

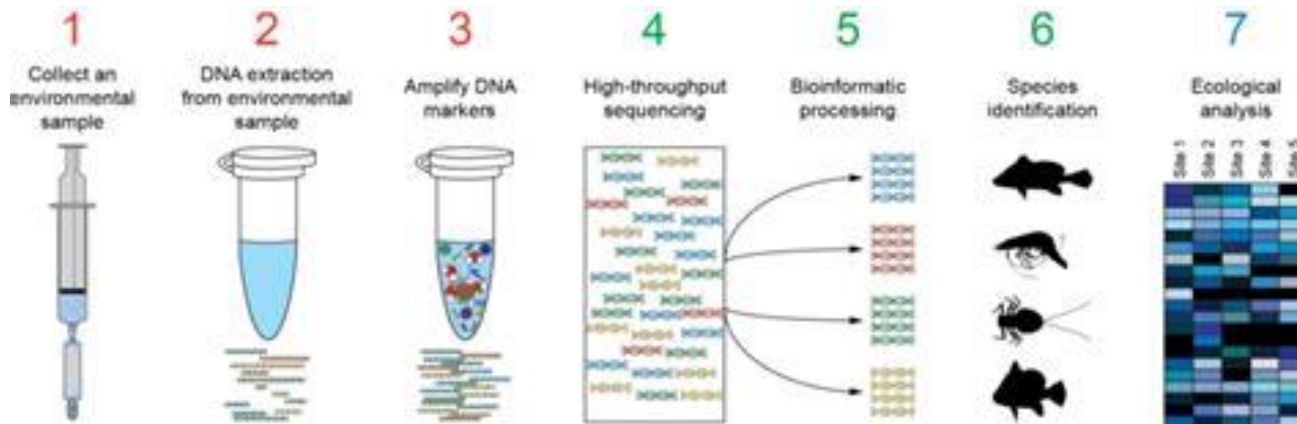
# Could eDNA be a transformative change in the way to operate the monitoring and assessment of exploited fish populations?

Jean-Marc Fromentin and Quentin Schull



# eDNA: What are we talking about?

- **environmental DNA (eDNA)**: traces of DNA released by different living organisms into their environment, such as soil, sediment, (sea)water, air, snow...
- eDNA come from mucus, gametes, shed skin, feces, carcasses, etc.
- eDNA can now be easily detected and collected eDNA samples can be analyzed, after extraction and purification, by high-throughput DNA sequencing methods, such as metabarcoding

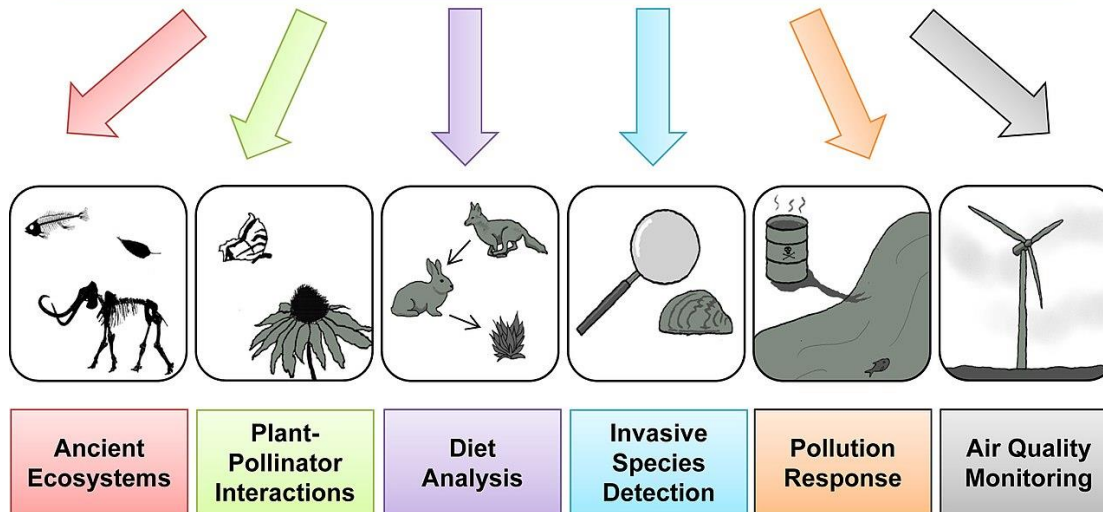




# eDNA for various applications

eDNA allows to reliably and exhaustively identify which species are present in a given sample. eDNA has been applied widely

