



## What and where? Predicting invasion hotspots in the Arctic marine realm

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Keywords:	Aquatic invasive species, Risk of invasion, Shipping, Species distribution model, Habitat suitability, Maxent, Climate warming
Abstract:	<p>The risk of aquatic invasions in the Arctic is expected to increase with climate warming, greater shipping activity and resource exploitation in the region. Planktonic and benthic marine aquatic invasive species (AIS) with the greatest potential for invasion and impact in the Canadian Arctic were identified and the 23 riskiest species were modelled to predict their potential spatial distributions (using Maximum Entropy) at pan-Arctic and global scales. Modelling was conducted under present environmental conditions and two intermediate future (2050 and 2100) global warming scenarios. Hotspots – regions of the Arctic where habitat is predicted to be suitable for a high number of potential AIS – were located in Hudson Bay, Northern Grand Banks/Labrador, Chukchi/Eastern Bering Seas, and Barents/White Seas, suggesting that these regions could be more vulnerable to invasions. Most benthonic and planktonic organisms showed a trend for a positive poleward shift in suitable habitat in the future. At a pan-Arctic scale, planktonic and, in particular, benthic organism, showed positive predicted suitable habitat gains under future conditions. However, at the global scale, habitat loss was predicted in more tropical regions for some taxa, particularly planktonic species. Results from the present study can help prioritize management efforts in the face of climate change in the Arctic marine ecosystem. Moreover, this particular approach provides information to identify present and future high-risk areas for AIS in response to global warming.</p>



# What and where? Predicting invasion hotspots in the Arctic marine realm

**Running head:** Arctic marine invasion hotspots

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## 22 Abstract

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40

## 41 Introduction

42 Invasive species are considered to be one of the main drivers of biodiversity loss and recent  
43 extinctions (Bellard, Cassey, & Blackburn, 2016; Blackburn, Bellard, & Ricciardi, 2019). In

addition, they may cause great ecological and economic impacts and, in some cases, even impact human health (Cook, Payne, MacLeod, & Brown, 2016; Hewitt, Campbell, & Gollasch, 2006; Ricciardi, Hoopes, Marchetti, & Lockwood, 2013; Simberloff et al., 2013). Estimates suggest that their presence may entail costs of up to 12% of the gross domestic product of affected countries (Marbua, Gren, & McKie, 2014).

The greatest numbers of aquatic invasions have been documented in temperate regions (Ruiz & Hewitt, 2009). However, high latitude areas are generally warming at a faster rate than other areas (Overland et al., 2018) and various climate change scenarios predict that the ice-free season will continue to lengthen (Barnhart, Miller, Overeem, & Kay, 2016; Jahn, 2018; Niederdrenk & Notz, 2018; Sigmond, Fyfe, & Swart, 2018). If warming is limited to 1.5 °C, as proposed in the Paris Agreement, ice-free summers in the Arctic will continue to rise even if global warming ceases (Screen, 2018). Moreover, temperature extremes at regional scales could be much greater than the global mean with some models predicting a rise greater than 7°C in the Arctic with a global average increase of only 1.5°C at peak warming (Seneviratne et al., 2018). Aquatic invasions in Arctic ecosystems have thus been identified as an emerging issue (Ricciardi et al., 2017) as the area is becoming increasingly susceptible due to regional climate change and associated increases in shipping activity and resource exploitation (Melia, Haines, & Hawkins, 2016; Miller & Ruiz, 2014; Niimi, 2004; Smith & Stephenson, 2013).

One of the leading causes of increasing invasion risk is the expansion of transportation networks (Early et al., 2016). Aquatic transportation, in particular, is highly relevant given that the shipping network is responsible for 90% of global trade (Kaluza, Kölzsch, Gastner, & Blasius, 2010; Xu et al., 2014), with ballast water and biofouling being the main vectors for transport of organisms (Bailey, 2015; Drake & Lodge, 2007; Ruiz, Fofonoff, Steves, & Carlton, 2015). Consequently,

67 marine taxa are one of the dominant groups that are unintentionally introduced at a global scale  
68 (Turbelin, Malamud, & Francis, 2017), and are predicted to contribute up to a 3- to 20-fold increase  
69 in global invasion risk (Sardain, Sardain, & Leung, 2019). In the Arctic, almost half of all known  
70 marine invasions to date have been due to shipping activities as a single-pathway means of  
71 transport (Chan et al., 2019). Greater opportunities for aquatic invasive species (AIS) transport are  
72 expected in the future as shipping traffic is also projected to grow given predicted ice-free  
73 conditions that will allow a more direct shipping corridor between the Pacific and the Atlantic  
74 oceans (Melia et al., 2016; Miller & Ruiz, 2014; Smith & Stephenson, 2013), reducing transit  
75 distances by up to 24% relative to current shipping routes (Buixadé Farré et al., 2014).

76 A recent study tallied a total of 34 non-indigenous species for the entire Arctic, with shipping  
77 activity being one of the main purported vectors (Chan et al., 2019). In addition, non-indigenous  
78 species have been identified from both ships *en route* to the Arctic and in the environment to which  
79 they arrive, highlighting the risk of new invasions in this region (Ashton, Riedlecker, & Ruiz,  
80 2008; Chan, MacIsaac, & Bailey, 2015; Dispas, 2019; Gíslason et al., 2014; Golder, 2018; Laget,  
81 2017; Lambert, Shenkar, & Swalla, 2010; Svavarsson & Dungal, 2008; Tremblay, 2017; Zimina,  
82 2014). Further, the origin of many newly observed species in Arctic locations is unknown and they  
83 have thus been classified as cryptogenic (Goldsmith, Howland, & Archambault, 2014; MacDonald,  
84 Bluhm, Iken, Gagaev, & Strong, 2010). These numbers are high compared to the other polar  
85 environment – the Antarctic – where there are no established AIS populations to date and only five  
86 non-indigenous marine species have potentially arrived through human activities (McCarthy,  
87 Peck, Hughes, & Aldridge, 2019). Although Hughes et al. (2020) suggest marine taxa pose the  
88 greatest potential invasion risk to the Antarctic Peninsula relative to other types of organisms.  
89 Commercial shipping is not expected to increase in the region and resource exploitation is

restricted under the Antarctic Treaty. However, the shortening sea ice season and increased shipping traffic due to tourism may increase risks of invasions (Ruiz & Hewitt, 2009; Hughes & Ashton, 2017; Jabour, 2017).

Given the vast size and remoteness of the Arctic, few baseline studies have been conducted (Archambault et al., 2010; CAFF and PAME, 2017; Piepenburg et al., 2011) and the resident fauna are thus poorly described relative to more accessible locations elsewhere in the world (Costello et al., 2017). Consequently, simply identifying newly arriving species can be challenging. To improve this detection gap, new methods and identification techniques are being used in remote regions, such as environmental DNA and metabarcoding (E. A. Brown, Chain, Zhan, MacIsaac, & Cristescu, 2016; Chain, Brown, MacIsaac, & Cristescu, 2016; Lacoursière-Roussel et al., 2018; Leduc, 2019). In addition, methods such as species distribution modelling (SDM) may be used to predict the potential distribution of suitable habitat for AIS (Barbosa & Schneck, 2015; Barbosa, Schneck, & Melo, 2012), including for high risk AIS in areas of concern such as in high latitude regions (Byrne, Gall, Wolfe, & Agüera, 2016; de Rivera, Steves, Fofonoff, Hines, & Ruiz, 2011; Goldsmit et al., 2018; Ware et al., 2016). Modelled results can inform pre-invasion management policies to avoid new arrivals and, potentially, subsequent issues with the establishment of the species and the consequent need to deal with eradication actions (Floerl, 2014; Locke & Hanson, 2009).

Although future invasions are expected to be enhanced by climate change (Bellard et al., 2013), predicted SDM-modelled distributions of environmental suitability for invasive species have been understudied in this context (Bellard, Jeschke, Leroy, & Mace, 2018), particularly for marine ecosystems (Barbosa et al., 2012; Bellard et al., 2018). Nevertheless, SDM tools such as MaxEnt, have been successfully applied to marine species (Lowen, McKindsey, Therriault, & DiBacco,

113 2016; Meißner et al., 2014; Reiss, Cunze, König, Neumann, & Kröncke, 2011; Robinson et al.,  
114 2011; Weinert et al., 2016; Robinson, Nelson, Costello, Sutherland, & Lundquist, 2017), including  
115 forecasting distributions under global change scenarios in high latitude regions (de Rivera et al.,  
116 2011; Goldsmit et al., 2018; Jueterbock, Smolina, Coyer, & Hoarau, 2016).

