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Evaluation of surplus production modelling in continuous time (SPiCT) for Greenland halibut in NAFO Division 1A Uummannaq

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Abstract

The Greenland halibut stock in NAFO Division 1A Uummannaq has previously been qualitatively assessed using index-based information. First attempts to provide analytical assessments with surplus production models were made since 2024. Here, sensitivity analyses are presented, i.e., an evaluation of several runs with surplus production models in continuous time (SPiCT) where input priors for r and B/K were varied while other model setup parameters were held constant. In addition, variations of truncated input catch time series were evaluated. These model evaluations were discussed in plenary and indicate a level of robustness in parameter estimates that provide an improved quantitative perception of the state of the stock compared to the previous qualitative assessment. A final model configuration is presented, which was accepted during the 2026 Scientific Council June meeting to provide advice.

Introduction

The inshore Greenland halibut stocks in NAFO Division 1A have been separated from the offshore Greenland halibut stock in Subarea 0+1 in 1994. The latter is assessed using a stochastic surplus production model in continuous time (SPiCT) as developed by Berg & Pedersen (2016) since 2024 (Nogueira et al., 2024). Advice for the inshore stocks in Division 1A has previously been provided without analytical assessment model, using index-based information only. Caution must be taken when applying surplus production models for these inshore Greenland halibut stocks as they are believed to rely on recruitment from the offshore stock. However, application of a SPiCT model may at least provide quantitative estimates of the exploitable biomass status and thus enable the application of the NAFO precautionary approach (PA) framework. An important consideration is then how sensitive the model reacts to the specification of different priors in terms of growth rate (r) and the initial state of the biomass of the stock in relation to its carrying capacity (B/K). Furthermore, if input time series vary in length, it should be explored whether this affects model results. Here, several (>30) model runs are evaluated and compared to investigate model sensitivity and develop an appropriate model configuration for the assessment of the Greenland halibut stock in Division 1A inshore Uummannaq.

Material and Methods

Input data

Catch data has been available since 1954, but the first years were characterized by very low or zero catches (Nygaard & Christiansen, 2026a). Since 1977 catches have gradually increased, except for one year, 1986, with missing data. This time series from 1977-2025 was used as input for the SPiCT model.

Fisheries-independent surveys were conducted in the Uummannaq area since the 1960s but only results from 1993 are currently presented due to uncertainty about earlier survey results (Nygaard & Christiansen, 2026b). Furthermore, the survey design changed from longline to gillnet in 2005 and several years in the time series are missing. An additional 90 mm mesh size section was added to the gillnet survey in 2015. Therefore, the time series from 2015 to 2025 was used as input for the SPiCT model. Details about the survey design are available in Nygaard & Christiansen (2026b).

In addition, two commercial CPUEs are available: one calculated from logbook data ("commercial logbook CPUE") and one calculated from factory landings data ("commercial factory CPUE"). The first is based on haul-by-haul information delivered to the Greenland Fisheries and Hunting Control Authority (GFJK) by fishing vessels. The latter is based on daily individual landings data that are recorded at the fish processing factories in the area. Both data sources contain metadata such as date, gear, position, effort, and more. The commercial logbook CPUE is available from 2006 to 2025, while the commercial factory CPUE is available from 2012 to 2025. Details about the CPUE calculations can be found in Nygaard & Christiansen (2026a).

All index input time series (survey CPUE, commercial logbook CPUE, and commercial factory CPUE) were shifted to the middle of the year for the model runs.

Base model configuration

All SPiCT runs were conducted using R package "spict" v1.3.9. All model runs used the four input time series described above. The production curve was fixed to the Schaefer model, a prior for the standard deviation of the biomass was set as logsdb = c(log(0.1), 0.5), and the alpha and beta priors were disabled. No prior for the initial state of the biomass (B/K) was applied. Initially, the prior for r was set at logr = c(log(0.2), 0.2). Otherwise default settings were applied. The exact R code to run the base model is available in Appendix A.

Sensitivity analyses

A series of model runs was conducted, which differed from the base model run in two parameters: the r prior was varied between 0.05 and 0.35 and a prior for the initial state of the biomass as a function of the stock's carrying capacity (B/K) was introduced and varied from 0.2 to 1 (Table 1). In total, this represents 35 individual runs with every possible combination of these tested values for r and B/K. Model runs were then checked for convergence and adherence to the points listed in Mildenberger et al. (2019). Matrices comparing the different parameter combinations were created with information about Akaike Information Criterion (AIC), ΔAIC, the biomass estimated at the end of the current year (B_{2025}), estimated K, estimated r, estimated maximum sustainable yield (MSY), and estimated relative biomass (B/B_{msy}).

Catch time series truncation

The catch time series used is 29 years longer than the longest used index time series. Therefore, SPiCT models using a shorter catch time series were tested. The base model configuration for this test was the same as described above, except that r was set as logr = c(log(0.25), 0.25). Two additional runs with a truncated time series were conducted. The first used a catch time series from 1991 to 2025, the same time period as used in the offshore Greenland halibut stock assessment (Hedges & Christiansen, 2025). The second used a catch time series from 2006 to 2025, thus with the same starting year as the longest used CPUE index time series. As in the sensitivity analyses above, the parameters B_{2025}, estimated K, estimated r, estimated MSY, and estimated B/B_{msy} were compared, as well as adherence to the checklist points of Mildenberger et al. (2019).

Final model configuration

After evaluation of the above-mentioned analyses a final model configuration was found. The long catch time series (1977-2025) was used and no prior for the initial state of the biomass (B/K) was imposed, rendering the final model setup nearly identical to the base model setup with the notable exception that the r prior was now set as logr = c(log(0.25), 0.25). The R code for the final model setup is available in Appendix B.

Results and discussion

All model runs converged successfully. The different runs are compared in more detail below.

