

Standardization of bigeye and yellowfin tuna CPUE by Japanese longline in the Indian Ocean which includes cluster analysis

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Abstract

Standardizations of Japanese longline CPUE for bigeye and yellowfin tuna in multiple Indian Ocean regions were conducted using generalized linear models (GLM) with log normal and delta-lognormal errors. The models incorporated fishing power based on vessel ID where available, and used cluster analysis to account for targeting. The variables year-quarter, vessel ID, latlong5 (five degree latitude-longitude block), cluster and number of hooks were used in the standardization. Dominant species differed depending on clusters. The effects of each covariate differed depending on species and region. The CPUE trends were similar to those estimated using ‘traditional’ method, though with some differences due to the inclusion of vessel effects and cluster variables.

1. Introduction

Until 2016, national scientists have mainly standardized Japanese longline CPUE for bigeye and yellowfin tuna in the Indian Ocean using generalized linear models (GLM), with log normal errors and either operational or aggregated catch and effort data (e.g. Matsumoto et al., 2016a, b). The standardizations have incorporated the effects of fishing season, area, fishing gear (number of hooks between floats and gear material) and an environmental factor (sea surface temperature). These may be termed ‘simple’ and ‘traditional’ methods.

In 2016, IOTC joint CPUE analysis (CPUE workshop) was conducted and ‘joint CPUEs’ were created for bigeye and yellowfin tuna, based on Japanese, Taiwanese and Korean longline operational data (Hoyle et al., 2016). These models account for fishing power based on vessel ID where available, and use cluster analysis to incorporate targeting. Joint CPUEs were considered to be more representative of status of the stocks and so were used for base models of stock assessment. At that time fleet-specific CPUE indices were prepared for Japanese longline using the same methods, but were not presented, so it was not possible to compare the joint and Japanese-only longline CPUE indices. In 2017 the joint CPUE analysis workshop was held and CPUE indices for each fleet as well as joint CPUE were created (Hoyle et al., 2017). Japanese longline CPUE for bigeye and yellowfin tuna created at that workshop was reported by Matsumoto et al. (2017). They reported that the trend of both CPUEs was mostly similar to those by traditional method, but there are some differences especially in the early period. Also in 2018 and 2019 the joint CPUE analysis workshop was again held and CPUE indices for each fleet as well as joint CPUE were created (e.g. Matsumoto et al., 2018). At those workshops it was aimed to create and consider CPUE for yellowfin, bigeye and/or albacore. This

document reports the standardization of bigeye and yellowfin tuna Japanese longline CPUE conducted at this year's joint CPUE analysis, using the same methods as that for joint CPUE.

2. Materials and methods

Data

Operational level (set by set) Japanese longline logbook data were used. The data were available for 1952-2018 (data for 2018 were preliminary), with the fields year, month and day of operation, location to 1° of latitude and longitude, vessel call sign, no. of hooks between floats (HBF), number of hooks per set, date of the start of the fishing cruise, logbook identifier, and catch in number of each species. Vessel call signs were available from 1979 onward and were used for the vessel identifier. The operations with hooks per set above 5000 and less than 200 were removed. Sets after 1975 with HBF missing or > 25 were removed. Sets before 1975 with missing HBF were allocated HBF of 5, according to standard practice with Japanese longline data.

Each set was allocated to bigeye and yellowfin regions (Fig. 1, Fig. 2). These regions are the same as those in the past studies.

Cluster analysis

We clustered the data using the approach applied by Hoyle et al. (2015). We removed all sets with no catch of any of the species, and then aggregated by vessel-month. Set level data contains variability in species composition due to the randomness of chance encounters between fishing gear and schools of fish. This variability leads to some misallocation of sets using different fishing strategies. Aggregating the data tends to reduce the variability, and therefore reduce misallocation of sets. For these analyses we aggregated the data by vessel-month, assuming that individual vessels tend to follow a consistent fishing strategy through time. One trade-off with aggregation in this way is that vessels may change their fishing strategy within a month, which will result in misallocation of sets. For the purposes of this paper we refer to aggregation by vessel-month as trip-level aggregation, although the time scale is (for distant water vessels) in most cases shorter than a fishing trip. In the data prior to 1979 vessel id was not available, but we were able to cluster them by vessel-month because the logbook id, available for the first time in the current data set, could be used to identify sets on the same vessel-trip.

We calculated proportional species composition by dividing the catch in numbers of each species by catch in numbers of all species in the vessel-month. Thus the species composition values of each vessel-month summed to 1, ensuring that large catches and small catches were given equivalent weight. The data were transformed by centering and scaling, so as to reduce the dominance of species with higher average catches. Centering was performed by subtracting the column (species) mean from each column, and scaling was performed by dividing the centered columns by their standard deviations.

We clustered the data using the hierarchical Ward hclust method, implemented with function hclust in R,

option 'Ward.D', after generating a Euclidean dissimilarity structure with function 'dist'. This approach differs from the standard Ward D method which can be implemented by either taking the square of the dissimilarity matrix or using method 'ward.D2' (Murtagh & Legendre 2014). However in practice the method gives similar patterns of clusters to other methods, more reliably than ward.D2 (Hoyle et al 2015).

Selecting the number of groups

We used several subjective approaches to select the appropriate number of clusters. In most cases the approaches suggested the same or similar numbers of groups. First, we applied hclust to transformed trip-level data and examined the hierarchical trees, subjectively estimating the number of distinct branches. Second, we ran kmeans analyses on untransformed trip-level data with number of groups k ranging from 2 to 25, and plotted the deviance against k. The optimal group number was the lowest value of k after which the rate of decline of deviance became slower and smoother. Third, following Winker et al (2014) we applied the nScree() function from the R nFactors package (Raiche & Magis 2010), which uses various approaches (Scree test, Kaiser rule, parallel analysis, optimal coordinates, acceleration factor) to estimate the number of components to retain in an exploratory PCA. Where there was uncertainty about the number of clusters, we selected the option with more clusters.

We plotted the hclust clusters to explore the relationships between them and the species composition and other variables, such as HBF, number of hooks, year, and set location. Plots included boxplots of a) proportion of each species in the catch, by cluster; b) the distributions of variables by cluster; and c) maps of the spatial distribution of clusters, one map for each cluster.

In some analyses clusters that caught very few of the species of interest were omitted, because they provide little relevant information and may cause analysis problems due to large numbers of zeroes, and memory problems due to large sample sizes. Cluster selection was based on review and discussion of the plots of covariates and species compositions by cluster. Also, in some analyses only clusters in which target species was dominant were selected to see the difference from the results in which all or almost all the clusters were used. Analyses were run both with and without these clusters.

For standardization of each region, data were selected for vessels that had fished for at least N1 quarters in that region. The standard level of N1 was 8 quarters in the equatorial regions and 2 quarters in the southern regions. Subsequently, vessels, 5° cells, and year-quarters were included if they had at least 100 sets. For analyses of the 1952-1979 period this criterion was reduced to 50 sets, to increase the size of the dataset. For datasets with more than 60,000 sets the number of sets in each stratum (5° square * year-quarter) was limited by randomly selecting 60 sets without replacement from strata with more than this number of sets. Testing suggested that this approach did not cause bias, and the effects on trends of random variation were reduced to very low levels at 30 sets per stratum (Hoyle & Okamoto 2011), suggesting that 60 sets was more than adequate.

CPUE standardization, and fleet efficiency analyses

CPUE standardization methods generally followed the approaches used by Hoyle et al. (2015). The operational data were standardized using generalized linear models in R.

GLM (generalized linear models) that assumed a lognormal and delta lognormal distribution was conducted, and in this report mostly the methods and results for delta lognormal distributions are shown with partly for lognormal distribution. In this approach the response variable $\log(\text{CPUE}+k)$ was used, and a Normal distribution assumed. The constant k , added to allow for modelling sets with zero catches of the species of interest, was 10% of the mean CPUE for all sets. CPUE was defined at the set level as catch in number divided by hooks set. The following models were used:

Lognormal

$$\ln(\text{CPUEs}+k) \sim \text{yrqtr} + \text{vessid} + \text{latlong5} + \text{cluster} + f(\text{hooks}) + \epsilon$$

Delta lognormal

$$(\text{CPUE}=0) \sim \text{yrqtr} + \text{vessid} + \text{latlong5} + f(\text{hooks}) + g(\text{HBF}) + \text{cluster} + \epsilon$$

$$\log(\text{CPUE}) \sim \text{yrqtr} + \text{vessid} + \text{latlong5} + f(\text{hooks}) + g(\text{HBF}) + \text{cluster} + \epsilon, \text{ for nonzero sets}$$

where *yrqtr*: year and quarter; *vessid*: effect of vessel ID; *latlong5*: effect of five degree latitude and longitude; *cluster*: effect of cluster; *f(hooks)*: function of number of hooks modelled with a cubic spline; *g(HBF)*: function of the number of hooks between floats modelled with a cubic spline; ϵ : error term.

Data periods

Vessel identity information was only available from 1979, so could not be applied uniformly across all years. The discontinuity in 1979 could be addressed in several different ways. We therefore analyzed the data in several ways so as to provide the assessment scientists with appropriate data. For each of the approaches above, four analyses were carried out as shown below.

Analysis	Years	Vessel effects
1	1952-1979	No
2	1979-end	Yes
3	1952- end	No
4	1952- end	Yes

It is possible to standardize the time series with vessel effects by assigning an identical dummy value to all vessels without vessel identity information. This was done for analysis 3). However, using a dummy value introduces several problems. First, not all vessels begin to report their callsign at once in 1979, and those that do are self-selected and not randomly selected from the vessel population. Therefore it cannot be assumed that fishing power remains constant after 1979 for the dummy vessel id, so the transition in 1979 may introduce a discontinuity into the time series. The discontinuity can be limited in scope by restricting the overlap between dummy and real vessel IDs to one year – 1979 – and removing sets with missing vessel IDs

after this time. Secondly, residuals may be more variable before 1979, without a true vessel ID in the model, which can introduce bias into the standardization.

One approach for addressing the discontinuity in analysis 3) is to adjust the time period 1952-1978 so that the relative averages in 1978 and 1979 are the same as they are in analysis 4), without vessel effects. However we considered that a better approach may be to estimate two time series 1952-1979 without vessel effects, and a second time series 1979-end with vessel effects (omitting all sets without vessel IDs). These are analyses 1) and 2) above. Subsequently the analyst can use them as desired, for example concatenating them after adjusting the averages so that the estimates for 1979 are the same.

The effects of covariates were examined using influence plots, using the R package `influ` (Bentley et al. 2011).

Indices of abundance

Indices of abundance were obtained by applying the R function `predict.glm` to model objects. Binomial time effects were obtained by generating time effects from the `glm` and adjusting them so that their mean was the proportion of positive sets across the whole dataset. The main aim with this approach is to obtain a CPUE that varies appropriately, since variability for a binomial is greater when the mean is at 0.5 than at 0.02 or 0.98, and the multiplicative effect of the variability is greater when the mean is lower. The outcomes were normalised and reported as relative CPUE with mean of 1.

Uncertainty estimates were provided by applying the R function `predict.glm` with `type = "terms"` and `se.fit=TRUE`, and taking the standard error of the year-quarter effect. For the delta lognormal models we used only the uncertainty in the positive component. Uncertainty estimates from standardizing commercial logbook data are in general biased low and often ignored by assessment scientists, since they assume independence and ignore autocorrelation associated with (for example) consecutive sets by the same vessels in the same areas. There may be a very large mismatch between the observation error in CPUE indices and the process error in the indices that is estimated in the assessment. This is particularly true for distant water longline CPUE, where very large sample sizes generate small observation errors.

Residual distributions and Q-Q plots were produced for all but the binomial analyses. For the lognormal positive analyses that included cluster in the model, median residuals were plotted by cluster. For all lognormal positive analyses, residuals by year-quarter were plotted by flag; median residuals by year-quarter were plotted by flag; and median residuals by 5° cell were mapped onto a contour plot for each flag.

We compared the indices with joint logline CPUE by Japanese, Taiwanese, Korean and Seychelles longline created at this year's CPUE collaborative analysis (Hoyle et al., 2019). The indices from 1979 onward with vessel effect were used. For each comparison, each dataset was normalized by dividing through by its mean, and the datasets plotted on the same axes.

3. Results and discussion

Cluster analysis

The aim of the cluster analysis was first to identify separate fishing strategies in the data for each species, regional structure, fleet, and region, and so to better understand the fishing practices; and second to assign each unit of fishing effort to a particular fishing strategy, so that the clusters could be used in standardization.

Species compositions were plotted by cluster for each region and fleet, as were the relative distributions of covariates (**Fig. 3- Fig. 8**). Dominant species differed depending on clusters. Clusters with low levels of the target species were excluded from standardization datasets.

Fig. 9 and **Fig. 10-Fig. 11** show the effect of each covariate for bigeye and yellowfin regions, respectively (from 1979 onward with vessel ID). For bigeye tuna, the vessel effect usually increased with time, but the trend differed depending on area. As for yellowfin tuna, vessel effect increased with time in several regions. At region 4 for regY2, large difference of the effect was observed among the clusters.

Fig. 12 and **Fig. 13-Fig. 14** show influence plot showing time series effect of each covariate for bigeye and yellowfin, respectively, with vessel effects. Historical difference of the effect of location ('latlong') was observed. Cluster effect was usually larger in the early period, indicating that targeting changed during these periods.

Fig. 15 and **Fig. 16-Fig. 17** show the trend of standardized CPUE for bigeye and yellowfin, respectively, without and with vessel effects. The trend differs between species and among regions, but CPUE usually shows decreasing trend with part of them increasing in the recent years.

Fig. 18 shows comparison of bigeye and yellowfin CPUE with joint logline CPUE. The trend of both CPUEs was mostly similar with small scale difference in several areas and period. In yellowfin tuna region 2, Japanese longline CPUE in recent years is not available due to the effect of piracy activities, but is supplemented by the data of other fleets.

Fig. 19 and **Fig. 20** show distribution of standardized residuals and QQ plots for bigeye and yellowfin, respectively.

4. References

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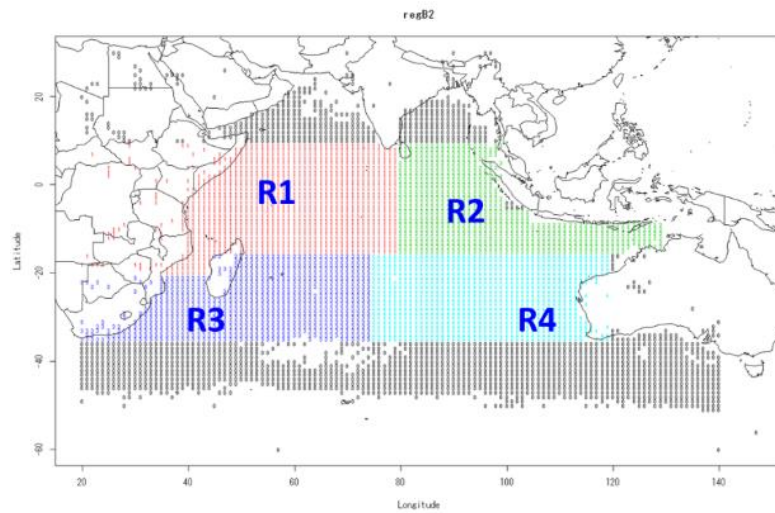


Fig. 1. Maps of the regional structures used to estimate bigeye CPUE indices, regB2.

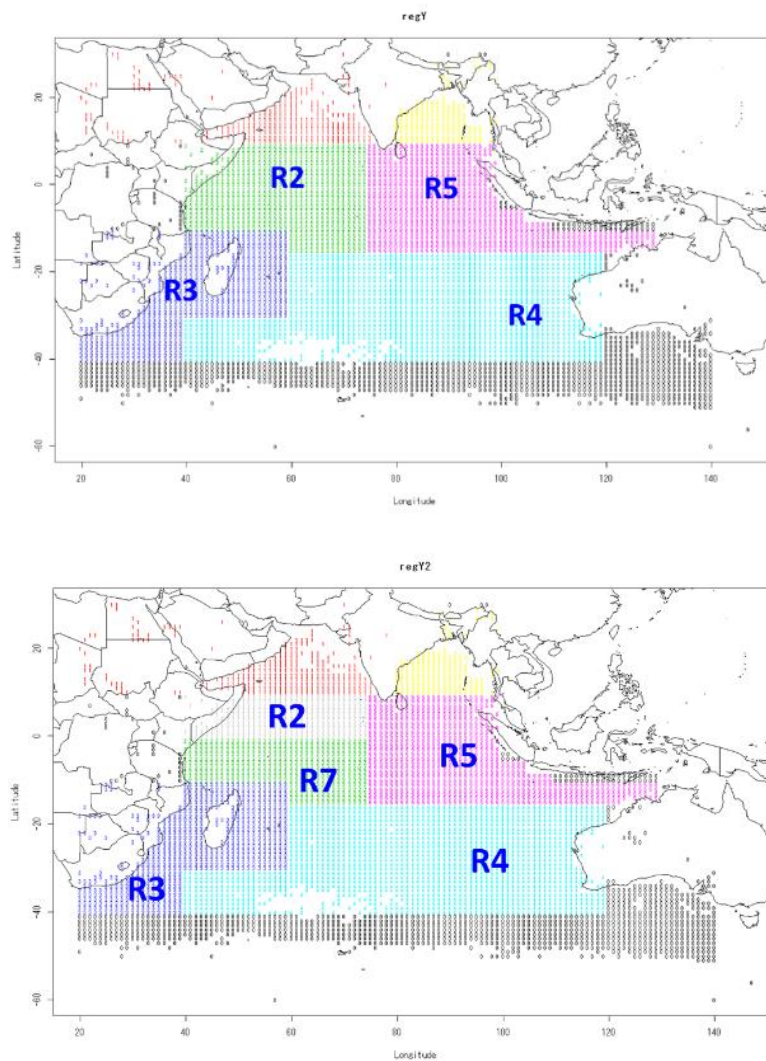


Fig. 2. Maps of the regional structures used to estimate yellowfin CPUE indices, regY (top) and regY2 (bottom). North of 10N was not used for the analyses.

