

Predicting toxin contamination in harvested marine species to guide dynamic ocean management

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Abstract

Harmful algal blooms (HABs) can produce toxins that accumulate in the tissue of seafood species and represent an increasing threat to seafood harvesters and consumers. Developing tools for predicting toxin contamination is critical to designing dynamic management strategies for mitigating risk to consumers while also minimizing impacts on harvesters. Here, we develop machine learning models for predicting daily coastwide domoic acid contamination in seven harvested marine invertebrates in California. Contamination in four wild capture species frequently exceeded management action thresholds. Models developed for these species were good predictors of contamination risk and hindcast high rates of contamination in historical catch. On the other hand, contamination in two aquaculture species rarely exceeded management action thresholds indicating that weekly testing and dynamic management have successfully eliminated public health risks for these species. We use our models to assess the appropriate spatial-temporal scales for toxin monitoring programs and dynamic fishery closures.

Keywords: harmful algal blooms; *Pseudo-nitzschia*; ecological forecasting; dynamic ocean management; climate change; domoic acid; machine learning; aquaculture; fisheries; biotoxins

Introduction

Harmful algal blooms (HABs) represent an increasingly significant threat to fisheries and aquaculture around the globe. They have been increasing in size, frequency, duration, and toxicity due to the combined effects of eutrophication and climate change (Glibert, 2020; Hallegraeff, 2010, 1993; Van Dolah, 2000) and these trends are expected to persist or worsen with continued climate change (“high confidence” in (IPCC, 2019)). Many HABs produce toxins that accumulate in the food web, including in species harvested in wild-capture fisheries and aquaculture, and can cause human illness or mortality when consumed in high doses (Grattan et al., 2016). HABs can reduce revenues from fisheries and aquaculture due to fish kills, closures to limit public health risk, and costly monitoring programs and mitigation responses (Hoagland et al., 2002; Hoagland and Scatasta, 2006). Furthermore, HABs can reduce tourism revenue from recreational fisheries (Dyson and Huppert, 2010), food provisioning in subsistence fisheries (Borbor-Córdova et al., 2018), and disrupt cultural practices, community identity, and social interactions associated with fishing (Bauer et al., 2010; Willis et al., 2018).

The impact of HABs on human society can be reduced through prevention, control, and mitigation (Anderson, 2009; Boesch et al., 1996). Although the prevention of HABs through reductions in nutrient runoff, pollution, and greenhouse gas emissions is optimal (Paerl et al., 2018, 2016), these pathways represent long-term projects that are outside the purview of fisheries and aquaculture managers. The control (a.k.a., suppression or destruction) of HABs through human interventions has received limited consideration (Anderson, 1997) due to unknown efficacy, low economic feasibility, and high potential for unintended consequences (Anderson, 2012, 2009). This leaves mitigation as the most actionable response to seafood operators and managers. Current HAB mitigation measures include: (1) temporary closure of fisheries and aquaculture facilities in areas with high contamination; (2) relocation of fishing grounds or aquaculture operations to uncontaminated areas; (3) depuration of toxic fisheries or aquaculture organisms in uncontaminated waters; or (4) evisceration of the most contaminated parts of the organism (Anderson et al., 2015, 2001). Although these procedures have generally been effective at keeping contaminated seafood off the market (Anderson et al., 2001), they can incur great economic and cultural costs to the people who depend on these resources (Bauer et al., 2010; Dyson and Huppert, 2010; Mao and Jardine, 2020).

The design and implementation of strategies that mitigate public health risks posed by HABs while also minimizing the burden placed on fishers and aquaculture farmers depends on a robust ability to detect and forecast the occurrence of HABs and accumulation of toxins in seafood species. Traditionally, the detection of HABs and seafood contamination has relied on *in situ* monitoring of phytoplankton community composition and toxin concentration and assay of contaminant concentrations in field-collected shellfish (Stauffer et al., 2019). Although these methods yield precise measurements of HAB and toxin dynamics, these programs are often opportunistic (i.e., not explicitly linked with an experimental design), costly, provide information on delay (i.e., after lab processing), and offer limited spatial and temporal resolution (Stauffer et al., 2019). Alternatively, statistical models that link *in situ* measurements with satellite observations and oceanographic model output can provide near real-time estimates of HAB

dynamics at daily intervals on large spatial scales (Anderson et al., 2019; Stauffer et al., 2019). Although predictions from these models are limited to the ocean surface and are less precise than *in situ* measurements (Anderson et al., 2016; Stumpf et al., 2009), they can provide early warning of HAB risk and guide dynamic ocean management, especially when interpreted in coordination with stakeholders (Anderson et al., 2019).

However, surface densities of harmful algae and toxins are not necessarily correlated with the accumulation of toxins in benthic organisms (Kvitek et al., 2008; Sekula-Wood et al., 2011; Umhau et al., 2018), which is the ultimate concern for managers and often the metric that triggers management action (US-FDA, 2019). Thus, a critical next step in the development of predictive modeling tools is to translate maps of near real-time surface HAB and toxin risk into maps of near real-time seafood contamination risk (Anderson et al., 2019). This has been challenging because the processes governing the uptake, retention, and depuration of toxins in aquatic food webs are highly complex (Granéli and Turner, 2006). For example, toxic algae cells can accumulate in benthic sediments, be resuspended later via bioturbation or bottom flow, and trigger contamination events that occur well after the termination of the original bloom (Vigilant, 2007). While mechanistic models for describing, predicting, and forecasting these complex processes evolve (CA-OST, 2016a; NOAA, 2015; Stauffer et al., 2019; Terseleer et al., 2013), statistical models employing state-of-the-art machine learning methods could provide mechanism-free approaches for predicting benthic seafood contamination from surface HAB and toxin dynamics.

In California, blooms of *Pseudo-nitzschia* genus are linked to warm ocean conditions (McKibben et al., 2017) and produce domoic acid, a neurotoxin that accumulates in the tissue of important seafood species (Lefebvre et al., 2002) and causes amnesic shellfish poisoning in humans when consumed in high doses (Perl et al., 1990). In 2015, an especially large bloom of *Pseudo-nitzschia* resulted in the prolonged closure of important commercial and recreational fisheries and aquaculture along the entire U.S. West Coast (McCabe et al., 2016). The direct economic impact from commercial closures was estimated to be \$25.6 million for the California Dungeness crab and rock crab fisheries (CDFW, 2018); the value of federal disaster relief funds issued to the state) with substantial but unquantified impacts to other commercial, recreational, and aquaculture fisheries (Moore et al., 2019; Ritzman et al., 2018). While aquaculture facilities are required to test for domoic acid weekly and have a clear domoic acid management plan (CDFW, 2017a), the monitoring and management of domoic acid in capture fisheries is more limited. Despite the importance of the Dungeness crab fishery and the consequences of its closure on the state economy, the biotoxin monitoring program that triggers these closures is limited to 72 individual pre-season crab samples divided among six sampling sites coastwide (CA-OST, 2016b; PSMFC, 2018). The sampling program for other wild species is ad-hoc, voluntary, and unfunded (CA-OST, 2016b).

In this study, we develop state-of-the-art machine learning models for predicting domoic acid contamination in seven commercially or recreationally important marine invertebrates in California (**Table 1**). The models relate predictions of daily surface water domoic acid risk from the California Harmful Algae Risk Mapping system (C-HARM; (Anderson et al., 2016)) (**Figure**

1; **Figures S1-S2**) to the domoic acid contamination of crabs and bivalves sampled by the California Department of Public Health (CDPH; (CDPH, 2019)) as part of its marine biotoxin monitoring program (**Figures 1-3**). By leveraging the spatial and temporal domain of the C-HARM system, our models can provide daily hindcasts (March 5, 2014 to present), daily nowcasts, and 3-day forecasts of domoic acid contamination on a 3-km grid spanning all of coastal California. We illustrate how our models could be used to: (1) guide studies into the biology of domoic acid accumulation in the food web; (2) identify low risk sites for aquaculture farms; (3) evaluate appropriate spatial-temporal scales for dynamic closures; and (4) build operating models for simulation testing candidate strategies for dynamic ocean management.

Results and discussion

Four of the five wild-capture species -- Dungeness crab, rock crab, spiny lobster, and razor clam -- exhibited high rates of domoic acid contamination above their FDA action thresholds (15-80% of samples; **Figure 3**) and the best performing models for these species were fair to good predictors of domoic acid contamination risk (**Figure 4; Table S1**). California sea mussel was the only wild-capture species to exhibit low rates of contamination above its action threshold (3.4% of samples; **Figure 3**) and models for this species were poor predictors of domoic acid contamination risk (**Figure 4; Table S1**). For the four wild-capture species with adequate models, we hindcast historical contamination risk inside fishing grounds from 2014 to present (**Figure 5**). We use these hindcasts to characterize the spatial and temporal variability of historical contamination events and provide guidance on (1) where expansions in field monitoring could improve ability to detect and monitor contamination events and (2) the appropriate size and duration of fishery closures in response to domoic acid contamination events.

