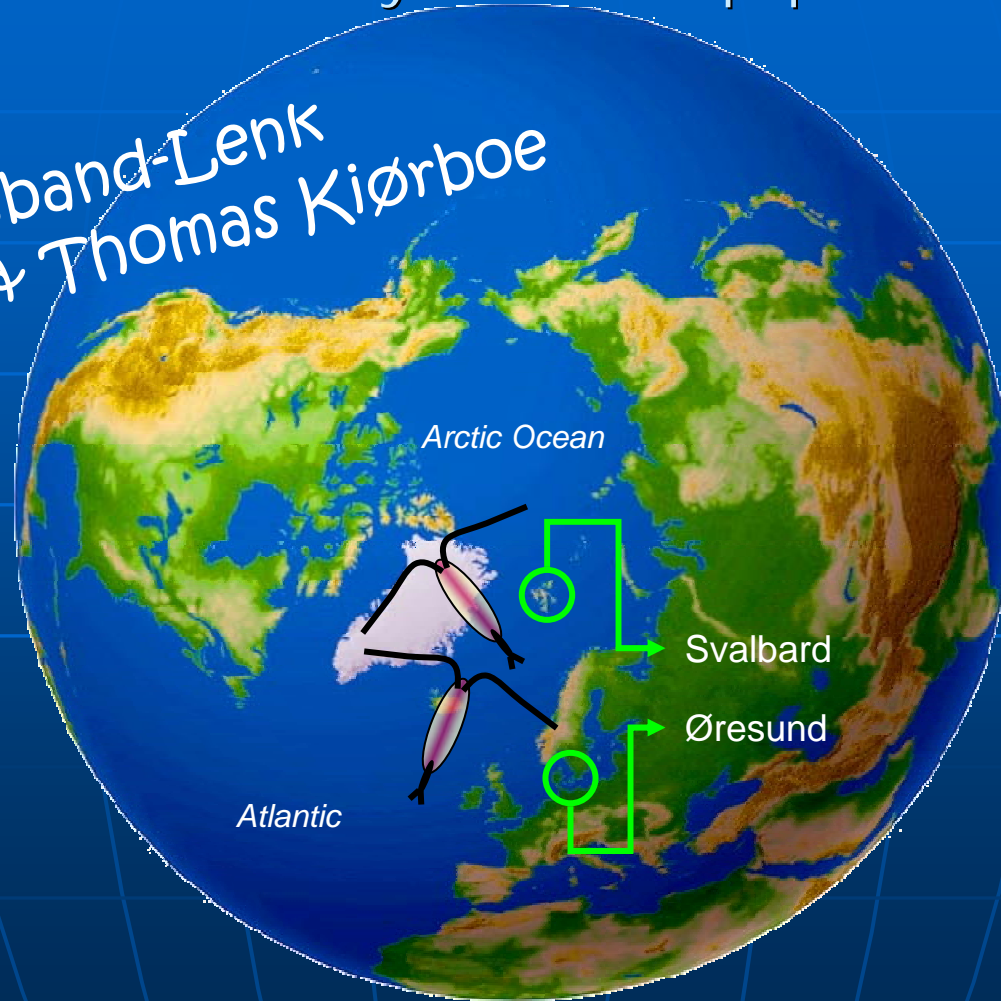


Phenotypic variability in quantitative life history traits

Does individual variability matter for population dynamics?

Claudia Halsband-Lenk
Ketil Eiane & Thomas Kiørboe



Background

- populations **evolve** over time
- due to **variations in vital rates** (birth, growth, development, death)
 - **population dynamics** (ecological scale)
 - **life history evolution** (long term)
- To quantify vital rates or co-varying traits is **difficult** in large plankton populations
- Limited understanding which **processes control population change** over time

Aims

- Contribute to the development of **individual based ecology** both **empirically and theoretically**
- approach **classical questions in population ecology** such as population **persistence and resilience**.
- Provide **quantitative information** about the **level of individual variability** in life-history traits within and between populations
- Provide indirect information on the **likelihood and strength of the genetic basis** for such differences
- Provide a sensible **starting point for later studies in quantitative genetics and adaptation/evolution** in large populations.

Methods

1. Intra-population variability
2. Comparison field \Leftrightarrow lab
3. Artificial selection
4. Comparison Arctic \Leftrightarrow Boreal
5. IBM

Methods

- suitable traits:
 - easy to **measure** (high n)
 - correlating with **vital rates** (e.g. growth)
 - **independent** of short term environmental variability
 - body size
 - stage duration/generation time
- comparison of populations from very different environments
 - **boreal** versus **arctic** → Øresund/Svalbard
 - potentially different **selective forces**

Methods

- collaboration



Ketil Eiane



Thomas Kiørboe



The University Centre in Svalbard

www.unis.no

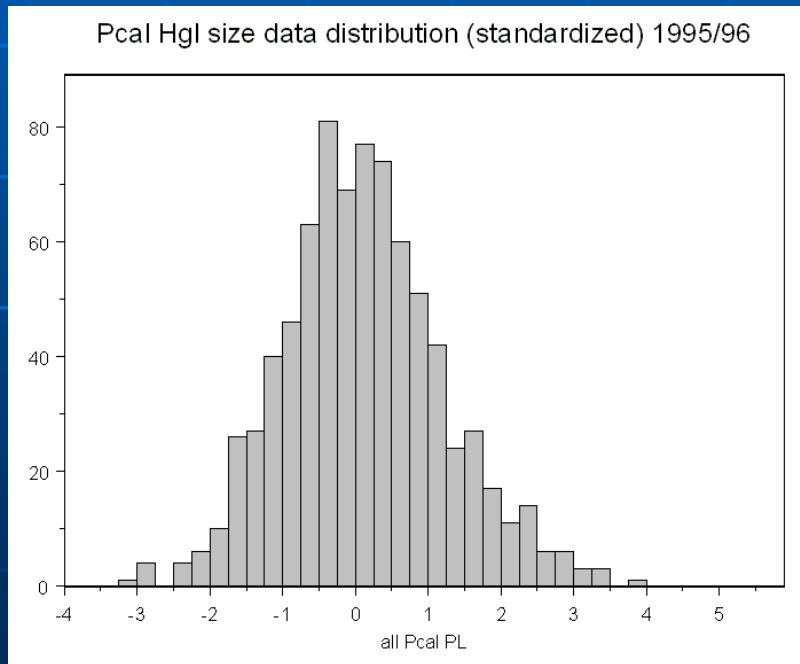
The logo for DFU, consisting of a green vertical bar to the left of the letters 'DFU' in a bold, serif font.

