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Applying a stochastic surplus production model (SPiCT) to the Greenland halibut Sub. 0+1 offshore

by

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Abstract

A Stochastic Surplus Production Model in Continuous Time (SPiCT) was applied to the Greenland halibut Subareas 0+1 offshore stock. Input data for the tuning model included catches in Subarea 0+1 offshore from 1965 to 2022 and two survey indices of the fishable biomass: the combined deep surveys index of Divisions 0A+1CD from 1999 to 2019 and the biomass of fish > 35 cm in the shallow survey in Divisions 1A-F). A prior for the shape parameter (n) was fixed at 2 (Schaefer). There is some concern regarding biomass scaling, especially at the start of the time series, which raised questions about some parameter estimates (e.g. r), and suggested that several priors need to be investigated further. The model was not accepted but model development is continuing.

Introduction

The SPiCT model is a stochastic surplus production model in continuous time (Pedersen & Berg, 2016). Previously no analytical assessment of the Greenland halibut Subareas 0+1 offshore stock has been accepted and the last assessment was based on a qualitative evaluation of fishery and survey data.

The model assumptions are:

1. The intrinsic growth rate represents a combination of natural mortality, growth, and recruitment.
2. The biomass refers to the exploitable part of the stock.
3. The stock is closed to migration.
4. Age and size-distribution are stable in time.
5. Constant catchability of the gear used to gather information for the biomass index.



We assume, when we run this model, that the stock is not migrating but we know there are some migrations. Tagging experiments show that migration mainly appears in individuals < 30 cm which is not part of the exploitable biomass. Only 2,5 % of the total recaptures (1.5%) migrated to different areas (Vihtakari et al. 2021)

Material and Methods

Catch data are available since 1965 (Treble and Nogueira 2022). Only data from 1987 are split by areas in both Subdivision 0 and 1. We considered that the first 22 years of the times series is more uncertain than the rest.

Two survey indices are available. A shallow survey was conducted in 1A-F (50-600m) for the period 1991-2022 (no survey was conducted in 2021) (Rasmus and Nogueira, 2022). The exploitable biomass, biomass of fish > 35 cm from the shallow water survey, and the total biomass from the combined deep water surveys in 0A-1CD were included in the model (Treble and Nogueira, 2022). The combined index is calculated using data from the Canadian 0A survey and the Greenland 1CD survey that are carried out in deep water (400-1500 m) where the exploitable biomass is found.

No surveys were carried out in 2018, 2020 and 2021. In 2019 surveys were carried out with a different vessel, so there is uncertainty in these index calculations; this was coded in the model. The research survey in 1AF is performed in June and the deep surveys in 0A and 1CD are performed in autumn, therefore, the biomass data are shifted a bit in time by adding 0.5 and 0.75 respectively in the model. The input time-series is shown in Figure 2.

Results and Discussions

The outcome of the SPiCT model is shown in Table 1. The intrinsic population growth rate (r) was estimated to be 0.49 and it is considered to be too high. The r estimated from the Greenland halibut stock in ICES Subareas 5,6,12 and 14 (Iceland and Faroes grounds, West of Scotland, North of Azores, East of Greenland) is $r = 0.16$ (ICES, 2022). The carrying capacity (K) is estimated to 320 811 t and B_{msy} was 160 151 t. Given the rule of thumb that B_{lim} is equal to 30% of B_{msy} , B_{lim} is estimated to 48 116.7 t. The relative Biomass/ B_{msy} is 1.4, which is well above 1, while the relative fishing mortality/ F_{msy} is 0.63, which is considerably lower than 1.

The main results of the model, the absolute biomass and absolute fishing mortality together with the relative biomass and fishing mortality, are shown in Figure 2.

Diagnostics of the model residuals are shown in Figure 3. In general, the residual diagnostics indicated the model formulation was appropriate. One Step Ahead (OSA) residuals were not significantly different from zero and therefore not biased (Figure 3, second row). Testing of multiple lags (here 4) found no significant autocorrelation in the residuals (ACF) of catches or the combined index, but we found autocorrelation in the shallow 1AF index (Figure 3, third row). The normality of the catch residuals is much lower than a p-value of 5% (Figure 3, fourth row). This is probably because catches at the beginning of the time series were very low. We considered this as only a slight violation of the assumptions and that it did not invalidate model results. Deviation from those criteria did not necessarily mean that the model results were invalid, but rather that the results should be examined further.

