Supplement 1: Raw results from fitting Von Bertalanffy growth curves

Table S1: Overview of the length-at-age data from the NS-IBTS SMALK data used for fitting the Von Bertalanffy growth model. Between brackets it is indicated which years for the model fit were subsequently used for further analysis.

|	area 1	area 2	area 3	area 4	area 5	area 6	area 7	area 8	area 9	area 10
Plaice	2007-2021 (2010-2013, 2015, 2017-2020)	2004-2021 (2008-2020)	2007-2021 (2007, 2009-2020)	1992-2021 (1992, 1993, 2003, 2006-2020)	1992-2021 (1992, 2008-2020)	1992-2021 (1992, 1993, 2003-2020)	1991-2021 (1991-1993, 2003-2020)	1991-2021 (all)	1991-2021 (all)	2008-2021 (2009-2020)
Witch	omitted	omitted	omitted	omitted	omitted	omitted	omitted	2005-2021 (2009-2020)	2011-2021 (2011, 2012)	omitted
Herring	1971-2021 (1972, 1974, 1975, 1977-2020)	1965-2021 (1965-1977, 1979-2020)	1967-2021 (1971-2020)	1966-2021 (all)	1967-2021 (1968, 1970-2002, 2005-2008, 2011-2020)	1965-2021 (1966-2020)	1966-2021 (all)	1967-2021 (1967, 1971, 1975-1978, 1980-2020)	1972-2021 (1975-2020)	2007-2021 (2009-2020)
Sprat	1978-2021 (1986, 1990, 1994, 1996, 1997, 2001)	1975-2021 (1977-1979, 1982-1986, 1988-1990, 1992-2004, 2010-21013, 2015, 2020)	1974-2021 (1977-2020)	1975-2021 (1975, 1976, 1979-1991, 1993-2020)	1976-2021 (1978, 1979, 1982-2020)	1976-2021 (all)	1975-2021 (1975-1977, 1980, 1982-1990, 1995-2020)	1972-2021 (1972-1981, 1984-1995, 1998-2020)	1972-2021 (1992-1975, 1978-1979, 1984-2020)	2007-2021 (2007-2018)
Mackerel	1978-2021 (1984, 1987, 1991, 1992, 1996-2020)	1978-2021 (1990, 1997, 1998, 2001-2003, 2012-2020)	1977-2021 (1983, 1997, 2001-2003, 2006, 2007, 2011, 2012, 2016, 2017, 2019, 2020)	omitted	omitted	1976-2021 (1977, 2015, 2018, 2020)	1978-2021 (2017-2020)	2018-2021 (2020)	omitted	2012-2016 (2012,2013)
Norway pout	1972-2021 (1976-2020)	1976-2021 (all)	1972-2021 (1974, 1977-2020)	1974-2021 (all)	omitted	omitted	1976-2021 (1976-1978, 1983-1985, 1987-1990, 1995, 1998, 2001, 2002, 2004, 2006, 2009-2013, 2015-2020)	1974-2021 (1974, 1975, 1991, 1995-1997, 2002-2020)	1991-2021 (1991, 1995-1997, 2002-2020)	omitted
Saithe	1977-2021 (1980, 1984, 1986, 1989, 1992-2020)	omitted	omitted	omitted	omitted	omitted	1981-2021 (1995-1999, 2012, 2014)	2003-2021 (2003-2006, 2009. 2013, 2014, 2017, 2018, 2020)	omitted	omitted
Whiting	1971-2021 (all)	1967-2021 (1971-2020)	1971-2021 (all)	1971-2021 (all)	1973-2021 (all)	1967-2021 (1971-2020)	1967-2021 (1971, 1974-2020)	1974-2021 (1974, 1975, 1978, 1991-1997, 2013-2020)	1991-2021 (1991-1997, 2013-2020)	2007-2021 (all)
Haddock	1971-2021 (all)	1967-2021 (1971-2020)	1971-2021 (all)	1972-2021 (all)	1973-2021 (1978-1980)	1972-2021 (1972-1986, 2001, 2002, 2020)	1957-2021 (1972-2017, 2019-2020)	1974-2021 (1980, 1991-1996, 2000-2020)	1991-2021 (2000-2018, 2020)	omitted
Cod	1973-2021 (all)	1972-2021 (1973, 1975-2020)	1972-2021 (1974-2020)	1971-2021 (1971-2004, 2006-2008, 2010-2020)	1972-2021 (1972-2004, 2007-2016)	1971-2021 (1971, 1973-2020)	1971-2021 (all)	1974-2021 (1974, 1975, 1978, 1980, 1981, 1985, 1986, 1991-2020)	1981-2021 (1981, 1985-2020)	2007-2010 (2007-2015)
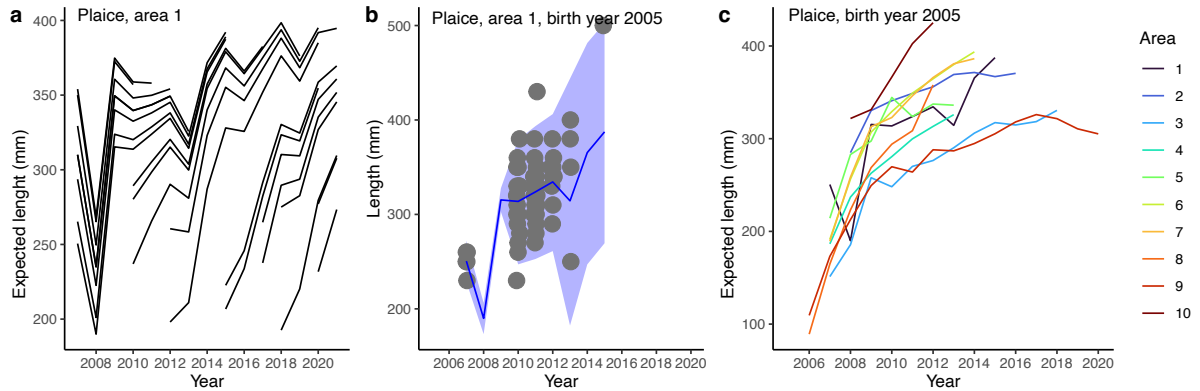
Figure S1: Overview of model predictions for plaice in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph. c) The right panel shows the predicted average length at age of cohorts born in 2005 in all areas with data.
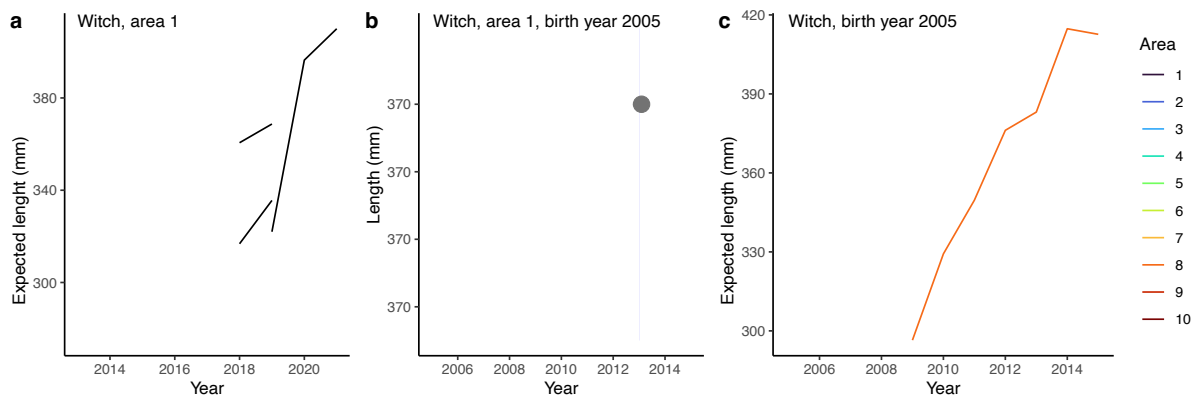

