

- 1 **Supplementary Information 1.** Assumptions applied in the simulations of ISAV dispersal and their
- 2 possible implications to the estimation of transmission risk and farm connectivity.

Assumptions	Possible implications
The decay rate of ISAV caused by UV is the same as IHNV	Uncertainty
The decay rate of ISAV caused by the ambient microbial communities is the same as IHNV in the Discovery Islands, BC aquatic environment	Uncertainty
The UV attenuation coefficient in varied water depth is the same as in the Discovery Islands, BC aquatic environment	Uncertainty
ISAV transmission risk within a farm follows a beta-PERT distribution with minimum, mean, and maximum values set as 0.8, 0.9, 0.99, respectively	Overestimate
Shedding rates of ISAV are estimated based on PCR detection results	Overestimate
Each farm has 300,000 fish, with an average weight of 5 kg per fish	Overestimate
All fish in the farm are susceptible to ISAV	Overestimate
No human interventions are included	Overestimate
A farm is considered as one homogeneous cage	Overestimate
No multiple outbreaks occur at the same time	Underestimate
The output of circulation model FVCOM can overall indicate the spatially and temporally varying in the studied region.	Uncertainty
No viral particles lost due to attaching land by applying a land avoidance scheme in PTrack	Overestimate

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5 **Supplementary Information 2. Determination of the shedding rate function**

6 Data from a laboratory experiment (Gregory et al. 2009) were used to simulate the shedding rate
7 of ISAV in Atlantic salmon in our modeling framework. In that study, they injected fish with an inoculum
8 of ISAV and monitored the concentration of ISAV every other day in 200 L of water over a 4 h period.
9 Their data showed that viral shedding started around day 7 post-infection, peaked around day 15, and
10 dropped afterward (Table S1.1). We attempted to fit a normal distribution to these data to model the
11 shedding rate of ISAV by Atlantic salmon. The normal distribution function is expressed as:

12
$$\theta(t) = \frac{\mu}{\sigma\sqrt{2\pi}} \exp\left(-\frac{(t-\beta)^2}{2\sigma^2}\right) \quad (\text{eq.S1.1})$$

13 where θ represents the viral load, t is time in days, μ , β , and σ are coefficients of the normal distribution
14 function, that represent the mean, amplitude, and variance, respectively. Values were obtained using the
15 solver function in EXCEL® software, with: $\beta = 14.18$, $\sigma = 2.94$, and $\mu = 27090335.11$. $R^2 = 0.99$. The
16 figure below shows the form of the normal distribution function overlaid on the raw data (Fig. S2.1).
17 Overall, during the time period covered by the data (days 5 to 19), the function fit the data very well. We
18 note that comprehensive laboratory experiments need be conducted in the future to optimize the function
19 and the coefficients.

20

21 **Table S2.1.** Laboratory experiment of ISAV virus shedding rate

Days post-infection	Shedding rate (TCID ₅₀ mL ⁻¹ kg ⁻¹) from Gregory et al. (2009)	Deduced Shedding rate (TCID ₅₀ kg ⁻¹ h ⁻¹)*
0	0	0
1	0	0
5	0	0

7	0.058	2,900
11	42	2,100,000
15	70	3,500,000
19	20	1,000,000
21	0	0

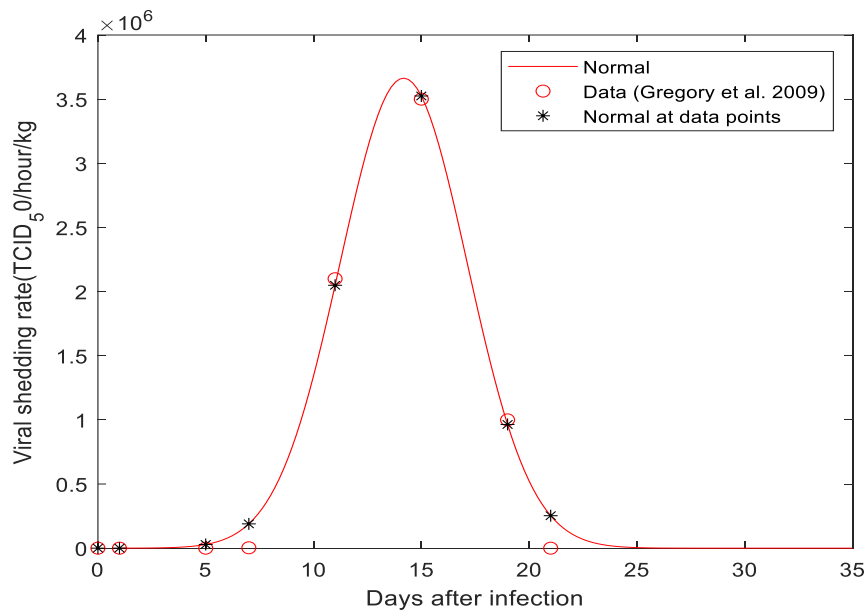
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23 *Deduced shedding rate per fish in $\text{TCID}_{50} \text{ kg}^{-1} \text{ h}^{-1}$ was calculated by modifying the virus shed per fish

24 biomass (in $\text{TCID}_{50} \text{ mL}^{-1} \text{ kg}^{-1}$) with the volume of water in fish tank (200 L), then dividing by the

25 shedding time (4 h), according to the method described in Gregory et al. (2009).

26



27

28 **Fig. S2.1** Virus shedding rate model. The normal distribution function is the red line; data from Gregory et

29 al. (2009) are in red circles; modeled values at the data time points of Gregory et al. (2009) are represented

30 by asterisks (*)

31

32 **Reference**

33 Gregory A, Munro L, Snow M, Urquhart K, Murray A, Raynard R (2009) An experimental investigation
34 on aspects of infectious salmon anaemia virus (ISAV) infection dynamics in seawater Atlantic
35 salmon, *Salmo salar* L. Journal of fish diseases 32:481–489.

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38 **Supplementary Information 3. Sensitivity analysis for PTrack time step**

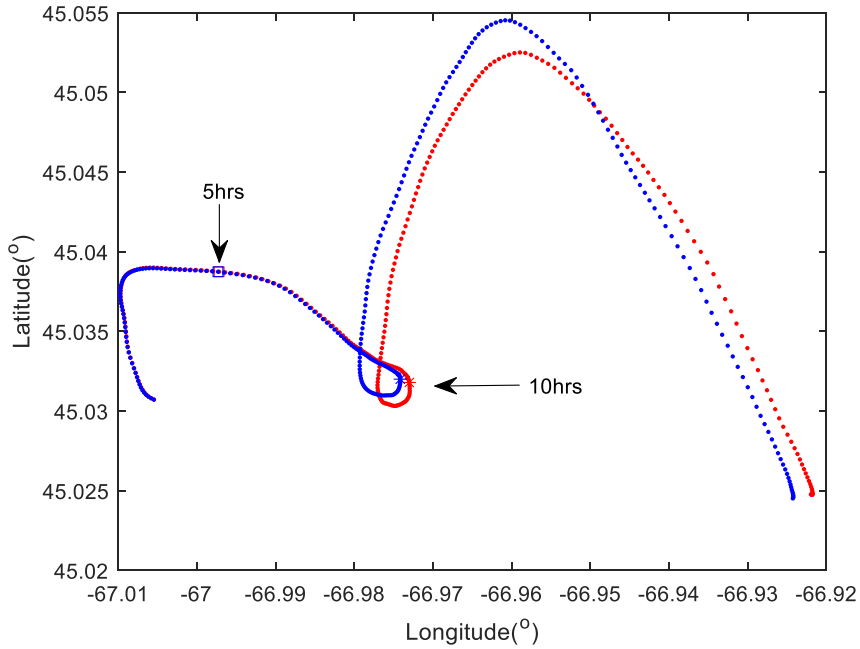
39 The spatial resolution for the physical model (FVCOM) used in this study is as small as 25 m in
40 shallow coastal waters and as large as 11 km in the deeper sea. As the time step retained to simulate particle
41 trajectories was set to 300 s (5 min) in this study, particles could easily move over the smallest grid size of
42 the model during an interval with currents speed exceeding 0.1 m s^{-1} . Hence, the potential of particles
43 jumping over grid cells may degrade the benefits of using a high resolution ocean circulation model and
44 can introduce uncertainties into the particle tracking results.

45 A finer temporal resolution of 30 s was thus used to repeat the particle tracking simulation and
46 compared with 300 s. To conduct the comparison, two groups of 100 particles were released at Farm 2
47 every hour for 48 hours, one group tracked at a 30 s time step, and the other at a 300 s time step. Each group
48 of 100 particles was tracked for 24 hours to cover the full tidal and light cycles, and to cover the estimated
49 viral survival time. The mean separation distance was then estimated by first computing the mean trajectory
50 of each group of 100 particles released at each hour from the two model settings (300 s and 30 s), followed
51 by computing the differences between the mean trajectory of the corresponding groups. The mean
52 differences of the 48 groups of particles were then calculated to represent the separation distance of the two
53 model settings.

