

UPDATED STANDARDIZED CPUE FOR SWORDFISH CAUGHT BY JAPANESE LONGLINE FISHERY IN THE ATLANTIC OCEAN

SCRS/1994/141

Col.Vol.Sci.Pap. ICCAT, 44 (3) : 231-237 (1995)

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SUMMARY

The standardized CPUE of Atlantic swordfish (*Xiphias gladius*) caught by the Japanese longline fishery was updated using the Generalized Linear Model (GENMOD), including the preliminary 1993 data. The data was made available for fish ages 5 and older with information on gear configuration. Two sets of standardized CPUE series were calculated for the north and south Atlantic, respectively.

RESUME

La CPUE standardisée de l'espadon Atlantique (*Xiphias gladius*) capturé par les palangriers japonais a été actualisée avec le Modèle Linéaire Généralisé (GENMOD) comprenant les données provisoires de 1993. On a pu obtenir des données pour les poissons des âges 5 et au-delà grâce aux informations sur la configuration des engins. Deux séries de CPUE standardisées ont été calculées respectivement pour l'Atlantique Nord et l'Atlantique Sud.

RESUMEN

Usando el Modelo Lineal Generalizado (GENMOD) se actualizó la CPUE estandarizada del pez espada atlántico (*Xiphias gladius*) capturado por la pesquería japonesa de palangre, incluyendo los datos preliminares de 1993. Los datos correspondían a peces de edades 5 y más con información sobre la configuración del arte. Se calcularon dos series de CPUE estandarizada, para el Atlántico norte y sur, respectivamente.

1. Introduction

Reliable CPUE series of the major fishing countries including Japan are required for the Atlantic swordfish stock assessment. The Japanese longline data were standardized using the General Linear Model (GLM) to various factors which affect CPUE (Miyabe 1992, Nakano 1993). However, some problems on the application of GLM model were noted, i.e., the treatment of zero catch observation and the interaction with YEAR-effect. Concerning with zero catch observation, adding small constant was used for multiplicative model on the GLM but the results were different according to the constants. Furthermore, if interaction with YEAR-effect was significant, it was difficult to estimate annual trend of the CPUE. Another approach using Generalized Linear Model, as defined by Nelder and Wedderburn (1972), was used to avoid the problems by Nishida et al (1994) and Miyabe (1994). They used Poisson distribution model with over-dispersion which can treat zero catch observation directly and weighted the estimates by area if YEAR-effect was significant. Nishida et al. (1994) called GGLM (Generalized General Linear Model) and Miyabe (1994) used GENMOD (procedure name of statistical analyzing package "SAS") for such a model. In this paper, the name "GENMOD model" is used for the Generalized Linear Model to avoid confusion with GLM.

This report updates CPUE series including the data of 1993. The data was made for fish 5 years and older (5+) with information of gear configuration. CPUEs were standardized for two sets of areas, the

North and South Atlantic following the two stock hypothesis.

2. Materials and methods

The Japanese longline fishery statistics including additional information on gear configuration compiled at the National Research Institute of Far Seas Fisheries (NRIFSF) and length frequency data collected by NRIFSF were used for the analysis. The catch for 5+ fish were separated from the catch statistics using length frequency. The data are aggregated into month and 5-degree area. CPUE was calculated as catch in number of fish per 1000 hooks. Observations with less than 5,000 hooks in a month area stratum were excluded and zero catch operations were included for the analysis.

Year, quarter, area, gear configuration and CPUE of bigeye tuna were included as main effects in the model. After several preliminary runs, areas aggregated into 5 areas in each Atlantic as shown in Figure 1 where significant catches and effort were made. Areas outside of these areas were not included for analysis because of model inability to estimate parameter due to small number of observations. With regard to gear configuration, 4 to 20 hooks between floats were observed in the data base. These 17 levels were categorized to 4 levels (4-7, 8-11, 12-15 and 16-20 hooks between the floats). Considering the two stocks hypothesis for the Atlantic swordfish, CPUEs were estimated for two units, North Atlantic (north of 5°N) and South Atlantic (south of 5°N). Number of observation for the North and South Atlantic used in the analysis are shown in Table 1 and 2, respectively. Years covered from 1975 to 1993.

