

A HIERARCHICAL BAYESIAN LIFE CYCLE MODEL FOR ATLANTIC SALMON STOCK ASSESSMENT AND PROVISION OF CATCH ADVICE AT THE NORTH ATLANTIC BASIN SCALE

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Table of contents

EXTENDED ABSTRACT	1
1 BACKGROUND	4
2 OUTLINES OF THE MODEL USED TO FIT THE HISTORICAL SERIES OF DATA (HINDCASTING PHASE)	7
2.1 POPULATION DYNAMIC PROCESS	7
2.1.1 Spatial structure	7
2.1.2 Stage structure and variability of life histories	8
2.1.3 Hypotheses to help partitioning the sources of temporal variability when estimating transition rates	9
2.1.4 River phase	9
2.1.5 Marine phase	10
2.1.6 Covariation among SUs	11
2.2 DATA INTEGRATION	12
2.2.1 Data integrated as fixed values	12
2.2.2 Observation equations (likelihood)	12
2.3 MCMC SIMULATIONS SETTINGS AND CONVERGENCE	17
2.3.1 Recommended MCMC settings	17
2.3.2 Note on computational time	18
2.4 EVALUATION OF THE FIT TO THE DIFFERENT DATA SOURCES	18
3 FORECASTING AND RISK ANALYSIS FRAMEWORK	19
3.1 USING THE SAME LCM FOR BOTH HINDCASTING AND FORECASTING	19
3.1.1 Nimble code - Option hindcast = TRUE/FALSE	20
3.2 PROPAGATION OF UNCERTAINTY IN THE FORECASTS	20
3.3 RISK ANALYSIS FRAMEWORK FOR THE WESTERN GREENLAND AND THE FAROES FISHERY	21
3.3.1 Parameterizing scenarios	21
3.1 PROBABILITY TO REACH MANAGEMENT OBJECTIVES	22

4	RESULTS	24
4.1	HINDCASTING - FITTING THE LCM TO THE TIME SERIES OF DATA.....	24
4.1.1	<i>Convergence of MCMC chains and model fit to the data.....</i>	24
4.1.2	<i>A widespread decline of abundances in all CSG</i>	25
4.1.3	<i>Coherence in temporal variations of post-smolt survival and proportion of fish maturing as 1SW</i> <i>25</i>	
4.2	FORECASTING AND RISK ANALYSIS.....	26
4.2.1	<i>An example of forecast for Quebec</i>	26
4.2.2	<i>Catch options for the West Greenland mixed stock fishery.....</i>	27
4.2.3	<i>Catch options for the Faroes mixed stock fisheries</i>	28
5	REFERENCES	84
6	APPENDIX 1. - PROCESS AND OBSERVATION EQUATIONS OF THE BAYESIAN LIFE CYCLE MODEL.....	88
6.1	POPULATION DYNAMICS.....	88
6.1.1	<i>Simplified life history</i>	88
6.1.2	<i>Eggs deposition</i>	88
6.1.3	<i>Egg-to-smolt transition</i>	89
6.1.4	<i>Marine phase.....</i>	90
6.2	OBSERVATION EQUATIONS.....	93
6.2.1	<i>Returns</i>	93
6.2.2	<i>Homewater catches.....</i>	94
6.2.3	<i>Catches at sea for sequential distant marine fisheries operating on mixture of stocks.....</i>	95
7	APPENDIX 2 - SENSITIVITY TO KEY STRUCTURAL HYPOTHESES (BACKGROUND INFORMATION).....	99
7.1	EGG-TO-SMOLT SURVIVAL	99
7.2	NATURAL MORTALITY RATE AFTER THE PFA STAGE	100
7.2.1	<i>Sensitivity to the average value of M.....</i>	100
7.2.2	<i>Time variations of M</i>	100
8	APPENDIX 3 - DATA SOURCES.....	101
9	APPENDIX 4 - CONVERGENCE MCMC CHAINS.....	114
10	APPENDIX 5 - FIT TO THE DIFFERENT DATA SOURCES	124
10.1	RETURNS.....	125

10.1.1	<i>North America – 1SW</i>	125
10.1.1	<i>North America – 2SW</i>	126
10.1.2	<i>Northern Europe – 1SW</i>	127
10.1.1	<i>Northern Europe – 2SW</i>	128
10.1.2	<i>Southern Europe – 1SW</i>	129
10.1.1	<i>Southern Europe – 2SW</i>	130
10.2	HOMEWATER CATCHES	131
10.2.1	<i>North America – 1SW</i>	131
10.2.1	<i>North America – 2SW</i>	132
10.2.2	<i>Northern Europe – 1SW</i>	133
10.2.1	<i>Northern Europe – 2SW</i>	134
10.2.2	<i>Southern Europe – 1SW</i>	135
10.2.1	<i>Southern Europe – 2SW</i>	136
10.3	CATCHES AT SEA	137
10.3.1	<i>LB/Newfoundland in SFA zones (3-7) (NAC fish only; no allocation among SU)</i>	137
10.3.2	<i>LB/Newfoundland/SPM – SFA zones (8-14) (NAC fish only; allocation fish from Labrador / other SU)</i>	139
10.3.3	<i>Faroese Fisheries (NEAC fish only)</i>	141
10.3.4	<i>West Greenland Fisheries (NAC and NEAC fish)</i>	144

Extended abstract

This working paper presents a new modelling framework for the stock assessment of Atlantic salmon in the North Atlantic basin. The core of the framework is a Bayesian hierarchical life cycle model which tracks the abundance of fish through time and life stages from eggs to adults that return to spawn in their homewater after one or two winters spent at sea, and for all stock units (SU) in Northern Europe, Southern Europe and North America (total 25 SU). The new model comes together with the WGNAS-SalmoGlob ToolBox that simplifies and strengthens the robustness of the stock assessment workflow from the input data to the production of catch advices (Fig. 1; Fig. 2). The new framework brings a major contribution to improve the scientific basis of Atlantic salmon stock assessment, and constitutes a benchmark for the assessment and forecast models used by ICES for Atlantic salmon stock assessment in the North Atlantic.

- In the new model, the dynamics of all SU in Northern Europe, Southern Europe and North America (25 SU) are considered within a single unified model where all SU follow a similar life history process. This represents a major improvement and a paradigm shift from the Pre Fishery Abundance (PFA) stock assessment and forecasting approach currently used by ICES. Indeed, three different and independent PFA models are currently used for Northern Europe, Southern Europe and North America and these models have different demographic structures (Chaput, 2012; ICES, 2018; Olmos et al., 2019; Olmos et al., XXX) Some core demographic hypotheses are not harmonized among these models. Specifically, the two European models explicitly consider 1SW and 2SW fish in the population dynamics, while the model for North America only considers the dynamics of 2SW fish (Chaput et al., 2005; Chaput, 2012). The North American model implicitly assumes that 2SW spawners only produce 2SW fish in future cohorts, and excludes contributions of 1SW and multi-sea-winter spawners. Temporal variations of productivities from eggs to PFA consider only the 2SW component and are therefore not comparable to productivities estimated for the European SU considering both 1SW and 2SW components of the PFA. Because of those differences one cannot evaluate the commonality in temporal trends among all SU in the North Atlantic. By contrast, the new life cycle model provides a singular harmonized framework to simultaneously assess two sea-age classes of Atlantic salmon for all SU in North America and Europe and hence allows for analyzing the commonality in the population dynamics among the 25 SU of the North Atlantic basin.
- The new model hence constitutes an important tool for future improvement of our understanding of the mechanisms driving the response of Atlantic salmon populations to variations in biological and environmental factors in a hierarchy of spatial scales. Formulating the dynamics of all SU in a single hierarchical model provides a tool for modelling covariations among different populations that may share part of their migration routes at sea and may be exploited by the same marine fisheries. It is a framework for quantifying the spatial coherence in the temporal variations of post-smolt survival and of the sea-age composition of returns for SU distributed across a broad gradient of longitude and latitude in the North Atlantic basin as a response to global scale environmental changes in the North Atlantic basin.
- The model provides estimates of marine survival from smolts to PFA stages and of the probability to mature as 1SW for the 25 SU and over more than 50 years (since 1971). Results

exhibit clear temporal signals and strong covariations among the 25 SU. The smolt-to-PFA survival exhibit an overall decreasing trend, with the survival divided by about 3 in 50 years. The probability to mature as 1SW first increases (which means a decline in the proportion of 2SW fish in the returns) and then seems to reach a plateau or even decline (especially for European fish) starting the end of the 1990's. Further statistical analysis revealed that the shared signal between the SU explains about 40% of the variability, with covariation that increases with the spatial proximity of the migration routes, which is fairly consistent with a response of populations to some large-scale synchronizing factors (Olmos et al., 2020).

- Results can be used to quantify the amount of temporal variation in those key life history traits that is accounted for by changes in sea surface temperature and primary productivity (Olmos et al., 2020). As a proof of concept, in Olmos et al., 2020, we explored if time variations of survival correlate with proxies of environmental/trophic conditions integrated over foraging habitats occupied by multiple populations during the late summer/fall, that is around the Norwegian sea for European populations and around Labrador Sea for North American populations. We found that time variations in survival was significantly negatively correlated with time variations in Sea Surface Temperature, and positively correlated with time variations in Primary productivity. These results re-enforce the hypotheses of a response of populations to large scale environmental changes. The LCM framework provide a tool to further test those hypotheses in the future and explore the opportunity to propose climate-enhanced stock assessment and advice.
- The same life cycle model is used for both the hindcasting (e.g., fitting the model on time series of historical data) and forecasting phases (forecast of the dynamics in future years after the last year of fitting) (Fig. 1; Fig. 2). All model properties are readily integrated into the forecast process: i) The model is used to forecast the population dynamics of all SU simultaneously, which is of particular interest when assessing catch options for mixed stock fisheries operating on a mixture of stocks from both North America and Europe; ii) Temporal variations in post-smolt survivals and in the proportions of fish maturing as 1SW incorporate the covariation among SU in both the hindcasting and forecasting phases. iii) All sources of stochasticity in the model (temporal variability) and parameters uncertainty (joint posterior distribution) are readily integrated in the inference and are propagated in the forecasting phases; Specifically we demonstrate the use of the life cycle model to evaluate the probability that returns in all SU achieve management objectives (expressed as total egg deposition > conservation limits or management objectives) for different catch options in both the Western Greenland and Faroes mixed stock fisheries. But the model could also be used to provide catch options for other fisheries, or to assess conservation measures for the different sea-age classes or the SU separately;
- The integrated life cycle framework is expandable and provides an opportunity to assimilate new sources of data to make the best use of all available biological and ecological information. For instance, it incorporates the possibility to provide time series of biological characteristics data to capture any potential trends (for instance any trend in the average fecundity of females that would result from trend in body size). The model also incorporates likelihood functions to assimilate genetic data to allocate mixed stock fisheries to the different stock complex. For instance, a two-stage likelihood function is used to allocate catches at West Greenland first between the North American and European stock complexes, and then between the Northern and Southern European Stock complexes. The structure is flexible and could be enhanced. For instance, as a proof of concept, another version of the model developed in Olmos et al. (2019) demonstrates the possibility to include a new likelihood function to assimilate genetic data to

allocate catches at West Greenland among all the individual SU in NAC and NEAC. Provided that the genetic data are reliable, this would provide valuable option to make the best use of the available data.

- The new framework is embedded within the WGNAS-SalmoGlob ToolBox (Hervann et al. 2021) that considerably simplifies and strengthens the robustness of the stock assessment workflow from the input data to the production of catch advices. A suite of programs in R using the Nimble package (for Bayesian estimation using MCMC algorithms) provides a consolidated streamline from hindcasting to forecasting. The suite or R-program is completed by a database and a web application accessible online via any web browser at http://sirs.agrocampus-ouest.fr/discardless_app/WGNAS-ToolBox/. The data base collates all inputs and data needed to feed the life cycle model. This represents a huge improvement as all the data and input for all SU of both Europe and North America are centralized within a single and secured data base. The web app proposes interactive tools to visualize, export and update the data (including versioning). Updated data are then automatically formatted in the appropriate format to be passed to the Bayesian life cycle model. This increases transparency in the way the data are used, and strengthens data quality control. It also provides a tool to visualize and to communicate model outputs among WGNAS members and with stakeholders, what builds confidence in stock assessment results among experts and managers.

Note on the data used

The version of the model presented in this working paper is run with the data of the ICES WGNAS report 2023. The time series of data is therefore 52 years from 1971 to 2022 (hindcasting phase). Following WKBSalmon discussions, these data are supplemented by new data on the origin of fish caught at Faroes (proportions to allocate Faroes catches among three subcomplex, Southern European complex, southern and northern and part of the Northern European complex; G. Bolstad, com pers.) and on the origin of fish caught at West Greenland (proportions to allocate European fish to the northern and the southern European complex; Tim Sheehan, com pers.). Forecasting to assess catch options at West Greenland and Faroes was performed for 3 additional years (2023-2024-2025).

1 Background

Atlantic salmon (*Salmo salar*) (hereafter A. salmon) that reproduce in rivers of eastern North America and Northeast Atlantic countries of Europe undertake wide-ranging migrations to common feeding grounds in the North Atlantic, where they are exposed to common marine environmental conditions and fisheries (Beaugrand and Reid, 2003; Beaugrand and Reid, 2012; Friedland et al., 2014; Mills et al., 2013; Olmos et al., 2019; Olmos et al. 2020). A. salmon are susceptible to be harvested at several stages in their life cycle. Some fisheries operate in high seas when population originating from various continental habitat regroup on high seas foraging areas, in coastal areas when salmon navigate before entering their natal river, or in freshwater (estuarine or river areas) during the final stages of their spawning migration. In particular, when present in the feeding grounds of West Greenland or in the vicinity of the Faroe Islands, they may be harvested in mixed stock fisheries, referred to as the high seas (or distant water) fisheries (Chaput, 2012; ICES, 2017a). A. salmon populations had been overfished during the 1960s through the 1990s with total catch in the North Atlantic maxima of about 12 000t in 1967 and 1973. Thus catches have participated to a decline of numbers of salmon returning to home rivers (Mills, 1989; Parrish et al., 1998). Catches at the West Greenland fishery reached a peak of just under 2700t in 1971 following the high development of offshore driftnet fishery in the 1960s (Dunbar and Thomson, 1979; Horsted, 1988).

The regulation of mixed stock high seas fishery was of sufficient concern that an international body (the North Atlantic Salmon Conservation Organization (NASCO; <http://www.nasco.int/>)) was formed in 1982 and a treaty subsequently signed by participating countries to manage the marine fisheries impacting different stock of A. salmon (Windsor and Hutchinson, 1994). The annual stock status reports developed by the Working Group on North Atlantic Salmon of the International Council for the Exploration of the sea (ICES/CIEM WGNAS) and the subsequent scientific advices provided to the NASCO have formed the basis for the negotiations and subsequent management of these fisheries.

To manage West Greenland and Faroes fisheries, ICES provides catch advice based on a forecast of A. salmon abundance prior to the high sea fisheries exploitation (Pre Fishery Abundance, measured at the January 1 of the first winter spent at sea, hereafter denoted PFA). A fixed escapement strategy has been adopted with the objective of achieving the spawner (or egg) requirements for the contributing stocks on both sides of the Atlantic Ocean (Chaput, 2012; Crozier et al., 2003; Crozier et al., 2004; Potter et al., 2004a).

Stock assessment models for Atlantic salmon have been developed based on data aggregated at the scale of regional or national stock units (SU) over the North Atlantic area within three continental stock groups (CSG): eastern North America (NA), Southern European (SE) and Northern European (NE) (Crozier et al., 2004; Potter et al., 2004a; Chaput et al. 2012).

These models were designed to reconstruct long term series (starting in the early 1970's) of abundance at sea before any marine fisheries (PFA) and to forecast the returns of adult salmon to their natal rivers (homewaters). These models have been incorporated in a risk analysis framework to assess the consequences of mixed stock marine fisheries at West Greenland and Faroes on the returns (Friedland et al., 2005; ICES, 2018) and to assess compliance of realized spawning escapement to conservation

limits (biological references point below which the stock should not pass) at both the SU and CSG scales.

However, PFA models suffer from three weaknesses that hinder their relevance for analyzing the demographic processes driving the population's dynamics of European and North American A. salmon populations and should be addressed in order to improve the scientific basis of A. salmon population assessment (Olmos et al., 2019; Olmos et al., XXX).

- First, PFA models used for formulating catch advice rely on a coarsely constructed stock-recruitment dynamic. Forecasts of the returns during the three years after the last assessment are based on forecasts of the productivity parameter defined as the productivity between a spawning potential (measure of the stock; expressed as a number of eggs potentially spawned each year for the two European CSG and as the potential number of spawners in the North American CSG) and abundance at the PFA stage (measure of the recruitment). This framework does not explicitly represent the population dynamics as a life cycle. Statistical inferences on the time series of productivity parameters are susceptible to time series bias because the dynamic link between PFA (the measure of recruitment) and subsequent egg depositions (measure of stock) is not represented (Massiot-Granier et al., 2014; Su and Peterman, 2012). The lack of flexibility in the statistical modelling framework also restricts the integration of the large amount of available data and knowledge on A. salmon demographics and population dynamics. As such, hypotheses on drivers and mechanisms of changes cannot be easily tested (Massiot-Granier et al., 2014; Olmos et al., 2019).
- Second, the PFA modelling workflow actually works as a combination of three models, what makes the streamlines from input data to outputs hard to handle. (1) A first model, the *run reconstruction* model relies on estimates of the abundance of fish returning to spawn and biological parameters (sex ratio, fecundity and mean proportion of smolts ages) to estimate the potential number of spawners or eggs (measure of the Stock) for each year of the time series. The same model is used to estimate the abundance of fish at the PFA stages (measure of the Recruitment), through a back-calculation procedure (similar to a Virtual Population Analysis) using data on catches at sea and hypothesis on natural mortality rates at sea. Hence, the measures of the stock and the recruitment are derived from the same data, whilst they are considered independent in the rest of the process. (2) A second part of the workflow consists of estimating the productivity parameters between the Stock and the Recruitment for all years of the historical time series, and uses time series hypothesis (random walk) to forecast the evolution of the productivity parameter during three years after the last year of the assessment. (3) In a third phase, this forecast of the productivity parameters serves as a basis to forecast the PFA and the number of fish that return to homewater based on catches scenarios at sea.
- Third, three different and independent PFA models were developed for the three CSG. Some core demographic hypotheses are not harmonized among these models. Specifically, the two European models explicitly consider 1SW and 2SW fish in the population dynamics, while the current model for NA, which was developed for catch advice purposes at West Greenland, only considers the dynamics of 2SW fish (Chaput et al., 2005; Chaput, 2012). The NA model implicitly assumes that 2SW spawners only produce 2SW fish in future cohorts, and excludes contributions of 1SW and any fish older than 2SW. Temporal variations of productivities for NA SU consider only the 2SW component and are therefore not comparable to the PFA models built for the European CSG considering both 1SW and 2SW components in marine productivity. Because of those differences one cannot evaluate the commonality in temporal trends

between all SU in the North Atlantic. This approach also ignores any covariance structure in the dynamics of the SU even though the SU may share common environments at sea and be jointly exploited in sea fisheries, and precludes evaluation of the consequences of scenarios on multiple stock complexes simultaneously (mixed stock fisheries, environmental factors).

In this working paper, we develop a Bayesian life cycle modelling framework for the combined analysis of Atlantic salmon population dynamics across all SU in the North Atlantic Ocean. We extend the framework developed by Massiot-Granier et al. (2014) (a life cycle model for one single SU) and Olmos et al. (2019) (all SU from North America and Southern Europe) to include the dynamics of 25 SU of the three CSG (North America, Southern Europe and Northern Europe). The new model brought major contributions to improve the scientific basis for Atlantic salmon stock assessment:

- The dynamic of all SU are jointly analyzed within a single unified hierarchical Bayesian life cycle approach with all populations following a similar life history process.
- It provides a framework for analyzing the mechanisms that shape population responses to variations in marine ecosystems. In particular, it allows for modelling covariations among all SU and for partitioning the effects of fisheries from the effects of environmental factors at a hierarchy of spatial scales, including at the level of the North Atlantic, of each CSG, and for each SU within a CSG.
- The integrated life cycle framework is also expandable and provides an opportunity to assimilate new sources of information to improve the ecological and biological realism of the model.
- Last, the life cycle model is a natural framework for forecasting population dynamics. The same model is used for both the inferences hindcasting (inferences) and forecasting phases, and all the model properties and sources of uncertainties are readily integrated into the forecast process. This model is a new tool to provide catch options for any marine fisheries that operate on a mixture of stocks (e.g. the West Greenland salmon fishery) and can also be used to evaluate catch options for other fisheries, or to assess conservation measures for the different sea-age classes or the SU separately.

2 Outlines of the model used to fit the historical series of data (hindcasting phase)

The life cycle model is a stage-based population model formulated in a Bayesian hierarchical state-space framework (Buckland et al., 2004; Cressie et al. 2009; Parent & Rivot, 2012; Rivot et al., 2004) that incorporates stochasticity in population dynamics as well as observation errors. We first detail the main hypotheses of the population dynamics process (the latent state process). Then we detail information on the data used to fit the model, that are directly integrated as fixed values or through likelihood function to integrate observation errors (the observation process).

All model equations and data sources are detailed in Appendix 1. A summary of background information on the sensitivity analyses to some key demographic hypotheses is provided in Appendix 2. This report doesn't detail all the data used in the model. The main data sources are given in Appendix 3. All data are available online at https://sirs.agrocampus-ouest.fr/discardless_app/WGNAS-ToolBox/.

2.1 Population dynamic process

2.1.1 Spatial structure

The model considers the dynamics of 25 SU (subscript $r = 1, \dots, N$ with $N=25$) (Fig. 3).

SU are defined on the basis of freshwater areas. All salmon within a SU are assumed to have the same demographic parameters and to undertake a similar migration route at sea. A strong hypothesis is that there is no exchange of abundance among the different SU (no straying represented among the different SU). However, the population dynamics are not independent among SU as the model includes the possibility of covariations in the temporal variation of key transition rates (e.g. marine survival, proportion of fish that mature as 1SW; see more details hereafter) to represent the effect of external factors susceptible to influence multiple population simultaneously.

The 25 SU are grouped in three large stock complexes:

- 6 SU from NA CSG, indexed by $r = 1, \dots, 6$: 1 = Labrador, 2 = Newfoundland, 3 = Quebec, 4 = Gulf, 5 = Scotia-Fundy, 6 = USA;
- 8 SU from the SE CSG, indexed by $r = 7, \dots, 14$: 7 = France, 8 = UK England and Wales, 9 = Ireland, 10 = UK Northern Ireland - FO, 11 = UK Northern Ireland - FB, 12 = UK Scotland East, 13 = UK Scotland West, 14 = Iceland South-West;
- 11 SU from NE CSG, indexed by $r = 15, \dots, 25$: 15 = Iceland North-East, 16 = Sweden, 17 = Norway South-East, 18 = Norway South-West, 19 = Norway Middle, 20 = Norway North, 21 = Finland, 22 = Russia Kola Barents, 23 = Russia Kola White Sea, 24 = Russia Arkhangelsk Karelia and 25 = Russia River Pechora.

The NE CSG is itself separated in two subcomplex to consider differences in the migration routes (which in particular results in different availability of the fishes at the Faroes fisheries):

- The southern part of the NE CSG, that comprises Iceland North-East, Sweden, Norway South-East, Norway South-West and Norway Middle (indexed by $r = 15, \dots, 19$).
- The northern part of the NE CSG, that comprises Norway North, Finland, Russia Kola Barents, Russia Kola White Sea, Russia Arkhangelsk Karelia and Russia River Pechora (indexed by $r = 20, \dots, 25$).

Note that Denmark, Netherland, Germany, Spain and Portugal (all being part of the SE CSG) are not considered in the current version of the assessment model because no complete series of data were provided to ICES WGNAS by these two jurisdictions so far.

2.1.2 Stage structure and variability of life histories

The population dynamic of each of the 25 SU is represented by an age- and stage-structured life cycle model (Fig. 4). Key demographic hypotheses are summarized in Table 1.

The model is built in discrete time on a yearly basis (subscript $t = 1, \dots, n$). It tracks the abundance of fish, males and females confounded ($N_{s,t,r}$) for each SU (r) by year (t) and life stage (s), sequentially from eggs (N_1) to 1SW (N_7) or 2SW (N_{10}) spawners for the period considered (starting in 1971, year of return to rivers) (Fig. 4; Table 2). Spawners are fish that contribute to reproduction and that survived all sources of natural and fishing mortality. All transition rates between stages s for each SU (r) in year t are denoted $\theta_{s,t,r}$.

For each SU, the model incorporates variations in the age of out-migrating juveniles from freshwater (i.e., smolt ages) and the sea-age of returning adults. Smolts migrate to sea after 1 to 6 years in freshwater (with variations among SUs). An important hypothesis is that there is no tracking of smolt-age once at sea, meaning that all transition rates applied to post-smolts at sea only depend on the migration year but are independent upon the smolt age.

Following the approach used by ICES for catch advice purposes (ICES 2020), only two sea-age classes are considered: maiden salmon that return to homewaters to spawn after one year at sea, referred to as one-sea-winter (1SW) salmon, or grilse, and maiden salmon that return after two winters at sea (2SW). This is a simplification of the larger diversity of life history traits as some maiden fish may spend more than two winters at sea before returning to spawn, and some salmon return as repeat spawners. However, the six smolt-age combined with the maiden 1SW and 2SW spawners (12 potential combinations total) already represent the essence of life history variation in North America and Europe. Also note that not all combinations really exist for all SU as the smolt-ages are generally concentrated on 2 or 3 ages in each SU (for instance, mostly age-1 and age-2 smolts in France; and mostly age-4 and age-5 in Labrador).

The model is not explicitly structured by sex. The abundance at each life-stage represents both sexes confounded. The proportion of females is only used to calculate the eggs deposition based on the spawners abundance (separately for the two sea-age classes).

Another fundamental hypothesis is that there is no heritability in the life histories. In particular, 1SW and 2SW spawners contribute to a single pool of eggs each year with all eggs considered equivalent, independently of the spawners life history.

2.1.3 Hypotheses to help partitioning the sources of temporal variability when estimating transition rates

As recognized by the data constraints already expressed in the existing PFA models used by ICES (ICES 2020) and discussed by Chaput (2012), Massiot-Granier et al. (2014) and Olmos et al. (2019), the quality and information provided by the data are limited, which restricts the number of transition rates that can actually be estimated.

The framework is primarily designed to provide estimates of *i*) abundance at various life stages along the life cycle; *ii*) exploitation rates of all fisheries; *iii*) post-smolt marine survival rates from out-migrating smolts to the PFA stage; *iv*) and proportion of fish that mature at the PFA stage, for each SU and with temporal variation over the time series (Fig. 4; Table 1 and 2).

To partition the temporal variability in the natural and fishing mortality during the freshwater and marine phase and in the proportion of fish that mature at the PFA stage, we use the framework described by Massiot-Granier et al. (2014) and Olmos et al. (2019):

- The survival rate from eggs to smolts is stochastic among years (lognormal) but with average value and variance fixed and homogeneous among all SU. Lognormal stochastic variations are independent across time (no temporal autocorrelation) and across SU (no spatial covariation).
- The allocation of the total number of smolts in a cohort to different smolt-ages is deterministic using fixed (provided in the data) proportions of smolt ages.
- Temporal variability of the transition rates of the marine phase only occurs between smolt migration and the PFA stage (defined as abundance of post-smolts at January 1 of the first winter at sea). This transition is decomposed in two steps: natural survival rate from smolt to the PFA stage (estimated), and the proportion of fish that mature at the PFA stage (estimated). After the PFA stage, all transition rates result from the combination of the fishing and natural mortality. The natural mortality (mortality rate per month) after the PFA stages is fixed and homogenous among all SU. The fishing mortality rate are estimated and can vary over time.

The sensitivity of model results to these hypotheses has already been explored by Massiot-Granier et al. (2014) and Olmos et al. (2019) in previous versions of the model. Summary of the main results is provided in the Appendix 2.

2.1.4 River phase

The number of eggs spawned in each SU by year are derived from the annual number of returning 1SW and 2SW spawners, multiplied by the proportion of females and the fecundity of females. 1SW and 2SW spawners contribute to a single pool of eggs each year with all eggs are considered equivalent, independently of the spawners life history (Fig. 4; Table 1 and 2). Both the proportion of females and the fecundity are provided in the data specifically for each sea-age class, SU and year. Note however

that for almost all SU, no information on the time variation of those biological characteristics are available in the data series so far.

In the absence of information on the total smolt production at the scale of SU, the average value of the transition rates between eggs and out-migrating smolt is fixed. In the configuration presented here (but see Olmos et al. (2019) for a sensitivity analysis to other modelling option, including density dependence), the eggs-to-smolt survival is density-independent, and modelled as lognormally distributed around an average of 0.007 (0.7%) with random variations ($CV=0.4$) independent across SU (no spatial covariation) and years (no temporal autocorrelation). As fecundity and average freshwater survival are fixed, the only source of stochasticity in the freshwater phase of the life cycle is due to these lognormal independent random deviations.

The total number of smolts produced by a cohort is attributed to river-age classes using SU specific smolt age proportions which are fixed in the data. The allocation to the different smolt ages is deterministic. The proportion of smolt-ages in the data are potentially variable in time depending on the data provided for each SU.

2.1.5 Marine phase

Smolts of different ages migrating seaward in any year t are pooled together once at sea (Fig. 4; Table 1 and 2). An important hypothesis is that there is no tracking of smolt-age once at sea, meaning that all transition rates applied to post-smolts at sea are independent upon the smolt age. Return rates from smolts to 1SW and 2SW adults result from the combination of natural mortality, fishing mortality, and a maturation schedule. The natural mortality before and after the PFA stages are partially confounded (see Massiot-Granier et al. (2014) and Olmos et al. (2019) for a discussion). To avoid statistical confusion, temporal variability is allowed in the natural mortality before the PFA stage and in the proportion of maturing PFA, but the natural mortality at sea after the PFA stage is fixed.

Survival from smolts to the PFA stage is estimated with temporal variability and variability among SUs (Table 2 and 3). Fish at the PFA stage can then mature (and return as 1SW adults) or delay maturation until the following winter (and return as 2SW adults). The proportion of fish maturing as 1SW is estimated with temporal variability and variability among SUs. The model explicitly incorporates spatial covariations among SU in those two key demographic parameters (see hereafter).

After the PFA stage (mature and non-mature PFA), transitions are modelled as a sequence of stages until the spawners with alternation of period of migration with natural mortality only and fisheries operating at sea on mixture of SU, as well as final homewater fishery (between return and spawner stage) specific to each SU. The sequence of those different periods varies depending on the North American or European origin of fish, with the West Greenland fishery that is common to all fish. Details on those sequence are provided in Fig. 5 and Tables 5 (for North American fish) and & Table 6 (for European fish).

The natural mortality rate at sea after the PFA stage is fixed, assumed constant in time, homogeneous among all SUs, and identical for maturing and non-maturing fish ($M = 0.03 \cdot month^{-1}$). This natural mortality rate is weighted by the duration of the different period fixed in the data (in months; Table 5 and 6). Under this assumption, the difference in natural mortality after the PFA stage between SU and between 1SW and 2SW fish is entirely conditioned by the difference in the duration between PFA and

1SW and 2SW returns. An additional natural mortality rate (with values fixed in the data) is added between the returns and the spawner stages.

Fishing mortality is modelled as a sequence of fisheries operating on mixtures of SU along the migration routes, as well as on each SU in homewaters (Fig. 5; Tables 5 & Table 6; but see more details on the marine fisheries in the Data Integration section below).

For each fishery and each year, catches (number of fish that die from the fishery) are calculated by multiplying the abundance of fish before the fishery with the harvest rate associated with the fishery and year under concern. Those catches are then considered to be observed with observation errors (see hereafter). Fisheries exploitation rates are estimated and are assigned weakly informative priors (Table 3). They vary by year and SU or group of SU depending on the available data to allocate the catches to the different SU or groups of SU.

2.1.6 Covariation among SUs

The model explicitly incorporates two components of temporal covariation among all SUs (Fig. 5).

First, the post-smolt survival (denoted $\theta_{3,t,r}$) and the proportion of fish maturing as 1SW (denoted $\theta_{4,t,r}$) are modelled as multivariate random walks in the logit scale which captures spatial covariation associated with environmental stochasticity. Random variations are drawn from multivariate Normal distributions in the logit scale with variance-covariance matrices Σ_{θ_3} and Σ_{θ_4} (Minto et al., 2014; Ripa and Lundberg, 2000) (Table 3):

$$(1) \quad \left(\text{logit}(\theta_{3,t+1,r}) \right)_{r=1:N} \sim \text{MVNormal} \left(\left(\text{logit}(\theta_{3,t,r}) \right)_{r=1:N}, \Sigma_{\theta_3} \right)$$

$$(2) \quad \left(\text{logit}(\theta_{4,t+1,r}) \right)_{r=1:N} \sim \text{MVNormal} \left(\left(\text{logit}(\theta_{4,t,r}) \right)_{r=1:N}, \Sigma_{\theta_4} \right)$$

with N = the number of SU in the model (here $N=25$). The pairwise correlation matrix ρ can be calculated from the variance-covariance matrix:

$$(3) \quad \rho = \sqrt{\text{diag}(\Sigma)}^{-1} \times \Sigma \times \sqrt{\text{diag}(\Sigma)}^{-1}$$

The multivariate RW is a simple and flexible structure for modelling trends and shifts over time. Previous studies have used RW assumptions with covariation to model coherence in temporal variations among populations (Minto et al., 2014; Peterman et al., 2000). No a priori hypothesis on the sign of covariation among SUs is made in our approach, and inferences on covariation and correlation among SUs are derived directly from the posterior distribution of the model parameters.

The second source of covariation among SU is the harvest dynamics of the sequential marine fisheries that operate on mixtures of SUs, with the portfolio of SU available for each fishery dependent on marine migration route hypotheses (Fig. 5 and section below describing the data used to allocate the proportion of catches among the different SU). In particular, when allocating catches at sea among different SU, using the hypothesis of a homogeneous harvest rate among SU generates strong covariation in the fishing mortality among the different SU.

2.2 Data integration

Two different streams are used to integrate data in the modeling approach : i) some data are directly integrated as fixed values ; ii) data are integrated through likelihood function to integrate observation errors (the observation process) (Table 4). Appendix 3 provides the main data sources. All data are available at https://sirs.agrocampus-ouest.fr/discardless_app/WGNAS-ToolBox/.

2.2.1 Data integrated as fixed values

The model integrates data in the form of fixed parameters values:

- The average value and the CV of the eggs-to-smolt survival rate, fixed to 0.7% and 0.4, respectively;
- The proportion of smolt-age (between 1 and 6). They are specific to each SU and may vary among years;
- The natural mortality rate at sea (after the PFA stage), fixed to $M = 0.03 \cdot month^{-1}$;
- The duration (in months) of the different period separating the sequential fishery at sea (see Table 5 and 6). They are used to calculate the natural mortality during the different period at sea. They are fixed over time (no variation among years) but may vary among SU;
- Additional mortality rates between returns and spawners. They are specific to each SU and may vary in time. In practice (data set WGNAS 2023) 0 for all SU except Scotland West and East;
- The proportion of delayed spawners. These are fish that return year t but delay spawning to the year after. They are specific to each SU and may vary among years. In practice 0 for all SU except the four Russian SU;
- The biological characteristics of fish at the spawner stage. These include the proportion of females and the average egg deposition per female. These are defined for 1SW and 2SW fish separately, specific for each SU and may vary among years.

2.2.2 Observation equations (likelihood)

2.2.2.1 A sequential approach used to integrate data with observation errors

The model is fitted to time series of data for years $t = 1, \dots, n$ (n being the last year of the hindcasting phase) with observation errors. This includes data on the returns and catches (marine and homewater fisheries) for each year and sea-age class separately (Table 4). The full likelihood function for the general state-space model is built from the combination of all observation equations for the returns, homewater catches, and catches at sea, for 1SW and 2SW separately.

A sequential approach (Michielsens et al., 2008; Staton et al., 2017) is used that consists of (i) processing observation models separately to reconstruct probability distributions that synthesize

observation uncertainty around the time series of catches and returns for the 25 SUs; and (ii) using those distributions as likelihood approximations in the population dynamics state-space model.

Using such a sequential approach represents a trade-off between model realism and computational efficiency (Maunder and Punt, 2013; Staton et al., 2017) and has two main advantages. First, it enhances computational efficiency. Indeed, building an integrated model that explicitly integrates specific observation models for each SU (Maunder and Punt, 2013; Rivot et al., 2004; Schaub and Abadi, 2011; but Massiot-Granier et al., 2014 for an application to a bayesian salmon life cycle fitted to the Scotland data) would dramatically increase the complexity of the full model. It would considerably increase the computational cost and the calculation time needed to reach convergence of MCMC chains. In addition, such a sequential approach considerably enhances modelling flexibility. Indeed, separating out the population dynamics itself from the models that integrate the raw data to provide estimates of returns or catches at the scale of each SU provides a flexible framework where any improvements of the observation models can be done without impacting the structure of the population dynamics model. Hence, continuous improvement of the models developed locally to maximize the use of available data and knowledge can be envisaged with minimum impacts on the population dynamics model and on the entire workflow.

Probability distributions for returns and catches are derived from a variety of raw data and observation models, specific to each SU (except for the mixed stock fisheries at sea) as originally developed by ICES to provide input for PFA models. These are directly derived from the Run Reconstruction (RR) models run by ICES WGNAS, separately for the three continental stock grouping.

The version of the model presented in this WP is fitted to the data of the ICES WGNAS 2023 report (ICES, 2023). Subscript $t = 1, \dots, n$ hence stands for the time series 1971 to 2022 with $n=52$.

ICES (2023) provides a shorter time series of data for Northern NEAC SU because some data are missing for Norway for the first time of the time series before 1982. In order to have the same length of data series for all SU (1971-2022), the Norwegian data were complemented using some best guest hypotheses (*Com pers.* Geir Bolstad and Peder Fiske, NINA; see details in Appendix 1).

2.2.2.2 Abundance of returns

Lognormal distributions were used to approximate the likelihood of the returns (Table 4; see data in Appendix 3). Observations errors are considered as independent among sea-age, year and SU. Lognormal distributions are fitted to the Monte Carlo draws of estimated returns provided by Run Reconstruction models. Expected mean and the standard deviation of those lognormal distributions (for each sea-age class, year and SU) are provided as input for the life cycle model. We forced the CV of those lognormal to have a minimum value of 0.05 as too small $CV < 0.05$ seriously limit mixing and convergence of MCMC chains.

2.2.2.3 Homewater fisheries

The homewater fisheries pool all fisheries capturing returning fish in coastal, estuarine and freshwater areas. Lognormal distributions are used to approximate the likelihood of the homewater catches (Table 4; see data in Appendix 3). Observations errors are considered as independent among sea-age, year and SU. The expected mean for each sea-age class, year and SU are extracted from Run Reconstruction models. Because homewater catches are generally provided with small observation

errors, and to avoid double count of observation errors in both the returns and the homewater catches, we use lognormal likelihood with the expected mean provided by the RR models and relative errors arbitrarily fixed to a CV = 0.05 around the point estimates.

2.2.2.4 Distant marine fisheries

The model represents the different fisheries at sea where the fish from the different SU are susceptible to be caught at different life stages along their migration route (Fig. 5; Table 5 & 6).

Fish from North American SU may be exploited in the marine fisheries of Newfoundland (NFLD), Labrador (LAB) and at Saint-Pierre et Miquelon (SPM) at different life stages. LAB, NFLD and SPM fisheries exploit a mixture of SU from North America only. Fish from North America are also susceptible to be exploited in the West Greenland (WG) marine fishery, together with fish from European SU.

Salmon from all European SU may be caught in the Faroes (FA) marine fishery at different life stages, and are also susceptible to be exploited in the WG fishery (together with fish from North America). Although a small (but non-negligible) proportion of fish originating from North America are caught at FA, the present version of the model supposes no fish from North America are caught there, and fish originating from NA in the catches have been retrieved from the Faroes catch data.

Fish originating from North America and Europe can eventually reach the common feeding grounds in WG after the 1st winter at sea. The WG fishery hence potentially harvests non-maturing salmon from a mixture of stocks from all SU from North American and Europe (although the proportion of fish originating from Northern Europe is low).

Distant marine fisheries operate on mixture of stocks. For each of the marine distant fishery, the likelihood equations associated with catches at sea essentially consist of two sets of likelihood terms:

- lognormal distributions of observation errors of the total catches by sea age class (in number of fish), summed over all SU exploited by the fishery under concern;
- complemented by Dirichlet likelihood for the proportion of catches allocated to different groups of SU when those data are available (Faroes and West Greenland fisheries). When those data are not available (or considered not reliable enough to be used), the catches are allocated to the different SU exploited by the fishery under concern using the hypothesis of a homogeneous harvest rate among SU. This is equivalent to considering that the different SU are harvested proportionally to their abundance in the mixture of stocks at the stage just before the fishery.

In this version of the model, data are only available to allocate catches to large groups of SU. Those data are then used in a multilevel allocation rules, where a Dirichlet likelihood functions are first used to allocate the catches among large groups of SU. Then, the allocation of catches at a lower level within groups is done assuming a homogeneous harvest rate among all SU within each group.

Observation errors on the total catches and on the proportions are considered independent across fisheries, years and SU.

Newfoundland, Labrador and Saint-Pierre et Miquelon fisheries exclusively operating on a mixture of North American SUs

Fish from North American SUs maturing in the first year at sea (1SWm) may be exploited on their return migrations to rivers in the marine fisheries of NFLD, LAB and SPM (Table 5; Fig. 5; see data in Appendix 3). One can actually distinguish three different fisheries:

- The Labrador fishery (commercial catches and subsistence fishery) that operate on 1SWm and 2SW fish but that is supposed to not impact the 1SWnm stage;
- The fishery operating in South-Western Newfoundland (SFA zones 8-14) and Saint Pierre et Miquelon that also operates on 1SWm and 2SW fish but that is supposed to not impact the 1SWnm stage;
- The fishery operating in North-Eastern Newfoundland (SFA zones 3-7) that is supposed to operate on 1SWm, 1SWnm and 2SW fish.

To simplify the approach, the Labrador fishery and the South-Western Newfoundland + SPM (SFA zones 8-14) fishery were pooled in the data as they operate on the same life stages.

Labrador and South-Western Newfoundland + SPM fishery (SFA zones 8-14)

The data of those fisheries operating in two different areas are pooled to simplify the model. and to impact all North American SU. Those fisheries operate on 1SWm and 2SW only. Data and expert opinion are first used to partition catches of 1SWm and 2SW fish originating from Labrador from those originating from the five other North American SU (ICES 2017a; 2017b) (Table5; Fig. 5).

For 1SWm and 2SW separately, and for each year, total catches of fish originated from Labrador, and the total catches of fish originated from the five other SU are considered to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty essentially due to the conversion from catch in weight to number of fish.

A specific harvest rate is estimated for fish originating from LB. In the absence of data to differentially allocate catches to each of the five other North American SU (all except Labrador), catches of fish originating from the five other North American SU are assigned assuming that harvest rates are homogeneous among the five SU (ICES 2017a; 2017b).

North-Eastern Newfoundland fishery (SFA zones 3-7)

This fishery is supposed to operate on 1SWm, 1SWnm and 2SW and to impact all North American SU (Table 5; Fig. 5).

Total catches of fish originated from all SU in North America are considered to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty essentially due to the conversion from catch in weight to number of fish.

In the absence of data to differentially allocate catches to each of the six North American SU, catches of fish originating from the six North American SU are assigned assuming a harvest rate homogeneous among all SU (ICES 2017a; 2017b).

Faroes Fishery exclusively operating on mixtures of European SUs

Fish from European SUs maturing in the first year at sea (1SWm) may be exploited on their return migrations to rivers in the Faroes marine fishery (Fig. 5; Table 6; see data in Appendix 3). Salmon that

do not mature during the first year at sea (1SWnm) may be caught in the Faroes fishery as 1SWnm. 1SWnm that survive to the Faroe fishery then migrate to the WG feeding grounds where they are susceptible to be harvested together with fish from North America. Survivors may finally be caught as 2SW salmon on their migration to home waters in the Faroes fishery. Even if the three stages 1SWm, 1SWnm and 2SW are impacted by this fishery, most of the catches at Faroes are realized on 2SW fish.

For each of the three age-class separately (1SWm, 1SWnm and 2SW), and for each year, total catches of fish caught at Faroes are assumed to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty essentially due to the proportion of unreported catches and of wild fish in the catches.

Total catches of 1SWm and 1SWnm and 2SW at Faroes are then allocated to the different SU following a two levels allocation rule (Fig. 6):

- **Level 1.** First, the total catches are allocated to three large groups of SU using proportion based on the relative harvest rate estimated from genetic assignment data (Geir Bolstad, com pers. 2023):
 - The Southern European CSG (France, UK England and Wales, Ireland, UK Northern Ireland - FO, UK Northern Ireland - FB, UK Scotland East, UK Scotland West, and Iceland South-West).
 - The southern part of the Northern European CSG, that comprises Iceland North-East, Sweden, Norway South-East, Norway South-West and Norway Middle.
 - The northern part of the Northern European CSG, that comprises Norway North, Finland, Russia Kola Barents, Russia Kola White Sea, Russia Arkhangelsk Karelia and Russia River Pechora. Genetic data indicate that proportion of those fish in the FA catches is much less than their proportion in the abundance, which indicates different (further east and north) migration routes.
- **Level2.** Second, within each of the three groups, catches are assigned to the different SU that compose the group assuming that exploitation rates are homogeneous among SU.

West Greenland fishery operating on mixture of North American and European SU

This fishery is assumed to operate on the 1SWnm component of the populations. Catches of 1SWnm at WG may originate from any of the 25 SU from all CSG (Fig. 5; Table 5 & Table 6; see data in Appendix 3). The total number of 1SWnm fish caught at WG is assumed to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty due to the conversion from catch in weight to number of fish.

Total catches are then allocated to the different SU following a three levels allocation rule (Fig. 7):

- **Level 1.** First, total catches are allocated to the North American or European complexes using proportions calculated from a compilation of individual assignment data based on discriminant analyses of scale characteristics and genetic analyses(ICES 2017a; 2017b).
- **Level 2.** Second, within the European stock complex, catches are allocated to the Southern or Northern European CSG using proportions calculated from a compilation of individual assignments (Tim Sheehan, com pers. 2023).
- **Level 3.** Third, within each of the three groups, catches are assigned to the different SU that compose the group assuming that exploitation rates are homogeneous among SU.

2.3 MCMC simulations settings and convergence

Bayesian posterior distributions were approximated using Monte Carlo Markov Chain (MCMC) methods in *Nimble* (<https://r-nimble.org/>) through the *rnimble* (www.Rproject.org) package.

Sampling efficiency for this model is relatively low, meaning that a long MCMC simulation is needed to obtain reasonable convergence to the posterior distribution and reliable results.

2.3.1 Recommended MCMC settings

- Use well-chosen initial values for the MCMC chains. To minimize numerical issues, we recommend simulating initial values directly from the Nimble model to ensure the consistency of initial values with the model. We also recommend using initial values close to the posterior to avoid initializing the model in a region of the parameters space where the likelihood is too low. An R-code using the Nimble model to simulate appropriate initial values for the MCMC chains is provided.
- Run multiple independent MCMC chains (e.g., 10 chains) with different initialization values. Running multiple chains (>2) is needed to check mixing and convergence. Also, running multiple chains in parallel on multiple cores saves computational time as the total number of MCMC iteration resulting from the collation of all the chains can be used as if they were generated from a single (but much longer) chain.
- Run the model during a relatively long period before storing the results to let the algorithm adapt and optimize. We recommend to discard the first 25000 iterations before storing (burnin = 25000).
- For each chain, use at least 250000 MCMC iterations after the burnin period for final inferences. In any case do not reduce the size of MCMC chains without carefully checking the convergence and the effective sample size of MCMC samples for all variables.
- The level of autocorrelation of MCMC chains is very high (still significant at lag 250), and we then recommend using a large thinning of MCMC chains to avoid storing too large MCMC samples with poor information. We recommend a thinning of at least 250. Running 250000 iterations with a thin=250 will result in a sample of 1000 iterations/chain kept for inferences.
- Monitor mixing of the chains for all parameters and variables in the model, and formally assess convergence. We especially recommend to assess convergence of key transitions rates, the smolt-to-PFA survival (θ_3) and the proportion maturing PFA (θ_4), but also of the abundance of fish in key life stages like the total abundance of smolts per cohort, the abundance at the PFA stage (total, mature and non-mature), and the abundance of returns (1SW and 2SW).

We recommend assessing convergence of MCMC chains using the *Rhat* Gelman-Rubin statistic (Brooks and Gelman, 1998) as implemented in the R Coda package (*gelman.diag()*). This statistic calculates the ratio between the variance calculated between MCMC chains and within MCMC chains. MCMC chains that have converged should generate values close to 1. The value 1.05 is commonly accepted as a rule of thumb and values greater than 1.05 may signal a lack of convergence. We also recommend to complement convergence assessment through visual checking of the mixing of multiple chains using *traceplot* of MCMC chains.

Running 10 MCMC chains in parallel under this configuration should ensure convergence of MCMC chains for all variables in the model. Note however that the *Rhat* statistics is calculated by assessing the mixing of 10 chains, but that final inferences are derived from a much larger sample resulting from the collation of the 10 chains. Then a *Rhat* statistics above 1.05 (based on the length of one chain) does not necessarily mean the sample resulting from the collation of the 10 chains does not provide a good approximation of the posterior distribution. Visual inspection of the mixing of MCMC chains can be used to confirm the good mixing.

The MCMC settings should also ensure the final MCMC sample (resulting in collating the MCMC samples of the 10 chains) has a minimum effective sample size as implemented using R Coda package (*effectiveSize()*) of at least 1000 for all variables, which is usually large enough to make good Monte Carlo approximations for any key management quantities, including probabilities in the tails of the posterior (Monnahan et al. 2019).

2.3.2 Note on computational time

The MCMC settings described above (10 chains in parallel; burnin = 25000; 250000 iterations; thin = 250 → resulting in 1000 iterations/chain saved) takes ~ 12 hours to run with a personal Laptop (Intel Core i9-9880H - 2.30Ghz). But due to the number of core as well as the memory required, we advise running the model on a server.

2.4 Evaluation of the fit to the different data sources

The whole likelihood function of integrated models results from the combination of multiple likelihood terms associated to the different data sources. In addition to the data directly integrated as fixed values in the model (e.g., biological characteristics) the LCM integrates four main data sources through likelihood terms (with observation errors):

- Abundance at the return stage (1SW and 2SW) - Lognormal likelihood
- Homewater catches (1SW and 2SW and delayed spawners) - Lognormal likelihood
- Catches of all fisheries at sea (1SW mature, 1SW non-mature, 2SW) - Lognormal likelihood
- Proportion of the different origins in the catches at sea - Dirichlet likelihood

The quality of fit of the model to the different data sources is assessed through the comparison between the posterior distribution of state variables in the model and the associated data. When observation errors are associated to one data source, the posterior distribution of the state variable is compared to the probability distribution that corresponds to observation errors (e.g., lognormal distribution of returns with known expected mean and standard deviation).

In this version of the model, comparisons are only qualitative. In a previous version of the model, Olmos et al. (2019) have implemented the calculation of Bayesian *p-values* for posterior checking. Those are useful synthetic indicators of the capacity of the model (once fitted a posteriori) to replicate data similar to the one that are used to fit the model. Similar diagnostics of quality of fit will be developed in the future.

3 Forecasting and risk analysis framework

Once fitted to the data, the life cycle model can be used to forecast the population dynamics during n_f years starting after the last year of the assessment, under any specific scenario. Forecasts are probabilistic and allow to compute, for any scenario, the probability distribution of any quantity in the model.

Following ICES WGNAS practices, the life cycle model is used to forecast the population dynamics during n_f years starting after the last year of the assessment, under different catches scenarios in the Faroes and Greenland mixed stock fisheries (Fig. 1, Fig. 2). We used probabilistic forecasts from the model to evaluate the probability that future returns of adult fish (after the last years of the hindcasting phase) fall above management objectives for different catch options in the Western Greenland and the Faroes fisheries.

In this application, the population dynamics is forecasted during $n_f = 3$ years. Forecast is therefore 2023-2025. But note that n_f is a parameter that can be changed easily if longer or shorter forecast are required.

3.1 Using the same LCM for both hindcasting and forecasting

A critical advantage of the LCM framework is that the same life cycle model is used for fitting the historical time series and forecasting. In practice, one unique life cycle model code written in Nimble is used for both the hindcasting and the forecasting phases. This ensures model consistency between the two phases and limits errors as no re-coding is required between the two phases. In addition, because the same model is used for hindcasting and forecasting, the posterior MCMC samples from the hindcasting phase can be easily re-used to propagate parameters uncertainty in the forecasts.

Note however that the Nimble code used for hindcasting should be slightly adapted to simulate the population dynamics under catches scenarios (forecasting).

First, the observation equations that are critical part in the hindcasting phase to assimilate the data in the Bayesian model must be deleted (or “muted”) when the model is used for forecasting.

Second, all equations for the transitions that involve a fishing mortality must be modified. Indeed, for the hindcasting phase, the following modelling structure applies for any marine fishery: for any marine fishery f , operating in year t on a number of fish $N_{f,t,r}$ originated from the stock unit r with an exploitation rate $h_{f,t,r}$, the catches $C_{f,t,r}$ (considered as unknown states) and the number of fish that escape the fishery $N_{f,esc,t,r}$ are modelled as:

$$(4.1) \quad C_{f,t,r} = h_{f,t,r} \times N_{f,t,r}$$

$$(4.2) \quad N_{f,esc,t,r} = (1 - h_{f,t,r}) \times N_{f,t,r}$$

Harvest rates $h_{f,t,r}$ and catches $C_{f,t,r}$ are both unknown and estimated from the data. A likelihood function relates the true catches $C_{f,t,r}$ to observed catches, so as to estimate the catches and the harvest rates.

In the forecasting phase, catches are no more unknown states variables but fixed quantities $C_{f,t,r}^{Scenarios}$ defined by the scenario. They are a fixed control variable for the population dynamics. Equations (4.1) and (4.2) should then be changed as:

$$(5) \quad N_{f,esc\ t,r} = N_{f,t,r} - C_{f,t,r}^{Scenarios}$$

The catches assigned to each stock unit r , $C_{f,t,r}^{Scenarios}$, are defined by allowing the total catches defined by the scenario (for instance the total catches at West Greenland) to the different stock units following the same rule that the one defined during the hindcasting phase (see details in section 3.3.1 below).

3.1.1 Nimble code - Option *hindcast* = TRUE/FALSE

In practice, a Nimble syntax trick is used to modify the Nimble code so that it can be used in both hindcasting and forecasting mode. This mainly consists in using “if (*hindcast*=TRUE) {}” tags in the code that indicate the lines of codes that should be deleted (or “muted”) and eventually replaced when passing from the hindcasting to the forecasting mode. More specifically, when the model is used in forecasting mode, all observation equations (likelihood) are deleted, and transitions involving fishing mortality are modified.

3.2 Propagation of uncertainty in the forecasts

Forecasts integrate and propagate all sources of uncertainty from the hindcasting phase. It integrates both process errors, e.g., environmental stochasticity due to the stochastic temporal variations of key transitions rates, and parameters’ uncertainty quantified by the joint Bayesian posterior distribution of all estimated parameters (Fig. 2).

For any given scenario, uncertainty is integrated through Monte Carlo simulations, by simulating a large number (denoted N_{simul}) of population trajectories with parameters and the abundance in different life stages randomly drawn in the joint posterior distribution which captures the covariance structure among all unknowns in the model. This is realized in practice by repeating the sequence below N_{simul} times:

- randomly draw values for a set of parameters and estimated abundance in different life stages in the joint posterior MCMC samples stored from the hindcasting phase
- given these parameters values, simulate one population trajectory using the Nimble code for the LCM set in its “forecasting mode”

When forecasting during 3 years as it is the case in this application, most of the uncertainty in the forecasts comes from the uncertainty in the key transition rates that control the smolt-to-PFA survival (the marine productivity) and the proportion of fish at the PFA stage that mature the first year at sea.