54 A single particle from the two groups generally follows the exact same trajectory within 10 hours
55 after release, before separating further over time (Fig. S3.1 for an example). The mean separation distance
56 was estimated for each one of the 48 groups. On average, there was a 24.7 m separation between the two
57 groups three hours after release, and 38.6 m five hours after release (Fig. S3.2). The average variation over
58 the entire tracking time was determined (Fig. S3.2).

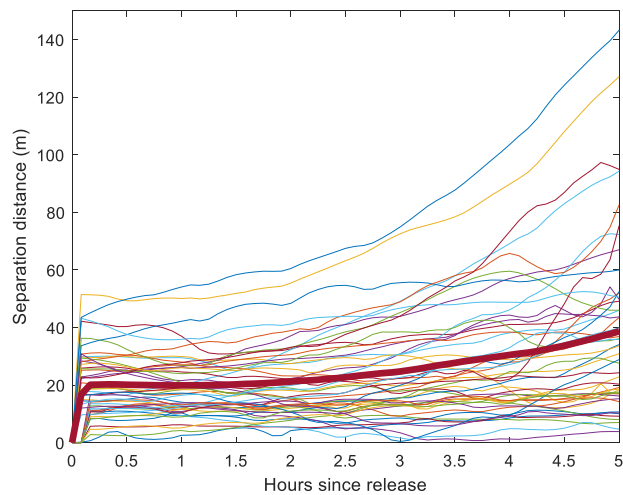
59 Laboratory data suggested that ISAV generally loses its infectivity within three hours in the
60 presence of UV. In this case, the 24.7 m trajectory difference found after three hours tracking between the
61 temporal resolution of 300 s and 30 s is generally within the minimal spatial grid of the ocean circulation

62 model applied in this study (i.e. 25 m). Thus, the impact of the smaller temporal resolution on the particle
63 trajectory is expected to be low.



64

65 **Fig. S3.1** An example of the mean particle trajectory difference of a group of 100 particles simulated with
66 a 300 s (red) and 30 s (blue) time step. Positions of particles at five hours and ten hours after release are
67 indicated.



68

69 **Fig. S3.2** Separation distances between particle groups modeled with the 300 s and 30 s time step, over a
 70 tracking time of five hours. Each line represents the differences between the mean trajectories of the
 71 corresponding groups from the two model settings (300 s and 30 s), and groups were released every hour
 72 for 48 h (100 particles in each group). The bold red curve is the average of all 48 groups of particles.

73

74 **Table S3.1.** Average separation distances between particle groups modeled with a 300 s and 30 s time
 75 step, calculated based on groups of 100 particles released hourly for 48 hours (i.e., 100×48 particles), with
 76 each group tracked for 24 h.

77

Hours after release (h)	0	1	2	3	4	5	6	7
Separation distance (m)	0.0	19.9	21.2	24.7	30.5	38.6	48.2	66.3
Hours after release (h)	8	9	10	11	12	13	14	15
Separation distance (m)	87.0	115.0	141.2	164.7	192.8	230.0	281.3	344.5
Hours after release (h)	16	17	18	19	20	21	22	23
Separation distance (m)	424.0	480.9	527.1	577.2	608.3	656.2	698.0	741.4

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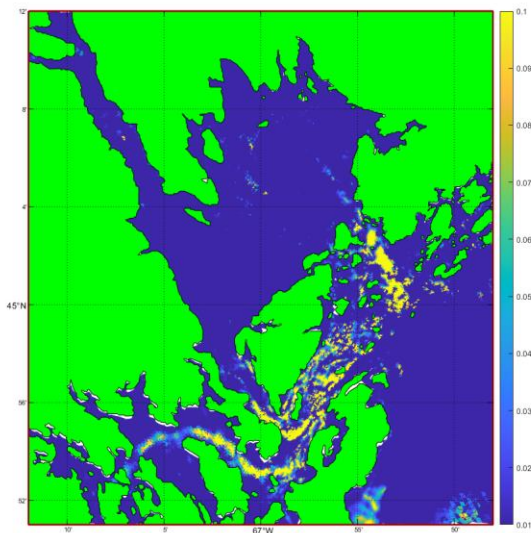
81 **Supplementary Information 4. Sensitivity analysis for the vertical diffusion coefficient**

82 In this study, the vertical diffusion coefficient for the random walk was set to $0.1 \text{ m}^2 \text{ s}^{-1}$ in the
83 PTrack module. While this parameter can be over $0.1 \text{ m}^2 \text{ s}^{-1}$ in the water near channels and islands, the
84 vertical diffusion coefficient from the outputs of FVCOM indicate that it is likely around $0.01 \text{ m}^2 \text{ s}^{-1}$ in
85 the main part of Passamaquoddy Bay (Fig. S4.1). To demonstrate the impact of the vertical diffusion
86 coefficient on the dispersal of ISAV, we compared the trajectories of particles experiencing vertical
87 diffusion coefficients of $0.01 \text{ m}^2 \text{ s}^{-1}$ and $0.1 \text{ m}^2 \text{ s}^{-1}$. To conduct the comparison, a group of 100 particles
88 were released at Farm 2 every hour for 48 hours. Each group of particles was tracked for 24 hours.

89 The results indicated that the dispersal scale of the $0.01 \text{ m}^2 \text{ s}^{-1}$ group was larger than that of the 0.1
90 $\text{m}^2 \text{ s}^{-1}$ group (Fig. S4.2). An average difference of 198.4 m was found 3 hours after release, and 333 m at
91 5 hours after release (Fig. S4.3). These results indicate that the vertical diffusion coefficients may impact
92 the trajectory results substantially, and higher vertical diffusion can result in an underestimation of the
93 horizontal particle dispersion.

94 Given that most farms are scattered in the higher vertical diffusion area, we considered $0.1 \text{ m}^2 \text{ s}^{-1}$
95 to be acceptable for our main simulations. Although it seems logical to apply a dynamic vertical diffusion
96 coefficient, such as one determined from the ocean circulation model, to better capture the spatial
97 variation of the vertical turbulent mixing of the area, applying a fixed space-independent value does
98 provide flexibility for optimal modelling performance (Page et al. 2005). The vertical diffusion
99 coefficient impacts the depth of particles, which can impact the UV attenuation process in our inactivation
100 module. Viral concentration can be impacted due to UV degradation at different depths. To demonstrate
101 how the vertical diffusion coefficient impacts the viral concentration, a comparison between the $0.01 \text{ m}^2 \text{ s}^{-1}$
102 1 and $0.1 \text{ m}^2 \text{ s}^{-1}$ groups was produced (Fig. S4.4). The results indicated that, although the dispersal scales
103 were larger for the $0.01 \text{ m}^2 \text{ s}^{-1}$ group, the viral concentration near the farm area was relatively lower for
104 this group compared with the $0.1 \text{ m}^2 \text{ s}^{-1}$ group. Besides the potential dilution effects caused by wider
105 dispersion, the lower concentration can be explained by particles likely being closer to the water surface

106 with a lower vertical diffusion, which enhanced their decay by UV radiation. Consequently, on the daily
107 concentration map, less virus were infectious in this case.



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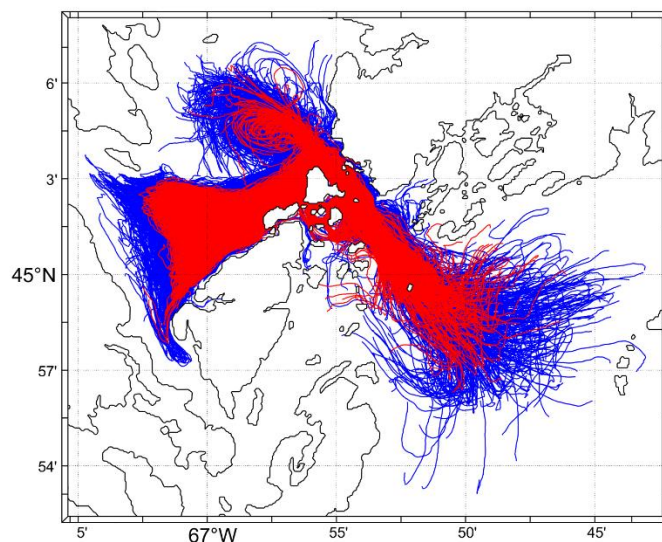
110 **Fig. S4.1** Simulated vertical diffusion coefficients of the surface layer, retrieved from the FVCOM output.

111 Colors on the map represent the values of the modeled vertical diffusion coefficient. (Note: Farms 1, 2,

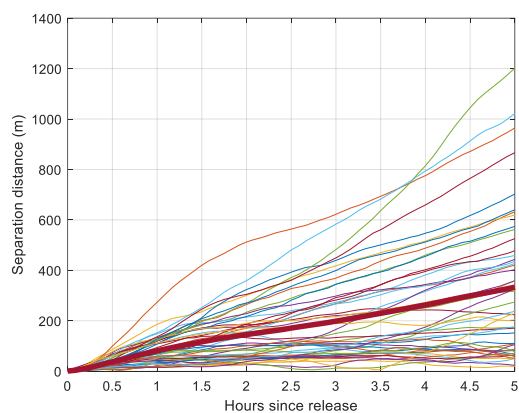
112 and 4 are in the area with lower vertical diffusion coefficients, and the other 10 farms are in areas with

113 higher vertical diffusion coefficients).

