Co-funded by the European Union

PAMBAS

STOCK IDENTITY OF *PARAPENAEUS LONGIROSTRIS* AND *ARISTEUS VARIDENS* IN WEST AFRICA

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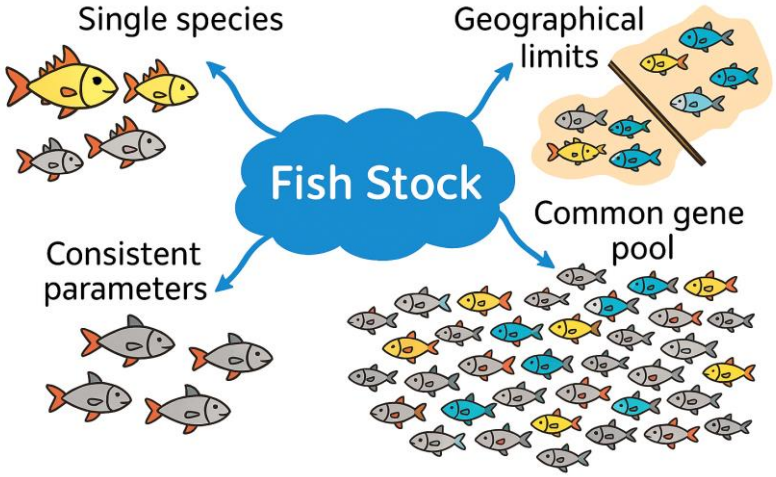
1.- INTRODUCTION

WHAT IS A STOCK?

In fisheries science, a stock refers to a group of individuals of the same species that is **self-sustaining**, usually occupying a **defined region** and showing **limited mixing with other conspecific groups**. A stock typically shares **similar life-history characteristics**, reproduces within the same area and responds collectively to natural and human-induced pressures.

- *Self reproducing and no breeding with other populations.*
- *Similar life history characteristics.*
- *Reproduction in the same area.*
- *Respond collectively to fishing pressure.*



PROCESSES SHAPING STOCK STRUCTURE

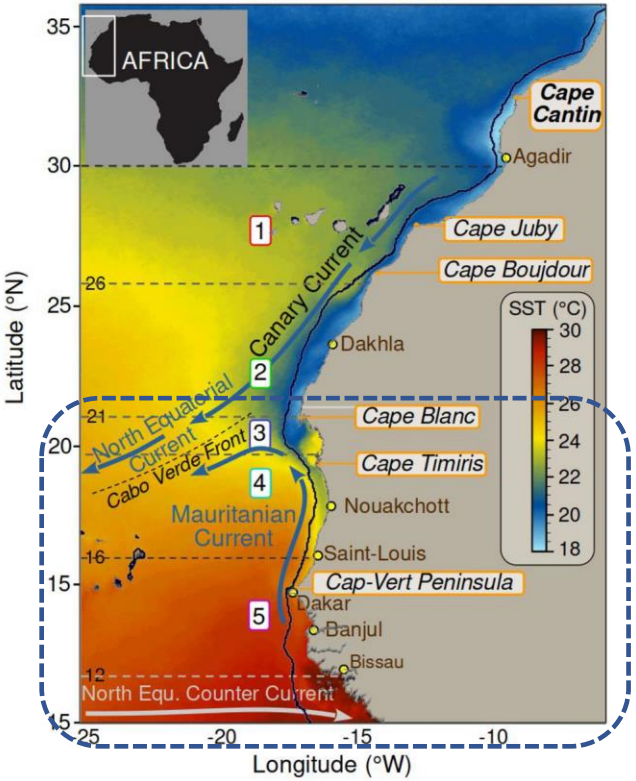
Several factors can drive stock differentiation:

- Oceanographic features (currents, fronts, barriers).
- Life-history traits (larval dispersal, mobility of adults).
- Geographic distance and limited gene flow.

These factors determine whether populations are connected or partially isolated, and therefore whether they should be managed as single or multiple stocks.

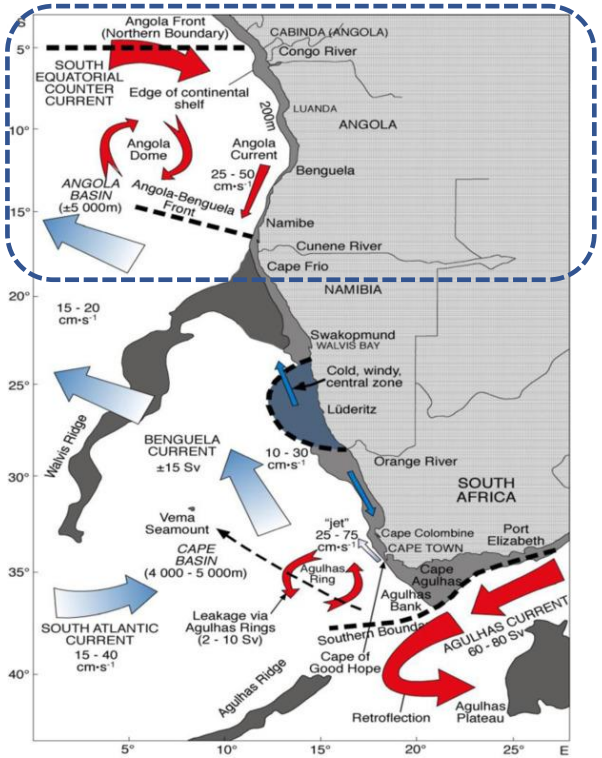
In addition, intra-population/stock complexity beyond stock differentiation can have strong impact in the population dynamics.

CCLME



Sarré et al., 2024

BCLME

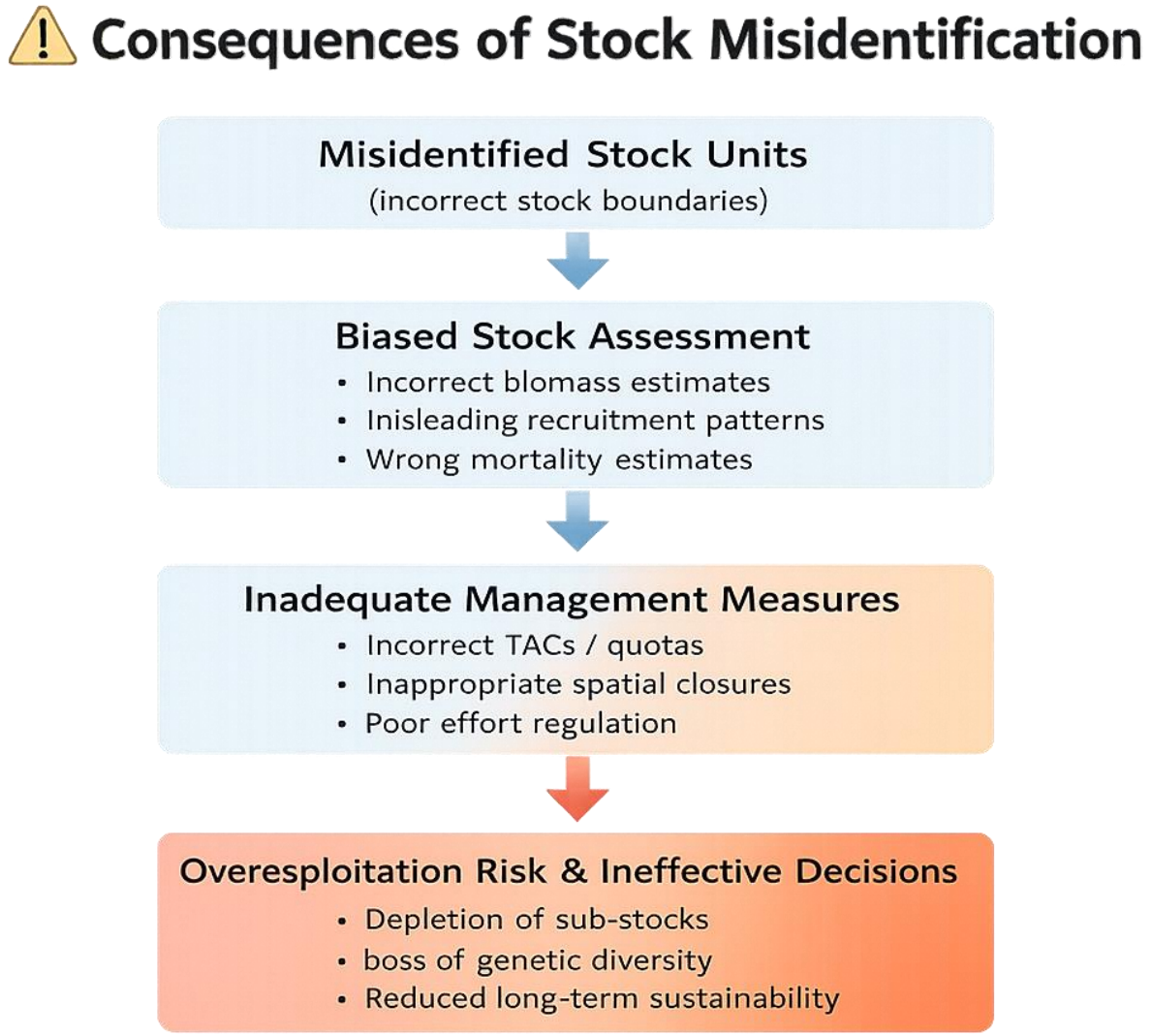


Hamukuaya et al., 2016

WHY DOES STOCK IDENTITY MATTER?

Identifying stock boundaries is essential for effective stock assessment and sustainable fisheries management because stocks:

1) Follow their own life-history cycle, including distinct spawning grounds.
2) Experience specific demographic influences, such as predation, recruitment, and mortality.
3) Can become partially or completely isolated, developing distinct morphological or genetic traits.
4) Respond differently to fishing pressure, environmental changes, and habitat degradation meaning each stock requires tailored management measures.



