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## Population size estimation of swordfish through Close-Kin Mark Recapture

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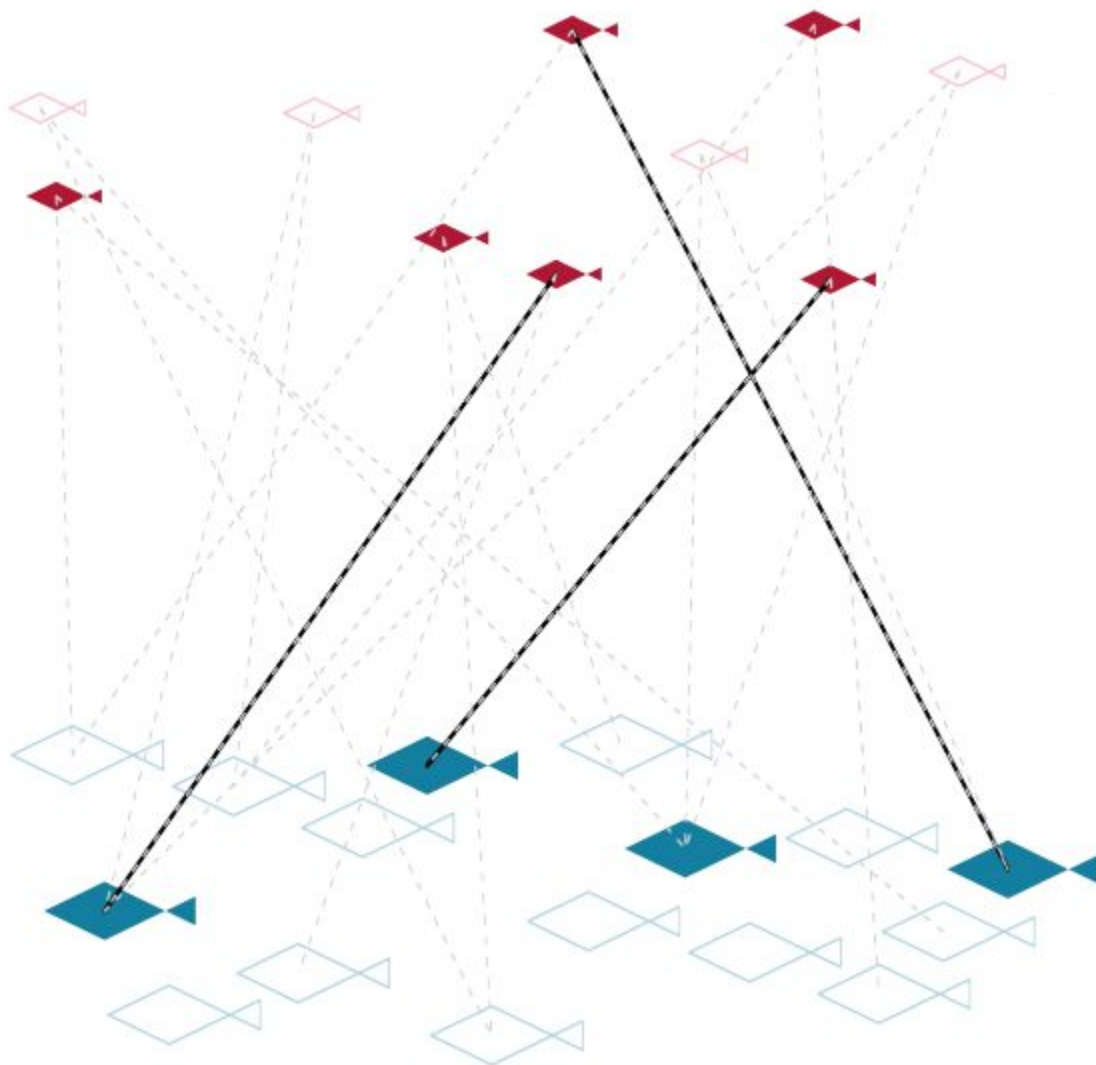
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# Swordfish Close Kin Mark Recapture (CKMR) in the Indian Ocean