Danmarks Fiskeriundersøgelser

www.difres.dk

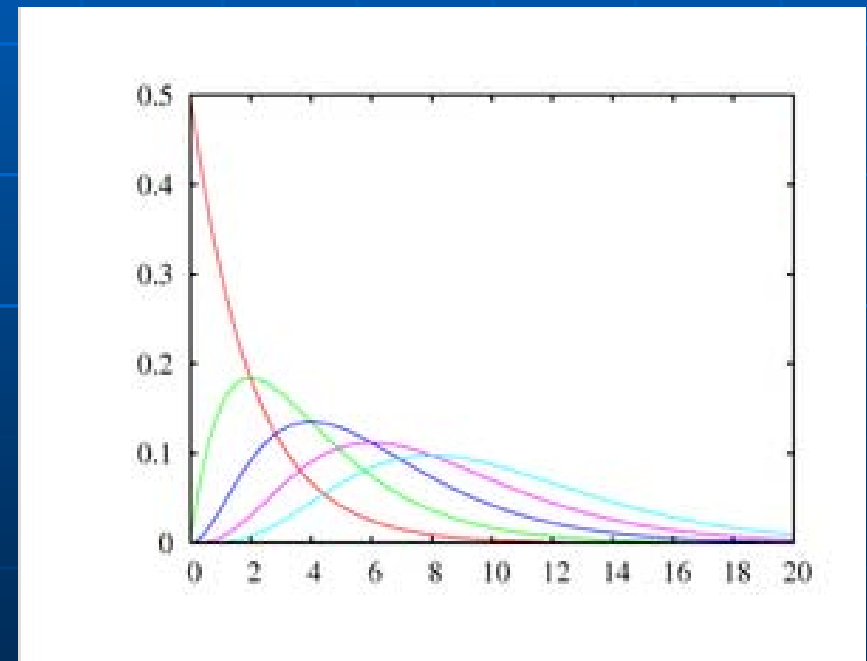
What level of variability can be expected?

Body size



symmetric

Development time



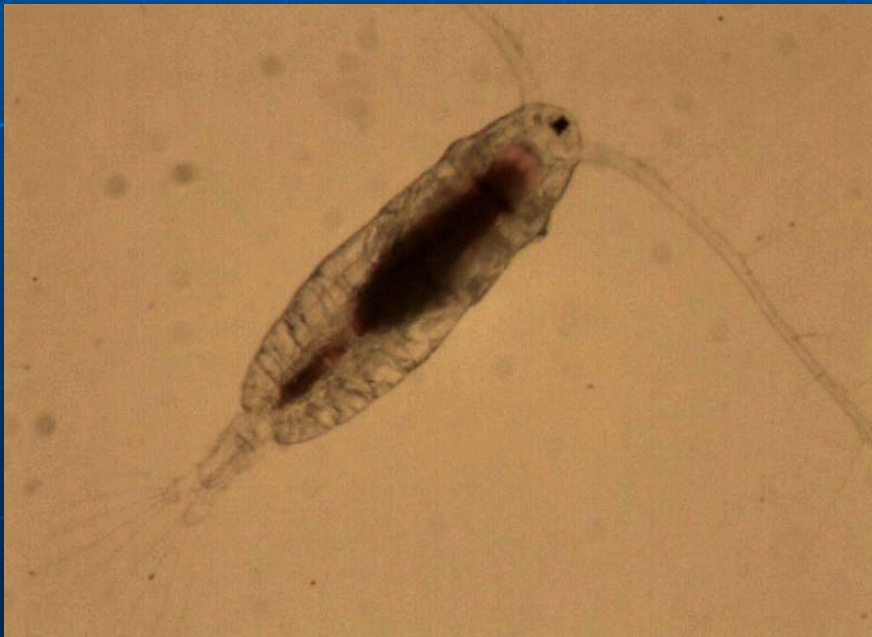
asymmetric

Model organisms

Acartia spp. (*A. tonsa*/*A. longiremis*)

↙ ↘
baltic arctic

- very common in coastal areas
- short generation times ~ a month (T-dependent!)
- relatively easy to culture (food: *Rhodomonas* sp.)



Sampling...

... in the Baltic is straightforward.



Sampling...

In the high Arctic however, one meets certain obstacles...



Sampling...

In the high Arctic however, one meets certain obstacles...



Sampling...

In the high Arctic however, one meets certain obstacles...



Sampling...

Methods of travel are rather unusual...



Sampling...

Methods of travel are rather unusual...



Sampling...

Methods of travel are rather unusual...



Sampling...

...as are the sampling procedures...



Sampling...

...as are the sampling procedures...



Sampling...

...as are the sampling procedures...