Sensitivity analyses

Model runs were checked for adherence to the points listed in Mildenberger et al. (2019), although some of these criteria are qualitative evaluations and thus cannot be reported in a simple categorical table. However, all models passed the simpler checks, i.e. models converged, all variance parameters were finite, the main variance parameter intervals did not span more than one order of magnitude, and initial values did not influence the parameter estimates. The one-step ahead residuals varied to some extent between runs, as did the retrospective patterns. Production curves remained relatively similar between runs.

The model with r prior = 0.2 and B/K prior = 0.2 had the lowest AIC value, closely followed by the model with r prior = 0.25 and B/K prior = 0.2 (Table 2). Eight model runs were within +/- 2 AIC of the model run with the lowest overall AIC (Table 3). In these eight model runs B_{2025} ranged from 27,815 t to 43,094 t (Table 4) and B/B_{msy} ranged from 0.57 to 0.71 (Table 5). Importantly, maximum sustainable yield (MSY) varied relatively little, from 4,705 to 6,338 t in these eight model runs. But even at higher B/K priors MSY did not exceed 6,337 t (Table 6). These results therefore indicate a certain stability in parameter estimates that are relevant for providing advice in the NAFO PA framework.

Catch time series truncation

The catch time series was truncated to evaluate how this affects model estimates. For these three runs (catch time series start at 1977, 1991, and 2006, respectively) the r prior was relaxed again and set at 0.25. All three model runs converged, showed finite variance parameters, main parameter intervals did not span more than one order of magnitude, and initial values did not influence the parameter estimates. MSY was very similar between these three runs, ranging from 6,701 t (1977 start) to 6,965 t (1991 start, Table 7), indicating again a degree of stability in a crucial metric. Residuals and retrospective analyses showed acceptable results in all three runs. However, Mohn's Rho was smaller in the catch time series from 1977 compared to the 1991 time series for both B/B_{msy} and F/F_{msy} (Table 8). In addition, the time series from 1991 estimated unrealistically high r at 0.31 (Table 7). It was therefore concluded that the time series starting in 1977 is the most promising model configuration.

Final model configuration

The final model configuration was thus using the catch time series from 1977, a relaxed (±0.25) r prior at 0.25 and no initial B/K prior. The final model configuration was thus using the catch time series from 1977, a relaxed (±0.25) r prior at 0.25 and no initial B/K prior. This final model estimated median relative B/B_{msy} at 0.6 in 2025 (Fig. 1, Table 9) and median relative F/F_{msy} at 1.9 in 2025 (Fig. 2, Table 9). Estimated parameters and relative reference points from the model are listed in Table 9. The prior and posterior distributions of the estimated parameters n (fixed to 2, i.e. Schaefer production curve), r (intrinsic growth), and sdb (standard deviation of the biomass) is given in Fig. 3. The posterior r is shifted slightly compared to the prior r. The production curve was generally characterized by the large fluctuations that the stock has experienced in the past decade (Fig. 4).

The final SPiCT model showed slight residual patterns (p = 0.026 and p = 0.049 for the catch ACF and Shapiro quantiles, respectively) in the commercial CPUE from factory-landings data (Fig. 5), but slight deviations do not necessarily invalidate model results (Mildenberger et al., 2019). A five-year retrospective analysis was performed also on the final model configuration. As in all performed model runs, the model is sensitive to peels of ≥3 years, but retros are well within confidence intervals. Mohn's rho is at 0.058 for B/B_{msy} and at -0.118 for F/F_{msy} (Fig. 6). The signal observed when peeling off three or more years is likely related to the particularly strong reduction in all stock indices in the past three years.

Conclusion

The final configuration of the surplus production model in continuous time is a valid tool to assess the stock of Greenland halibut in Division 1A Uummannaq. It may be expected that the model can be further improved when the survey and CPUE time series become longer. As time progresses, more data will likely be available, but it may also be an option to revisit older catch and survey data and explore whether these could be included. The approach presented here may also serve as an example to further develop similar assessments for the DiskoBay and Upernavik Greenland halibut stocks in NAFO Division 1A.

Tables

Table 1. Greenland halibut in Division 1A inshore Uummannaq, SPiCT sensitivity analyses : parameters tested. All combinations of the tested values listed below were run, i.e., a total of 35 runs.

Parameter	R code	Description	Tested values
r	priors$logr <- c(log(r), 0.05, 1)	Prior for the intrinsic growth rate	0.05, 0.1, 0.15, 0.20, 0.25, 0.3, 0.35
B/K	priors$logbkfrac <- c(log(bk), 0.2, 1)	Prior for the initial state of the stock in terms of B/Kt	0.2, 0.4, 0.6, 0.8, 1

Table 2. Greenland halibut in Division 1A inshore Uummannaq, SPiCT sensitivity analyses results : AIC values for the 35 runs with different priors for r and B/K as described in Table 1.

AIC		B/K				
	priors	0.2	0.4	0.6	0.8	1
	0.05	29.34	30.11	30.89	31.61	32.27
	0.1	26.19	27.58	28.88	29.97	30.91
	0.15	24.03	26.02	27.55	28.76	29.78
r	0.2	23.01	25.22	26.67	27.84	28.86
	0.25	23.02	24.85	26.06	27.13	28.11
	0.3	23.55	24.63	25.57	26.55	27.51
	0.35	24.16	24.46	25.18	26.08	27.02

Table 3. Greenland halibut in Division 1A inshore Uummannaq, SPiCT sensitivity analyses results : ΔAIC values for the 35 runs with different priors for r and B/K as described in Table 1. Values within 2 ΔAIC of the lowest AIC are marked in yellow.

min(AIC)-AIC		B/K				
	priors	0.2	0.4	0.6	0.8	1
	0.05	-6.33	-7.10	-7.88	-8.60	-9.26
	0.1	-3.18	-4.57	-5.87	-6.96	-7.90
	0.15	-1.02	-3.01	-4.54	-5.75	-6.77
r	0.2	0.00	-2.21	-3.66	-4.83	-5.85
	0.25	0.00	-1.84	-3.05	-4.12	-5.10
	0.3	-0.54	-1.62	-2.56	-3.54	-4.50
	0.35	-1.15	-1.45	-2.17	-3.07	-4.01

Table 4. Greenland halibut in Division 1A inshore Uummannaq, SPiCT sensitivity analyses results : B_{2025} values for the 35 runs with different priors for r and B/K as described in Table 1. Runs within 2 ΔAIC of the lowest AIC are marked in yellow (see Table 3).