Indeed, because of the time delay between the egg deposition and the smolt production (minimum 2 years for age 1 smolts), uncertainty coming from the forecasted egg deposition and subsequent cohorts will impact returns later on that three years after the last year of the hindcasting phase. Forecast are therefore mostly conditioned by the hypotheses made to model the temporal variation of key demographic parameters during the hindcasting phase. In particular, for each simulated trajectory, stochastic variations of the smolt-to-PFA survival and the proportion of maturing PFA are forecasted following the multivariate random walks defined at equations (1)-(2). Because of the random walk hypothesis, the forecasted smolt-to-PFA survival and proportion maturing PFA during the forecasting period will remain at the same average level than the last year of the fitted time series, but with an uncertainty that increases quickly with time due to error propagation through the random walk (Fig. 8).

3.3 Risk analysis framework for the Western Greenland and the Faroes fishery

SUs from North American and Europe are all potentially harvested by the West Greenland fishery (although the proportion of fish originating from Northern Europe is very low in West Greenland catches). A risk framework for the provision of catch advice for the West Greenland fishery has been applied since 2003 by NASCO and ICES (ICES, 2013). Only fish from European origin are potentially harvested at the Faroes fisheries. There is currently no agreed framework for the provision of catch advice for the Faroes fishery adopted by NASCO. However, NASCO has asked ICES, for a number of years, to provide catch options or alternative management advice with an assessment of risks relative to the objective of exceeding stock conservation limits for salmon in the European area.

Probabilistic forecasts from the model are used to evaluate the probability that future returns of adult fish reach management objectives for different catch options in the Western Greenland and the Faroes fisheries. As an important contribution, our new life cycle model provides a unified framework for evaluating catch options for the Faroes and West Greenland for all SU separately or simultaneously.

3.3.1 Parameterizing scenarios

In this WP, we illustrate the framework by simulating catches scenarios ranging from 0 to 500 tons (11 scenarios with values every 50 tons) for both the Faroes and the West Greenland catches.

Catch options. For each scenario, catch options (defined in tons) are converted to number of fish really caught after consideration of unreported catches rates, the conversion from weight to number of fish (using mean weight of fish) and sharing agreement rule. There is no uncertainty in this conversion so far.

Sharing agreement. The current version of the model uses sharing agreement options as defined historically as management options funded on a social agreement on what might be equitable use of resources. Implementation in the LCM consists in setting homewater catches and all other marine fisheries at zero and scaling the total fish caught at Faroes or West Greenland following the sharing agreement rule. For the West Greenland fishery, sharing agreement rule were defined historically as 40%/60%. This means that a scenario of say, 100 tons, actually corresponds to $100/0.4 = 250$ tons of

fish caught. For the Faroes fishery, sharing agreement rule were defined historically as 8.4%/91.6%. This means that a scenario of say, 100 tons, actually corresponds to $100/0.084 = 1190$ tons of fish caught.

Catches allocation. In forecasting, catches at Faroes and West Greenland from the scenarios are allocated to the different continental stock groups and SU the same way Faroes and West Greenland catches are partitioned in the model during the hindcasting phase. Proportions used to allocate the catches among stock complexes (proportions at Level 1 for the Faroes fisheries and at Level 1 and 2 for the W. Greenland fishery) are considered constant during the forecasting phase (no time variations). They are directly derived from the hindcasting phase, and set equal to the average realized proportions calculated in the model over the last five years of the hindcasting phase. The posterior uncertainty (from MCMC draws) around those proportions is therefore considered in the simulations. Within each stock complex, proportions used to allocate the catches among SU (proportions at Level 2 for the Faroes fishery and at Level 3 for the West Greenland fishery) are calculated in the model as the relative proportions of abundance. This is therefore equivalent to the homogeneous harvest rate hypotheses used in the forecasting phase. The posterior uncertainty (from MCMC draws) around those proportions is also considered in the simulations.

All other fisheries. In all scenario, all other fisheries except the Faroes and Greenland are set to 0 catches. This means that the framework is not expected to provide any advice on the way the total catches should be managed by the different countries.

Other settings. All other parameters needed to define the population dynamics during the forecasting phase (e.g., smolt-age proportions, proportion of females in returns, fecundity ...) are set to their average calculated over the last five years of the hindcasting phase, and considered constant (no time variation) during all forecasted years.

3.1 Probability to reach management objectives

As a purpose of illustration in this WP, management objectives (MO) are defined in number of eggs and are directly deduced from the values provided by ICES (2021) (see Table 7). Management objectives are based on Conservation Limits (CLs) as defined by ICES and NASCO or using other rules agreed by ICES.

For any scenario, the forecasted egg deposition by spawners (e.g. after all potential fisheries) is then compared to the management objectives expressed in number of eggs as defined above. Forecasts are probabilistic and allow to compute, for any scenario, the probability that the egg deposition overreach management objectives. The probability are directly calculated from Monte Carlo trials.

Sea-age class

It is straightforward to calculate the total egg deposition realized by 1SW and 2SW fish, or for the two sea-age class separately. The compliance to the management objectives can be provided for all sea age class combined or for the two sea-age class separately. The model can also assess the proportion of eggs spawned by 2SW fish. Assessing the compliance to MO for 2SW specifically or the proportion of eggs spawned by 2SW fish allows investigating the sensitivity of this component of populations to the catch scenarios. This is especially the case of the West Greenland fishery that exclusively target the

non-mature component of the salmon abundance at sea, and the Faroes fishery that preferentially target the 2SW fish on their returning migration to homewaters. The sensitivity of the proportion of eggs spawned by 2SW to these fisheries is an indicator of the selectivity of the fishery relative to the sea-age class and of its potential evolutionary impact.

Spatial aggregation and probability that several SU reach MO simultaneously.

The model works at the scale of SU (25 SU) but results can be aggregated at any scale. This allows managers to evaluate both individual (country level), aggregated and simultaneous achievement of MO.

- **Country scale.** Management objectives used by ICES are only available at a more aggregated spatial scale than SU defined in our life cycle model (Table 7). Specifically, one MO is available for Scotland (sum of Eastern Scotland and Western Scotland in our model), one MO for Northern Ireland (sum of Northern Ireland FO and Northern Ireland FB), one MO for Norway (sum of 4 SU in our model, South-East Norway, South-West Norway, Middle Norway and North Norway) and one MO for Russia (sum of 4 SU in our model, Russia Kola Barents Russia Kola White Sea, Russia Arkhangelsk Karelia and Russia River Pechora). To be compared to the MO defined by ICES, returns of spawners (and associated eggs deposition) in our model are then summed to match with the spatial scale considered for MO.
- **Stock grouping.** One can also calculate the probability of achieving MO at the scale of any stock grouping (e.g., sum of all SU in north American, Southern Europe, Northern Europe)
- **Simultaneously.** One can also calculate the probability of MO being achieved by all management units simultaneously within a same stock grouping (i.e. in the same given year). This probability integrates the spatial covariation in the return among SU.

4 Results

Those results were obtained using the data from ICES WGNAS report 2023. The time series of data is therefore 52 years from 1971 to 2022 (hindcasting phase). Following WKBSalmon discussions, these data are supplemented by new data on the origin of fish caught at Faroes (proportions to allocate Faroes catches among three subcomplex, Southern European complex, southern and northern and part of the Northern European complex; G. Bolstad, com pers.) and on the origin of fish caught at West Greenland (proportions to allocate European fish to the northern and the southern European complex; Tim Sheehan, com pers.). Forecasting to assess catch options at West Greenland and Faroes was performed for 3 additional years (2023-2024-2025).

4.1 Hindcasting - Fitting the LCM to the time series of data

4.1.1 Convergence of MCMC chains and model fit to the data

4.1.1.1 Convergence of MCMC chains

Results of convergence diagnostics indicate that with the MCMC settings mentioned above, MCMC chains of all variables in the model have converged.

The Gelman-Rubin *Rhat* statistics stands well below the 1.05 rule of thumb for almost all variables (Appendix 4). Note however that *Rhat* is greater than 1.05 for N_8 (abundance at the non-maturing PFA stage) for some SU and some years. This indicates that the convergence is more difficult for this variable than for other ones, but is not to be interpreted as a worrying lack of convergence signal. Indeed, the calculation of *Rhat* is based on the mixing of the 10 chains, but the final inferences are derived from a much larger sample resulting from the collation of the 10 chains that provides a much stable approximation of the posterior distribution. Visual inspection of the mixing of MCMC chains confirm the good mixing of the 10 chains (not shown).

4.1.1.2 Quality of fit to the different data sources

The quality of fit of the model to the different data sources is assessed through the comparison between the posterior distribution of state variables in the model and the associated observations for the four main sources of data (Appendix 5):

- Abundance at the return stage (1SW and 2SW)
- Homewater catches (1SW and 2SW)
- Catches of all marine fisheries (1SW mature, 1SW non mature, 2SW)
- Proportion of the different origins in the catches at sea

Results show that the model fits well to all data sources. The fit to the homewater catches is very tight, which is directly explained by the very low variance imposed on observation errors around the point estimates of homewater catches (lognormal with CV arbitrarily fixed to 0.05%).

4.1.2 A widespread decline of abundances in all CSG

The model estimates time series of all key life stages in the model for all SU or for any aggregation of SU at the scale of SU or countries (Fig. 9; here results are plotted for the 17 countries) or aggregated at the scale of stock complexes (Fig. 10a-b-c).

When examining trends of all SU together, posterior estimates of returns (total 1SW + 2SW; Fig. 11a) show consistent declining trends from the early 1970s to the 2010s in all CSG. Returns at the end of the time series were estimated to be ~50% of the abundances at the beginning of the 1970s for NA and SE CSG and ~30% for NE CSG. In NA CSG returns show an increase in abundance from 2003 (mostly due to an increase in Labrador and Newfoundland) that is not observed for the two other CSG.

The average proportion of 1SW fish in returns is different between the three CSG (Fig. 11b). The proportion of 1SW in returns is lower in the NE CSG, which is characterized by a high proportion of fish spending more than one winter at sea. The Southern European CSG has the highest average proportion of 1SW in returns. The three CSG exhibit similar temporal trends in the proportions of 1SW salmon in returns (Fig. 11b). The average time trend shows a consistent increasing trend from the early 1970s to the early 1980s, followed by a plateau or even a slight decline for the NE CSG.

Trends in spawner and return abundances may differ due to variations in homewater fishery exploitation rates (Fig. 11c-d). Egg depositions follow the same general temporal trends as spawners (Fig. 11e). The proportion of eggs spawned by 1SW is highly variable between the three CSG (Fig. 11f). Contrast between the three CSG corresponds to the contrast in the proportion of 1SW in the return augmented by the difference in the average number of eggs spawned per fish that is particularly high for 2SW fish in NE (because of higher female-biased sex ratio and higher average size of fish in NE).

Time series of total PFA in each CSG show very similar continuous declines by a factor 3, between the 1970s and the 2010s (Fig. 12) with a stronger decline for the NA CSG. The decline in PFA is marked by a strong decrease in abundances in the 1990s.

4.1.3 Coherence in temporal variations of post-smolt survival and proportion of fish maturing as 1SW

4.1.3.1 Post-smolt survival rate

The time-series of post-smolt survival for the 25 SU show a common decreasing trend over years (Fig. 13, Fig. 14). The trends averaged over all SU of the same CSG exhibit slightly different tendencies over the years (Fig. 13). Those patterns are consistent with the decline observed in the abundance at the PFA stage. The post-smolt survival in NA exhibit a strong decline by a factor 3 in the period 1985-1995. This decline is also observable in SE with a sharp decline by a factor ~1.8 in 1987. The sharp decline in

the late 80's-early 90's is less visible in NE. Trend in NE shows a continuous and smoothed decline over the period.

The majority of pairwise correlations are positive (Fig. 15; correlations are calculated in the logit scale). In general, correlations are stronger between geographically close SU. The results show strong correlations for SU within NA, followed by SE and NE. Correlations between the NE SU are stronger for the block of SU going from Sweden (East) to Russia-KB (West).

4.1.3.2 Proportion of fish maturing as 1SW

Time trends in the proportion of fish that mature as 1SW also show a strong coherence among SU (Fig. 16, Fig. 17). These are in accordance with the expectation of higher correlations between SU of the same CSG.

Overall, there is an increasing trend from the 1970s to the 1990s that corresponds to declines in the proportions of 2SW fish in the returns followed by a levelling off or even a decline from the 2000s (Fig. 16).

Consistently with the low proportion of 1SW observed in the returns, the two most eastern SU, Russia-AK and Russia-RP, and US differ from the others SU with a very low probability of maturing (Fig. 17). Some SU like Newfoundland have very high proportion of fish maturing as 1SW.

As observed for the post-smolt survival, most of the pairwise correlations are positive across the 25 SU (Fig. 18; correlations are calculated in the logit scale). In general, the correlations are stronger for geographically close SU. The results show strong correlations for SU within NA, followed by SE and NE.

4.2 Forecasting and risk analysis

4.2.1 An example of forecast for Quebec

The model allows for forecasting abundances for all life stages in the model under the different catch options at Faroes or West Greenland.

As an example of forecasts results obtained for Quebec under the scenarios of 0 catches in both Faroes and West Greenland (Fig. 9, Figure for Québec), results show how uncertainty in the forecasts increases with forecasting horizon. The propagation of uncertainty is mostly the consequence of uncertainty propagation through time in forecasts of the post-smolts survival and proportion maturing PFA modelled as multivariate random walks (Fig. 8).

Figure 19 shows the results of the forecasts obtained for Quebec under different catch options at West Greenland. The forecasted abundance of 2SW returns and the subsequent egg deposition decline when increasing the catches at West Greenland. The figure also shows that the abundance of 1SW returns is not impacted by the catch options at West Greenland. Accordingly, the proportion of eggs spawned by 2SW fish declines when increasing the catches at West Greenland, which is expected as this mixed stock fishery exclusively impacts the non-maturing component of the population.

From those forecasts it is straightforward to compute the probability that the egg deposition, total (1SW + 2SW component of the returns) or separately for the two sea-age class 1SW and 2SW, is greater than the management objectives defined for any country/regions in the model or at any higher aggregation level (country/regions, aggregated at the scale of stock complex, or simultaneously for all SU in the same stock complex).

4.2.2 Catch options for the West Greenland mixed stock fishery

Note. For West Greenland catch options, the probability to achieve management objectives are only illustrated by comparing the eggs deposition by 2SW fish only with the 2SW management objectives.

4.2.2.1 Regions/country scale

As expected, stocks from North America such as Labrador, Quebec, and Gulf are highly sensitive to catch options at West Greenland (Fig. 20a). The probability of achieving 2SW management objectives for those stock units dramatically decreases when catches increase. This is expected as the North American fish represent the majority of the catches at WG in the recent years and their relative harvest rate is much higher than for European fish in the recent years. The sensitivity to catch options is further increased for SU where returns are dominated by 2SW as only this component of the population is impacted by the WG fishery.

Stock units from southern Europe are less sensitive to catch options at WG. This mostly results from a relative harvest rate at WG that is much lower than for North American stock units in the recent years.

Catch options at WG have only minimal influence on the probability of achieving management objectives for northern European stocks. This is expected as these stocks represent only a very low proportion of the catches at WG (less than 5% of the total fish harvested in WG).

Finally, the proportion of eggs spawned by 2SW may also reveals highly sensitive to catch options at WG (Fig. 20d). This is expected because this fishery is extremely selective as it exclusively operates on the non-maturing component of the populations. This is especially visible for some North American stock units. The proportions of eggs spawned by 2SW drops very quickly when catches increases for SU with high proportion of 2SW in the returns (e.g., Quebec). This proportion remains low for all SU for which returns are dominated by 1SW fish (e.g., Newfoundland).

4.2.2.1 Stock complex scale

When assessed at the scale of stock complexes (i.e. by comparing the total egg deposition with the management objectives aggregated at the scale of stock complex), the North American stock complex logically reveals the most sensitive to catches scenarios at WG (Fig. 20b). Sensitivity of the southern European stock complex is limited, and the north European stock complex reveals nearly unsensitive.

As expected, the probability that all SU in the same continental stock grouping achieve their management objectives simultaneously is even lower (Fig. 20c). This probability is near zero for North America and Southern Europe whatever the catch options.

When assessed at the scale of the continental stock groups, the proportions of eggs spawned by 2SW overall follow the same patterns than the probability to achieve 2SW management objectives, with a higher sensitivity for the North American stock complex, a limited sensitivity for Southern Europe and no sensitivity for Northern Europe (Fig. 20e).

4.2.3 Catch options for the Faroes mixed stock fisheries

Note. For Faroes catch options, the probability to achieve management objectives is illustrated by comparing the total egg deposition (by 1SW + 2SW fish) with the management objectives expressed in total number of eggs.

4.2.3.1 Regions/country scale

Catch options at Faroes influence the probability of achieving management objectives for European SU only (Fig. 21a). As expected, SU from North America are totally insensitive to catch options at Faroes as fish from North America are not supposed to be caught there. The sensitivity is slightly higher for country/regions with the high proportion of 2SW in their returns (e.g. England and Wales, Scotland).

The proportion of eggs spawned by 2SW also reveals highly sensitive to catch options at Faroes (Fig. 21d). This is expected because this fishery is extremely selective as the highest proportion of the catches are realized on 2SW fish. The proportions of eggs spawned by 2SW drops quickly when catches increase. This is even more sensitive for the country/regions with the highest proportion of 2SW in their return (e.g. England and Wales, Scotland).

4.2.3.1 Stock complex scale

When assessed at the scale of stock complexes (i.e. by comparing the total egg deposition with the management objectives aggregated at the scale of stock complex), the southern and northern European stock complexes reveal similar sensitivity to Faroes catch options (Fig. 21b).

As expected, the probability that all SU in the same continental stock grouping achieve their management objectives simultaneously is even lower (Fig. 21c). This probability is notably lower for Southern Europe than for Northern Europe.

When assessed at the scale of the continental stock groups, the proportions of eggs spawned by 2SW overall follow the same patterns than the probability to achieve 2SW management objectives, with a similar sensitivity between Southern and Northern Europe, but a higher proportion for north European stock complex (Fig. 21e).

Table 1. Summary of the core demographic hypotheses in the stage-based population dynamic model

Core demographic hypotheses	
■	12 potential life histories resulting from the combination of 6 smolts ages, and 2 sea-ages (1SW and 2SW)
■	No sex-specific life histories. Abundance at all stage are modelled females and males confounded. The proportion of females in 1SW and 2SW are only used to calculate the number of eggs potentially spawned by spawners
■	No heritability of life histories (“an egg is an egg”)
■	All smolts of different river age migrating the same year are pooled. There is no tracking of smolts ages once at sea. All transition rates at sea depends on migration year but are independent on smolts age
■	No data on smolts production available at the scale of SU. Smolt production is modelled as a linear function of eggs deposition with lognormal stochasticity with fixed expected mean (=0.007) and CV (=0.4)
■	Natural mortality rate at sea after the PFA stage is fixed, constant and homogeneous among SU, fixed to $M = 0.03 \cdot \text{month}^{-1}$
■	Inferences on Smolt → PFA survival (“marine productivity”) and on the proportion of PFA maturing as 1SW are relative to those hypotheses
■	No exchange of abundance among the different SU (no straying among the different SU). But the model includes the possibility of covariations in the temporal variation of key transition rates (e.g. marine survival, proportion of fish that mature as 1SW) to represent the effect of external factors susceptible to influence multiple population simultaneously
■	No environmental/ecosystem variables used in the model. Forecasts are based on statistical time series model fitted on historical time trends

Table 2. Summary of the main life stages and transitions of the life cycle model. To simplify the notations, subscript r for the SU does not appear in the table.

Stages	Transitions	Parameters / Transition rates		Observation equations (likelihood)
N1: Eggs	$N7_t \rightarrow N1_t$ $N10_t \rightarrow N1_t$	Sex-ratio and fecundity	Fixed Proportion of females and the fecundity are fixed (provided in the data) and specific for each sea-age class, SU and year	No
N2: Total number of Smolt	$N1_t \rightarrow N2_t$	Freshwater survival (θ_{1t})	Estimated Stochastic Lognormal with average value = 0.007 and CV = 0.4 fixed for all SU and all years Random variations independent across years and SU	No
N3: Number of smolts in each age class (6 age classes)	$N2_t \rightarrow \begin{cases} N3_{t+1+1} \\ \dots \\ N3_{t+1+a} \\ \dots \\ N3_{t+1+6} \end{cases}$	Proportion of smolt age in the cohort c ($\theta_{2c,a=1:6}$)	Fixed Proportion of smolt ages are fixed (provided in the data) and specific for each SU and cohort c	No
N3tot: Total number of smolts migration year t	$N3_{tot_t}$	$N3_{tot_t}$ is calculated as the sum of all smolt age classes migrating year t		No
N4: PFA (Pre Fishery Abundance)	$N3_{tot_t} \rightarrow N4_{t+1}$	Post-smolt survival (θ_{3t})	Estimated Temporal variations specific to each SU Modelled as a Multivariate random walk with covariation among all SU	No

N5 : PFA maturing N8 : PFA non maturing	$N4_t \rightarrow \begin{cases} N5_t \\ N8_t \end{cases}$	<i>Proportion maturing PFA</i> (θ_{4_t})	Estimated Temporal variations specific to each SU Modelled as a Multivariate random walk with covariation among all SU	No
N6 : Returns 1SW	$N5_t \rightarrow \dots \rightarrow N6_t$	Harvest rates of the different sequential marine fisheries	Estimated (non-informative prior), with variations across years. Depending on the fishery, harvest rates are variable across SU or homogeneous across SU	Catches of the different sequential marine fisheries observed with Lognormal errors and fixed variance For some fisheries - additional Dirichlet likelihood function to allocate catches among groups of SU
		Natural mortality (M)	Fixed ($0.03 \cdot \text{month}^{-1}$)	Returns 1SW observed with Lognormal errors and fixed variance
N9 : Returns 2SW	$N8_t \rightarrow \dots \rightarrow N9_t$	Harvest rates of the different sequential marine fisheries	Estimated Temporal variations Depending on the fishery, harvest rates are variable or homogeneous across SU	Catches of the different sequential marine fisheries observed with Lognormal errors and fixed variance For some fisheries - additional Dirichlet likelihood function to allocate catches among groups of SU
		Natural mortality (M)	Fixed ($0.03 \cdot \text{month}^{-1}$)	Returns 2SW observed with Lognormal errors and fixed variance
N7 : Spawners 1SW	$N6_t \rightarrow N7_t$ Deterministic	Harvest rates of the homewater fisheries	Estimated Temporal variation and variations across SU	1SW homewater catches observed with Lognormal errors and fixed variance
		Additional natural mortality between returns and spawners	Fixed (depends on the SU)	

N10 : Spawners 2SW	$N9_t \rightarrow N10_t$ Deterministic	Harvest rates of the homewater fisheries	Temporal variation and variations across SU	2SW homewater catches observed with Lognormal errors and fixed variance
		Additional natural mortality between returns and spawners	Fixed (depends on the SU)	

Table 3. Prior distributions on key estimated transition rates. Note that harvest rates for the West Greenland and Faroes fishery are defined at the scale of groups of SU (see Table 5 and Table 6 for more details on the harvest rates).

Survival rate between the eggs deposition and the total number of smolts produced in the cohort c (corresponding to egg deposition of year c)

$$\log(\theta_{1,c,r}) \sim \text{Normal}(\log(\mathbb{E}_{\theta_1}) - \frac{1}{2}\sigma_{\theta_1}^2, \sigma_{\theta_1}^2)$$

$$\text{with } \mathbb{E}_{\theta_1} = 0.007 \text{ and } \sigma_{\theta_1}^2 = \log(\text{CV}_{\theta_1}^2 + 1) \text{ with } \text{CV}_{\theta_1} = 0.4$$

Temporal variations of the post-smolt survival ($\theta_{3,t,r}$) and the proportion of fish maturing as 1SW ($\theta_{4,t,r}$) modelled as multivariate random walks in the logit scale with variance-covariance matrices Σ_{θ_3} and Σ_{θ_4}

$$\left(\text{logit}(\theta_{3,t+1,r})\right)_{r=1:N} \sim \text{MVNormal}\left(\left(\text{logit}(\theta_{3,t,r})\right)_{r=1:N}, \Sigma_{\theta_3}\right)$$

$$\left(\text{logit}(\theta_{4,t+1,r})\right)_{r=1:N} \sim \text{MVNormal}\left(\left(\text{logit}(\theta_{4,t,r})\right)_{r=1:N}, \Sigma_{\theta_4}\right)$$

Non diagonal (plain) $N \times N$ variance-covariance matrix ($N=25$)

$$\Sigma_{\theta} = \begin{pmatrix} \sigma_{\theta_{1,1}}^2 & \dots & \sigma_{\theta_{1,N}}^2 \\ \dots & \dots & \dots \\ \sigma_{\theta_{N,1}}^2 & \dots & \sigma_{\theta_{N,N}}^2 \end{pmatrix}$$

Note: Two different matrices for the post-smolt survival (Σ_{θ_3}) and for the proportion of fish maturing as 1SW (Σ_{θ_4})

$\Sigma_{\theta}^{-1} \sim \text{Wishart}(\Omega, \delta)$ with scale matrix Ω set as the $N \times N$ identity matrix and δ the degree of freedom set to N

The pairwise correlation matrix ρ is $\rho = \sqrt{\text{diag}(\Sigma)}^{-1} \times \Sigma \times \sqrt{\text{diag}(\Sigma)}^{-1}$

Exploitation rates of all fisheries f (marine fisheries and homewater fisheries) for any year t and stock unit or group of stock unit g (see details in Tables 4 and 5)

$$h_{f,t,g} \sim \text{Beta}(1,2)$$

all years and stock unit or group of stock units g are independent

Table 4. Summary of the data used in the life cycle model. Most of the data are provided as time series specific to each of the 25 SU (indicated Year x SU) and eventually for the two sea-age classes of returns separately. Some data are integrated as fixed values, other are integrated through likelihood functions to consider observation errors. In this case, data come in the form of a mean and standard deviation. See details of the main data sources in Appendix 3. All data are available at https://sirs.agrocampus-ouest.fr/discardless_app/WGNAS-ToolBox/

Data type	Dimension	Likelihood (observation errors)
Average value and CV of the eggs-to-smolt survival rate	1	Fixed in the data
Proportion of smolt ages (1-6)	Year × SU	Fixed in the data
Natural mortality rate at sea	1	Fixed in the data
Durations (in months) of the different period separating the sequential fishery at sea	SU	Fixed in the data
Additional mortality rates between return and spawner stages	Year × SU	Fixed in the data
Proportion of delayed spawners	Year × SU	Fixed in the data
Proportion of females at spawner stage	Sea-age (1SW/2SW) × Year × SU	Fixed in the data

Eggs spawned per female	Sea-age (1SW/2SW) \times Year \times SU	Fixed in the data
Returns (number of fish)	Sea-age (1SW/2SW) \times Year \times SU	\sim Lognormal with mean and CV from the run-reconstruction models
Homewater catches (number of fish)	Sea-age (1SW/2SW) \times Year \times SU	\sim Lognormal with mean from the run-reconstruction models and CV fixed to 5%
Total catches at sea on mixture of stocks (number of fish)	Sea-age (1SW/2SW) \times Year \times SU	\sim Lognormal with mean and CV from the run-reconstruction models
Proportions to allocate catches at sea among different SU	Sea-age (1SW/2SW) \times Year \times SU	\sim Dirichlet with proportions from genetic data or allocation based on the homogeneous harvest rate hypothesis

Table 5. Summary of the duration among stages and the sequential fisheries (operating on mixed stocks at sea and homewater fisheries) for stock units in the North American continental stock grouping (Source: ICES 2018; Prévost et al., 2009).

North American continental stock grouping		
Stages/Fisheries	Migration duration	Exploitation rate
PFA maturing		
↓	7 months	Variable among years
1SWm NFDL/LB/SPM Fisheries		2 fisheries: - (NFDL SFA zones 3-7). Homogeneous among SU - (NFDL SFA zones 8-14, LAB, SPM). Specific estimate for SU = Labrador + homogeneous among all other SU
↓	1 month	
Returns 1SW		
↓	0	
1SW homewater Fishery		Variable among years Variable among SU
↓	0	
Spawners 1SW		
PFA non maturing		
↓	7 months	Variable among years Homogeneous among SU
1SWnm NFDL/LB Fisheries (SFA zones 3-7 only)		
↓	2 months	Variable among years and SU Allocation to the SU in two steps: 1) allocate fish from North America and Europe based on data 2) Within North America, allocate fish among SU using homogeneous harvest rates
1SWnm West Greenland Fishery		
↓	8 months	Variable among years 2 fisheries: - (NFDL SFA zones 3-7): Homogeneous among SU - (NFDL SFA zones 8-14, LAB, SPM): Specific estimate for SU = Labrador + homogeneous among all other SU
2SWm NFDL/LB/SPM Fisheries		
↓	1 month	
Returns 2SW		
↓	0	
2SW homewater Fishery		Variable among years Variable among SU
↓	0	
Spawners 2SW		

Table 6. Summary of the duration among stages and the sequential fisheries (operating on mixed stocks at sea and homewater fisheries) for stock units in the Southern and Northern European continental stock groupings (Source: ICES 2018; Potter, 2016).

Southern and Northern Europe continental stock groupings		
Stages/Fisheries	Migration duration	Exploitation rate
PFA maturing		
↓	0.5 months	<ul style="list-style-type: none"> - Variable among years - Variable among the 3 sub complexes: Southern Europe, northern part of Northern Europe and southern part of Northern Europe based on data - Homogeneous among SU within each subcomplex
1SWm Faroes Fishery		
↓	7.5 months	
Returns 1SW		
↓	0	Variable among years Variable among SU
1SW homewater Fishery + fishery on delayed spawners		
↓	0	
Spawners 1SW		
PFA non maturing		
↓	0.5 months	<ul style="list-style-type: none"> - Variable among years - Variable among the 3 sub complexes: Southern Europe, northern part of Northern Europe and southern part of Northern Europe based on data - Homogeneous among SU within each subcomplex
1SWnm Faroes Fishery		
↓	8.5 months	<ul style="list-style-type: none"> - Variable among years - Variable among the three stock complexes: north America, Southern European and Northern European - Homogeneous among SU within each stock complex
1SWnm West Greenland Fishery		
↓	5 months	<ul style="list-style-type: none"> - Variable among years - Variable among the 3 sub complexes: Southern Europe, northern part of Northern Europe and southern part of Northern Europe based on data - Homogeneous among SU within each subcomplex
2SWm Faroes Fishery		
↓	3.5 months	Variable among years Variable among SU
Returns 2SW		
↓	0	
2SW homewater Fishery + fishery on delayed spawners		
↓	0	
Spawners 2SW		

Table 7. Conservation limits or management objectives (for North America) used in this application. CL or management objectives in fish are directly derived from ICES WGNAS 2021 report (Europe: Table 3.2.1.1; North America: Section 4.2). For Russia and Iceland, CL are estimated using the pseudo stock-recruitment approach relating lagged eggs and PFA estimates. Management objectives are different from Spawners requirement for Scotia Fundy (spw requirement = 24705 MSW fish) and USA (spw requirement = 29199 MSW fish). Biological characteristics used to convert a number of fish into eggs are data from WGNAS 2023 (last year of data = year 2022).

		CL or management objective (for NAC) in number of fish			Biological characteristics of				CL in eggs		
		1SW	MSW	Prop 1SW	Prop females		eggs/female		1SW	MSW	Total
					1SW	MSW	1SW	MSW			
NAC	LB	missing	34746		0.505	0.859	2500	5000		149234070	149234070
	NF	missing	4022		0.713	0.836	2500	5000		16811960	16811960
	QB	missing	32085		0.131	0.662	3653	8620		183042107	183042107
	GF	missing	18737		0.113	0.740	3354	7979		110662110	110662110
	SF	missing	10976		0.350	0.889	3194	6434		62801128	62801128
	US	missing	4549		0.000	0.640	3167	7838		22817192	22817192
S.NEAC	FR	17400	5100	0.77	0.450	0.800	3450	6900	27013500	28152000	55165500
	EW	53988	29918	0.64	0.450	0.700	3000	6500	72883800	136126900	209010700
	IR	211471	46943	0.82	0.600	0.850	3400	7000	431400840	279310850	710711690
	N.IR	34880	6152	0.85	0.570	0.600	3459	6781	68770454	25030027	93800482
	SC	102592	84990	0.55	0.495	0.714	3184	5909	161693199	358575020	520268219
	IC.SW	16660	1632	0.91	0.420	0.570	5954	10787	41661329	10034499	51695828
N.NEAC	IC.NE	5019	1851	0.73	0.330	0.630	5982	11666	9907807	13604073	23511880
	SW	1731	2714	0.39	0.500	0.700	3000	6000	2596500	11398800	13995300
	NO	54105	73770	0.42	0.341	0.687	2433	7879	44854544	399186397	444040941
	FI	14946	9521	0.61	0.120	0.770	5000	13000	8967600	95305210	104272810
	RU	62285	34412	0.64	0.225	0.675	4250	12500	59560031	290351250	349911281

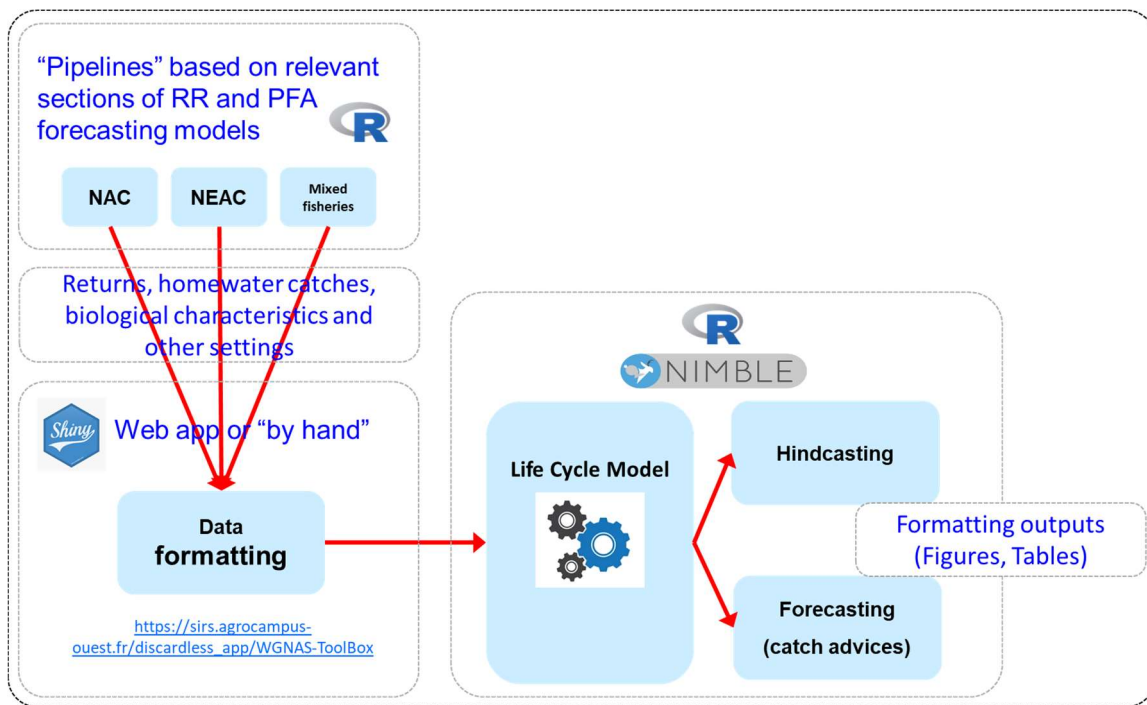


Figure 1. Streamline for stock assessment and catch advice using the life cycle model

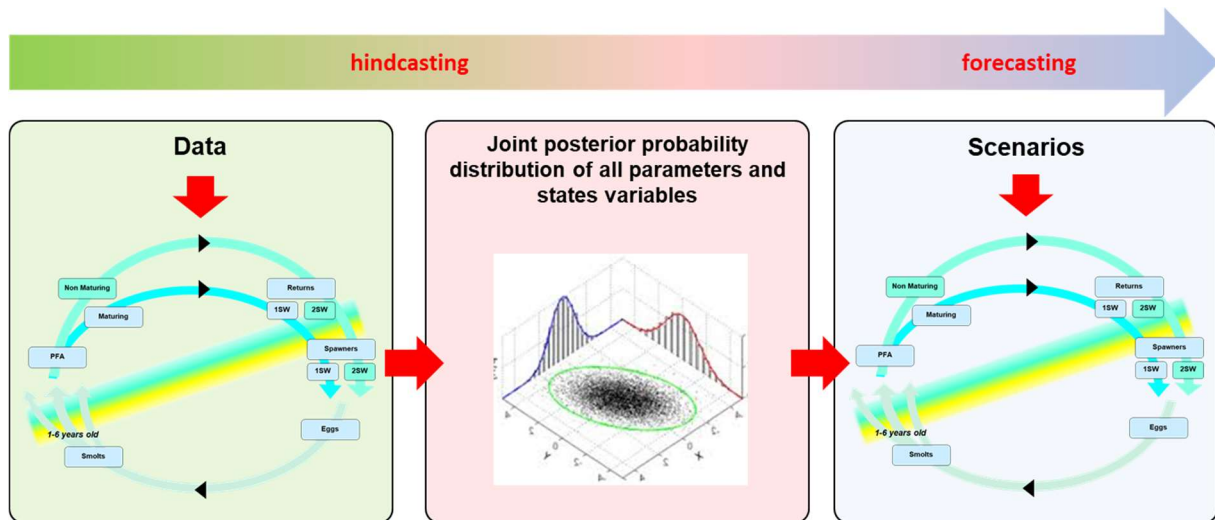


Figure 2. Workflow hindcasting → forecasting. The life cycle is first fitted to the historical time series of data (in the present application, 1971-2022), and then used to forecast abundances for each stock unit (SU) under different scenarios of catches at West Greenland and Faroes fisheries. All sources of uncertainty in both the model and the parameters estimates (joint posterior distribution derived from the hindcasting phase) are integrated out in the forecasting through Monte Carlo simulations.

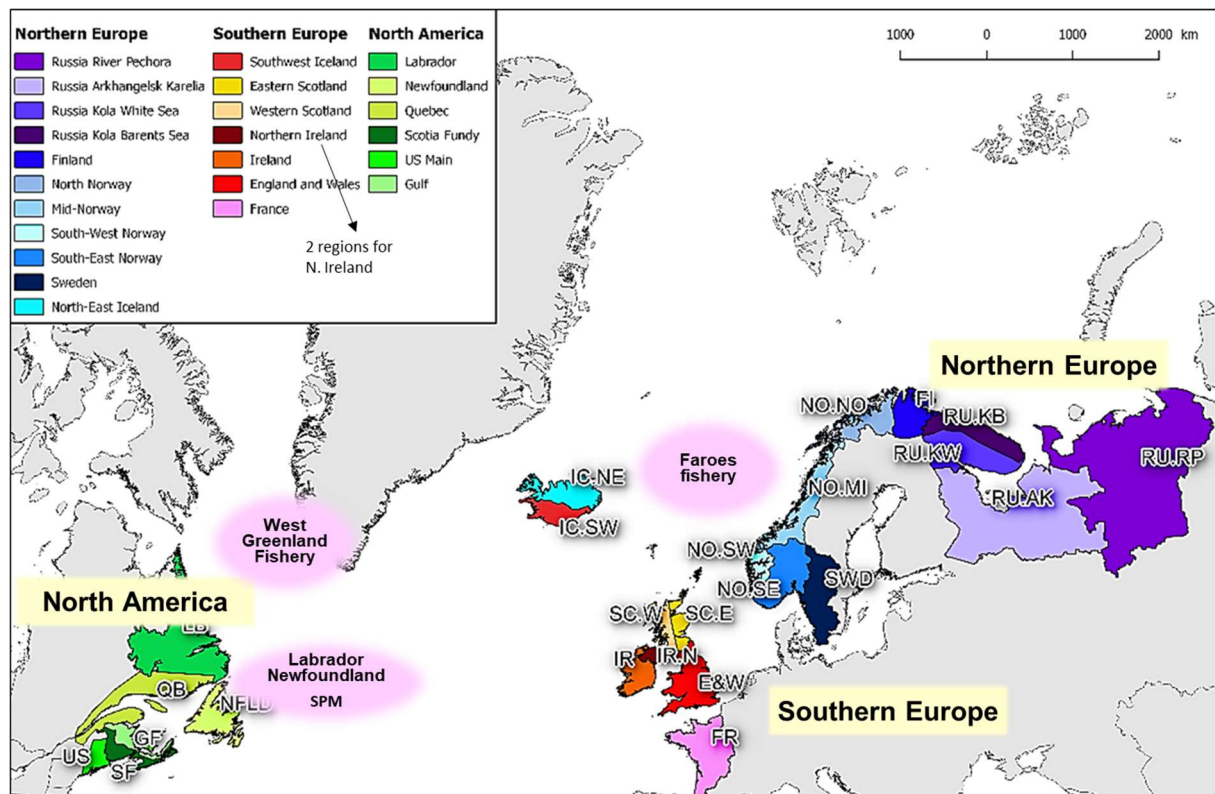


Figure 3. The 25 stock units considered in North Atlantic. Stock units of North America: NFDL=Newfoundland, GF=Gulf, SF=Scotia-Fundy, US=USA, QB=Quebec and LB=Labrador ; Stock units in Southern Europe: IR=Ireland, E&W=England&Wales, FR=France, E.SC=Eastern Scotland, W.SC=Western Scotland, N.IR=Northern Ireland FO and FB (note that the split between FO and FB is not represented on the map), IC.SW=South-West Iceland ; Stocks units in Northern Europe: FI=Finland, IC.NE=North-East Iceland, NO.MI=Middle Norway, NO.NO=North Norway, NO.SE=South-East Norway, NO.SW=South-West Norway, RU.AK=Russia Arkhangelsk Karelia, RU.KB=Russia Kola Barents Sea, RU.KW=Russia Kola White Sea, RU.RP=River Pechora, SWD=Sweden. Germany, Netherland, Denmark, Spain and Portugal are not included in the model. Pink ellipses indicate the main fisheries at sea operating on mixed stocks: Faroes, West Greenland, Labrador and Newfoundland (LAB/NFLD), and Saint Pierre and Miquelon (SPM).

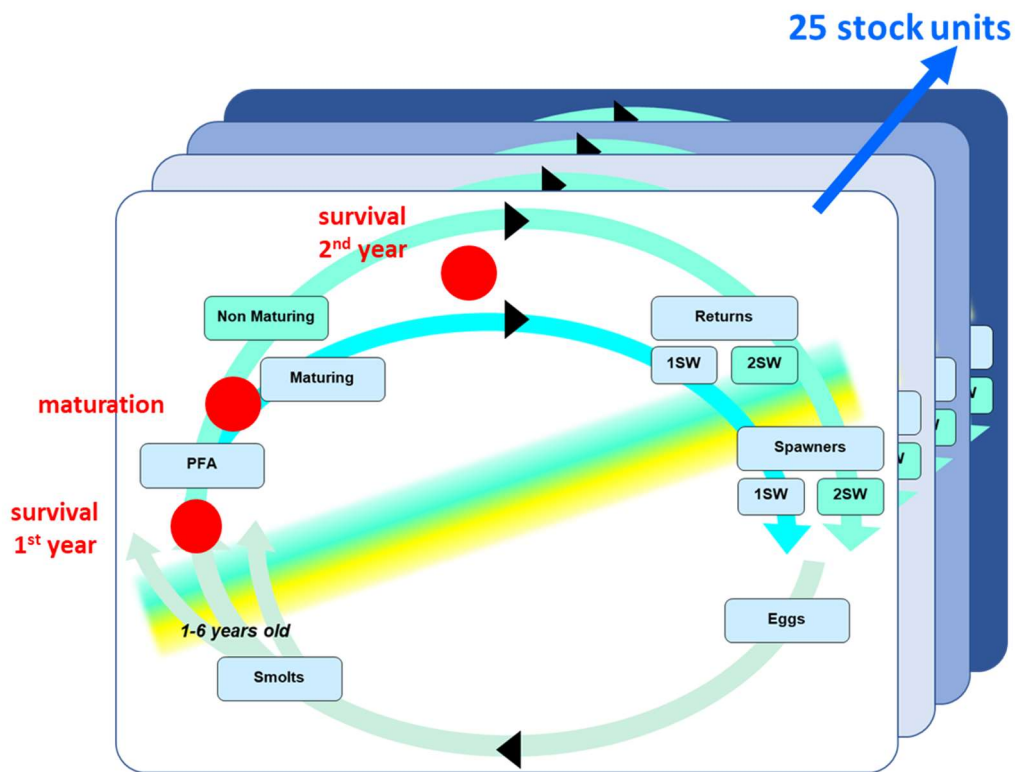


Figure 4. Scheme of the stage-based structured life cycle model. for the 25 SU. Blue boxes: different life stages. For each SU, the model tracks the abundance of fish, males and females confounded by year and life stage, sequentially from eggs to 1SW or 2SW spawners (fish that survived all sources of natural and fishing mortality and that contribute to reproduction). The model incorporates variations in the age of out-migrating smolts (after 1 to 6 years in freshwater) and the sea-age of returning adults. Only two sea-age classes are considered: maiden salmon that return to homewaters to spawn after one year at sea (one-sea-winter (1SW)), and maiden salmon that return after two winters at sea (2SW). All fish within a SU are assumed to have the same demographic parameters and to undertake a similar migration route at sea. There is not no exchange of abundance among the different SU. Red dots indicate the key demographic transition rates that are the main target of the statistical estimation: survival between smolt and PFA stage, the proportion of fish maturing at the PFA stage (fish that will return as maiden 1SW fish), and the survival during the second year at sea. Mortality during the second year at sea results from the combination of natural mortality (fixed) and fishing mortality (estimated).

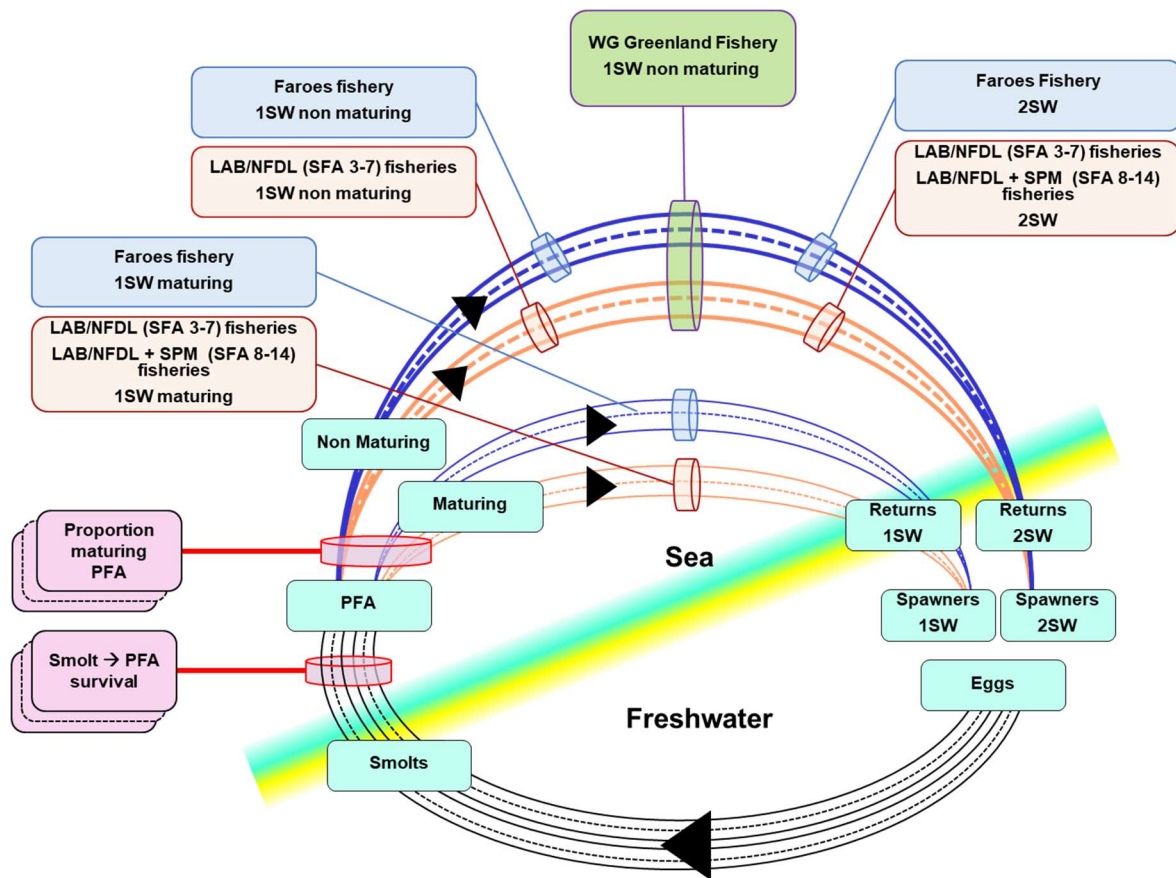


Figure 5. Structure of the age- and stage-based life cycle model for the 25 SU highlighting the joint structure among the SU. Sources of covariation among the SU are two-fold: 1) covariations in the time series of post-smolt survival and proportion maturing as 1SW; 2) covariations through fisheries operating on mixtures of SU at sea. Blue boxes: different life stages. Blue arrows: North American stock units. Orange arrows: European stock units (Southern and Northern European). Thin line: marine phase for the 1SW fish. Bold lines: Marine phase for the 2SW fish. Cylinders: sources of covariations among the 25 SU. Red cylinders: key parameters (post-smolt survival and maturing probability). Orange cylinders: fisheries operating on mixture of European stock units. Blue cylinders: fisheries operating on mixture of North American stock units. Green cylinder: Fishery operating on mixture of both North American and European stock units. (adapted from Olmos et al., 2019).

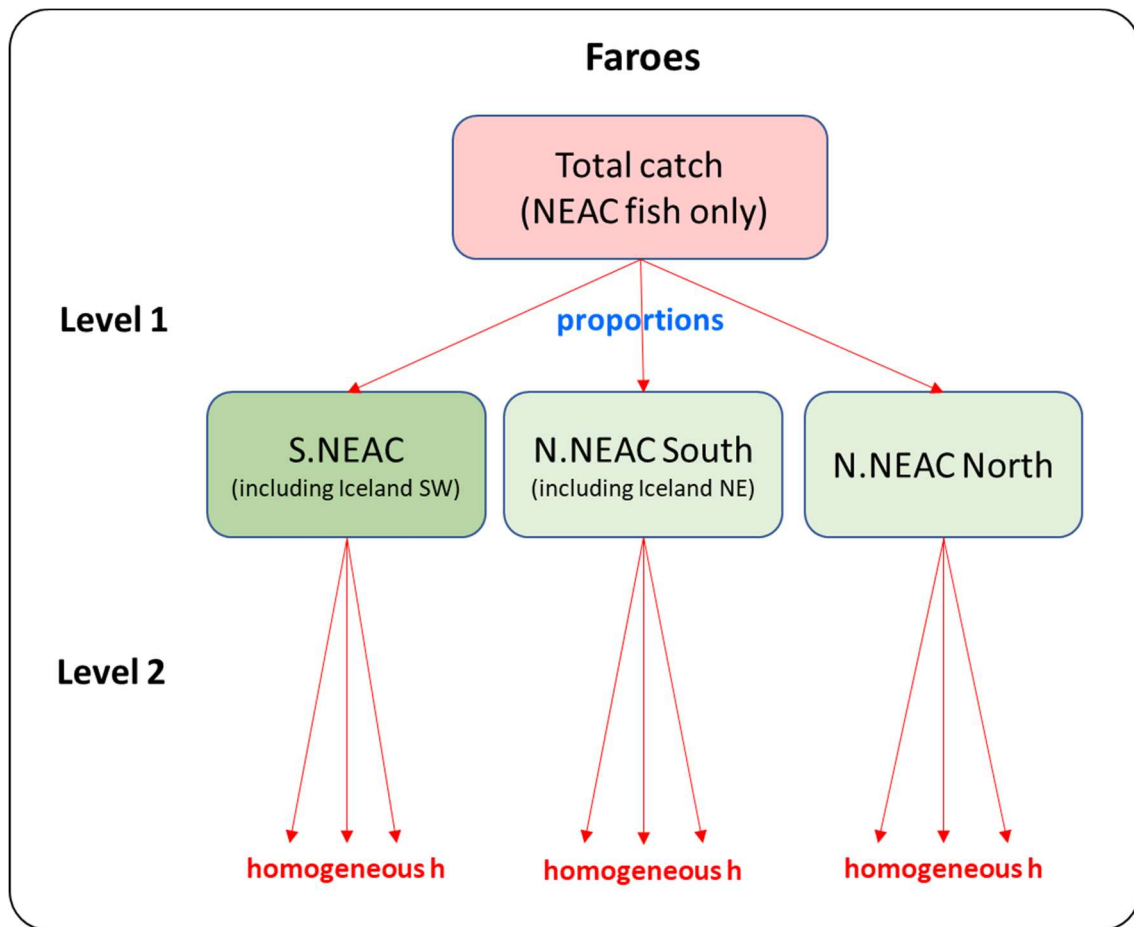


Figure 6. Faroes fishery. Data and hypotheses used to allocate the catches to the different SU. Total catches of 1SWm and 1SWnm and 2SW at Faroes are allocated to the different SU following a two levels allocation rule. Level 1. The total catches are allocated to three large groups of SU using proportion based on the relative harvest rate estimated from genetic assignment data (Geir Bolstad, com pers. 2023): The Southern European CSG (France, UK England and Wales, Ireland, UK Northern Ireland - FO, UK Northern Ireland - FB, UK Scotland East, UK Scotland West, and Iceland South-West); The southern part of the Northern European CSG (Iceland North-East, Sweden, Norway South-East, Norway South-West and Norway Middle); the northern part of the Northern European CSG (Norway North, Finland, Russia Kola Barents, Russia Kola White Sea, Russia Arkhangelsk Karelia and Russia River Pechora). Level2. Within each of the three groups, catches are assigned to the different SU that compose the group assuming that exploitation rates are homogeneous among SU.

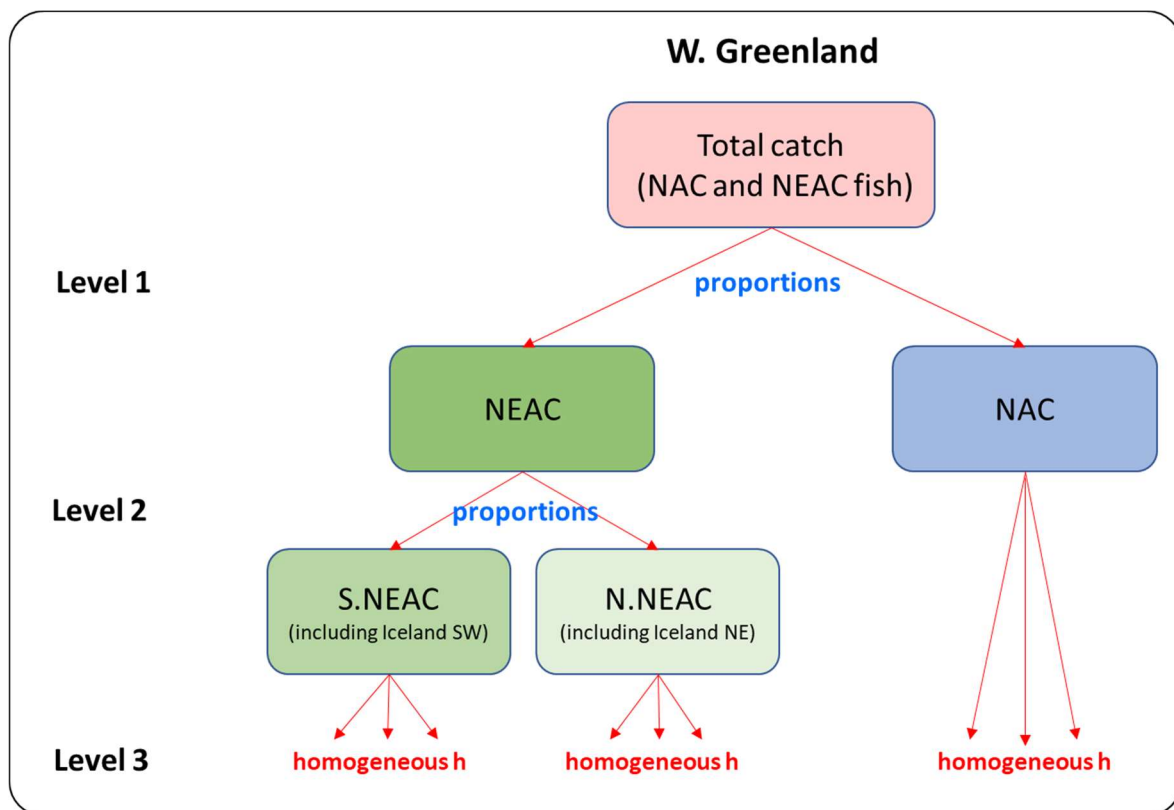


Figure 7. West Greenland fishery. Data and hypotheses used to allocate the catches to the different SU. Total catches of 1SWnm are allocated to the different SU following a three levels allocation rule. Level 1. Total catches are allocated to the North American or European complexes using proportions calculated from a compilation of individual assignment data based on discriminant analyses of scale characteristics and genetic analyses (ICES 2017a; 2017b). Level 2. Within the European stock complex, catches are allocated to the Southern or Northern European CSG using proportions calculated from a compilation of individual assignments (Tim Sheehan, com pers. 2023). Level 3. Within each of the three groups, catches are assigned to the different SU that compose the group assuming that exploitation rates are homogeneous among SU.

