

# Genetics in support of fisheries and aquaculture management

17-19 September  
Faro, Portugal



# Largest ever polar expedition will soon be frozen in drifting sea ice



**ENVIRONMENT** 13 September 2019

By [Adam Vaughan](#)

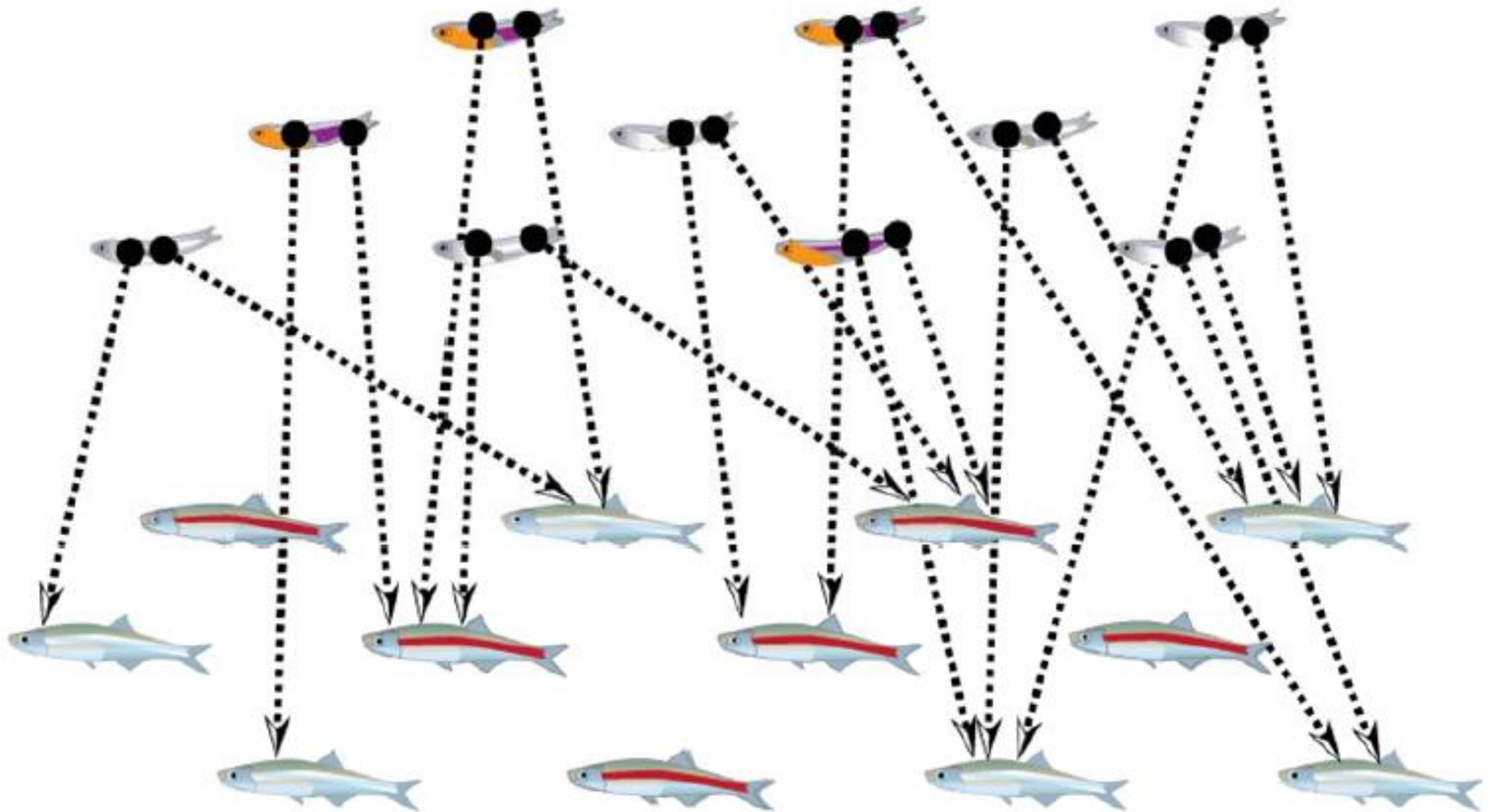


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# Close-Kin Mark Recapture

With the kind support of Ilaria Coscia and CSIRO Australia





# Close-Kin Mark Recapture

- **There are others out there ...**
- **Glossary**
- **Introduction and principles**
- **Underlying assumptions**
- **Needs**
- **Examples**
- **Does it really work?**
- **A roadmap**
- **On the need to scope**
- **Managing expectations**
- **Conditions**
- **GECKA**
- **Becoming an expert**



