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1	Prediction of Alexandrium and Dinophysis algal blooms and shellfish
2	contamination in French Mediterranean Lagoons using decision trees and
3	linear regression: a result of 10 years of sanitary monitoring
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20 Abstract

French Mediterranean lagoons are frequently subject to shellfish contamination by Diarrheic 21 Shellfish Toxins (DSTs) and Paralytic Shellfish Toxins (PSTs). To predict the effect of 22 23 various environmental factors (temperature, salinity and turbidity) on the abundance of the major toxins producing genera, *Dinophysis* and *Alexand*rium, and the link with shellfish 24 contamination, we analysed a 10-year dataset collected from 2010 to 2019 in two major 25 shellfish farming lagoons, Thau and Leucate, using two methods: decision trees and Zero 26 Inflated Negative Binomial (ZINB) linear regression models. Analysis of these decision trees 27 revealed that the highest risk of *Dinophysis* bloom events occurred at temperature <16.3°C 28 and salinity <27.8, and of *Alexandrium* at temperature ranging from 10.4 to 21.5°C and 29 salinity >39.2. The highest risk of shellfish contaminations by DSTs and PSTs occurred 30 31 during the set of conditions associated with high risk of bloom events. Linear regression prediction enables us to understand whether temperature and salinity influence the presence of 32 Alexandrium and affect its abundance. However, Dinophysis linear regression could not be 33 validated due to overdispersion issues. This work demonstrates the tools which could help 34 sanitary management of shellfish rearing areas. 35

36 Keywords

37 Alexandrium, Dinophysis, Toxic blooms, Temperature, Salinity, Prediction

38 I. Introduction

Abbreviations : DT: Decision tree, IRR : Incidence Risk Ratio, LD : Limit of Detection, LQ: Limit of Quantification, OR: Odds Ratio, REPHY: French Observation and Monitoring program for Phytoplankton and Hydrology in coastal waters, REPHYTOX: French Monitoring Program for Phytotoxins in marine organisms, ZINB: Zero Inflated Negative Binomial

The geographical expansion of harmful algae and their durable settlement in many marine 39 ecosystems has become a major concern all over the world (Hallegraeff et al. 2003; Drake et 40 al. 2005; Hallegraeff 2010; Casas-Monroy et al. 2015; Glibert 2020). Harmful algae (HA) 41 proliferation or HABs (Harmful Algal Blooms) leads to observable negative effects on marine 42 resources, economics and human health (Granéli and Turner, 2006). Many HA produce toxins 43 that can contaminate marine resources and lead to human intoxication (Pulido 2016). For this 44 reason, the proliferation of HAs in water is frequently monitored near shellfish farming areas 45 (Anderson et al. 2001). Studies showed that blooms can be impacted by many environmental 46 factors such as temperature and salinity (Anderson and Keafer, 1987; Laabir et al. 2011), light 47 48 (Figueroa et al. 2018), oxygen concentration in sediment and nutrient availability (Collos et al. 2007, 2009; Xu et al. 2010; Ishikawa et al. 2014). Blooms are generally triggered by the 49 synergic combination of several factors (Accoroni et al. 2015; Raso et al. 2012) among which 50 51 temperature and salinity play a key role as they can influence every phases of bloom dynamics, including initiation, growth and termination (Figueroa et al. 2018; Granéli and 52 Turner 2006). Many dinoflagellates including Alexandrium show planktonic and benthic 53 forms, and initiation of the blooms depends on the success of cysts germination which occurs 54 after a dormancy period. The duration of this phase was shown to be influenced by 55 56 temperature, and some HA cysts germinate only within specific ranges of temperature (Anderson and Keafer 1987; Genovesi et al. 2009). Moreover, germination can be linked with 57 water agitation leading to sediment resuspension (Laanaia et al. 2013) which is generally 58 associated with variations in water temperature and salinity. Growth corresponds to biomass 59 increase which duration and maximum concentration can be influenced by temperature and 60 salinity along with other factors such as nutrients (Bill et al. 2016; Collos et al. 2007; Davis 61 et al. 2015; Ishikawa et al. 2014; Laabir et al. 2011; Ralston et al. 2015; Raso et al. 2012; Xu 62 et al. 2010). Bloom termination happens when environmental conditions are no longer 63

favourable, which can be attributed to nutrient depletion or inadequate temperature leading to
mortality or encysment (Ralston et al. 2014; Verity et al. 1988).