The routine pre-season monitoring of domoic acid contamination in Dungeness crabs has relatively good spatial coverage from Monterey Bay north (**Figure 5**), where approximately 97% of Dungeness crab landings have been caught over the past five years (**Figure S5**). As a result, pre-season monitoring has successfully detected and tracked many of the historical early season contamination events predicted by the model (**Figure 5**). However, sampling has been limited south of Monterey Bay despite high predicted domoic acid risk in this area (**Figure 5**). Although this southern region generates only a small portion of state-wide landings (~3%), it is the source of catch for the majority of Dungeness crab landed in Avila Beach/Port San Luis and Morro Bay, and may disproportionately expose these communities to domoic acid risk (**Figure S5**). Furthermore, the model predicts that a number of late season contamination events went undetected following the termination of pre- or early-season testing. Although the majority of the catch in this derby fishery is caught at the beginning of the season (**Figure S5**), unmonitored late season catch still presents a public health risk. Overall, the largest benefits for public health might be the expansion of pre-season monitoring south of Monterey Bay and routine late season monitoring coastwide whereas the largest benefits for fishers, via more nimble management, might be the expansion of early-season monitoring between Eureka and Bodega Bay (**Figure 5**).

Historically limited monitoring of rock crab and spiny lobster for domoic acid contamination is likely to have overlooked a number of large contamination events. This is particularly true for spiny lobster, for which sampling has been sparse, yet is predicted to have experienced extensive contamination risk (**Figures 5&6**). In six years, only 173 spiny lobster have been tested for domoic acid contamination (**Figures 2&3**) and the majority of these samples (95%) were collected during three sampling campaigns (**Figure 5**). This limited sampling program likely failed to detect extensive contamination events occurring north of Los Angeles (34°N), especially during the 2016-17, 2017-18, and 2018-19 seasons (**Figure 6**). However, the timing of the commercial and recreational lobster season (Oct 1-Mar 15) reduces contamination risk, with more pronounced contamination events occurring during the off-season summer months than during the in-season winter months (**Figures 5&6**). Rock crab were predicted to experience frequent contamination events but at smaller spatial and shorter temporal scales than either Dungeness crab or spiny lobster (**Figures 5&7**). The rapid turnover in rock crab contamination events constrains the feasibility of dynamic management in this fishery. Domoic acid closures for rock crab may be necessarily less nimble and more precautionary than for Dungeness crab or spiny lobster.

Razor clams, which exhibit slow domoic acid depuration rates (Schultz et al., 2008) and can retain domoic acid for up to a year after a HAB event (Wekell et al., 1994), were predicted to have the highest frequency and intensity of historical contamination events (**Figures 6-8**). In response to this risk, the California Department of Fish and Wildlife (CDFW) has closed the recreational razor clam fishery since April 2016 in Humboldt and Del Norte counties (CDFW, 2017b), which are home to Clam Beach and Crescent Beach, respectively (**Figure 2**), the two most productive, popular, and well-monitored clamping beaches in the state (Moore, 2001). The CDFW currently recommends that clammers visit Doran Beach in Sonoma County and Dillon Beach in Marin County while the closure remains in place (Wilson, 2017). However, these beaches have received little to no monitoring (**Figure 2**) and contamination at these beaches has likely been high since 2014 (**Figure 5**). Our model predictions could be used to identify low risk razor clam beaches that -- following validation through targeted field sampling and laboratory testing -- could be recommended for recreational clamping.

Our hindcasts of historical contamination risk could be used to compare the performance of alternative strategies for mitigating the impact of HABs on wild-capture fisheries and public health through a process called management strategy evaluation. A management strategy evaluation (MSE) simulates the entirety of the resource--harvester--management loop to measure the performance of and tradeoffs between alternative management strategies (Punt et al., 2016). As an example, our hindcasts could be used to simulate domoic acid contamination and to quantify the ability of alternative management strategies to maximize fishing opportunities (e.g., amount of catch or profits, length or timing of season, etc.) while minimizing contaminated catch (i.e., amount above the action threshold). The evaluated management strategies could include combinations of: (1) expanded or redesigned monitoring programs; (2) management triggers based on monitoring or other indicators of elevated risk; and/or (3) management actions such as fishery closures, evisceration orders, or timing of the open season. The MSE process can also incorporate other, potentially, synergistic, fishery risks. For

example, delays in the Dungeness crab and rock crab trap fisheries due to domoic acid risk during the 2015-16 fishing season resulted in greater overlap in areas of high fishing effort and high humpback whale density, which resulted in a sharp increase in the number of whale entanglements in crab fishing gear (Santora et al., 2020). Solutions to these interconnected management challenges could be explored by jointly simulating domoic acid contamination, humpback whale distributions, and crab fleet dynamics in a management strategy evaluation framework.

Both aquaculture species -- Pacific oyster and bay mussel -- exhibited low rates of domoic acid contamination above the FDA action threshold (<4% of samples; **Figure 3**) and models of contamination risk were either unreliable or impossible to estimate. No Pacific oyster samples exceeded the action threshold (the highest observed domoic acid contamination was 9.6 ppm; **Figure 3**) and contamination risk models were not pursued for this species. Only 3.3% of bay mussel samples exceeded the action threshold and models for these species were poor predictors of contamination risk (**Figure 3; Table S1**). The low rate of contamination in aquacultured organisms is likely driven by fast depuration rates (<96 hours) in these species (Blanco et al., 2002; Mafra et al., 2010; Novaczek et al., 1992; Schultz et al., 2008), and the frequent testing and dynamic management employed by aquaculture farms in collaboration with the CDPH. All commercial shellfish facilities are required to submit weekly tests to the state, conduct even more frequent testing on their own, and shut down sales when individuals test above the FDA action threshold (CA-OST, 2016b).

Although the lack of significant domoic acid contamination in aquaculture species is good at face value, the absence of a robust contamination signal prevents the development of predictive models that could otherwise be used to give farmers advance warning of contamination events and identify low risk sites for new aquaculture farms. The use of sentinel organisms, i.e., the experimental placement of aquaculture species in areas representative of potential farm locations (Backer and Miller, 2016), would advance the collection of data required to develop effective models for predicting contamination for existing or emerging aquaculture species. Aquaculture is the fastest growing food sector in the world (FAO, 2018, 2016) and is likely to become an even more important source of food as the human population and its demand for animal-based protein grows (Costello et al., 2019). The ability for aquaculture to meet these demands will be challenged by increasing HAB frequency, storm intensity, ocean warming, salinity fluctuations, deoxygenation, and ocean acidification (Barange et al., 2018; IPCC, 2019; Weatherdon et al., 2016). Thus, developing tools for identifying locations for aquaculture farms that are subject to minimal risk will be necessary for expanding aquaculture under climate change (Gaines et al., 2019).

Our framework for predicting and forecasting seafood contamination risk is transferable to existing marine and freshwater biotoxin monitoring programs (see (Anderson et al., 2019) for examples) as the basis for statistical “shortcuts” while more mechanistic models for predicting the production and flow of toxins through the food web are developed and tested. For example, the machine learning approach developed here could be used to relate brevetoxin contamination in wild and aquaculture shellfish (Pierce and Henry, 2008) to gridded predictions

of *Karenia brevis* risk produced by the Gulf of Mexico Harmful Algal Bloom Operational Forecast System (GOM HAB-OFS; (Stumpf et al., 2003; Tomlinson et al., 2004)). In places without gridded predictions of HAB or toxin risk, contamination in seafood species could instead be predicted from more conventional data, such as field measurements of HAB or toxin densities or field or satellite measurements of the oceanographic processes driving HAB and toxin dynamics. (Finnis et al., 2017) provide a good example of the ability for machine learning models to predict toxin contamination from underlying oceanography. They show that contamination of mussels (*Mytilus* spp.) with saxitoxin, a neurotoxin produced by dinoflagellates in the genus *Alexandrium* that can cause paralytic shellfish poisoning, can be predicted from environmental variables such as temperature, salinity, and freshwater discharge.

The use of predictive statistical or mechanistic models to guide the dynamic management of domoic acid contamination could dramatically reduce the burden of closures on fishers and aquaculture farmers while minimizing the public health risk of contamination events. The economic benefits of such advancements are highly likely to outweigh the costs of expanded monitoring, data sharing platforms, and personnel required to develop and maintain these tools (Stauffer et al., 2019). Although the economic impacts of HABs are challenging to estimate (Sanseverino et al., 2016), a recent evaluation suggests that marine and freshwater HABs result in approximately US\$10 billion of economic losses annually (Bernard et al., 2014). Given the rule-of-thumb that the value of information on a resource is worth at least 1% of the resource (Macauley, 2006), annual investments in HAB monitoring, forecasting, and communication of at least US\$100 million annually are warranted (Stauffer et al., 2019). The importance of and return on this investment will only increase as HAB frequency, intensity, and impact on fisheries and aquaculture increase under climate change.