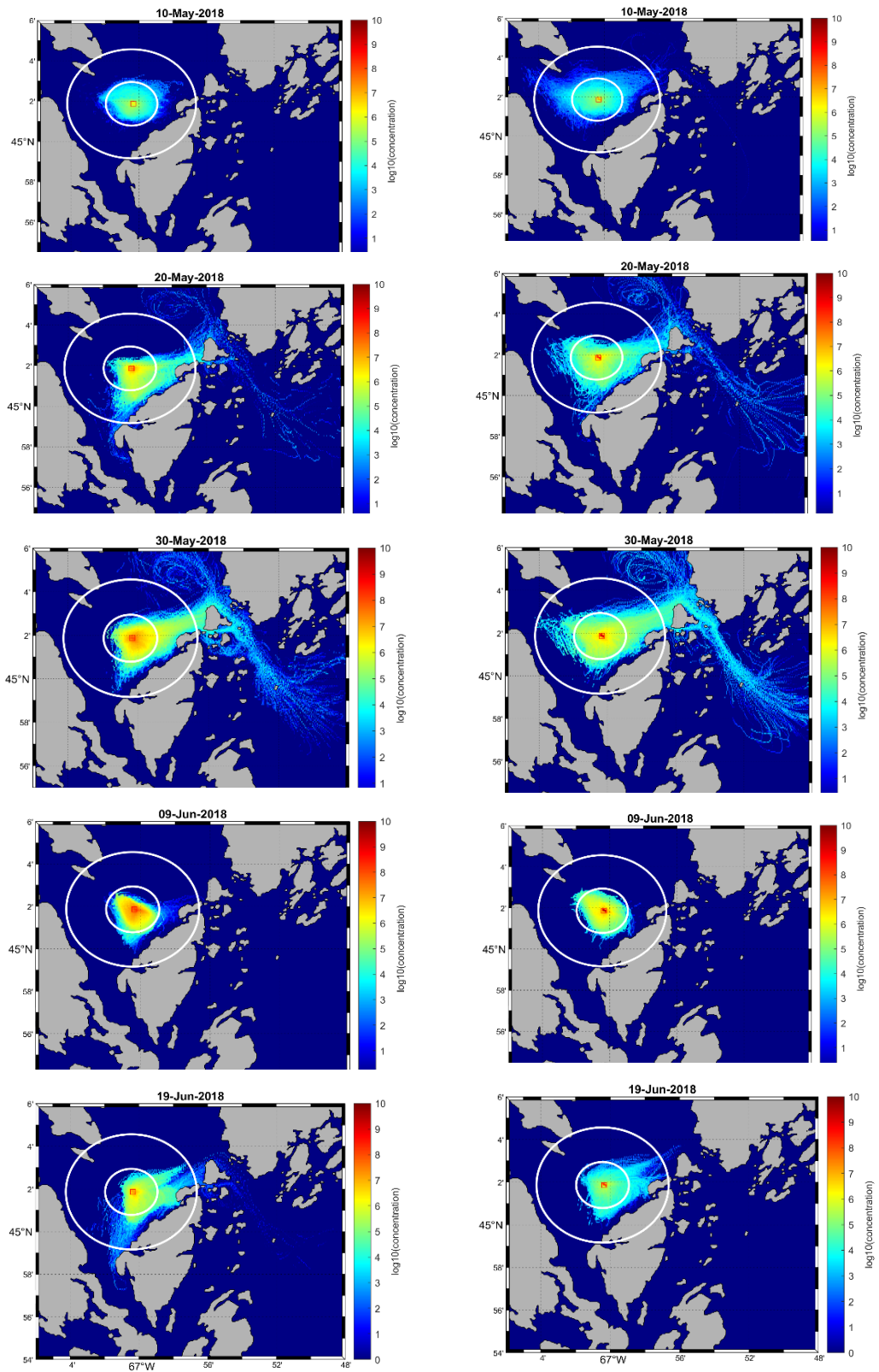
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 116 **Fig. S4.2** Trajectory differences for particles simulated at different vertical diffusion coefficients: 0.1 m²
 117 s⁻¹ (red) and 0.01 m² s⁻¹ (blue) during 48 hours of tracking.
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 120 **Fig. S4.3** Distances separating particle groups with different vertical diffusion coefficients over a tracking
 121 time of 5 hours. Each line represents the differences between the mean trajectory of the corresponding
 122 groups from the two model settings (0.1 m² s⁻¹ and 0.01 m² s⁻¹), as one of 48-hourly released groups (100
 123 in each group). The bold red curve is the average of all 48 groups of particles.
 124



A : $0.1 \text{ m}^2 \cdot \text{s}^{-1}$

B : $0.01 \text{ m}^2 \cdot \text{s}^{-1}$

126 **Fig. S4.4** ISAV concentration ($\log_{10}(\text{TCID}_{50} \text{ m}^{-3})$) released from Farm 2 in the top 15 m of the water
127 column and summed over a 24-h period on different days (10, 20, 30, 40, 50 days) post-outbreak and
128 simulated with different vertical diffusion coefficients. A side: $0.1 \text{ m}^2 \text{ s}^{-1}$ and B side : $0.01 \text{ m}^2 \text{ s}^{-1}$. The red
129 square represents Farm 2 location. The radii of the two white circles centered at Farm 2 are 2 km and 5
130 km, respectively.

131

132 **References**

133 Page FH, Chang B, Losier R, Greenberg D, Chaffey J, McCurdy E (2005) Water circulation and
134 management of infectious salmon anemia in the salmon aquaculture industry of southern Grand
135 Manan Island, Bay of Fundy, Canada. Canadian Technical Report of Fisheries and Aquatic
136 Sciences 2595.

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139 **Supplementary Information 5. UV radiation conversion**

140 The viral decay caused by ultraviolet light is mainly from the UV_A (315-400 nm) and UV_B (280-
141 315 nm) bands (Garver et al. 2013; Häder et al. 2015). However, direct measurements of UV radiation
142 were not available for the studied area. Hence, we used a UV index from the closest available operational
143 UV monitoring station from Environment Canada, in Toronto, Ontario (Canada). (Data available at:
144 <https://exp-studies.tor.ec.gc.ca/>). The UV index is an irradiance scale computed by multiplying the
145 erythemal irradiance (286.3-363 nm) integral in Watts m⁻² by 40 (McKinley and Diffey 1987).

146 It should be noted though that the UV index covers a narrower range of wavelengths compared to
147 UV_A and UV_B. As a result, the UV index was converted to total UV radiation using the empirical equation
148 provided by Foreman et al. (2015) based on an experiment conducted by Garver et al. (2013) using a
149 Davis UV sensor (#6490) that measured erythemal UV (280 to 360 nm, the UV Index) and a Davis solar
150 radiation sensor (#6450) that measured total solar radiation (110 to 400 nm) as:

$$151 \quad UV_{AB} \text{ (W m}^{-2}\text{)} = (a1 \times UV_{\text{index}} \times 0.025 + b1) \times (1 - 0.08) \quad (\text{eq. S5.1})$$

152 where the UV index was multiplied by 0.025 to get the erythemal UV radiation (W m⁻²); a1 = 302.8926,
153 b1 = 3.6671.

154 It must be noted that the empirical relationship between the UV index and UV radiation can vary
155 with different atmospheric parameters, e.g., ozone profile, aerosol properties, and Solar Zenith Angle
156 (Allaart et al. 2004), as well as with the experimental conditions. In addition, ocean albedo may be
157 adjustable, as the average ocean albedo was reported to be between 0.05 and 0.10 (Seitz 2011). These
158 introduce some uncertainties for the calculation of UV radiation applied in our current model.
159 Measurements of the incident UV radiation in the local area of our study is needed to better estimate the
160 viral decay caused by UV.

161

162 **References**

163 Allaart M, van Weele M, Fortuin P, Kelder H (2004). An empirical model to predict the UV-index based
164 on solar zenith angles and total ozone. *Meteorological Applications* 11:59-65.

165 Garver KA, Mahony AA, Stucchi D, Richard J, Van Woensel C, Foreman M (2013) Estimation of
166 parameters influencing waterborne transmission of infectious hematopoietic necrosis virus
167 (IHNV) in Atlantic salmon (*Salmo salar*). *PLoS One* 8:e82296.

168 Häder D-P, Williamson CE, Wängberg S-Å, Rautio M, Rose KC, Gao K, Helbling EW, Sinha RP,
169 Worrest R (2015) Effects of UV radiation on aquatic ecosystems and interactions with other
170 environmental factors. *Photochemical and Photobiological Sciences* 14:108–126.

171 McKinlay AF and Diffey BL (1987) A reference action spectrum for ultraviolet induced erythema in
172 human skin. pp. 83-87 in Passchier WF, Bosnjakovic BFM [eds]. *Human Exposure to Ultraviolet
173 Radiation: Risks and Regulations*, Elsevier, Amsterdam.

