A framework for examining climate-driven changes to the seasonality and geographical range of coastal pathogens and harmful algae

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ABSTRACT

Climate change is expected to alter coastal ecosystems in ways which may have predictable consequences for the seasonality and geographical distribution of human pathogens and harmful algae. Here we demonstrate relatively simple approaches for evaluating the risk of occurrence of pathogenic bacteria in the genus *Vibrio* and outbreaks of toxin-producing harmful algae in the genus *Alexandrium*, with estimates of uncertainty, in U.S. coastal waters under future climate change scenarios through the end of the 21st century. One approach forces empirical models of growth, abundance and the probability of occurrence of the pathogens and algae at specific locations in the Chesapeake Bay and Puget Sound with ensembles of statistically downscaled climate model projections to produce first order assessments of changes in seasonality. In all of the case studies examined, the seasonal window of occurrence for *Vibrio* and *Alexandrium* broadened, indicating longer annual periods of time when there is increased risk for outbreaks. A second approach uses climate model projections coupled with GIS to identify the potential for geographic range shifts for *Vibrio* spp. in the coastal waters of Alaska. These two approaches could be applied to other coastal pathogens that have climate sensitive drivers to investigate potential changes to the risk of outbreaks in both time (seasonality) and space (geographical distribution) under future climate change scenarios.

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Introduction

The most recent assessment by the Intergovernmental Panel on Climate Change provided unequivocal evidence for warming of the climate system. Emissions of greenhouse gases from human activities are the highest in history, and have caused unprecedented warming (IPCC, 2014). During the period from 1880 to 2012, mean global land surface air temperatures have increased by 0.85 °C with a greater rate of change in the period from 1970 to present (IPCC, 2014). Similarly, over the last four decades, surface waters of our oceans have warmed at a rate of 0.11 °C per decade, and alterations in precipitation patterns have increased salinity in the Atlantic Ocean and decreased salinity in the Pacific and Southern Oceans (IPCC, 2014). From 1901 to 2010, mean global sea level has risen 0.19 m and the rate of ice loss from glaciers around the

world has also increased (IPCC, 2014). While much progress has been made in documenting historical changes in climate and generating future climate projections based on various greenhouse gas concentration trajectories, understanding the ecological and human health impacts, especially in coastal systems, and developing strategies for addressing them has (necessarily) lagged behind.

Most assessments of climate change impacts on human health have focused on direct impacts such as the potential for more frequent and severe heat events causing heat stroke, worsening air pollution causing respiratory disease, and more frequent extreme events (e.g., flood, wild fire) causing loss of life (Haines et al., 2006). Of equal concern, but arguably more difficult to predict, are the indirect impacts of climate change, including changes to vector-, food- and waterborne diseases arising from the disruption of natural systems (Hunter, 2003; Noyes et al., 2009; Tirado et al., 2010). Naturally occurring pathogens and harmful algae in coastal environments are very likely to be affected by climate change, resulting in changes in their distribution, abundance, and perhaps virulence or toxicity (Moore et al., 2008; Mahoney et al., 2010; Baker-Austin et al., 2012; Vezzulli et al., 2013). However, the inherent complexity of coastal systems can complicate projections of the pathogen and algae responses. Experts agree that changes are highly likely to occur, but quantitative analyses of the direction, magnitude, and timing of these changes are often lacking (e.g., Anderson et al., 2012). Decision makers responsible for protecting human health need quantitative information on how the risk of illness from coastal pathogens and harmful algae will change in the future, with estimates of uncertainty, to inform the development of preparedness, mitigation, and adaptation strategies.

For some human pathogens and harmful algae in coastal systems, temperature exerts strong constraints on their physiology (e.g., Paerl and Huisman, 2008), controlling their distribution and abundance in space and time. These organisms cannot grow outside of certain temperature windows, and optimal temperatures within the window support proliferative growth. Because changes to temperature in the U.S. and globally are among the most confident projections of climate change with high agreement among climate models in both the direction and magnitude of change (IPCC, 2014; Walsh et al., 2014), the pathogen and algae responses to climate change may have predictable outcomes. Here we evaluate the impacts of climate change on the potential for outbreaks of toxin-producing harmful algae in the genus *Alexandrium* and occurrence and abundance of bacteria in the genus *Vibrio* that threaten human health.

Harmful algal blooms (HABs) are becoming increasingly frequent in U.S. coastal waters and some have expanded into new geographic locations (e.g., Tester et al., 1991; Campbell et al., 2010; Nishimura et al., 2013), consistent with an apparent worldwide trend (Hallegraeff, 1993, 2010; Van Dolah, 2000; Lewitus et al., 2012). Some harmful algae produce toxins that cause disease in humans that contact them. Paralytic shellfish poisoning (PSP) is perhaps the most widespread of the HAB-related diseases (Erdner et al., 2008) and is caused by potent neurotoxins that are produced by dinoflagellates in the genus *Alexandrium*. The toxins accumulate in filter feeding shellfish when *Alexandrium* bloom and human consumption of contaminated shellfish can cause PSP, characterized by gastrointestinal and neurological symptoms. In severe intoxications, muscle paralysis can develop and death can occur (Quayle, 1969; Kao, 1993). In Puget Sound, Washington State, *Alexandrium* blooms have increased in geographic scope since the 1950s (Trainer et al., 2003) and it is very likely that the 20th century warming trend contributed to the increasing trend in shellfish toxicity (Moore et al., 2011). The timing of blooms is sensitive to weather and climate variations, with toxic blooms largely driven by warm air and water temperatures (Moore et al., 2009).