Methods

Overview

We developed, tested, and compared machine learning models for predicting domoic acid contamination in seven marine invertebrate species in California. We developed the models by relating estimates of domoic acid risk from the California Harmful Algae Risk Mapping (C-HARM) system (Anderson et al., 2016) to the domoic acid concentrations of crabs and bivalves sampled by the California Department of Public Health (CDPH) as part of its biotoxin monitoring program. We trained candidate models on 80% of the data for each species and tested the models on the remaining 20% of the data. We identified the best performing model for each species and used these models to hindcast the proportion of historical harvest likely to have been contaminated with domoic acid above the U.S. Food and Drug Administration (FDA) action threshold for each species (US-FDA, 2019).

Domoic acid contamination data

We modeled domoic acid contamination using contamination measurements from the California Department of Public Health (CDPH) biotoxin monitoring program as the response

variable. California has been monitoring marine biotoxins since 1927 (longer than any other U.S. state), has been monitoring domoic acid levels since 1991, and has publicly available contamination data from July 2015 to present. We evaluated the seven species with more than 100 measurements of domoic acid concentration (**Table 1**). These measurements were collected through a mixture of voluntary to mandatory and routine to ad-hoc coastwide sampling programs (CA-OST, 2016b) (**Figure 1**). Dungeness crab are routinely sampled from twelve sites before each season opens and are sampled at a wider array of sites on an ad-hoc basis throughout the season in response to indicators of elevated contamination risk. Rock crab, spiny lobster, razor clam, and sea mussel are sampled on an ad-hoc basis by California state biologists and a network of volunteers in response to elevated risk. The majority of samples for Pacific oyster and bay mussel are provided by commercial growers who are required to submit samples for weekly toxin testing. See **Table 1** for the number of samples for each species.

C-HARM predictions of domoic acid risk

We modeled domoic acid contamination using historical daily predictions of surface water domoic acid risk from the California Harmful Algae Risk Mapping (C-HARM) system (Anderson et al., 2016) as the predictor variables (**Figure 1**). C-HARM uses regressions developed from field observations (Anderson et al., 2011) to estimate the probability of *Pseudo-nitzschia* blooms ($>10^4$ cells/ml), high particulate domoic acid (pDA) concentrations (>500 ng/l), and high cellular domoic acid (cDA) concentrations (>10 pg/cell) from a combination of ocean reflectance, sea surface temperature, salinity, chlorophyll, and month variables. Historical daily predictions are available from March 5, 2014 to present (~6 years) on a 3 km resolution grid spanning the entire California coastal ocean from north of Crescent City, CA to Ensenada, Mexico to approximately 1000 km offshore (**Figure S1**). We imputed values for 125 days (5% of days) without C-HARM pDA and cDA predictions (due to failed ROMS model runs during server outages) using linear interpolation. C-HARM has been shown to be a relatively good predictor of nearshore *Pseudo-nitzschia* and domoic acid dynamics when tested against data from seven piers along the California coast (Anderson et al., 2016). C-HARM's pDA predictions have been shown to be moderately correlated with domoic acid concentrations in experimental monitoring resins (SPATT) and marine mammal strandings but only weakly correlated with domoic acid concentrations in mussel tissue (Anderson et al., 2016).

Model development and testing

We evaluated the ability of three classification models -- logistic regression, random forests, and boosted regression trees -- to estimate the probability that an individual of each study species is contaminated above its FDA management action threshold (US-FDA, 2019) based on each of the previous 30 days of cellular domoic acid (cDA) risk. For both the random forest and boosted regression tree models, we performed grid searches for the tuning parameter combinations that maximize Cohen's kappa using repeated 10-fold cross validation (**Figures S3-S5**). The models were fit using a combination of the *tidymodels* (Kuhn and Wickham, 2020), *caret* (Kuhn, 2020), *gbm* (Greenwell et al., 2019), and *randomForest* (Liaw and Wiener, 2002) packages in R (R Core Team, 2020).

We considered 30 days of domoic acid risk given laboratory experiments showing that contaminated Dungeness crabs took 21 days to depurate 89% of their initial domoic acid load ((Lund et al., 1997)). Although the depuration rates for rock crab and spiny lobster are unknown, they have similar diets to Dungeness crab and may therefore have similar uptake kinetics. Although the depuration rates of Pacific oyster and mussels are much faster (~96 hours), the performance of machine learning models is insensitive to the inclusion of uninformative variables. The depuration rate of razor clam is much longer (1 year) but we use only 30 days to maintain consistency across models. We did not evaluate particulate domoic acid (pDA) risk as a predictor of domoic acid contamination risk because the algorithm for calculating pDA risk changed when C-HARM switched hosts in 2018 (C. Anderson, personal communication).

We measured model performance in terms of accuracy, Cohen's kappa, and the area under the receiver operating characteristic curve. Accuracy measures the proportion of correct classifications. Cohen's kappa measures the proportion of correct classifications accounting for the probability of being correct by chance (Cohen, 1968). Although there are no definitive rules for interpreting Cohen's kappa, general guidelines suggest that values >0.70 are 'excellent', 0.4–0.7 are 'good', 0.2–0.4 are 'fair', and <0.2 are 'poor' (Fleiss, 1973, p. 1; Landis and Koch, 1977). The receiver operating characteristic (ROC) curve depicts classification performance by plotting the true positive rate (probability of detection) against the false positive rate (probability of false alarm) at various threshold settings. The area under the curve (AUC) thus measures how well a classifier can distinguish between two groups (i.e., contaminated vs. uncontaminated) where 1.0 means that the classifier is perfect and 0.5 means that the classifier performs no better than a coin flip. Although there are no definitive rules for interpreting AUC values, general guidelines suggest that values >0.9 are 'outstanding', 0.8–0.9 are 'excellent', and 0.7–0.8 are 'acceptable' (Hosmer and Lemeshow, 2000).

Hindcasting historical contamination risk

For species with models with fair to good accuracy (Cohen's kappa > 0.35), we used the best performing model based on AUC (**Table S1**; **Figure 4**) to hindcast historical contamination risk (March 5, 2014 to May 20, 2020) throughout the species fishing grounds (**Figure 2**). The majority of fishing occurs within 100 fathoms (600 ft or 183 m; (Miller et al., 2017)) and fishing grounds were delineated as the portion of a species range inside this area. We examined spatial-temporal variability in contamination by calculating mean daily contamination risk along each latitudinal band and identified distinct contamination events from these data by contouring space-time windows where an individual would have greater than a 50% probability of being contaminated above the FDA action threshold. This not only reflects areas where the probability of being contaminated is greater than the probability of not being contaminated but is also the management trigger for Dungeness crab zonal closures (CA-OST, 2016b). We characterized the spatial and temporal scales of each contamination event by measuring its coastal span (latitudinal extent) and duration (number of days above the action threshold), respectively. Finally, we identified opportunities for improving the sampling program design by comparing the alignment between the locations of sampling sites and the areas of high contamination risk.

Acknowledgements

We are grateful to Christina Grant (CDPH) and Duy Truong (CDPH) for sharing the crab domoic acid data, Vanessa Zubkousky (CDPH) for sharing the mollusc domoic acid data, and Morgan Ivens-Duran (CDFW) and Christy Juhasz (CDFW) for sharing the Dungeness crab landings data. This work was supported by TNC California.

Competing interests

The authors declare that they have no competing interests.

Data availability

The data that support this study are available here: <https://github.com/cfree14/dungeness>

Code availability

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Tables and figures

Table 1. Study species sample size, fishery type, and open season information.

Species	# of samples	Fishery type ¹ and season
<i>Crustaceans</i>		
Dungeness crab (<i>Metacarcinus magister</i>)	1582 (all wild)	Commercial (99%): Dec 1 - Jul 15 (north), Nov 15 - Jun 30 (central) Recreational (1%): Nov 2 - Jul 30 (north), Nov 2 - Jun 30 (central)
Rock crab ² (<i>Cancer</i> spp.)	861 (all wild)	Commercial: Year-round Recreational: Year-round
California spiny lobster (<i>Panulirus interruptus</i>)	167 (all wild)	Commercial (75%): Oct 1 - Mar 15 Recreational (25%): Early Oct - Mar 15
<i>Bivalves</i>		
Razor clam (<i>Siliqua patula</i>)	567 (all wild)	Recreational: Year-round (with occasional even/odd year closures)
California sea mussel ³ (<i>Mytilus californianus</i>)	1330 (566 sentinel, 764 wild)	Recreational: Year-round (with frequent summer domoic acid quarantines)
Bay mussel (a.k.a., Mediterranean mussel) ³ (<i>Mytilus galloprovincialis</i>)	448 (315 cultured, 133 wild)	Aquaculture
Pacific oyster (<i>Crassostrea gigas</i>)	668 (all cultured)	Aquaculture

¹ Percentages for Dungeness crab (CDFA, 2011) and spiny lobster (CDFA, 2017c) indicate the percent of total landings derived from commercial and recreational fisheries.

² Includes red (*Cancer productus*), yellow (*Cancer anthonyi*), and brown (*Cancer antennarius*) rock crabs, which overlap in range but are most abundant in northern, central, and southern California, respectively.

