

CCSBT 2025 collaborative risk assessment

Summary of modelling to date

ERS Tech meeting – 7 to 11 April 2025

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Summary

- Compilation of combined observed overlap and captures dataset
- Summary of analyses to date (2024 inputs), including models fitted to:
 - ‘Original’ taxonomic resolution of captures
 - Genus-level captures
 - Models with family and genus-specific π vectors
 - Seabird distributions informed by density and BLI range maps
 - Updated density maps
 - Preliminary models with species-level catchabilities
- Modelling choices

Updated fishery inputs

- Updated datasets for fishery inputs received from:
 - Australia
 - New Zealand
 - South Africa
 - Taiwan
 - Japan
- Korea have provided CSV files with observed captures and observed effort
 - Has not been processed for incorporation into combined dataset as yet

Key model parameters

$$\underbrace{\text{captures}}_{C_{f,s}}_{f,s} = q_{f,z} \cdot \mathbb{O}_{f,s}$$

$$\boldsymbol{\pi}_f = (\pi_{\text{sub-genus}}, \pi_{\text{genus}}, \pi_{\text{family}}, \pi_{\text{class}})$$

- Catchability (q) - accounts for how likely a taxa is to be caught (e.g., behaviour around vessel)
- Probability of identification at a given taxonomic resolution ($\boldsymbol{\pi}$) - accounts for the ease of identification
- Estimated captures are a function of catchability and overlap
- For a given species, estimated observed captures per capture code calculated from:
 - Estimated captures of the species (from observed density overlap)
 - Probability of identifying those captures at different taxonomic resolutions ($\boldsymbol{\pi}$)
- Taxonomic resolutions of catchabilities (q 's) and $\boldsymbol{\pi}$'s do not need to be consistent

Improvement to π vectors

- The π vector gives the probability of identifying a capture at each taxonomic resolution
- Implemented an improvement to π vector:

$$\boldsymbol{\pi} = (\pi_{\text{sub-genus}}, \pi_{\text{genus}}, \pi_{\text{family}}, \pi_{\text{class}}) \quad \text{where} \quad \sum_i \pi_i = 1$$

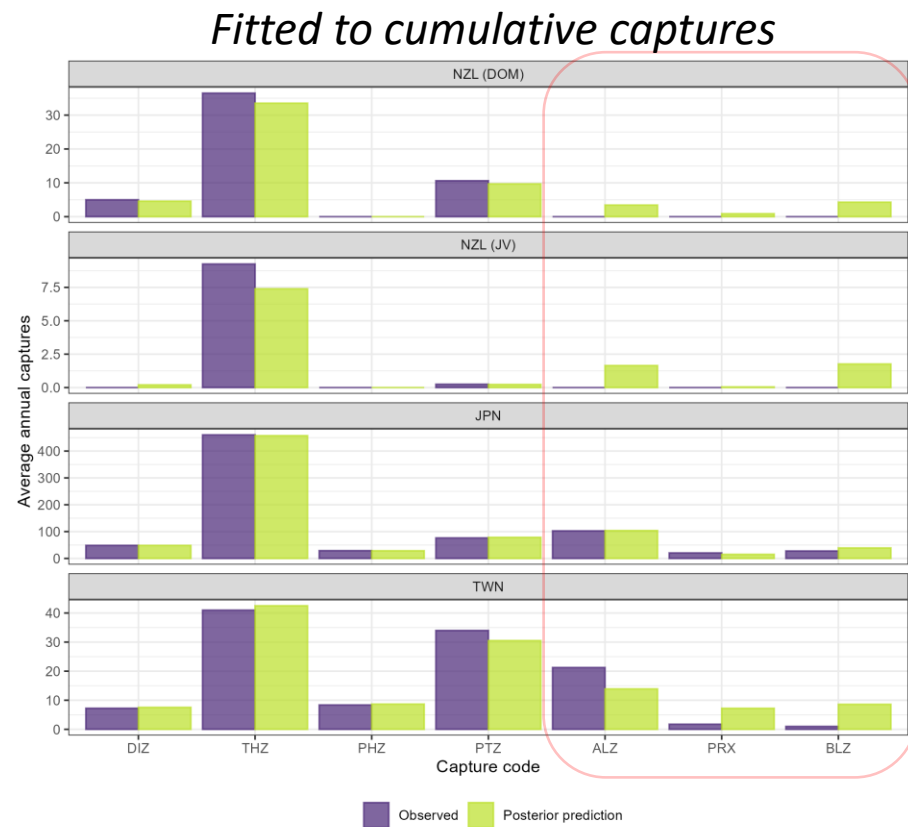
- All species have **one** corresponding capture code at each taxonomic resolution
- For taxa with a complex-level capture code, and no species-level capture code:
 - $\pi_{\text{sub-genus}}$ gives probability of identification to a complex-level
- For taxa with a species-level capture code, and no complex-level capture code:
 - $\pi_{\text{sub-genus}}$ gives probability of identification to a species-level

