



SCW16 / Paper 05

# JM Biology

Biological data used in the joint jack mackerel assessment

What was checked in model 1.14

## Core message

**The paper turns biology inputs from static model files into a reproducible audit: what is fixed, what differs by stock hypothesis, and where the Far North weight-at-age update needs benchmark attention.**

### Inputs

1.14.dat plus h1/h2 control files

### Focus

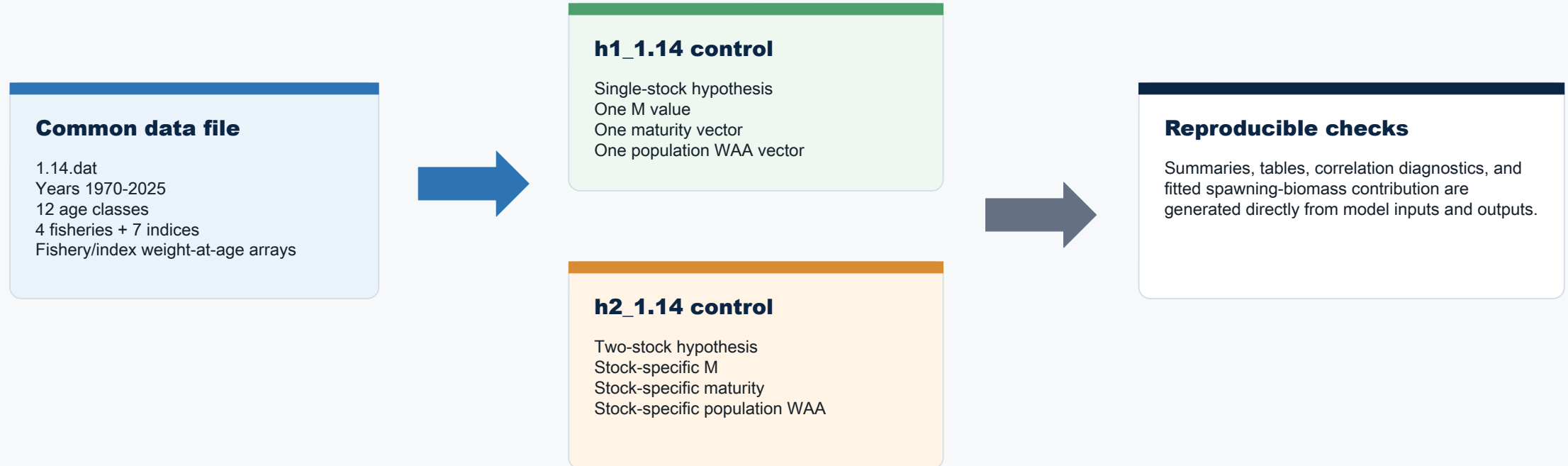
M, maturity, population WAA, fishery/index WAA

### Use

Benchmark decisions and MSE readiness

# The review is anchored to model 1.14 source files

The same common data file feeds both stock hypotheses; control files determine the biological assumptions.





# Biological assumptions diverge under the two-stock hypothesis

The single-stock model uses Stock 1 biology; h2 separates Stock 1 and Stock 2 natural mortality, maturity, and population WAA.

**0.28**

**Natural mortality: h1 and h2 Stock 1**

Configured under #N\_Mort

**0.33**

**Natural mortality: h2 Stock 2**

Stock-specific assumption

**10.5**

**Spawning month**

SSB calculated after 0.792 of annual mortality

**12**

**Age classes**

Includes age-12 plus group

## Stock 1 maturity

Age 1 is partially mature (0.52); ages 2+ are fully mature. This schedule is also used by the single-stock model.

## Stock 2 maturity

Age 1 is immature, age 2 is partial (0.37), age 3 is near mature (0.98), and ages 4+ are mature.

