Oregon State University
College of Earth, Ocean, and Atmospheric Sciences

NOAA FISHERIES

Impacts of temporal and spatial variability in somatic growth on fish stock assessment models

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Quantitative Seminar Series

Outline

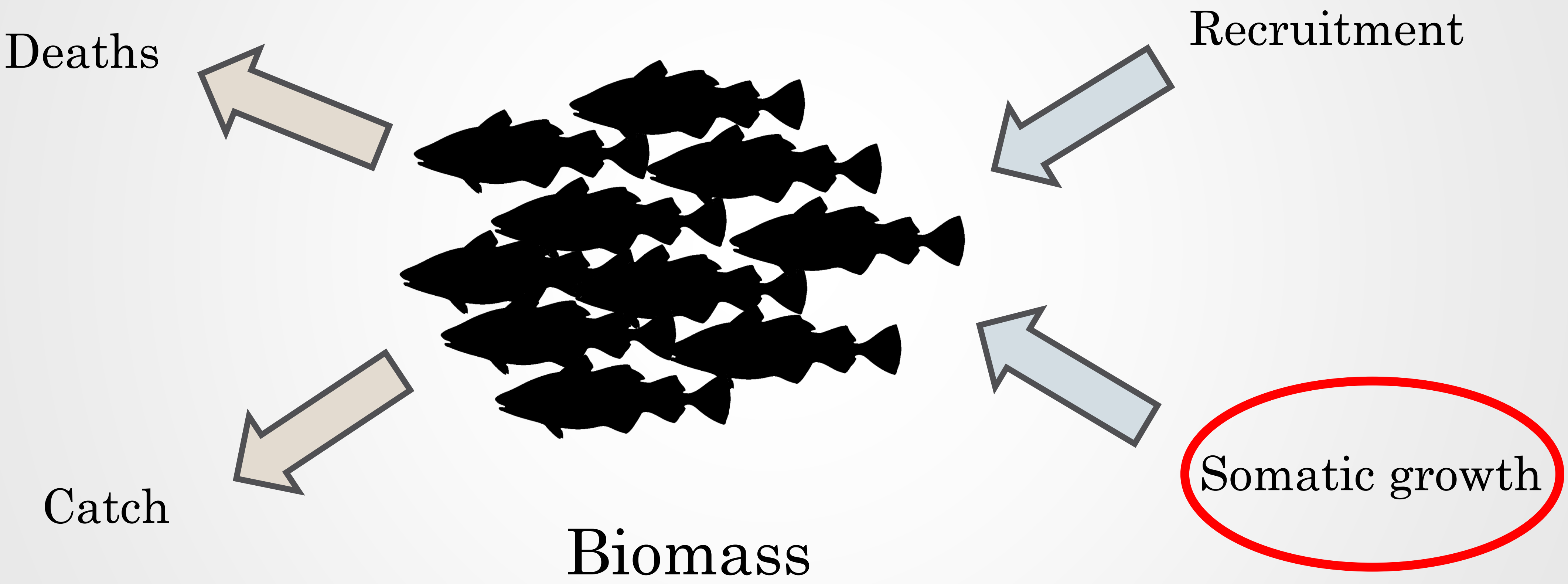
- Somatic growth in fish populations

1. Impacts of temporal and spatial variability in somatic growth rates on age composition estimation
2. Consequences of somatic growth misspecification on stock assessment outcomes

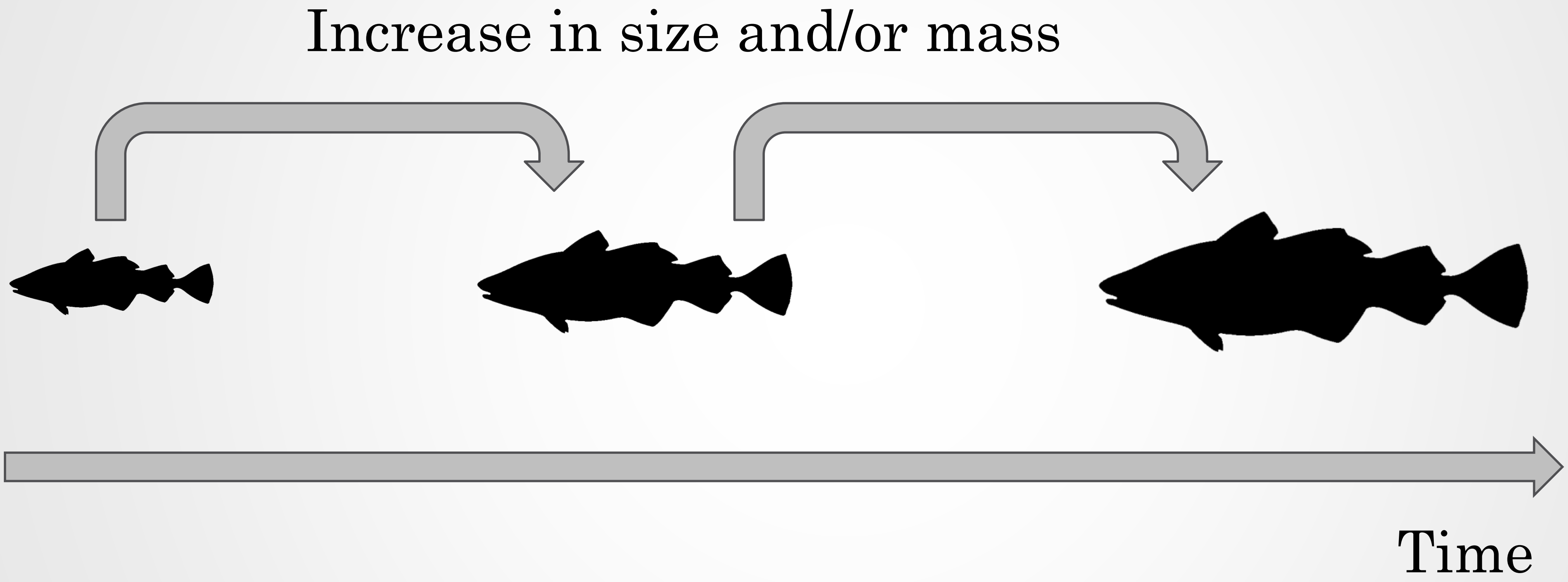
- Conclusions

Populations dynamics

Exploited closed population:



Somatic growth

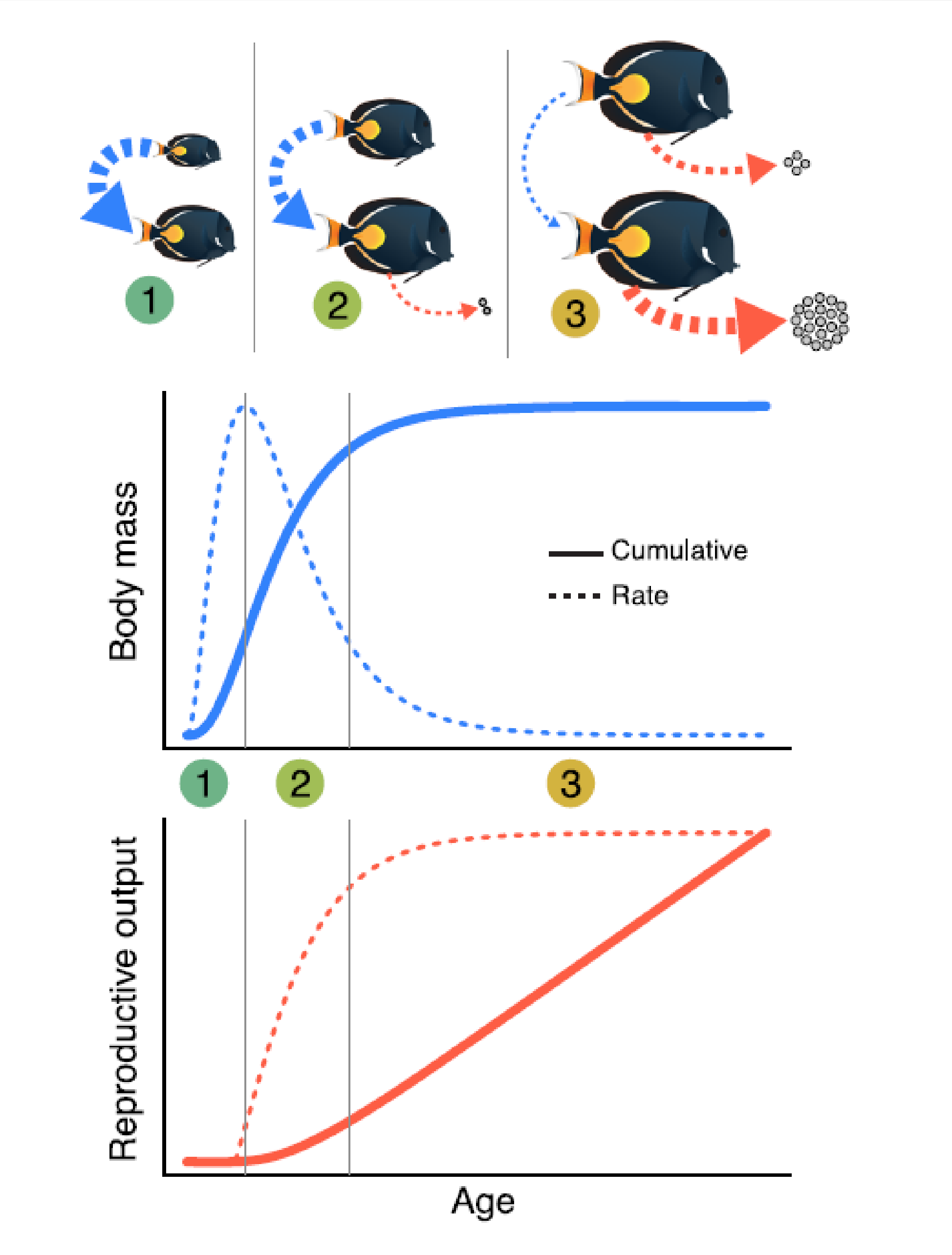


Somatic growth

Trade-off between reproduction and growth:

- Faster growth in younger ages
- Energy allocated in reproduction in older ages

Growth rate can vary in space and time.



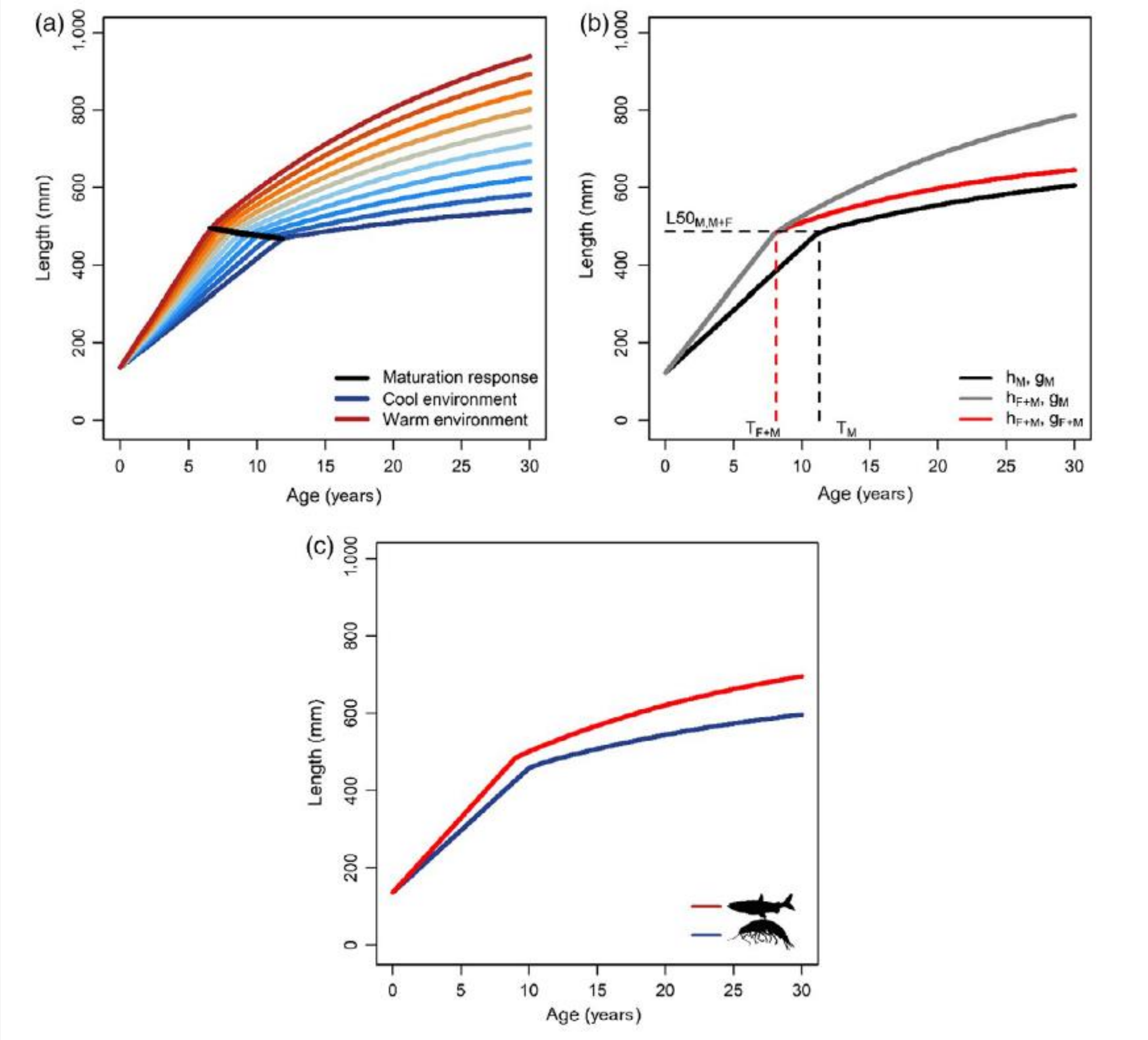
Morais and Bellwood (2020)

Somatic growth variability

Factors that vary somatic growth rates:

1. Environment
   - Temperature
   - Food quality and concentration
2. Predators
3. Fishery
4. Density-dependence
5. Genetics

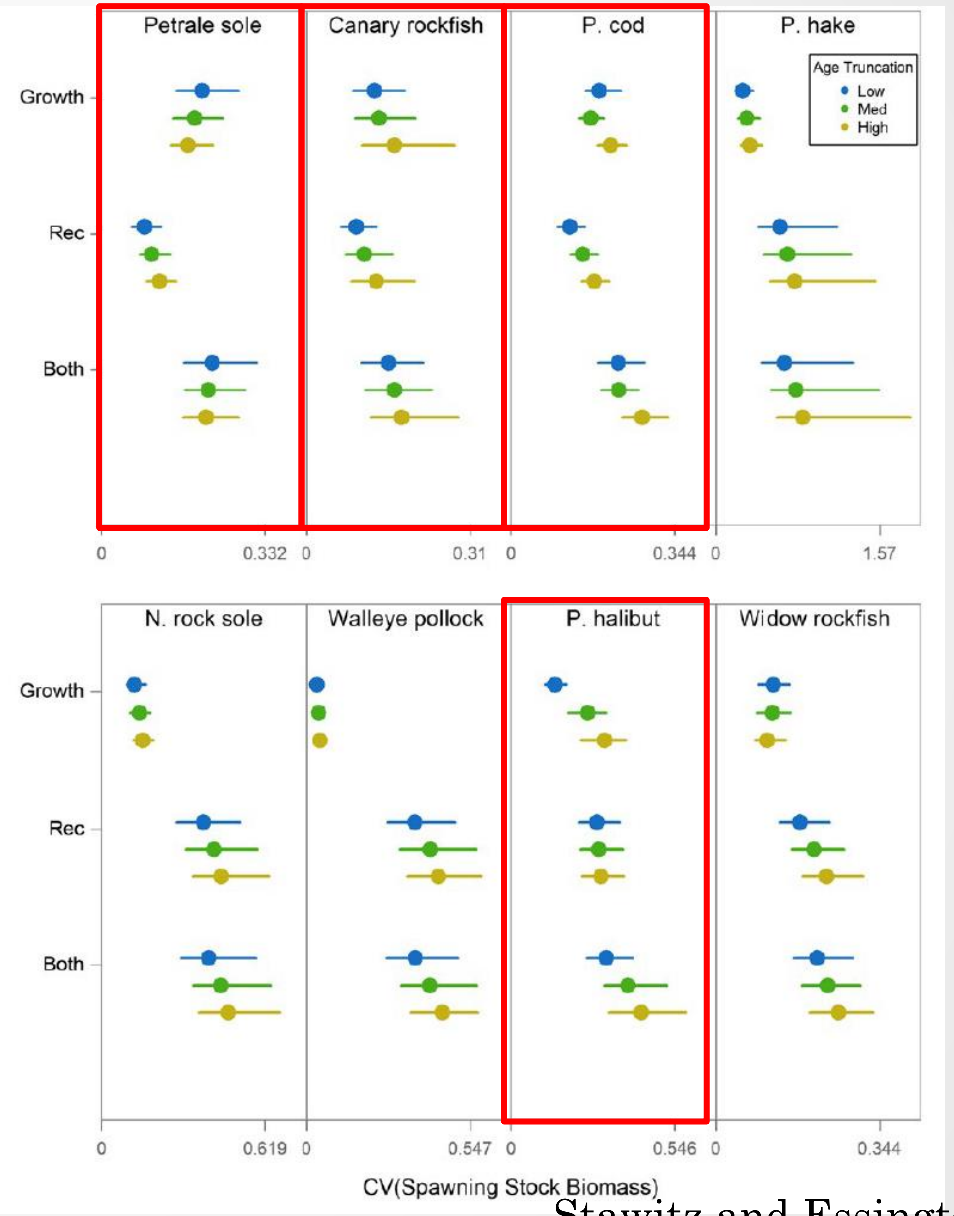
Somatic growth variability



Wilson et al. (2019)

Somatic growth: why is important?

Growth, as recruitment, can drive the variability in stock spawning biomass.

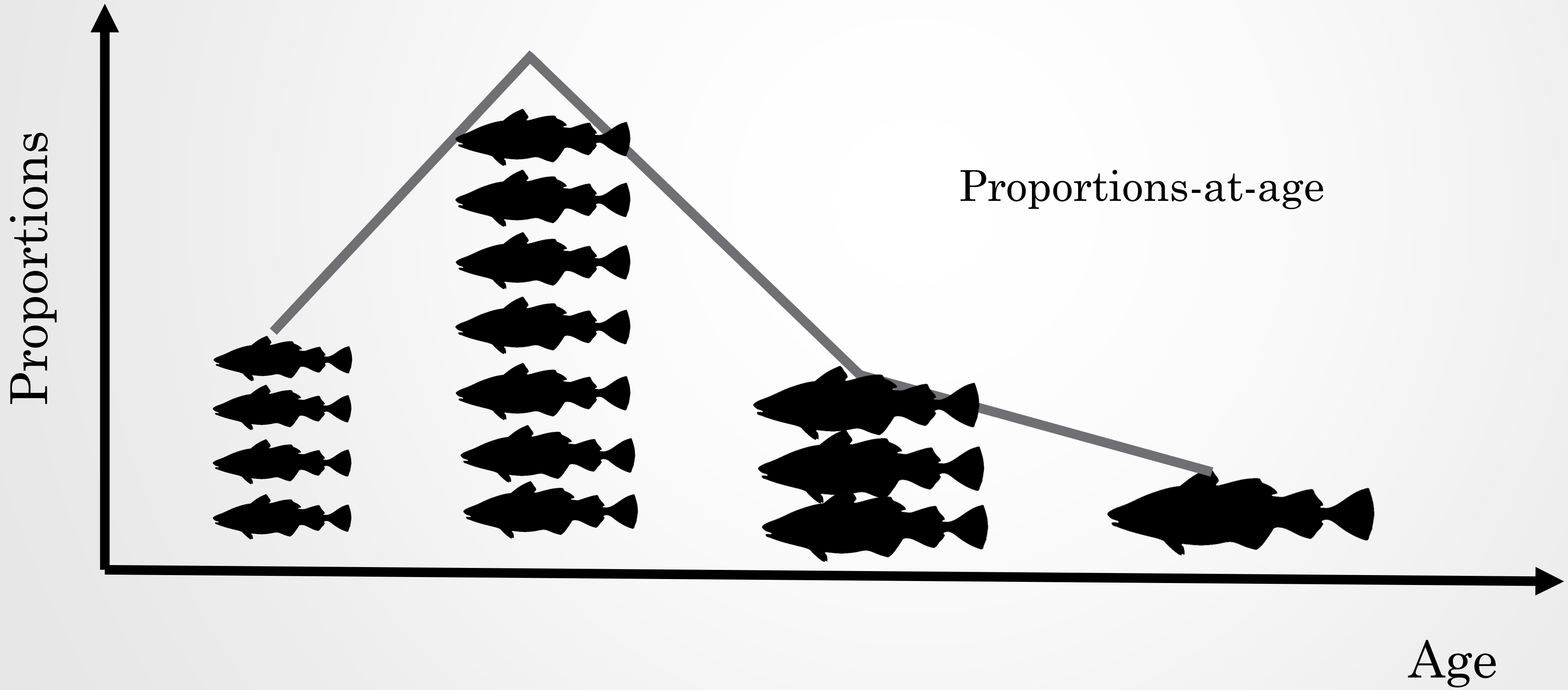


Stawitz and Essington (2018)

