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Executive Summary
<p>This report records the outcomes of the workshop on modelling data requirements held on 10-11 March 2019 (MEESO Milestone 18). The workshop brought together representatives of the research groups working on the four models being deployed in MEESO Work-package 5 (Estimating mesopelagic resources and their resilience to harvesting and climate change). The models are the S6 stock assessment model, the single-species spatial population model StrathSPACE, the NORWECOM.E2E end-to-end ecosystem model, and the global mid-trophic-level SEAPODYM-MTL model. Based on the presentations given at the workshop, this report gives an overview of the models and identifies input parameters and fitting data required for each model. The intention is that this report forms a basis for the wider MEESO community to comment on, or make suggestions regarding, the modelling work, and especially to maximise the possibility of new data gathered by the project being directly inputted to the modelling effort. Each of the models have different specific data requirements, but a common feature is the need for good estimates of the length distributions of the stocks of the target species (<i>Maurollicus muelleri</i> and <i>Benthoosema glaciale</i>) and information on individual growth rates.</p>



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1. Introduction

On March 10-11, 2020, a workshop was convened to discuss the data requirements of the models used in MEESO Work Package 5 (WP5: Estimating mesopelagic resources and their resilience to harvesting and climate change). This workshop was MEESO Milestone 18 (MS18), and this report of it is MEESO Deliverable 5.1 (D5.1). The workshop was originally scheduled to be held at Strathclyde University (STRATH) at its Ross Priory conference venue. However, the lead-up to the event coincided with increasing concerns about international travel during the deteriorating situation of the coronavirus (COVID-19) pandemic. Although official travel restrictions had yet to be implemented at that point, they were anticipated. The workshop participants unanimously agreed that the workshop should be re-arranged as a virtual meeting, which went ahead online on the same dates.

The main purpose of the meeting was to get together representatives from each of the four groups doing modelling work in WP5 in order to discuss the data requirements for each model. The agenda for the meeting is supplied in Appendix 1, and a list of participants is supplied in Appendix 2. There were four main sessions, each focussing on presentations about the four main models being deployed in WP5. Additionally, the meeting heard a presentation by Silvia Paoletto (DTU) on her ongoing work she reviewing the published literature on the biology of *Maurolicus muelleri*, one of the two programme target species.

The four models that formed the basis for the workshop presentations and discussions, and which are presented in more detail the following sections, are S6 (Developed by DTU), StrathSPACE (STRATH), NORWECOM.E2E (IMR), and SEAPODYM-MTL (CLS). Broadly, these form a progression in model complexity, and deliver distinct outputs for the programme. The S6 model is a single species stock assessment model designed to provide information on stock status based on minimal data i.e. data poor situations. The StrathSPACE model is also a single species model, but it is spatially explicit and includes transport (water currents) and temperature effects from physical models. It is not a stock assessment model, but can be used to explore spatial scenarios of harvesting. The NORWECOM.E2E model is a spatial ecosystem model, hence unlike the single species model it can be used to explore the wider, food-web level, impacts of harvesting. The SEAPODYM-MTL model is also a spatial ecosystem model, but one with a focus on highly migratory top predators (Atlantic albacore), and hence may be used to explore the effects of harvesting mesopelagic stocks on this commercially important group.

The main purpose of this report is as a resource for the wider MEESO programme in order to maximise the possibility of new data gathered by the project being directly inputted to the modelling effort. A secondary purpose is to give an overview of the models at a level of detail that is beyond that possible in the project proposal. This will provide a basis for other participants to comment on, or make suggestions regarding, the modelling work. To this end, the following sections will briefly outline the main elements of, and identify the parameters required for, each of the four models.



2. The S6 Model (Alex Kokkalis, DTU)

The S6 model is a single-species stock assessment model motivated by the need to manage data-limited stocks using only size-based estimation of biological reference points. The underlying theory was proposed by Anderson and Beyer (2013), and developed in further applications by Kokkalis et al. (2014), and Kokkalis et al. (2017). It is available as an R package, on the GitHub software development platform (<https://github.com/alko989/s6model>).