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**Juveniles  
(immature)**

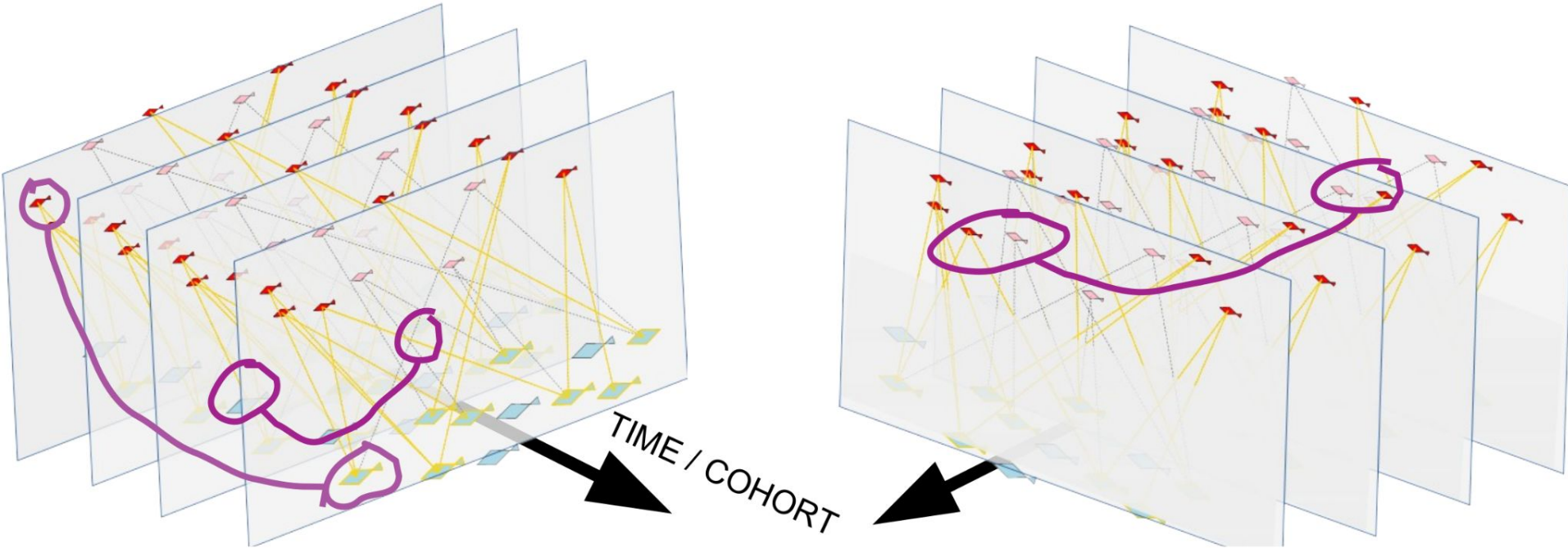
Each offspring genetically “marks” or “tags”  
its two parents among the total adult  
population

