Modelling of aquaculture impacts: what scales do we need to resolve?

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Tweetable abstract: #MASTSasm2020.

Modelling of aquaculture impacts: what scales do we need to resolve? We compare a suite of nested model simulations with high resolution mooring data and evaluate the model complexity/resolution required to resolve aquaculture-relevant physics like transport and dispersion.

@maxhollo

The aquaculture sector contributed £1.8 billion to the Scottish economy during 2016 and is targeted to double by 2030 [1]. Consenting of new marine pen fish farm sites is dependent on demonstrating, through numerical modelling, that the proposed site will comply with minimum environmental standards for the build-up/dispersion of waste products and the spatial extent and intensity of impacts. The industry is thus increasingly moving from sheltered and constrained inshore waters to more exposed, energetic and dispersive environments to mitigate or lower the environmental impact.

A number of modelling approaches are available to determine discharge licenses. The level of modelling is case-dependent and occasionally may not require full-scale three-dimensional hydrodynamic models. However, transport and dispersion in the coastal ocean are multi-scale process and potentially highly dependent on small scale physics. It is thus important to ensure that the modelling approach used adequately resolves or parameterises aquaculture-relevant physical processes near the site of interest.

Here, using a hierarchy of nested hydrodynamic model simulations, with horizontal resolutions varying in a range of 5-200 m at the site of interest, we explore the scales required to adequately represent the dispersive environments near existing and contrasting fish farm sites. Model simulations are evaluated against mooring deployments that resolve velocity, temperature and salinity at high temporal frequencies close to the farm sites.

Upcoming work will investigate application of model outputs and integration with particle tracking tools to examine how interactions between physical and biological processes influence dispersal of agents such as parasites and harmful algae in contrasting environments.

References
[1] A Strategic Plan for farming Scotland's seas. https://aquaculture.scot/wp-content/uploads/2017/11/Aquaculture_Growth_2030.pdf
[2] Aleynik et al 2016, *Harmful Algae*, 53, 102-107

Figure 1. Horizontal (surface, **a**) and vertical (**b**) temperature distribution reveals the structure of the coastal currents near the aquafarm site: RUM-FVCOM model nested into WeStCOMS [2].
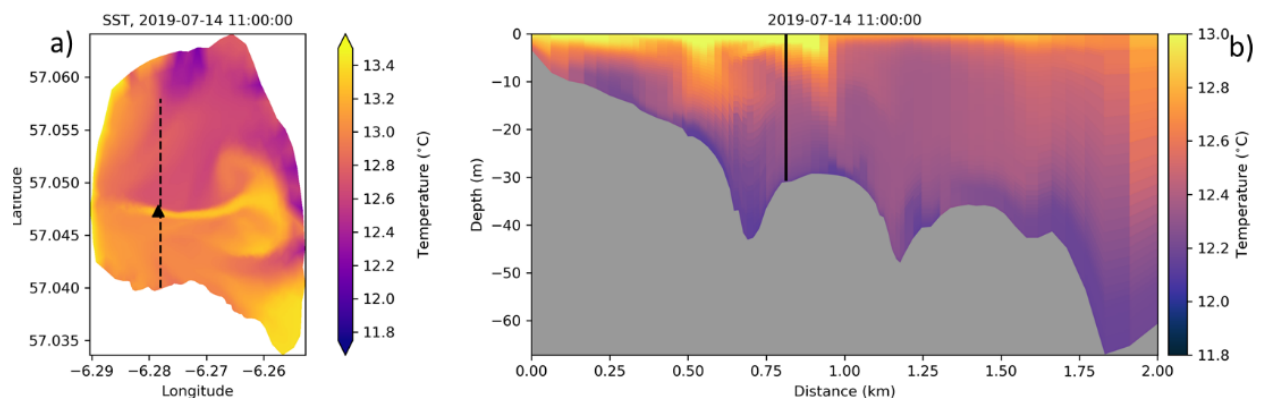
Using remotely-sensed oceanographic products to enhance epidemiological models for Atlantic salmon aquaculture in Scotland.