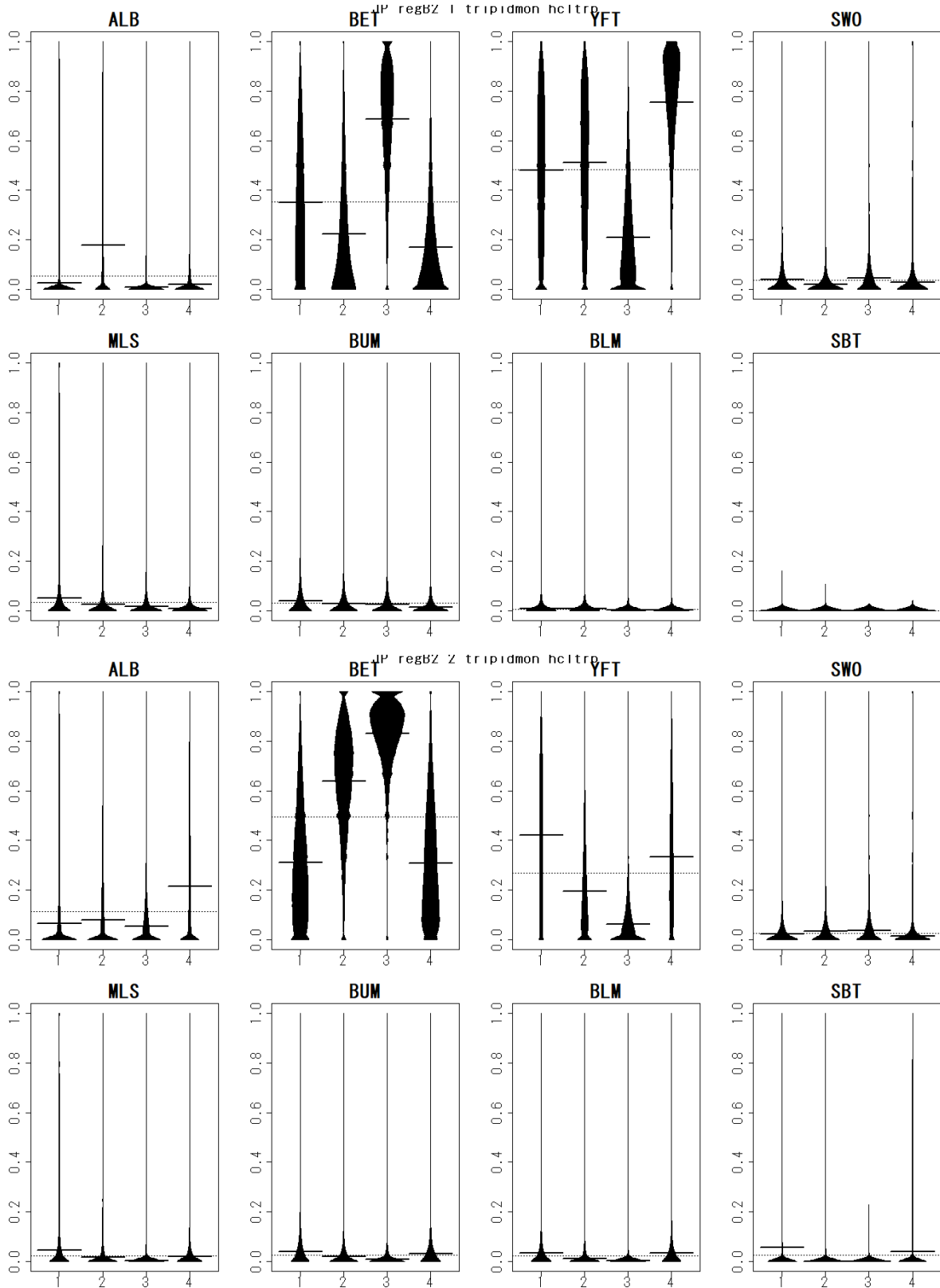


Fig. 3. Beanplots for bigeye region showing species composition by cluster. The horizontal bars indicate the medians.

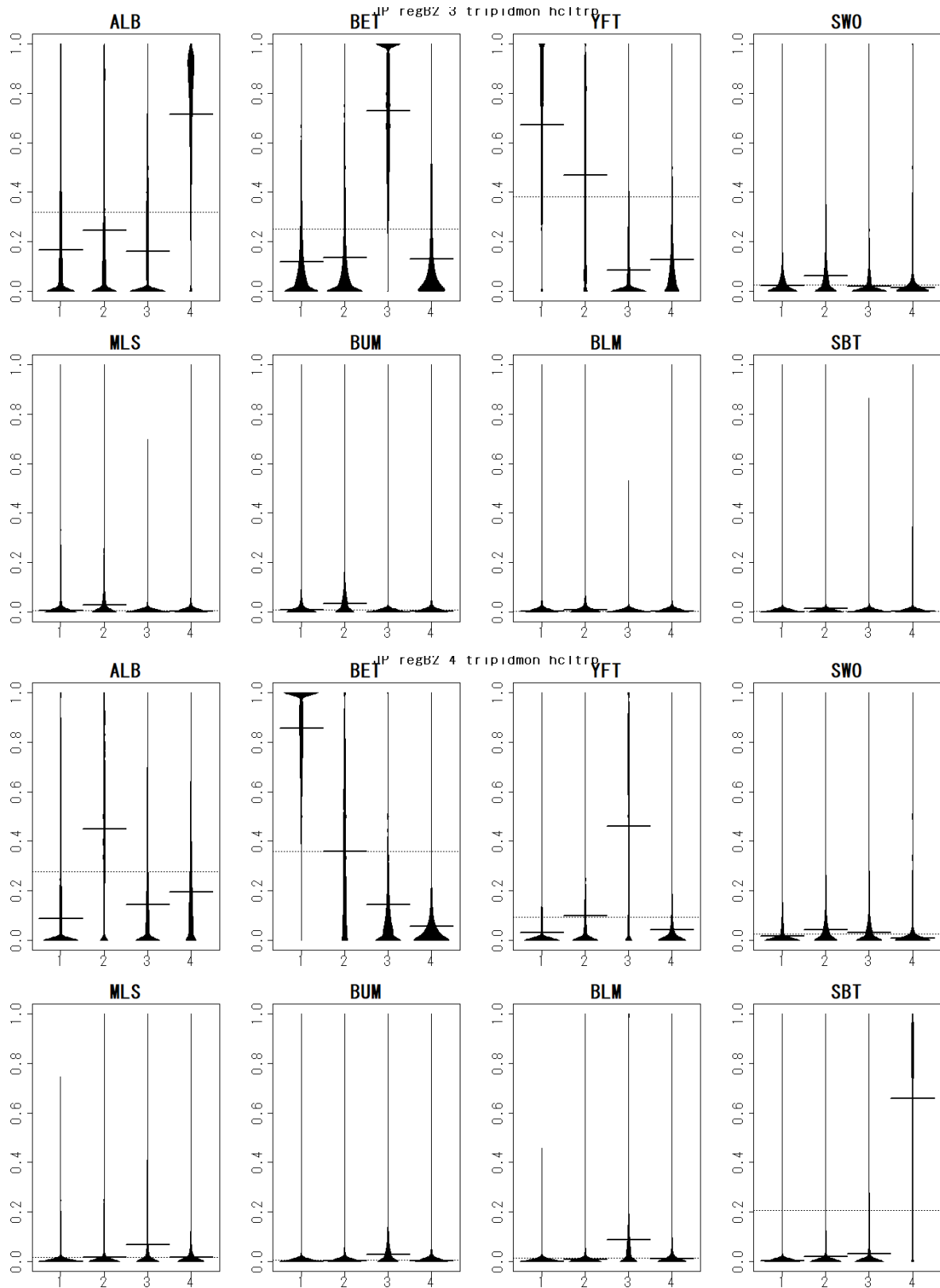


Fig. 3. Beanplots for bigeye region showing species composition by cluster. The horizontal bars indicate the medians. (continued)

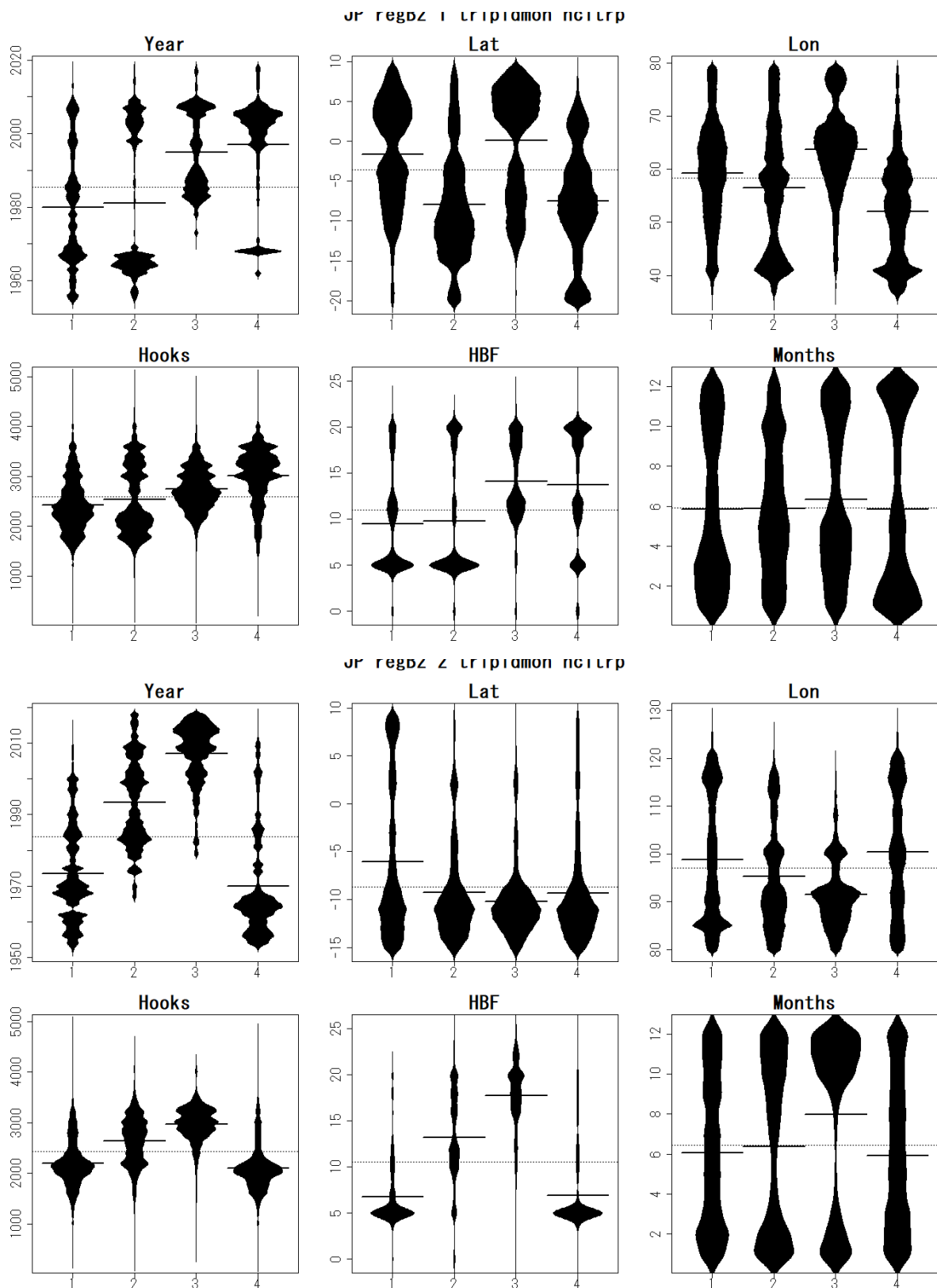


Fig. 4. Beanplots for bigeye region showing number of sets versus covariate by cluster. The horizontal bars indicate the medians.

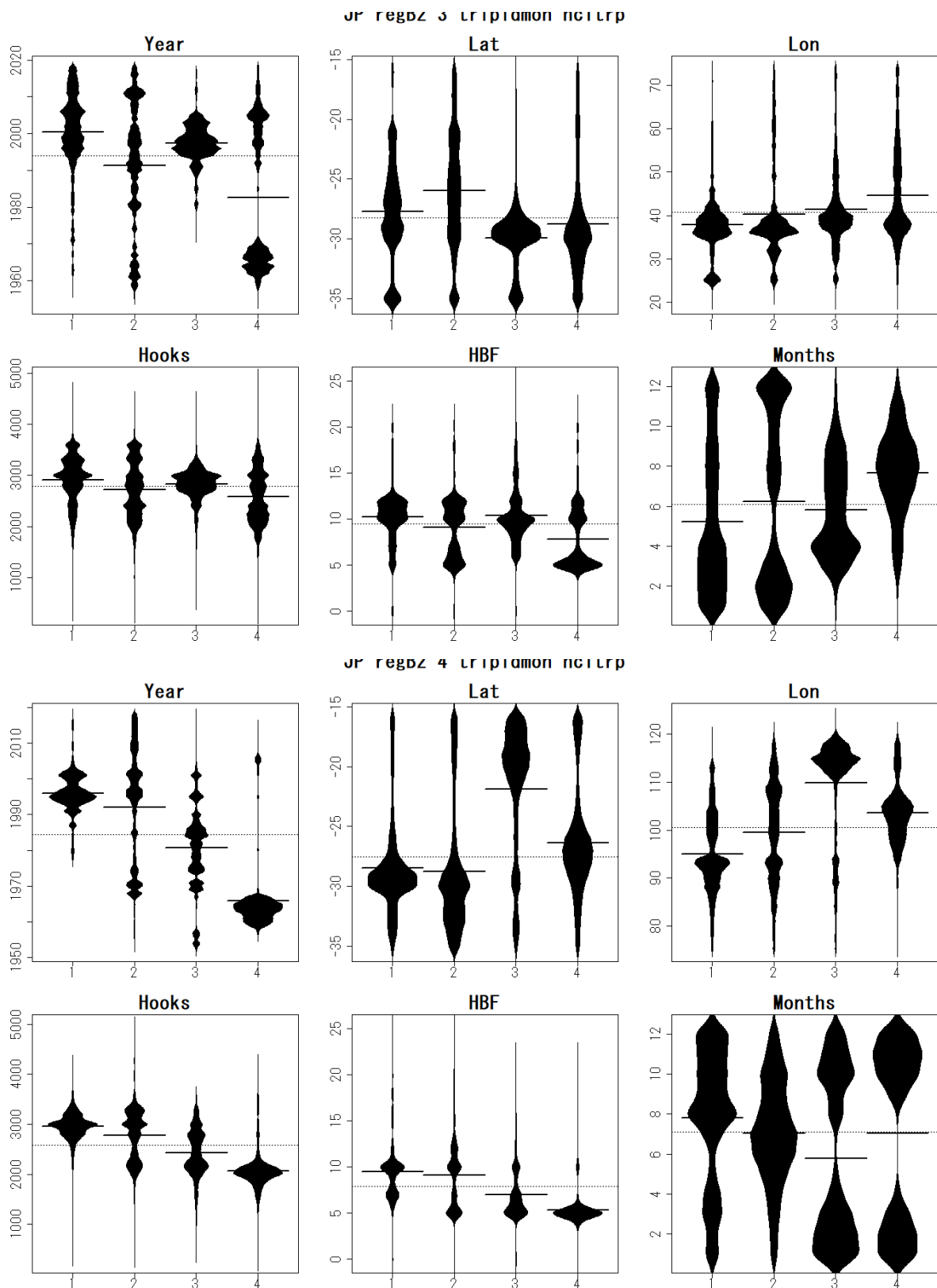


Fig. 4. Beanplots for bigeye region showing number of sets versus covariate by cluster. The horizontal bars indicate the medians. (continued)

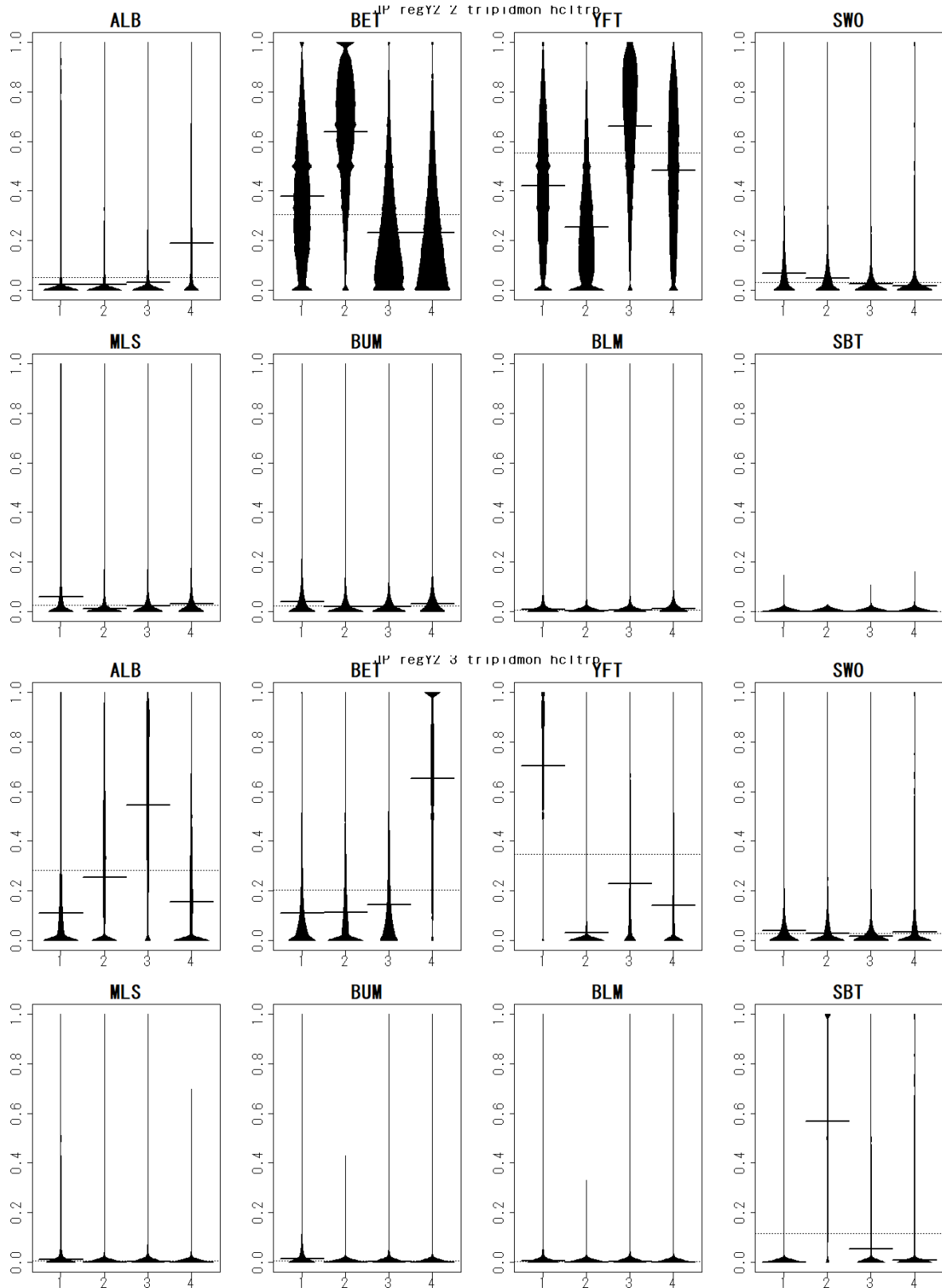


Fig. 5. Beanplots for yellowfin region regY2 showing species composition by cluster. The horizontal bars indicate the medians.

