



Advancing the SEAPODYM modelling framework: *methodology, validation, and analyses*

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SC21 Recommendations

676 – validation against other approaches; include fitting to simulated data (e.g. Indian Ocean yellowfin, Goethel et al. 2024).

677 – reporting of the tropical-tuna reference models to include: convergence diagnostics, sensitivity to fixed parameters and key assumptions, likelihood profiles, sensitivity to the optimisation period, uncertainty in estimates.

***2019 SEAPODYM Review** – the remaining recommendation: a bridging analysis.*

Paper delivers

SC21 / review ask	§ Finding
Bridging analysis (2019 review, 676)	(3) Each mechanism is required by a distinct data type
Fitting to simulated data (676)	(4) Parameters are recovered within their standard errors
Likelihood profiles (677)	(5) Reported MLEs provide minimal stock size compatible with observed fishing
Sensitivity to fixed parameters (677)	(6) Integrated in model development workflow
Convergence diagnostics and uncertainty estimation (677)	(7) Hessian-based scale-invariant diagnostics, standard errors from inverse Hessian
Model validation against independent data, sensitivity to optimisation period (676, 677)	(8) Tested via validation outside of the fitting window

Bridging analysis: the design

- Environmental variables are **drivers** of the population dynamics and the **shape and magnitude** of the relationships between population processes and the environment **are estimated**, not assumed.
- A standard fishery model $\neq$ a reduced case of SEAPODYM with the spatial and environmental terms disabled.

SEAPODYM underlying equation:

$$\frac{\partial N}{\partial t} + \frac{\partial N}{\partial a} = -\nabla \cdot [(\mathbf{v}_0 + \chi_a \nabla H_a) N] + \nabla \cdot [D(H_a) \nabla N] - [M(a, H) + F(a, t, \mathbf{x})] N, \quad N(0, t, \mathbf{x}) = H_s(t, \mathbf{x}) \frac{r \bar{N}(t, \mathbf{x})}{1 + b \bar{N}(t, \mathbf{x})}$$

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Q1. Can **movement** be modelled with passive drift and constant diffusion rate?

B1 (Passive drift + Constant D) $\rightarrow$ B1+ habitat-dependent D(Ha) $\rightarrow$ **Ref** (B1+ D(Ha) + taxis)

Q2. Can SST explain tuna larval survival and so be a single environmental driver of **recruitment**?

B2 (ref. movement, Hs = f1(SST)) $\rightarrow$ B2 + larval food f2(NPP) $\rightarrow$ **Ref** (+ predation f3)

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Bridging analysis: results

– *Tagging data inform movement, and fisheries data inform recruitment*

Movement

- Passive drift with currents only – **worse fit**, mainly for tags, but also for catch likelihood
- variable diffusion alone – **small gain** (6.92 to 6.76)
- **active movement** (6.76 to 4.89) halves the tagging misfit (2.91 to 1.38) *and* removes the catch deterioration (0.72 to 0.51)

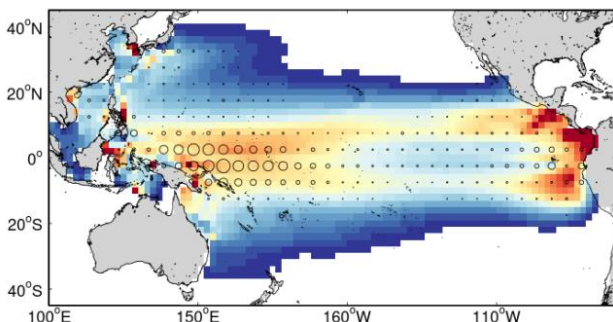
Recruitment

- SST-only larval survival cannot fit catch likelihood (0.51 to 1.11)
- larval food halves it (0.57) and predation removes the residual misfit(0.51)

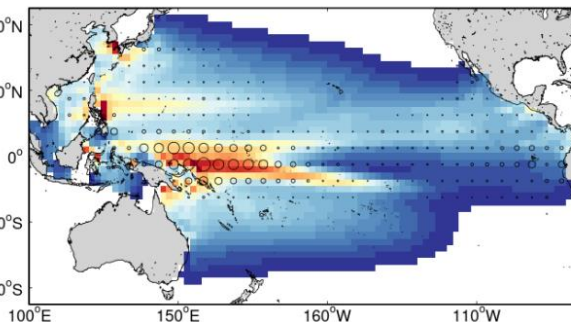
Table 1. Estimated negative log-likelihood ($\times 10^5$) in the skipjack models.