Puget Sound strains of *Alexandrium* grow over a range of temperatures from ~7 to 24 °C, with optimal growth occurring at temperatures between ~10 and 21 °C (Bill et al., submitted for publication). Temperatures exceeding 13 °C have been associated with increased risk of Puget Sound shellfish being contaminated with toxins produced *Alexandrium* (Nishitani and Chew, 1984). The species of *Alexandrium* thought to be responsible for blooms in Puget Sound has historically been identified as *Alexandrium catenella*; however, the name *Alexandrium fundyense* has recently been proposed to replace all Group I strains of the *Alexandrium tamarense* species complex that includes *A. catenella* (John et al., 2014).

Cases of *Vibrio* related illness have increased in the U.S. over the past decade (Newton et al., 2012). *Vibrio* are gram negative, flagellated bacteria that serve as functional members of the natural heterotrophic community in coastal waters. They freely associate with a variety of biotic and abiotic surfaces including water, sediment, fish, shellfish, algae, and zooplankton (Depaola et al., 1994; Maugeri et al., 2006; Turner et al., 2009; Johnson et al., 2010). Several species of *Vibrio* are known to cause illness in humans, with symptoms ranging from skin irritation and gastroenteritis, to bullous lesions, septicemia and mortality. Principal among these are strains of *Vibrio cholerae*, *Vibrio vulnificus*, and *Vibrio parahaemolyticus*. *V. cholerae*, the causative agent of cholera, is endemic to US coastal waters, but nearly all cases of toxigenic 01 and 0139 serotypes are associated with foreign travel (CDC_COVIS, 2014). Some non 01 and 0139 serotypes however, are diarrheagenic and are isolated in 5–10% of reported *Vibrio* related illnesses (Newton et al., 2012). *V. parahaemolyticus* and *V. vulnificus* are associated with the majority of the estimated 80,000 illnesses annually in the US (Scallan et al., 2011).

Temperature strongly controls *Vibrio* growth, generally being inhibitory <10 °C and optimal at ~37 °C (Martinez-Urtaza et al., 2010). As such, it is highly likely that warming of our coastal oceans will accelerate the spread of *Vibrio* to northern latitudes, where the warming effect is projected to be most pronounced. In the past decade alone, outbreaks have been documented in Alaska, Spain, Europe, and north Atlantic states of the U.S. and correlatively linked to warming trends (González-Escalona et al., 2005; McLaughlin et al., 2005; Baker-Austin et al., 2012; García et al., 2013; Martinez-Urtaza et al., 2013). For example, Baker-Austin et al. (2012) recently provided statistical evidence of the relationship between sea surface temperature (SST) and increasing illnesses in the Baltic. In Alaska, a 2004 outbreak of *V. parahaemolyticus* among cruise ship passengers was associated with an anomalous SST event pushing warm waters into Prince William Sound (McLaughlin et al., 2005). In the Chesapeake, several statistical models have been developed relating SST and other variables

to *Vibrio* occurrence and abundance (Constantin de Magny et al., 2010; Jacobs et al., 2010, 2014) and have been used to demonstrate the impact of climate variability on local scale distribution (Banakar et al., 2012). By 2012, the annual number of cases of *Vibrio* infection had steadily risen in Chesapeake watershed states to nearly 100 (CDC_COVIS, 2014, MD, VA, and PA combined), and a burgeoning oyster aquaculture industry has raised much concern related to *Vibrio* control with increased summer harvest.

Few studies have investigated the potential effects of climate change on coastal water-borne pathogens and toxic HABs in an ecologically relevant context. Laboratory studies have provided information on the growth and toxicity of some of these organisms in response to one or a few parameters that are sensitive to climate change, but the experimental conditions are typically *static* with the organisms exposed to constant conditions that may be representative of a 'low', 'medium', and 'high' scenario (e.g., Peperzak, 2005; Sun et al., 2011). In other cases, growth and/or toxicity relationships with climate are gleaned from historical data already collected, but challenges associated with the temporal and spatial resolution of the data as well as the potential effects of other non-climate drivers of change can hamper efforts to establish cause and effect. Consequently, there has been limited application of these relationships to *dynamic* projections of coastal and marine systems, and usually only one or a few climate models, years, and/or greenhouse gas concentration trajectories are examined (Moore et al., accepted for publication), limiting confidence in the projections.

Here we present ecologically relevant approaches that provide new insights into climate change effects on water-borne pathogens and toxic HABs in coastal waters. The approaches allow for a *quantitative* evaluation of the likelihood of projected impacts to human health. Approaches such as these that provide decision support on climate change and health have been termed 'data mashups' (Fleming et al., 2014) and integrate different types and sources of data to better target management needs and promote the development of more effective adaptation and mitigation strategies to climate change. To demonstrate these approaches, we employ previously developed empirical models relating the growth, abundance, or probability of occurrence of two species of *Vibrio* (*V. parahaemolyticus* and *V. vulnificus*) and the harmful alga *A. fundyense* to environmental parameters that are sensitive to climate (USFDA, 2005; Jacobs et al., 2014; Bill et al., submitted for publication) to provide first order estimates of changes in both time (seasonality) and space (geographical distribution) under future climate change scenarios.