Figure S2: Overview of model predictions for witch in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel does not show a fitted line because the data for witch in area 1 was insufficient to fit the growth model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph. c) The right panel shows the predicted average length at age of cohorts born in 2005 in all areas with data.
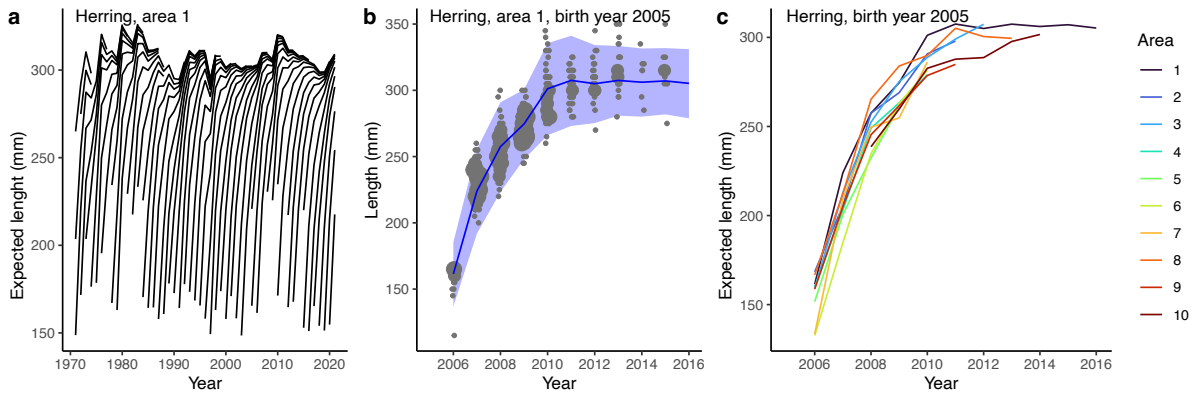
Figure S3: Overview of model predictions for herring in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph. c) The right panel shows the predicted average length at age of cohorts born in 2005 in all areas with data.
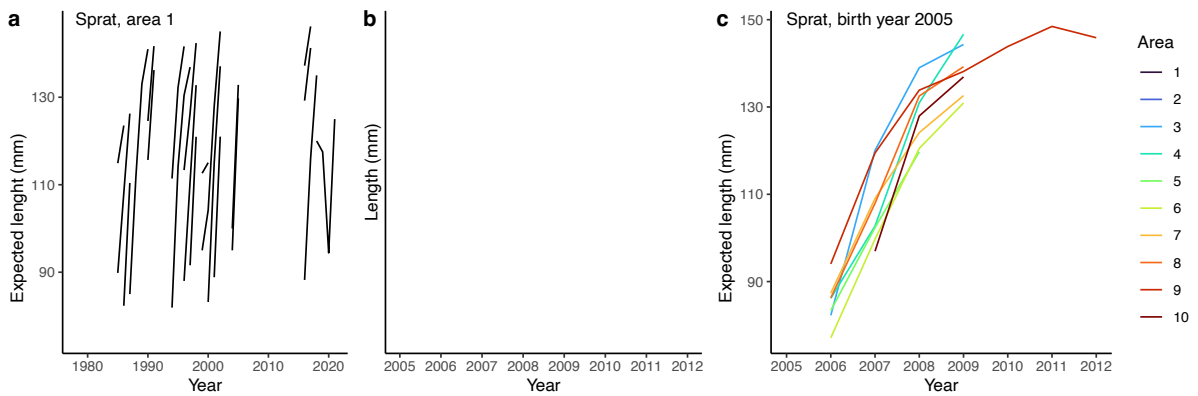