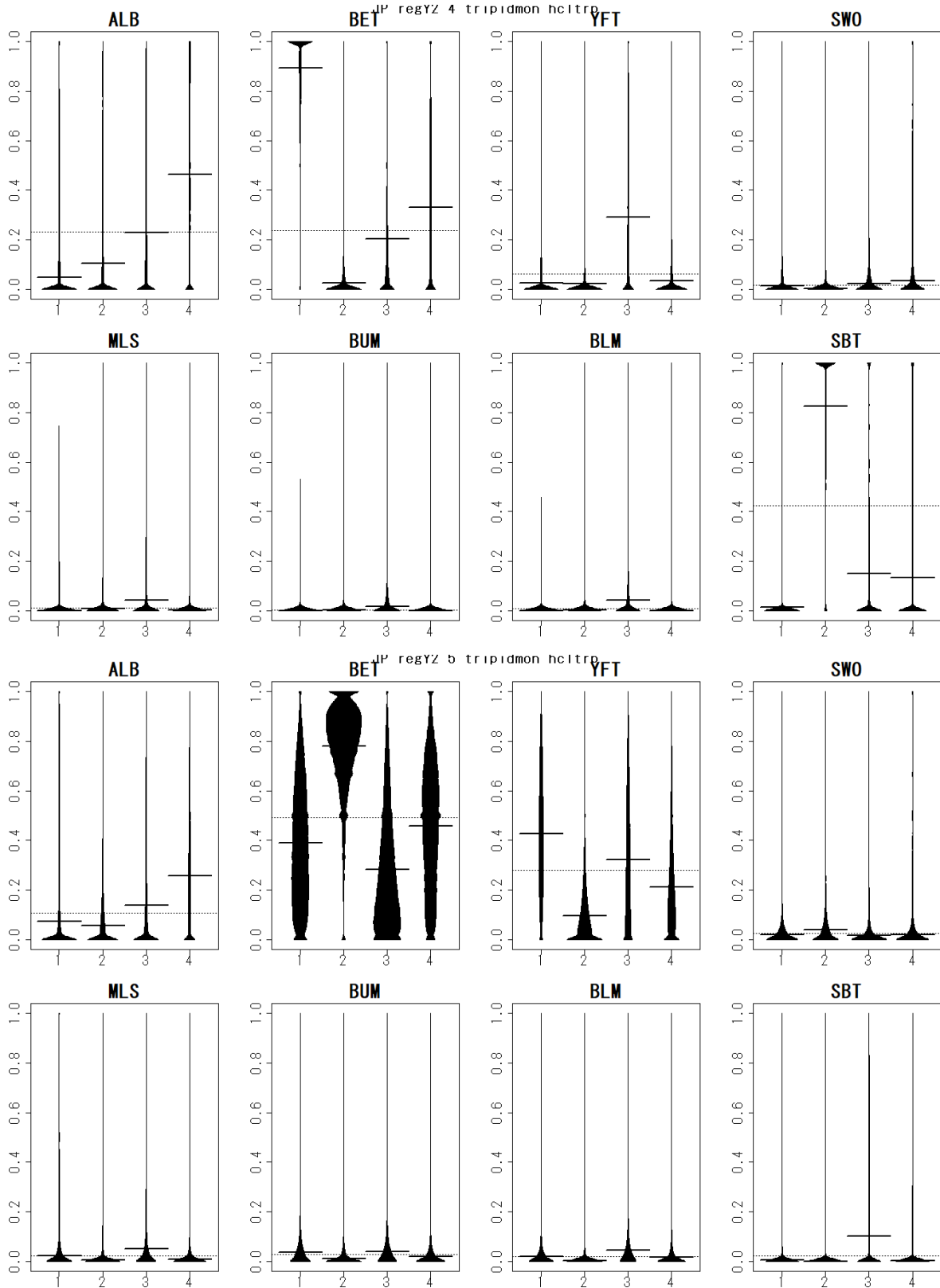


Fig. 5. Beanplots for yellowfin region regY2 showing species composition by cluster. The horizontal bars indicate the medians. (continued)

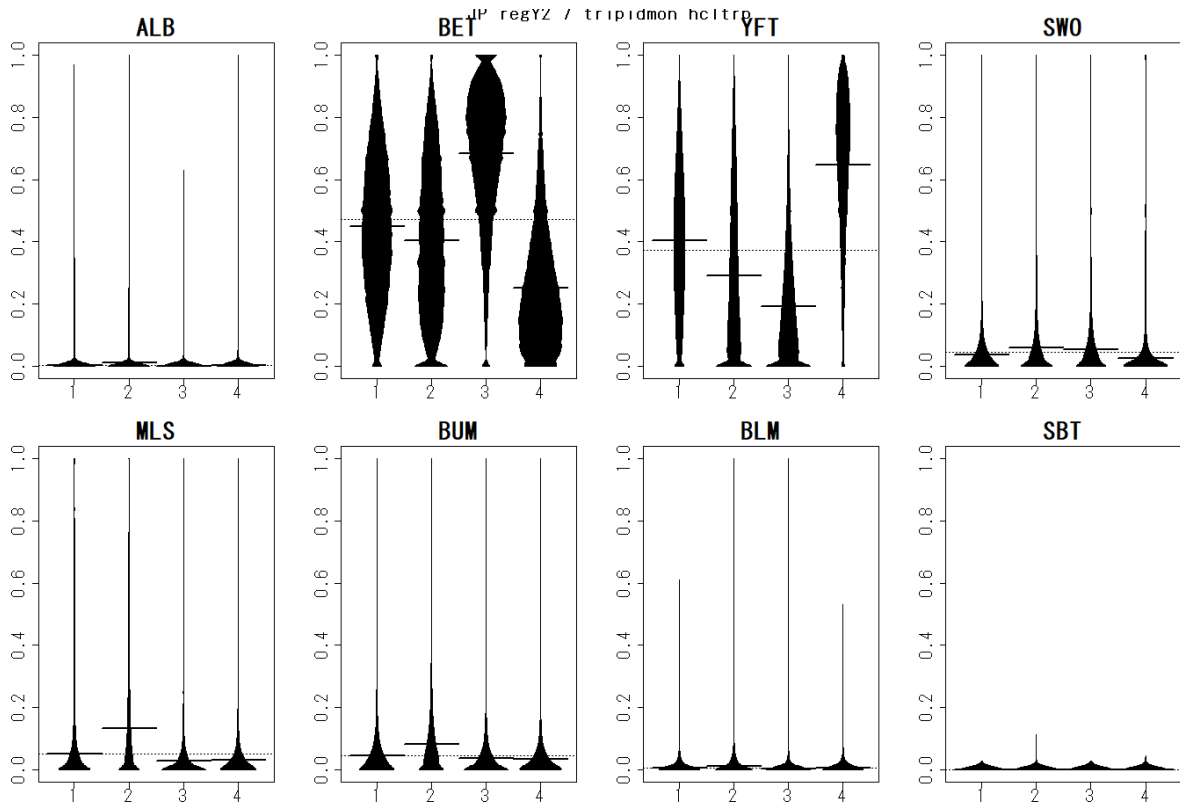


Fig. 5. Beanplots for yellowfin region regY2 showing species composition by cluster. The horizontal bars indicate the medians. (continued)

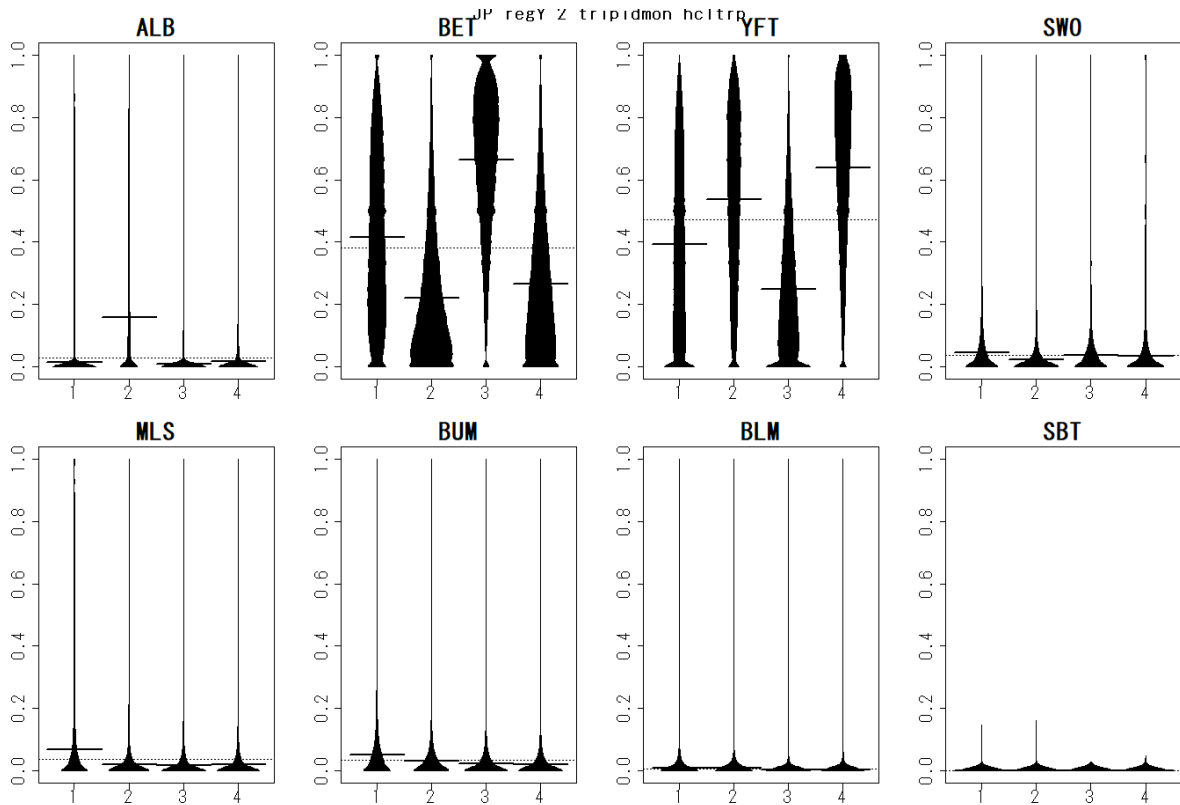


Fig. 6. Beanplots for yellowfin region regY (only R2) showing species composition by cluster. The horizontal bars indicate the medians.

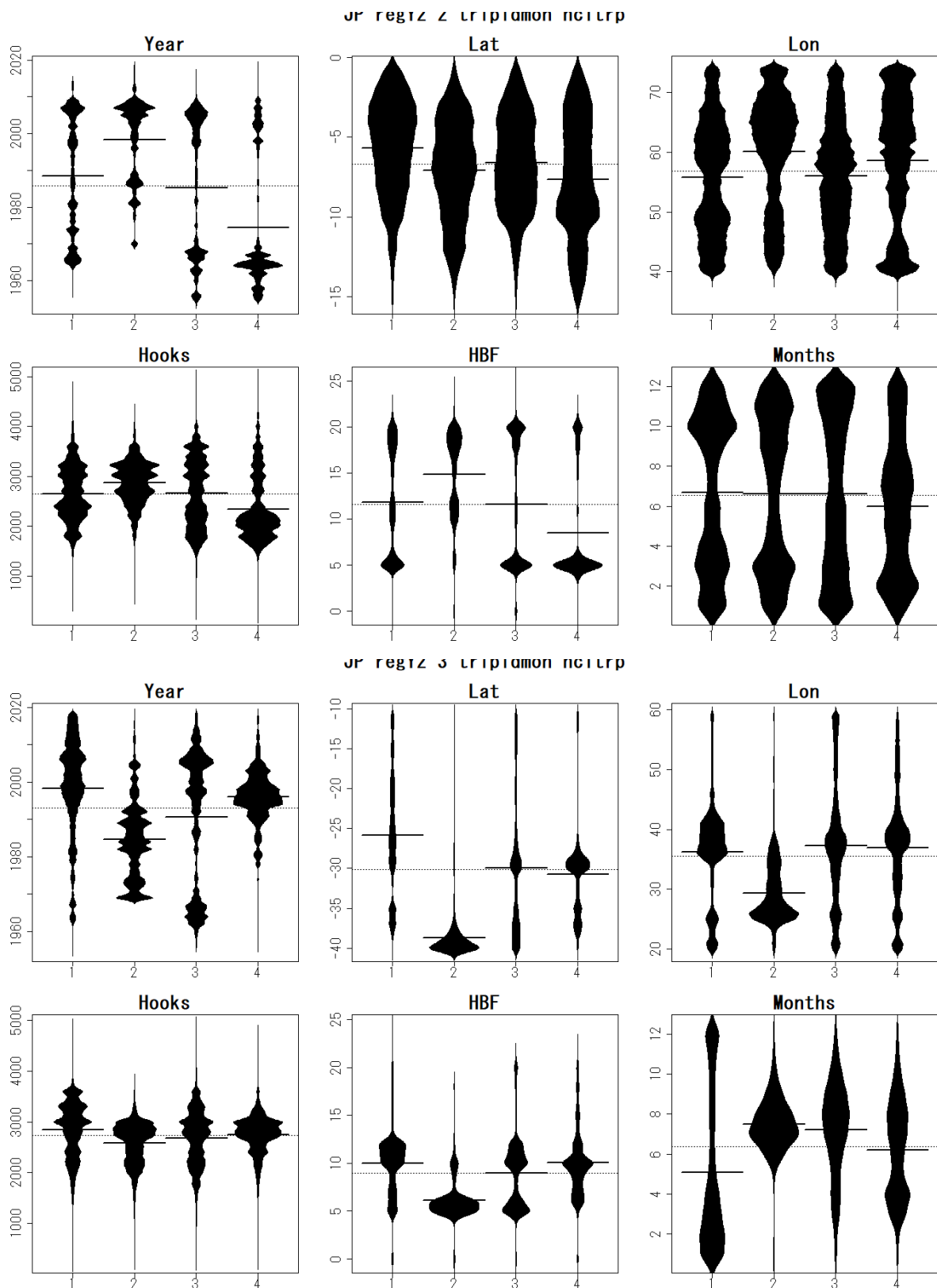


Fig. 7. Beanplots for yellowfin region regY2 showing number of sets versus covariate by cluster. The horizontal bars indicate the medians.