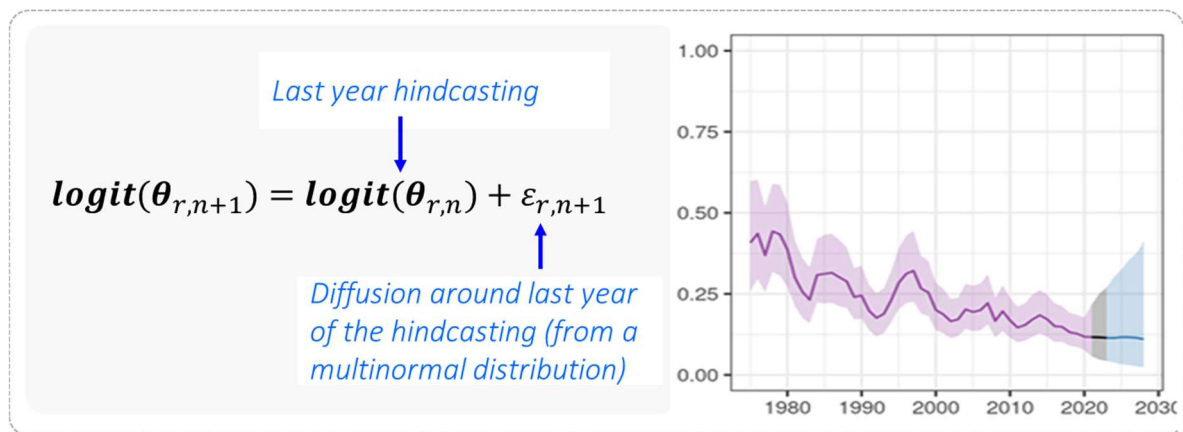


Figure 8. Illustration of the propagation of uncertainty in a putative example of the smolt-to-PFA survival rate θ . Pink shaded: hindcasting on the historical time series (here 1971-2022). Blue and grey shaded: forecasting during 5 additional years (2023-2027).

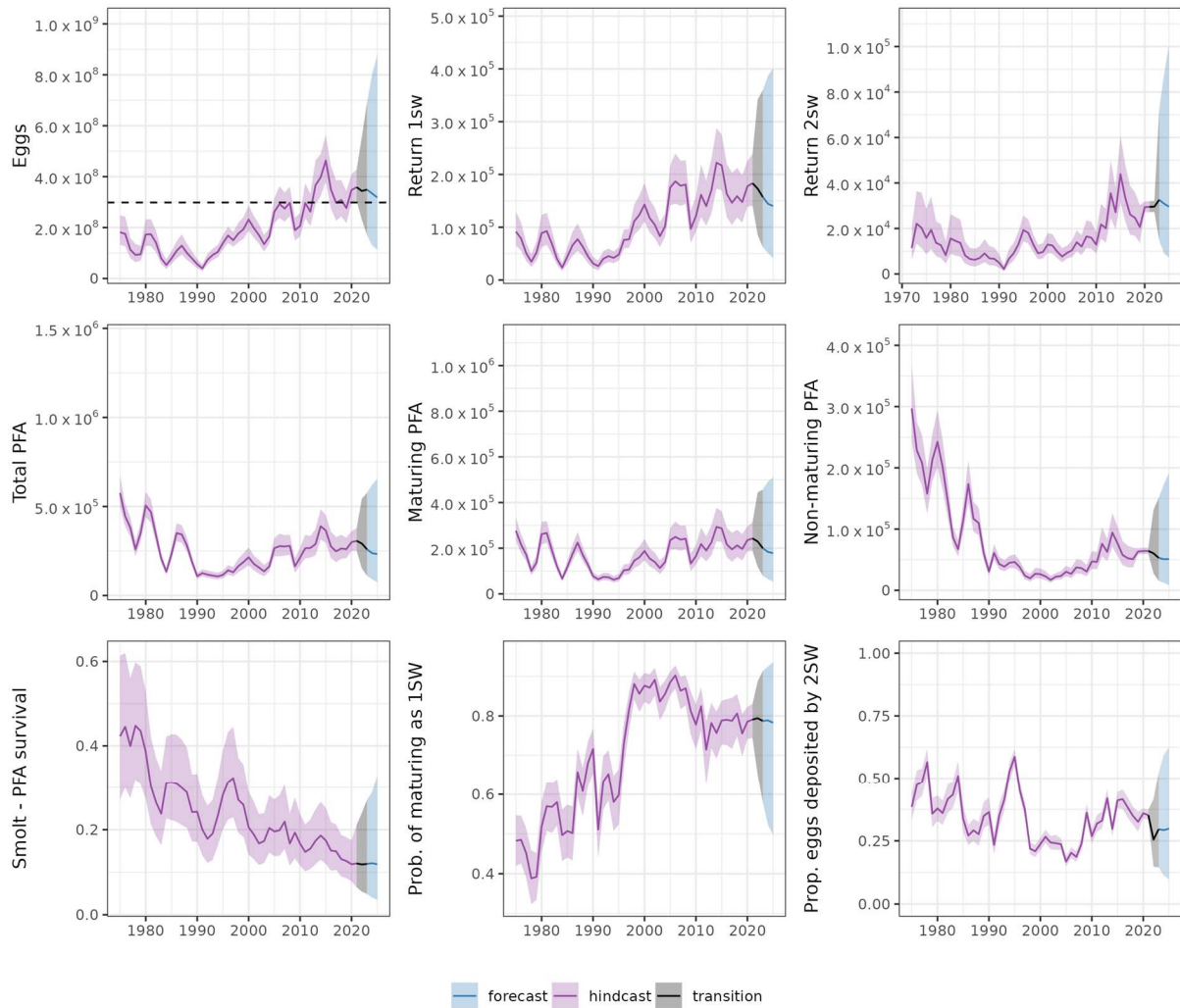
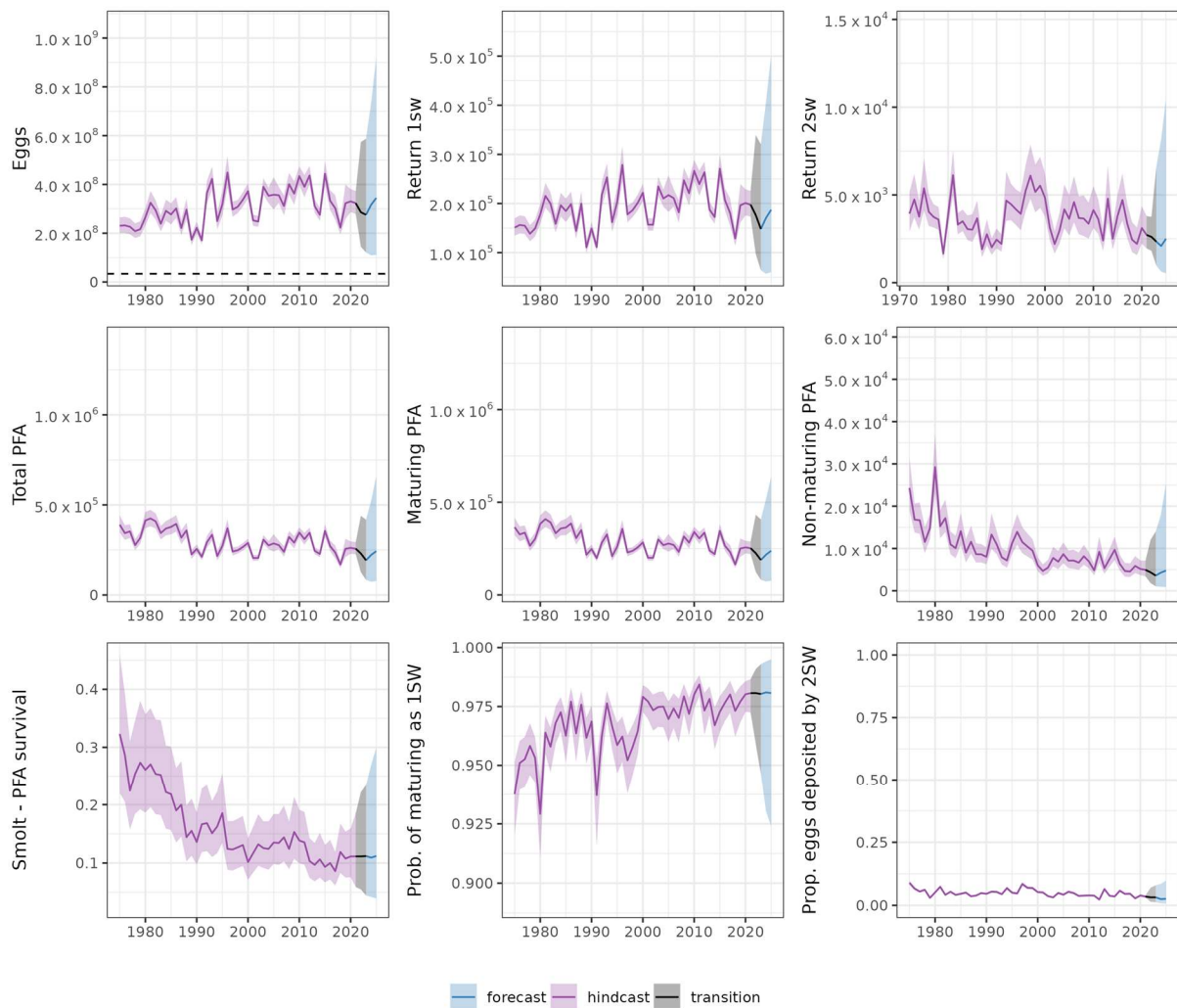
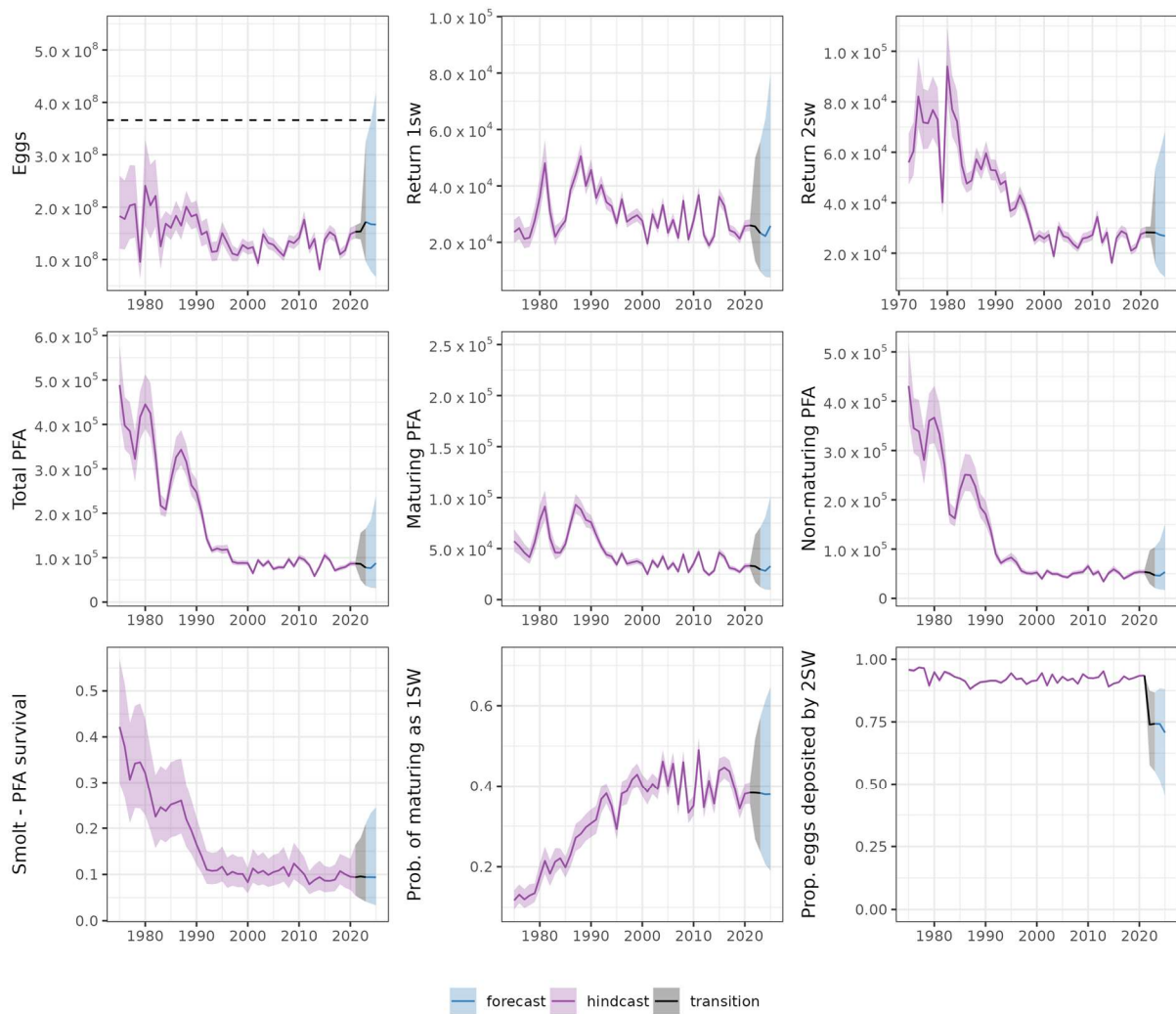
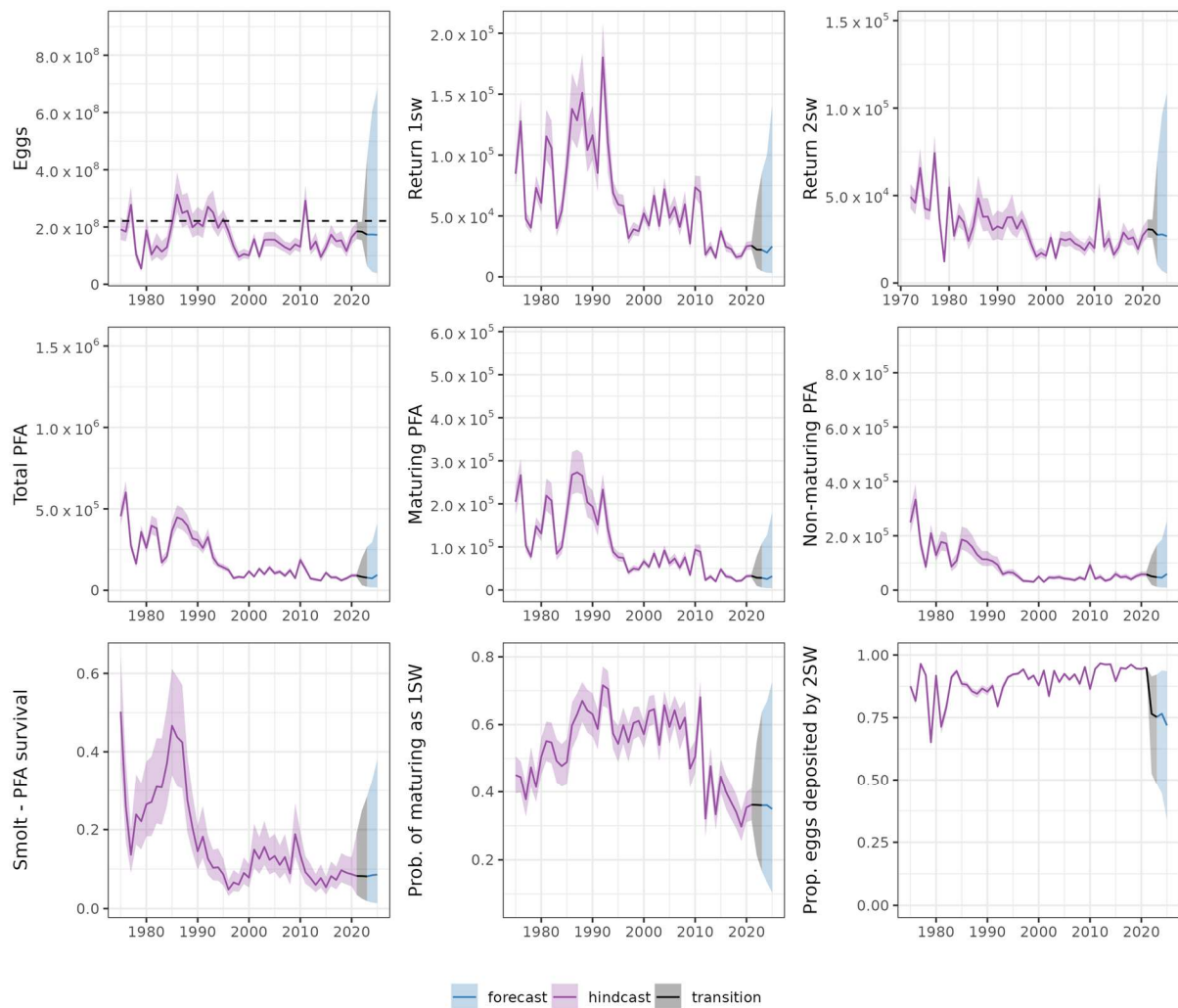
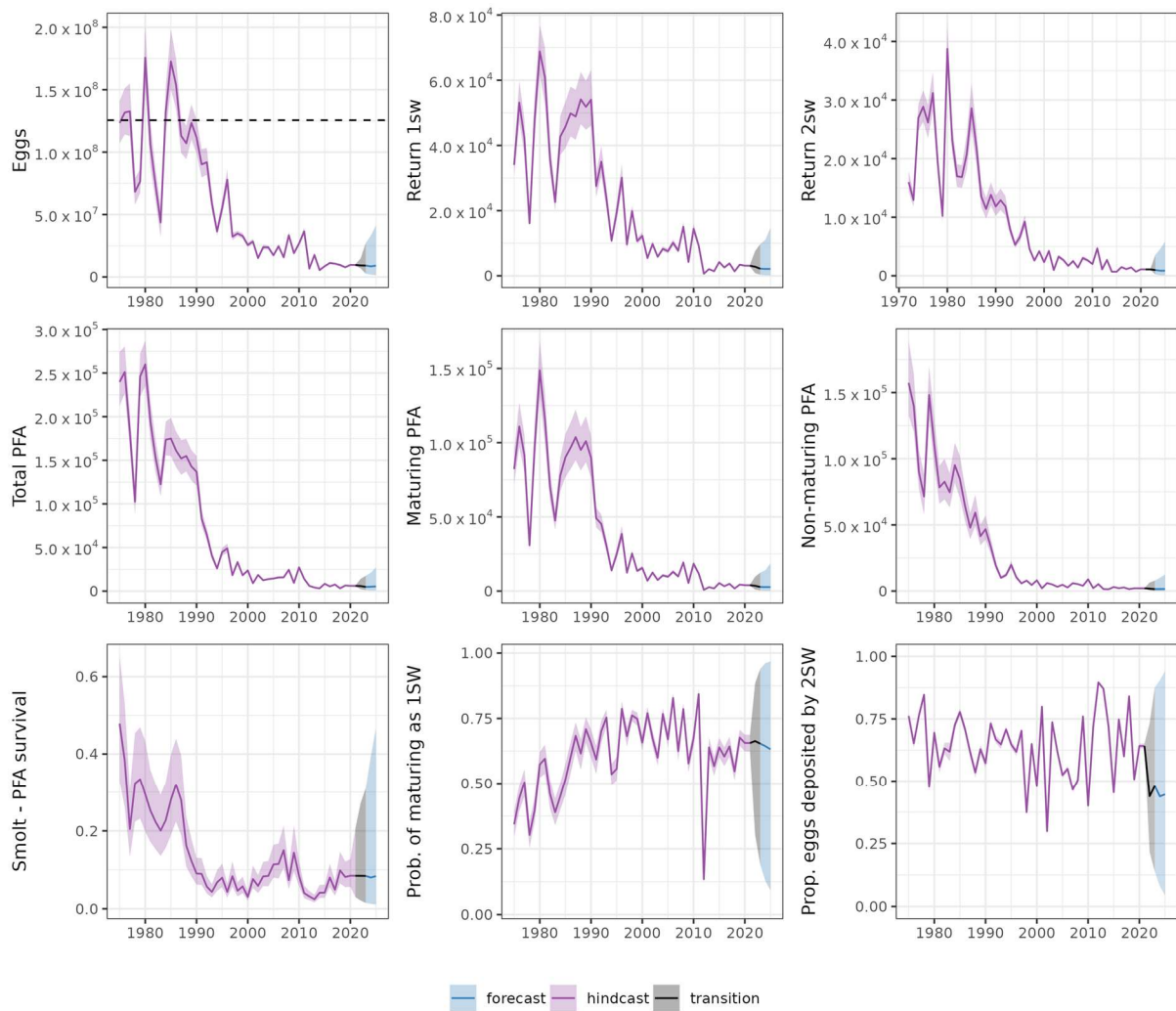
Labrador (NAC)

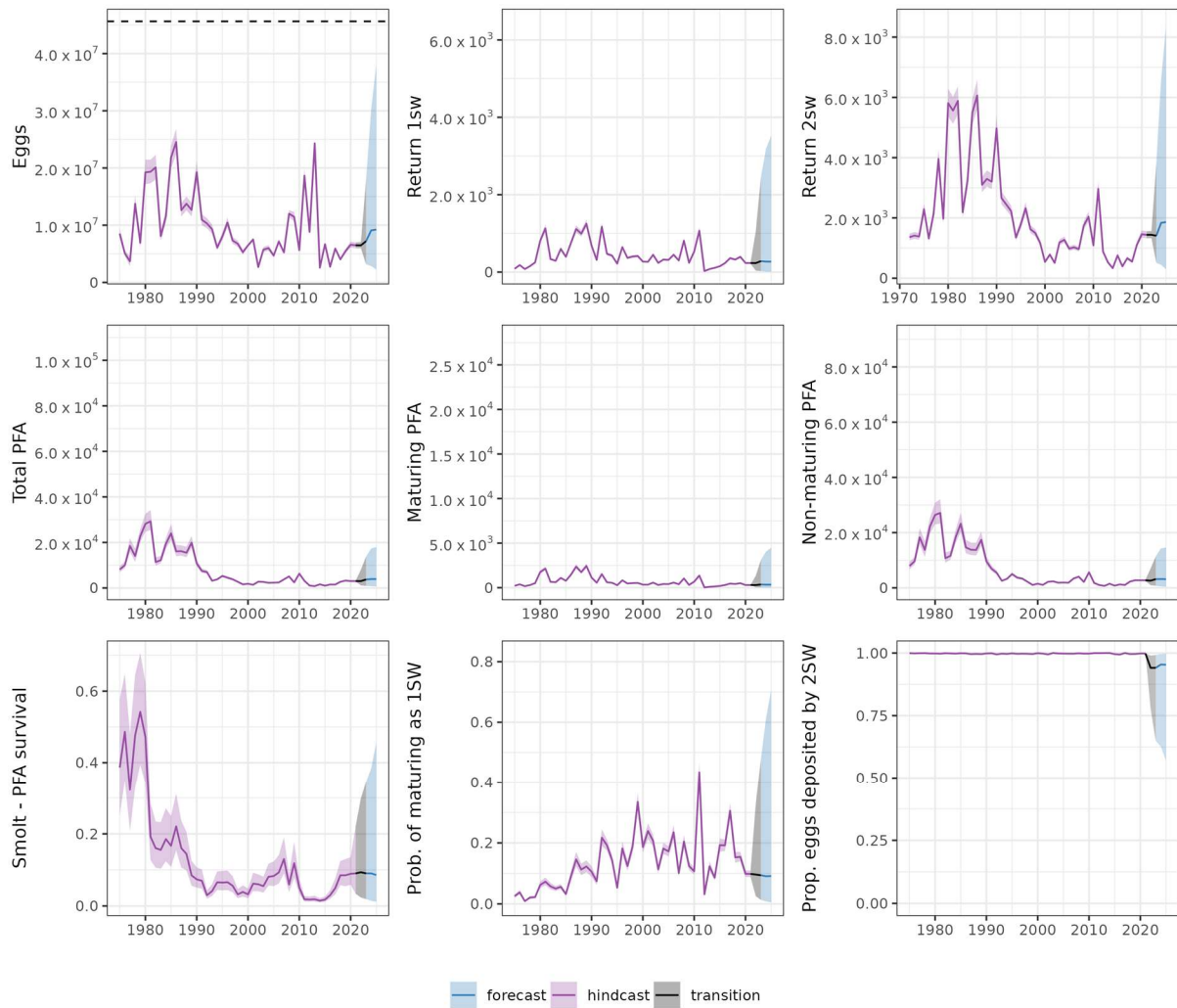
Figure 9. SU = Labrador. Posterior probability distributions for the key life stages for all SU (or aggregate of SU at the scale of countries). Pink shaded: hindcasting on the historical time series 1971-2022. Blue and grey shaded: forecasting obtained under a scenario with 0 catches in all fisheries. Horizontal dotted lines in the top left panel is the management objectives (in total eggs 1SW + 2SW).

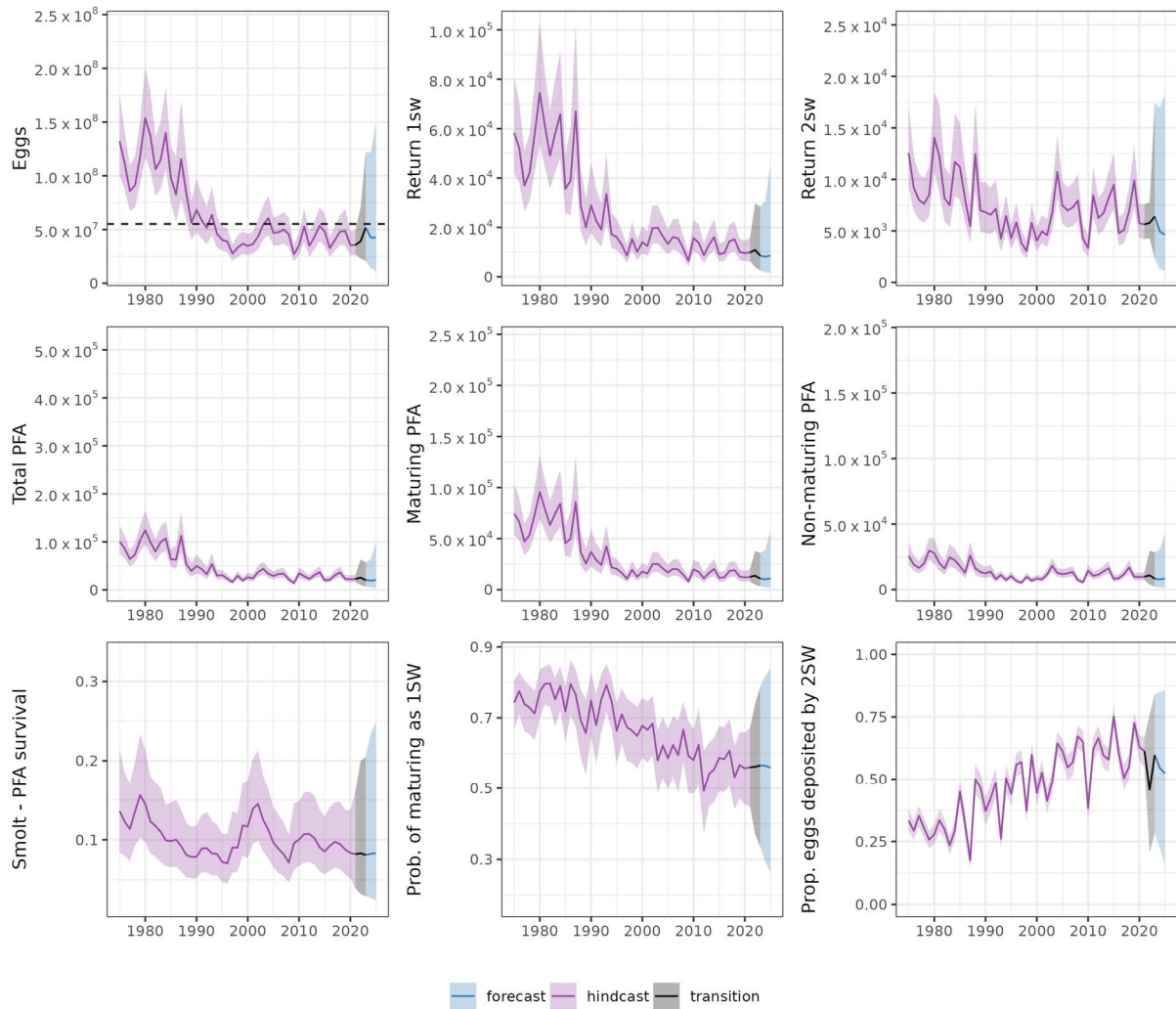
Newfoundland (NAC)**Figure 9 (continuing). SU = Newfoundland.**

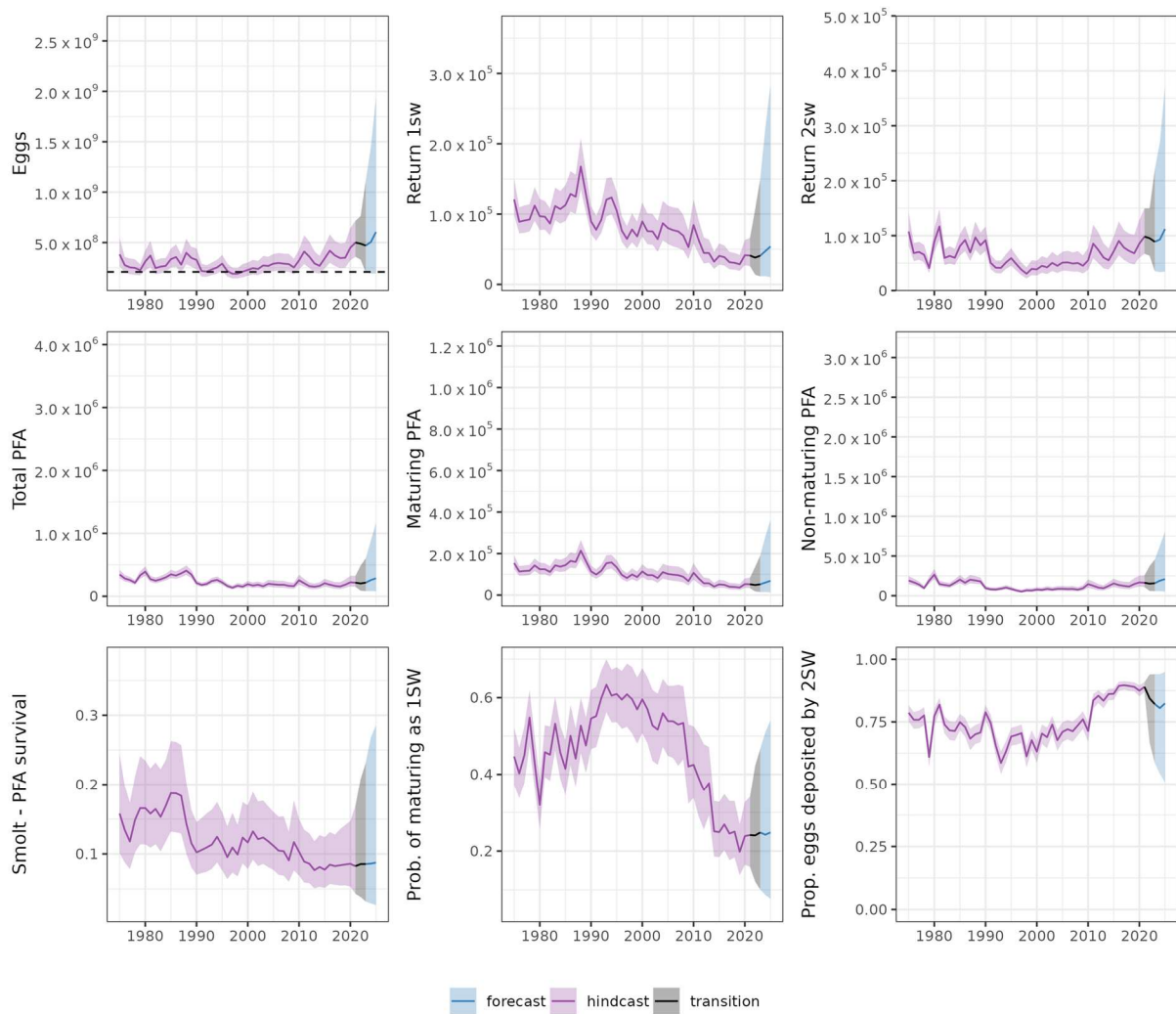
Quebec (NAC)**Figure 9 (continuing). SU = Quebec.**

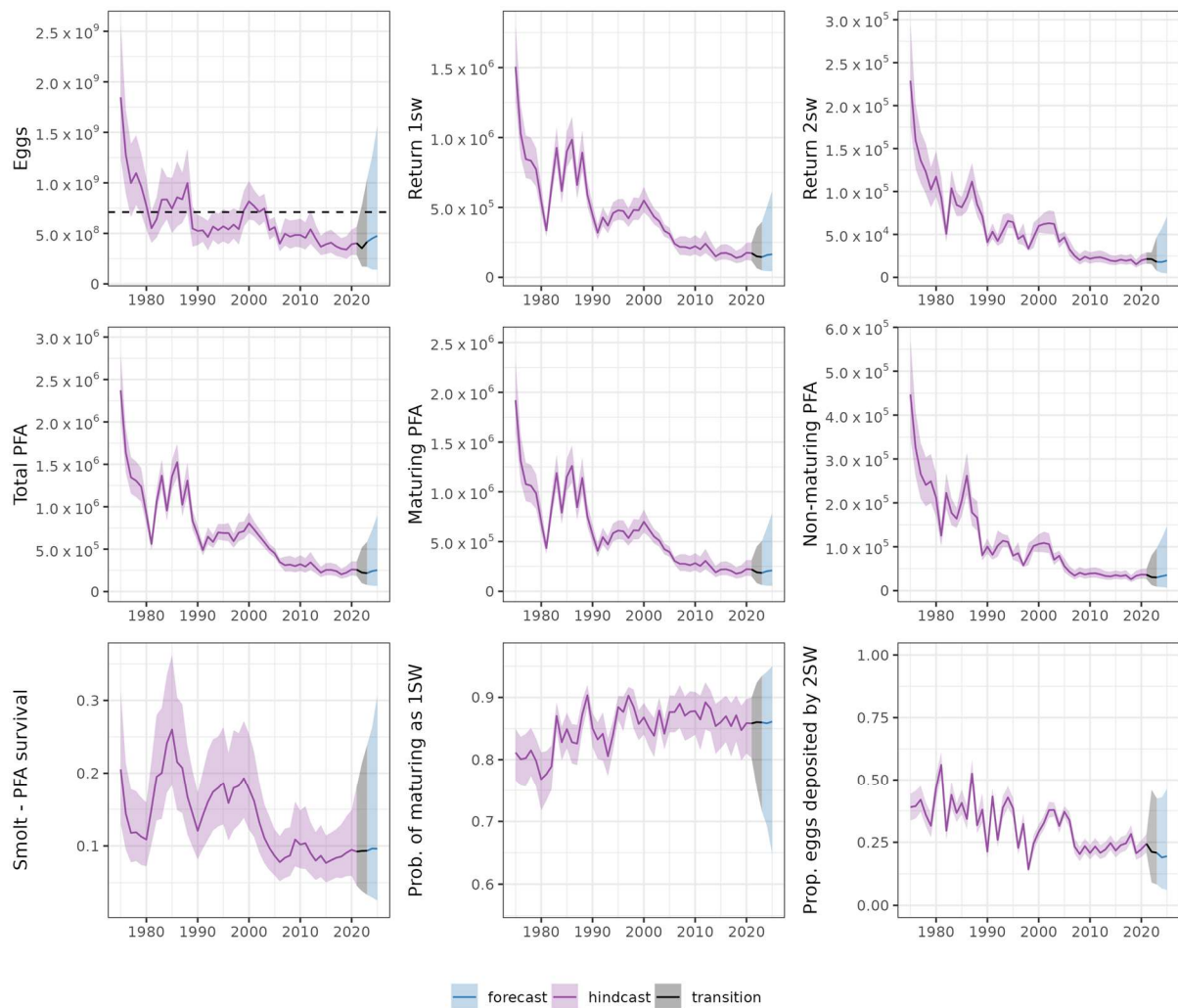
Gulf region**Figure 9 (continuing). SU = Gulf region.**

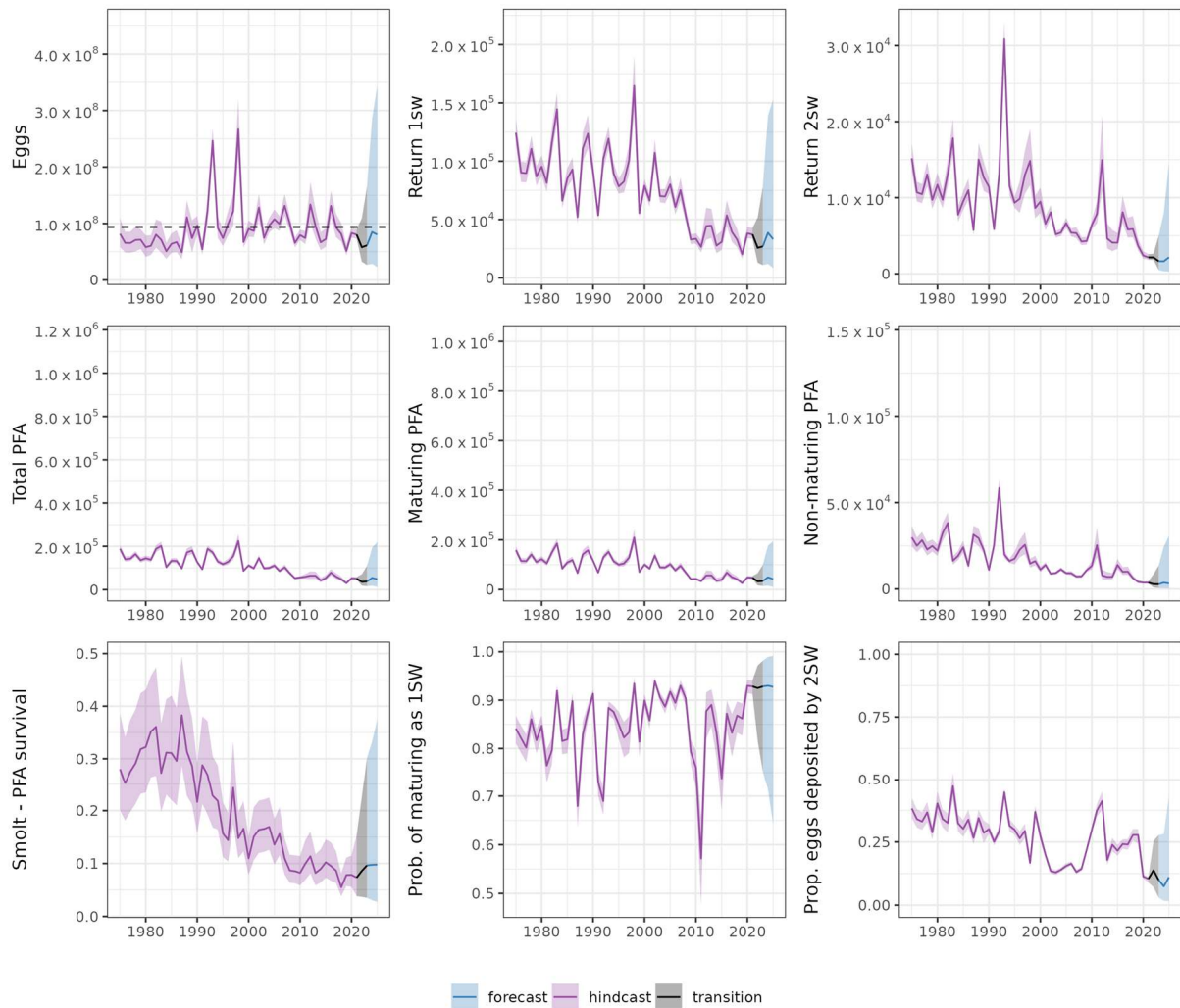
Scotia Fundy (NAC)**Figure 9 (continuing). SU = Scotia Fundy.**

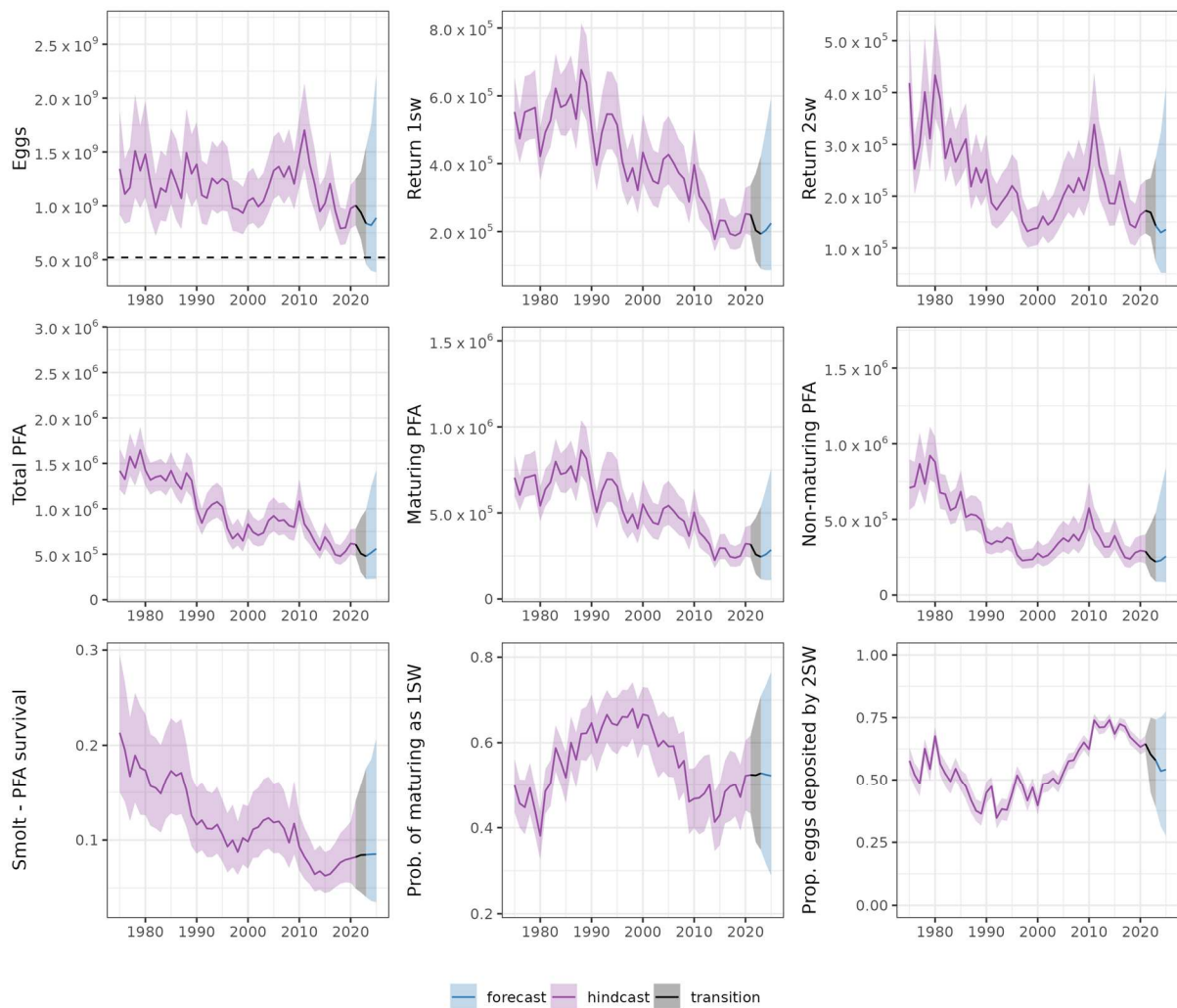
USA (NAC)**Figure 9 (continuing). SU = USA.**

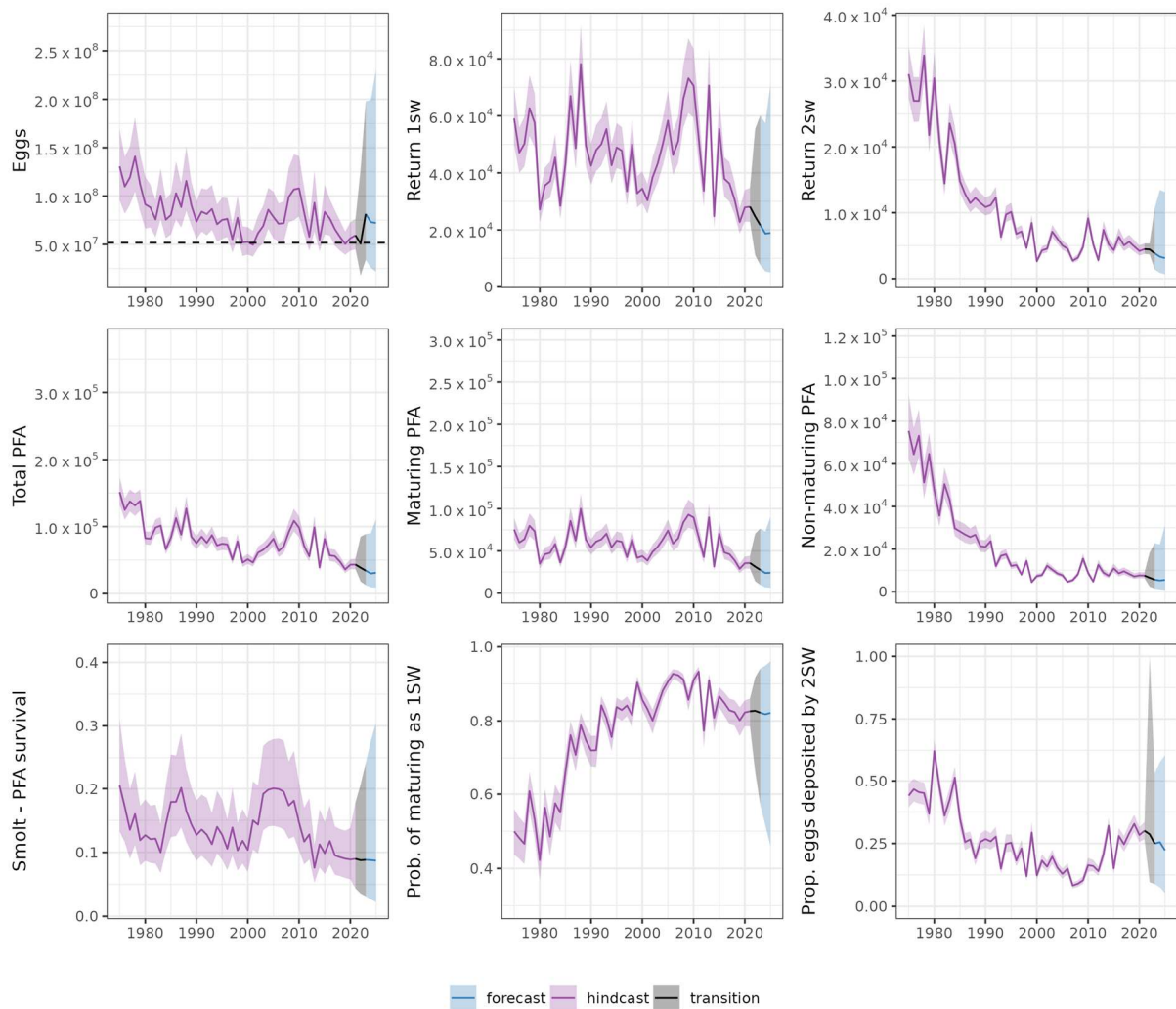
France (Southern NEAC)**Figure 9 (continuing). SU = France.**

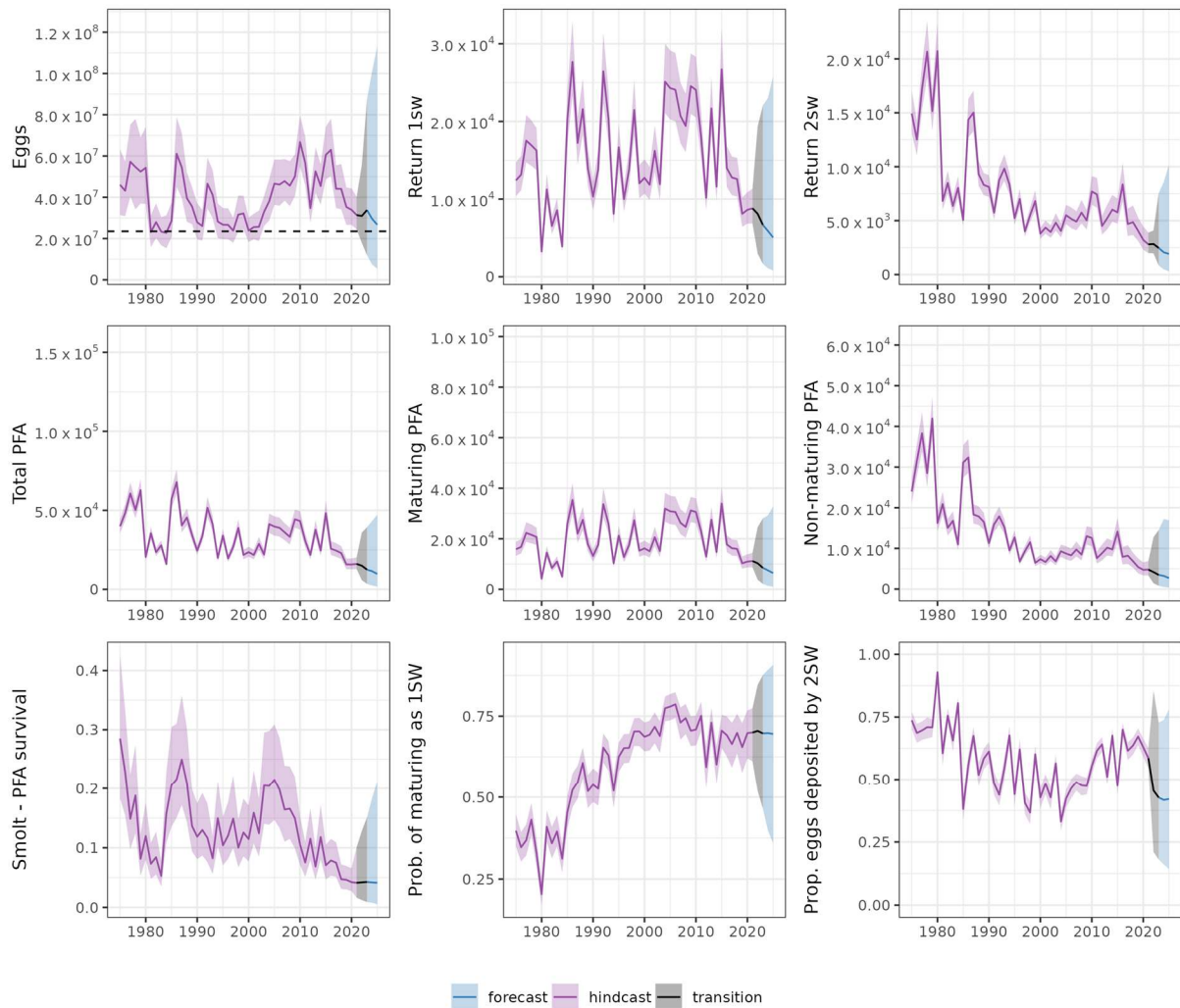
England & Whales (Southern NEAC)**Figure 9 (continuing). SU = UK England & Whales.**

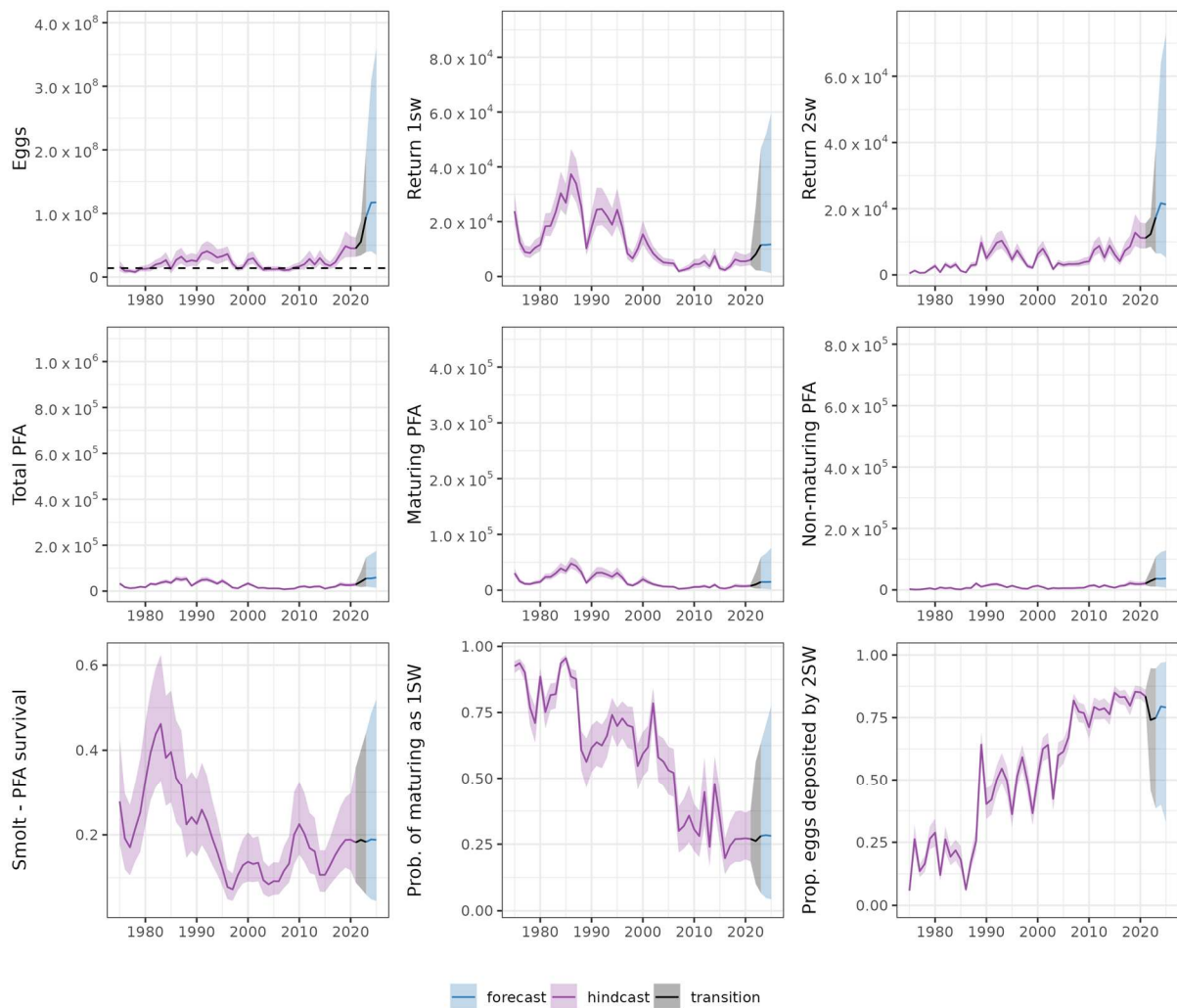
Ireland (Southern NEAC)**Figure 9 (continuing). SU = Ireland.**

