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

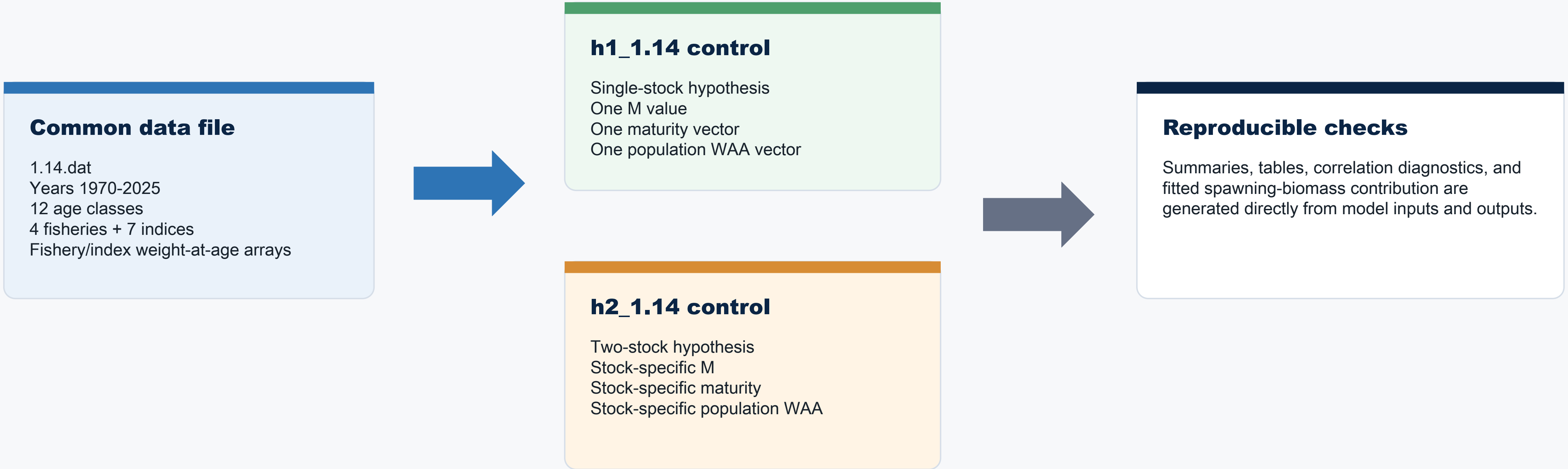
Use

Benchmark decisions and MSE readiness

Source: SCW16-Doc05_JM_Biology.qmd

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.



Common data file

1.14.dat
Years 1970-2025
12 age classes
4 fisheries + 7 indices
Fishery/index weight-at-age arrays

h1_1.14 control

Single-stock hypothesis
One M value
One maturity vector
One population WAA vector

h2_1.14 control

Two-stock hypothesis
Stock-specific M
Stock-specific maturity
Stock-specific population WAA

Reproducible checks

Summaries, tables, correlation diagnostics, and fitted spawning-biomass contribution are generated directly from model inputs and outputs.

Source: SCW16-Doc05_JM_Biology.qmd; model 1.14 inputs from jjm/assessment

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.