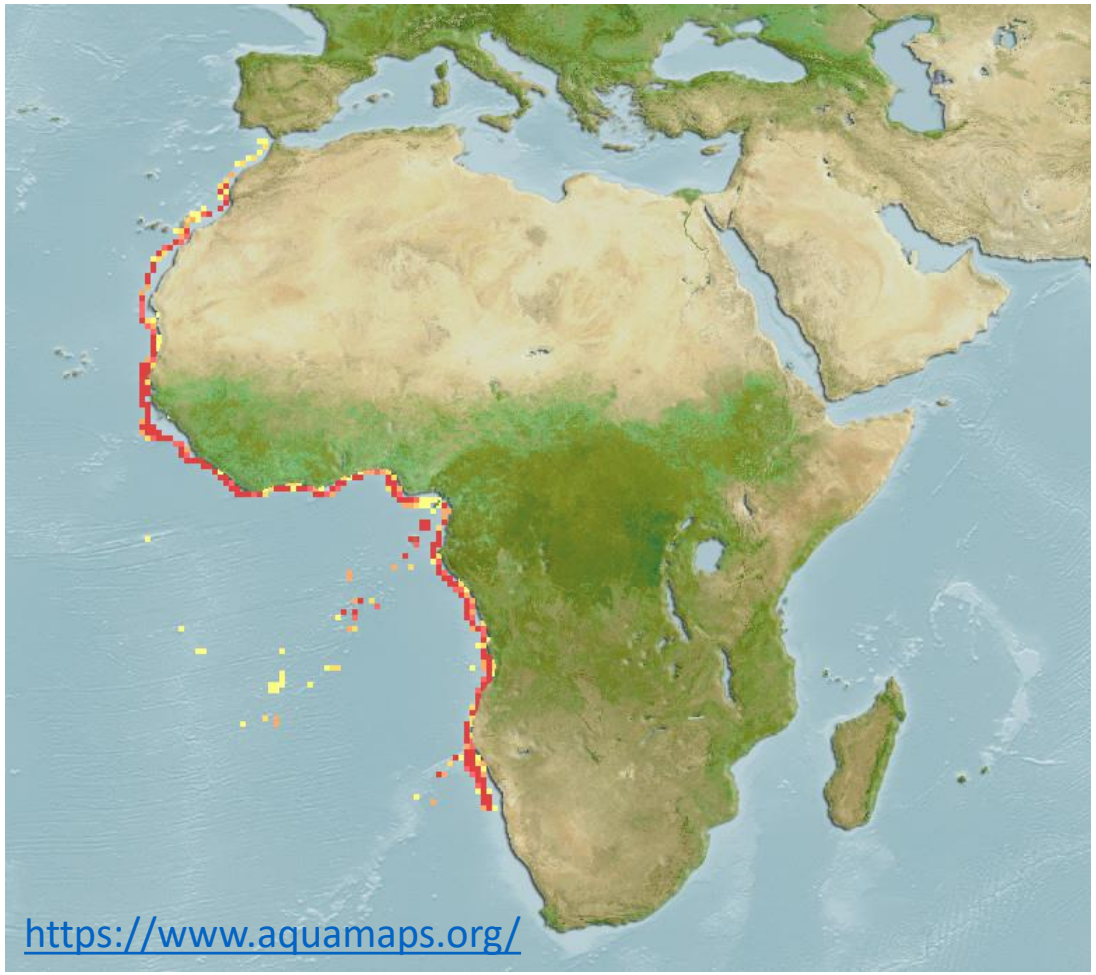
SPECIES DISTRIBUTION

Parapenaeus longirostris

Distribution: Atlantic and the Mediterranean: from USA to French Guiana, the entire Mediterranean and from Portugal to Namibia.

SPECIES DISTRIBUTION

Aristeus varidens



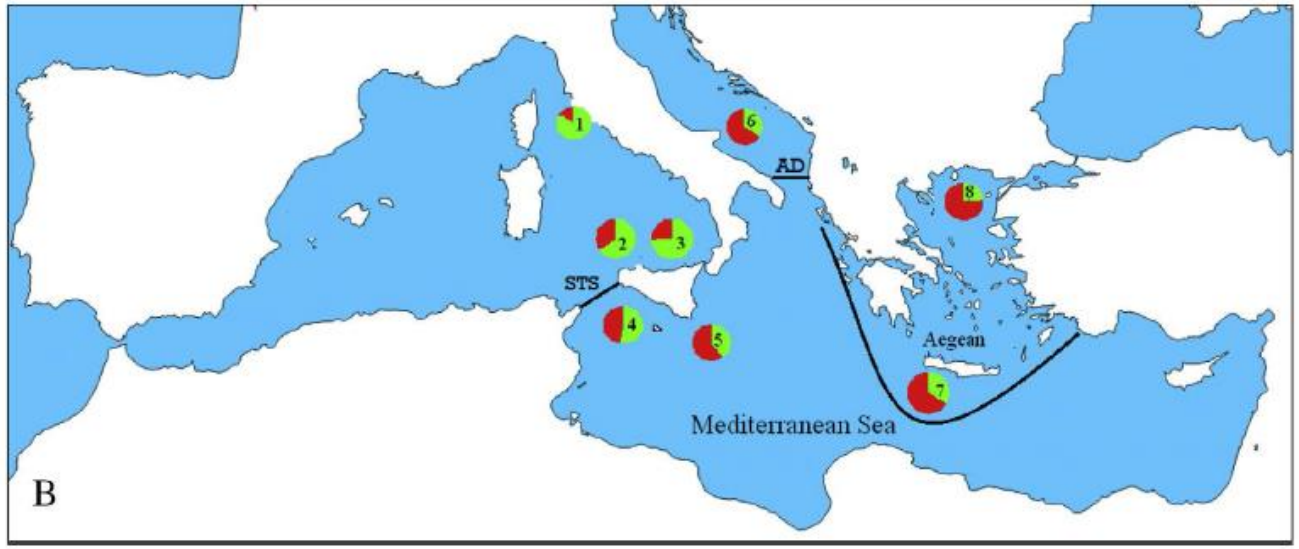
Distribution: Eastern Atlantic: from Morocco to Namibia.

PREVIOUS STUDIES ON STOCK IDENTITY

Parapenaeus longirostris

Genetic structure of *P. longirostris* in the central and eastern Mediterranean Sea revealed:

- Significant and **gradual differentiation** from the Tyrrhenian, Adriatic, Strait of Sicily, to the Aegean area, along a west-east axis.
- Although some homogeneity was evident within the different population of the Mediterranean, **some degree of isolation** was found between different areas.
- The differences observed are consistent with existence of **physical barriers or connectivity facilitators**, such as oceanographic fronts (STS, Adriatic barrier, Levantine isolation).



Distribution of the two Amplified Fragment Length Polymorphism (AFLP) clusters of *P. longirostris* population sub units and the main oceanographic fronts and boundaries (STS, Siculo Tunisian Strait; AD, Adriatic barrier; Aegean or Levantine isolation) affecting genetic pattern of the deep-water rose shrimp.

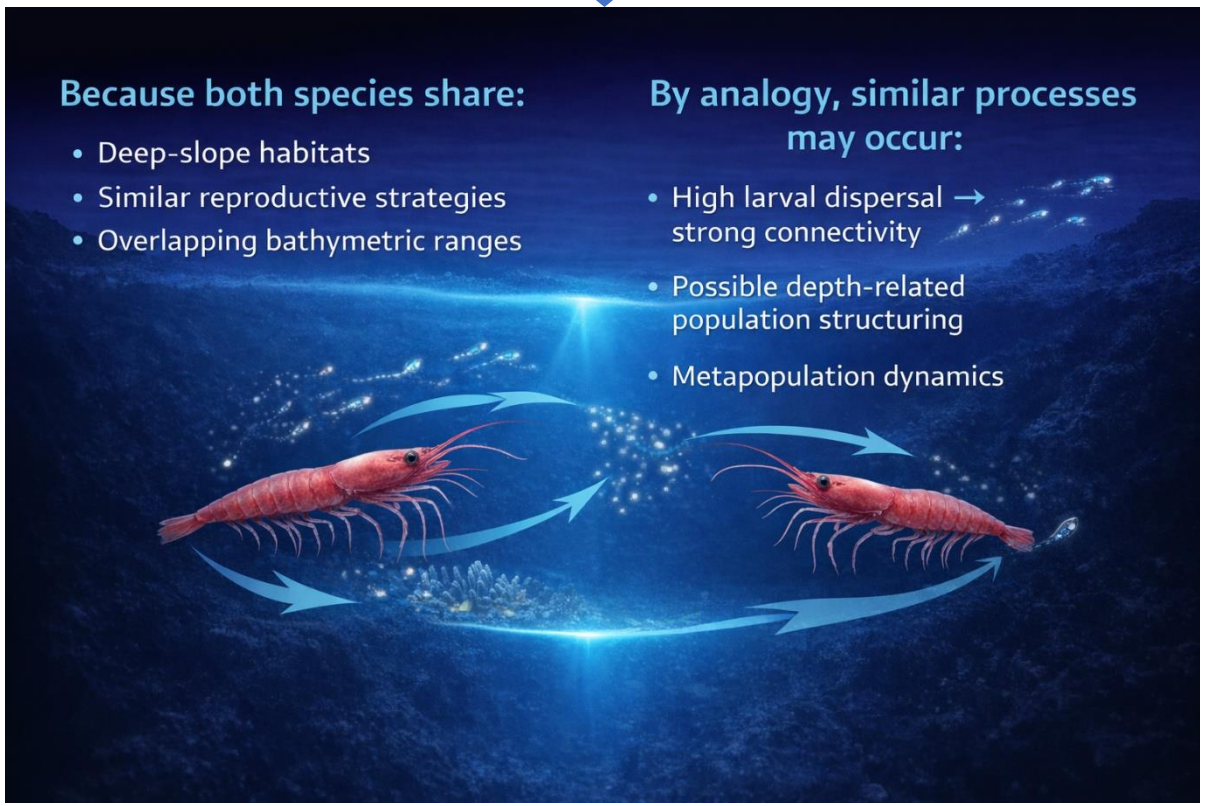
Lo Brutto *et al.*, 2013

PREVIOUS STUDIES ON STOCK IDENTITY

Aristeus varidens

Aristeus varidens

No stock identity studies available→ Major knowledge gap.



Aristeus antennatus

- *A. antennatus* in the Mediterranean is described as a single genetic stock forming a depth-structured metapopulation with multiple demographic subgroups connected by larval drift.
- Larval dispersal ensures high connectivity.

WHY PAMBAS?

- *P. longirostris* shows structure elsewhere, so it may be structured in West Africa.
- *A. varidens* has zero stock information, requiring a full baseline.
- Both species are important in regional fisheries.
- Understanding stock identity is essential for defining assessment and management units.

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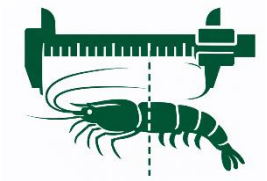
2.- OBJECTIVES

GENERAL OBJECTIVE:

To provide the first biological basis for defining stock structure of *Parapenaeus longirostris* and *Aristeus varidens* in West Africa, using a holistic approach that integrates spatio-temporal dynamics, life-history traits, morphometry and genetic information as baseline support for stock assessment and management.