Methods

Seasonal shifts

Changes to the timing of growth of *Vibrio* and outbreaks of *Alexandrium* were evaluated on a monthly timescale to identify the potential for broadened seasonal windows of increased risk for illness in Chesapeake Bay and Puget Sound (Fig. 1). Existing empirical models for the abundance and probability of occurrence of *Vibrio* and for growth of *Alexandrium* are driven in part by SST (described below). By applying historical records of SST in these locations to the existing empirical models for *Vibrio* and *Alexandrium*, a 'present-day' seasonal window of increased risk for illness was identified that could be compared with a range of future scenarios.

Fig. 1. Geographic locations of the projections for coastal pathogens and HABs, showing Alaskan coastal waters, Quartermaster Harbor in Puget Sound (QMH), and the Chesapeake Bay. Main-stem Chesapeake Bay water quality monitoring stations used for downscaling efforts in this study are denoted (●).

Future scenarios for SSTs in Chesapeake Bay and Puget Sound were developed by combining surface air temperature changes simulated by global climate models (GCMs) with observed time series of SSTs used in the development of historical climate-pathogen and climate-HAB relationships. Generally, twenty-one GCMs from the fifth phase of the Coupled Model Intercomparison Project (CMIP5) were used to provide a full range of projections for Chesapeake Bay and Puget Sound under scenario RCP6.0 (Table 1). RCP 6.0 is one of four greenhouse gas concentration trajectories that describe alternative futures based on assumptions about economic activity, energy sources, population growth and other socio-economic factors. RCP 6.0 assumes that global annual greenhouse gas emissions peak around 2080 and then decline (Meinshausen et al., 2011).

GCMs generally are not of high enough spatial resolution to include the Chesapeake Bay and Puget Sound water bodies. These locations are simulated as land in models; thus, there are no model SST data available for those locations. Instead, scenarios are developed using baseline historical observations of SSTs and assuming that future changes in SSTs will be similar to the model-simulated relative changes in near surface air temperatures. Specifically, future scenarios are constructed by comparing the historical model-simulated air temperatures for the model grid boxes covering the water body locations with the SST observations, and adjusting the future model projections by the difference (bias) between the observations and model simulations.

Near surface temperatures historically correlate strongly with SST in the Chesapeake Bay (Najjar et al., 2010; Preston, 2004; Cronin et al., 2003). Because this relationship is critical to our approach, we further examined the correlation of monthly mean SST and air temperature at a single location in Chesapeake Bay. SST was obtained for a 15 year period from station LE 3.2 of the Chesapeake Bay Programs water quality monitoring network (Mid Bay, near Annapolis, MD, Fig. 1). Corresponding air temperature was obtained from NOAA for the Annapolis, MD Police Barracks (Station GHCND:USC00180193). SST and surface air temperature was significantly and positively correlated ($r = 0.96$, $n = 183$, $P < 0.001$). Similarly in Puget Sound, surface air temperature has been found to be the strongest driver of variability in SST during all seasons (Moore et al., 2008). These results indicate that air temperature deviance can be used as bias correction for SST projections in Chesapeake Bay and Puget Sound (see below).

Baseline observations of SST were obtained from the Chesapeake Bay Program Data Hub (http://www.chesapeakebay.net/data/downloads/cbp_water_quality_database_1984_present) for all mainstem monitoring stations for the period of 1985–2000. In Puget Sound, baseline monthly SST data were obtained from the King County Department of Natural Resources and Parks at Dockton (47.38 N, 122.46 W, Quartermaster Harbor), from 2006 to 2014. Quartermaster Harbor has a history of PSP toxicity in shellfish (Nishitani and Chew, 1984). It was first identified to be an important initiation site for *Alexandrium* blooms in Puget Sound during a survey in 2005 when it was found to contain >12,000 cysts/cm^3 (Horner et al., 2011) and remains an important initiation site relative to other Puget Sound sites (Greengrove et al., 2012).

The near surface air temperature data from climate model simulations will generally be characterized by biases in both the mean and variance when compared to historical baseline observations of SSTs. Two bias adjustment methods were applied: quantile mapping for Chesapeake Bay and the simple 'delta' method with variance adjustment for Puget Sound

Table 1

Global climate models used in this study and modeling groups participating in CMIP5. All models were used to force empirical models for *Alexandrium* and *Vibrio* to project seasonal shifts in growth and occurrence. An asterisk (*) denotes the four models used in projecting geographic range shifts for the Alaskan shoreline.

Model	Institute
bcc_csm1_1	Beijing Climate Center, China Meteorological Administration
bcc_csm1_1_M	Beijing Climate Center, China Meteorological Administration
CCSM4	National Centers for Atmospheric Research
CESM1_CAM5*	Community Earth System Model Contributors
CSIRO_Mk3	Commonwealth Scientific and Industrial Research Organization and Queensland Climate Change Centre of Excellence
FIO_ESM	First Institute of Technology, SOA
GFDL_CM3*	NOAA, Geophysics Fluid Dynamics Laboratory
GFDL_ESM2G	NOAA, Geophysics Fluid Dynamics Laboratory
GFDL_ESM2 M	NOAA, Geophysics Fluid Dynamics Laboratory
GISS_E2_H	NASA, Goddard Institute for Space Studies
GISS_E2_R	NASA, Goddard Institute for Space Studies
HadGEM2_AO	Met Office Hadley Centre
HadGEM2_ES	Met Office Hadley Centre
IPSL_CM5A_LR	Institut Pierre-Simon Laplace
IPSL_CM5A_MR	Institut Pierre-Simon Laplace
MIROC_ESM	Japan Agency for Marine-Earth Science and Technology, Atmosphere and Ocean Research Institute (The University of Tokyo), and National Institute for Environmental Studies
MIROC_ESM_CHEM	Japan Agency for Marine-Earth Science and Technology, Atmosphere and Ocean Research Institute (The University of Tokyo), and National Institute for Environmental Studies
MIROC5	Atmosphere and Ocean Research Institute (The University of Tokyo, National Institute for Environmental Studies, and Japan Agency for Marine-Earth Science and Technology
MRI_CGCM3	Meteorological Research Institute
NORESM1_M*	Norwegian Climate Centre
NORESM1_ME*	Norwegian Climate Centre

(e.g., Hay et al., 2000). The more sophisticated quantile mapping method was not applied to the Puget Sound data because the observed data record was not of sufficient duration (i.e., <10 years).

