

CHALLENGES AND SOLUTIONS WHEN IMPLEMENTING GENETICS AND PARASITE DATA INTO MODELS

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WHO AM I?

An impostor

Blame Anna!

BUT

I have been party to many discussions related to fishery assessment and management questions where the use of genetics/parasite data has been under consideration

OUTLINE

I. The key questions

II. Genetics

- a) Low discriminatory power
- b) Lack of significant differences
- c) Improving power
- d) Estimating overlap proportions
- e) Novel usages

III. Parasites

KEY QUESTIONS

- How many demographically distinct populations (stocks) are present?

Different stocks should be managed separately

- What are the boundaries between them? (Other than “political” defaults)

- Where stocks overlap, in what relative proportions are they present?

GENETICS – low discriminatory power

m proportion of stock migrating per generation

Key management question:

Is $m >$ or < 0.1 (are stocks coupled or separate?)

N_e effective population size

F_{st} measure of genetic difference

$$F_{st} = 1 / (1 + 4 m N_e)$$

Doesn't give m directly

GENETICS – low discriminatory power

$$F_{st} = 1 / (1 + 4 m N_e)$$

Usually N_e is large, so that F_{st} is small

Though note that N_e/N can range from 10^{-1} to 10^{-6}

If $N_e > 10^4$, F_{st} has little ability to distinguish amongst key values of m .

GENETICS – lack of significant difference

Failure to find significant differences

does **NOT** imply

NO stock structure

- Type II error – power depends on sample size (and effect size)
- Use other information (e.g. tagging)
- If in doubt, treat as separate stocks to be precautionary? – **yes/no?**

GENETICS – improving power

History: allozymes
mtDNA (maternal only)
microsatellites
SNPs

Successive increase in power

However, there has been a tendency in the past to oversell potential utility

Differences that “disappeared” (the “Oslo bump”)

GENETICS – estimating overlap proportions

FREQUENCY-BASED METHODS

- Determine allele frequency distributions for regions where only a single stock (is considered to be) present
- Estimate proportions in overlap areas by MLE
- Widely used for whale and salmon population models
- Problems with > 2 stocks with one large and one small difference

GENETICS – estimating overlap proportions

ASSIGNMENT –BASED METHODS

- Don't need “pure stock” assumptions
- Based on minimising departures from Hardy-Weinberg equilibrium
- Again problems with > 2 stocks with one large and one small difference – difficult to detect the third stock reliably

ASSIGNMENT-BASED EXAMPLE

Shallow-water hake off Namibia and South Africa
(Unpublished data, courtesy Romina Henriques)

2012

2013

2014

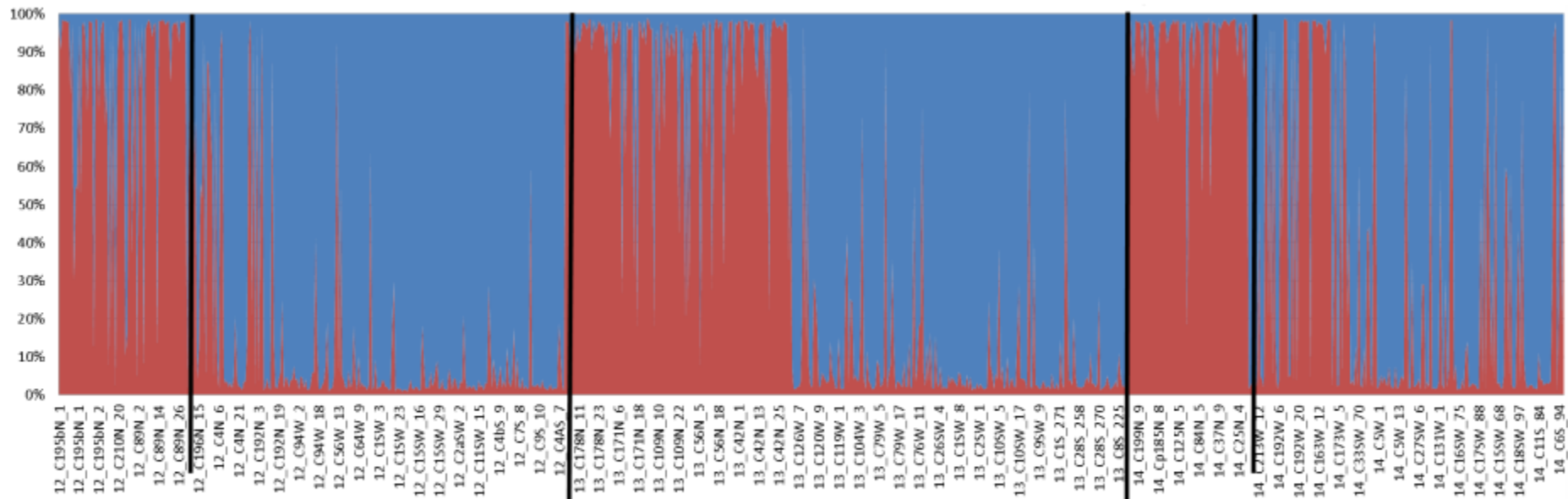
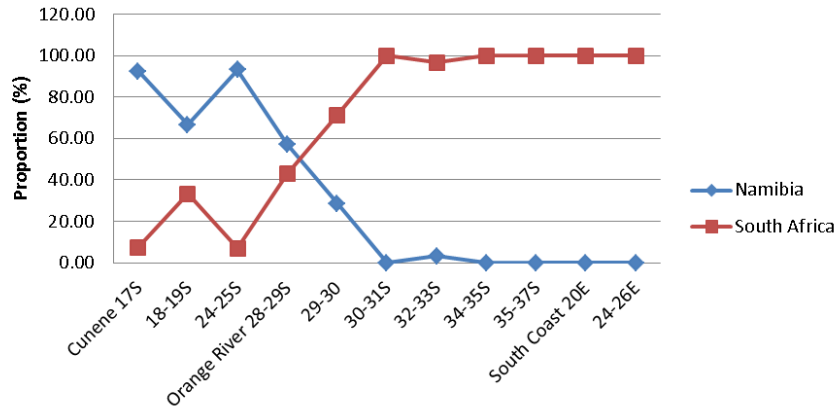