UK Northern Ireland (Southern NEAC)**Figure 9 (continuing). SU = UK Northern Ireland (aggregate FO + FB)**

Scotland (Southern NEAC)**Figure 9 (continuing). SU = Scotland (aggregate East and West).**

Iceland South West (Southern NEAC)**Figure 9 (continuing). SU = Iceland South-West (belongs to the South European stock grouping).**

Iceland North East (Northern NEAC)**Figure 9 (continuing). SU = Iceland North-East (belongs to the North European stock grouping).**

Sweden (Northern NEAC)**Figure 9 (continuing). SU = Sweden.**

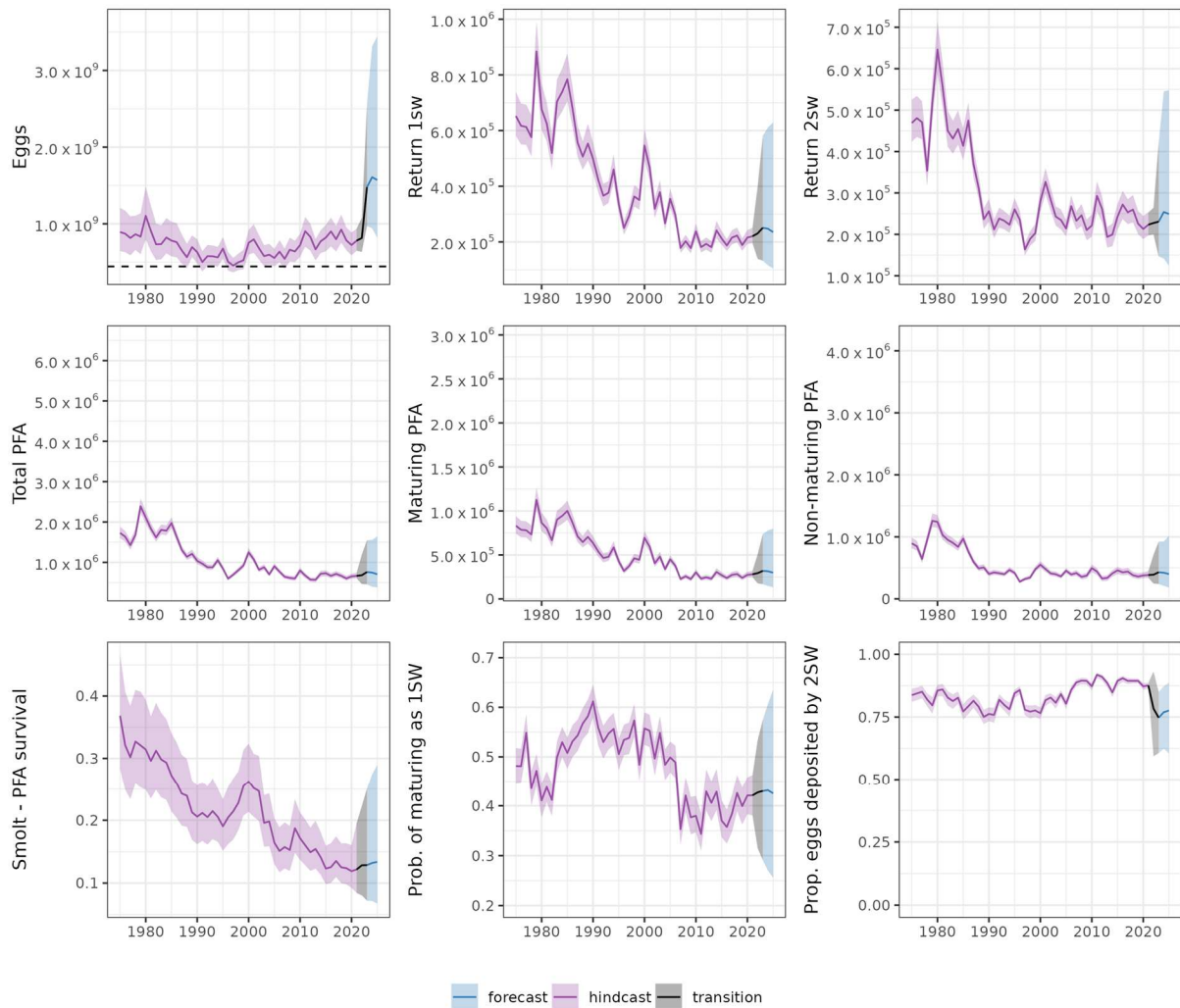
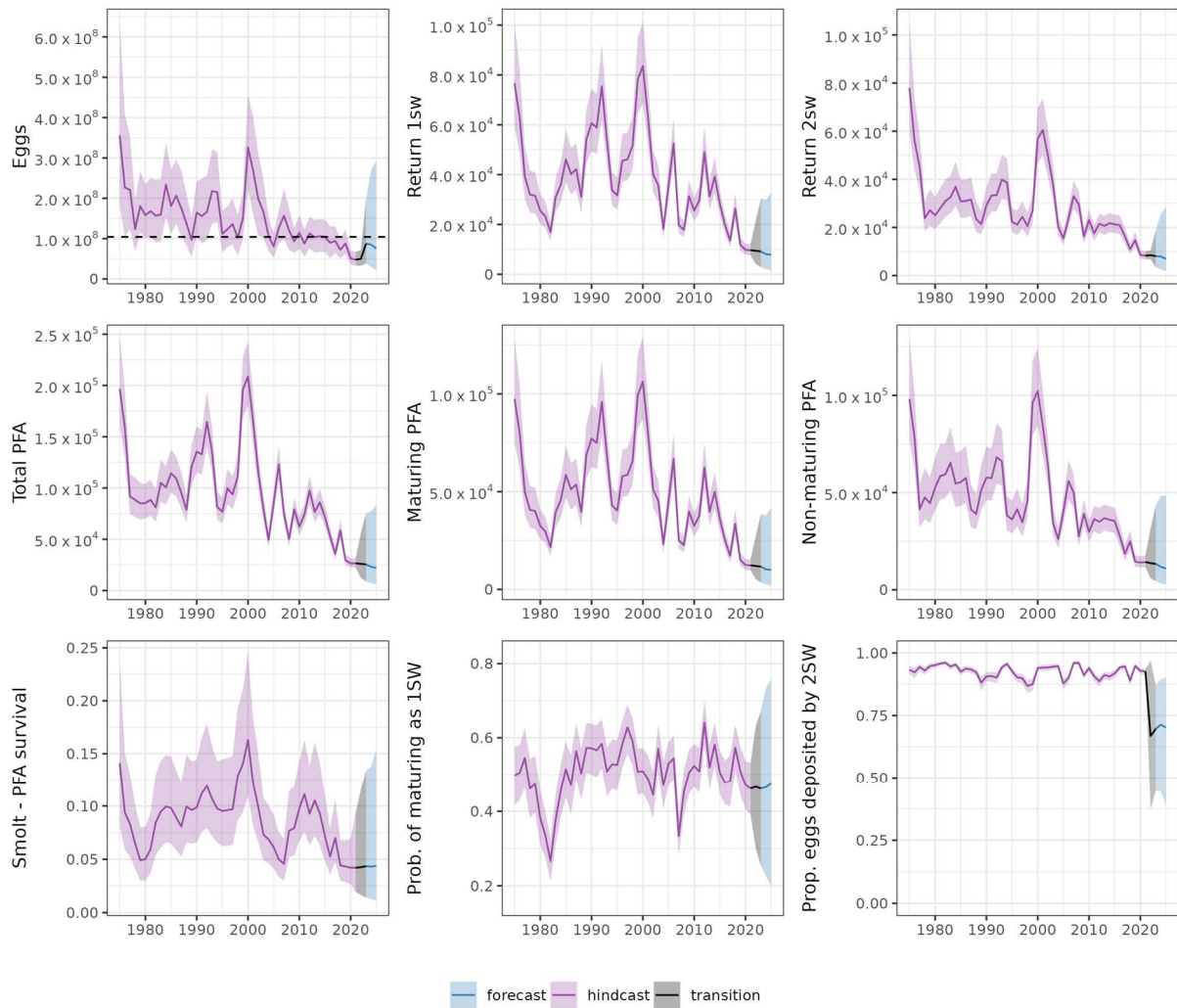
Norway (Northern NEAC)

Figure 9 (continuing). SU = Norway (aggregate Norway South-East, Norway South-West, Middle Norway, Norway North).

Finland (Northern NEAC)**Figure 9 (continuing). SU = Finland.**

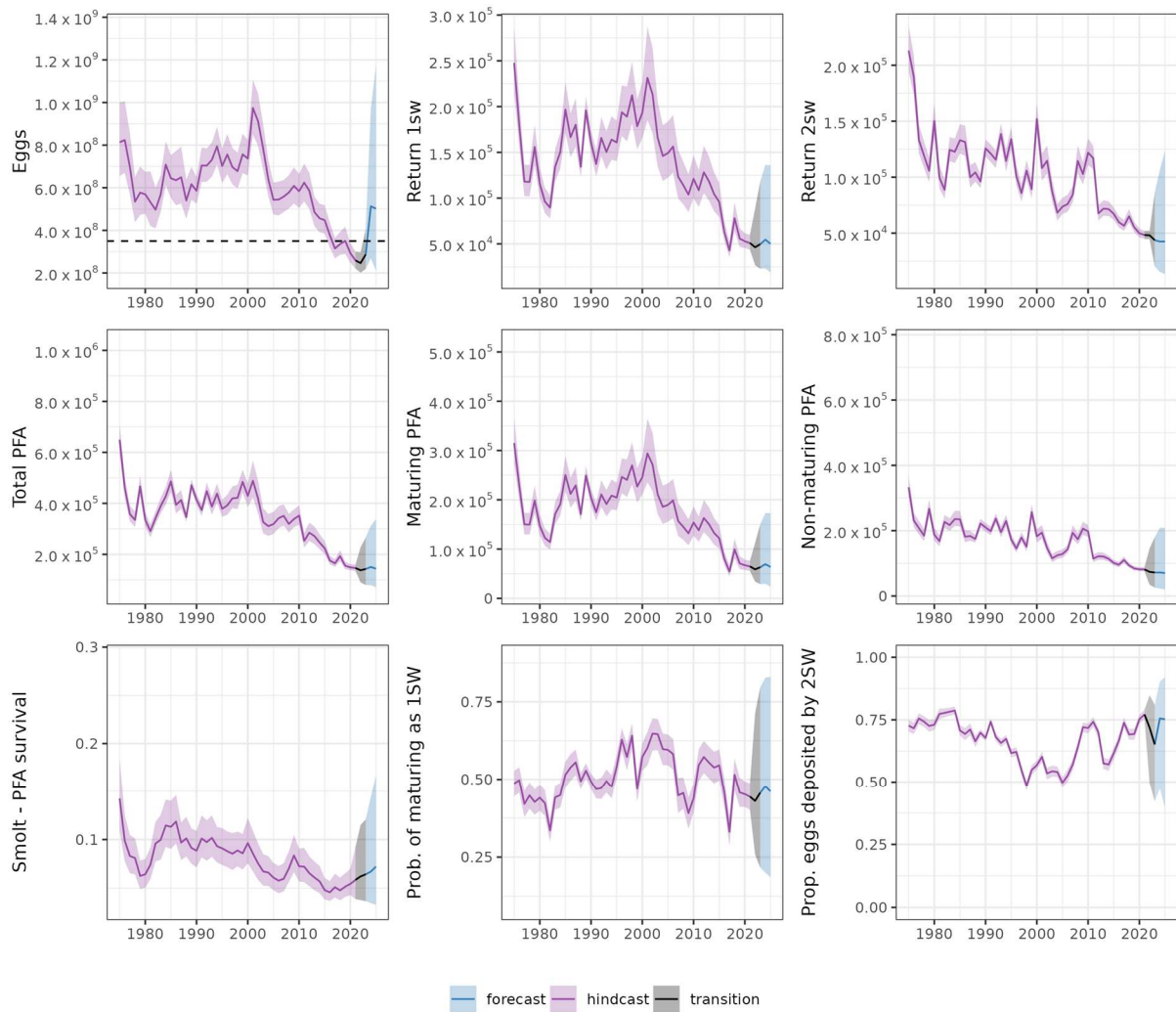
Russia (Northern NEAC)

Figure 9 (continuing). SU = Russia (aggregate Russia Kola Barents, Russia Kola White Sea, Russia Arkhangelsk Karelia and Russia River Pechora).

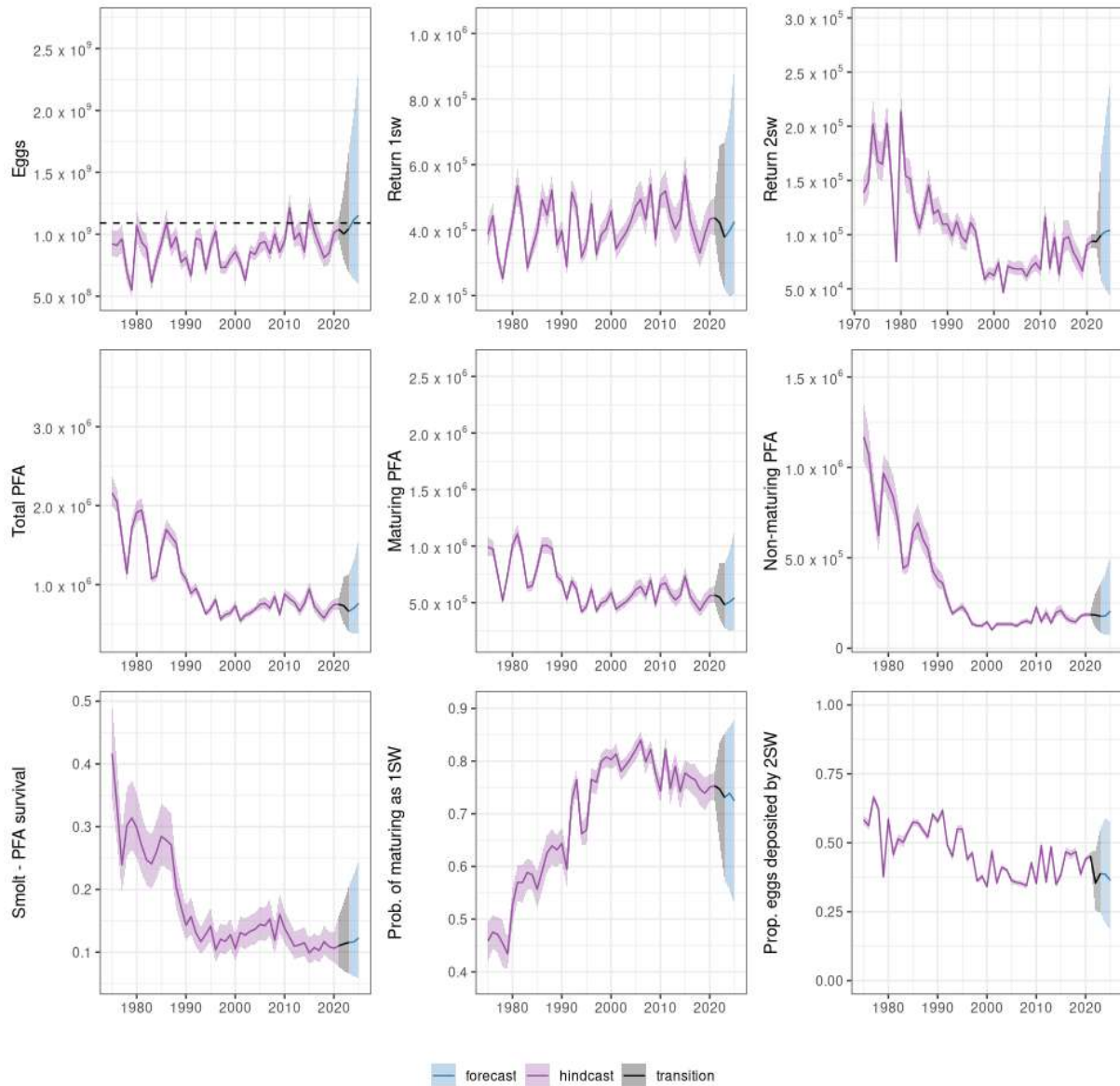
North America (aggregated)

Figure 10a. Posterior probability distributions for the key life stages aggregated for all stock units of North America. Pink shaded are: hindcasting on the historical time series 1971-2022. Blue and grey shaded area = forecasting obtained under a scenario with 0 catches in all fisheries. Horizontal dotted lines in the top left panel is the management objective in eggs (total 1SW + 2SW).

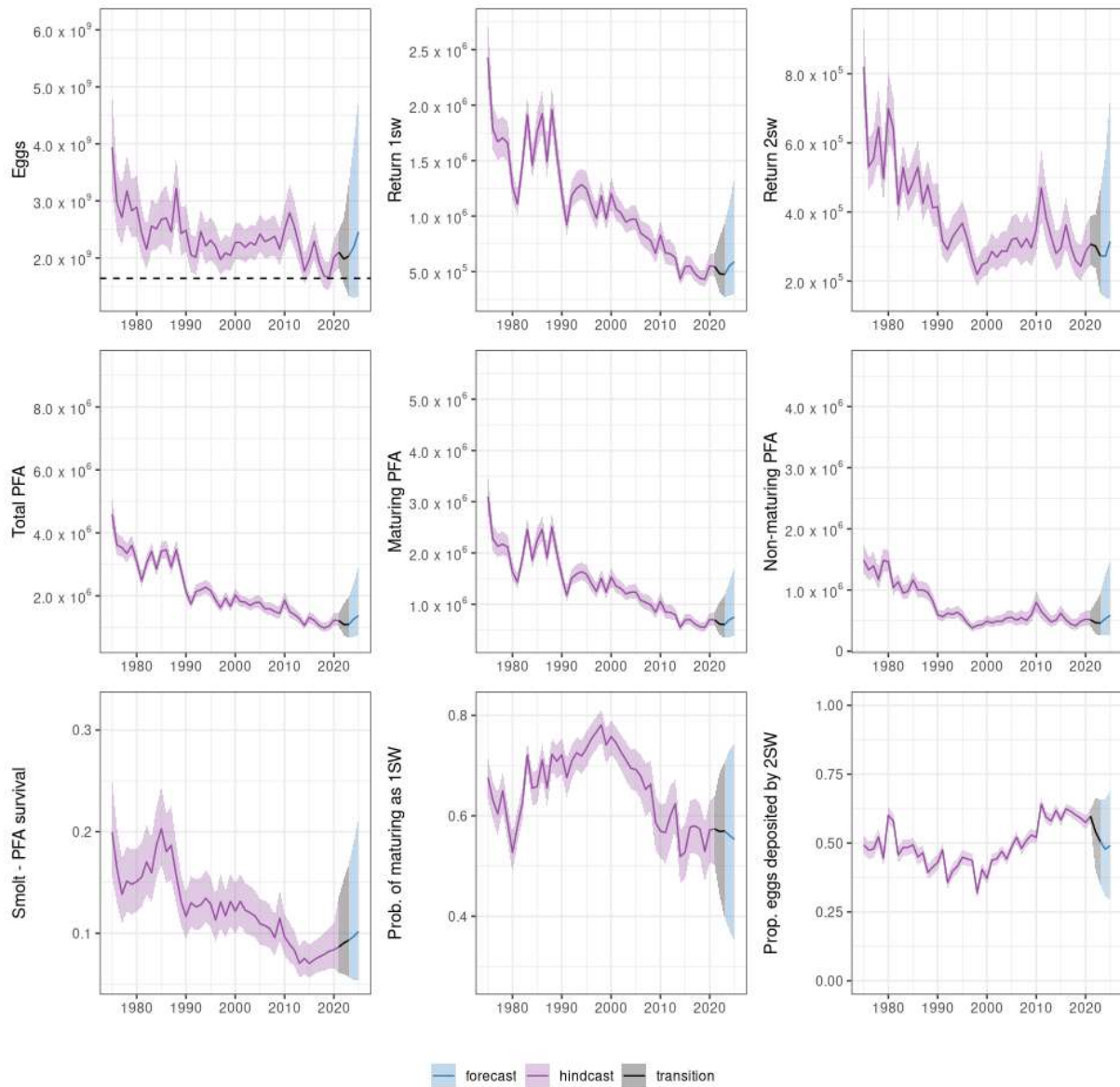
Southern Europe (aggregated)

Figure 10b. Posterior probability distributions for the key life stages aggregated for all stock units of Southern Europe. Pink shaded are: hindcasting on the historical time series 1971-2022. Blue and grey shaded area = forecasting obtained under a scenario with 0 catches in all fisheries. Horizontal dotted lines in the top left panel is the management objective in eggs (total 1SW + 2SW).

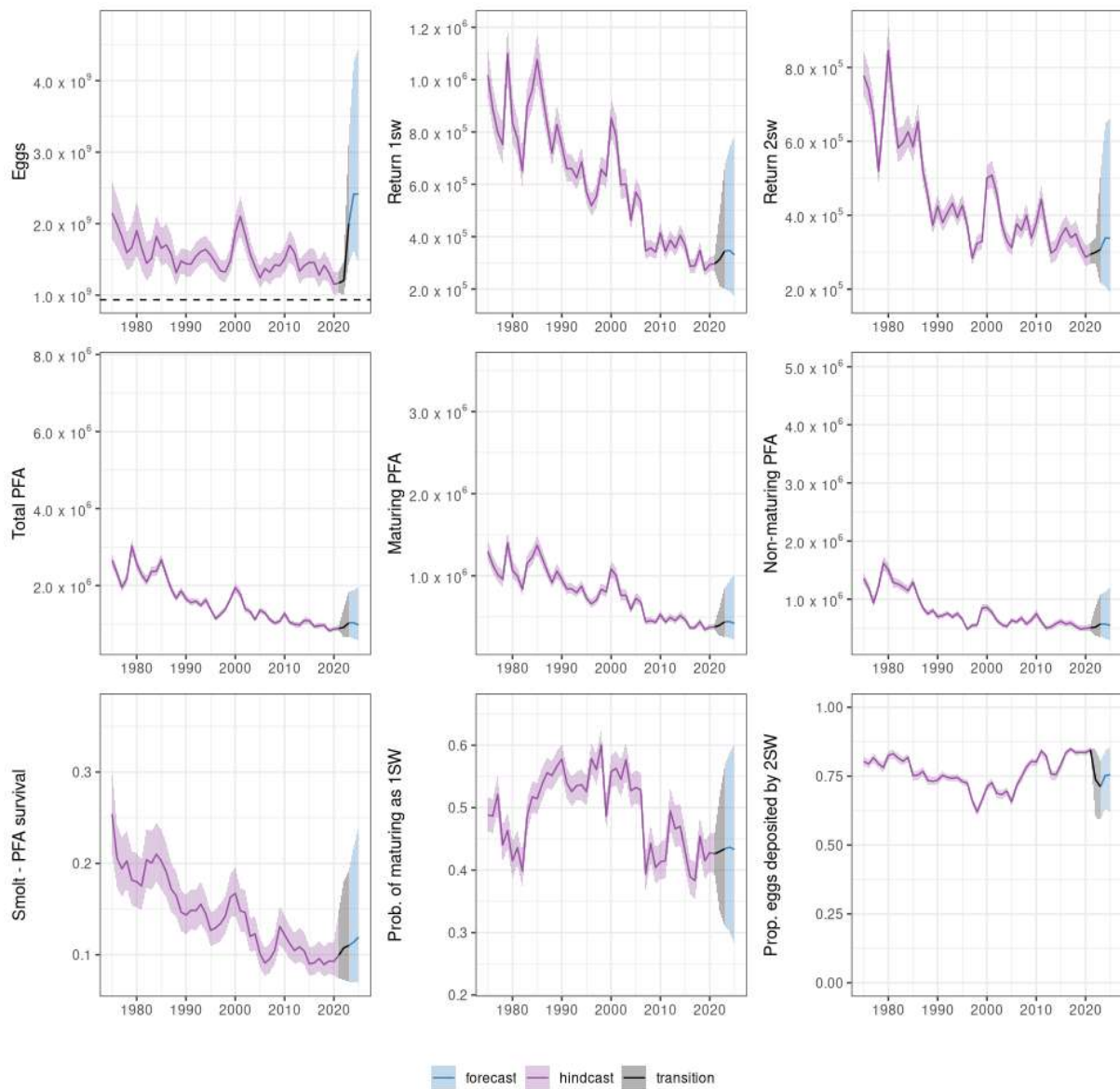
Northern Europe (aggregated)

Figure 10c. Posterior probability distributions for the key life stages aggregated for all stock units of Northern Europe. Pink shaded are: hindcasting on the historical time series 1971-2022. Blue and grey shaded area = forecasting obtained under a scenario with 0 catches in all fisheries. Horizontal dotted lines in the top left panel is the management objective in eggs (total 1SW + 2SW).

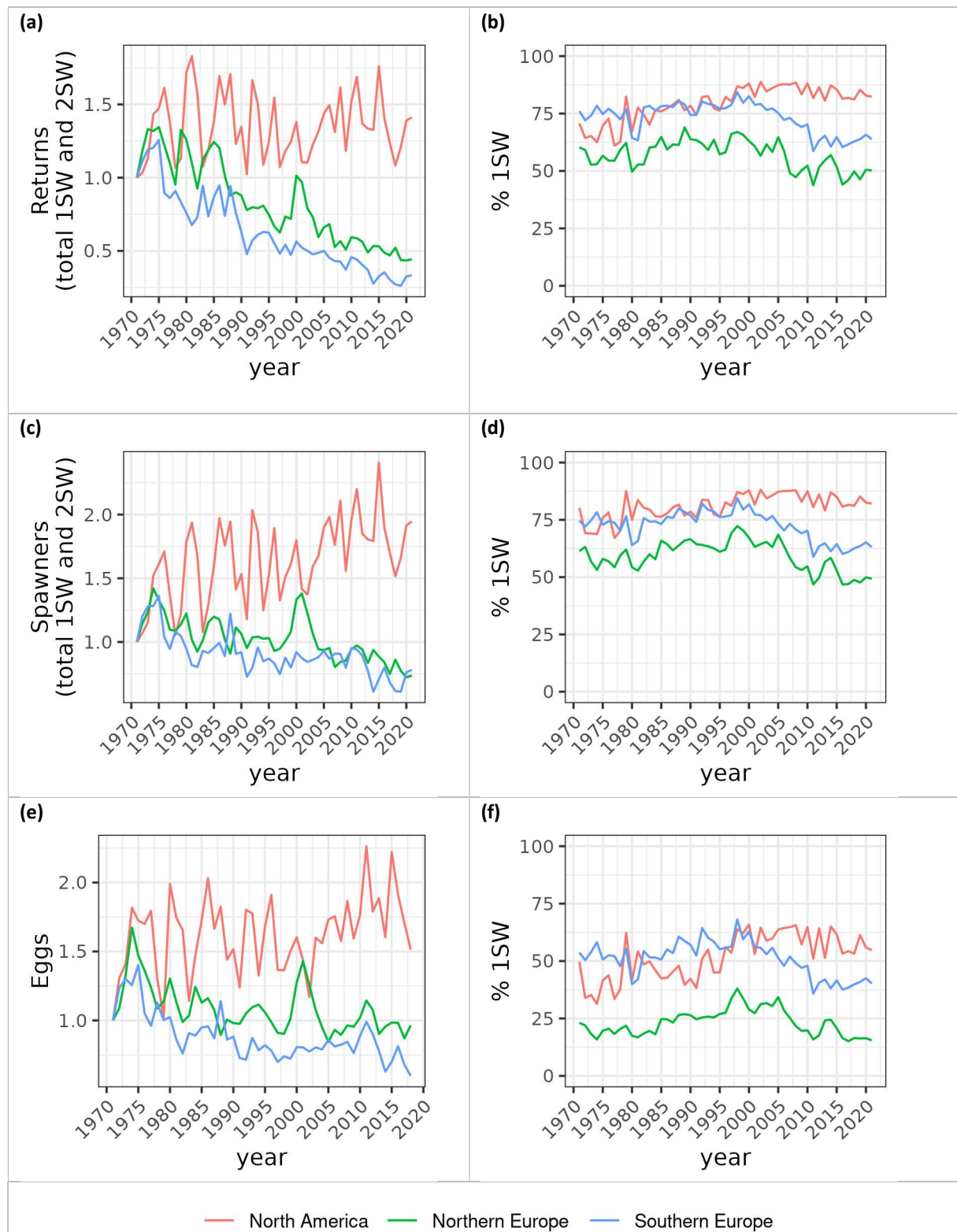


Figure 11. Abundances aggregated per CSG at four stages in the life cycle (medians of marginal posterior distributions; All standardized to the first year values): (a) total returns to homewater (1SW + 2SW); (b) proportion of 1SW in returns; (c) total spawners (1SW + 2SW); (d) proportion of 1SW in spawners; (e) total egg deposition by spawners; (f) proportion of eggs spawned by 1SW.

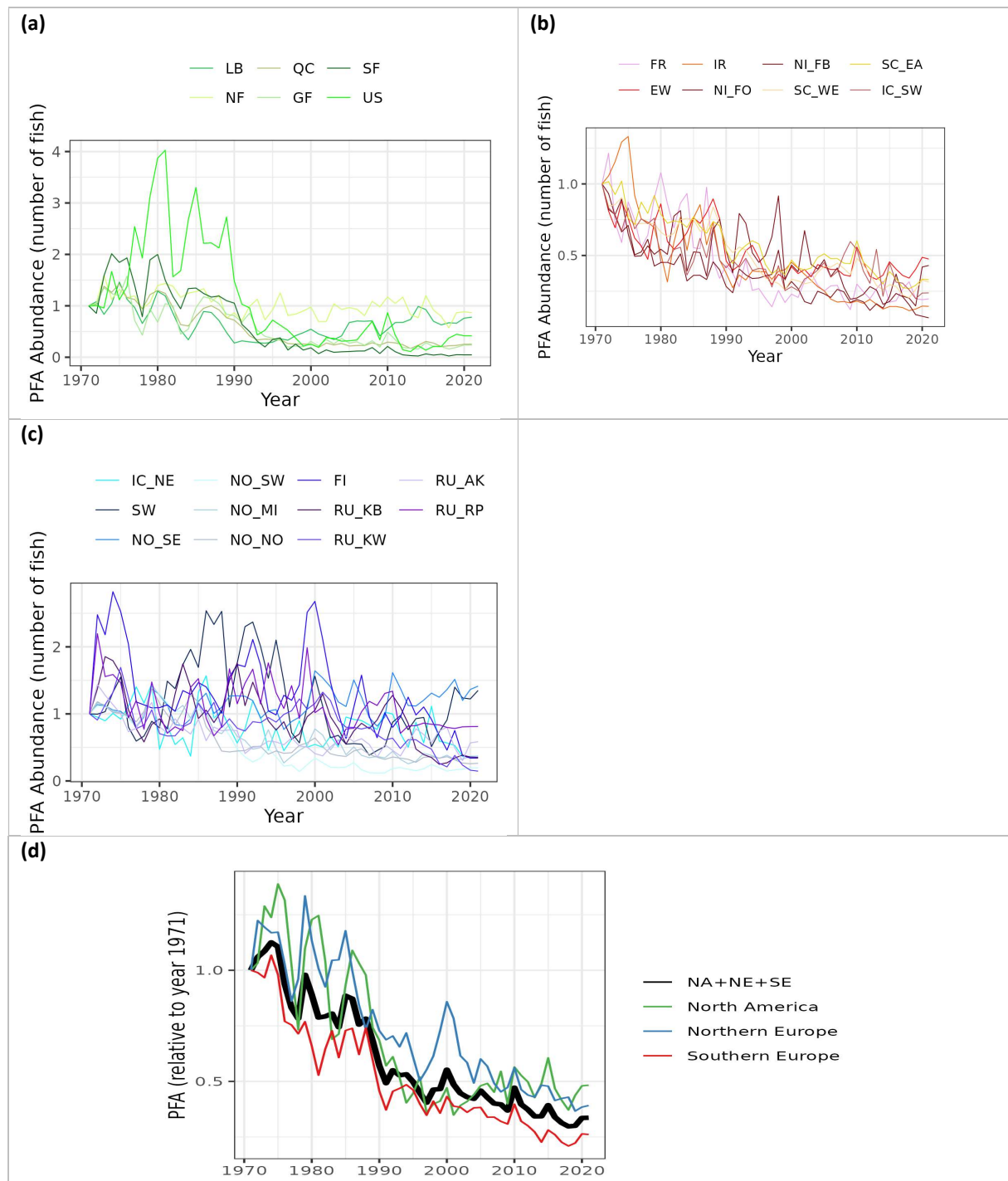


Figure 12. Abundances estimated at the PFA stage (maturing + non maturing PFA) for all SU for the three continental stock groups (median of the marginal posterior distributions; all standardized to the first year values): (a) North America, (b) Southern Europe; (c) Northern Europe; (d) summed by CSG.

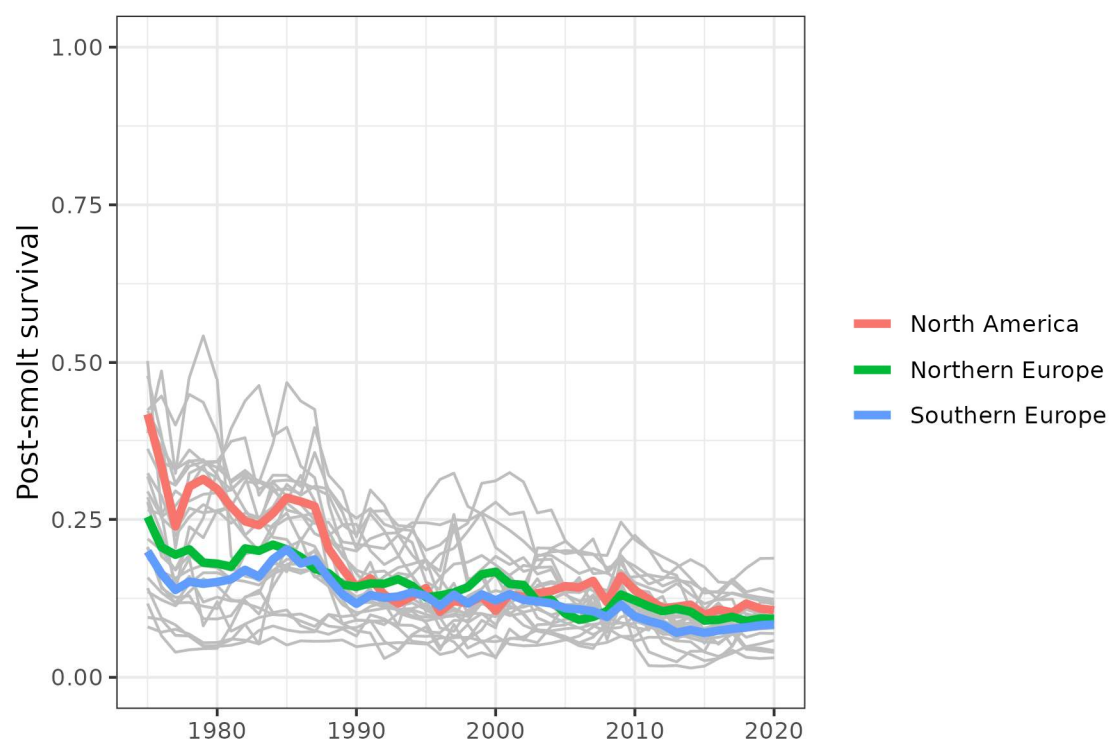


Figure 13. Smolt-PFA survival (in the natural scale) for the 25 SU (thin grey lines) and averaged over the three continental stock groups (thick color lines) (median of the marginal posterior distributions). The first 5 years are not represented as the inferences are too sensitive to initialization of the first cohorts.

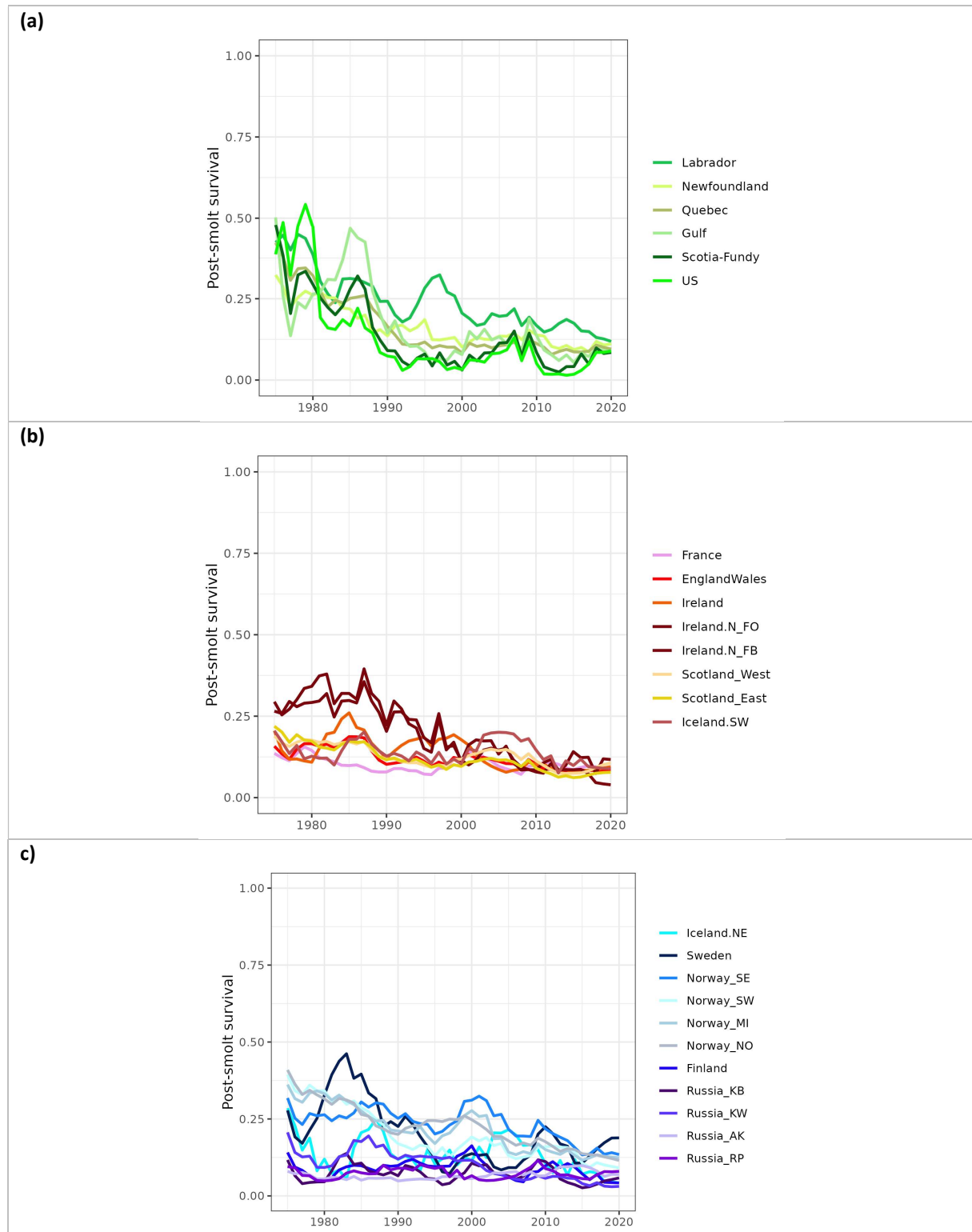


Figure 14. Smolt-PFA survival (in the natural scale) for the 25 SU grouped by continental stock groups (median of the marginal posterior distributions). The first 5 years are not represented as the inferences are too sensitive to initialization of the first cohorts.

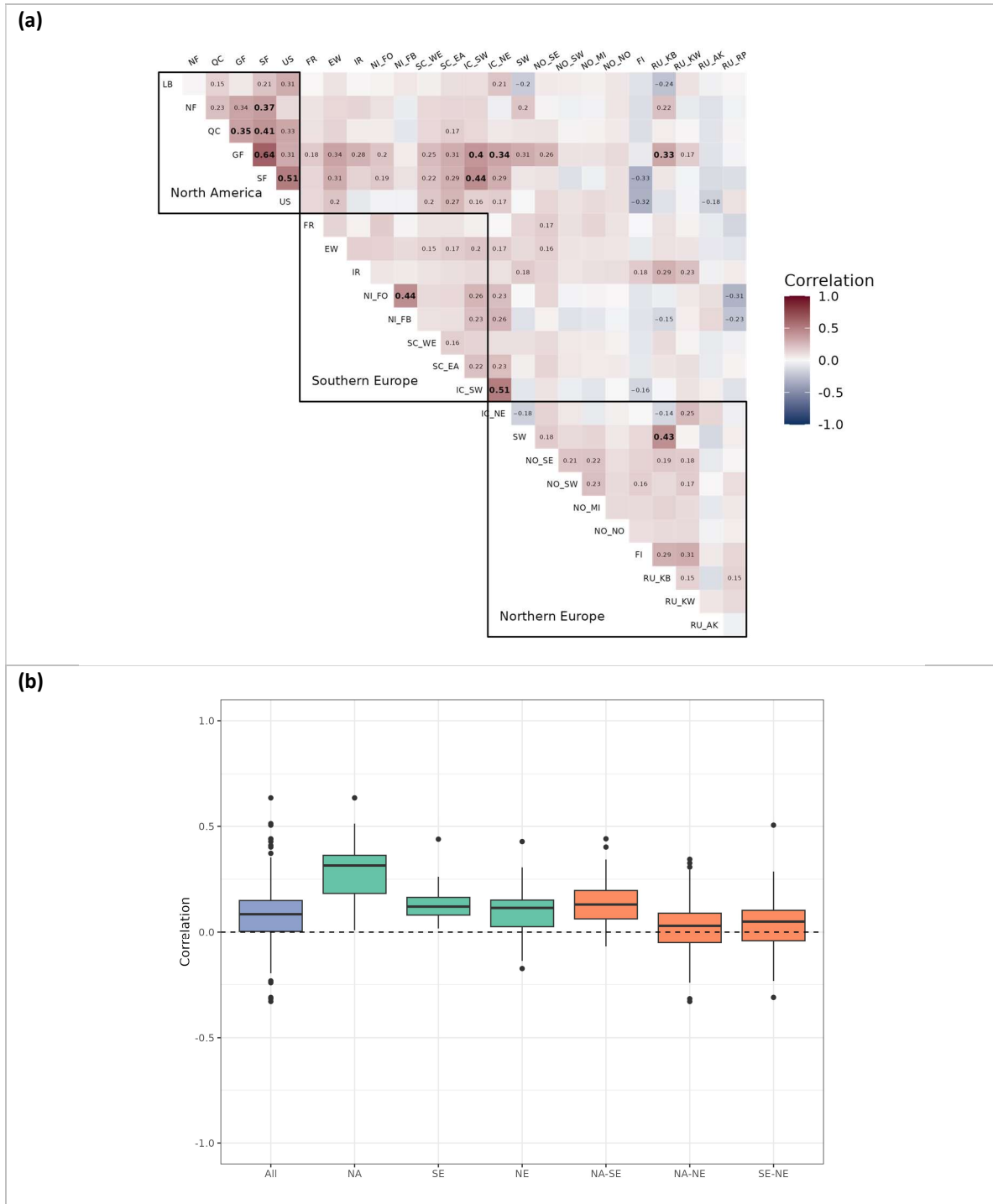


Figure 15. Smolt-PFA survival. a) Pairwise correlations calculated between all SUs (median of the posterior distribution from the variance-covariance matrix in the logit scale). The posterior median of the correlation is indicated when the Bayesian credibility interval (BCI) does not contain 0 (BCI 50% and 90% for bold numbers). **b)** Pairwise correlations (calculated in the logit scale) averaged over all SUs, over SU within the same CSG (NA, SE, NE) and over pairs of SU that belong to two different CSG (NA-SE, NA-NE and SE-NE).

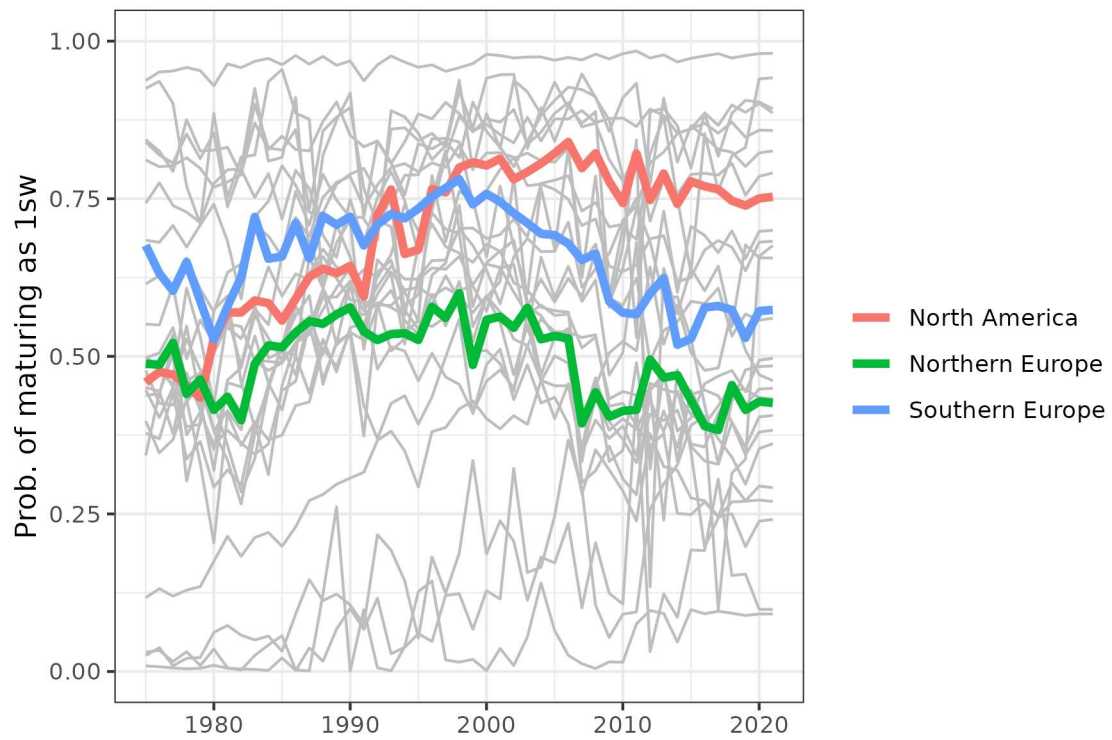


Figure 16. Proportion PFA maturing as 1SW (in the natural scale) for the 25 SU (thin grey lines) and averaged over the three continental stock groups (thick color lines) (median of the marginal posterior distributions). The first 5 years are not represented as the inferences are too sensitive to initialization of the first cohorts.

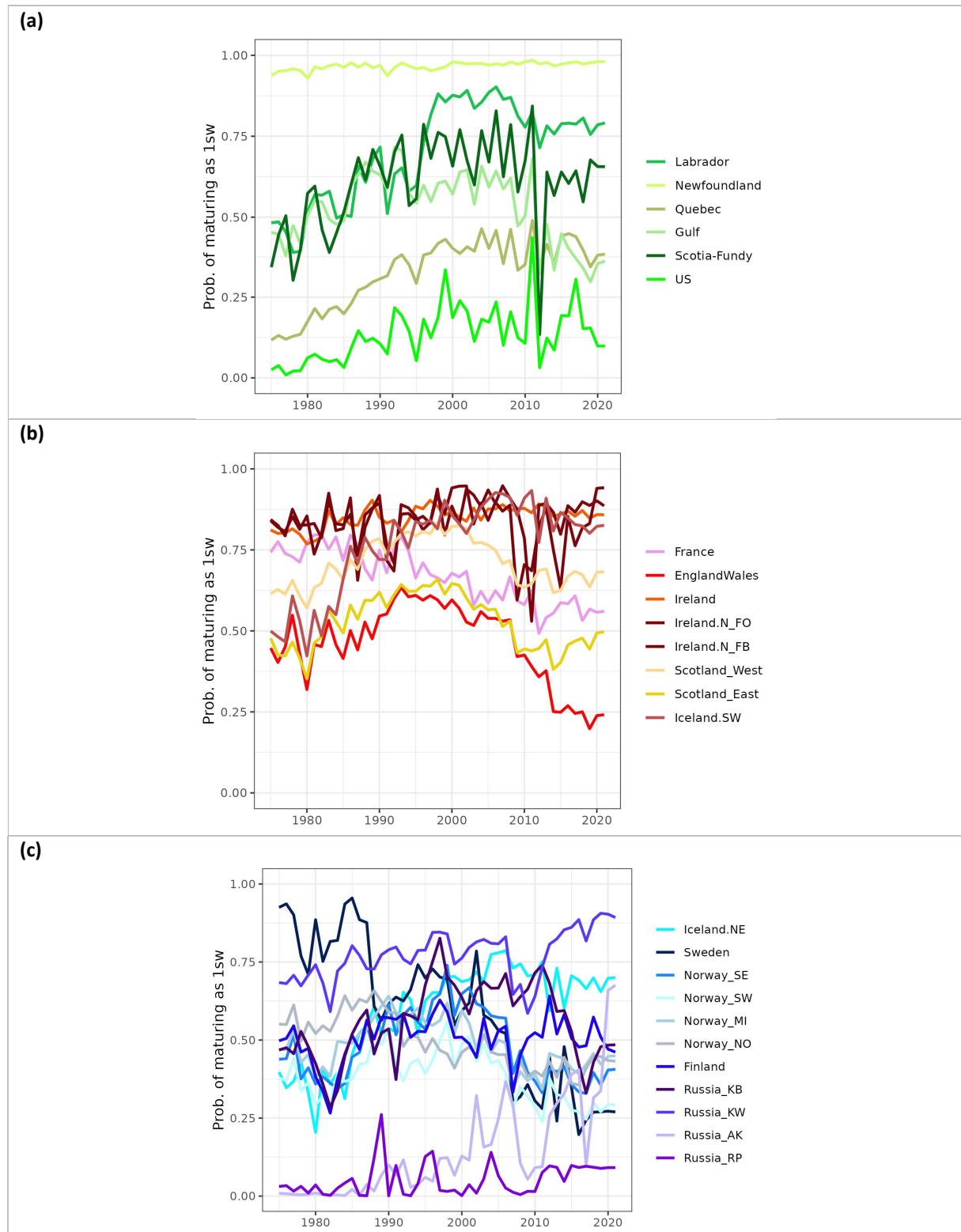


Figure 17. Proportion maturing PFA (in the natural scale) for the 25 SU grouped by continental stock groups (median of the marginal posterior distributions). The first 5 years are not represented as the inferences are too sensitive to initialization of the first cohorts.

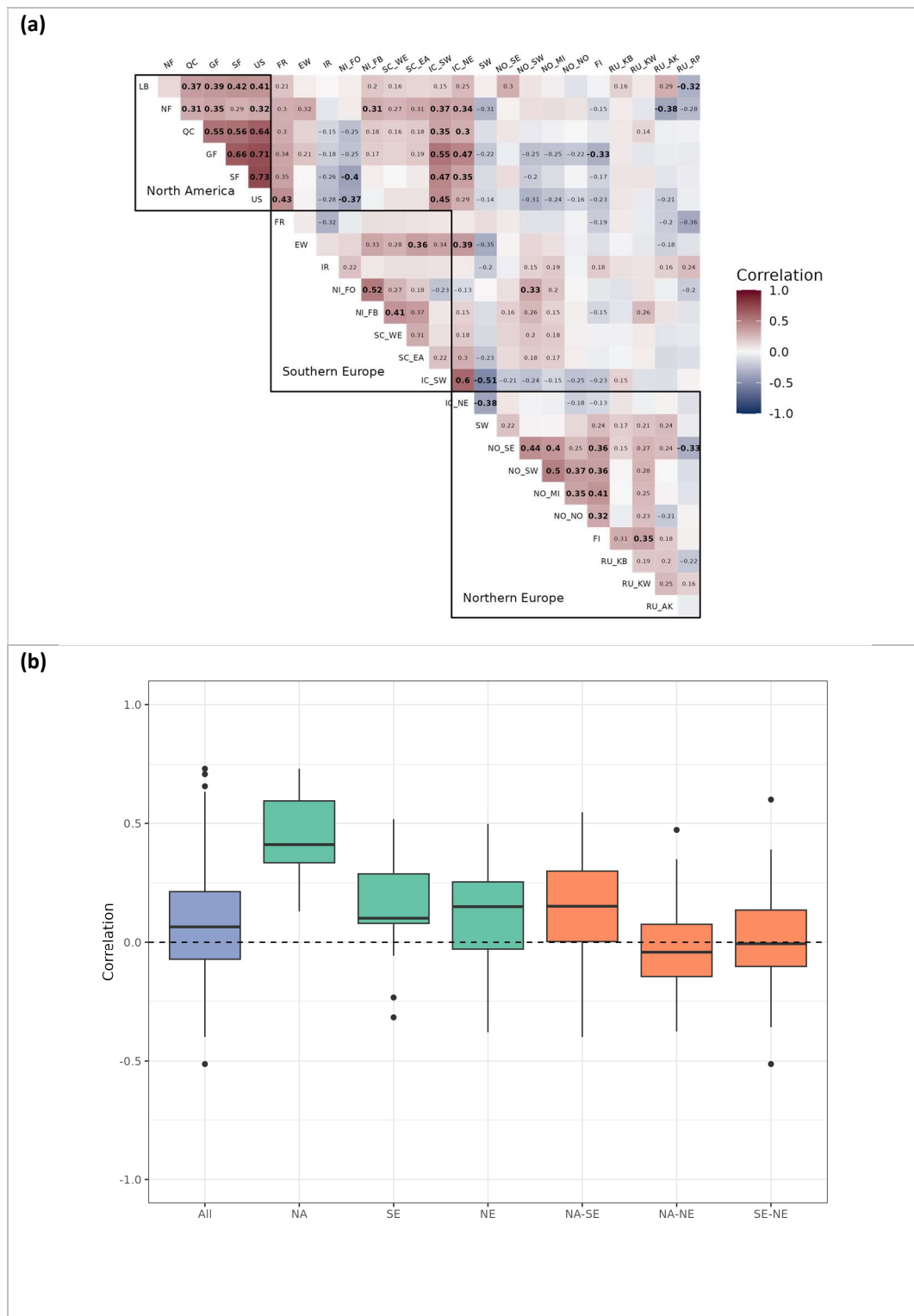


Figure 18. Proportion of PFA maturing as 1SW. a) Pairwise correlations calculated between all SUs (median of the posterior distribution from the variance-covariance matrix in the logit scale). The posterior median of the correlation is indicated when the Bayesian credibility interval (BCI) does not contain 0 (BCI 50% and 90% for bold numbers). b) Pairwise correlations (calculated in the logit scale) averaged over all SUs, over SU within the same CSG (NA, SE, NE) and over pairs of SU that belong to two different CSG (NA-SE, NA-NE and SE-NE).