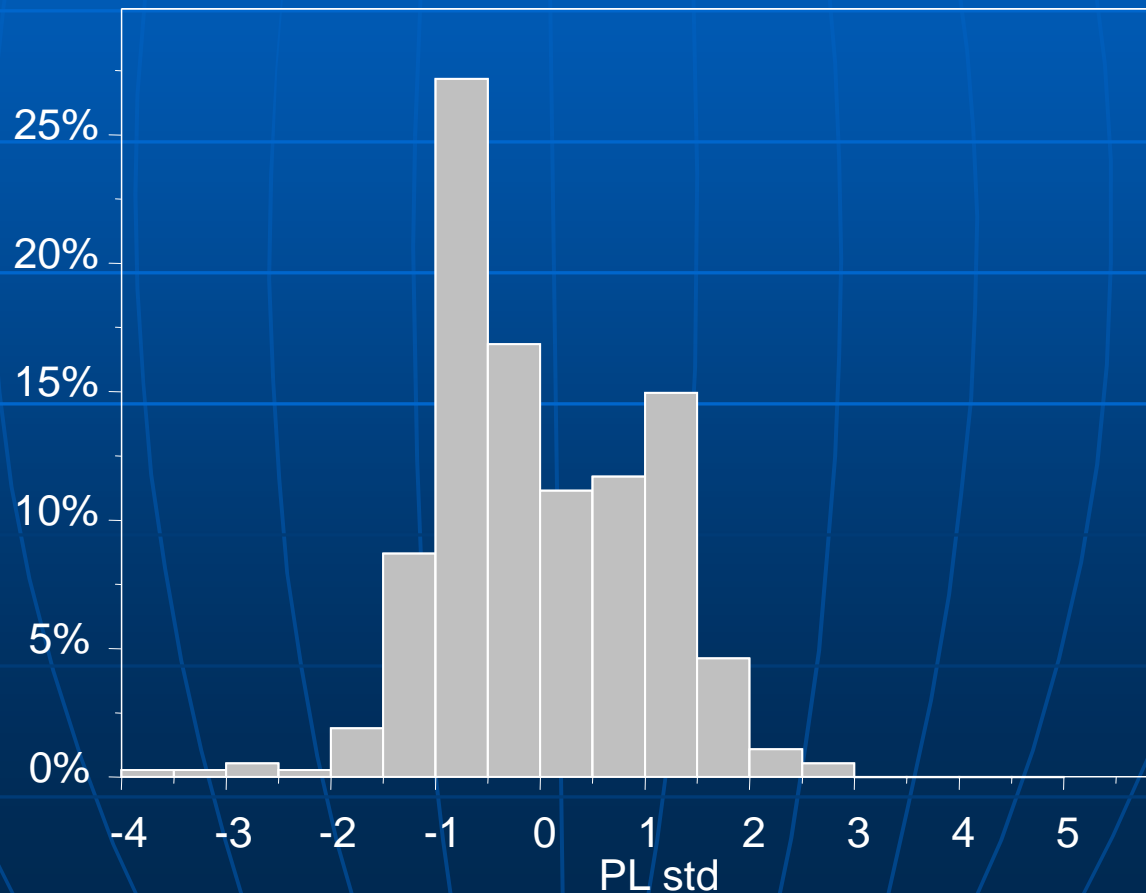


1. Intra-population comparison

- variability within populations
 - *Acartia* sp. reared under controlled conditions
 - range of body sizes
 - range of development times
 - differences of siblings from known females

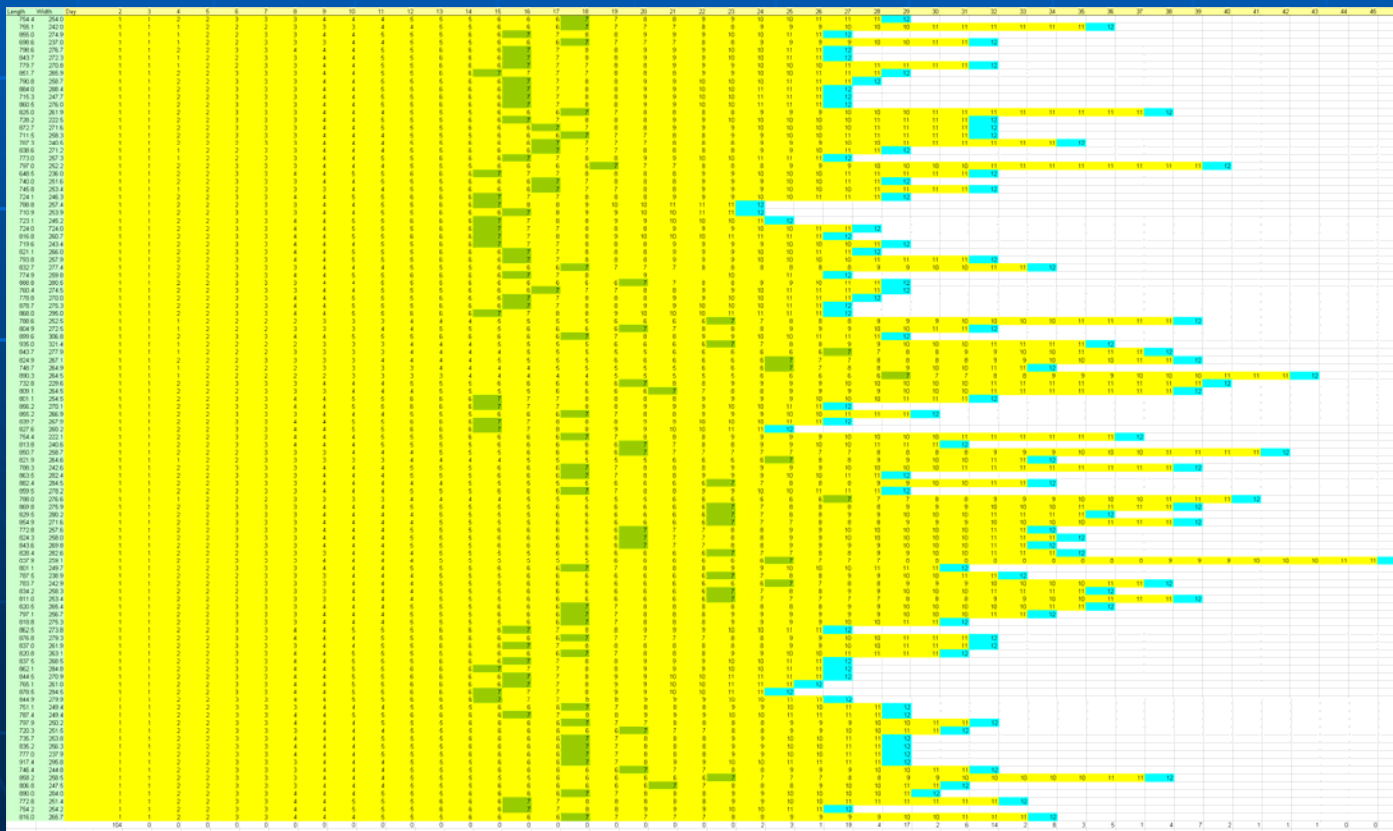
1. Intra-population comparison

body size *Acartia tonsa*_{Øresund}



1. Intra-population comparison

individual development *Acartia tonsa*_{DFU}



172 individuals
from 15 ♀♀

green: reached
stage C1

blue: reached
adulthood

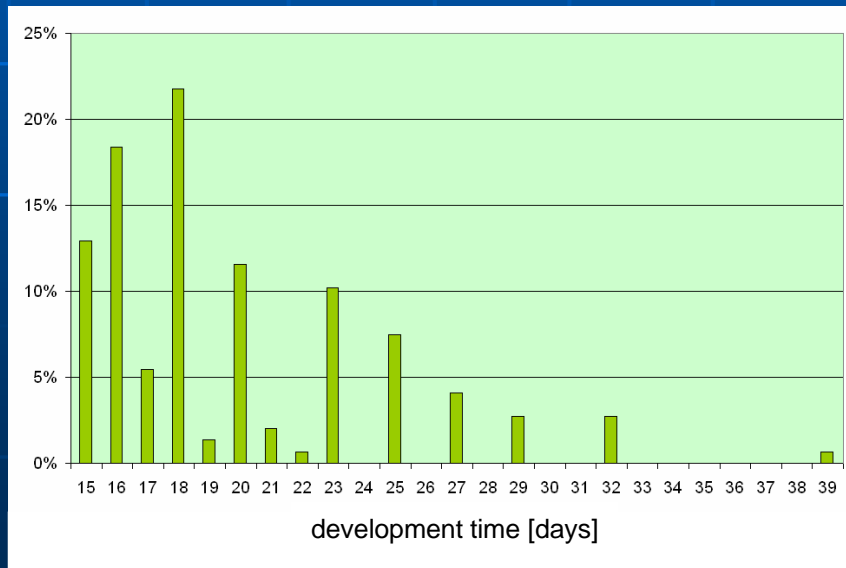
67 died
(=38.2%)