Figure I: Structure assignment plots for the complete dataset (2012-2014) of *M. capensis* based on nine microsatellite markers for K=2: Namibia – blue; South Africa – red

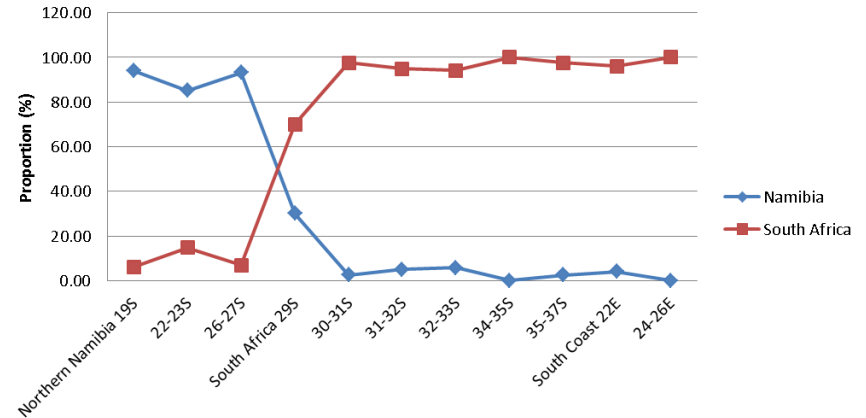
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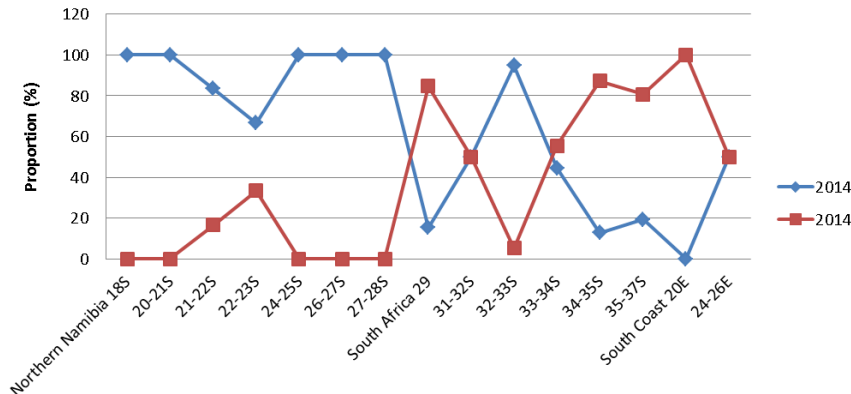


Figure IIa: Proportion (in %) of *M. capensis* individuals assigned to both the Namibian and South African populations per year, based on nine microsatellites and using a sampling interval of 1^0

GENETICS – novel usages

■ TOSSM

IWC MSE testing of different genetic approaches to determine stock boundaries

■ “CLOSE KIN”

“Genetic fingerprinting” approach to use parent/offspring identifications on a mark-recapture basis to estimate population size (avoids standard problem of estimating recovery reporting rate) – Bravington, SBT