From the observed SST data [$SST_{obs}(y,m)$] where m = month and y = year, monthly mean values [$SST_{obs,mean}(m)$] were computed by averaging the data for the period 1985–2000 for Chesapeake Bay and 2006–2013 for Puget Sound. For each GCM, we identified the nearest grid point to Chesapeake Bay or Puget Sound and used the data for that grid point in subsequent calculations. We then applied similar calculations to the model air temperature data [$T_{model}(y,m)$]. Monthly anomalies [$SST'_{obs}(y,m)$, $T'_{model}(y,m)$] were computed by subtracting the monthly means:

$$SST'_{obs}(y,m) = SST_{obs}(y,m) - SST_{obs,mean}(m)$$

$$T'_{model}(y,m) = T_{model}(y,m) - T_{model,mean}(m)$$

Cumulative distribution functions [$CDF_{obs}(m,x)$, $CDF_{model}(m,x)$ where x is the percentile] for Chesapeake Bay were computed for each month by ranking the anomaly values, using the common period of 1895–2000 for the model and observations CDF. For Puget Sound, standard deviations [$\sigma_{obs}(m)$, $\sigma_{model}(m)$] were calculated, for the common period of 2006–2013.

The SST scenarios were computed out to 2099. First, for each month, a trend [$A_{model}(m)$] was computed for the model's time series (1985–2099 for Chesapeake Bay, 2006–2099 for Puget Sound). The model values were detrended by subtracting the trend line values for each month.

$$T'_{model,detrend}(y,m) = T'_{model}(y,m) - A_{model}(m) * (y - y_{beg})$$

where y_{beg} = beginning year of observed data (1985 for Chesapeake Bay, 2006 for Puget Sound). For Chesapeake Bay, quantile mapping is applied by comparing each detrended value [$T'_{model,detrend}(y,m)$] to $CDF_{mod}(m,x)$ and the percentile (x) is determined. Next the value of $CDF_{obs}(m,x)$ is determined from the percentile x. Let $delta(y,m)$ denote the mapped value. In the case where $T'_{model,detrend}(y,m)$ is beyond the range of $CDF_{mod}(m,x)$, the CDFs are extrapolated with the assumption that the ratio, CDF_{obs}/CDF_{mod}, at the tails of the distribution is constant beyond the tails. For example, if $T'_{model,detrend}(y,m) < CDF_{mod}(m,0)$, then $delta(y,m) = T'_{model,detrend}(y,m) * CDF_{obs}(m,0)/CDF_{mod}(m,0)$. For Puget Sound, the 'mapped' value is just the variance-adjusted detrended value:

$$delta(y,m) = T'_{model,detrend}(y,m) * \sigma_{obs}(m)/\sigma_{model}(m)$$

The projected value of temperature for month and year incorporates the mapped value plus the trend. The future estimate of SST [$SST_{est}(y,m)$] is then given by:

$$SST_{est}(y,m) = SST_{obs,mean}(m) + delta(y,m) + A_{model}(m) * (y - y_{beg})$$

The above downscaling approach includes several assumptions and limitations. One assumption is that the future trend in temperature is linear, and thus a simple linear trend adjustment (A) is appropriate. Fig. 2 shows the future multi-model mean and range of temperature for Chesapeake Bay and Puget Sound. The temperature change is indeed highly linear. This is a consequence of the choice of scenario, RCP6.0, which is characterized by an approximate linear increase in greenhouse gas forcing over the 21st Century. Choice of another scenario with non-linear changes in greenhouse gas forcing, such as RCP4.5, would necessitate the use of a non-linear fit to the temperature change. A second assumption is that the present and future CDFs are similar in shape. When there are significant differences, Li et al. (2010) suggest an alternate method that incorporates the future CDF in the mapping. We compared our method with that of Li et al. (2010) and found average differences of less than 0.2 °C in the future projections, approximately an order of magnitude smaller than the model range (Fig. 2). Thus, the simpler method above was employed. One limitation is the short observational record for Puget Sound, the small sample size leading to high uncertainty in the variance estimate. An analysis of air temperature data from nearby Seattle-Tacoma Airport shows that the monthly variance for 2006–2013 averages about 90% of the variance for a standard 30 year period (1981–2010), a relatively small difference. Since the model variance is calculated over the same period and thus subject to similar uncertainties, errors associated with this uncertainty will be random and should roughly cancel over the 21-model ensemble.