Source: SCW16-Doc05_JM_Biology.qmd; model 1.14 inputs from jjm/assessment

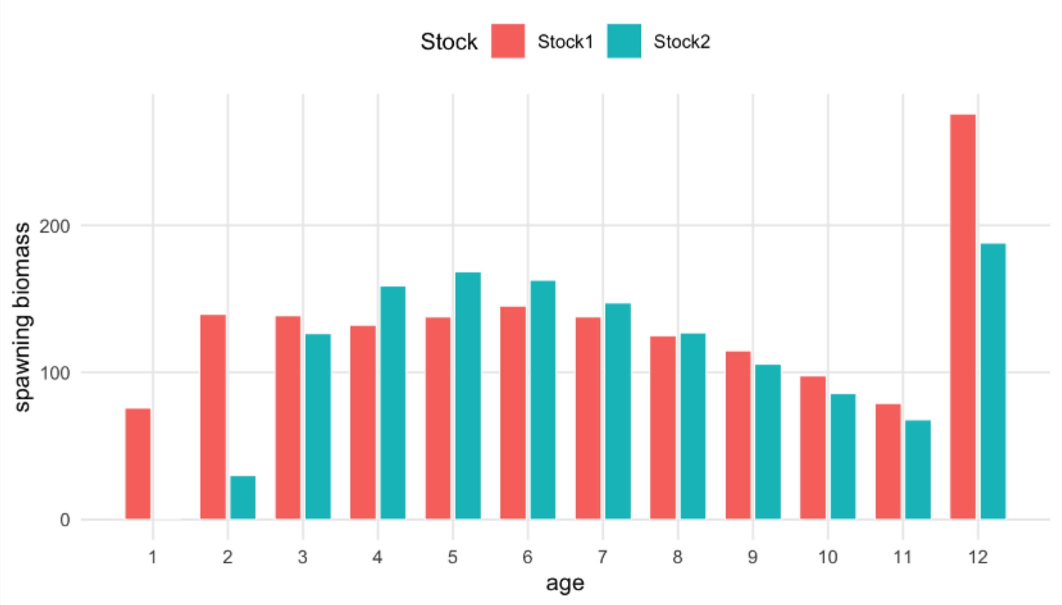
The paper makes the SSB calculation explicit

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

SSB ingredient chain

N at age → **Survival to spawn** → **WAA x maturity**

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.

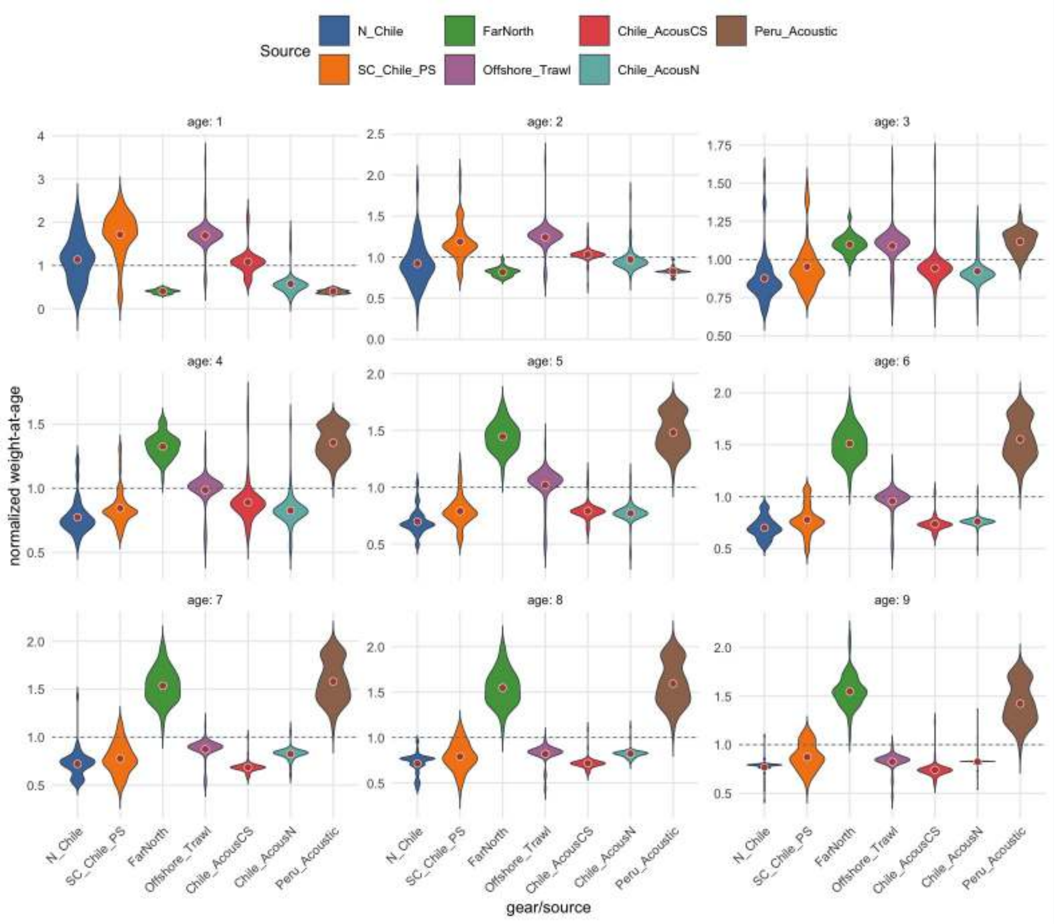


Age-specific spawning biomass per recruit highlights that h2 biology is not interchangeable between stocks.

