

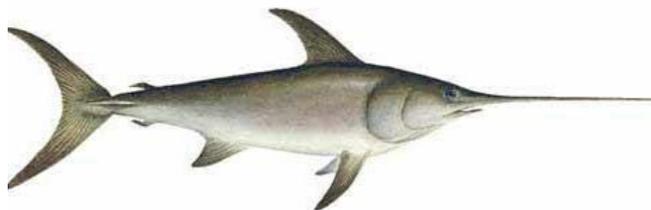
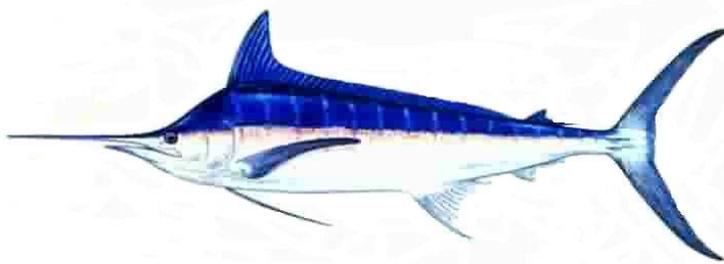


ISC/09/BILLWG-3/03

Preliminary analysis on possible stock boundary of striped marlin in the north Pacific using fisheries data of Japanese longliners

Momoko Ichionkawa
National Research Inst. of Far Seas Fisheries
5-7-1 Orido, Shimizu, Shizuoka, Japan 424-8633

Kotaro Yokawa
National Research Inst. of Far Seas Fisheries
5-7-1 Orido, Shimizu, Shizuoka, Japan 424-8633



Introduction

This document review possibility of existence potential stock boundary of striped marlin in the North Pacific. This document used cluster analysis (Cope and Punt 2009) as well as same method that was applied in determining swordfish stock boundary (Ichinokawa and Brodziak 2008).

Materials and Methods

Fishery data and considered oceanic region

The fishery data were from Japanese offshore and distant water longline fisheries operating in the Pacific. The time period covered by the data in this study was from 1960 to 1990. The time period was determined because longline efforts decreased in the eastern Pacific, main fishing ground of striped marlin, after 1990. The fishery data have been collected and compiled by National Research Institute of Far Seas Fisheries (NRIFSR), Fisheries Agency of Japan. Japanese longline data are originally reported by fishermen in the style of log-book recording details, such as fishing locations, day for the operation, ship ID and gear for fishing, by every operation. NRIFSR aggregates the log-book data into the data stratified with 5x5 degree cells and months in order to average erratic data and keep the size of data small. In this study, the aggregated data with 5x5 spatial resolutions were used.

Nominal CPUE of the striped marlin caught by Japanese longliners in the Pacific is shown in Fig. 1. Considering the CPUE distributions, this study assumed 3 different spatial domain to be separated: spatial domain (A) as used in swordfish analysis (Ichinokawa and Brodziak 2008), and smaller two domains (B) and (C).

Determination of single boundary with computer intensive method

Details of the algorithm are described in Ichinokawa and Brodziak (2008).

The statistical model for calculating standardized CPUE of striped marlin was generalized linear model (GLM) assuming a lognormal error distribution. The GLM includes explanatory variables of year (Y), quarter (Q) and area (A).

$$\log(\text{CPUE}_{yijk} + \mu / 10) = Y_y + Q_j + A_k + (\text{interaction terms})$$

The parameter of μ was added to CPUE (number of striped marlin per 1000 hooks, CPUE_{yijk}) in order to avoid negative infinity caused from the natural logarithm of zero. The μ is determined as overall average of the nominal CPUE (Campbell et al. 1996). The effect of quarter are defined as Jan-March (1st quarter), April-June (2nd quarter), July-Sep (3rd quarter) and Oct-Dec (4th quarter). Because stepwise model selection with BIC in preliminary analysis selected the interaction terms of Y*A, Q*A but not Y*Q, models including two interaction terms of Y*A and Q*A, one of Y*A, one of Q*A and no terms are considered in this study.