Figure S4: Overview of model predictions for sprat in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel is empty because sufficient length-at-age data for sprat was missing to fit the growth model in area 1. c) The right panel shows the predicted average length at age of cohorts born in 2005 in all areas with data.
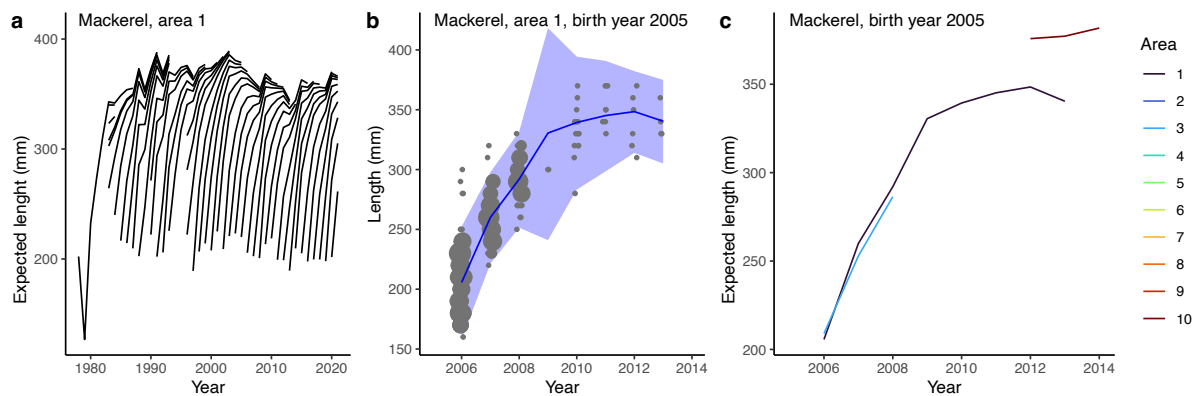
Figure S5: Overview of model predictions for mackerel in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph.
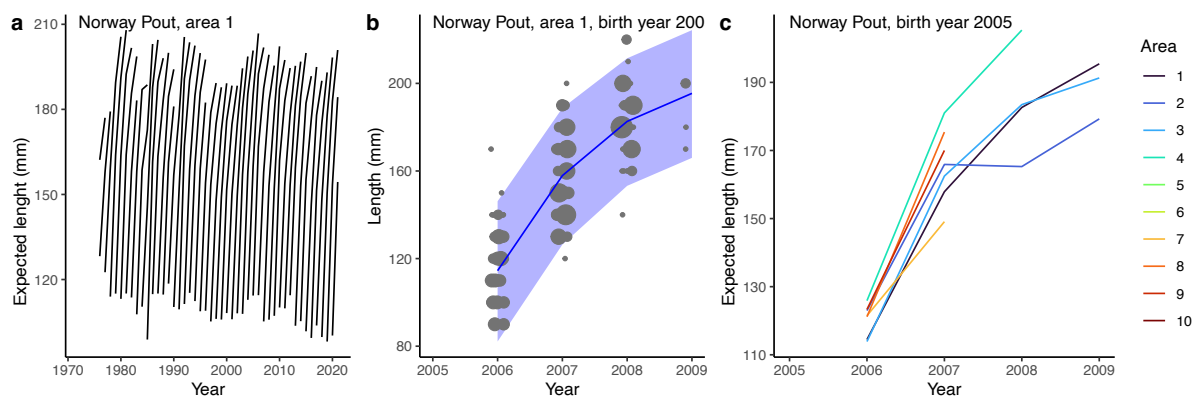

Figure S6: Overview of model predictions for Norway pout in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph.
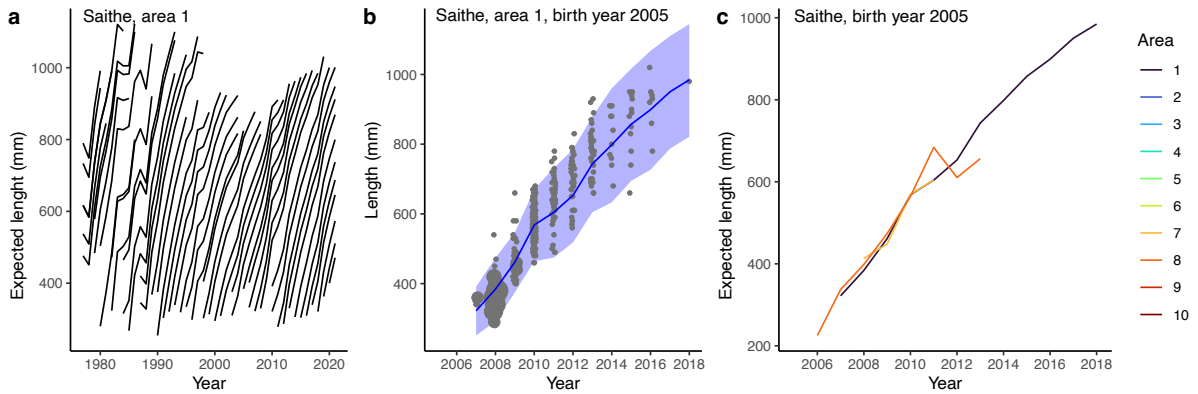
Figure S7: Overview of model predictions for saithe in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph.
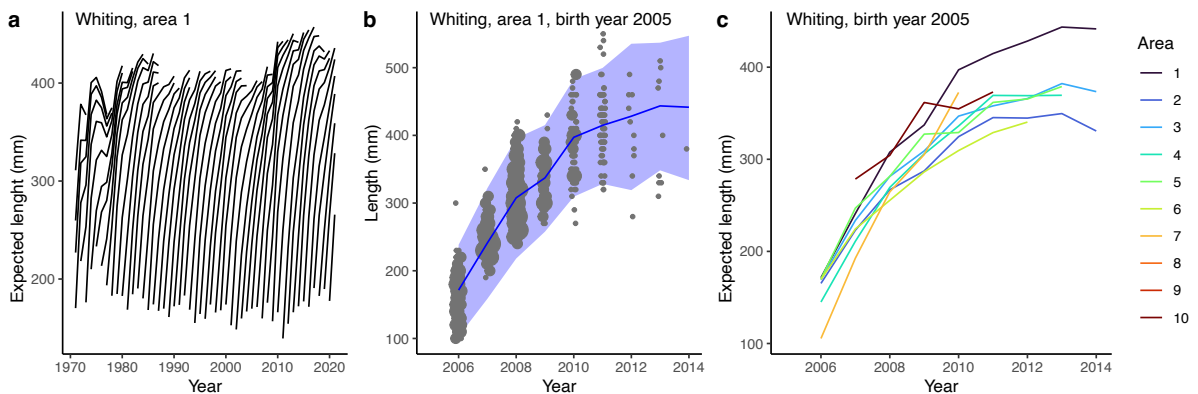