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Environmental factors, such as water temperature and salinity, have a large impact on salmon production. Most open-pen salmon production sites monitor environmental factors *in situ* at the farm locations to help make management decisions. There is much variation, however, among companies regarding their monitoring regimes. Not all sites use similar tools, or measure at similar frequencies, times during the day, or water depths. Likewise, not all environmental factors are measured at all sites.

Because these environmental factors affect fish health, it is often desirable to include them in epidemiological studies, one common type of which is the risk-factor analysis. The goal of such a study is to elucidate the relationship between an independent variable (i.e., the outcome of the study such as mortality), and dependent variables of interest, such as presence of a pathogen, application of a certain type of mitigation measure, or environmental factors or conditions. It is therefore valuable to include environmental factors in such analyses, if they can be uniformly measured and provided

A cost-effective solution to be able to include environmental factors into risk-factor studies it to use remotely-sensed satellite products. Such products are often available open-sourced and therefore easy to obtain. They have drawbacks, as they are less precise as *in situ* measurements, and may not fully cover all geographical areas of interest, such as sea lochs.

As an example of the use of remotely-sensed satellite products, we present a risk-factor analysis in which we investigated factors that affect monthly site level mortality on Scottish salmon farms. Results show that location in space and time (production cycle, site and local authority) affected mortality, and that of the environmental factors included in the analysis (phytoplankton concentrations, salinity and sea surface temperature), only sea surface temperature affected mortality, and there was no significant effect of a lag between the environmental factors and mortality. Monthly site-level mortality is a large scale outcome, and we suspect that at a smaller scale, such as daily or weekly site- or pen level there could be a larger effect and possibly lag effect of the environmental parameters. It is important to compare *in situ* observations taken on the sites and remotely-sensed satellite products to ensure they provide similar values and trends.

Tweetable abstract: Salmon aquaculture in open net-pens is affected by environmental factors. Open-sourced remotely-sensed satellite products, such as salinity and sea surface temperature, can enhance epidemiological models.

The Role of Stokes Drift in Shoreline Accumulations of Infective Sea Lice Larvae

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Sea lice are naturally-occurring copepod crustaceans, which have evolved over millennia to live on salmonids (salmon and trout), feeding on mucus, skin and blood to survive. The lice life cycle includes a short, free-swimming larval phase, during which the lice larvae (copepodids) must find and attach to a fish host.

Salmon farms hold fish in pens at higher densities than in the wild. Sea lice also infect farmed fish and farms can provide an environment in which lice can proliferate. When lice numbers on farms are uncontrolled they can pose a potential risk to local wild salmonid populations as well as to the health and welfare of farmed fish; controlling their numbers on site limits these risks.

For the protection of local wild salmonid population, it is important to understand how lice are dispersed from salmon farms, but the mechanisms by which lice larvae locate wild fish hosts are poorly understood. Dispersal of the free-swimming larval stage in coastal waters is thought to be important, but capturing infective sea lice copepodids in the water column is difficult, as densities are low, typically less than 1 copepodid m^{-3} (e.g. Penston and Davies, 2009). Yet at some shoreline locations, much higher densities have been measured, exceeding 100 copepodids m^{-3} (McKibben and Hay, 2004). These high densities were found in Loch Torridon, Scotland, in water depths less than 2m (some of the sampling was done by wading) very close to the mouth of the river Shieldaig, which has an indigenous sea trout population.

These copepodid accumulations are concerning and puzzling: concerning because these high densities must pose an infection risk to migrating post-smolt sea trout from the River Shieldaig; and puzzling because accumulation close to a river mouth, with seaward-flowing brackish water, seems physically and biologically counter-intuitive (lice do not tolerate low salinity water).

Computer modelling studies did not reproduce these high densities close to the river mouth, except by using a "sticky" lateral boundary condition, which is an artificial numerical representation of the physical processes that must be involved. Here, we explore the role that Stokes drift, due to wave action, may play in producing the high shoreline densities of larval lice. Copepodids are thought to remain close to the sea surface and will thus be exposed to shoreward drift under landward-propagating waves and seaward drift under seaward wave action.