The model is similar multiplicative one but predicts catch itself rather than CPUE as shown below:

$$E(C) = H \cdot \exp(\mu + YR + QT + AR + BR + CLBET + \text{Inter})$$

Where $E(C)$: expectation of catch

H : number of hooks

μ : intercept

YR : effect of year

QT : effect of quarter

AR : effect of area

BR : effect of gear (number of branch line between floats)

$CLBET$: effect of bigeye tuna caught

Inter : any combination of two way interaction term.

Analysis was made through computer software, 'SAS Ver. 6.09' on the UNIX workstation. The fitting of Poisson distribution to model catch was done by GENMOD procedure of SAS/STAT statistical package (Ver. 6.09), which fits Generalized Linear Model. Under this procedure, many other distributions of exponential family such as normal, binomial, gamma and inverse Gaussian can be included in a model very easily. Parameters are obtained by maximum likelihood estimation with the algorithm of a ridge-stabilized Newton-Raphson method (SAS 1993).

In most case, overdispersion was observed, then DSCALE option which estimates dispersion parameter was included. All statistics were adjusted according to the dispersion parameter appropriately.

3. Results and Discussion

The final model and factors chosen for North and South Atlantic were as follows:

$$\text{North Atlantic: } YR + QT + AR + BR + CLBET + YR * QT + QT * AR$$

$$\text{South Atlantic: } YR + QT + AR + BR + CLBET + YR * QT.$$

The goodness of fit is shown in Table 3. Deviance (twice the difference between the maximum achievable log likelihood and the log likelihood at the maximum likelihood estimates) is much larger than the degree of freedom. Therefore, it might be possible to improve fitting of the model. The distributions of residuals for each model are shown in Figure 2. The distribution pattern of residual for North and South Atlantic appears similar with a slight skewness toward negative direction. The F statistics of effects used for both models are statistically significant (Table 4).

Since interaction term including Year became significant, annual abundance indices were calculated with weighting by Area. The equation of area-weighted abundance indices is as follows:

$$E(\text{CPUE}_y) = \sum q \sum \text{area} (P(\text{CPUE}) \cdot \text{Area index})$$

where $E(\text{CPUE}_y)$: area weighted annual abundance index,

$P(\text{CPUE})$: predicted CPUE by the model,

Area index : index of area.

The scaled annual index (calculated the value of 1975 as 1.0) is shown in Table 5. CPUE trends obtained by the GENMOD were shown in Figure 3 with the results of General Linear Model (GLM).

Both estimates from GENMOD and GLM model show similar trends, although the results of GENMOD indicate smooth and small fluctuation.

The result of updated CPUE indicates downward trend until 1983, then shows relatively stable state with slight decline in the North Atlantic. The CPUE trend for South Atlantic shows stable states until 1987 with fluctuation, then decline about one third to 1992 and significantly increase in 1993. The increase of CPUE in 1993 is due to the change of length frequency in the South Atlantic. Preliminary Japanese swordfish length frequency data shows the increase of mean length in the area (Uosaki and Uozumi 1994).

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Table 1. Number of observations used in GENMOD for the North Atlantic.