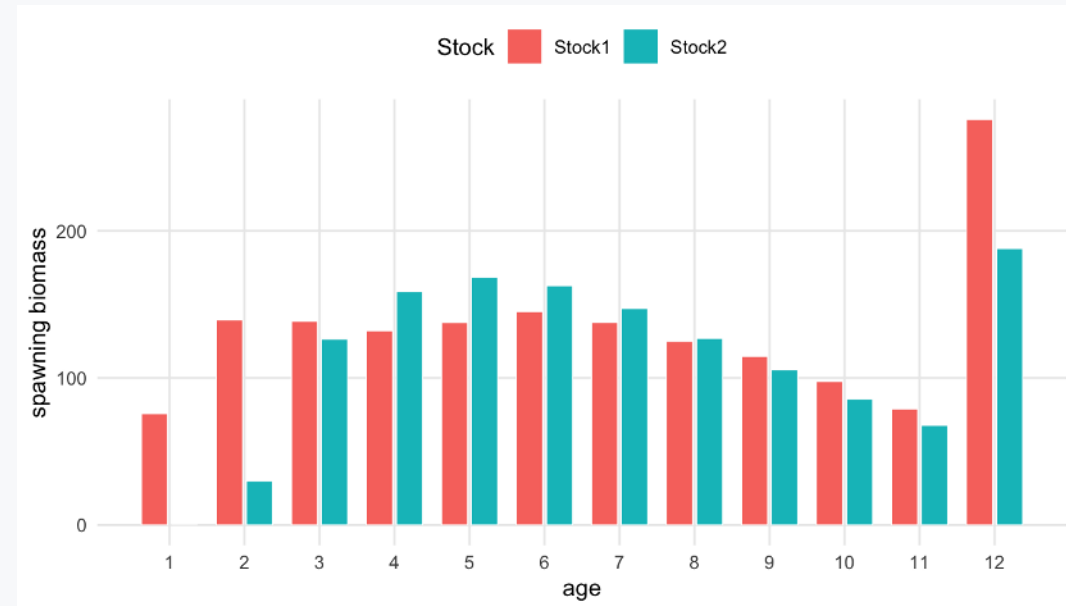
# The paper makes the SSB calculation explicit

Spawning biomass is tied to numbers-at-age, survival to the spawning month, population weight-at-age, and maturity-at-age.

## SSB ingredient chain



Population WAA is fixed by stock in the control file; fishery/index WAA arrays are used for predicted catch and index biomass, not for SSB.



Age-specific spawning biomass per recruit highlights that h2 biology is not interchangeable between stocks.

# Weight-at-age is the central update in model 1.14

The defining change from 1.13 is an update to historical Far North weight-at-age, so the paper treats WAA as the main biological data issue.

## What was separated

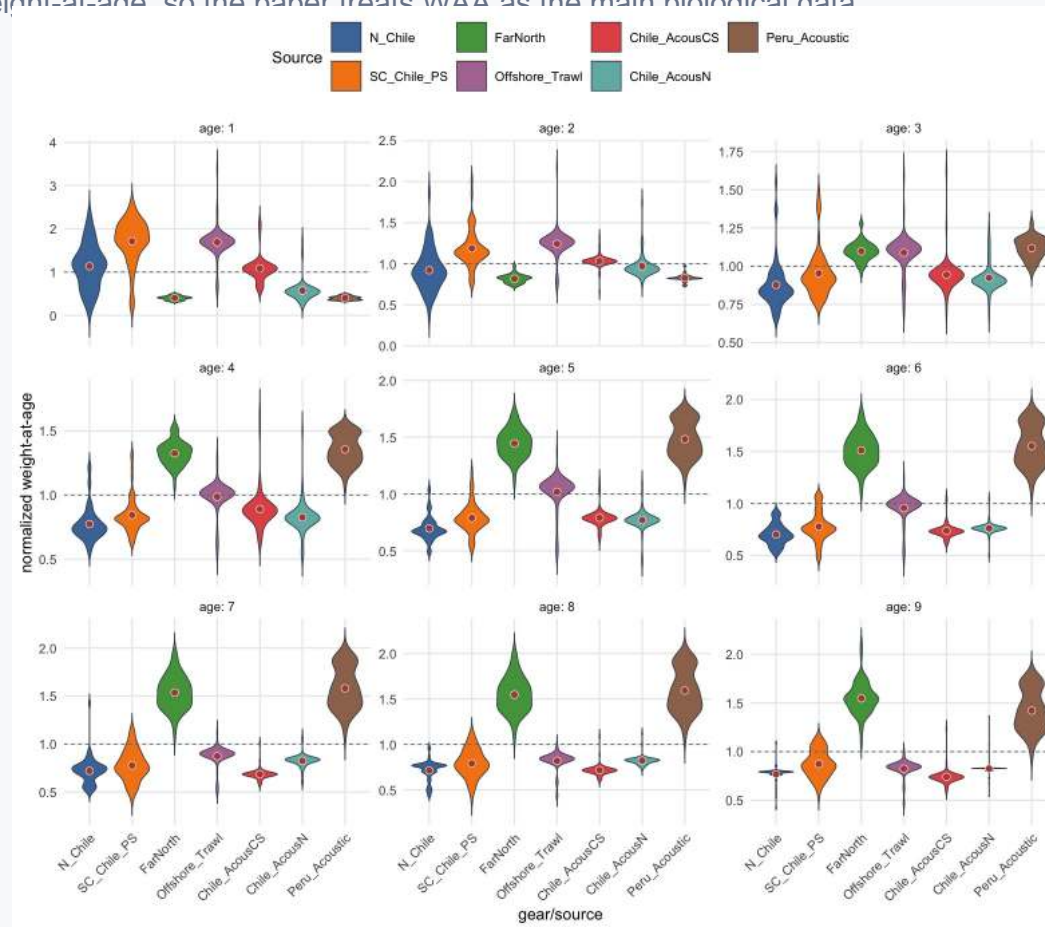
Population WAA used for SSB vs. time-varying fishery and index WAA used for catch/index biomass.