SPECIFIC OBJECTIVES:

1. To characterize spatial variation in key **life-history traits** for each species in different countries/zones. Evaluate whether these biological traits differ geographically, which may indicate separate management units.



2. To analyse **morphometric variation** as a tool for stock discrimination. Apply morphometrics to detect phenotypic differentiation among zones that may indicate distinct stock units.

3. To explore **genetic structure** with available genetic tools to confirm or refute observed life-history- and morphometric- based stock structure.

4. To **integrate multiple lines of evidence** into a holistic stock identity evaluation. Combine life-history traits, morphometry, spatial distribution and genetics to infer stock structure.

5. To identify **potential population units** within each species across the study area.

6. To **integrate** the stock units identified into the **assessment** models and **management** process.

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3.- METHODS

HOLISTIC APPROACH

LIFE HISTORY TRAITS (LHT)

GENETICS

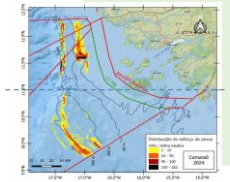
SPATIO-TEMPORAL PATTERNS ??

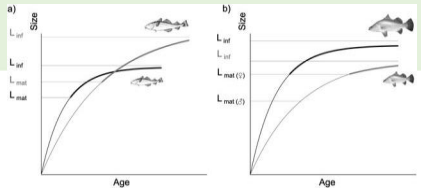
MORPHOMETRY

HOLISTIC APPROACH

Life History Traits

- Growth, recruitment, reproduction, distribution patterns



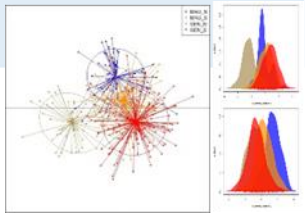


Morphometry

- Analyses based on morphometric measurements of the species.

Genetics

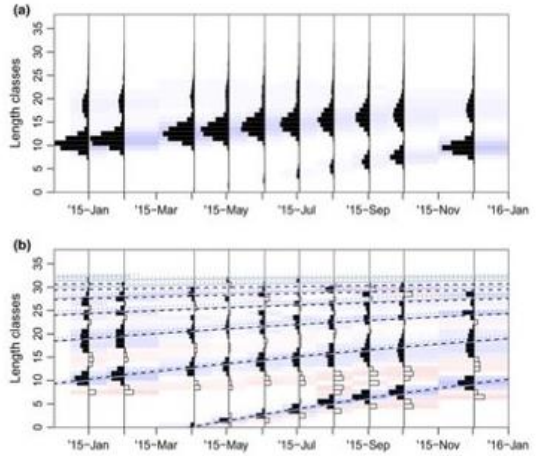
Study of the genetic structure of populations to identify the geographical limits of stocks using microsatellite markers.

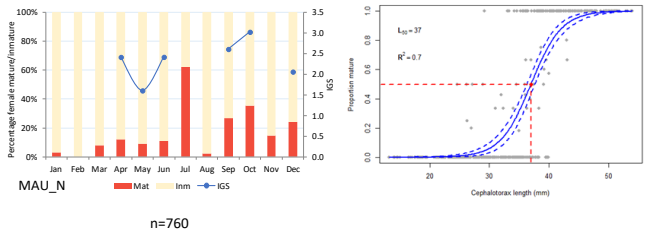


1- LIFE HISTORY TRAITS (LHT)

LHT are used to distinguish stocks because they are phenotypic expressions of the interaction between genotypic and environmental influences.

1. **Data collection:** Compile biological data from national partners (samples collected by observers and sampled in the labs). Monthly samples (2 years), by defined zones.
2. **Data analysis** for:
   - Growth: from LFD → the Von Bertalanffy growth function parameters (L∞, K, t0),
   - Reproduction → spawning periods and areas, length at first maturity.
   - Demographic structure.
   - Distribution.
   - Abundance.
3. Estimate **spatial and temporal variation** in the LHT.
4. Detect **biological differences among zones** as indicators of potential stock structure.





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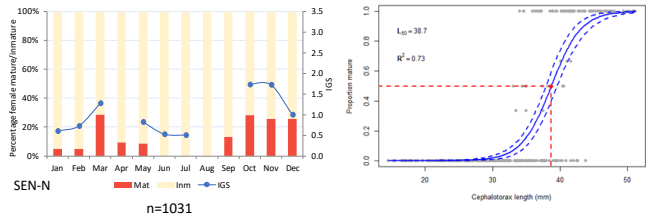

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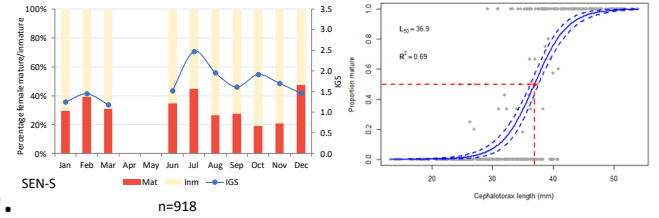

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1- LIFE HISTORY TRAITS (LHT)

LHT to be calculated/described for:

- Each zone
- Sex
- Month of sample collection

→ to investigate the spatial and temporal stability of LHT as indicators of stock structure.

Comparison by Multiple Comparison Test (MCT) (Tukey, Bonferroni methods)

- LHT provide the first biological signal of possible population subdivision.
- Understanding LHT is a fundamental first step to identify stocks, before applying more specific stock identification analyses.

2- MORPHOMETRY

The body-shape analysis will be based on Truss Network morphometrics and/or geometric morphometrics. The images of the two target species sent by partner institutions will be analysed at IEO using these two approaches based on the analysis of anatomical reference points (**landmarks**).

Both methods will rely on the same homologous anatomical landmarks, but they differ in the way body shape is characterised:

Truss Network morphometrics:

- Based on measuring **linear distances** between landmarks.
- Provides a **simple and robust** description of body proportions.
- Suitable for **rapid comparisons** of body proportions across zones.

Geometric morphometrics:

- Analyses the exact **landmark coordinates** (x, y).
- Maintains the integrity of **body geometry**.
- Allows the detection of **finer-scale** shape variation.

2- MORPHOMETRY

1- **Digital photographs** of each specimen will be taken following the standardized protocols (1/year by defined zones).

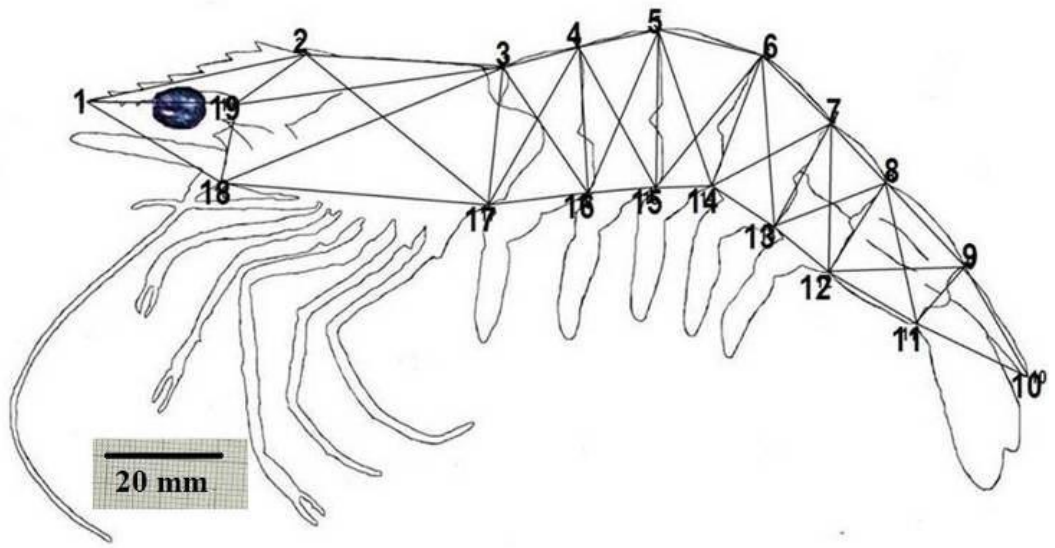
- 50 by sex for selected length ranges
- Immature females.

2- MORPHOMETRY

2.- Locate landmarks on the pictures (ImageJ). Preliminary set of **19 anatomical landmarks** selected (to be readjusted, if needed).

Landmarks

1. Base of the rostrum
2. Teeth of the first rostrum
3. Upper part of the base of the first segment
4. Upper part of the base of the second segment
5. Upper part of the base of the third segment
6. Upper part of the base of the fourth segment
7. Upper part of the base of the fifth segment
8. Upper part of the base of the sixth segment
9. Upper part of the base of the final segment
10. Caudal base
11. End of the sixth segment (ventral)
12. End of the fifth segment (ventral)
13. End of the fourth segment (ventral)
14. End of the third segment (ventral)
15. End of the second segment (ventral)
16. End of the first segment (ventral)
17. Base of the first walking leg
18. Base of the antenna
19. Base of the carapace



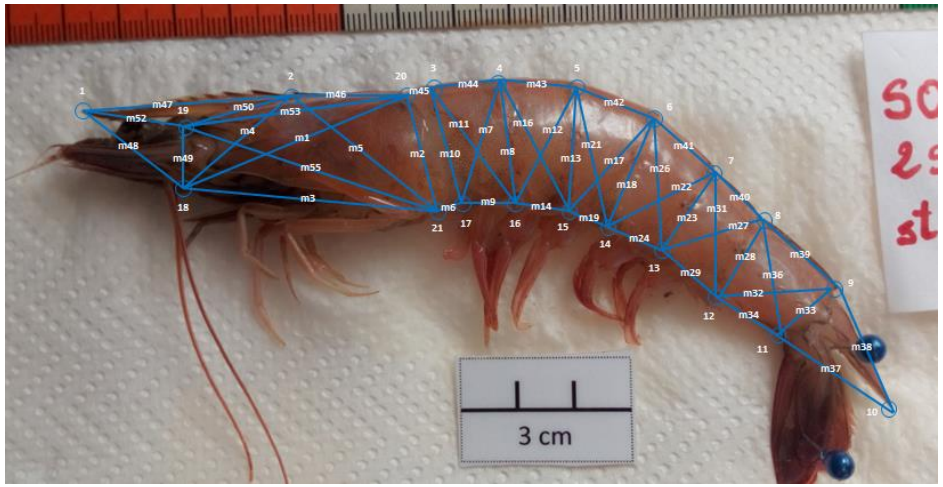
Marini et al., 2016

2- MORPHOMETRY

Truss Network

3- A **truss network** will be constructed by interconnecting the anatomical landmarks to generate a set of linear distances that will represent the entire body outline .