174 Seitz R (2011) Bright water: hydrosols, water conservation and climate change. *Climatic
175 Change* 105:365-381.

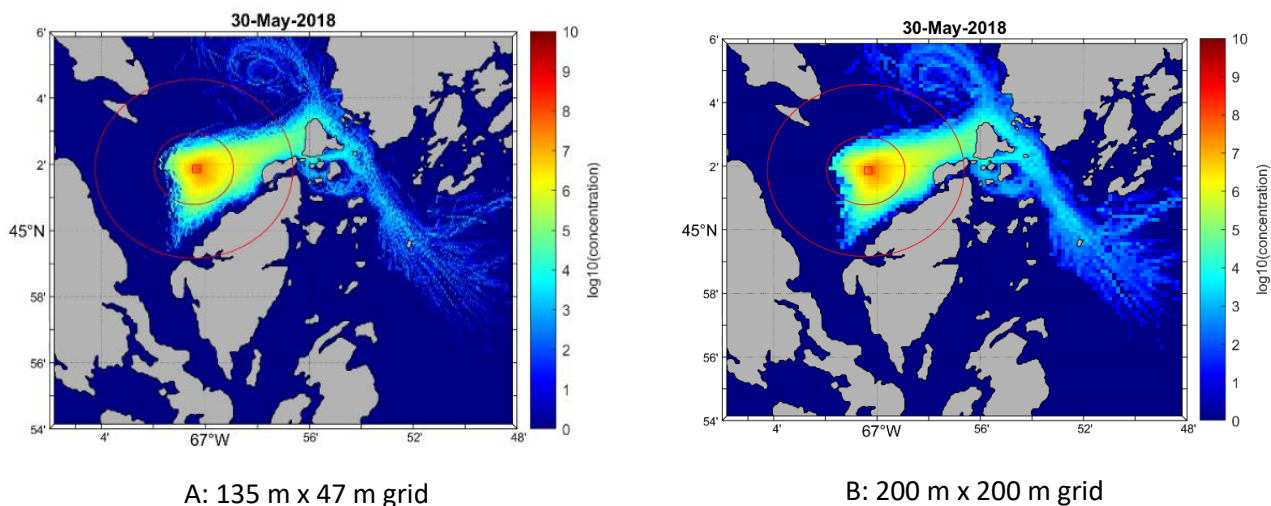
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178 **Supplementary Information 6. Sensitivity analysis for the size of secondary grid cells**

179 To facilitate the calculation and visualization of particle concentrations, we applied a secondary
180 grid different from that of the particle tracking output generated by PTrack. It should be noted that this
181 secondary grid does not affect the particle tracking results, but could have an effect on the estimated
182 concentration in some areas. To test how the selection of the secondary grid cell size impacts viral
183 concentration calculation, we compared the results obtained when using a larger grid size (i.e., 200 m ×200
184 m) to the one retained for our analyses (i.e., 135 m ×47 m). The viral tracking results of Farm 2 were used
185 as an example for this sensitivity analysis. A daily map of May 30, 2018 was produced for illustration
186 purposes (Fig. S6.1).

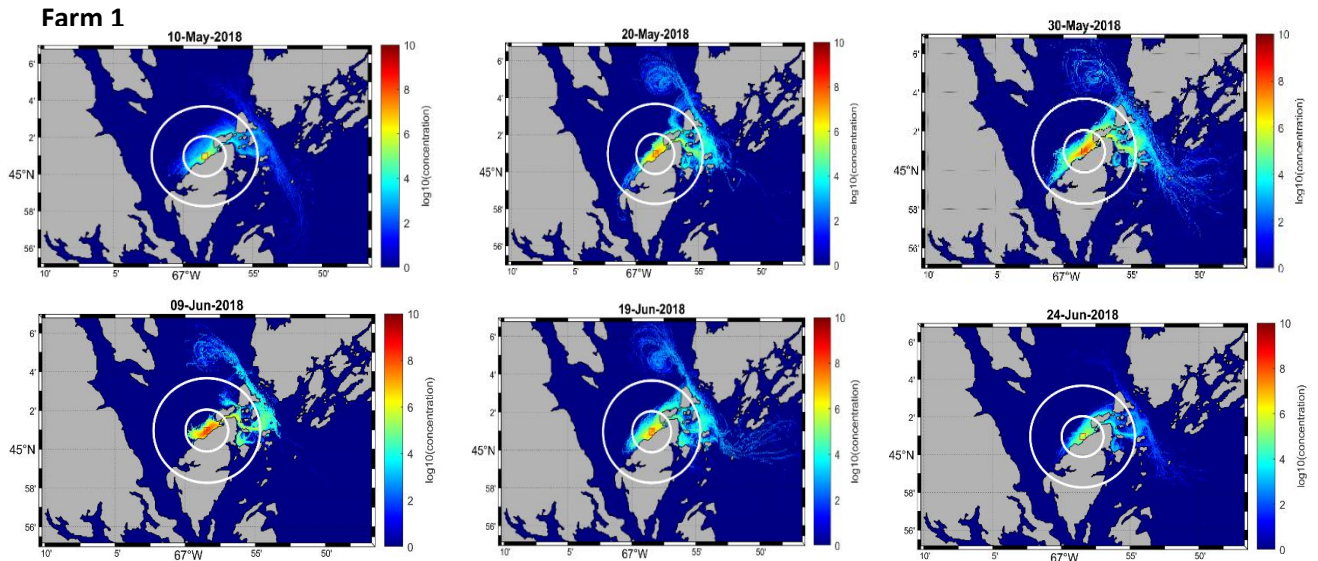
187 The viral concentration map created with the 200m × 200m secondary grid resulted in a more
188 spatially continuous distribution. However, given the large number of particles released, i.e., 100 particles
189 at each hour for 55 days, the current 135 m × 47 m secondary grid was also able to provide a similar
190 continuity, with comparable concentration values shown on the maps.



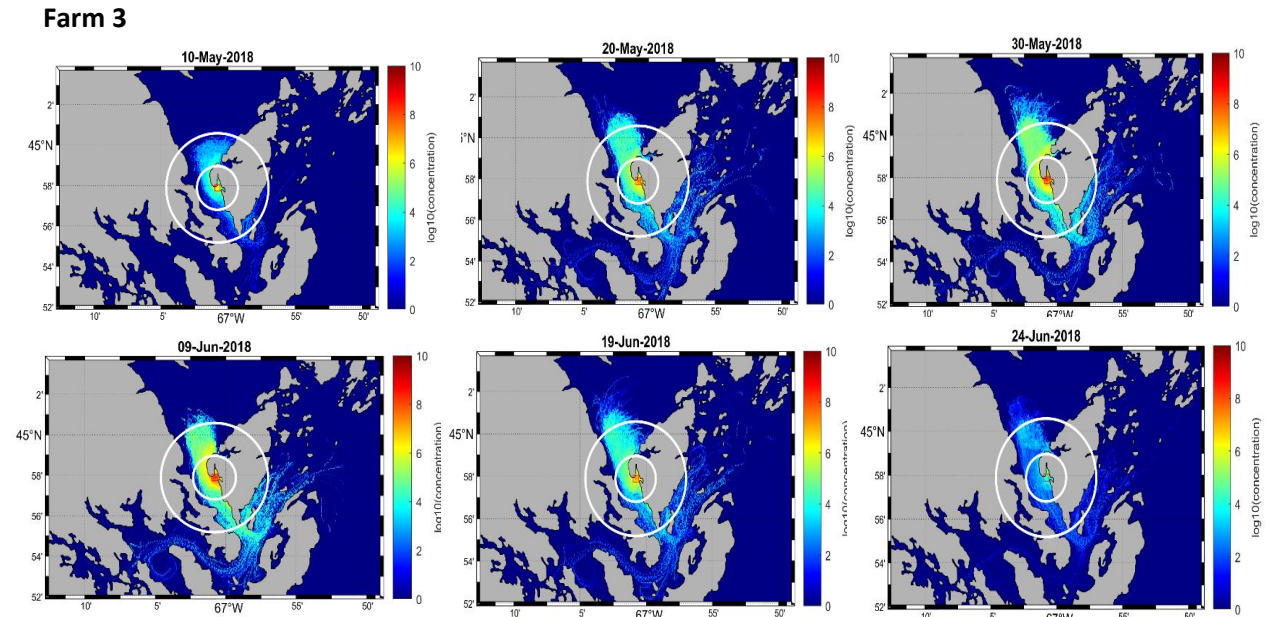
192 **Fig. S6.1** Average daily ISAV concentration ($\log_{10}(\text{TCID}_{50} \cdot \text{m}^{-3})$) released from Farm 2 over the top 15 m
193 of the water column at day 30 post-outbreak and using two different secondary grids. A: 135 m \times 47 m
194 and B: 200 m \times 200 m. The radii of the two red circles centered at Farm 2 are 2 km and 5 km,
195 respectively.
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198 **Supplementary Information 7. Concentration maps for all selected farms**

199 Daily dispersal maps with the average viral load over the top 15 m of the water column were
200 produced for all selected farms following a simulated outbreak, and are posted below to provide the
201 reference ISAV dispersal predictions from our framework.