117 Regions where many species coincide are known as biodiversity hotspots and may provide  
118 information about species richness, endemism and/or threatened taxa, and may be of importance  
119 for conservation (Myers, Mittermeier, Mittermeier, Da Fonseca, & Kent, 2000). Based on this  
120 concept, potential invasion hotspots may be identified as areas that are hospitable to and thus at  
121 risk to invasion by a greater than average numbers of AIS for a given region (Ruiz, Fofonoff,  
122 Steves, Foss, & Shiba, 2011). The use of a biological invasions hotspot approach has been limited  
123 to date (but see Bellard, Leroy, Thuiller, Rysman, & Courchamp, 2016; Catford, Vesk, White, &  
124 Wintle, 2011; Ibanez, Silander Jr, Allen, Treanor, & Wilson, 2009, O'Donnell et al., 2012; Torres  
125 et al., 2018) with few studies in marine environments. Most analyses of AIS hotspots in marine  
126 ecosystems have focused on vectors (Davidson et al., 2010; Drake & Lodge, 2004; Pearce, Peeler,  
127 & Stebbing, 2012; Semmens, Buhle, Salomon, & Pattengill-Semmens, 2004; Tidbury, Taylor,  
128 Copp, Garnacho, & Stebbing, 2016) and current AIS richness (Edelist, Rilov, Golani, Carlton, &  
129 Spanier, 2013; Katsanevakis et al., 2014; Kelly, Leach, Cameron, Maggs, & Reid, 2014; Rilov &  
130 Galil, 2009; Ruiz et al., 2011; Verlaque, 2001), although a few have also predicted hotspots of  
131 potential marine biological invasions (Cheung et al., 2009; Gallardo, Zieritz, & Aldridge, 2015;  
132 Jones & Cheung, 2015).

133 This study aims to identify potential high risk AIS and predict hotspots of invasion for these under  
134 current and projected future environmental conditions in Arctic environments. Cold-tolerant  
135 planktonic and benthic AIS were scored to produce a list of the top species with the highest relative



likelihood of invasion and impact, since these ecological groups include the dominant known highest risk marine invasive species (Molnar, Gamboa, Revenga, & Spalding, 2008). The distribution of suitable habitats for this set of species was then modelled to predict regions of overlap under current and future projected conditions, thus identifying hotspots of potential biological invasions. Although all analyses were done globally, there was an emphasis at the Canadian and pan-Arctic scales.

## Materials and methods

### Study region

Distribution model outputs were produced with global coverage to allow evaluation of global and pan-Arctic patterns although analyses were focussed on the potential highest-risk species for the Canadian Arctic. The rationale for this approach is the vast expanse of the Canadian Arctic (Archambault et al., 2010), its vulnerability to invasion (Chan, Bailey, Wiley, & MacIsaac, 2013; Chan, MacIsaac, & Bailey, 2016; Goldsmit et al., 2018; Goldsmit, McKindsey, Archambault, & Howland, 2019), the ambiguous status of new species that have potentially arrived through human transport (Goldsmit et al., 2014), and the unprecedented warming that it has experienced over the last decade (Bush & Lemmen, 2019). The region is immense, accounting for eight of 19 Arctic ecoregions (Figure 1) (Spalding et al., 2007). In fact, Canada has the longest coastline in the world, the majority of which is situated in the Arctic (it accounts for almost 2,000,000 km<sup>2</sup> of the territorial sea) (Archambault et al., 2010). Even though few AIS have been identified in Canada relative to other Arctic regions, Chan et al. (2019) suggest that this accounts for ca. 20% of all AIS recorded from marine Arctic waters. At the same time, additional species have been identified for the first time in the Canadian Arctic using molecular tools (E. A. Brown et al., 2016; Chain et al.,

2016; Lacoursière-Roussel et al., 2018) or identified as cryptogenic as their origin is unclear (Goldsmith et al., 2014). Moreover, Canadian Arctic ports (especially those in the Hudson Complex) (Figure 1) have been identified as being of moderate to high ecological risk of invasion since they could provide suitable habitat for various AIS (Goldsmith et al., 2018; Goldsmith, Nudds, et al., 2019) and there is evidence that a number of non-indigenous species are already being transported by shipping traffic into the region (Chan et al., 2015; Dispas, 2019; Laget, 2017; Tremblay, 2017).

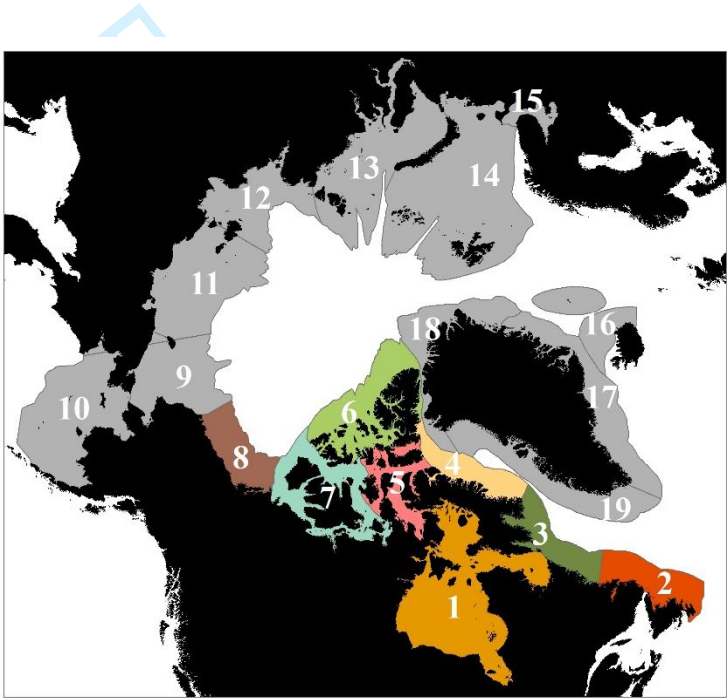


Figure 1: Arctic ecoregions as delineated by Spalding et al. (2007). Canadian Arctic ecoregions are coloured. 1: Hudson Complex; 2: Northern Grand Banks-Southern Labrador; 3: Northern Labrador; 4: Baffin Bay-Davis Strait; 5: Lancaster Sound; 6: High Arctic Archipelago; 7: Beaufort-Amundsen-Viscount Melville-Queen Maud; 8: Beaufort Sea-continental coast and shelf; 9: Chukchi Sea; 10: Eastern Bering Strait; 11: East Siberian Sea; 12: Laptev Sea; 13: Kara Sea; 14: Northern and East Barents Sea; 15: White Sea; 16: North and East Iceland; 17: East Greenland Shelf; 18: North Greenland; 19: West Greenland Shelf.

## Species selection

A three-step procedure was used to select potential marine AIS (zoobenthos, **phytobenthos** and zooplankton) for modelling (Figure **S1**). The majority were species that are considered AIS in other regions of the world and have the possibility **of being** transported through shipping to the Canadian Arctic; **several other AIS had been** previously detected in other Arctic environments. These steps included: 1) pre-screening analysis and selection; 2) ranking a subset of these species using a semi-quantitative screening-level risk assessment tool, the Canadian Marine Invasive Screening Tool (CMIST) (Drolet et al., 2016); and 3) selecting a final list of higher risk species based on CMIST.

The first step of the pre-screening analysis considered biological and ecological characteristics that could allow a given organism to survive Arctic conditions (e.g., temperature and salinity tolerance of the species needed to generally fall within the range of expected Arctic conditions) and information on the potential of it arriving in the region via shipping (Figure **S1.1**). One hundred species were thus pre-screened using a combination of data sources including published articles (Chain et al., 2016; Chan et al., 2012; **Chan et al., 2015**; Chan et al., 2016; Geller & Ruiz, 2013; Hines, Ruiz, & Fofonoff, 2000; Molnar **et al.**, 2008; Ruiz et al., 2006; Turbelin et al., 2017; Ware et al., 2016; Young, 2016), grey literature and web-based global invasive species databases such as the National Exotic Marine and Estuarine Species Information System (NEMESIS; [www.invasions.si.edu/nemesis/](http://www.invasions.si.edu/nemesis/)), Invasive Species Compendium ([www.cabi.org/isc](http://www.cabi.org/isc)), the European Network on Invasive Alien Species NOBANIS ([www.nobanis.org/](http://www.nobanis.org/)) and the Global Invasive Species Database GISD ([www.issg.org/database](http://www.issg.org/database)).

A total of 31 species were identified as being of potential risk to the area using this pre-screening process (Figure **S1.2a**). These species were then ranked to evaluate risk of **invasion** using CMIST

(Drolet et al., 2016) — a rapid screening-level risk assessment tool to quantify the risk of existing or potential marine invaders in a given area. The semi-quantitative tool uses existing information and expert opinion to evaluate the potential for arrival, establishment, spread, and impact by a given species and has been applied in a number of eco-regions within Canada (DFO, 2017; Drolet et al., 2016; A. M. Moore, Lowen, & DiBacco, 2018; Therriault et al., 2018). CMIST scores are computed based on responses to 17 questions related to the likelihood and impact of invasion (see Figure S1.2a). The information used to answer CMIST questions included published articles, governmental reports, grey literature, and the global invasive species websites listed above for each species. Expert assessor knowledge on the risk assessment areas was used to score the potential impact of a given species based on its known impacts observed elsewhere and the availability of suitable habitats and environmental conditions. Uncertainty is scored for each risk question by assigning a qualitative score reflecting the quality of information available to answer each CMIST question. A Monte Carlo randomization procedure is then used to obtain adjusted risk scores that include uncertainty (Drolet et al., 2016).

CMIST-ranked species with medium and high mean risk scores (N=18; Table 1) were retained for more detailed assessment using SDM. To this list, five potentially harmful phytoplankton species were added (Table 1, Figure S1.2b). These dinoflagellate species have been found in ballast water tanks and/or in ballast water exchange zones of Canadian domestic ships that discharge their water in Canadian Arctic ports (Laget, 2017). All are known to have the capacity to produce toxins and have been implicated in harmful algal events throughout the world (Harmful Algal Information System, from the Intergovernmental Oceanographic Commission of UNESCO, <http://haedat.iode.org/>).