Cluster analysis

Another approach with cluster analysis was also tried referring Cope and Punt (2009). Although Cope and Punt (2009) evaluate uncertainty of clustering using CV of the standardized CPUE, this document conduct only single cluster analysis using R function ‘pam’. This is because CV of the estimated standardized CPUE derived from Japanese longline data is generally very small owing to large sample size. Area stratification for calculating regional specific abundance indices was given by glm-tree method (Ichinokawa and Brodziak, submitted). The number of cluster is also assumed as 2 or 3. Cluster analysis was conducted with scaled index of least squares mean derived from GLM.

Results and Discussion

Boundaries determined under the 3 spatial domains of A-C are determined as Fig 2-4. The boundaries under spatial domains of (A) and (B) separated the domains into two regions with higher CPUE in the northeastern area and with lower CPUE in the southwestern area (Fig. 2 and Fig. 3). The spatial domain of (C) in Fig. 4 was separated into two of coastal areas off California and region around Hawaii Islands. However, the boundary in Fig. 4 is sensitive to the assumed model comparing Fig. 4a and Fig 4b-c. In addition, results of 50 time bootstrap simulations show uncertainty of the boundary especially in the area south to 10N and east to 230E (Fig. 5).

Standardized CPUEs calculated in the separated regions show similar trends each other (right panels in Fig. 6), while magnitude of the CPUEs is distinctly different (left panels in Fig. 6). Those results indicate there would be synchrony in population dynamics of striped marlin in the North Pacific, even though our algorithm may determine single boundary in a given spatial domain.

Results of cluster analysis are also shown in Fig. 7 under the assumption of 3 clusters and boundary A. Other results are also available with pdf file of “cluster_areaB-2.pdf” under the assumption of 2 clusters and boundary B, and pdf file of “cluster_areaB-3.pdf” under the assumption of 3 clusters and boundary B.

References

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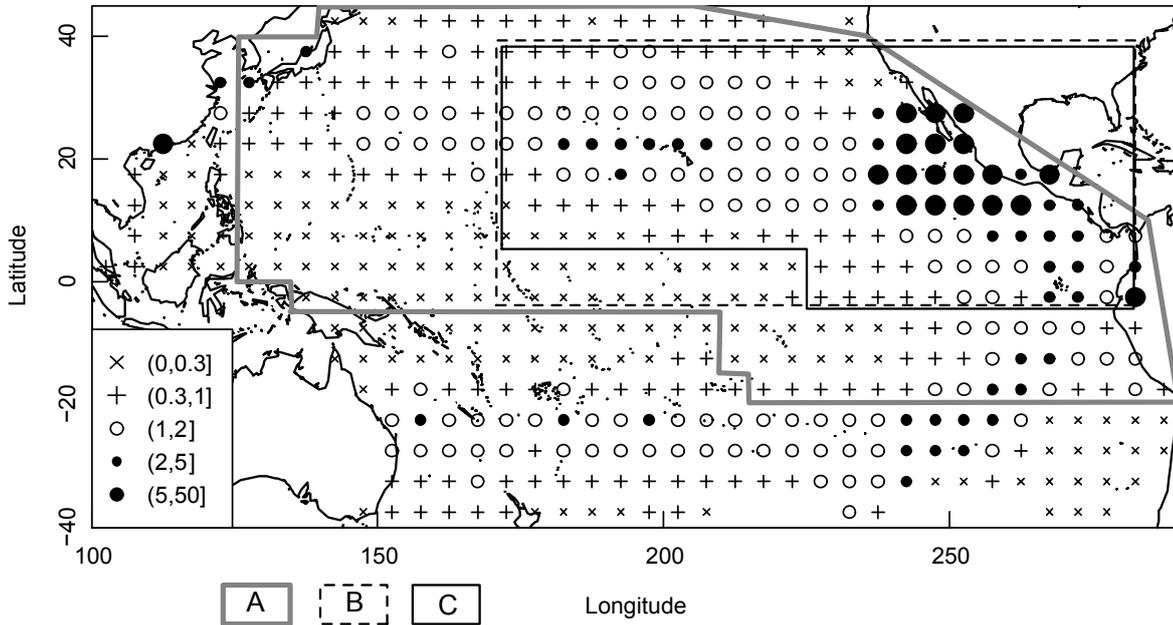