B_{2025}		B/K				
	priors	0.2	0.4	0.6	0.8	1
	0.05	71,095	81,382	88,471	93,447	97,077
	0.1	51,053	58,779	62,266	64,164	65,313
	0.15	43,094	47,483	48,959	49,587	49,888
r	0.2	37,863	40,242	40,735	40,850	40,857
	0.25	33,876	35,003	35,066	35,009	34,935
	0.3	30,624	31,007	30,940	30,849	30,766
	0.35	27,815	27,915	27,834	27,752	27,680

Table 5. Greenland halibut in Division 1A inshore Uummannaq, SPiCT sensitivity analyses results : B/B_{msy} values for the 35 runs with different priors for r and B/K as described in Table 1. Runs within 2 ΔAIC of the lowest AIC are marked in yellow (see Table 3).

B/Bmsy		B/K				
	priors	0.2	0.4	0.6	0.8	1
	0.05	0.34	0.56	0.70	0.79	0.85
	0.1	0.46	0.62	0.68	0.72	0.74
	0.15	0.57	0.66	0.69	0.70	0.71
r	0.2	0.63	0.68	0.69	0.70	0.70
	0.25	0.67	0.70	0.70	0.70	0.70
	0.3	0.70	0.71	0.70	0.70	0.70
	0.35	0.71	0.71	0.71	0.71	0.71

Table 6. Greenland halibut in Division 1A inshore Uummannaq, SPiCT sensitivity analyses results : MSY values for the 35 runs with different priors for r and B/K as described in Table 1. Runs within 2 ΔAIC of the lowest AIC are marked in yellow (see Table 3).

MSY		B/K				
	priors	0.2	0.4	0.6	0.8	1
	0.05	3,000	3,022	3,008	2,985	2,961
	0.1	3,999	4,150	4,197	4,217	4,226
	0.15	4,705	4,855	4,901	4,918	4,924
r	0.2	5,230	5,368	5,396	5,401	5,399
	0.25	5,647	5,762	5,773	5,769	5,762
	0.3	5,999	6,076	6,077	6,070	6,061
	0.35	6,287	6,338	6,337	6,329	6,320

Table 7. Greenland halibut in Division 1A inshore Uummannaq, SPiCT catch time series truncation analyses results : three runs with catch time series starting in 1977 (t1), 1991 (t2), and 2006 (t3) were compared. Selected estimated parameters for each run are shown, i.e. B_{2025}, K, r, MSY, and B/B_{msy}.

	t1 1977	t2 1991	t3 2006
B_{2025}	30,671	27,626	28,372
K	102,144	90,834	101,087
r	0.26	0.31	0.27
msy	6,701	6,965	6,739
B/Bmsy	0.61	0.62	0.57

Table 8. Greenland halibut in Division 1A inshore Uummannaq, SPiCT catch time series truncation analyses results : three runs with catch time series starting in 1977 (t1), 1991 (t2), and 2006 (t3) were compared. Adherence to the criteria described in Mildenberger et al. (2019) is summarized.

	t1 1977	t2 1991	t3 2006
convergence	yes	yes	yes
var parameter finite	TRUE	TRUE	TRUE
residuals	okay	okay	okay
retro	okay	okay	okay
mohn's rho b/bmsy	0.058	0.072	0.037
mohn's rho f/fmsy	-0.118	-0.141	-0.052
production curve	okay	okay	okay
calc.om	1	1	0-1
check.ini	good	good	good

Table 9. Estimated parameters and relative reference points of the final SPiCT model configuration for Greenland halibut in Division 1A inshore – Uummannaq.

Parameter	Estimate	CI lower	CI upper	Log.est
alpha2 (α = SDIndex/SDBiomass)	0.85	0.22	3.31	-0.17
Beta (β = SDCatch/SDF)	1.05	0.50	2.17	0.04
r (intrinsic growth rate)	0.26	0.17	0.40	-1.34
m (deterministic MSY)	6,701	5,208	8,621	8.81
K (Carrying capacity)	102,144	66,416	157,093	11.53
q1 (Catchability for survey)	0.0005	0.0002	0.0009	-7.68
q2 (Catchability for logbook CPUE)	0.0007	0.0004	0.0014	-7.24
q3 (Catchability for factory CPUE)	0.0011	0.0006	0.0020	-6.82
sdb (Standard deviation biomass)	0.08	0.04	0.16	-2.49
sdf (Standard deviation fishing mortality)	0.14	0.08	0.25	-1.95
sdi1 (Standard deviation survey)	0.35	0.23	0.54	-1.05
sdi2 (Standard deviation logbook CPUE)	0.07	0.03	0.17	-2.66
sdi3 (Standard deviation factory CPUE)	0.13	0.08	0.23	-2.02
sdc (Standard deviation catch)	0.15	0.11	0.21	-1.91
B (Biomass 2025)	30,671	14,006	67,164	10
F (Fishing mortality 2025)	0.24	0.11	0.51	-1.42
B/Bmsy (relative biomass 2025 in %)	0.61	0.32	1.18	-0.49
F/Fmsy (relative fishing mortality 2025 in %)	1.87	0.96	3.65	0.63