Truss distance				
D01. 1→2	D11. 4→5	D21. 6→14	D31. 9→10	D41. 17→18
D02. 1→18	D12. 4→15	D22. 6→15	D32. 9→11	D42. 17→19
D03. 1→19	D13. 4→16	D23. 7→8	D33. 9→12	D43. 18→19
D04. 2→3	D14. 4→17	D24. 7→12	D34. 10→11	
D05. 2→17	D15. 5→6	D25. 7→13	D35. 11→12	
D06. 2→19	D16. 5→14	D26. 7→14	D36. 12→13	
D07. 3→4	D17. 5→15	D27. 8→9	D37. 13→14	
D08. 3→16	D18. 5→16	D28. 8→11	D38. 14→15	
D09. 3→17	D19. 6→7	D29. 8→12	D39. 15→16	
D10. 3→19	D20. 6→13	D30. 8→13	D40. 16→17	



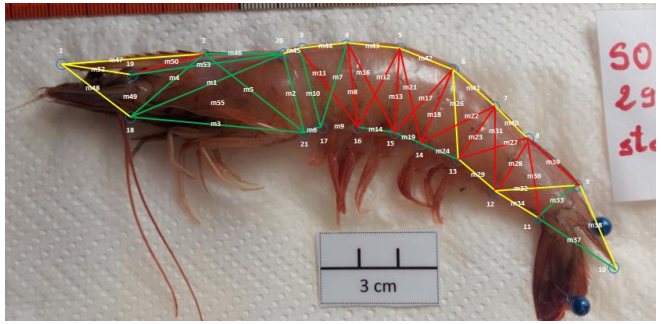
Distances will be extracted from images using ImageJ.

Check measurement consistency and image quality before analysis.

2- MORPHOMETRY Truss Network

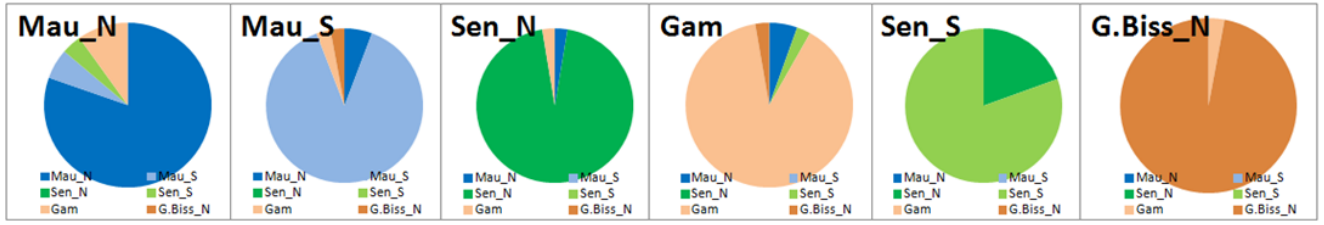
4. Multivariate analyses

- **Principal Components Analysis (PCA)** will be used to summarise the major axes of shape variability.
- **Linear Discriminant Analysis (LDA)** will be applied to evaluate the ability of morphometric variables to discriminate among zones.
- **Cross-validation procedures** will be used to estimate the percentage of correctly classified individuals ("**confusion matrix**") and therefore the strength of morphometric separation among regions.



Morphometric variables of *P. notialis* with meaningful loadings in the PCA, corresponding to the first (red), second (green) and third factor (yellow).

Country area	Predicted Group Membership					
	Mau_N	Mau_S	Sen_N	Gam	Sen_S	G.Biss_N
Mau_N	80,4	5,9	0	9,8	3,9	0
Mau_S	5,7	88,6	0	2,9	0	2,9
Sen_N	2,6	0	94,9	2,6	0	0
Gam	5,4	0	0	89,2	2,7	2,7
Sen_S	0	0	19,4	0	80,6	0
G.Biss_N	0	0	0	2,9	0	97,1



Classification of *P. notialis* individuals (%) into their original population using classification matrix of the LDA based on truss morphometry.

This morphometric approach will detect subtle spatial patterns in body shape and provide a robust tool for identifying potential stock units.

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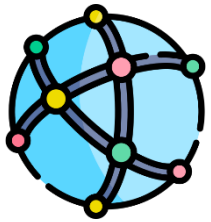
3- GENETICS: Why?/ Pourquoi?

To understand **how biological diversity is distributed across space and time**

- **Who is breeding with whom? Connectivity.**
- **How different are two groups from each other? Differentiation.**
- **How much 'genetic health' does the group have? Variability to survive environmental changes.**



Comprendre **comment la diversité biologique se répartit dans l'espace et dans le temps.**

- **Qui se reproduit avec qui ? Connectivité.**
- **À quel point deux groupes sont-ils différents l'un de l'autre ? Différenciation.**
- **Quelle est la «santé génétique» du groupe ? Variabilité pour survivre aux changements environnementaux.**

Icons by Freepik, Nualnoi Kinkaeo

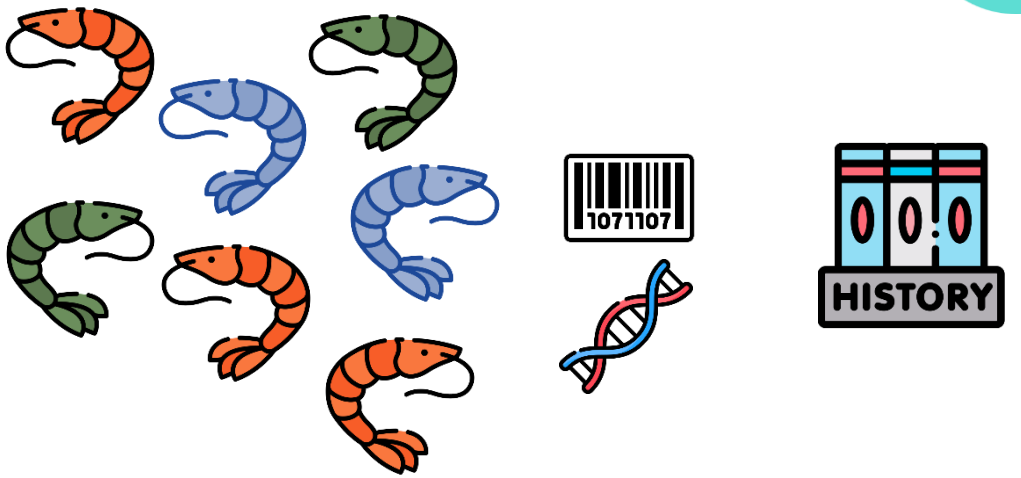
3- GENETICS: Why?/ Pourquoi?

	Without Genetics (Traditional Management)	With Genetics (Modern Management)
Vision	"There is tuna throughout the Atlantic."	"There is one stock in the Mediterranean and another in the Gulf of Mexico."
Action	A single fishing quota for the entire ocean.	Separate quotas based on the health of each group.
Risk	Depleting a population without realizing it.	Biodiversity conservation and profitable fisheries.
	Sans Génétique (Gestion traditionnelle)	**Avec Génétique (Gestion moderne)**
Vision	« Il y a du thon dans tout l'Atlantique. »	« Il y a un stock en Méditerranée et un autre dans le golfe du Mexique. »
Action	Un quota de pêche unique pour tout l'océan.	Des quotas séparés selon la santé de chaque groupe.
Risque	Épuiser une population sans s'en rendre compte.	Conservation de la biodiversité et pêche rentable.

3- GENETICS How does it work?/Comment ça marche?

Each prawn has a unique barcode (its DNA) that tells its story: where it comes from, what family it belongs to, and how it has adapted.

Chaque crevette possède un code-barres unique (son ADN) qui raconte son histoire: d'où elle vient, à quelle famille elle appartient et comment elle s'est adaptée.



To read the code, we need a tissue sample.
Pour lire le code, nous avons besoin d'un échantillon de tissu.

Icons by surang, Tru3 Art, Good Ware, HAJICON, Freepik, mangsaabguru, Smashicons

3- GENETICS Objective/objectif

Study of the genetic structure of populations to identify geographical boundaries of stocks using **microsatellite markers**.

Etude de la structure génétique des populations pour identifier les limites géographiques des stocks à l'aide des **marqueurs microsatellite.**

3- GENETICS Starting Point/Point De Départ

- *P. longirostris* shows structure elsewhere, so it may be structured in West Africa.
- ***A. varidens* has zero stock information**, requiring a full baseline.
- Both species are important in regional fisheries.
- Understanding stock identity is essential for defining assessment and management units.

Genetics/ Génétique

Icons by Freepik

3- GENETICS Sampling/Echantillonage

Collecting **high-quality tissue** (muscle), preserved in **undenatured ethanol**.
Representative sample size
trained technical staff to ensure the integrity of the sample for DNA análisis
Simultaneous Sampling Protocol

Prélèvement de tissus (muscles) de haute qualité, conservés dans de **l'éthanol non dénaturé**
Échantillon représentatif
Personnel technique qualifié pour garantir l'intégrité de l'échantillon pour l'analyse ADN
Protocole d'échantillonnage simultané