Parameterisation of π

- In 2024, π vector was assumed to be shared across all taxa
- Agreed to explore relaxing this assumption, i.e., account for variation in taxonomic resolutions of capture identifications between taxa
 - Genus-specific π vectors as a starting point
 - Family-specific π vectors as an alternative
- Models fitted to 2024 input suggests that estimated catchabilities are reasonably insensitive to parameterisation of π

Fitting to cumulative vs empirical captures

- Tendency to over-estimate captures identified to coarser taxonomic resolutions when fitting to cumulative captures
- **Agreed that fitting to empirical captures preferred**



Implausible updates to N_{BP} and P_B – part 1

- Strong (and biologically implausible) updates to N_{BP} and P_B occurred in 2024 risk assessment for some species (particularly mollymawk taxa)
- Updates to N_{BP} or P_B adjust estimated population size, and so observed overlap
 - Allows model to better fit to observed captures of taxa within a species group (that are assumed to share the same catchability)
- A variety of potential drivers for these updates, including:
 - Inaccuracies in density maps, resulting in biased estimates of observed overlap
 - Errors in identification of seabird captures, i.e., bias in estimates of observed catch
 - Also variability in catchabilities among taxa (within a species group)
 - Though appears unlikely to explain the magnitude of updates observed for some species

Implausible updates to N_{BP} and P_B – part 2

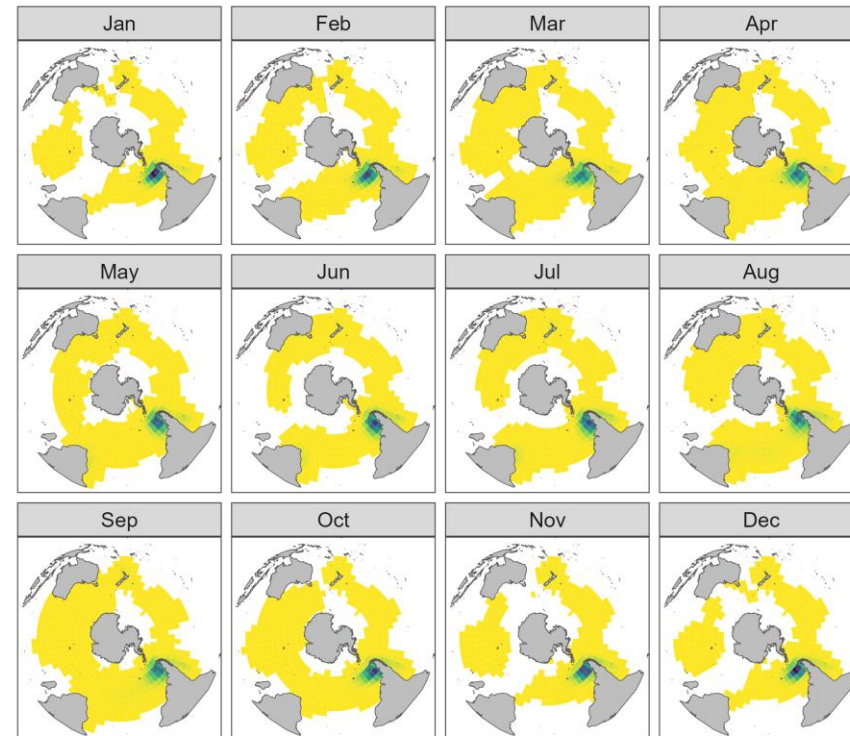
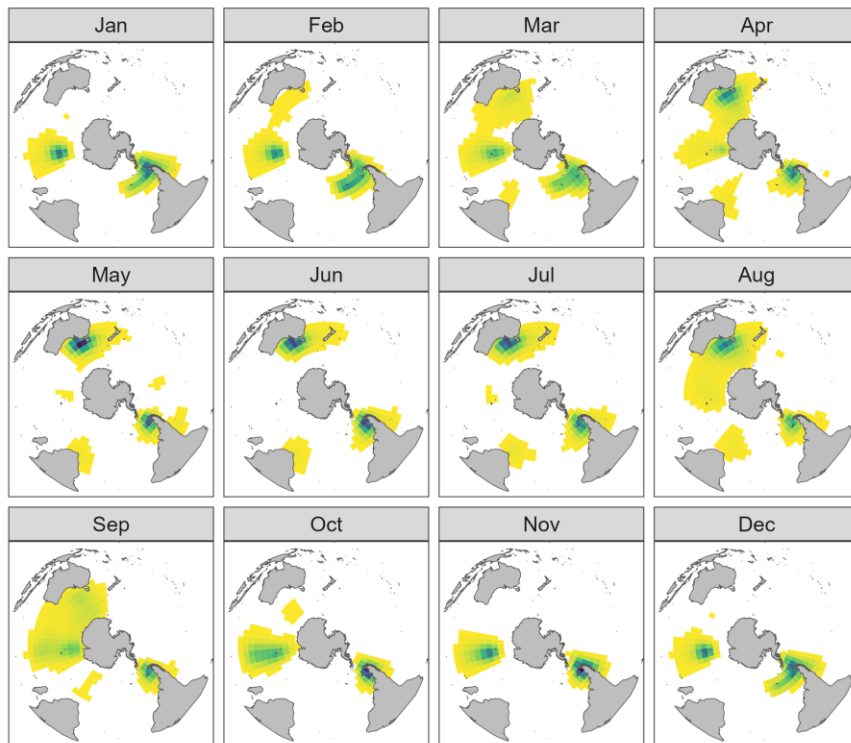
- **Inaccuracies in density maps (impacting overlap)**
 - Captures in areas of zero observed overlap
 - Review of density maps in 2024 (issues with known foraging areas absent from maps, etc)
 - Maps are adults only, colonies without tracking data etc.
- **Errors in identification of seabird captures**
 - Captures in areas of zero observed overlap
 - Very difficult for observers to discriminate between different seabird taxa at sea
 - Necropsy and photo-based identifications more accurate, but not available for all fleets (and time periods), more difficult for birds alive at vessel
 - Errors in identifications in CCSBT analysed dataset likely