The downscaled values of SST in Puget Sound and Chesapeake Bay from the 21 GCMs were applied to empirical models for *Alexandrium* and *Vibrio*, respectively, to evaluate climate-driven changes to human health risk through the 21st century. The empirical model for *Alexandrium* is a specific growth rate function that was developed using two local strains from Puget Sound (Bill et al., submitted for publication). The function indicates that Puget Sound *Alexandrium* growth is inhibited at temperatures below 7 °C, but then increases with warmer temperatures. Above 10 °C, the growth response is slightly less sensitive to temperature and a broad range of temperatures between 10 and 21 °C support optimal growth. Growth is strongly inhibited at temperatures above 25–26 °C, and growth ceases completely at 28 °C. Puget Sound *Alexandrium* are euryhaline and growth is sensitive to salinity changes only in the range of 10–20 psu (practical salinity units) (Bill et al., submitted for publication). The historical record of sea surface salinity (SSS) at the Dockton site in Quartermaster Harbor never fell below 21.87 psu, indicating that changes in SST are more important in regulating *Alexandrium* at this location. Therefore, we do not project changes to SSS here and instead use the climatological monthly mean values of SSS in the empirical growth function (Table 2). As such, we assume that potential changes to SSS in Quartermaster Harbor will be minimal and that *Alexandrium*
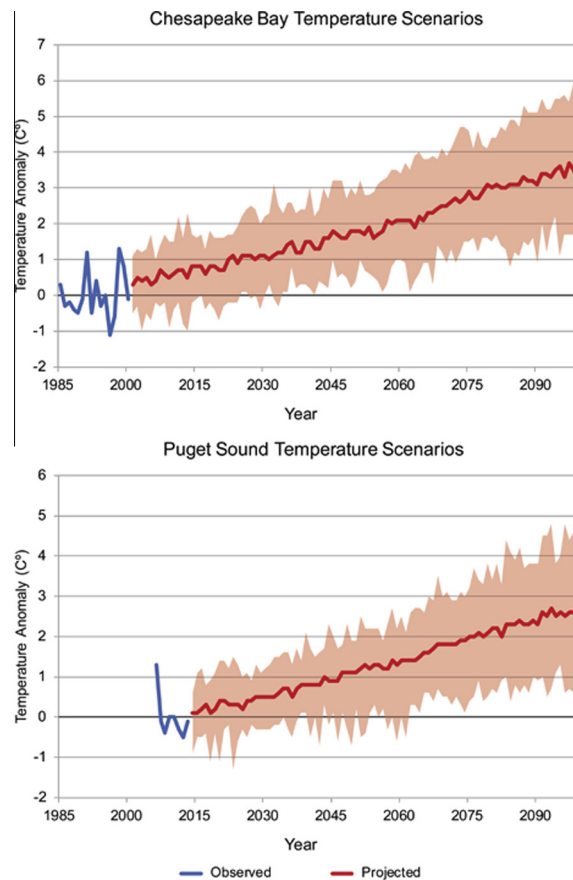
Fig. 2. Observed (blue) and projected (red) mean annual temperature for Chesapeake Bay (top panel) and Puget Sound (bottom panel). Projected data are multi-model means for 21 CMIP5 models for the RCP6.0 scenario. Observed data for Chesapeake Bay (Puget Sound) cover the period 1985–2000 (2006–2013). Projected data are relative to the mean of the observed period. Shaded area gives the range of future projections.

growth will continue to be sensitive to changes in SST only at this site. This is a reasonable assumption since there are few freshwater inputs to Quartermaster Harbor and salinity variations are small.

Two empirical models for *Vibrio* in Chesapeake Bay were used in this study. The first is a previously published statistical model relating probability of occurrence of *V. vulnificus* to SST and SSS (Jacobs et al., 2014). For the purpose of this exercise, salinity was held constant at 12 psu, or approximately optimal salinity for *V. vulnificus* in Chesapeake Bay (Jacobs et al., 2010, 2014). Concentrations of *V. parahaemolyticus* in oysters were modeled based on empirical relationships with SST and SSS established by the US Food and Drug Administration (USFDA, 2005). SSS was held constant at 20 psu, or approximately the optimal salinity for *V. parahaemolyticus* growth in oysters identified by the FDA *V. parahaemolyticus* risk assessment (USFDA, 2005).

Relative to the present day, which is defined by the duration of the baseline periods of observations in Puget Sound and Chesapeake Bay, changes in the seasonality of *Alexandrium* and *Vibrio* spp. growth were examined for the 2030s, 2050s, and 2090s defined by the periods 2025–2035, 2045–2054, and 2090–2099.

Geographic range shifts

Changes to the geographical distribution of *Vibrio* in Alaskan coastal waters (Fig. 1) were evaluated using GIS tools for spatial mapping. Water temperatures of 15 °C or greater are generally suitable for *Vibrio* growth and offer a threshold for examining potential changes in habitat availability with future warming (McLaughlin et al., 2005; Martinez-Urtaza et al.,

Table 2
Climatological monthly mean surface salinity for the Dockton site, Quartermaster Harbor, WA used to force the empirical growth model for *Alexandrium*.

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
SSS (psu)	27.68	28.72	28.52	28.24	27.38	28.03	28.71	29.28	29.63	29.97	29.23	29.22

2010). Of the suite of CMIP5 GCMs given in Table 1, four were selected to demonstrate a range of future climate projections and represent uncertainty (ISPL_CM5A_MR, NORESM1_M, NORESM1_ME, and GFDL_CM3). This approach allows for estimating climate trends where running all GCM's is not feasible. For each GCM, a mean August 'hindcast' SST layer was created in GIS using historic modeled data from 1971 to 2000 and observed data for the same time period. The month of August was chosen to demonstrate this landscape approach for evaluating changes to the risk of outbreaks of *Vibrio* since this is generally a present-day high risk month when SSTs are elevated during the summer. Similar to the approach described above for Puget Sound and Chesapeake Bay, the delta method was employed by subtracting predicted from observed temperatures for the baseline period and applying the bias correction to annual CGM model predictions for the month of August. After resampling to reduce the effect of land areas, the resulting layer was reclassified into areas where SST was above and below 15 °C. The reclassified areas were then overlaid with the Alaska coastline to obtain the shoreline area (M) with SSTs above and below 15 °C. For each GCM, a mean length was calculated for the 2030s, 2050s, and 2090s, and results reported as percentage of Alaskan shoreline with suitable SST for *Vibrio* growth.