**Adults  
(mature)**

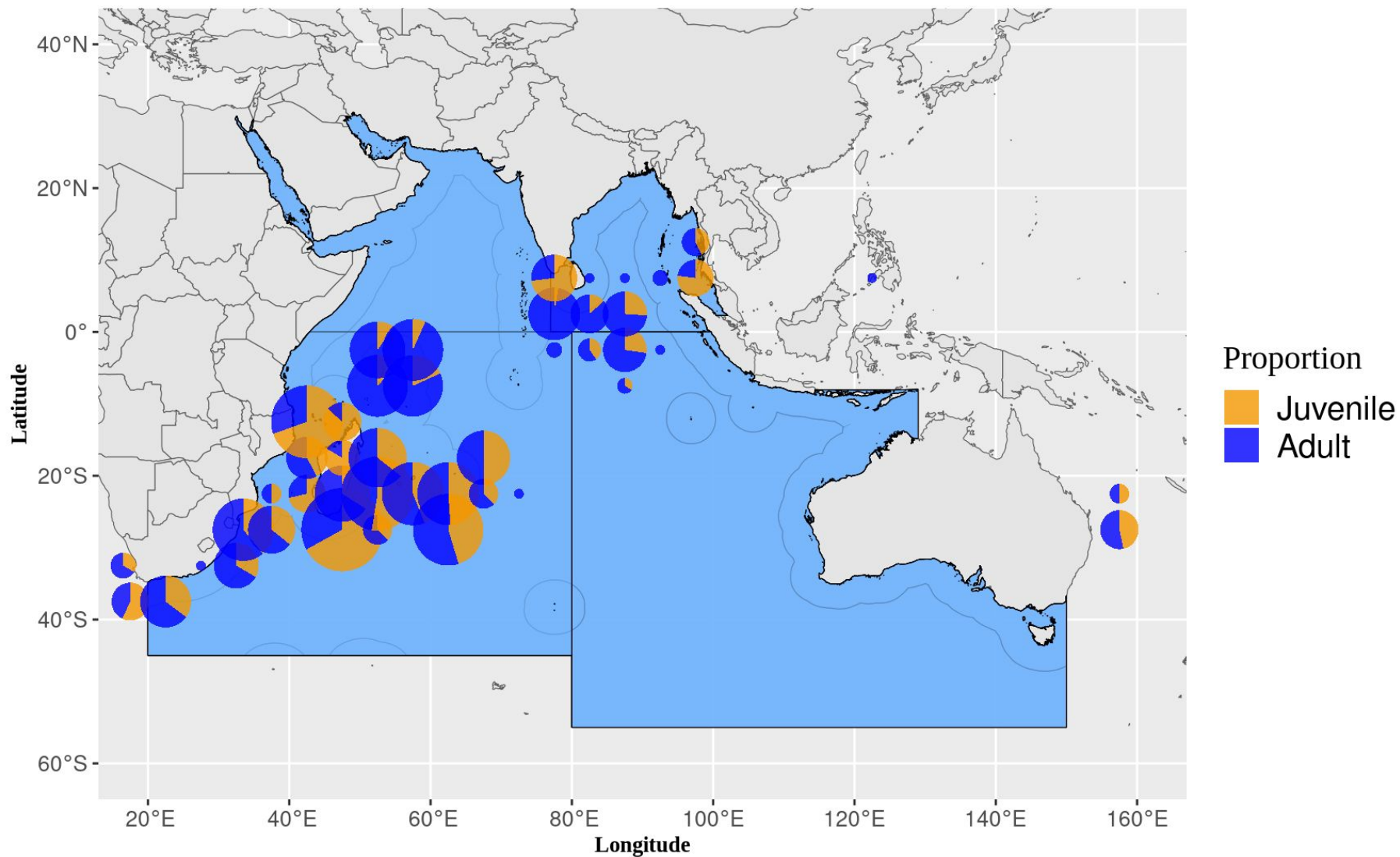
Tags: **direct** (POPs)

or

**indirect** (HSPs)



Mature individuals are “recaptured” **directly** via sampling themselves and their offspring or **indirectly** by sampling at least two offspring