Source: SCW16-Doc05_JM_Biology.qmd; model 1.14 inputs from jjm/assessment

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.

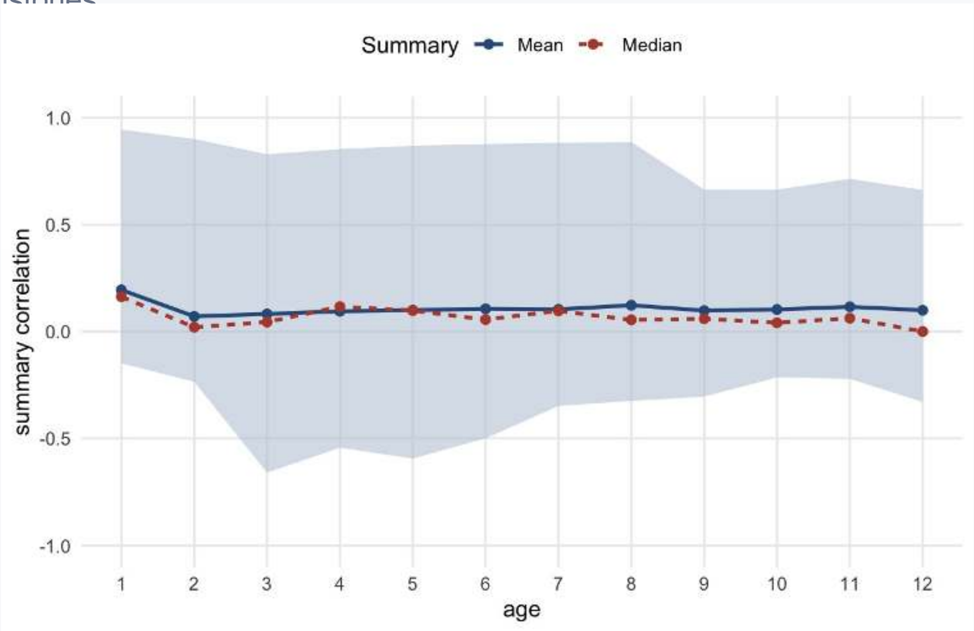
What still needs review

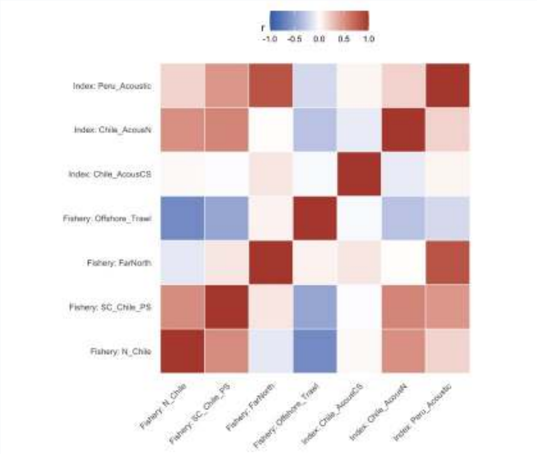
Explicit comparison with model 1.13 and interpretation of how Far North updates affect biomass signals.

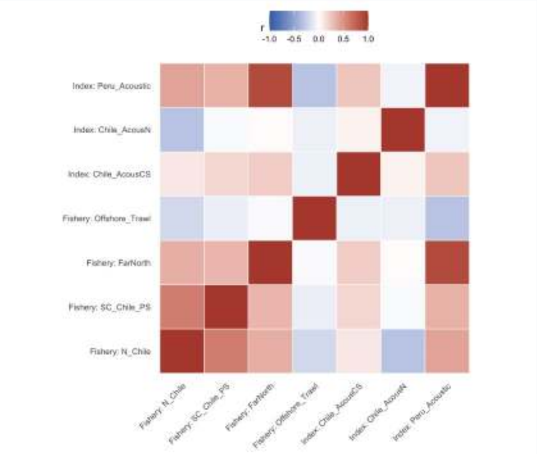
Source: SCW16-Doc05_JM_Biology.qmd; model 1.14 inputs from jjm/assessment

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.