Exploration of density maps

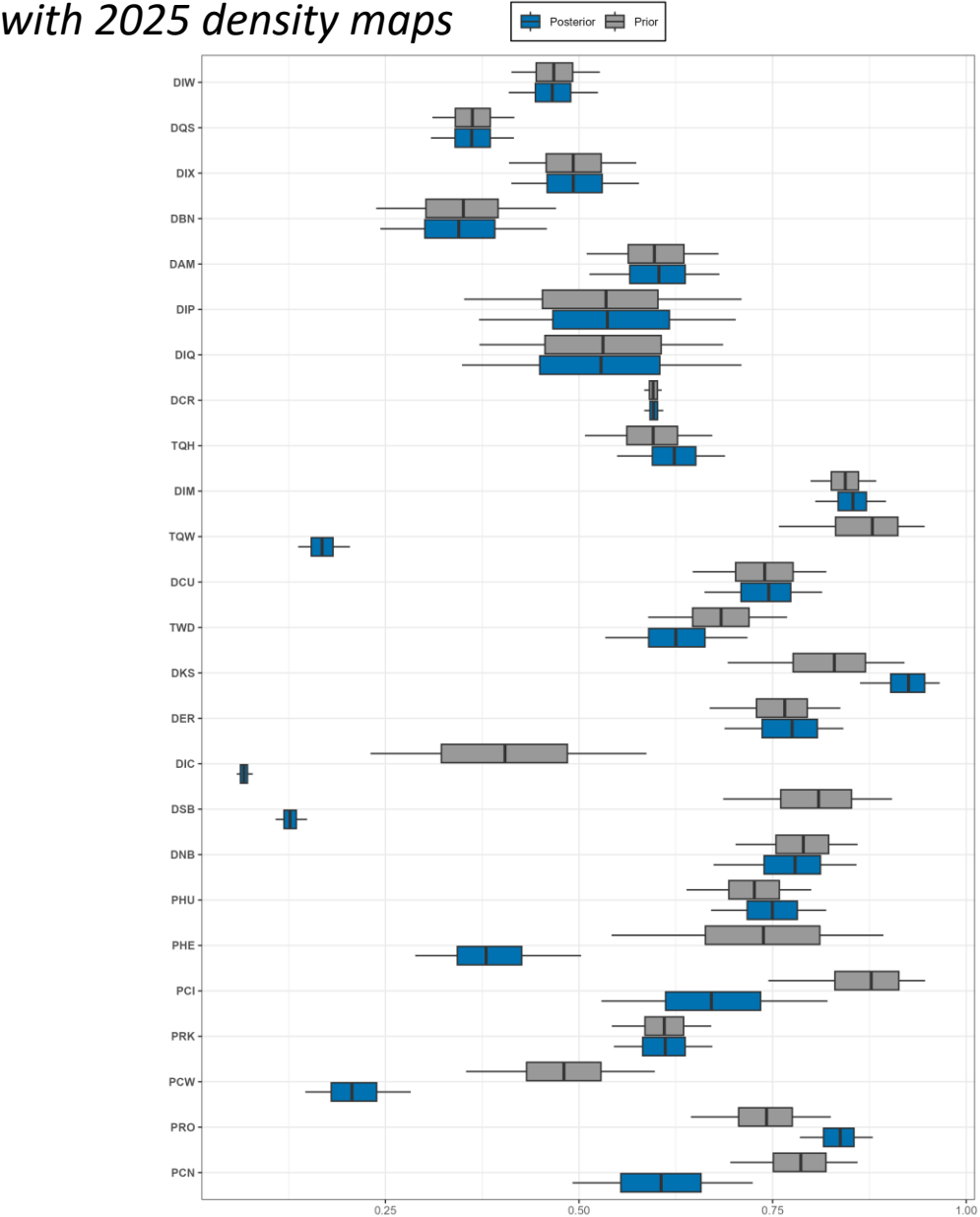
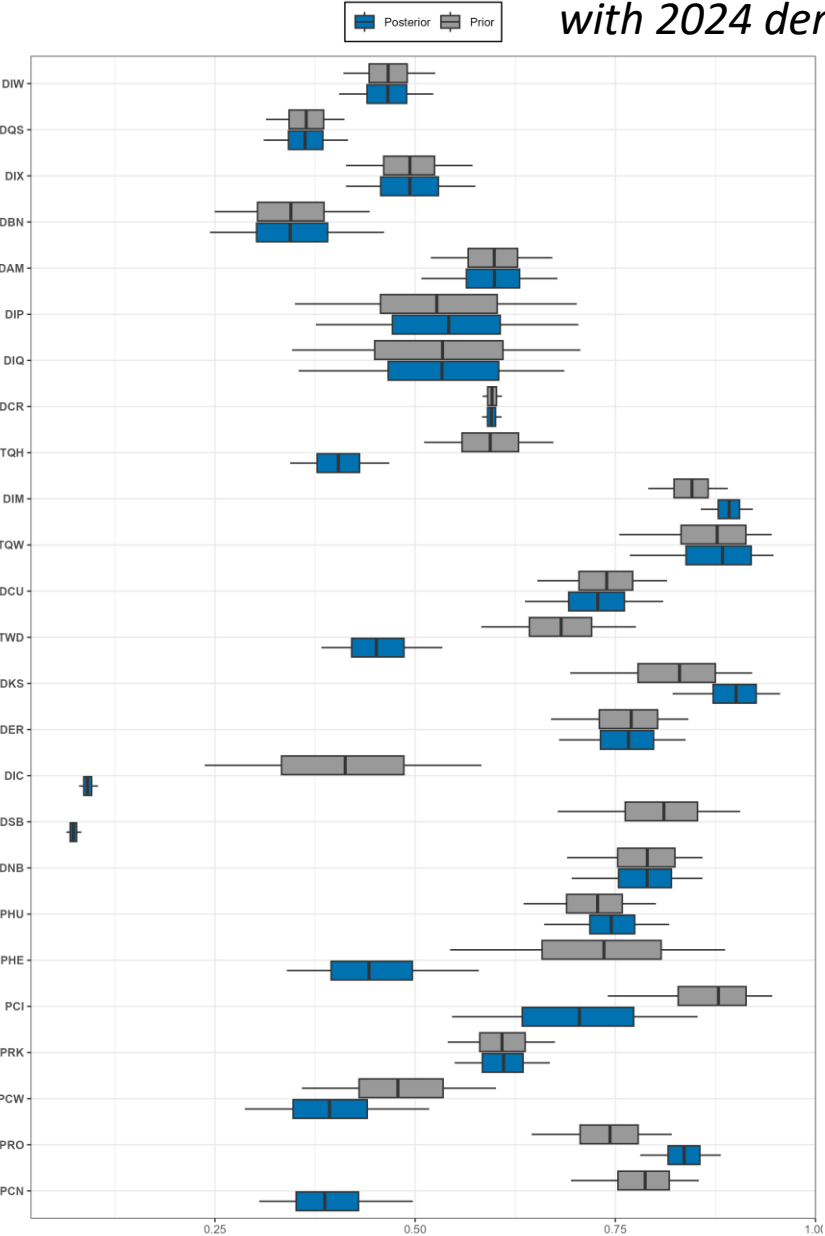
- At 21 March Progress meeting, requested to review available information (eBird sightings data, banding data etc.)
 - Assess evidence for deficiencies in density maps
 - E.g., presence of birds in areas estimated to have zero density based on tracking data
- Focussed on taxa with strong posterior updates to biological priors
- No compelling evidence for inconsistencies between density maps and other information sources
- Also reviewed updated density maps against feedback from experts on 2024 density maps
 - Updates to density maps appears to have addressed concerns raised by experts for some taxa