Table 2 shows correlations between model parameters for fixed effects. Most of the parameters are well separated i.e., relatively low correlations. The highest correlations were between K and m , q and m , and q and k . Parameter estimates should not be influenced by initial values (Millenberger et al. 2019), which appears to be the case in the present assessment (Table 3).

Retrospective plots of fishing mortality and fishable biomass over five years all fall within the confidence limits and Mohn's rho values are relatively low (-0.004 and -0.003 for B/B_{msy} and F/F_{msy} , respectively) (Figure 4).

Conclusion:

Biomass of Greenland halibut at the beginning of the times series is very low and needs to be investigated. No survey data are available before 1991 and catches at the beginning of the time series were very low. Priors about the initial depletion were included in other runs, but with limited success; this needs to be further investigated. The intrinsic population growth rate is also very high and a smaller value can be added with priors. The model was not accepted by NAFO SC in 2023 but model development is continuing.

References

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Table 1. Results from the SPiCT model.

Convergence: 0 MSG: relative convergence (4)
 Objective function at optimum: 53.5896558
 Euler time step (years): 1/4 or 0.25
 Nobs C: 58, Nobs I1: 11, Nobs I2: 31

Residual diagnostics (p-values)

	shapiro	bias	acf	LBox	shapiro	bias	acf	LBox
C	0.0012	0.9462	0.0468	0.1256	**	-	*	-
I1	0.2146	0.9615	0.5228	0.8977	-	-	-	-
I2	0.9972	0.9102	0.0074	0.0096	-	-	**	**

Priors

logn ~ dnorm[log(2), 0.001^2] (fixed)
 logalpha ~ dnorm[log(1), 2^2]
 logbeta ~ dnorm[log(1), 2^2]

Model parameter estimates w 95% CI

	estimate	cilow	ciupp	log.est
alpha1	3.488580e+00	7.336232e-01	1.658915e+01	1.2494947
alpha2	7.775102e+00	1.714490e+00	3.525959e+01	2.0509266
beta	1.489237e+00	9.461547e-01	2.344042e+00	0.3982639
r	4.900076e-01	3.534513e-01	6.793226e-01	-0.7133343
rc	4.900093e-01	3.534546e-01	6.793209e-01	-0.7133309
rold	4.900110e-01	3.534538e-01	6.793272e-01	-0.7133275
m	3.930004e+04	2.454637e+04	6.292145e+04	10.5789808
K	3.208110e+05	1.639426e+05	6.277788e+05	12.6786073
q1	6.384212e-01	2.873007e-01	1.418659e+00	-0.4487570
q2	6.437500e-02	2.856560e-02	1.450745e-01	-2.7430307
n	1.999993e+00	1.996077e+00	2.003917e+00	0.6931438
sdb	3.456120e-02	7.718300e-03	1.547600e-01	-3.3650234
sdf	2.936089e-01	2.100895e-01	4.103307e-01	-1.2255067
sdi1	1.205695e-01	7.600320e-02	1.912684e-01	-2.1155287
sdi2	2.687169e-01	2.083878e-01	3.465115e-01	-1.3140968
sdc	4.372532e-01	3.380036e-01	5.656459e-01	-0.8272429

Stochastic reference points (Srp)

	estimate	cilow	ciupp	log.est	rel.diff.Drp
Bmsys	1.601514e+05	8.176064e+04	3.137018e+05	11.983875	-0.001585401
Fmsys	2.447119e-01	1.766786e-01	3.389425e-01	-1.407674	-0.001196324
MSys	3.919086e+04	2.446019e+04	6.279280e+04	10.576199	-0.002785699

States w 95% CI (inp\$msytype: s)

	estimate	cilow	ciupp	log.est
B_2022.75	2.260292e+05	8.874357e+04	5.756947e+05	12.3284195
F_2022.75	1.563502e-01	5.664230e-02	4.315744e-01	-1.8556571
B_2022.75/Bmsy	1.411347e+00	1.045252e+00	1.905666e+00	0.3445448
F_2022.75/Fmsy	6.389154e-01	2.716498e-01	1.502717e+00	-0.4479832

Predictions w 95% CI (inp\$msytype: s)

	prediction	cilow	ciupp	log.est
B_2024.00	2.231499e+05	8.535624e+04	5.833889e+05	12.3155990
F_2024.00	1.563502e-01	4.699650e-02	5.201534e-01	-1.8556568
B_2024.00/Bmsy	1.393369e+00	9.979003e-01	1.945561e+00	0.3317244
F_2024.00/Fmsy	6.389156e-01	2.191010e-01	1.863128e+00	-0.4479829
Catch_2023.00	3.509392e+04	2.053257e+04	5.998193e+04	10.4657831
E(B_inf)	2.175422e+05	NA	NA	12.2901482