³ Note: hybridization of wild mussels (*Mytilus* spp.) introduces error in the identification of wild mussels collected for toxin monitoring.

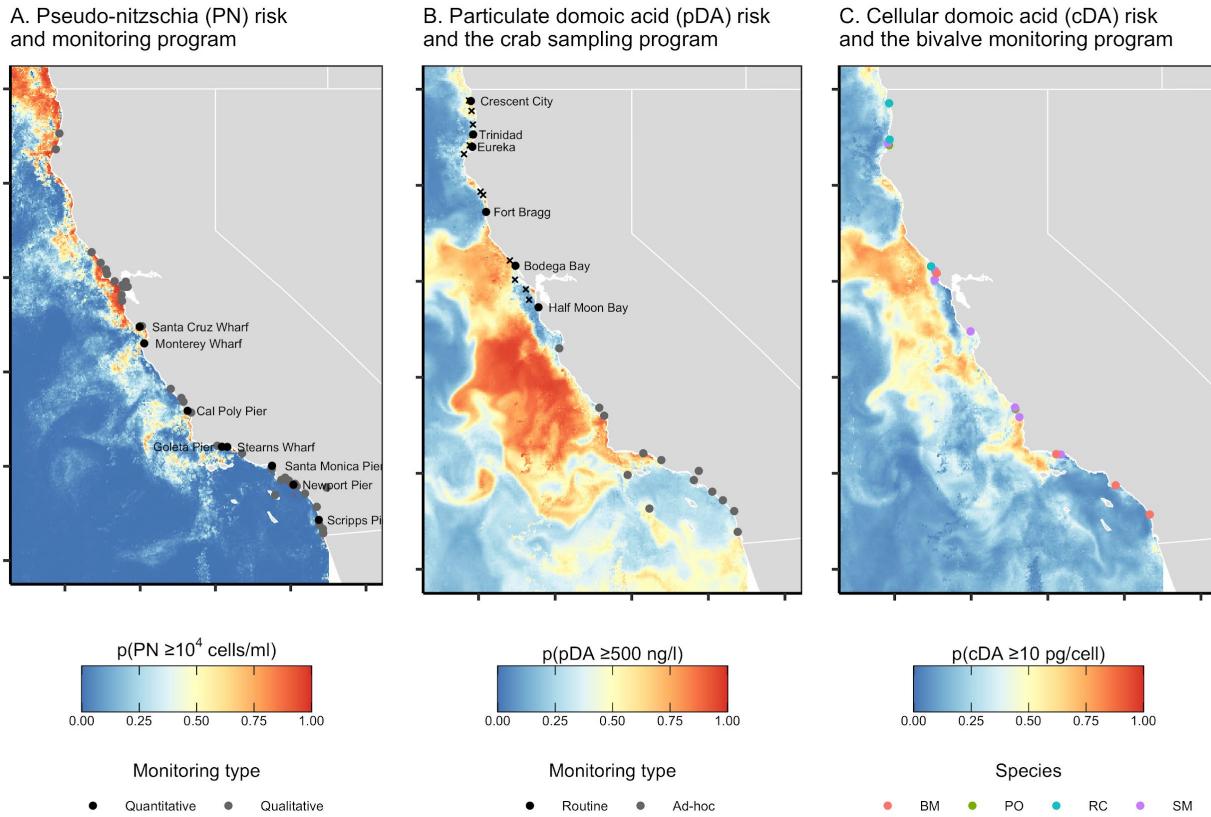


Figure 1. Distribution of (A) *Pseudo-nitzschia* (PN), (B) particulate domoic acid (pDA), and (C) cellular domoic acid (cDA) risk predicted by C-HMM on an example date (July 1, 2015). Panel A shows the network of quantitative (8 piers; black circles) and qualitative (40 locations; grey circles) *Pseudo-nitzschia* monitoring sites. Panel B shows the routine pre-season (6 ports, black circles; 2 sites per port, black x's) and ad-hoc mid-season (13 ports, grey circles) monitoring sites for domoic acid in Dungeness crabs. Panel C shows the routine monitoring sites for domoic acid in bivalves (BM=bay mussel, PO=Pacific oyster; RC=razor clam; SM=sea mussel).

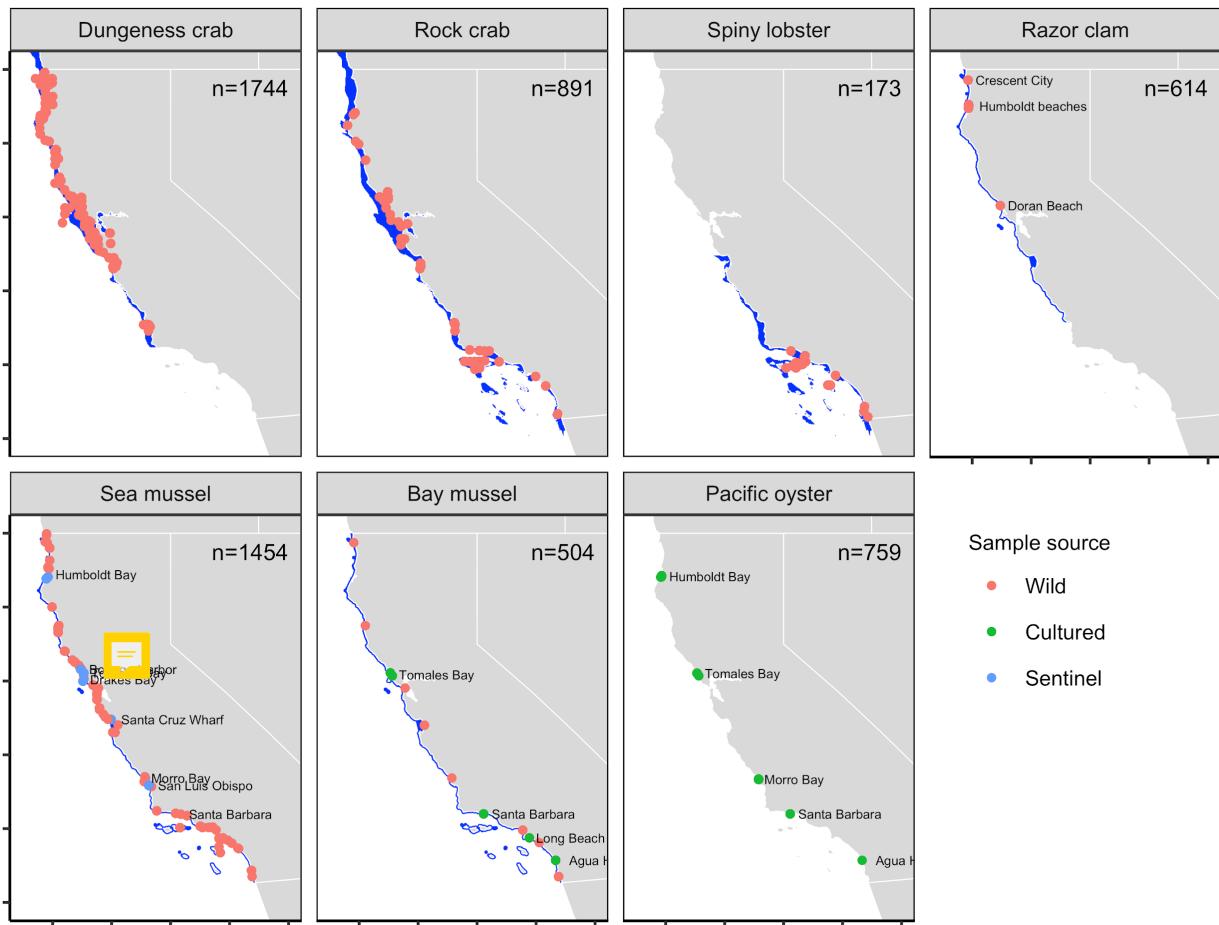


Figure 2. The geographical range of the study species (blue shading) in California and the origin of samples collected for domoic acid contamination monitoring. Dungeness crab, rock crab, and spiny lobster mainly occur within 100 fathoms (600 feet) depth; razor clam, sea mussel, and bay mussel mainly occur in intertidal areas; and Pacific oyster only occur at aquaculture farms . The sample size is printed in the top right corner of each plot.