The final species list for modelling thus included a total of 23 known marine AIS or harmful algal species from 4 ecological groups (zoobenthos, phytobenthos, zooplankton and phytoplankton) that pose potential risks for invasion in the Canadian Arctic. To simplify terminology, hereafter when referring to this suite of species they will be termed as ‘AIS’. (See Table S1 for information on species’ characteristics and impacts). Likewise, the term “invasion” is used to make reference to the complete process of a species transitioning all invasion stages (transport, arrival, establishment, and spread) (Lockwood, Hoopes, & Marchetti, 2007).

Table 1: List of modelled species and the methodology for species selection. Ecological groups were classified as zoobenthos, phytobenthos, zooplankton, and phytoplankton. Selection methods were the Canadian Marine Invasive Screening Tool (CMIST) (Drolet et al., 2016), and harmful dinoflagellate species found in ballast of vessels discharging in the Canadian Arctic (Laget, 2017).

Species	Common name	Taxa	Ecological group	Selection method	Predictors included in SDM
<i>Amphibalanus eburneus</i>	Ivory barnacle	Crustacea	Zoobenthos	CMIST	Bottom temperature Sea surface temperature Bottom salinity Sea surface salinity Ice thickness Depth Distance to land
<i>Botrylloides violaceus</i>	Violet tunicate	Tunicata	Zoobenthos	CMIST	
<i>Botryllus schlosseri</i>	Golden star tunicate	Tunicata	Zoobenthos	CMIST	
<i>Carcinus maenas</i>	Green crab	Crustacea	Zoobenthos	CMIST	
<i>Chionoecetes opilio</i>	Snow crab	Crustacea	Zoobenthos	CMIST	
<i>Ciona intestinalis</i>	Vase tunicate	Tunicata	Zoobenthos	CMIST	
<i>Littorina littorea</i>	Common periwinkle	Mollusca	Zoobenthos	CMIST	
<i>Membranipora membranacea</i>	Coffin box bryozoan	Bryozoa	Zoobenthos	CMIST	
<i>Molgula manhattensis</i>	Sea grape	Tunicata	Zoobenthos	CMIST	
<i>Mya arenaria</i>	Soft shell clam	Mollusca	Zoobenthos	CMIST	
<i>Paralithodes camtschaticus</i>	Red king crab	Crustacea	Zoobenthos	CMIST	

<i>Codium fragile</i> <i>spp. fragile</i>	Dead man's fingers	Chlorophyta	Phytobenthos	CMIST	Bottom temperature Sea surface temperature Bottom salinity Sea surface salinity Ice thickness Depth Distance to land Photosynthetically active radiation Dissolved oxygen pH Minerals and nutrients (calcite, iron, nitrate, phosphate, and silicate)
<i>Dumontia</i> <i>contorta</i>	Dumont's tubular weed	Rhodophyta	Phytobenthos	CMIST	
<i>Sargassum</i> <i>muticum</i>	Japanese wireweed	Phaeophyceae	Phytobenthos	CMIST	
<i>Undaria</i> <i>pinnatifida</i>	Wakame	Phaeophyceae	Phytobenthos	CMIST	
<i>Acartia</i> ( <i>Acanthacartia</i> ) <i>tonsa</i>	No common name found	Copepoda	Zooplankton	CMIST	Sea surface temperature Bottom salinity Sea surface salinity Ice thickness Depth Distance to land Chlorophyll concentration Dissolved oxygen pH
<i>Aurelia</i> <i>limbata</i>	Brown- branded moon jelly	Cnidaria	Zooplankton	CMIST	
<i>Mnemiopsis</i> <i>leidy</i>	Warty comb jelly	Ctenophora	Zooplankton	CMIST	
<i>Alexandrium</i> <i>tamarense</i>	No common name found	Dinoflagellata	Phytoplankton	Laget (2017)	
<i>Dinophysis</i> <i>caudata</i>	No common name found	Dinoflagellata	Phytoplankton	Laget (2017)	Sea surface temperature Sea surface salinity Ice thickness Distance to land Photosynthetically active radiation Dissolved oxygen pH Minerals and nutrients (iron, nitrate, phosphate, and silicate)
<i>Dinophysis</i> <i>dens</i>	No common name found	Dinoflagellata	Phytoplankton	Laget (2017)	
<i>Gonyaulax</i> <i>polygramma</i>	No common name found	Dinoflagellata	Phytoplankton	Laget (2017)	
<i>Kryptoperidinium</i> <i>triquetrum</i>	No common name found	Dinoflagellata	Phytoplankton	Laget (2017)	

235

236 Species data

237 Global scale occurrence data of marine invaders selected for modelling was compiled for both  
 238 native and invaded ranges using global biodiversity databases such as the Global Biodiversity  
 239 Information Facility (GBIF - [www.gbif.org](http://www.gbif.org)), Ocean Biogeographic Information System (OBIS -

[www.obis.org](http://www.obis.org)), and invasive species lists with coordinate location information and specific literature (Table S1). An effort was made to maximize the number and quality of occurrence records to best predict potential distributions by doing a vast and complete search of occurrence records and by checking information to find the original source of those records (García-Roselló et al., 2015; Guisan, Graham, Elith, & Huettmann, 2007; Guisan, Zimmermann, et al., 2007; Lobo, 2008). The inclusion of both native and invaded ranges was used to improve predictions for the extent of suitable habitat (Broennimann & Guisan, 2008). A single presence record was counted per grid cell to decrease the possibility of over-prediction, hence, occurrence points were considered at the same resolution as the corresponding environmental layers (García-Roselló et al., 2015). All points were verified to ensure that they were in sea grids (and not over land). When necessary, points were moved to the closest sea grid using the Near Proximity tool in ArcMap v10.2.2.

#### Environmental data

Marine data layers, prepared specifically for ecological modelling, were used as environmental predictors and downloaded at a global scale from Bio-ORACLE v2 (<http://www.bio-oracle.org/>). These layers were produced with climate data describing monthly averages for the period from 2000 to 2014 representing recent (hereafter referred to as present) conditions (Assis et al., 2018). They were obtained from pre-processed global ocean re-analyses combining satellite and *in situ* observations at regular two- and three-dimensional spatial grids (Assis et al., 2018). A set of 37 environmental layers was used from this source comprising bottom and sea surface temperature and salinity, ice thickness, chlorophyll, dissolved oxygen, pH, photosynthetically active radiation, and minerals and nutrients (iron, calcite, nitrate, phosphate, and silicate) (Table 1 and Table S2). Long-term maximum, minimum and mean values were used for most of the predictors when

available (Table S2). For example, the layer of long-term maximum temperature takes the average of records that correspond to the average of the warmest months between 2000 and 2014 (Assis et al., 2018). Resolution of environmental layers was 5 arcmin (approximate 9.2 km at the equator). Bathymetry and land distance obtained from Aquamaps (<http://www.aquamaps.org/>) (Kaschner et al., 2016), were also added as layers, but with a resolution of 30 arcmin (approximate 55 km at the equator) (Table S2). Bottom substratum type was not included in the analysis due to the lack of availability of a high-resolution global scale database, however suitable benthic habitat was assumed to be present within each study region.

#### Habitat suitability model

Habitat suitability for selected AIS was modelled using MaxEnt v3.3.3k (Phillips, Anderson, & Schapire, 2006), a machine learning method based on maximum entropy. It predicts the potential geographic distribution of suitable habitat for species using species occurrence data (presence-only) and various potential combinations of environmental data layers as input. MaxEnt is one of the most widely used SDM algorithms because of its high predictive accuracy and efficiency in modelling range shifts under future climate change scenarios (Bucklin et al., 2015; Elith et al., 2006; Elith et al., 2011; Hijmans & Graham, 2006; Pearson, 2007). In addition, it has recently been shown to outperform other modelling techniques to accurately predict the distributions of invasive species (Battini, Farías, Giachetti, Schwindt, & Bortolus, 2019).

A limitation of using presence-only data in SDM is the effect of sample selection bias whereby sampling is more intensive in some areas than others (Phillips et al., 2009). To control for this, the Gaussian kernel density of sampling localities tool was used to reduce spatial sampling biases (J. L. Brown, 2014). Bias files were included in model building using the SDMtoolbox package in



ArcGIS (J. L. Brown, 2014). This method assigns a higher weighting to presence-only data points with fewer neighbors in the geographic landscape for inclusion in the SDM.