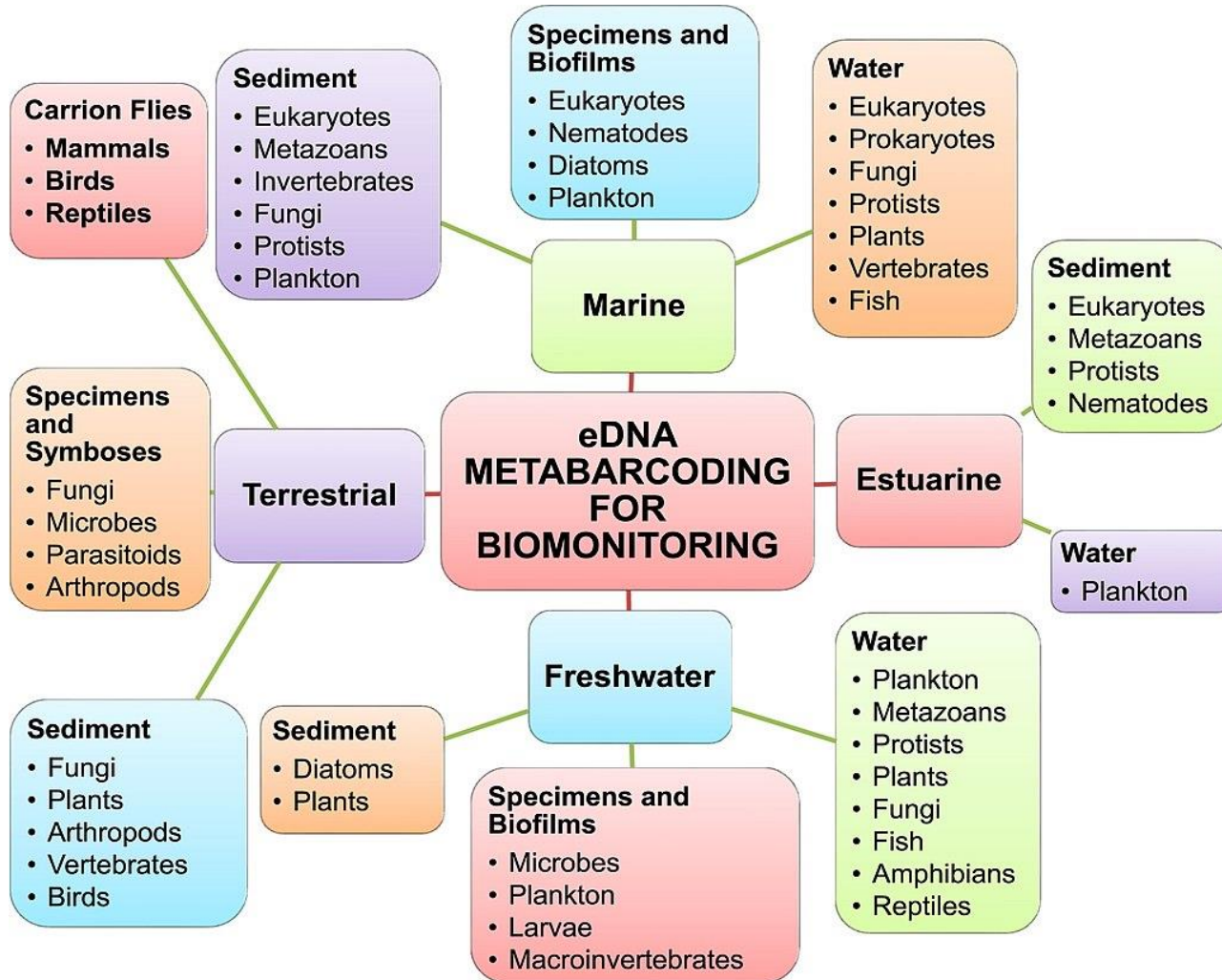
## eDNA Metabarcoding Applications





# eDNA for biomonitoring and assessing biodiversity

eDNA has proved to be reliable and effective for all ecosystem types, and offers enormous potential for biological monitoring