	B1	B1+	B2	B2+	Ref
Total	6.92	6.76	5.54	5.09	4.89
catch C	0.76	0.72	1.11	0.57	0.51
length L	2.74	2.75	2.65	2.79	2.64
tagging T	3.04	2.91	1.42	1.33	1.38

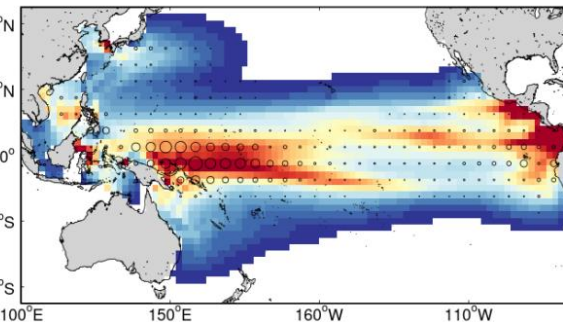
B1



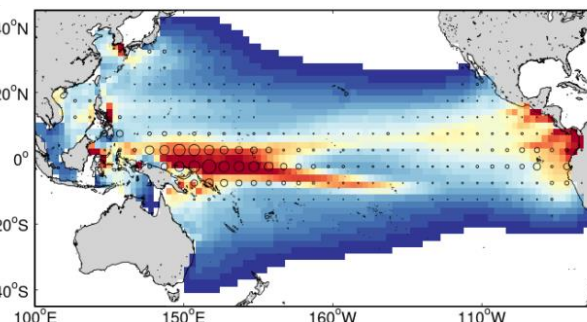
B2



B2+



Reference



Fitting to simulated data

Why not the Goethel et al. (2024) dataset

Five structural mismatches, three are critical:

- **SPM spatio-temporal resolution** is too coarse for SEAPODYM ADRE, both in terms of numerics and estimation.
- **No fishing effort.** SEAPODYM infers spatial biomass from CPUE via the catch equation.
- **Tags pre-aggregated** to 5 degrees by quarter. SEAPODYM treats each recapture as a point observation, with exact release position and date as the initial condition and source term of the PDE.

Recommendation 676 is therefore answered by the i) bridging analysis, ii) within-SEAPODYM twin experiments and iii) model validation against independent observational datasets rather than modelled ones.

Identical-twin experiments

Does the estimation method recover the truth? Sample size?

1) South Pacific albacore, 16 fisheries

- synthetic catch generated from a known parameter set
- 10 jitter starts: **8 converged, all identical to 4 significant figures**
- biological parameters recovered within relative error 9%
- catch fit at the recovered solution **$r^2 = 1.00$, $nRMSE = 0.02$**

2) Continuous vs. categorical larval data

- Established sampling size needed to recover spawning-habitat parameter estimates;
- Proved that categorical data sample size has to be $\times 10^2$ bigger to allow successful parameter recovery.

3) Density data

- Example shows how the model absorbs forcing biases via MLE

Convergence: gradient threshold and Hessian

$$\theta_{\text{mle}} = \underset{\theta \in (\underline{\theta}, \bar{\theta})}{\operatorname{argmin}} (-\ln L) \quad \frac{\partial(L^-)}{\partial \theta} \simeq 0 \quad \mathbf{H}_{++}$$

The gradient is **not scale-invariant** – a fixed threshold confounds the objective's scale with proximity to the minimum.

$$\max_i |g_i| < \delta$$

Two Hessian-based diagnostics instead: a **positive-definite Hessian**, and the **Newton decrement** (the relative improvement still attainable).

$$\mathbf{H}_{++} \quad \lambda^2 = g^\top H^{-1} g \quad \left(\frac{1}{2} \lambda^2 / L \right)$$

Example, tag-only fit, 5 parameters ($\max_i |g_i| = 5.7; 0.07$):

Table 2. Estimated parameters of the tag movement model of SEAPODYM

θ	Parameter description	Estimate	Std. error	CV
σ_0	std. dev. of SST Gaussian (age 0), °C	2.000	0.0170	0.85%
b_T	Allometric power in thermal preferences at age	2.285	0.0025	0.11%
σ	diffusion-rate multiplier	0.0542	0.0136	25.2%
V_m	max. sustainable speed (taxis), BL s ⁻¹	1.176	0.0018	0.16%
c	diffusion-habitat coefficient	0.191	0.0238	12.5%

Model Validation

- Fit to the data via maximum-likelihood estimation;
- Validation of the model dynamics and estimated parameter values;
- Goodness of fit of the MLE solution against *independent* datasets.