sex ratio 2:1

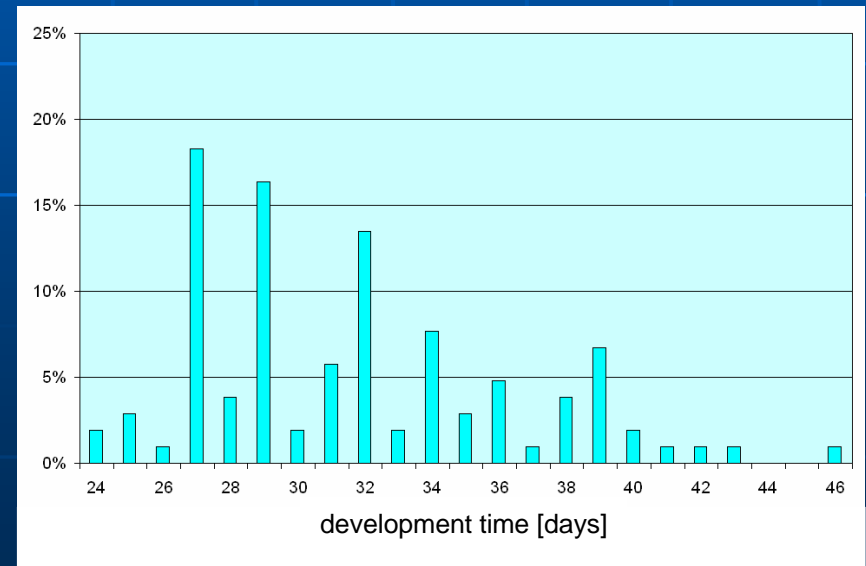
1. Intra-population comparison

individual development *Acartia tonsa*_{DFU}

to C1



to adult



2. Comparison Field-Lab

- variability within populations
 - compare lab-reared *Acartia tonsa* with their relatives from the wild
 - range of body sizes

2. Comparison Field-Lab



Field = high environmental variability



Lab = low environmental variability due to controlled conditions

Reduction of variability??

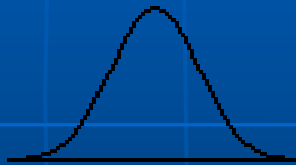
2. Comparison Field-Lab

Generation 1



Field = high environmental variability

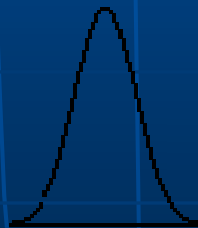
Generation 2



Lab = low environmental variability due to controlled conditions

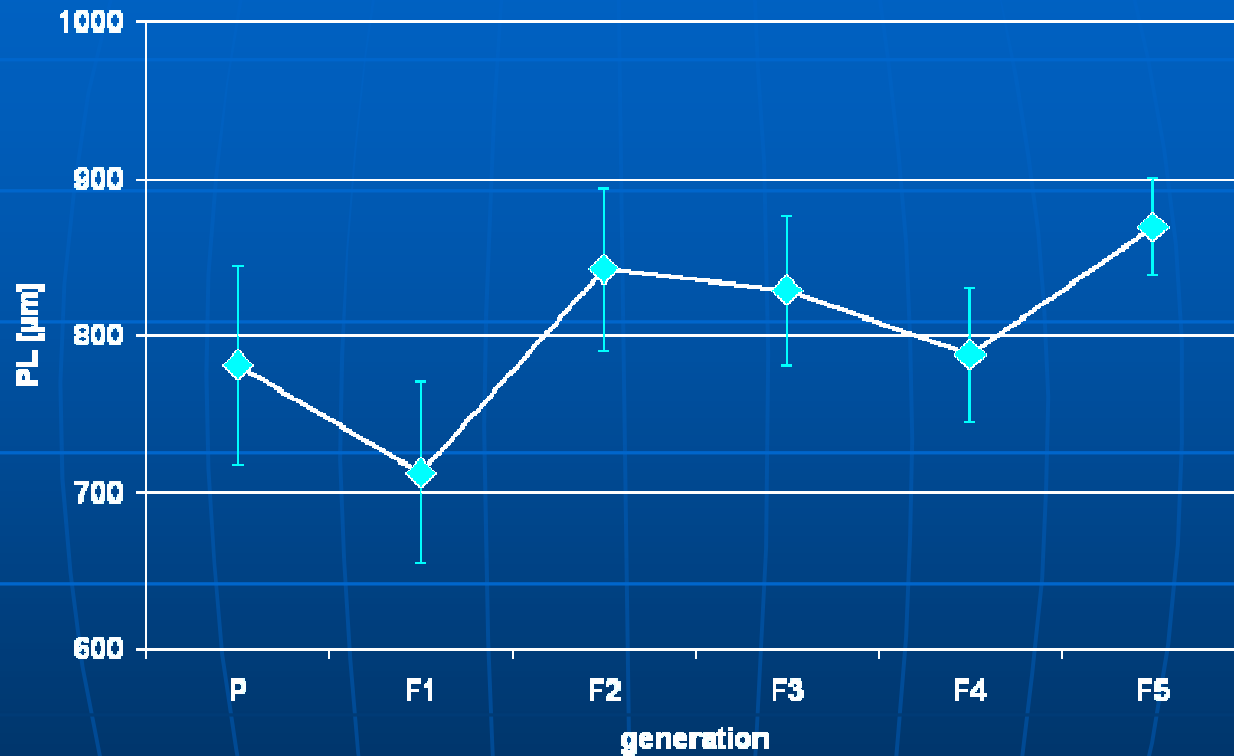
...