As a consequence of these various and contrasted impacts of environmental factors on HAB 66 67 dynamic, efforts have been made to develop early HABs warning systems based on environmental predictors. Conventionally, statistical numerical modelling has been used for 68 HABs prediction (González Vilas et al. 2014). Through linear regression, these models can 69 70 efficiently predict phytoplankton dynamics because they are capable of integrating many predictors and can be adapted to different data distributions (Davidson et al. 2016). Given the 71 cyclic and seasonal pattern in HABs, they have mainly been investigated through time series 72 73 modelling based on a range of variables measured over time (Cruz et al., 2021). For instance, several studies have applied linear regression to forecasting the blooms of *Pseudo-nitzschia* 74 (Anderson et al. 2010; Lane et al. 2010; Seubert et al. 2013). The interest in alternatives like 75 Machine Learning (ML) models has recently increased. ML methods consist of using 76 computer systems that are able to learn and draw inference from data patterns without explicit 77 78 instructions. One of the many advantages of ML methods is their ability to predict highly dynamic and complex phenomena and to handle big and non-linear data. A wide variety of 79 machine learning approaches has been used over the past years to forecast HABs (Franks 80 81 2018; Cruz et al. 2021). Among them, decision trees (DTs) seem to be highly relevant tools. A DT is a tree-like structure in which the leaves represent outcome labels and the branches 82 represent conjunctions of the input features that resulted in those outcomes. Aside from 83 overcoming the problems due to missing data, they are easy to interpret since they provide 84 concrete thresholds that can be used by marine stakeholders. In South Korea, Shin (2017) 85 86 used DTs to forecast cyanobacteria blooms and (Park et al. 2011) applied this method to predict red tide blooms. 87

French Mediterranean lagoons are special ecosystems as they are semi-enclosed marine 88 89 systems, containing many shellfish farming areas, and they are frequently subject to HAB events and particularly proliferation of the dinoflagellates Alexandrium pacificum and 90 91 Dinophysis acuminata complex responsible for intoxication events threatening human health and resulting in economic losses (Deslous-Paoli et al. 1998; Collos et al. 2009; Laabir et al. 92 2011; Laanaia et al. 2013; Belin et al. 2021; Séchet et al. 2021). Until now, no machine 93 94 learning approach has been developed to quantify and predict the risks of HABs proliferations and shellfish contamination in these ecosystems. Based on a ten-year dataset of parameters 95 (temperature, salinity and turbidity) and of HA taxa, using both decision trees and a Zero-96 97 Inflated Negative Binomial regression model, this study aimed at providing robust tools to predict the risk of bloom of the two major HA genera in French Mediterranean lagoons, 98 Dinophysis and Alexandrium, and the subsequent shellfish contamination in exploited semi-99 100 enclosed marine systems.

101 **2. Materials and methods**

102 *2.1. Data recovery*

103 Data were collected from the framework of the REPHY and REPHYTOX monitoring net-

104 works (REPHY - French Observation and Monitoring program for Phytoplankton and Hy-

drology in coastal waters 2019; REPHYTOX - French Monitoring program for Phytotoxins in
marine organisms 2019).

107 Briefly, the data comes from field surveys carried out by Ifremer in two exploited French

108 Mediterranean lagoons, Thau (7000ha, mean depth 4m, water temperature range : 3.9-29.6°C;

- salinity range : 27.4-42.9) and Leucate (5400ha, mean depth 1.9m water temperature range
- 110 0.9-29.3°C, salinity range: 8.4-42.3) (Fiandrino et al. 2017; Ladagnous and Le Bec 1997)
- from January 2010 to December 2020 (Fig 1). The concentration of phytoplankton species

was measured using the Utermöhl method (Utermöhl 1931) with a 10 mL Hydrobios cham-112 113 ber. The limit of quantification (LQ) and the threshold limit of detection (LD) are both 100 cell/L. Temperature, salinity, turbidity, total phytoplankton including the lipophilic toxins 114 producer *Dinophysis* spp. and the paralytic shellfish toxins producer *Alexandrium* spp., were 115 monitored twice a month at three stations in shellfish farming areas in the Thau lagoon (Mar-116 seillan, Bouzigues and Crique de l'Angle), and two stations in the Leucate lagoon (Parc and 117 118 Grau) (Fig 1). Mussels and oysters were sampled in these stations twice a month. At least 1 kg of shellfish, composed of a minimum of ten individuals, were sampled randomly and Lipo-119 philic toxins (Okadaic Acid (OA), Dinophysistoxins (DTXs) and Pectenotoxins (PTXs)) were 120 121 measured by Liquid Chromatography coupled to tandem Mass Spectrometry (LC-MS / MS) (ANSES LSA-INS-0147, Standards and Reference Material were provided by the NRC-122 CNRC, Marine Analytical Chemistry Standards Program. Institute for Marine Biosciences). 123 Each of the constitutive toxins was corrected by a TEF (Toxic Equivalent Factor) to account 124 for its potential toxicity. The quantification of PSTs was carried out by mouse bioassay, cali-125 brated and validated to give quantitative results (Anses PBM BM LSA-INS-0143). 126

127 2.3. Data processing and analyses

128 2.3.1. Preliminary processing

All data analyses were performed using R software (R Core Team 2020). Since *Alexandrium pacificum* and *Alexandrium tamarense* are difficult to distinguish by light microscopy,

abundances of both species were added to each other and were thereafter named *Alexandrium*

tamarense/pacificum. As for *Dinophysis*, regulatory monitoring considers all species that can

- be identified in the lagoons because they are all likely to contaminate shellfish. Thus, even
- though the *D. accuminata* complex represents the vast majority of the species found in Thau
- and Leucate, we chose to consider data at the genus level. The value of toxin concentrations

below the detectable threshold was estimated to be the detectable threshold divided by 2 since
a non-detectable value does not mean that there is no toxin in shellfish. When toxins were
detectable but not quantifiable, the value was estimated by the means of the detectable and
quantifiable thresholds.