Samples were collected over 2006-2007 and 2009-2011



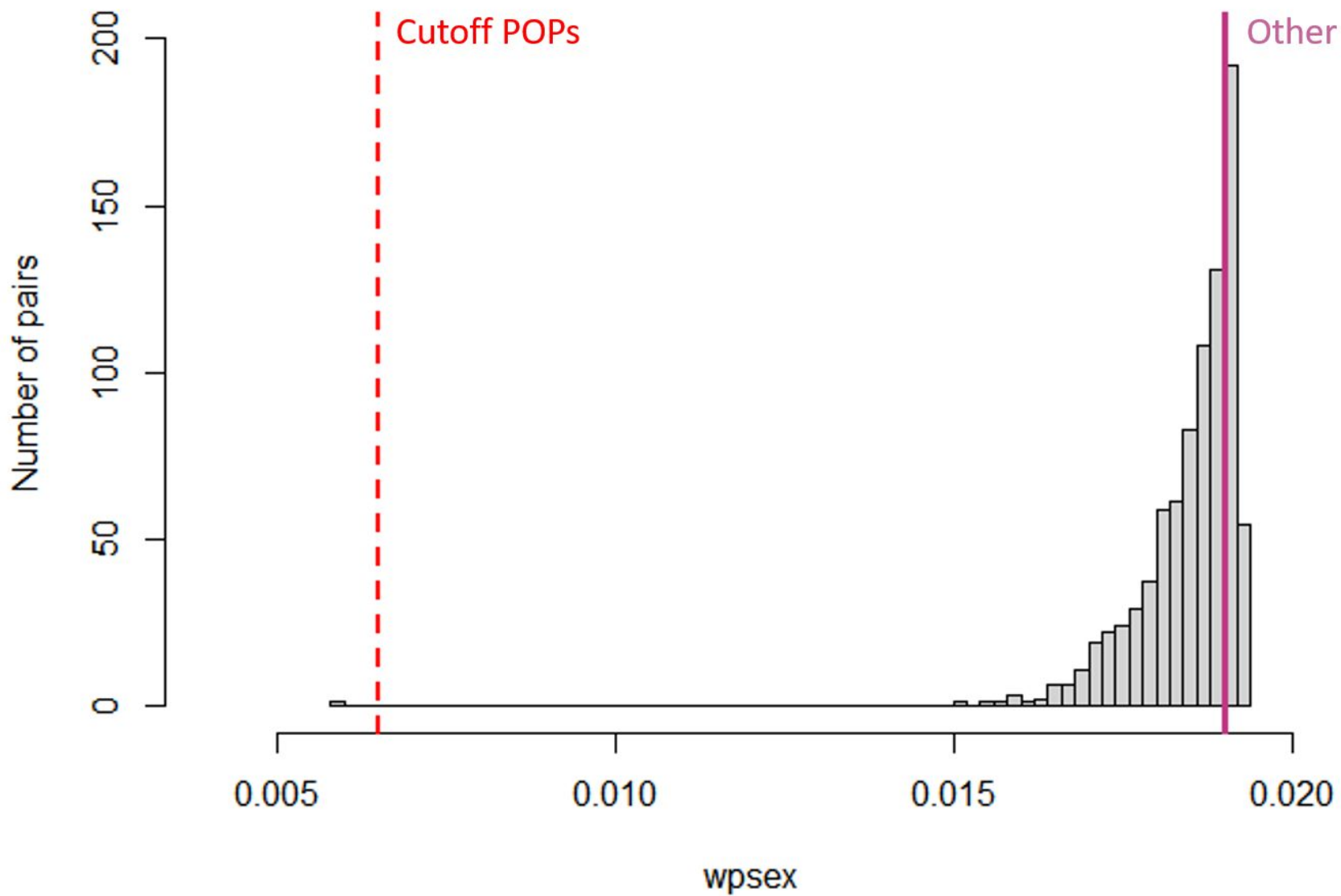
WPSEX is a weighted sum across loci of the number of pseudo-exclusions where one genotype is AA and the other BB, which could either be a true exclusion in a non-POP, a co-inherited null, or a genotyping error where AB is mis-called.

$$WPSEX_{ij} = \sum_l w_l I[(g_{il}, g_{jl}) = (AA, BB)]$$

where the indicator  $I[]$  function is 1 if its condition is met and 0 otherwise, and  $w_l$  is a locus-specific weight.

On average, POPs will have fewer pseudo-exclusions (because no true exclusions) and thus lower WPSEX's than will Unrelated Pairs (UPs).

$$WPSEX_{POP} < WPSEX_{FSP} < WPSEX_{HSP} < WPSEX_{UP}$$



$$\text{PLOD}_{\text{HSP:UP}}(i, j) = \sum_{\ell \in \text{loci}} \log \frac{\mathbb{P}[g_{i\ell}, g_{j\ell} | k_{ij} = \text{HSP}]}{\mathbb{P}[g_{i\ell}, g_{j\ell} | k_{ij} = \text{UP}]}$$