Figure S8: Overview of model predictions for whiting in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph.
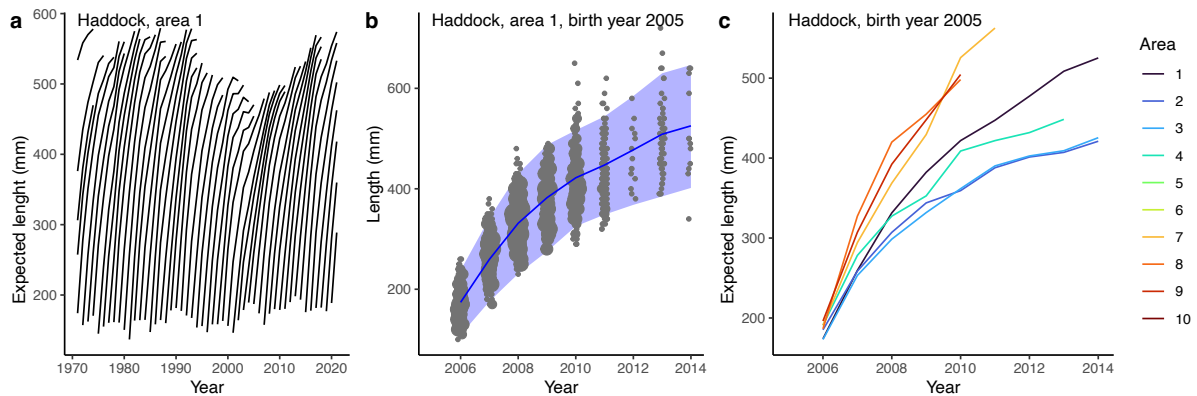
Figure S9: Overview of model predictions for haddock in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph.
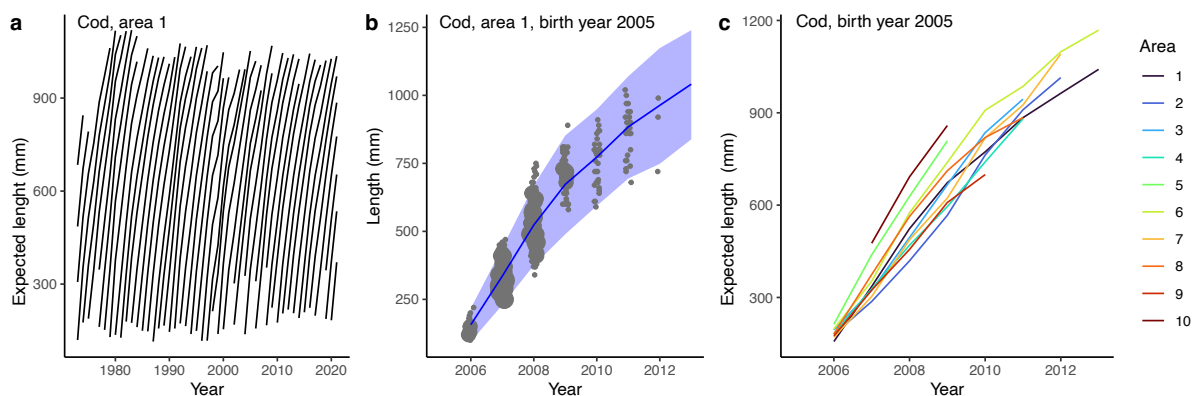