Figures

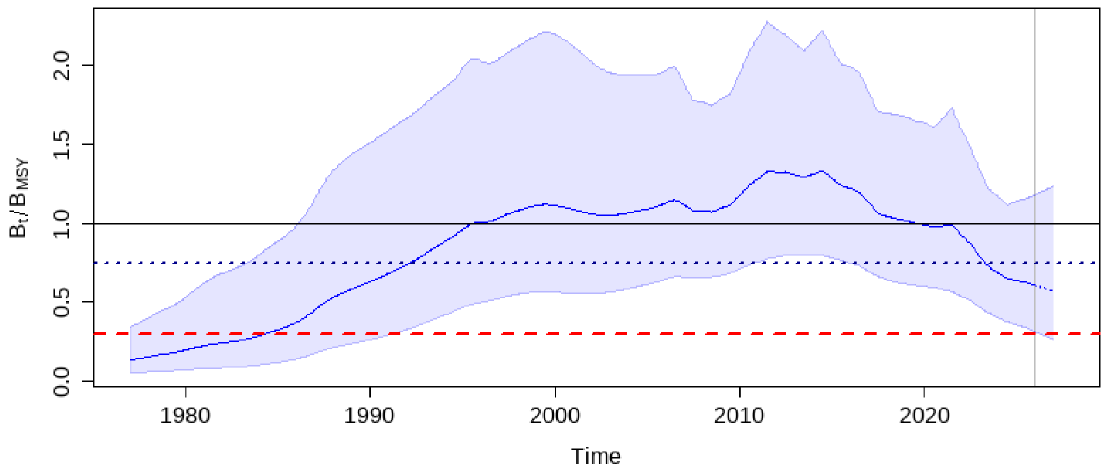

Figure 1. Greenland halibut in Division 1A inshore Uummannaq, final model configuration: estimated relative biomass B/B_{msy} (blue line) with 95 % confidence interval (blue shaded area). The dotted line is $B_{trigger}$ = 0.75 B_{msy} and the red dashed line is B_{lim} = 0.3 B_{msy}.

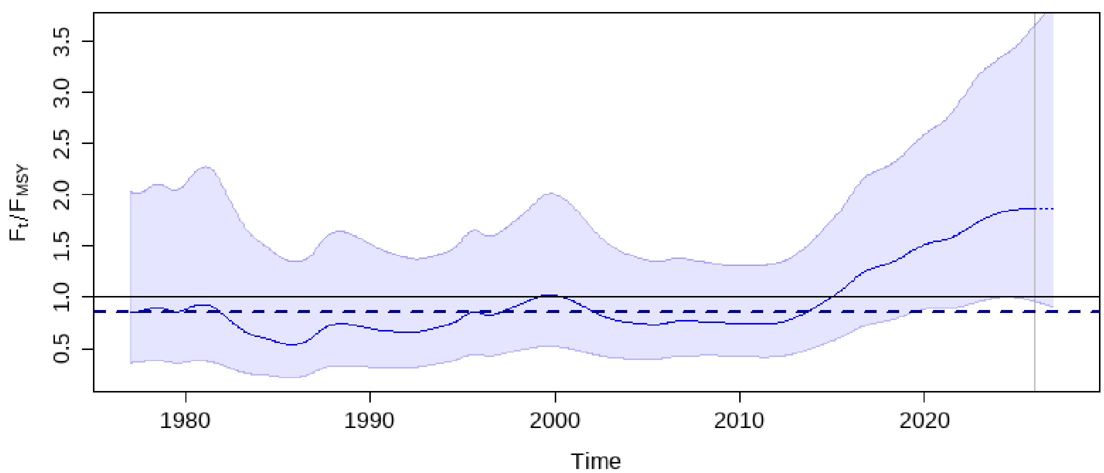

Figure 2. Greenland halibut in Division 1A inshore Uummannaq, final model configuration: estimated relative fishing mortality F/F_{msy} (blue line) with 95 % confidence interval (blue shaded area). The solid line is F_{lim} = F_{msy} and the dashed line is F_{target}.