Fig. 1. Average nominal CPUE (inds/1000 hooks) of striped marlin in the Pacific, caught by Japanese longliners during 1970-1990. The area surrounded by gray tick line (A), black broken (B) and black solid (C) lines are defined spatial domain to be separated into two in this study.

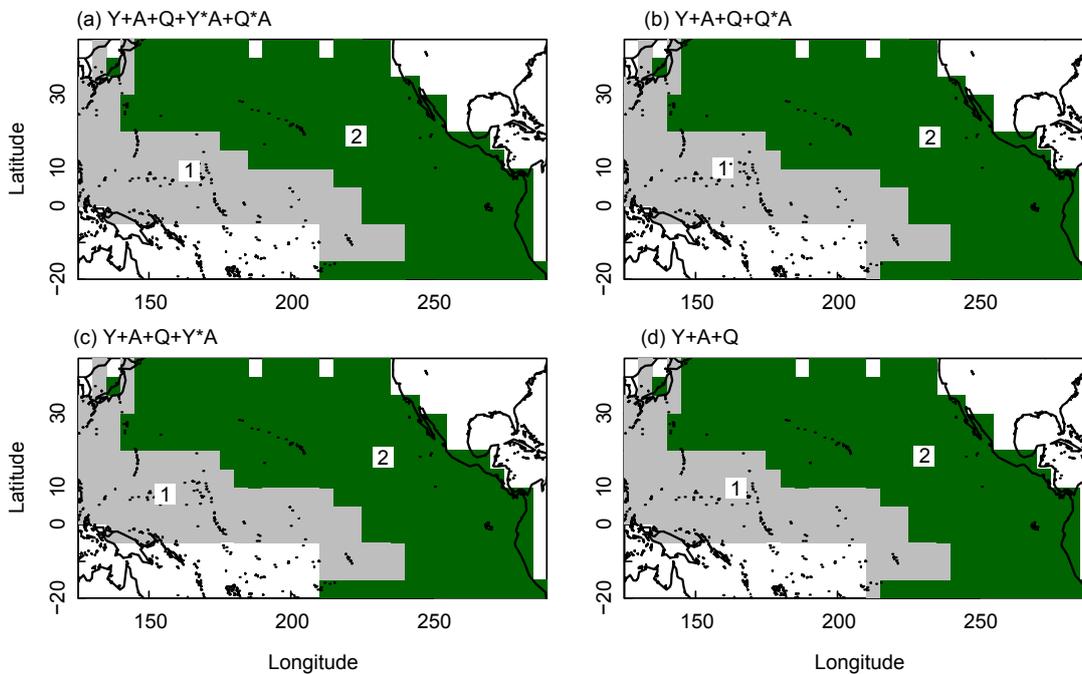


Fig. 2. Boundaries separating spatial domain (A).