3- GENETICS Genetic analysis

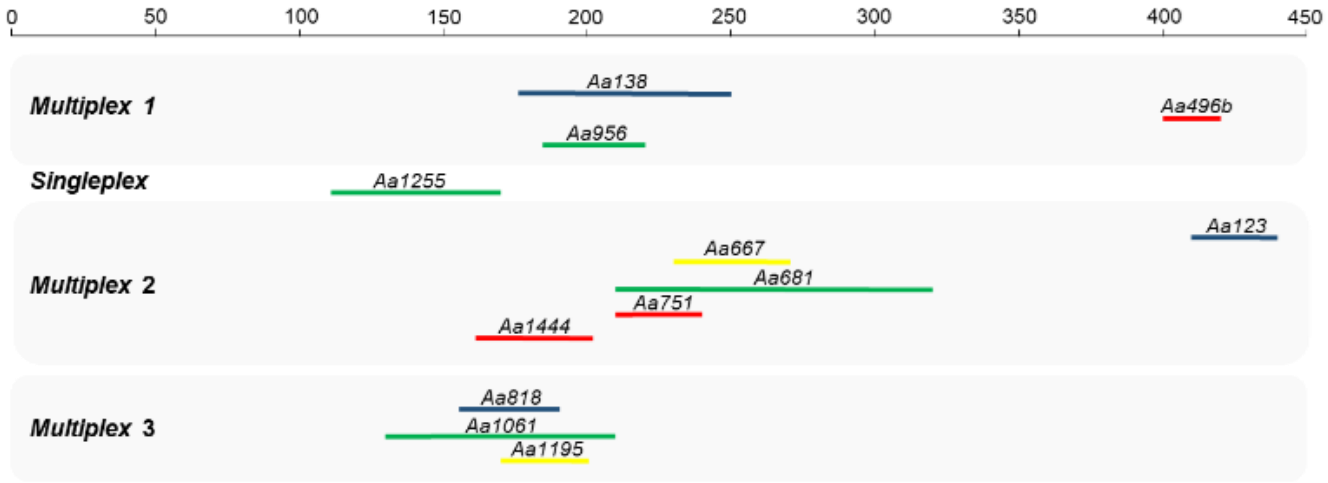
1- MOLECULAR MARKERS SELECTION/ SÉLECTION DES MARQUEURS MOLÉCULAIRES

PeerJ

Development and characterization of novel microsatellite markers by Next Generation Sequencing for the blue and red shrimp *Aristeus antennatus*

Sandra Heras, Laia Planella, Ilaria Caldarazzo, Manuel Vera, José-Luis García-Marín and Maria Ines Roldán

Heterologous primers/ amorceurs hétérologues (Heras et al., 2016)



Parapenaeus longirostris

Aristeus varidens

3- GENETICS Genetic analysis

2- GENOTYPING/GÉNOTYPAGE

Amplify several selected microsatellites to determine the multilocus genotype of individuals.

Amplifier plusieurs microsatellites sélectionnés afin de déterminer le génotype multilocus des individus.

Statistical power (POWSIM) and Null alleles (Micro-Cheker or Freena)

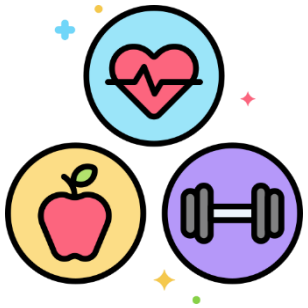
3- SEQUENCING/ SÉQUENÇAGE (Activité Complementaire)

Scarce information

3- GENETICS Data analysis

Genetic diversity

- Number of alleles (N_A)
- Allelic Richness (A_R)
- Observed Heterozigosity (H_O)
- Expected Heterozigosity (He)

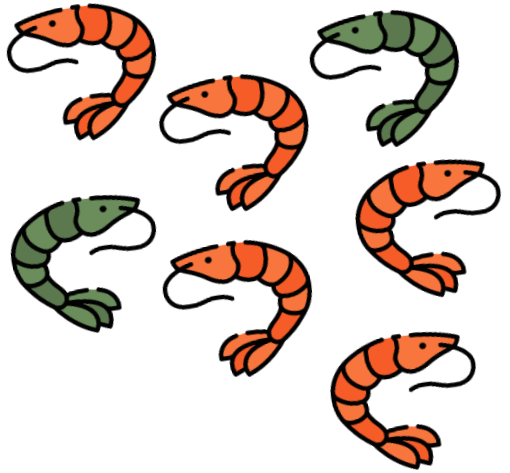


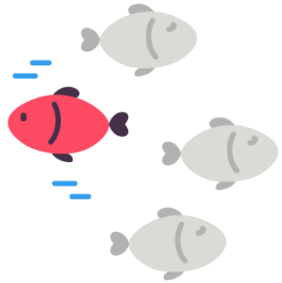
F_{IS}

Genetic Effective Size (Ne)

Genetic differentiation

- F_{ST} (genetic drift/ dérive génétique)
- Structure
- Isolation by distance
- Number of migrants (Nm)





Icons by Flat Icons, Freepik, Victoruler

3- GENETICS The future

Genetics is no longer just a descriptive tool; it provides quantitative indicators to define ***Evolutionary Significant Units (ESUs)*** *that must be protected across borders.*

La génétique n'est plus seulement un outil descriptif ; elle fournit des indicateurs quantitatifs permettant de définir les unités évolutives significatives (UES) qui doivent être protégées au-delà des frontières.

Icons by Freepik

3- GENETICS Genetic Key Indicators for Fisheries Management

Genetic Connectivity Index (GCI)

Evaluates how much shrimp larvae or adults move between the four African countries.
Management Goal: Determines if a Shared Management Plan is mandatory or if local measures suffice.

Effective Population Size (Ne)

Measures the number of "genetically active" shrimp contributing to the next generation (not just total biomass).
Management Goal: Sets a "red line" to avoid Genetic Erosion and ensure the long-term recovery of the stock.

Population Assignment Power

Uses DNA to trace a shrimp back to its country of origin
Management Goal: A vital tool for IUU Fishing Control in transboundary waters.

Seijas-Díaz and Presa, 2025

Genetic Reference Points (GRPs) in Fisheries Assessment/Points de Référence Génétiques (PRG) dans l'évaluation des pêcheries

Seijas-Díaz and Presa, 2025

Integration into Assessment/ Intégration dans l'évaluation:

Indicators must be integrated into fisheries evaluations as Genetic Reference Points (GRPs) to monitor long-term viability /Les indicateurs doivent être intégrés aux évaluations halieutiques en tant que Points de Référence Génétiques (PRG) afin de surveiller la viabilité à long terme

Advanced Metrics for Impact Quantification/ Mesures avancées pour la quantification des impacts:

Genetic Resilience Index (GRI): To assess the population's ability to recover from environmental stress.
Indice de Résilience Génétique (IRG) : Pour évaluer la capacité de la population à se rétablir après un stress environnemental.

Effective Genetic Mortality (Fe): To quantify the loss of genetic variation specifically caused by fishing pressure.
Mortalité Génétique Effective (Fe) : Pour quantifier la perte de variation génétique spécifiquement causée par la pression de pêche.

3- GENETICS Genetic Reference Points (GRPs)

BGRP (Baseline): The original genetic state of the shrimp before intense fishing.
TGRP (Target): The ideal genetic diversity level we want to maintain.
LGRP (Limit): The "danger zone"; if we cross this, the stock may never recover.
tGRP (Threshold): The "early warning" signal to reduce fishing pressure.

BGRP (Référence) : L'état génétique originel de la population de crevettes avant la pêche intensive.
TGRP (Cible) : Le niveau idéal de diversité génétique que nous souhaitons maintenir.
LGRP (Limite) : La zone de danger ; si nous franchissons ce seuil, le stock risque de ne plus se reconstituer.
tGRP (Seuil) : Le signal d'alerte précoce pour réduire la pression de pêche.

Seijas-Díaz and Presa, 2025

3- GENETICS The innovation-Modern Metrics/ L'innovation - Mesures modernes

We are not just counting shrimp; we are measuring Genetic Resilience (GRI) and Effective Genetic Mortality. This project positions the region at the global forefront of genetic-based fisheries management.

Nous ne nous contentons pas de compter les crevettes ; nous mesurons la résilience génétique (IRG) et la mortalité génétique effective. Ce projet positionne la région à l'avant-garde mondiale de la gestion des pêcheries basée sur la génétique.

TABLE OF CONTENTS

4- SPATIO-TEMPORAL PATTERNS

Coherent fluctuating dynamics can be a signal of independent population dynamics, and then stock.

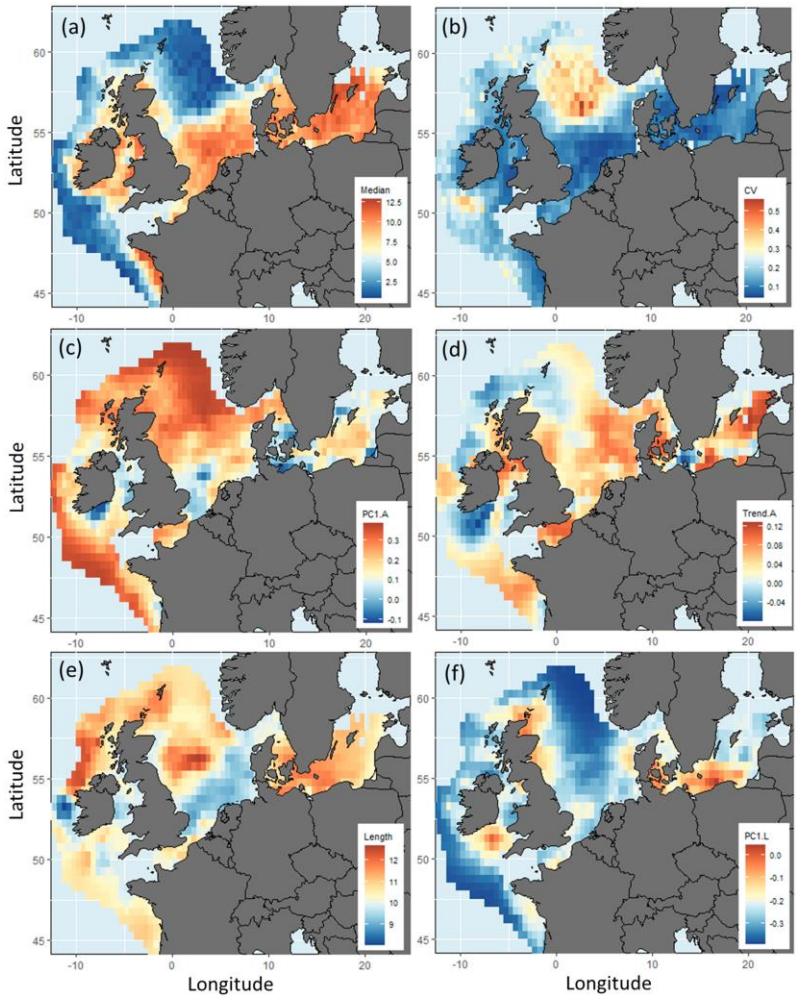
Regional differences in spatial abundance patterns, temporal dynamics and population demographics, can be unified to inform on stock identification

Combining:

- A **Spatial Distribution Modeling** (SDM; vector autoregressive spatio-temporal package, VAST) with
- an **Hierarchical Spatial Clustering (HSC).**

Six variables for the HSC→ differences in :

- **abundance distributions** (median, and CV of log-abundance)
- **temporal dynamics** (trend and first mode of variability in log-abundance)
- **demographics** (trend and first mode of variability in average length).