# eDNA for various applications

A tremendous interest in the ecological community since a decade (emerging around 2000)  
There is even an eDNA journal since 2019 (CiteScore-Scopus: 9.9)

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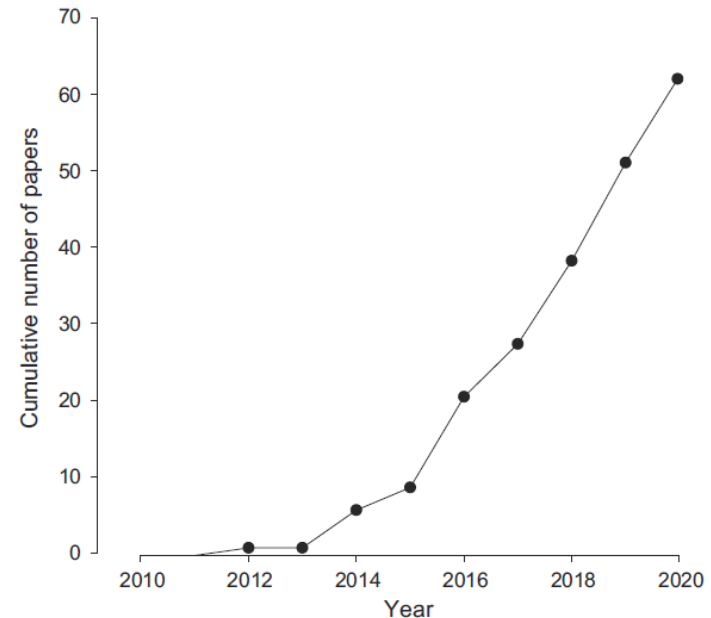
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## eDNA to estimate biomass of a given population

eDNA can also be used to reliably estimate the biomass, or even abundance, of a given population, using quantitative or digital PCR

Cumulative number of articles published from 2012 to 2020 assessing the utility of eDNA for estimating the abundance and/or biomass of fish across all environments



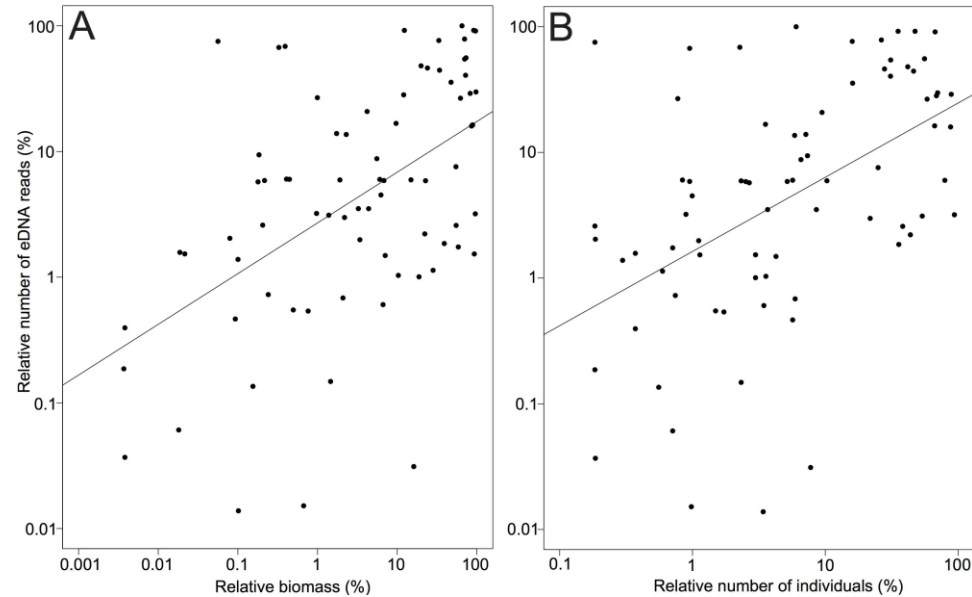
Rourke et al. 2022 reviewed 63 studies published between 2012 and 2020 using eDNA for monitoring fish populations. They found 90% identified positive relationships between eDNA concentrations and the abundance and/or biomass of the given species