Initial simulations from a particle-tracking dispersal model, coupled to a 3D hydrodynamic model, are presented, comparing lice densities with and without the effects of Stokes drift. The period chosen for study was May – August 2019, when lice levels on nearby farms were moderate but relatively steady. Despite this, the weekly shoreline sampling recorded high variability in the lice densities. The variability in weekly lice density was only reproduced when Stokes drift was included in the model simulations; the wind-driven circulation alone did not reproduce the observed variability.

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It's all FYNE: How a novel management tool for the salmon aquaculture industry brings together nutrition and environment

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[Twitter abstract: The #FYNE GUI is a management tool for #aquaculture businesses to achieve targets for seafood fatty acid nutritional quality and harvestable weight, while estimating environmental impact and complying with farm discharges' regulation.   https://bit.ly/2Y29i3n #salmon #kelp #mussels]

Atlantic salmon, *Salmo salar,* is a key source of polyunsaturated fatty acids (PUFA), essential to human health, which is vastly fulfilled by the aquaculture industry worldwide. With salmon farming representing an important sector to the Scottish economy, there is considerable interest in ensuring its environmental sustainability, from the control of farm discharges and minimisation of benthic impacts, to improved animal health and decreased reliance on wild-caught fish for feed.

In recent years, this has prompted research into the potential of integrated multi-trophic aquaculture (IMTA) as an option to reduce the local footprint of fish farms and industry efforts to replace wild-caught fish in feeds with terrestrial ingredients. However, the continued decrease of wild-caught fish in the salmon feeds has reduced the PUFA content in the final product (Sprague et al., 2016), affecting the key marketable and health attribute. It is also unclear how varying the diet composition translates into changes in the farm-level environmental footprint of salmon production, a crucial issue to the sector's regulation and social license to operate. We therefore propose an holistic approach to farm management, which simultaneously considers the nutritional quality of final products and the local environmental impacts at farm-level.

We present a new application for industry to quantify the environmental and nutritional output of both monoculture and IMTA, given multiple operational changes. The FYNE graphical user interface (GUI) allows the user to create a virtual IMTA (currently for Atlantic salmon, blue mussels, sugar kelp) farm or monoculture (one of the aforementioned species) and predict the consequence of operational changes to the local environment and nutritional output. The user can vary farm location, abundance of cultured and co-cultured species, as well as salmon feed proximate composition. Values selected by the user are input into underlying ecosystem and PUFA models. Modelled outputs include harvestable weight, salmon fatty-acid content and total organic carbon and nitrogen concentrations on the sediment over time. The concentration of the latter nutrients can be used as a proxy for the farm-level environmental footprint.

The FYNE model was designed to support aquaculture operators and feed manufacturers to achieve targets for fatty-acid nutritional quality and harvestable weight, while helping to comply with regulatory frameworks on farm discharges. Current work is being done on model validation and parameterisation of the ecosystem component. To ensure that the GUI offers a comprehensive approach to optimise trade-offs between product nutritional value and local environmental impacts during grow-out stage, future work will include user testing of the GUI by businesses to improve features and enhance user experience,

Acknowledgements

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Optimizing nutritional programming stimulus duration in Atlantic salmon (*Salmo salar*) for more efficient utilization of vegetable based feeds.

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The Scottish farmed salmon industry continues to expand, with benefits for both rural communities and the national economy. Nevertheless, traditional feeds formulated with high levels of marine raw materials fishmeal (FM) and fish oil (FO) are unsustainable, due to the high demand for these finite ingredients and the large environmental footprint associated with harvesting and processing the fish to produce them. One alternative is to produce feeds with higher proportions of vegetable-derived oils and proteins. However, feeds with a high vegetable content can lead to reduced feed utilization and also have lower levels of essential long chain polyunsaturated fatty acids (n-3 LC-PUFA), eicosapentaenoic acid (EPA; 20 : 5n-3) and docosahexaenoic acid (DHA; 22 : 6n-3). One solution to this problem is an early nutritional intervention or "stimulus": fish are fed a predominantly vegetable-based diet for a short period, to induce a more efficient uptake and utilization of nutrients from a similar diet later in development. Recently, it was demonstrated that Atlantic salmon (*Salmo salar*) fed a predominantly vegetable-based diet, from first exogenous feeding, during a three-week stimulus phase had greater growth, feed efficiency (Clarkson et al. 2017) and accompanying upregulation in key pathways of intermediary metabolism (Vera et al. 2017). However, at the end of stimulus and intermediate phases fish fed the vegetable-based diet had significantly lower body weight than those fish fed a standard marine diet (Clarkson et al. 2017). This present work sought to investigate the optimum duration of a first feeding stimulus to ascertain whether initial phenotypic differences at the end of the stimulus phase could be avoided. As such, this trial specifically aimed to confirm if nutritional programming could be successfully triggered following a shorter stimulus duration.