The theory is based on individual body size and uses a species independent set of life-history invariants, which together with the asymptotic body weight define the stock. Growth is described by a von Bertalanffy-type of growth equation and natural mortality is size-dependent. Recruitment is described by a Beverton–Holt stock-recruitment function and the theory provides a prediction of the parameter that determines the steepness of the recruitment function.

A key assumption of the model is that the stock is at a steady state, i.e. that the stock biomass is not fluctuating in time due to variations in recruitment or mortality. For our currently unexploited target species (*Maurolicus muelleri* and *Benthoosema glaciale*) this is as likely to be true as for any fish stock. In essence, it can be shown that the steady state of the size spectrum ($N(w)$, number density at weight w) is given by

$$N(w) = \frac{R}{g(w)w_r} \exp\left(-\int_{w_r}^w \frac{\mu(x)}{g(x)} dx\right) \quad (1)$$

where R is the (steady state recruitment), w_r is the weight of a recruit (egg size), $g(w)$ is the growth of an individual as a function of size, and $\mu(w)$ is the mortality rate as a function of size. Growth depends on assimilation and losses to activity and maturation according to

$$g(w) = A w^n - \epsilon_a w - \epsilon_r \psi_m(w) w$$

where A is the a growth constant, n is an allometric exponent, ϵ_a is the allocation to activity, ϵ_r is the recruitment efficiency, and $\psi_m(w)$ is the maturity ogive (the proportion of the population mature at size). The size dependence of the mortality rate is given by

$$\mu(w) = aA w^{n-1} + F\psi_F(w)$$

where a is the physiological mortality parameter, F is the fishing mortality scalar and $\psi_F(w)$ is the size-dependent selectivity.

By applying species-independent life-history invariants it is possible (see Andersen and Beyer, 2013) to define the recruitment rate, R , in terms of the other parameters of the model. The model is further simplified by assuming a characteristic sigmoid curve for the “switching” functions giving the maturity ogive $\psi_m(w)$ and for the fishing selectivity $\psi_F(w)$. These are defined by a body size η_m at which 50% of the population is mature, and a body size η_F at 50% retainment by fishing gear (both expressed as proportional to the asymptotic body weight, W_∞), and corresponding



parameters defining the width of the curves (u_m, u_F). These simplifications allow the number of input parameters to be reduced to those given in Table 1.

Table 1. *Input parameters for the S6 model.*

Symbol	Description	Units
a	physiological mortality	dimensionless
A	growth parameter	$g^{-n}y^{-1}$
η_m	size at maturation relative to W_∞	dimensionless
n	allometric exponent	dimensionless (=3/4)
ϵ_a	allocation to maintenance	dimensionless
ϵ_r	recruitment efficiency	dimensionless
W_r	egg weight	g
u_m, u_F	width of maturity ogive and fishing selectivity function, relative to W_∞	dimensionless

By fitting either the predicted size distribution (Equation 1), or the predicted catch-at-size distribution, to input data the remaining unknown parameters may be estimated (Table 2). The input data is either observed size distributions from surveys, to the size distribution of a commercial catch.

Table 2. *Parameters normally estimated for the S6 model.*

Symbol	Description	Units
F	Fishing mortality	y^{-1}
η_F	50% retainment size relative to W_∞	dimensionless
W_∞	Asymptotic individual weight	g

The main output is normally F/F_{MSY} . If total catch is available it is also possible to estimate spawning stock biomass and recruitment. If data from multiple years are available, each year is treated separately, and a time series subsequently assembled. For example, Figure 1 shows some model validation outputs comparing S6 estimates with those from ICES assessment for two cod stocks.