# eDNA to estimate biomass of a given population

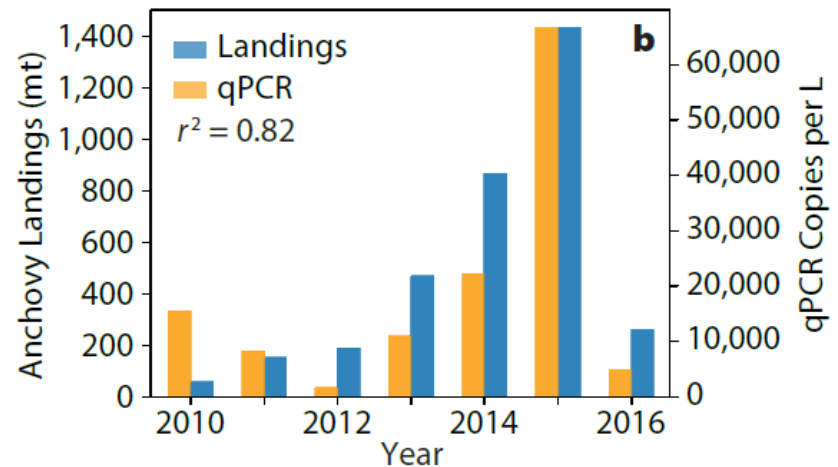
An example comparing eDNA frequencies and relative biomass (A) and relative abundance (B) for various fish families sampled at the same 20 locations

Thomsen, P. F., et al. (2016). "Environmental DNA from Seawater Samples Correlate with Trawl Catches of Subarctic, Deepwater Fishes." *PLoS ONE* 11(11): e0165252



An example comparing annual **anchovy landings** in tons (Monterey Bay) and annual **anchovy qPCR** copies