Generation x

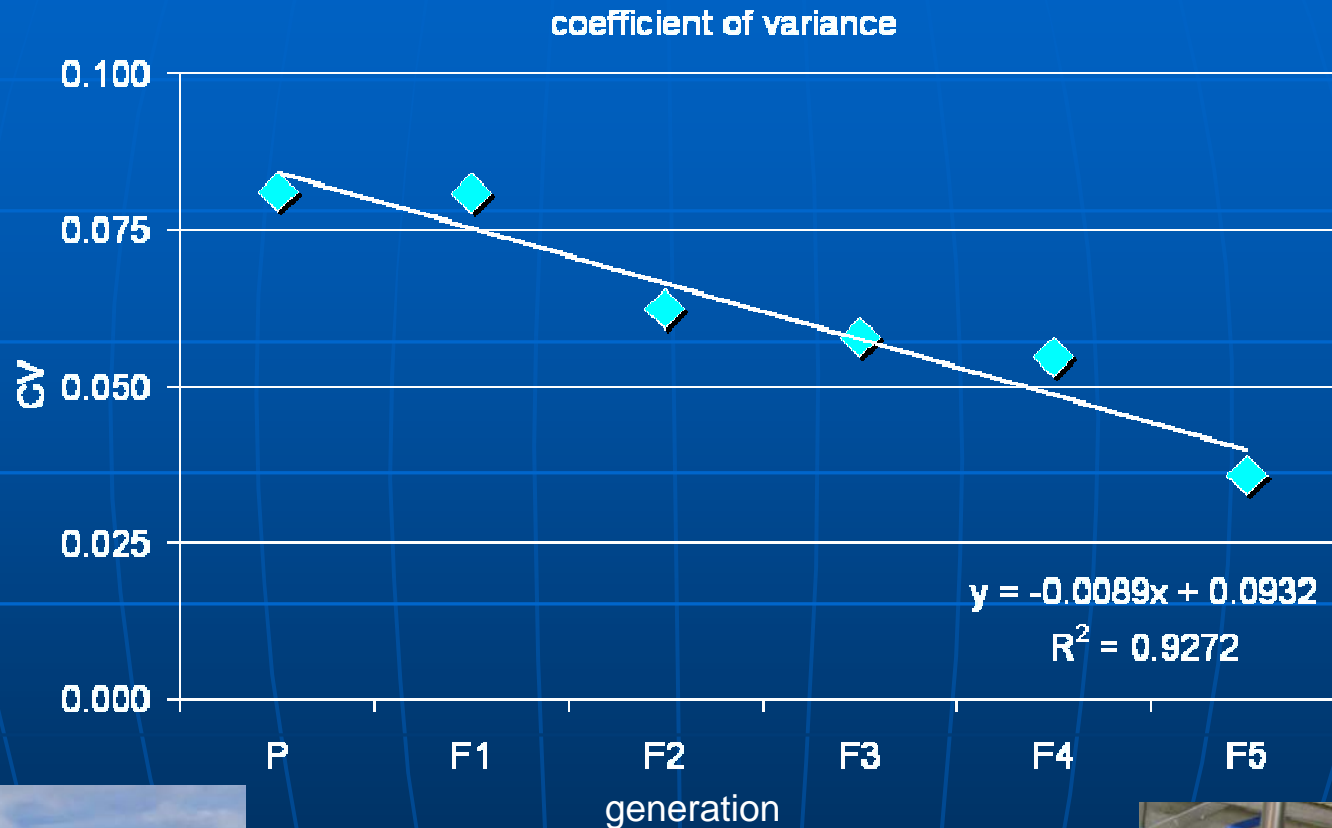


Reduction of variability??

2. Comparison Field-Lab



2. Comparison Field-Lab



variability decreases

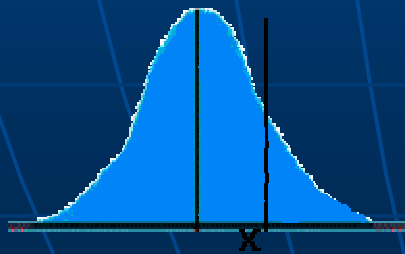
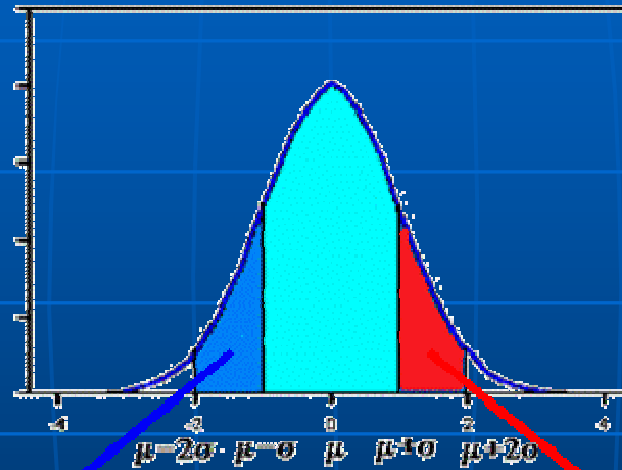


3. Artificial Selection

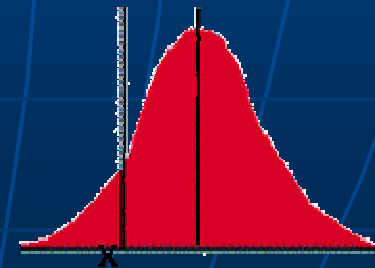
- induce variability in size within populations
 - manually select „large“ and „small“ females to start cohorts
 - monitor size distribution of offspring → heritability

3. Artificial Selection

body size



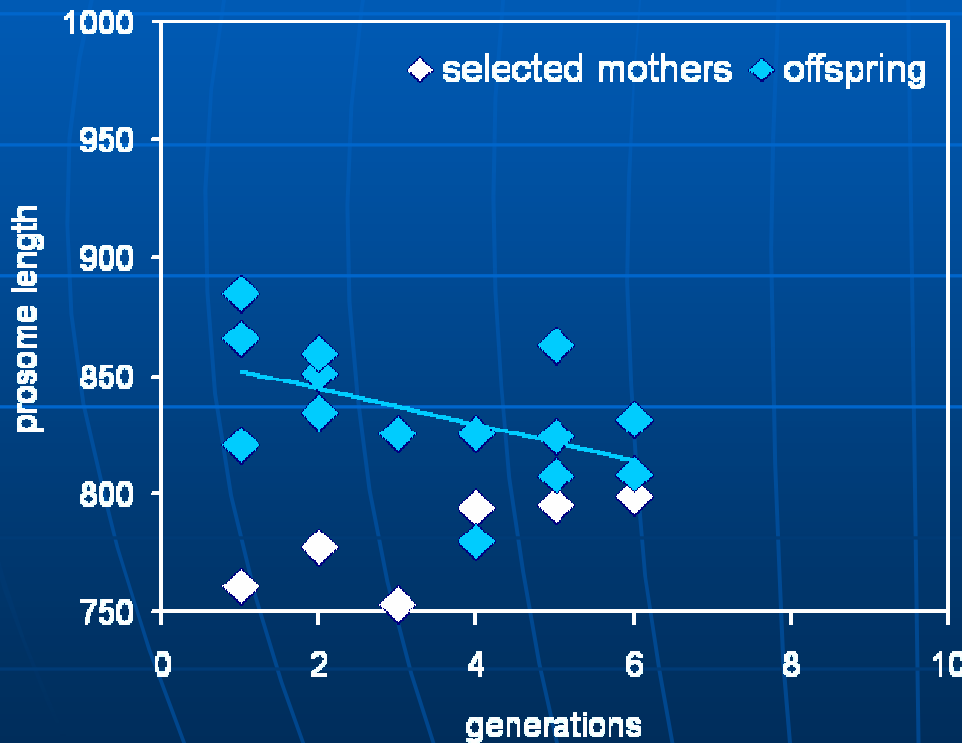
„small“?