GENETICS – novel usages

■ “CLOSE KIN”

“Genetic fingerprinting” approach to identify an individual repeatedly or identify parent-offspring linkages to establish extent of movement and hence inform about stock structure

■ BOTTLENECKS

Number alleles present establishes minimum number present at the time of a recent substantial reduction (used for humpback whales)

LIMITATION

Populations cannot be too large

PARASITES

BASIC IDEA

If a particular parasite is found on fish in a certain region only, *and that parasite remains on the fish after infestation*, that region contains a separate stock

SUCCESS RATE

Generally poor

HAKE PARASITES OFF NAMIBIA

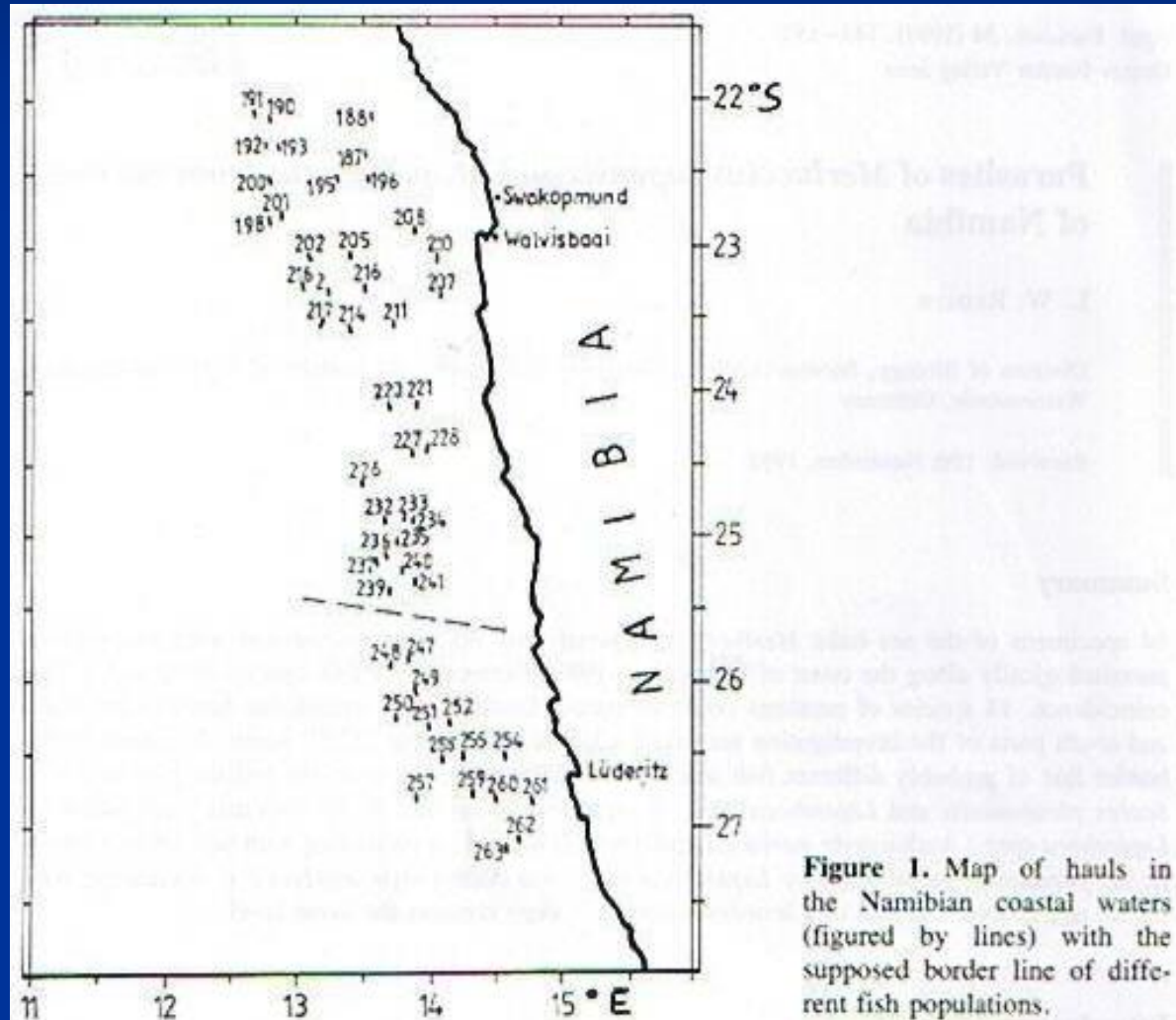


Figure 1. Map of hauls in the Namibian coastal waters (figured by lines) with the supposed border line of different fish populations.