Results

Seasonal shifts

Projections of SST for Chesapeake Bay estimate an average warming of 3.4 °C compared to the baseline period by the 2090s. The range of projections varied from 1.8 °C (FIO_ESM) to 4.6 °C (MIROC_ESM), and are similar to previously reported estimates for Chesapeake Bay (Najjar et al., 2009). This warming is projected to increase the abundance of V. parahaemolyticus in oysters by an average of 0.3 (±0.08) log cfu/g from the baseline period by the 2090s (Fig. 3). The projected increases in *V. parahaemolyticus* concentrations are relatively consistent seasonally although slightly elevated in the month of September (0.4 log cfu/g increase). While 2090s projected concentrations remain below criteria provided by the US Food and Drug Administration (10,000/g) to reduce illness risk, they are similar to those recently reported for regions of the Gulf of Mexico (Givens et al., 2014). In addition, with increasing air temperature, post-harvest growth will be of increasing concern. The probability of occurrence of *V. vulnificus* in mesohaline waters of Chesapeake Bay is projected to increase by 10.4% (±2.4%) by the 2090s (Fig. 3). The greatest changes are for the months of May (+16.2%) and September (+16.6%) which shoulder the present-day season for increased risk of illness, with the least change occurring in the winter months of January and February. Thus, assuming similar patterns of recreational and occupational use, risk of exposure to *V. vulnificus* is likely to increase.

By the 2090s, SST projections for Quartermaster Harbor, Puget Sound suggest an average 2 °C increase over the baseline period (2006–2014; Fig. 3). When these changes in SST are applied to the empirical model of *Alexandrium* growth, the results indicate that blooms could develop up to 2 months earlier in the year and persist for up to 2 months longer compared to the present day (Fig. 3). Following Bill et al. (submitted for publication), we define bloom-favorable conditions as those sustaining growth rates that exceed 0.25 μ d^{-1}. All model projections indicate that the *Alexandrium* bloom season will expand by at least 1 month on either side of the present-day bloom season by 2100. Therefore, this projection has high confidence and it is highly likely that the risk of shellfish being contaminated with potent toxins produced by *Alexandrium* blooms, making them unsafe for human consumption, will increase. This finding is consistent with previous studies on the potential impacts of climate change on *Alexandrium* in Puget Sound using climate model output from CMIP4 (Moore et al., 2011, accepted for publication).

Geographic range shifts

Projections for Alaskan coastal waters indicate that 60% of shoreline will have temperatures favorable SST for *Vibrio* growth for the month of August by the 2090s (Table 3). However, model projections vary considerably. This is not surprising,
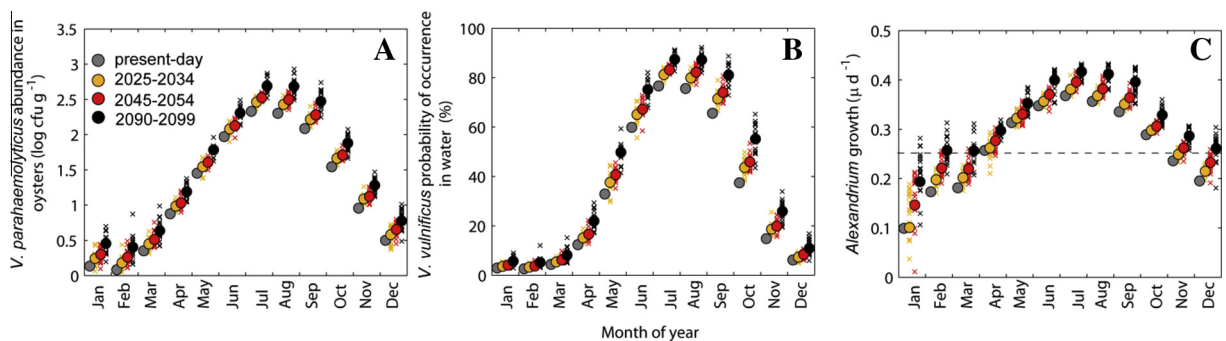

Fig. 3. Seasonal and decadal projections of the (A) concentration of *V. parahaemolyticus* in oysters of Chesapeake Bay, (B) probability of occurrence of *V. vulnificus* in Chesapeake Bay, and (C) growth of *Alexandrium* in Puget Sound. Mean values are plotted by decadal period, and the corresponding range of model projections are indicated by 'x'.

Table 3
Minimum, maximum, and average projections of percent of Alaska coastline with projected sea surface temperatures >15 °C in the month of August.