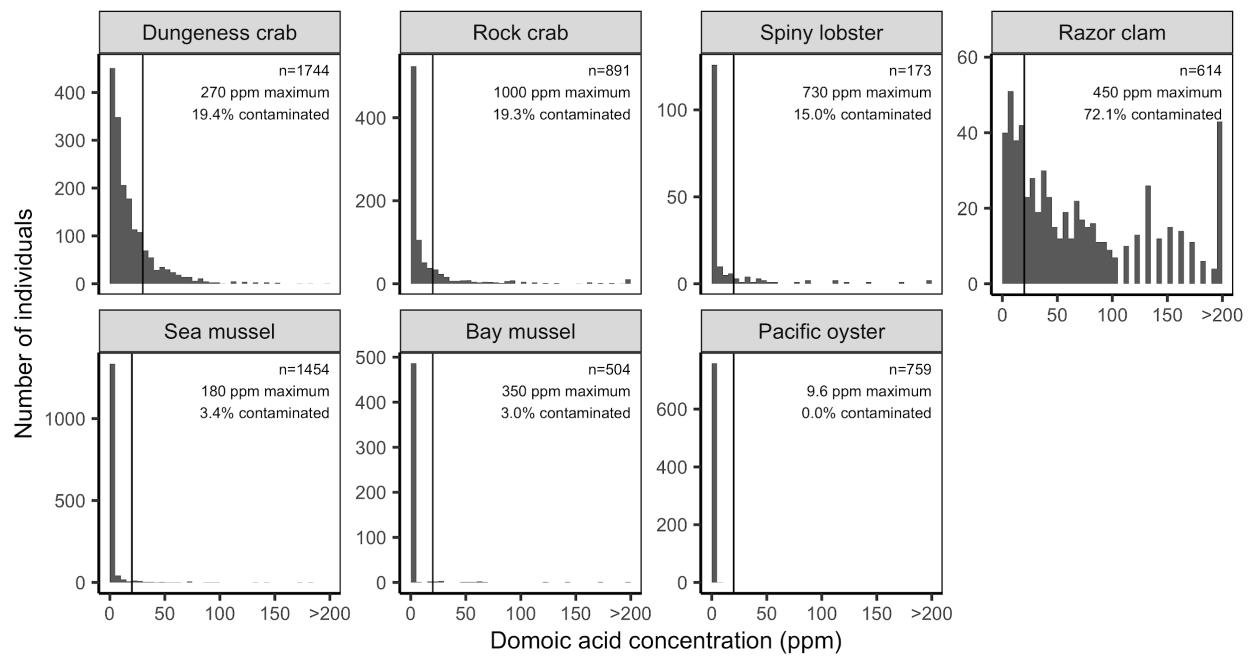


Figure 3. Domoic acid concentrations in samples collected by the CDPH as part of its biotoxin monitoring program. The domoic acid FDA action threshold (vertical line) is 30 ppm for Dungeness crab and 20 ppm for all other species. The sample size, percent of samples above the FDA action threshold, and maximum observed concentration are printed in the top right corner of each panel.

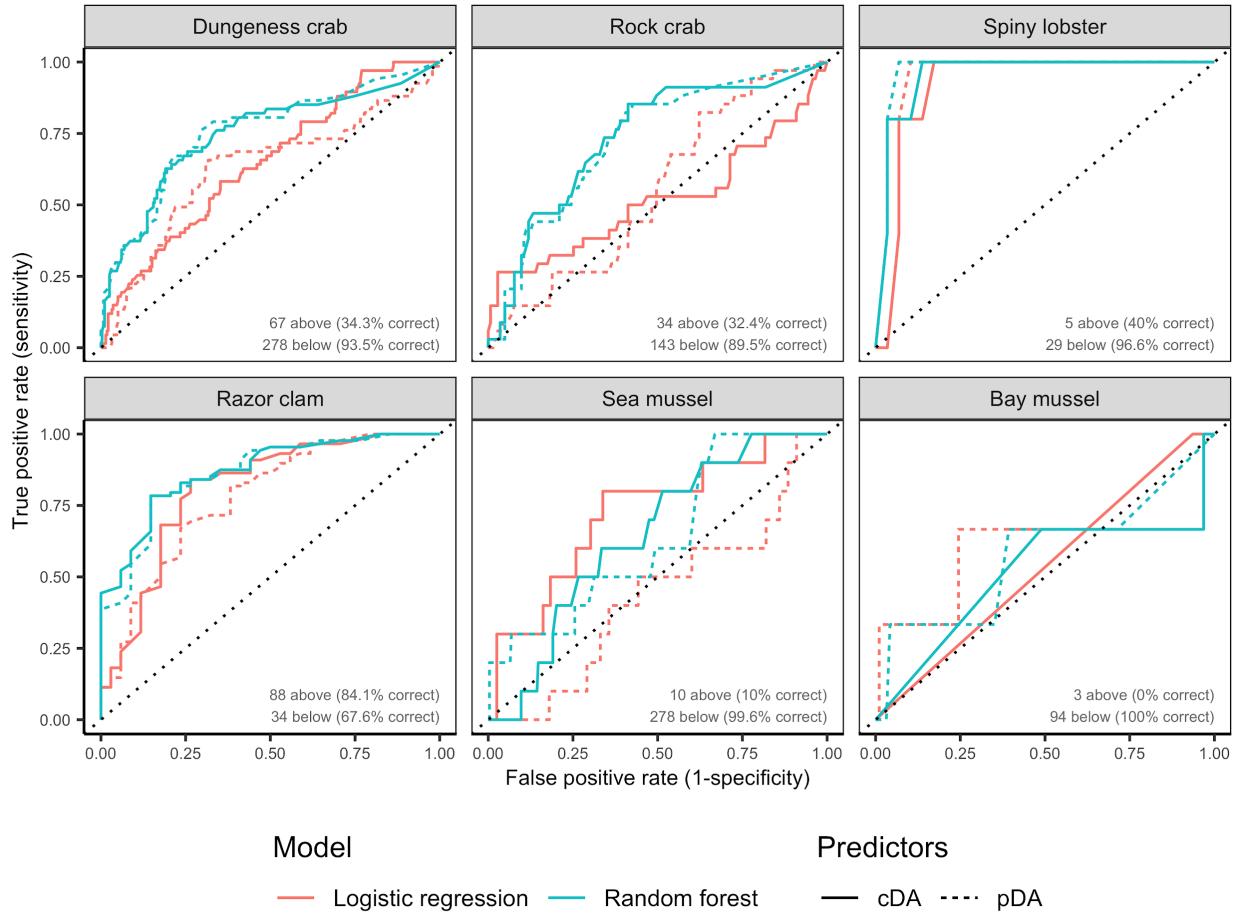


Figure 4. Receiver operating characteristic (ROC) curves for logistic regression, random forest, and boosted regression tree models that estimate the probability a crab is contaminated above or below the management action threshold (>30 ppm domoic acid) based on each of the previous 30 days of cDA risk estimated by C-HARM. The best performing model is inundated in the bottom right corner (see Table S1 for more details). The size of the test dataset and the performance of the best model on the test dataset is indicated in the bottom right corner.