TABLE OF YR BY QT					
YR	QT				Total
Frequency	1	2	3	4	
75	78	75	76	34	263
76	39	62	64	32	197
77	40	47	36	41	164
78	55	71	50	36	212
79	64	52	42	37	195
80	51	72	112	111	346
81	94	109	109	160	472
82	140	149	117	183	589
83	95	55	58	54	262
84	93	104	57	63	317
85	91	114	97	178	480
86	110	55	58	101	324
87	76	31	83	76	266
88	98	44	78	124	344
89	165	133	159	222	679
90	173	97	111	133	514
91	136	83	134	119	472
92	161	70	87	41	359
93	189	96	107	80	472
Total	1948	1519	1635	1825	6927

TABLE OF YR BY AREA						
YR	AREA					Total
Frequency	1	2	3	4	5	
75	31	102	48	39	43	263
76	50	67	26	22	32	197
77	29	68	20	25	22	164
78	47	61	30	44	30	212
79	81	57	11	42	4	195
80	114	43	59	72	58	346
81	194	57	53	83	85	472
82	111	59	70	196	153	589
83	72	60	36	53	41	262
84	66	76	28	71	76	317
85	111	37	70	122	140	480
86	102	44	40	44	94	324
87	111	39	44	19	53	266
88	113	38	50	37	106	344
89	158	58	99	184	180	679
90	128	86	81	72	147	514
91	140	87	59	82	104	472
92	79	81	51	38	110	359
93	85	83	72	79	153	472
Total	1822	1203	947	1324	1631	6927

Table 1. Number of observations used in GENMOD for the North Atlantic, continued.

TABLE OF YR BY BR					
YR	BR				Total
Frequency	1	2	3	4	Total
75	263	0	0	0	263
76	181	16	0	0	197
77	163	1	0	0	164
78	164	48	0	0	212
79	146	32	17	0	195
80	210	132	4	0	346
81	215	237	20	0	472
82	176	342	71	0	589
83	104	150	7	1	262
84	122	175	20	0	317
85	109	262	109	0	480
86	117	142	65	0	324
87	85	127	52	2	266
88	92	150	102	0	344
89	156	160	309	54	679
90	164	102	200	48	514
91	143	98	115	116	472
92	121	57	107	74	359
93	135	50	168	119	472
Total	2866	2281	1366	414	6927

TABLE OF YR BY CLBET				
YR	CLBET			Total
Frequency	1	2	3	Total
75	161	53	49	263
76	116	44	37	197
77	68	27	69	164
78	69	59	84	212
79	84	39	72	195
80	92	86	168	346
81	208	136	128	472
82	162	199	228	589
83	117	61	84	262
84	135	68	114	317
85	142	141	197	480
86	142	72	110	324
87	124	59	83	266
88	144	60	140	344
89	272	161	246	679
90	247	159	108	514
91	205	120	147	472
92	165	86	108	359
93	201	145	126	472
Total	2854	1775	2298	6927

Table 2. Number of observations used in GENMOD for the South Atlantic.

TABLE OF YR BY QT					
YR	QT				Total
Frequency	1	2	3	4	Total
75	15	3	39	38	95
76	7	0	10	24	41
77	4	5	25	25	59
78	5	1	34	16	56
79	1	4	48	75	128
80	53	42	115	108	318
81	66	30	66	105	267
82	126	55	76	141	398
83	91	5	21	153	270
84	144	17	139	163	463
85	132	68	187	191	578
86	170	35	80	107	392
87	96	56	45	96	293
88	179	122	159	271	731
89	227	170	221	272	890
90	254	217	244	245	960
91	213	176	193	216	798
92	217	80	106	170	573
93	226	184	176	164	750
Total	2226	1270	1984	2580	8060

TABLE OF YR BY AREA						
YR	AREA					Total
Frequency	1	2	3	4	5	Total
75	1	8	1	59	26	95
76	0	0	0	29	12	41
77	0	1	0	44	14	59
78	2	0	0	40	14	56
79	0	24	0	85	19	128
80	2	63	0	220	33	318
81	12	25	23	159	48	267
82	30	57	52	214	45	398
83	19	68	47	123	13	270
84	42	128	56	206	31	463
85	111	175	109	163	20	578
86	57	41	112	150	32	392
87	43	60	72	106	12	293
88	154	144	158	213	62	731
89	245	137	219	227	62	890
90	244	205	271	196	44	960
91	185	85	243	218	67	798
92	136	44	203	130	60	573
93	189	103	153	235	70	750
Total	1472	1368	1719	2817	684	8060

Table 2. Number of observations used in GENMOD for the South Atlantic, continued.