Volume 89, Issue 6

Special Issue: Fish, Genes and Genomes: Contributions to Ecology, Evolution and Management

Pages: 2471-2767


December 2016

JOURNAL OF **FISH BIOLOGY**



SYMPOSIUM PAPER

## Can estimates of genetic effective population size contribute to fisheries stock assessments?<sup>†</sup>

J. R. Ovenden , G. M. Leigh, D. C. Blower, A. T. Jones, A. Moore, C. Bustamante, R. C. Buckworth, M. B. Bennett, C. L. Dudgeon

First published: 11 October 2016 | <https://doi.org/10.1111/jfb.13129> | Cited by: 14

<sup>†</sup> This paper was presented at the FSBI Symposium, Bangor, in July 2016. Its content may not follow the usual style and format of the *Journal of Fish Biology*.

# A Glossary

**CKMR:** Close-Kin Mark Recapture

**CPUE:** Catch Per Unit Effort

**POPs:** Parent-Offspring pairs

**HSPs:** Half-sib pairs

**SBT:** Southern Bluefin Tuna

**SNP:** Single Nucleotide Polymorphism (a genomic marker)

# In a Nutshell

**Officially Introduced  
in 2016**

*Statistical Science*  
2016, Vol. 31, No. 2, 259–274  
DOI: 10.1214/16-STS552  
In the Public Domain

## **Close-Kin Mark-Recapture**

Mark V. Bravington, Hans J. Skaug and Eric C. Anderson

- **Proposes an alternative, fisheries-independent way to calculate abundance of a population.**
- **Based on the principle of mark-recapture, - offspring to ‘mark’ two parents, by their genetic make-up.**

# In Principle



**Population:**  
10 Juveniles; 12 Adults  
**Matches:**  
4

**Sampled and analysed:**  
4 Juveniles; 6 Adults  
**Nest(adult) =  $(2 \times 24) / 4 = 12$**   
**Ntrue(adult) = 12**

**Comparisons:**  
 $4 \times 6 = 24$



# In Principle

**“DNA tagging”: One juvenile marks two parents.**

- 1. The bigger the population, the less likely to find kin-pairs (*recaptures*).**
- 2. The **higher** the adult survival rate, the **longer** the time to recapture a parent after sampling its offspring**
- 3. Other complications: adult mortality before being sampled, reproductive variability...**

# Assumptions

- **Each individual has a mother and a father**
- **You can reliably find POPs and HSPs via genetics/genomics**
- ***“Everything else is just maths and logistics!”***  
***(Bravington, pers. comm.)***

**CKMR is a flexible tool that can and should be adapted to each specific case.**

# Needs

- **Covariates: year, length, age (?), rough location**
- **\*Enough\* samples (to get enough kin-pairs)**
- **Juvenile samples, and (for teleosts) samples across full size range of adults**
- **Helps to know total catches-at-size over time**
- **But NO need for CPUE, selectivity assumptions, surveys...**

# In a Nutshell for Nerds ...

*Statistical Science*  
2016, Vol. 31, No. 2, 259–274  
DOI: 10.1214/16-STS552  
In the Public Domain