	Skipjack	Yellowfin	Bigeye	Albacore
MLE	1995-2012	1999-2018	1995-2019	1980-2013
Validation	1979-1994 2013-2022	1983-2018 2019-2022	1960-1994	1960-1979



Catch & CPUE

Time/space (total or by fishery):

- Sq. Pearson correlation
- Variance ratio
- Centred NRMSE
- Mean of residuals

Within-cell:

- R-squared goodness of fit
- Sq. Pearson correlation
- MARE

EEZ-level:

- NRMSE seasonal series



Length Frequency

LF distributions by quarter, by qtr/year, total by fishery:

- NRMSE (normalized by LF mean)
- SMD - standardised bias of the mean lengths



Tagging Data

Lon/lat profiles for all recaptures or by tag group:

- NRMSE (normalized by sd)
- Pattern correlation
- Kling-Gupta efficiency

Time/space (total recaptures)

- Sq. Pearson correlation
- Variance ratio
- Centred NRMSE



Larval CPUE

Seasonal larval CPUE:

- Pearson correlation

Larval counts at SST, dissolved oxygen, primary production and micronekton density

- NRMSE (normalized by sd)

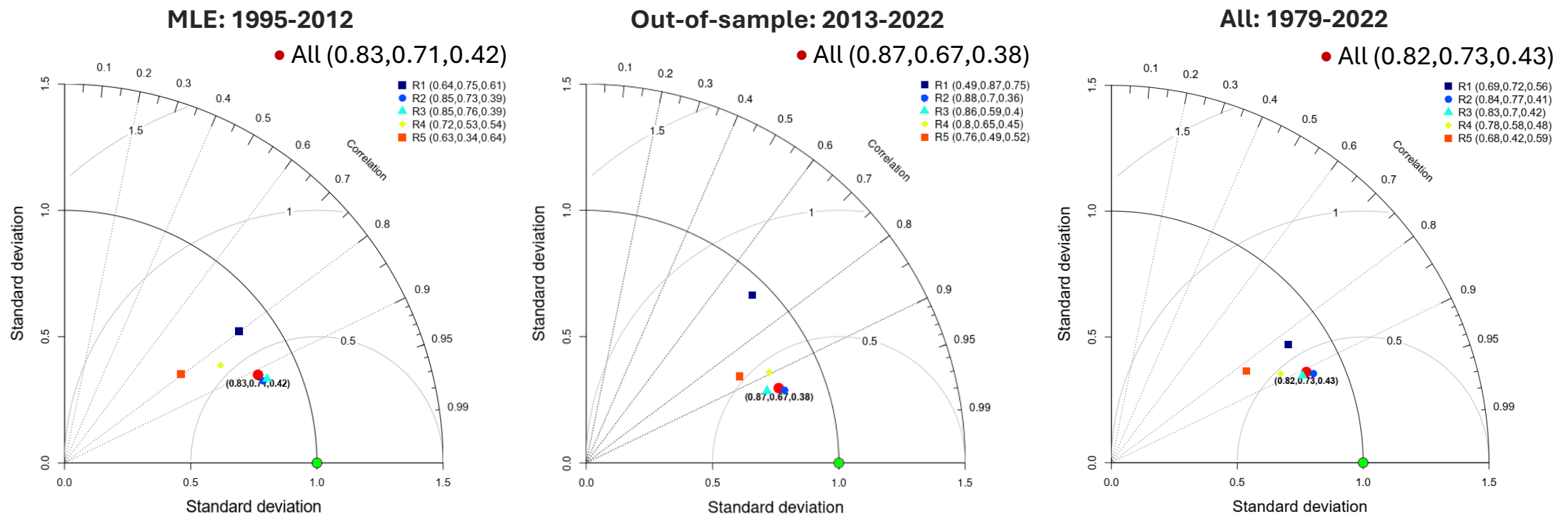
Validation outside the fitting window

WCPFC-SC21-2025/SA-IP-20

Tagging data: $(r^2, VR, err) = (0.65, 1.0, 0.62)$ for MLE (no EPO) and $(0.72, 0.7, 0.53)$ for out-of-sample data (including EPO).

Length data: $NRMSE$ (by fishery) = 0.19–0.48 for MLE and 0.18–0.48 over 1979–2022.