TABLE OF YR BY BR

YR	BR				Total
Frequency	1	2	3	4	
75	95	0	0	0	95
76	41	0	0	0	41
77	59	0	0	0	59
78	56	0	0	0	56
79	111	17	0	0	128
80	128	154	36	0	318
81	80	158	26	3	267
82	90	250	50	8	398
83	55	171	44	0	270
84	53	254	156	0	463
85	36	229	313	0	578
86	40	129	217	6	392
87	13	69	172	39	293
88	18	120	512	81	731
89	28	130	549	183	890
90	68	115	425	352	960
91	28	98	271	401	798
92	52	66	158	297	573
93	5	72	242	431	750
Total	1056	2032	3171	1801	8060

TABLE OF YR BY CLBET

YR	CLBET			Total
Frequency	1	2	3	
75	9	40	46	95
76	2	14	25	41
77	4	11	44	59
78	3	17	36	56
79	11	43	74	128
80	49	129	140	318
81	55	111	101	267
82	86	152	160	398
83	41	129	100	270
84	51	208	204	463
85	78	227	273	578
86	41	108	243	392
87	14	46	233	293
88	88	198	445	731
89	179	348	363	890
90	204	490	266	960
91	228	372	198	798
92	132	261	180	573
93	174	380	196	750
Total	1449	3284	3327	8060

Table 3. Criteria for assessing goodness of fit.

North Atlantic

Criterion	DF	Value	Value/DF
Deviance	6797	33892.1603	4.9863
Scaled Deviance	6797	6797.0000	1.0000
Pearson Chi-Square	6797	38986.5373	5.7358
Scaled Pearson X2	6797	7818.6664	1.1503
Log Likelihood	.	40352.9680	.

South Atlantic

Criterion	DF	Value	Value/DF
Deviance	7976	77713.4631	9.7434
Scaled Deviance	7976	7976.0000	1.0000
Pearson Chi-Square	7976	88428.1301	11.0868
Scaled Pearson X2	7976	9075.6831	1.1379
Log Likelihood	.	99508.1874	.

Table 4. Likelihood ratio statistics for type 3 analysis.

North Atlantic

Source	NDF	DDF	F	Pr>F	ChiSquare	Pr>Chi
YR	18	6797	96.7537	.0000	1741.5662	0.0000
QT	3	6797	5.4135	.0010	16.2404	0.0010
AR	12	6797	31.0398	.0000	372.4782	0.0000
BR	3	6797	166.7766	.0000	500.3299	0.0000
CLBET	3	6797	26.7087	.0000	80.1261	0.0000
YR*QT	54	6797	24.9707	.0000	1348.4163	0.0000
QT*AR	36	6797	26.1923	.0000	942.9239	0.0000

South Atlantic

Source	NDF	DDF	F	Pr>F	ChiSquare	Pr>Chi
YR	18	7976	65.7861	.0000	1184.1489	0.0000
QT	3	7976	16.7324	.0000	50.1972	0.0000
AREA	4	7976	453.6201	.0000	1814.4803	0.0000
BR	3	7976	102.8832	.0000	308.6497	0.0000
CLBET	2	7976	83.0761	.0000	166.1521	0.0000
YR*QT	53	7976	30.2476	.0000	1603.1245	0.0000

Table 5. Scaled abundance indices.