1. Impacts of temporal and spatial variability in somatic growth on age composition estimation

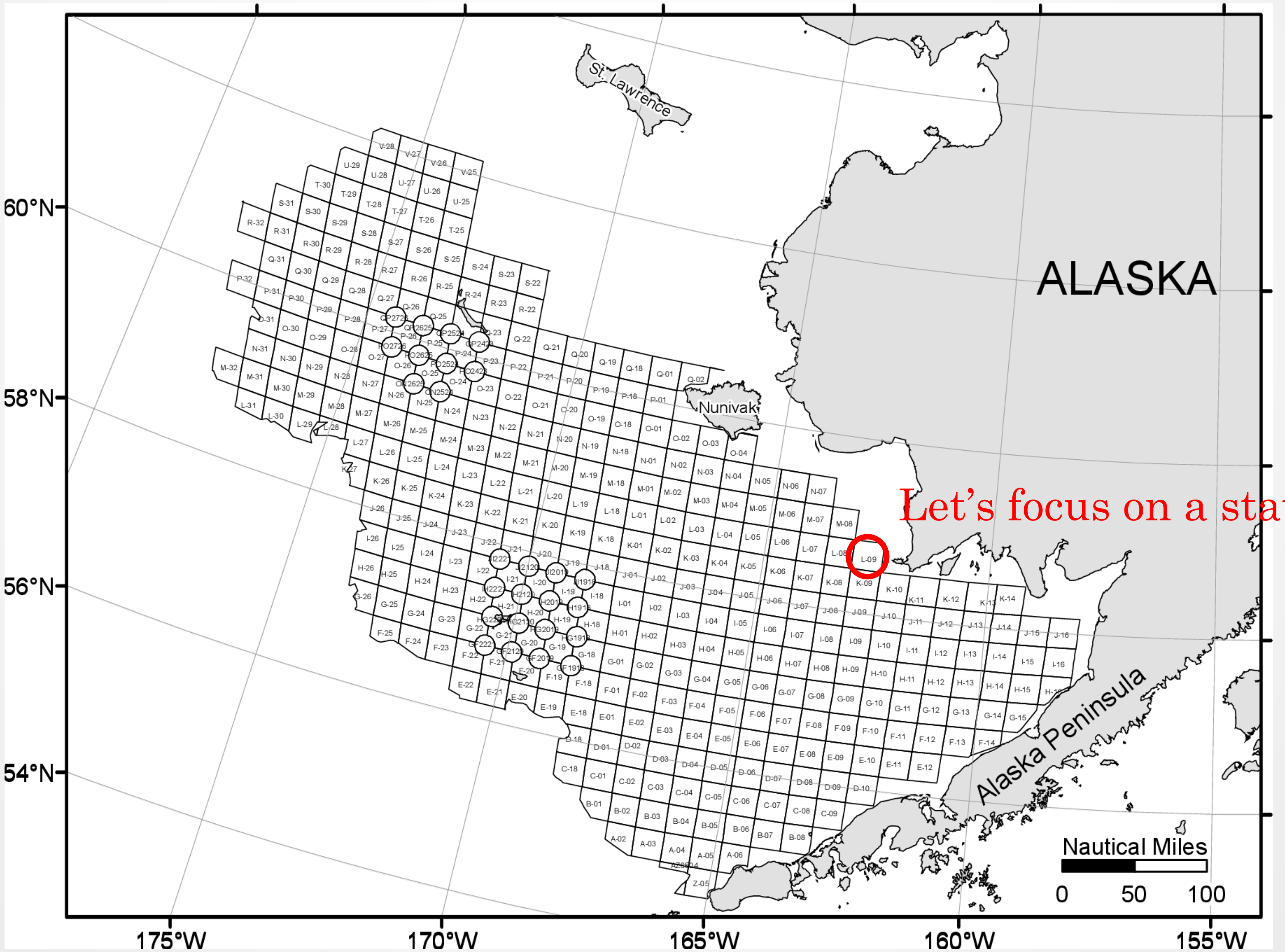
Age composition estimation

Age compositions:



Age composition estimation

Estimated from the fishery or a survey:



Let's focus on a station

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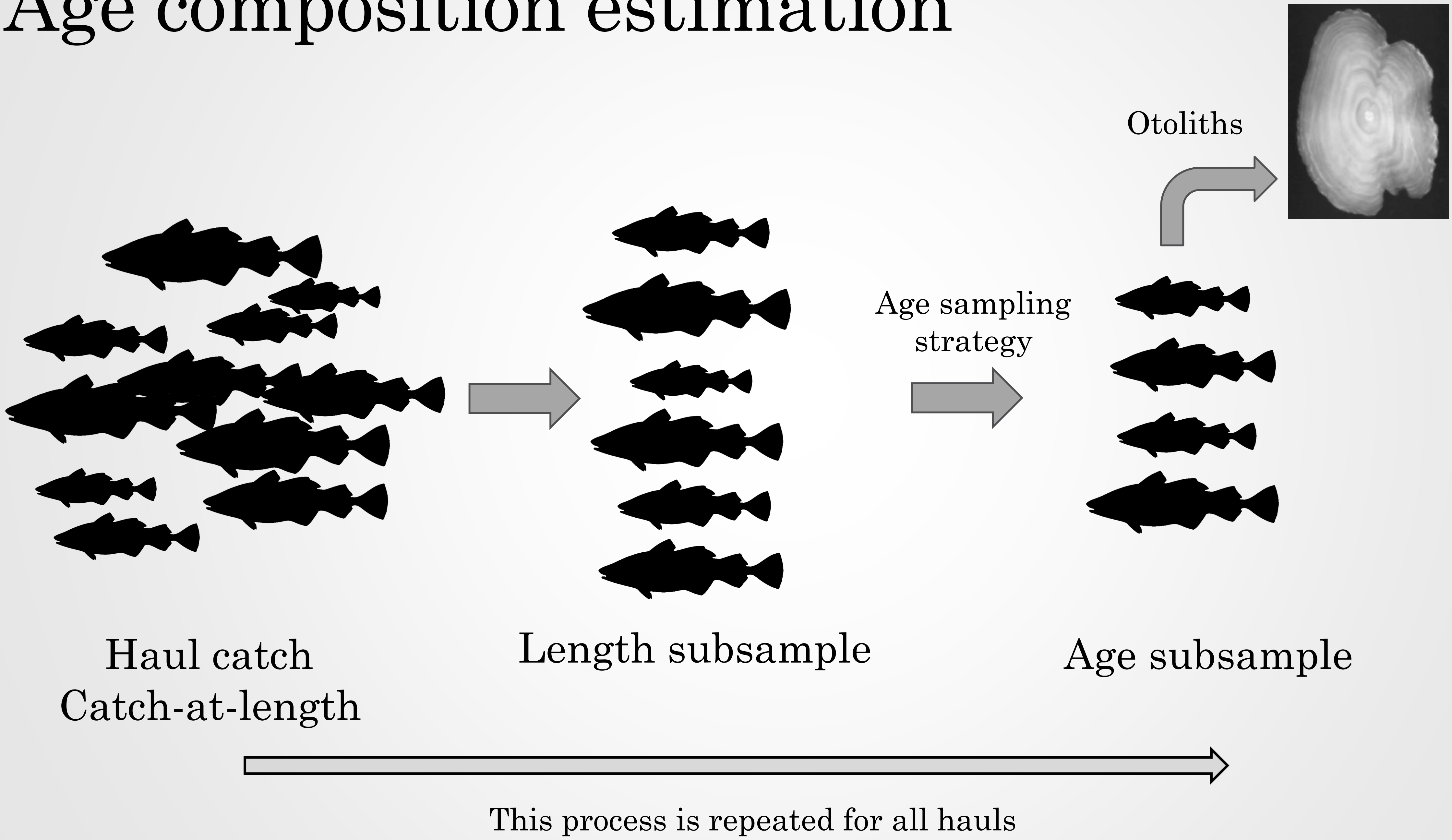
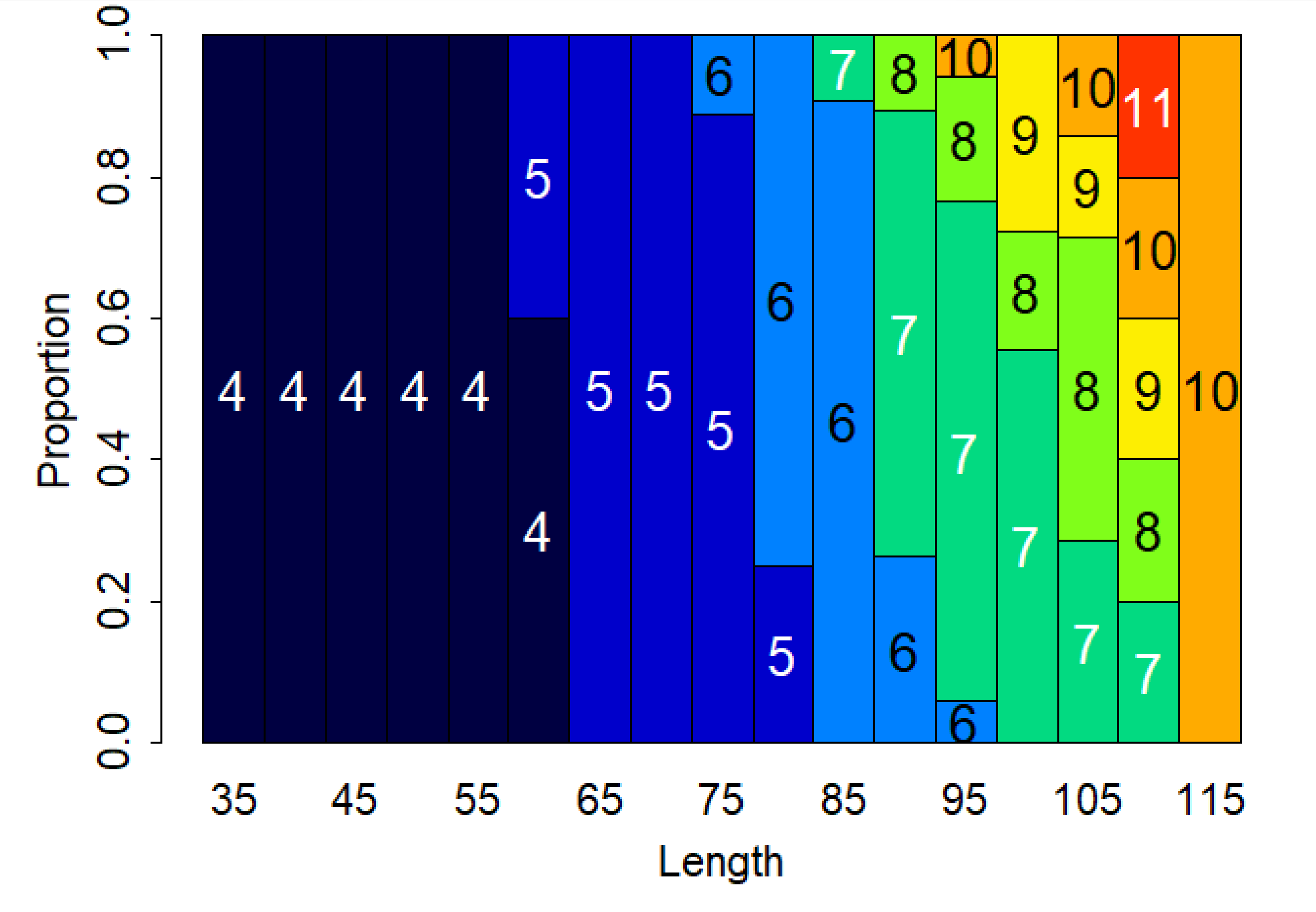
Age composition estimation

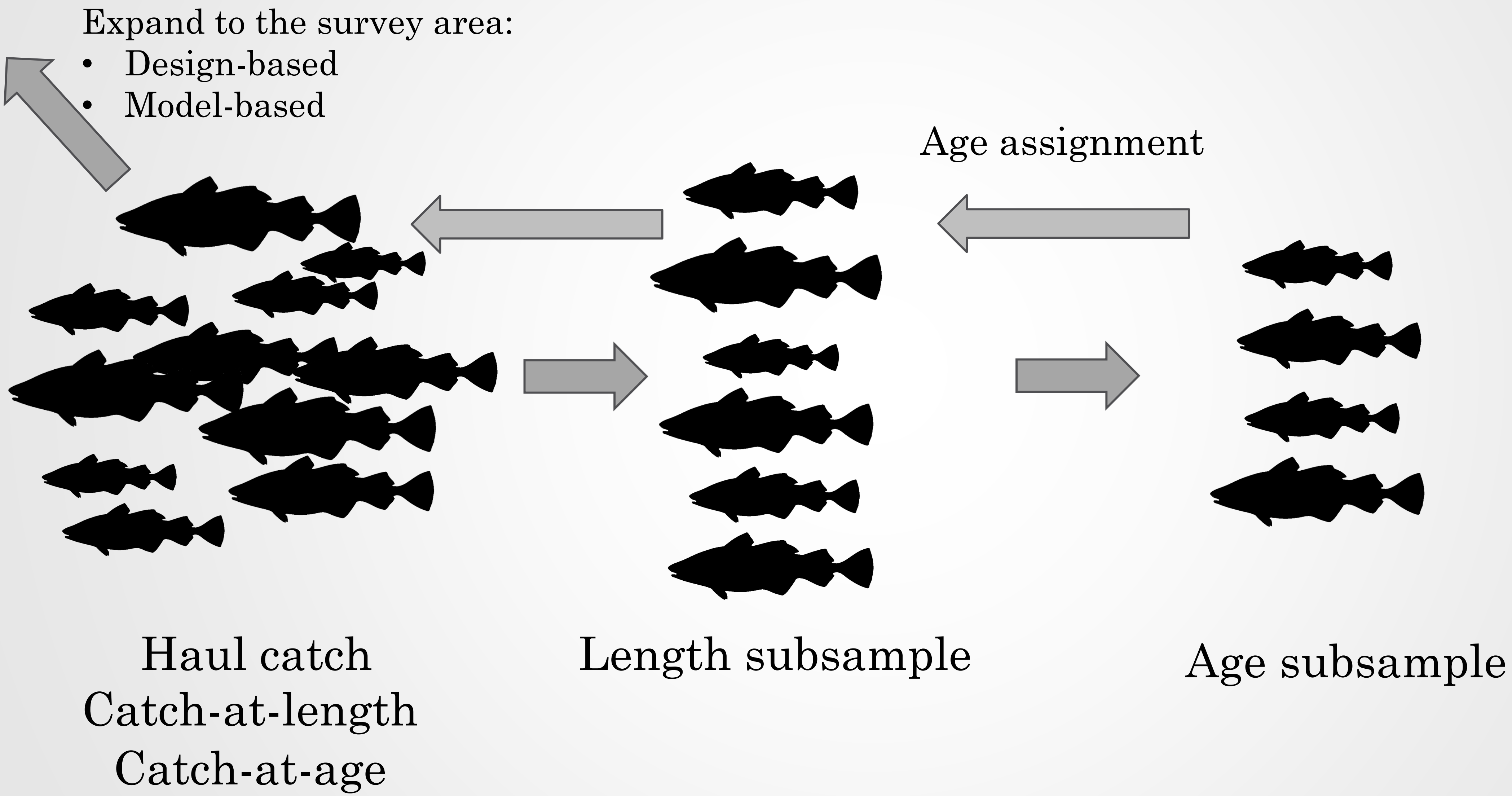


Age composition estimation

Age-length key (ALK) construction from information in the age subsample

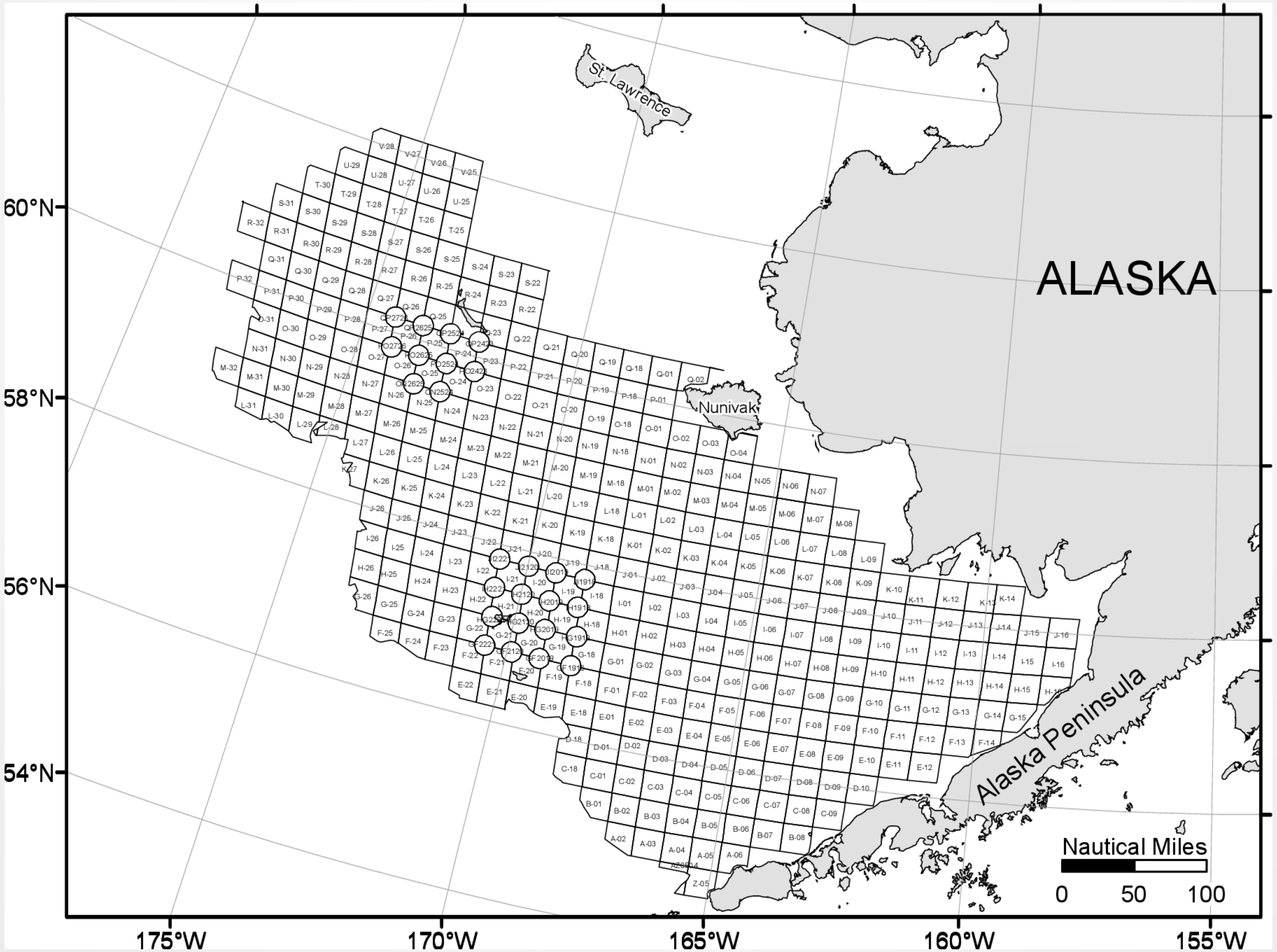


Age composition estimation



Age composition estimation

Age composition for the entire survey area



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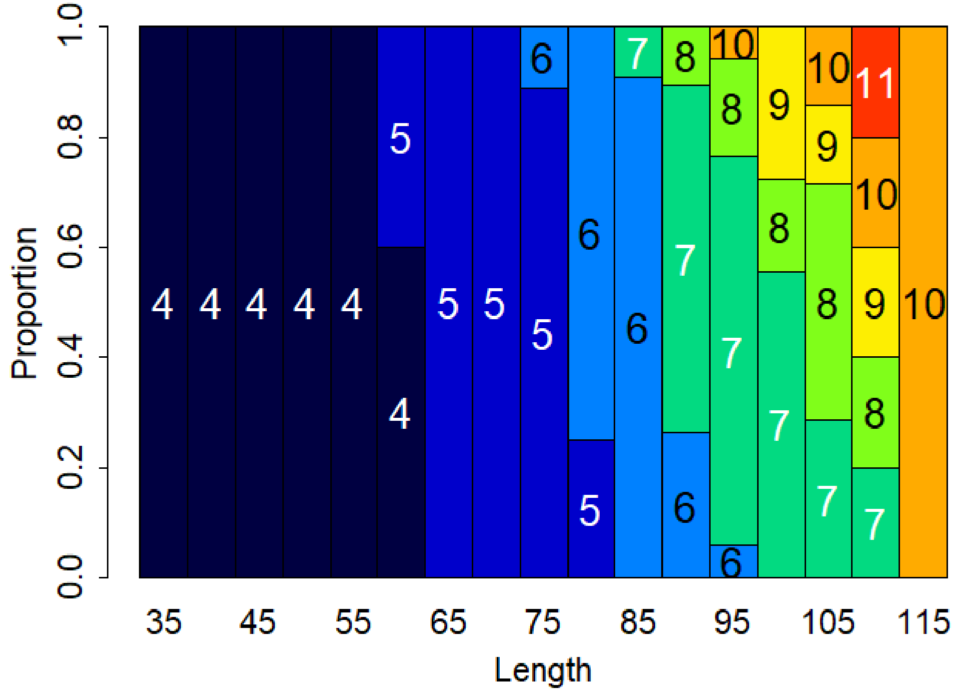
Age composition estimation

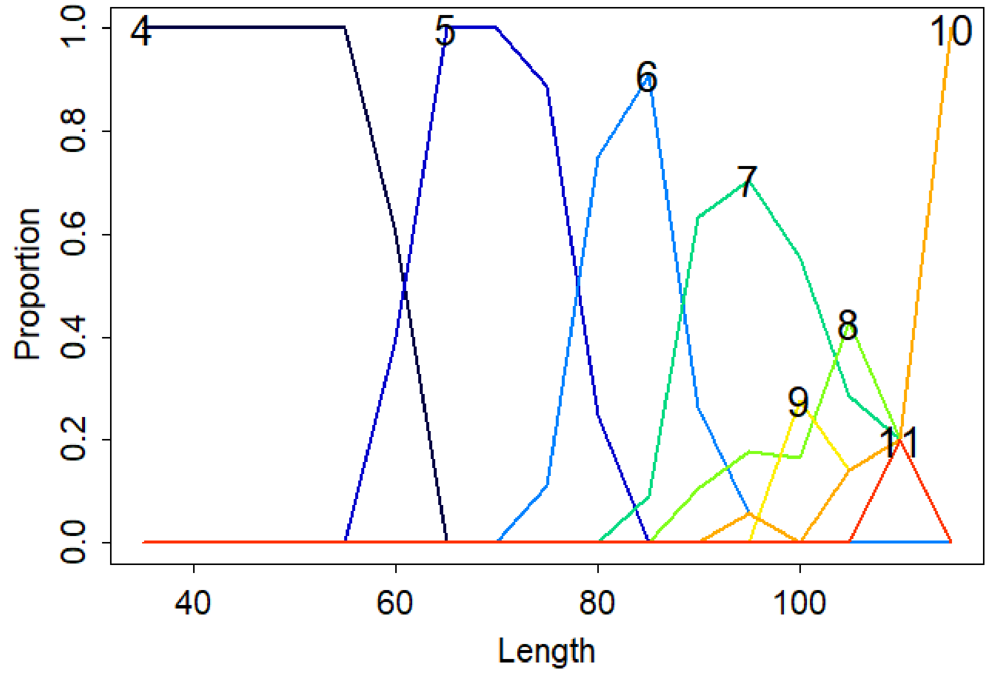
Impacted by three main factors:

1. Age sampling strategy
2. $\boxed{\text{Age assignment in the length subsample}}$
3. Catch-at-age expansion to the entire survey area

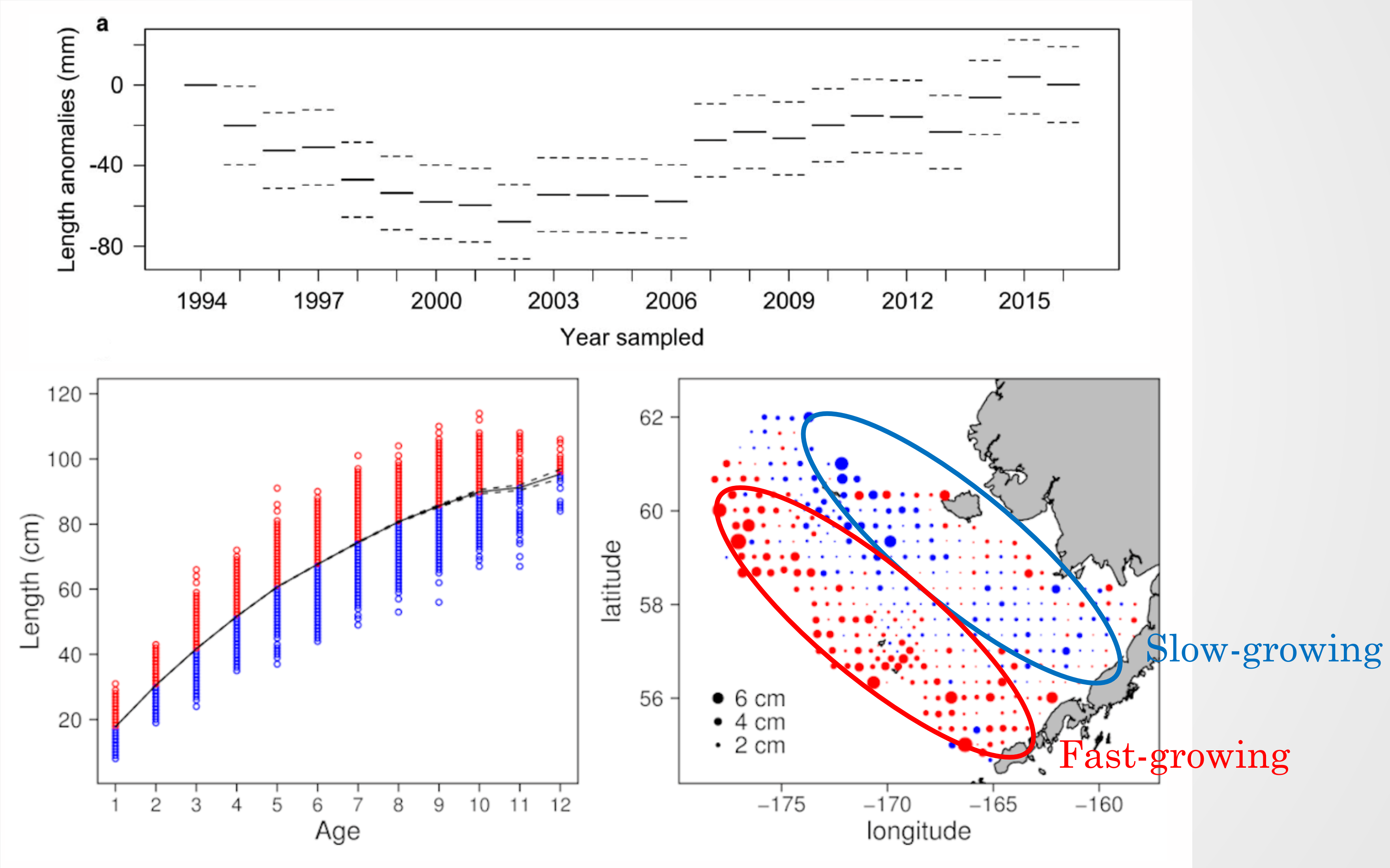
Age-length key

- Simple construction
- Used worldwide
- Needs good amount of data
- Normally pools data from the entire study area
- Data gaps for some lengths
- In some cases, pools data from different times





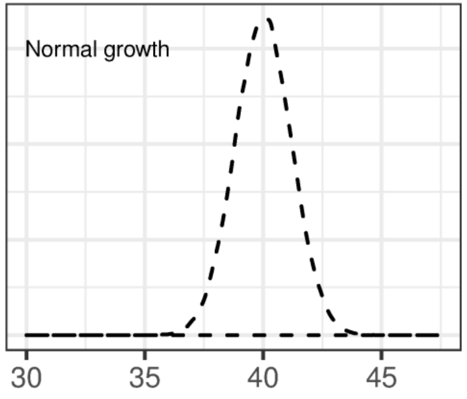
Pacific cod in the eastern Bering Sea



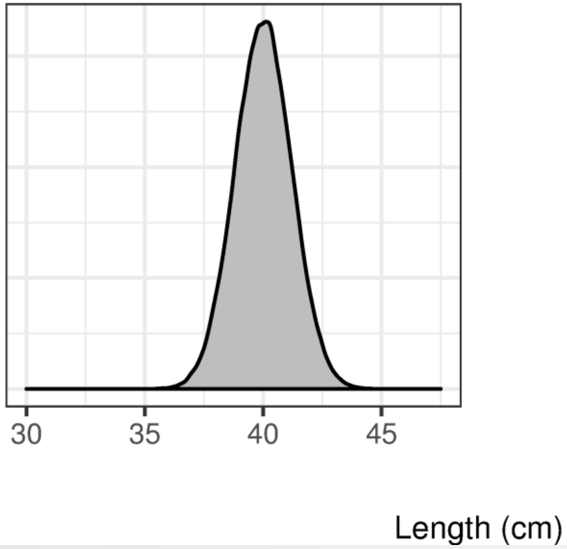
Ciannelli et al. (2019)

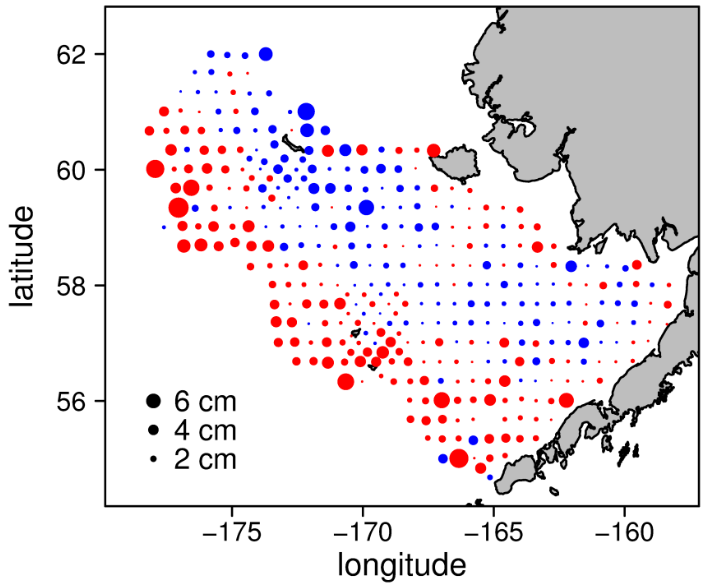
Variability in size-at-age

At a given location:



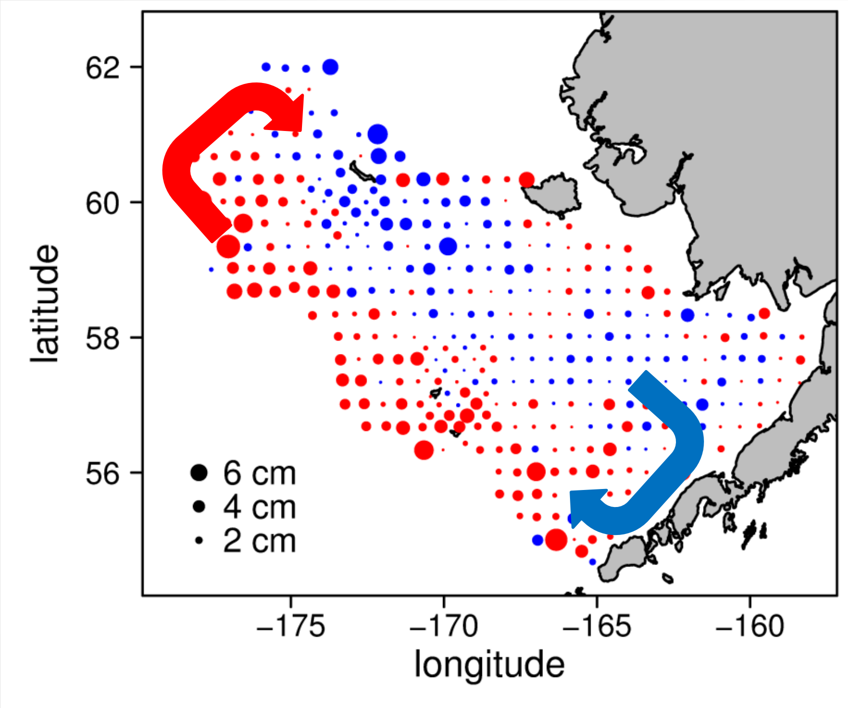
At the population:

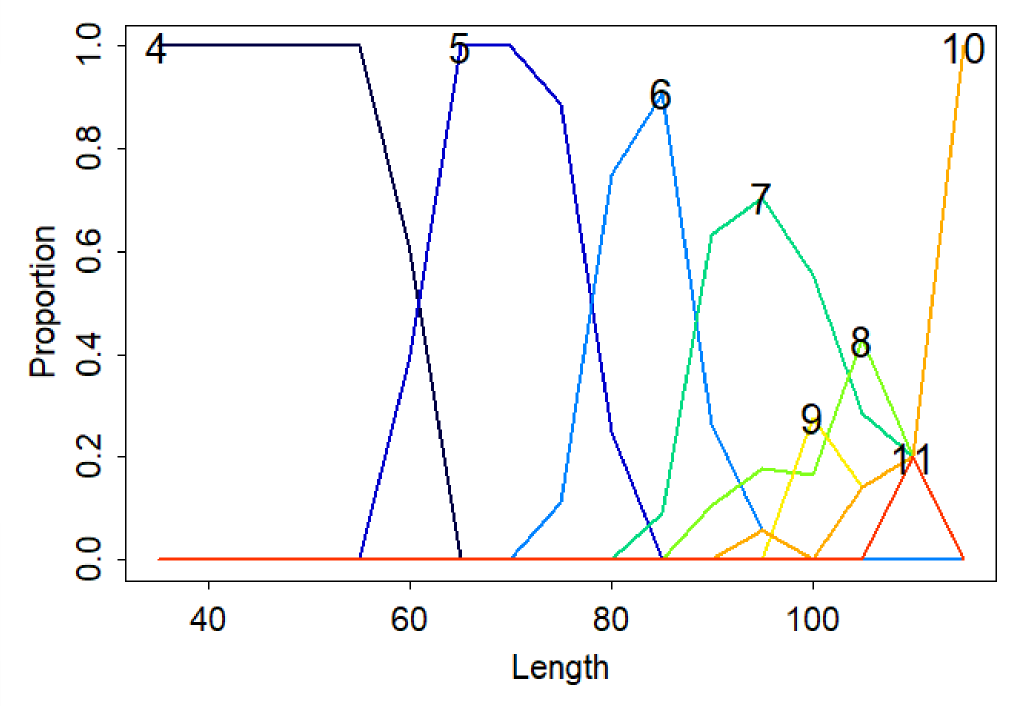




Correa et al. (2020)

Spatial variation in somatic growth impacts age-length keys





Age-length key

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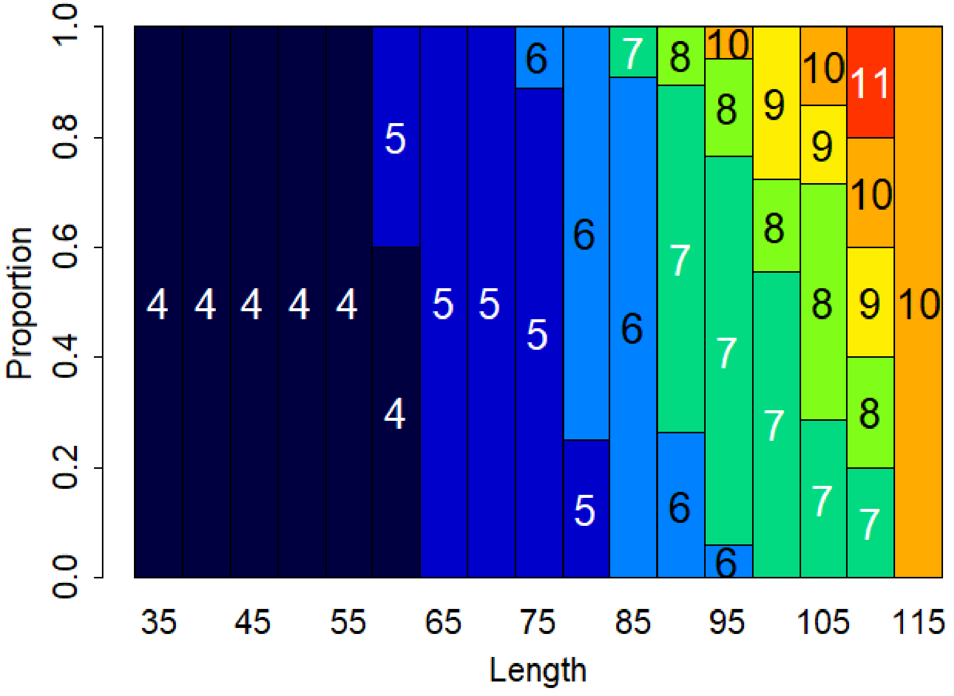
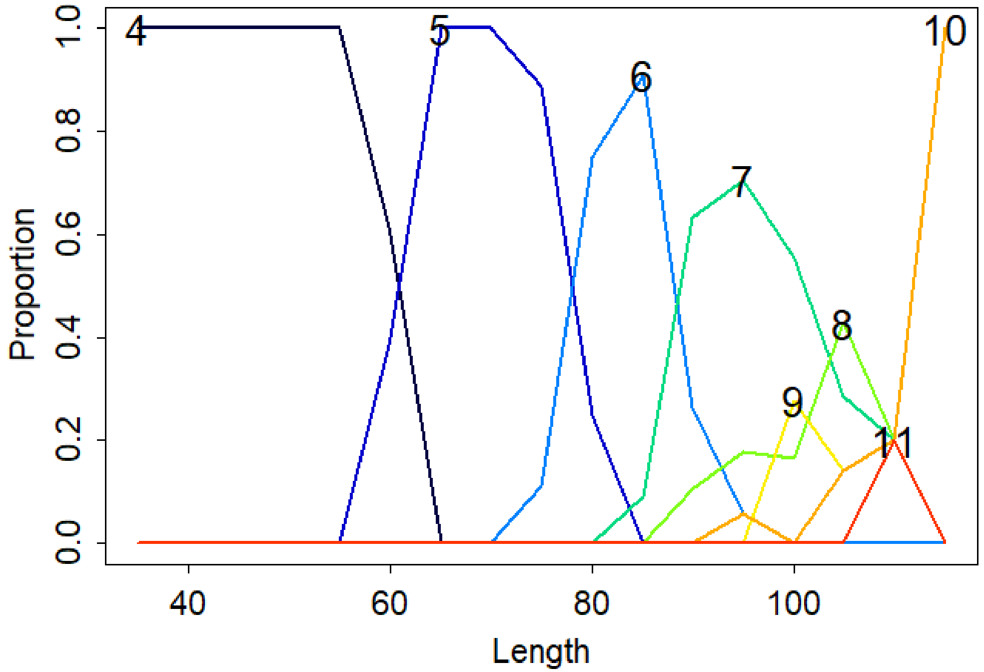
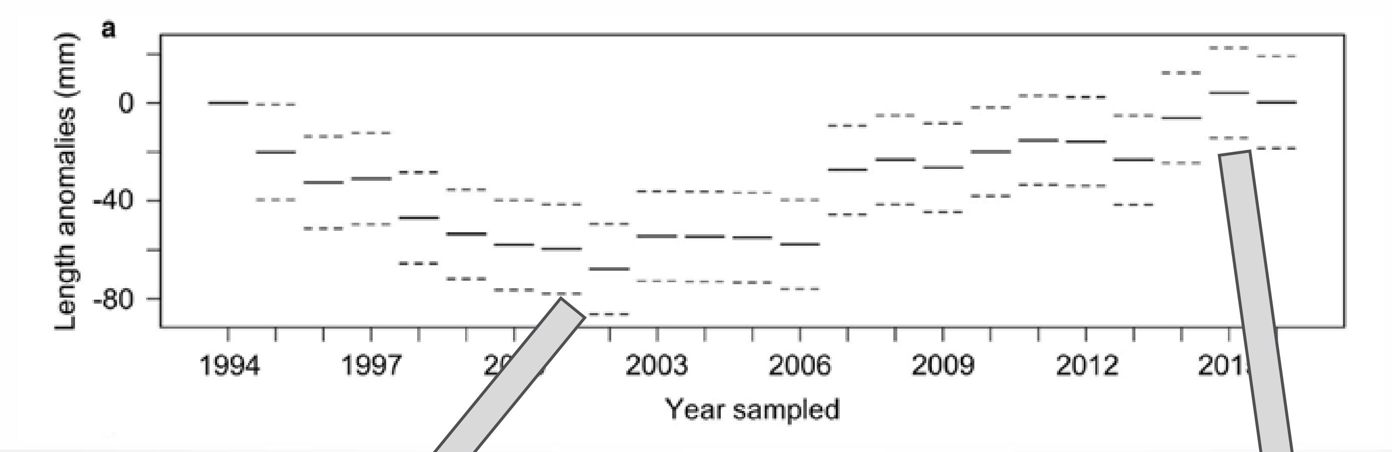
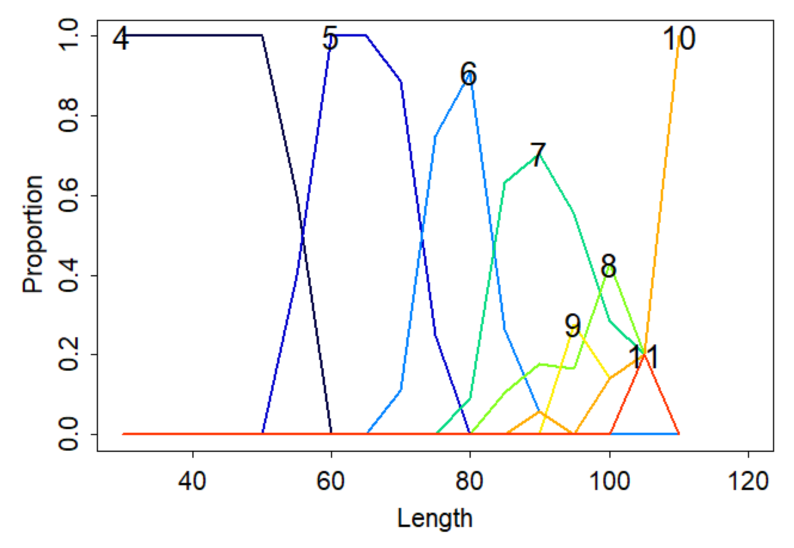


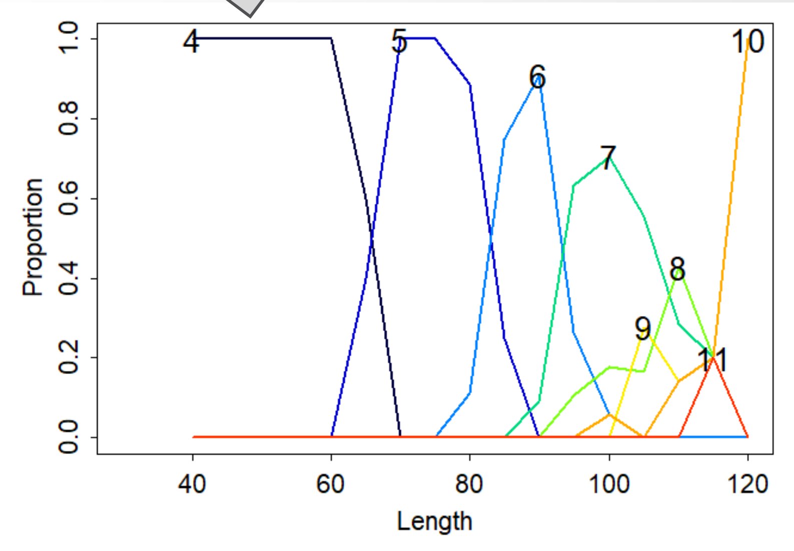


Temporal variation in somatic growth impacts age-length keys





Combine information from periods with different somatic growth rates



Alternative approaches to ALK?