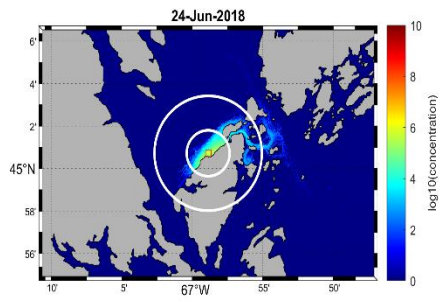
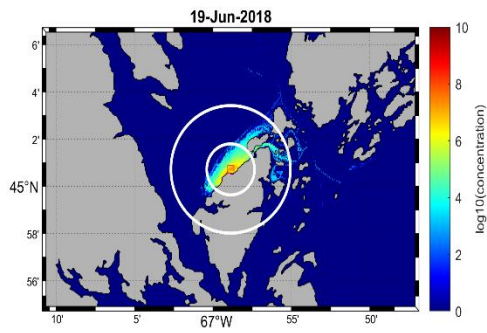
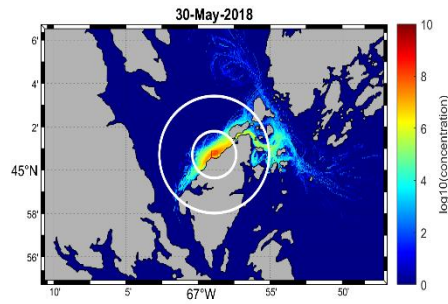
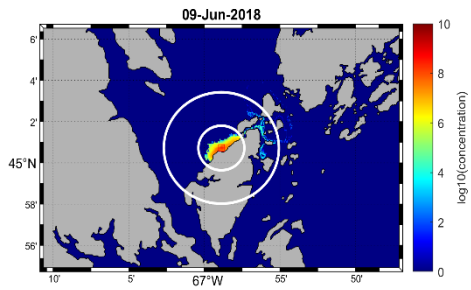
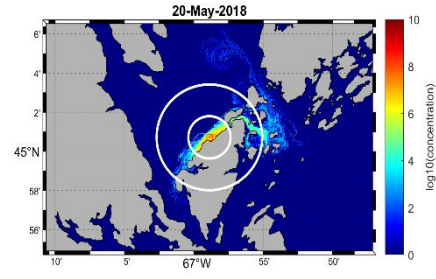
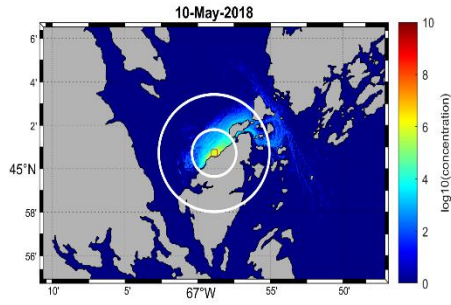
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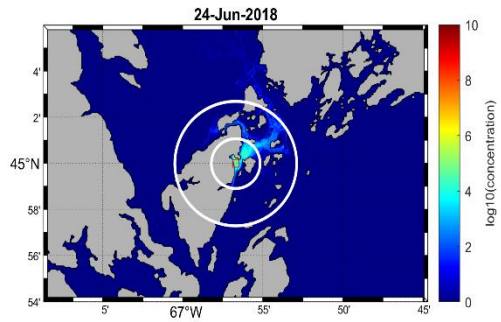
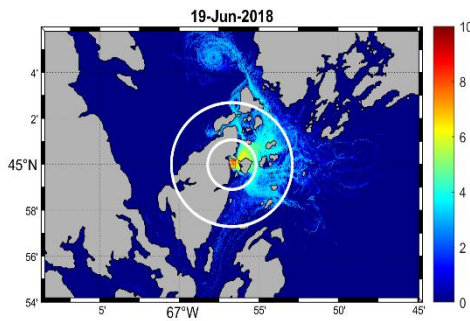
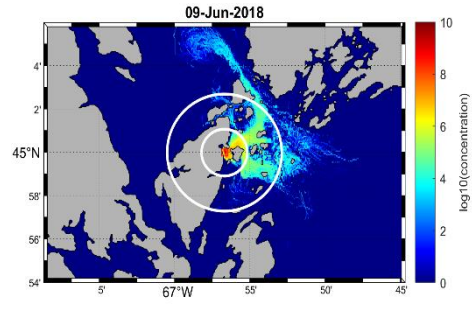
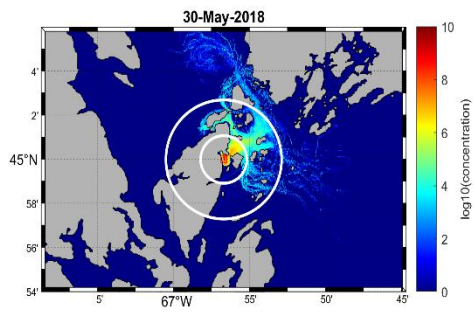
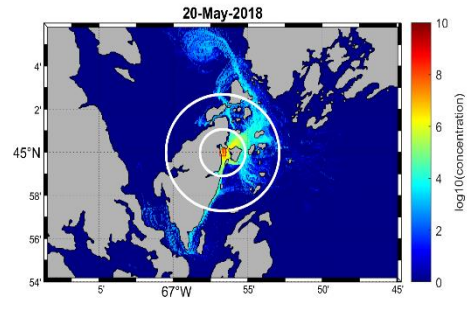
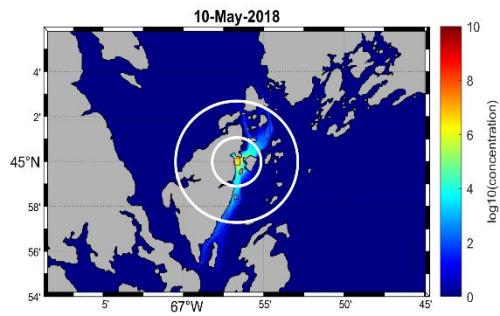