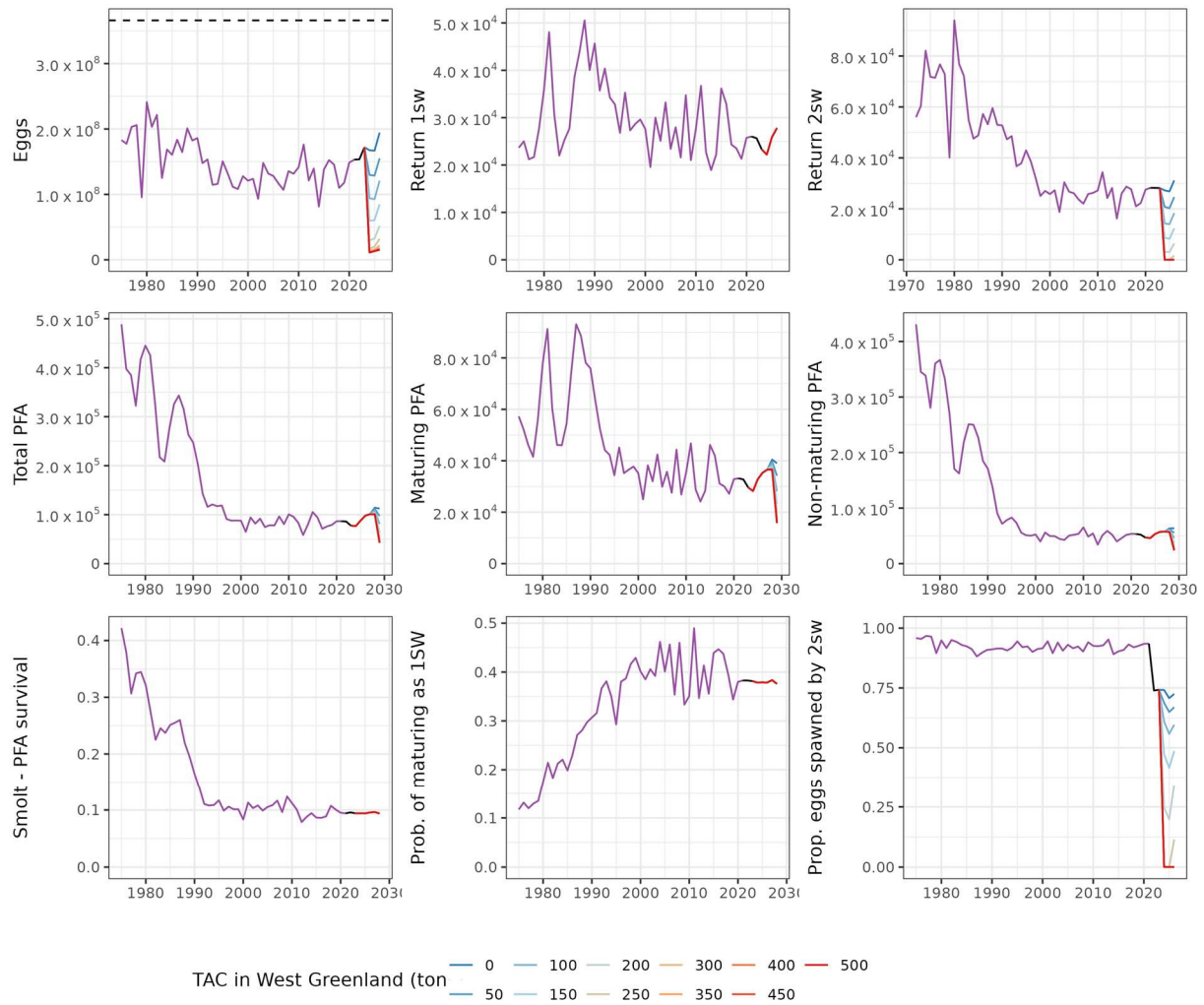
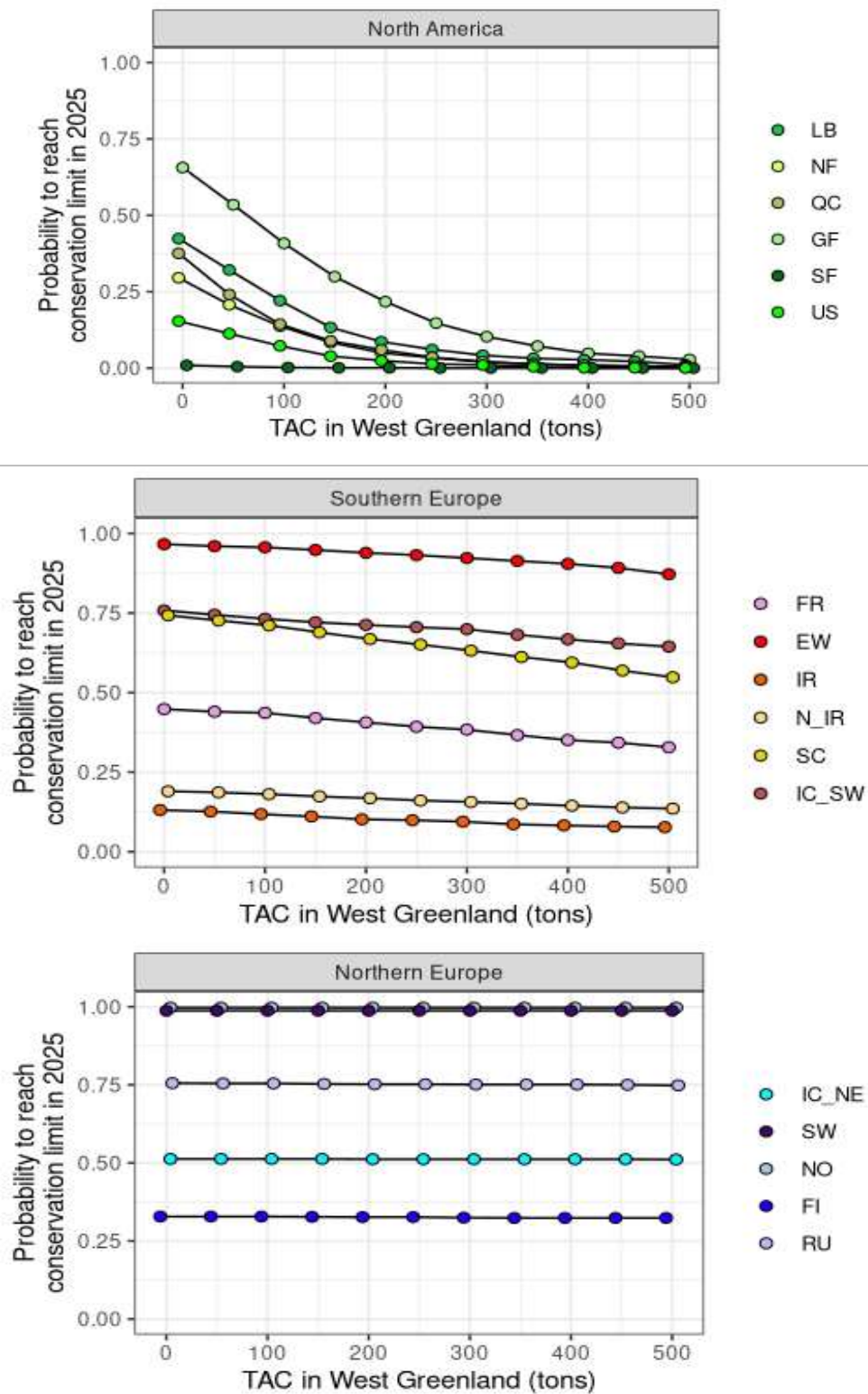


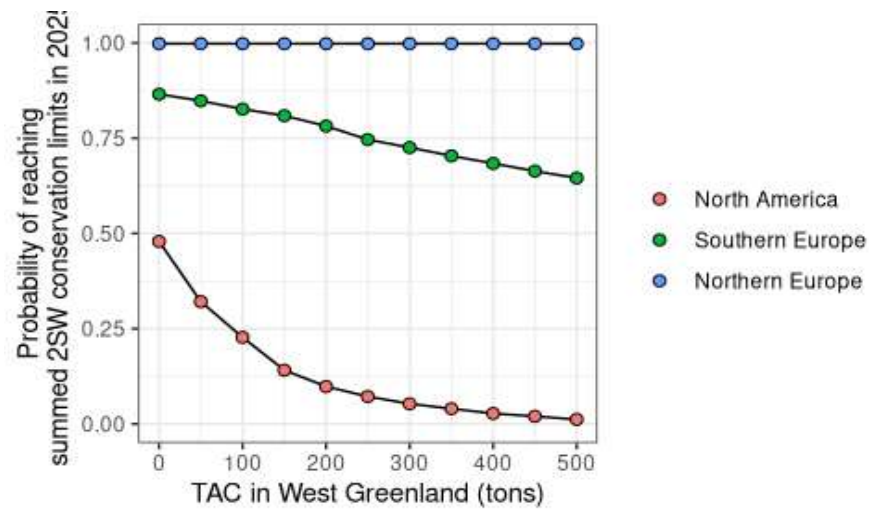
Figure 19. Example for Quebec - Estimation of the key life stages and transition rates obtained during the hindcasting phase (1971-2022) and for the 3 years forecast 2023-2025 after the last assessment year (2022) for different catch options at West Greenland. Plain lines indicate the posterior mean of the posterior predictive distributions obtained under different catch options at West Greenland.

West Greenland catch options

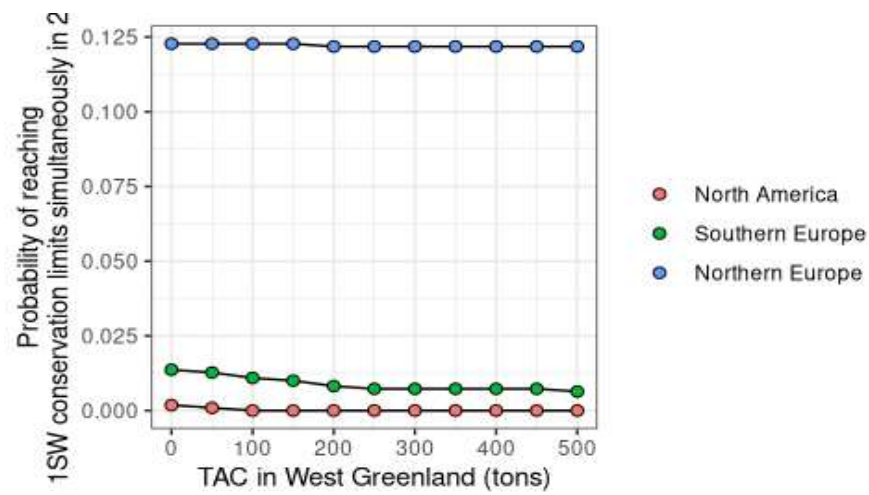
(a)



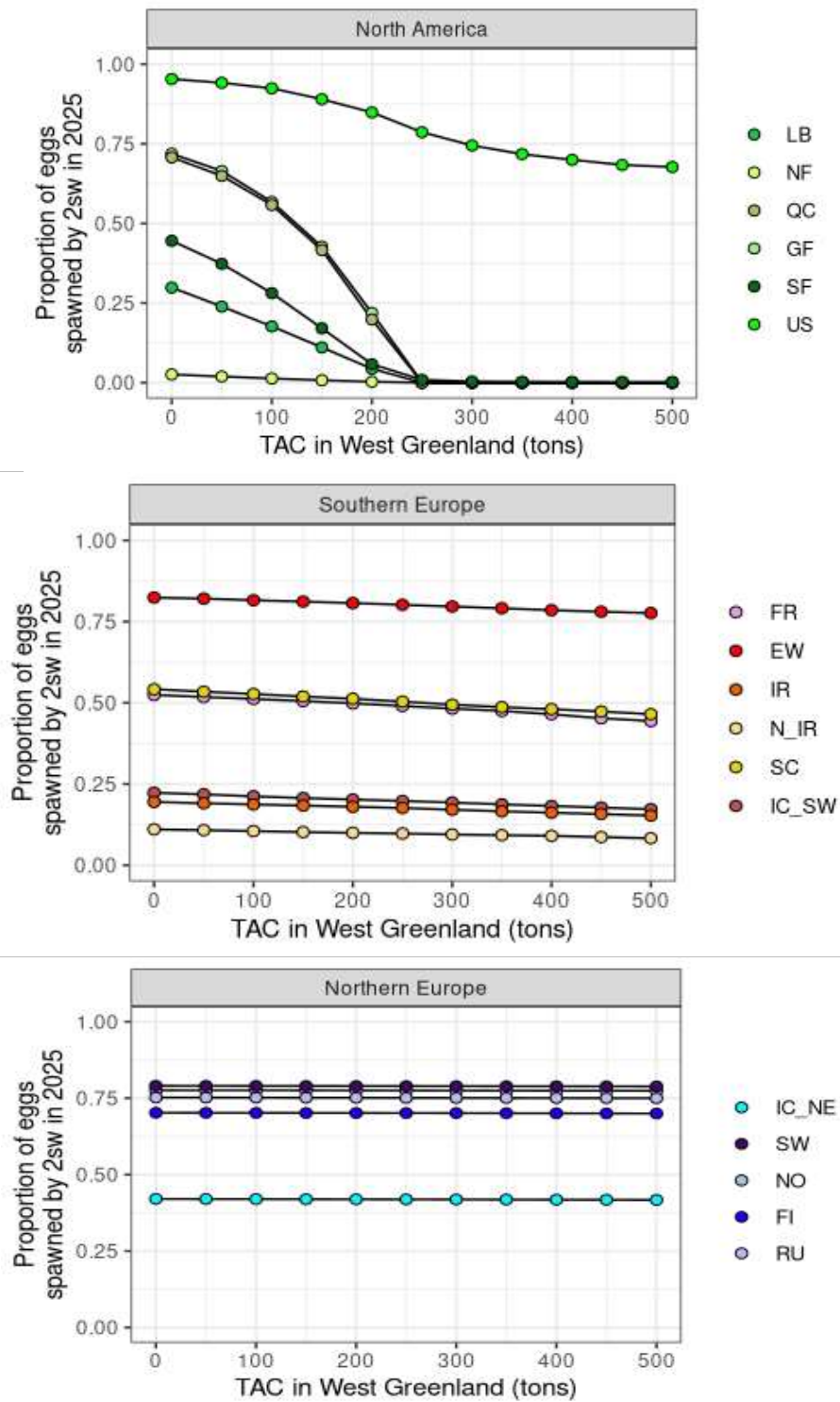
(b)



(c)



(d)



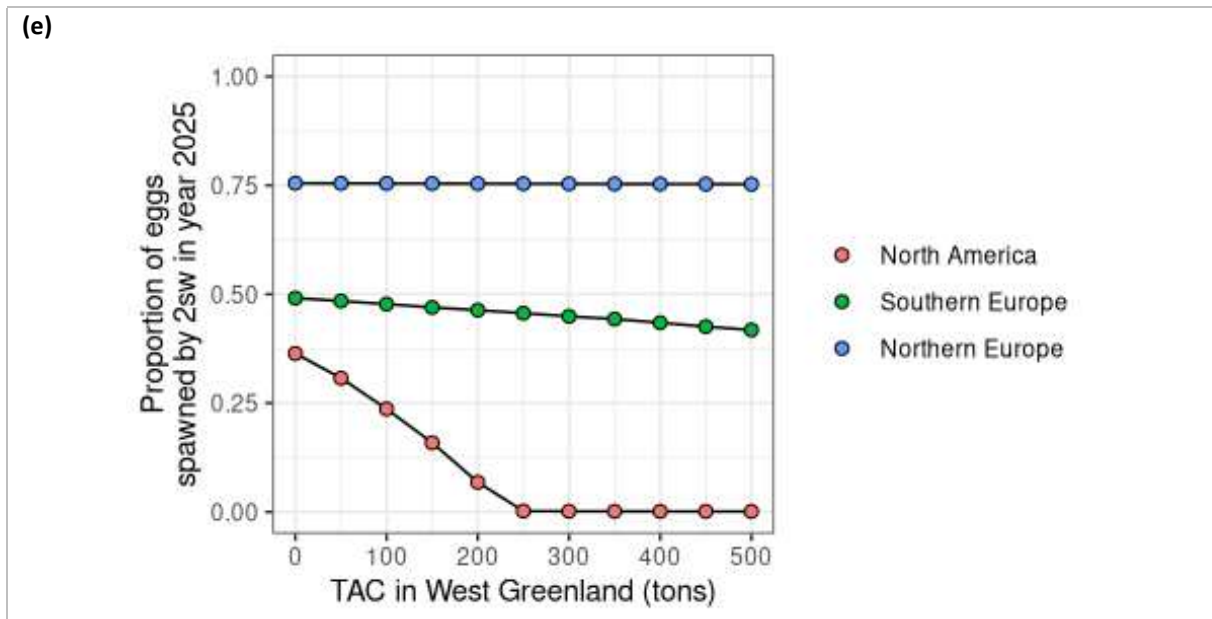
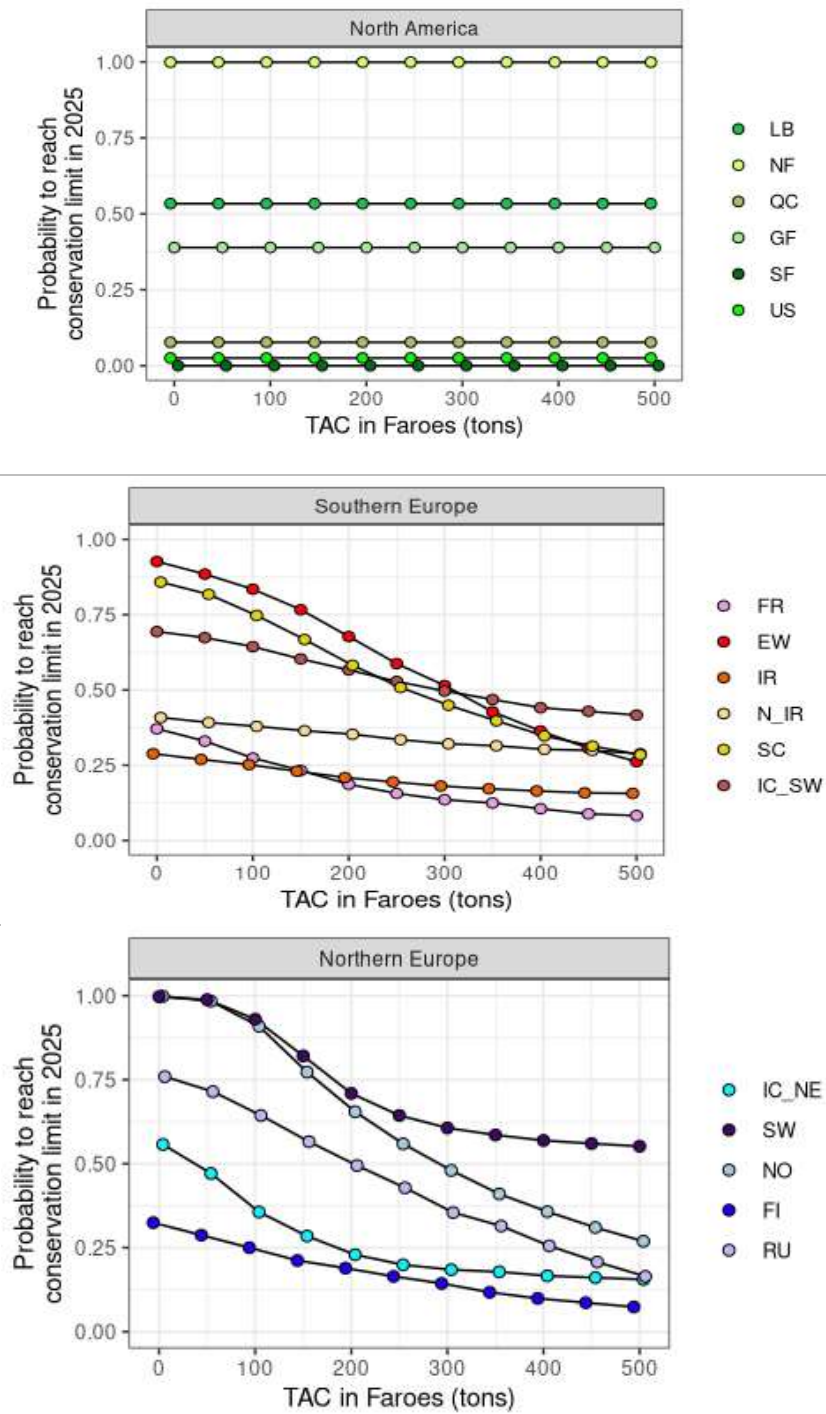


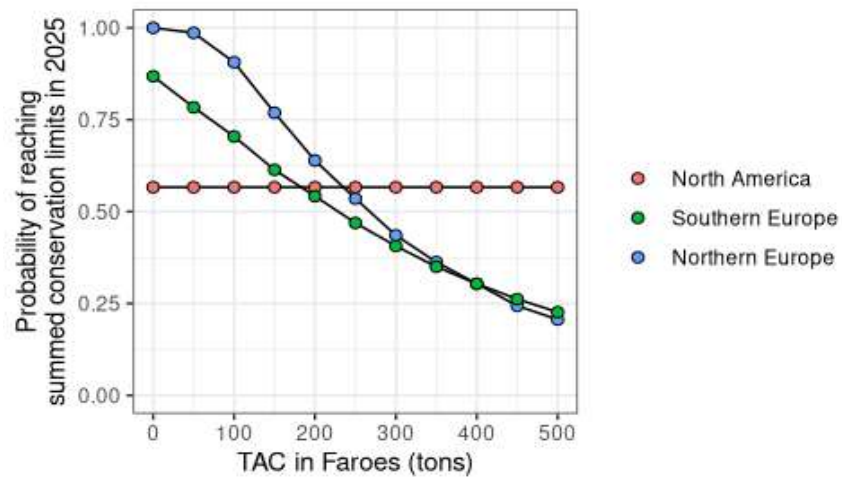
Figure 20. Catches options at West Greenland (catches options 0-500 tons; 0 catches for all other fisheries). (a-b-c) Probability to achieve 2SW Conservation Limits obtained under different catch options after 3 years of forecasting (year 2025; last assessment year = 2022) (a) for all countries/regions individually; (b) aggregated by stock complex; (c) simultaneously for all SU of the same complex. (d-e) Proportion of eggs spawned by 2SW fish (relative to the total eggs deposition by 1SW + 2SW the same spawning year) calculated under different catch options, (d) for all countries/regions individually; (e) aggregated by stock complex. Only very few fish originated from Northern Europe are caught at West Greenland. This explains why the probability to achieve CL for northern European SU is fairly insensitive to WG catch scenarios.

Faroes catch options

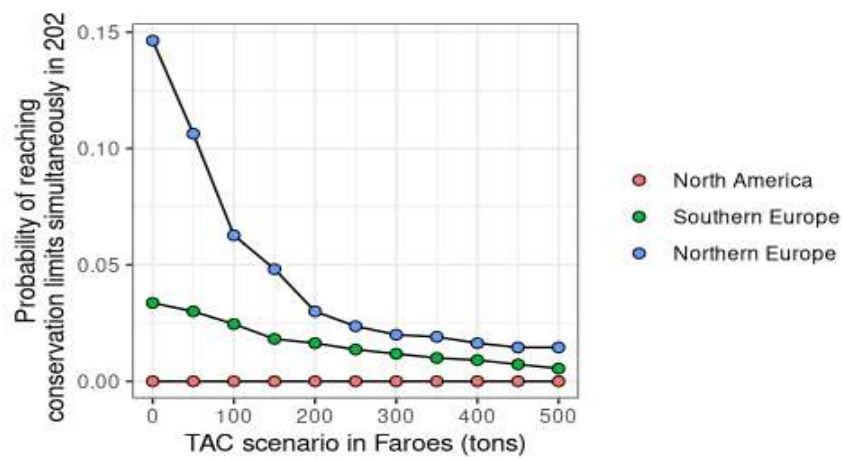
(a)



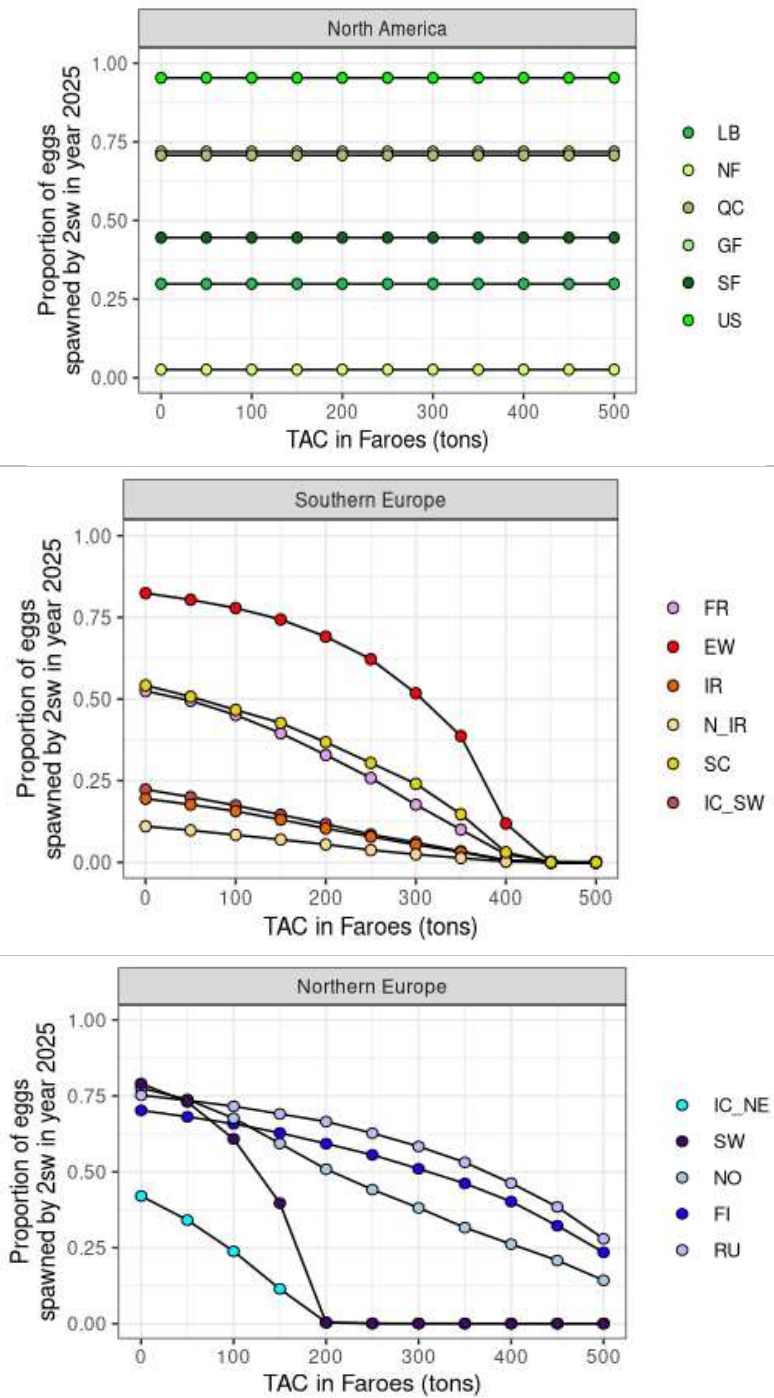
(b)



(c)



(d)



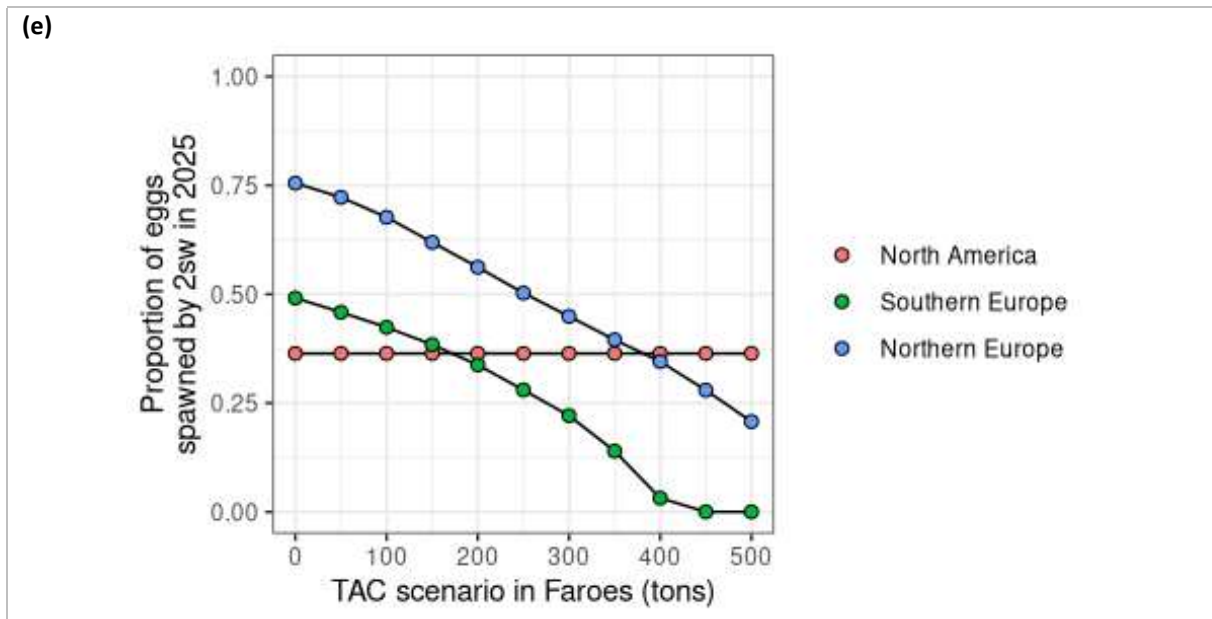


Figure 21. Catches options at Faroes (catches options 0-500 tons; 0 catches for all other fisheries). (a-b-c) Probability to achieve the Conservation Limits (1SW+2SW) obtained under different catch options after 3 years of forecasting (year 2025; last assessment year = 2022) (a) for all countries/regions individually; (b) aggregated by stock complex; (c) simultaneously for all SU of the same complex. (d-e) Proportion of eggs spawned by 2SW fish (relative to the total eggs deposition by 1SW + 2SW the same spawning year) calculated under different catch options, (d) for all countries/regions individually; (e) aggregated by stock complex. The model assumes no fish from North America are caught at Faroes. The probability to achieve CL for North American fish therefore is totally insensitive to Faroes catch scenarios (not shown).

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6 Appendix 1. - Process and observation equations of the Bayesian life cycle model

6.1 Population dynamics

6.1.1 Simplified life history

The age- and stage-structured life cycle model has a similar structure for each SU. It includes variation in the age of juveniles out-migrating from freshwater (i.e. smolts) and the sea-age of returning adults. Smolts migrate seaward after 1 to 6 years spent in freshwater (depending on SU). Two sea-age classes are considered in the model: Maiden salmon that return and reproduce after one year at sea, referred to as one-sea-winter (1SW) salmon or grilse, and maiden salmon that return after two winters spent at sea (2SW). This is a simplification of the variety of life history as some maiden fish may spent more than two winters at sea before returning to spawn, or some may be repeat spawners. However, those fish are rare and the 6 smolt-ages \times 2 sea-ages combinations capture the essence of life history variations.

6.1.2 Eggs deposition

The total number of eggs potentially spawned in year t for SU r by the two age classes confounded is denoted $N_{1t,r}$ and is the sum of eggs spawned by 1SW females ($N_{11,t,r}$) and 2SW females ($N_{12,t,r}$):

$$(A1.1) \quad N_{1t,r} = N_{11,t,r} + N_{12,t,r}$$

The model considers that 1SW and 2SW spawners contribute to a single pool of eggs each year with all eggs considered equivalent, independently of the spawners life history.

The number of eggs potentially spawned by 1SW spawners in year t for SU r is calculated by combining the number of 1SW spawners escaping the homewater fisheries ($N_{7t,r}$; state variable of the model) with the proportion of females $prop.fem_{1,t,r}$ (fixed in the data) and the average number of eggs potentially spawned per 1SW female, denoted $eggs_{1,t,r}$ (fixed in the data):

$$(A1.2) \quad N_{11,t,r} = N_{7t,r} \times prop.fem_{1,t,r} \times eggs_{1,t,r}$$

Symmetrically, the total number of eggs potentially spawned in year t for SU r by 2SW spawners ($N_{10t,r}$) is:

$$(A1.3) \quad N_{12,t,r} = N_{10t,r} \times prop.fem_{2,t,r} \times eggs_{2,t,r}$$

6.1.3 Egg-to-smolt transition

The egg-to-smolt transition consists of two steps:

- the survival from egg-to-smolt per cohort;
- and the distribution of the surviving smolts according to their age at downstream migration.

6.1.3.1 Egg-to-smolt survival

Because no smolt production data is available at the scale of SU, it is difficult to separate the variability of the egg-to-smolt survival from that of the post-smolt survival, and parameters of the egg-to-smolt transitions have to be fixed.

The egg-to-smolt survival is density independent, with average survival rate \mathbb{E}_{θ_1} arbitrarily fixed to 0.007 (Hutchings & Jones, 1998; Massiot-Granier et al. 2014) for all years and all SU (Table 1, Table 2). Environmental stochasticity is modelled by lognormal random noise with variance $\sigma_{\theta_1}^2$ fixed to an arbitrarily value corresponding to $CV_{\theta_1}=0.4$ ($\sigma_{\theta_1}^2 = \log(CV_{\theta_1}^2 + 1)$) which is a median values for the inter-annual variability found in the literature (Prevost et al., 2003; Pulkkinen et al., 2013). The total number of smolts produced in the cohort c (corresponding to egg deposition of year $t = c$), denoted $N_{2c,r}$ is then modelled as:

$$(A1.4) \quad \log(N_{2c,r}) \sim \text{Normal}(\log(\mathbb{E}_{\theta_1} \times N_{1c,r}) - \frac{1}{2}\sigma_{\theta_1}^2, \sigma_{\theta_1}^2)$$

Lognormal random variations of the egg-to-smolt survival rate are considered independent across SU (no spatial covariation) and years (no temporal autocorrelation).

This model configuration only allows for lognormal random stochasticity in the egg-to-smolt survival and does not account for any compensation neither (but see Olmos et al. 2019 for a sensitivity analysis to inclusion of density dependence). This also implicitly assumes that any trends in the stock productivity over time are a response to changes in the marine phase, what may inflate the importance of trends in the post-smolt survival.

6.1.3.2 Distribution according to smolt ages

The proportion of smolt in the cohort c migrating at age $a = 1, \dots, 6$ at year $t = c + a + 1$, denoted $\theta_{2c,a,r}$, are fixed to their averaged proportions $psm_{c,1:6,r}$ fixed in the data with values specific to each SU and that may vary between cohorts c .

Given $\theta_{2c,a,r}$, the number of smolts from the cohort c that migrate at age a year $t = c + a + 1$ is modelled as:

$$(A1.5) \quad N'_{2c,a,t=c+a+1,r} = \theta_{2c,a,r} \times N_{2c,r}$$

Last, the number of smolts migrating in the spring of year t is the sum of all smolts of six different ages (and therefore of six different cohorts) migrating the same year t :

$$(A1.6) \quad N_{3t,r} = \sum_{a=1}^{a=6} N'_{2c=t-a-1,a,t,r}$$

An important hypothesis underlying equation (A1.6) is that there is no tracking of smolt-age once at sea, meaning that all transition rates applied to post-smolts at sea only depend on the migration year but are independent upon the smolt age.

Note. In a previous model version, smolt ages distribution ($\theta_{2_{c,a,r}}$) was estimated. Proportion of smolt ages were set a tight Dirichlet prior distribution. However, this transition revealed serious bottleneck for computational time needed to reach convergence. A simpler solution using fixed proportions is then adopted to keep reasonable model execution time.

6.1.4 Marine phase

The marine phase is modelled as a sequence of three blocks of transitions:

- survival from smolts to the PFA stage;
- the maturation of fish at the PFA stage;
- and the fishing and natural mortality between PFA and returns.

6.1.4.1 Post-smolt survival and proportion of fish maturing as 1SW

Time series of post-smolt survivals ($\theta_{3_{t,r}}$) and the proportion of fish maturing as 1SW ($\theta_{4_{t,r}}$) are modelled as multivariate random walks in the logit scale. Random variations are drawn from multivariate Normal distributions with variance-covariance matrix Σ_{θ_3} and Σ_{θ_4} that define the covariations among the SU (Minto et al., 2014; Ripa and Lundberg, 2000):

$$(A1.7) \quad \begin{cases} \text{First year (for } r = 1:N): \text{logit}(\theta_{3_{t=1,r}}) \sim \text{Normal}(0,1) \\ \text{Then } (\text{logit}(\theta_{3_{t+1,r}}))_{r=1:N} \sim \text{MVNormal}((\text{logit}(\theta_{3_{t,r}}))_{r=1:N}, \Sigma_{\theta_3}) \end{cases}$$

$$(A1.8) \quad \begin{cases} \text{First year (for } r = 1:N): \text{logit}(\theta_{4_{t=1,r}}) \sim \text{Normal}(0,1) \\ \text{Then } (\text{logit}(\theta_{4_{t+1,r}}))_{r=1:N} \sim \text{MVNormal}((\text{logit}(\theta_{4_{t,r}}))_{r=1:N}, \Sigma_{\theta_4}) \end{cases}$$

Then, given the number of smolts migrating in year t ($N_{3_{t,r}}$) and the post-smolt survival ($\theta_{3_{t,r}}$), the number of posts-smolts that survive to the PFA stage ($N_{4_{t+1,r}}$) in January of year $t + 1$ is modelled as:

$$(A1.9) \quad N_{4_{t+1,r}} = \theta_{3_{t,r}} \times N_{3_{t,r}}$$

Given the number of fish at the PFA stage ($N_{4_{t+1,r}}$) and the maturation rate ($\theta_{4_{t+1,r}}$), mature ($N_{5_{t+1,r}}$) and non mature fish ($N_{8_{t+1,r}}$) at the PFA stage are modelled as:

$$(A1.10) \quad N_{5_{t+1,r}} = \theta_{4_{t+1,r}} \times N_{4_{t+1,r}}$$

$$(A1.11) \quad N_{8_{t+1,r}} = (1 - \theta_{4_{t+1,r}}) \times N_{4_{t+1,r}}$$

Note. In a previous model version, those transitions were modelled as stochastic, using lognormal distribution with standard deviation fixed to a very low value. However, those transitions revealed serious bottlenecks for computational time needed to reach convergence. Those transitions are now modelled as deterministic to keep reasonable model execution time.

6.1.4.2 Sequential marine fisheries and natural mortality

Catches

After the PFA stage, both maturing and non-maturing fish are subject to natural mortality and sequential fisheries mortalities operating on mixed stocks (Tables 5, Table 6). The following modelling structure applies for each of those transitions. For any marine fishery f , operating year t on a number of fish $N_{f,t,r}$ originated from the stock unit r with an exploitation rate $h_{f,t,r}$, the catches $C_{f,t,r}$ (considered here as an unknown states) and the number of fish that escape the fishery $N_{f,esc,t,r}$ are modelled as:

$$(A1.12) \quad C_{f,t,r} = h_{f,t,r} \times N_{f,t,r}$$

$$(A1.13) \quad N_{f,esc,t,r} = (1 - h_{f,t,r}) \times N_{f,t,r}$$

Exploitation rates

Exploitation rates $h_{f,t,r}$ are modelled as variable over time. The way the variability across SU is modelled depends on the data available to allocate catches to each SU and on expert knowledge about migration routes (Table 5, Table 6).

West Greenland fishery (WG; operating on a mixture of SU from North America and Europe). Proportion data are available to allocate catches among three large stock groupings:

- **Level 1.** Between the North American CSG and the European CSG;
- **Level 2.** Within European CSG, between Southern and Northern European CSG.

Hence, for year any year t , three different exploitation rates are estimated for each of these three groups, and harvest rates are then supposed to be homogeneous among all SU within these three groups.

Faroes fishery (FA; operating on SU from Europe only). Proportion data are available to allocate catches among three large stock groups:

- **Level 1.** Split among The Southern European CSG, the Southern part of the Northern European CSG and the Northern part of the Northern European CSG

Hence, for year any year t , three different exploitation rates are estimated for each of these three groups, and harvest rates are then supposed to be homogeneous among all SU within these three groups.

Fisheries specific to the North American SU. No proportion data are available to allocate catches among SU. Catches were allocated to each SU by considering a single h homogeneous for all SU.

There is however an exception to this general rule (Prévost et al., 2009). For the Labrador/Newfoundland (LAB/NFDL) in zones (8-14) and Saint-Pierre et Miquelon (SPM) fisheries operating on 1SWm and 2SW fish, data are available to separate the catches of fish originated from Labrador from those originated from other North American SU. Hence, a separate h is estimated for Labrador SU, and a single homogeneous h is considered for the five other North American SU.

Natural mortality

All fisheries at sea are separated by periods of time where only natural mortality occurs (ICES, 2018; Potter, 2016; Prévost et al., 2009). Fish that escape the fishery f at year t hence suffer natural mortality rate (all denoted $\theta_{5_{t,f}} = e^{-M \times \Delta_{t,f}}$) before entering the next fishery $f + 1$ where the monthly mortality rate M is fixed, constant across years and SU's ($M = 0.03 \cdot month^{-1}$; Table 2) and the duration $\Delta_{t,f}$ (in months) are assumed known and constant across years but with some variations among SU to account for variability in migration routes (Tables 5, Table 6):

$$(A1.14) \quad N_{f+1\ t,r} = (1 - \theta_{5_{t,f}}) \times N_{f,esc\ t,r}$$

6.1.4.3 From returns to spawners

Homewater catches

Fish that escape all marine mortality and return as 1SW fish ($N_{6_{t,r}}$) or 2SW fish ($N_{9_{t,r}}$), are subject to homewater fisheries that operate locally on each SU.

Homewater fisheries are modelled with exploitation rates $h_{HWf_{t,r}}$ that are assumed to vary with years and SU and for the two sea-age classes separately (Tables 5 & 6). Homewater fishery harvest rates are estimated from observation of homewater catches provided in the data.

Delayed spawners

After homewater fishery, a proportion of fish may potentially delay spawning to the next year. The proportion of delayed spawners are fixed in the data, and may vary with SU, years and sea-age classes and are denoted $p_{delSp_{t,r}}$ (specific for 1SW and 2SW). Fish that delay spawning to the next year may then be subject to a specific fishery with (estimated) exploitation rates $h_{delSp_{t,r}}$ (specific to 1SW and 2SW). These additional exploitation rates are estimated from catches of delayed spawners provided in the data. In practice, the proportion of delayed spawners and the associated additional catches are 0 for all SU except for Russian stock units. But these transitions are modelled uniformly for all stock units with zero proportion of delayed spawners in the data and zero additional catches for almost all SU.

Stocking

Last, the number of 2SW spawners may also be eventually supplemented by stocking. The number of fish stocked $n_{Stock,2SW_{t,r}}$ fixed in the data. In practice, it is null for all SU except USA. But the transition is modelled uniformly for all SU.

Additional natural mortality before spawning

An additional survival rate ($\theta_{6_{t,r}}$ or $\theta_{9_{t,r}}$, for 1SW and 2SW, respectively; fixed in the data) is then finally applied on all remaining fish before spawning. In practice, it is 1 for all SU except Scotland West and East. But the transition is modelled uniformly for all SU.

Finally, the number of fish that escape the homewater fishery and potentially spawn as 1SW ($N_{7_{t,r}}$) and 2SW ($N_{10_{t,r}}$) are modelled as:

$$(A1.15)$$

$$\begin{aligned}
 N_{7,t,r} &= \left((1 - h_{HWf.1S_{t,r}}) \times (1 - p_{delSp.1SW_{t,r}}) \times (1 - h_{sup.1SW_{t,r}}) \times N_{6,t,r} + (1 \right. \\
 &\quad \left. - h_{HWf.1SW_{t-1,r}}) \times p_{delSp.1SW_{t-1,r}} \times (1 - h_{delSp.1SW_{t,r}}) \times N_{6,t-1,r} \right) \times \theta_{6,t,r} \\
 (A1.16) \\
 N_{10,t,r} &= \left((1 - h_{HWf.2S_{t,r}}) \times (1 - p_{delSp.2SW_{t,r}}) \times N_{9,t,r} \right. \\
 &\quad \left. + (1 - h_{HWf.2SW_{t-1,r}}) \times p_{delSp.2SW_{t-1,r}} \times (1 - h_{delSp.2SW_{t,r}}) \times N_{9,t-1,r} \right) \times \theta_{9,t,r} + n_{Stock.2SW_{t,r}}
 \end{aligned}$$

6.2 Observation equations

The model incorporates observation errors for all the time series of returns and catches. A sequential approach (Michielsens et al., 2008; Staton et al., 2017) is used that consists of two steps:

- In a first step, observation models are processed separately to reconstruct probability distributions that synthesize observation uncertainty around catches and returns for each year and each of the 25 SU. Probability distributions for returns and catches are derived from a variety of raw data and observation models, specific to each SU and each year and originally developed by ICES to provide input for PFA models for north American (Rago et al., 1993) and European (Potter et al., 2004b) stock units.
- In a second step, those distributions are used to approximate likelihoods in the population dynamics state-space model.

6.2.1 Returns

6.2.1.1 Estimation from the run reconstruction models

Returns are estimated for each year, each SU and for the two sea-age classes separately. Raw data used to estimate return essentially consist in homewater catches available at the scale of rivers or regional fishery jurisdictions, scaled by harvest and declaration rates and then aggregated at the scale of larger stock units. Uncertainties then essentially arise from a numerical (Monte Carlo) integration of uncertainties about harvest and declaration rates. Other fishery independent information like counting fences or mark and recapture data can also be used. Detailed description of the raw data and models used in each SU is provided in several papers (Crozier et al., 2003; ICES, 2002, 2015b; Potter et al., 2004b; Rago et al., 1993) and in the WGNAS Stock Annex for Atlantic salmon.

The case of Northern NEAC SU

ICES provides a shorter time series of data for Northern NEAC SU because some data are missing for Norway before 1982. The Norwegian data for the period 1971-1982 were completed using the following hypotheses (*Com pers.* Geir Bolstad and Peder Fiske, NINA):

- Homewater catches - Catch data for Norway (homewater catches, 1SW and 2SW separately) for the period 1971-1982 were extracted from the ICES WGNAS report of year 2002 (table 3.3.3.1f. Allocations of catches among the four regions of Norway was done using averages proportions calculated from the first five years for which data are available 1983-1987.

- Returns – The probability distribution of returns (1SW and 2SW, separately) was estimated by dividing the catches by guesstimates of exploitation rates and unreported catches for the period 1982-1971. Harvest rates and unreported catches were extrapolated backwards in time from year 1983. Uncertainty about those rates was bumped by 20% to account for the additional uncertainty due to extrapolation.
- Note that all MSW were considered as 2SW as for all other European SU.

6.2.1.2 Observation equations

The resulting probability distributions of returns are shown in Appendix 3. Numerical integration of uncertainty overall supports the hypothesis that the returns are lognormally distributed, allowing to approximate the likelihood for the returns as follows. For any year t and SU r , the expected mean of the distribution derived from the observations models for 1SW (respectively, 2SW) returns in log scale, denoted $\mathbb{E}_{\log(R_{1SW_{t,r}})}$ (resp. $\mathbb{E}_{\log(R_{2SW_{t,r}})}$), is considered as an observed realization of a Normal distribution of non-observed returns (in log-scale) $N_{6_{t,r}}$ (resp. $N_{9_{t,r}}$), with known variance $\sigma_{1SW_{t,r}}^2$ (resp. $\sigma_{2SW_{t,r}}^2$) set to the value derived from the observation errors models. These observation errors are considered independent across years, SU and sea-age classes.

$$(A1.17) \quad \mathbb{E}_{\log(R_{1SW_{t,r}})} \sim \text{Normal}(\log(N_{6_{t,r}}), \sigma_{1SW_{t,r}}^2)$$

$$(A1.18) \quad \mathbb{E}_{\log(R_{2SW_{t,r}})} \sim \text{Normal}(\log(N_{9_{t,r}}), \sigma_{2SW_{t,r}}^2)$$

6.2.2 Homewater catches

6.2.2.1 Estimates from the run reconstruction model

The homewater fisheries take adult fish that are mainly returning to the natal rivers to spawn. Point estimates of total catches reported by ICES (ICES 2018) pool all homewater fisheries capturing returning fish in coastal areas, estuaries and freshwater, for each SU, each year and each sea-age class separately. Available knowledge supports that homewater catches are known with only few errors.

6.2.2.2 Observation equations

The resulting probability distributions of returns are shown in Appendix 3. Point estimates of total catches of all homewater fisheries, for each SU, each year and each sea-age class separately are denoted $\mathbb{E}_{\log(C_{HW.1SW_{t,r}})}$ and $\mathbb{E}_{\log(C_{HW.2SW_{t,r}})}$ for 1SW and 2SW fish, respectively (in log scale). The likelihood term for homewater catches is built from lognormal observation errors with known observation error. Relative error is then arbitrarily fixed to CV=0.05 for both sea-ages, for all years and all SU (but note this value can be changed to acknowledge for greater observation errors). Observation errors are considered independent across years, SU and sea-age classes. The likelihood terms associated with homewater catches are:

$$(A1.19) \quad \mathbb{E}_{\log(C_{HW.1S_{t,r}})} \sim \text{Normal}(\log(h_{HWf.1SW_{t,r}} \times (1 - p_{delSp.1S_{t,r}}) \times N_{6_{t,r}}), \sigma_{HW.1SW}^2)$$

$$(A1.20) \quad \mathbb{E}_{\log(C_{HW.2SW_{t,r}})} \sim \text{Normal}(\log(h_{HWf.2SW_{t,r}} \times (1 - p_{delSp.2SW_{t,r}}) \times N_{9_{t,r}}), \sigma_{HW.2SW}^2)$$

with $\sigma_{\text{HW.1SW}}^2 = \sigma_{\text{HW.2SW}}^2$ the variance corresponding to CV=0.05.

Observation model for the delayed catches are modelled similarly with the same CV of observation errors.

6.2.3 Catches at sea for sequential distant marine fisheries operating on mixture of stocks

6.2.3.1 General rule

Distant marine fisheries exploit mixtures of stocks. For each of the distant marine fishery f , the likelihood equations associated with catches at sea essentially consist of two sets of likelihood terms:

- lognormal distributions of observation errors of the total catches by sea age class (in number of fish), summed over all SU exploited by the fishery under concern;
- complemented by Dirichlet likelihood for the proportion of catches allocated to different group of SU when those data are available (Faroes and West Greenland fisheries). When those data are not available (or considered not reliable enough to be used), the catches are allocated to the different SU exploited by the fishery under concern using the hypothesis of a homogeneous harvest rate among SU. This is equivalent to considering that the different SU are harvested proportionally to their abundance in the mixture of stocks at the stage just before the fishery.

In this version of the model, data are only available to allocate catches to large groups of SU. Those data are then used in a multilevel allocation rules, where Dirichlet likelihood functions are first used to allocate the catches among large groups of SU. Then, the allocation of catches at a lower level within groups is done assuming a homogeneous harvest rate among all SU within each group.

Data are detailed in the Appendix 3.

Likelihood on total catches

For each fishery f , observation models are built independently from the state-space model to estimate lognormal probability distributions of total catches for each year t , with expected mean and variance (in log-scale) denoted $\mathbb{E}_{\log(C_{ft})}$ and σ_{ft}^2 , respectively. Variances σ_{ft}^2 are derived by integrating uncertainty in the catch declaration rates, the proportions of fish of wild origin in the catches, and sampled biological characteristics of the catches including average weight of a fish used to convert catches in weights to number of fish, and scale samples used to separate the two sea-age classes in the catches.

By denoting $C_{ft} = \sum C_{ft,r}$ the total catches from the state process summed over all SU on which the fishery f is operating, the likelihood term for the total catch is modelled as:

$$(A1.20) \quad \mathbb{E}_{\log(C_{ft})} \sim \text{Normal}(\log(C_{ft}), \sigma_{ft}^2)$$

Likelihood to allocate catches to different groups

For any fishery f , let's denote $g = 1, \dots, k$ the subscript of groups of SU that compose the mixture of stock on which the fishery f is operating. When available, observed proportions of groups of SU in the catches, denoted $p_{f,t,g}^{obs}$ (with for any year t , $\sum_{g=1}^k p_{f,t,g}^{obs} = 1$) are used to allocate the catches using a Dirichlet likelihood term:

$$(A1.21) \quad (p_{f,t,g=1}^{obs}, \dots, p_{f,t,g=k}^{obs}) \sim \text{Dirichlet}(\eta_{sample} \times (p_{f,t,g=1}, \dots, p_{f,t,g=k}))$$

where $p_{f,t,g} = \frac{c_{f,t,g}}{c_{f,t}}$ is the proportion of fish from the group g in the total catches calculated from the state process. η_{sample} is a scaling factor that controls the precision of the observation equation (the larger η_{sample} , the lower the variance of the observation errors). The value of η_{sample} is fixed to 100 in the model thus ensuring a very low observation error on those proportions and then a tight fit of the proportion $p_{f,t,g}$ in the model to the observed proportions $p_{f,t,g}^{obs}$.

6.2.3.2 Specificities of the different fisheries

Newfoundland, Labrador and Saint-Pierre et Miquelon fisheries exclusively operating on a mixture of North American SUs

Fish from North American SUs maturing in the first year at sea (1SWm) may be exploited on their return migrations to rivers by three fisheries: i) the Labrador fishery (commercial catches and subsistence fishery), that operate on 1SWm and 2SW fish but that is supposed to not impact the 1SWnm stage, ii) the fishery operating in South-Western Newfoundland (SFA zones 8-14) and Saint Pierre et Miquelon that also operates on 1SWm and 2SW fish but that is supposed to not impact the 1SWnm stage, iii) the fishery operating in North-Eastern Newfoundland (SFA zones 3-7) that is supposed to operate on 1SWm, 1SWnm and 2SW fish.

To simplify the approach, the Labrador fishery and the South-Western Newfoundland (SFA zones 8-14) fishery were pooled in the data as they operate on the same life stages.

Labrador and South-Western Newfoundland fishery (SFA zones 8-14)

The data of those fisheries were pooled. They operate on 1SWm and 2SW only.

Data and expert opinion are used to partition catches of 1SWm and 2SW fish originating from Labrador from those originating from the five other North American SU (ICES 2017a; 2017b).

For 1SWm and 2SW separately, and for each year, total catches of fish originated from Labrador, and the total catches of fish originated from the five other SU are considered to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty essentially due to the conversion from catch in weight to number of fish.

A specific harvest rate is estimated for fish originating from LB. In the absence of data to differentially allocate catches to each of the five other North American SU (all except Labrador), among the six North American SU, we assume harvest rates are homogeneous among the five other North American SU (ICES 2017a; 2017b).

North-Eastern Newfoundland fishery (SFA zones 3-7)

This fishery is supposed to operate on 1SWm, 1SWnm and 2SW.

Total catches of fish originated from all SU in North America are considered to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty essentially due to the conversion from catch in weight to number of fish.

In the absence of data to differentially allocate catches to each of the six North American SU, we assume harvest rates are homogeneous among the six North American SU (ICES 2017a; 2017b).

Faroes Fishery exclusively operating on mixtures of European SUs

Fish from European SUs maturing in the first year at sea (1SWm) may be exploited on their return migrations to rivers in the FA marine fishery. Fish that do not mature during the first year at sea (1SWnm) may be caught in the FA fishery as 1SWnm. 1SWnm that survive to the Faroe fishery then migrate to the WG feeding grounds where they are susceptible to be harvested together with fish from North America. Survivors may finally be caught as 2SW salmon on their migration to home waters in the FA fishery.

For each of the three age-class separately (1SWm, 1SWnm and 2SW), and for each year, total catches of fish caught at FA are assumed to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty essentially due to the proportion of unreported catches and of wild fish in the catches.

Total catches of 1SWm and 1SWnm and 2SW at FA are then allocated to the different SU following a two levels allocation rule.

- **Level 1.** First, the total catches are separated in three large groups of SU. The relative proportions of those three groups are fitted to observed proportions (estimated from genetic assignment data) using 3-dimensional Dirichlet likelihood function:
 - The Southern European CSG (France, UK England and Wales, Ireland, UK Northern Ireland - FO, UK Northern Ireland - FB, UK Scotland East, UK Scotland West, and Iceland South-West);
 - The southern part of the Northern European CSG, that comprises Iceland North-East, Sweden, Norway South-East, Norway South-West and Norway Middle;
 - The northern part of the Northern European CSG, that comprises Norway North, Finland, Russia Kola Barents, Russia Kola White Sea, Russia Arkhangelsk Karelia and Russia River Pechora. Genetic data indicate that proportion of those fish in the FA catches is much less than their proportion in the abundance, which indicates different (further east and north) migration routes.
- **Level 2.** At the second lower level, within each of the three groups, we assume exploitation rates are homogeneous among all SU that compose the group.

West Greenland fishery operating on mixture of North American and European SU

Catches of 1SWnm at WG may originate from any of the 25 SU from all CSG. The total number of 1SWnm fish caught at WG is assumed to be observed with lognormal errors, with relative error (CV) derived from specific models that integrate the uncertainty due to the conversion from catch in weight to number of fish (note however the CV is fixed to 0.2 for all years in this application).

Total catches are then allocated to the different SU following a three level allocation rule.