Model predictive power was evaluated using cross-validation with 70% of the occurrence points chosen randomly and used to train the model and the other 30% to test it (Araújo, Pearson, Thuiller, & Erhard, 2005). In this validation procedure, data were partitioned by a random process of  $k=500$  iterations of training and validation (Hijmans, 2012). Both native and invaded ranges were used for training and evaluating the models (Verbruggen et al., 2013), since invaded area provides valuable information on species' tolerance to climatic conditions that may not be present in its native range (Marcelino & Verbruggen, 2015). Training points were selected by random seeding with the convergence threshold set at 0.00001. The hinge feature was used as it produces complex yet smoothed and ecologically meaningful response curves and has been shown to improve model performance (Merow, Smith, & Silander, 2013; Phillips & Dudík, 2008). **MaxEnt generates background data to compare with known presence points. This study used the default option, which generates 10000 random background points.**

Initial models were run for each species individually with pre-selected environmental layers. The selected layers were those known to typically be the most important limiting factors for each type of taxa, to have been used in other modelling studies (Table 1) (Barnes, 1999; Belanger et al., 2012; Chust et al., 2016; Cusson, Archambault, & Aitken, 2007; Gallardo et al., 2015; Jensen, Mousing, & Richardson, 2017; Leidenberger, Obst, et al., 2015; Wagner, 1977), or that were identified as being important by personal communications with taxonomic experts (G. Winkler pers. comm. 2017, and A. Rochon pers. comm. 2018). After the first run, layers with a relative contribution score of  $<4\%$  were excluded (Jueterbock et al., 2016). Special attention was made to layers that were highly correlated (correlation coefficient  $\geq 0.7$ ) (Dormann et al., 2013), as

308 correlated predictors can lead the model to produce erroneous response curves to layers that do not  
309 reflect species physiological tolerances (Marcelino & Verbruggen, 2015). Correlation was  
310 calculated using the SDMtoolbox (J. L. Brown, 2014) (Table S2) and only one such correlated  
311 predictor – that with the highest contribution to the modelling exercise – was retained for model  
312 construction. As per Goldsmit et al. (2018), predictors were identified by evaluating the  
313 combination of: a) the response curves for each species – to evaluate if the predictor behaves in a  
314 biologically meaningful way in the model (Marcelino & Verbruggen, 2015); b) a species-specific  
315 Jackknife test – to evaluate the contributions of the various parameters and analyse importance of  
316 variables; and c) the estimates of the contribution of each variable to model prediction. A minimum  
317 of three environmental layers was included in each model. Each species was then modelled again  
318 with the selected layers (Table S3). Model performance was evaluated as the area under the curve  
319 (AUC) and true skill statistic (TSS). In presence-only models, AUC is the probability that the  
320 model correctly ranks a random presence site versus a random site from the study area (Phillips et  
321 al., 2009). Values close to 1 indicate good prediction in site discrimination, while a value of 0.5  
322 indicates a prediction equal to random and values lower than 0.5 indicate a performance that is  
323 worse than random predictions. TSS assesses the accuracy of predictions using sensitivity  
324 (proportion of correctly predicted presences) and specificity (proportion of correctly predicted  
325 absences) in its equation ( $TSS = sensitivity + specificity - 1$ ). TSS is an appropriate evaluation  
326 alternative for model predictions converted to binary (presence-absence) maps using a threshold  
327 (Allouche, Tsoar, & Kadmon, 2006). It ranges from -1 to +1, where values between 0 and -1  
328 indicate performance no better than random, while a statistically reliable model performance is  
329 indicated by values  $> 0.4$ , excellent models by a minimum of 0.7, and 1 indicates perfect agreement  
330 with the model (Allouche et al., 2006).

Model runs were replicated five times and the averages of those runs used as the outcome of the modelling exercise. Continuous values were transformed to binary values to identify predicted suitable and unsuitable habitat since continuous model projections may present some difficulties for interpretation. In addition, binary presence/absence maps are more useful for risk assessment exercises. This transformation was done using the maximum training sensitivity plus specificity threshold, which has been shown to produce the most accurate predictions, especially for presence-only datasets (Jiménez-Valverde & Lobo, 2007; Liu, White, & Newell, 2013). All binary models were then delimited using a threshold for the maximum depth each species could inhabit according to their ecological requirements (Goldsmit et al., 2018) (Table S4). An exception was made for phytoplankton as they were all surface dinoflagellates; thus, there was no need to consider maximum depth for their distribution (A. Rochon pers. comm. 2018). Heat maps showing the total number of modelled AIS that may find suitable habitat in a region – hereafter AIS richness – were then created using combined maps representing the cumulative number of species (of the 23 modelled) predicted to find suitable habitat in a given grid cell at global and pan-Arctic scales. It should be kept in mind that, at a global scale, richness includes native and invaded ranges of all species modelled, while at pan-Arctic scale, richness includes mainly predicted invaded ranges.

#### Future projections

Once all models were run, tested, and validated, predicted habitat suitability was evaluated under projected global change scenarios at global and pan-Arctic scales. The same set of environmental layers that were used for contemporary models were used for projected future models although only temperature, salinity, and ice layers were available for projected future scenarios (Table S3). Future environmental layers were obtained from Bio-ORACLE v2 for RCP4.5 emission scenario for the years 2050 and 2100. The average and range of climatic anomalies for temperature, salinity

and sea ice thickness of this scenario at the end of the century are given in Assis et al. (2018). In short, it represents an intermediate greenhouse emission (temperature anomaly of 2.4 °C by 2100) (Moss et al., 2008) and stabilization scenario resulting from the implementation of appropriate mitigation strategies (Clarke et al., 2007). This anomaly also coincides approximately with the expected increase in temperature in Arctic regions under the proposed efforts of the Paris Agreement in 2015 (Solecki et al., 2018). Future layers were produced for 2040–2050 and 2090–2100 by averaging data from distinct atmosphere–ocean general circulation models provided by the Coupled Model Intercomparison Project 5, which was developed by the World Climate Research Programme’s Working Group on Coupled Modelling (see Assis et al. 2018 for more information).

Resulting distribution models of each individual species were compiled by **ecological** groups (zoobenthos, **phytobenthos**, zooplankton and phytoplankton) and these combined models were then used to compare present with forecasted distributions for the years 2050 and 2100. This was achieved by spatially analyzing species richness and distribution change between present and future climate scenarios using ArcMap v10.2.2 and SDMtoolbox (J. L. Brown, 2014). Overlap of regions were analyzed at both global and pan-Arctic scales, to evaluate predicted latitudinal shifts in suitable habitat. **Changes in the distribution of suitable habitat over time were evaluated independent of natural or anthropogenic habitat overlap** to identify regions of loss, gain, and no change in time, for both timeframes.

## Results

### Analysis of environmental predictors and model evaluation

Varying combinations of predictors contributed to explaining the species distribution models of the **ecological** groups analyzed (Figure 2). Sea surface temperature and land distance contributed

to models for all ecological groups, although in varying proportions. Bottom temperature and depth were important in explaining models for zoobenthos and phytobenthos, in addition to ice concentration for the latter. Other main predictors for zooplankton included sea surface salinity, ice, and depth, whereas important phytoplankton predictors included nutrients and minerals (especially iron) (Figure 2, Table S3). All environmental predictors used to construct the final model for each species were within training ranges. Most AUC values were >0.91 and TSS >0.81 indicating good prediction in site discrimination, with the exception of four modelled species that were somewhat lower (*Chionoecetes opilio*, *Dinophysis caudata*, and *Gonyaulax polygramma* with AUC between 0.76 and 0.83; and *G. polygramma* and *Aurelia limbata* with TSS between 0.75 and 0.79), but still well above the thresholds for random site prediction (Table S5). Analysis of unimodal environmental response curves indicated that environmental conditions were within suitable ranges for all modelled species.

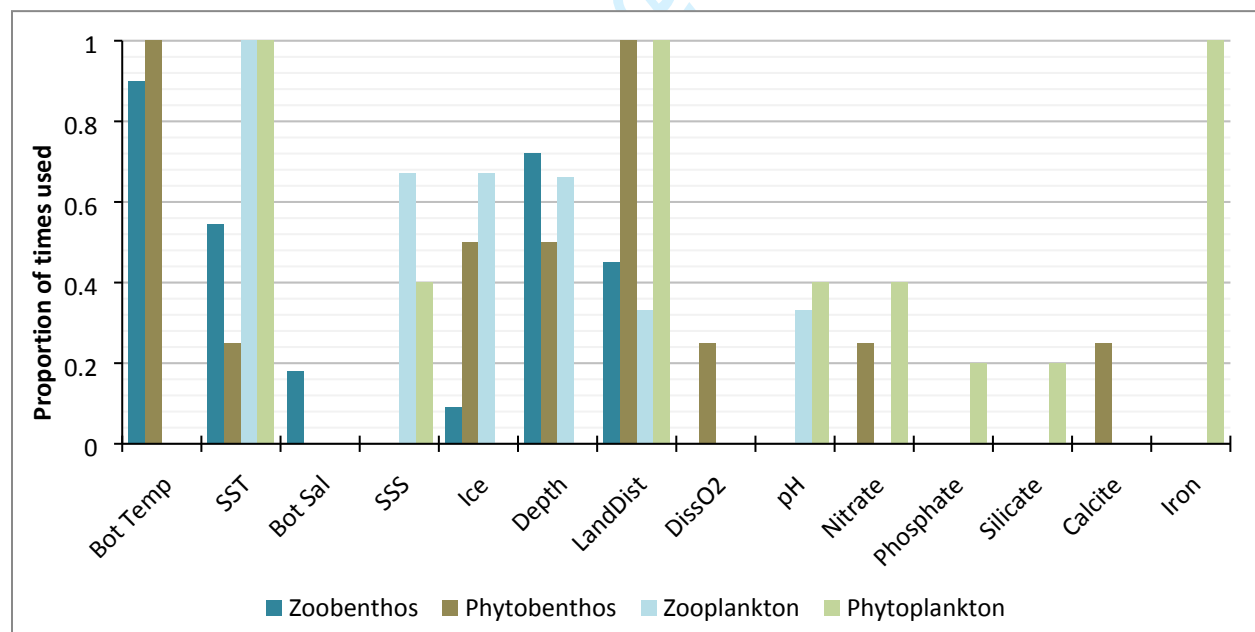


Figure 2: Proportion of times individual predictors were used for model building per ecological group. Bot Temp = Bottom temperature; SST = Sea surface temperature; Bot Sal = Bottom salinity; SSS = Sea surface salinity; LandDist = Land distance; DissO<sub>2</sub> = Dissolved oxygen.