„large“?

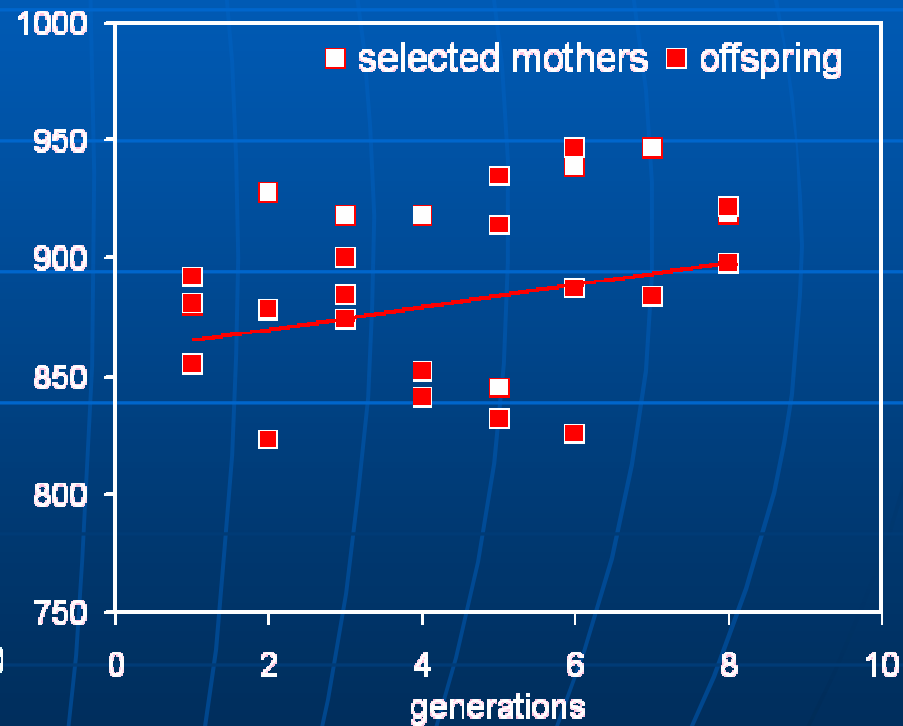
3. Artificial Selection

„small“



$$y = -7.63x + 860.04$$
$$R^2 = 0.262$$

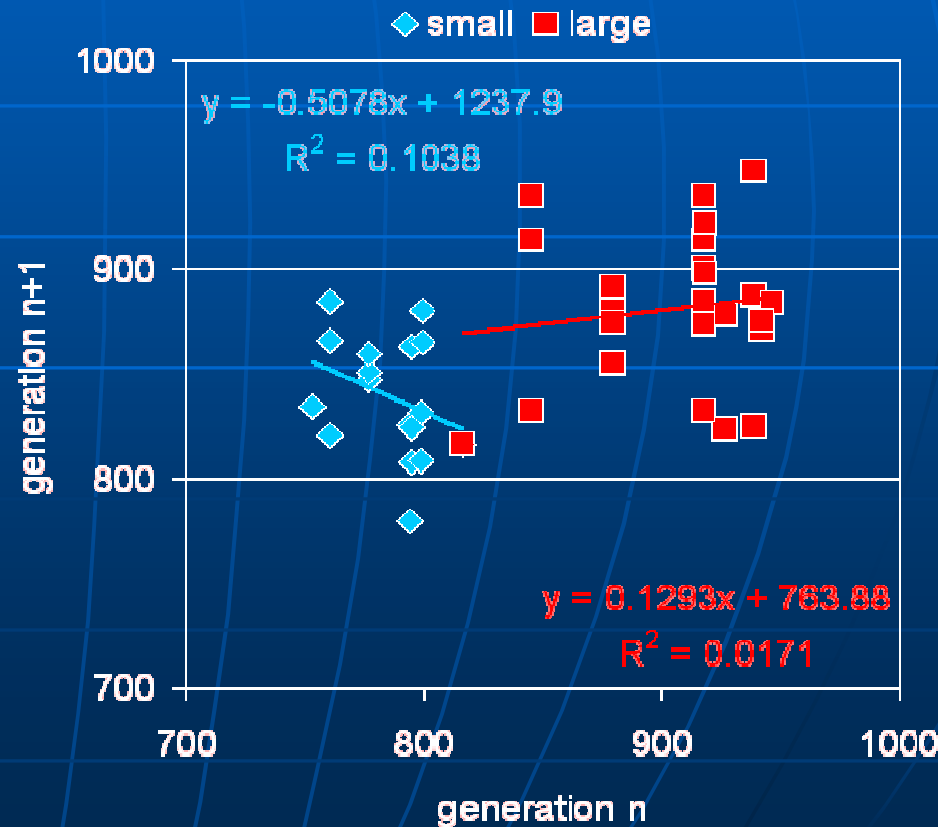
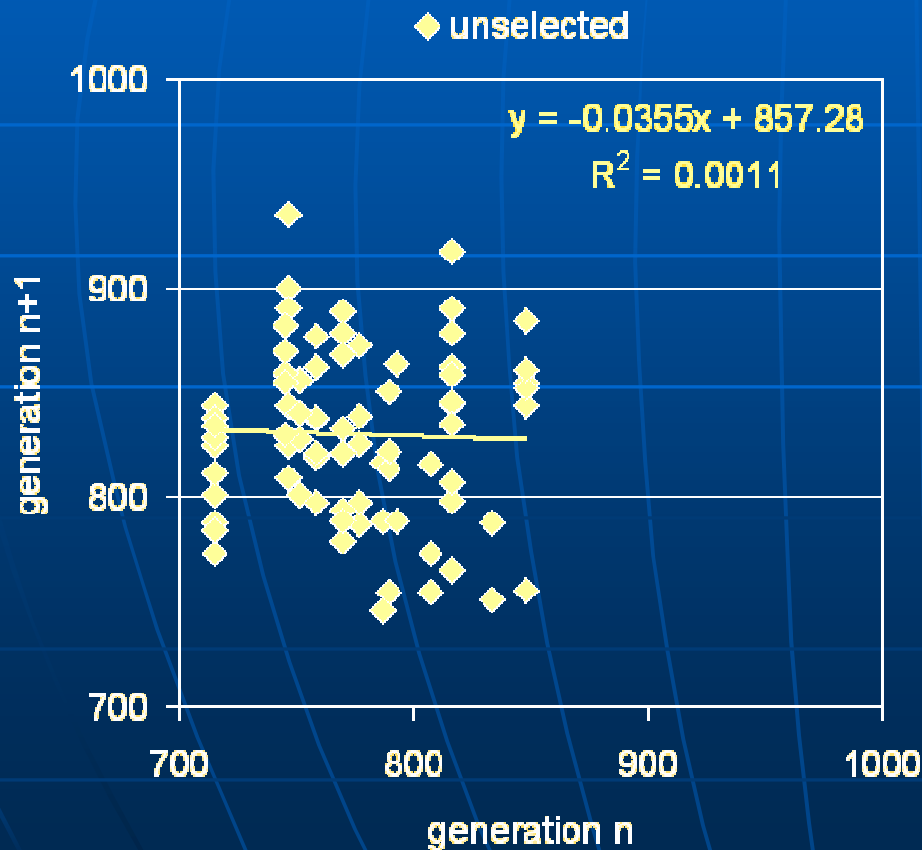
„large“