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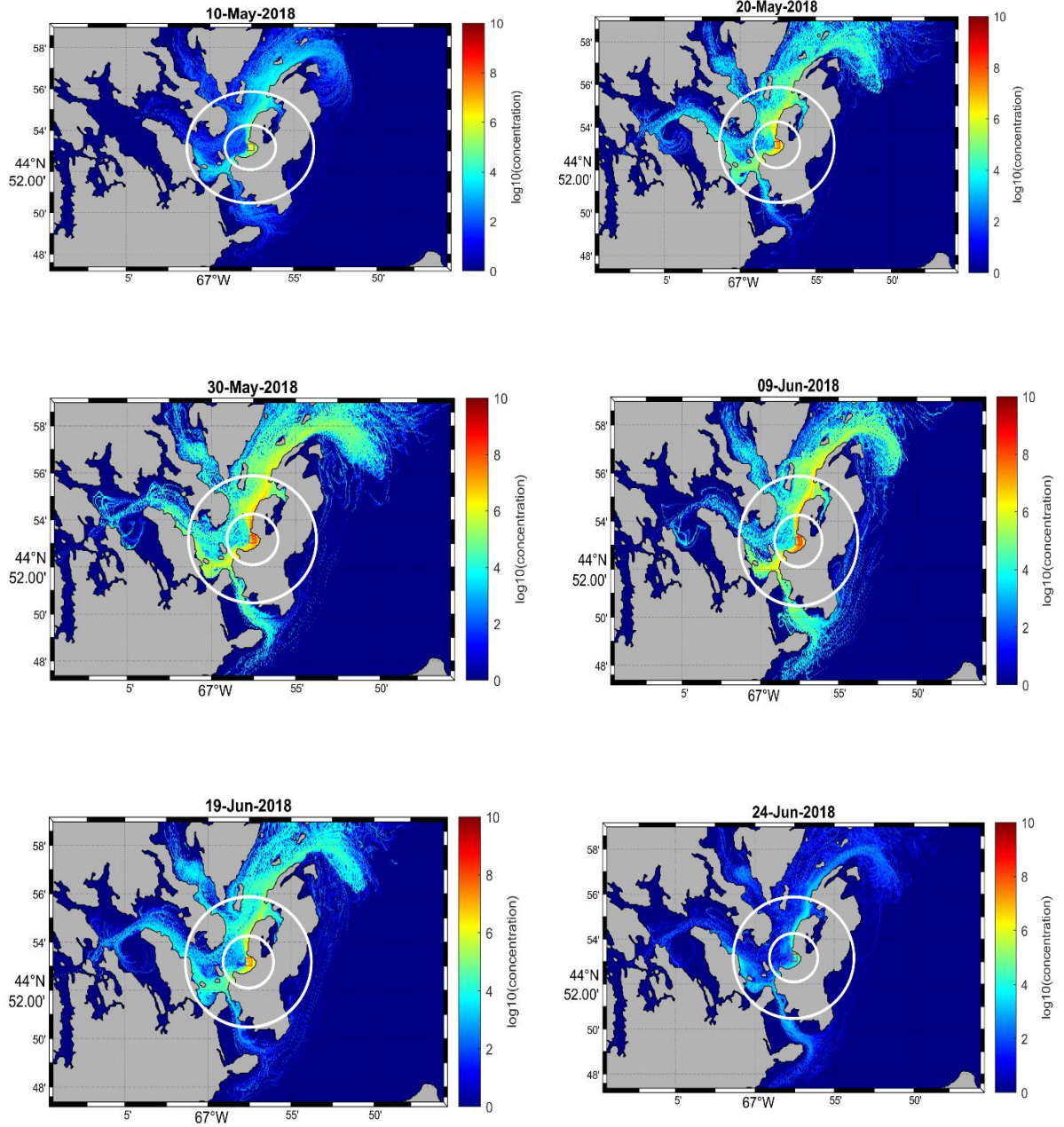
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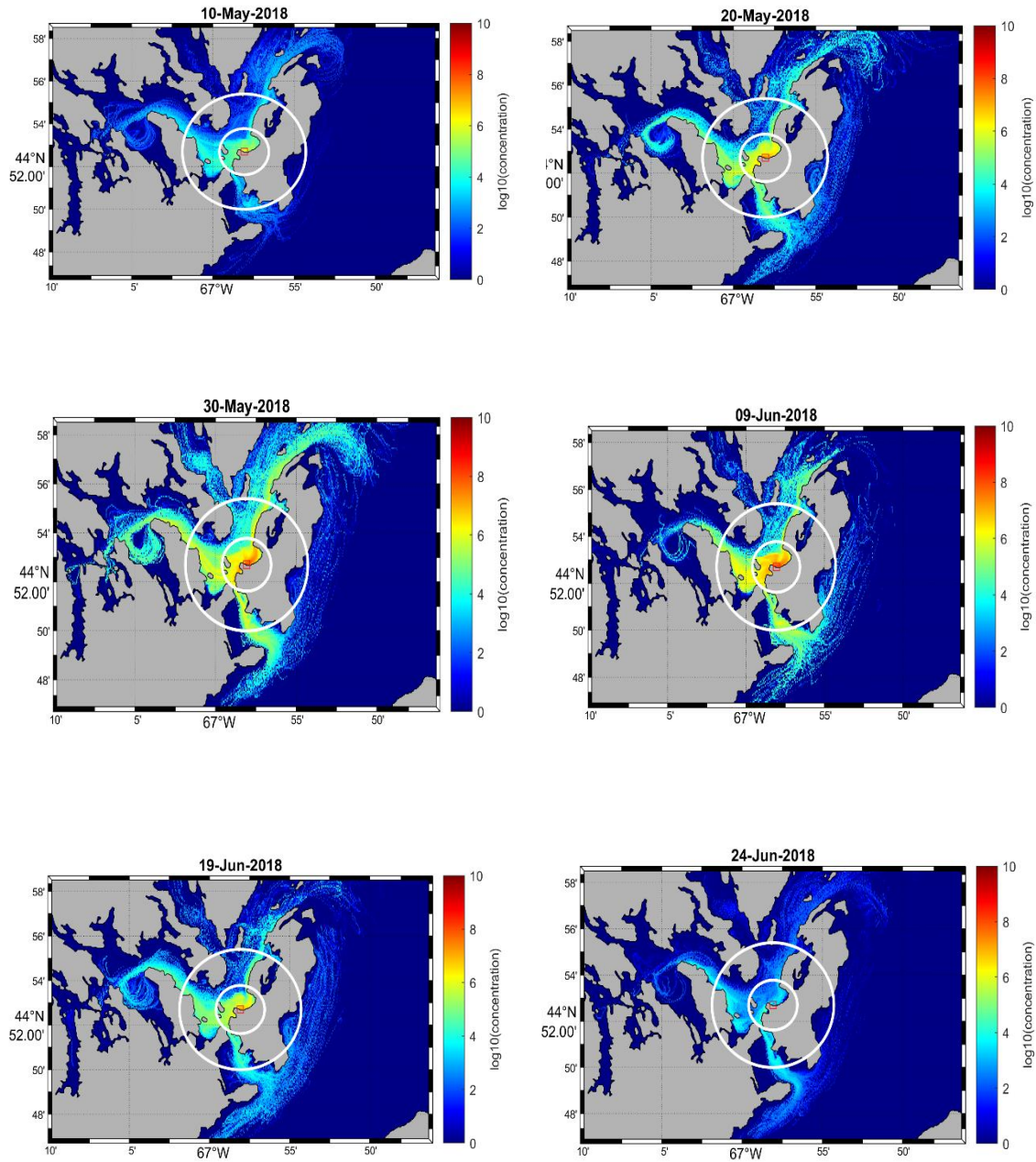
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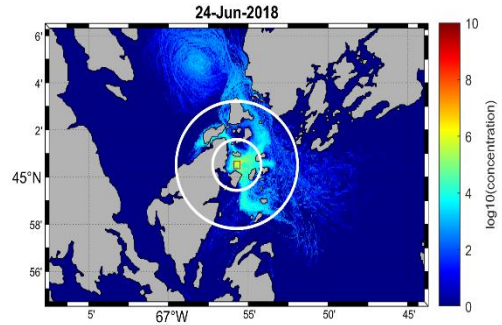
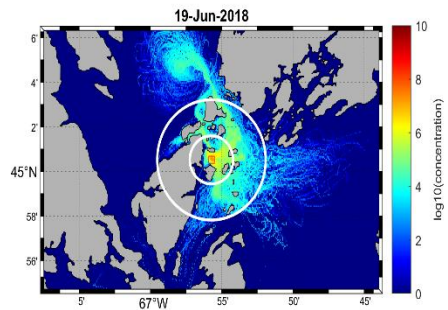
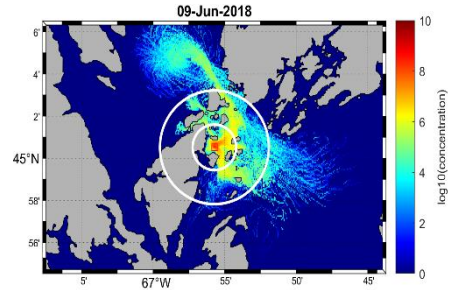
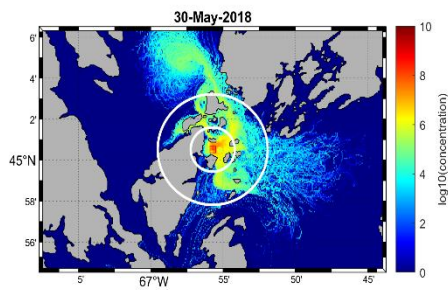
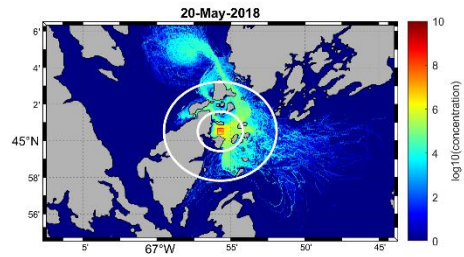
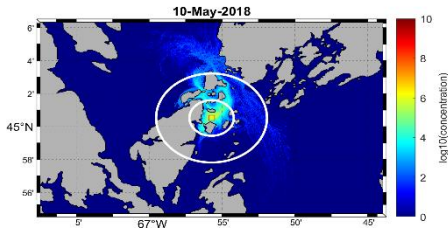
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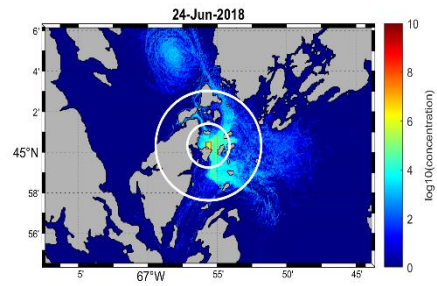
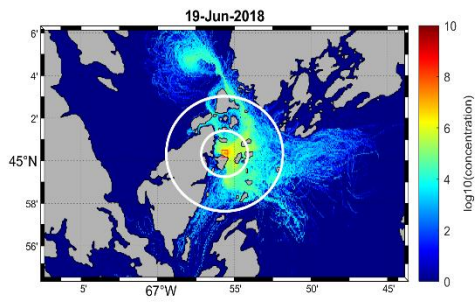