***“Everything else is just maths...”***

## Close-Kin Mark-Recapture

Mark V. Bravington, Hans J. Skaug and Eric C. Anderson

accordingly. The kinship probability becomes

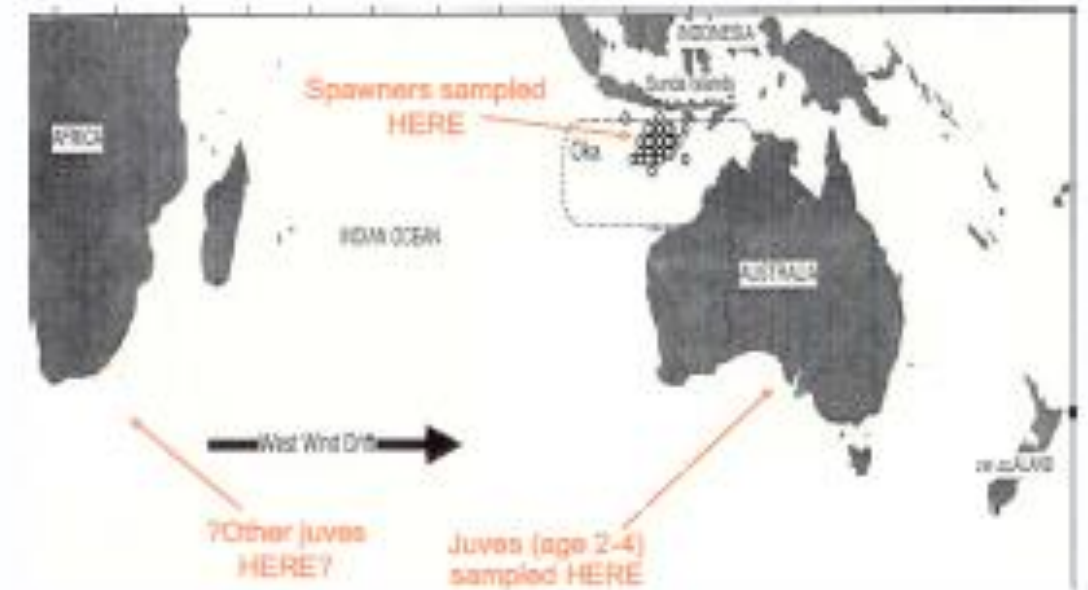
$$(3.3) \quad \begin{aligned} & \mathbb{P}[K_{ij} = \text{MO} | z_i, z_j] \\ &= \frac{\mathbb{I}[y_i + \alpha \leq y_j]}{N_{\ominus y_j}} \times \begin{cases} 1; & t_i > y_j, \\ \phi_i(t_i, y_j); & t_i < y_j, \end{cases} \end{aligned}$$

where  $\phi_i(t_i, y_j)$  is the probability that  $i$  survives from  $t_i$  to  $y_j$ .

# Example

## southern bluefin tuna (SBT)

- Aus' ex-most valuable fishery
- W/wide \$1-2B p.a.
- Heavily depleted, prior to this study, absolute N highly uncertain
- "Challenging" conventional data



- Main catch:
  - juveniles (Australia)
  - subadults (Indian ocean)
  - few adult spawners (Indonesia)
- Maturity age ~ 10
- Lives to 40+ if allowed





# Example

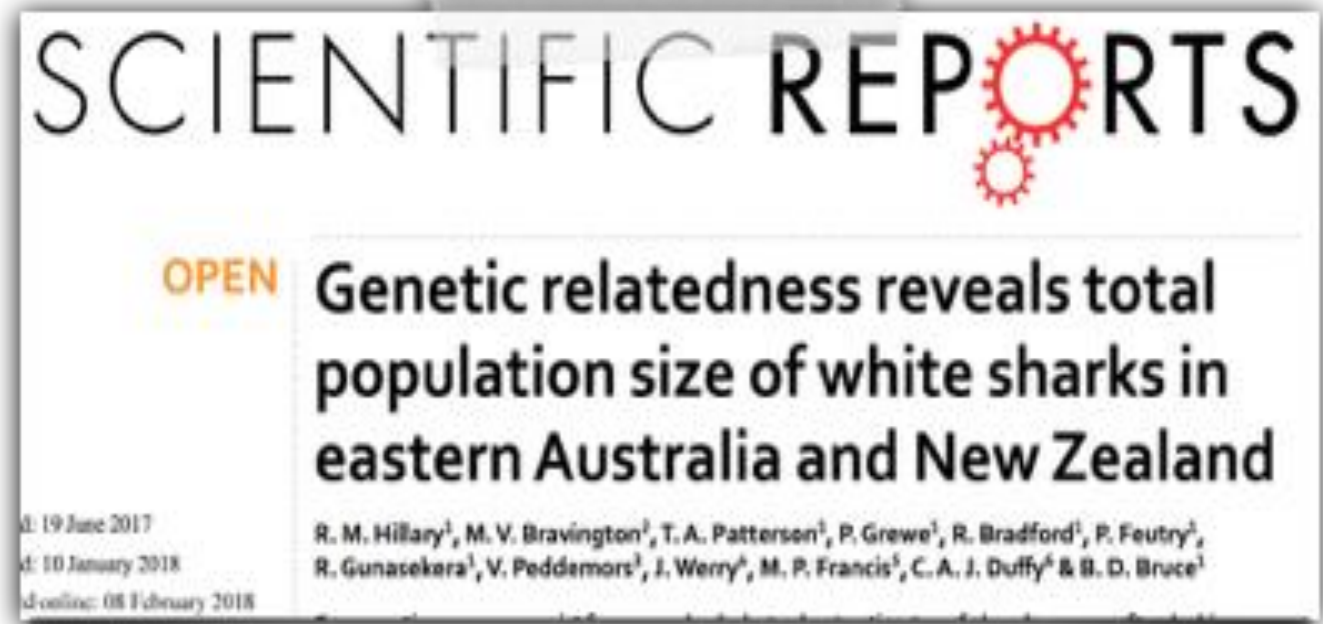
## southern bluefin tuna (SBT)