$$y = 4.8x + 860.33$$
$$R^2 = 0.099$$

3. Artificial Selection

heritability



4. Comparison Arctic-Boreal

- compare variability patterns between populations
 - arctic individuals
 - boreal individuals } of closely related species
bred under identical conditions

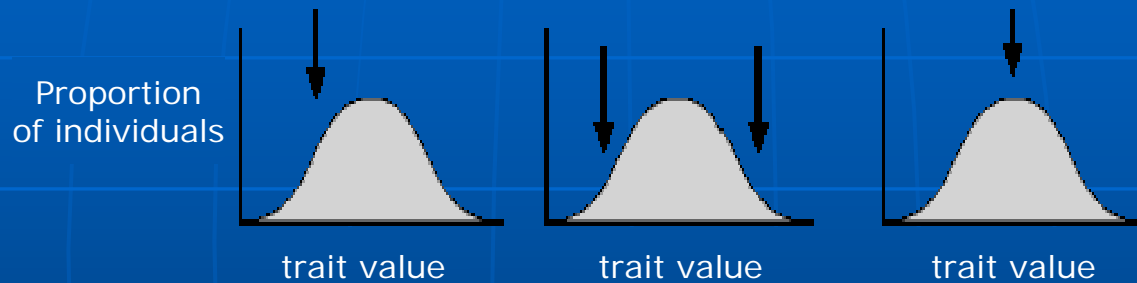
4. Comparison Arctic-Boreal



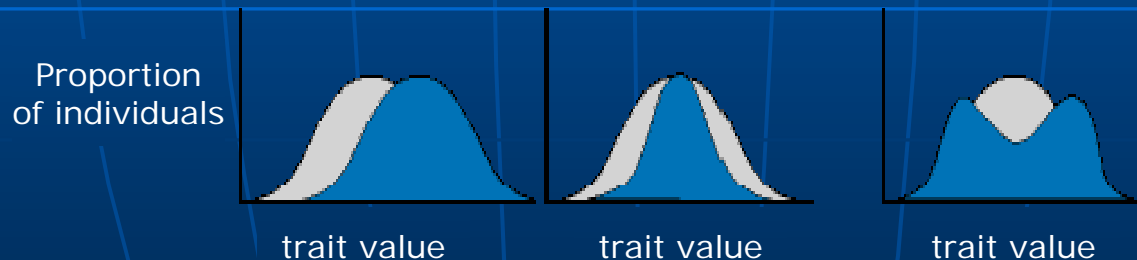
4. Comparison Arctic-Boreal

- repeat 1. and 2. with Arctic populations
 - intra-population variability in *Acartia longiremis*
 - body size
 - development times
 - reduction of variability field → lab?
 - differences in variability patterns due to different selection pressure?
- compare with *A. tonsa*_{Øresund}
- estimate strength of life history evolution

4. Comparison Arctic-Boreal



?? – work in progress...



**Directional
Selection**

**Stabilizing
Selection**

**Disruptive
Selection**

5. Model (IBM)

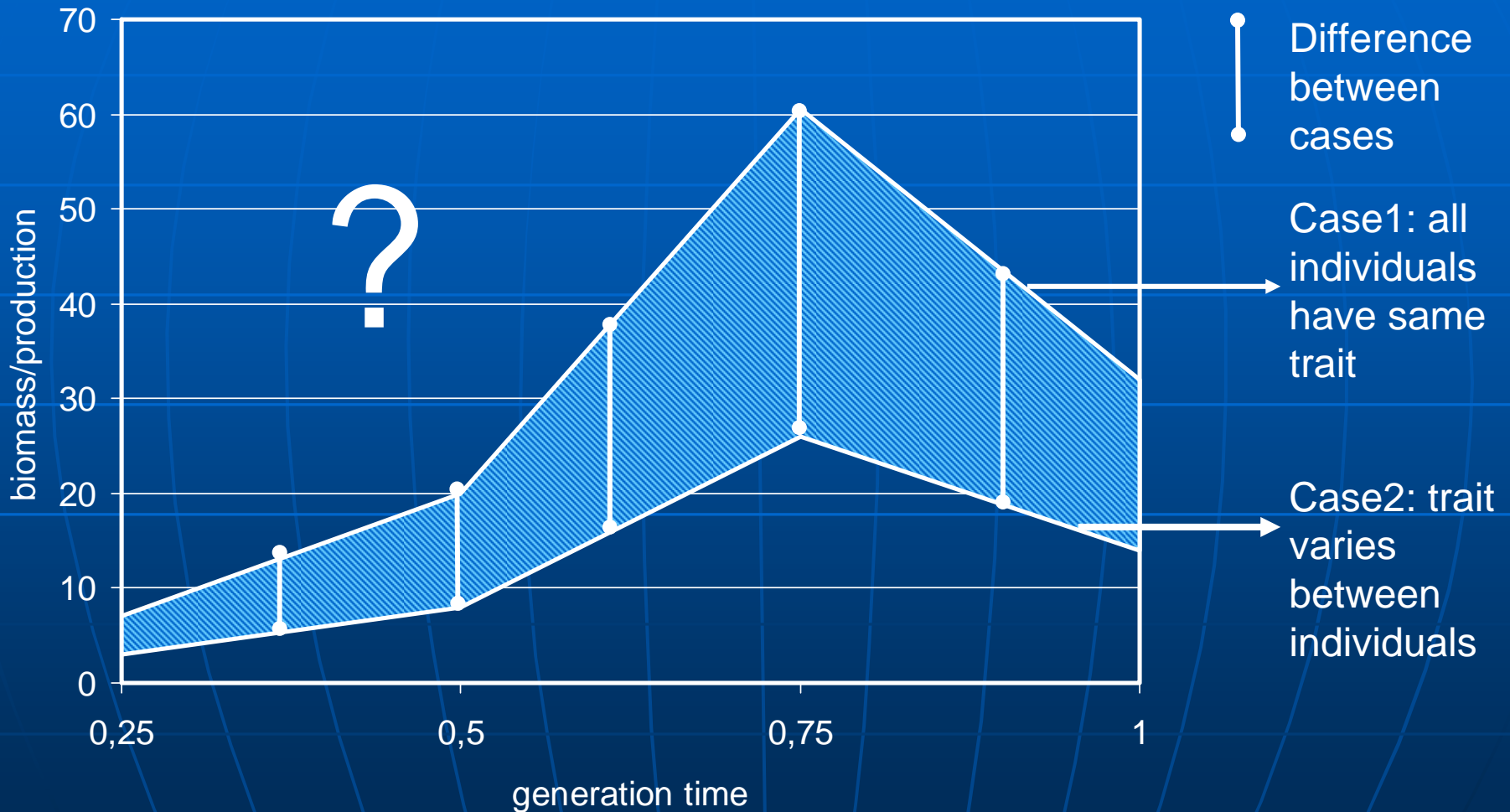
- develop an **individual based model (IBM)**
 - series of model runs where **only the level of individual variability varies**
 - monitor model **outputs over time**
- does individual variability **alter** model outputs on **ecologically relevant time-scales?**

