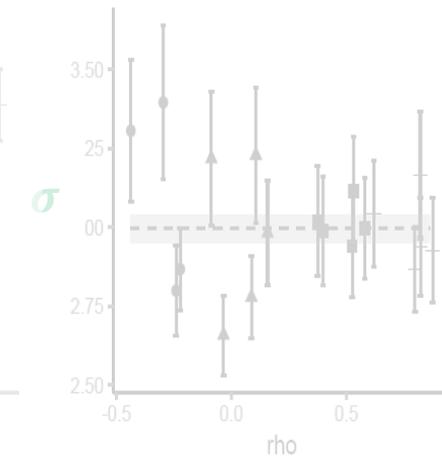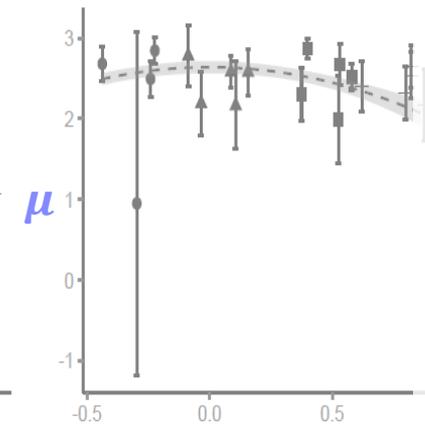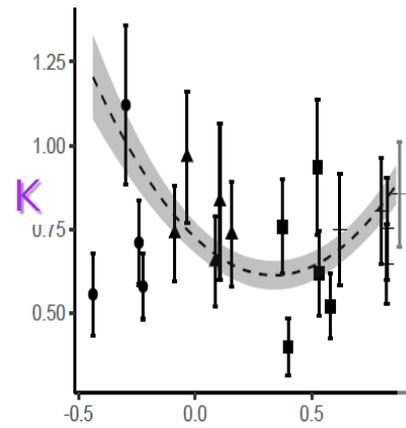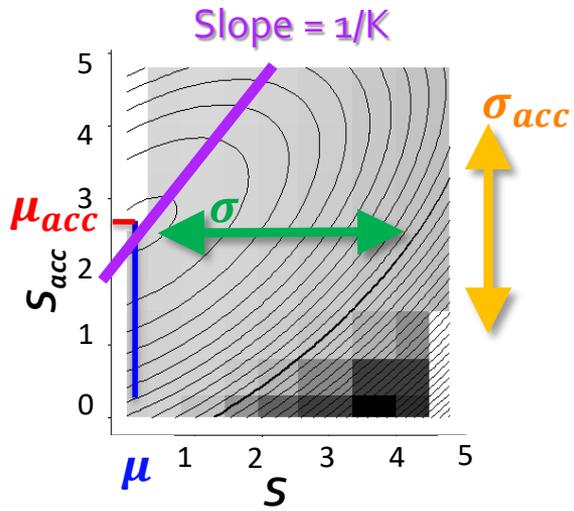
Strain A, $\rho = -0.5$
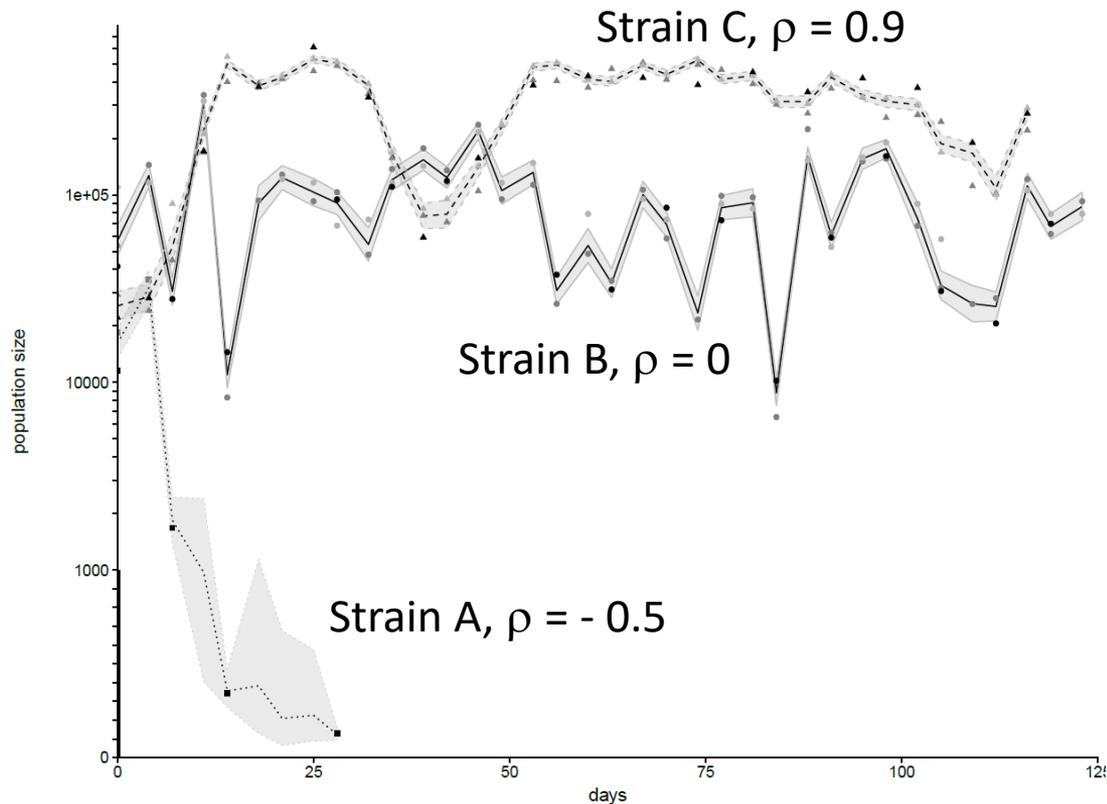
Experimental evolution
of trans-generational tolerance curves