Lindegren et al. 2022

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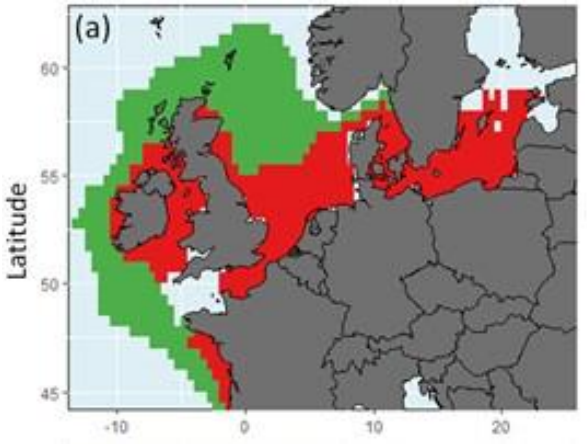
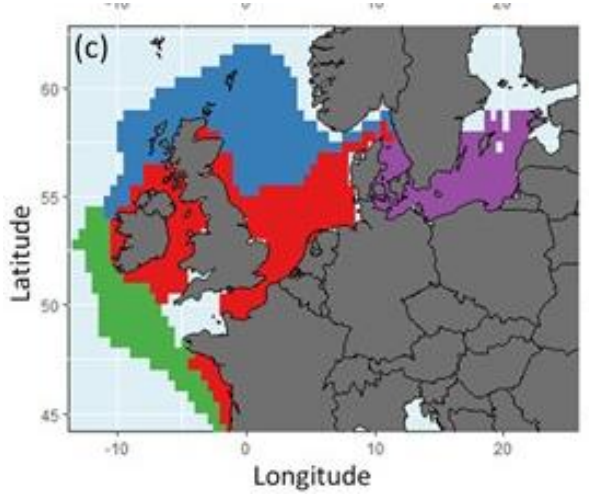


Two clusters

Four clusters



Lindegren et al. 2022

TABLE OF CONTENTS

4- HOLISTIC APPROACH

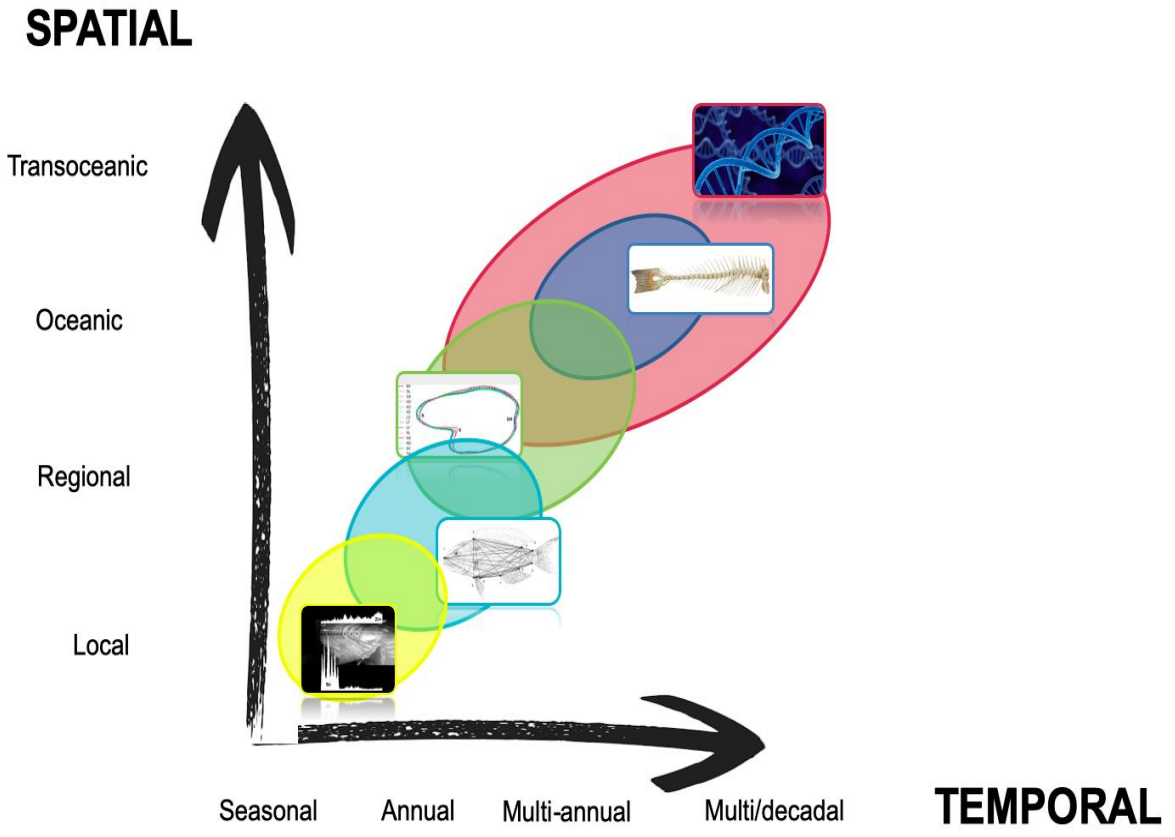
Stock ID techniques provide information at contrasting **spatial and temporal scales**.

Two main **components**:

- Broad spatial patterns of differentiation (evolutionary scale).
- Local adaptation and demographic processes.

Plastic and genetic (i.e. adaptive) components of life history may balance (or not) their importance.

One technique ≠ One indicator.



Populations recently isolated or have adapted to local conditions on an evolutionary timescale may **not exhibit genetic differences** but may rather show **demographic independence at ecological timescales**: those of relevance for fisheries assessment

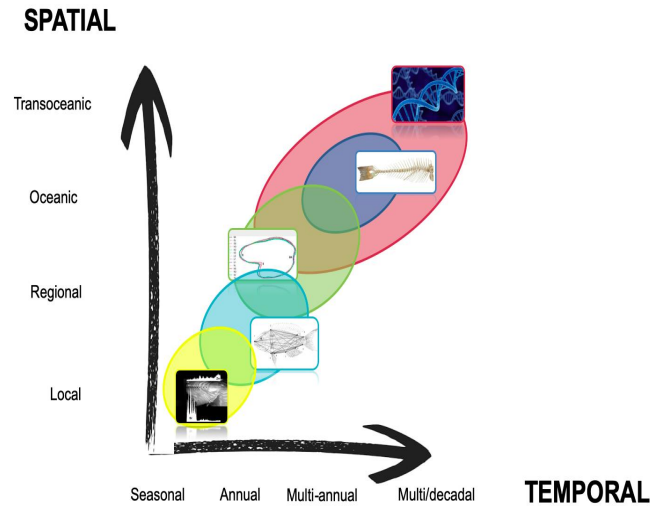
4- HOLISTIC APPROACH

Several methods for **muldisciplinary integration:**

1) **Semiquantitative:** Based on pair wise comparisons.

2) **Multivariate approaches:** Gradient analysis methods such as the Redundancy analysis (RDA) or Principal Components Analyses (PCA).

3) **Clustering algorithms:** Fuzzy K-means – a commonly used approach for exploring the structure of a set of patterns, especially when the clusters are overlapping or fuzzy.



CRITERIA TO CONSIDER

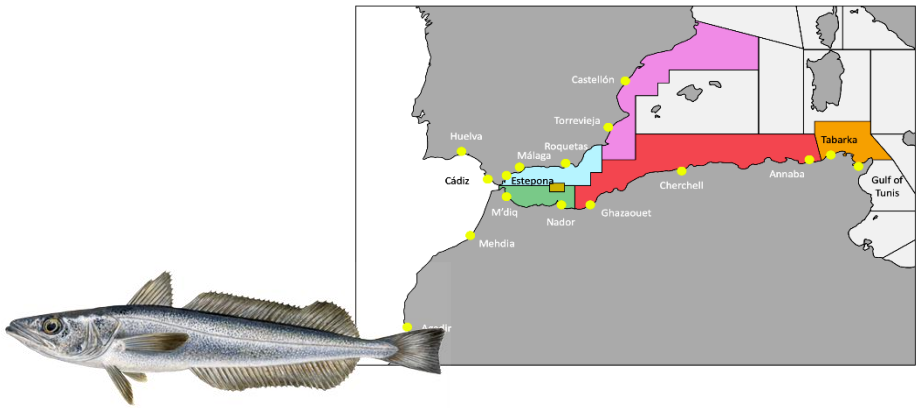
- Data quantity (number of methods) and resolution.
- Robustness
- Communication to managers.
- Combination of methods.

4- HOLISTIC APPROACH

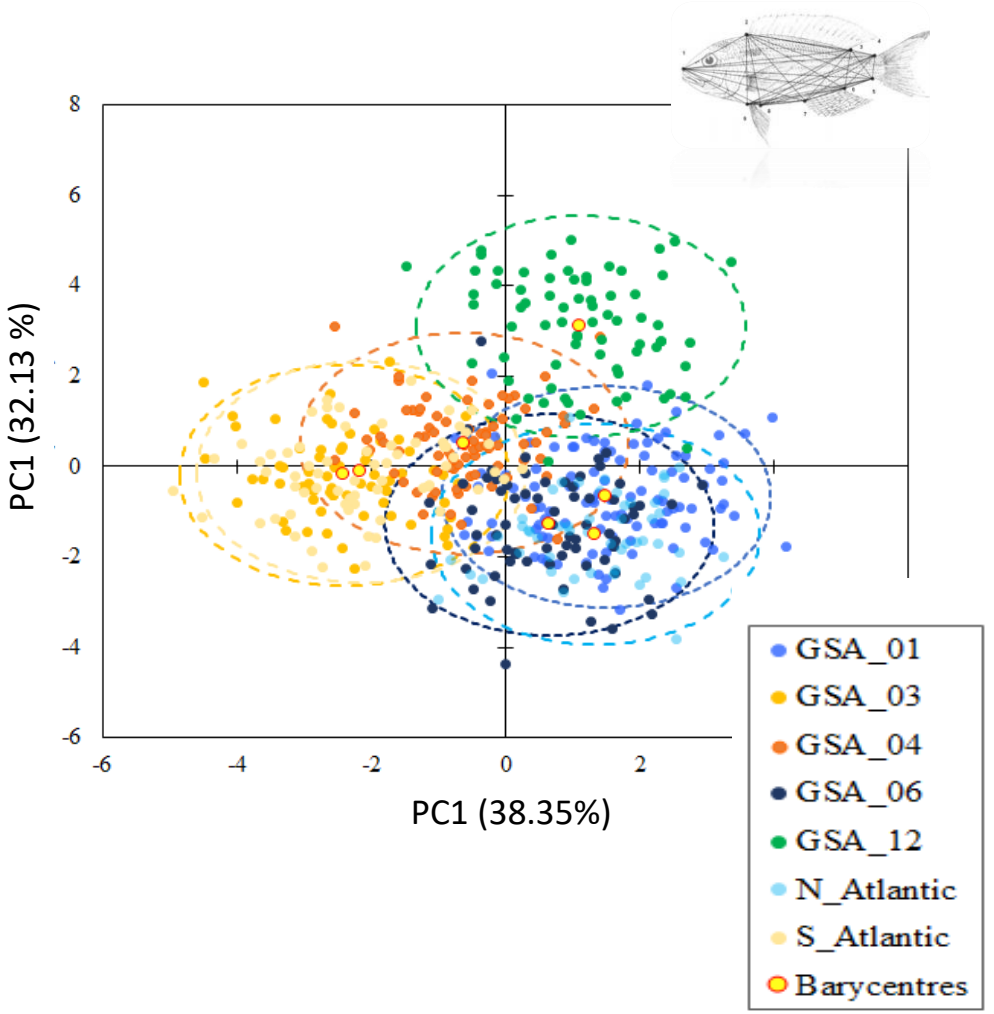
Redundancy analysis (**RDA**) or Principal Components Analyses (**PCA**).