Hotspots vulnerable to invasions

Arctic regions with an elevated number of modelled AIS having overlapping suitable habitat were located in coastal regions surrounding Hudson Bay, Northern Grand Banks/Labrador, Chukchi/Eastern Bering Seas, and Barents/White Seas (Figure 3a). These hotspots are predicted to have potentially greater AIS richness compared to other Arctic regions in the present and both modelled future scenarios. The areal extent of hotspots vulnerable to invasion is predicted to increase over time; this increase is predicted not only in total area covered, but also in the number of species projected to encounter appropriate habitat there (Figure 3b).

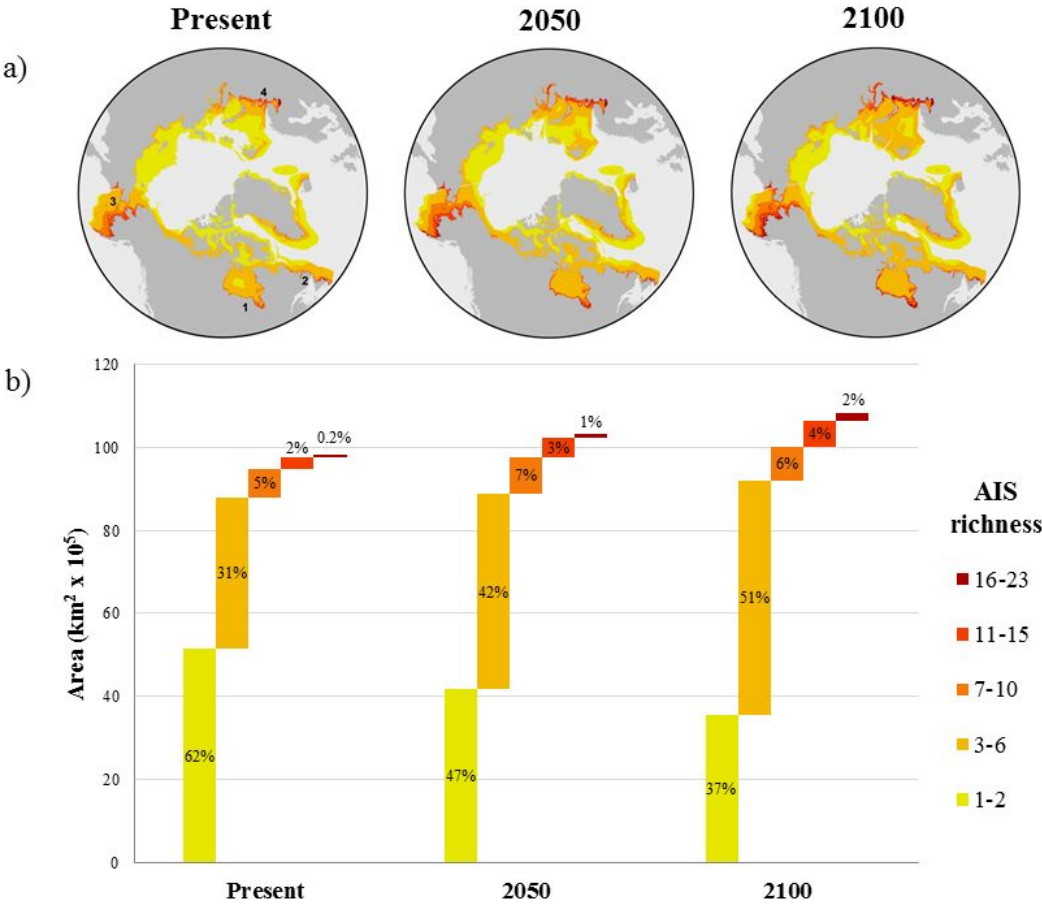


Figure 3: Predicted total AIS richness at an Arctic scale: a) Predicted hotspots of AIS richness for present and future (2050 and 2100) conditions in the Arctic (1. Hudson Bay, 2. Northern Grand

Banks/Labrador, 3. Chukchi/Eastern Bering Seas, 4. Barents and White Seas). Colors represent the number of overlapping species with predicted suitable habitat in a given area; b) Predicted future extension of suitable habitat by area for each category (natural breaks Jenks) of AIS richness. Values shown in the bars are the net percentages of suitable habitat at each level of AIS richness within each projected time period.

These same regions are predicted to be hotspots for individual ecological groups, particularly zoobenthos, phytobenthos, and phytoplankton (Figure 4a, 4b and 4d). When evaluated independently, these groups showed the same pattern of future increased areal extent in the predicted suitable habitat, but at varying taxa-dependent scales (absolute area extent: zoobenthos and phytoplankton  $\sim 100 \times 10^5 \text{ km}^2$ , phytobenthos and zooplankton  $\sim 20 \times 10^5 \text{ km}^2$ ) (Figure 4a-d). Despite these differences in magnitude for absolute predicted future suitable habitat, at a relative scale the percentage change in suitable habitat was predicted to be greater through time for some groups (e.g., phytobenthos). Further, the relative change in predicted suitable habitat for various categories of AIS richness differed between ecological groups (Figure 4e-h). For example, zoobenthos are predicted to have greater future increases in the areal extent of habitats suitable for a high number of overlapping species (i.e., with high AIS richness).

Only one species of zooplankton (*Aurelia limbata*) was predicted to have extended suitable habitat in the Arctic; hence, no potential hotspots with overlapping species was observed (Figure 4c). It should be highlighted that few zoobenthic species have native ranges included in the area of analysis: i) *C. opilio*: Beaufort Sea, Bering Sea and Northern Grandbanks/Labrador; ii) *Littorina littorea*: White Sea; iii) *Mya arenaria*: Northern Grandbanks/Labrador; and iv) *Paralithodes camtschaticus*: Bering Sea (Figure 1, Table S1).



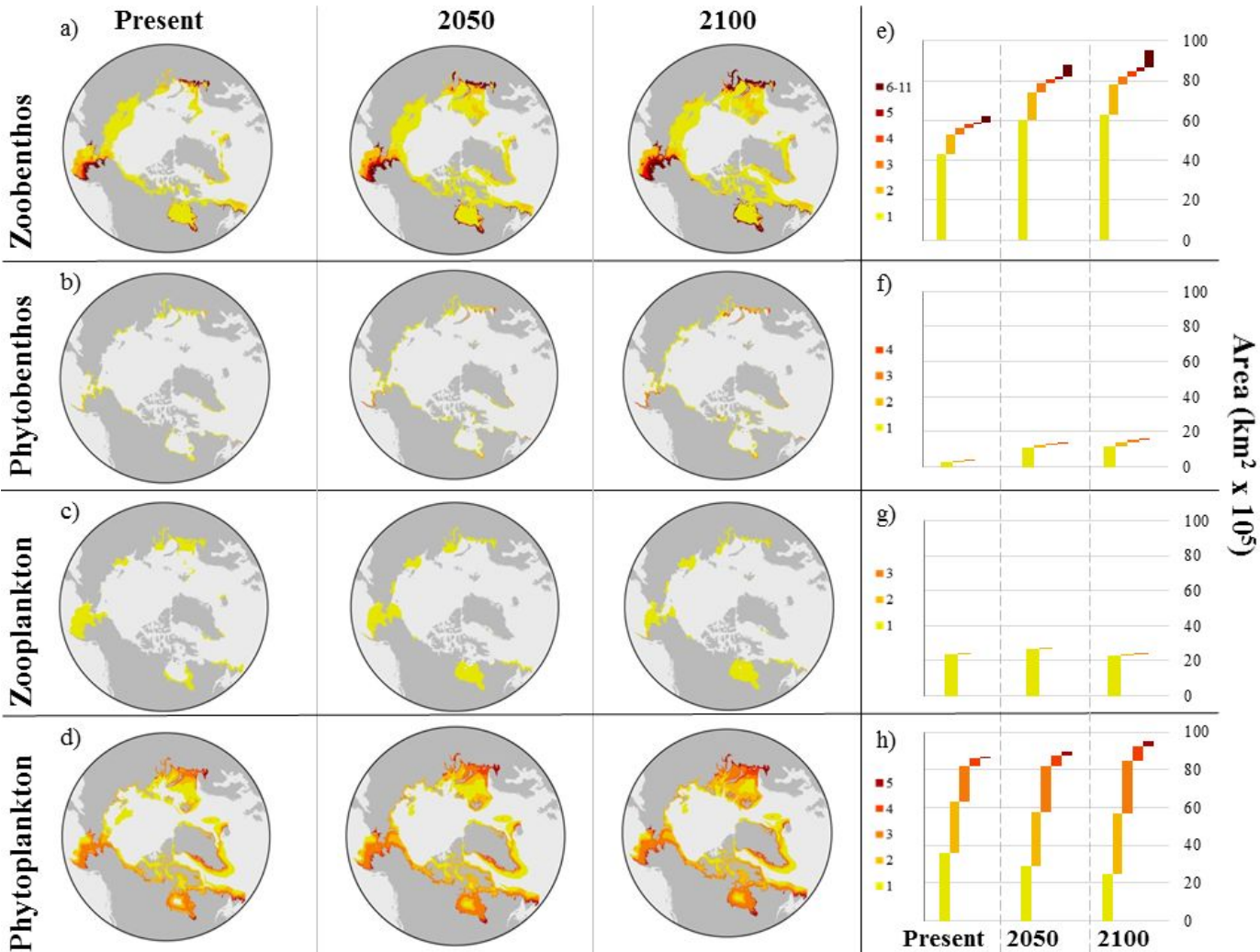


Figure 4: a-d) Predicted hotspots of AIS richness per ecological group under present and future (2050 and 2100) conditions at an Arctic scale. Colors represent the number of overlapping species with suitable habitat in a given area. e-h) Predicted future change of suitable habitat for each category of AIS richness.