140 2.3.1. Exploratory analysis

Bivariate analyses were performed in order to identify which factors were mainly related to
phytoplankton and toxin concentrations. Pairwise Spearman and Pearson coefficients were
calculated between phytoplankton and environmental factors, and between toxins and
environmental factors.

145 *2.3.2. Building decision trees*

146 Variable selection and encoding

147 Decision trees (DT) were used to predict the risks of HABs and of bivalve contamination considering temperature, salinity and turbidity as predictors. Prior to the analysis, Dinophysis 148 and A. tamarense/pacificum concentrations were converted to binary variables: the abundance 149 of cells was encoded by 1 when the concentration exceeded 1000 cells/L for A. 150 tamarense/pacificum (value inducing the sanitary warning protocol) and 500 cells/L for 151 Dinophysis (estimated value indicating a bloom, the sanitary warning protocol being induced 152 by a concentration of cells \geq LD), and by 0 when the abundances were beyond these 153 154 concentrations. Toxin concentrations were converted to categorical variables based on the regulatory thresholds: they were encoded by 0 when concentrations were below 80 μ g per kg 155 of shellfish flesh) for lipophilic toxins and below 340 µg/kg for PSTs, by 1 when they were 156 between 80 μ g/kg⁻¹ and 160 μ g/kg for lipophilic toxins, and between 340 μ g/kg and 800 157 μ g/kg for PSTs, and by 2 when they were above 160 μ g/kg for lipophilic toxins and above 158 800 μ g/kg for PSTs. 159

161	The DTs building process is described in Fig 2. DTs were set up with the <i>rpart package</i>
162	(Therneau and Atkinson 2019) using the CART algorithm (Breiman et al. 1984). As a
163	supplementary constraint, a minimum of 10 observations was imposed for a branch to become
164	a branch node and there had to be at least 5 observations per leaf node. A maximum of 10
165	nodes per tree was imposed. In order to set up a robust tool: for each predicted variable, the
166	experiment with DT was repeated 100 times; each time, the data set was split into two sets, 80
167	% made up the training set and 20% the testing set. The split algorithm allowed all the
168	different pairs of training and testing sets to have approximately the same proportion of 0, 1
169	(and 2 for the toxins) in the predicted variables. The structures of the 100 trees were then
170	compared in order to find the most common one. For each node the process consisted of:
171	- Finding the most frequent variable
172	- Finding the most frequent threshold for this variable
173	- Selecting the trees with this variable and threshold
174	- Repeating the process at the next children nodes for the selected trees only.
175	Secondly, the most common structure was determined and an average of the trees presenting
176	this structure was then calculated. To this end, the mean of the number of observations for
177	each node and the average proportions of 0, 1 or 2 were calculated. In order to test the trees'
178	performance outside the training data sets, the selected structures were tested on the testing
179	data sets. The average testing trees were then processed in the same way as for the average
180	learning trees.

181 Finally, pruning analysis was applied in order to prevent overfitting by reducing the size of

the trees and to prevent overtraining. Pruning a tree consists in removing the redundant and/or

less important nodes to improve its predictive accuracy. The pruning process followed theserules:

- The proportion of 1 or 2 in at least one of the nodes of the testing trees should be above 20%

- The number of observations in each node of the testing trees should be above 3

187 *2.3.3. Linear models*

188 *Type of regression*

Mixed linear models were set up to predict phytoplankton concentrations in the Thau and 189 Leucate lagoons based on hydrological factors. The distributions of HA abundance were 190 characterized with a very high frequency of 0, meaning that HA were not detected most of the 191 time. In addition, abundances are discrete variables, hence the Zero Inflated Negative 192 Binomial (ZINB) model (Greene 1994) appeared to be the most suitable regression for this 193 dataset. ZINB regression is used for data that exhibits excess zeros and over dispersion. In 194 Zero Inflated (ZI) models (Lambert 1992), theory suggests that the excess zeros are generated 195 196 by a separate process from the count values and that the excess zeros can be modelled 197 independently. Thus, the ZINB model has two parts, the negative binomial count model and the logit model for predicting excess zeros. The process explaining the excess zeros could 198 correspond to an absence of HA cyst germination, when count values would represent the 199 200 proliferation of vegetative cells once germination had occurred. Type 2 ZINB were used for the models because the Akaike Information Criteria (AIC) (Akaike 1974) were lower than 201 type 1 ZINB. As the variables were time series data sampled in different stations, it was 202 203 necessary to check the influence of the stations, and to check that the relationships between the variables would still be significant without this influence. Mixed models were thus 204 205 performed, using the stations as grouping factors. Only random-intercept models were performed because random-slope models did not converge. The significance of Random 206 effects was tested by performing an Anova between the models with and without random 207

effects. Random effects were kept for the logistic and/or the negative binomial part only when
it was significant it when it allowed the model to fit the data better; this was shown on the
residuals graphs.