## What was compared

Fishery and acoustic-survey WAA sources by age, excluding duplicated CPUE and DEPM series.

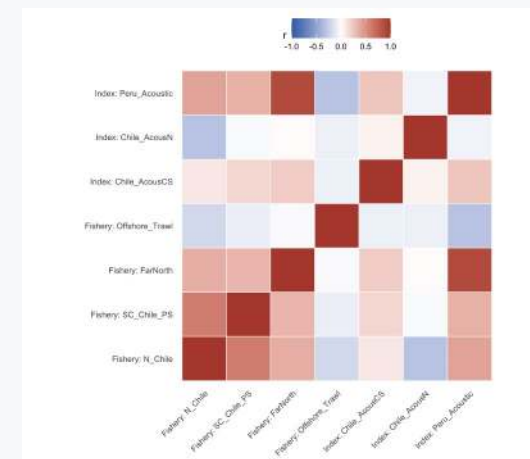
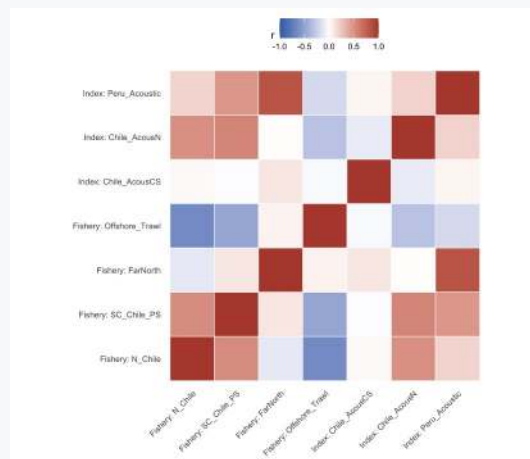
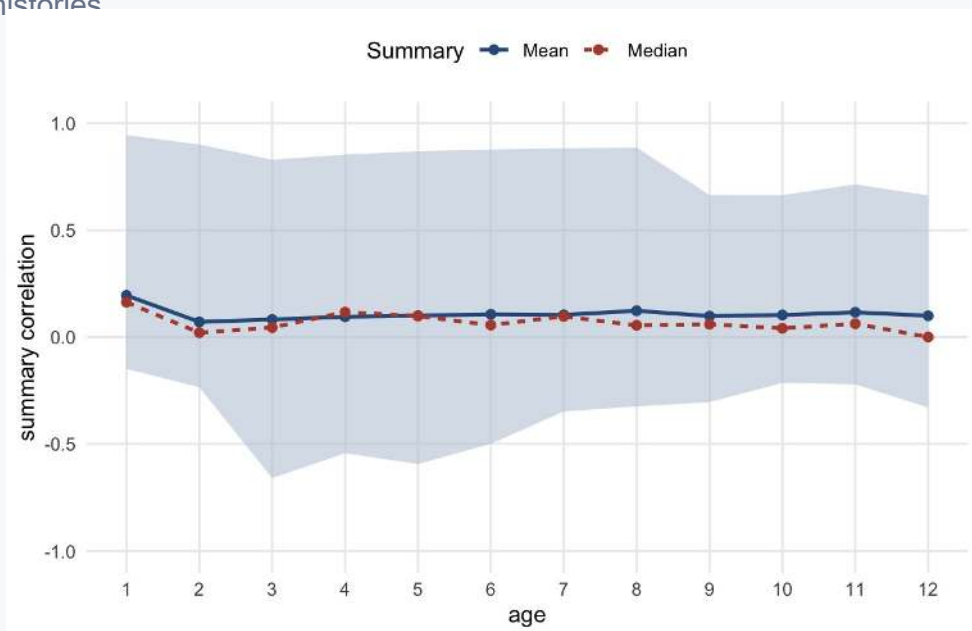
## What still needs review

Explicit comparison with model 1.13 and interpretation of how Far North updates affect biomass signals.