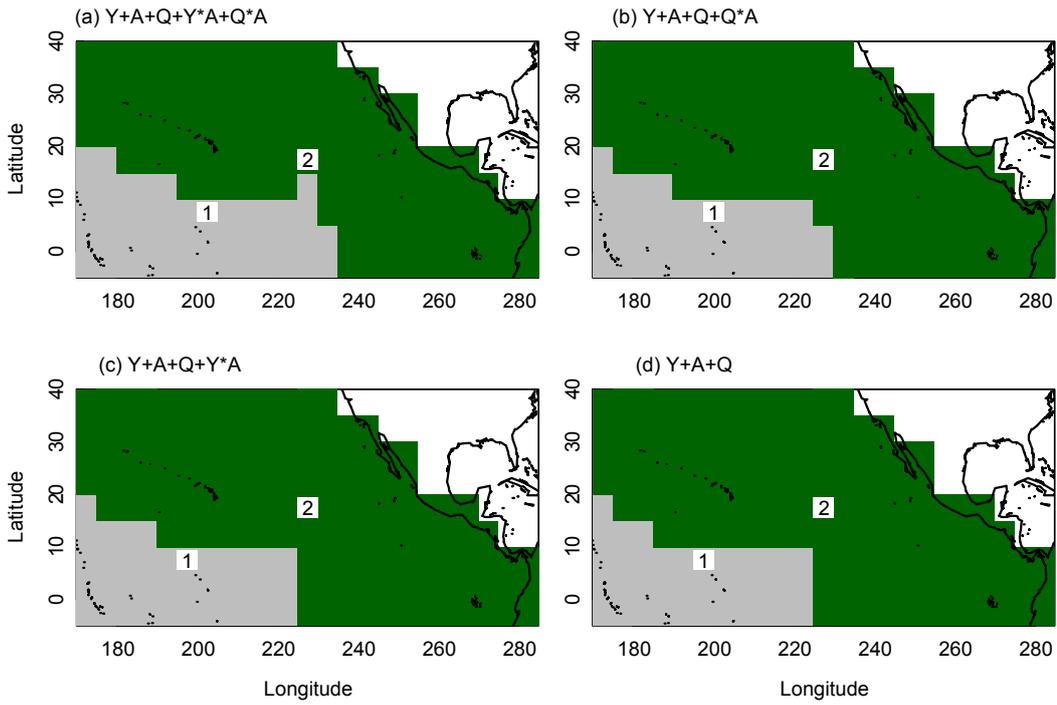


Fig. 3. Boundaries separating spatial domain (B).

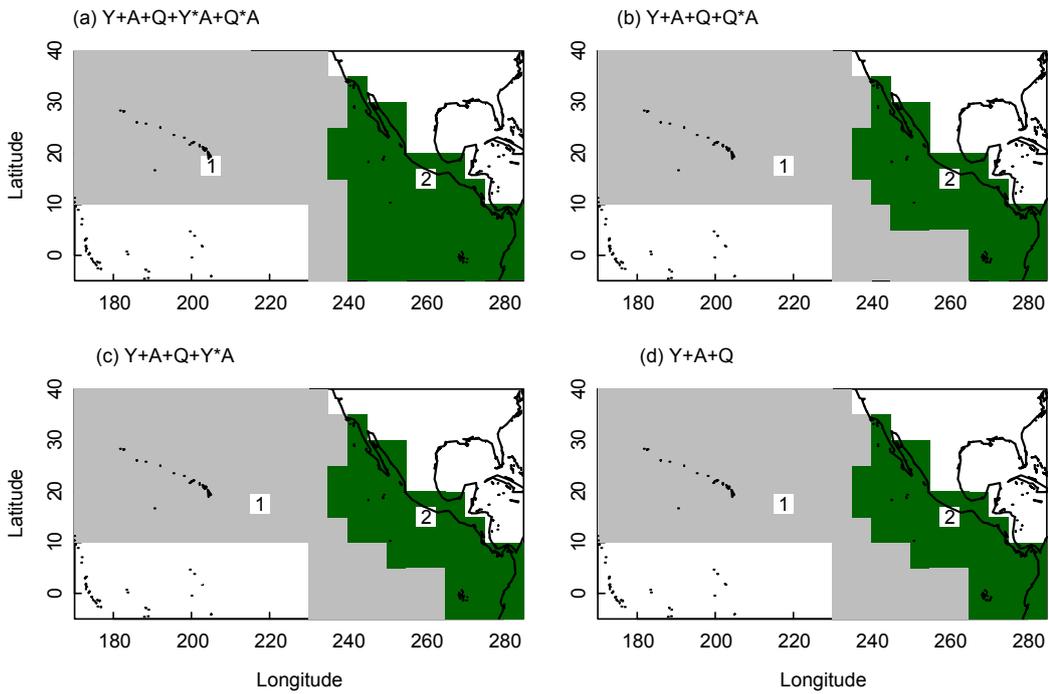


Fig. 4. Boundaries separating spatial domain (C).