211 Variable selection and encoding

The model building process is described in Fig 3. A model was set up to predict HA 212 concentrations using the hydrological factors as predictors (i.e the predictive variables) and 213 214 showing a Spearman or a Pearson coefficient with a *p*-value lower than 20%. The linearities of the relationships were tested by performing maximum likelihood tests between models 215 before and after having transformed the factors to categorical variables. When non-linear 216 relationships were found, the variables were encoded as categorical variables, the levels being 217 determined by the ranges depicted by the DT and by visual examination of the distribution 218 219 graphics. Several combinations of variables and of levels were tested and the AIC was used to select the best fitting model. The Incident Risk Ratio (IRR) was calculated for the negative 220 221 binomial part (IRR = exp (coefficient)). An IRR >1 means an increase of the average 222 microalgae's abundance. As for the logit part, a particularity in the ZI model is that the coefficient and the Odds Ratio (OR = exp(coefficient)) characterize the probability of zero, in 223 this case the probability of absence of the HABs. To make it easier to understand, we choose 224 to depict the Odds Ratio of the presence of the algae: OR (Presence) = 1/OR. An OR 225 (presence) >1 means an increase of the probability of presence of the alga. 226

227 Validation

228 The validation of the model was based on the standardized residuals simulated with the

229 *DHARMa* package (Hartig 2020). The resulting simulated residuals graphics obtained with

this package are interpretable the same way as the residuals graphics for simple linear models

231 (Hartig 2020). Specialized goodness-of-fit tests were performed on the simulated residuals

with the DHARMa package: the Kolmogorov-Smirmnov test, a non-parametric dispersion test
based on the standard deviation of the simulated residuals, testing whether the simulated
dispersion is equal to the observed dispersion, and an outlier test that tests whether there are
more simulation outliers than expected. Finally, Nakagawa's conditional and marginal R²
were calculated to show how much of the variability was explained by the global model and
by random effects.

238 **3. Results**

239 *3.1. Exploratory data analysis*

Correlation coefficients between phytoplankton abundance, abiotic factors and toxins in Thau 240 241 and Leucate lagoons were calculated as shown in Tab 1A and 1B respectively. In both 242 lagoons, the coefficients showed significant correlations between phytoplankton and abiotic factors: In Thau, the Spearman coefficient showed a positive correlation (*p*.val<0.001) 243 between A. tamarense/pacificum and salinity (Sal.). In Leucate, Dinophysis was negatively 244 245 correlated to temperature (Temp.) and Sal. (p.val<0.001), whereas it was positively correlated to Temp. in Thau (p.val<0.001) (Tab. 1). Dinophysis was also positively correlated to 246 turbidity (Turb.) (Spearman coefficient 0.15, p.val < 0.001) (Tab. 1). When significant, the 247 correlations between A. tamarense/pacificum, Dinophysis and abiotic factors were quite low, 248 absolute values ranged from 0.15 to 0.31 (Tab. 1). In both lagoons, whenever significant, the 249 250 Spearman coefficients between the environment and toxic phytoplankton species were always stronger than the Pearson coefficients, suggesting non-linear relationships. Furthermore, 251 toxins were highly correlated to the abundance of the microalgae which produce them. The 252 significant correlations between A. tamarense/pacificum and PSTs in Thau ranged from 0.41 253 to 0.58 and the Pearson coefficients were stronger than the Spearman coefficients, with 254 *p*.val<0.001, suggesting a linear relationship (Tab. 1). The lipophilic toxins (OA, PTX, DTX) 255

were positively correlated with the abundance of Dinophysis, the significant coefficients 256 257 ranged from 0.45 to 0.69 (p.val<0.00) (Tab 1). Furthermore, abiotic factors seemed to have similar impact on the toxins as on the microalgae producing them. In Thau, PSTs were 258 positively correlated to Sal. (significant correlation coefficients ranged from 0.3 to 0.41, 259 *p*.val<0.05) (Tab. 1). In Leucate, lipophilic toxins were negatively correlated to both Temp. 260 (coefficients ranging from -0.38 to -0.57) and Sal. (significant coefficients ranging from -0.14 261 to -0.35) and positively correlated to Turb. (significant coefficient ranging from 0.27 to 0.28, 262 p.val<0.001) (Tab. 1). The Spearman coefficients showed that A. tamarense.pacificum and 263 Dinophysis abundances were non-linearly but positively correlated with the abundance of 264 265 dinoflagellates and diatoms, and that these correlations were stronger for A. tamarense/pacificum (coefficients ranging from 0.18 to 0.29, p.val<0.001) than for 266 *Dinophysis* (coefficients ranging from 0.08 to 0.09, *p*.val<0.05) (Tab. 1). 267