- **2006: Sampling for CKMR starts;**
- **One juvenile ground - One spawning ground;**
- **2012: about 8000 juveniles and 5000 adults had been genotyped (20–25 microsatellite loci);**
- **2019: 22000 samples - switch to SNPs;**
- **Estimated size of adult population =  $2 \times 10^6$  (higher than previously known).**

# Example

**white shark**



- **Introducing the use of Half Sibling Pairs (HSP)**
- **Sampling adults is very difficult**

**If you sample two juveniles a few years apart that are an HSP, we can estimate the probability of them having the same mother or father - suitable modelling will estimate adult abundance and its trend, plus adult survival rate.**

# Does it Work?

**Apparently so!**

**Further validation: populations of brook trout  
(2400 individuals over 5 years)**

**CKMR results compared to those obtained through  
electrofishing 📍 **very consistent****

Methods in Ecology and Evolution



RESEARCH ARTICLE

**Validation of close-kin mark–recapture (CKMR) methods for  
estimating population abundance**

Daniel E. Ruzzante✉, Gregory R. McCracken, Brage Førland, John MacMillan, Daniela Notte, Colin Buhariwalla, Joanna Mills Flemming, Hans Skaug

First published: 18 June 2019 | <https://doi.org/10.1111/2041-210X.13243>

# BUT!

- **CKMR is NOT ‘just’ genotyping thousands of individuals!**
- **Required: Background knowledge on the biology of target species.**
- **Required: Careful design of study in question.**

**Where and how to start?**



# GECKA

Genetic close-kin analysis on white anglerfish (*Lophius piscatorius*) for abundance estimates in support of deep sea fisheries management under the Common Fisheries Policy



University of  
**Salford**  
MANCHESTER



## CLOSE-KIN MARK RECAPTURE FOR STOCK ASSESSMENT *a survival guide*



### IS CKMR *applicable*?

NO, without a good knowledge of the biology of the species or for certain life-histories

### IS CKMR *useful*?

Given the biology of the species:

- is it too costly?
- is the the stock too small?
- is it already well assessed?

### *scoping study, FIRST*

*it is useful, but is it feasible?*

Is age data reliably available?  
Would you be able to sample enough across age classes?

### *assemble a team*

you need lab technicians, geneticists, bioinformaticians and stock assessment expert...

## the **5** steps to success

### 2. Sampling

Once you have a rough idea of how many samples are needed, go out and get them...

### 4. Kin-finding

Strict control for false positives and estimate of false negatives

### 1. Design

How many samples are necessary to find enough POPs/HSPs? The better the design, the more precise the result

### 3. Genotyping

It needs to be **repeatable, reliable** and with low error-rate

### 5. Statistics

Consider covariates -age structure, population structure, site-fidelity, lucky litters etc...