Climate models	Average (%)	Minimum (%)	Maximum (%)
2030 projection results for percent of Alaska coastline in August with projected sea surface temperature > 15°C			
GFDL	22.0	0.2	73.2
IPSL	30.7	0.0	60.9
NorESM1_M	13.1	0.0	28.6
NorESM1_ME	20.7	0.0	56.8
*2050** projection results for percent of Alaska coastline in August with projected sea surface temperature > 15°C*			
GFDL	39.2	11.3	60.8
IPSL	30.2	0.6	76.2
NorESM1_M	33.6	6.4	65.5
NorESM1_ME	28.0	8.1	50.5
*2090*** projection results for percent of Alaska coastline in August with projected sea surface temperature > 15°C*			
GFDL	79.6	65.1	87.2
IPSL	62.1	38.0	77.1
NorESM1_M	51.5	21.0	73.1
NorESM1_ME	38.9	3.6	75.8

[*] Based on evaluation of projection data for 2026–2035.
[**] Based on evaluation of projection data for 2046–2055.
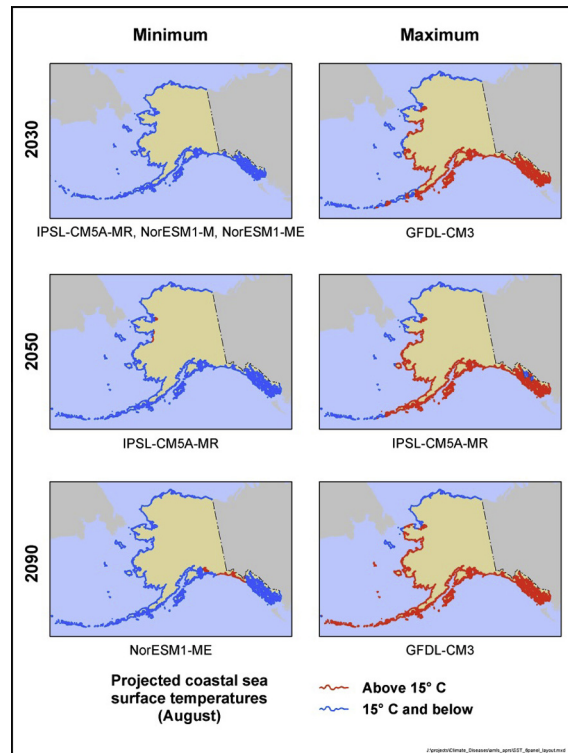[***] Based on evaluation of projection data for 2086–2095.

Fig. 4. Projected area of Alaskan coastline with suitable SST for *Vibrio* growth (SST > 15 °C) during August for the 2030s, 2050s, and 2090's.

as the four models used in this analysis were chosen to demonstrate the possible range expected for RCP6.0. Minimum and maximum projections of the percentage of coastline with increased risk for *Vibrio* infections range from 0 to 73.2% for the 2030s, 0.6 to 76.2% for the 2050s, and 3.6 to 87.2% for the 2090s (Table 3). While the range of possible outcomes is considerable, even the most conservative model suggests that the geographical distribution of *Vibrio* may extend from north of Juneau to Prince William Sound by the 2090s (Fig. 4). In southern Alaskan coastal waters, SST > 15 °C already occur during the summer, and in the Gulf of Alaska, SSTs have increased at a rate of 0.04 °C/y over the period 1976–2004 (McLaughlin et al., 2005).

Discussion

Using relatively simple approaches, we provide first order projections of the effects of climate change on the growth and distribution of pathogens and HABs that impact human health in U.S. coastal waters. The projections show the potential for changes to the seasonal window of growth and geographical range of coastal pathogens in Chesapeake Bay, Puget Sound, and Alaskan coastal waters. Importantly, the approaches described here use multiple GCMs and include estimates of uncertainty around the projections. This allows managers responsible for protecting coastal resources and human health to consider a range of possible outcomes in their decision-making. Together, the approaches can provide valuable information in both space and time to inform the development of adaptation strategies to increase the resiliency of coastal communities to the effects of climate change.

An example of how modeling approaches such as those described here can inform adaptation strategies is through changes in industry practices and education. A survey of vibriosis cases and medical practitioners in Japan revealed that while there are an estimated 425 cases annually of *V. vulnificus* septicaemia, only 15.7% of physicians had a basic knowledge of the infection (Osaka et al., 2004). Projections of changes in the risk for *Vibrio* infections such as those highlighted here allow for regionally focused education of emergency care physicians and general practitioners in regions of emerging concern, and awareness of expectations of early and later seasonal cases in endemic regions. Another example of how this information might be applied is to inform industry practices to minimize the risk of disease associated with contacting waterborne pathogens. Regulations and controls on oyster harvest and post-harvest treatment may also need to adapt to expanding seasons and geographic range shifts of coastal pathogens. Modeling approaches, such as presented here, will continue to improve and reduce uncertainty around these projections allowing for integrated approaches to risk management.

Expansion of seasonal windows of increased risk for *Vibrio* infections and elevated abundance of *Vibrio* in U.S. coastal waters has been associated with warming in recent years. In the oyster market survey used to develop the *V. parahaemolyticus* harvest model used in these projections, a log difference in abundance of both *V. vulnificus* and *V. parahaemolyticus* was noted between the sampling years of 1998 and 1999 and was associated with a ~3–4 °C temperature increase between years (Cook et al., 2002; Martinez-Urtaza et al., 2010). A review of *V. vulnificus* illness associated with oyster consumption from 1989 to 1997 and 1998 to 2007 also demonstrated an increase in illnesses associated with an elevated proportion of days warmer than 20 °C in the months of April and November (Martinez-Urtaza et al., 2010). While short-term studies have consistently linked warm temperature to increased *Vibrio* growth, only recently has evidence become available over time scales relevant to climate variability and change (i.e., ~30+ years). Vezzulli et al. (2012) demonstrated increased prevalence of plankton associated *Vibrio* in the North Sea over a 50 year time frame, correlating significantly with a concurrent rise in SST.