Catch data: $r^2 = 0.82$ -0.87; $VR = 0.67$ -0.73; $err = 0.38$ -0.43.



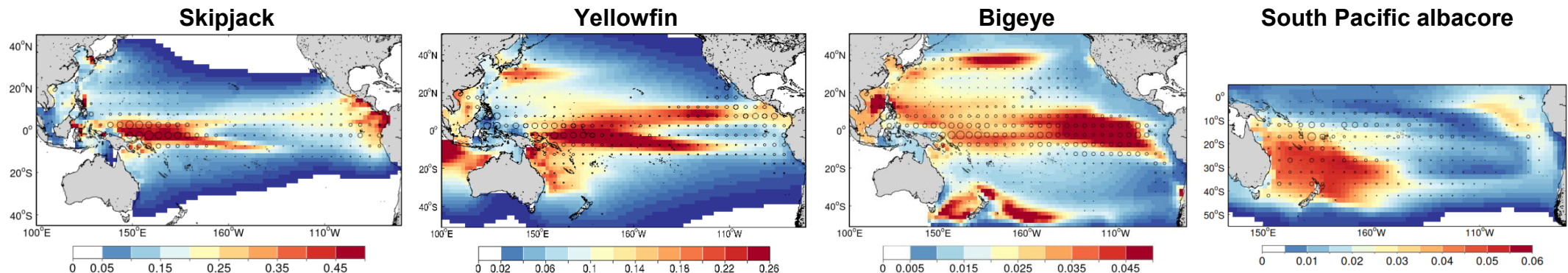
Updated vs previous reference models

WCPFC-SC22-2026/EB-IP-04

- *Of validation window 1986-2010, first decade is **out-of-sample** for updated models of skipjack, bigeye and yellowfin whereas it is included in fitting in the previous models.*
- **Catch scores improve for all four species.**
- **Length scores improve for skipjack and bigeye but deteriorate for yellowfin and albacore.**
- **Tagging data scores improve for skipjack and bigeye, deteriorate for yellowfin.**
- **Early-life scores improve for albacore, good for skipjack.**

Table 3. Global validation scores by data type

Data	Metric	Skipjack		Yellowfin		Bigeye		Albacore	
		Prev.	Upd.	Prev.	Upd.	Prev.	Upd.	Prev.	Upd.
Catch (<i>C</i>)	r^2	0.93	0.95	0.45*	0.51*	0.71	0.81	0.71	0.72
	VR	0.88	0.92	0.50*	0.94*	0.67	0.85	0.6	0.73
	<i>err</i>	0.27	0.23	0.75*	0.75*	0.54	0.43	0.54	0.53
Length (<i>L</i>)	NRMSE $\bar{x}$	0.40	0.39	0.47	0.53	0.68	0.41	0.44	0.52
	SMD	0.11	0.00	0.08	-0.07	0.15	0.02	-0.061	0.058
Tagging (<i>T</i>)	NRMSE σ	0.57	0.52	0.36	0.5	0.74	0.70	—	—
	KGE	0.73	0.77	0.85	0.73	0.35	0.55	—	—
	PC	0.86	0.89	0.93	0.87	0.64	0.76	—	—
Early-life (<i>E</i>)	NRMSE σ	—	0.45	0.68	0.67	—	—	0.98	0.72



Conclusions

- **Essential, Data-Driven processes:** each process and environmental link is necessary, informed by specific data (e.g., tagging for movement, catch for recruitment).
- **Reliable Reference Models:** grounded in robust and reproducible estimation methods.
- **Convergence Diagnostics:** established using scale-invariant diagnostics.
- **Strict Validation Rules:** models must pass out-of-sample validation and yield biologically sound parameters to ensure robustness.
- **Stock Size Estimation:** not the primary focus; the MLE solutions provide the minimal stock size compatible with observed fishing.
- **Primary Challenges:** high dimensionality and sensitivity to ocean forcings (which requires full re-estimation).
- **An Evolving Framework:** Continuously integrating new data and capabilities (progressing from now implemented *simulation application with 85% parallel efficiency toward parallel estimation*).

Acknowledgments

WCPFC Project 62 (Commission Data, Advice)

Oceanic Fisheries Programme (OFP) SPC

Climate Change and Tuna Project
coordinated by the OFP SPC

FAO ABNJ2 Tuna Project funded by the
Global Environmental Fund

GCF Regional Tuna Programme, Component
B, Activity 3.1.

Thank you!