Year	North	South
75	1.0000	1.0000
76	0.7537	0.7079
77	0.5604	1.1173
78	1.1259	1.2491
79	0.4734	0.7037
80	0.6138	1.2745
81	0.4524	1.3730
82	0.5428	0.8724
83	0.3353	0.8415
84	0.4011	1.1134
85	0.3273	0.8453
86	0.3427	1.0738
87	0.3002	0.9482
88	0.3467	0.6963
89	0.2684	0.5515
90	0.2707	0.5956
91	0.3826	0.4932
92	0.2687	0.3636
93	0.2349	0.6888

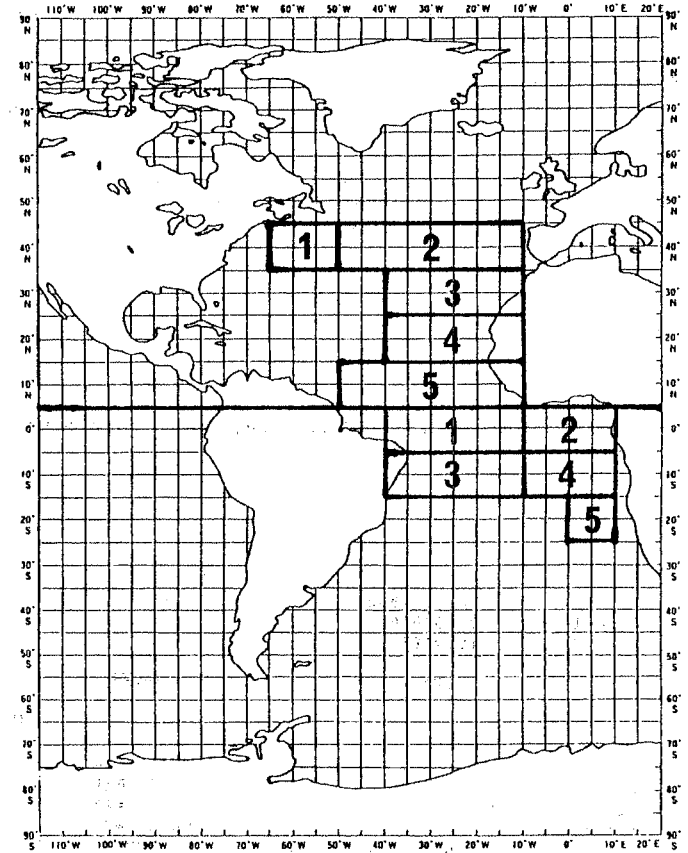
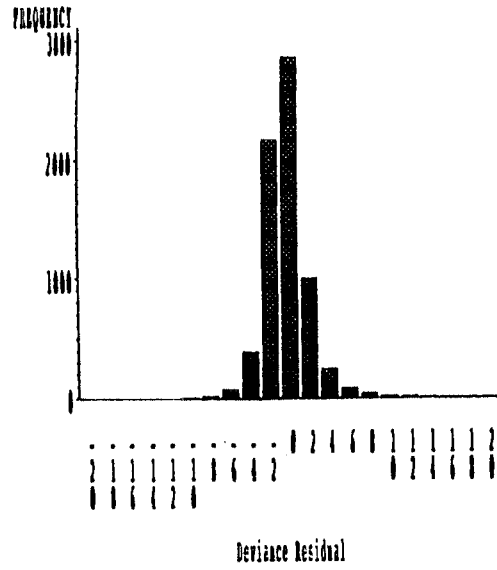


Fig. 1. Area division used for the analysis to swordfish of the North and South Atlantic