- **PC** values were also averaged **by sub-areas for each technique**.

- From each metric we can get **two independent metrics** (PC1, PC2; no correlated)



Multivariate approaches



(Hidalgo et al 2024)

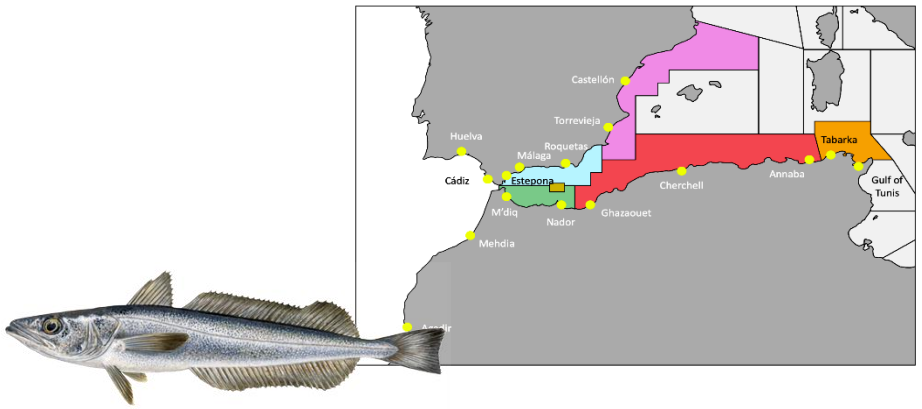
4- HOLISTIC APPROACH

Stock Differentiation Index (SDI, Welch et al. 2015, Izzo et al. 2017)

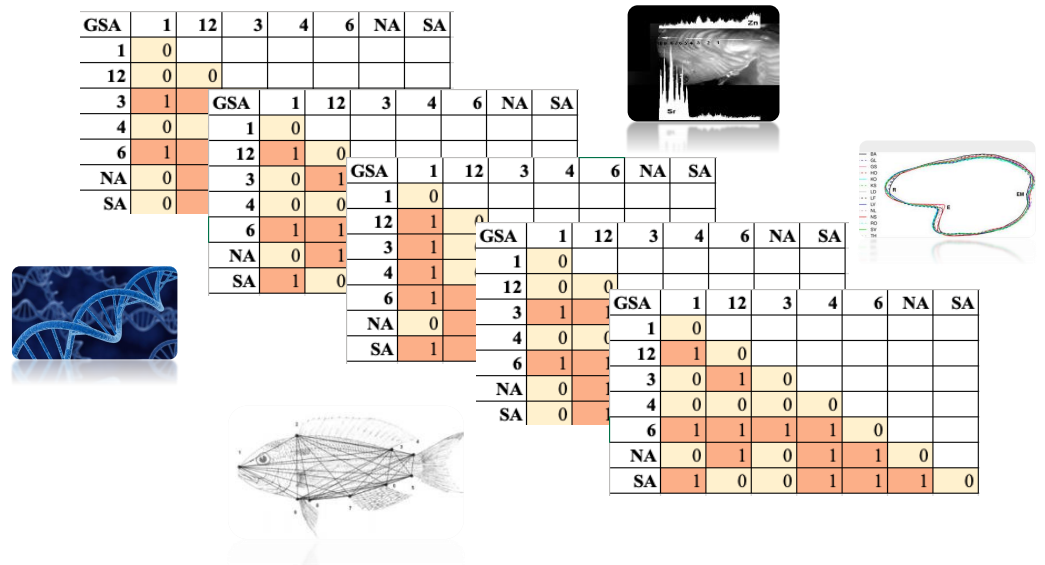
- Based a **semi-quantitative** approach, assigns difference values (0,1) to each **pairwise comparison** for each of the considered tracers based on the results obtained in the previous analysis

- **Simple** but **robust**.

- **Easy to communicate**, often used to support other more complex methods



Semiquantitative



GSA	1	12	3	4	6	NA	SA
1	0.15						
12	0.69	0.14					
3	0.89	0.75	0.00				
4	0.83	0.29	0.44	0.14			
6	0.54	0.36	0.92	0.61	0.00		
NA	0.81	0.93	0.78	1.00	0.79	0.13	
SA	0.78	0.82	0.53	0.75	0.79	0.53	0.00

$SDI_{WHOLE} = 0.71$

STRONG

SDI > 0.66

MODERATE

0.33 < SDI < 0.66

WEAK

SDI < 0.33

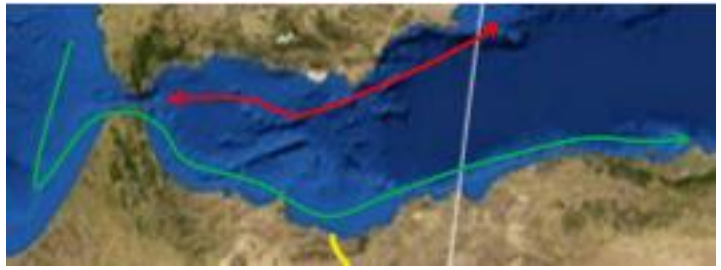
(Hidalgo et al 2024)

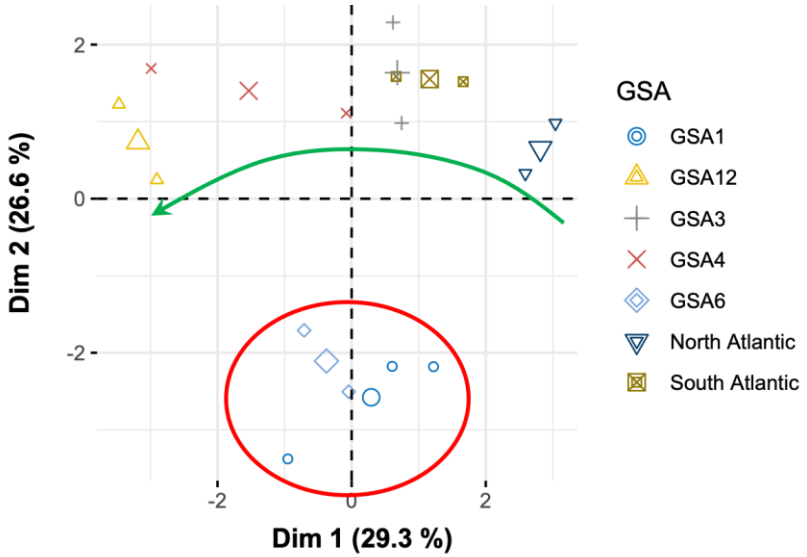
4- HOLISTIC APPROACH

Multivariate approaches

- **Six techniques** applying any kind of **discriminant analyses**.

- Two first axes explain **> 70% variance** in all techniques.

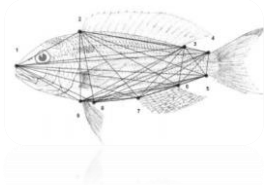




GENETICS

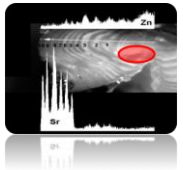
MERISTICS

BODY MORPHOMETRICS

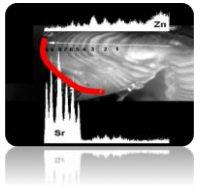


SHAPE ANALYSES

MICROCHEMISTRY CORE



MICROCHEMISTRY EDGE



(Hidalgo et al 2024)

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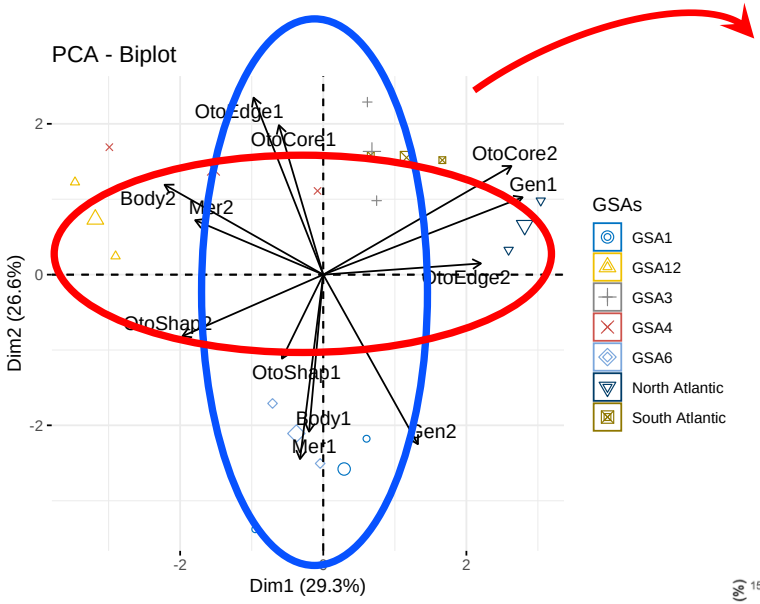
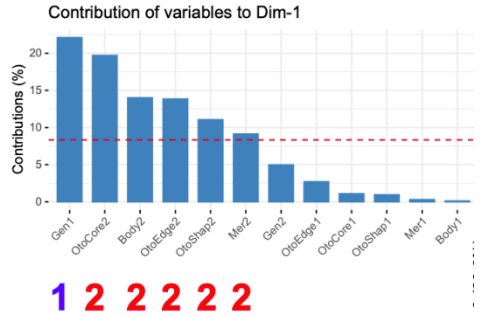
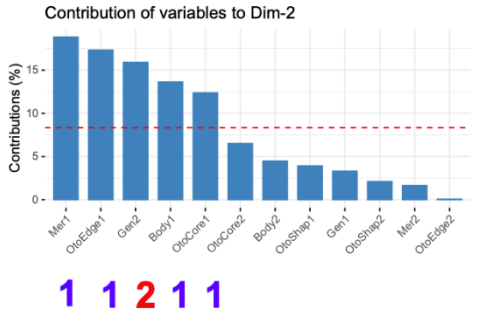
- **Contribution** of each axis: **confluence on** the spatial **scales**.