Fish in triplicated tanks (300/tank) were fed an experimental vegetable-based diet (Vstimulus) for one or two weeks from first exogenous feeding. A control group was fed a standard marine-based diet (Mstimulus). All groups were then transferred to a standard marine based formulation, for an intermediate grow out phase of 10 weeks, prior to a "challenge" phase of six weeks when all fish were administered a vegetable-based diet. Growth rates and size of individual fish were significantly lower ($p<0.05$) in fish fed Vstimulus compared to Mstimulus at the end of the stimulus phase. However, no significant differences in any other growth parameters evaluated were observed, during the remainder of trial, between any of the sample groups. Retention EPA and DHA were significantly reduced ($p<0.05$; 60% for EPA and 120% for DHA respectively) in fish fed the Vstimulus diet for two weeks compared to groups fed Mstimulus. Furthermore, expression of genes relating to fatty acid metabolism in pyloric caeca were significantly reduced ($p<0.05$) in groups fed Vstimulus diet for one or two weeks. The latter result could indicate nutritional programming in Vstimulus fish, as fish fed the Mstimulus diet may have been upregulating genes to compensate for the lower EPA and DHA levels in challenge feeds.

Taken together these results suggest that a shorter stimulus period may induce nutritional programming, although further work is required to provide a more definitive conclusion. A current trial is investigating the longer term post-smoltification effects of nutritional programming after a stimulus phase of three weeks. It is hoped that this work will increase sustainability in the Scottish salmon sector leading to enhanced consumer confidence and demand.

Clarkson, M., Migaud, H., Metochis, C., Vera, L. M., Leeming, D., Tocher, D. R. and Taylor J. F. (2017) Early nutritional intervention can improve utilisation of vegetable-based diets in diploid and triploid Atlantic salmon (*Salmo salar* L.), British Journal of Nutrition, doi:10.1017/S0007114517001842

Vera, L. M., Metochis, C., Taylor J. F., Clarkson, M., Skjærven, K. H., Migaud, H., and Tocher, D. R. (2017) Early nutritional programming affects liver transcriptome in diploid and triploid Atlantic salmon, *Salmo salar*, BMC Genomics (2017) 18:886

Tweetable abstract: Programming fish to eat their greens for a more sustainable future#MASTSasm2020. Twitter handle:@Chef2Beaker and @Nutriprog

Profiling microbial communities for healthier oyster hatcheries.

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Pacific oyster cultivation, worth £7.5M per annum to the UK, also provides high quality produce to a global market and skilled employment in rural areas. The benefits of water clarification and increased local biodiversity associated with these filter-feeders is well documented. The biggest threat to Pacific oyster aquaculture at present is the devastating Ostreid herpesvirus (OsHV-1). Unlike neighbouring countries in Europe, UK waters remain largely free from this pathogen. As such, the majority of UK oyster farmers must source their oysters from disease-free oyster hatcheries in the UK, of which there are currently two. Hatcheries commonly experience significant sporadic early life mortalities, which are suspected to be associated with microbial contamination. Possible sources of contamination include, for example, the seawater intake (via compromised filtration systems), the adult oysters (simultaneously with gametes) or the algal culture system. To elucidate the perturbations associated with mortality events, we designed a sampling strategy to capture microbial genomic DNA at all stages of the hatchery process: pre- and post- water filtration, the larvae themselves and their environment at various stages of development. By sampling through multiple spawning cycles, we have captured samples from larvae cohorts with and without major early life mortality events. These samples are sequenced using a metabarcoding approach for prokaryotic and eukaryotic microbes with the Nanopore MinION system. Microbial diversity and abundance will be correlated against metadata, comprising local weather conditions, water quality analysis, hatchery water conditions (temperature, algal content, salinity and pH), in addition to the number of larvae present. Selected samples will be processed for whole genome sequencing to describe the core microbiome of the hatchery and to fully characterise interesting microbes. To date, we have described microbes associated with normal functioning hatchery water systems. By continuing to analyse the microbial components of these samples, we will describe variations in the hatchery system, identify its compromised areas, and provide the first atlas of microbes associated with healthy/unhealthy larval culture.