At a global scale, total species richness was higher and largely concentrated on the coasts of Northern Europe and the White Sea, Northwest Atlantic, some regions of Northwest and Northeast Pacific, and southern regions of Temperate South America and Temperate Australasia (Figure S2).



## Distribution change

Suitable habitat was projected to increase in the future for all AIS combined as well as for all individual **ecological** groups in the Arctic realm under both climate change scenarios (Figures 5 and 6), although benthic species showed greater potential habitat gains (Figures 5a, 5b, and 7) than did planktonic species (Figure 5c, 5d, and 7) under future climate scenarios. The overall predicted future suitable habitat changes at the pan-Arctic scale for all AIS combined were net habitat gains of +5.8% and +14.1% by 2050 and 2100, respectively (Figures 6 and 7). However, the same analysis predicted an overall suitable habitat loss at a global scale in both future scenarios (-4% by 2050 and -4.2% by 2100) (Figures 6 and 7).

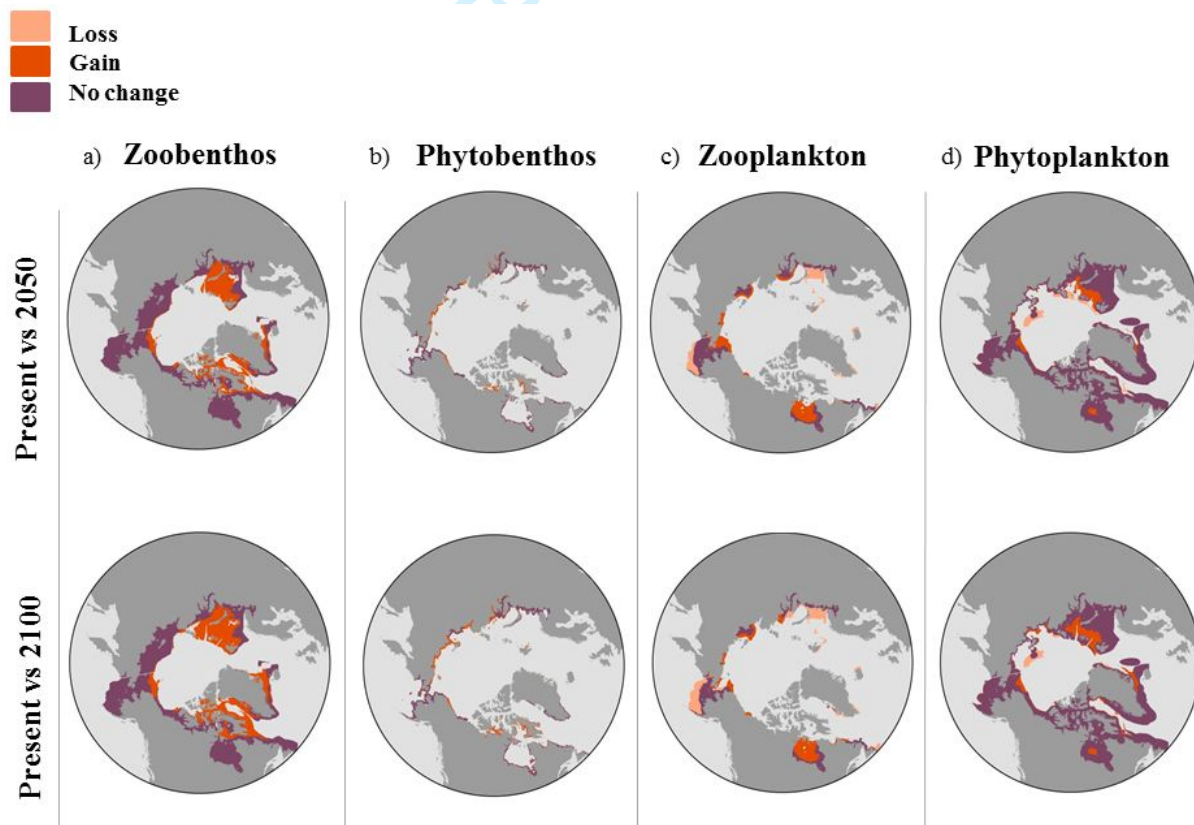


Figure 5: Overall change in predicted suitable habitat for each **ecological** group at an Arctic scale between present and future scenarios (2050 and 2100): a) zoobenthos, b) **phytobenthos**, c) zooplankton, and d) phytoplankton.

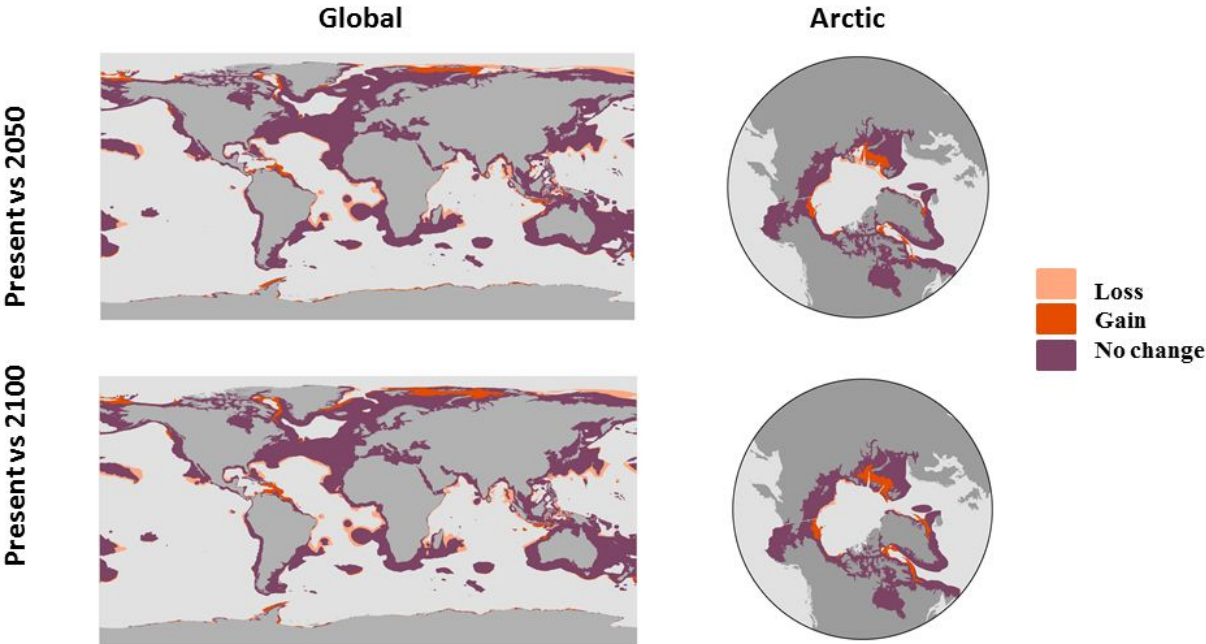


Figure 6: Overall change in predicted suitable habitat of all AIS combined at global and pan-Arctic scales between present and future scenarios (2050 and 2100).

These results show that most modelled species are predicted to find suitable habitats in colder regions, with a trend towards a positive pole-ward shift in future distributions, particularly in northern latitudes (the pole-ward shift to the south is predicted to be lower) (Figure 6). At a global scale, however, planktonic species are predicted to experience habitat loss, while benthic species are predicted to have a positive and higher habitat gain (Figure 7 and S3).