268 *3.2. Decision trees*

269 Decision trees were able to predict when blooms of *A. tamarense/pacificum* and *Dinophysis* 270 could occur (Fig 4). Turb. was never kept in pruned DTs and appeared thus to be a nondeterminant risk factor in Dinophysis and A. tamarense/pacificum blooms. Results showed 271 that, for Temp. between 10.4°C and 21.5 °C and Sal. >39.2, the mean risk of a bloom of A. 272 273 tamarense/pacificum occurrence was over 50% (Fig 4A). The mean risk was less than 12% when Sal. is <39.2 and, even with a high salinity, it was near 0% when Temp. was <10.4 °C. 274 The decision tree for *Dinophysis* (Fig 4B) indicated that Sal. <27.8 and Temp <16.3°C led to 275 a mean risk of bloom over 50%. This situation was however quite rare (only 21 observations 276 over the 10 years monitoring). Sal. >32.0 along with Temp. <16.3°C also led to a high 277 probability of bloom (in average 26% of the testing datasets). Temp. >16.3 °C led to a low 278 risk (on average 4.2% of the testing data sets). No low threshold of temperature was found for 279 Dinophysis. 280

Decision trees were able to predict when shellfish contaminations could occur (Fig 5). The 281 282 trees showed that toxins were usually found in animals in the conditions promoting a bloom event (Fig 5). Again, Turb. was never kept in the pruned DTS. In Thau, the risk of 283 contamination of mussels and oysters by PSTs was significant for seawater Sal. > 37.7 and 284 39.9, respectively (Fig 5 A/B). Low Temp. also promoted risks of shellfish contamination. 285 For mussels, Temp. <18.5°C combined with Sal. >37.7 yielded a total mean risk of 286 287 contamination of 92% (44.9% between 340 µg/kg and 800 µg/kg (labelled 1 on the figure) and 47.1% exceeding 800 µg/kg (labelled 2 on the testing data sets). For oysters, Temp. 288 <16°C combined with Sal. >39.9 led to a 57% mean risks of contamination, the latter being 289 290 mainly comprised between 340 μ g/kg and 800 μ g/kg (52.3% of the observations in the testing dataset). It is possible that the contaminations were rare below a low Temp. threshold, but 291 were not represented on the decision trees because of a low number of observations. In 292 293 Leucate, the risks of mussel and oyster lipophilic contamination was higher when Temp. is <16.3 °C and <13.5 °C, respectively (Fig 5 C/D). The 16.3 °C threshold showed that mussels 294 295 would become contaminated as soon as Temp. allowed Dinophysis blooms. Under this Temp., the risk of contamination was high independently of the Sal. (56.7% and 31.1% risk of a 296 contamination over 160 μ g/kg (labelled 2 on the figure) for a Sal. respectively > and <33.5). In 297 oysters, contamination by lipophilic toxins happened at Temp. <13.5°C and Sal. < 27.8 that 298 led to 30.7% mean risk of contamination (over 160 µg/kg) in the testing data sets. In all, these 299 trees showed that the conditions in which oysters were contaminated were more restrictive 300 than for mussels: the Temp. and Sal. ranges were systematically narrower for oysters. 301

302 *3.3. Linear regression*

In order to predict *A. tamarense/pacificum* abundance in Thau, a ZINB model was set up using two categorical predictors (temperature, split into four levels, and salinity, split into three levels) and one continuous predictor, turbidity (Tab 2). The splits have been selected

thanks to the results of decision trees and from visual examination of data distribution. The 306 307 negative binomial part of the model, which depicted how predictors impact cell abundance, showed that the reference Temp. level, 14.6 to 21.5 °C, was associated with the highest 308 average microalgal abundance. The IRR revealed that the average abundance was multiplied 309 by 0.15 when Temp. was \geq 25°C (*p*.val 4.38e-3), and by 0.010 when Temp. was \leq 10.4°C 310 (p, val < 7.73e-5). A Sal. >36 was associated with the highest average abundance of A. 311 312 *tamarense/pacificum*: the average abundance was multiplied by 0.25 when Sal. was <36 compared with a Sal. >39.2, but no difference was shown when Sal. was comprised between 313 36 and 39.2. Turb. did not significantly impact A. tamarense/pacificum abundance. It should 314 315 be noted, before interpreting the logit part of the model, the coefficients were conversely related to the presence of the alga. In order to depict how the predictors affect the probability 316 317 of presence of the alga, we choose to calculate OR (presence) = $1/(\exp(\text{coefficient}))$. This part 318 of the model showed that the reference Temp. level was associated with the highest probability of presence of A. tamarense/pacificum. For instance, the odds of its presence were 319 320 multiplied by 0.14 when the temperature was <10.4°C and by 0.15 when it was >25. The reference Sal. (over 39.2) led to the highest likelihood of the presence of A. 321 tamarense/pacificum: the odds of the presence were multiplied by 0.21 when Sal. was <36 322 and by 0.44 when it was between 36 and 39.2. Turb. was not associated with the presence of 323 this alga. Overall, what emerged from the two parts of the models was that the conditions in 324 which A. tamarense/pacificum usually reached higher abundances were generally the same as 325 those in which the probability of finding it were the highest. 326 Random effects were significant for both parts of the model (*p*.val of the Anovas describing 327

random effects for the log and negative binomial parts were respectively 1.82e-7 and 4.88e-3)

- which indicated that a part of the variability in *A. tamarense/pacificum's* presence and
- abundance was due to the location. The conditional Nakagawa R² was 0.402 whereas the

marginal Nakagawa R² was 0.206. The model thus described almost 40.2% of the data
variability, with 19.6% (0.402-0.206) being explained by random effects.