- Puerta et al. (2018): used a generalized additive model (GAM):

At a given year:

$$g[\mathbb{E}(a_j)] = \alpha + s_1(l_j) + s_2(lon_j, lat_j) + \varepsilon_j$$

g is the log-link function
a_j is the age of the sampled individual j in the age subsample
l_j is the length of the sampled individual j in the age subsample
lon_j, lat_j is the spatial location where the j individual was sampled
ε_j is the error term

The response variable is **age (discrete)**

Alternative approaches to ALK?

- Berg et al. (2012): used continuation ratio logits (CRL) and GAM for estimation:

At a given year:

$$g[\mathbb{E}(\pi_{a,j})] = \alpha_a + \beta_a l_j + s_a\left(lon_j, lat_j\right) + \varepsilon_{a,j}$$

g is the logit-link function
$\pi_{a,j}$ is the conditional probability of a fish of being age a given that it is at least that age:

$$\pi_a = P(Y = a | Y \geq a) = \frac{p_a}{p_a + \cdots + p_{A^*}}$$

A^* is the maximum estimable age
J is the minimum estimable age

Then, the unconditional probabilities at age are estimated:

$$\tilde{p}_J = \hat{\pi}_J \qquad \tilde{p}_a = \hat{\pi}_a \prod_{j=J}^{a-1}(1 - \hat{\pi}_j), \quad a > J$$

The response variable is **proportions-at-age**

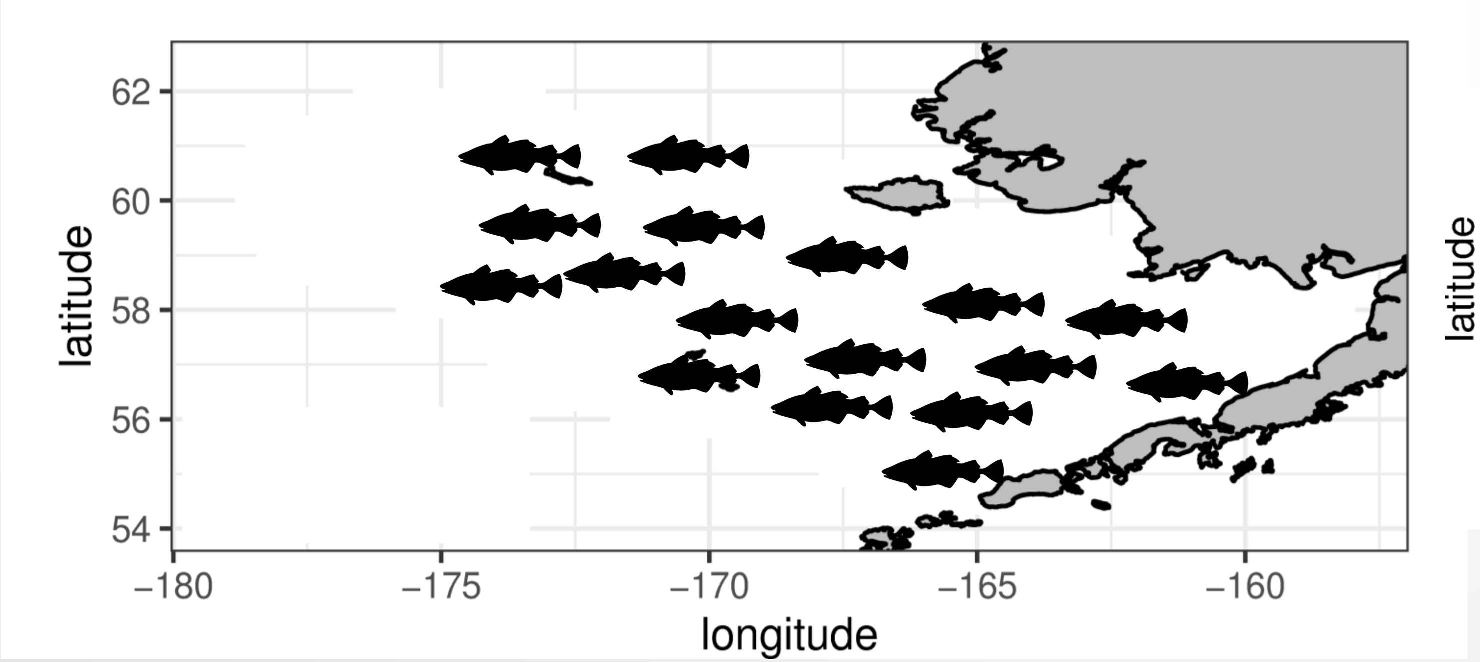
Objectives

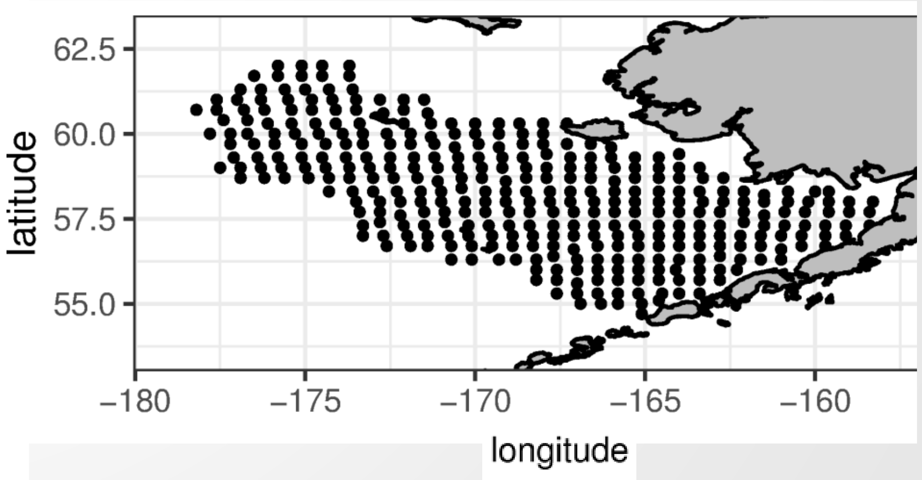
Evaluate the performance of classic age-length keys (design-based) and two alternative approaches (model-based) to estimate age compositions of a fish population with spatial and temporal variability in somatic growth

Evaluate how age compositions estimated using different approaches perform in a stock assessment model

Simulation experiment

- Spatial and temporal population dynamics of a Pacific cod-like species
- A survey per year (Bottom-trawl survey-like)
  - Haul catches
  - Length subsamples
  - Age subsamples
  - Age composition estimates per survey





Spatial and temporal variability in somatic growth

Two somatic growth scenarios:

- No spatial / No temporal (No S / No T)
- Spatial / Temporal (S / T)

$$L_a = L_\infty(1 - e^{-k^*(a-t_0)})$$

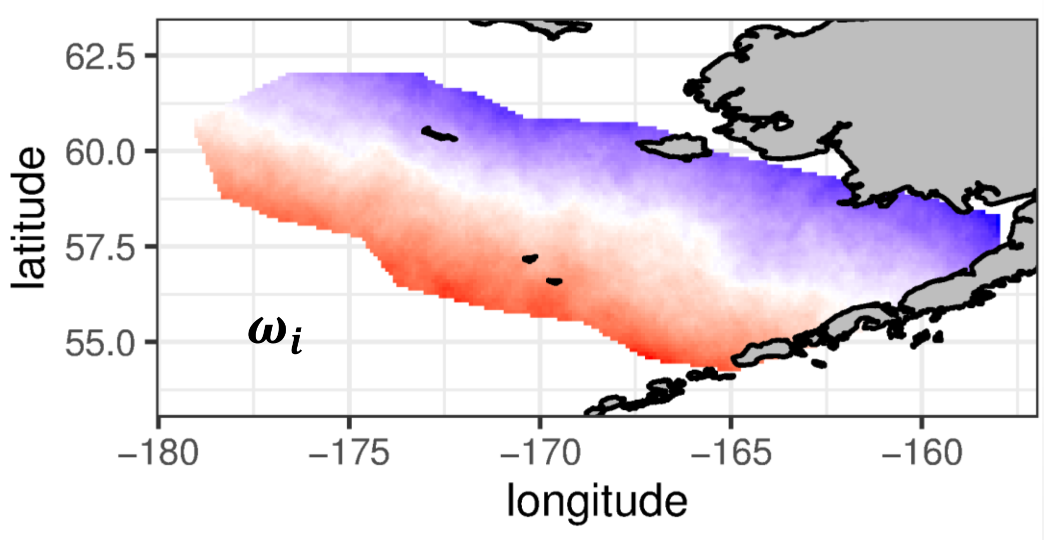
No S / No T:

$$k^* = k$$

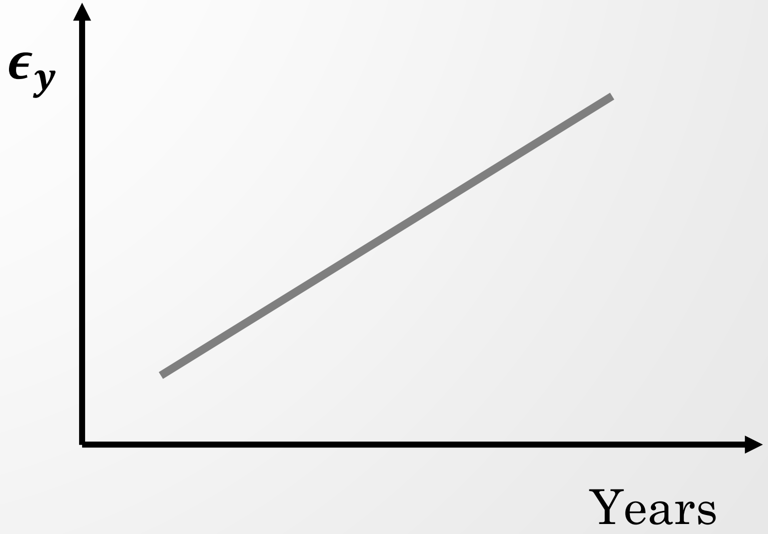
S / T:

$$k^* = k + \boxed{\omega_i} + \boxed{\epsilon_y}$$

Spatial variability:

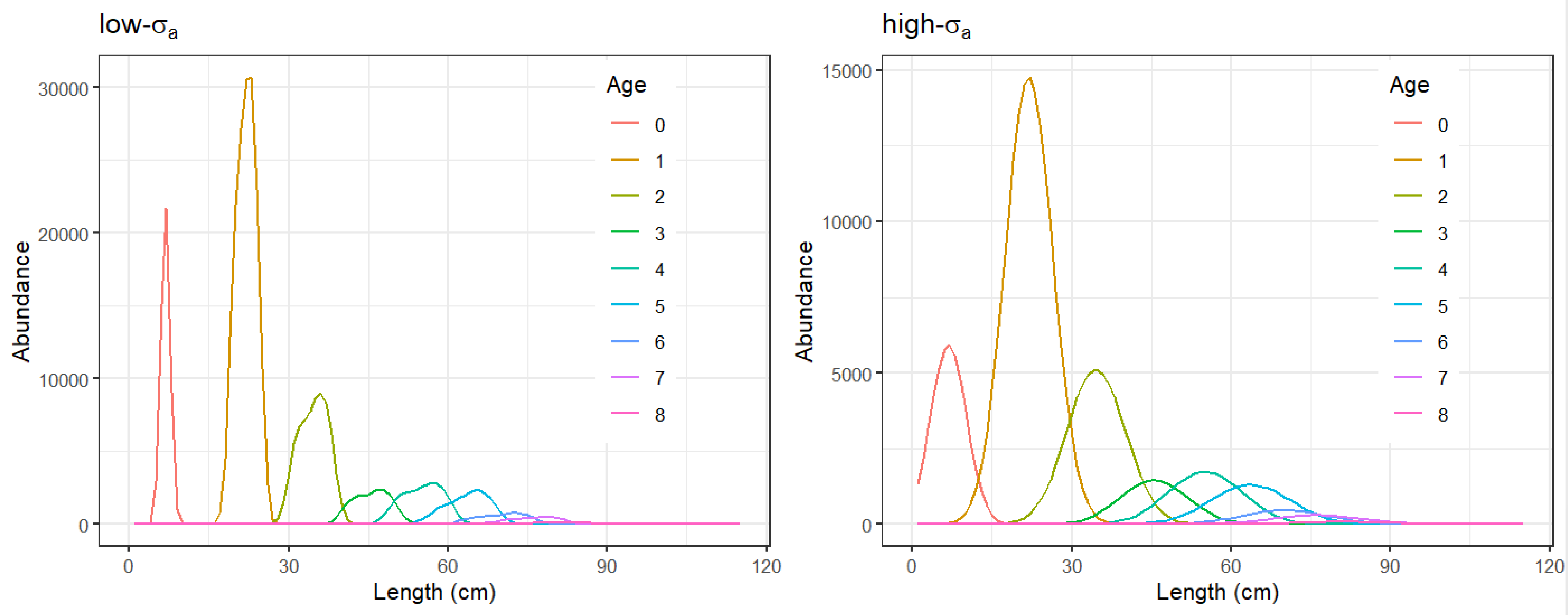


Temporal variability:



Degree of overlap in size-at-age

At a given location:



Correa et al. (2020)

σ_a = Variance of size-at-age

Age assignment

1. **Pooled age-length key (pooled ALK):** length and age information from different years is combined to construct a single ALK.
2. **Annual age-length key (annual ALK):** uses year-specific length and age information to construct ALKs.
3. **Generalized Additive Models (GAM):** is the Puerta's approach. Age is the response variable.
4. **Continuation Ratio Logits (CRL):** is the Berg's approach. Proportion-at-age is the response variable.

Age assignment

a-b) Pooled or annual ALK

Length subsample

l	$\hat{c}_l$

Age assignment

J	...	A^*
$q_{l,J}$	...	q_{l,A^*}

Abundance-at-age estimation

$$\hat{c}_J = \hat{c}_l * q_{l,J}$$
$$\dots$$
$$\hat{c}_{A^*} = \hat{c}_l * q_{l,A^*}$$

c) GAM

Length subsample

l	$\hat{c}_l$	lon	lat

Age assignment

$$\hat{a} \in \{J, \dots, A^*\}$$

Abundance-at-age estimation

$$\hat{c}_a = \hat{c}_l$$
where $a = \hat{a}$

d) CRL

Length subsample

l	$\hat{c}_l$	lon	lat

Age assignment

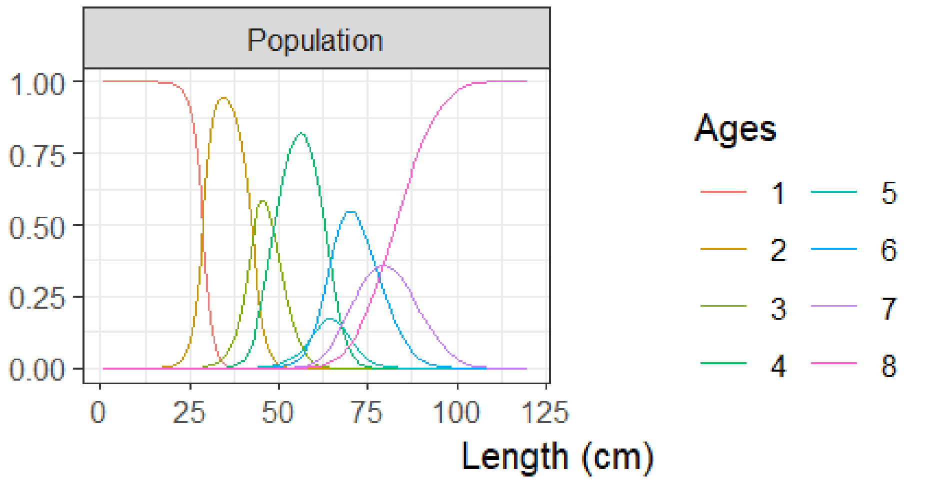
J	...	A^*
$\tilde{p}_J$	...	$\tilde{p}_{A^*}$

Abundance-at-age estimation

$$\hat{c}_J = \hat{c}_l * \tilde{p}_J$$
$$\dots$$
$$\hat{c}_{A^*} = \hat{c}_l * \tilde{p}_{A^*}$$

Correa et al. (2020)

Age assignment



Correa et al. (2020)

Age compositions in stock assessment models

Age compositions are an informative input to stock assessment models:

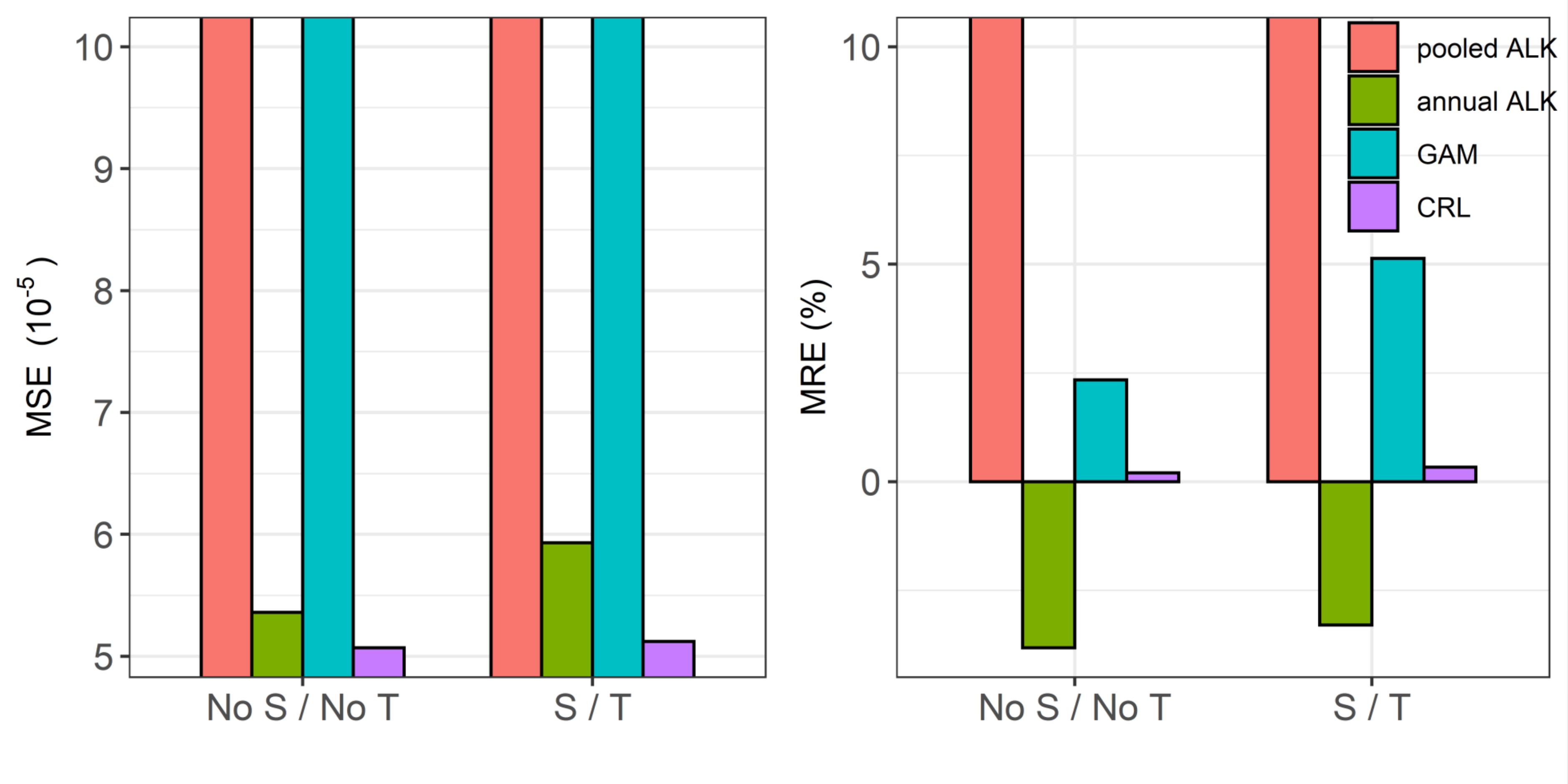
- Recruitment
- Mortality
- Somatic growth
- Selectivity

Using survey data of Pacific cod in the eastern Bering Sea (1994 - 2016):

1. Estimate age compositions using the four evaluated approaches
2. Include these age compositions in the Pacific cod stock assessment model separately
3. Compare consistency among data inputs in the stock assessment model

Results

High-σ_a case:

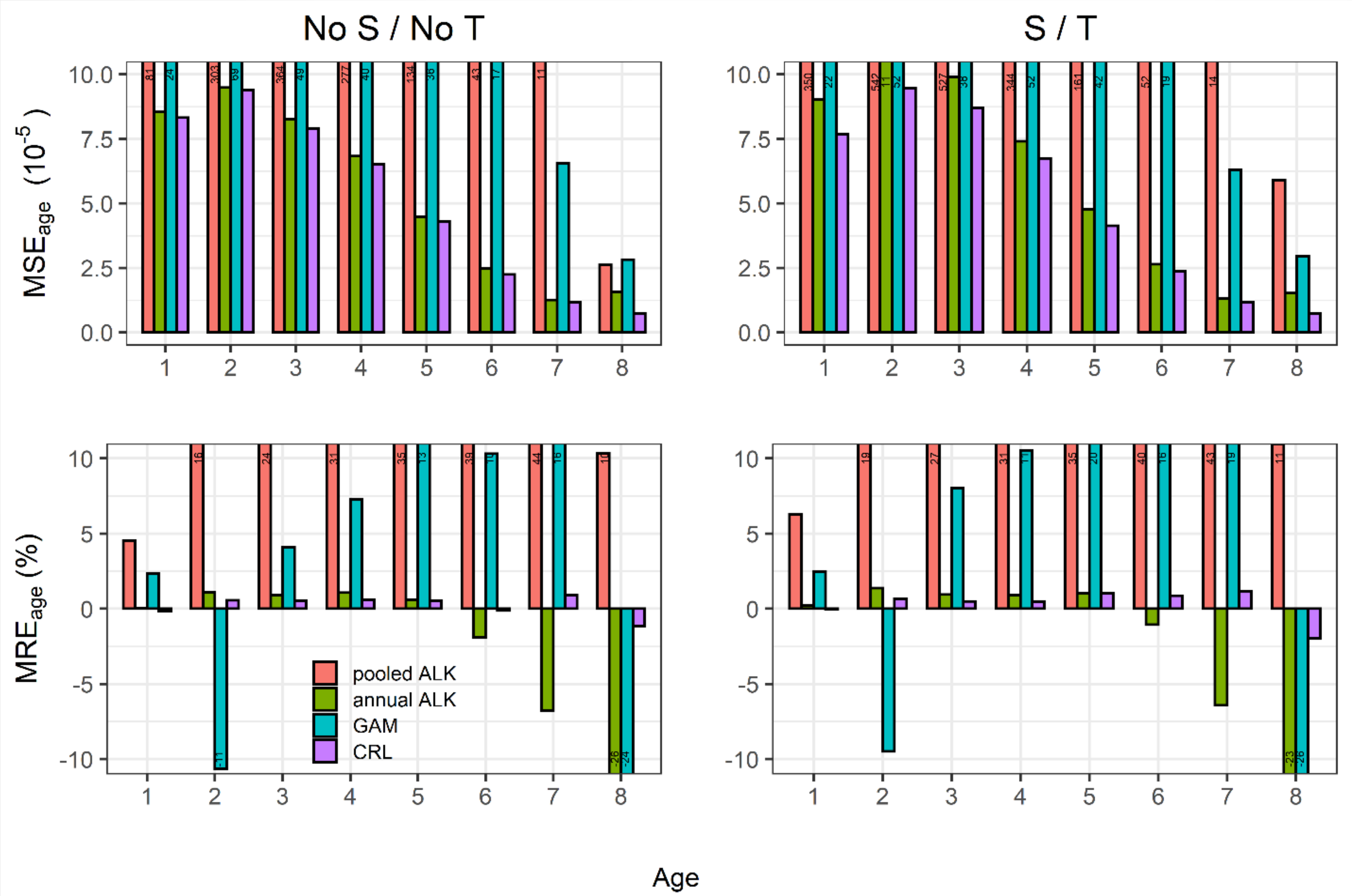


Correa et al. (2020)

MSE: Measure of error
MRE: Measure of bias

Results

High-σ_a case, indicators per age:

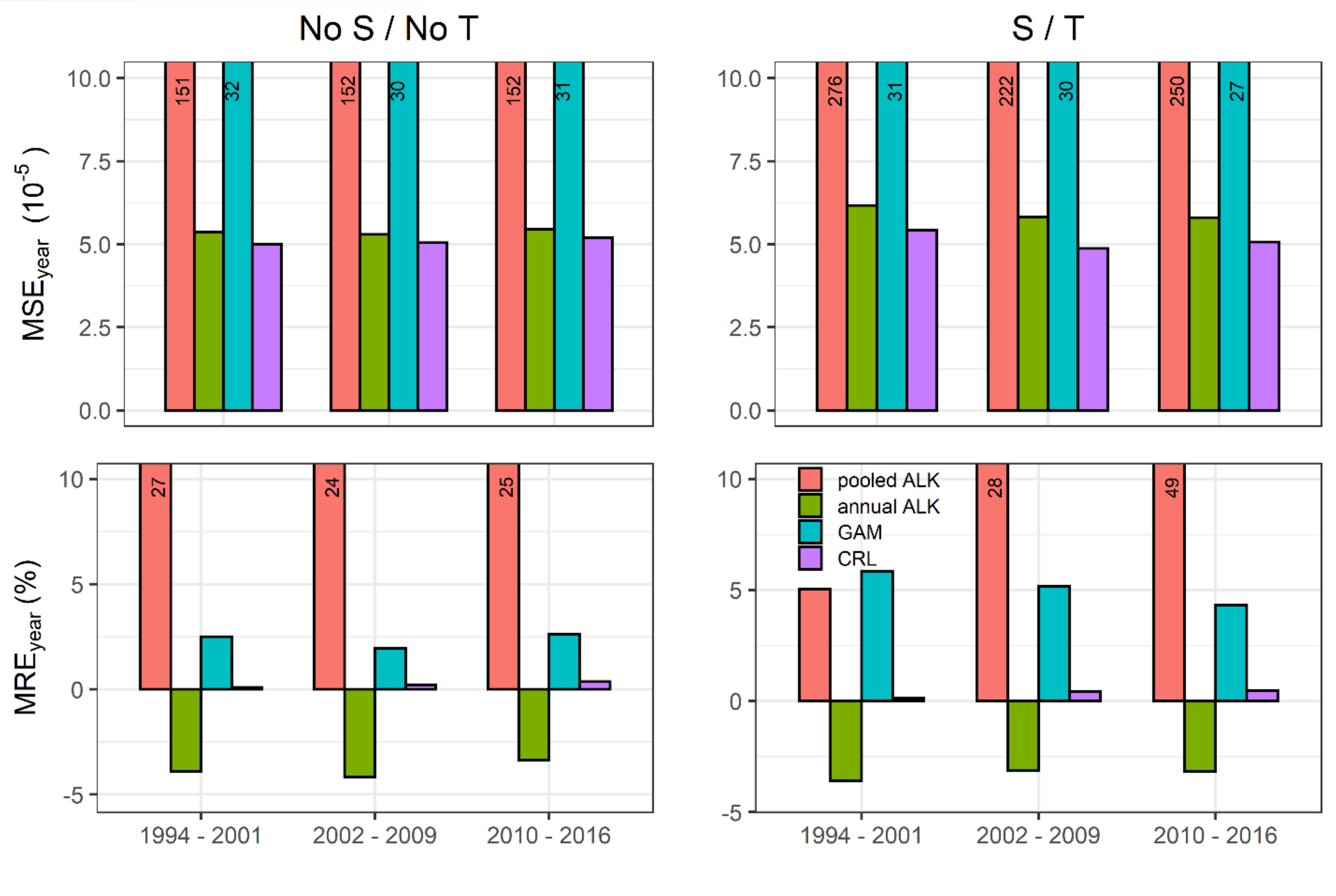


Correa et al. (2020)

MSE: Measure of error
MRE: Measure of bias

Results

High-σ_a case, indicators per period:

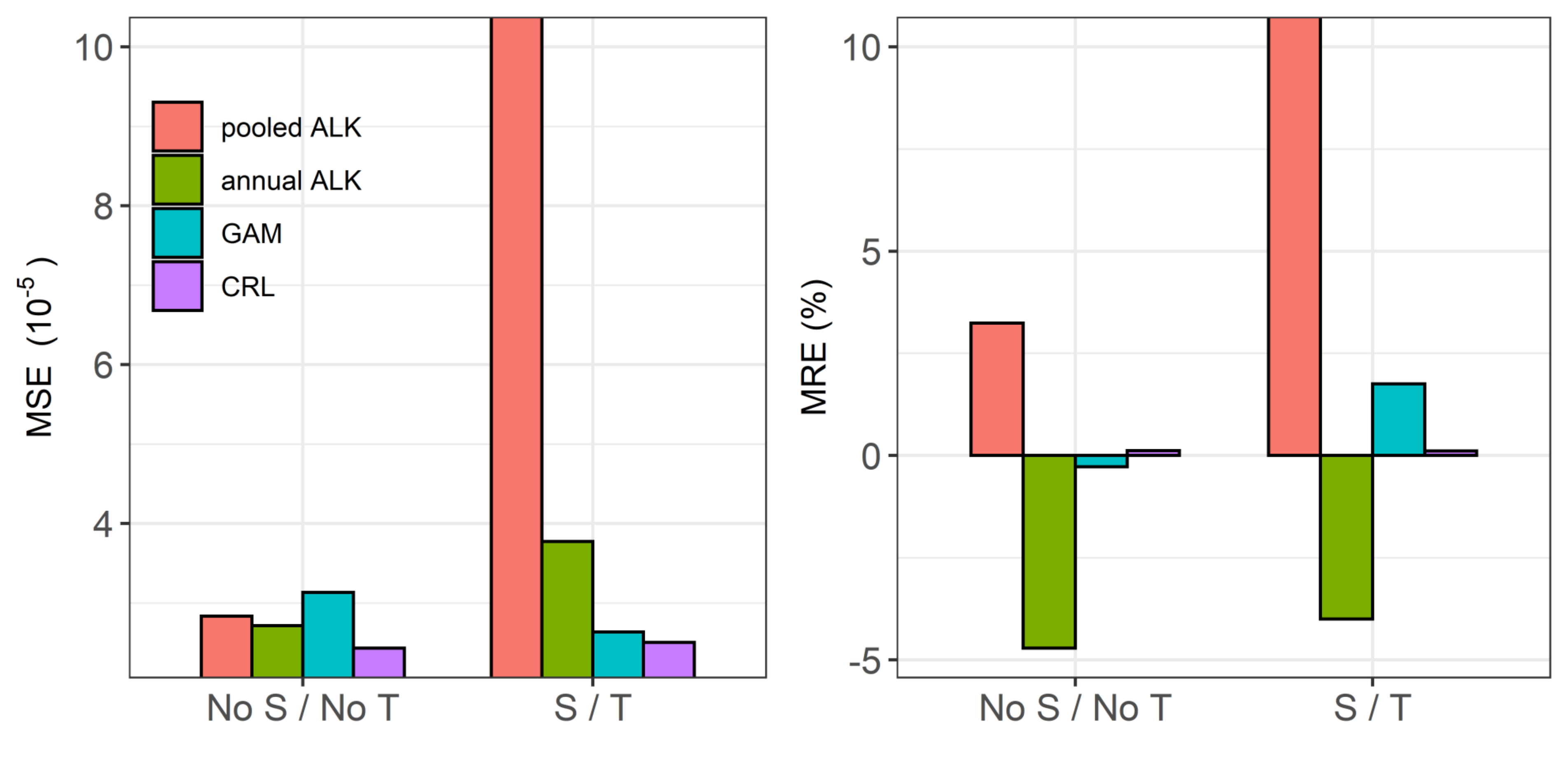


Correa et al. (2020)

MSE: Measure of error
MRE: Measure of bias

Results

Low-σ_a case:



Correa et al. (2020)

MSE: Measure of error
MRE: Measure of bias

Results

Age compositions in stock assessment models:

- Look at likelihood components

Component	SS pooled ALK	SS annual ALK	SS GAM	SS CRL
Total	92.53	75.18	88.96	$\boxed{72.93}$
Catch	5.9e–13	0.0105e–13	0.06e–13	0.35e–13
Equilibrium catch	11.4e–05	6.3e–05	9.6e–05	6.8e–05
Survey	–29.7	–40.7	–40.05	–40.15
Length composition	74.27	72.1	72.66	71.77
Age composition	76.32	61.83	71.26	59.43
Recruitment	–29.23	–19.03	–16.08	–19.09

Correa et al. (2020)

Conclusions

- CRL approach was the most robust method to estimate age compositions
- Pooled ALK was the worst method
- Annual ALK was affected by data gaps in older ages
- GAM approach highly affected by the degree of overlap in size-at-age across ages
- Evidence that CRL approach might improve data consistency and fit in stock assessment models

https://github.com/gmoroncorrea/STageCompsEstimation

2. Consequences of somatic growth misspecification on stock assessment outcomes

Stock assessment models

Stock assessment: process of collecting and analyzing biological and statistical information to determine the changes in the abundance of fisheries stocks in response to fishing and to predict future trends of stock abundance.

Data:

- Catch
- Abundance indices
- Length compositions
- Age compositions
- Environmental indices

Parameters:

- Mortality
- Somatic growth
- Stock-recruitment
- Selectivity
- Fecundity

Stock assessment model:

- Population model
- Observation model
- Statistical model

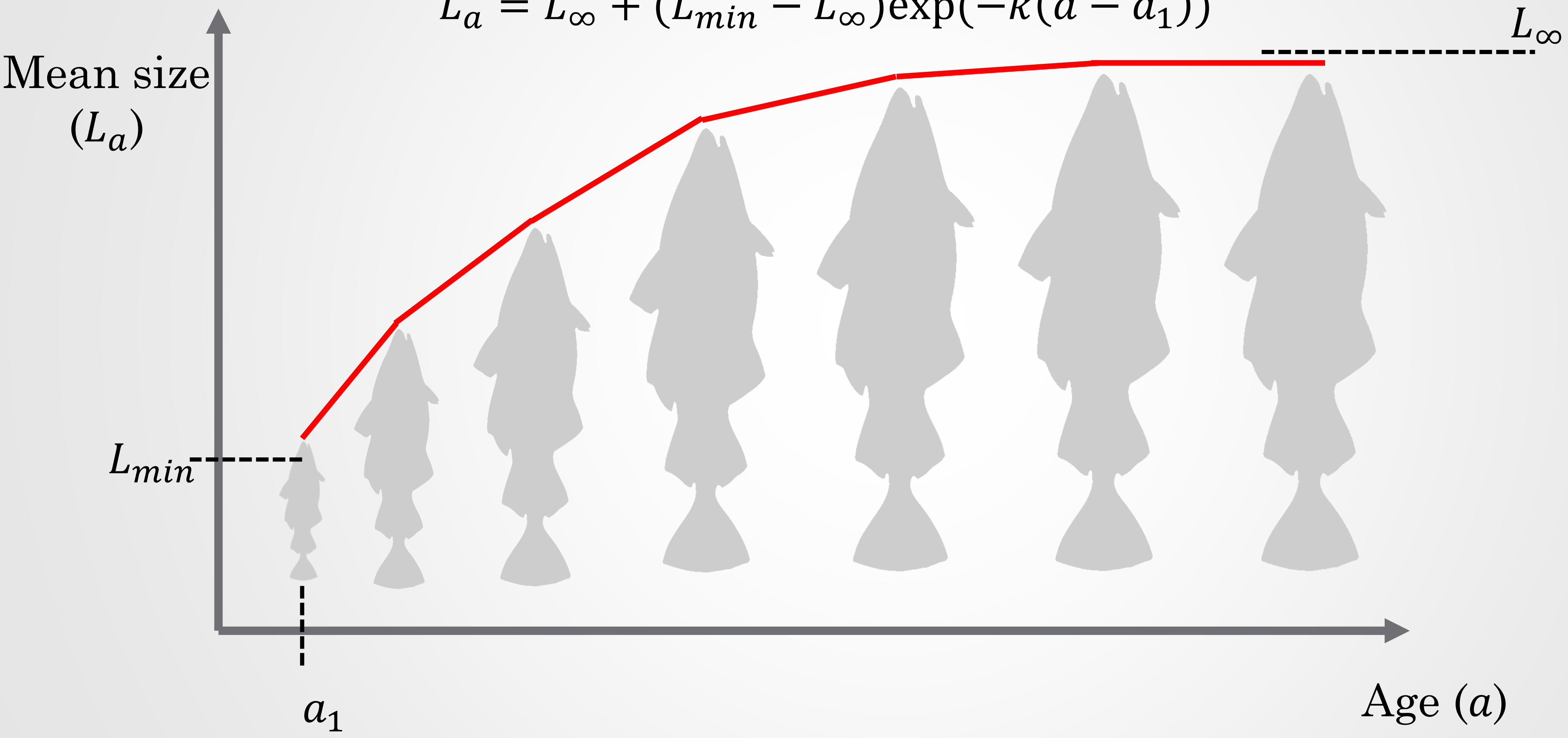
Stock assessment outcomes:

- Biomass estimates
- Parameter estimates
- Stock status
- Reference points

Fisheries management

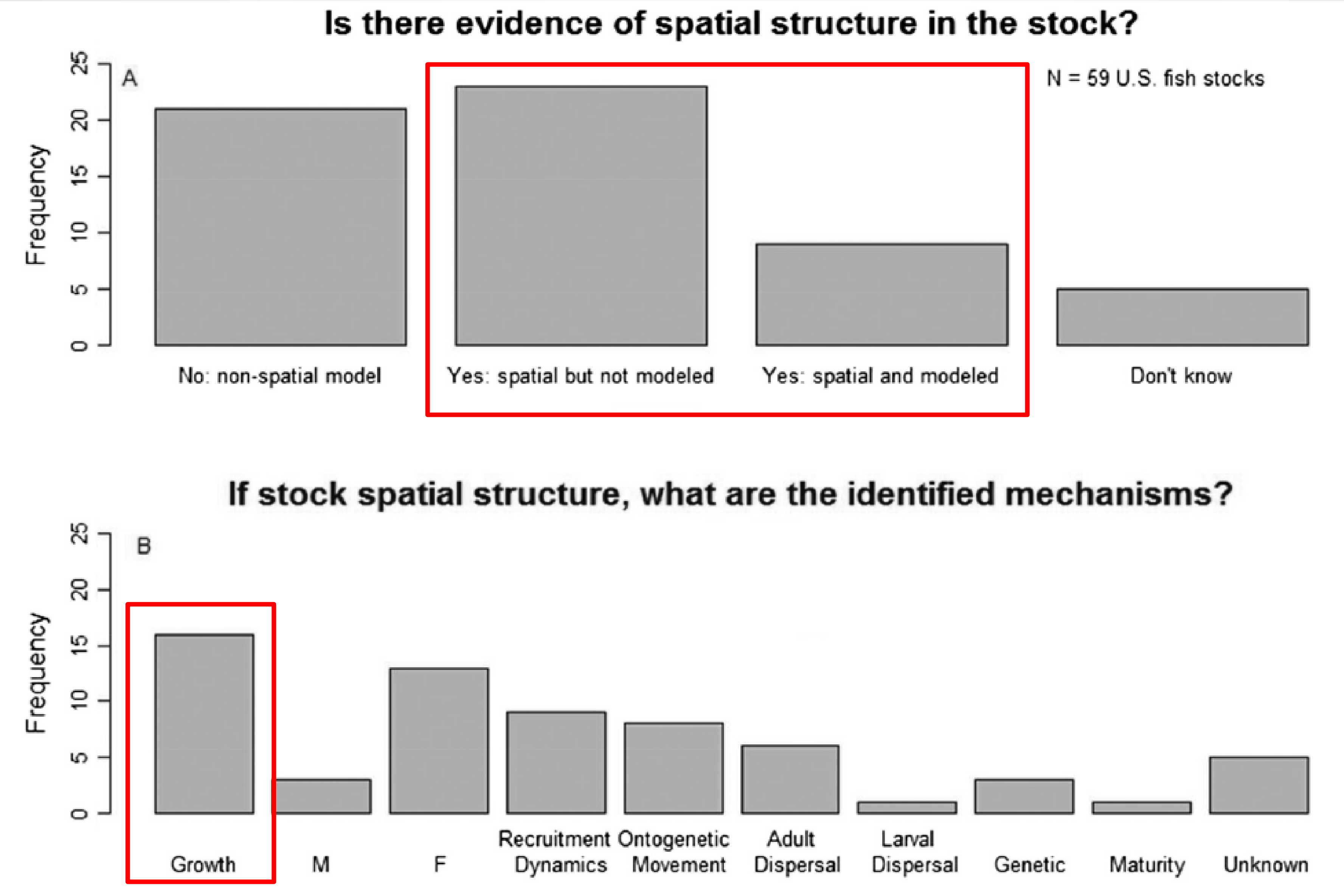
Growth in stock assessment models

$$L_a = L_\infty + (L_{min} - L_\infty)\exp(-k(a - a_1))$$



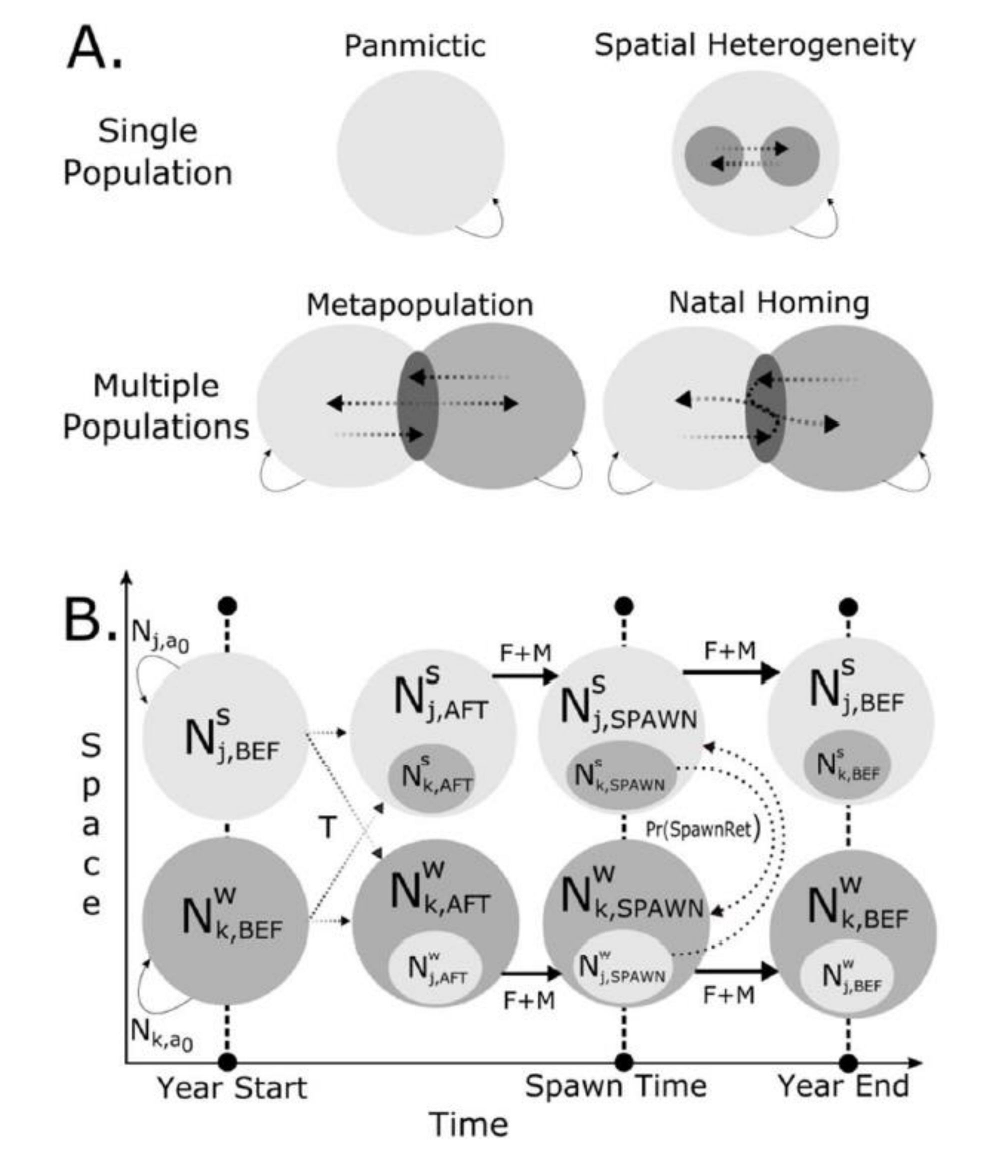
Growth parameters should be assumed constant in space and time?