$g_{i\ell}$  is genotype of  $i$  at locus  $\ell$  : AA, AB or BB

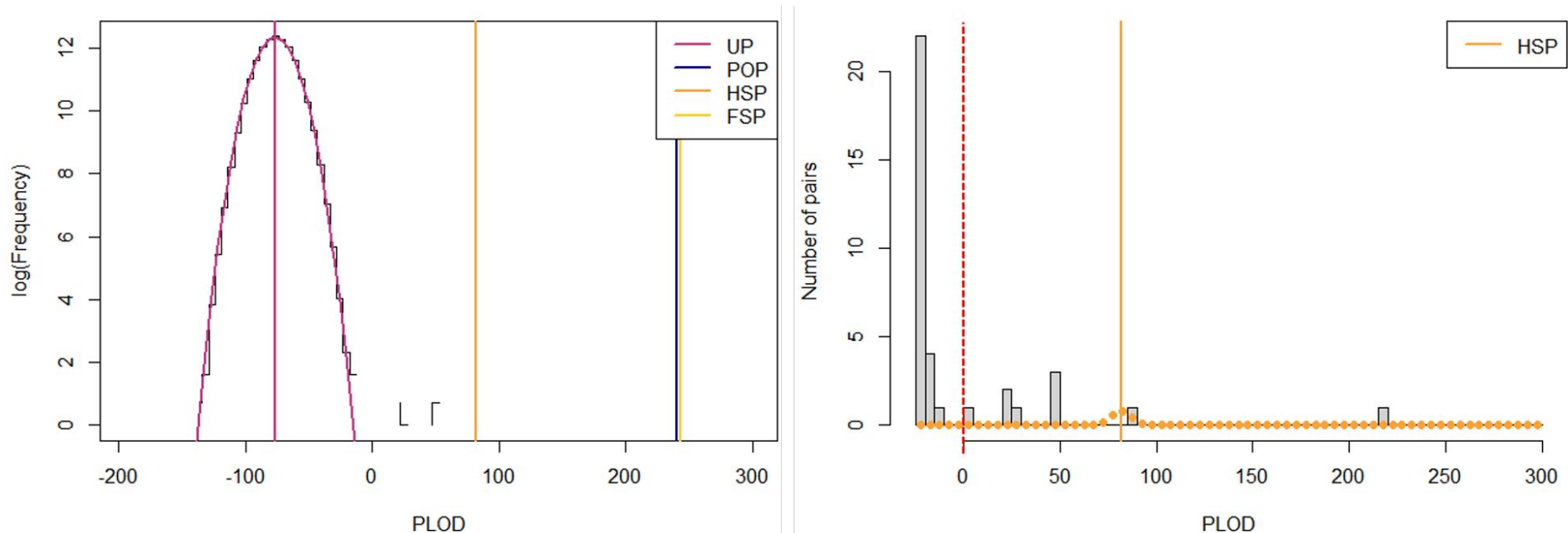
$$\begin{aligned} & \mathbb{P}[g_{i\ell}, g_{j\ell} | k_{ij} = \text{HSP}] \\ &= \frac{1}{2} \mathbb{P}[g_{i\ell}, g_{j\ell} | \kappa_{ij\ell} = 0] + \frac{1}{2} \mathbb{P}[g_{i\ell}, g_{j\ell} | \kappa_{ij\ell} = 1] \\ & \mathbb{P}[g_{i\ell}, g_{j\ell} | k_{ij} = \text{UP}] = \mathbb{P}[g_{i\ell}, g_{j\ell} | \kappa_{ij\ell} = 0] \end{aligned}$$