A variety of empirical (statistical) and in some cases mechanistic (process based) models have been developed for specific pathogens in U.S. waters. Examples include models for species of *Vibrio* (Constantin de Magny et al., 2010; Froelich et al., 2013; Jacobs et al., 2014), HABs (Milroy et al., 2008; Anderson, 2009; Moore et al., 2009; Brown et al., 2013), and indicator bacteria (Nevers and Whitman, 2011). In many cases, such models have been used in hydrodynamic modeling systems or used in conjunction with remotely sensed data to provide short term predictions, or early warning (Phillips et al., 2007; Brown et al., 2013; Grimes et al., 2014). These approaches offer a basis for first order projections of climate impacts. For example, Moore et al. (2011) identified environmental parameters associated with favorable bloom conditions for the toxic dinoflagellate *Alexandrium* in Puget Sound, termed the window of opportunity. Scenario modeling based on 20 GCM (CMIP4) simulations of the A1B scenario was used to demonstrate that conditions appropriate for bloom events may appear 2 months earlier and persist for 1 month later by the end of the 21st century. In other regions of the world, fully coupled GCM-oceanographic modeling systems have been employed to offer greater spatial resolution of climate impacts. Glibert et al. (2014) demonstrated this approach using a single GCM applied in a coupled oceanographic-biogeochemical model for two species of harmful algae in Northern Europe and Southeast Asia. The coupling of biological models with earth system modeling approaches offers much potential for projecting changes in waterborne pathogens, and undoubtedly will be further pursued in future efforts.

Modeling projected changes in waterborne disease burden has similarly progressed, but faces many challenges. In some cases, simple models relating environmental variables to the incidence rate can provide first order estimation. For example, Baker-Austin et al. (2012) provided a statistical model relating elevated SST to *Vibrio* infections in the Baltic Sea. Similarly, Gingold et al. (2014) used time series analysis to relate SST and tropical storm frequency to ciguatera fish poisoning. As with pathogen habitat models, these relationships can be used for climate projection, but have several caveats. They do not capture many of the issues which affect disease epidemiology such as changing demographics, intervention strategies and sanitation practices. Nor in the case of the disease agents themselves do they account for the ecology of the system and complex and evolving interactions among host, pathogen and the environment.

Temperature is a well-established driver of microbial growth in the environment, but other climate related factors not accounted for in this exercise may also influence future concentrations and distribution. For example, salinity is an important determinant of habitat suitability for *Vibrio*, which may be influenced by sea level rise and changing precipitation patterns. Gibson and Najjar (2000) developed statistical models for salinity in Chesapeake Bay and applied them to four GCM's demonstrating potential range shifts in freshwater and overall isohalines. Increases in freshwater flow would potentially provide more habitat for *V. cholerae*, while distributing *V. vulnificus* and *V. parahaemolyticus* further down Bay. These changes would also alter the ecology of the system in numerous ways including the potential for increased loading of dissolved organic

carbon and nutrients, providing substrate for algal and pathogen growth, changes in preferred habitat for oysters, and the timing and location of spring blooms. However, robust projections of the likelihood, direction and magnitude of these changes are not presently available. Equally speculative are changes associated with ocean acidification. Huq et al. (1984) demonstrated that attachment of *V. cholerae* to copepods was greatest under alkaline (pH 8.5) conditions, declining with decreasing pH. However, Sperling et al. (2013) found that high CO_2 levels in mesocosm experiments enhanced the diversity of the bacterial community in particle attached bacteria, but not in free living. While more research is clearly needed in this area, projections of 0.3–0.4 decline in pH by 2100 (IPCC, 2014) will likely have taxon specific implications (Flynn et al., 2012) which may influence the dynamics and diversity of phytoplankton blooms and consequently *Vibrio* growth and distribution (Vezzulli et al., 2012). Over the next several decades, the coupling of climate and epidemiological models holds much promise for enhanced prediction over time and spatial scales relevant to public health intervention (Rodó et al., 2013). Seasonal changes and climate indices such as ENSO are being incorporated into waterborne disease and epidemiological models (Koelle, 2009; Lal et al., 2013). Such approaches allow for the concurrent evaluation of environmental conditions suitable for pathogen growth, influences on transmission rate, and proportion of the population that is susceptible (Koelle, 2009). Efforts to develop finer scale spatial resolution of climate model projections will also enhance local scale epidemiological modeling approaches. Nevertheless, the approaches described here use the best available science at the highest resolution available to us for the regions of concern. We cannot claim to predict actual impacts or the pathogen and HAB responses to all possible forcing factors. Rather, we are characterizing relative differences compared to the present-day.

In summary, we present an environmentally relevant approach that provides new insights into climate change impacts on waterborne pathogens and toxic HABs in U.S. coastal waters. This approach allows a quantitative evaluation of the likelihood of projected changes in the seasonal windows of growth and geographic range shifts of coastal pathogens, with implications for human health risk. This information can be used in decision support around climate change and public health to guide adaptation and mitigation efforts to minimize the risk of disease. For example, public health managers can use this information to proactively plan for the increased economic cost associated with expanded monitoring for waterborne pathogens and toxic HABs outside of the historical seasonal window and/or in new geographic regions with no prior history of disease. This will minimize the risk of being caught off-guard by an unexpected outbreak or bloom.

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