Genmod, North Atlantic Swordfish, 1975-1993, BR



Genmod, South Atlantic Swordfish, 1975-1993, BR

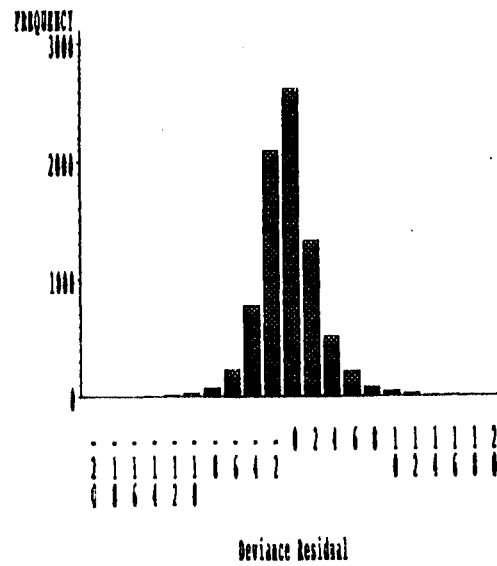


Fig. 2. Residual distributions of the model for the North and South Atlantic.

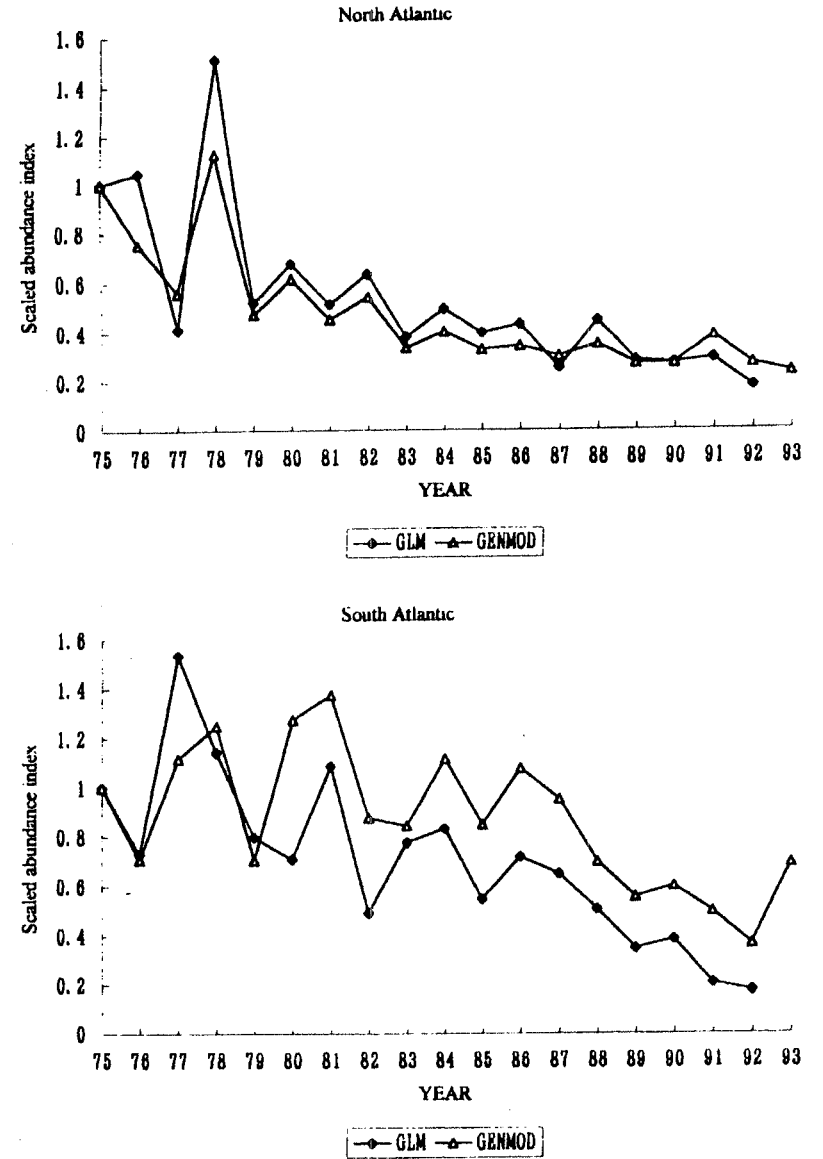


Fig. 3. Scaled annual abundance indices for the Atlantic swordfish calculated by GENMOD and GLM.