Multivariate approaches







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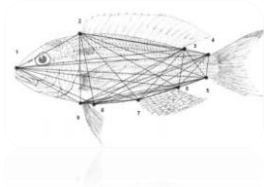

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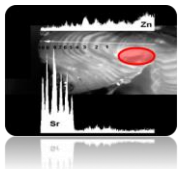

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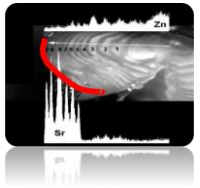

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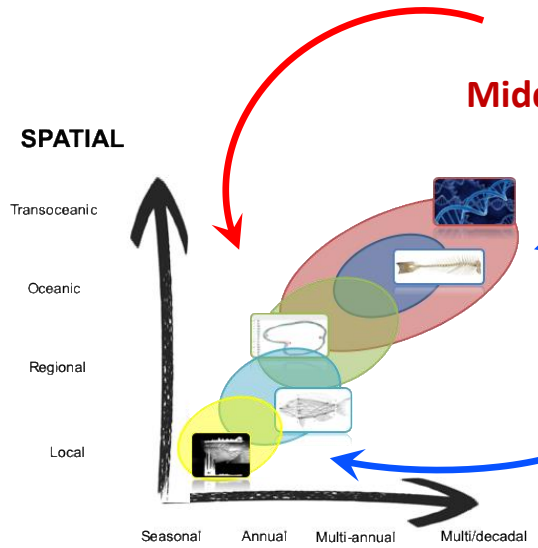
All techniques give **information at different scales**, while **one** being always **more prevalent**

Multivariate approaches



DYNAMIC

Middle/regional/Multiannual/annual Scale:

- Regional environmental influence.
- Regional/local adaptation.

Large and short scales:

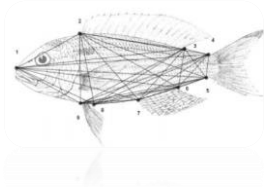
PERSISTANT

- Evolutionary connectivity.
- Genetic differentiation
- Spawning/demographic aggregations.

GENETICS

MERISTICS

BODY MORPHOMETRICS



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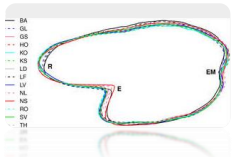

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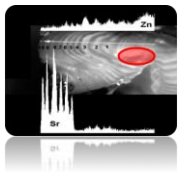

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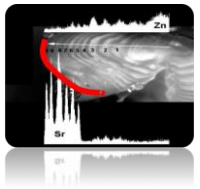


(Hidalgo et al 2024)

4- HOLISTIC APPROACH

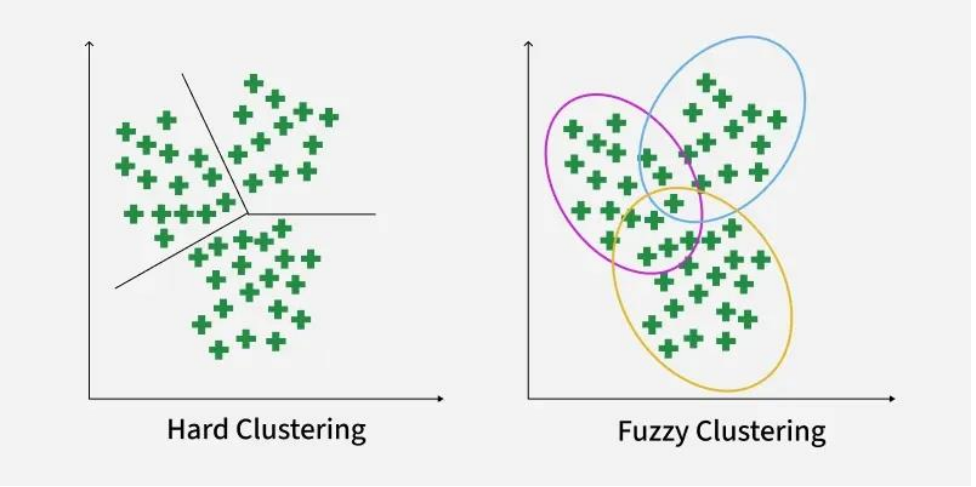
Fuzzy K-means clustering (FKM)

- Clustering algorithm that allows **data points to belong to multiple clust**ers simultaneously with varying degrees of membership (0,1)

- FKM identify **discontinuities in the data** (i.e., clusters), but it also assesses the **level of fuzziness** in the association of data to clusters.

- It represents an intermediate solution **between clustering methods and gradient analysis** methods.

- FKM membership grades, as variables to be explained, as **predictors**, can be used in the **Redundancy Analysis** (RDA) along with environmental variables.



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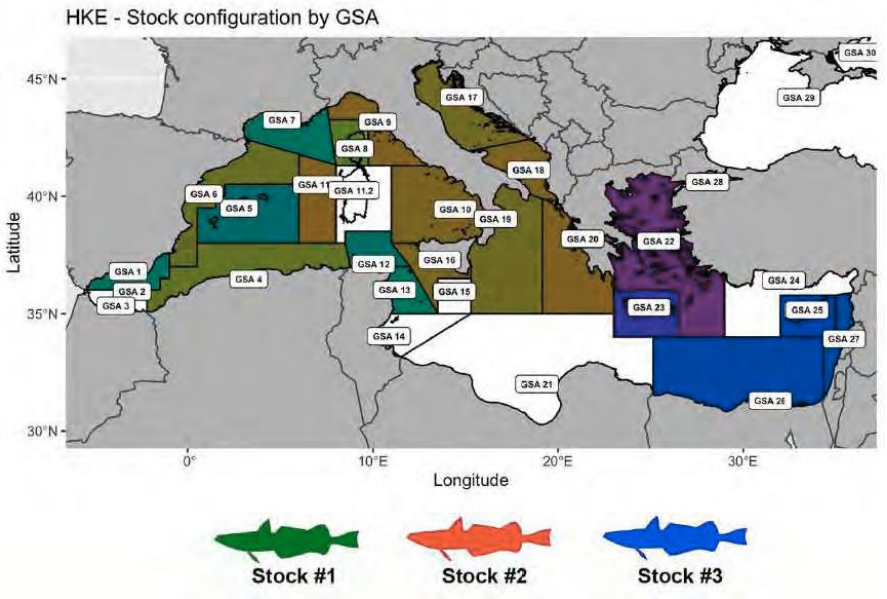
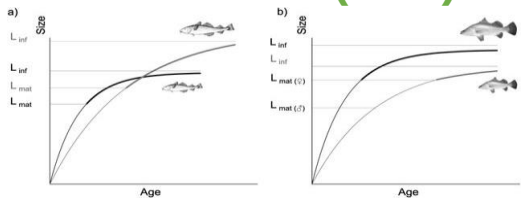
Probability of membership of hake samples to the three stocks identified



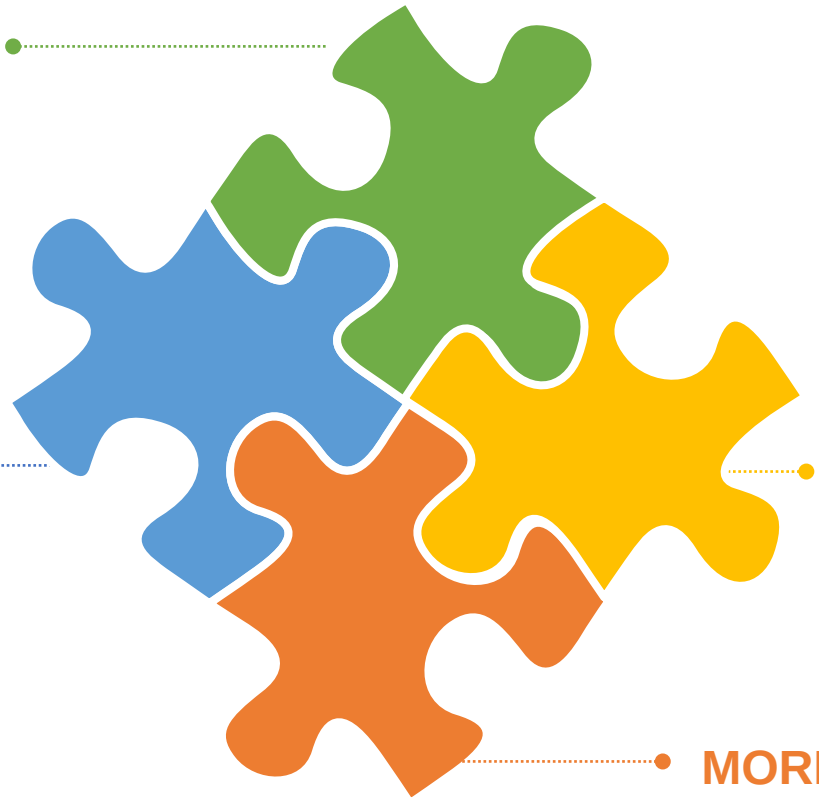
Spadicato et al 2024

4- HOLISTIC APPROACH

LIFE HISTORY TRAITS (LHT)

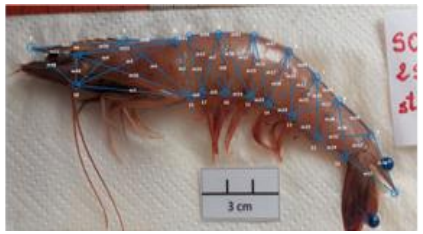


GENETICS



SPATIO-TEMPORAL PATTERNS ??

MORPHOMETRY



Merci pour votre attention

Obrigada pela vossa atenção

Gracias por vuestra atención

Thanks for your attention