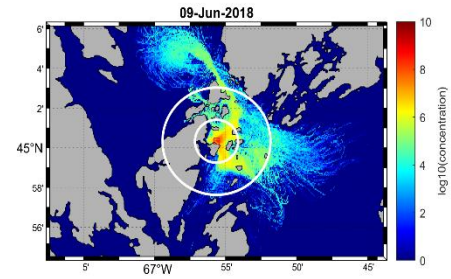
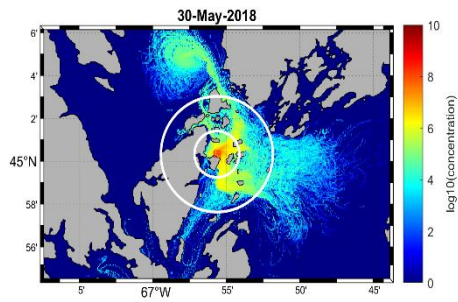
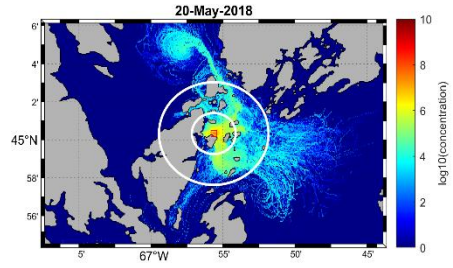
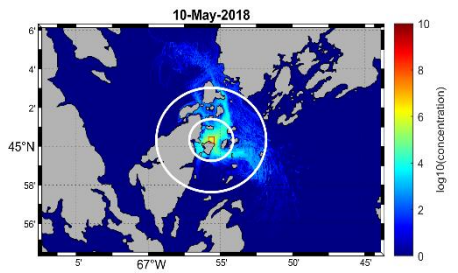
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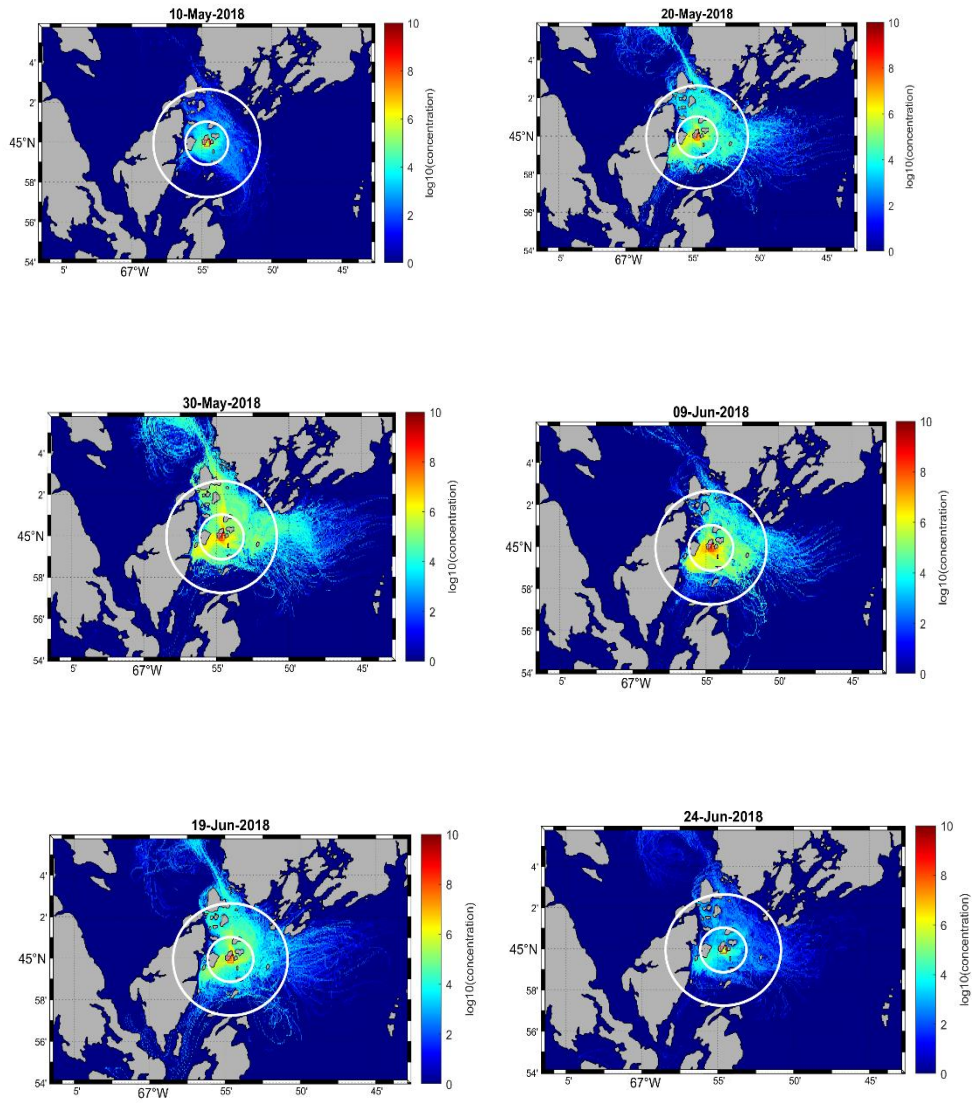
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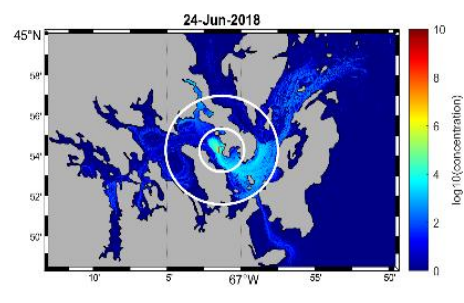
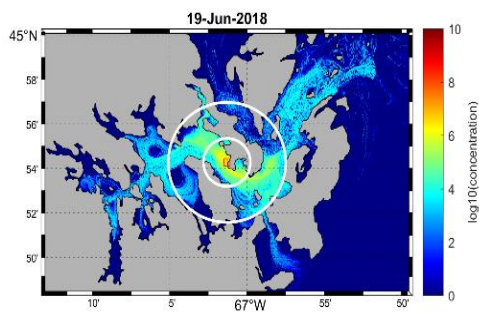
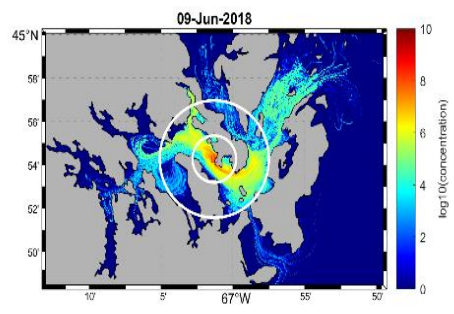
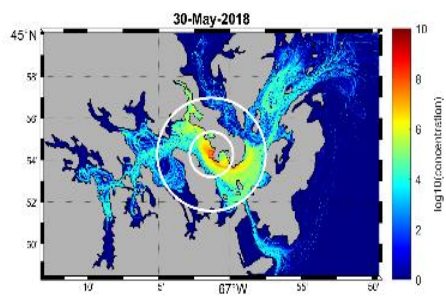
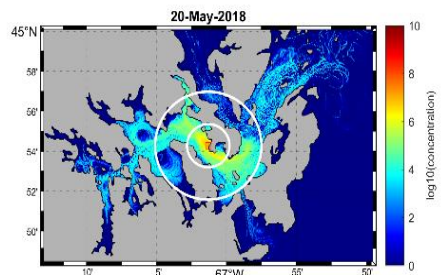
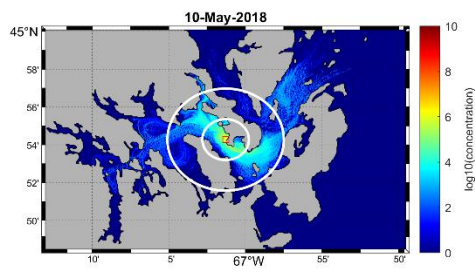
Farm 9