Table 2. Correlation matrix for the estimated SPiCT model parameters

	logm	logK	logq	logq	logq
logn					
logm	1.000000000	0.8948589892	-0.9331208447	-0.9205623033	0.0016527643
logK	0.894858989	1.000000000	-0.9858039532	-0.9830580912	0.0000133857
logq	-0.933120845	-0.9858039532	1.000000000	0.9869480779	-0.0006688433
logq	-0.920562303	-0.9830580912	0.9869480779	1.000000000	-0.0006742963
logn	0.001652764	0.0000133857	-0.0006688433	-0.0006742963	1.000000000
logfdb	-0.117098119	-0.2646161491	0.2361920144	0.2347260038	0.0004469741
logfdf	0.210732799	0.2290432087	-0.2295581316	-0.2288642283	0.0006775867
logfdi	-0.169232213	-0.1800531897	0.1854224583	0.1789052627	-0.0002164786
logfdi	-0.035874484	-0.0316432646	0.0322053131	0.0348685929	0.0001247413
logfsc	0.012482682	0.0457607466	-0.0372575366	-0.0388749320	0.0002973214
	logfdb	logfdf	logfdi	logfdi	logfsc
logm	-0.1170981188	0.2107327987	-0.1692322129	-0.0358744835	0.0124826815
logK	-0.2646161491	0.2290432087	-0.1800531897	-0.0316432646	0.0457607466
logq	0.2361920144	-0.2295581316	0.1854224583	0.0322053131	-0.0372575366
logq	0.2347260038	-0.2288642283	0.1789052627	0.0348685929	-0.0388749320
logn	0.0004469741	0.0006775867	-0.0002164786	0.0001247413	0.0002973214
logfdb	1.000000000	-0.0909702766	0.0210284896	0.0347694659	-0.0253599333
logfdf	-0.0909702766	1.000000000	-0.0424270491	-0.0131949323	-0.1592545419
logfdi	0.0210284896	-0.0424270491	1.000000000	-0.0188646021	-0.0084923373
logfdi	0.0347694659	-0.0131949323	-0.0188646021	1.000000000	0.0069049152
logfsc	-0.0253599333	-0.1592545419	-0.0084923373	0.0069049152	1.000000000

Table 3. Checking the influence of initial values on parameter estimates with 20 random selected initial values. Distance from the estimated parameter vector to the base run parameter vector (should be close to 0).

	Distance	m	K	q	q	n	sdb	sdf	sdi	sdi	sdc
Basevec	0.00	39300.04	320810.97	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 1	0.28	39300.12	320811.24	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 2	0.00	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Trial 3	0.63	39300.05	320810.34	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 4	0.17	39300.11	320811.12	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 5	316067.40	55286.71	5148.23	256.56	24.32	2	0.13	0.02	0.28	0.49	0.40
Trial 6	0.72	39300.07	320811.69	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 7	0.00	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Trial 8	0.21	39300.09	320810.77	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 9	0.00	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Trial 10	0.36	39300.12	320811.32	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 11	0.41	39300.13	320811.37	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 12	0.23	39300.22	320811.11	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 13	0.38	39300.12	320811.34	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 14	0.08	39300.10	320811.02	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 15	0.06	39300.08	320810.93	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 16	0.37	39300.13	320811.32	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 17	0.00	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Trial 18	0.19	39300.12	320811.14	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 19	0.42	39300.13	320811.38	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44
Trial 20	0.64	39300.10	320810.34	0.64	0.06	2	0.03	0.29	0.12	0.27	0.44