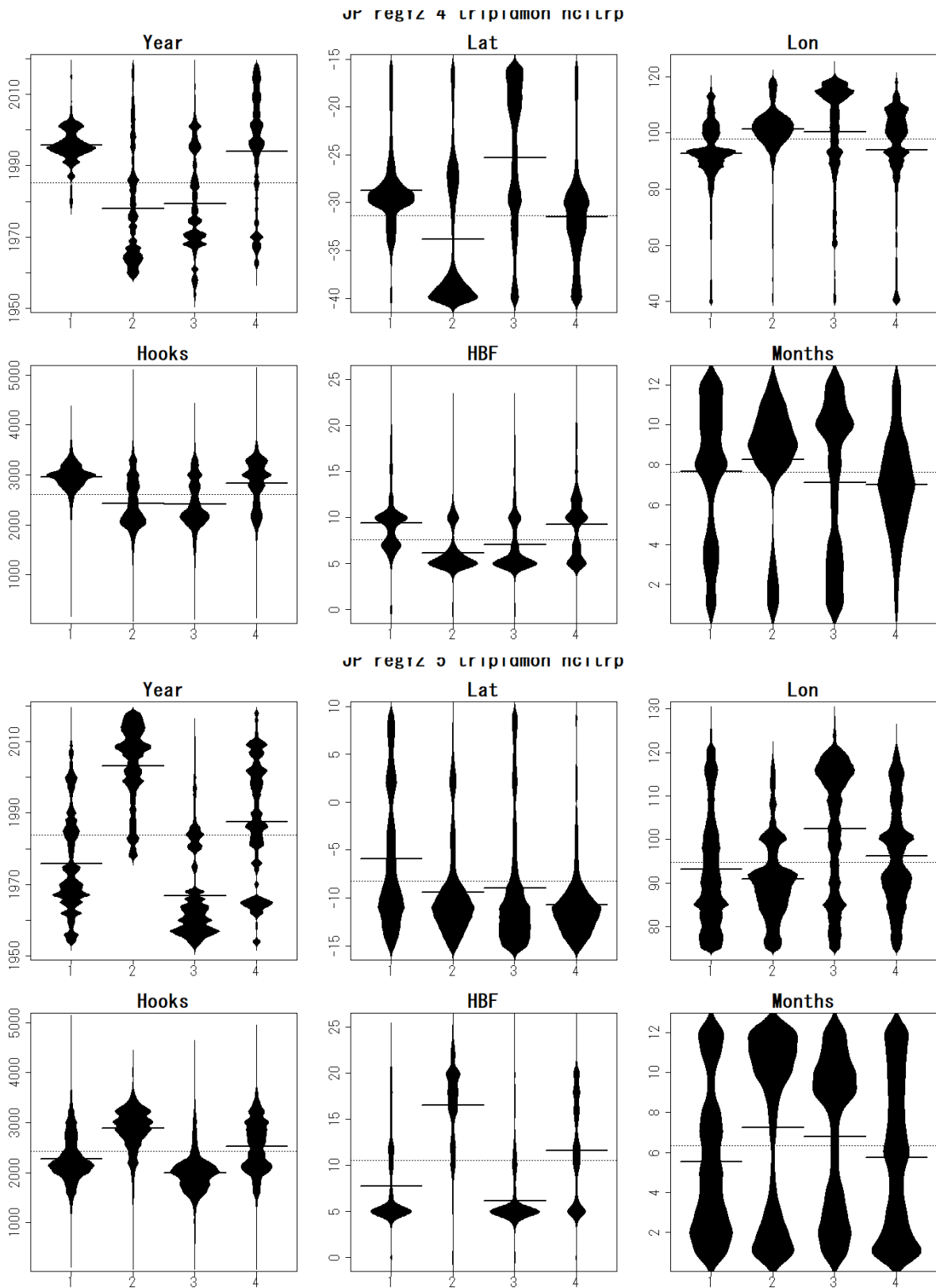


Fig. 7. Beanplots for yellowfin region regY2 showing number of sets versus covariate by cluster. The horizontal bars indicate the medians. (continued)

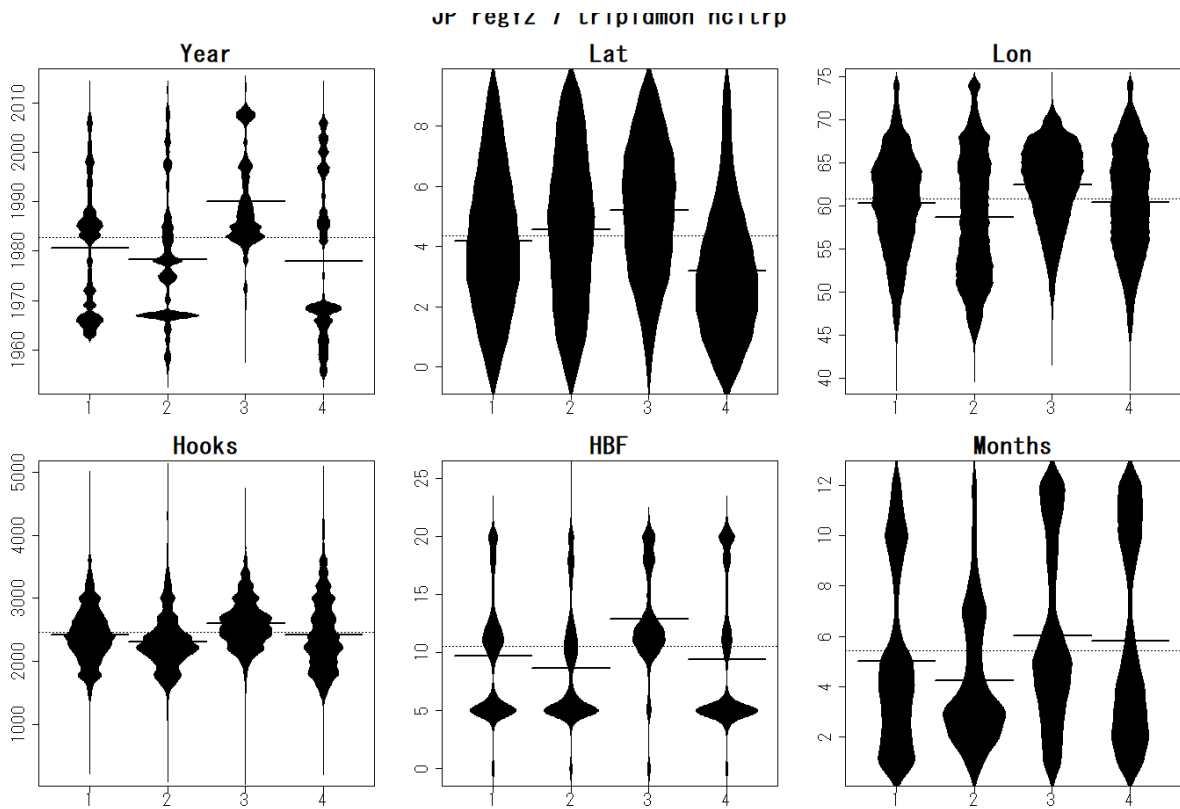


Fig. 7. Beanplots for yellowfin region regY2 showing number of sets versus covariate by cluster. The horizontal bars indicate the medians. (continued)

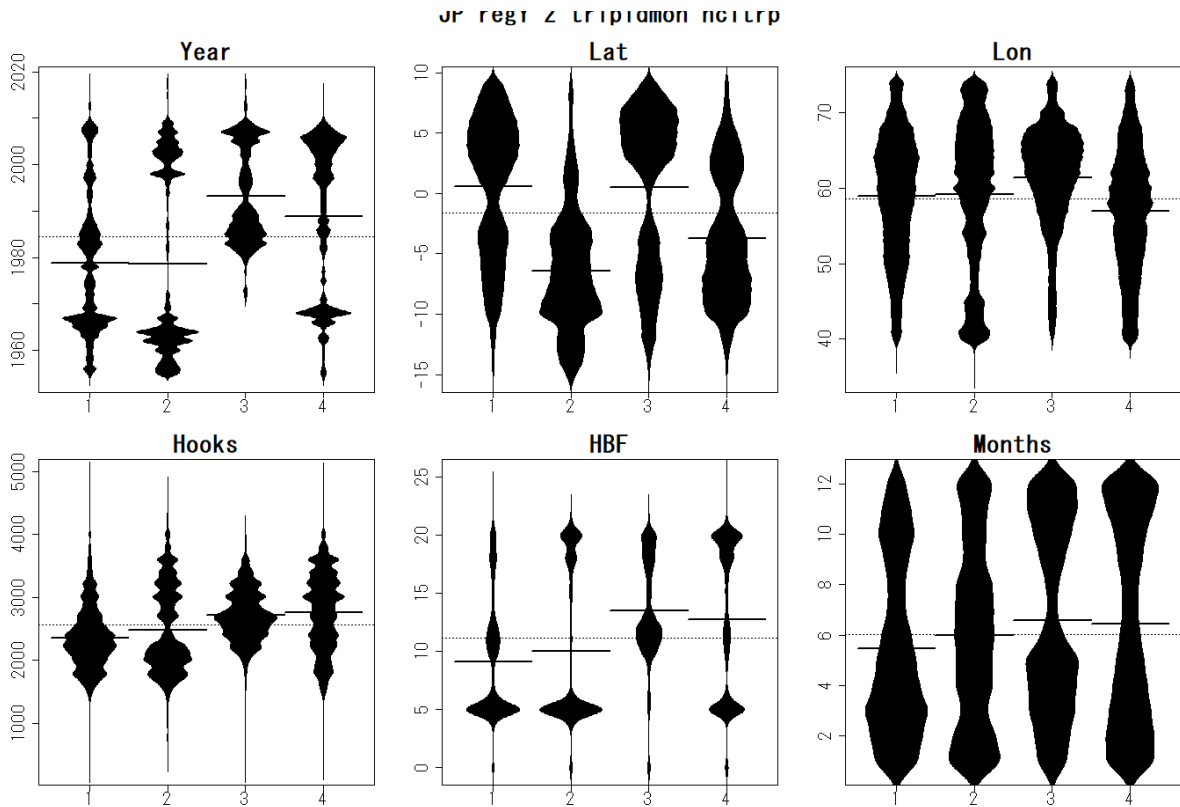
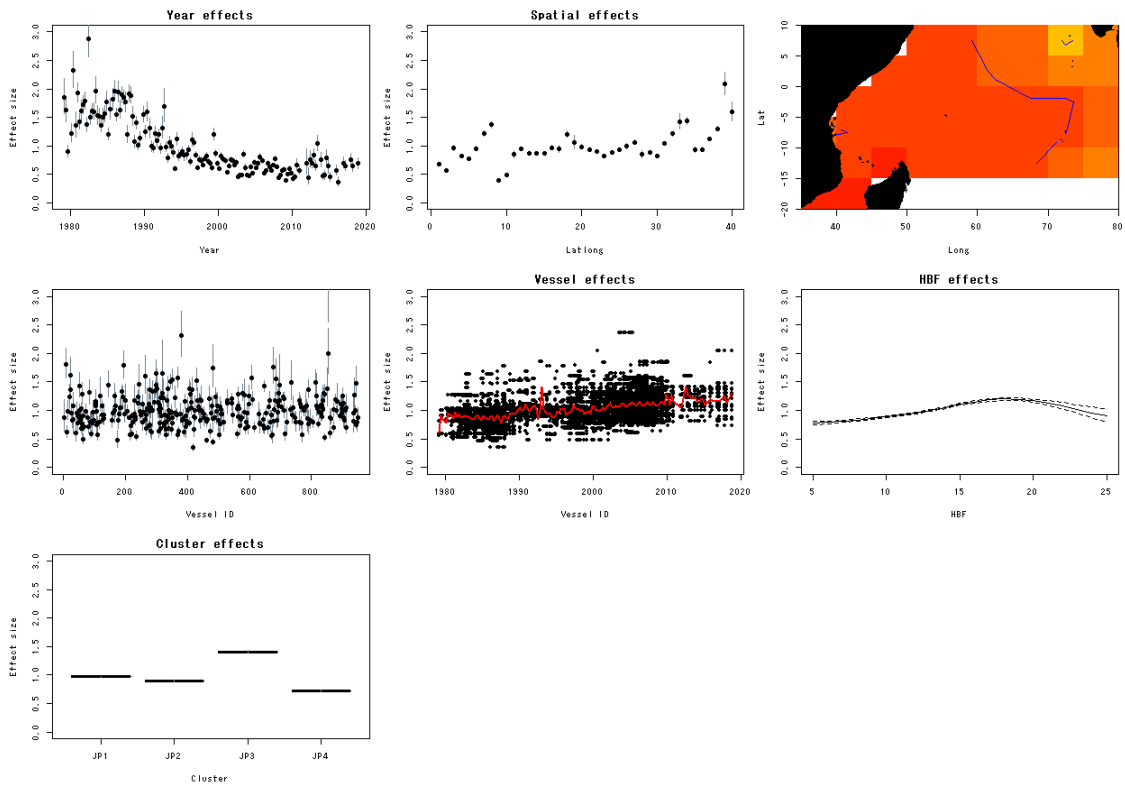


Fig. 8. Beanplots for yellowfin region regY (only R2) showing number of sets versus covariate by cluster. The horizontal bars indicate the medians.

Region 1



Region 2

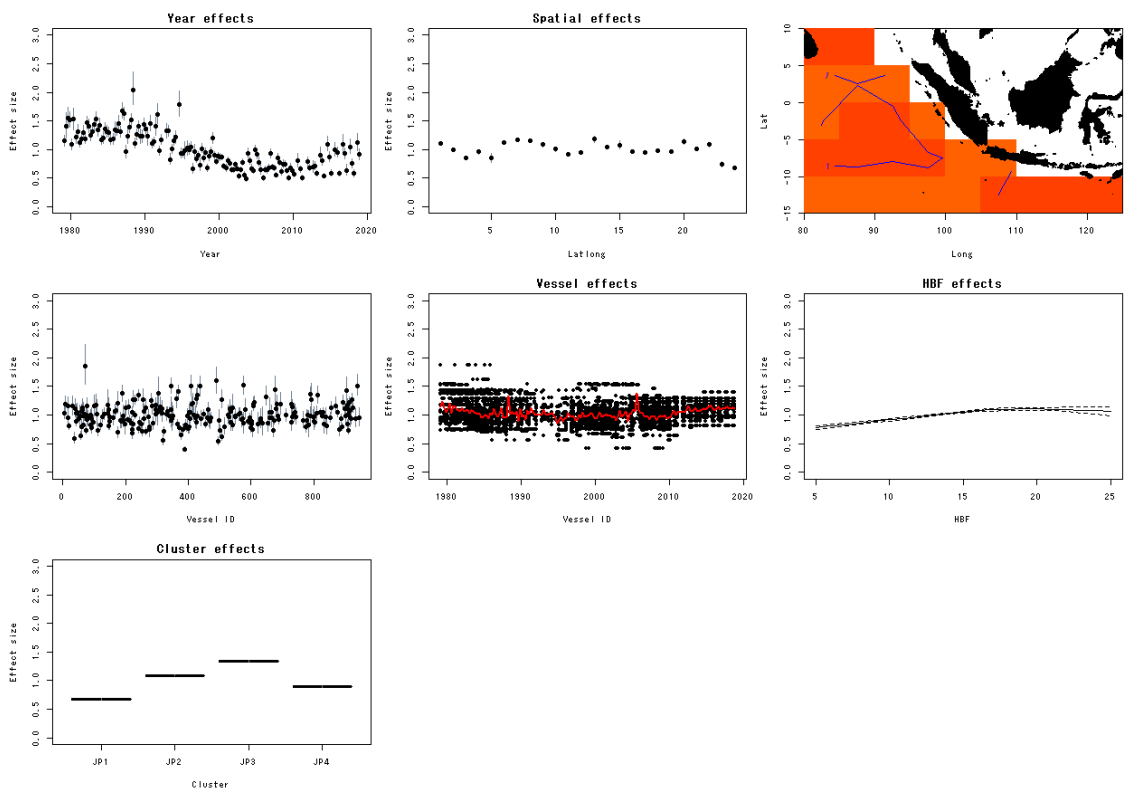
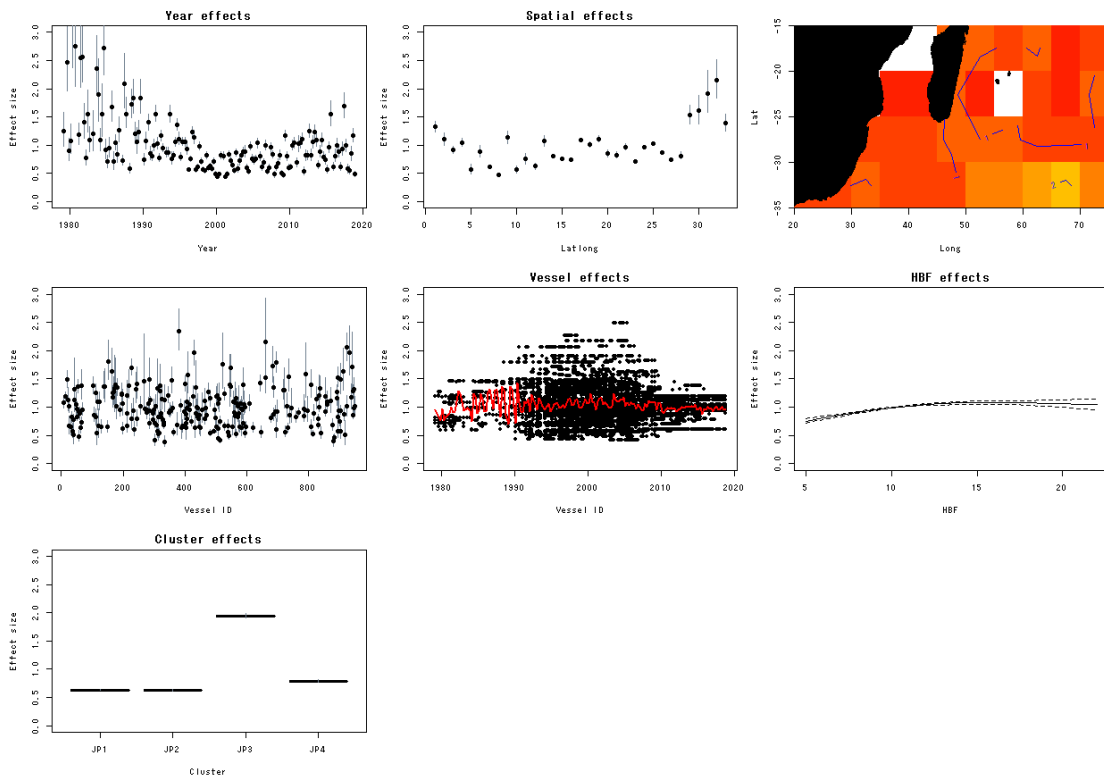


Fig. 9. Effect of each covariate for bigeye region (from 1979 onward with vessel ID).