# Key

- **Good, *qualitative* knowledge of target species biology.**
- **Aging is important**
  - **at least for juveniles;**
  - **best “guesses” (e.g. from length) are useful too.**
- **Obtaining necessary number of samples feasible?**

# Better Not If

- **Too costly – compared to fishery value.**
- **Target stock is too small.**
- **Target stock is already well assessed?**

# Before the Start: Scope

- **Biology okay?**
- **Sampling feasible?**
- **Value of fisheries?**
- **How many individual to sample (roughly) to expect a useful number of kin-pairs?**
  - (R package *Microscoping* - under development)
- **If yes: more detailed design, to look at precision, optimality, how much ageing, etc.**
  - (R package *optides* – under development)



# Before the Start: Scope

- **TIME and BUDGET:**

- **CKMR study in 6 months**

- **without a team of geneticists, statisticians, stock assessment experts**

**= wishful thinking!**

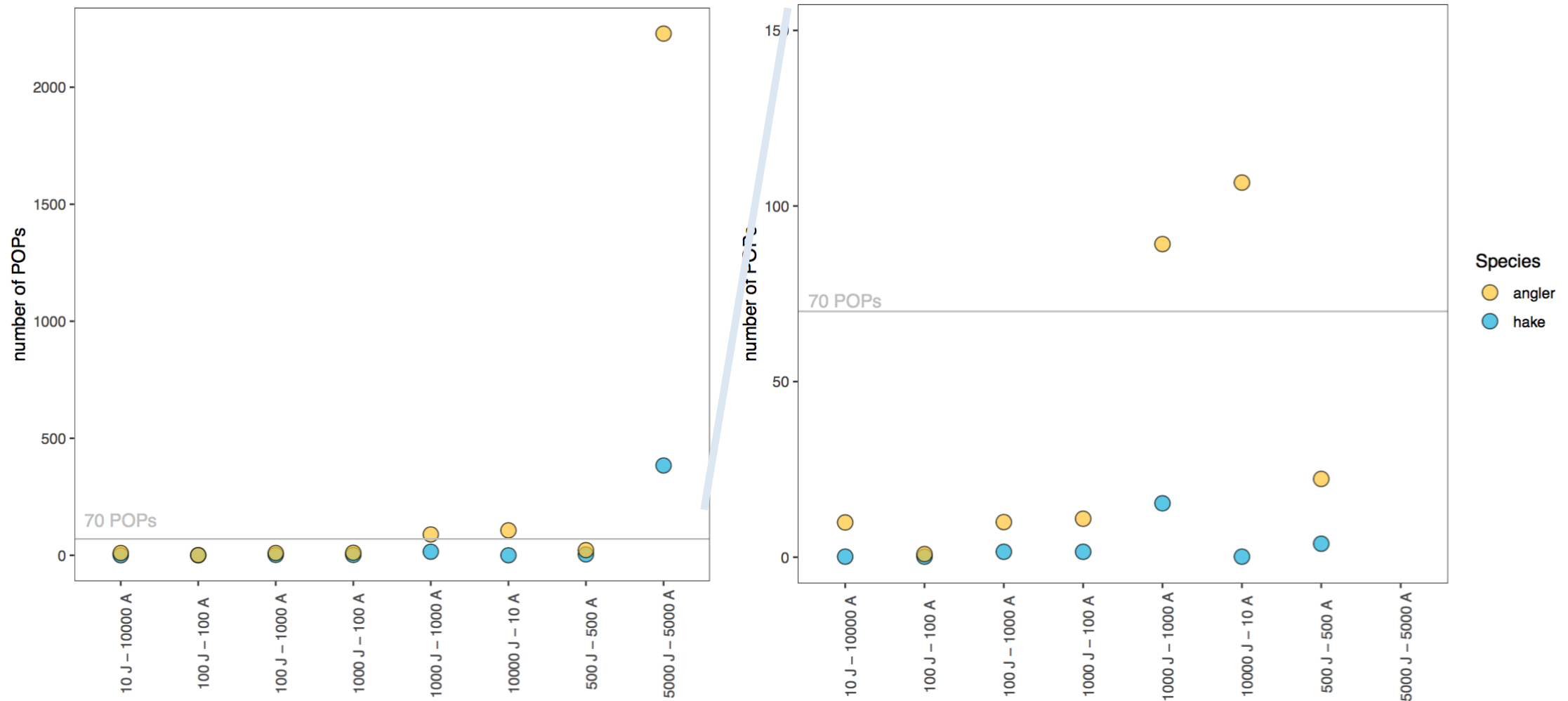
- **Most projects: >3 years [Start to CKMR estimate]**