Spatial structure in stock assessment models



Berger et al. (2017)

Spatial structure in stock assessment models



Goethel and Berger et al. (2019)

Modeling the spatial structure of a stock is a complex process.

In general:

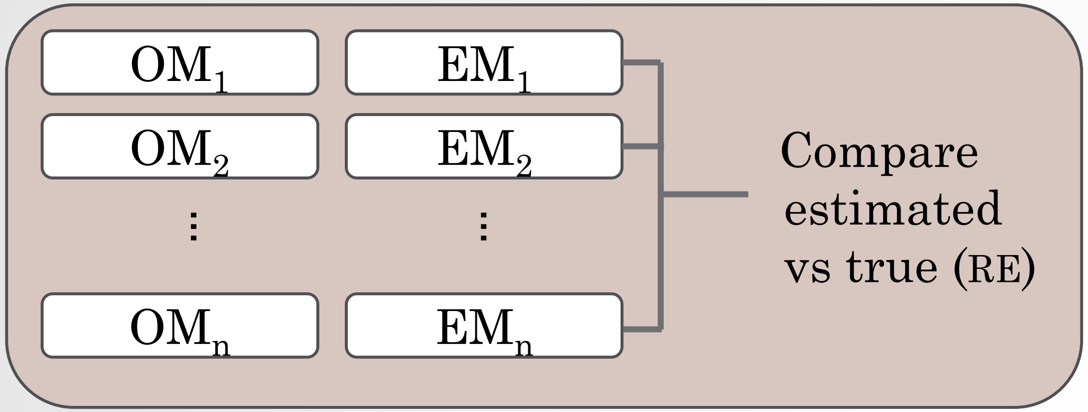
- Spatially explicit models improve model outcomes.
- Becoming popular when data permit.

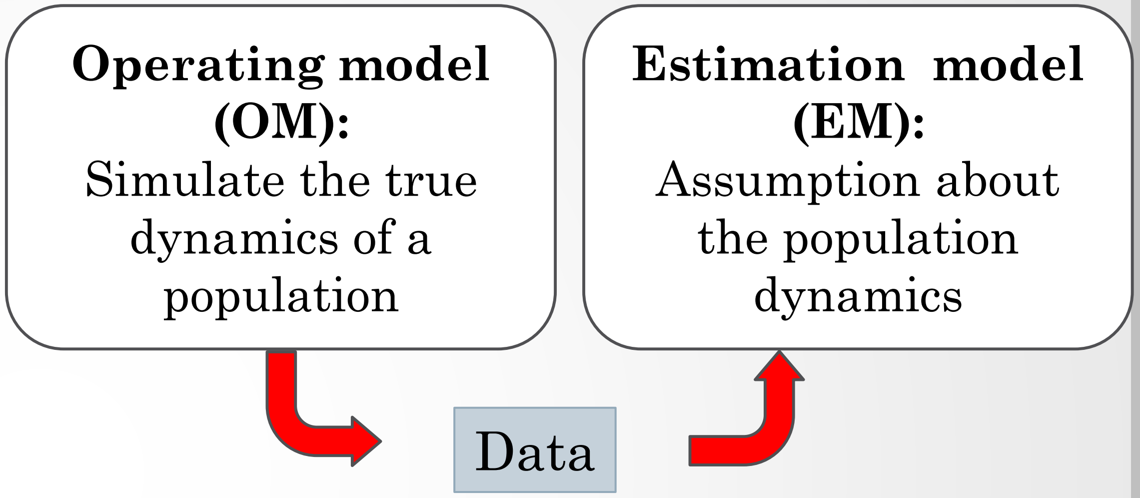
Challenges (Punt et al. 2019):

- Lack of data
- Lack of biological information (movement data!)
- Political boundaries ≠ biological boundaries
- Computational demands

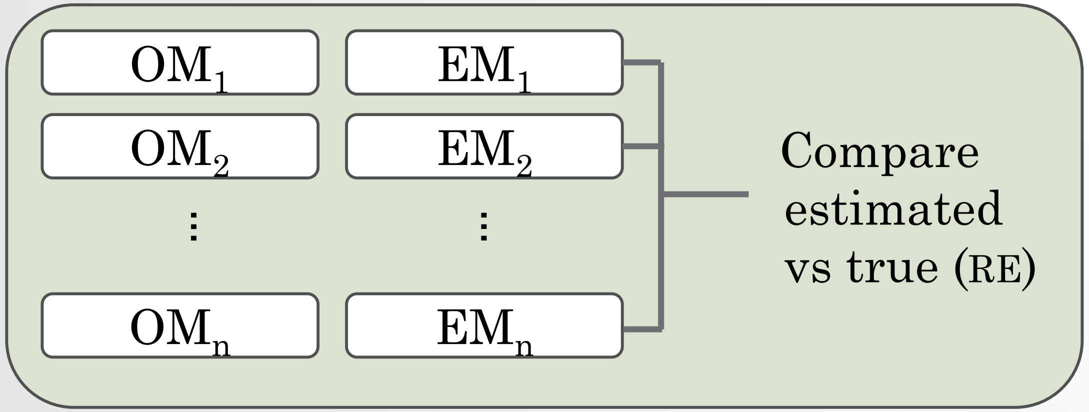
Simulation experiments in stock assessment models

Scenario 1:





Scenario 2:



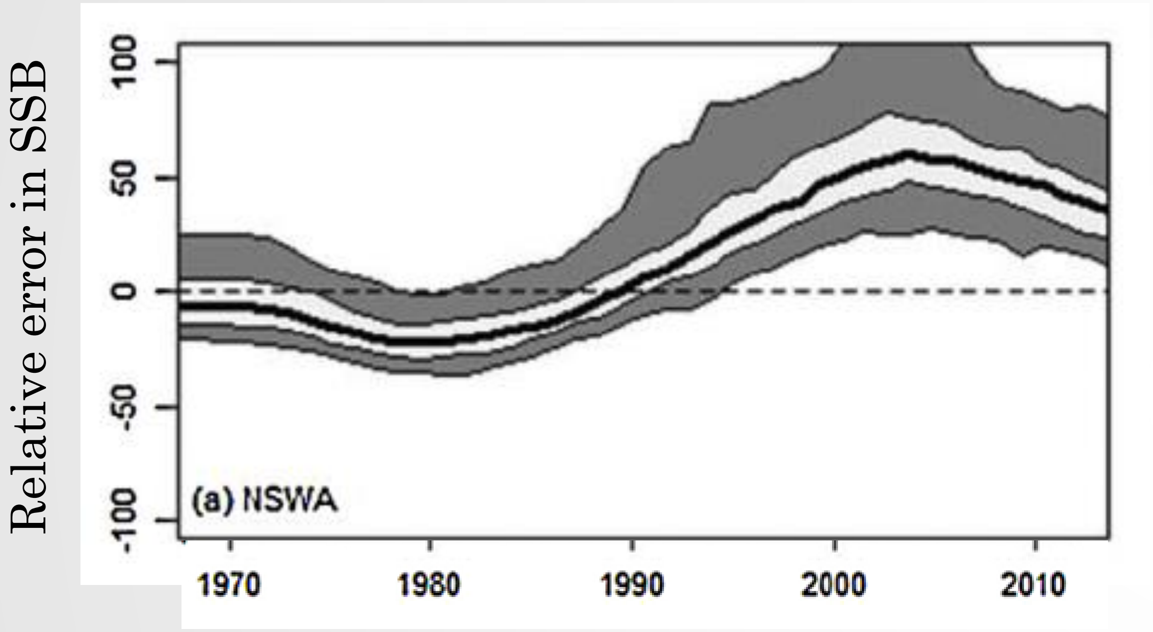
⋮

Scenario k:

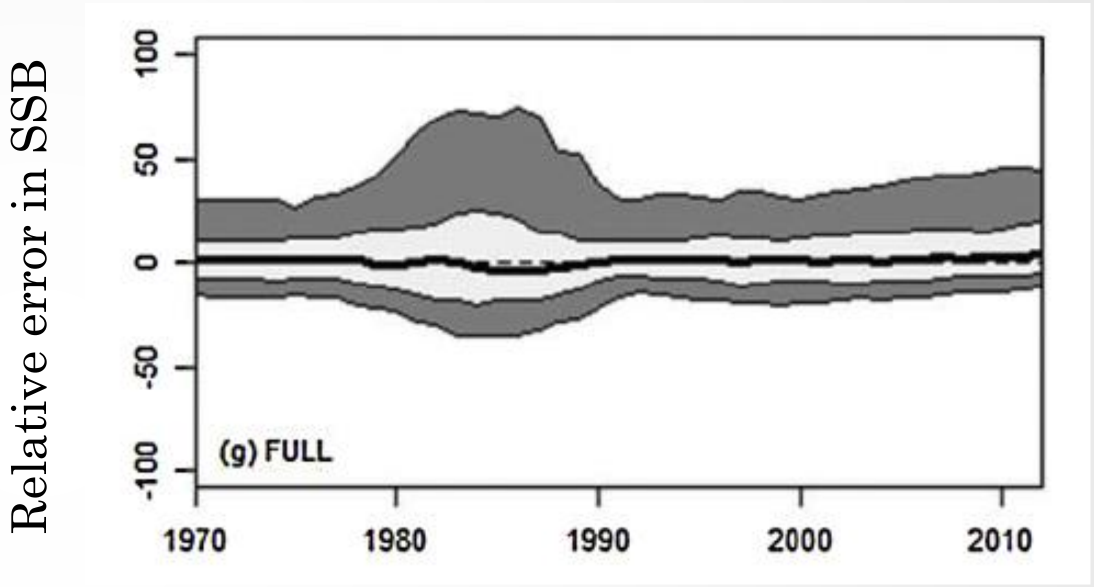
- Simulation-estimation process
- Different 'realities' can be simulated
- Used for different purposes:
  - Movement
  - Recruitment
  - Natural mortality
  - Data quantity and quality
  - Somatic growth

Spatial variability in somatic growth

Ignore spatial variability in somatic growth:



Include spatial variability in somatic growth:



Using parameters from pink ling (*Genypterus blacodes*) in Australia and a simulation experiment:

- Ignoring spatial structure: more biased estimates but precise
- Considering spatial structure (i.e., spatially explicit model): unbiased estimates

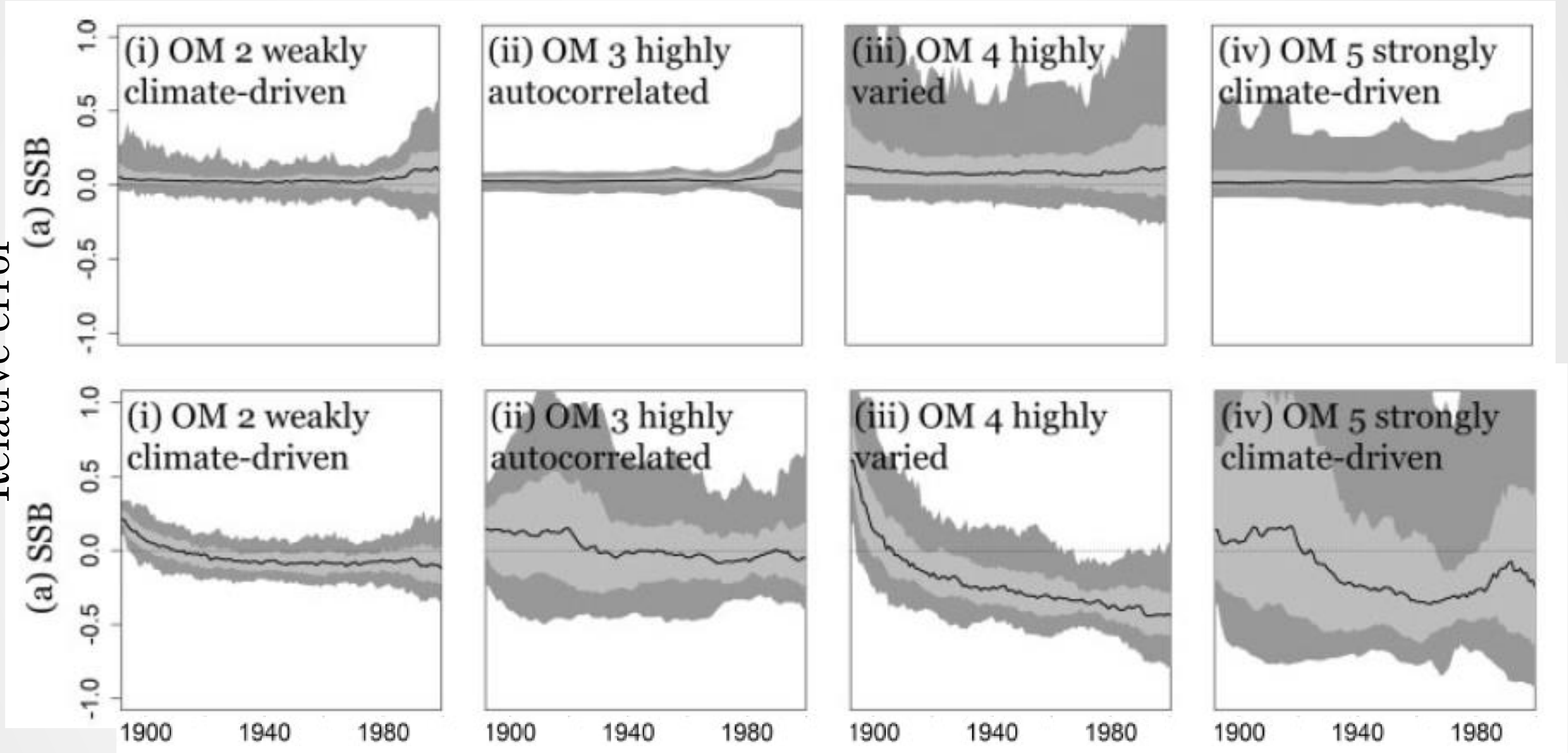
Punt et al. (2015)

Temporal variability in somatic growth

EM correctly specified including an environmental index

EM misspecified

Relative error

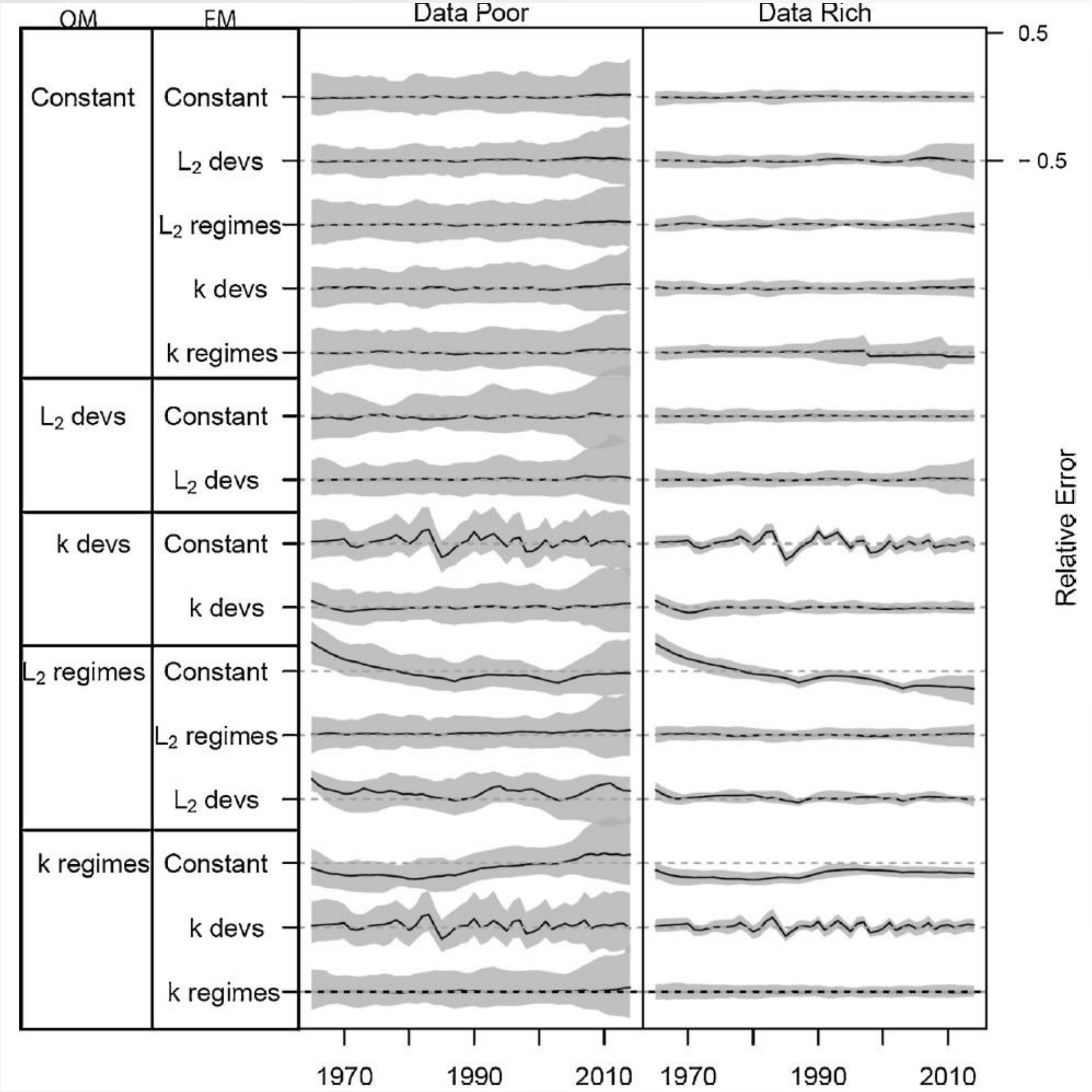


Using parameters from splitnose rockfish (*Sebastes diploproa*), they simulated temporal variability in somatic growth:

- Highly biased SSB estimates when EM was misspecified

Lee et al. (2018)

Temporal variability in somatic growth



Using parameters petrale sole (*Eopsetta jordani*) in the California Current, they simulated temporal variability in somatic growth (deviates and regime-like):

- Data poor vs data rich: data rich scenarios were more precise.
- Unbiased estimates when EM accounted for temporal variability

Stawitz et al. (2019)

Sardine (*Sardinops sagax*)
Cod (*Gadus macrocephalus*)
Rockfish (*Sebastes diploproa*)

Objectives

What if the stock has a substantial spatial and temporal variability in somatic growth but we ignored them?

Evaluate the consequences of misspecification in somatic growth in stock assessment models

- Spatial and temporal variability
- Three life-histories: sardine – cod – rockfish

Simulation experiment using ss3sim (Anderson et al. 2014)

Somatic growth variability simulation

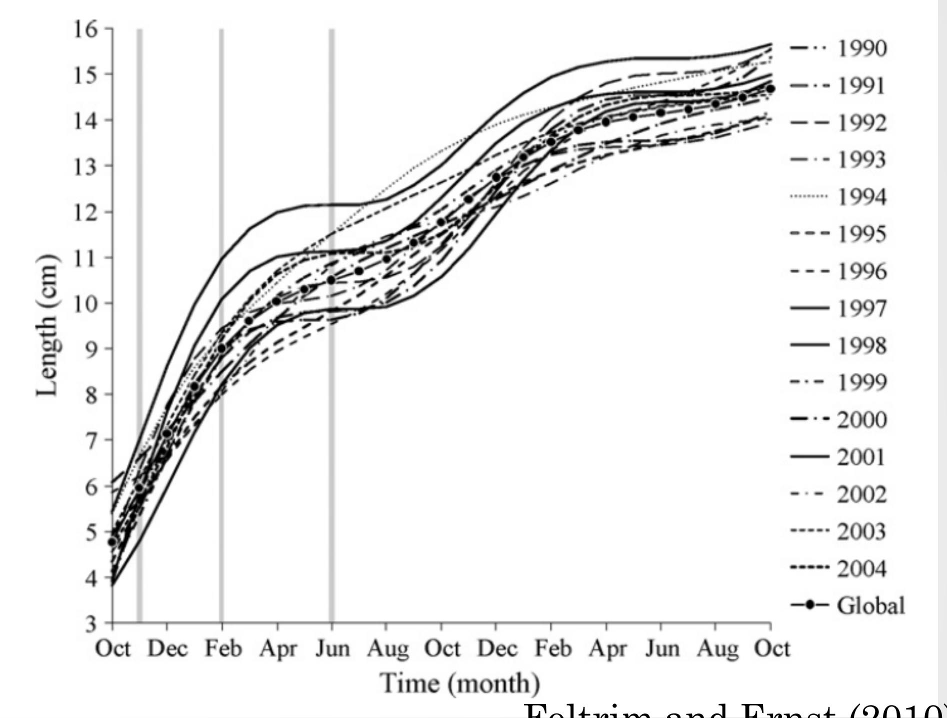
Operating model (OM)

Changes in mean size-at-age
- Changes in k or L_∞

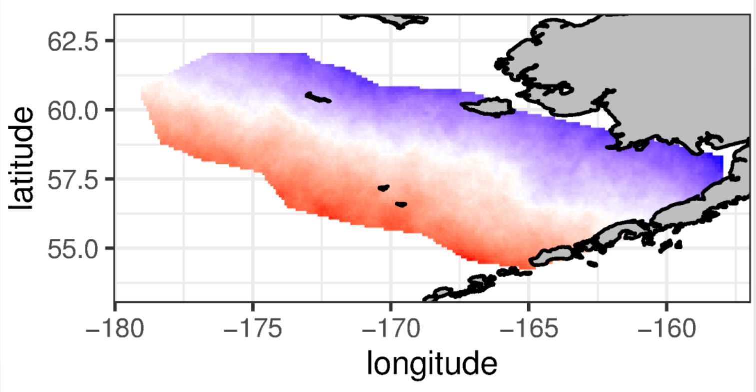
Temporal variability Mean size-at-age varies by:
- Year (year-specific)
- Cohort (cohort-specific)

Follows the PDO trend.