Updates to density maps – part 1

- Density maps updated this year for 16 of the 25 species
 - Additional tracking datasets
 - Weighting of tracks by colony population size
- Resulted in substantial changes for some species, e.g., black-browed albatross



Updating of density maps – part 2

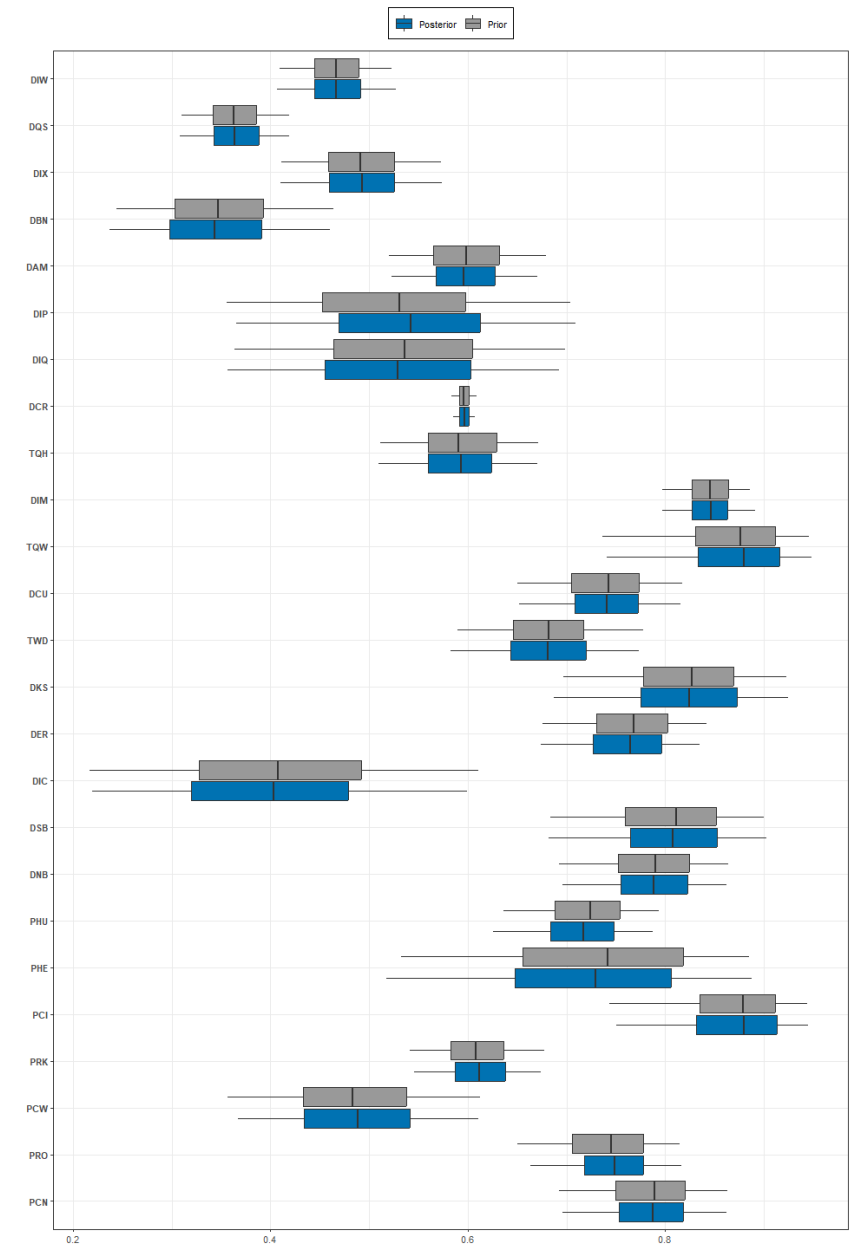


How to move forward

- Reducing taxonomic resolution of captures dataset appears appropriate
 - But to what level? Are identifications to genus level likely to be sufficiently accurate
 - Trade-off with parameterisation of catchabilities. E.g., capture identifications at family-level would preclude genus-specific catchabilities
- Interest in pursuing models with species-level catchabilities?