The study of residuals (Fig 6) showed no significant problem: the QQplot curve was straight, the Kolmogorov-Smirnov and Dispersion tests were not significant (respectively *p*.val: 0.36 and 0.056). The graph of residuals against predicted values showed that residuals followed a uniform law (no particular shape was revealed) and the predicted quantile curves were aligned with the observed quantile curves. Five outliers were revealed by this graph, but did not invalidate the model (*p*.val of the outlier test: 0.088). No significant problems were detected through these graphics.

340 **4. Discussion and conclusion**

341 *4.1. Discussion*

In this work, we developed an innovative approach to forecast the risk of HABs and shellfish
contamination occurring in the marine environment. Our study was based on a solid long-term
database integrating ten years of sanitary monitoring results. After having explored the data
through exploratory bivariate analyses, we used two complementary methods, DTs and
statistical ZINB models, in order to reveal the relationships between environmental
parameters such as temperature and salinity, HABs and shellfish contamination.
First, the exploratory bivariate analyses indicated an impact of temperature and salinity on

HABs. These results were in accordance with several studies showing that temperature and
salinity influence the occurrence of *Alexandrium* and *Dinophysis* blooms (Abdenadher et al.
2012; Anderson and Keafer 1987; Gomis et al. 1996; Itakura et al. 2002; Ninčević Gladan et
al. 2008; Swan et al. 2018). The correlation coefficients were medium to low, but were not
expected to be much higher as they depicted the influence of only one variable on the HA

354

abundances variability. The exploratory analyses showed thus that temperature and salinity 355 were to be adequate predictors in following multivariate analyses.

By using decision trees, we determined the range of optimum temperature and salinity 356 357 associated with high risks of blooms. The proportion of blooms with a salinity above 39.2 and temperature ranging between 10.4 and 21.5 for A. tamarense/pacificum, and when salinity 358 was below 27.8 for *Dinophysis* spp. exceeded 50%, which could trigger safeguard measures 359 360 of the reared shellfish. If the optimal ranges of temperature and salinity may appear wide, they only represent 9.7% and 3.1% of the data in Thau and Leucate, respectively, which has to do 361 with the broad ranges of temperature and salinity in Mediterranean lagoons. The temperatures 362 363 were congruent with previous observations showing that A. tamarense/pacificum blooms mainly occur from October to December and April to June but were rarely observed in 364 summer and winter (Laabir et al. 2011, 2012). Laanaia (2013) highlighted that Alexandrium 365 blooms occurred mainly during periods when salinity was below 39.3 from 2002 to 2006. 366 Even though substantial risks could subsist outside the optimum ranges depicted by the DTs 367 368 (11.9% risk of A. tamarense/pacificum bloom below 39.2), this study could thus reveal a change in *A. tamarense* populations composition together with a variation in intra-species 369 physiological constants in Thau over the past few years. Our work also showed positive 370 371 correlations between toxins in bivalves and the HAs producing them, as well as with the environmental factors that impact these algae. The optimal temperature and salinity ranges 372 associated with high risks of shellfish contamination by phycotoxins were congruent with the 373 ranges increasing the risks of blooms. In Mediterranean lagoons, all referenced Dinophysis 374 species were potentially toxic. Recently, qPCR analyses the Alexandrium species in Thau 375 lagoon showed that the proportion of non-toxic Alexandrium species during a bloom were 376 very low (Sectox project, Eric Abadie, unpublished data). This could explain the high 377 correlations between algae and toxins. The correlation coefficients and the DTs showed that 378

relationships between phytoplankton and toxins were stronger in mussels than in oysters.
Mussels are considered as sentinel organisms for lipophilic toxins as they are known to be
contaminated more easily than the other bivalves (Levinton et al. 2002). However, a strong
inter-individual variability in the accumulation of toxins has been documented in oysters
(Pousse et al. 2018), meaning that sanitary risks remain substantial even in shellfish other than
mussels. Together, our results suggested that the DT is a tool which can provide relevant
information that will be useful in sanitary monitoring.