SARDINE PARASITES OFF SOUTH AFRICA

Imply eastward movement

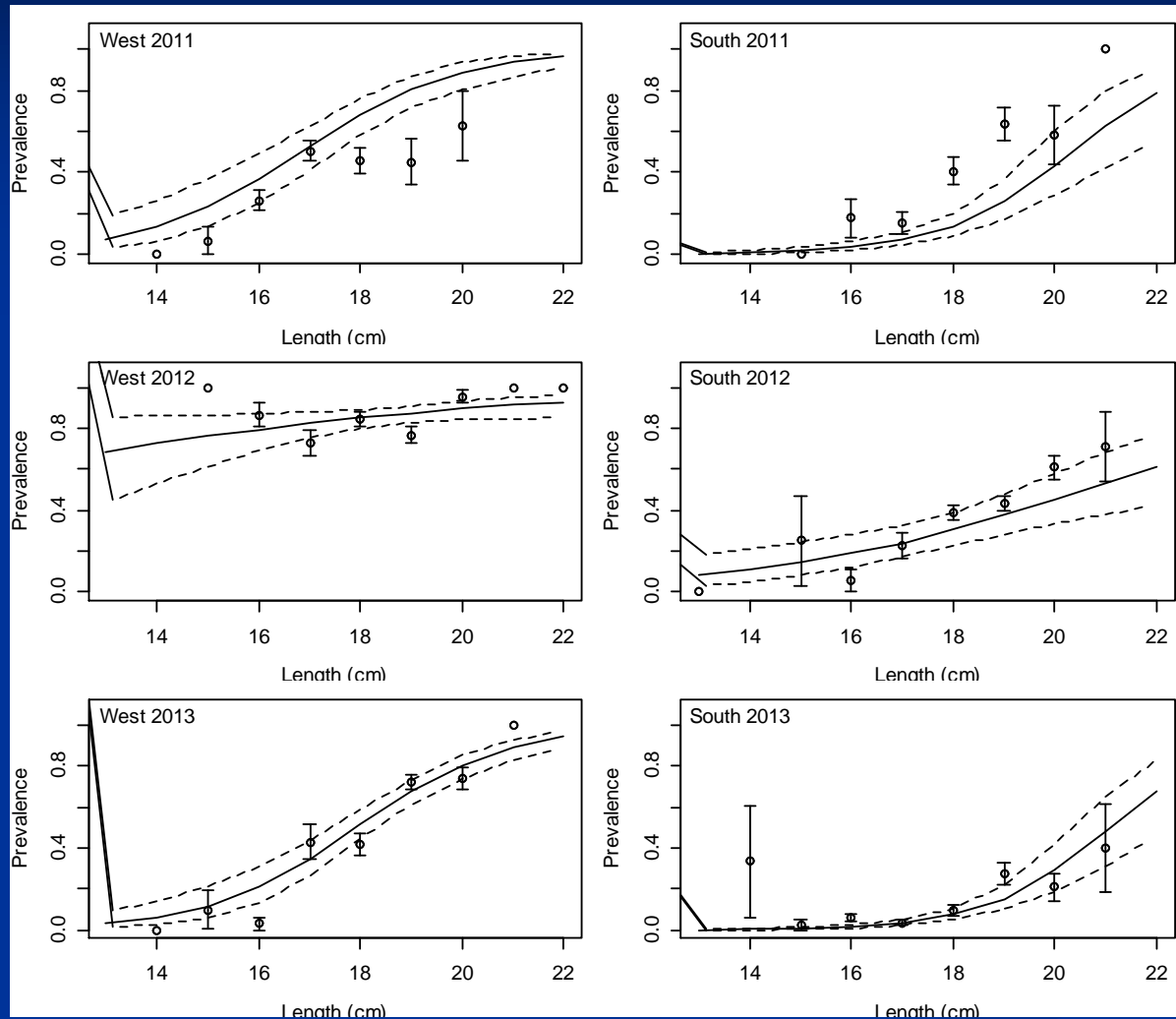


Figure 1: Outputs from the updated prevalence of infection GLM showing predicted prevalence (proportion; solid lines with 95% confidence limits shown as dashed lines) by CL for each stock during each year. Open circles denote the mean observed prevalence of infection-at-CL by year and stock with binomial standard error bars shown.

Thank you for your attention

With acknowledgements to

Waples, Punt and Cope – Fish and Fisheries 9 (2008) 423-49

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Carl van der Lingen – South African sardine parasite data

Rebecca Rademeyer – assistance with slides

Numerous geneticists for interchanges during IWC workshops in particular