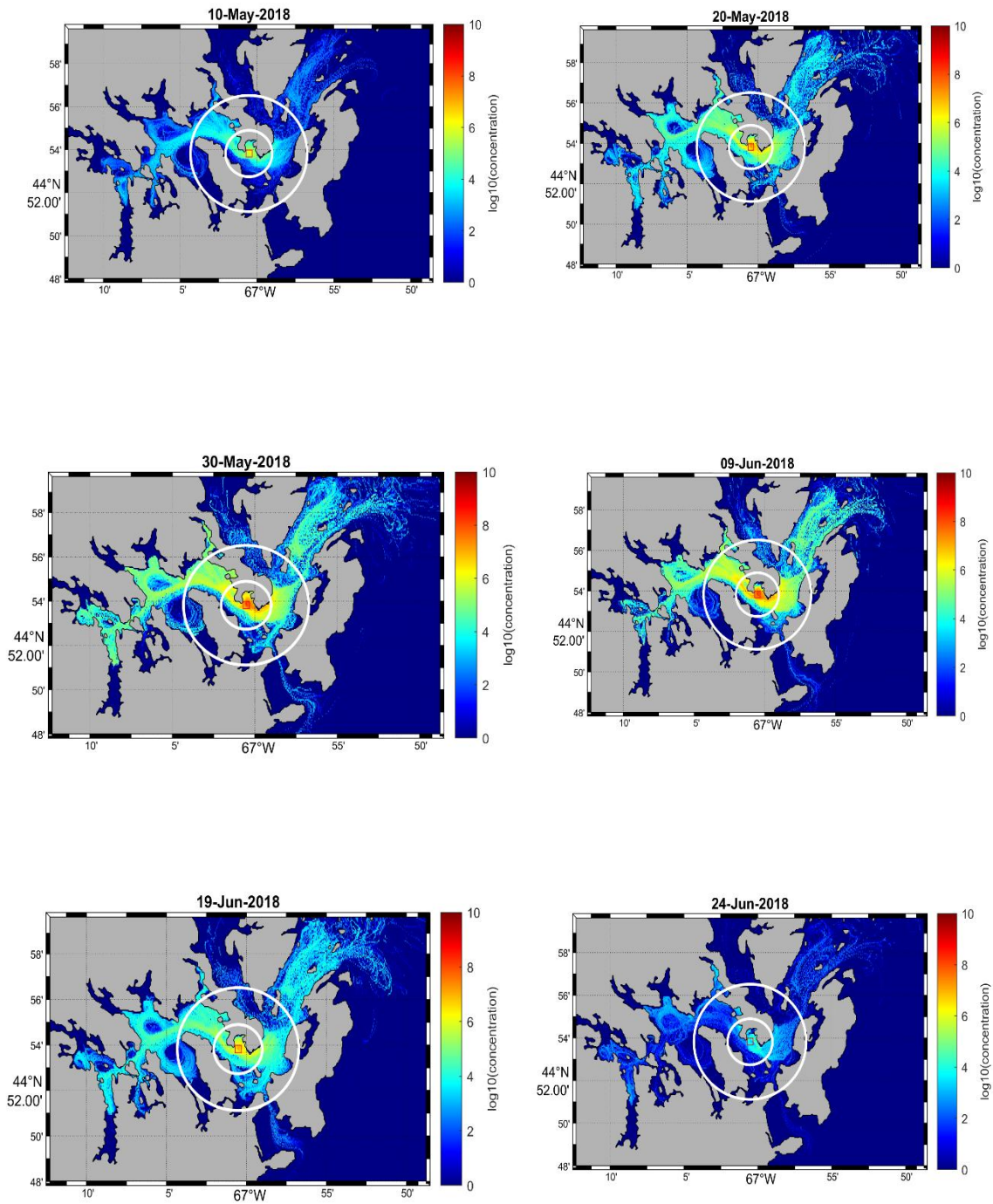
Farm 10



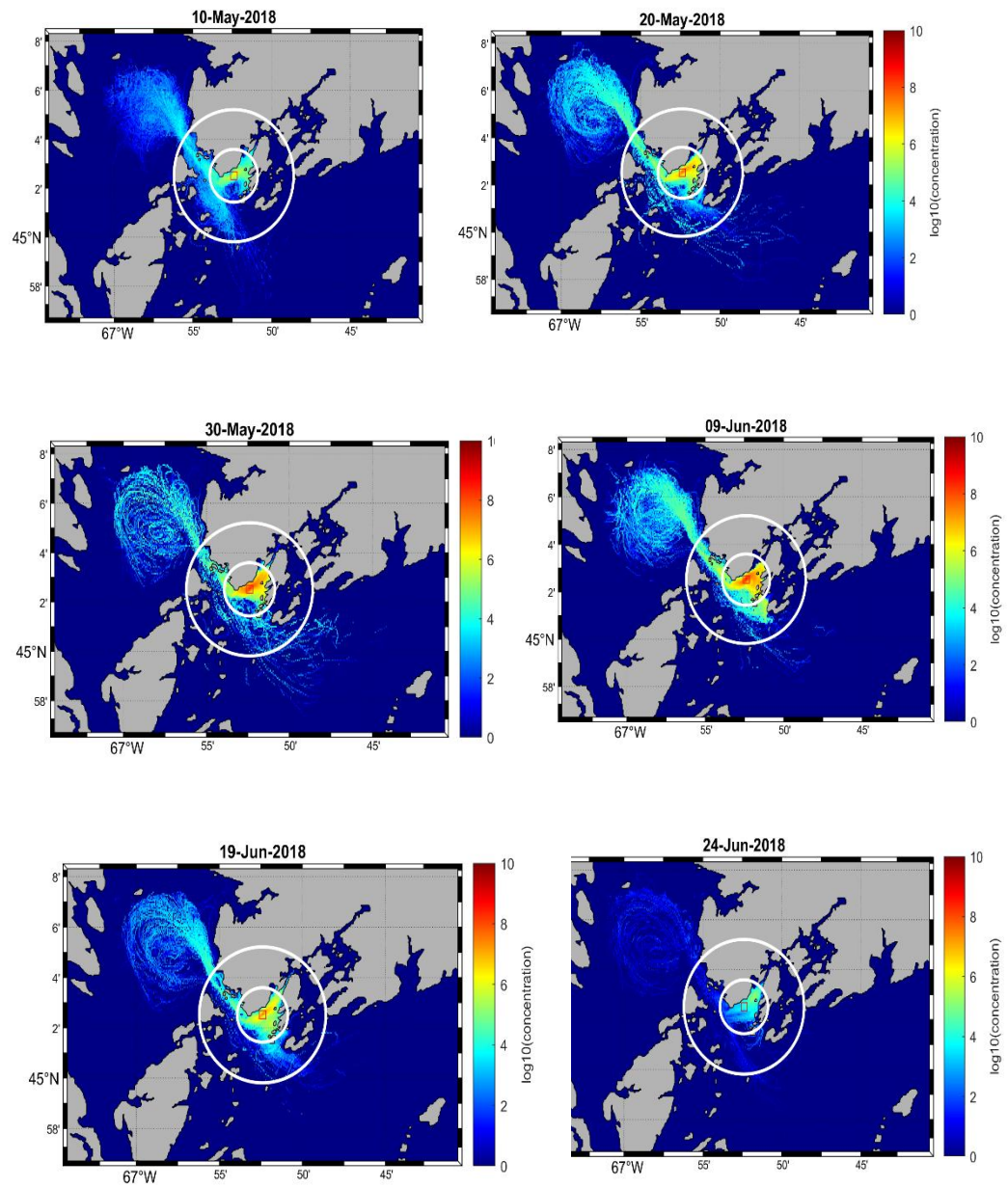
Farm11



Farm12

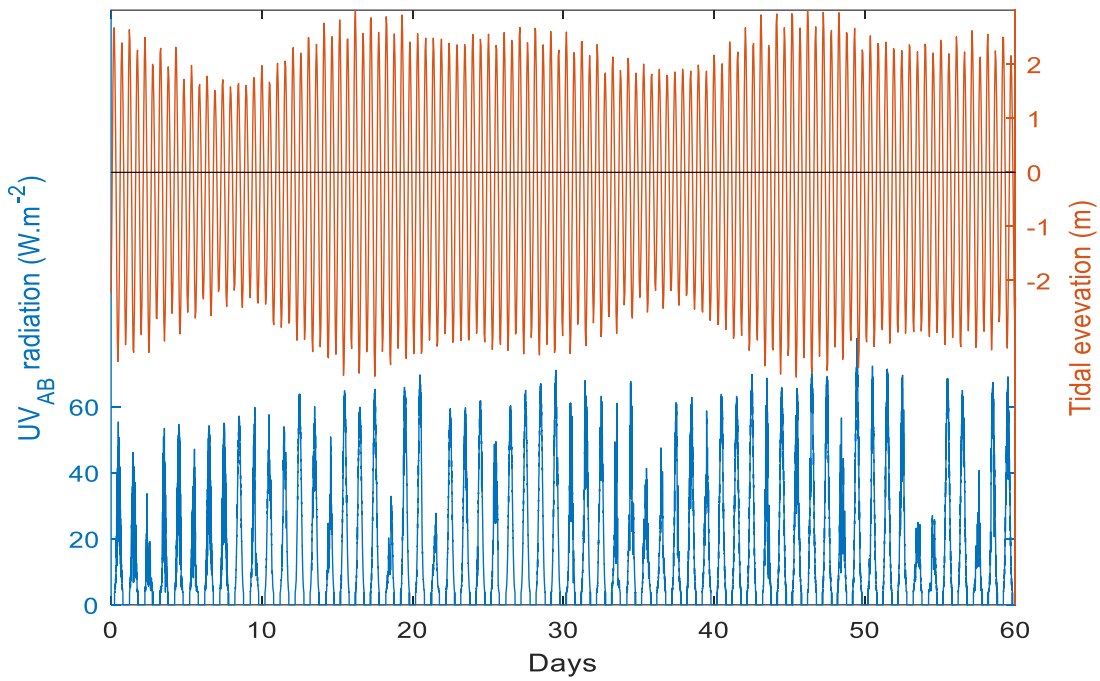


Farm13



217 **Fig. S7.1** ISAV concentration ($\log_{10}(\text{TCID}_{50} \text{ m}^{-3})$) in the top 15 m of the water column and summed over
218 a 24-h period on (10, 20, 30, 40, 50, and 55 days) post-outbreak, released from Farms 1 and 3-13. For
219 each the red square represents the Farm's location. The radii of the two white circles centered at the
220 Farms are 2 km and 5 km, respectively.
221

222 **Supplementary Information 8. Tidal elevation in Passamaquoddy Bay and UV radiation.**



223

224 **Fig. S8.1** Tidal elevation in Farm 2 from the ocean circulation module (red line) and UV_{AB} radiation
225 (blue line) during May 1 to Jun 30, 2018.

226 Note: Ultraviolet (UV) index raw data is from the closest available UV monitoring station in Toronto, ON
227 (Canada). Data available at: <https://exp-studies.tor.ec.gc.ca/>. The conversion method from UV index to
228 UV_{AB} radiation is detailed in Supplementary Material.

229