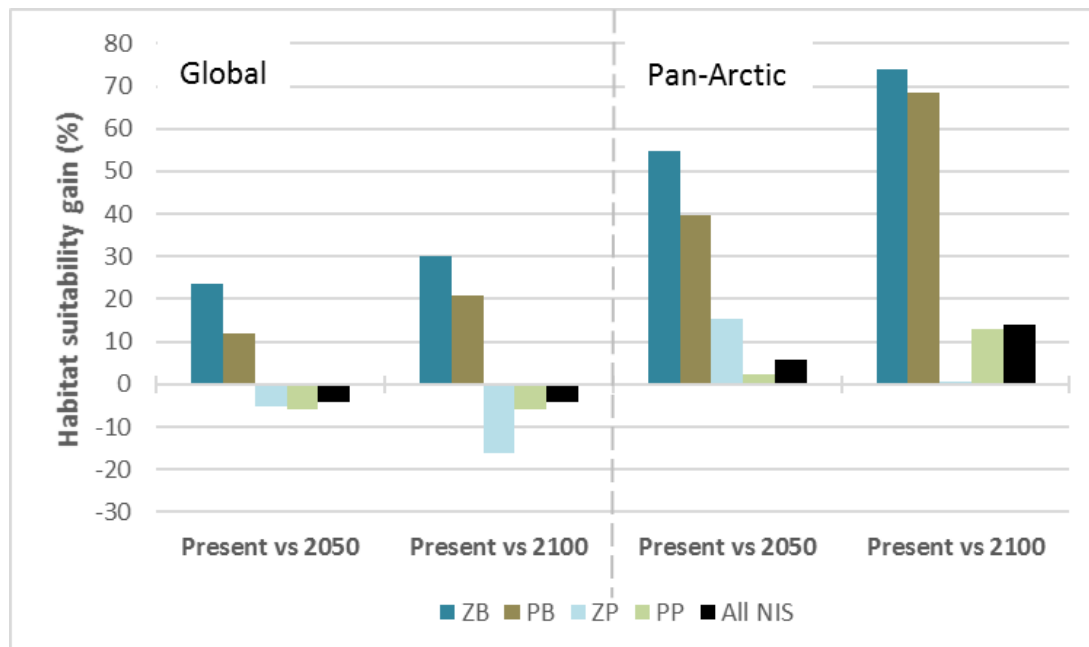


Figure 7: Percentage of predicted habitat suitability change (gain or loss) for the four ecological groups and all AIS together at global and pan-Arctic scales. ZB= zoobenthos; PB= phytobenthos; ZP= zooplankton; PP= phytoplankton.

## Discussion

This study predicted the distribution of suitable habitat for 23 high-risk AIS at pan-Arctic and global scales and identified hotspots of suitable habitats for multiple species. Overall, results indicate that suitability will increase over time in Arctic regions, particularly in Hudson Bay, Northern Grand Banks/Labrador, Chukchi/Eastern Bering Seas, and Barents/White Seas regions. Gradually, these regions could become more vulnerable to invasions not only due to the increased extent of suitable habitat but also due the increased number of species that may find suitable habitat there (i.e., AIS richness). This trend was observed across all assessed ecological groups which showed gains in suitable habitat in future scenarios, especially benthic organisms, which exhibited particularly high distributional changes as compared to planktonic organisms.

477 Interestingly, predicted shifts under future climate scenarios differed at pan-Arctic and global  
478 scales. When all species were considered collectively, there was a predicted increase in suitable  
479 habitat at the pan-Arctic scale. In contrast, the net result at a global scale was a predicted loss of  
480 suitable habitat, suggesting a marked northward shift with global change. Projected future  
481 scenarios considered only the direct effect of climate change. However, projected increases of  
482 shipping to the area will likely exacerbate the risk as new transport routes open due to longer ice-  
483 free conditions that increase opportunities for natural resource extraction (Melia et al., 2016; Miller  
484 & Ruiz, 2014; Smith & Stephenson, 2013). Likewise, the Antarctic, could be affected by native  
485 and invasive species in northern regions, given that environmental conditions are similar. Arctic  
486 ports could act as possible sources of AIS to the Antarctic given that some ships transit between  
487 poles and could act as a potential pathway of transportation, although survival and establishment  
488 in such scenarios are unknown (McCarthy et al., 2019).

489 The use of CMIST as a screening tool to identify high-risk species for specific ecoregions is a  
490 recent approach to stay ahead of the invasion process (Drolet et al., 2016; A. M. Moore et al.,  
491 2018; Therriault et al., 2018). Although the use of CMIST combined with habitat modelling as  
492 done in this study places more emphasis on the likelihood of invasion risk component of risk, the  
493 tool may be used as a first step in developing a ranked watch list to guide early detection and  
494 monitoring efforts and to prioritize species for detailed risk assessments and potential regulations  
495 (Locke et al., 2011). CMIST provided the opportunity to identify potential AIS of greater risk to  
496 the Arctic by considering known species' characteristics and impacts in other regions of the world  
497 where they have already invaded. Eighty-seven percent of the species included in the present  
498 modelling assessment belong to groups with the greatest numbers of known invasions in the  
499 marine Arctic ecosystem (Chan et al., 2019). The uneven emphasis of organisms retained for

modelling (i.e., those scored as higher risk based on CMIST) from the different ecological groups (maximum of 11 zoobenthic species vs. a minimum of 3 zooplankton species) may, in part, be explained by the fact that most known introduced marine organisms are benthic species (Streftaris, Zenetos, & Papathanassiou, 2005). These proportions are comparable with previous assessment studies (Leidenberger, Obst, et al., 2015), although the uneven coverage does make general trends more difficult to interpret.

Sea surface temperature and land distance were retained in all models, consistent with other studies that found these predictors to contribute significantly to explaining species distributions (Leidenberger, Obst, et al., 2015; Stelzer, K, Bourlat, & Obst, 2013). Water temperature has been identified as the most relevant predictor of global marine species distribution and land distance of moderate importance for both benthic and planktonic species (Bosch, Tyberghein, Deneudt, Hernandez, & De Clerck, 2018). Depth was an important predictor, as shown by Bosch et al. (2018) who suggested that bathymetry is of high relevance for modelling various taxa. Ice concentration was moderately important for phytobenthos and zooplankton, perhaps reflecting limits on distribution of the former due to ice abrasion, changes in light exposure and a preference of ice-free waters for the latter (Clark et al., 2013; Kube, Postel, Honnef, & Augustin, 2007; Pascual et al., 2015; Richardson, 1979). Iron was an important predictor for all modelled phytoplankton species, likely as it is known to be important to phytoplankton growth, abundance, dominance, and species distributions (Hecky & Kilham, 1988; C. M. Moore et al., 2013) and plays a role in the development of harmful algal bloom species (Doucette & Harrison, 1990; Wells, Mayer, & Guillard, 1991). In Arctic regions, meltwater can be a significant bioavailable source of iron to surrounding coastal oceans (Bhatia et al., 2013; Tovar-Sánchez et al., 2010) and evidence suggests a link between ice and iron from glacial meltwater leading to blooms in some

523 phytoplankton taxa (Aguilar-Islas, Rember, Mordy, & Wu, 2008; Joli et al., 2018). This is  
524 important given that increased iron due to a shift from an ice-covered to an open water Arctic  
525 Ocean (Screen, 2018; Seneviratne et al., 2018) could create favourable conditions for harmful  
526 species that may arrive in the region.

527 Four Arctic regions (i.e., Hudson Bay, Northern Grand Banks/Labrador, Chukchi/Eastern Bering  
528 Seas, and Barents/White Seas) were identified as potential hotspots for invasions. Invasion  
529 hotspots could pose even greater risks if they coincide with major shipping routes, biodiversity  
530 hotspots or areas of special interest/importance, which is the case for most of the invasion hotspots  
531 predicted in the present study. The predicted invasion hotspots overlap with regions that have been  
532 highlighted for being special (with regards to their uniqueness, importance for species life  
533 histories, threatened species and/or habitats, biological productivity, diversity, etc.). For example,  
534 some Ecologically and Biologically Significant Areas (also known as EBSAs) and Marine Refuges  
535 coincide with the predicted invasion hotspots in Northern Grand Banks/Labrador, Chukchi/Eastern  
536 Bering Seas and Barents/White Seas (Kenchington et al., 2011; Speer & Laughlin, 2011;  
537 Templeman, 2007; [www.dfo-mpo.gc.ca/oceans/oeabcm-amcepz/refuges/index-eng.html](http://www.dfo-mpo.gc.ca/oceans/oeabcm-amcepz/refuges/index-eng.html)), as well  
538 as in the southern part of Hudson Bay, which has been identified as being an area of high biological  
539 importance (Stephenson & Hartwig, 2010). Ecoregions with a high concentration of polynyas  
540 could also be at greater risk, given that they may act as important biological hotspots due to their  
541 increased productivity and biodiversity (Marchese, 2015). This may be the case for the Chukchi  
542 and Eastern Bering Seas, which are known to have concentrations of polynyas (CAFF, 2013). This  
543 is consistent with previous studies that have identified biodiversity hotspots in marine and  
544 terrestrial ecosystems as being at particular risk to future invasions (Bellard et al., 2014; Li, Liu,  
545 Kraus, Tingley, & Li, 2016) and climate change (Ramírez, Afán, Davis, & Chiaradia, 2017). The

546 presence of AIS in biological hotspots could endanger native and endemic species as AIS are  
547 considered to be one of the leading causes of biodiversity loss and contemporary extinctions  
548 (Bellard, Cassey, et al., 2016; Blackburn et al., 2019) with impacts on ecosystem structure and  
549 functioning, including changes in food webs, biomass, flux rates, etc. (Ehrenfeld, 2010). Relating  
550 where invasion hotspots overlap with biological hotspots could be crucial for prioritizing  
551 conservation efforts.