Figure S10: Overview of model predictions for cod in area 1 and cohorts born in 2005 to obtain insight in the Von Bertalanffy growth model. a) The left panel shows the predicted average length-at-age for every cohort in area 1. b) The middle panel shows the predicted average length-at-age of the cohort born in 2005 in area 1 as a blue line. The blue area shows the length range at which the model predicts that 95% of the individuals fall into based on the predicted variance in size-at-age. For comparison, grey dots indicate datapoints from this cohort used for fitting the model. The size of the dots indicates the number of individuals with a specific size and age combination in the given year and cohort in the dataset. Note that data from other cohorts and years also influences the model fit resulting in the predictions shown in the graph.
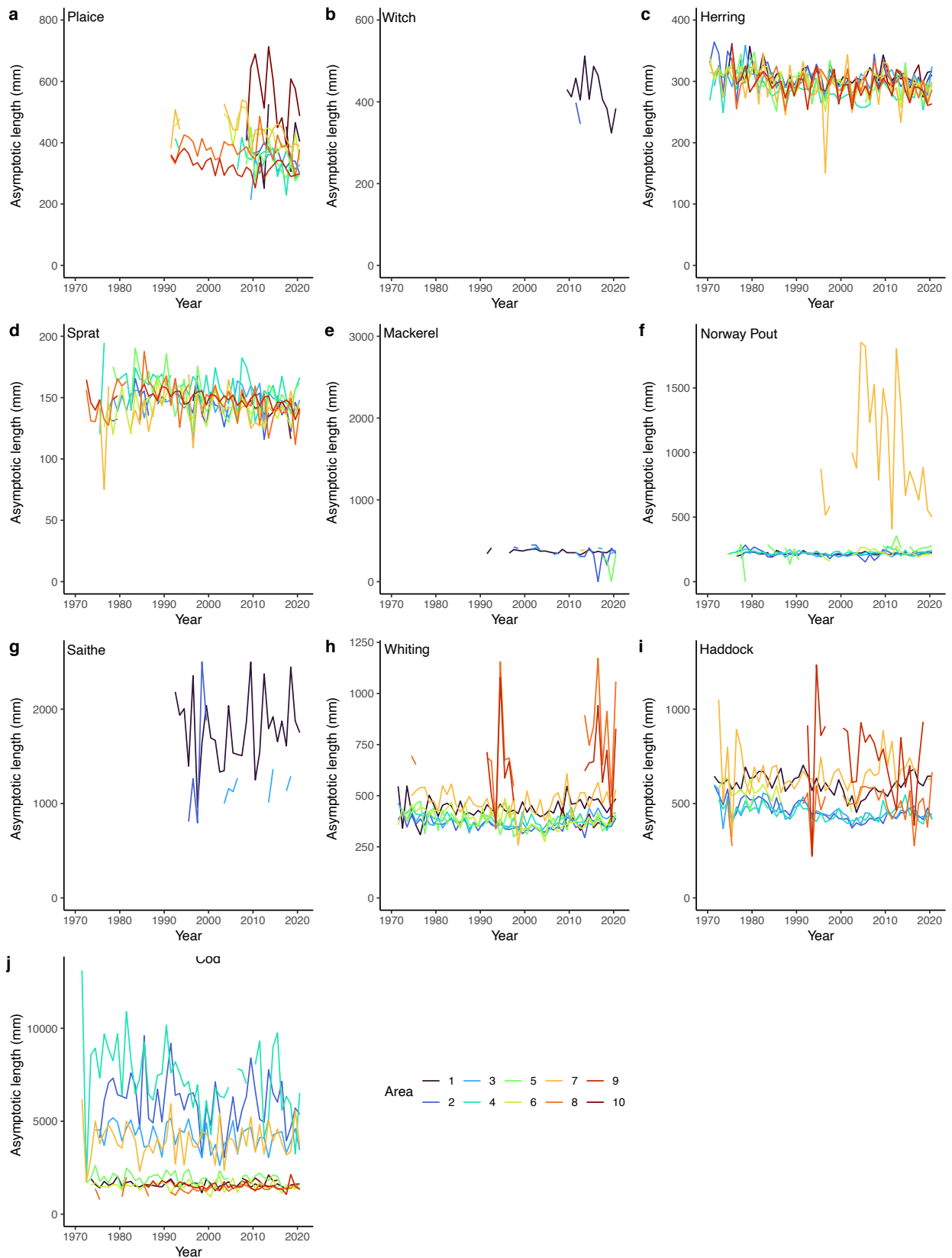
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Figure S11: Fitted annual asymptotic lengths of ten commercially exploited fish species in ten roundfish areas in the North Sea. Time series are interrupted for years in which data was insufficient to provide a reliable estimate of the asymptotic length.

Supplement 2: Correction of asymptotic size to obtain the corrected EGC

The fitted asymptotic length must be corrected to be comparable between areas and species. The first correction deals with the spurious relationship between the fitted asymptotic length and the von Bertalanffy growth scalar. The correlation between the value of the asymptotic length and the growth scalar is corrected by fitting a linear regression with the equation:

$$\bar{\mu}_{T,area}\ell_\infty \sim \alpha_0 + \alpha_1\, 1/r_{B_{area}} + \epsilon_{T,area} \qquad\qquad \text{(eq S2.1)}$$

In which α_0 and α_1 represent the regression coefficients and $\epsilon_{T,area}$ is the random error term accounting for all unexplained variation. The results of this regression are presented in supplementary figure S2.1. For further analysis, we use the residuals of this linear model. These residuals represent the asymptotic length without the spurious correlation with the growth scalar can be calculated as:

$$R_{T,area} = \bar{\mu}_{T,area}\ell_\infty - \alpha_0 - \alpha_1\, 1/r_{B_{area}} \qquad\qquad \text{(eq S2.2)}$$

We represent the variation in the residual asymptotic length within an area by the standard deviation of the residuals, calculated as:

$$SD(R_{area}) = \sqrt{\frac{\sum(R_{T,area} - \overline{R_{area}})^2}{n_{area}}} \qquad\qquad \text{(eq S2.3)}$$

in which $\overline{R_{area}}$ is the average residuals in an area and n_{area} is the number of residual asymptotic lengths in an area. The correlation between the variation in asymptotic length is quantified with a regression between this standard deviation of the residuals and the growth scalar is corrected by fitting a linear regression with the equation:

$$SD(R_{area}) \sim \beta_0 + \beta_1\, 1/r_{B_{area}} + \epsilon_{area} \qquad\qquad \text{(eq S2.4)}$$

In which β_0 and β_1 represent the regression coefficients and ϵ_{area} is the random error term accounting for all unexplained variation. The results of this regression are presented in supplementary figure S2.2. The effect of the growth scalar on the asymptotic length is corrected by dividing the residuals by the predicted value from this regression. This corrected quantity is the corrected environmental growth condition (EGC), calculated as:

$$EGC_{corrected} = \frac{\bar{\mu}_{T,area}\ell_\infty - \alpha_0 - \alpha_1 1/r_{B_{area}}}{\beta_0 + \beta_1 1/r_{B_{area}}} \qquad\qquad \text{(eq S2.5)}$$

