

A REMOTE SENSING AND REGIONAL DOWNSCALING APPROACH TO THE ECOLOGICAL FORECASTING OF POTENTIALLY TOXIC DIATOM BLOOMS IN CALIFORNIA AND THE CHESAPEAKE BAY

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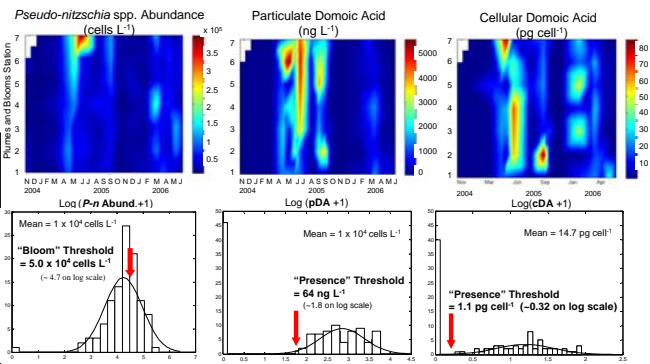
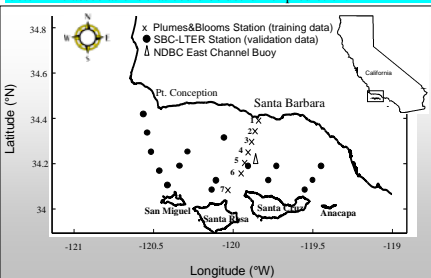
Recent downscaling efforts for the Southern California Bight (SCB) and the Chesapeake Bay have led to hydrodynamic models currently being applied to empirical habitat models for the neurotoxin-producing diatom group, *Pseudo-nitzschia* (Amnesic Shellfish Poisoning). Statistical models for predicting the occurrence of potentially toxic diatom blooms in the Santa Barbara Channel (SBC) and the Chesapeake Bay were developed with *in situ* monitoring observations and then used to create hindcasts of bloom probabilities using SCB-ROMS and ChesROMS. Environmental parameters significantly associated with toxic blooms off the coast of central California are similar to those for the Chesapeake Bay, suggesting certain commonalities across ecosystems. The Chesapeake Bay is a highly-eutrophied estuarine system structured by riverine inputs and oceanic intrusions, while the SBC is a region where wind-driven upwelling and mesoscale eddies are important processes driving phytoplankton blooms. In both systems, *Pseudo-nitzschia* blooms pose an increasing threat to human and wildlife health, rendering possible mitigation by bloom prediction a desired goal for public health and resource managers.

The views, opinions, and findings contained in this report are those of the authors and should not be construed as an official National Oceanic and Atmospheric Administration U.S. Government position, policy, or decision.

THE SANTA BARBARA CHANNEL – California Current System

STUDY SITE & DATA

Monthly cell abundance and toxin data were collected at 7 stations in the Santa Barbara Channel, off the coast of central CA, from November 2004 - June 2006. Concurrent hydrographic, chemical, and optical properties were measured and examined in relation HAB data to determine associations that could be useful for prediction.

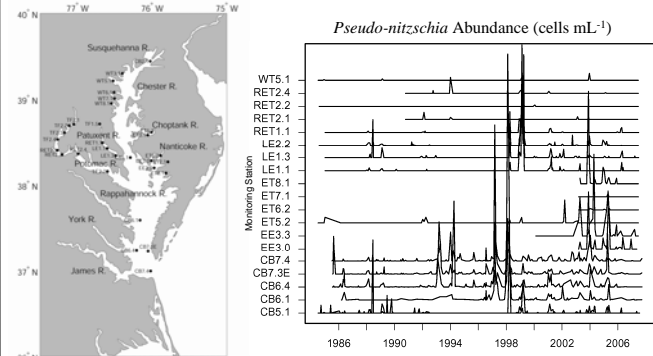


Histograms of the lognormal response variables: (a) *Pseudo-nitzschia* abundance, (b) pDA, and (c) cDA (note the bi-modal distributions for pDA and cDA) overlaid with the approximated normal density distribution. Red arrows indicate placement of designated thresholds used in evaluating model performance (Table 2 below).

THE CHESAPEAKE BAY -- Maryland, Virginia, D.C.

STUDY SITE & DATA

Habitat suitability models are being developed for a variety of HABs in the Chesapeake Bay as part of a NOAA MERHAB project (see poster by Christopher Brown). *Pseudo-nitzschia* cell abundance and water quality data were acquired for 30 stations from the MD Dept. of Natural Resources and the USEPA Chesapeake Bay Program monitoring datasets spanning 1985-2007 (N=6,989). The poly- and oligohaline regions are the most comprehensively represented salinity regimes in the pre-selected dataset, with fewer observations available for the mesohaline, or middle portion of the Bay. A suite of 21 physical, chemical, and biological properties were used to determine significant predictors for blooms. To date, the Chesapeake Bay has no recorded outbreaks of ASP or domoic-acid poisoning but does have algal blooms capable of toxin production.



The majority of blooms in the record occur in the middle and lower bay- mouth region (CB5.1, CB6.1, CB6.4, CB7.3E, CB7.4) with notable hotspots for bloom development in tidal estuarine zones (EE3.0, EE3.3, LE1.1, LE3.1, LE2.2, RET1.1). Although several large blooms were recorded for the lower Bay during the 1980s and 1990s, blooms at the mouths of major tributaries such as the Potomac, Choptank, and Patuxent Rivers are relatively small and infrequent prior to 1997 at which point the lower bay and tidal estuaries appear to become synchronized.