552 The Barents Sea has been highlighted as a region that already has a substantial number of **invasions**  
553 and environmental conditions that increase the probability of successful establishment (Chan et  
554 al., 2019). Two of the species modelled in the present study, *C. opilio* and *P. camtschaticus*, are  
555 already established there (Chan et al., 2019; Dvoretzky & Dvoretzky, 2009; Hansen, 2015). **The**  
556 **former is thought to have been introduced by ballast water, while the latter was an intentional**  
557 **introduction (Alvsvåg, Agnalt, & Jørstad, 2009; Jørgensen & Nilssen, 2011).** The Barents Sea  
558 appears to be in transition from a cold Arctic to warm Atlantic climate regime (Lind, Ingvaldsen,  
559 & Furevik, 2018), making it particularly vulnerable to invasion. **Indeed, it is predicted to suffer**  
560 **one of the largest future habitat losses by endemic species in the Arctic (Renaud et al., 2019),**  
561 **leaving potential niches available for novel species to occupy. Additionally,** Arctic ecoregions will  
562 be more exposed to potential future **arrivals** with further ice reduction and increased navigability  
563 of the Northern Sea Route and the Northwest Passage, although much greater investment in  
564 infrastructure, navigation and communications would be needed to this end (Buixadé Farré et al.,  
565 2014). Nonetheless, both human activities and AIS are likely to increase over time in the Arctic,  
566 as has been observed over the last few years (Chan et al., 2019; Dawson, Pizzolato, Howell,  
567 Copland, & Johnston, 2018).



At a global scale, planktonic organisms showed a marked loss of suitable habitat that exceeded predicted gains. This may be due to their being dispersive pelagic organisms which have the capability of expanding rapidly and show extensive distribution changes in response to temperature increases related to global warming (Poloczanska et al., 2013). Predicted future changes in sea surface temperatures, in particular, which are expected to outpace shifts in bottom temperature (Levitus et al., 2012) may be driving this pattern. Indeed, models in the present study showed that sea surface temperature was more important for planktonic organisms whereas bottom temperature was an important variable for benthic organisms. However, the pattern of predicted change by taxa is different at the pan-Arctic scale where both planktonic and particularly benthic AIS showed positive suitable habitat gains coinciding with other modelling studies (de Rivera et al., 2011; Goldsmit et al., 2018; Jueterbock et al., 2013; Townhill et al., 2018; Villarino et al., 2015; Ware et al., 2016). This could be explained by the fact that temperature increases have been shown to be greater in the Arctic than in other areas (Bush & Lemmen, 2019; Pendleton et al., 2019) and thus predicted gains in suitable habitat there would be expected to be relatively greater than losses elsewhere.

A marked poleward shift was predicted, consistent with other forecasting studies for various types of marine organisms, including invertebrates, algae and fish (Byrne et al., 2016; Chust et al., 2013; Goldsmit et al., 2018; Jones & Cheung, 2015; Mackey et al., 2012; Townhill et al., 2018; Valle et al., 2014; Wisz et al., 2015). Poleward shifts may serve as an early warning signal of ecosystem change due to climate warming. Multiple studies across different taxa are showing consistency between observed responses of marine organisms to climate change, particularly in high-latitude regions (Poloczanska et al., 2013). Cold-adapted species typically have narrow thermal windows and low energy-demand lifestyles, making them more sensitive to temperature changes



(Poloczanska et al., 2016). Poleward shifts in predicted future suitable habitat in the present study are disproportionately located in Arctic areas, such as has been shown in Cheung et al. (2009), García Molinos et al. (2015), and Jones & Cheung (2015). Invasive species in the Antarctic region have been limited by physiology at cold temperatures rather than geographic limits, but global warming may remove those physiological barriers and alter limitations (Aronson et al 2007). However, it should be noted that a substantial number of the species modelled here are already distributed in northern/cold regions, which may bias observed patterns. Although, three modelled species (*C. intestinalis*, *B. schlosseri*, and *U. pinnatifida*) are among the most likely to become invasive in the Antarctic Peninsula according to a recent horizon scanning study (Hughes et al., 2020).

The locations with greater reductions of the sea ice season over the last 40 years (Stammerjohn, Massom, Rind, & Martinson, 2012) coincides with the regions of predicted invasion hotspots in the present study, suggesting that these areas are already experiencing changing environmental conditions and that such variations are projected to continue in time, including the probability of a complete ice-free Arctic during summer (Screen, 2018; Sigmond et al., 2018). The combination of species invasions and predicted reductions in sea-ice cover could alter reproduction/phenology timing, energy pathways, and food-web dynamics with subsequent impacts on production at higher trophic levels (Poloczanska et al., 2013; Haug et al., 2017 and references therein). In this context, AIS could take advantage of new habitats and resources and outcompete native species, which are generally expected to be more sensitive to temperature changes given that they live within a narrow low-temperature range (Peck, 2005). Invasive, non-native, and native boreal species could thus expand their ranges as suitable habitats in polar regions become more common (de Rivera et al., 2011; Goldsmit et al., 2018; Ware et al., 2016;

614 [Renaud et al., 2019](#)) with subsequent impacts on richness, community composition, and Arctic  
615 ecosystems. However, it remains unknown whether biogeographic boundary locations will  
616 change (Costello et al., 2017).

617 The model used in this study, MaxEnt, is robust and performs well to predict suitable habitats for  
618 invasive species currently and to project range shifts under future climate change scenarios (Battini  
619 et al., 2019; Hijmans & Graham, 2006). Special attention was taken in the selection of  
620 environmental predictors for modelling. Correlation between predictors was accounted for as  
621 including all available predictors may lower predictive power due to model over-parameterization  
622 (Bradie, Pietrobon, & Leung, 2015; Tyberghein et al., 2012). Nevertheless, modelling studies  
623 always have some restrictions and limits that should be recognized in results interpretation. One  
624 main limitation of the present study is that potential species occurrences and range changes are  
625 based solely on abiotic factors and do not reflect the realized distribution of a species, assuming  
626 that species are in equilibrium with their environment (Bellard et al., 2018; Guisan &  
627 Zimmermann, 2000). Biotic interactions, potential resources, and life history traits were not  
628 included in the modelling exercise, even though they are known to be important in shaping the  
629 spatial distribution of species (Wisz et al., 2013). Moreover, including physiological data such as  
630 reproductive temperature to represent phenology, can significantly change SDM predictions.  
631 Including this type of data has been shown to strongly limit predicted northward shifts under future  
632 climate change scenarios (Chefaoui, Serebryakova, Engelen, Viard, & Serrão, 2019). However,  
633 this particular aspect was somewhat offset by the fact that environmental conditions for  
634 reproduction, together with conditions needed for different life stages, were considered in this  
635 study during the species selection using CMIST scores. Given that the present study modelled the  
636 potential distribution of suitable habitat in a new environment, biotic interactions may not be

realistic if applied in a different context, such as different regions or time periods (Anderson, 2017 and references therein). Moreover, biotic interactions are known to affect distributions at local spatial scales (Pearson & Dawson, 2003). Another potential limiting factor in modelling future distributions was the availability of projected environmental predictors under global warming scenarios, since it has been recently shown that including projections using multi-factor models can result in better performance predictions (McHenry, Welch, Lester, & Saba, 2019). Temperature, salinity and sea ice thickness were the only environmental predictors available to use as future projected environmental layers, although including only these factors is common practice in similar modelling exercises (e.g., Goldsmit et al., 2018; Jueterbock et al., 2016; Leidenberger, De Giovanni, Kulawik, Williams, & Bourlat, 2015, and Weinert et al., 2016). Despite limitations and restrictions, SDM can provide valuable information to help manage resources in a marine ecosystems that will face increasing anthropogenic pressures (Reiss et al., 2014) and has been shown to be a useful predictive tool to assess various taxa concurrently (Gallardo et al., 2015; Leidenberger, Obst, et al., 2015). SDM may also be particularly useful for regions such as the Arctic, where predicting biodiversity changes under global warming effects is challenging due to the paucity of baseline data for most organisms (Wassmann, Duarte, Agusti, & Sejr, 2011; Renaud et al., 2019).

Distributional change of AIS may increase risk in previously unimpacted areas, potentially creating new problems for wildlife and even human health (such as harmful algal blooms). These types of episodes are being facilitated by climate change (Hallegraeff, 2010; Kordas, Harley, & O'Connor, 2011; Poloczanska et al., 2013; Poloczanska et al., 2016). The present study predicts changes over such an extensive area (more than  $1 \times 10^7$  km<sup>2</sup>, equivalent to almost 5.5 times the size of Greenland) that altered community structure may be widespread. Results presented here

provide information on AIS that pose some of the greatest threats to the Arctic, with areas at greatest risk identified as hotspots. This information is valuable given that aquatic invaders are understudied in the context of climate change (Bellard et al., 2018). The Arctic is predicted to be affected by increased habitat suitability for a number of potential AIS and given its vast area, it could be severely impacted by AIS accumulating in specific locations under both current and future environmental conditions. Identification of hotspots through SDM, predictions on habitat vulnerability and particular areas of concern could guide ballast water practices and other management actions, including prevention, early detection monitoring, rapid response, and conservation planning. Information such as that provided by the present study should help guide how best to prioritize management efforts in this unique and vast region.

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High Arctic Research Station, and Quebec-Ocean. The author sequence follows the ‘first-last author-emphasis’ norm.

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