Region 3



Region 4

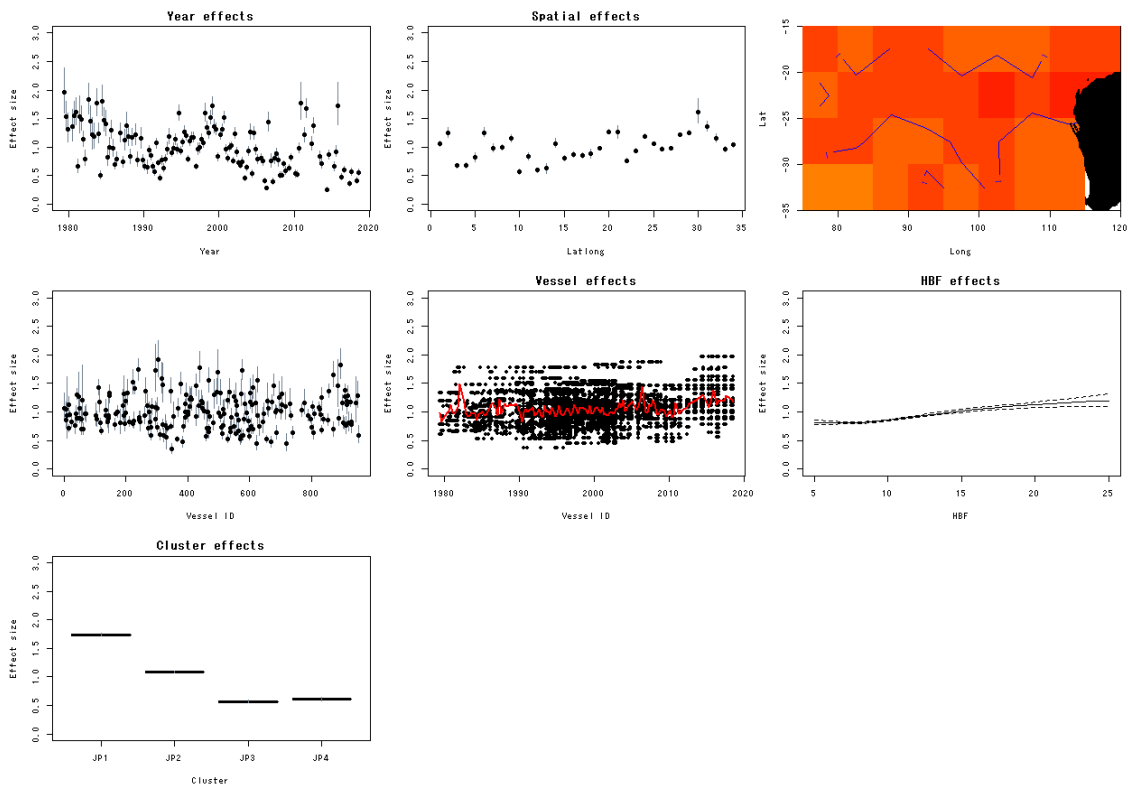
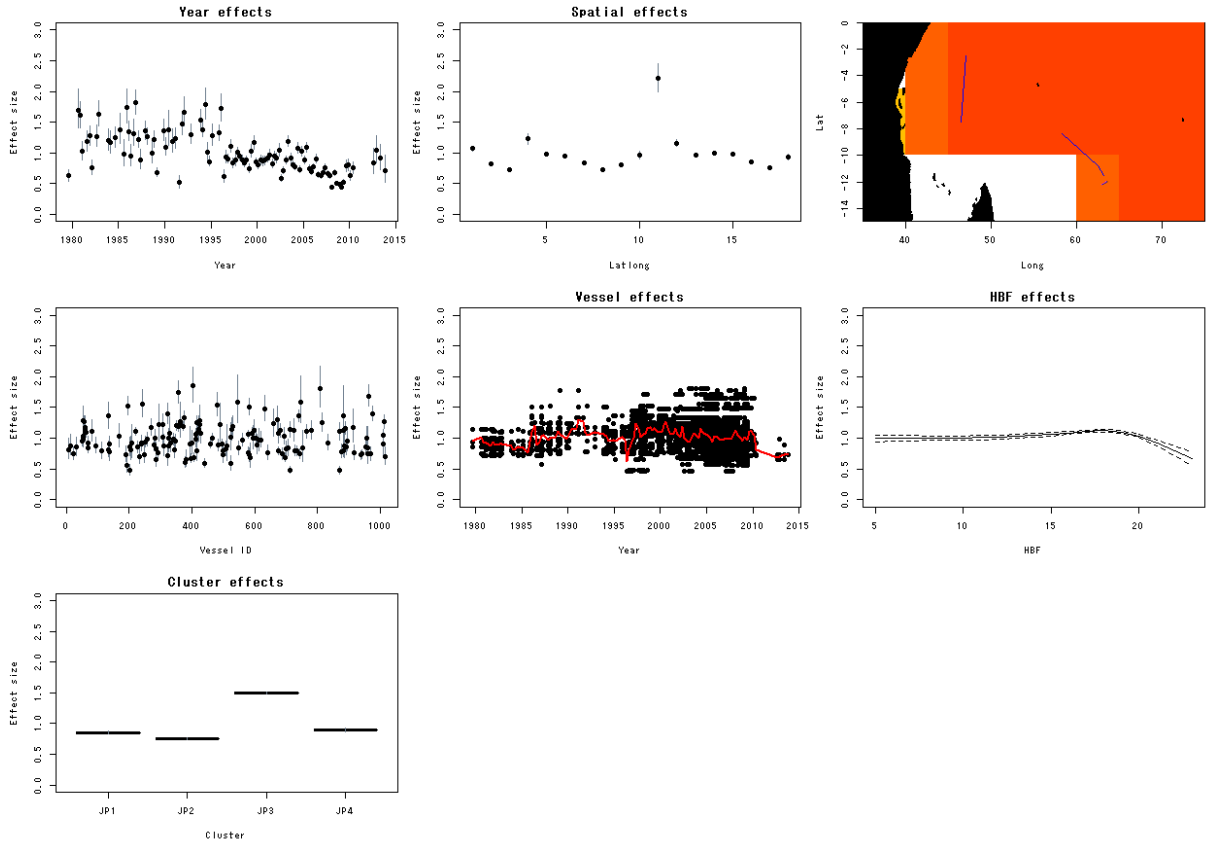


Fig. 9. Effect of each covariate for bigeye region (from 1979 onward with vessel ID). (continued)

Region 2



Region 3

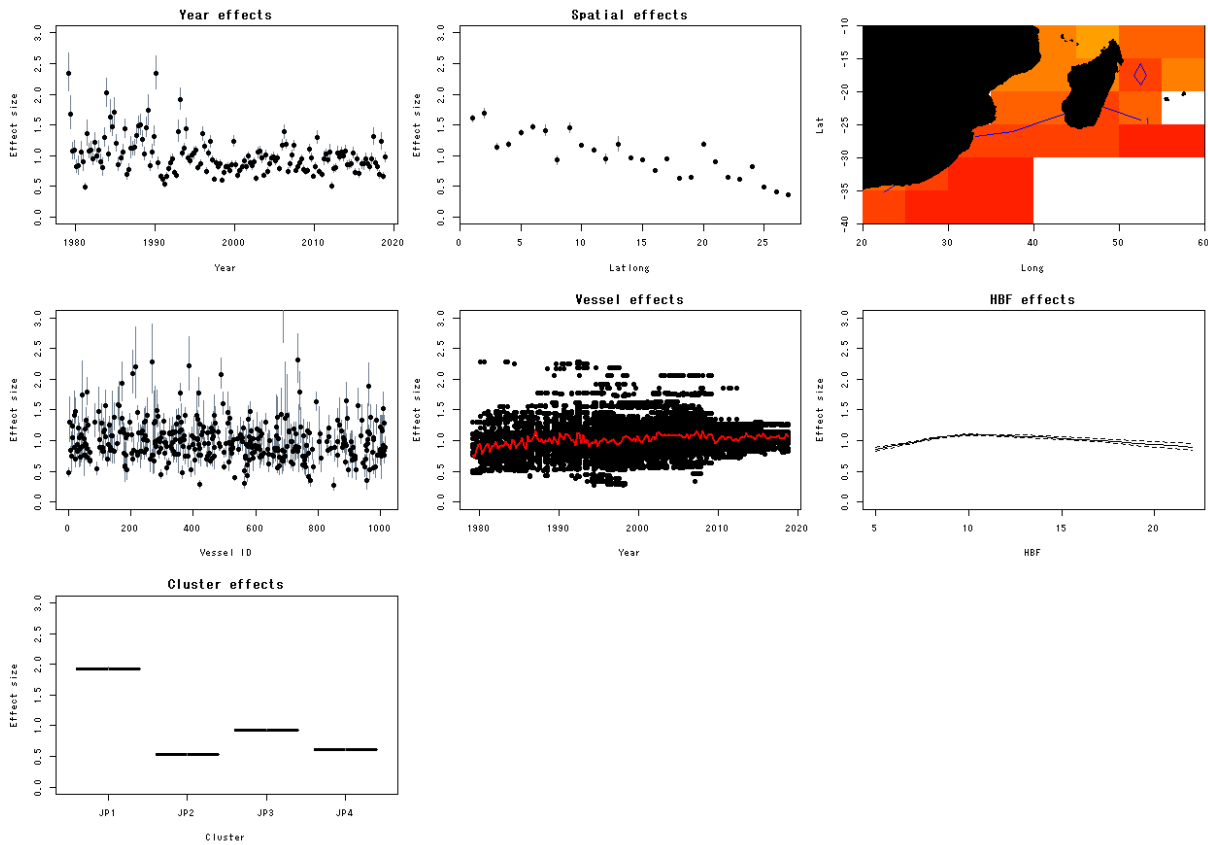
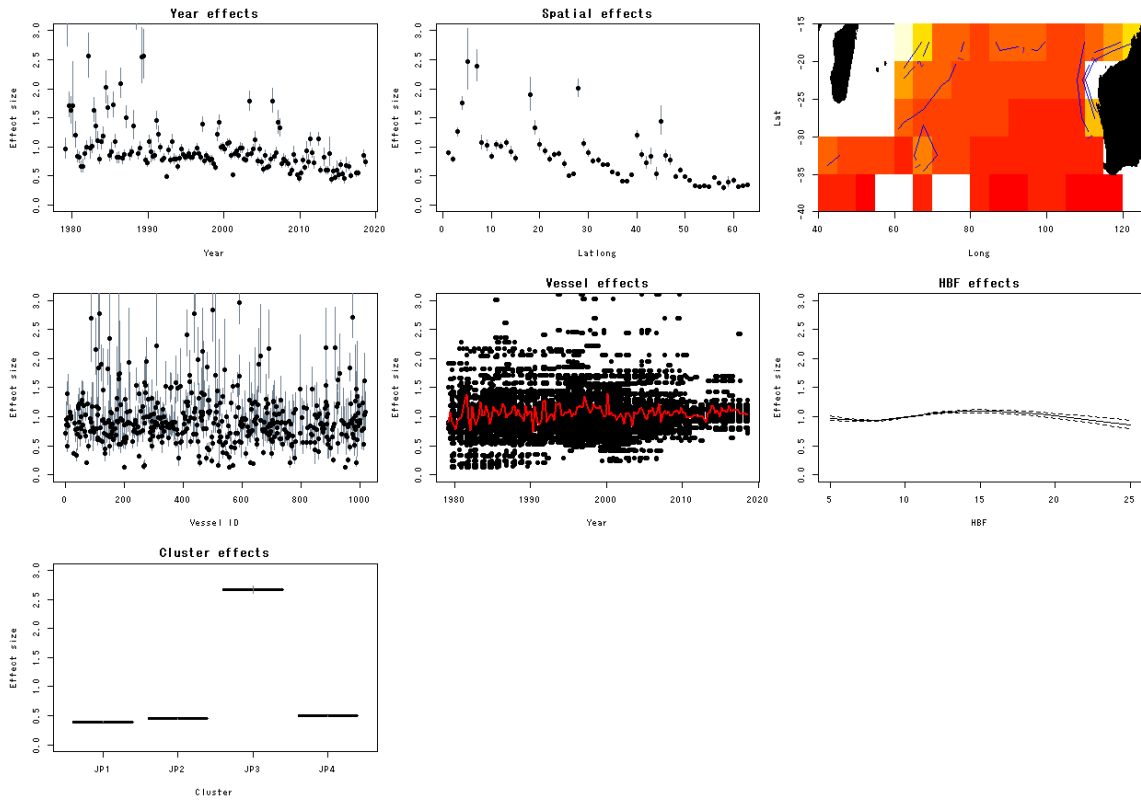


Fig. 10. Effect of each covariate for yellowfin region regY2 (from 1979 onward with vessel ID).

Region 4



Region 5

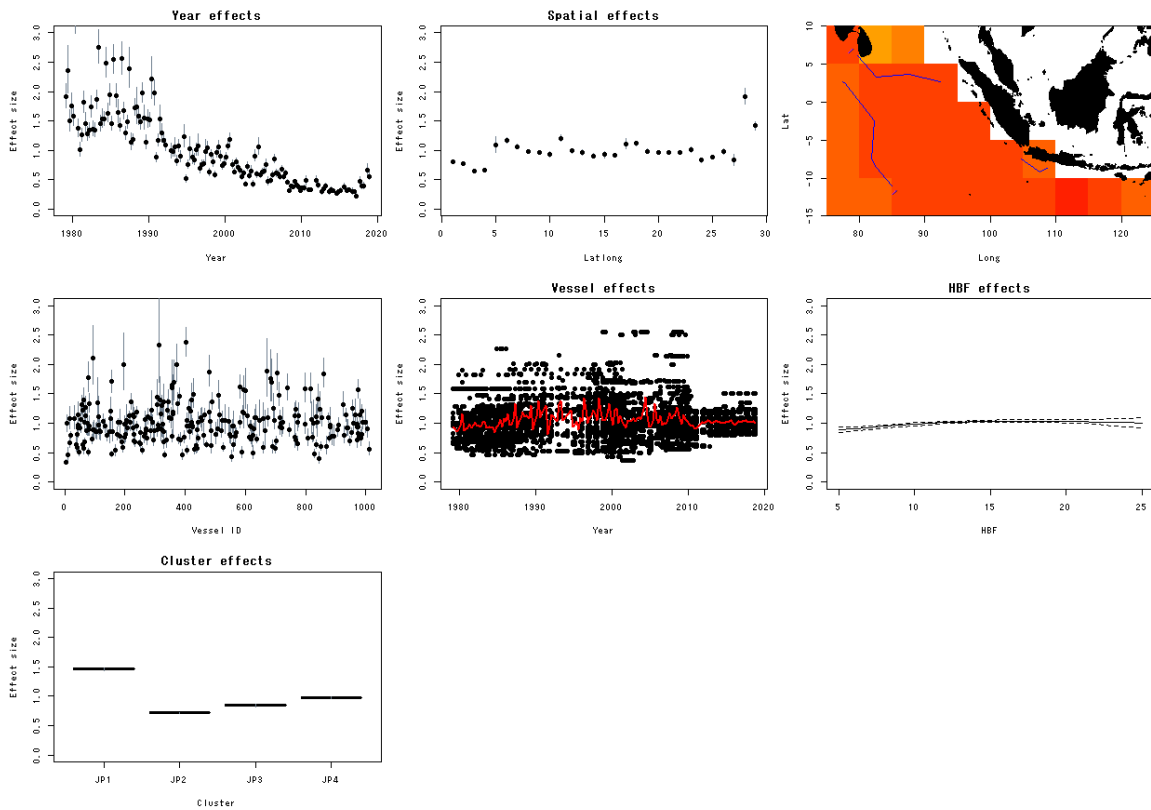


Fig. 10. Effect of each covariate for yellowfin region regY2 (from 1979 onward with vessel ID).
(continued)

Region 7

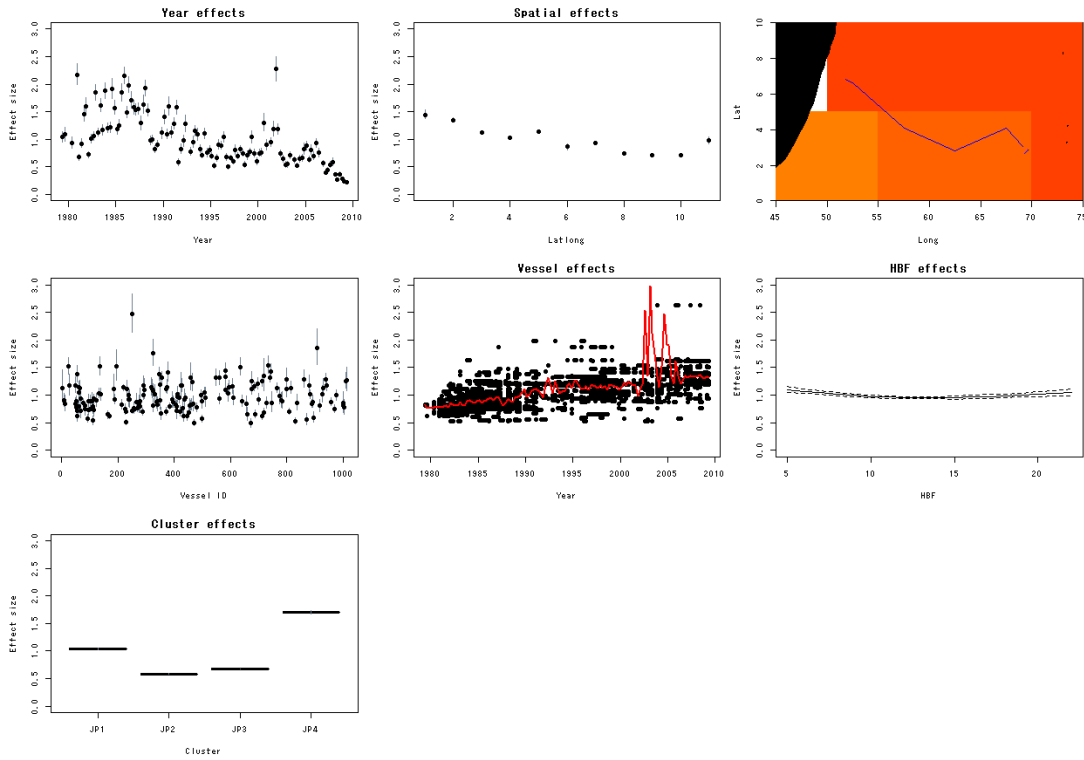


Fig. 10. Effect of each covariate for yellowfin region regY2 (from 1979 onward with vessel ID). (continued)