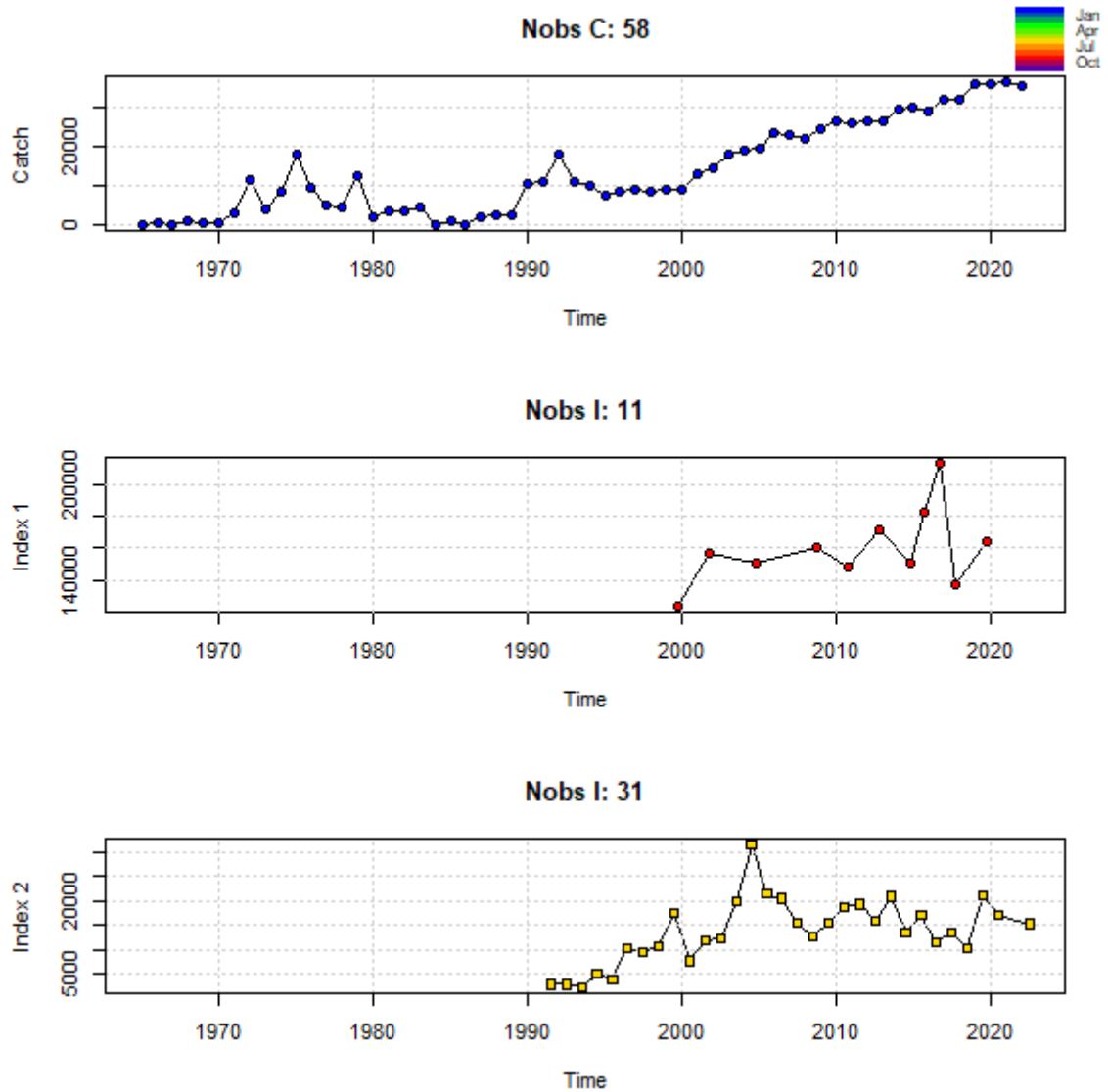


Figure 1. Input data for SPiCT models of the Greenland halibut Subareas 0+1 offshore stock. Top: Catch, middle: 0A-1CD combined index, Bottom: 1AF Survey index (biomass > 35 cm). spict_v1.3.7@cdf315