$\kappa_{ij\ell}$  : number of coinherited alleles



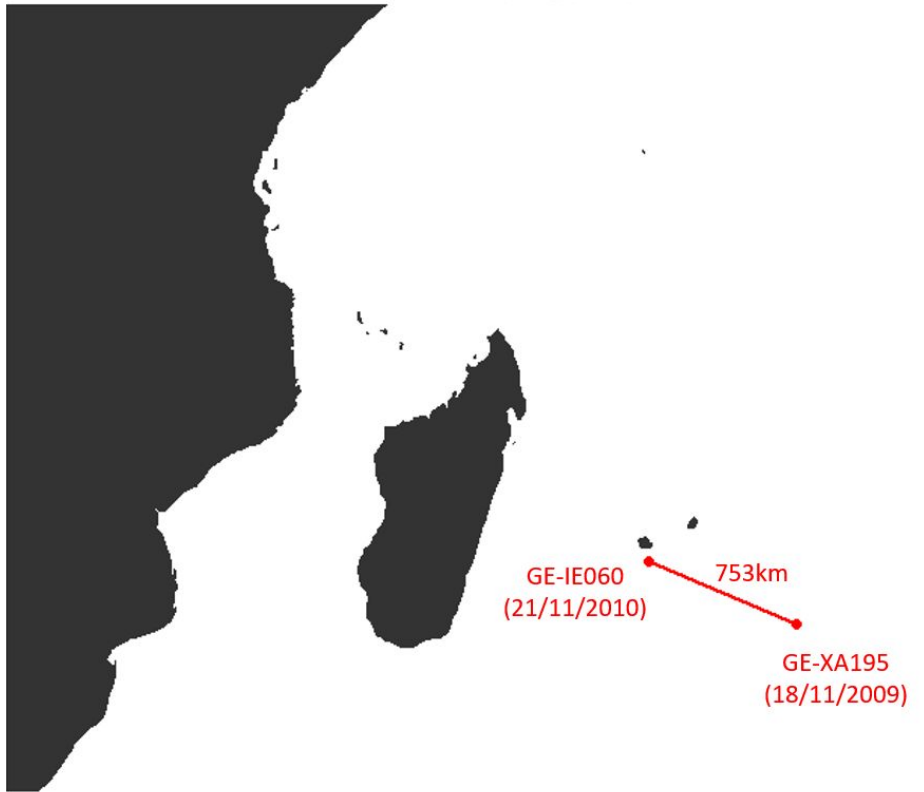


- ❖ Histogram correspond to field data and color line are predicted one
- ❖ Negative bump for Unrelated Pairs (UP) → perfect match
- ❖ 1 POP as for WPSEX with same fish
- ❖ 1 HSP (PLOD = 85) and 6 weaker kin ( $20 < \text{PLOD} < 50$ )



## Both pairs from South-Western Indian Ocean

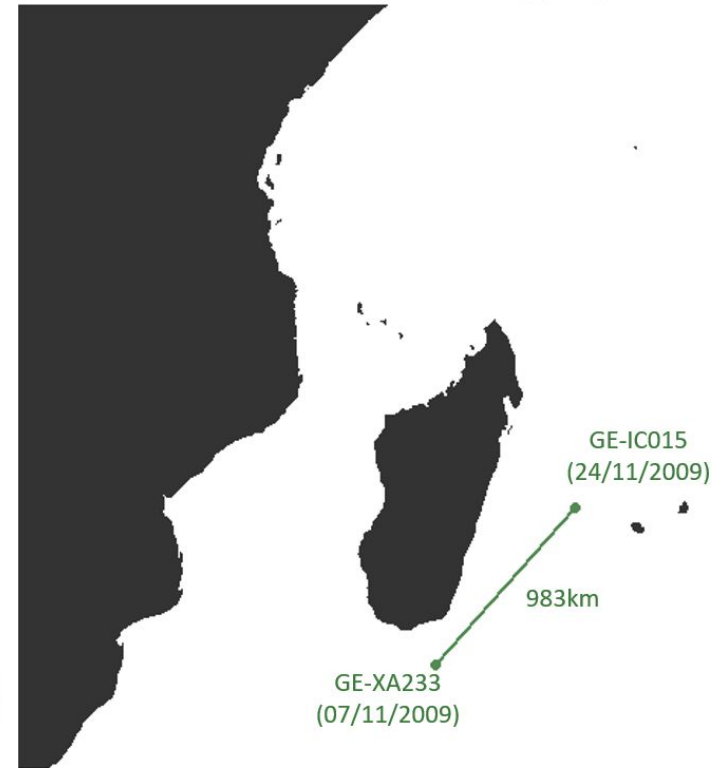
Pairs of Parent-Offspring (POP)



GE-XA195 : 233 cm - Female

GE-IE060 : 155 cm - Male -Maturity stage : 2

Pairs of Half-Sibling (HSP)



GE-IC015 : 188 cm - Female

GE-XA233: 252 cm - Female -Maturity stage : 7

Data source: DArT



*We are currently working on it with Sylvain, we hope that the model will work before the presentation we are very close. Otherwise we will use the first equation we presented in the paper for this slide.*