Region 2

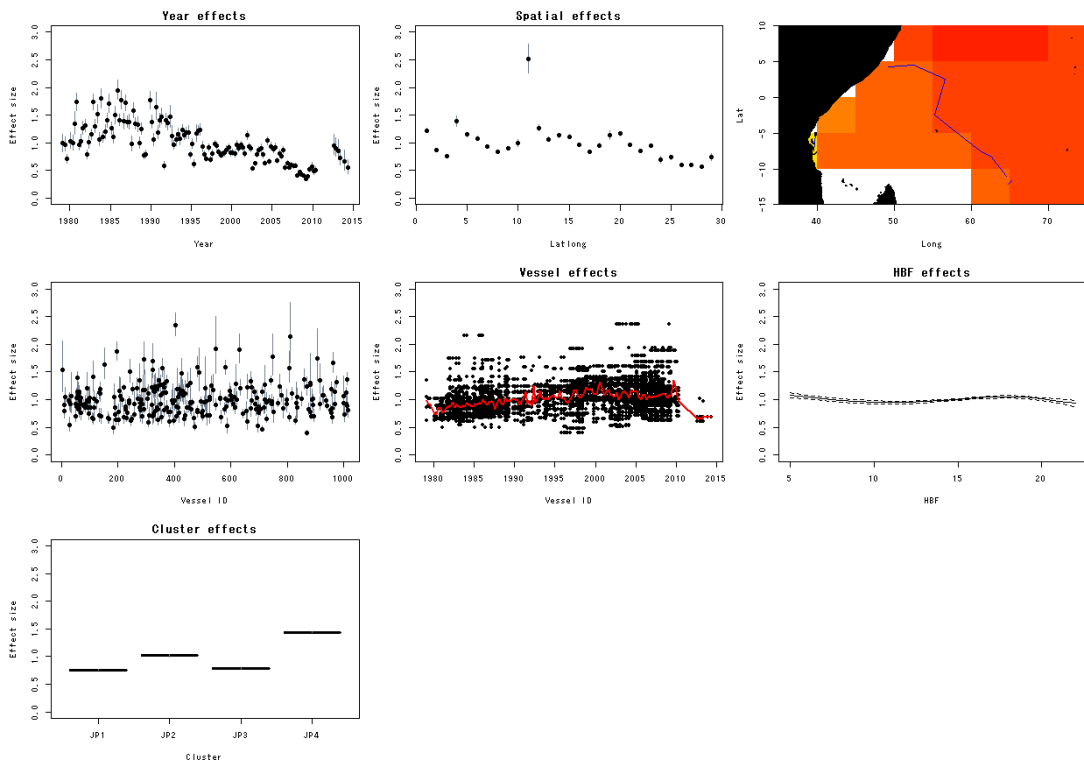
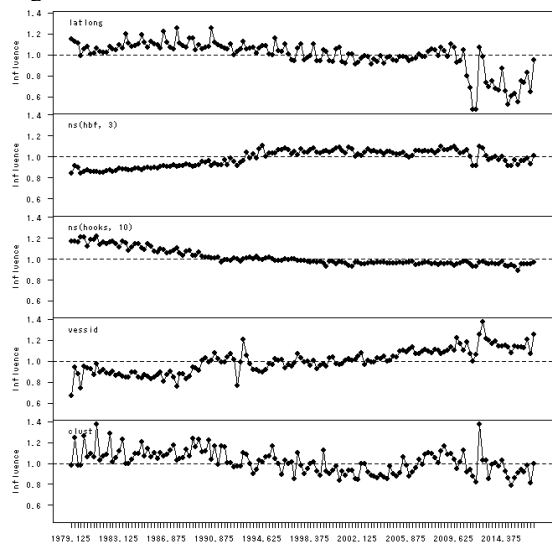
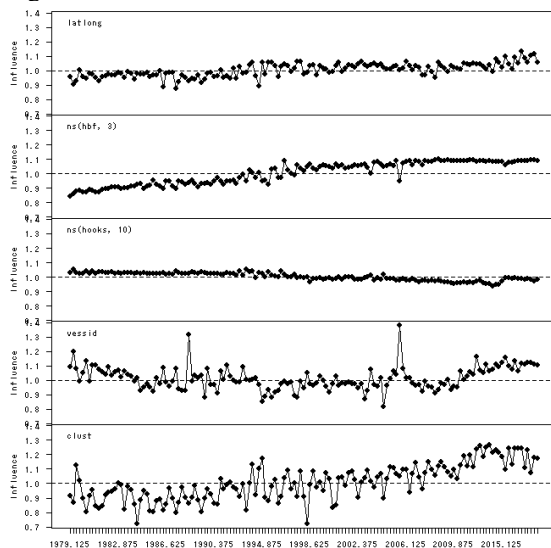


Fig. 11. Effect of each covariate for yellowfin region regY (only R2) (from 1979 onward with vessel ID).

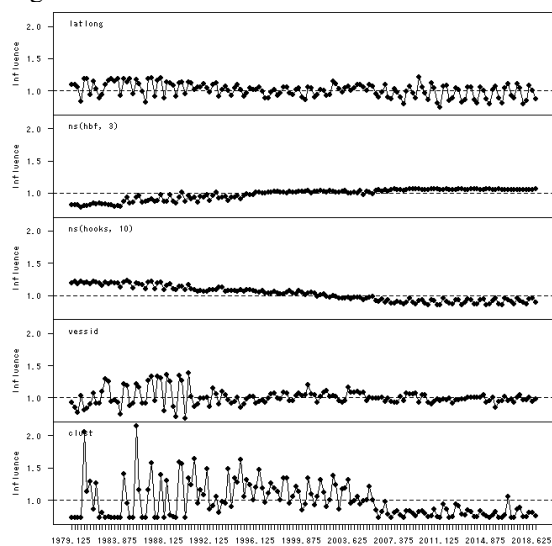
Region 1



Region 2



Region 3



Region 4

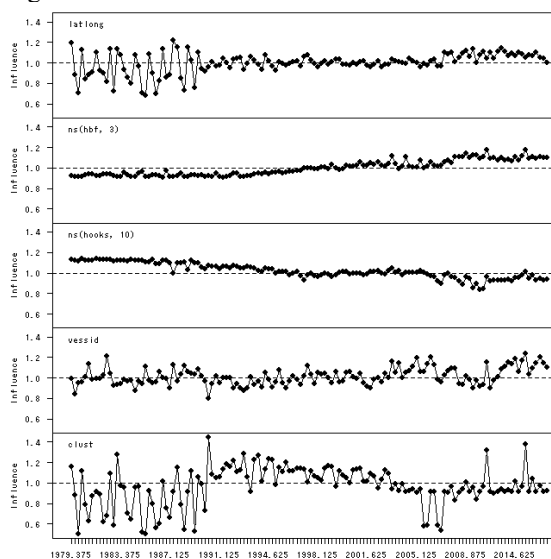
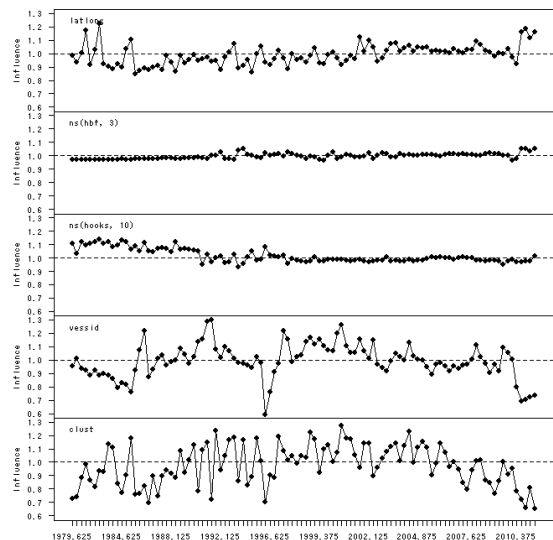
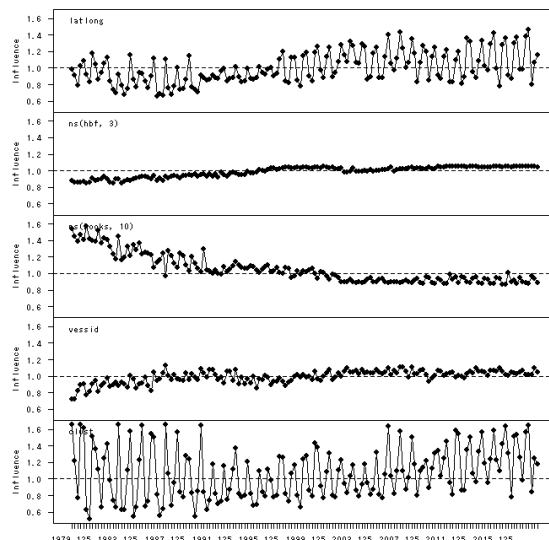


Fig. 12. Influence plot (time series effect of each covariate for bigeye region regY2, late period with vessel ID).

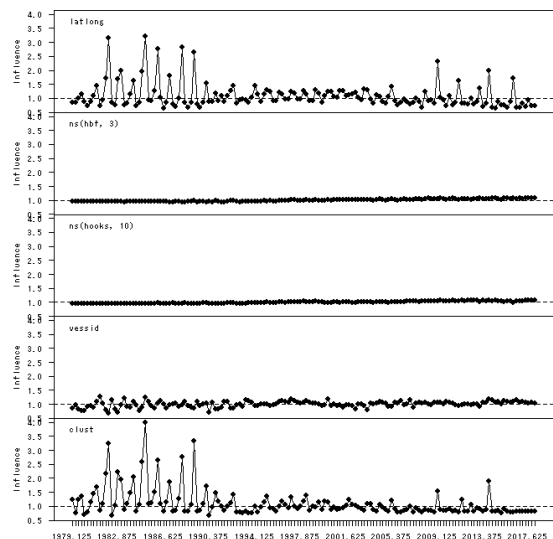
Region 2



Region 3



Region 4



Region 5

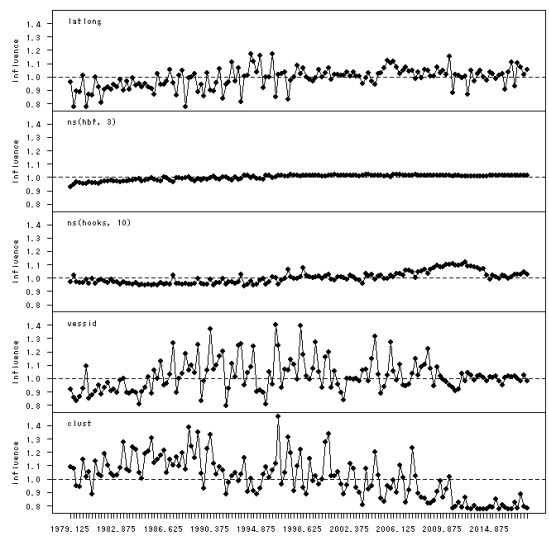


Fig. 13. Influence plot (time series effect of each covariate for yellowfin region regY2, late period with vessel ID).

Region 7

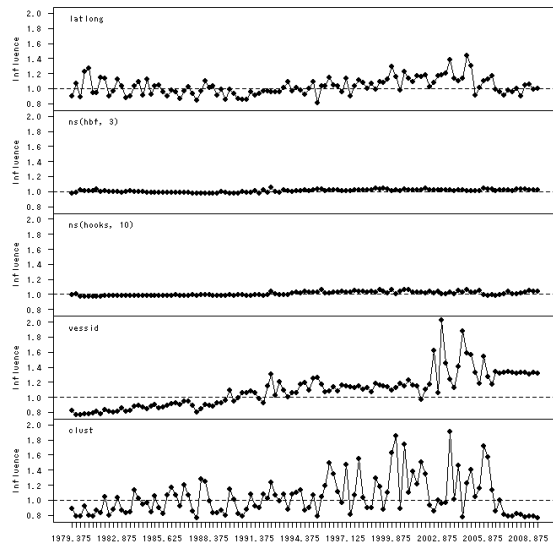


Fig. 13. Influence plot (time series effect of each covariate for yellowfin region regY2, late period with vessel ID). (continued)

Region 2

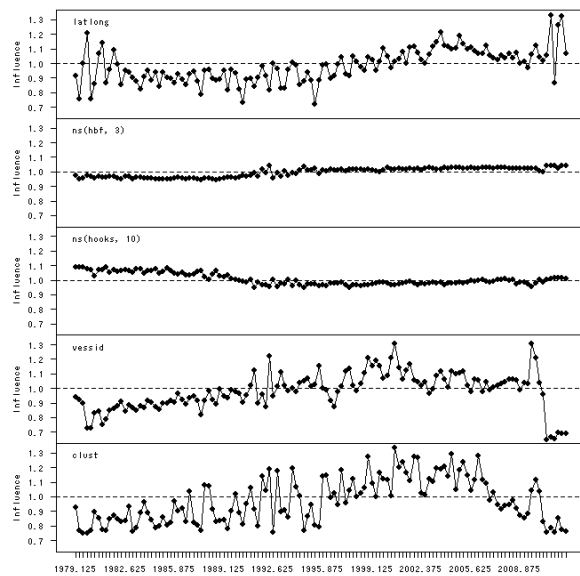


Fig. 14. Influence plot (time series effect of each covariate for yellowfin region regY (only R2), entire period with vessel ID).

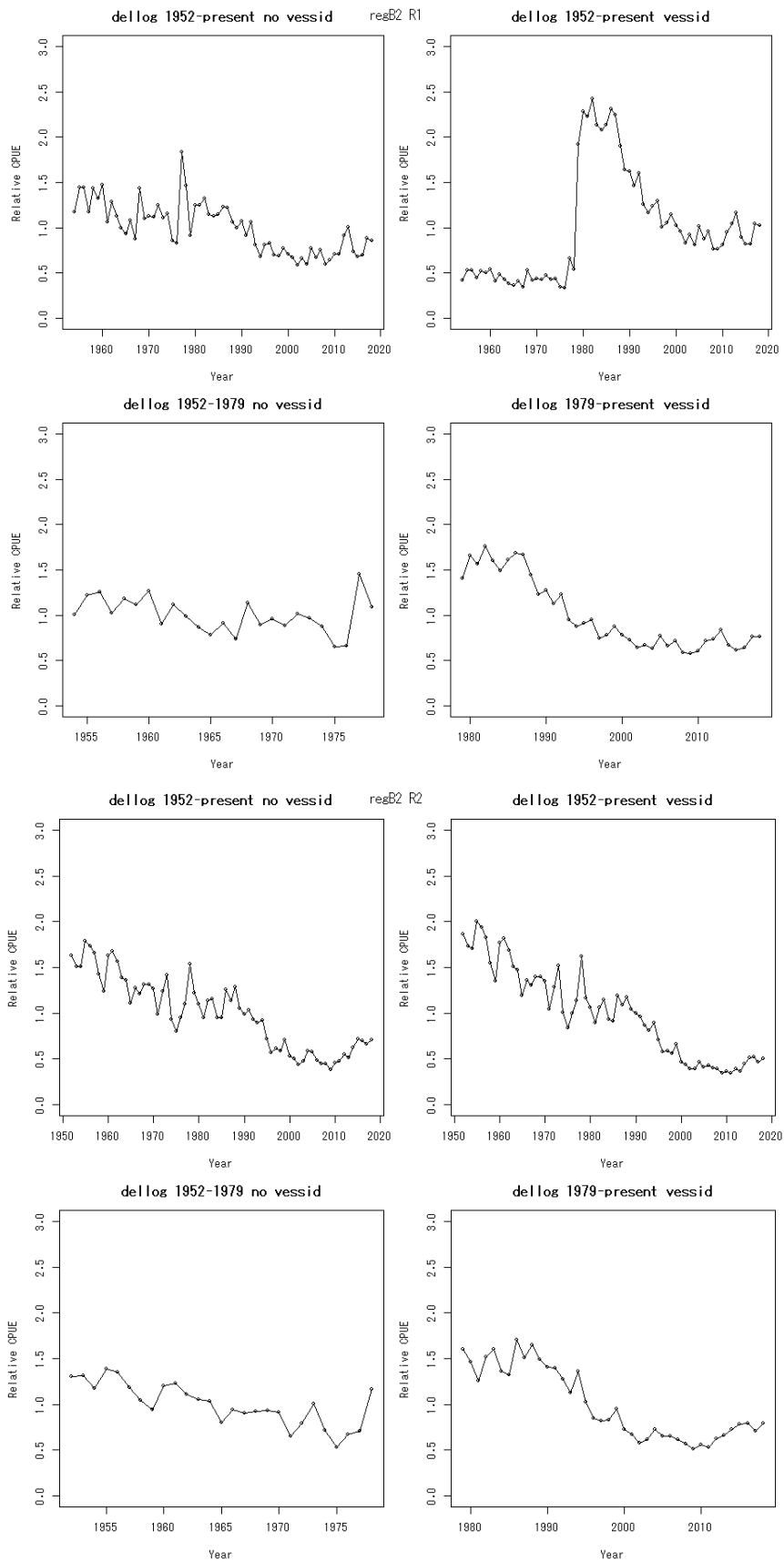


Fig. 15. Trend of annual CPUE of bigeye.