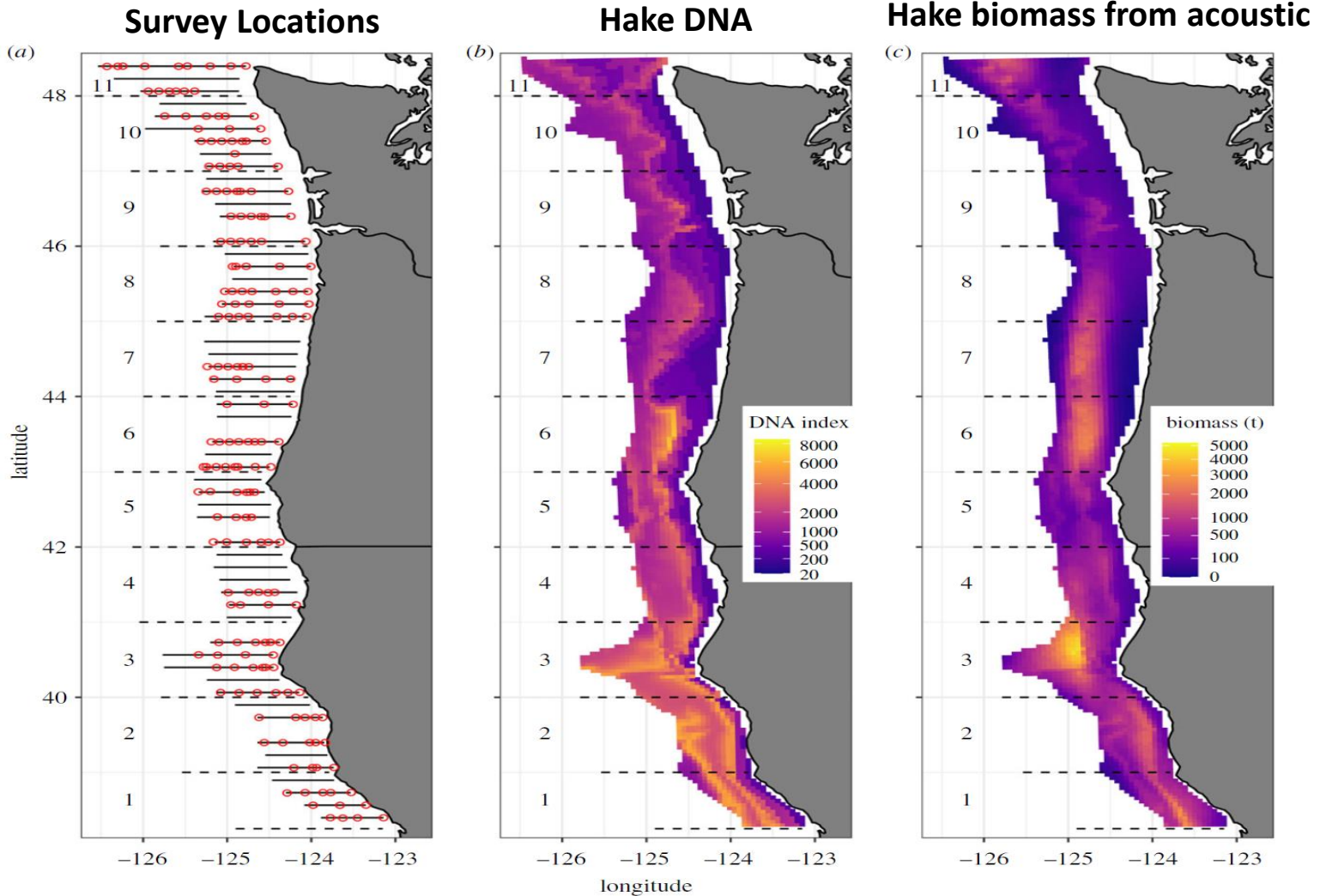
Chavez, F. P., et al. (2021). "Observing life in the sea using environmental DNA." *Oceanography* 34(2): 102 - 119





# eDNA to estimate biomass of a given population

Another example based on **Pacific hake** (*Shelton et al. 2022*)



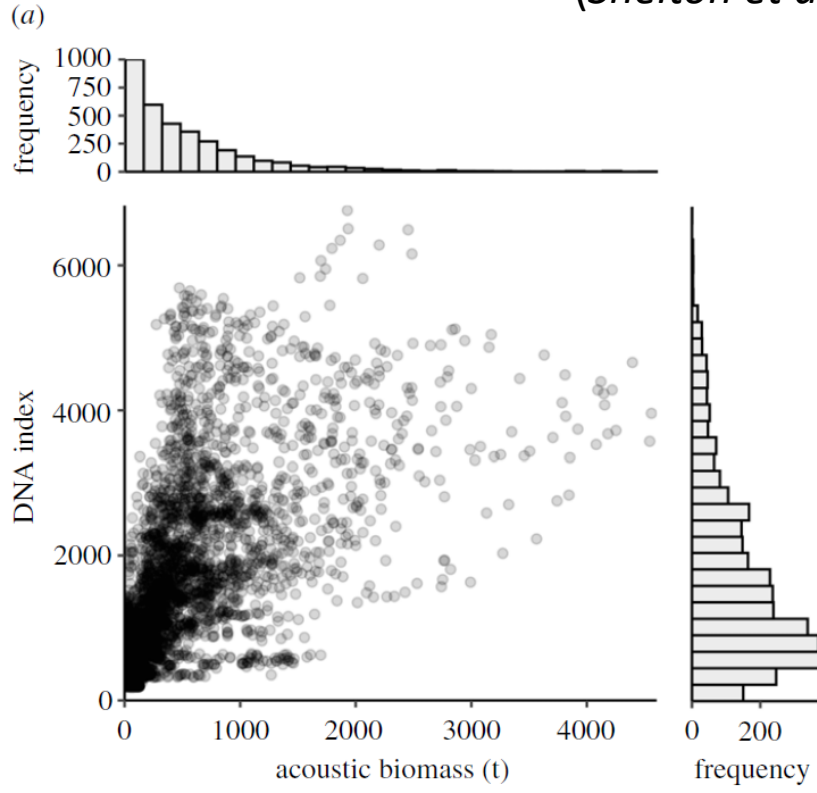
*Shelton, A. O., et al. (2022). "Environmental DNA provides quantitative estimates of Pacific hake abundance and distribution in the open ocean." Proc R Soc B 289: 20212613.*