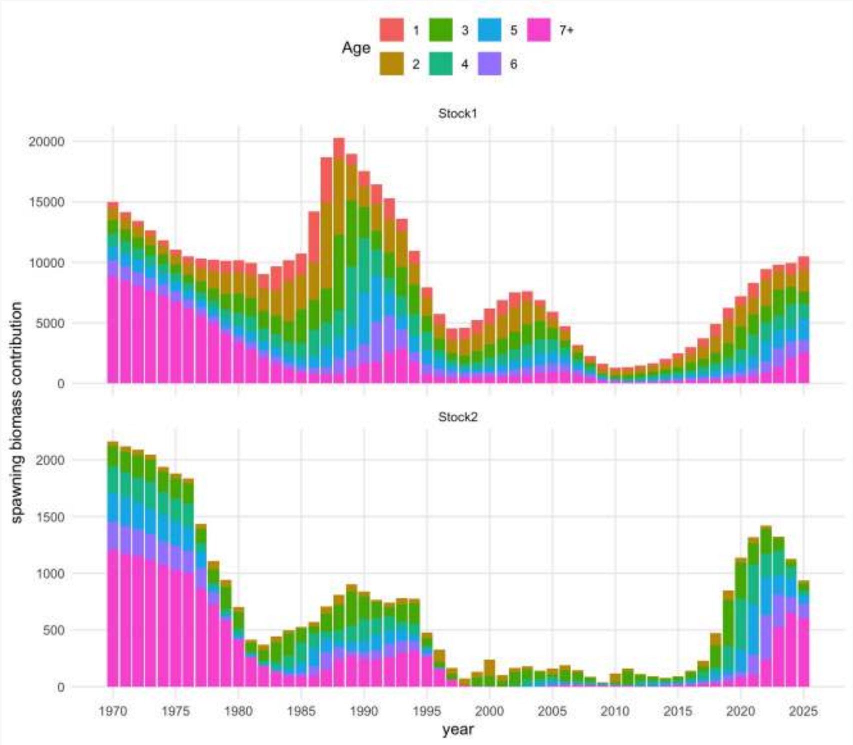
Interpretation

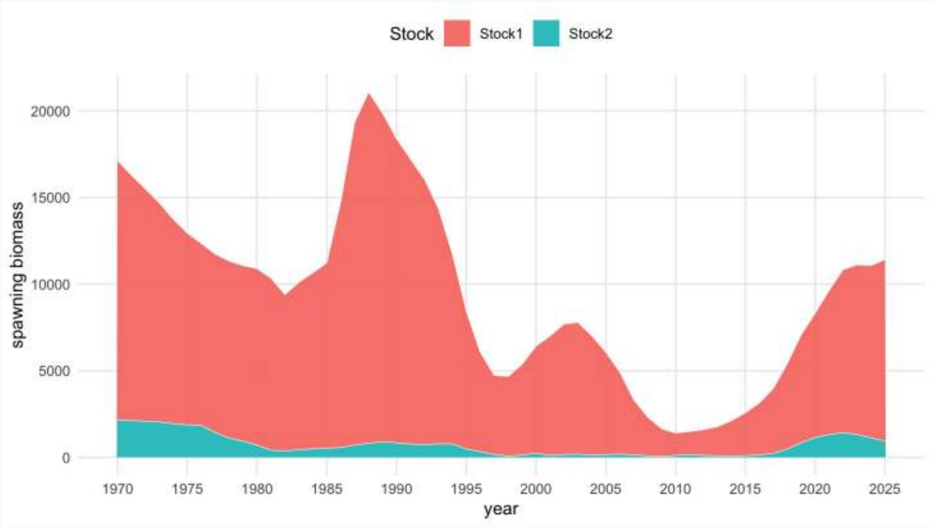
Correlation structure is diagnostic, not a decision by itself; source provenance matters.

Source: SCW16-Doc05_JM_Biology.qmd; model 1.14 inputs from jjm/assessment

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.

Source: SCW16-Doc05_JM_Biology.qmd; model 1.14 inputs from jjm/assessment

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.

Source: SCW16-Doc05_JM_Biology.qmd; model 1.14 inputs from jjm/assessment