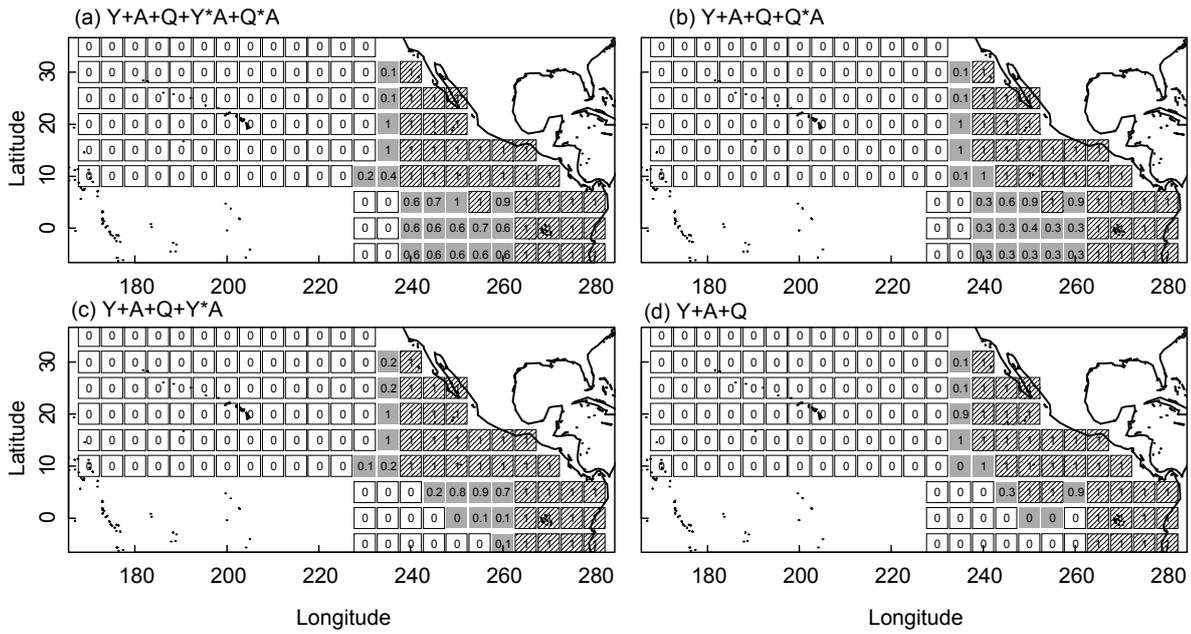


Fig. 5. Uncertainty of the selected boundaries evaluated from 50 time bootstrap simulations with spatial domain (C). The number at each 5x5 blocks shows the probability that the 5x5 block belongs to the eastern Pacific area: the areas colored with white and hatched color are the regions that always belong to the western and eastern region in the north Pacific, respectively, and areas shaded by gray color are uncertain region.