- **Level 1.** First, the total catches are separated between the North American and the European stock complexes (north and south). The relative proportions of those two groups are fitted to observed proportions (estimated from a compilation of individual assignment data based on discriminant analyses of scale characteristics and genetic analyses (ICES 2017a; 2017b)) using a two dimensional Dirichlet likelihood.
- **Level 2.** Second, catches of fish from the European stock complex are separated in two sub-groups, the southern and the northern European CSG. The relative proportions of those two groups are fitted to observed proportions using a two dimensional Dirichlet likelihood.
- **Level 3.** Third, within each of the three groups, we assume exploitation rates are homogeneous among all SU that compose each group.

7 Appendix 2 - Sensitivity to key structural hypotheses (background information)

Strong hypotheses are made in the model to offset the lack of data on some key demographic transitions. In particular:

- The egg-to-smolt survival rate is density independent, random around a fixed average value
- The natural mortality rate after the PFA stage (M) is fixed and with no time variation

The sensitivity of model results to these hypotheses has already been explored by Massiot-Granier et al. (2014) and Olmos et al. (2019) in previous versions of the model. Below we summarize the main results.

7.1 Egg-to-smolt survival

The smolt-to-PFA survival is partly confounded with the egg-to-smolt survival in the model. In the absence of smolt production data on the smolt production at the scale of SUs, the parameters of the freshwater-phase dynamic were assumed to vary randomly (lognormal with CV=0.4) around a fixed average value (0.7%).

Olmos et al. 2019 have explored the sensitivity of the results to the value of amount of between years stochastic variation in the egg-to-smolt survival. As expected, because part of the overall interannual variability in the survival is captured by the egg-to-smolt survival, increasing (decreasing) the coefficient of variation of the interannual variability in the egg-to-smolt survival results in greater (lower) temporal variation in egg-to-smolt survival estimates. However, the overall time trends in post-smolt survival time series revealed robust to an increase in the egg-to-smolt interannual variance. Spatial covariances among the time series of post-smolt marine survivals also revealed fairly robust to an increase in the egg-to-smolt interannual variance, although high values of the CV (0.6, 0.8) diminished the amount of spatial covariation of the time series of the smolt-to-PFA survival. Trends and spatial covariance in the time series of proportions of 1SW maturing were robust to an increase in the interannual variability in the egg-to-smolt survival.

Massiot-Granier (2014) and then Olmos et al. (2019) explored the sensitivity of the results to the introduction of density-dependence in the egg-to-smolt survival. The effect of introducing density dependence revealed marginal relative to change in the interannual stochasticity in egg-to-smolt survival. Inferences on trends and spatial covariances of post-smolt survivals and proportions maturing as 1SW were found to be fairly robust to introduction of density dependence.

7.2 Natural mortality rate after the PFA stage

Importantly, the differential in natural mortality between 1SW and 2SW fish is partly confounded with the proportion maturing as 1SW (Chaput, 2012). Because of the absence of abundance audit point between the smolt and the return stage, the natural mortality rate after the PFA stage was fixed (drawn in a very tight informative prior distribution), assumed identical for maturing and non-maturing fish, and constant in time.

7.2.1 Sensitivity to the average value of M

Massiot-Granier et al. (2014) explored the sensitivity of the results to the average value of M . As expected, M is a scaling factor in the model that balances the smolt-to-PFA survival rate. The lower the expected mean of the prior on M , the lower the posterior estimates of the smolt-to-PFA survival. Changing the expected value of M also affects the probability of maturing as 1SW. A higher M slightly decreases the differential of cumulated natural mortality between 1SW and 2SW fish, which leads to higher estimates of the proportion maturing as 1SW.

7.2.2 Time variations of M

Under the baseline model hypotheses, the temporal variability of the smolts return rates for both 1SW and 2SW fish combined is captured by temporal variations in the smolt-to-PFA survival, and the variability of the ratio of return rates of 2SW relative to 1SW fish is captured by temporal variations in the proportion maturing.

Massiot-Granier et al. (2014) explored an alternative hypothesis where changes in the ratio of return rates of 2SW relative to 1SW fish result from variations in the natural mortality rate of 2SW fish after the PFA stage, rather than from changes in the proportion maturing. The proportion maturing is assumed constant, as is the natural mortality rate of 1SW fish, but between-year variability of the natural mortality rates of 2SW relative to 1SW fish is accounted for. Results revealed that estimates of abundance and transition rates from eggs to PFA were not sensitive to changing from the baseline to this alternative hypothesis. But the mortality rates of non-maturing fish after the PFA stage varies notably, with a pattern of variation very similar to that of the proportion maturing.

This is a critical issue that future research should address. Indeed, the alternative hypotheses may have important implications for the management of high seas fisheries. Considering a higher mortality rate for 2SW fish after the PFA stage would reduce the expected impact of catch regulations for the distant water fisheries aimed at preserving future 2SW fish. The alternative hypothesis of different temporal variation in natural mortality between 1SW and 2W fish could also be interpreted as a response to environmental changes that would affect differently 1SW and 2SW fish during their migration routes.

8 Appendix 3 - Data sources

Data presented below are from ICES WGNAS report 2023. The time series of data is therefore 52 years from 1971 to 2022 (hindcasting phase).

Following WKBSalmon discussions, these data are supplemented by new data on the origin of fish caught at Faroes (proportions to allocate Faroes catches among three subcomplex, Southern European complex, southern and northern and part of the Northern European complex; G. Bolstad, com pers.) and on the origin of fish caught at West Greenland (proportions to allocate European fish to the northern and the southern European complex; Tim Sheehan, com pers.).

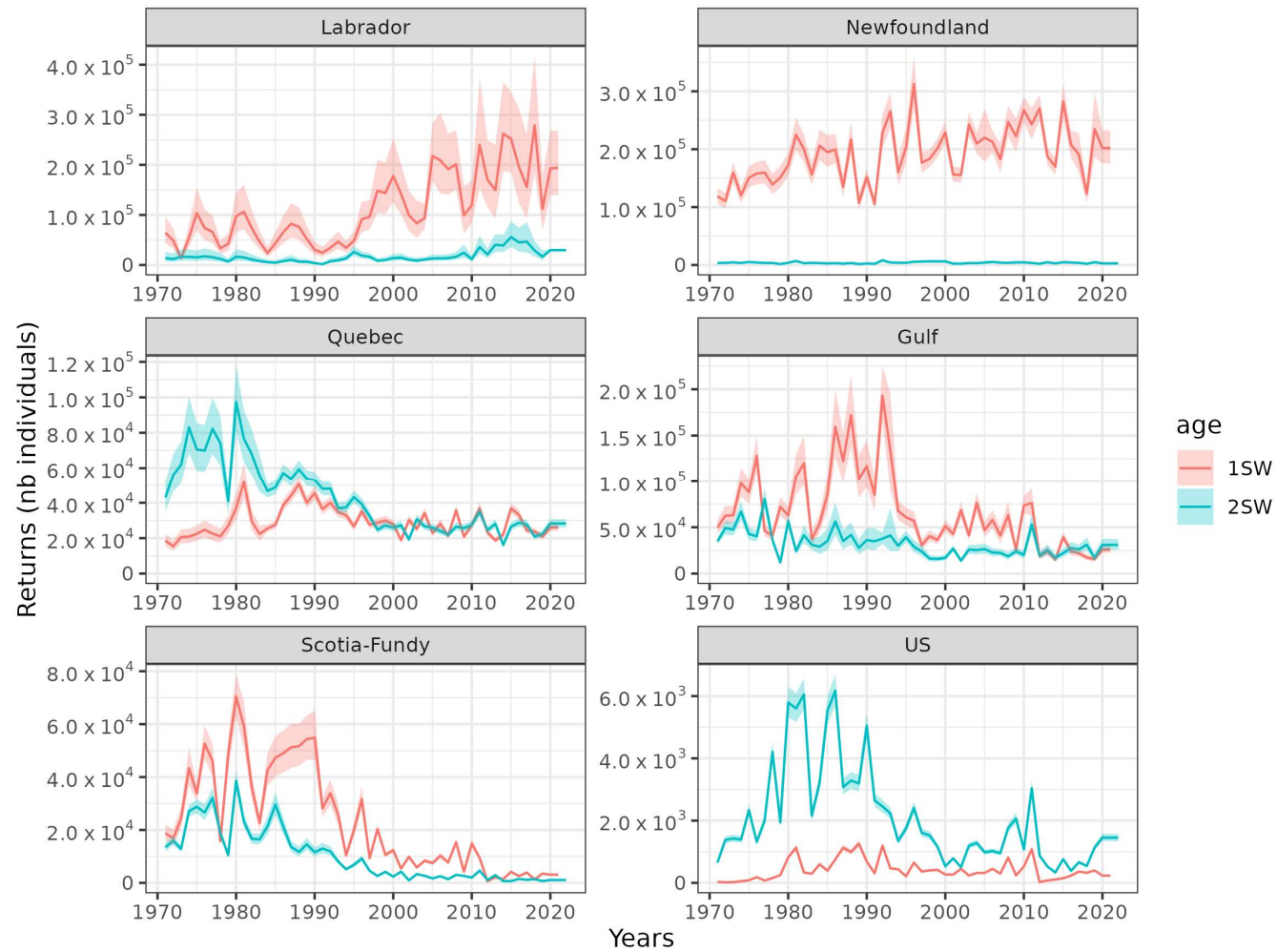


Figure A3.1. Number of fish returning as 1SW (red) and 2SW (blue) in the 6 SU of North America (median, quantiles 5% and 95% of lognormal distributions). (Source: ICES 2023).

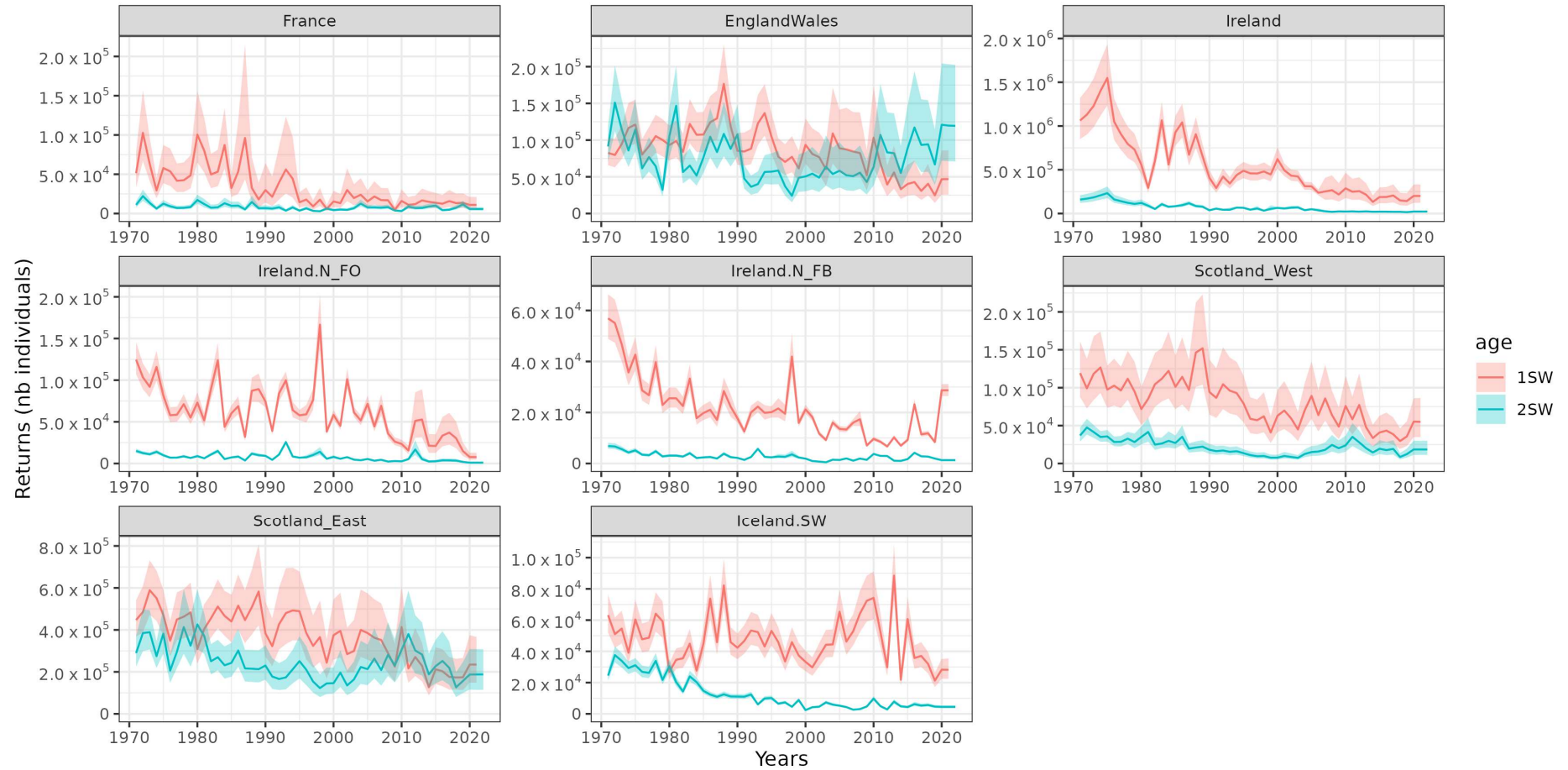


Figure A3.1 (Continuing). Number of fish returning as 1SW (red) and 2SW (blue) in the 8 SU of Southern Europe (median, quantiles 5% and 95% of lognormal distributions). (Source: ICES 2023).

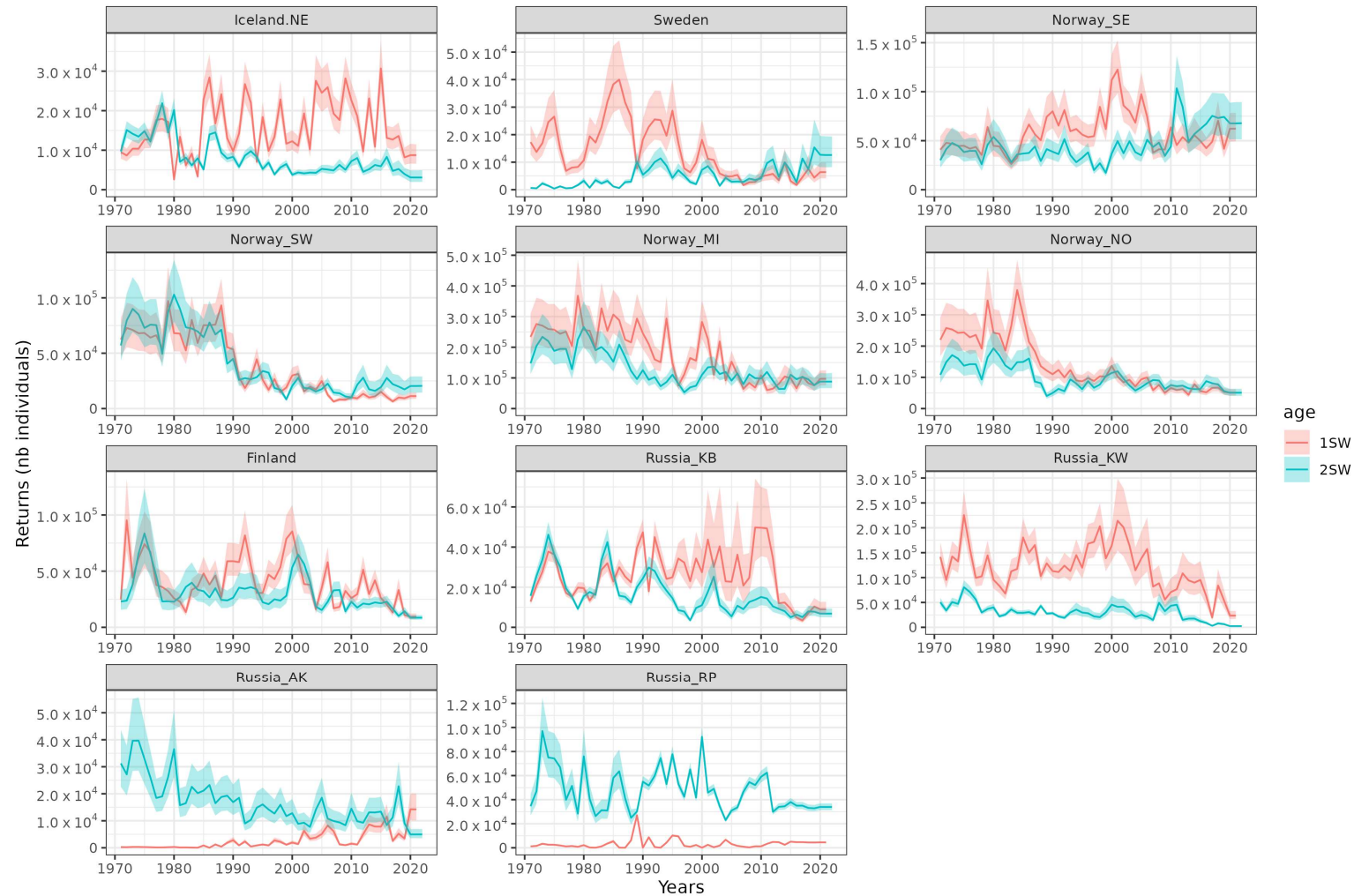


Figure A3.1 (Continuing). Number of fish returning as 1SW (red) and 2SW (blue) in the 11 SU of Northern Europe (median, quantiles 5% and 95% of lognormal distributions). (Source: ICES 2023).

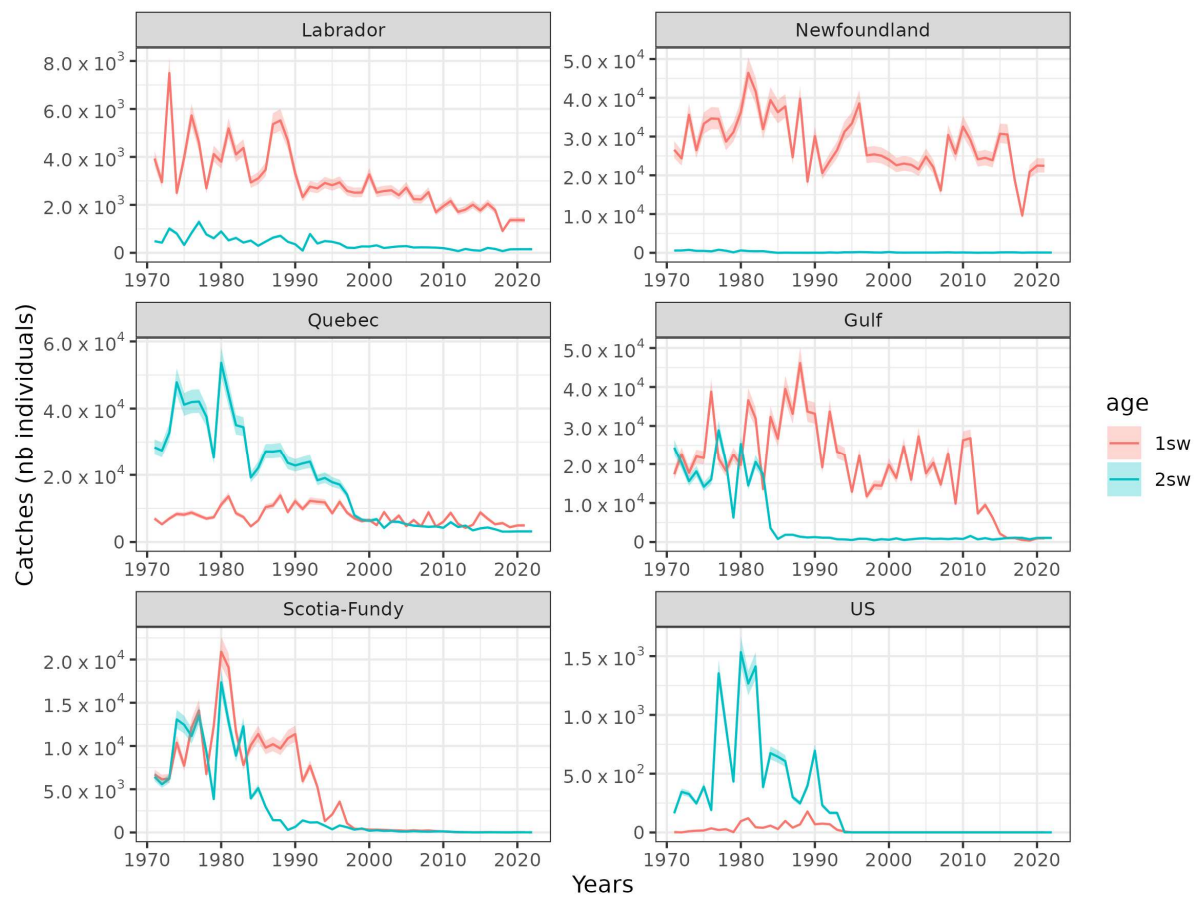


Figure A3.2. Homewater catches (median and 90% credibility intervals of logNormal probability distributions with CV arbitrarily fixed to 5%) for the 6 SU of North America (Source: ICES 2023).

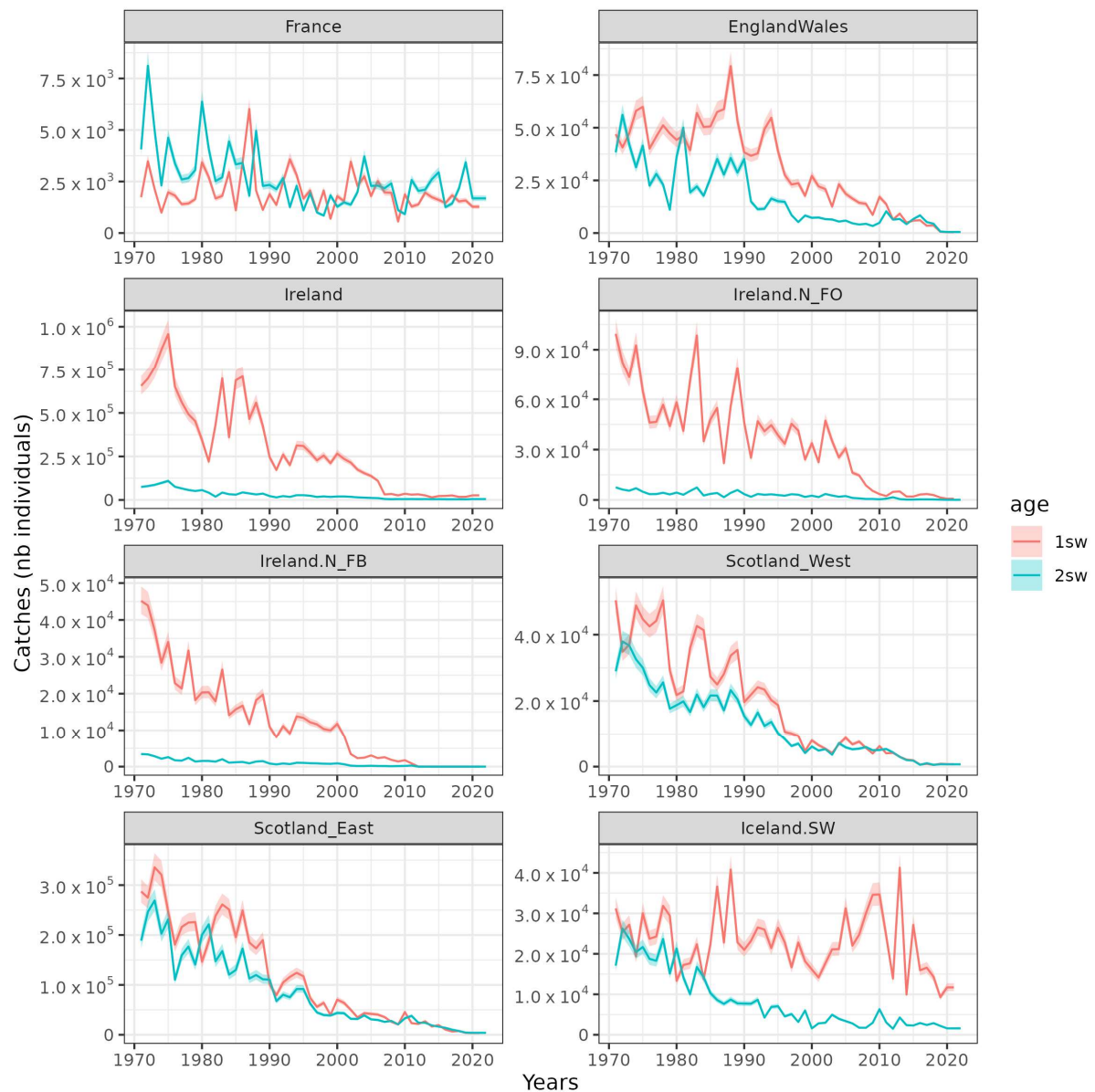


Figure A3.2 (continuing). Homewater catches (median and 90% credibility intervals of logNormal probability distributions with CV arbitrarily fixed to 5%) for the 8 SU in Southern Europe (Source: ICES 2023).

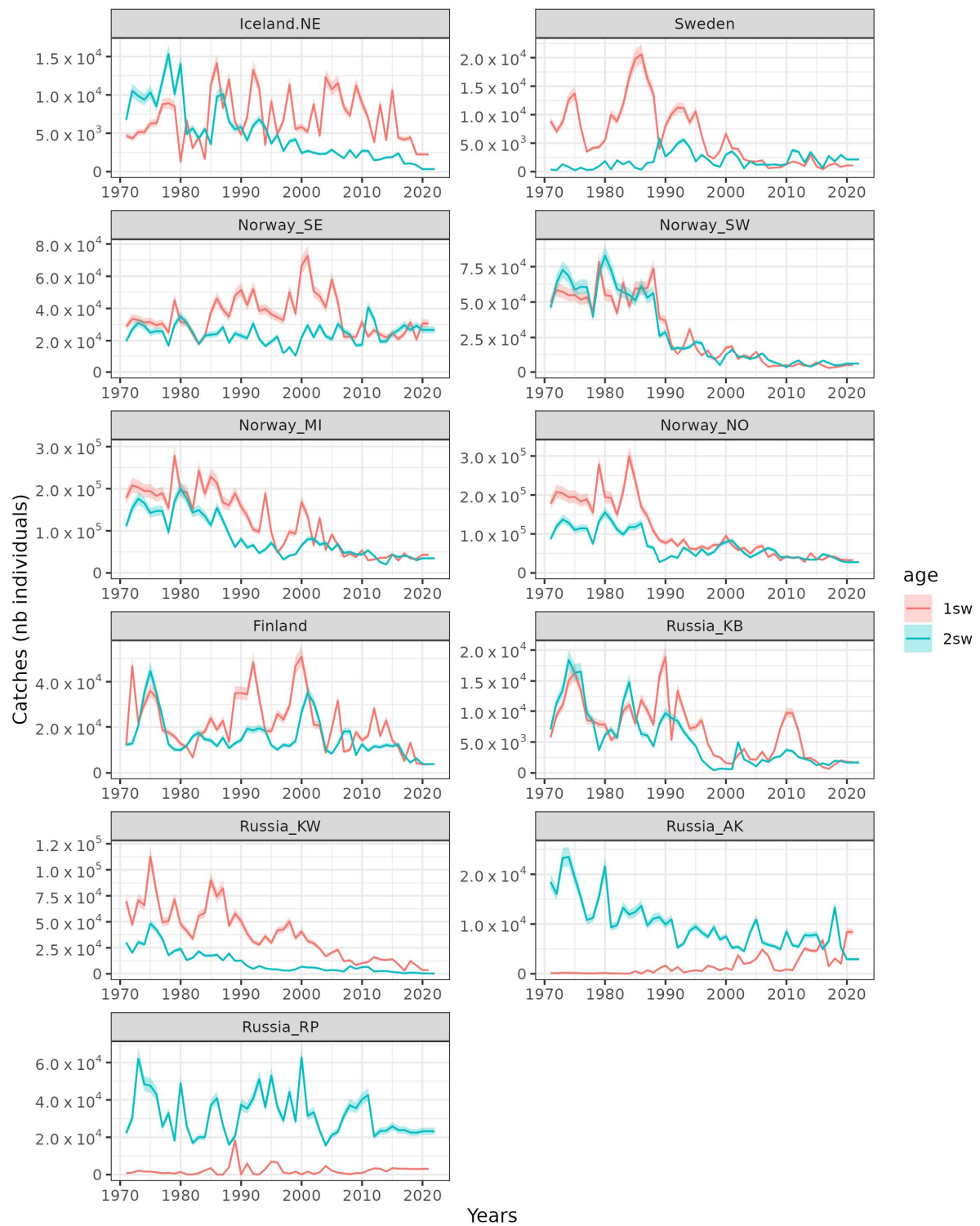


Figure A3.2 (continuing). Homewater catches (median and 90% credibility intervals of logNormal probability distributions with CV arbitrarily fixed to 5%) for the 11 SU in Northern Europe (Source: ICES 2023; See text for the hypotheses used to complete the time series for the period 1971-1982).

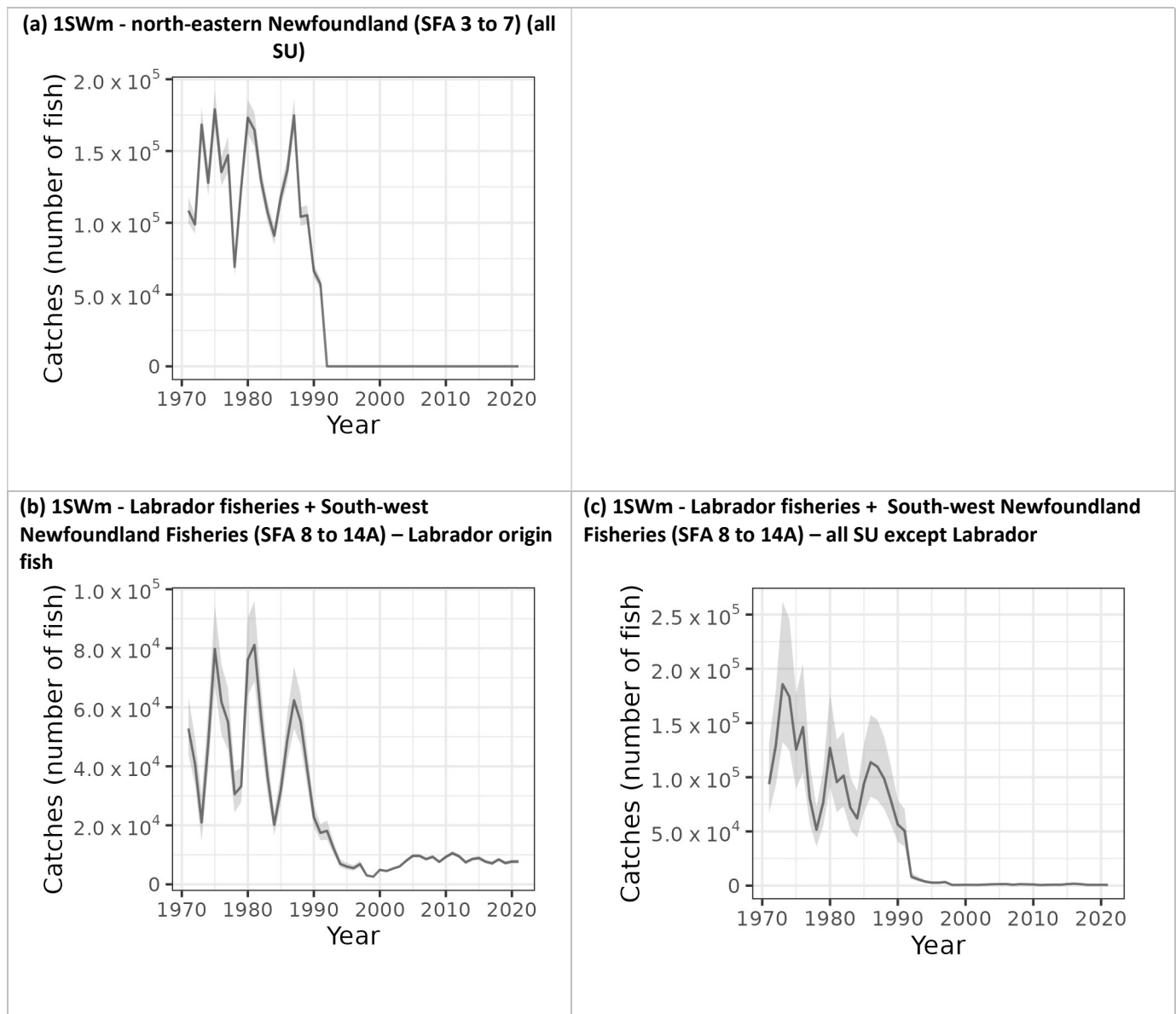


Figure A3.3. Catches (median and quantiles 5% and 95% of logNormal distributions) of the sequential fisheries at sea occurring on mixed stocks of North American 1SW maturing fish. (a) catches of all SU in north-eastern Newfoundland (SFA 3 to 7); (b) Labrador origin catches in Labrador Fisheries; (c) catches of SU 1-5 in Labrador fisheries, South-west Newfoundland Fisheries (SFA 8 to 14A) and in the Saint Pierre and Miquelon fisheries. (Source: ICES 2023).

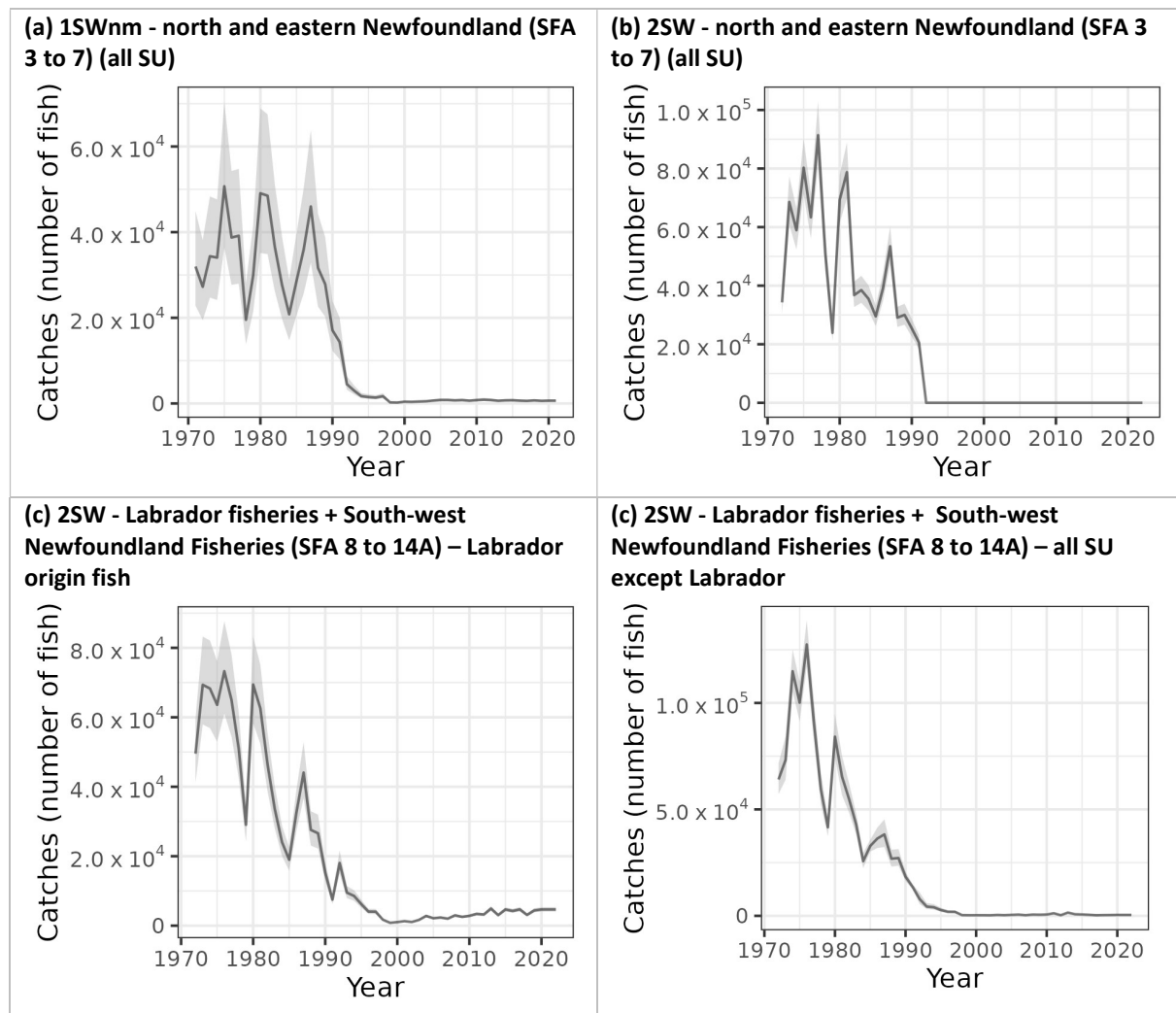


Figure A3.3. (Continuing). Catches (median and quantiles 5% and 95% of logNormal distributions) of the sequential fisheries at sea occurring on mixed stock fisheries, on North American 1SW non-maturing fish. (a) 1SWnm catches for all SUs in north and eastern Newfoundland (SFA 3 to 7); (b) 2SW catches for all SUs in north and eastern Newfoundland (SFA 3 to 7); (c) 2SW catches – Labrador origin fish in the catches in the Labrador fisheries; (d) 2SW – all other SU origin fish in catches in Labrador fisheries, south and west Newfoundland Fisheries (Salmon Fishing Areas 8 to 14A) and in the Saint Pierre and Miquelon fisheries. (Source: ICES 2023).

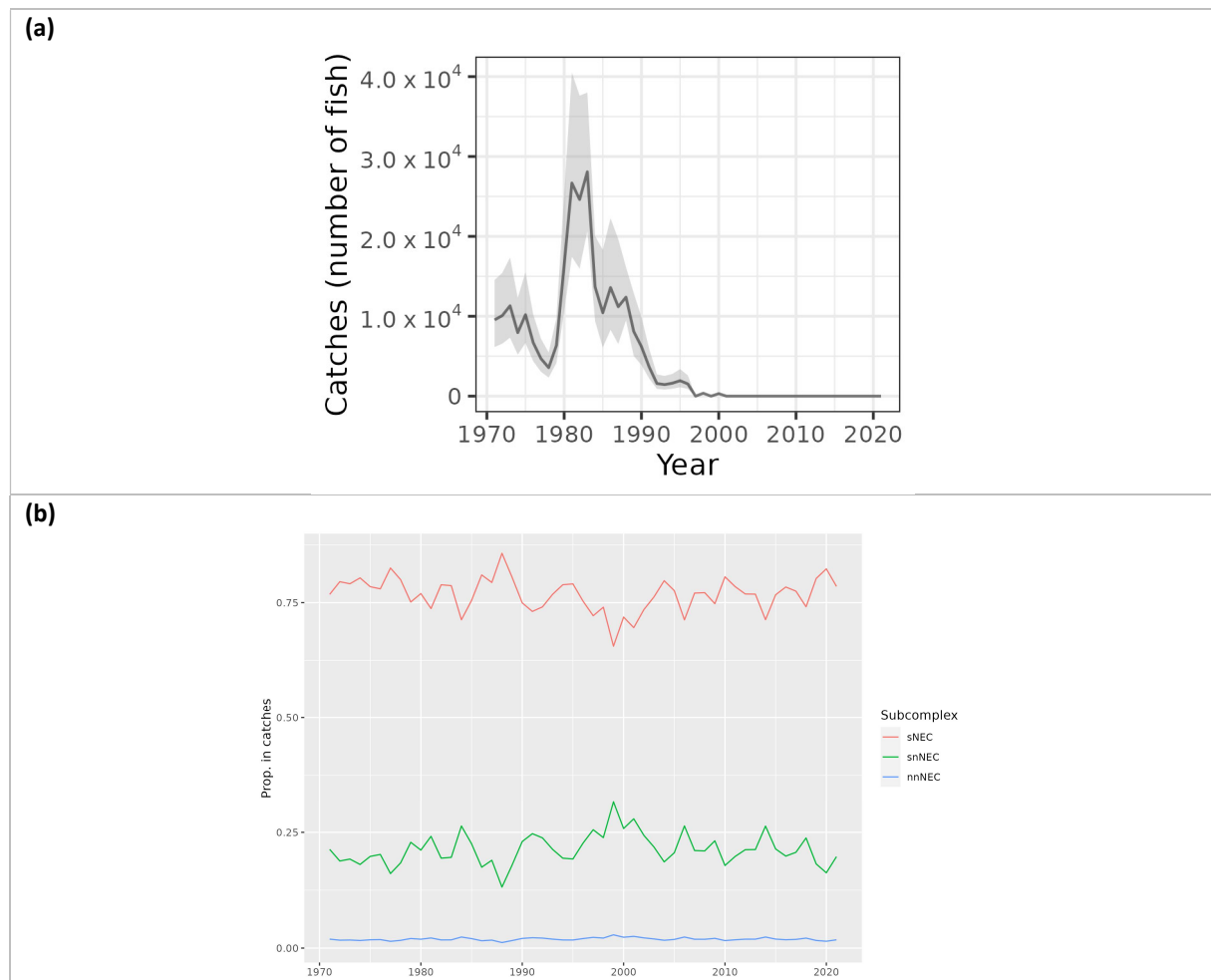
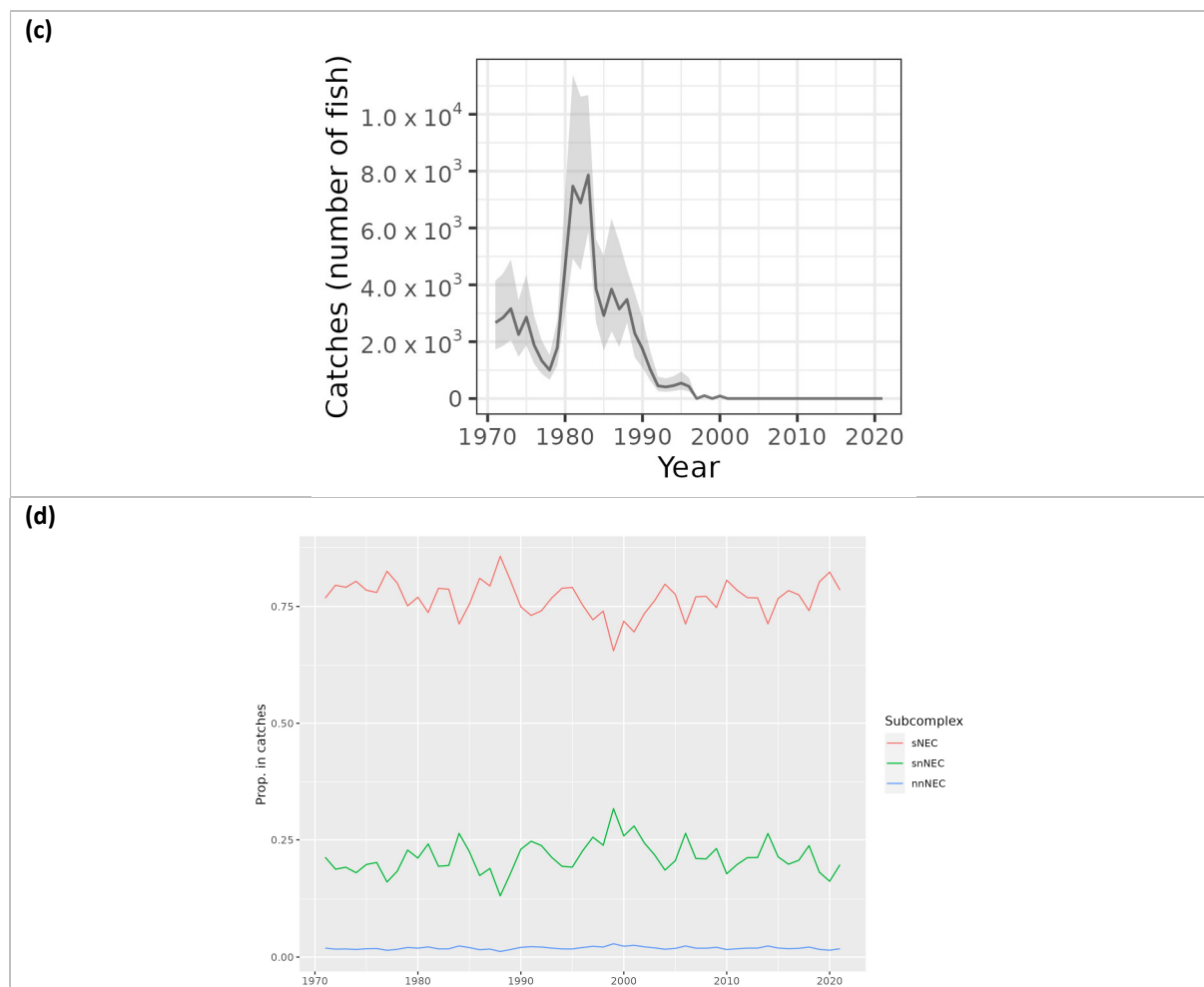


Figure A3.4. (a) Total catches of the 1SW maturing stage in the Faroes fishery. Catches of fish originating from North America have been retrieved; (b) Proportions of the catches attributed to South European, southern and northern part of the North European stock complex (Source: ICES 2023).



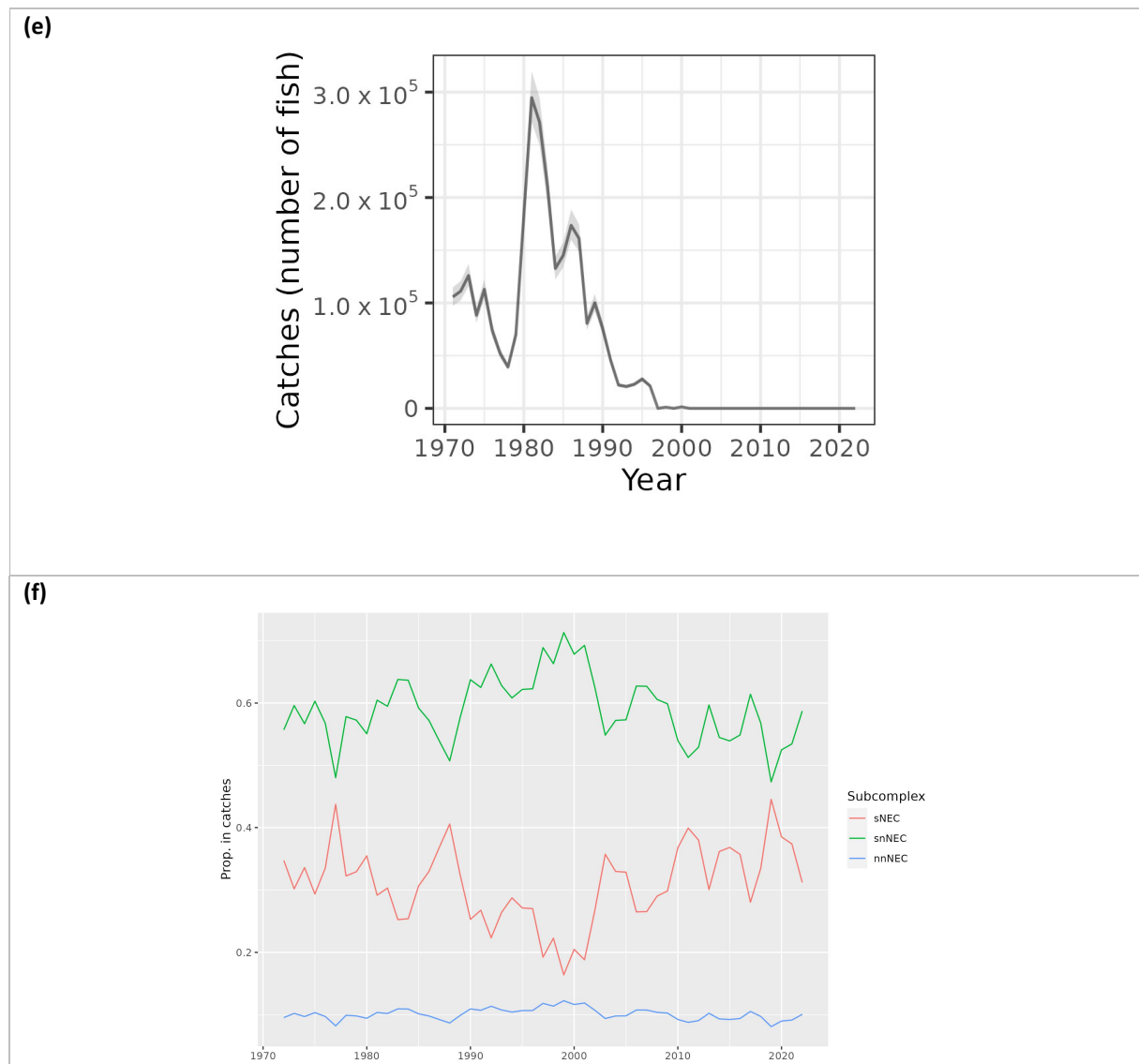


Figure A3.4. (continuing). (e) Total catches of the 2SW stage in the Faroes fishery. Catches of fish originating from North America have been retrieved; (f) Proportions of the catches attributed to South European, southern and northern part of the North European stock complex (Source: ICES 2023).

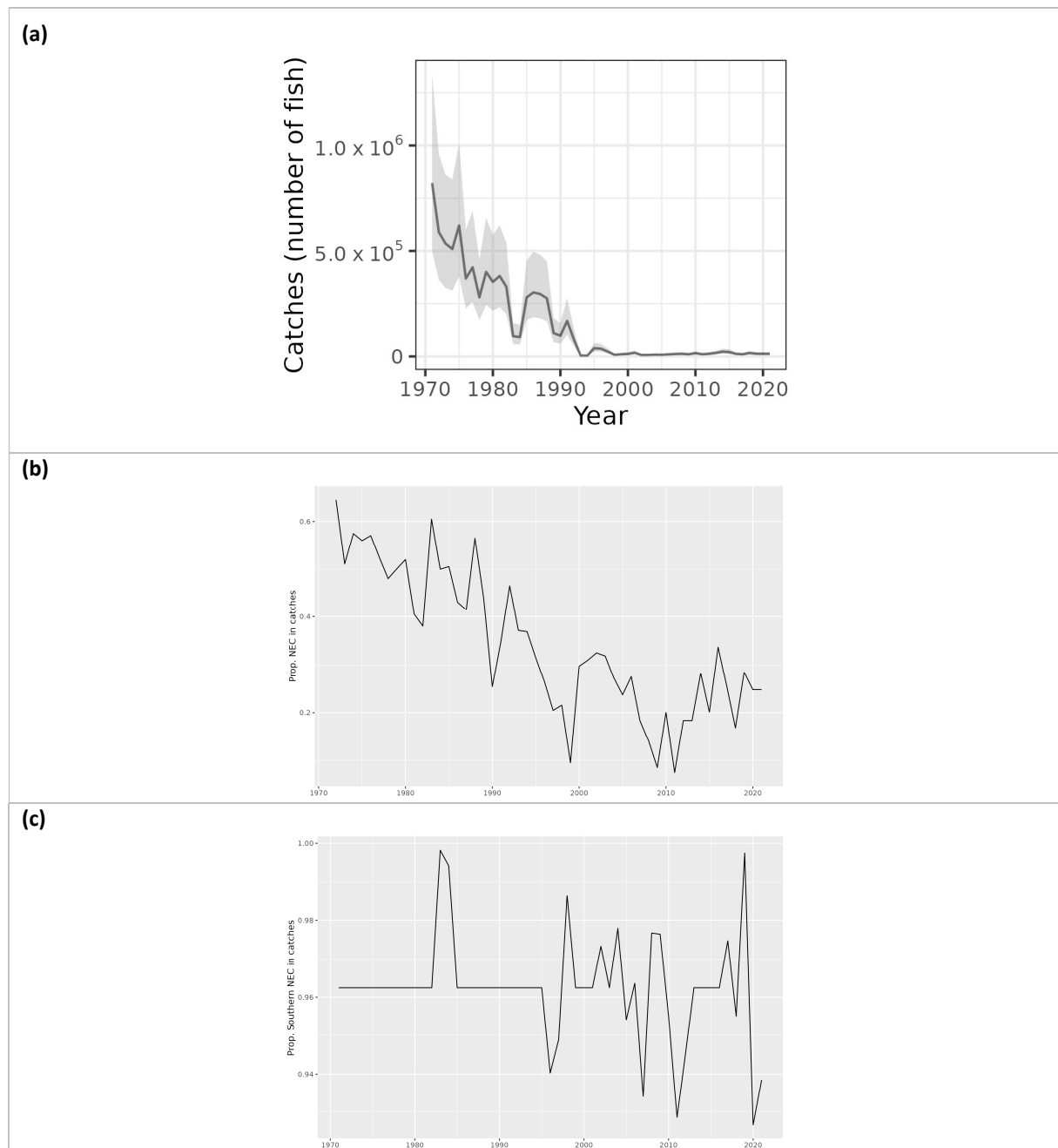


Figure A3.5. (a) Total catches (median and quantiles 5% and 95% of logNormal distributions) of 1SW non-maturing in the West Greenland fishery; (b) Proportions of the catches attributed to European stock complex (versus North American stock complex); (c) Proportion of the catches within the European stock complex attributed to the Southern European stock complex (versus northern European stock complex). (Source: ICES 2023).

9 Appendix 4 - Convergence MCMC chains

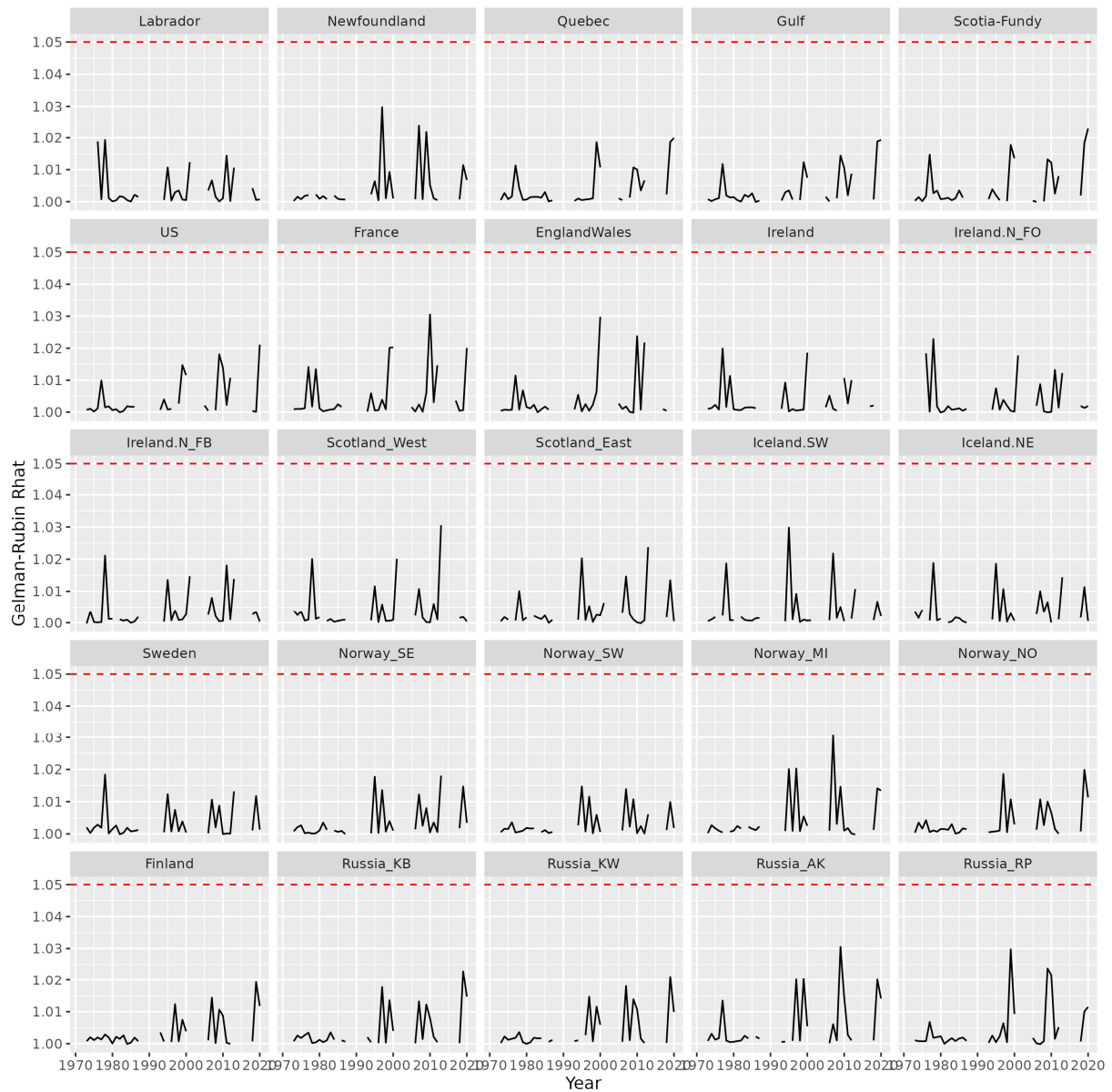


Figure A4.1. Summary of diagnostic convergence for the smolt-to-PFA transition rate (θ). The Gelman-Rubin R_{hat} value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of R_{hat} that are exactly 1).