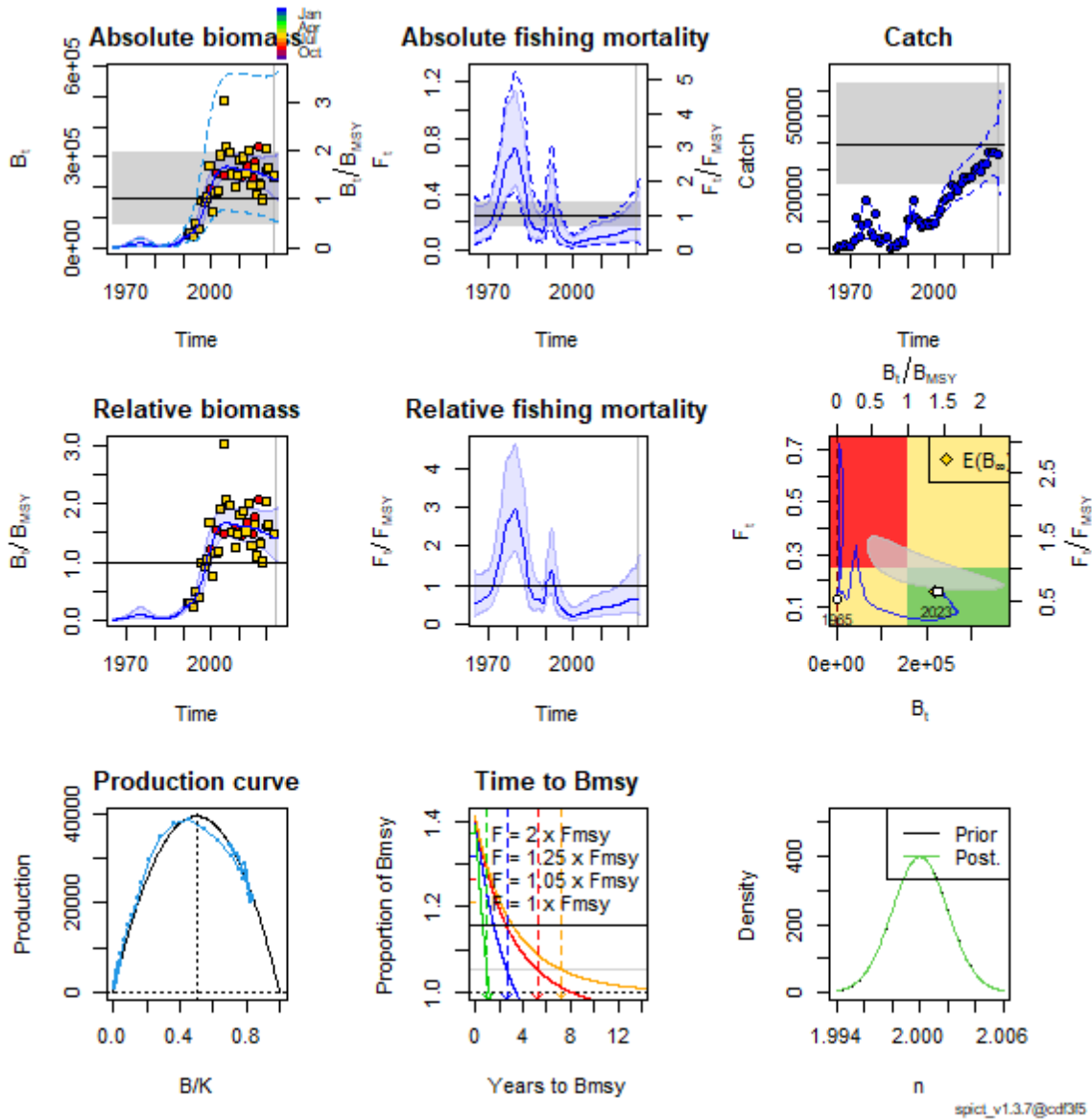


Figure 2. Main results of the model with prior to fix $n = 2$ (`inp$priors$logn <- c(log(2),1e-3)`)

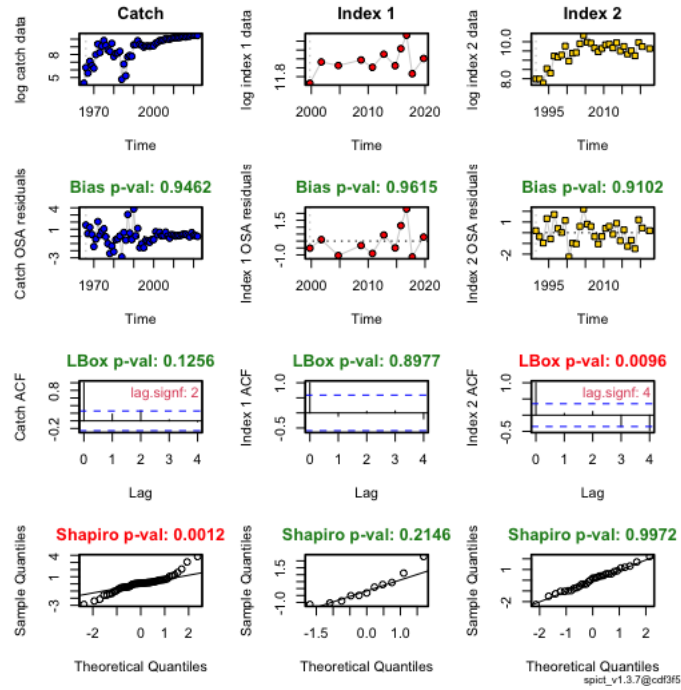


Figure 3. Diagnostics. First row show log of the input data series; catch, survey index 0A1CD and survey index 1AF. Second row “one-step ahead” (OSA) residuals and a test for bias. Third row show the autocorrelation of the residuals including Ljung-Box test of multiple lags and tests for the individual lags. Fourth row show the results of Shapiro test for normality of the residuals.