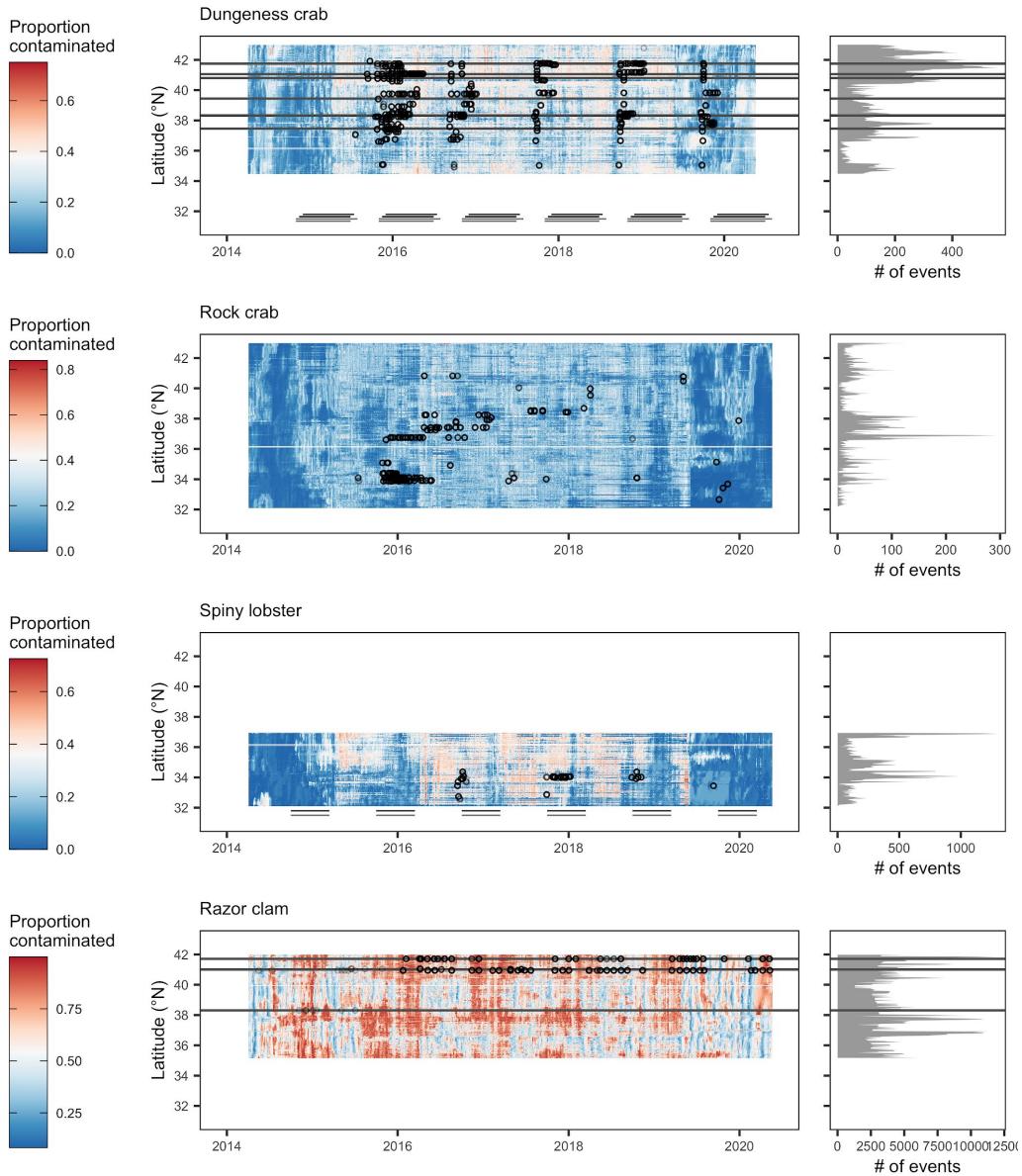


Figure 5. Spatial-temporal trends in contamination events within fishing grounds along the California coast. Each cell represents the mean proportion of the population contaminated with domoic acid above the action threshold in all cells in 0.03 degree latitude bands on each day from March 5, 2014 to May 19, 2020 as predicted by the best performing model for each species. Contamination events are identified as events where more than 50% of the population is contaminated with domoic acid above the action threshold (30 ppm for Dungeness crab and 20 ppm for the remaining species). The horizontal lines indicate latitudes with routine sampling programs and the points indicate location and timing of historical sampling.

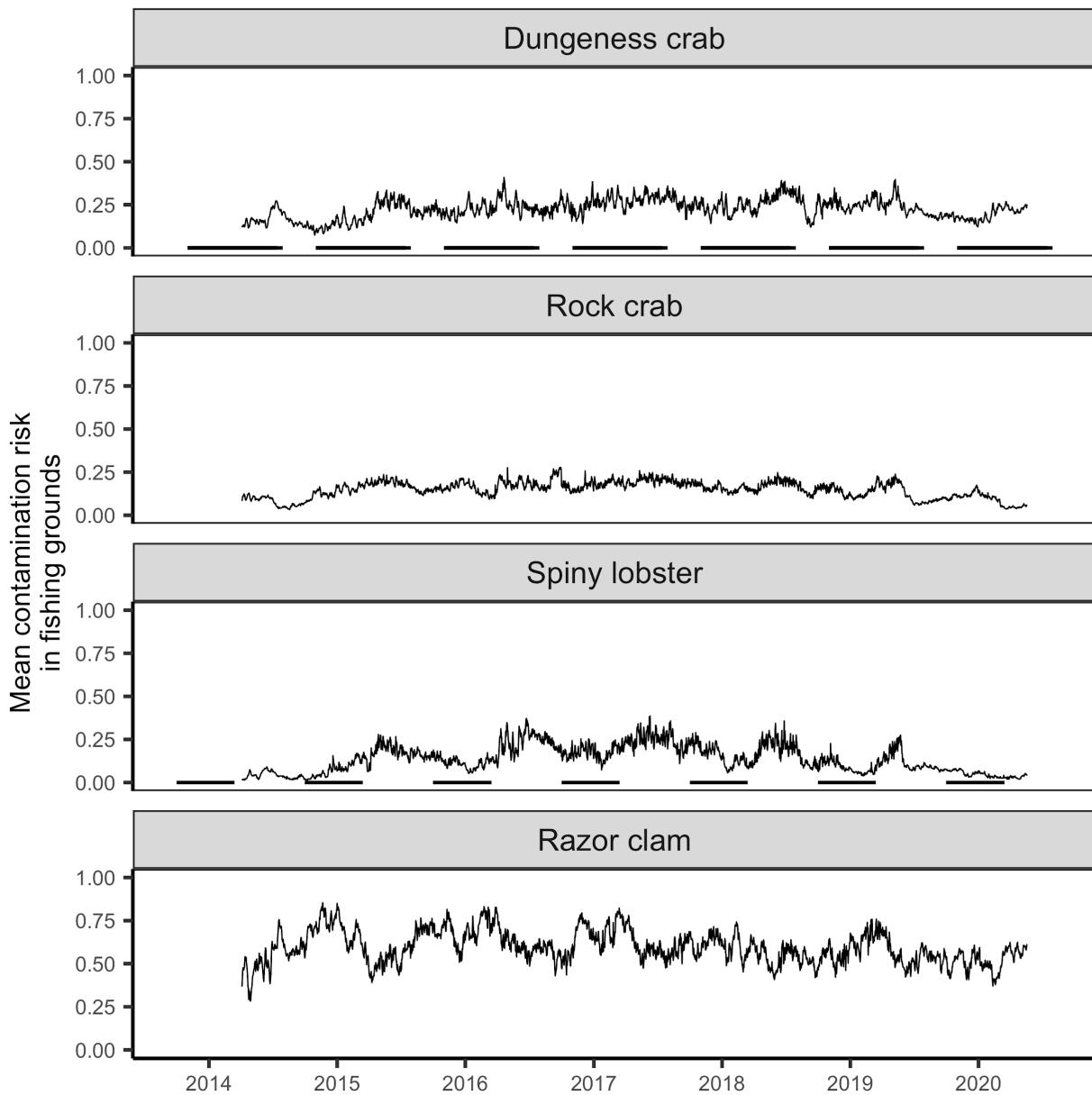


Figure 6. Mean daily contamination risk in each species fishing grounds. Lines indicate seasons for Dungeness crab and spiny lobster. Razor clam and rock crab are open year-round.

Supplementary material

Table S1. Domoic acid depuration rates for the study species or their phylogenetic analogs.

Species / reference	Depuration rate (as reported in source)	Depuration rate (%/day) (derived from source)
<i>Crustaceans</i>		
Dungeness crab (<i>Metacarcinus magister</i>)		
Lund et al. 1997	89% in 21 days	
Schultz et al. 2008	51 ± 13 hr half-life	
Rock crab (<i>Cancer</i> spp.)		
No studies known	-----	
California spiny lobster (<i>Panulirus interruptus</i>)		
No studies known	-----	
<i>Bivalves</i>		
Razor clam (<i>Siliqua patula</i>)		
Schultz et al. 2008	-----	
Jennings et al. 2020	2% / day	
California sea mussel (<i>Mytilus californianus</i>)		
Whyte et al. 1995	-----	
Bay mussel (<i>Mytilus galloprovincialis</i>)		
Blanco et al. 2002	56-88% in 4 days	
Pacific oyster (<i>Crassostrea gigas</i>)		
Mafra et al. 2010	25-88% / day	
<i>Phylogenetic analogs</i>		
Blue mussel (<i>Mytilus edulis</i>)		
Novaczek et al. 1992	50% eliminated in 24 hr	
Schultz et al. 2008;	55 ± 27 hr half-life	
Krogstad et al. 2009	87% / day	
Mafra et al. 2010	140-160% / day	

Table S2. Performance metrics for models that estimate the probability that an individual is contaminated above the domoic acid FDA action threshold (30 ppm for Dungeness crab and 20 ppm for all others) based on the previous 30 days of domoic acid risk estimated by C-HARM.*

Model	Predictors	AUC	Kappa	Accuracy
<i>Dungeness crab</i>				
Random forest	pDA	0.76	0.33	0.82
Boosted regression trees	pDA	0.75	0.32	0.81
Boosted regression trees	cDA	0.75	0.31	0.81
Random forest	cDA	0.75	0.33	0.82
Logistic regression	cDA	0.65	0.00	0.8
Logistic regression	pDA	0.63	-0.02	0.8
<i>Rock crab</i>				
Boosted regression trees	pDA	0.73	0.24	0.76
Random forest	cDA	0.73	0.24	0.79
Random forest	pDA	0.73	0.24	0.79
Boosted regression trees	cDA	0.73	0.22	0.76
Logistic regression	pDA	0.55	-0.02	0.8
Logistic regression	cDA	0.52	0.17	0.81
<i>Spiny lobster</i>				
Random forest	pDA	0.97	0.44	0.88
Boosted regression trees	cDA	0.97	0.44	0.88
Boosted regression trees	pDA	0.97	0.44	0.88
Random forest	cDA	0.96	0.44	0.88
Logistic regression	pDA	0.93	0.53	0.88
Logistic regression	cDA	0.92	0.53	0.88
<i>Razor clam</i>				
Random forest	cDA	0.87	0.52	0.8
Boosted regression trees	pDA	0.86	0.50	0.8
Random forest	pDA	0.86	0.50	0.8
Boosted regression trees	cDA	0.86	0.55	0.83
Logistic regression	cDA	0.81	0.45	0.79
Logistic regression	pDA	0.78	0.40	0.78
<i>Sea mussel</i>				
Logistic regression	cDA	0.72	-0.01	0.96
Random forest	cDA	0.64	-0.01	0.96
Random forest	pDA	0.64	0.16	0.97
Boosted regression trees	pDA	0.62	-0.01	0.96
Boosted regression trees	cDA	0.62	0.16	0.97
Logistic regression	pDA	0.43	-0.02	0.95
<i>Bay mussel</i>				
Logistic regression	pDA	0.59	0.26	0.95
Random forest	pDA	0.58	0.00	0.97
Logistic regression	cDA	0.53	-0.04	0.91
Random forest	cDA	0.51	0.00	0.97
Boosted regression trees	pDA	0.5	0.00	0.97
Boosted regression trees	cDA	0.47	0.00	0.97