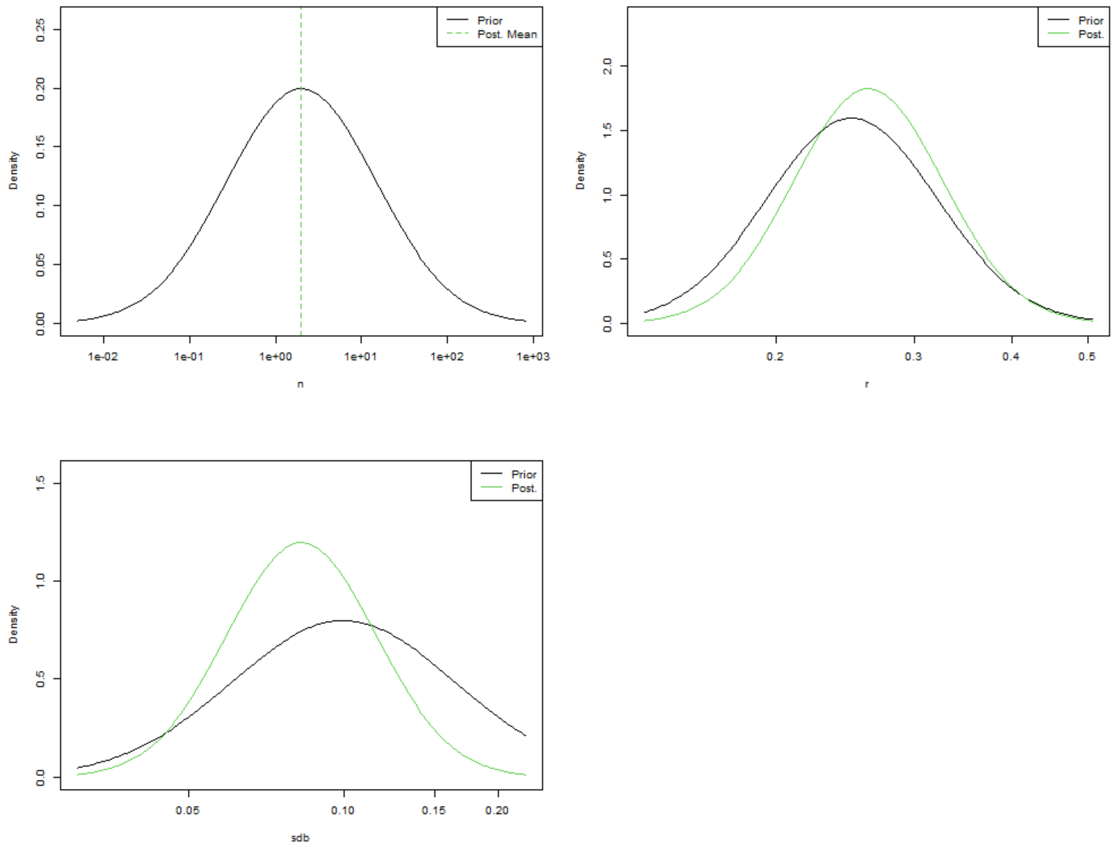

Figure 3. Greenland halibut in Division 1A inshore Uummannaq, final model configuration: prior and posterior distribution for the parameters *n*, *r*, and *sdb*.

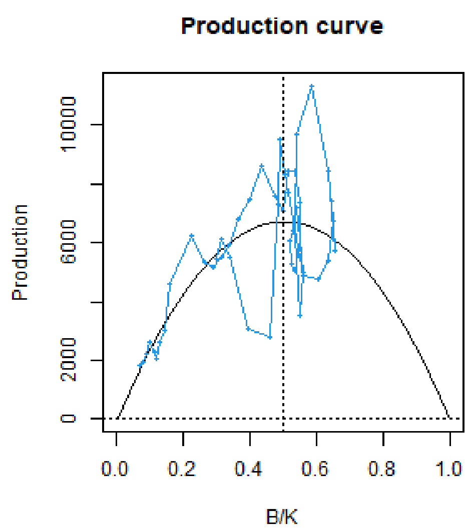

Figure 4. Greenland halibut in Division 1A inshore Uummannaq, final model configuration: production curve.