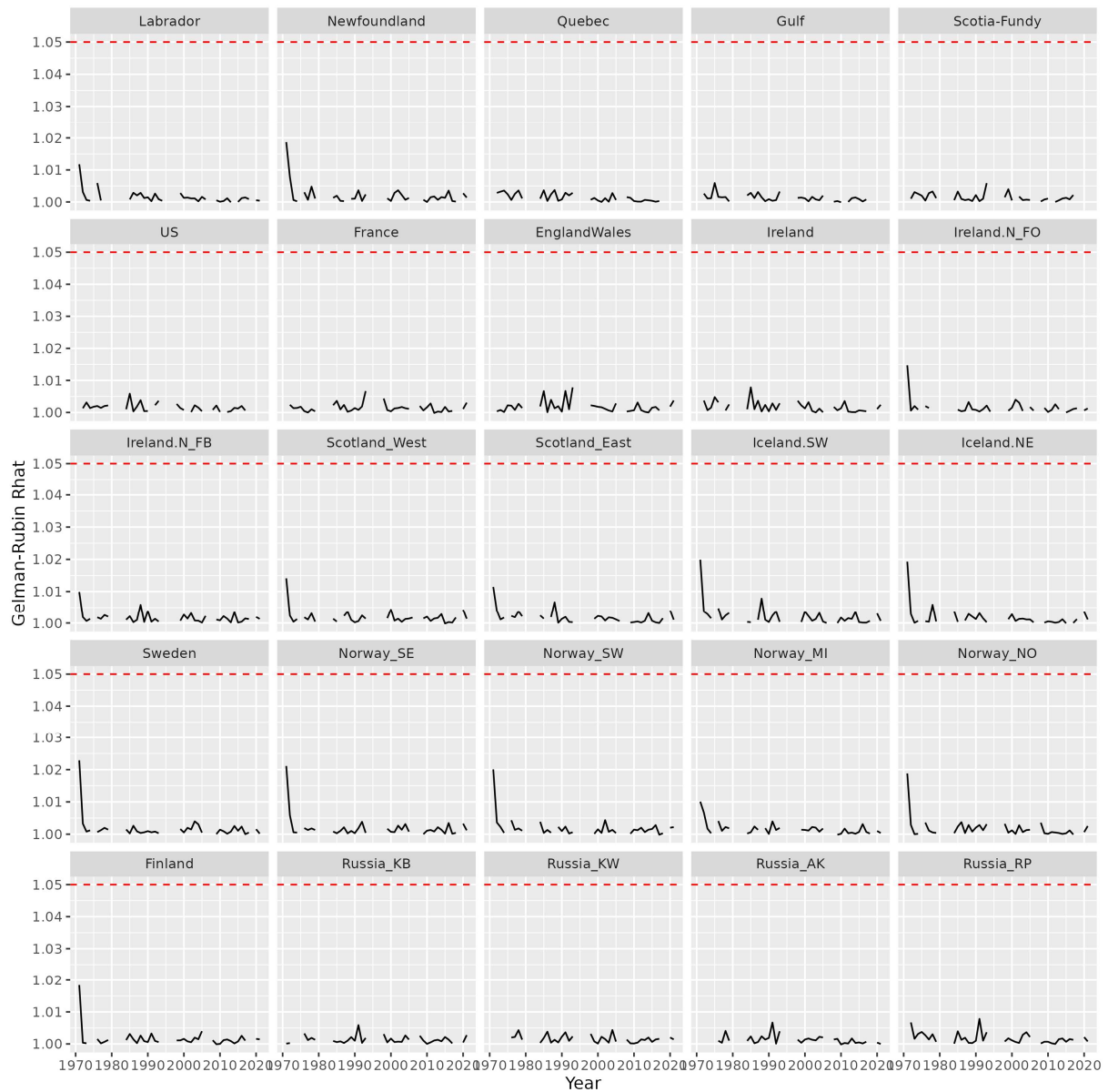


Figure A4.2. Summary of diagnostic convergence for the proportion of maturing PFA (θ_4). The Gelman-Rubin R_{hat} value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of R_{hat} that are exactly 1).

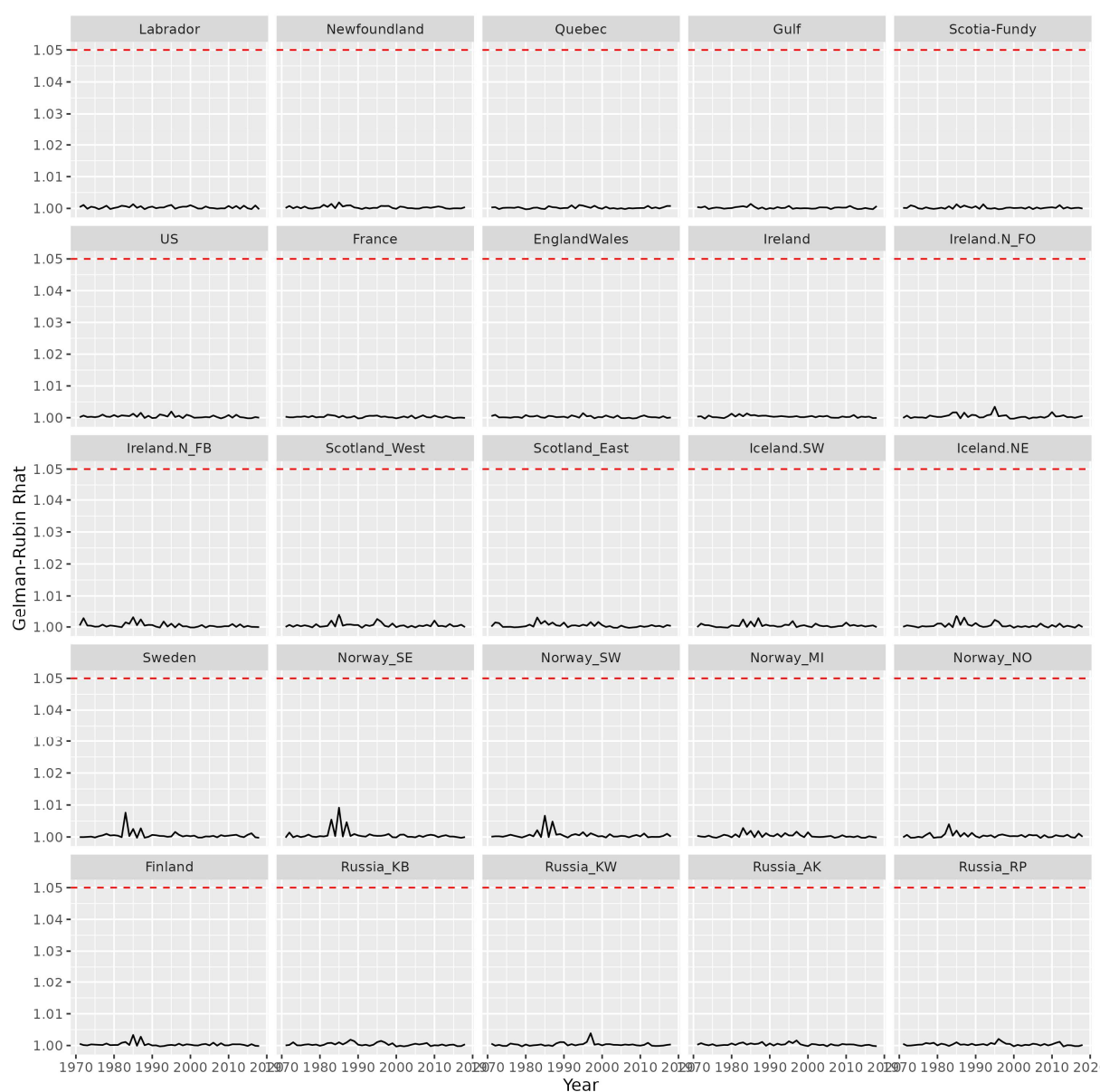


Figure A4.3. Summary of diagnostic convergence for the abundance of smolt-per cohort (variable N_2). The Gelman-Rubin R_{hat} value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of R_{hat} that are exactly 1).

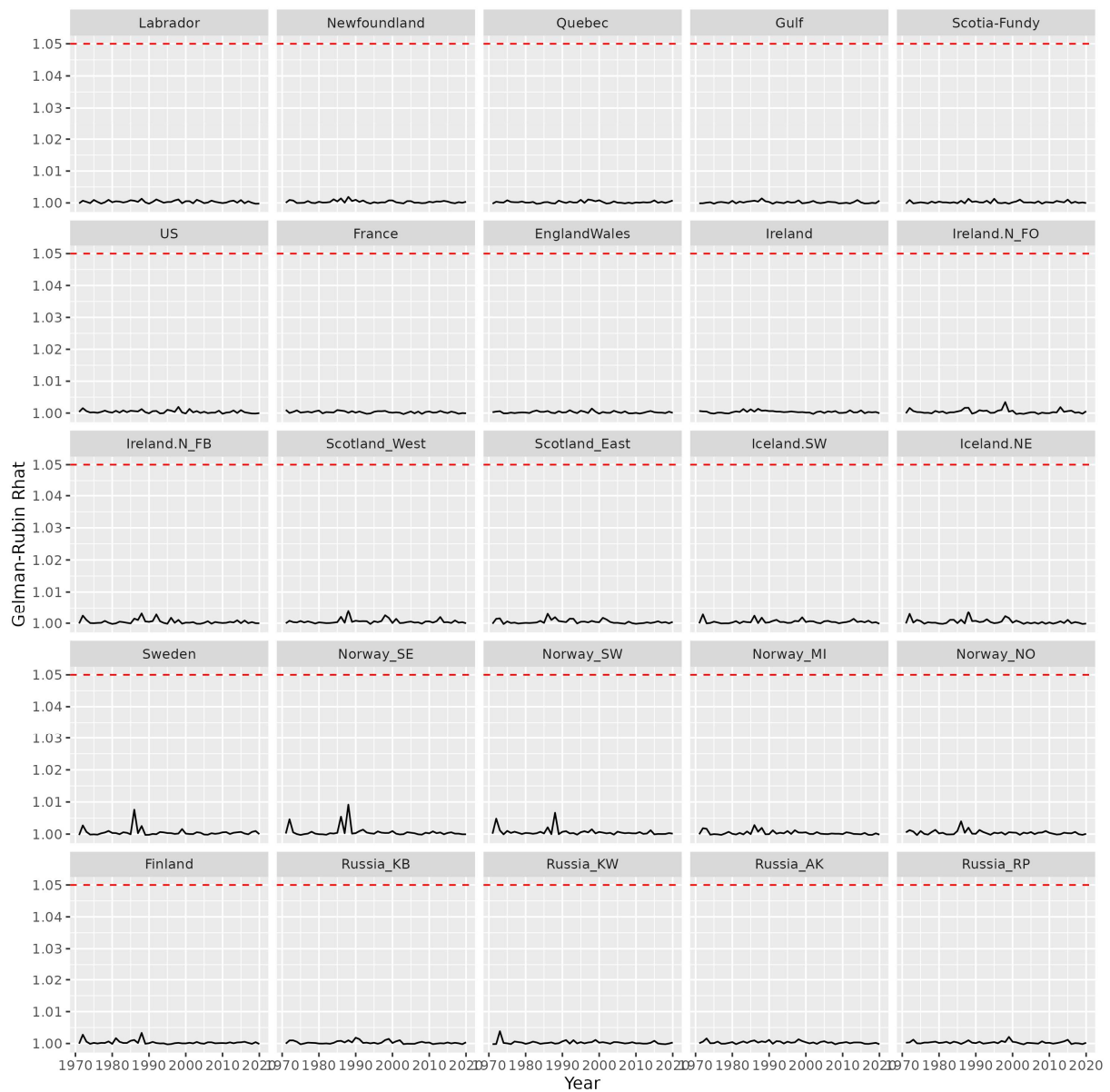


Figure A4.4. Summary of diagnostic convergence for the abundance of smolt-migrating year t calculated as the sum of smolts of multiple age migrating the same year (variable N_3). The Gelman-Rubin R_{hat} value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of R_{hat} that are exactly 1).

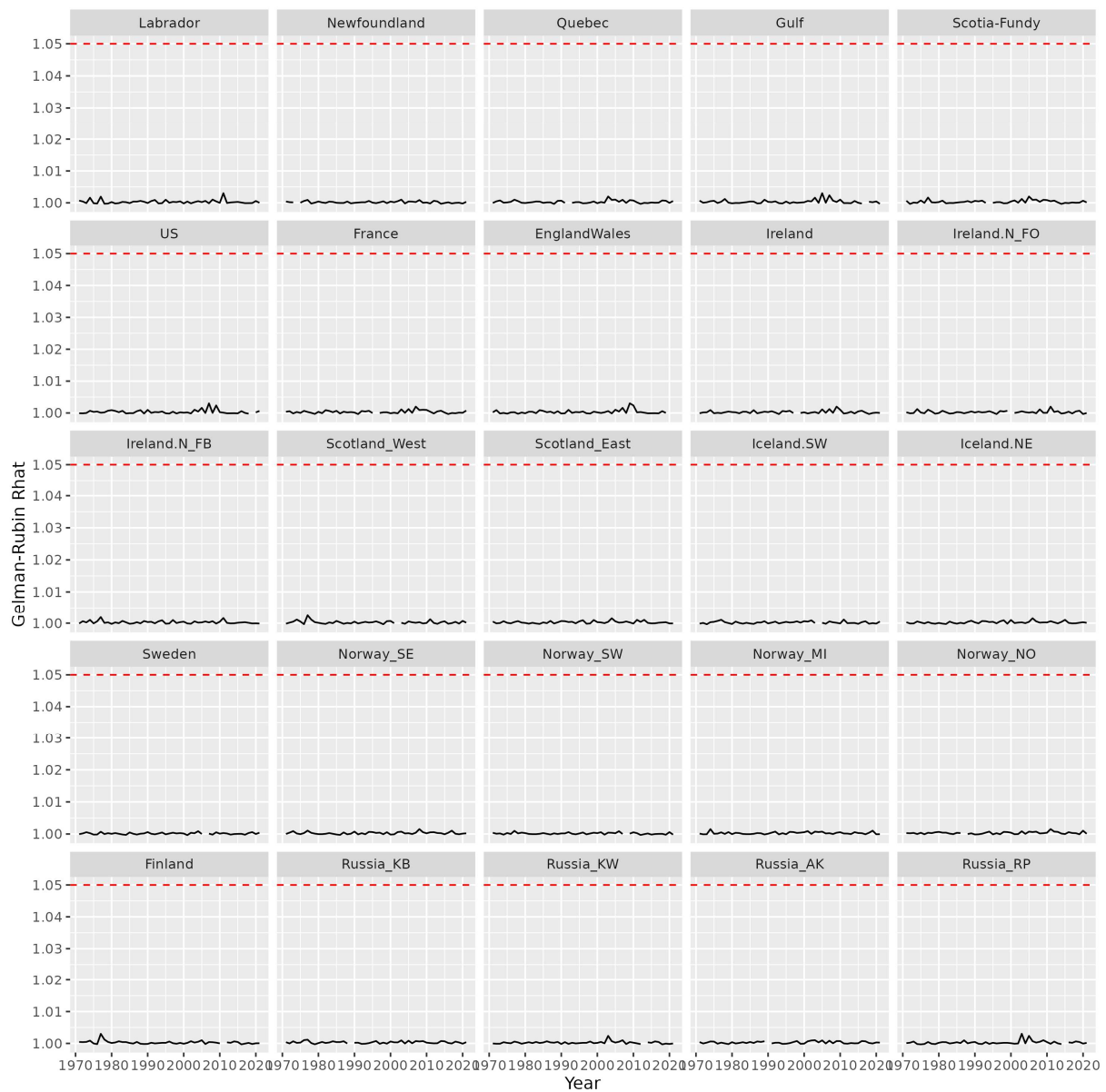


Figure A4.5. Summary of diagnostic convergence for the abundance of fish at the PFA stage (variable N_4). The Gelman-Rubin R_{hat} value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of R_{hat} that are exactly 1).

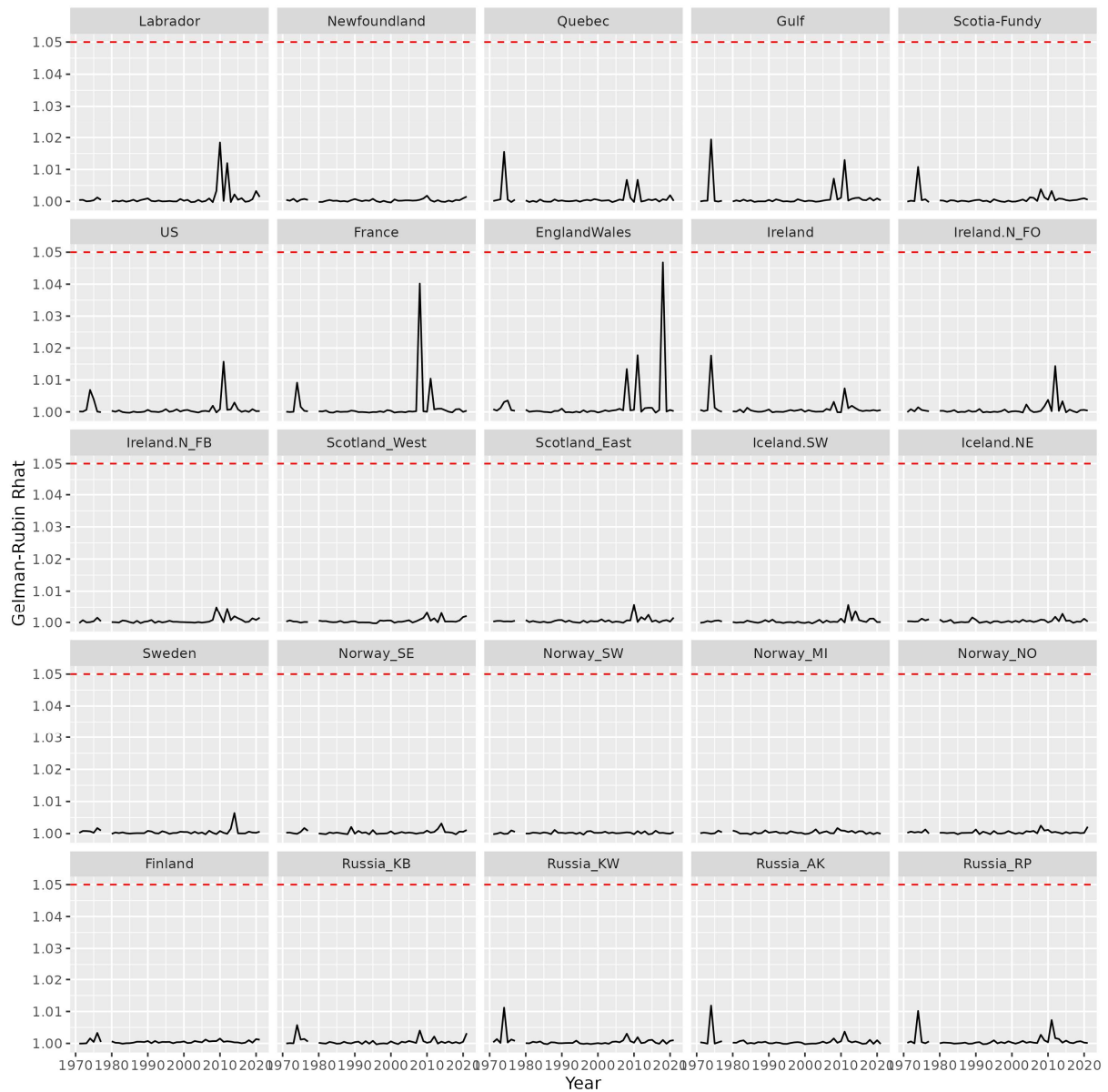


Figure A4.6. Summary of diagnostic convergence for the abundance of fish at the maturing PFA stage (variable N_5). The Gelman-Rubin R_{hat} value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of R_{hat} that are exactly 1).

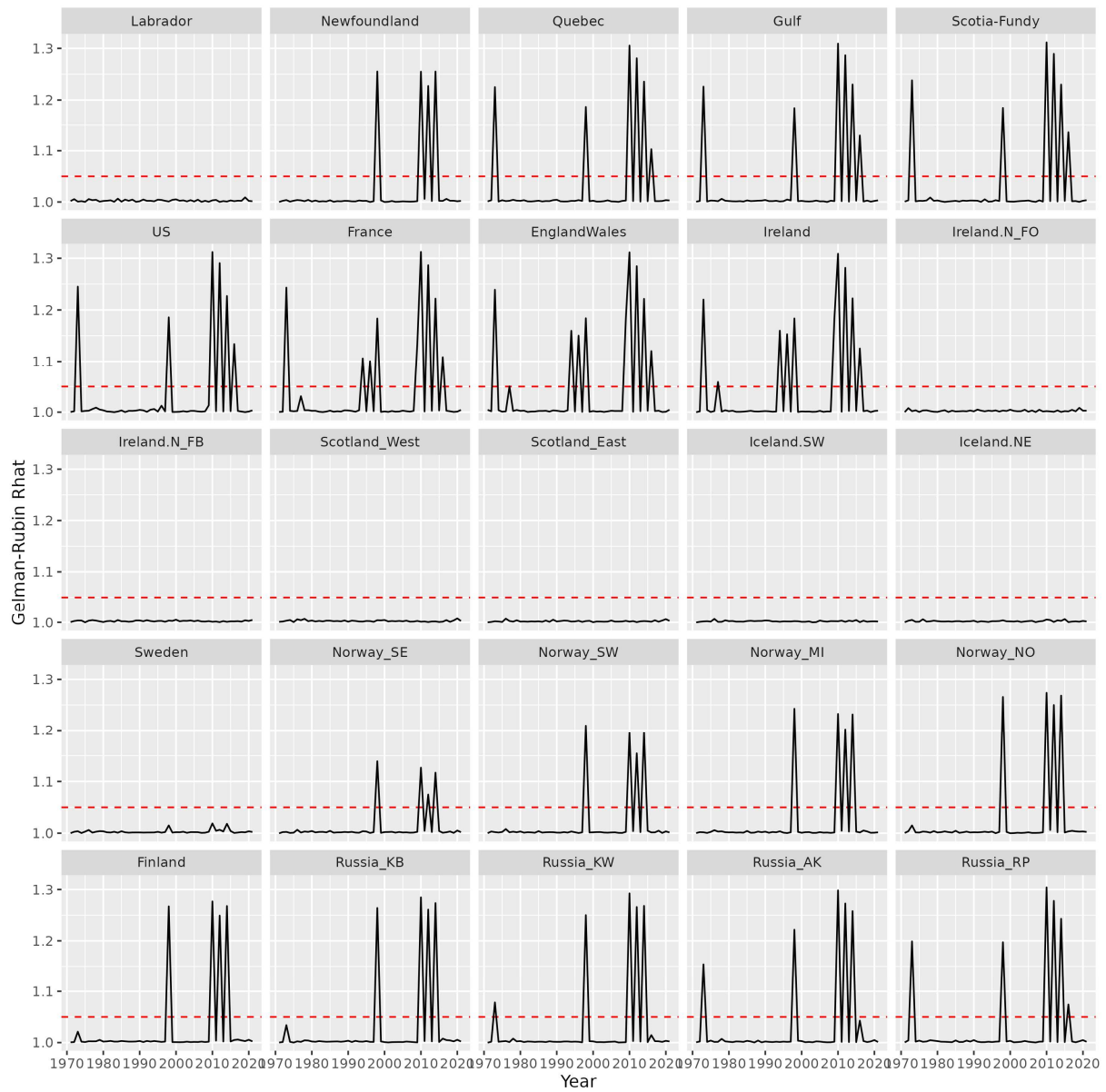


Figure A4.7. Summary of diagnostic convergence for the abundance of fish at the non-maturing PFA stage (variable N_8). The Gelman-Rubin $Rhat$ value is provided. The red dotted line indicates the empirical threshold of 1.05.

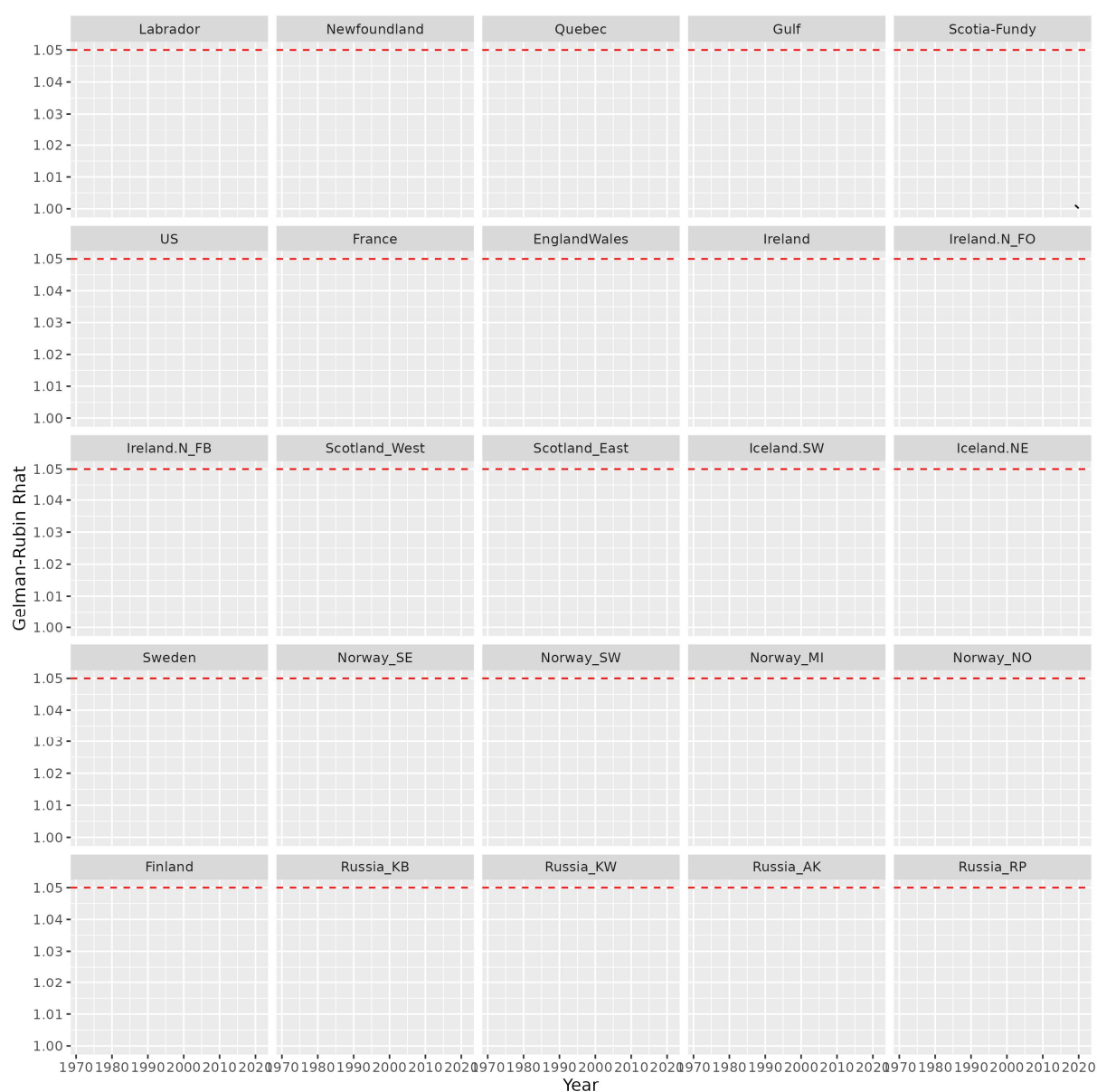


Figure A4.8. Summary of diagnostic convergence for the abundance of fish at the stage of 1SW returns (variable N_6). The Gelman-Rubin $Rhat$ value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of $Rhat$ that are exactly 1).

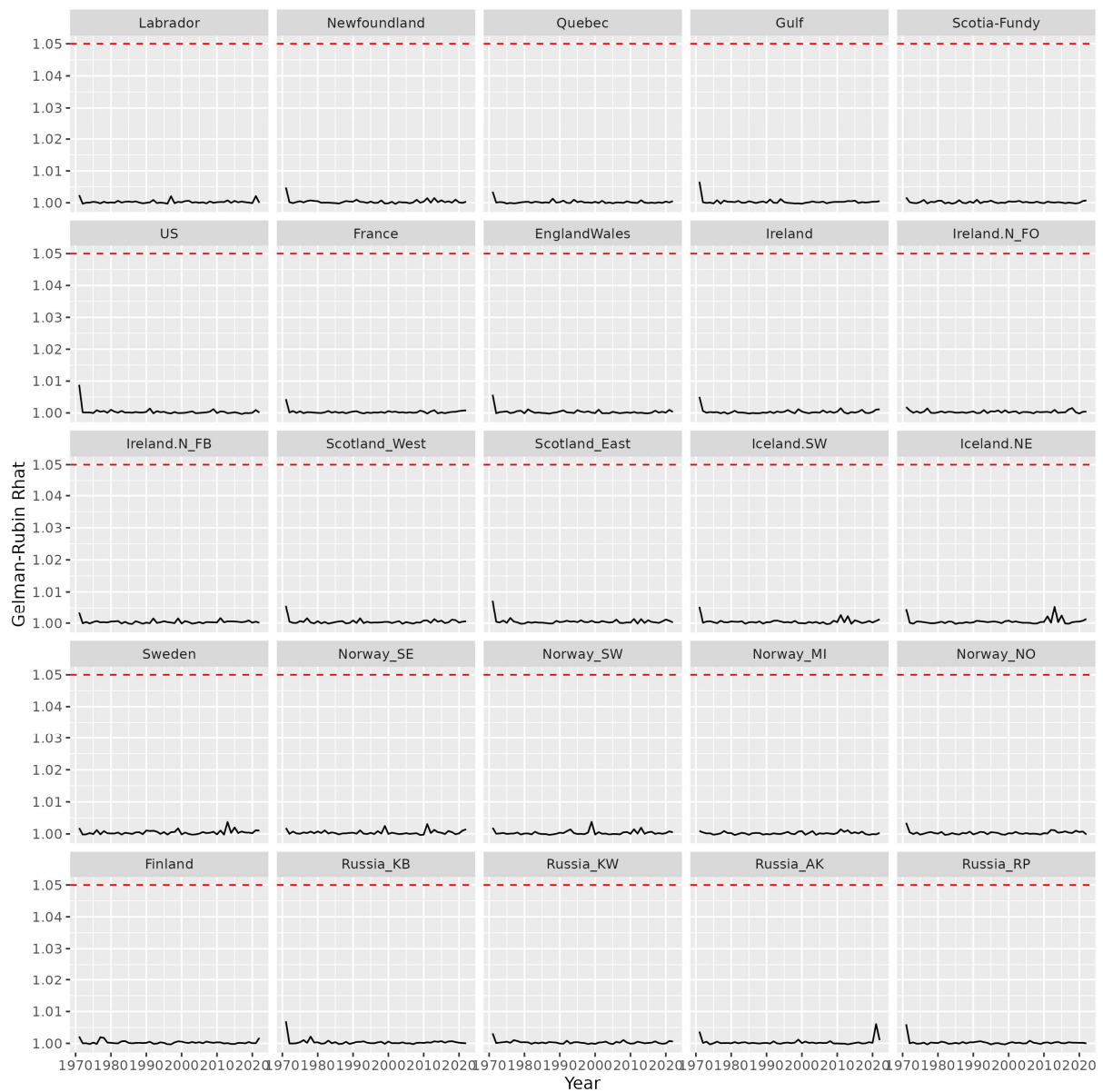


Figure A4.9. Summary of diagnostic convergence for the abundance of fish at the stage of 1SW returns (variable N_9). The Gelman-Rubin R_{hat} value is provided. The red dotted line indicates the empirical threshold of 1.05. (Note: Results of calculation that do not appear on the graph are values of R_{hat} that are exactly 1).

10Appendix 5 - Fit to the different data sources

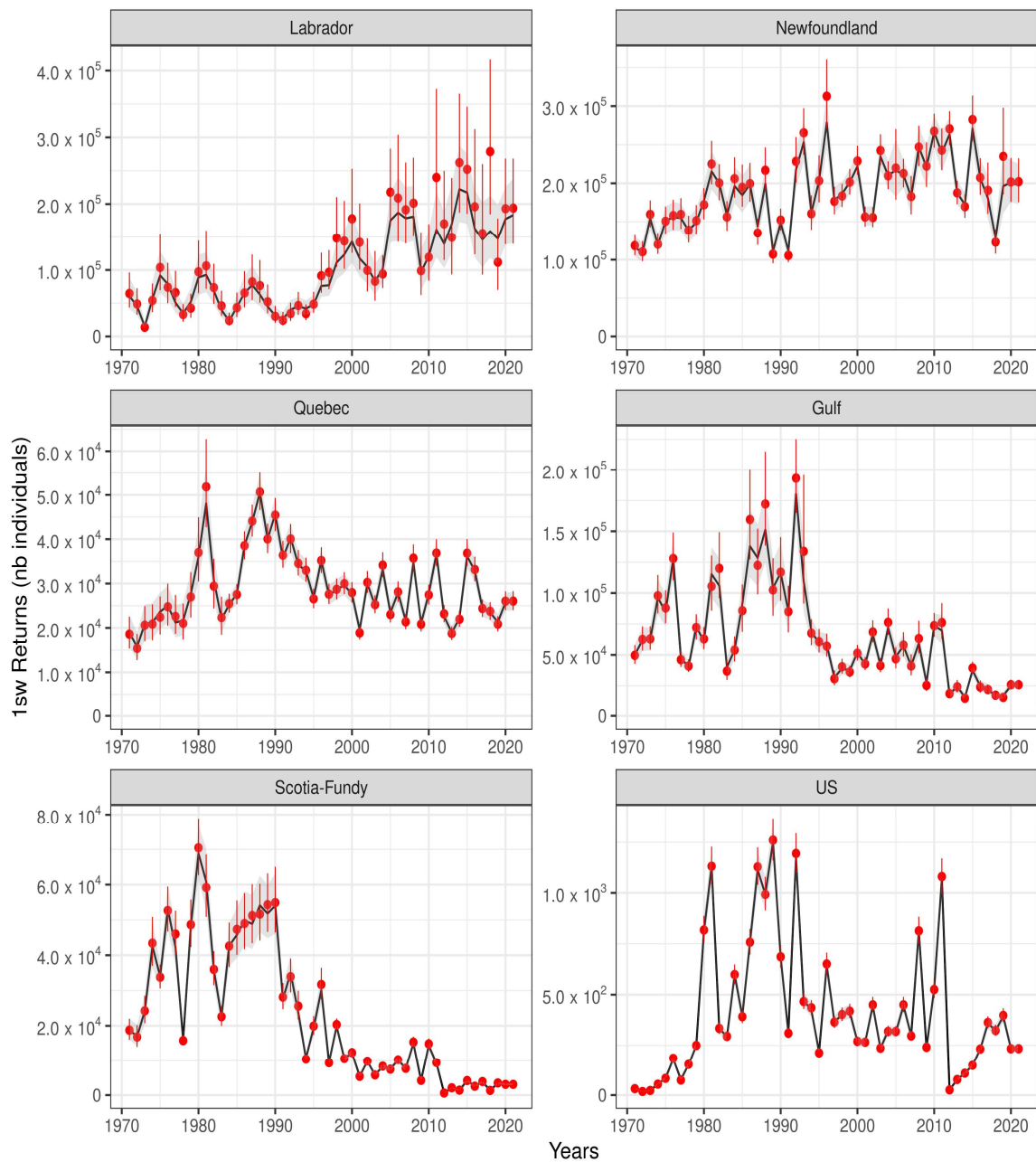
All figures below are used to assess the fit of the model to the four main sources of data integrated through likelihood functions.

- Abundance at the return stage (1SW and 2SW) - Lognormal likelihood
- Homewater catches (1SW and 2SW and delayed spawners) - Lognormal likelihood
- Catches of all fisheries at sea (1SW mature, 1SW non-mature, 2SW) - Lognormal likelihood
- Proportion of the different origins in the catches at sea - Dirichlet likelihood

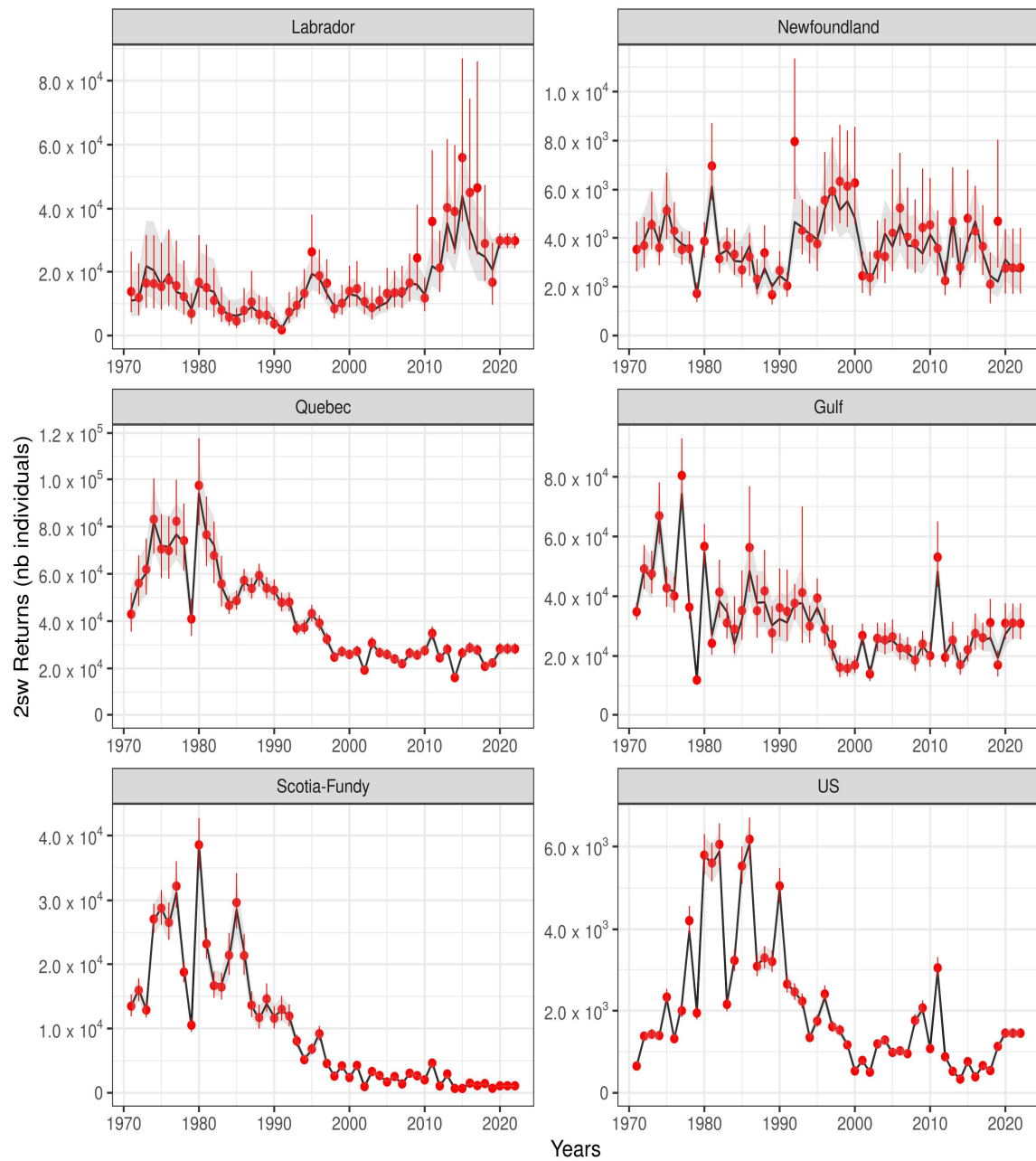
The quality of fit of the model to the different data sources is assessed through the comparison between the posterior distribution of state variables in the model (shaded areas) and the associated data. When observation errors are associated to one data source, the posterior distribution of the state variable is compared to the probability distribution that corresponds to observation errors (red dot and plain lines).