- These tolerance curves have evolved in response to our stochastic treatments
- Little to no effect on tolerance breadth **σ**, but effect on interaction *K* between past and current environment.

	Mean	Variance	ρ Autocorrelation	ρ^2 Predictability
Rmax	-		+	-
K			-	+
μ_{acc}		-		-
μ		-	+	-
σ_{acc}				
σ	-			

Experimental evolution
of trans-generational tolerance curves
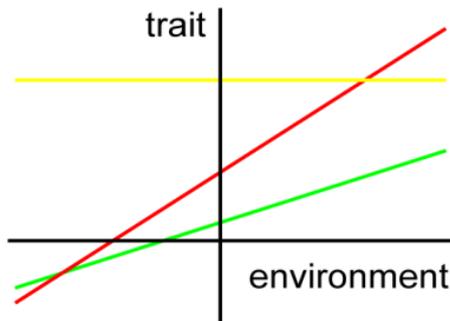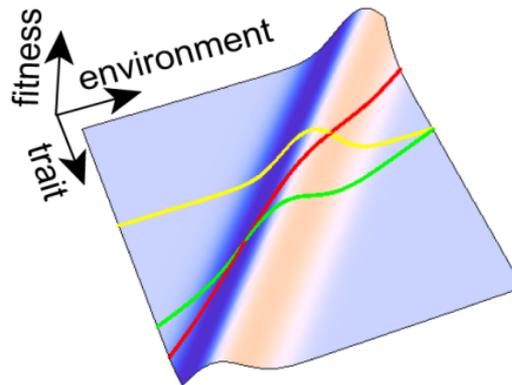
Plasticity, evolution and demography

- Phenotypic plasticity of traits under selection underlies environmental tolerance[1]

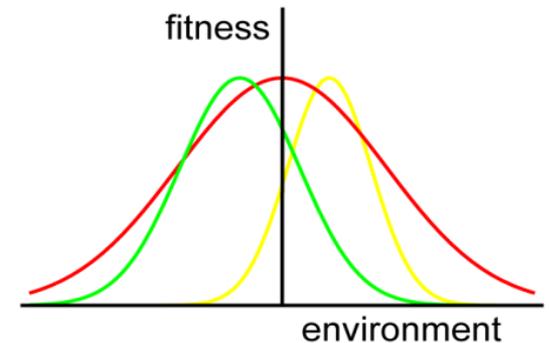- Fluctuating environments alter plastic responses, phenotype-fitness relationship (selection), and rates of evolution

- This largely drives populations dynamic fluctuations in a randomly changing environment

1: Chevin, Lande & Mace (2010 PLoS Biol)
Lande (2014 JEB)

Weak effect approximation

- **Weak mutation effect:** $\beta = -S(m + p'a - \theta) \approx -S(m - \theta)$

- Relates to curvature of fitness landscape: $\dfrac{\partial \beta}{\partial p} = 0 \Leftrightarrow \dfrac{\partial^2 \ln \overline{W}}{\partial m \partial p} = 0$

Large $a = -m_0/2$

Small $a = -m_0/5$