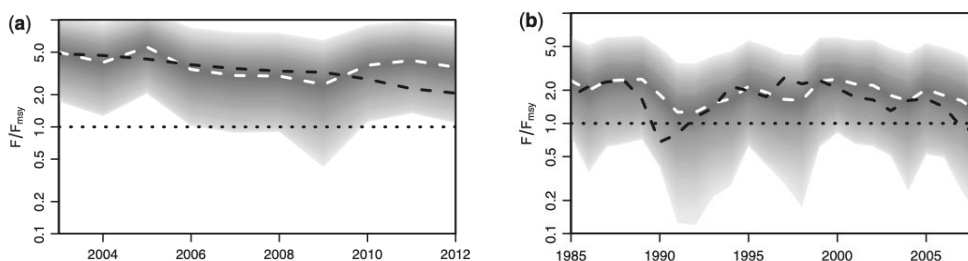


Figure 1. *Example S6 output showing the fishing status of two cod stocks: (a) North Sea, (b) Northeast Arctic, The estimated stock status (median: white dashed line, grey shading: sensitivity level—lighter grey represents higher confidence) compared with the official ICES*

assessment (black dashed line). Fishing at F_{MSY} is shown with the dotted line. From Kokkalis et al. (2017).

For the MEESO mesopelagic stocks, however, there is no existing fishery. This means that the essential input data for the assessments will require sample size distributions - specifically numbers at length from acoustic or catch data from scientific surveys or from catch data from trial fisheries. With F at zero, it may therefore be possible to estimate natural mortality from the size distributions rather than apply the scaling laws. Applications of S6 model typically used a “Robin Hood” approach (robbing estimates of parameters from data rich systems to supply data poor ones) to the input parameters (Table 1), but obviously any species-specific information that would improve values in that table would also be beneficial.

3. The StrathSPACE Model (Douglas Speirs, STRATH)

StrathSPACE is a framework for simulating the combined space and size structured dynamics of a single-species marine population, incorporating the effects of birth, death, growth, active migration and passive transport by water currents. This is achieved by modelling the transfers of numbers of individuals between and along sequences of size classes at each spatial location in a grid covering the model region. Transfer of numbers between different spatial locations to represent active migration or passive drift due to water currents are calculated from the outputs of particle tracking models, which are run separately beforehand. These make use of water flow data and environmental conditions simulated by 3-dimensional hydrodynamic models. Typically, StrathSPACE models are hand-tuned by adjusting a small number of key parameters (2-5) so as to achieve a best-match between model results and observed data. The tuned model is then been compared with other ‘independent’ data that were not involved in the tuning to check for consistency. The general framework has been used to model zooplankton (e.g. Speirs et al. 2006; Wilson, Heath and Speirs 2016) and fish (e.g. Andrews et al. 2006; Heath et al. 2014).

In its MEESO implementation, StrathSPACE will have

- a discrete time and discrete space closed life-cycle population model;
- a single depth layer representing average daily vertical position of the target species;
- a population structured by length (number of individuals per length class);
- growth represented by von Bertalanffy equation, but potentially dependent on temperature and food (e.g. from biogeochemical model outputs such as NEMO-MEDUSA);
- Planktonic larvae (turbulent diffusion and current driven);
- Passive (current driven) and biodiffusive (random movement) of adults.

The driving data required for StrathSPACE are flow fields required to calculate horizontal transport, temperature fields (for temperature dependence of biological processes such as growth), and food fields (for food dependent growth rates). These data from the NEMO-MEDUSA global model are currently being made available by the UK National Oceanography Centre (NOC) for the years 1980-2099, with RCP 8.5



for forward run, for the whole Atlantic. Figure 2 shows a sample projection of the meso-zooplankton functional group for the year 2025.