 - Adjustments to q can account for errors in observed overlap
 - Shouldn't bias estimates of total catch IF observed effort representative of total effort (spatially & temporally)
 - Preliminary model runs with species q effects
$$q_{f,s} = \beta_f + \beta_g + b_{fs} \quad \text{where} \quad b_{fs} \sim N(0, \theta)$$
 - Charlie can work towards a more robust approach (if required)

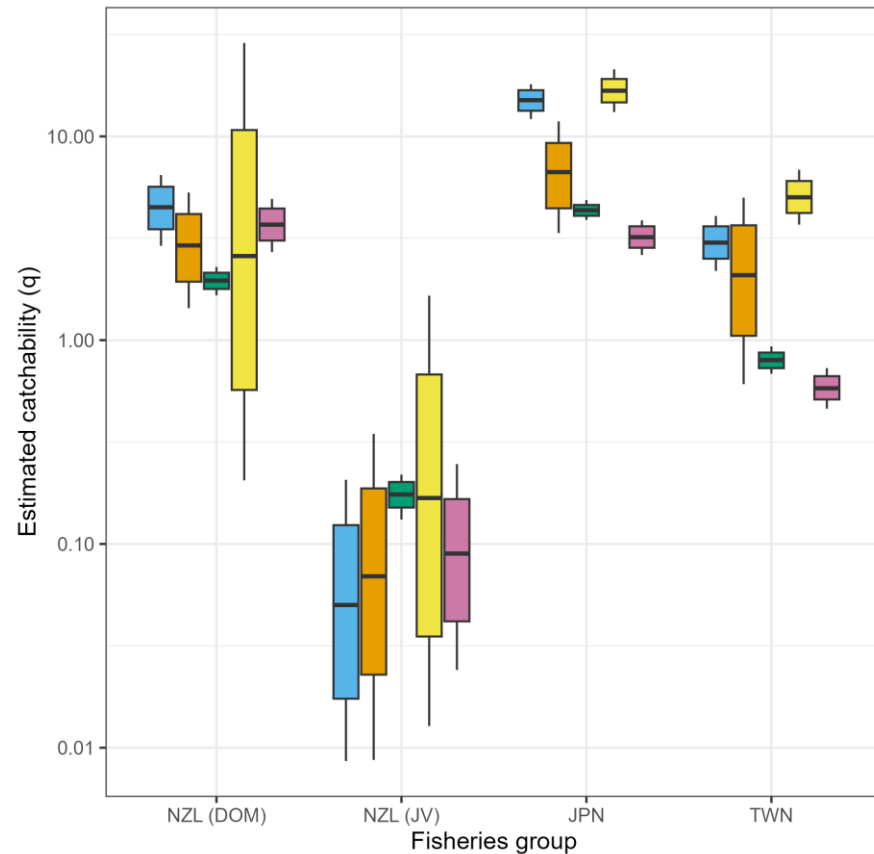
Lowering taxonomic resolution of captures – part 1

- Models fitted to captures data at a genus level have no posterior updates to breeding pairs (N_{BP}) or probability of breeding (P_B)
 - No need for adjustments to species-level numbers (through N_{BP} and/or P_B) to better fit to species (or complex) captures