- **Do not be intimidated: compare to the overall value of the target fishery**

- **Most effort/cost is invested in the first years**

# Before the Start: Scope

## Sampling effort





# Scope and Manage Expectations

**(Roughly)**

## **White anglerfish**

- **1000 juveniles + 1000 adults**
- **could result in ~90 POPs**

## **European hake**

- **5000 juveniles + 5000 adults**
- **could result in ~350 POPs**

# Conditions

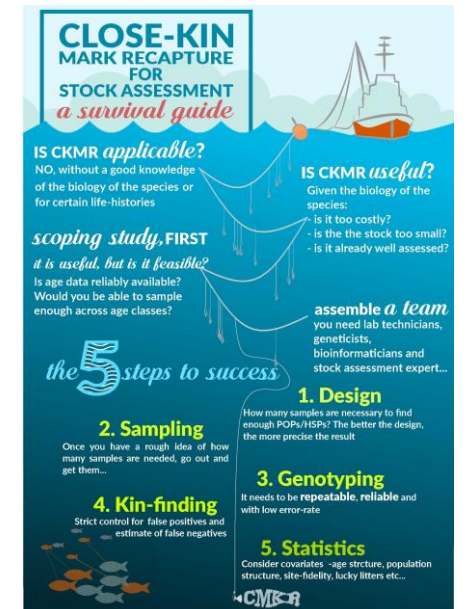
- **Genotyping has to be accurate (reducing error rate)**
- **Kin-finding must be controlled for false-positives (and false-negatives)**

# GECKA

## GECKA

Genetic close-kin analysis on white anglerfish (*Lophius piscatorius*) for abundance estimates in support of deep sea fisheries management under the Common Fisheries Policy

<https://www.azti.es/gecka/>



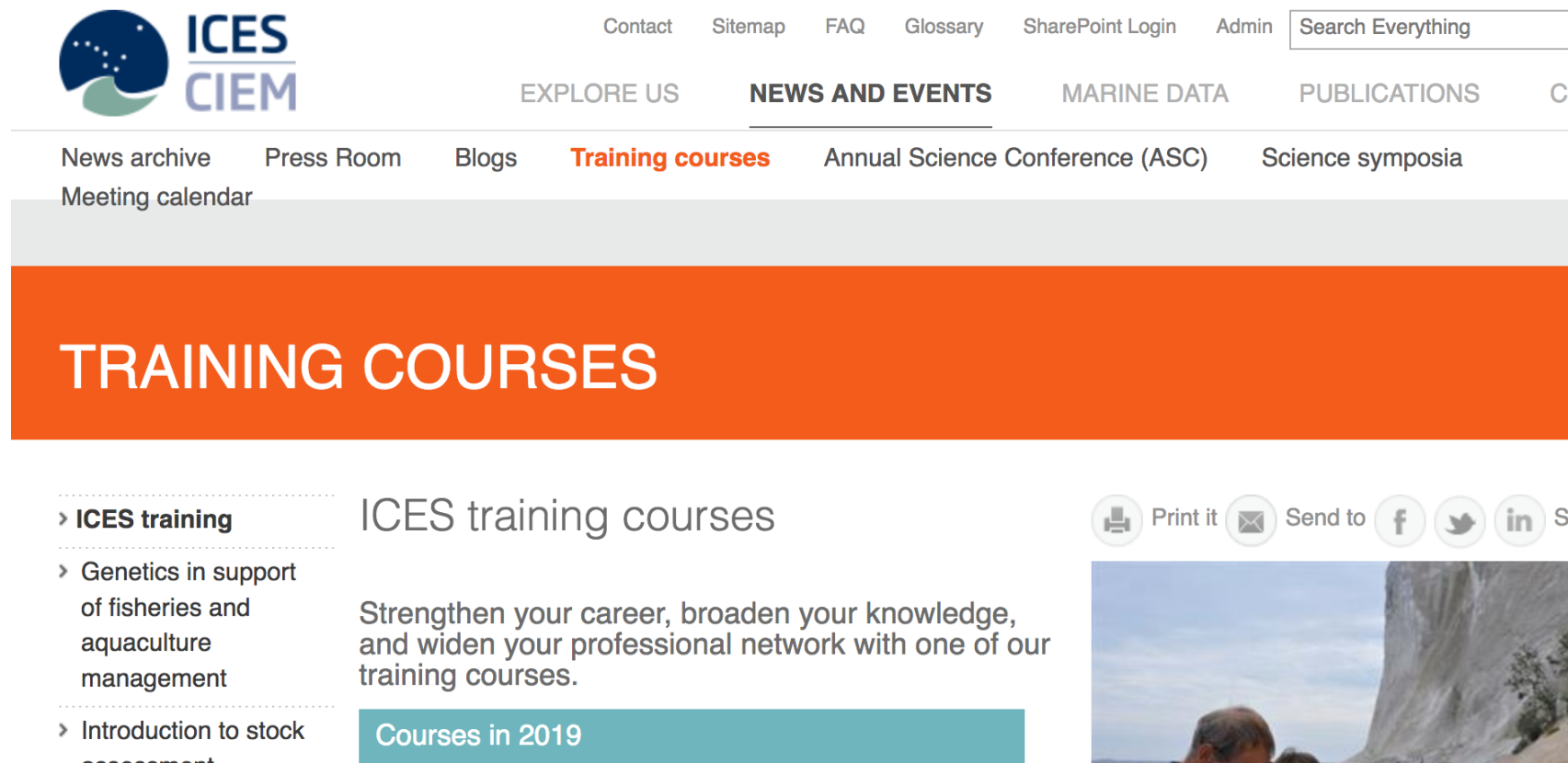
University of  
**Salford**  
MANCHESTER