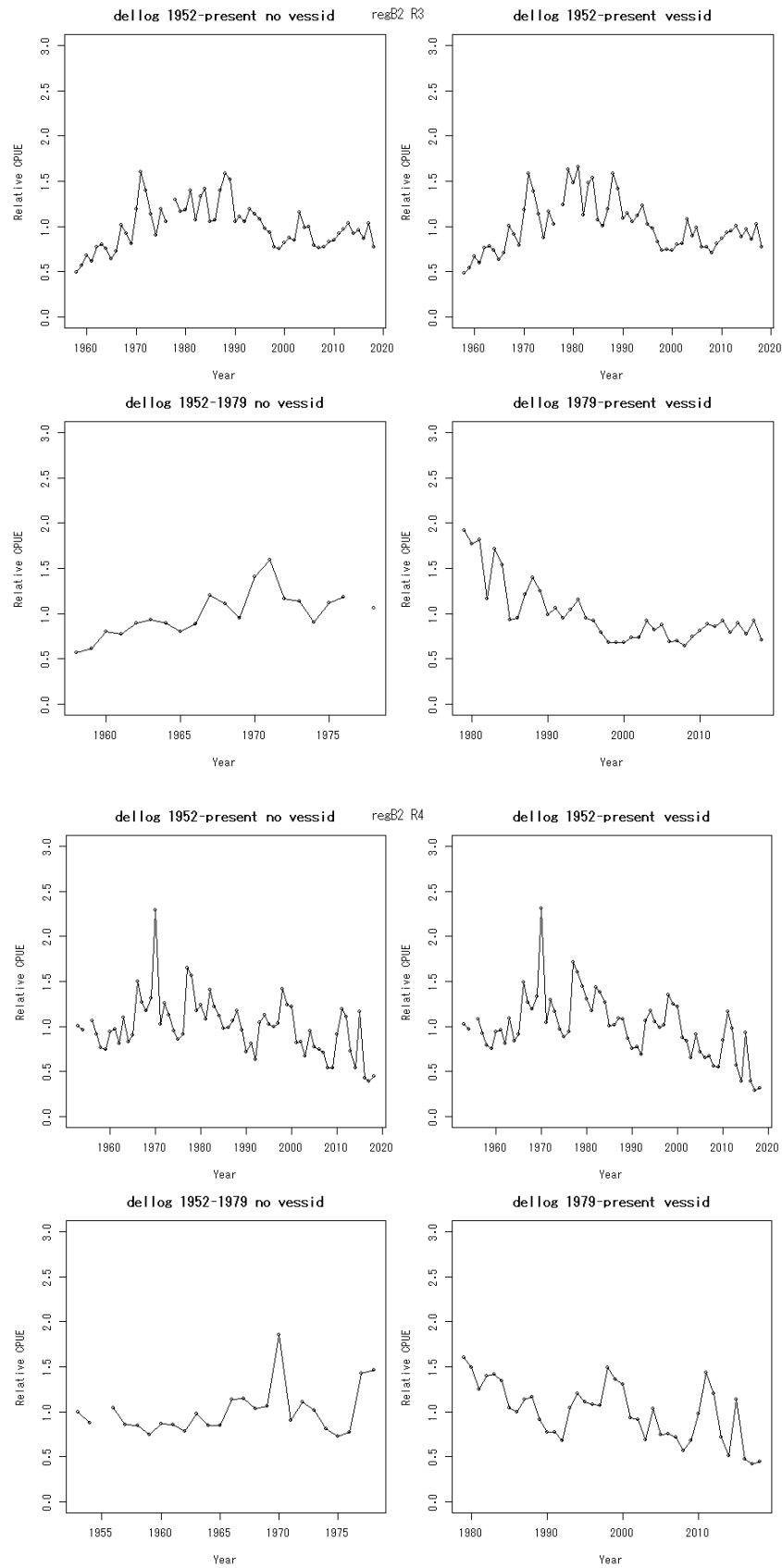


Fig. 15. Trend of annual CPUE of bigeye.(continued)

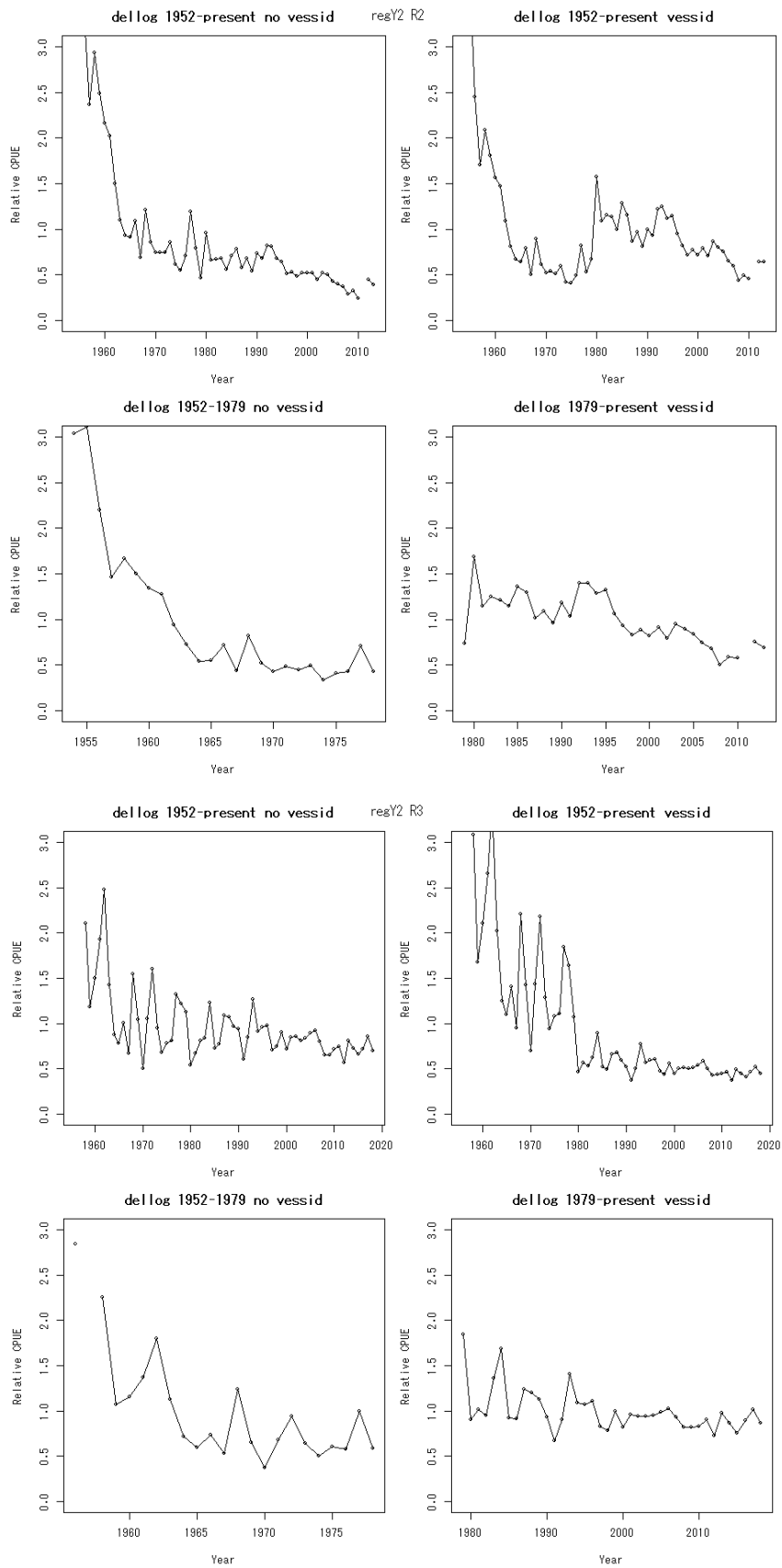


Fig. 16. Trend of annual CPUE of yellowfin region regY2.

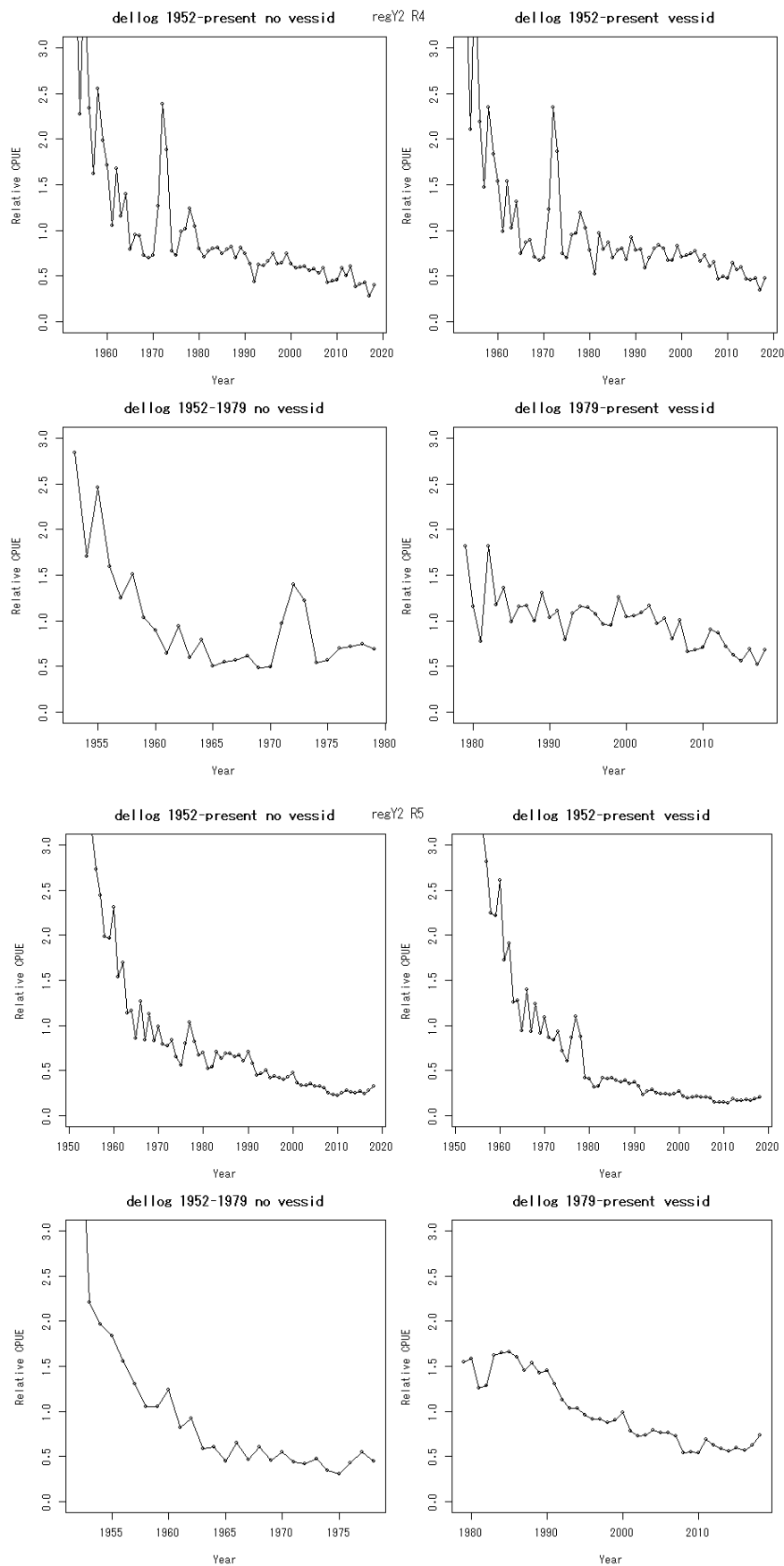


Fig. 16. Trend of annual CPUE of yellowfin region regY2.(continued)

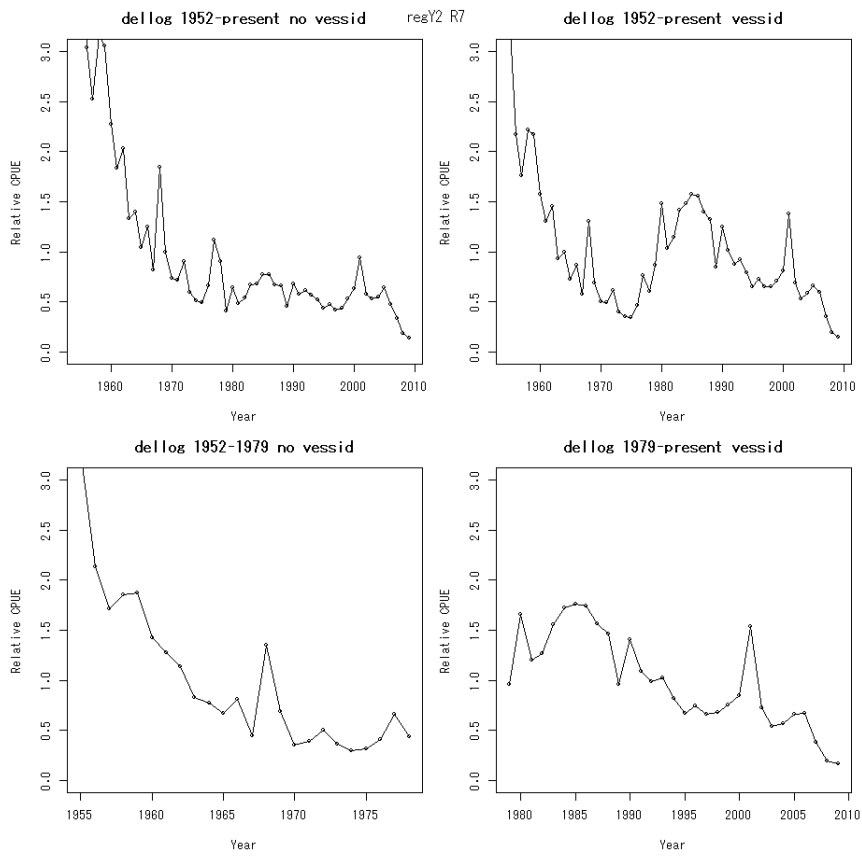


Fig. 16. Trend of annual CPUE of yellowfin region regY2.(continued)

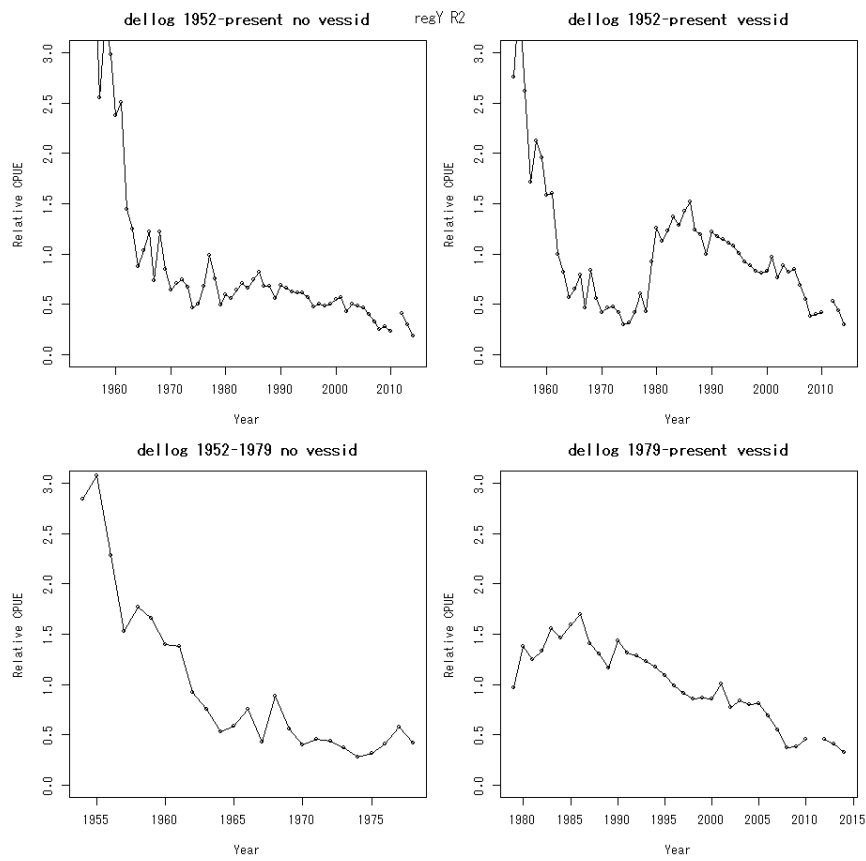
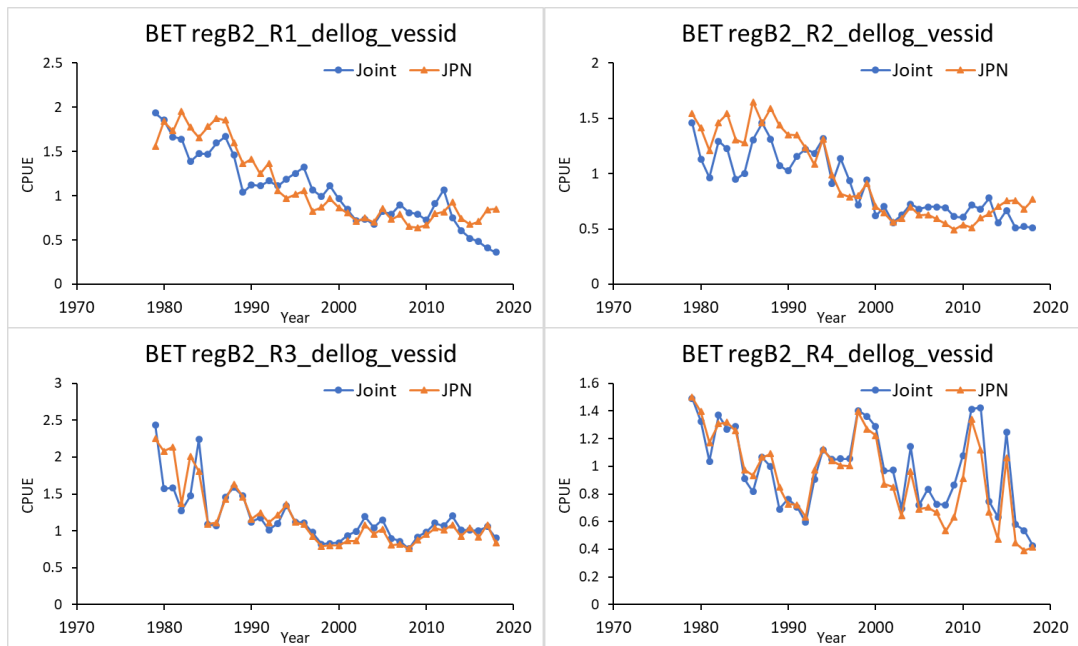


Fig. 17. Trend of annual CPUE of yellowfin region regY (only R2).