Spatial variability Mean size-at-age varies between two areas

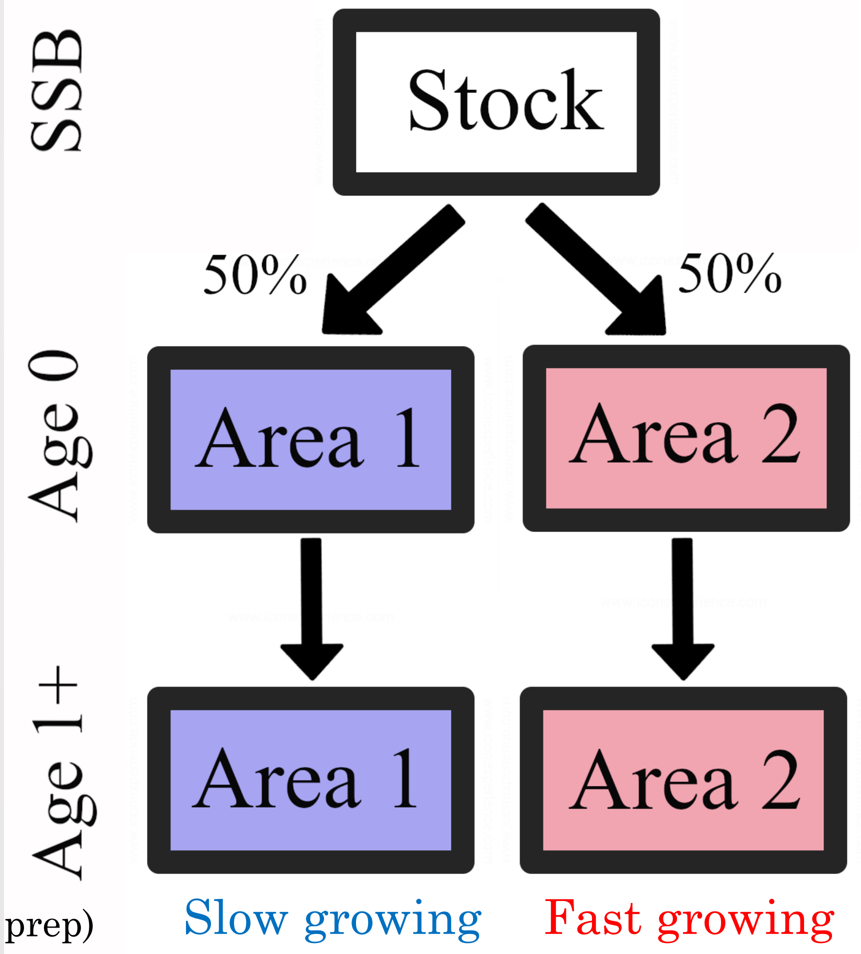


Feltrim and Ernst (2010)



Somatic growth variability simulation

Operating model (OM)

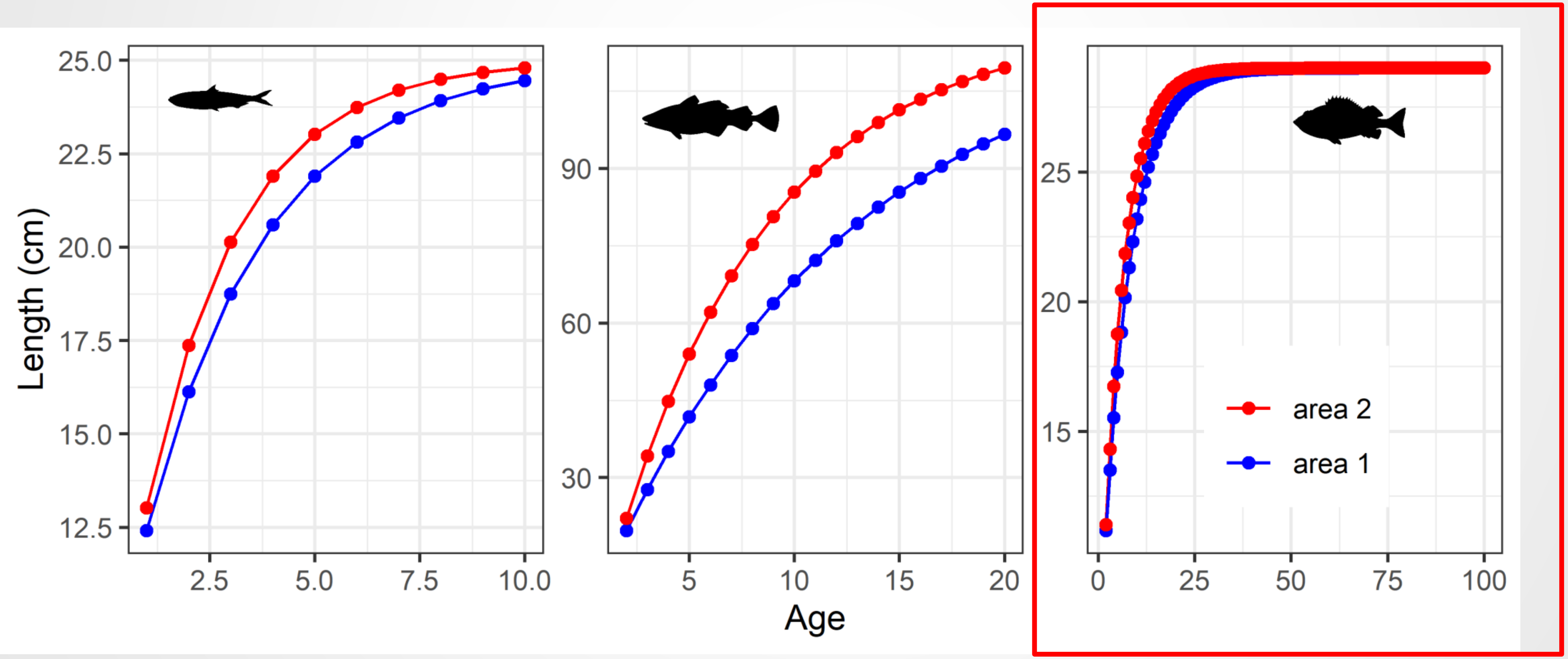


Correa et al. (in prep)

Somatic growth variability simulation

Operating model (OM)

Simulated changes in mean size-at-age by varying the *k* parameter (based on literature):

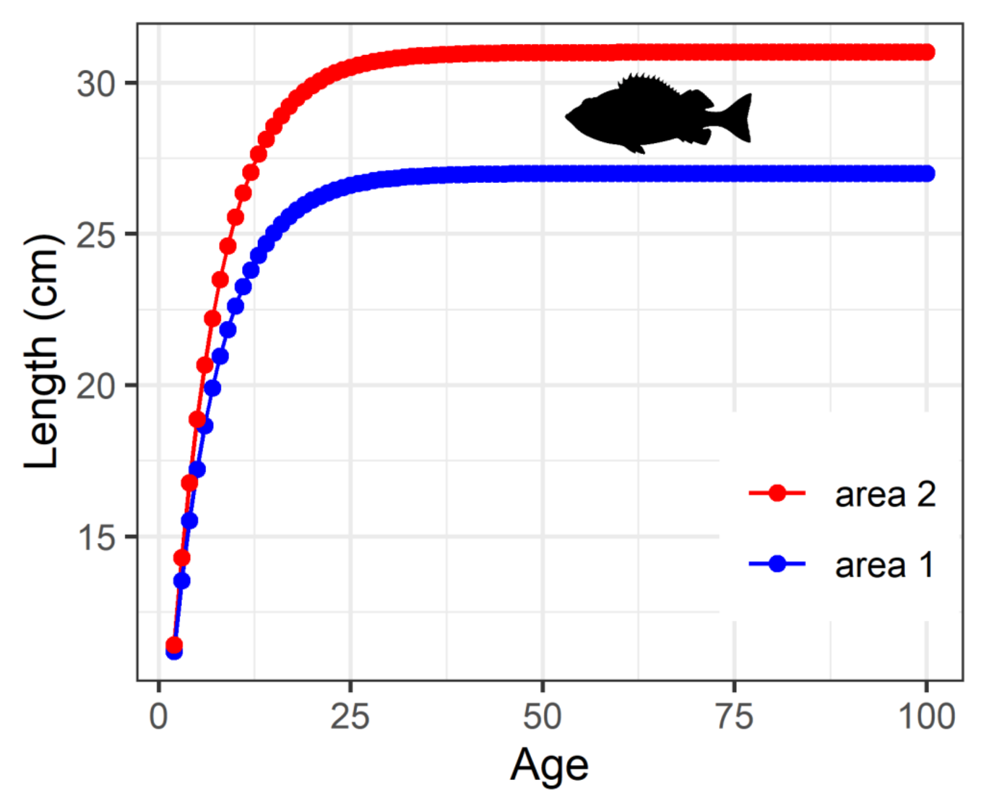


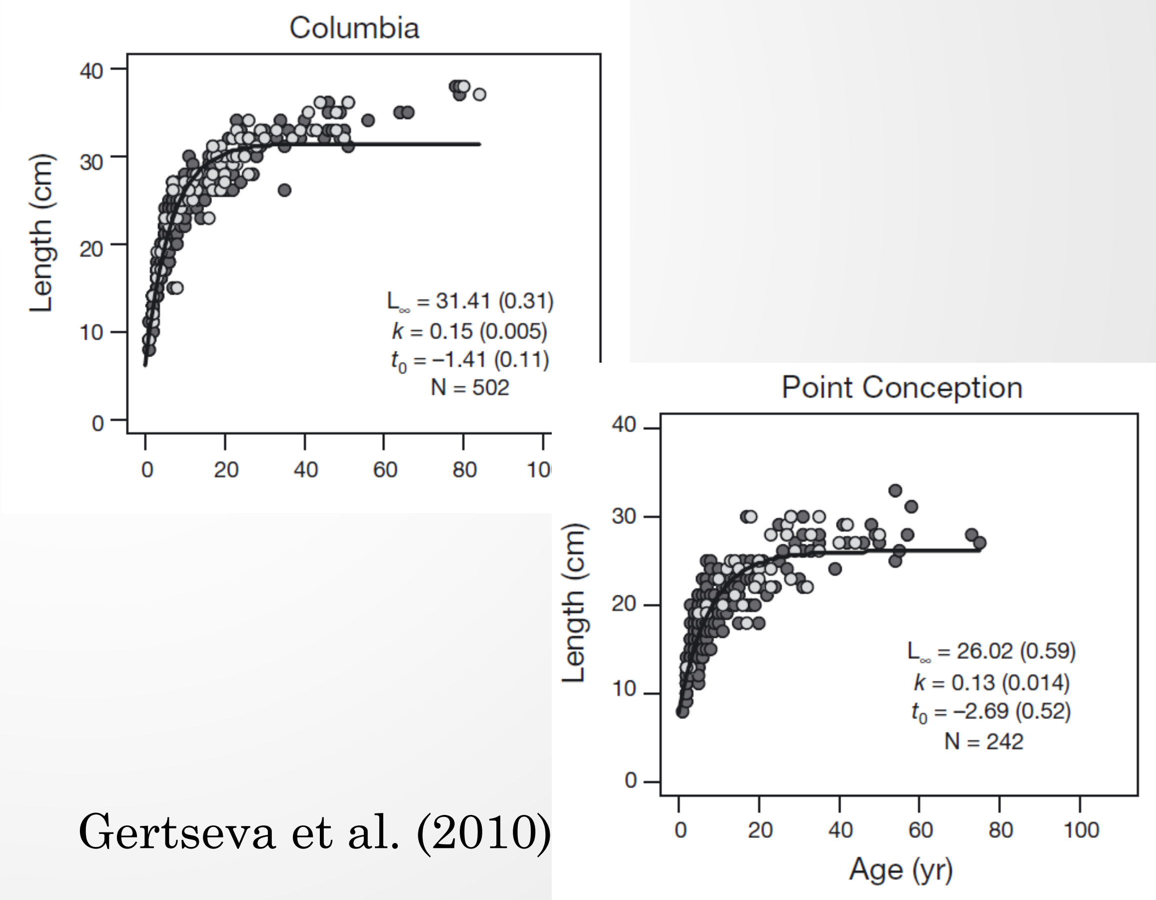
Correa et al. (in prep)

Somatic growth variability simulation

Operating model (OM)

Simulated changes in mean size-at-age by varying the L_∞ parameter (based on literature):





Gertseva et al. (2010)

Somatic growth variability estimation

Estimation model (EM)

When OM simulates **temporal** variability, EM:

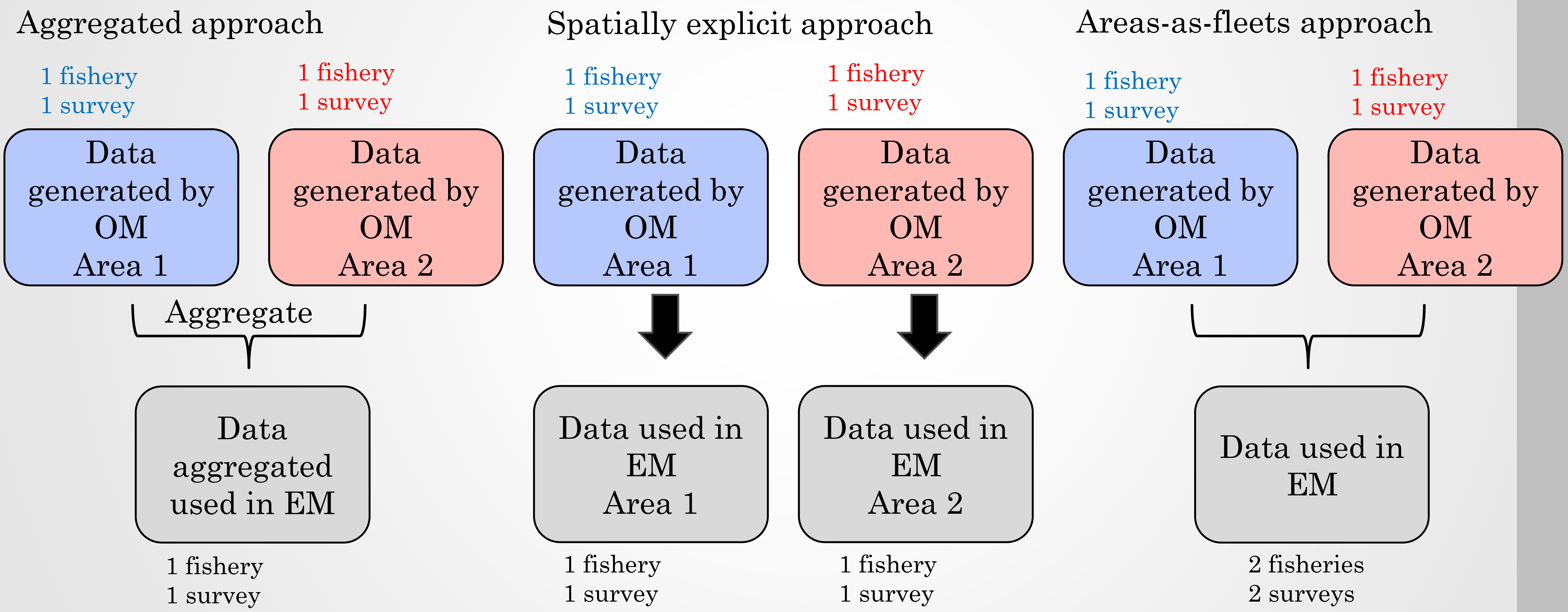
- Assumes k and L_∞ constant over time
- Includes an 'observed' environmental index (env_{obs})

When OM simulates **spatial** variability, EM:

- Aggregated: Assumes k and L_∞ constant over space. Data generated by the OM is aggregated.
- Spatially explicit: Two-area model, k and L_∞ are estimated by area.
- Areas-as-fleet: Like aggregated approach, but data is not aggregated.

Somatic growth variability estimation

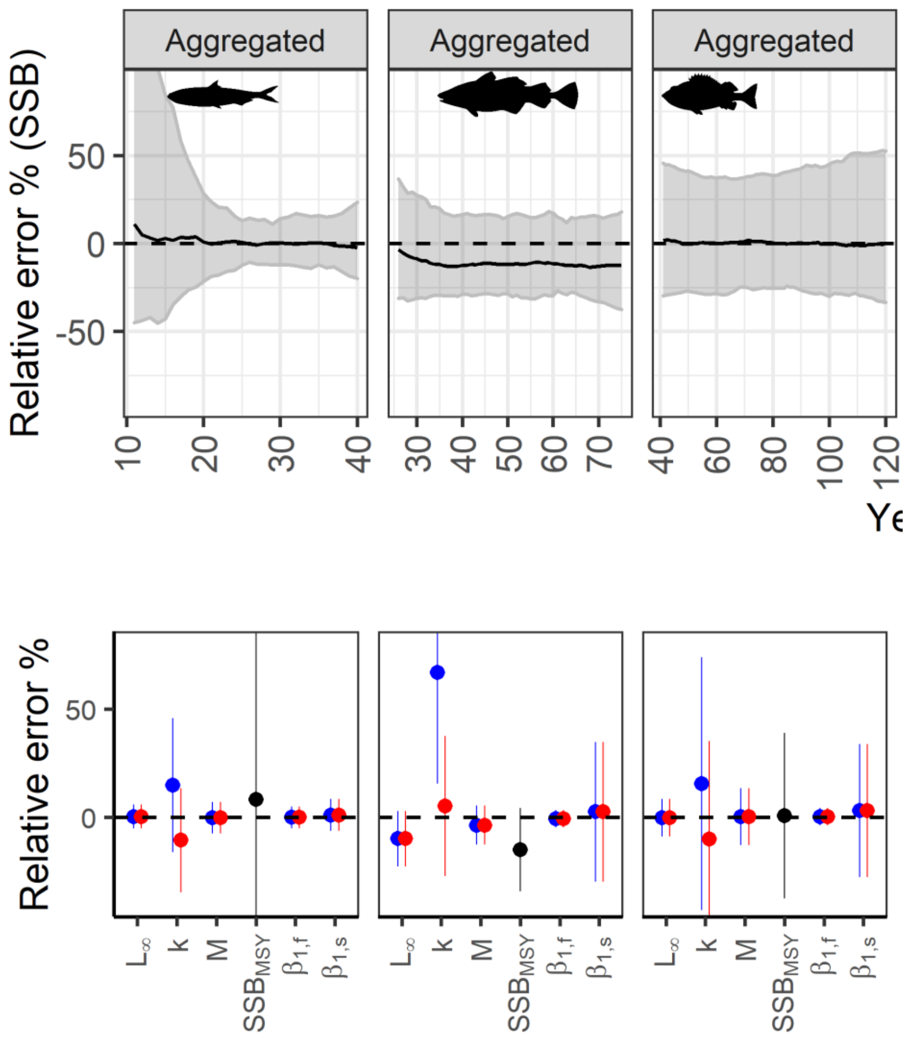
Estimation model (EM)



Results: Spatial variability

OM:

- Spatial variability in mean size-at-age by varying ***k*** between areas



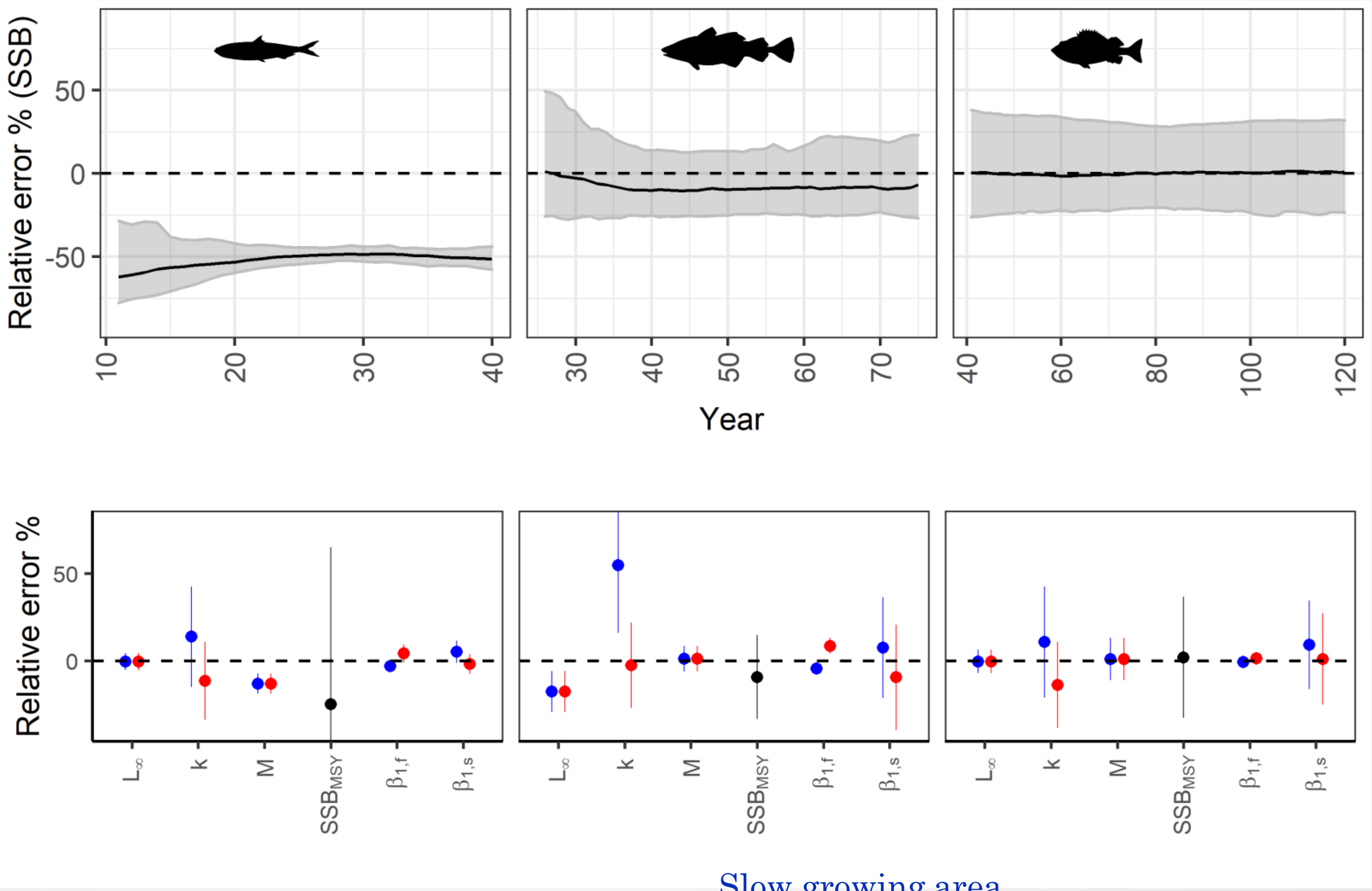
Slow growing area
Fast growing area

Correa et al. (in prep)