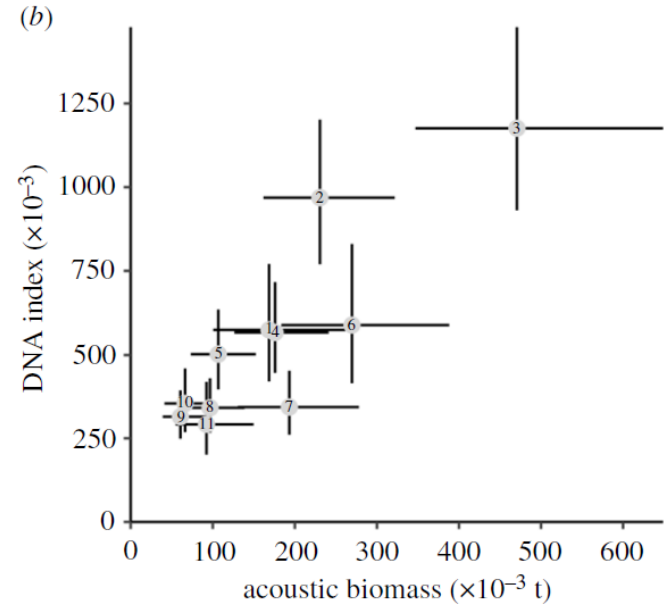


# eDNA to estimate biomass of a given population

Comparison between eDNA and acoustics-derived biomass for **Pacific hake**  
(*Shelton et al. 2022*)



Among the 3455 grid cells



Using 1 degree latitude means

Local differences, but comparable information about the broad-scale spatial distribution and abundance



# Main advantages and disadvantages of eDNA

## Advantages

- **Cost effective:** monitoring cost can be divided by 10 to 100
- **Lower GHG** (greenhouse gases) emission
- **Non-invasive** method (simple filtration of seawater): no mortality of wild fish and no impact on marine habitats
- **Easier and quicker to implement** than conventional fisheries surveys
- **Easily repeatable** and flexible (can be carried out by almost any scientist)
- **Scientific based information** that does not depend on fisheries information

## Disadvantages

- Key abiotic factors (temperature, currents...) that affect the **dispersal and persistence of eDNA** remain unquantified (as for many other sampling methods)
- Dynamics of **eDNA production** by living organisms not well known
- Dynamics of **eDNA degradation** also not well known

**An approach of great interest, especially for exploited stocks for which catch and/or effort are unknown (e.g. small-scale fisheries)**



## From eDNA to fisheries management advice

**How can an eDNA-based index of biomass be translated into an useful information for fisheries management ???**

An option might be to develop a **Harvest Control Rule (HCR)** based on the year-to-year changes in the eDNA-based index and whose performance is tested through a **Management Strategy Evaluation (MSE)**

- The **HCR** is usually a simple algorithm that converts variations in the biomass index into a quota. The HCR may be based other management measures, such minimum size, time/area closures (depending on the context).
- The **MSE** is based on an operating model, such an age-structured population dynamics model, which includes the salient aspects of species biology and ecology. The aim of MSE is to test the performances of various HCR against the simulated population dynamics of the given species. Economic aspects might be included as well!



# From eDNA to fisheries management advice

Such an approach has been performed by Edwards et al. (2014) for the African Lion hunting (data-poor)

1. The **OM** is a nonlinear matrix model  $\mathbf{N}_{t+1} = \mathbf{M}_t(\mathbf{N}_t - \mathbf{k}_t)$ ,

- $N_{t+1}$  is the number of adult lion at time t+1
- $M_t$ , the transition matrix function subdivided into birth, aging, and survival components.
- $k_t$  a vector of numbers of adult lion killed.
- The model includes 10 cohorts.