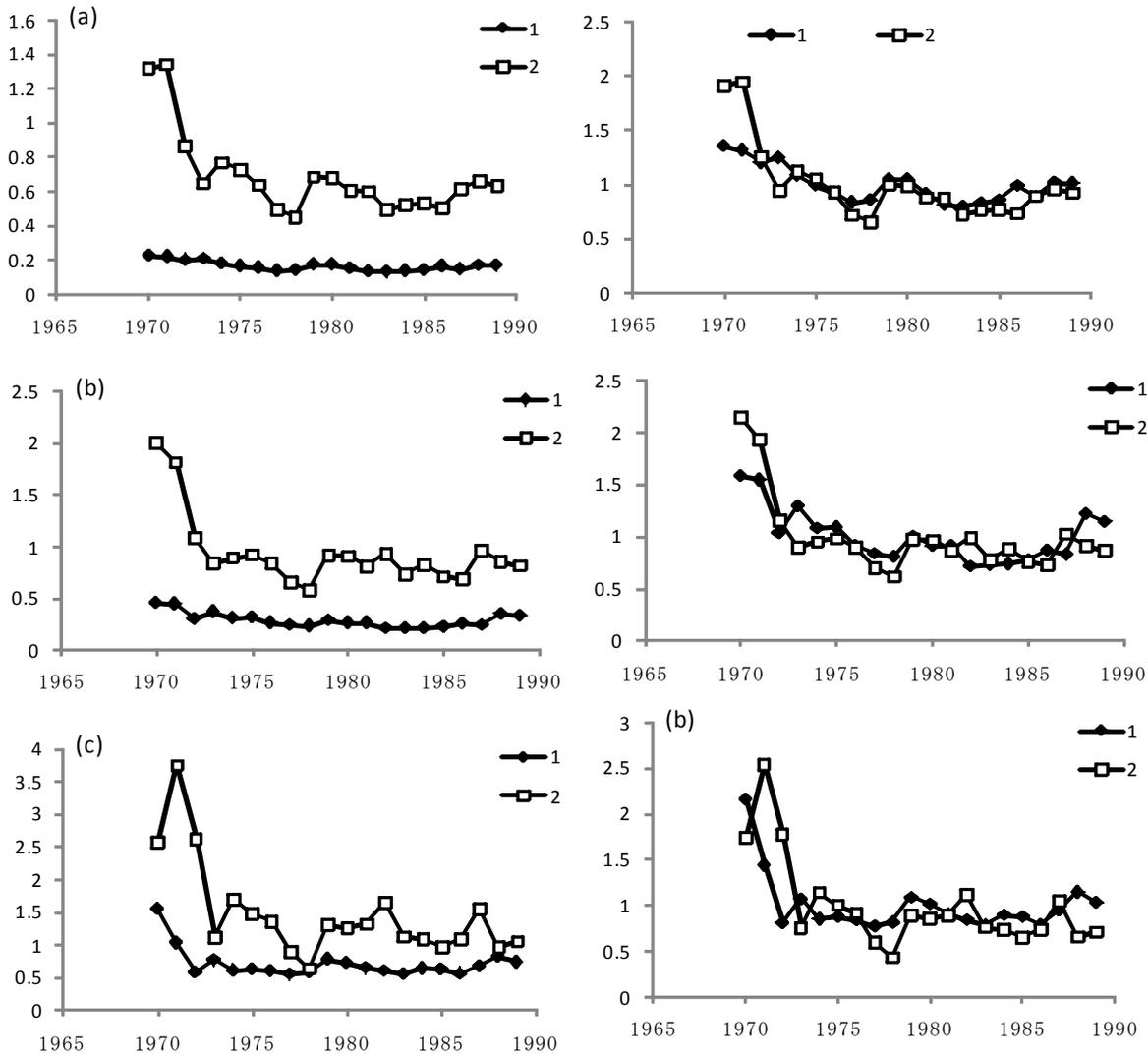


Fig. 6. Least squares mean of standardized CPUE in area 1 and 2 in Fig. 2 (a), Fig. 3 (b) and Fig. 4 (c) with the model including 2 interaction terms of $Y*A$ and $A*Q$.