STATISTICAL MODEL

I used a least-squares stepwise regression approach to identifying predictors for 1) *Pseudo-nitzschia* abundance 2) particulate domoic acid, and 3) cellular domoic acid from a suite of 37 hydrographic and optical variables. The results for models (1) and (2) shown in Table 2 reflect the significant associations seen between variables in the correlation analysis (Table 1). Blooms and high toxin levels are directly related to upwelling conditions and negatively related to nutrient ratios of Si:N and Si:P.

(Anderson et al. *Harmful Algae*, 2009)

Table 1.	<i>P.n</i> Abund.	pDA	cDA	SST	SSS	CHL	NO ₃	PO ₄	Si(OH) ₄	Si:N	Si:P
<i>P.n</i> Abund.	****	0.53	0.07	-0.34	-0.15	0.34	0.04	0.03	0.01	-0.06	-0.07
pDA		****	0.42	-0.16	0.14	0.18	0.03	-0.06	-0.08	-0.08	-0.12
cDA			****	-0.27	0.17	0.14	-0.03	-0.06	-0.05	-0.01	-0.12

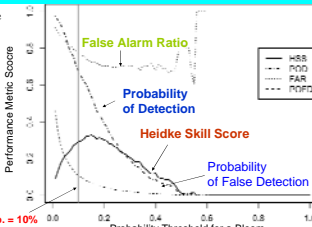
Table 2.	Significant Predictors For Full Models	Significant Predictors For Remote-Sensing Models
<i>P.n</i> spp. Abundance	-R _{si} (412/555) - Silicate:Nitrate ratio n = 75 + R _{si} (555) -a _{ph} (490) - R _{si} (510/555) 75% prob. of CORRECT bloom ID using 5.0 x 10⁴ cells L⁻¹ threshold	-R _{si} (412/555) 63% skill n = 89 - R _{si} (510) -Chlorophyll (level 2) - R _{si} (510/555) 53% prob. of CORRECT bloom ID using 5.0 x 10⁴ cells L⁻¹ threshold
	Particulate Domoic Acid	- R _{si} (510/555) 58% skill n = 80 - Silicate:Phosphate - Temperature + Salinity 83% prob. of CORRECT ID using 64 ng L⁻¹ threshold

STATISTICAL MODEL

I used a logistic regression approach to model cell abundance by creating a binary variable using the unofficial operational bloom threshold of 100 cells mL⁻¹. Model performance was judged by several metrics (Table 4) and outcomes optimized according to an adjustable probability threshold to aid managers in making forecasts.

Table 3. Significant Predictors of *P.n* Abundance

Predictor	Coefficients	p-val (Chi)
Intercept	-1.84	
PO ₄	-69.5	<<0.001
Salinity	0.101	<<0.001
Temp	-0.063	<<0.001
DOC	0.306	<<0.001
Si(OH) ₄	-0.373	<<0.001
Month	-0.079	0.002
NP	-0.753	0.008



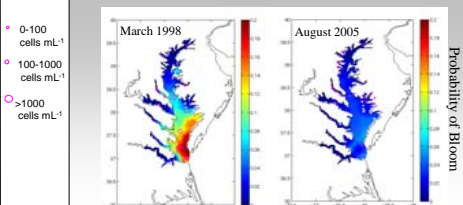
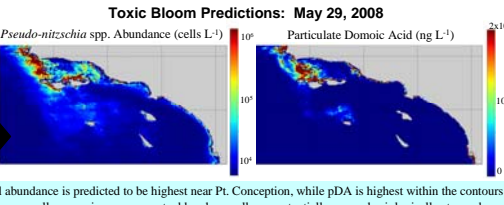
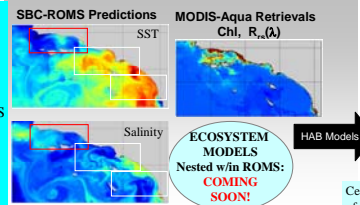
*DOC = Dissolved Organic Carbon
N:P = Nitrate:Nitrite: Phosphate
Prob. = 10%

Table 4.	HSS	POD	FAR	POFD	Nagelkerke's R ²
Absent if P _{bloom} < 0.50	0.01	0.01	0.83	0.003	0.10
Absent if P _{bloom} < 0.10	0.30	0.69	0.76	0.10	0.10
Cross-validation P _{bloom} = 0.10	0.31	0.69	0.76	0.10	0.10

(Anderson et al., in review)

HINDCASTS

Physical and optical data from the regional ocean model and satellite retrievals allow for preliminary prediction maps of cell abundance and toxin concentration using the RS Models (Table 2). An interpolative smoothing method (DINEOF) was applied to remote-sensing inputs to achieve better spatial resolution in the bloom prediction maps.



HINDCASTS
Grids maps of bloom probabilities were created using spatial interpolation of observations relevant to the logistic model and compared with observations (bubbles). Unfortunately, DOC measurements are not available for many of the tributary monitoring sites, precluding computation of the full GLM. An alternative model w/o DOC was used to make predictions of a large bloom (March 1998) and non-bloom (August 2005) event. The distribution of bloom observations above the 100 cells mL⁻¹ threshold is generally well-captured by the alternative GLM which assigns probabilities between 10-20% to the cluster of observations at or above 1,000 cells mL⁻¹ in the lower bay. In a forecast mode, the physical and chemical input parameters to the habitat model will be generated by The Chesapeake Bay Forecasting System (CBFS).

FUTURE WORK

An active area of current research is the selection and nesting of proper ecosystem models within ROMS. Validation is a key component to assessing predictive skill, and we are working closely with researchers and decision-makers to evaluate model performance. We will continue to refine the merging of satellite and regionally downscaled forecasting products with these empirical habitat models to assess forecasting capabilities and any potential connections to large-scale climate modes.

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