5. Model (IBM)

- Populations with **different variability patterns**
 - All individuals have the **same** (mean) trait
 - Trait **varies** between individuals
 - size = normal distribution
 - Development time = non normal (gamma)
- Assign **functions** for
 - mortality, growth, fecundity
- relate variability patterns to **fitness**: how does size/dev.time affect fecundity/mortality...
- Model **one trait** at a time over 1 generation
- **Combine traits**, more than one generation

→ Andrew Hirst, today 16:40!!

5. Model (IBM)



How realistic is case 1?

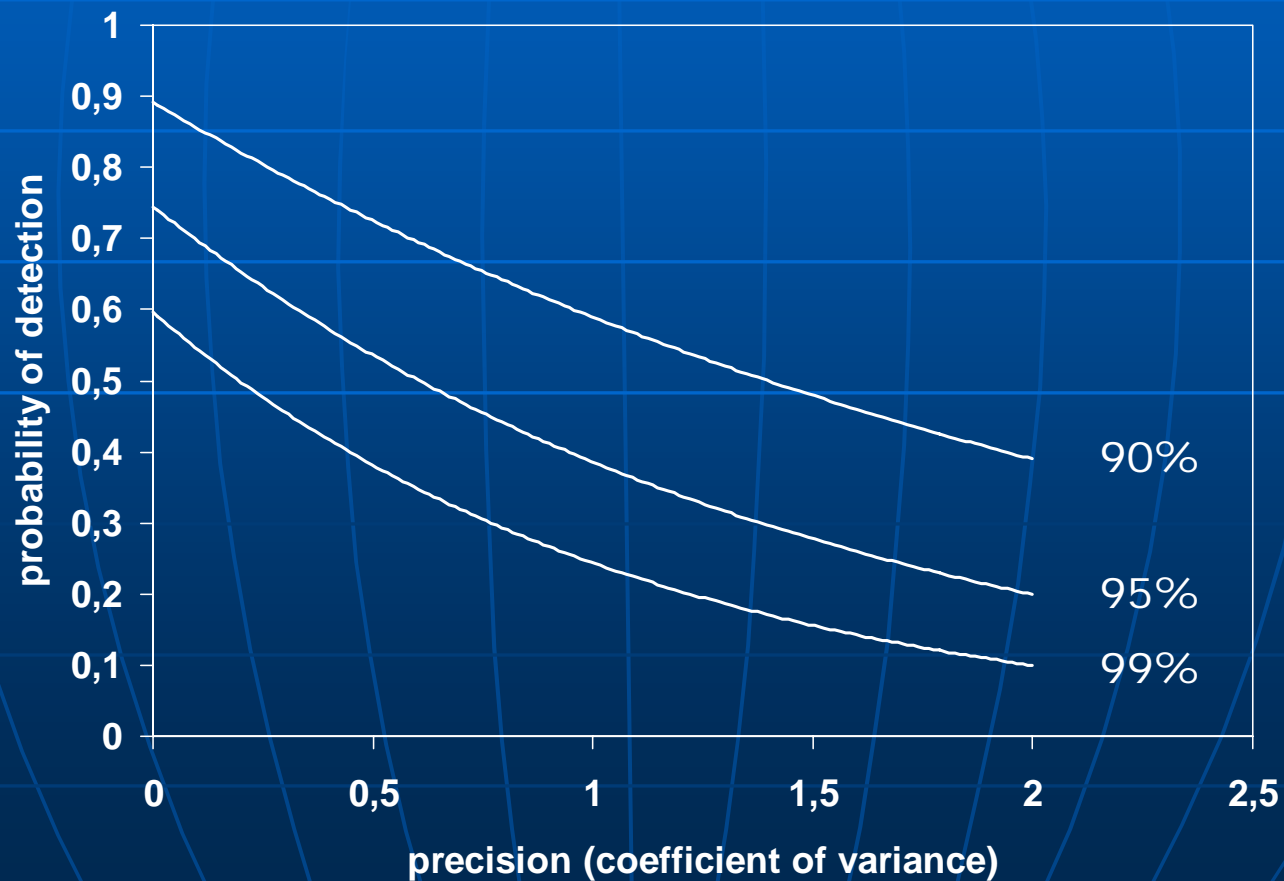
Does case 2 improve our ability to simulate/predict natural populations?

5. Model (IBM)

- how precise can we get?
 - what level of phenotypic variability **can be detected** with current methods
 - net **sampling**: space/time scales, replicates
 - **sources of variability** (real = patchiness, induced = inaccuracy of net/handling/data(n))
 - how **strong** does selection have to be to alter our results (so that we would notice)?
 - **naturally** (life history evolution)
 - due to **climate change** (e.g. warming, acidification,...)
 - due to other **anthropogenic effects** (e.g. pollution, invasive species, ...)

5. Model (IBM)

model output (hypothetical example)



The END

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