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@timtreegan: Oysters clarify water &⬆biodiversity. 🇬🇧Pacific Oyster⬜ aquaculture relies on hatcheries for robust spat supply, and is threatened by ⬜ disease. By sequencing DNA⬜from a hatchery environment & developing ⬜s over time ⬜, we correlate ⬜ health with microbial species present.

The full abstract should be submitted to masts@st-andrews.ac.uk, in an editable format, by 16:00 Friday 14th August 2020.

Neuroendocrine regulation of bivalve metamorphosis: applications for shellfish aquaculture industry

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Tweet for #MASTSasm2020 (max 280 characters): Understanding the neuroendocrine regulation of metamorphosis in bivalve species to improve bivalve aquaculture industry and predict adverse effects of environmental pollutants.

Abstract

Most of our commercial bivalve production comes from aquaculture in open water systems. For restocking bivalve populations, juveniles (spat) are also often produced in hatcheries, in which broodstock are conditioned and bivalve spat are cultured to desired size for grow-out. The bivalve life cycle, as for many invertebrates, is biphasic with a free-swimming larval phase followed by often sessile adult stage. The transition between these two life stages is known as metamorphosis, and includes the loss of larval organs and acquisition of adult structures. As a developmental process, metamorphosis is regulated by a complex interaction of neurohormones and neurotransmitters, but our knowledge on the actual pathways is limited (Joyce and Vogeler, 2018). Unfortunately, mortality rate can be high during metamorphosis, resulting in lowered survival. One of the strategies for hatcheries to improve spat survival is to induce metamorphosis with a chemical inducer, such as epinephrine, a common neurotransmitter. However, epinephrine only induces metamorphosis in certain species, and our limited understanding of the pathways involved makes it difficult to apply existing knowledge when developing hatchery protocols for new species. Further understanding regarding regulation of metamorphosis will also aid our understanding on how pollutants in coastal waters interfere with development in natural bivalve populations. Given that endocrine pathways are highly conserved among unrelated species, there is a global concern about pharmaceutical residues in the environment due to potential effects on non-target species.

As a novel divergence from existing theories regarding metamorphosis regulation, we provide a short overview about two previously unexplored pathways involving the NMDA receptor (NMDAR) and the nitric oxide (NO) pathway as potential regulators of metamorphosis in bivalve species. Our research has shown that antagonists to NMDAR, a transmembrane ion channel present in nerve cells and muscle junctions, induced metamorphosis in several oyster and clam species (Vogeler et al 2018). Using the Pacific oyster *Crassostrea gigas* as a model organism, we further investigated the relationship between NMDARs and a potential downstream NO pathway given that inhibitors to the NO pathway also induced metamorphosis in *C. gigas* (Vogeler et al, under review & submitted). NMDARs, NO producing synthases as well as NO itself were present larval structures prior to metamorphosis such as the velum (larval swimming organ), apical ganglion and nervous structure of the foot (for crawling on surfaces). These larval organs are suspected to sense for environmental cues to induce metamorphosis and are lost during the transition. Combining findings of these previous studies, we propose that the NMDAR and the NO pathways are regulators of metamorphosis presumably via inhibition of the larvae's locomotion ability, which can initiate metamorphosis when additional and not yet clearly understood, conditions apply.

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