10.1 Returns

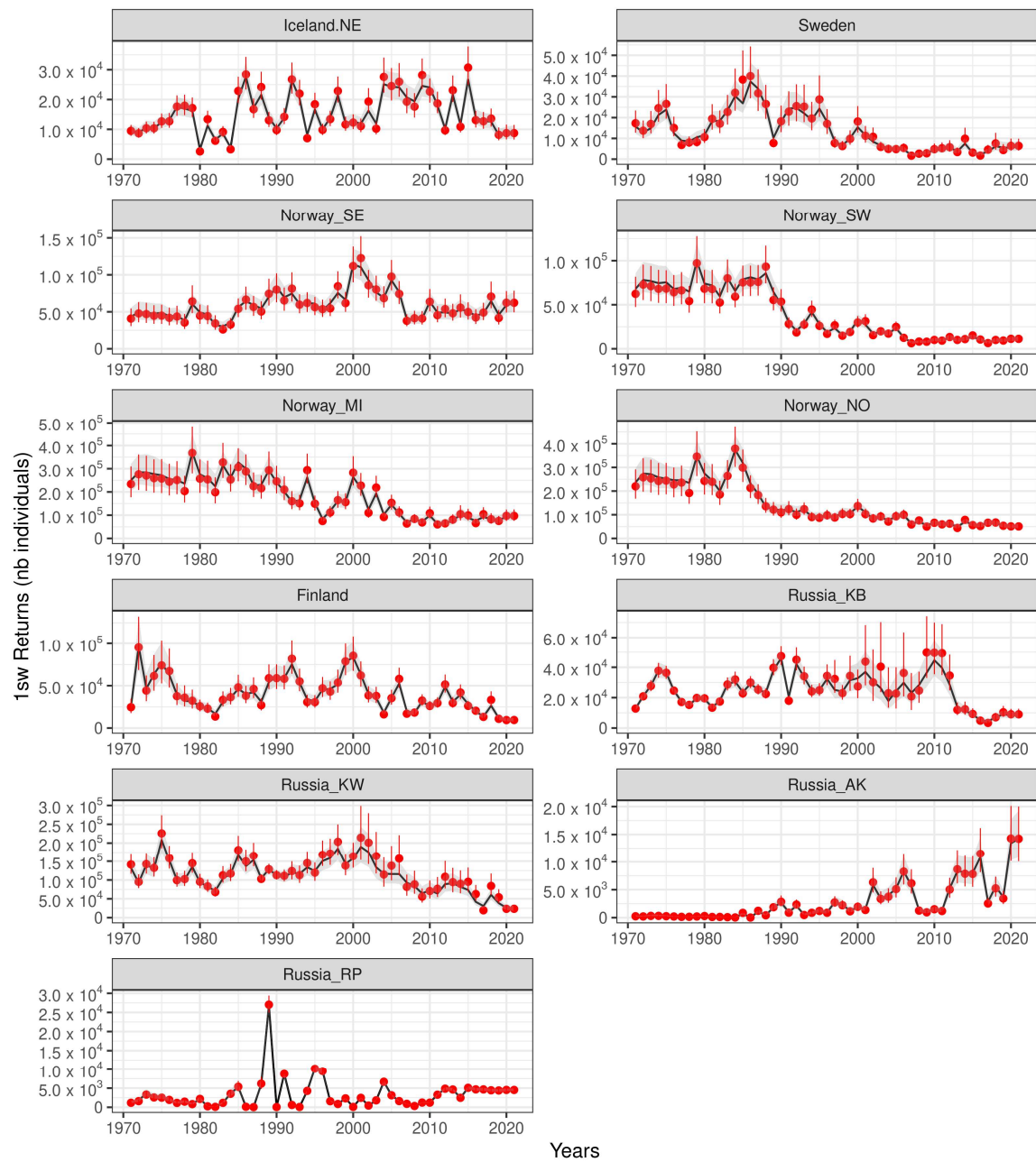
10.1.1 North America – 1SW



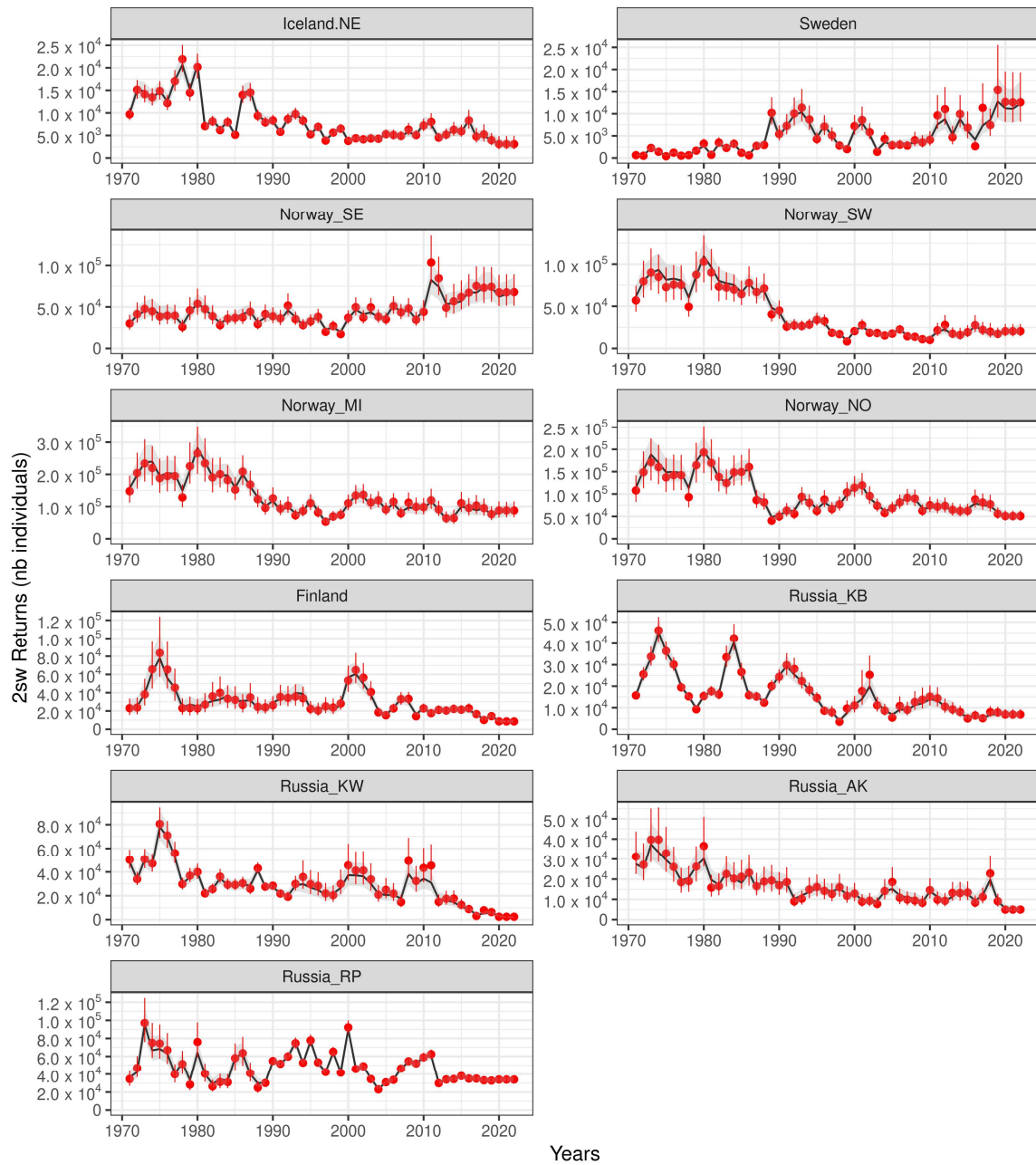
10.1.1 North America – 2SW



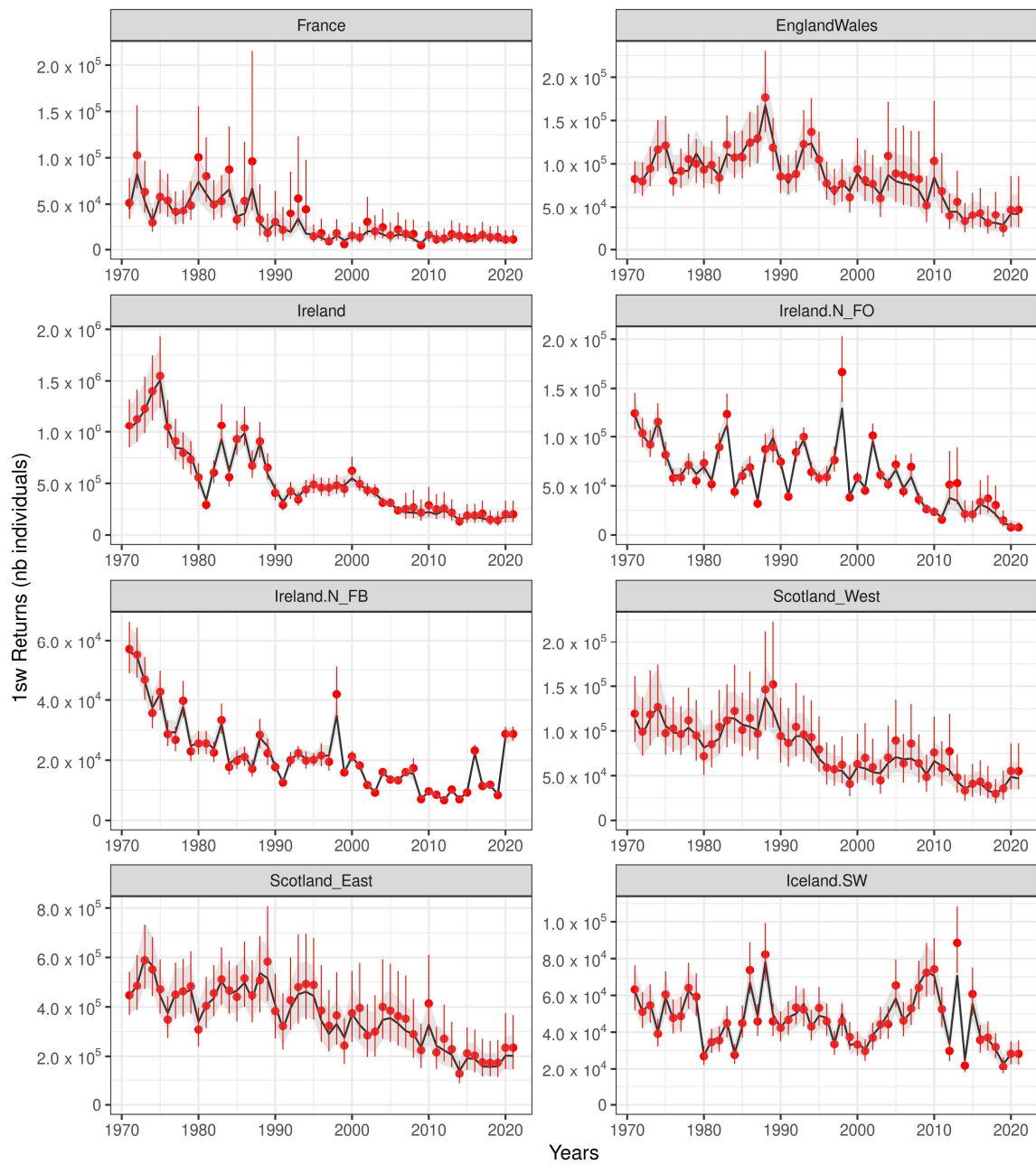
10.1.2 Northern Europe – 1SW



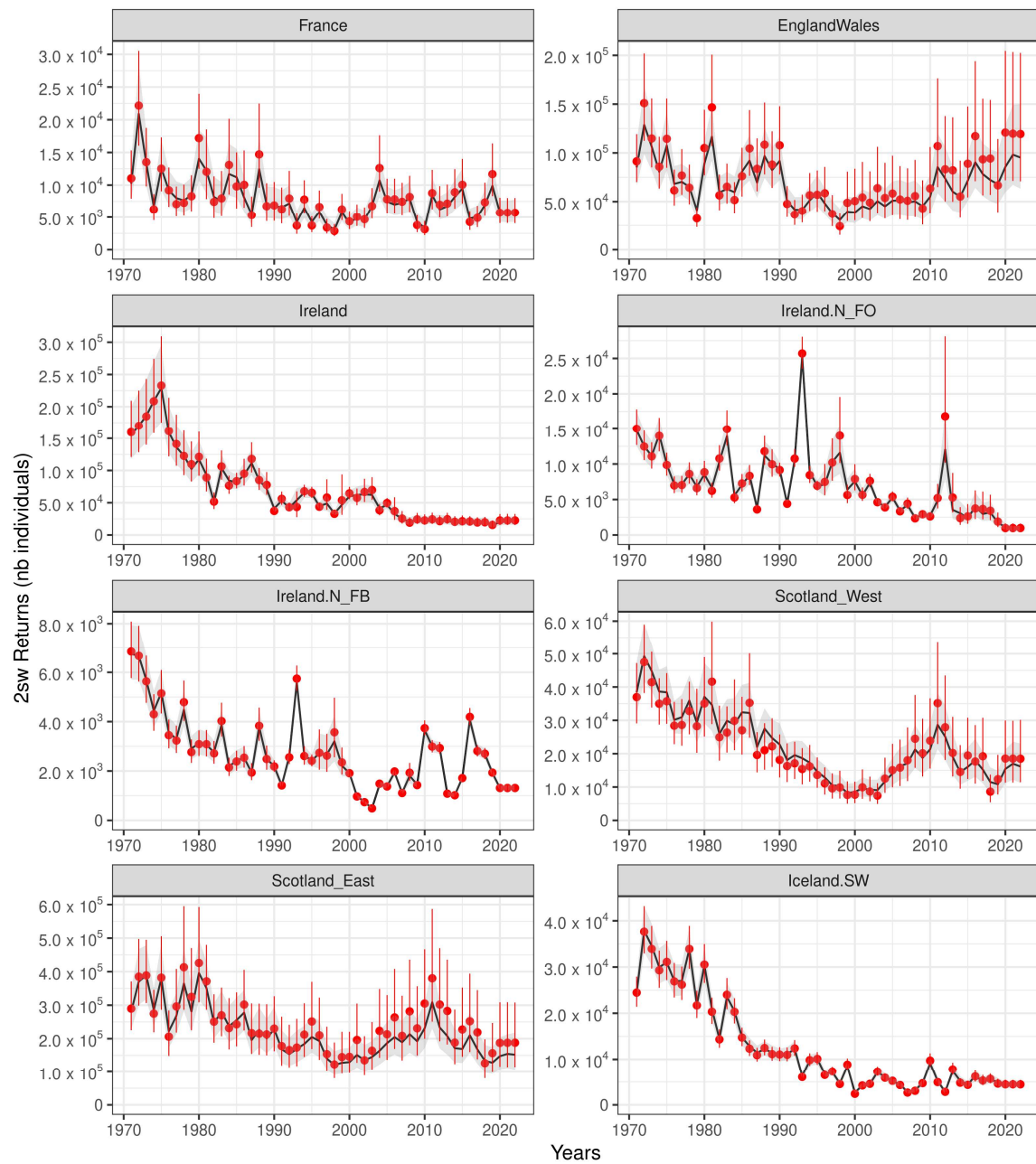
10.1.1 Northern Europe – 2SW



10.1.2 Southern Europe – 1SW

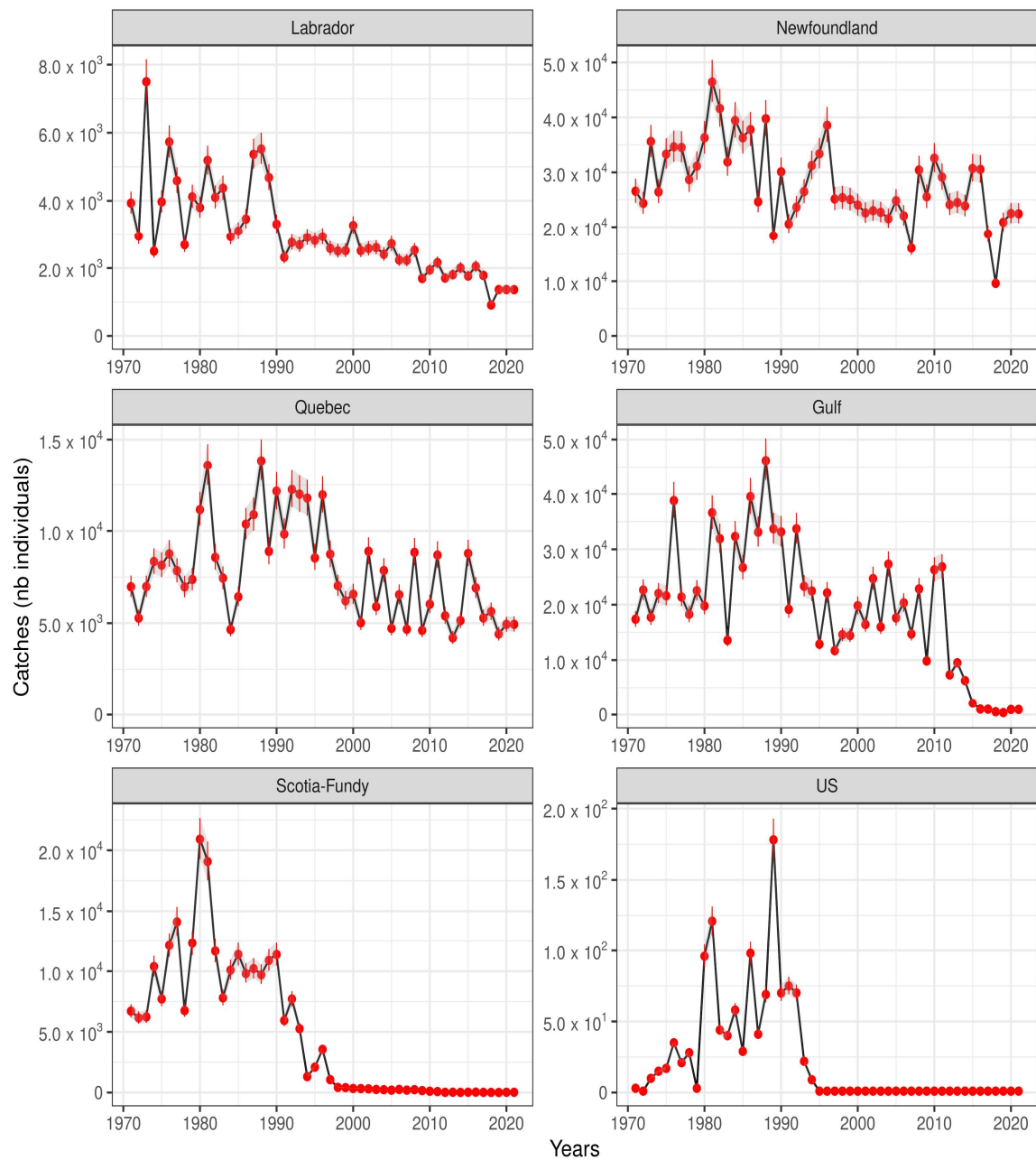


10.1.1 Southern Europe – 2SW

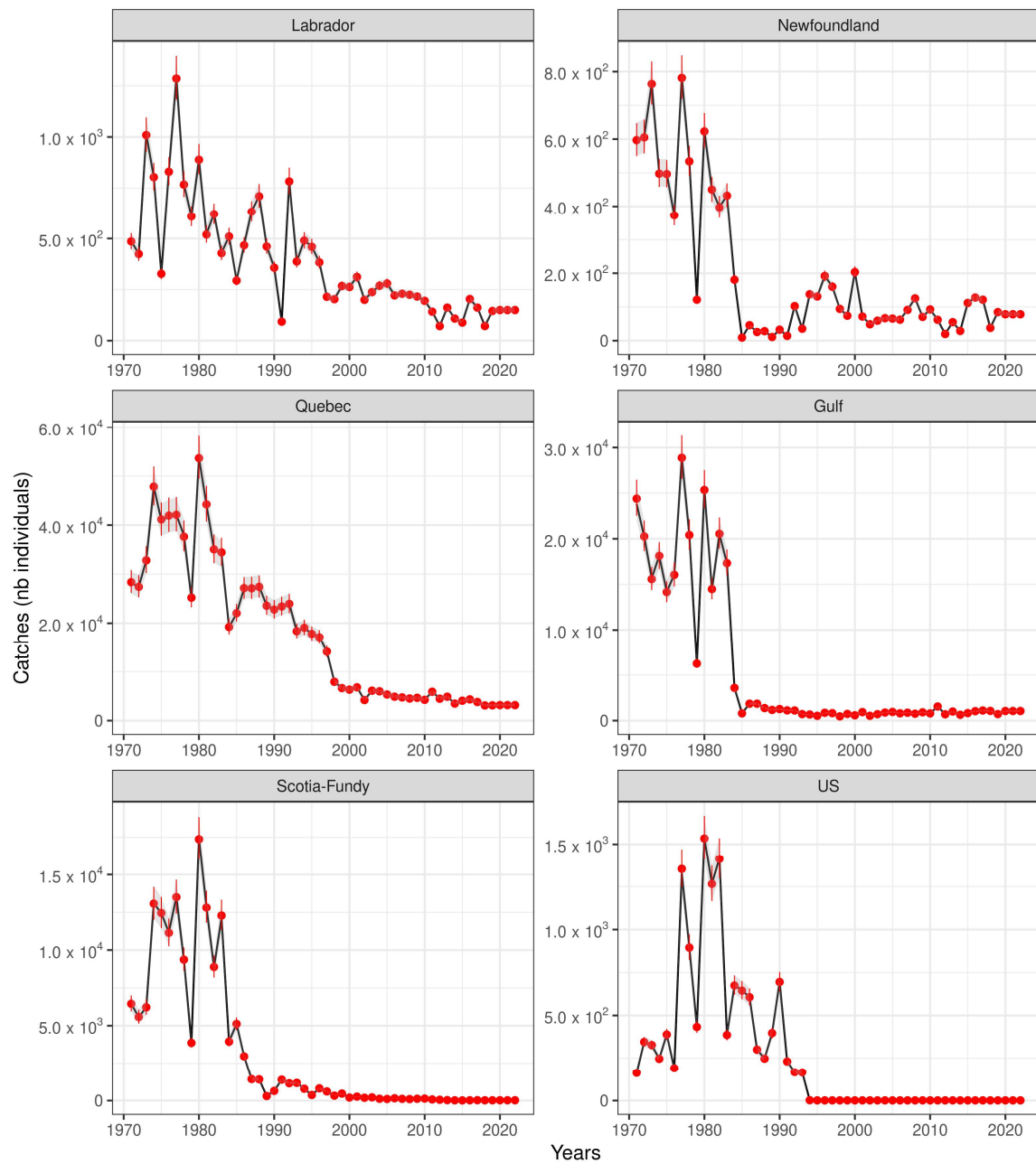


10.2 Homewater catches

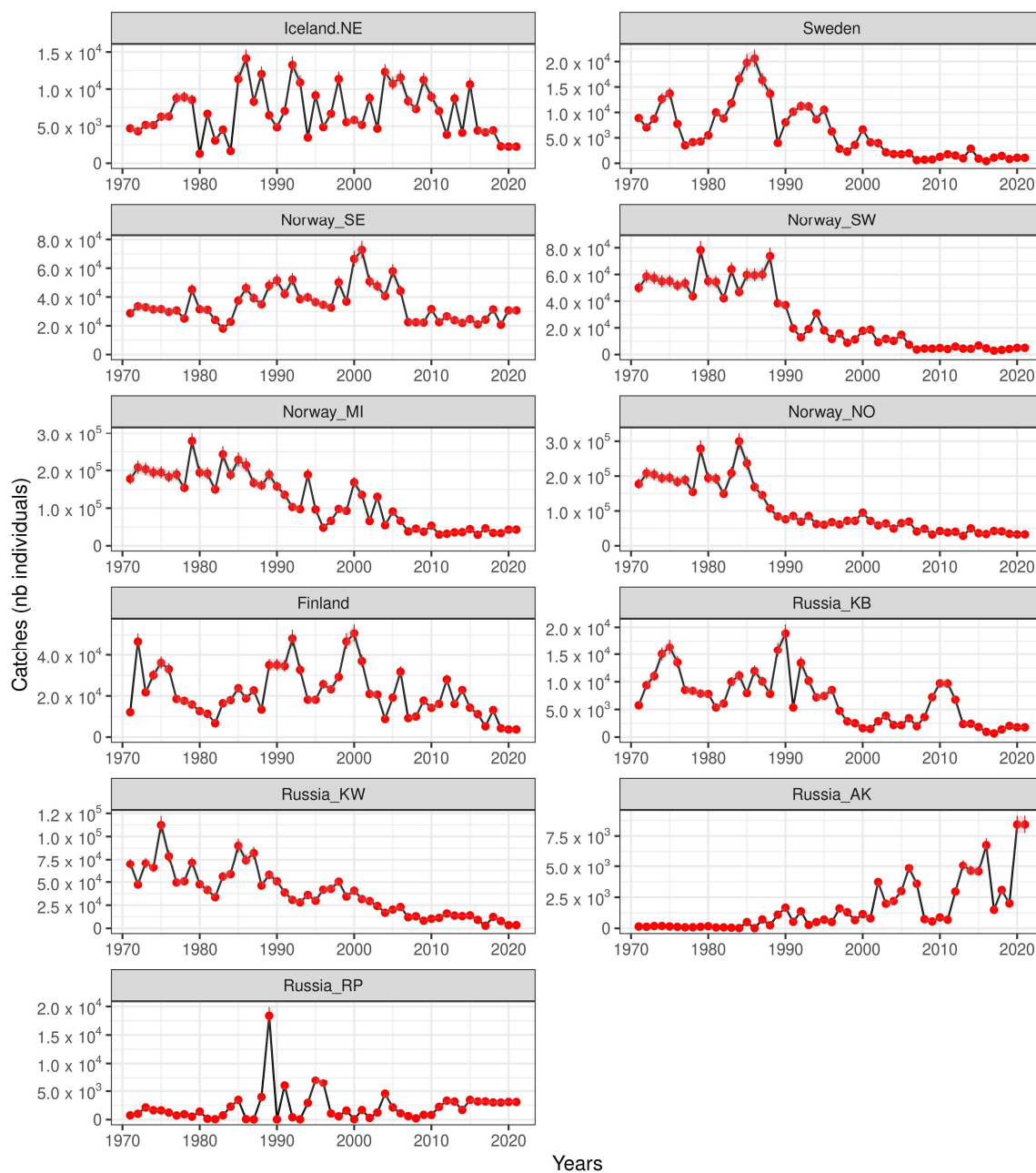
10.2.1 North America – 1SW



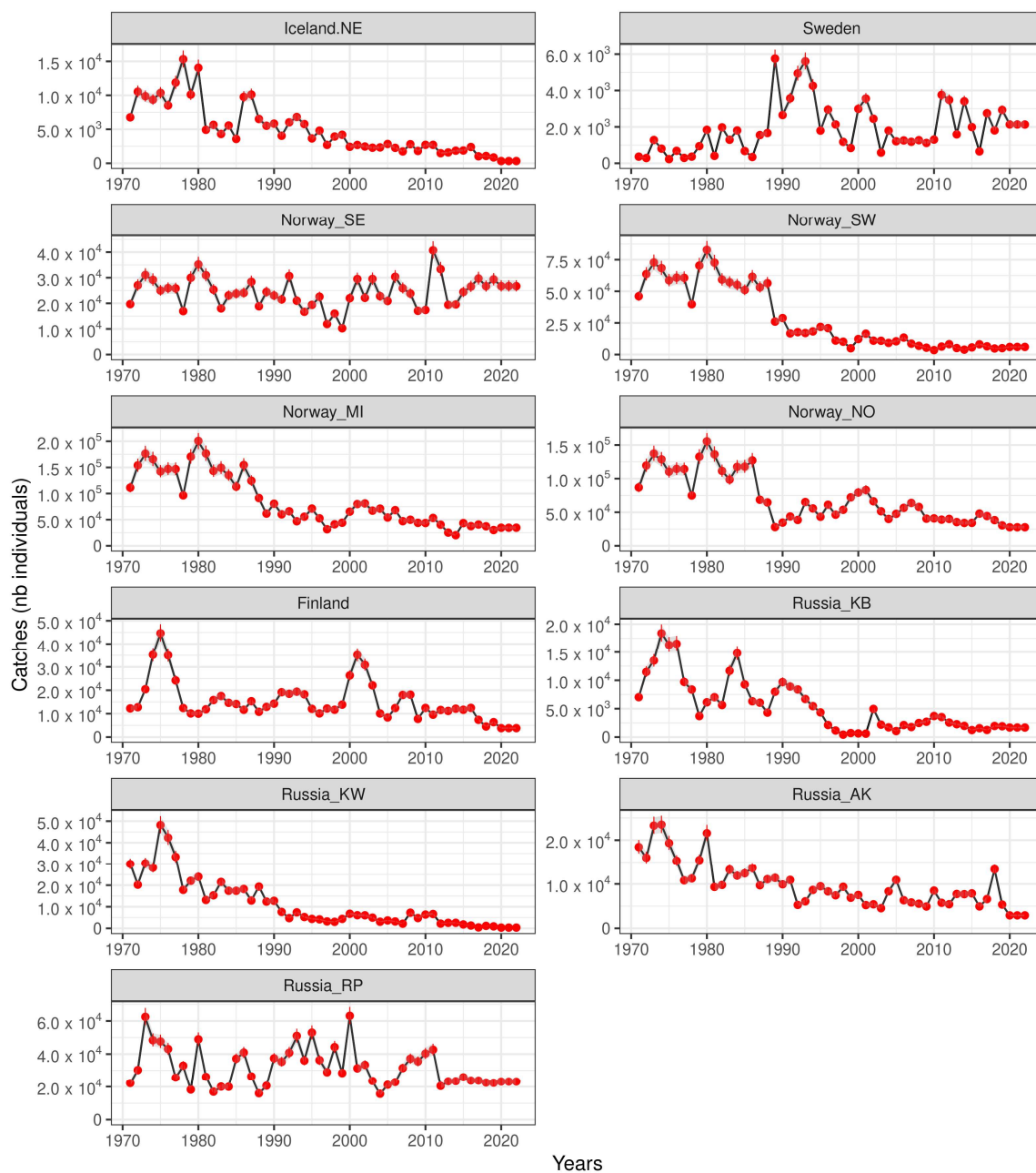
10.2.1 North America – 2SW



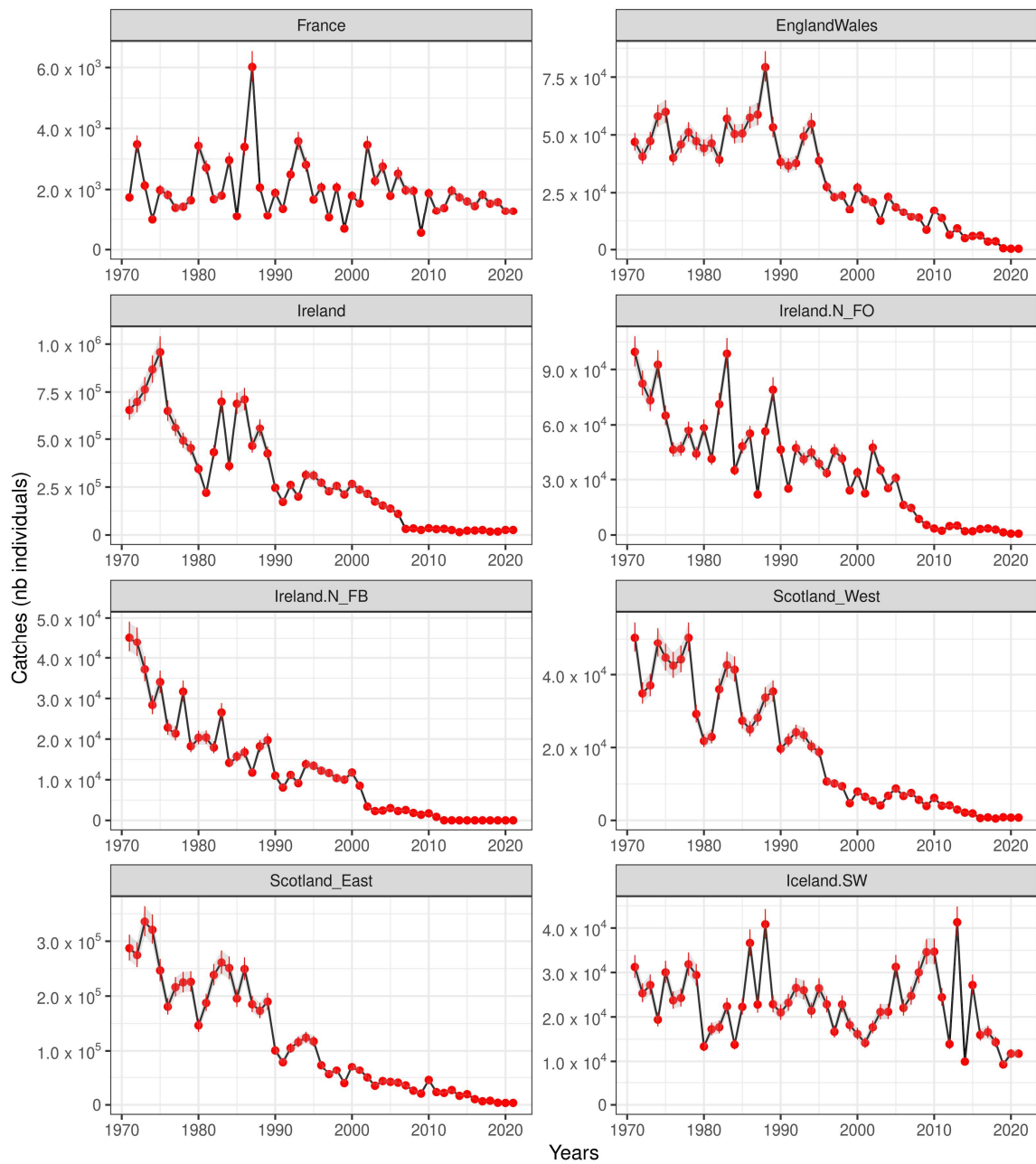
10.2.2 Northern Europe – 1SW



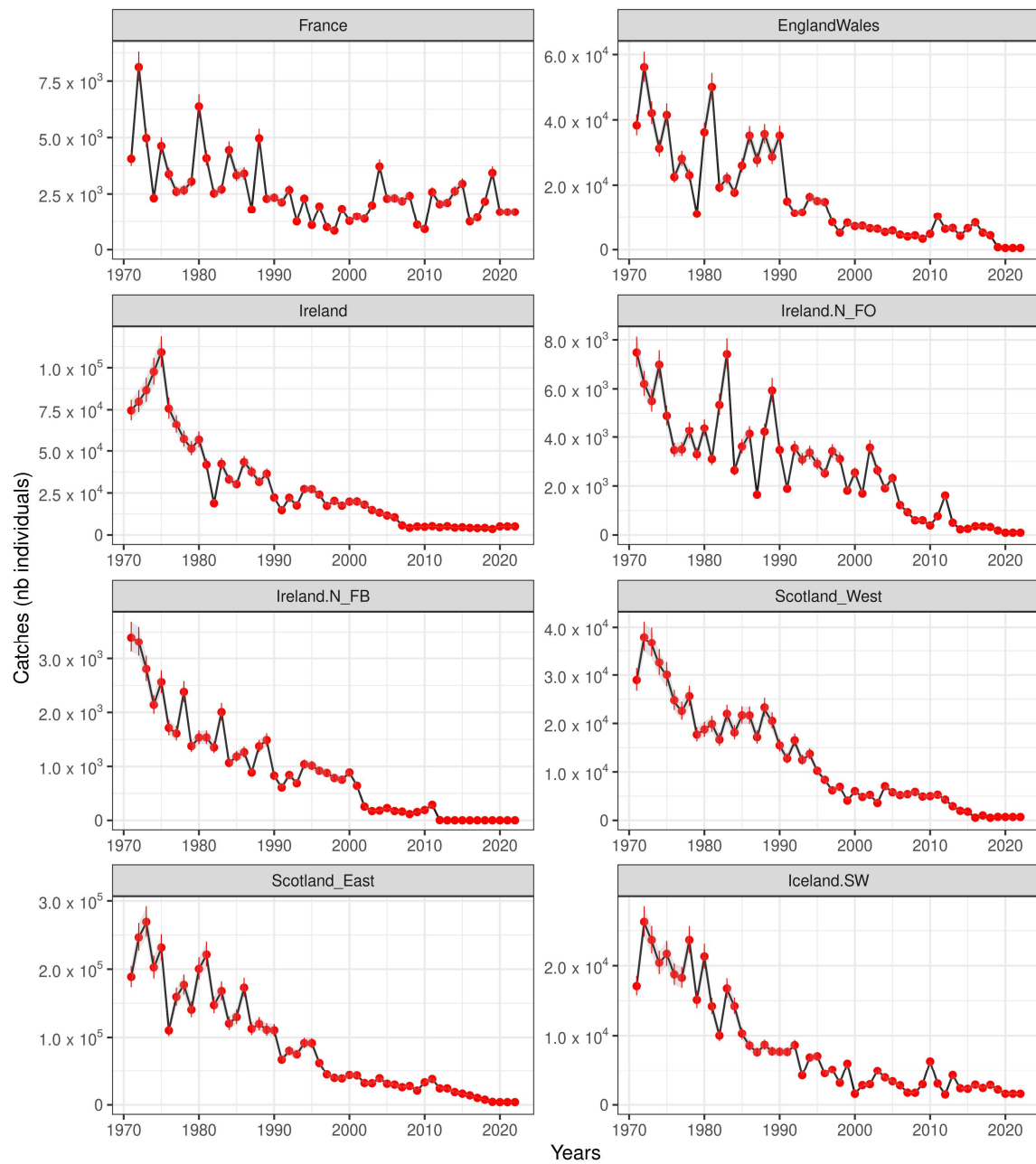
10.2.1 Northern Europe – 2SW



10.2.2 Southern Europe – 1SW



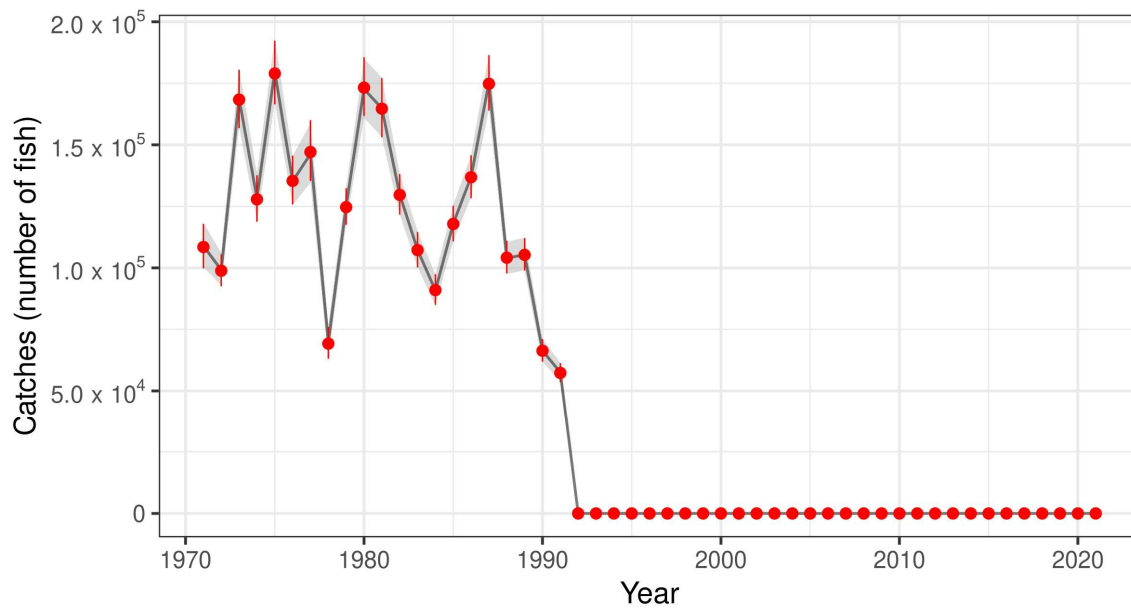
10.2.1 Southern Europe – 2SW



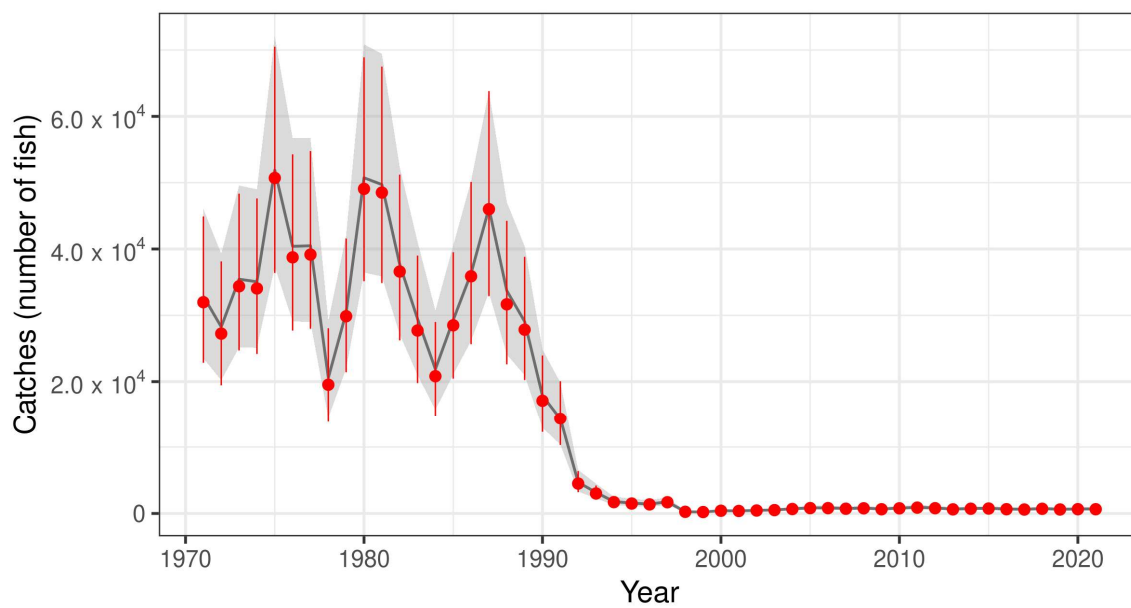
10.3 Catches at sea

10.3.1 LB/Newfoundland in SFA zones (3-7) (NAC fish only; no allocation among SU)

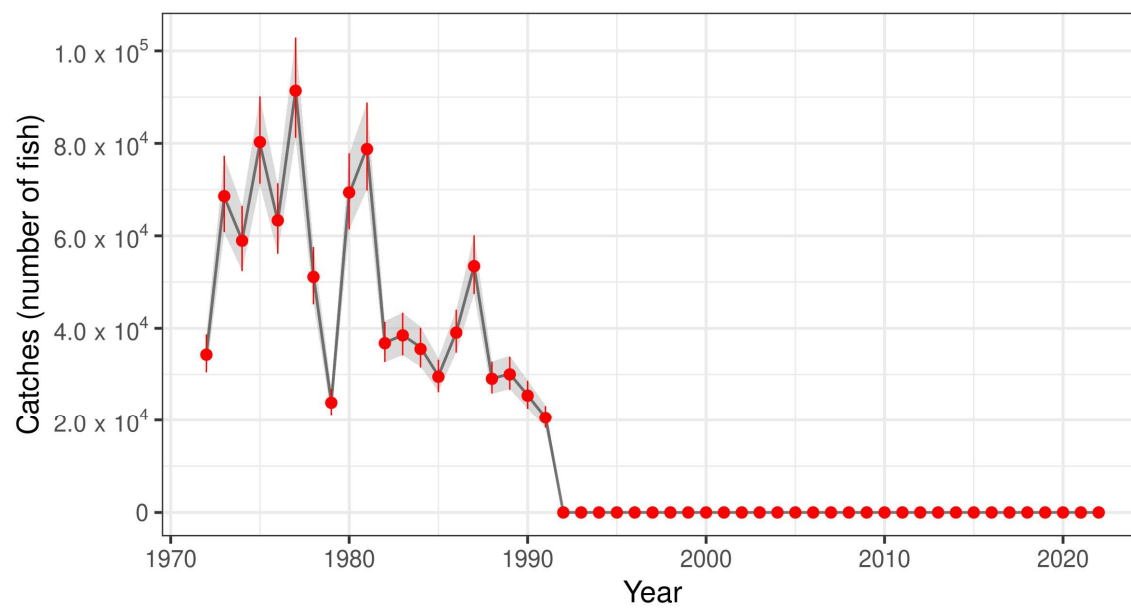
10.3.1.1 1SW mature



10.3.1.2 1SW non mature

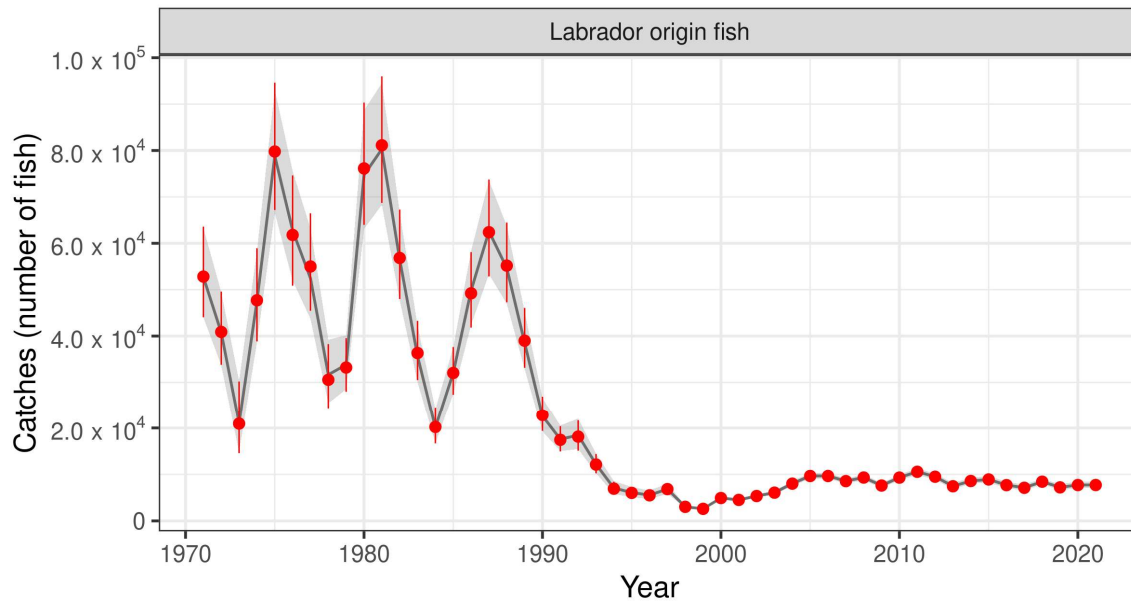


10.3.1.3 2SW

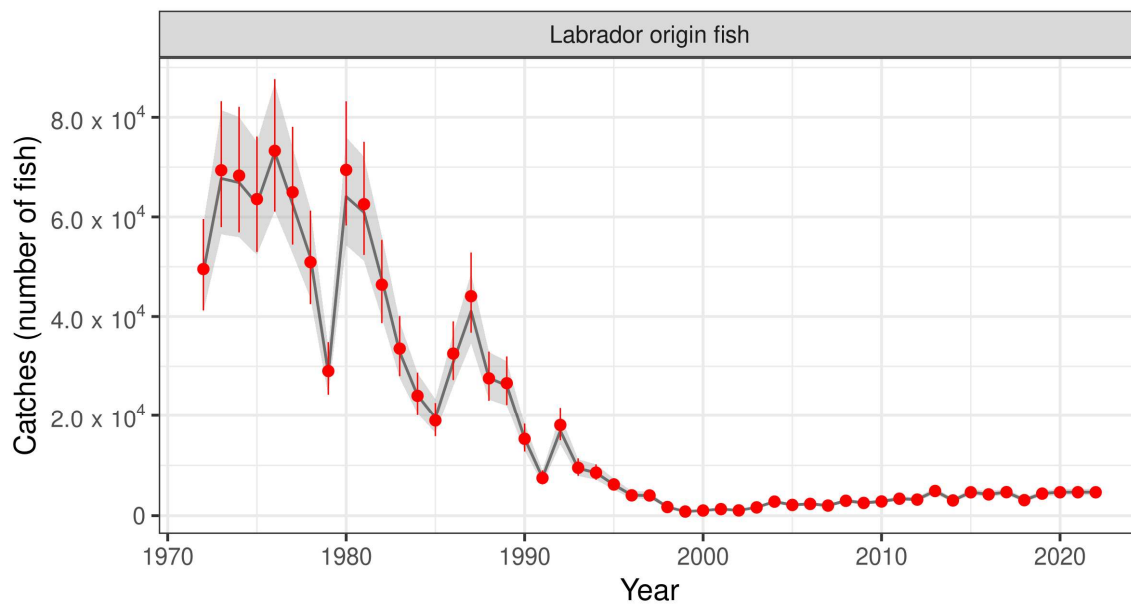


10.3.2 LB/Newfoundland/SPM – SFA zones (8-14) (NAC fish only; allocation fish from Labrador / other SU)

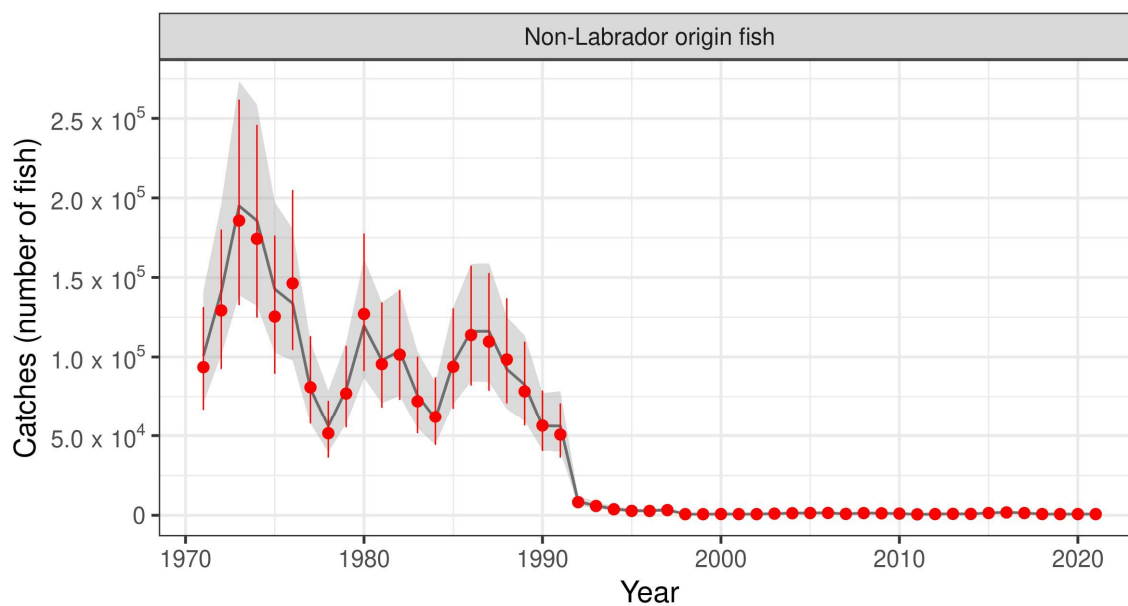
10.3.2.1 Labrador origin in the catches - 1SW mature



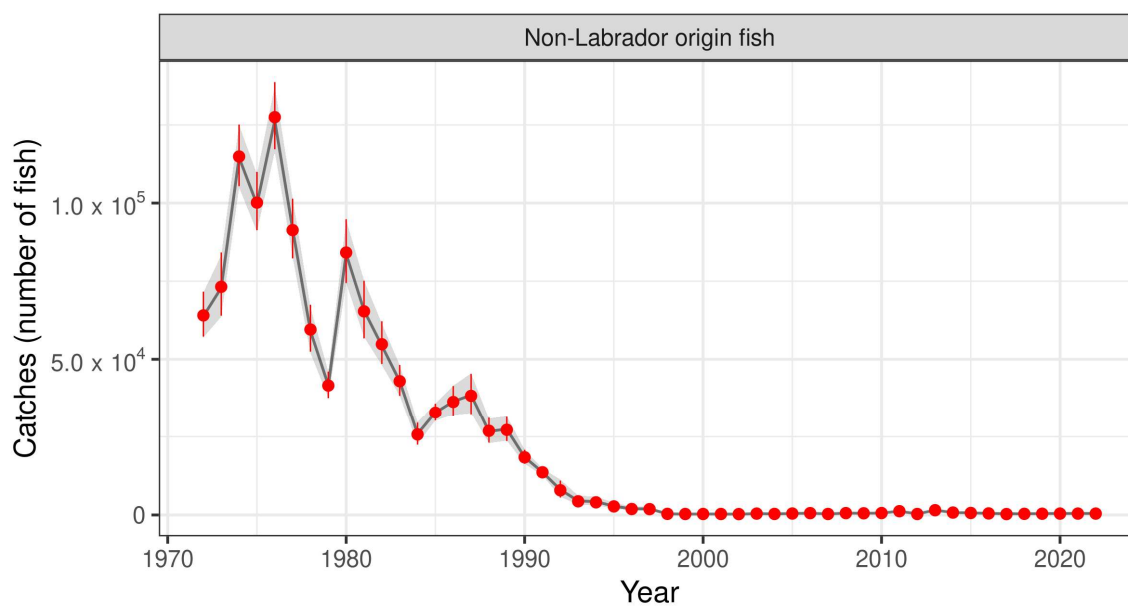
10.3.2.2 Labrador origin in the catches - 2SW



10.3.2.3 Non Labrador origin fishes in the catches - 1SW mature

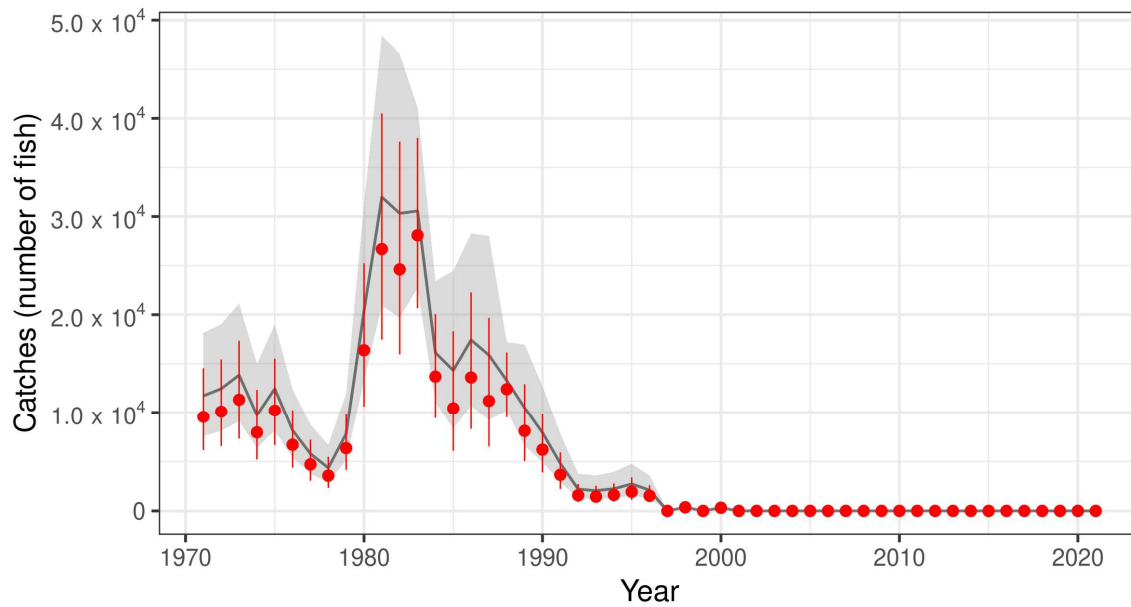


10.3.2.1 Non Labrador origin fishes in the catches - 2SW

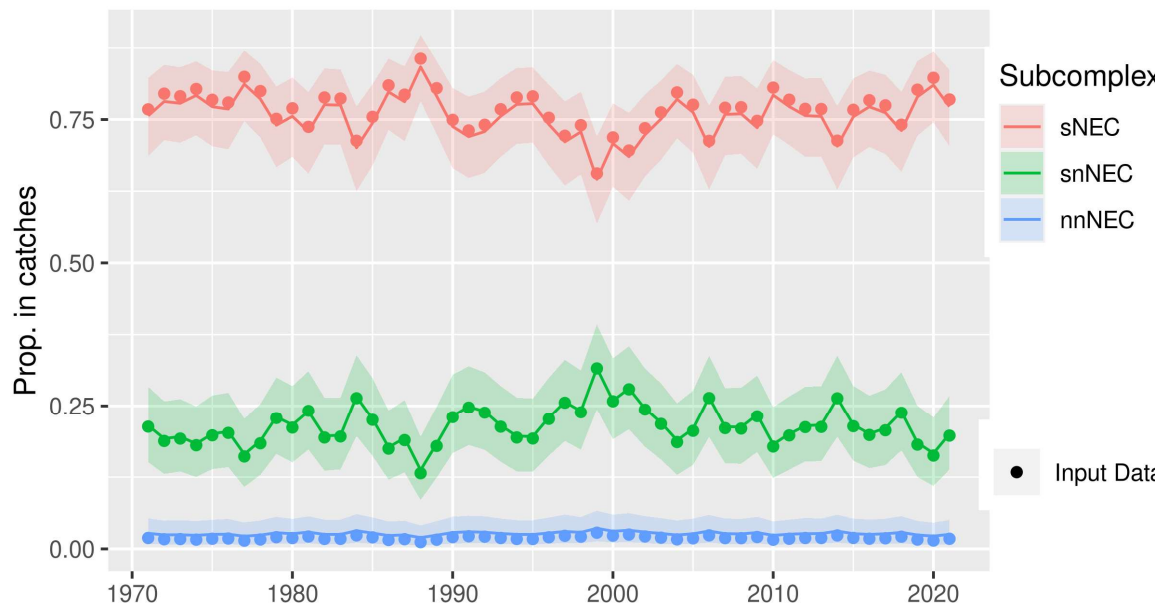


10.3.3 Faroes Fisheries (NEAC fish only)

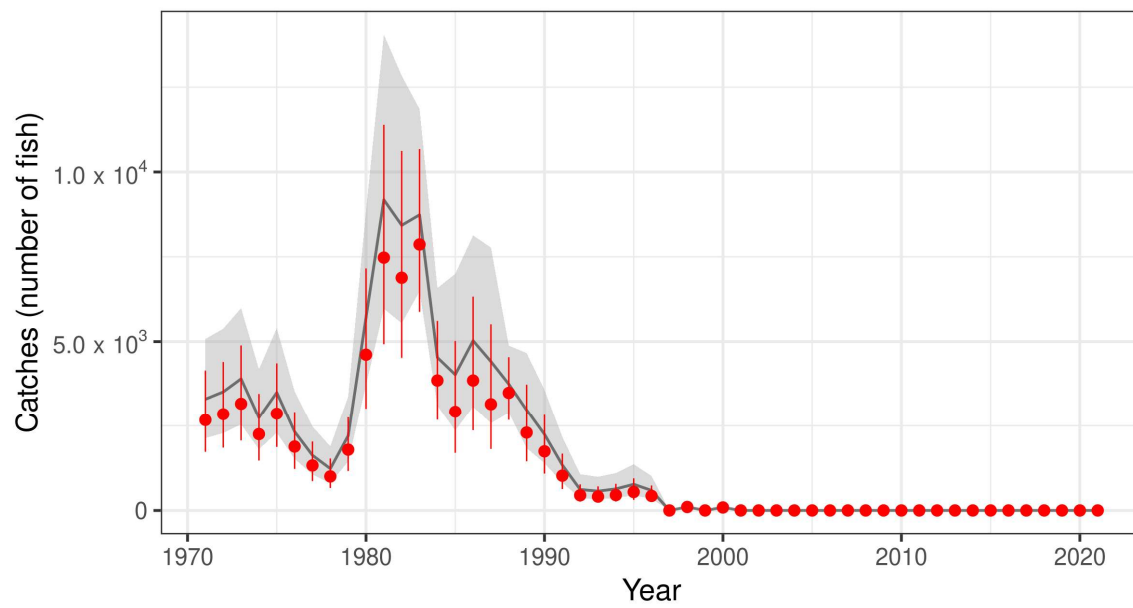
10.3.3.1 Total catches - 1SW mature



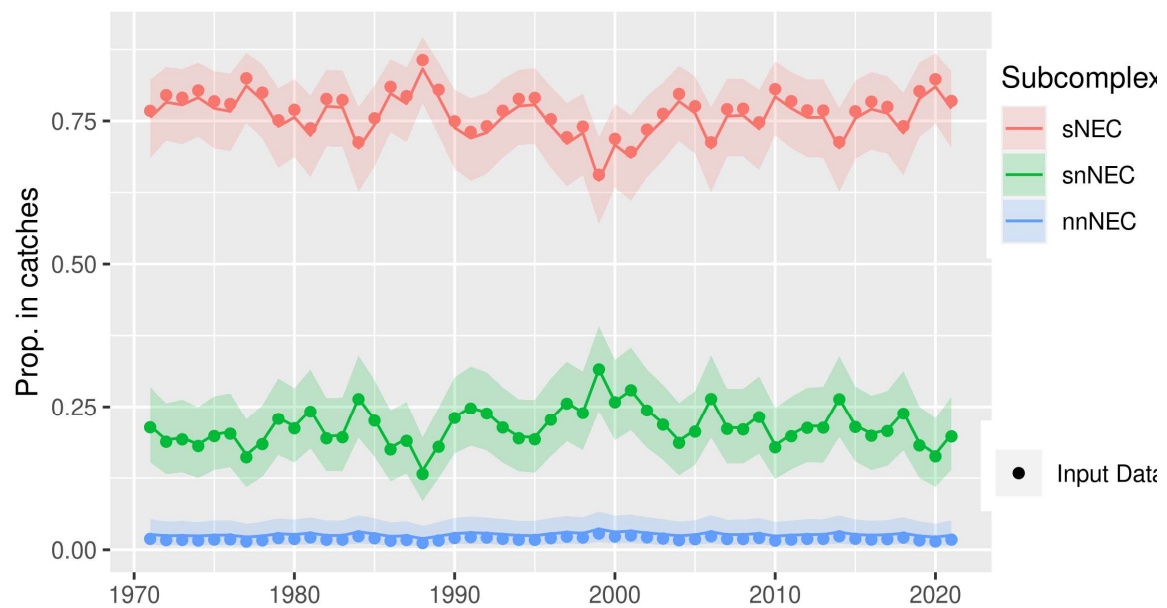
10.3.3.1 Proportions originated from the three sub-complexes – 1SW mature



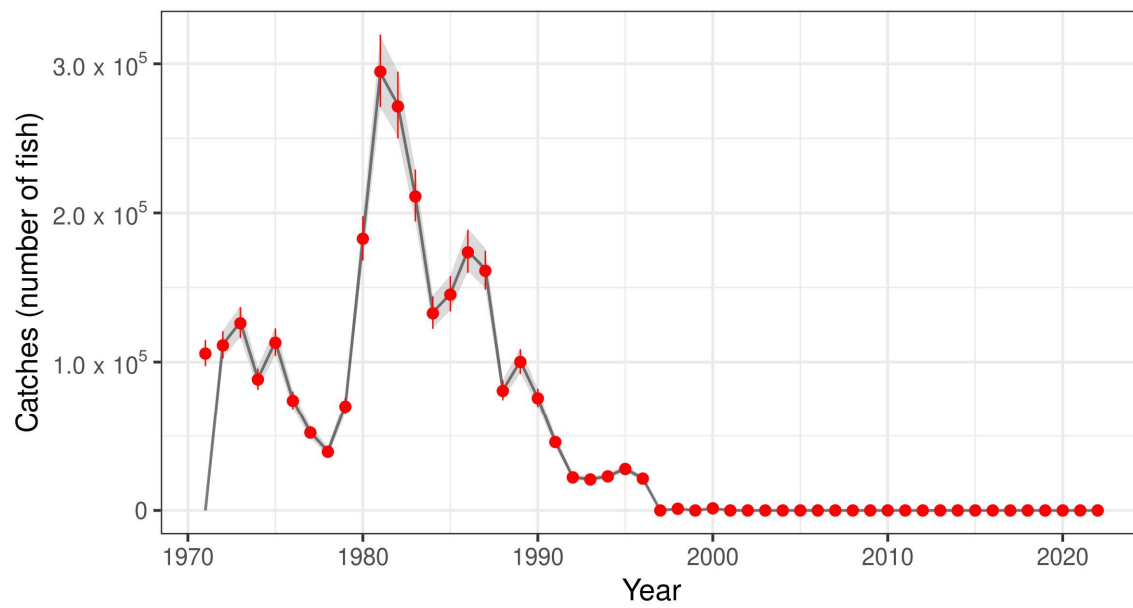
10.3.3.2 Total catches - 1SW non mature



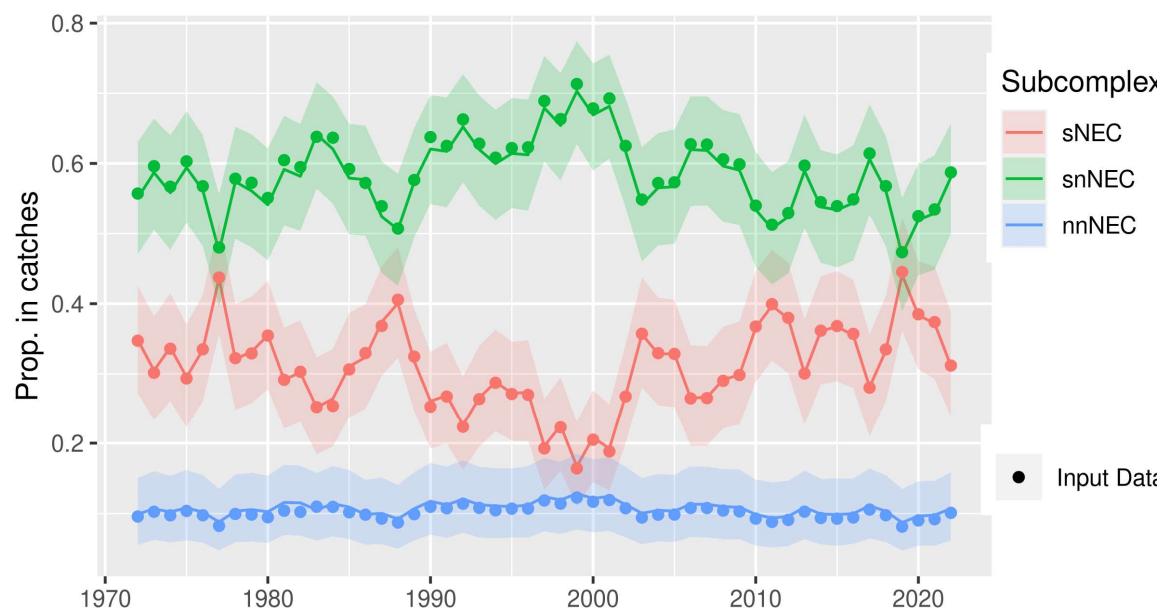
10.3.3.1 Proportions originated from the three sub-complexes – 1SW non mature



10.3.3.2 Total catches - 2SW

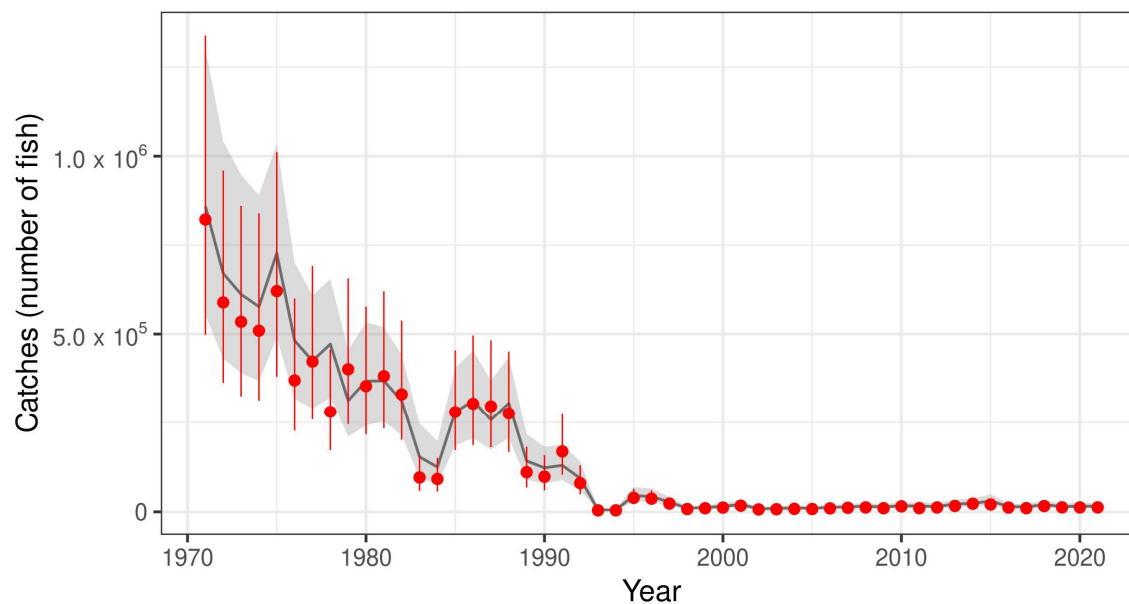


10.3.3.1 Proportions originated from the three sub-complexes – 2SW

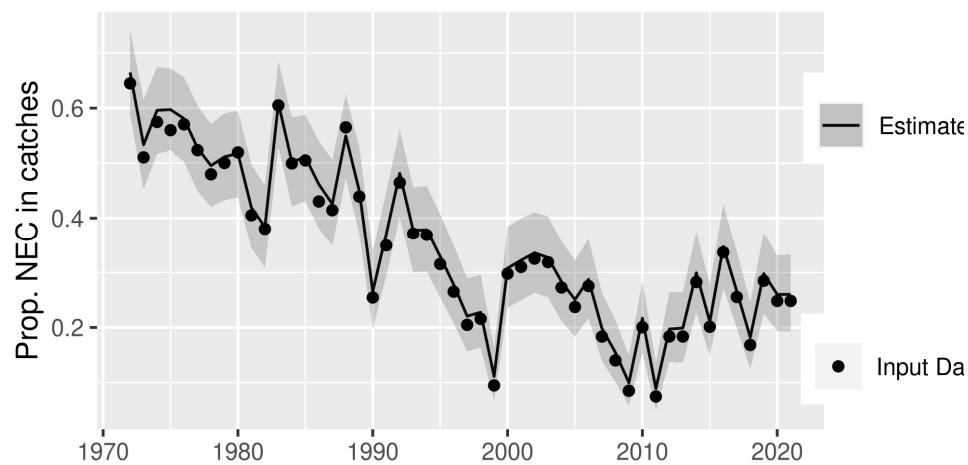


10.3.4 West Greenland Fisheries (NAC and NEAC fish)

10.3.4.1 Total Catches - 1SW non mature



10.3.4.2 Proportions to allocate among NEAC/NAC



10.3.4.3 Proportions to allocate among Southern/Northern NEAC within NEAC fish