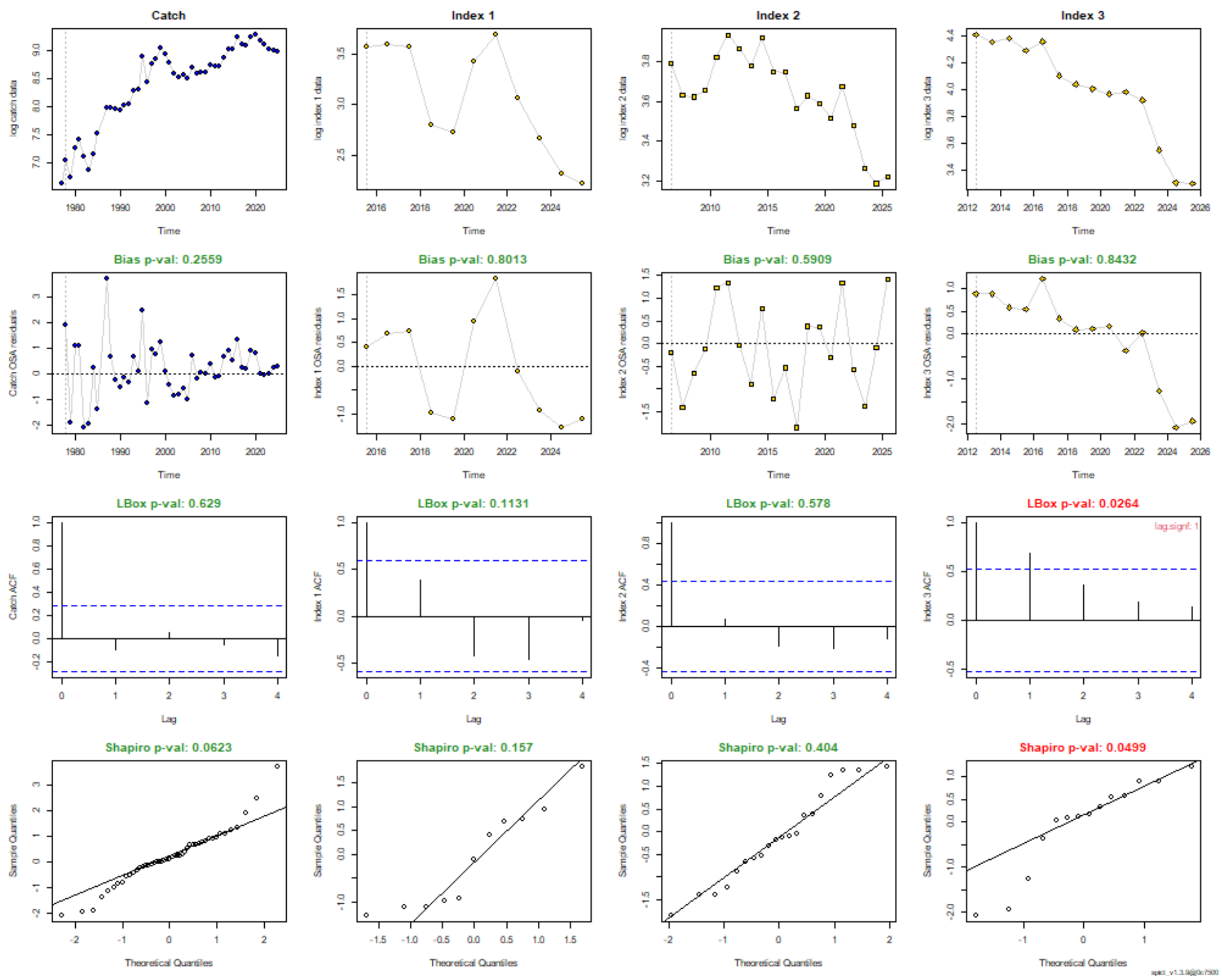

Figure 5. Greenland halibut in Division 1A inshore Uummannaq, final model configuration diagnostics: First row shows log of the input time series, second row shows "one-step-ahead" residuals and a test for bias, third row shows autocorrelation of the residuals including Ljung-Box tests, and fourth row shows Shapiro test results for normality of the residuals.

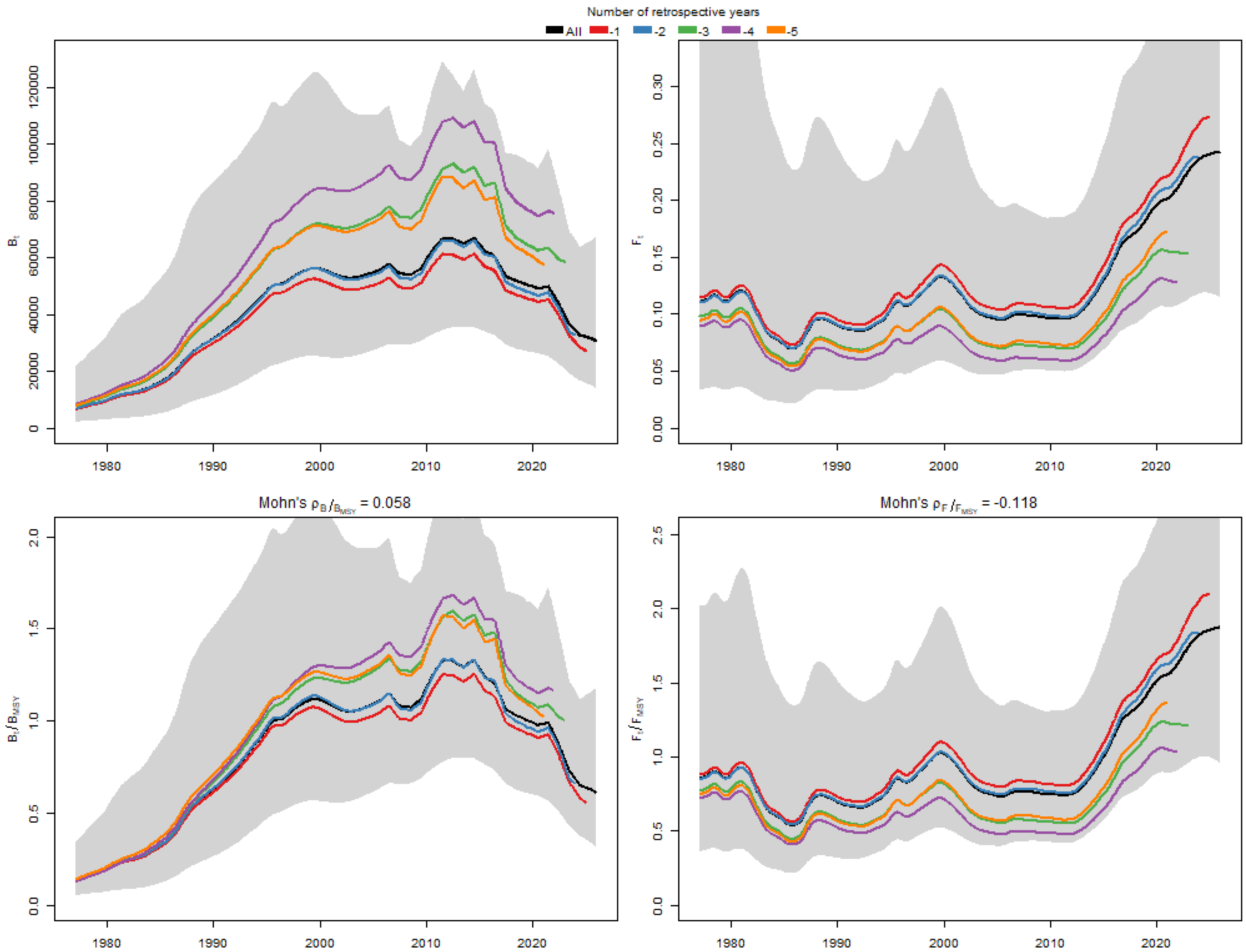

Figure 6. Greenland halibut in Division 1A inshore Uummannaq, final model configuration: five-year retrospective analysis of fishing mortality and biomass. Upper left : abosulte biomass B_t ; upper right : absolute fishing mortality F_t ; lower left : relative biomass B/B_{msy} ; lower right : relative fishing mortality F/F_{msy}. Mohn's rho values were calculated for relative values. Confidence intervals are 95 %.