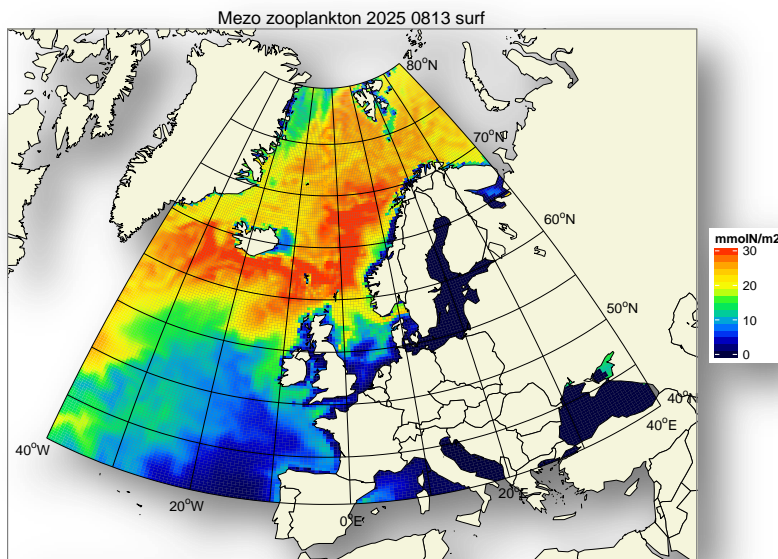


Figure 2. Projected surface layer meso-zooplankton abundance ($\text{mmol Nitrogen}/\text{m}^2$) from the NEMO-MEDUSA biogeochemical model for the year 2025 in the RCP 8.5 climate change forward run. These can be used in the StrathSPACE model as a proxy for food availability.

In addition to the driving data (physical-biogeochemical model outputs), the implementation of the StrathSPACE models for the MEESO target species (*Bethosema muelleri* and *Maurolicus glaciale*) requires input data to parameterize, for both species, the population model itself.

There will be two variants of the model. A basic model, with minimal input data requirements, and a model that includes temperature and food dependence of growth. The input data requirements for the basic StrathSPACE population model are:

- Von Bertalanffy growth parameters (3 parameters: L_0 , L_{inf} , K);
- Beverton-Holt (or Ricker) stock recruitment parameters (2 parameters);
- Natural mortality, possibly length dependent (1 parameter or more if length-dependent);
- Length at maturity (1 parameter or more for a maturity ogive);
- Length-weight relationship (2 parameters).
- Typical (daily-averaged) depth for each species.

Most of these could be obtained from literature, but natural mortality and recruitment are less certain. These could be treated as fitting parameters.

The additional input data requirements for the StrathSPACE population model with temperature-dependent growth are:

- Von Bertalanffy growth parameters from various locations with contrasting temperatures;
- Q10 for metabolic costs;
- Q10 feeding search rate;
- Holling Type II functional response parameters;
- Diet data (gut contents taxa);
- Fecundity (eggs per gramme).

Finally, in addition to the input data, StratSPACE requires fitting (or target) data for all the model variants:

- Sample length distributions (preferably from different contrasting regions);
- Regional total biomass estimates and/or biomass density estimates;
- Any distributional data – geographic range, presence/absence.

All requirements are for both target species *B. glaciale* & *M. muelleri*.

4. The NORWECOM.E2E Model (Morten Skogen, IMR)

The NORWECOM.E2E model is an end-to-end coupled 3 dimensional physical, chemical, and biological model originally applied to study primary production, nutrient budgets and dispersion of particles such as fish larvae and pollution. The chemical–biological nutrient–phytoplankton–detritus (NPD) model is coupled to the physical model through the subsurface light, the hydrography and the horizontal and the vertical movement of the water masses. It has been extended with individual-based models (IBMs) for *C. finmarchicus* (e.g. Skaret et al. 2014) and pelagic fish (Utne et al. 2012). These are fully coupled running in offline mode using physical fields (salinity, temperature, oxygen, velocities) from the ROMS model. The model resolution is 10-20 km grid horizontally and 21 vertical layers, covering the Nordic Seas (Northeast Atlantic). The model has already included a first version of a mesopelagic fish IBM (*Benthoosema glaciale*), but further tuning and validation of model will be based on inputs from WP4. The model will be used to produce hindcast simulations with a focus on trophic interactions and inter-annual variability in biomass, production and distribution. It will also be used to quantify vertical carbon flux and harvesting effects of climate change using downscaled CMIP5 or CMIP6 forcing. Figure 3 shows a schematic representation of the NORWECOM.E2E modules.