For comparison between species, this EGC is normalized by subtracting the mean and dividing by the standard deviation of the combined areas for every species.

$$EGC_{normalized} = \frac{\overline{EGC}}{SD(EGC)} \qquad\qquad \text{(eq S2.6)}$$

In which $\overline{EGC}$ is the mean environmental growth conditions for all years and areas of a species combined and $SD(EGC)$ is the standard deviation in environmental growth conditions for all years and areas of a species combined, calculated as:

$$SD(\overline{EGC}) = \sqrt{\frac{\sum(\overline{EGC} - \overline{\overline{EGC}})^2}{n_{spec}}} \qquad\qquad \text{(eq S2.7)}$$

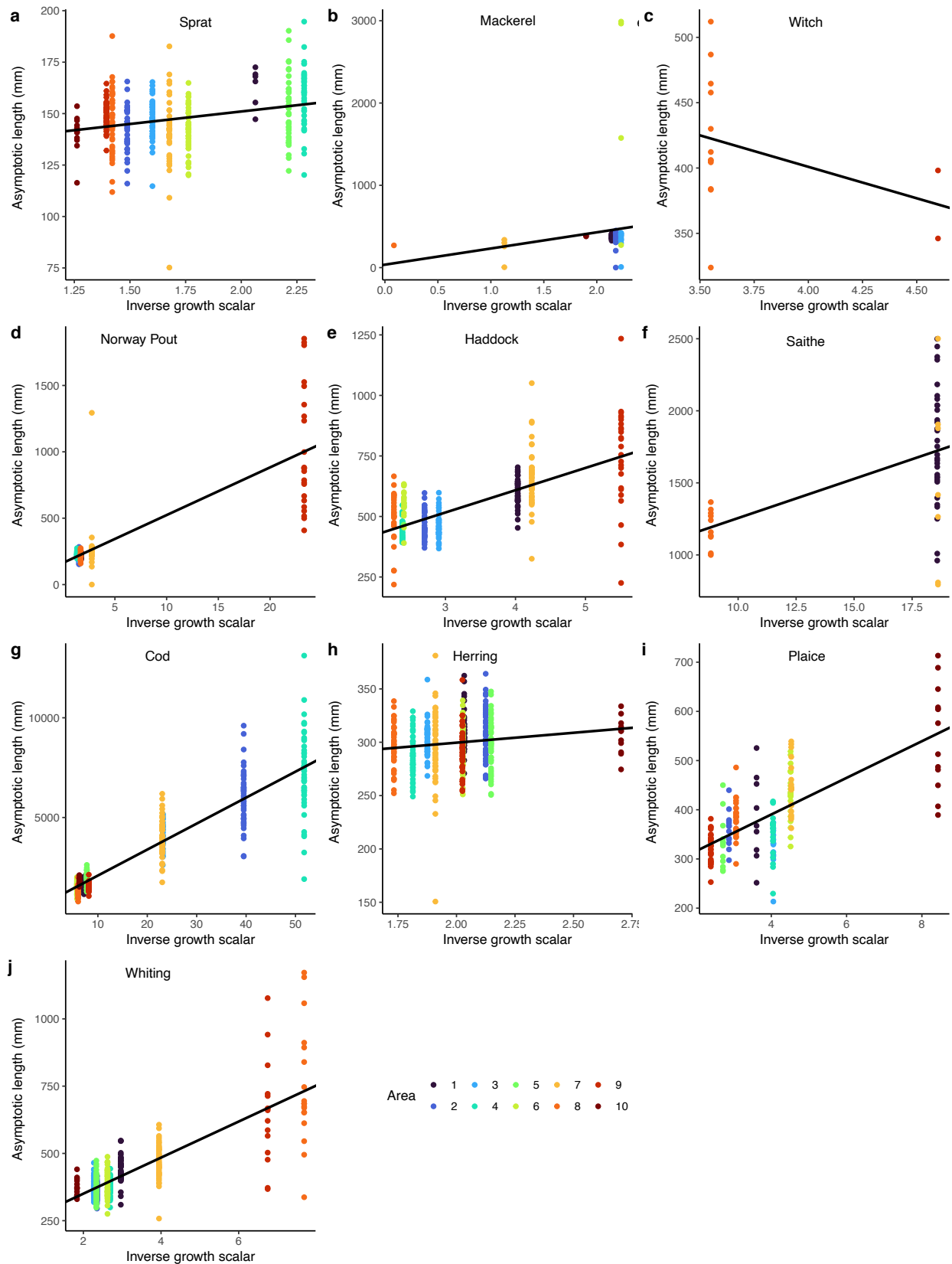in which n_{spec} is the total number of EGC calculated for a species.