References

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Appendix A

R code for the base SPiCT model run was as follows:

```
library(spict)
library(tseries)

### load catches in Uummannaq 1977 to 2025
obsC <- c(754,1144,835,1422,1662,1210,966,1259,1833,NA,2897,2920,2859,

2779,3045,3067,3916,4004,7234,4579,6293,6912,8425,7568,6558,5339,5039,5248,4856,5984,5
318,5426,5451,6226,6146,6130,7007,8199,8244,
          10304,9049,8839,10162,10677,9609,9007,8250,8028,7812)
timeC <- c(seq(1977,2025,1))

### load index (gillnet survey CPUE), 2015 to 2025 (no survey in 2021), all sizes (but
very few are < 35 cm, so this is approx. fishable biomass)
surI_1 <-
c(35.50407452,36.14421975,35.55292388,16.50023784,15.2701154,30.54837823,39.84290316,
            21.4527773,14.44491204,10.16803052,9.25169797)
surtime_1 <- c(seq(2015,2025,1))
surtime_1 <- surtime_1 + 0.5

### load index 2 (commercial longline CPUE from logbooks), 2006 to 2025, all sizes
cpueI <-
c(44.23,37.66,37.42,38.67,45.74,51.08,47.67,43.65,50.28,42.42,42.32,35.23,37.64,36.2,3
3.64,39.44,32.47,26.09,24.22,25.08)
cpuetime <- c(seq(2006,2025,1))
cpuetime <- cpuetime + 0.5

### load index 3 (commercial longline CPUE from factory landings), 2012 to 2025, all
sizes
cpueI_2 <-
c(81.83,77.71,79.85,72.91,77.84,60.41,56.66,54.72,52.68,53.35,50.33,34.69,27.17,27.03)
cpuetime_2 <- c(seq(2012,2025,1))
cpuetime_2 <- cpuetime_2 + 0.5

### input catch
inp<-list(timeC=timeC,obsC=obsC)

### input survey and commercial CPUE indices
inp$timeI<-list()
inp$timeI[[1]]<-surtime_1
inp$timeI[[2]]<-cpuetime
inp$timeI[[3]]<-cpuetime_2
inp$obsI<-list()
inp$obsI[[1]]<-surI_1
inp$obsI[[2]]<-cpueI
inp$obsI[[3]]<-cpueI_2

### check input and remove NA entry (1986 is missing)
inp<-check.inp(inp)

### priors
inp$priors$logsdb <- c(log(0.10),0.5,1)
inp$phases$logn <- -1
inp$priors$logalpha <- c(0,0,0)
inp$priors$logbeta <- c(0,0,0)
inp$priors$logr <- c(log(0.2),0.2,1)

### fit model
res <- fit.spict(inp,verbose=TRUE)
```

Appendix B

R code for the final SPiCT model run was as follows:

```
library(spict)
library(tseries)

### load catches in Uummannaq 1977 to 2025
obsC <- c(754,1144,835,1422,1662,1210,966,1259,1833,NA,2897,2920,2859,

2779,3045,3067,3916,4004,7234,4579,6293,6912,8425,7568,6558,5339,5039,5248,4856,5984,5
318,5426,5451,6226,6146,6130,7007,8199,8244,
          10304,9049,8839,10162,10677,9609,9007,8250,8028,7812)
timeC <- c(seq(1977,2025,1))

### load index (gillnet survey CPUE), 2015 to 2025 (no survey in 2021), all sizes (but
very few are < 35 cm, so this is approx. fishable biomass)
surI_1 <-
c(35.50407452,36.14421975,35.55292388,16.50023784,15.2701154,30.54837823,39.84290316,
            21.4527773,14.44491204,10.16803052,9.25169797)
surtime_1 <- c(seq(2015,2025,1))
surtime_1 <- surtime_1 + 0.5

### load index 2 (commercial longline CPUE from logbooks), 2006 to 2025, all sizes
cpueI <-
c(44.23,37.66,37.42,38.67,45.74,51.08,47.67,43.65,50.28,42.42,42.32,35.23,37.64,36.2,3
3.64,39.44,32.47,26.09,24.22,25.08)
cpuetime <- c(seq(2006,2025,1))
cpuetime <- cpuetime + 0.5

### load index 3 (commercial longline CPUE from factory landings), 2012 to 2025, all
sizes
cpueI_2 <-
c(81.83,77.71,79.85,72.91,77.84,60.41,56.66,54.72,52.68,53.35,50.33,34.69,27.17,27.03)
cpuetime_2 <- c(seq(2012,2025,1))
cpuetime_2 <- cpuetime_2 + 0.5

### input catch
inp<-list(timeC=timeC,obsC=obsC)

### input survey and commercial CPUE indices
inp$timeI<-list()
inp$timeI[[1]]<-surtime_1
inp$timeI[[2]]<-cpuetime
inp$timeI[[3]]<-cpuetime_2
inp$obsI<-list()
inp$obsI[[1]]<-surI_1
inp$obsI[[2]]<-cpueI
inp$obsI[[3]]<-cpueI_2

### check input and remove NA entry (1986 is missing)
inp<-check.inp(inp)

### priors
list.possible.priors()
inp$priors$logsdb <- c(log(0.10),0.5,1)
inp$phases$logn <- -1
inp$priors$logalpha <- c(0,0,0)
inp$priors$logbeta <- c(0,0,0)
inp$priors$logr <- c(log(0.25),0.25,1)

### fit model
res <- fit.spict(inp,verbose=TRUE)
```