Results: Spatial variability

OM:
- Spatial variability in mean size-at-age by varying ***k*** between areas

Areas-as-fleets



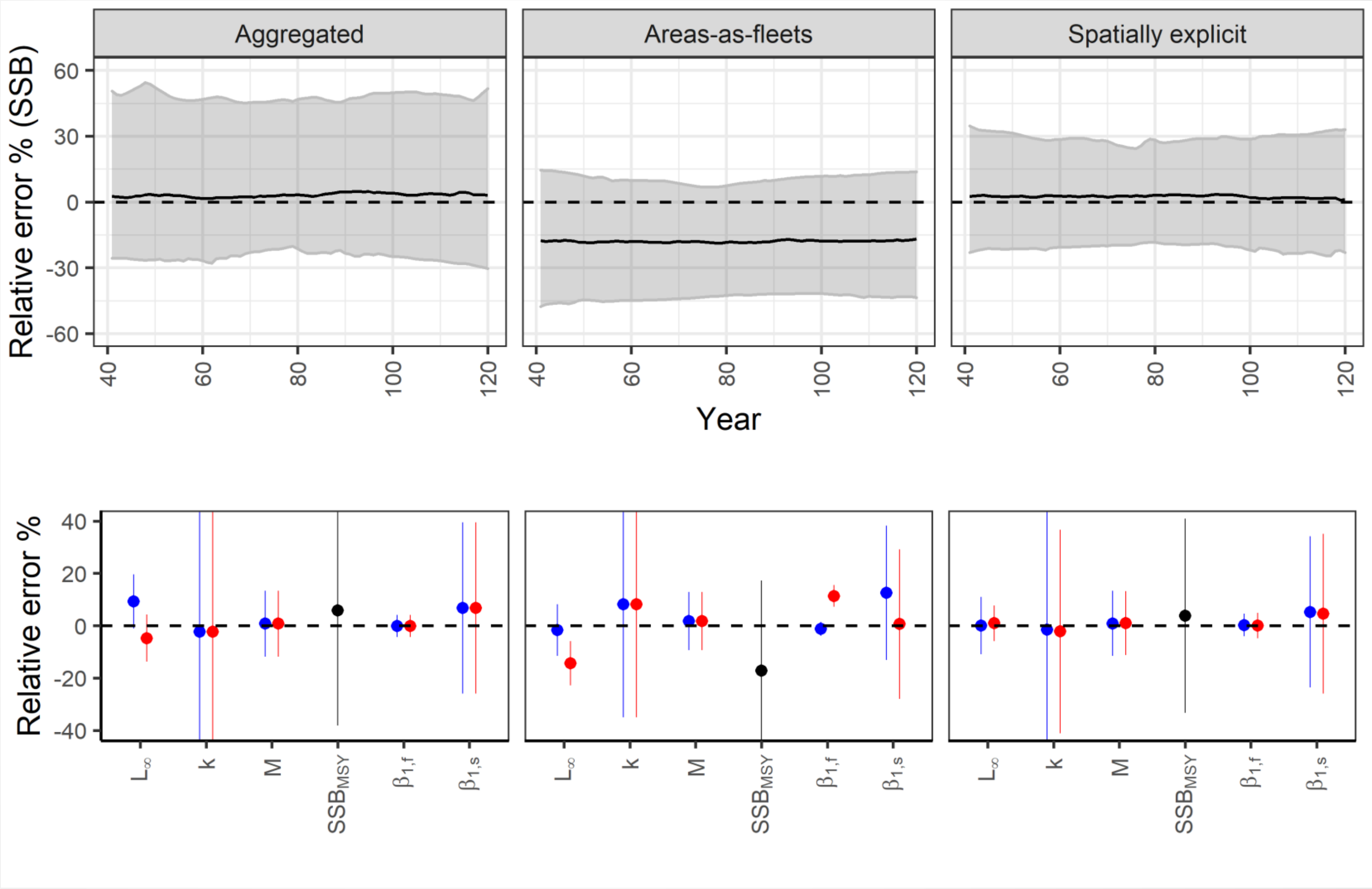
Slow growing area
Fast growing area

Correa et al. (in prep)

Results: Spatial variability

OM:

- Spatial variability in mean size-at-age by varying L_∞ between areas

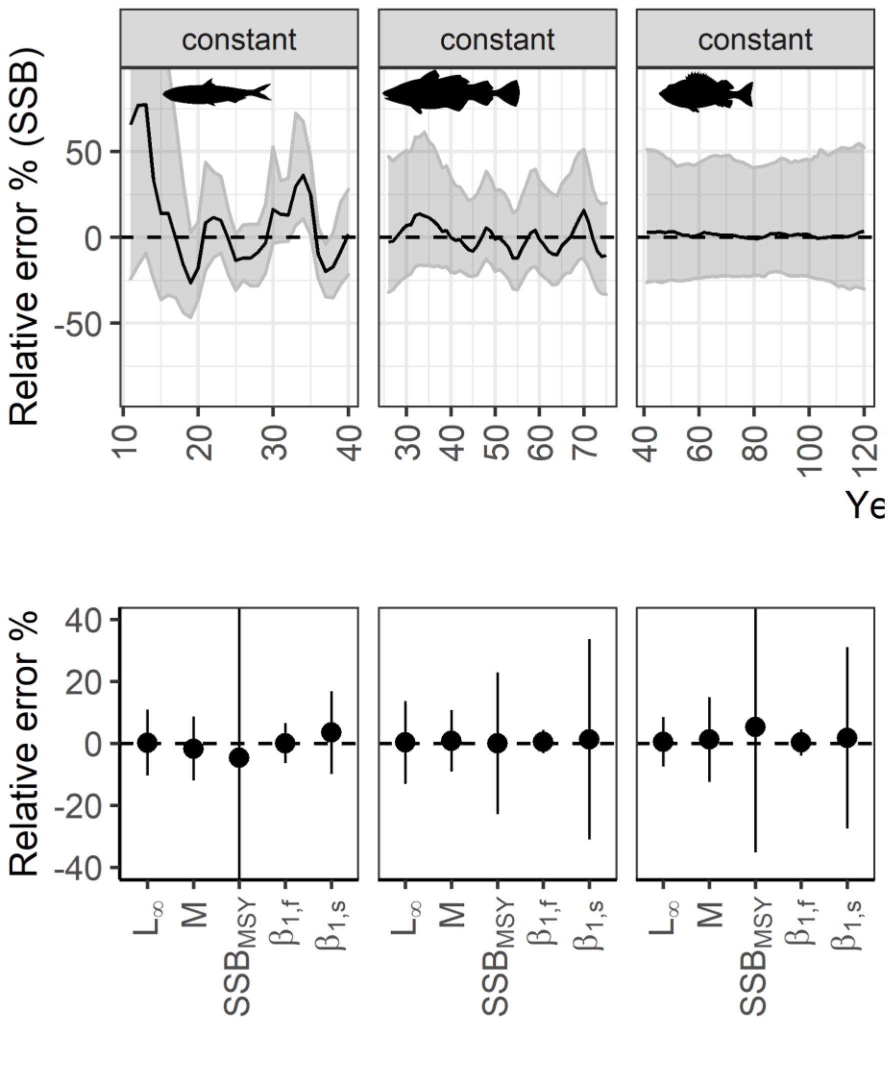


Slow growing area
Fast growing area

Correa et al. (in prep)

Results: Temporal variability

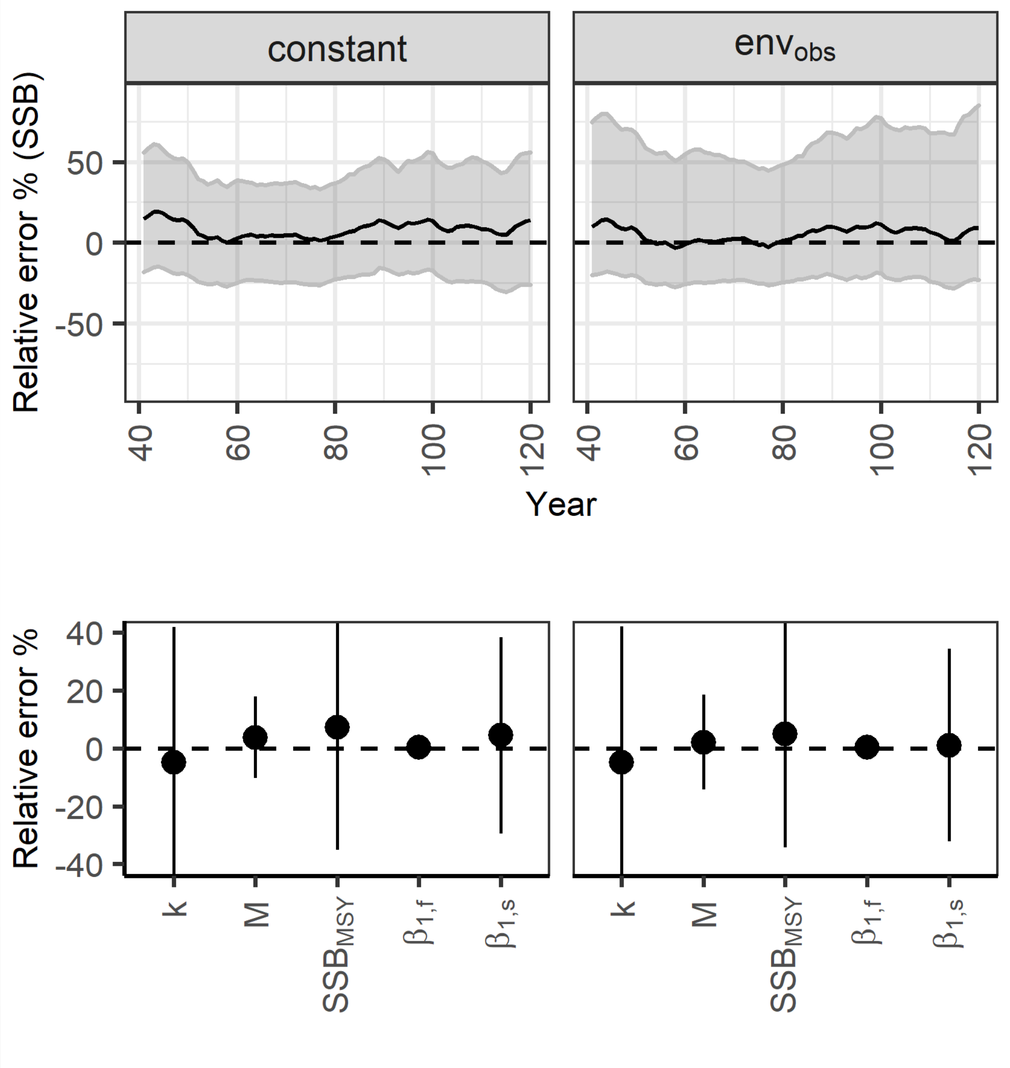
OM:
- Temporal variability (**year-specific**) in mean size-at-age by varying ***k*** over time



Correa et al. (in prep)

Results: Temporal variability

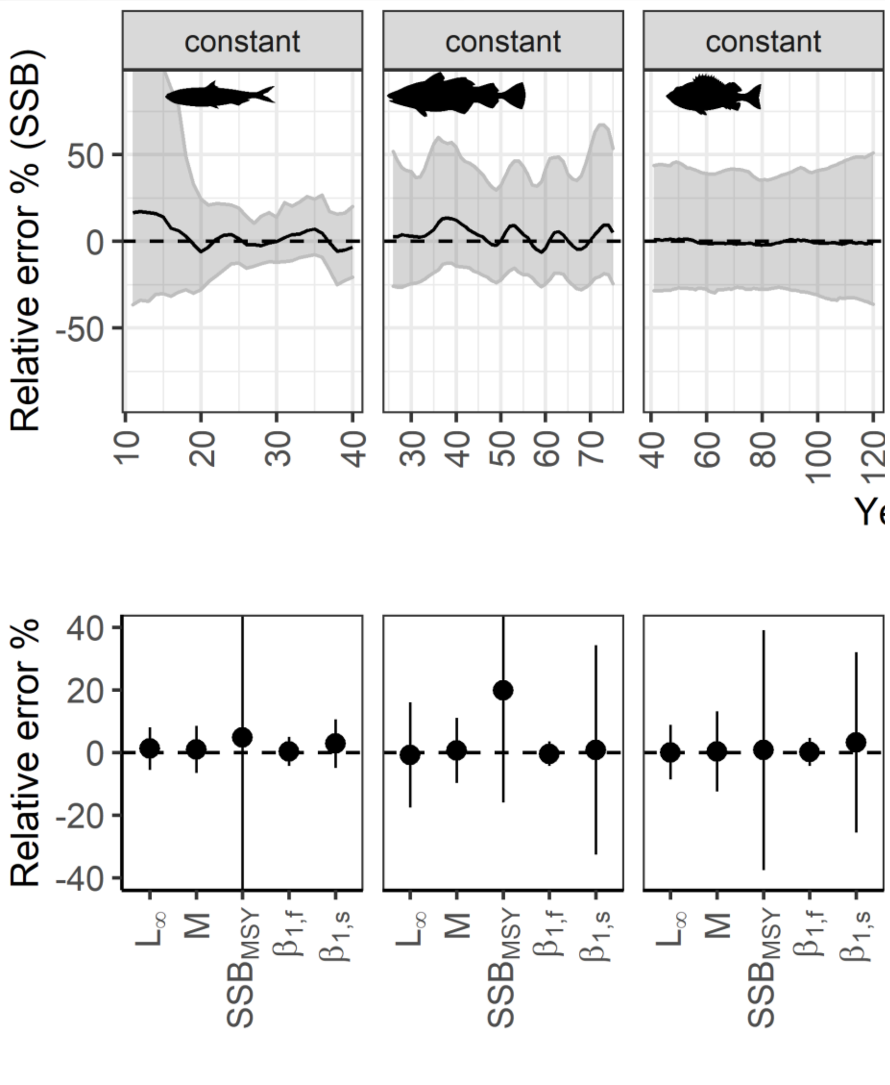
OM:
- Temporal variability (**year-specific**) in mean size-at-age by varying $\boldsymbol{L_\infty}$ over time



Correa et al. (in prep)

Results: Temporal variability

OM:
- Temporal variability (**cohort-specific**) in mean size-at-age by varying ***k*** over time



Correa et al. (in prep)

Conclusions

- Spatial variability in somatic growth:
  - Aggregated approach OK
  - Areas-as-fleet was the worst approach
  - Spatially explicit reported unbiased estimates
- Temporal variability in somatic growth:
  - Ignoring either year or cohort-specific variability produced biased SSB estimates
  - Including an environmental index produced unbiased SSB estimates

https://github.com/gmoroncorrea/spatiotemporal_growth

Caveats

- No movement assumed
- True values of parameters known
- Fishing mortality assumed equal for both areas (Spoiler: it worsened the aggregated and areas-as-fleets approach)
- Boundaries between slow and fast-growing areas known (Detection: Kapur et al. 2020)

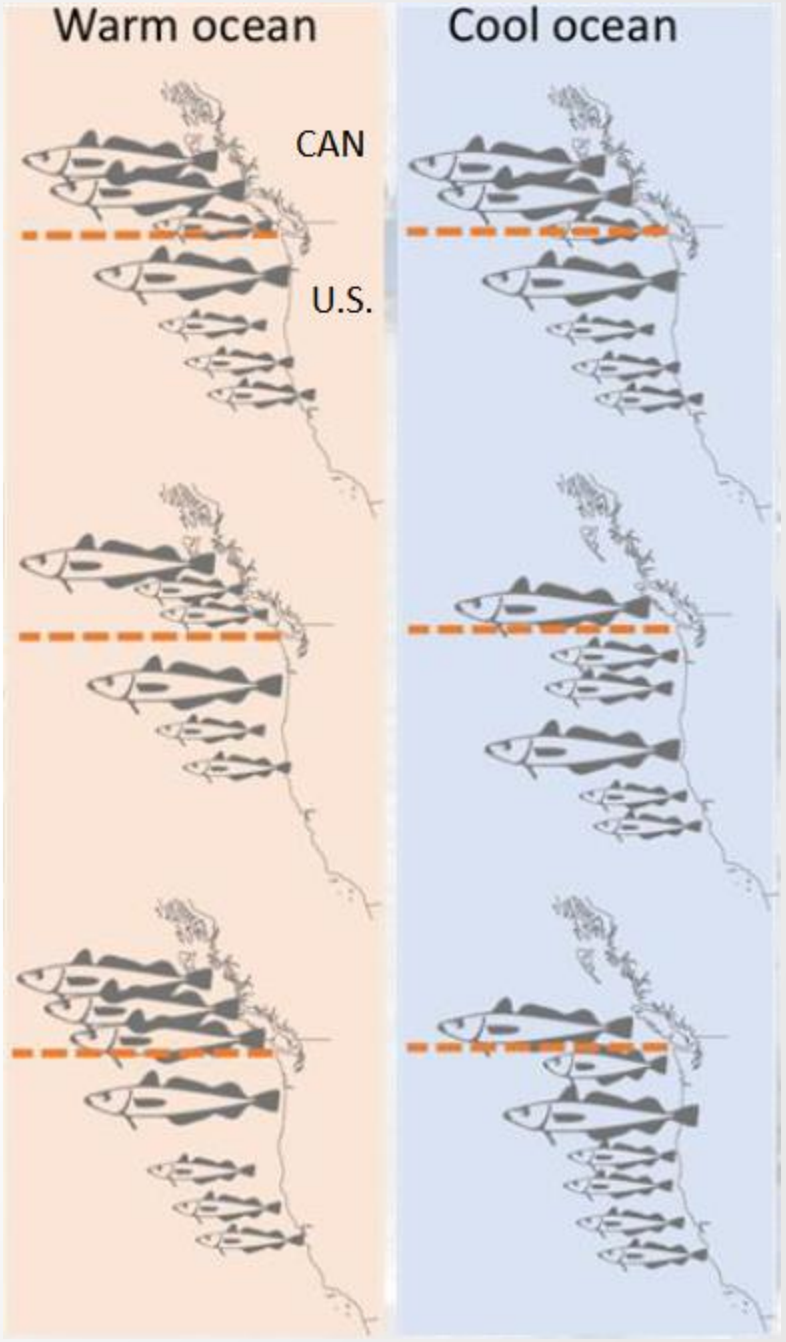


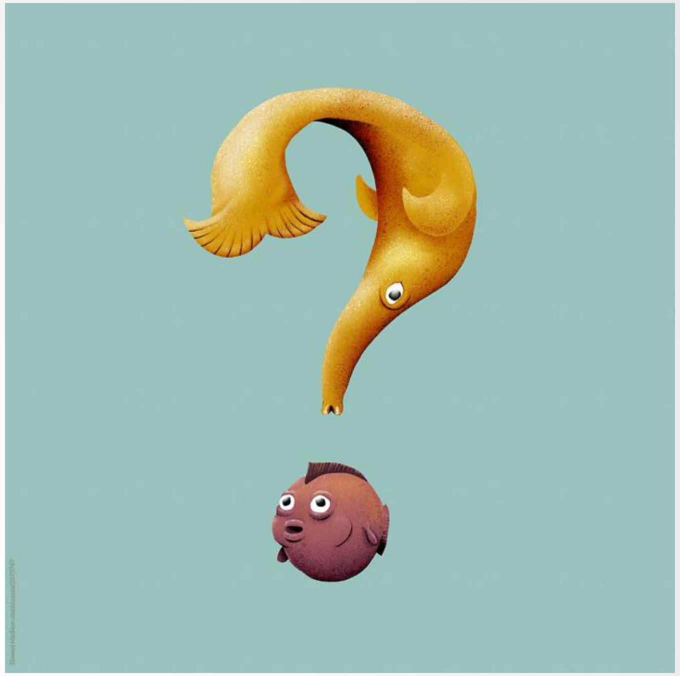
Figure from Aaron Berger's presentation

General conclusions

- Somatic growth is an important aspect of the population dynamics of a stock
- It contributes significantly to the variability in biomass in some cases
- Its variability affects the estimation of some data inputs used in stock assessment models
- Ignoring variability in somatic growth might lead to biased stock assessment outcomes

Acknowledgement

Lorenzo Ciannelli – Oregon State University
Stan Kotwicki – AFSC – NOAA
Lewis A.K. Barnett – AFSC – NOAA
Carey McGilliard – AFSC – NOAA
Claudio Fuentes – Oregon State University



Thanks for listening!

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