Figure S12: linear relationship describing the spurious correlation between the fitted asymptotic length and the inverse of the growth scalar as used to calculate the corrected environmental growth conditions for the ten fish species in ten roundfish areas.
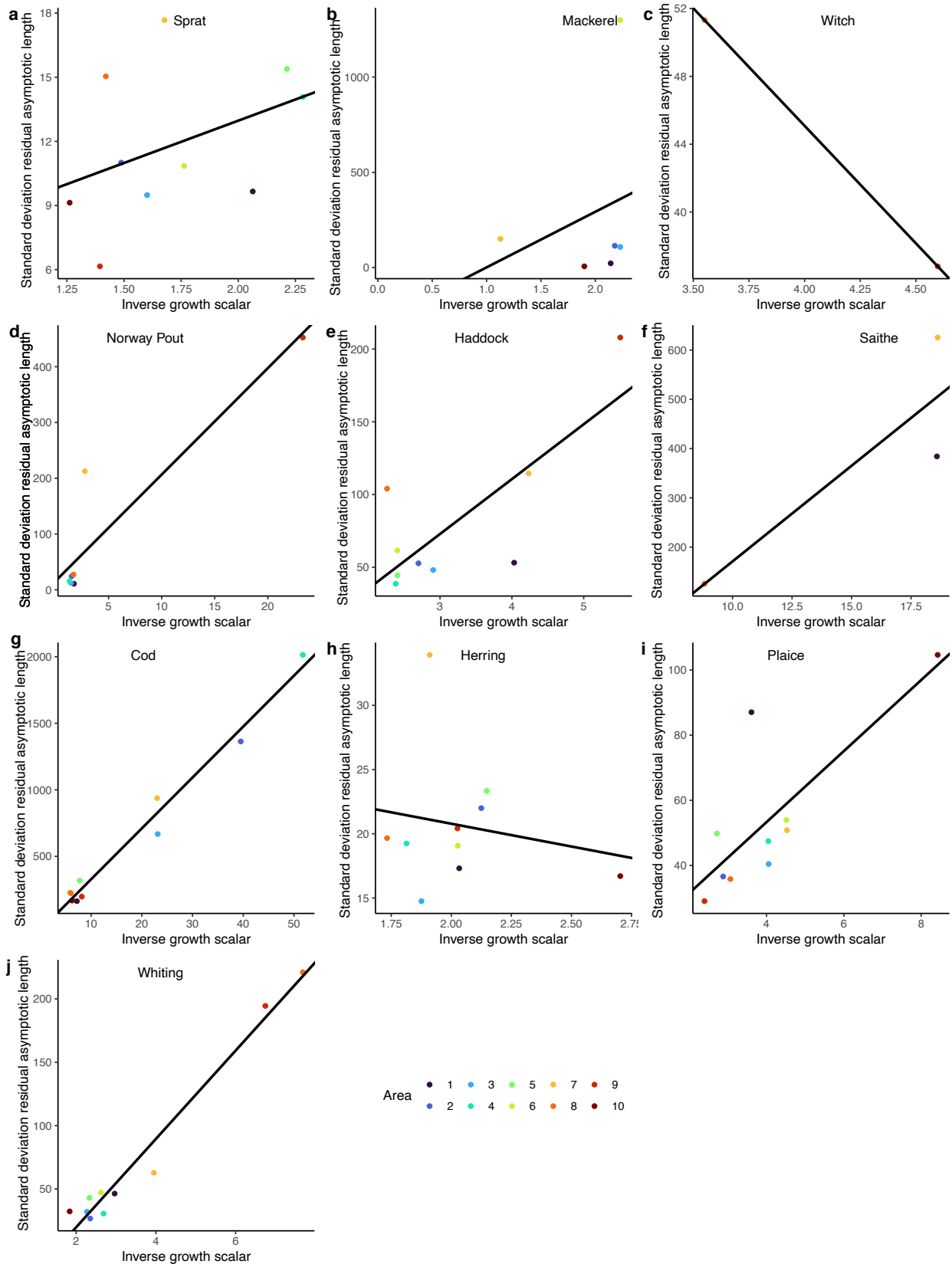
Figure S13: linear relationship describing the spurious correlation between the variation in asymptotic length represented as the standard deviation in the residual asymptotic length per area and the inverse of the growth scalar as used to calculate the corrected environmental growth conditions.

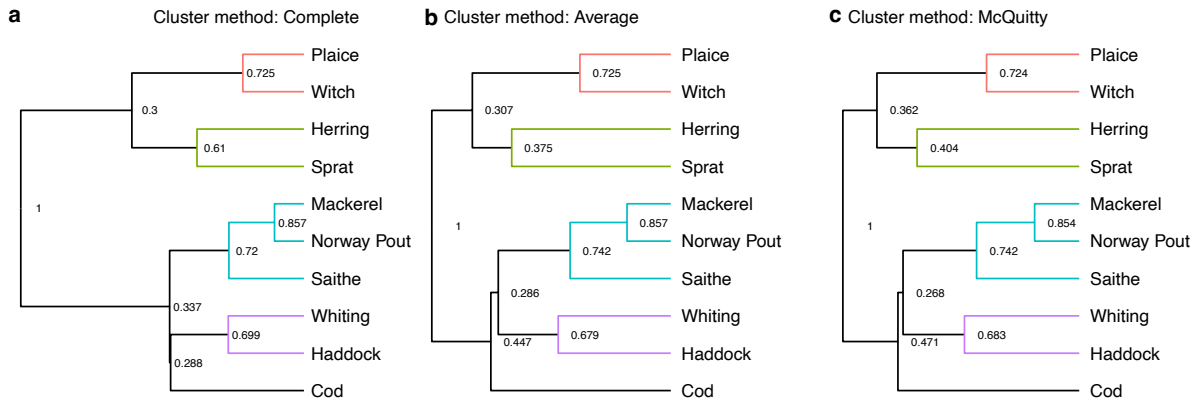## Supplement 3: Clustering results from all three methods