Colophon

The computational environment that was used to generate the final SPiCT run was as follows:

```
─ Session info ───────────────────────────────────────────────────────────────────────────────────────────────────────────────
 setting  value
 version  R version 4.5.2 (2025-10-31 ucrt)
 os       Windows 11 x64 (build 26100)
 system   x86_64, mingw32
 ui       RStudio
 language (EN)
 collate  Danish_Denmark.utf8
 ctype    Danish_Denmark.utf8
 tz       America/Godthab
 date     2026-06-07
 rstudio  2026.01.0+392 Apple Blossom (desktop)
 pandoc   NA
 quarto   ERROR: Unknown command
"TMPDIR=C:/Users/hech/AppData/Local/Temp/Rtmp63d4y6/file6758393e3f50". Did you mean
command "create"? @ C:\\PROGRA~1\\RStudio\\RESOUR~1\\app\\bin\\quarto\\bin\\quarto.exe

─ Packages ───────────────────────────────────────────────────────────────────────────────────────────────────────────────────
 package      * version date (UTC) lib source
 cachem         1.1.0   2024-05-16 [1] CRAN (R 4.5.2)
 cli            3.6.6   2026-04-09 [1] CRAN (R 4.5.3)
 curl           7.0.0   2025-08-19 [1] CRAN (R 4.5.2)
 devtools       2.5.2   2026-04-30 [1] CRAN (R 4.5.3)
 dplyr        * 1.2.1   2026-04-03 [1] CRAN (R 4.5.3)
 ellipse        0.5.0   2023-07-20 [1] CRAN (R 4.5.3)
 ellipsis       0.3.3   2026-04-04 [1] CRAN (R 4.5.3)
 farver         2.1.2   2024-05-13 [1] CRAN (R 4.5.2)
 fastmap        1.2.0   2024-05-15 [1] CRAN (R 4.5.2)
 forcats      * 1.0.1   2025-09-25 [1] CRAN (R 4.5.2)
 fs             2.1.0   2026-04-18 [1] CRAN (R 4.5.3)
 generics       0.1.4   2025-05-09 [1] CRAN (R 4.5.2)
 ggplot2      * 4.0.2   2026-02-03 [1] CRAN (R 4.5.2)
 glue           1.8.0   2024-09-30 [1] CRAN (R 4.5.2)
 gtable         0.3.6   2024-10-25 [1] CRAN (R 4.5.2)
 hms            1.1.4   2025-10-17 [1] CRAN (R 4.5.2)
 lattice        0.22-7  2025-04-02 [2] CRAN (R 4.5.2)
 lifecycle      1.0.5   2026-01-08 [1] CRAN (R 4.5.2)
 lubridate    * 1.9.5   2026-02-04 [1] CRAN (R 4.5.2)
 magrittr       2.0.4   2025-09-12 [1] CRAN (R 4.5.2)
 Matrix         1.7-4   2025-08-28 [2] CRAN (R 4.5.2)
 memoise        2.0.1   2021-11-26 [1] CRAN (R 4.5.2)
 mgcv           1.9-3   2025-04-04 [2] CRAN (R 4.5.2)
 nlme           3.1-168 2025-03-31 [2] CRAN (R 4.5.2)
 pillar         1.11.1  2025-09-17 [1] CRAN (R 4.5.2)
 pkgbuild       1.4.8   2025-05-26 [1] CRAN (R 4.5.3)
 pkgconfig      2.0.3   2019-09-22 [1] CRAN (R 4.5.2)
 pkgload        1.5.2   2026-04-22 [1] CRAN (R 4.5.3)
 purrr        * 1.2.1   2026-01-09 [1] CRAN (R 4.5.2)
 quadprog       1.5-8   2019-11-20 [1] CRAN (R 4.5.2)
 quantmod       0.4.28  2025-06-19 [1] CRAN (R 4.5.3)
 R6             2.6.1   2025-02-15 [1] CRAN (R 4.5.2)
 RColorBrewer   1.1-3   2022-04-03 [1] CRAN (R 4.5.2)
 readr        * 2.1.6   2025-11-14 [1] CRAN (R 4.5.2)
 rlang          1.2.0   2026-04-06 [1] CRAN (R 4.5.3)
 rstudioapi     0.18.0  2026-01-16 [1] CRAN (R 4.5.2)
```

```
 S7              0.2.1   2025-11-14 [1] CRAN (R 4.5.2)
 scales          1.4.0   2025-04-24 [1] CRAN (R 4.5.2)
 sessioninfo     1.2.3   2025-02-05 [1] CRAN (R 4.5.3)
 showtext        0.9-8   2026-03-21 [1] CRAN (R 4.5.3)
 showtextdb      3.0     2020-06-04 [1] CRAN (R 4.5.3)
 spict         * 1.3.9   2026-06-03 [1] Github (DTUAqua/spict@0c75000)
 stringi         1.8.7   2025-03-27 [1] CRAN (R 4.5.2)
 stringr       * 1.6.0   2025-11-04 [1] CRAN (R 4.5.2)
 sysfonts        0.8.9   2024-03-02 [1] CRAN (R 4.5.3)
 tibble        * 3.3.1   2026-01-11 [1] CRAN (R 4.5.2)
 tidyr         * 1.3.2   2025-12-19 [1] CRAN (R 4.5.2)
 tidyselect      1.2.1   2024-03-11 [1] CRAN (R 4.5.2)
 tidyverse     * 2.0.0   2023-02-22 [1] CRAN (R 4.5.2)
 timechange      0.4.0   2026-01-29 [1] CRAN (R 4.5.2)
 TMB           * 1.9.21  2026-03-23 [1] CRAN (R 4.5.2)
 tseries       * 0.10-61 2026-03-26 [1] CRAN (R 4.5.3)
 TTR             0.24.4  2023-11-28 [1] CRAN (R 4.5.3)
 tzdb            0.5.0   2025-03-15 [1] CRAN (R 4.5.2)
 usethis         3.2.1   2025-09-06 [1] CRAN (R 4.5.3)
 vctrs           0.7.1   2026-01-23 [1] CRAN (R 4.5.2)
 withr           3.0.2   2024-10-28 [1] CRAN (R 4.5.2)
 xts             0.14.2  2026-02-28 [1] CRAN (R 4.5.3)
 zoo             1.8-15  2025-12-15 [1] CRAN (R 4.5.3)

 [1] C:/Users/hech/AppData/Local/R/win-library/4.5
 [2] C:/Program Files/R/R-4.5.2/library
 * ── Packages attached to the search path.

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```