* pDA=particulate domoic acid; cDA=cellular domoic acid; AUC=area under the receiver operating curve

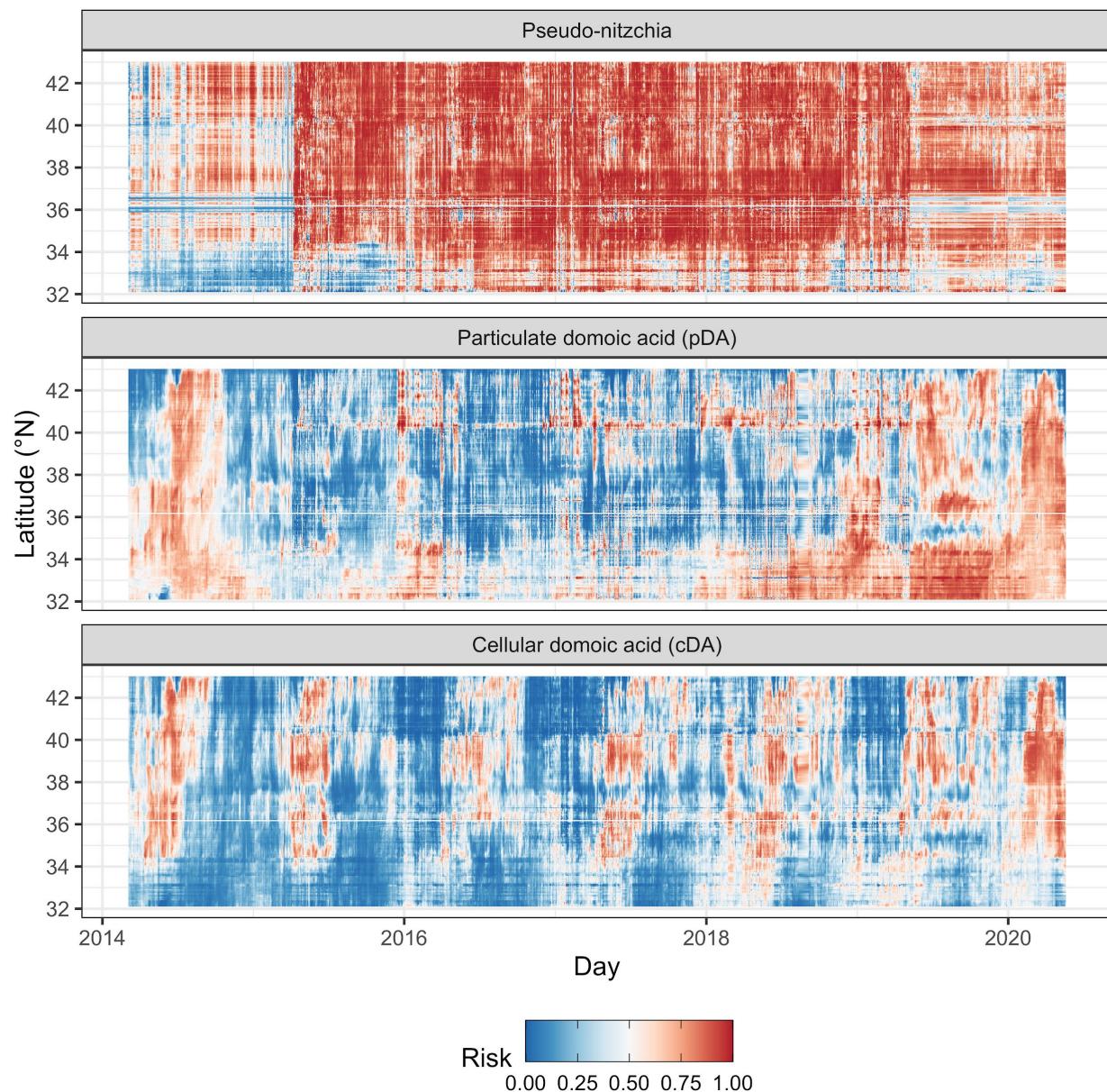


Figure S1. Spatial-temporal trends in mean *Pseudo-nitzschia*, particulate domoic acid (pDA), and cellular domoic acid (cDA) risk inside California fishing grounds (waters less than 100 fathoms) as predicted by C-HARM from 2014 to 2019.

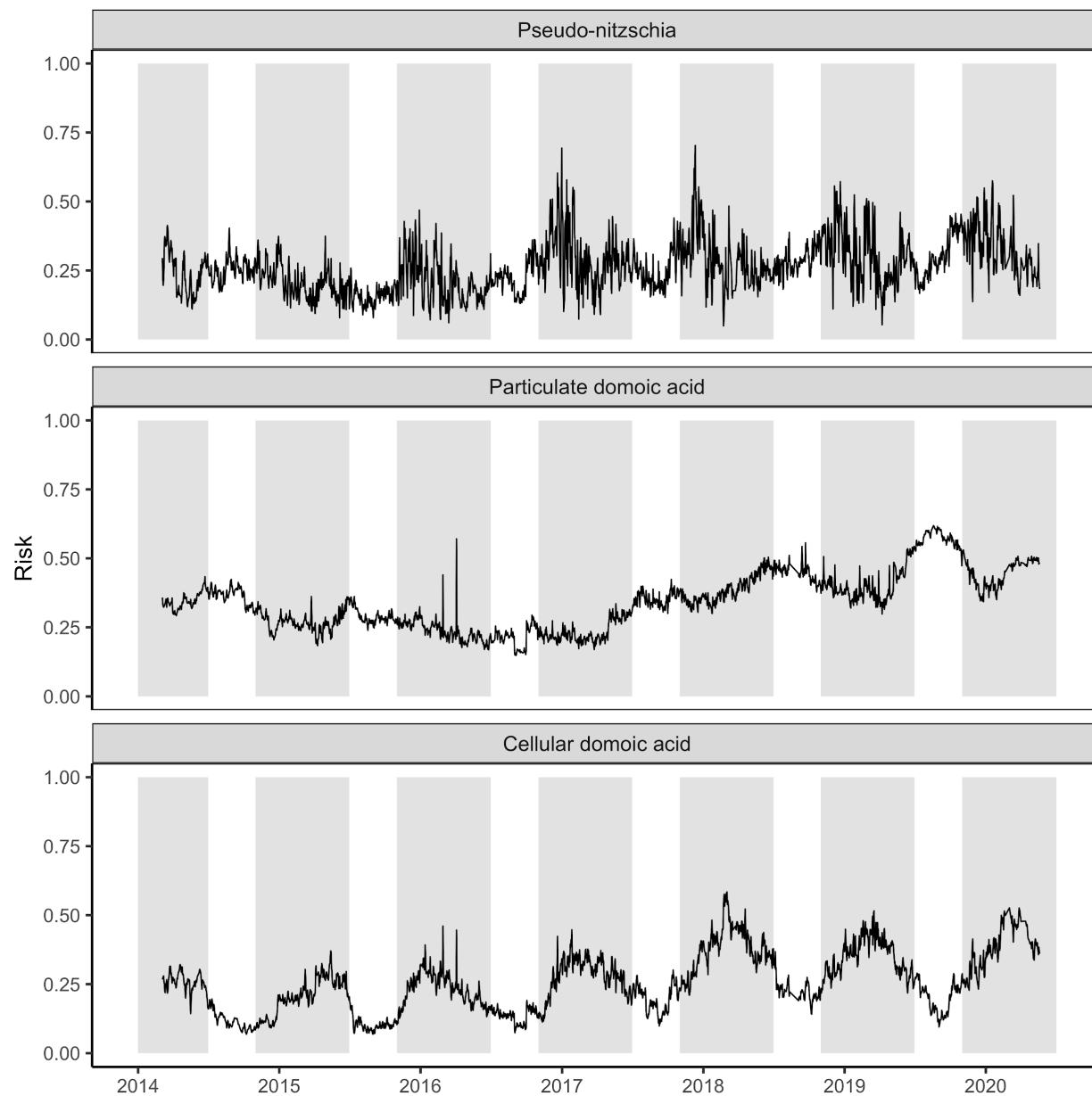


Figure S2. The mean daily *Pseudo-nitzschia*, particulate domoic acid (pDA), and cellular domoic acid (cDA) risk predicted by C-HARM from 2014 to 2019 on the California shelf (<100 fathoms). Dungeness crab commercial fishing seasons are shaded in grey.