$$\hat{N}_{\text{adult}} = 2 mJ mA/P$$

$mJ$  : number of genotyped offspring

$mA$  : number of genotyped adults

$P$  is the number of identified POPs

1 434 880 adults individuals in 2009  
(2 x 760 juveniles x 944 adults)/1



- ❖ Current design is good
- ❖ 1 POP obtained, simulation ~18% chance

## Perspectives

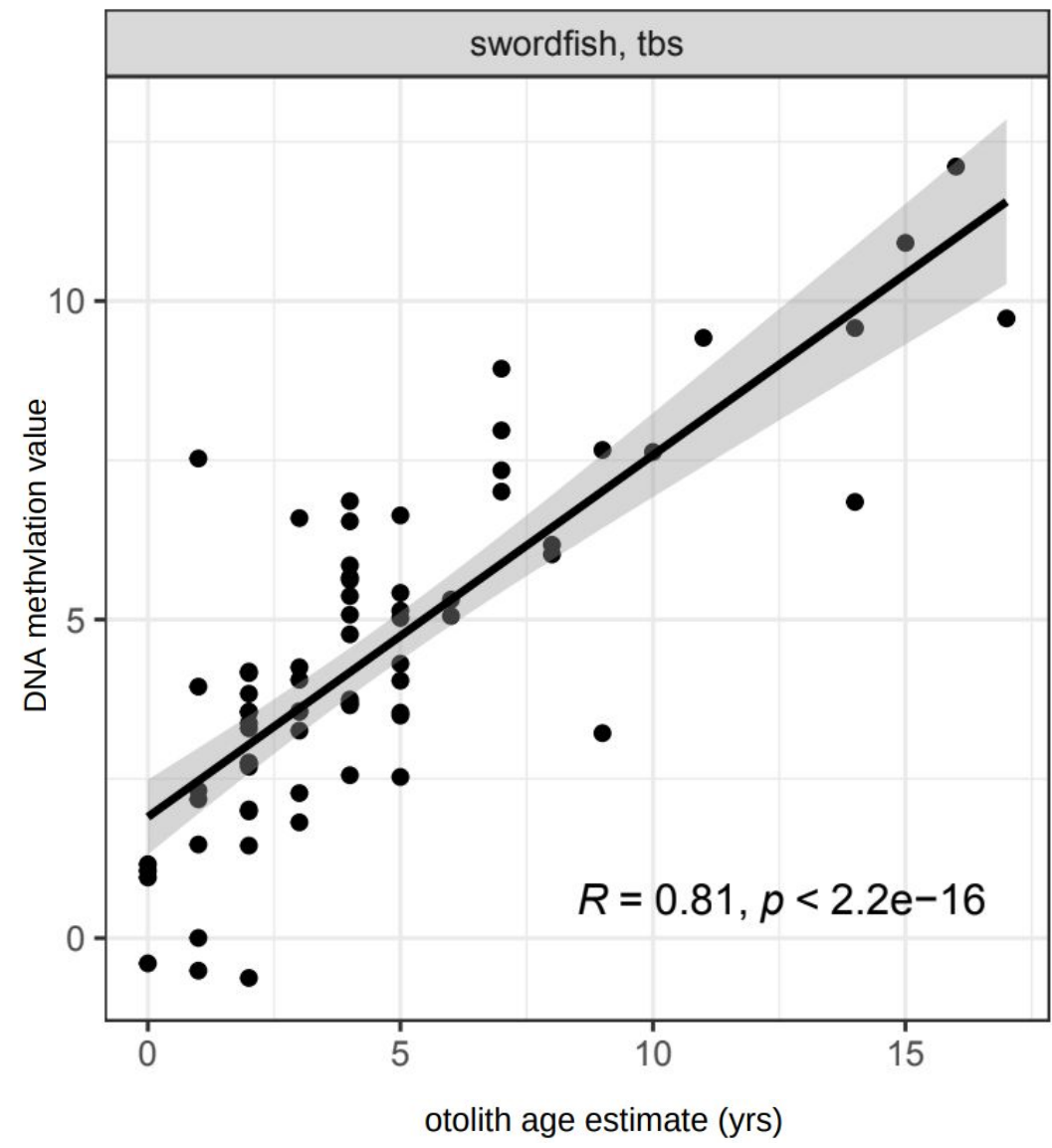
- ❖ Increasing number of samples
  - **Add PSTBS-IO samples from Grewe et al. 2020 ?**
  - **Continue sampling all around Indian Ocean**
- ❖ Targeting 50 POPs / XHSPs for good estimation and CV
  - **~ 15 000 swordfish (1:1 adults:juveniles)**

Differentiation between adult and juvenile :

- ❖ Length
  - LCK, LMF ...
  
- ❖ Otolith age
  - Time-consuming
  - Variability (technique, observer ...)

New approach :

- ❖ Epigenetic (methylation)
- ❖ Positive correlation of 0.81



Thank you for your  
attention!



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