# Cross-source WAA signals are generally modest

The diagnostics show low average pairwise correlations by age, with some strong pairs reflecting shared sampling and imputation histories



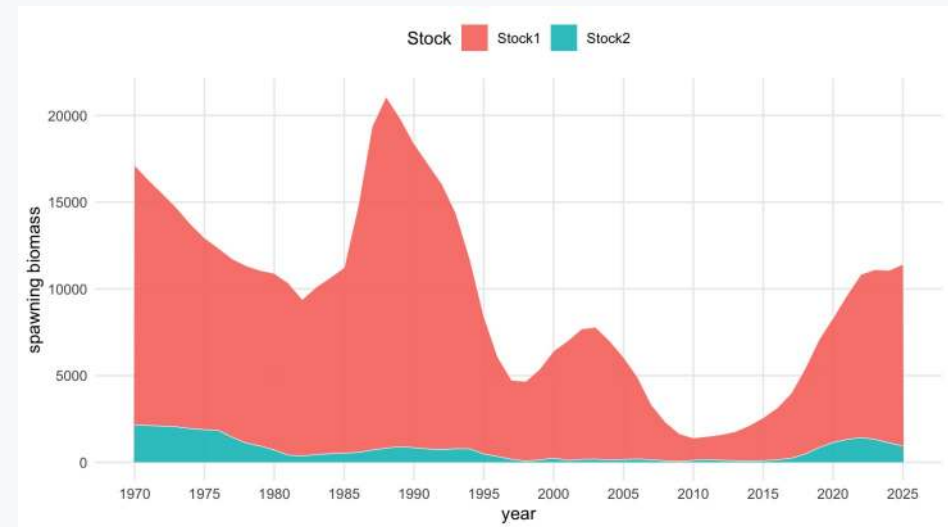
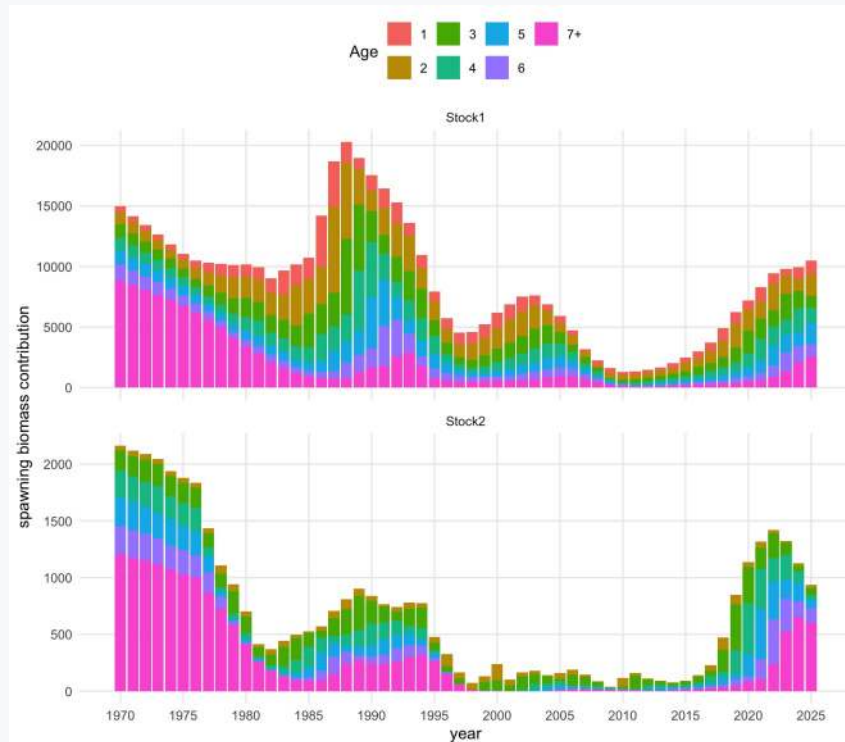
**Age 3**  
 Median pairwise  $r = 0.04$ ; 8 negative pairs among 21 source pairs.

**Age 8**  
 Highest mean pairwise correlation, but median remains low at 0.05.

**Interpretation**  
 Correlation structure is diagnostic, not a decision by itself; source provenance matters.

# Fitted h2 spawning biomass shows age and stock structure

The paper carries biology through to fitted SSB contribution so the implications are visible, not only listed as input vectors.



**Stock 1 has broader age contribution; Stock 2 is shifted older because early ages mature later.**

The stock-scale figure helps separate biological contribution from relative stock scale in h2.



# What Day 3 needs to decide from the biology review

The paper is ready to support benchmark decisions if the group converts checks into accepted inputs and targeted sensitivities.

## 1. Confirm base biology

Are the model 1.14 M, maturity, spawning month, and population WAA inputs acceptable for the base benchmark model?

## 2. Compare 1.13 vs 1.14

Quantify and explain the historical Far North WAA update before treating it as settled input.

## 3. Define sensitivities

Identify plausible alternatives for M, maturity, and WAA that affect SSB or reference points.

## 4. Link Peru papers

Connect Doc13 length-weight and Doc14 length-frequency evidence to Far North biology/composition treatment.

## 5. Update report text

Move from placeholders to clear accepted inputs, caveats, and follow-up owners.

## 6. MSE readiness

State which biology uncertainty dimensions should condition June 2026 operating-model work.

**Recommended closeout: accept model 1.14 biology where documented, run only high-value sensitivities, and keep the Far North WAA comparison as the critical unresolved check.**