BET



YFT

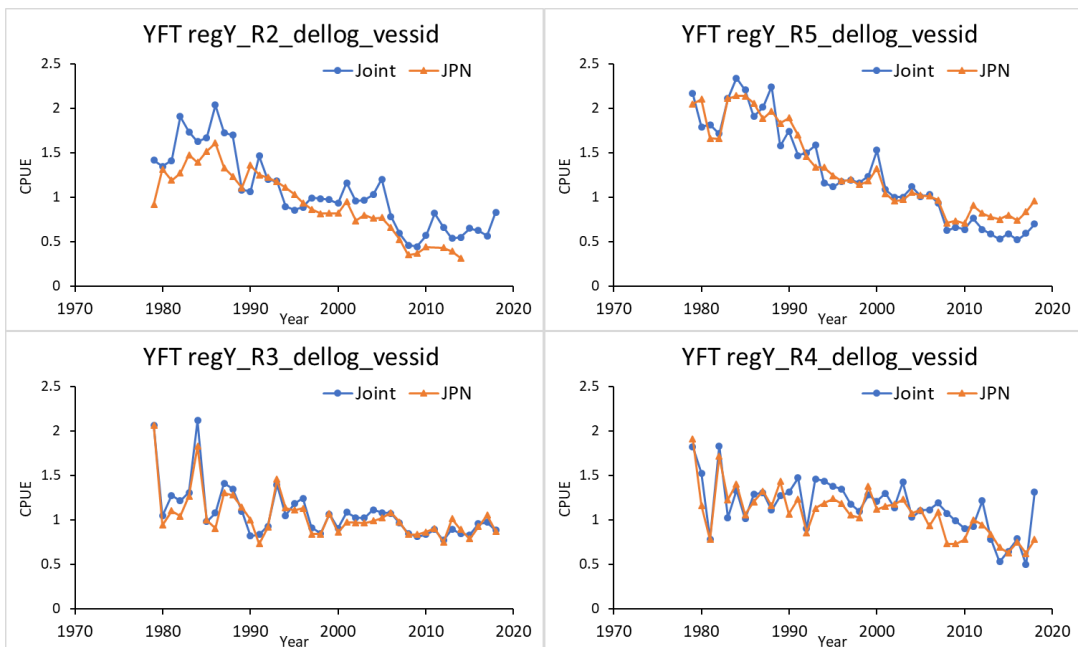


Fig. 18. Comparison of CPUE series of bigeye and yellowfin tuna with joint longline CPUE (Hoyle et al., 2019).

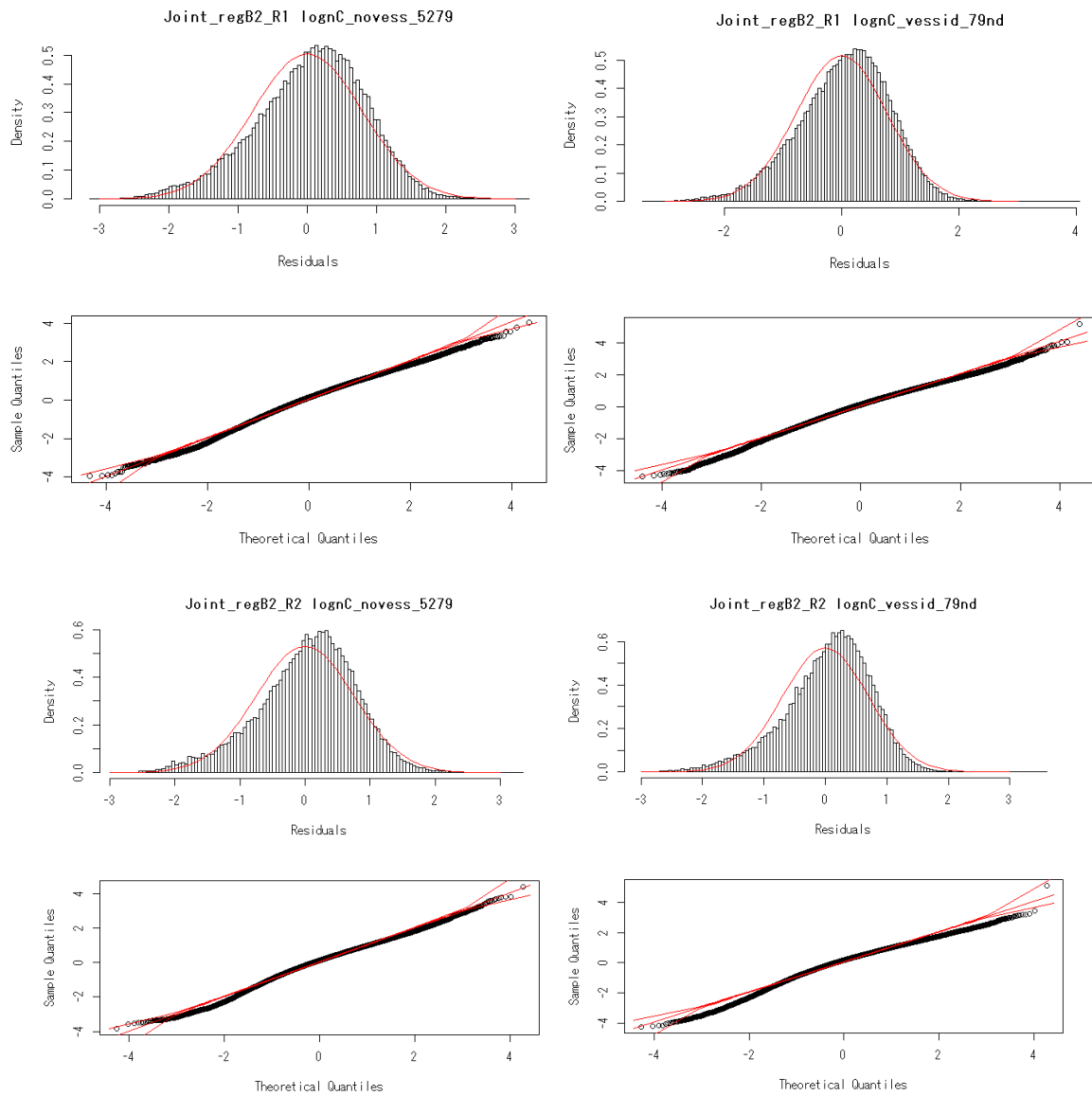


Fig. 19. Standardized residuals of CPUE standardization for bigeye.

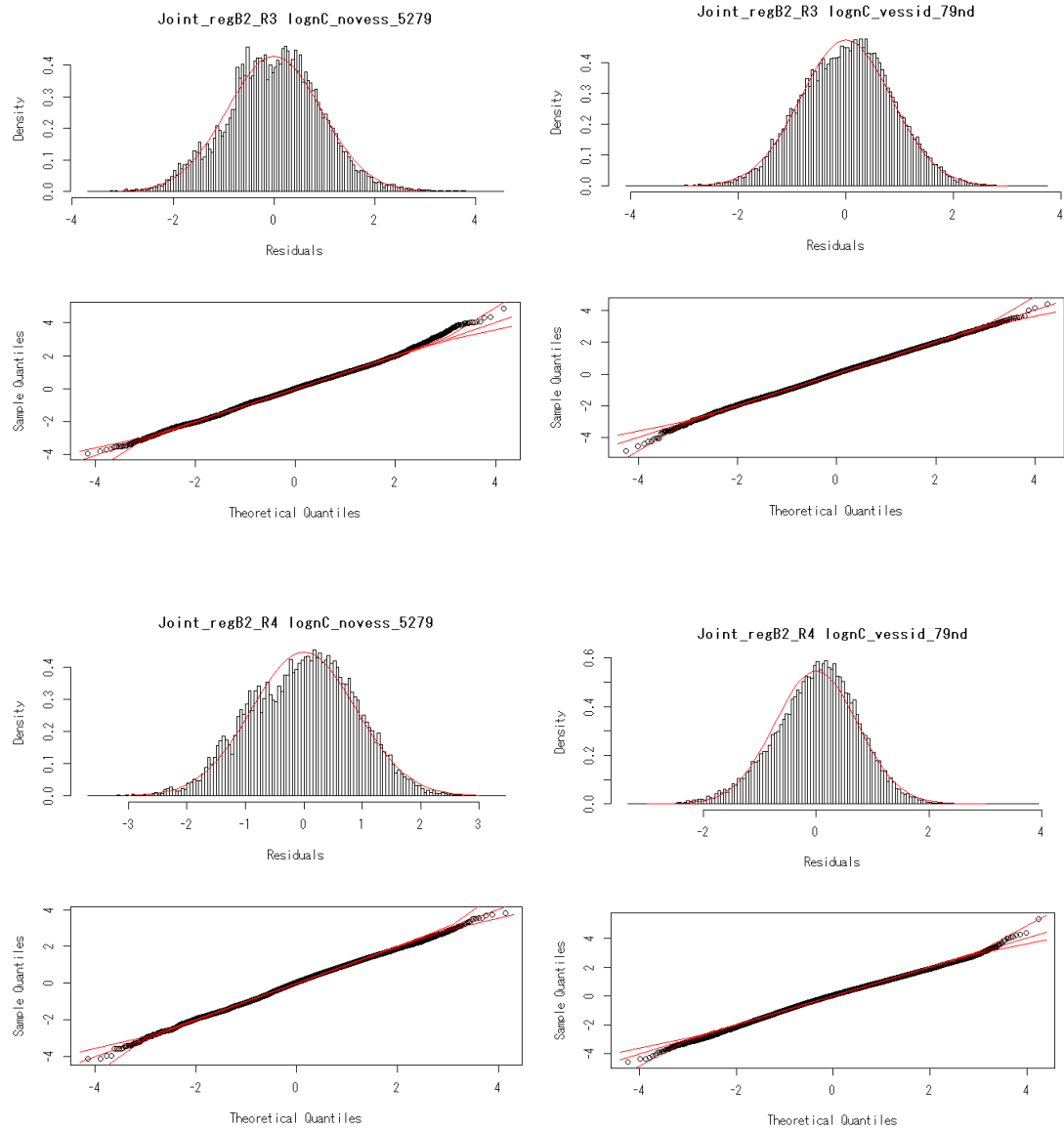


Fig. 19. Standardized residuals of CPUE standardization for bigeye. (continued)

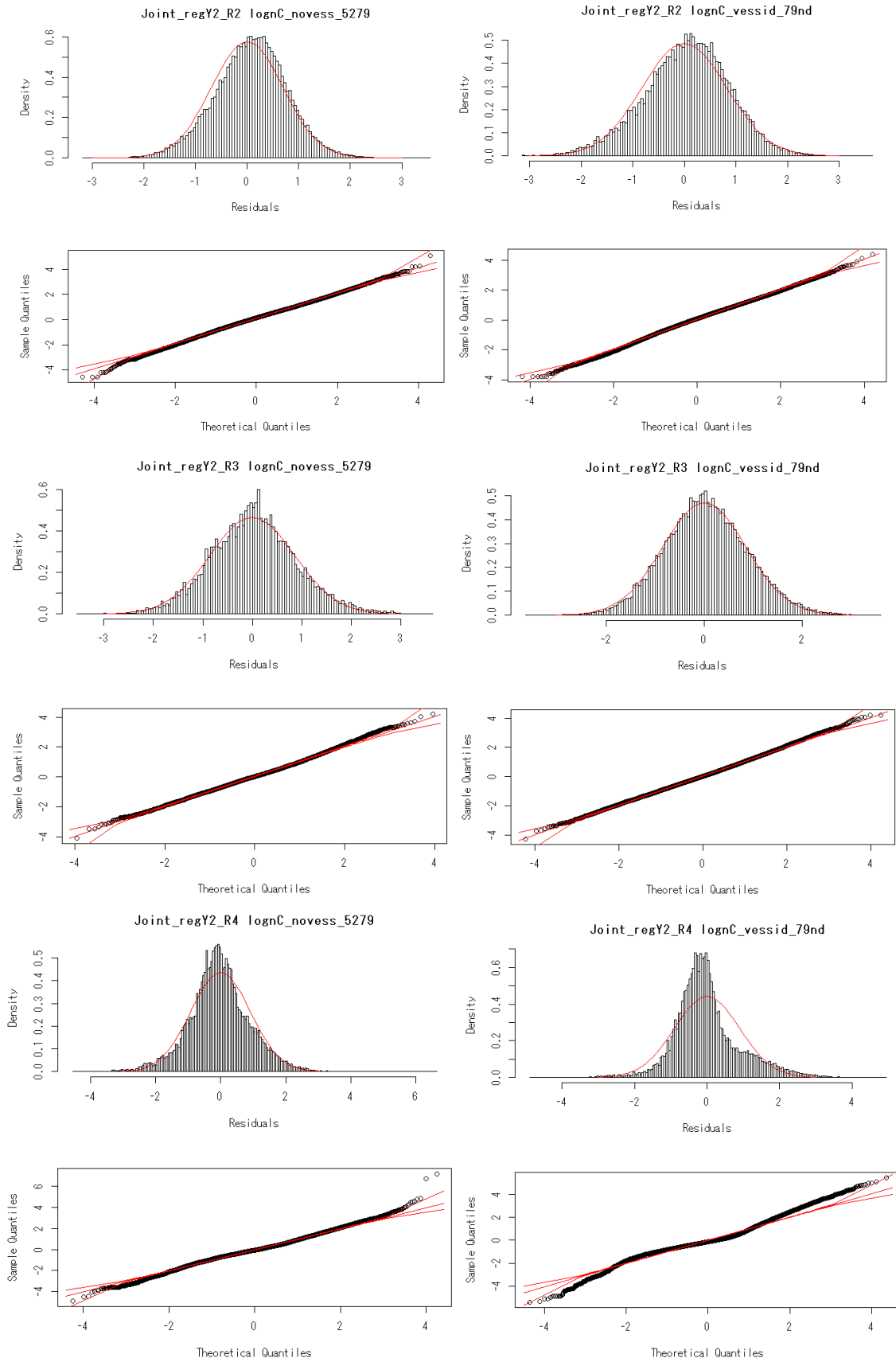


Fig. 20. Standardized residuals of CPUE standardization for yellowfin regY2.

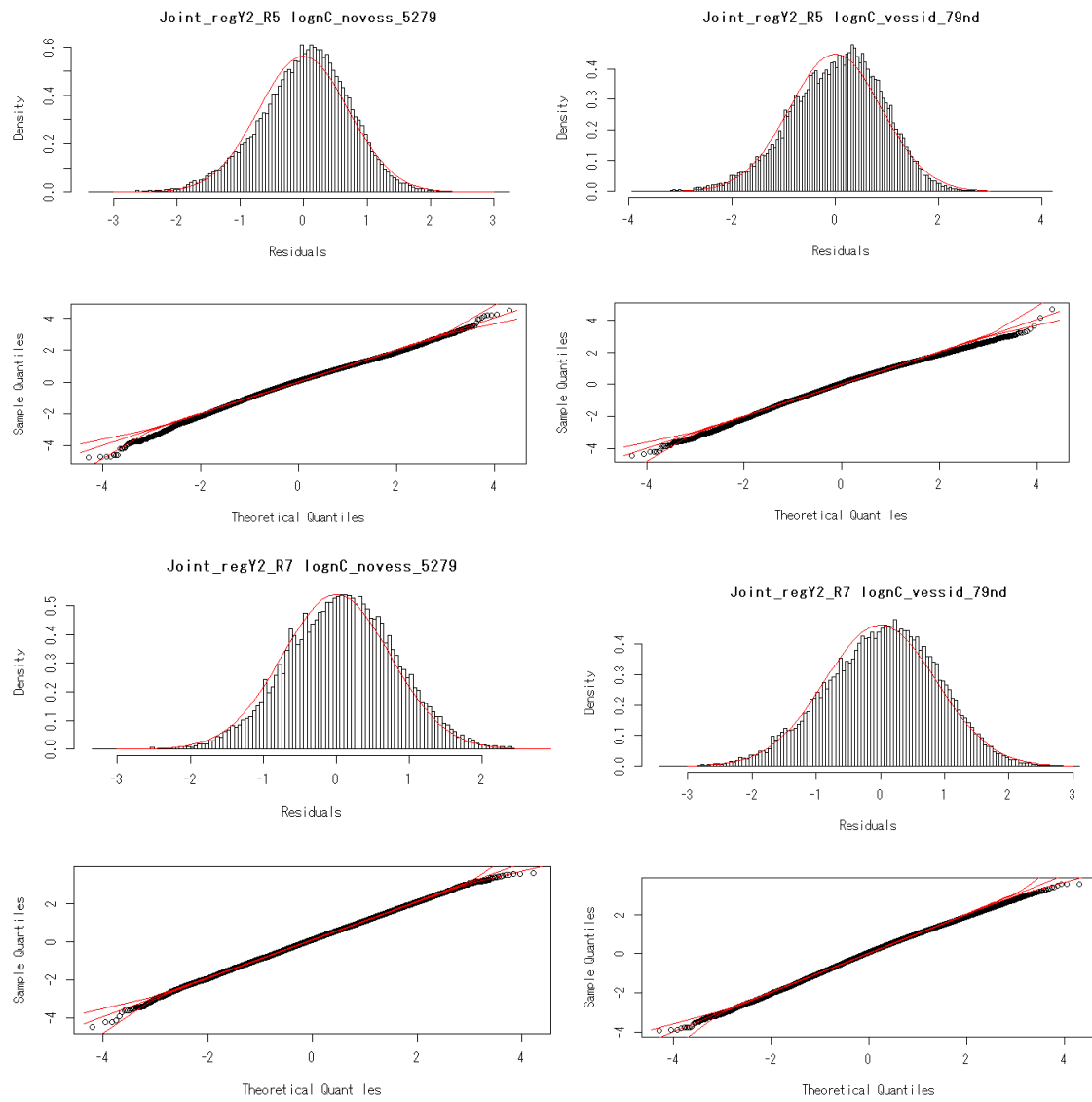


Fig. 20. Standardized residuals of CPUE standardization for yellowfin regY2. (continued)