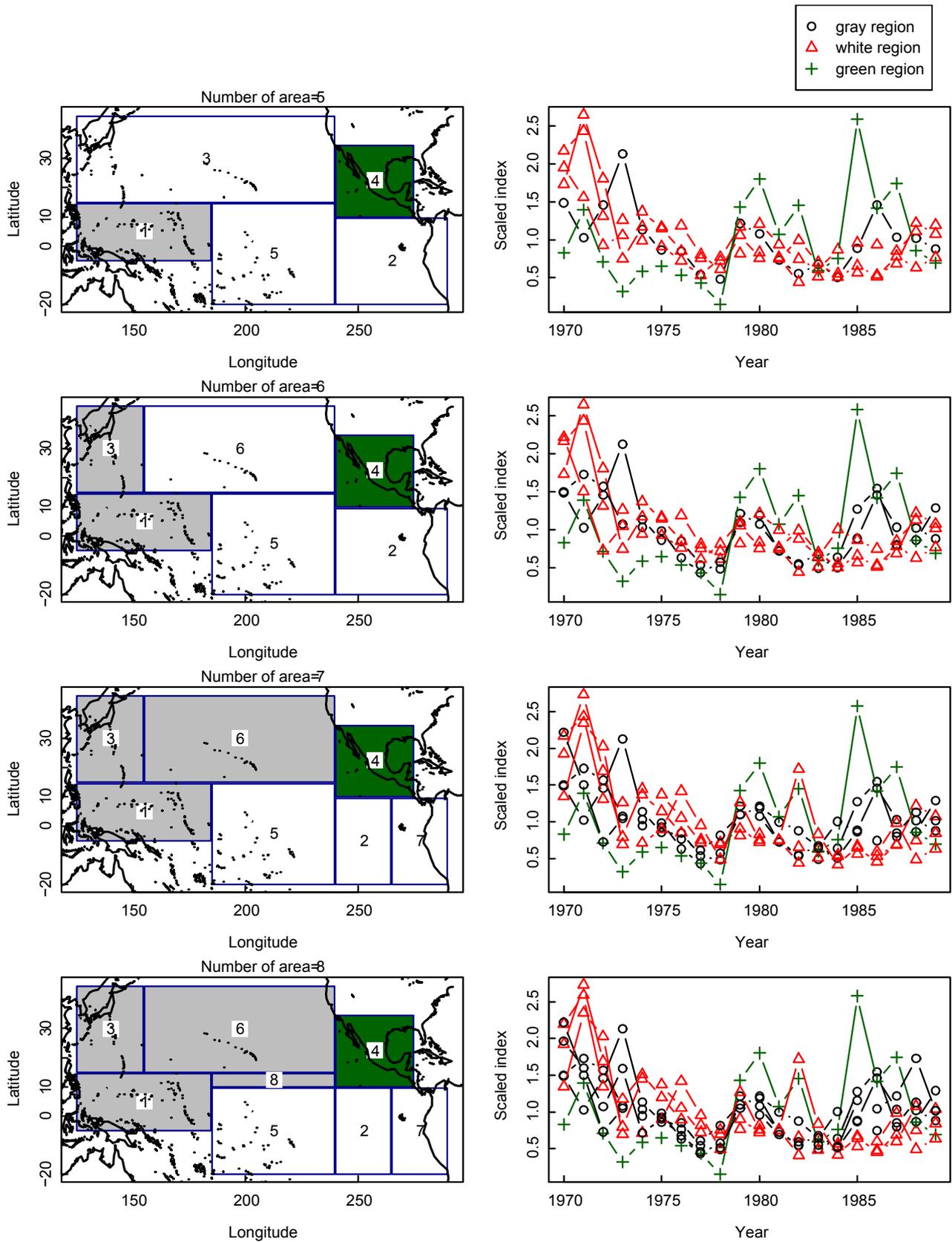


Fig. 7. Results of cluster analysis with different assumptions of area stratification. Regions with same color belong to same cluster. Because region numbered 4 always belong on lonely cluster, 3 clusters are assumed in this analysis.