**Data:** life history traits of lion (biology) and number of lion killed per area

2. The **HCR** is based on a sustainable quota (Q) defined as:  $Q=HN$

- $H$  the sustainable harvest rate
- $N$  the number of lions available to be hunted (here males)

Assuming a random search across space:  $Q=H/c\mu$

- $C$  is a constant of catchability
- $\mu$  is the waiting time to kill a lion

Finally, the quota at t+1 ( $Q_{t+1}$ ) is defined as:  $Q_{t+1} = \hat{H}_t [c(\hat{m} + \hat{\mu}_t)]^{-1}$ ,

- $\hat{H}$  is the proportion of quota filled
- $m$  is the gradient of  $\mu$  over the previous 5 years

**Data:** waiting time to kill a lion, catchability and number of lion killed

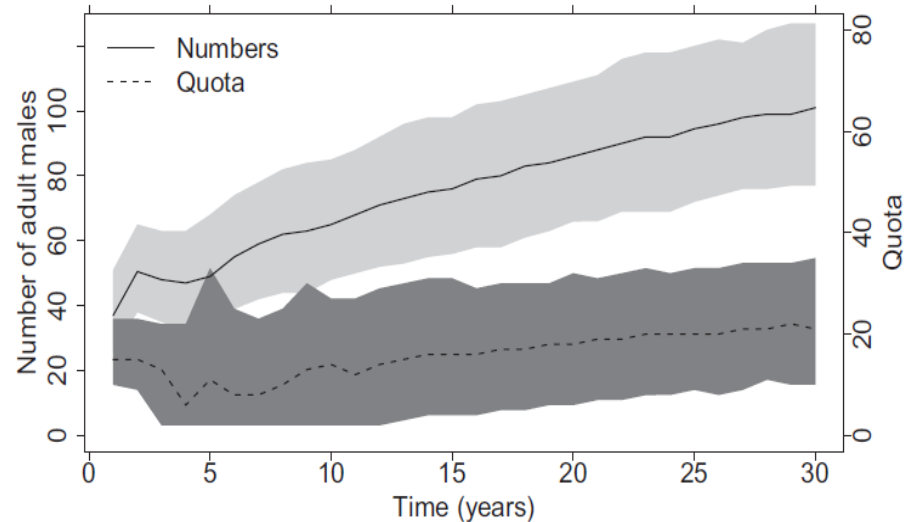


## From eDNA to fisheries management advice

The MSE process was iterated forward in time over a 30-y period, assuming a heavily depleted initial population, including uncertainties in demography, observation, and compliance to the minimum age rule

Simulations were repeated over a range of catchability values

Simulations confirmed that high harvest rates can be sustained for lions  $\geq 5$  years (maturity at 4 years) while the hunting of younger lions induced a decline in population size



Edwards, C.T.T. et al. (2014). "Data-poor management of African lion hunting using a relative index of abundance." *Proc Nat Acad Sci US* 111(1): 539-543

Such an approach is performed by CCSBT for the **Southern Bluefin tuna** (data-rich) where the HCR is based on 3 indices (1 CPUE index and 2 indices of abundance):

$$TAC_{y+1} = TAC_y (1 + \Delta_y^{\text{cpue}} + \Delta_y^{\text{ck}}) \times \Delta_y^{\text{gt}}$$



# An application to the Mediterranean seabream and seabass

## So why this presentation ??

Together with a colleague, Q. Schull, we would like to develop an eDNA approach to evaluate and monitor two flagship species of the French Mediterranean coastal fisheries, i.e. **gilthead bream and sea bass**



There is no advice on Mediterranean coastal species because landings are poorly known and subject to considerable uncertainties:

- **Catch and effort from artisanal fleets are incomplete** (despite decades of effort)
- Catch from **recreational fishing** is unknown, but suspected to be significant
- **Illegal fishing** is of an unknown nature, but also appears to be significant

Therefore, conventional methods in fisheries science can hardly be applied and an eDNA approach together with an HCR tested through MSE may be a good option

**Thanks for your attention !**