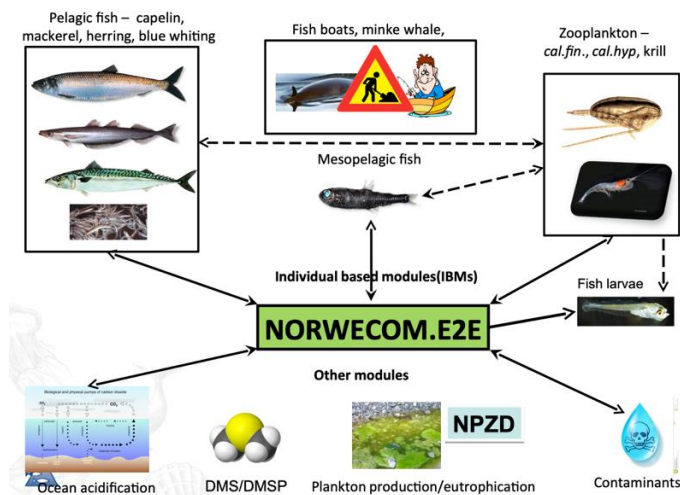


Figure 3. Schematic representation of NORWECOM.E2E modules.

IBMs representing mesopelagic fish species are characterised by state variables, including, but not restricted to position (x,y,z), weight, age, length, sex, fat content, swimming speed, egg production, and number of individual fish (where each IBM agent represents a super-individual i.e. a group of fish in the same location having experienced the same environmental history). The *Benthosema* IBM includes natural (background) mortality, starvation due to low weight, mortality due to outspawned individuals, and mortality due to pelagic and tactile predation. Their vertical behaviour is governed by following isolumens, and the horizontal movement is passive. They feed, using a Holling type 2 functional response, on the *Calanus finmarchicus* IBM and mesozooplankton from the underlying NPZD model. Four stages are classified by weight (egg, larvae, juvenile, adult). The model timestep is 1 hour.

For some processes, particularly those linked to movement, we do not know anything on causes and effects. This is defined as a gen open for selection/mutation. For such traits these are initiated randomly, and a fitness model selects the best strategies during the model set-up. For mesopelagic fish there are 2 gens (so far): an isolumen for juveniles, and an isolumen for adults, which govern the vertical positioning of juvenile and adult fish in relation to light.

Outputs include time series of total stock biomass, individual growth trajectories, average weights of individuals in year classes. Figure 4 shows some sample output of the time series of biomass divided by year class.

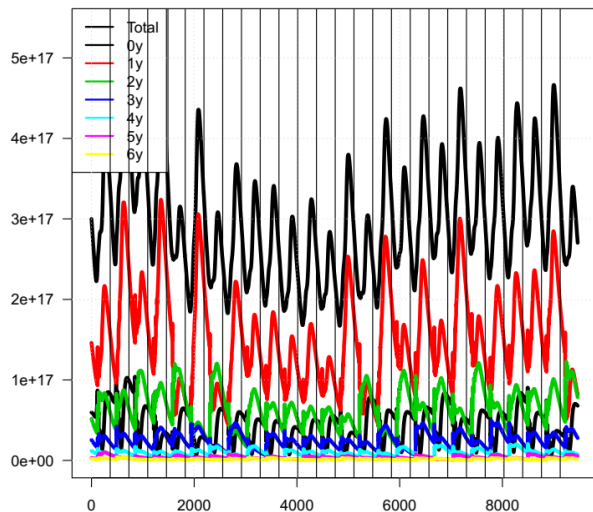


Figure 4. Sample output of the Benthosema module of NORWECOM.E2E, showing times series of the total stock biomass, and biomass by year class. The x-axis indicates model days (the vertical lines mark years). The y-axis is biomass in mgC.