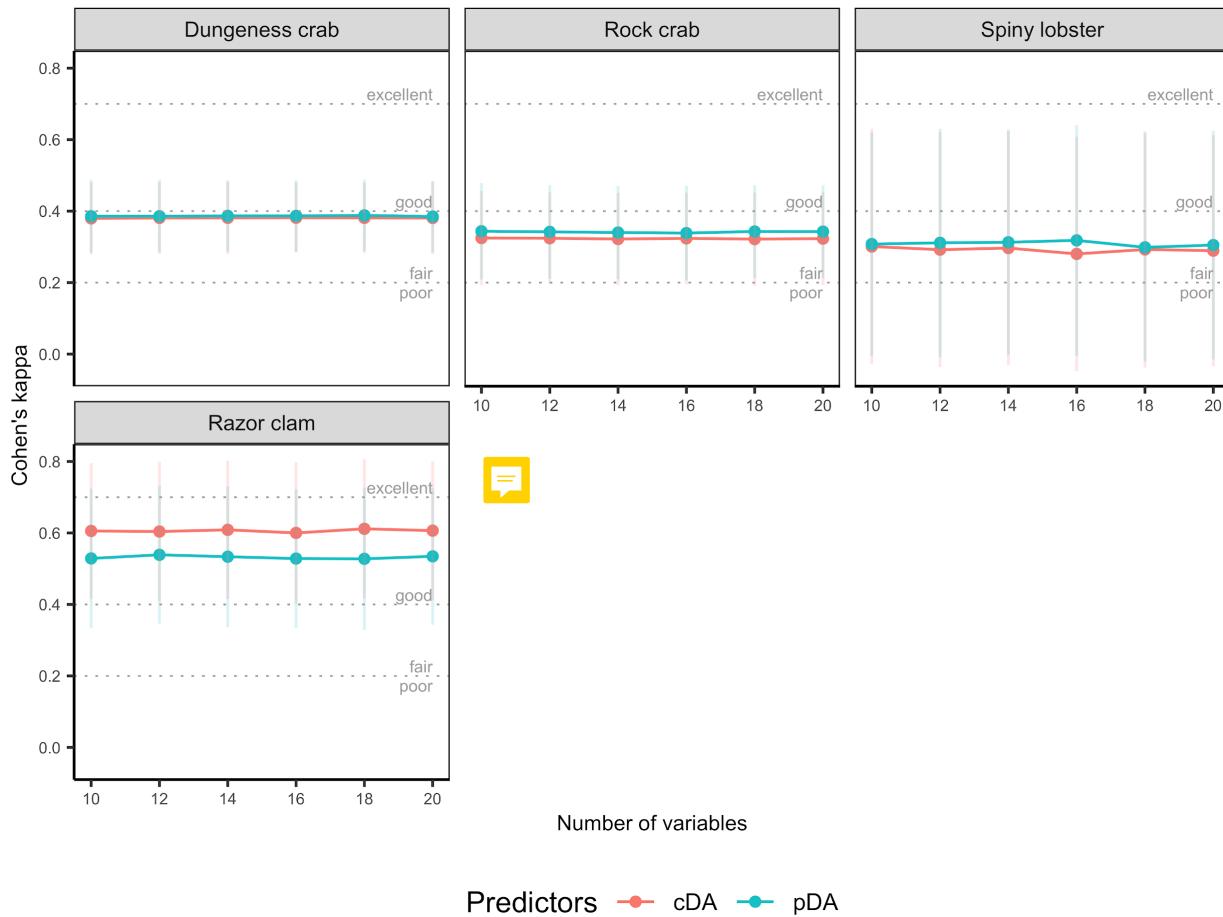


Figure S3. Performance of candidate random forest classification models used to estimate the probability that an individual organism is contaminated with domoic acid above its FDA action threshold. The candidate models consider two sets of predictors - particulate domoic acid (pDA) and cellular domoic acid (cDA) -- and six levels of the hyperparameter ("mtry") controlling the number of random variables at each split in the model. Performance is measured through 10-fold cross-validation using Cohen's kappa which measures the proportion of correct classifications accounting for the probability of being correct by chance. Although there are no definitive rules for interpreting Cohen's kappa, general guidelines suggest that values >0.70 are 'excellent', $0.40 - 0.70$ are 'good', $0.20 - 0.40$ are 'fair', and < 0.20 are 'poor'.

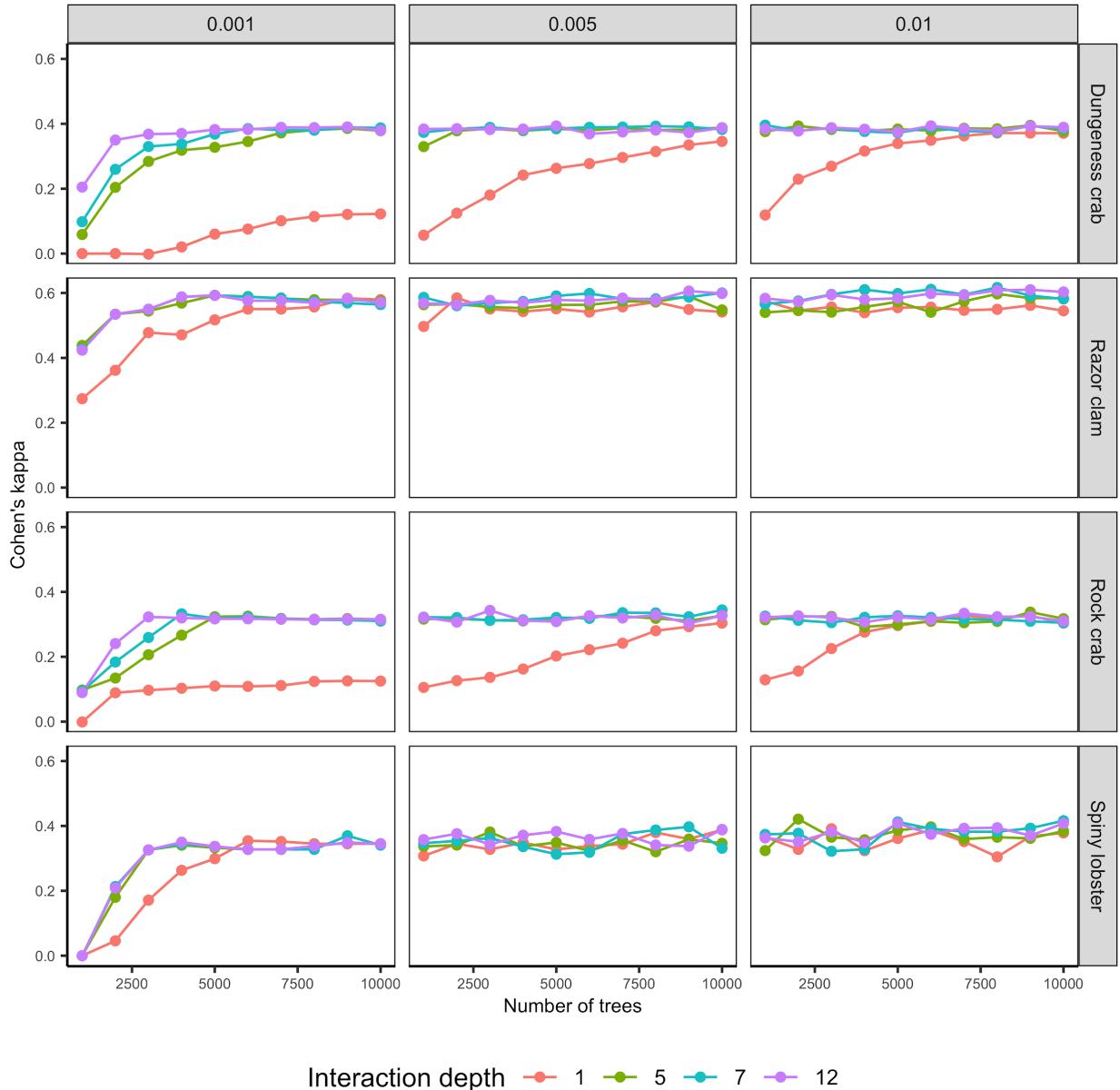


Figure S4. Performance of candidate boosted regression tree classification models used to estimate the probability that an individual organism is contaminated with domoic acid above its FDA action threshold. The candidate models consider two sets of predictors - particulate domoic acid (pDA) and cellular domoic acid (cDA) -- and six levels of the hyperparameter ("mtry") controlling the number of random variables at each split in the model. Performance is measured through 10-fold cross-validation using Cohen's kappa which measures the proportion of correct classifications accounting for the probability of being correct by chance. Although there are no definitive rules for interpreting Cohen's kappa, general guidelines suggest that values >0.70 are 'excellent', $0.4\text{--}0.7$ are 'good', $0.2\text{--}0.4$ are 'fair', and <0.2 are 'poor'.