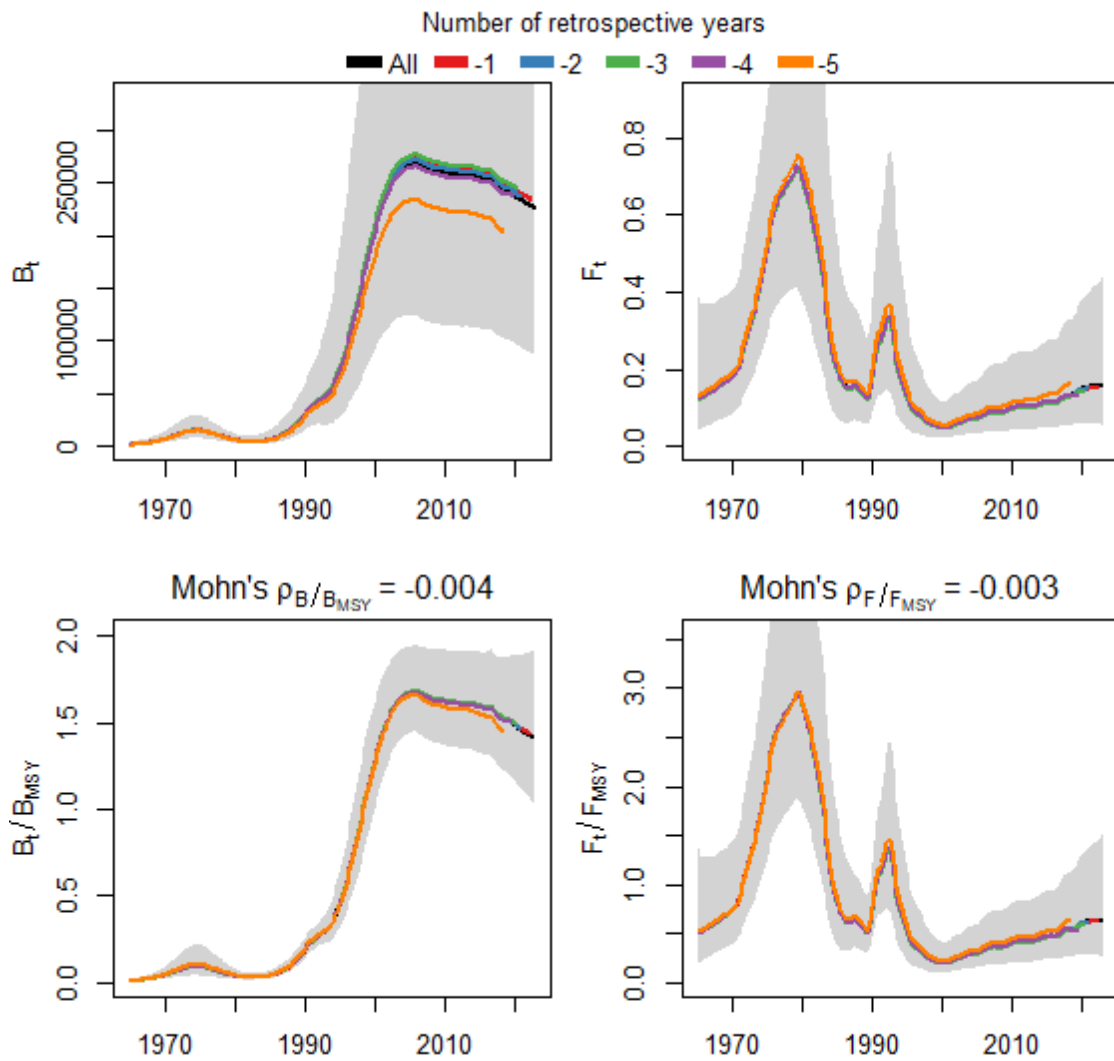


Figure 4. Five year retrospective plots of fishing mortality and fishable biomass.