The data requirements relevant for NORWECOM.E2E validation are observations on:

- Weight (and length) at age
- Biomass per year-class
- Distribution maps
- Mortality rates

Mortality rates are of course notoriously difficult to estimate in the field, but any data on age-dependent mortality, or size-dependent mortality, or indeed dependencies on environmental conditions would be useful.

5. The SEAPODYM-MTL Model (Patrick Lehodey & Anna Conchon, CLS)

The SEAPODYM Mid-Trophic Level model (SEAPODYM-MTL) is a pseudo-3D dynamical global model that simulates biomass distributions of 1 zooplankton and 6 micronekton functional groups, according to their diel vertical migration behavior (Dragon et al. 2015, and references therein). Their dynamics are driven by temperature and oceanic currents. The amount of energy allocated from primary production to each group can be estimated from observations within a Maximum Likelihood Estimation framework. The boundaries of the vertical layers are dynamically defined on the euphotic depth. The has been checked against various 38 kHz acoustic transects. Daily vertical migration is a ubiquitous phenomenon, observed globally from the equator to arctic regions. With the extension of the model to high latitudes, the definition has been modified. A methods has been developed (A. Conchon) to identify depths of layer boundaries from acoustic transects, mainly from the Southern Ocean. Then, relationships with environmental variables are explored. Key established macro-relationships are used to parameterize the functional groups. Specifically, the relationship between lifespan and age at maturity, the relationship between age at maturity and temperature, and the relationship between post-embryonic (hatching to adult) development time for zooplankton and temperature. As a result of time of development and relationship to temperature, the

predicted biomass distributions can be very different between groups and primary production (Figure 5).