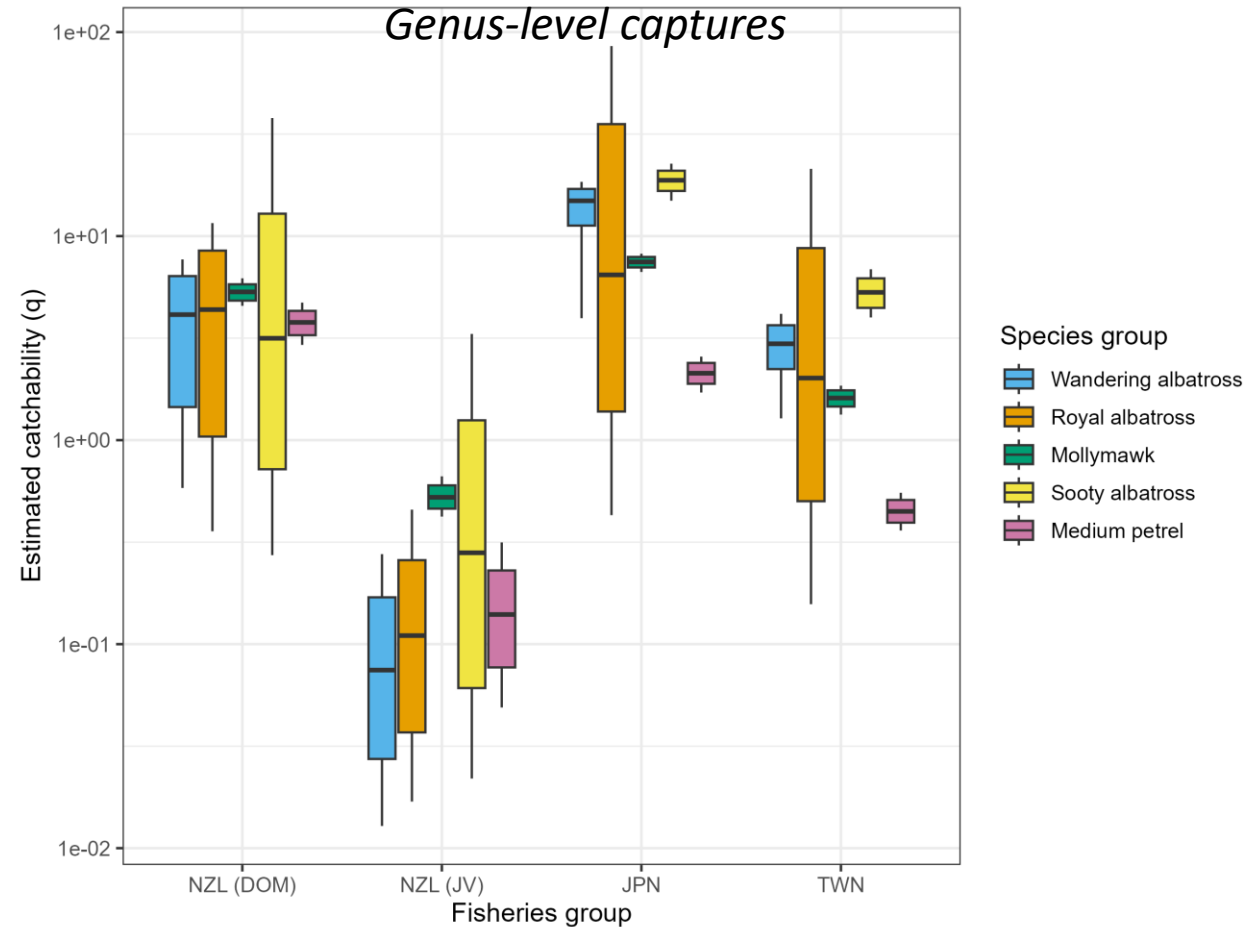


Lowering taxonomic resolution of captures – part 2

Original taxonomic resolution of captures



Genus-level captures



- Increased q's for mollymawks
 - Compensatory increase in q, as N no longer artificially increased for some taxa with updates to N_{BP} or P_B
- Increased uncertainty in royal albatross
 - Collapse wandering albatross and royal albatross catchability group to match resolution of captures

Modelling choices

- Appropriate taxonomic resolution for captures identifications
 - Which then informs how to parameterise catchabilities
- Appropriate taxonomic resolution for π
- Combine density maps with BLI range maps?
- Models fitted to:
 - 2012 to 2023, no temporal variation in q
 - 2012 to 2023, with time-blocked q (2012–2016, 2017–2019, 2020 to date)
 - 2012 to 2019 (for direct comparison with the 2024 all-data estimate)

Thank you!