386 Through linear regression, the model confirmed the DT results obtained with A.

tamarense/pacificum and showed how abiotic factors influence either its presence or its cell 387 388 abundance when present. The optimal set of parameters chosen by the CART algorithm was significantly associated with the maximum average abundance and odds of presence of the 389 algae. Moreover, this model specified the sets of parameters more accurately by 390 distinguishing significantly more levels of temperature and salinity than the DT. It also 391 revealed that the optimal sets of parameters are similar for the presence of the microalgae and 392 393 for their abundance when they were present: this could indicate that germination and proliferation occured in the same conditions (Temperature from 14.6 to 21.5°C and Salinity 394 >39.2). Actually, from 2010 to 2020, most of the substantial blooms occurred within these 395 396 conditions, as the bloom of October 2015 (820000 cells/mL) and October 2017 (35000 cells/mL). Few other blooms occurred for slightly lower salinities, as in June 2011 (250000 397 cells/mL; Salinity 36.6). This is however not in total contradiction with the model since the 398 latter shows that, even though a salinity over 39.2 increases the risk of *Alexandrium* presence, 399 its abundance when it's present could be increased by a salinity over 36. This brings to light 400 that, if this model shows conditions where risks are very important, it does not mean that 401 blooms cannot occur outside them. The model predicting *Dinophysis* spp. abundance could 402 not be validated due to overdispersion issues. In contrast to Alexandrium, Dinophysis feeds on 403

living prevs and acquires its kleptochloroplasts originating from a cryptophyte through 404 405 predation on the ciliate Mesodinium rubrum (Park et al. 2006; Reguera et al. 2012). Hence, its growth depends on the presence of cryptophyte preys and ciliates, which themselves depend 406 on environmental factors like light intensity (Kim et al. 2008; González-Gil et al. 2010). The 407 mixotrophic status of *Dinophysis* spp. and the influence of its predator make its dynamics 408 more complex and difficult to integrate in a linear regression model. Further studies 409 integrating more variables, abiotic as well as biotic, may allow to validate a model for 410 Dinophysis spp. 411

Several other environmental factors could have been integrated to increase the model's 412 413 performances regarding the mechanisms of blooms. Indeed, temperature and salinity changes may occur along with variations in other factors such as nutrients, water column conditions 414 and residence time which can trigger or deplete blooms. In addition to the direct impact of 415 temperature toward Alexandrium cyst germination (Anderson and Keafer 1987; Genovesi et 416 al. 2009), this factor is likely to be related with water stability or turbulence. In this regard, 417 418 winds seem to be a critical factor in lagoons by promoting turbulence and resuspension and decreasing temperature (Laanaia et al. 2013). As instance, an important bloom of 419 Alexandrium occurred in 2004 for a salinity of 36.5 (outside the optimal salinities depicted by 420 the DTs): this bloom was triggered by cysts germination resulting from water column 421 agitation by strong winds, also inducing a drop in temperature (Laanaia et al. 2013). 422 Moreover, salinity and temperature may be associated with nutrient availability as they can be 423 linked with nitrogenous and phosphorous fluxes between compartments (organic and 424 inorganic nutrients in water column, organisms and sediments) (Bougis 1974; Boynton and 425 Kemp 1985; Grenz et al. 1992). Many studies showed that nutrient availability is positively 426 associated with Dinophysis (Ajani et al., 2016) and Alexandrium growth (Collos et al., 2007; 427 2009; Natsuike et al., 2018) and that a lack of nutrients could lead to sexuality, and thus to the 428

decline of blooms (Anderson and Lindquist 1985). Unfortunately, nutrient measurements by 429 430 the REPHY network were not performed at the same time and stations than those of this work. Further studies including nutrient availability in water would allow to understand if 431 temperature and salinity have an indirect impact on cells abundance as their variation occur 432 along nutrients fluxes. Oxygen and light intensity are also known to influence Alexandrium 433 proliferations (Anderson and Keafer 1987; Keafer et al. 1992; Ajani et al. 2016; Valbi et al. 434 2019) and light increases toxin production by HA (Ogata et al. 1987). As nutrients, these 435 factors were not measured during the period or sites considered here but could be integrated in 436 further studies. We tried to integrate turbidity, although the linear regression showed no 437 438 significant impact and it never ended up as a remaining variable in the pruned DTs. In the Mediterranean lagoons as in all aquatic ecosystems, turbidity can result from a large panel of 439 environmental variations such as water turbulence (Baas et al. 2005) and surface winds (Arfi 440 441 et al. 1993). These different factors could have various impacts on Alexandrium and *Dinophysis* distribution, which may explain why turbidity appears to be a bad predictor of the 442 443 concentration of these species.

The approach developed here provided robust, easily interpretable, reliable results. At first, 444 the DTs highlighted the set of parameters in which blooms and shellfish contamination were 445 446 the most likely to happen, and provided an estimation of the risk within these sets. The models statistically confirmed the set for A. tamarense/pacificum, specified it by providing 447 narrower ranges, and linked them to the mechanisms of blooms. The robustness of the DTs 448 was ensured by repeating each experiment 100 times and calculating average DTs on both 449 learning and testing datasets, thus providing a very robust tool. The number of observations 450 used for toxins DTs was quite low, but the sets of parameters for phytoplankton and toxins 451 DTs were congruent which tends to validate the results. By validating the model's predictions 452 453 thanks to residuals graphs and to adequation, dispersion and outlier tests, this work confirmed that temperature and salinity did have an impact on *A. tamarense/pacificum's* presence and
abundance. Moreover, including random effects in the model by grouping on the sampling
sites allowed us to exclude the variability due to location, thus increasing its reliability.