# Want to become a CKMR Expert?

**March 2020 - Dates TBC**

**Instructors: Mark Bravington and Richard Hillary**



The screenshot shows the ICES CIEM website navigation menu and a training course announcement. The navigation menu includes: Contact, Sitemap, FAQ, Glossary, SharePoint Login, Admin, Search Everything, EXPLORE US, NEWS AND EVENTS (highlighted), MARINE DATA, PUBLICATIONS, and CIEM. Below the menu are links for News archive, Press Room, Blogs, Training courses (highlighted), Annual Science Conference (ASC), Science symposia, and Meeting calendar. A large orange banner reads "TRAINING COURSES".

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## TRAINING COURSES

› **ICES training**


- › Genetics in support of fisheries and aquaculture management
- › Introduction to stock assessment

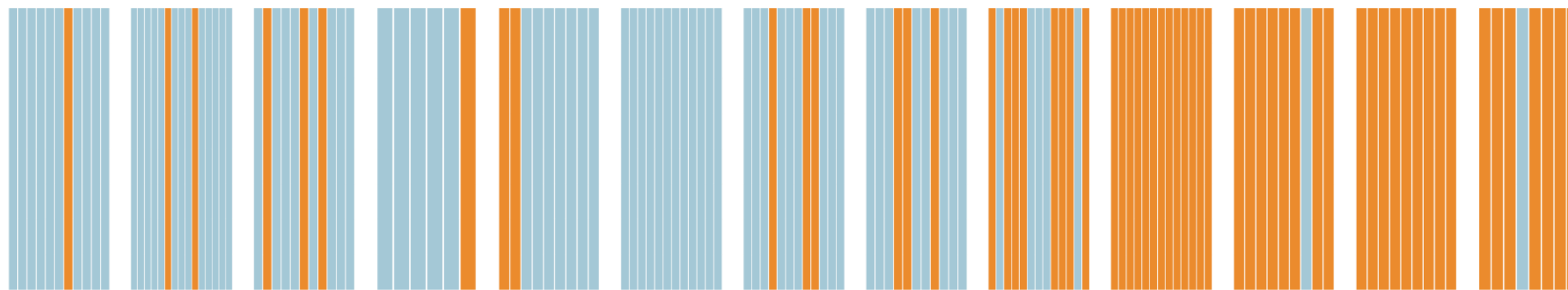
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