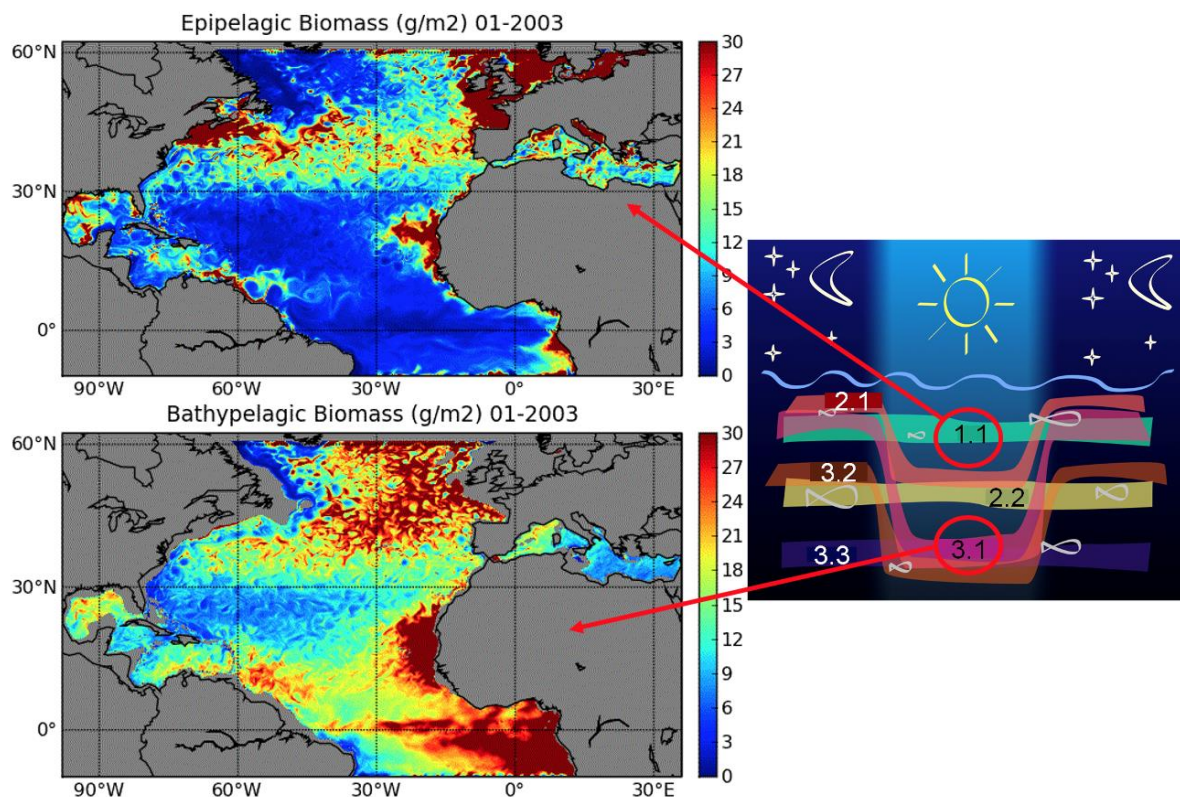


Figure 5. Sample biomass output from two SEAPODYM-MTL model depth layers.

The model is calibrated qualitatively against ADCP backscatter as a proxy of the density of organisms, and 38 kHz echo-sounders (more dedicated to micro-nekton). The model is also validated quantitatively against trawl sampling (requiring hard work at sea to cover all the main taxa by layer, day and night, but it is precious information), and acoustic data.

In MEESO, SEAPODYM-MTL will be used for global modelling and biomass estimation. It does not resolve individual species (specifically our target species *Bethosema muelleri* and *Maurolicus glaciale*), so there is a need to identify to which functional group these species belong, and to identify what percentage of the biomass of the functional group these species represent.

There is need for collaboration and shared information from past papers and datasets and new MEESO and other cruises on:

- Relative or quantitative biomass estimates of mesopelagics/target species;
- Vertical structure (layer boundaries);
- Habitat, any information allowing the delineation of the species distributions and variables that can help to define them;
- Key demographic parameters (age at maturity versus ambient temperature, lifespan);

- Vertical habitat;
- Composition in the functional group (% of target species versus other species).

6. Concluding remarks

Each of the four models discussed above have differing data requirements. The data used by all the models are, however, of two distinct types – input parameters, and fitting (or validation) data. The first type are parameter values that are independently measured, or whose values are assumed if data are unavailable. The second, by contrast, are target data that the models attempt to reproduce, often by tuning unmeasured, or unconstrained, parameters during a fitting process. Unsurprisingly, since all the models have very different structures, the main differences between them in terms of data requirements are in the input parameters. For example, the S6 model uniquely in this suite of models requires parameters that relate body size to reproduction costs and activity costs. There are, nonetheless, some common features. For example, all four models require information on either age (SEAPODYM-MTL), or size (S6, StrathE2E, NORWECOM.E2E) at maturity. Similarly, for fitting data, three of the models (S6, StrathE2E, and NORWECOM.E2E) all require length distributions estimated from survey or catch data for validation.



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8. Appendix 1

Agenda of MEESO WP5 Online Workshop on Modelling Data Requirements, 10-11 March 2020. The times are given in CET.

Tuesday 10th March

11.30 – 1pm – Session 1

- Introduction and overview – Douglas Speirs (STRATH)
- The S6 model – Alexandros Kokkalis (DTU)

1-1.30pm – Lunch

1.30-2.30pm – Session 2

- The SEAPODYM model – Patrick Lehodey (CLS)

2.30-2.45pm – Break

2.45-4pm – Session 3

- The NORWECOM model – Morten Skogen (IMR)
- General discussion

Wednesday 11th March

9-10.30am – Session 4

- The StrathSPACE model – Douglas Speirs (STRATH)
- Literature review of biology of *Maurolicus muelleri* – Silvia Paoletti (DTU)

10.30-10.45 – Break

10.45-12.30pm – Session 5

- Closing discussion
- Meeting end



9. Appendix 2

List of Attendees (including affiliation and contact email)

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Anna	Conchon	CLS	aconchon@groupcls.com
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