457 *4.2. Conclusion*

This study is a first step in forecasting the risks due to HABs in French Mediterranean 458 lagoons. Few variables were used, as they came from a network thought to trigger sanitary 459 alerts based on few parameters. Models were set up for two lagoons, including Thau which is 460 the fourth oyster farming area in France. They provided ranges of temperature and salinity 461 triggering blooms, and these ranges could be linked to the mechanisms of blooms. The robust 462 results could help stakeholders to manage the sanitary regulation of these lagoons in the future 463 according to network measurements. The methods developed in this study could be used to 464 investigate other data sets describing different ecosystems and integrating more biotic and 465 abiotic variables, which could allow to increase the model's performance. 466

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Table 1 : Correlation coefficients between A. tamarense/pacificum, Dinophysis, diatoms, other dinoflagellates,

			Thau Tagoon			
	A. tamarense/ pacificum	Diatoms	Dinoflagellates	Sal.	Temp.	Turb.
A. tamarense/ pacificum		-0.01 <u>0.18</u>	0.05 <u>0.29</u>	0.04 <u>0.17</u>	0.02 0.02	0.04 0.05
PST	0.41	-0.11	-0.2	0.3	-0.18	-0.14
(m)	0.17	-0.23	-0.05	0.33	<u>-0.38</u>	-0.31
(0)	<u>0.58</u> <u>0.44</u>	-0.18 -0.19	-0.12 -0.06	0.27 <u>0.41</u>	-0.04	-0.16

Thau lagoon

abiotic factors (temperature, salinity and turbidity) and toxins in Thau and Leucate lagoons from 2010 to 2019.

Temp.: Temperature; Sal.: Salinity; Turb.: Turbidity. Non-italics: Pearson coefficients. Italics: Spearman coefficients. Bold: *p*.val <0.05. Underlined: *p*.val < 0.01. Bold and underlined: *p*.val <0.001. Colorized in blue: Significant positive correlation coefficients. Colorized in red: Significant negative correlation coefficients. Paralytic Shellfish Toxins (PST); Okadaic acid (OA); Pectenotoxins (PTX); Dinophysis toxins (DTX); Toxins in the mussels (m); Toxins in the oysters (o).

Leucate lagoon

	Dinophysis	Diatoms	Dinoflagellates	Sal.	Temp.	Turb.
Dinophysis		-0.01	-0.04	$\frac{-0.21}{0.22}$	$\frac{-0.23}{0.31}$	0.03
OA	<u>0.45</u>	-0.06	-0.06	<u>-0.28</u>	<u>-0.38</u>	0.08
(m)	<u>0.67</u>	-0.15	-0.07	<u>-0.34</u>	<u>-0.51</u>	<u>0.27</u>
OA+PTX+DTX	<u>0.46</u>	-0.06	-0.06	<u>-0.28</u>	<u>-0.39</u>	0.08
(m)	<u>0.66</u>	-0.15	-0.08	<u>-0.35</u>	<u>-0.51</u>	<u>0.27</u>
OA	<u>0.5</u>	-0.08	-0.05	-0.14	<u>-0.39</u>	0.13
(o)	<u>0.69</u>	-0.2	-0.1	-0.19	-0.56	<u>0.28</u>
OA+PTX+DTX	<u>0.52</u>	-0.08	-0.06	-0.12	<u>-0.38</u>	0.12
(0)	<u>0.69</u>	- 0.22	-0.13	-0.17	-0.56	<u>0.28</u>

	Negative Binomial regression			Logistic regression		
Term	Coefficient	IRR	<i>p</i> .val	Coefficient	OR(presence)	<i>p</i> .val
Intercept	8.72	6.11e3	<2e-16 ***	-0.65	1.92	0.060
Temp. <10.4	-2.28	0.010	<7.73e-5 ***	1.93	0.14	1.60e-7 ***
Temp. €[10.4; 14.6[-0.78	0.45	0.030 *	0.76	0.46	6.02e-3 **
Temp. €[21.5; 25[-1.76	0.17	3.45e-7 ***	1.15	0.31	2.03e-5 ***
Temp. > 25	-1.92	0.15	4.38e-3 **	1.90	0.15	2.66e-5 ***
Sal. < 36	-1.38	0.25	4.85e-4 ***	1.53	0.21	7.45e-7 ***
Sal. c [36; 39.2[0.22	0.81	0.49	0.81	0.44	1.47e-3 **
Turb.	0.13	1.13	0.13	-0.094	1.09	0.051

Table 2 : Zero inflated negative binomial model predicting A. tamarense/pacificum concentrations in Thau

The sampling site nested are as random effects. IRR: Incident Risk Ratio. OR: Odds Ratio. Temp.: Temperature. Sal.: Salinity. Turb.: Turbidity.