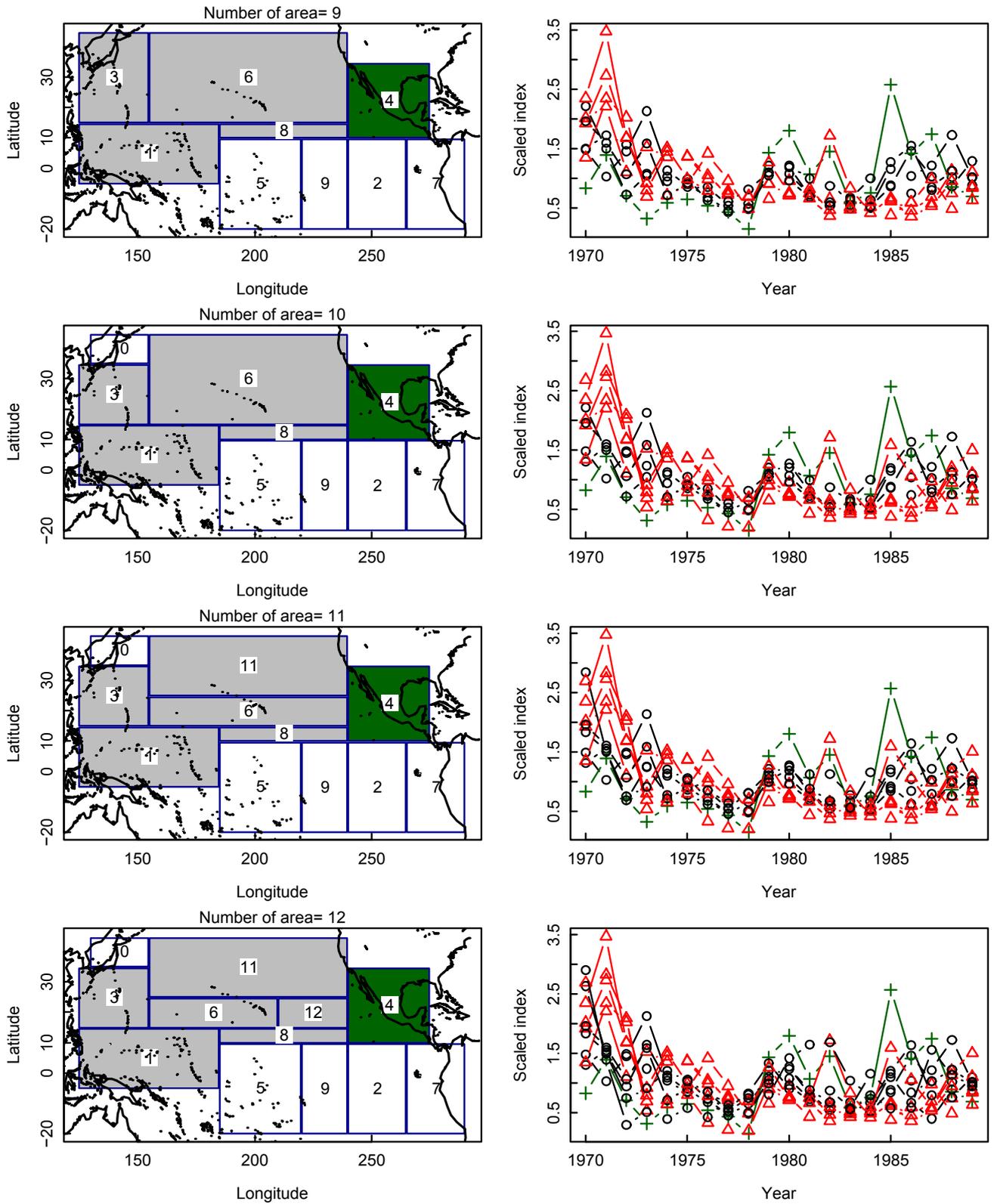


Fig. 7. Continued.