Figure S14: Clustering of ten North Sea fish species based on the normalized environmental growth condition for three different cluster methods. Small digits show the bootstrap probability, which is the fraction of bootstrap repeats in which a branch contained the depicted species. Coloured branches show clusters which arise in all clustering methods.
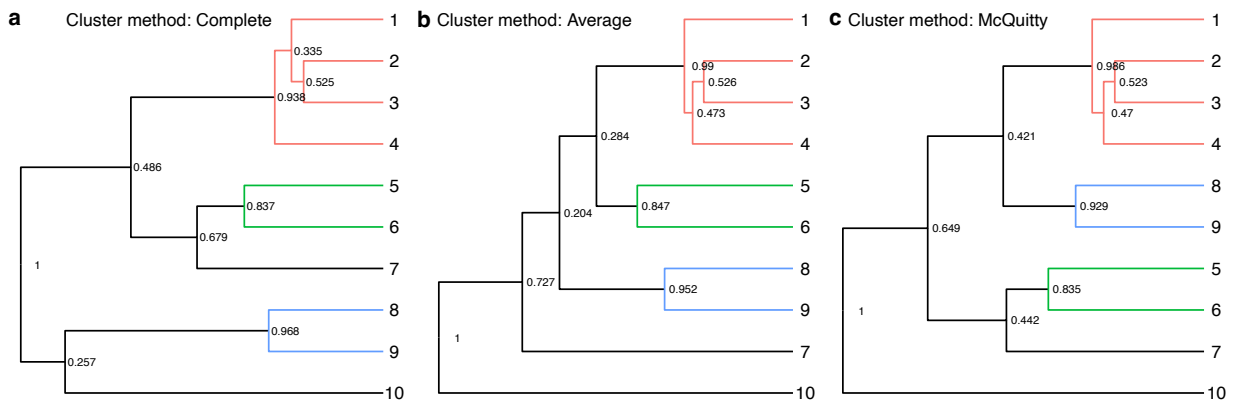

Figure S15: Clustering of ten roundfish areas based on the normalized environmental growth condition for three different cluster methods. Small digits show the bootstrap probability, which is the fraction of bootstrap repeats in which a branch contained the depicted areas. Coloured branches show clusters which arise in all clustering methods.

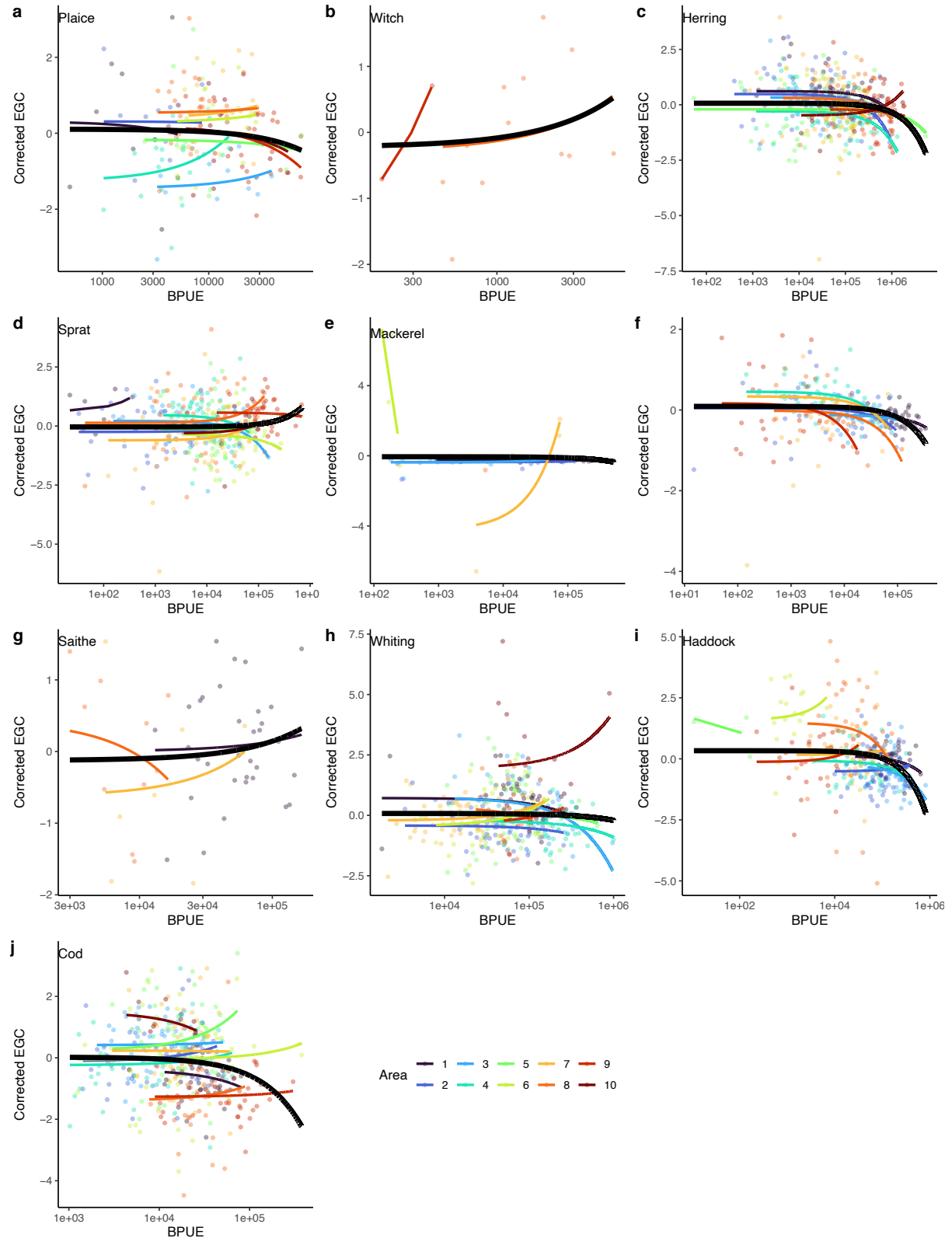**Supplement 4: Correlation between corrected EGC and BPUE**

Figure S16: Version of main figure 5 with logarithmically scaled axes showing the linear regression between the corrected EGC and the BPUE. Coloured lines show linear regressions for every area separately, while thick black lines show the linear regression of the corrected EGC with BPUE for all areas combined. circles indicate the datapoints on which the linear regression lines are based. Note that the regression lines show linear regressions but appear curved in these graphs due to the log-transformation of the BPUE axes