Mechanistic Modeling of Dynamics and Blooms of Jellyfish in the Northern Gulf of Mexico

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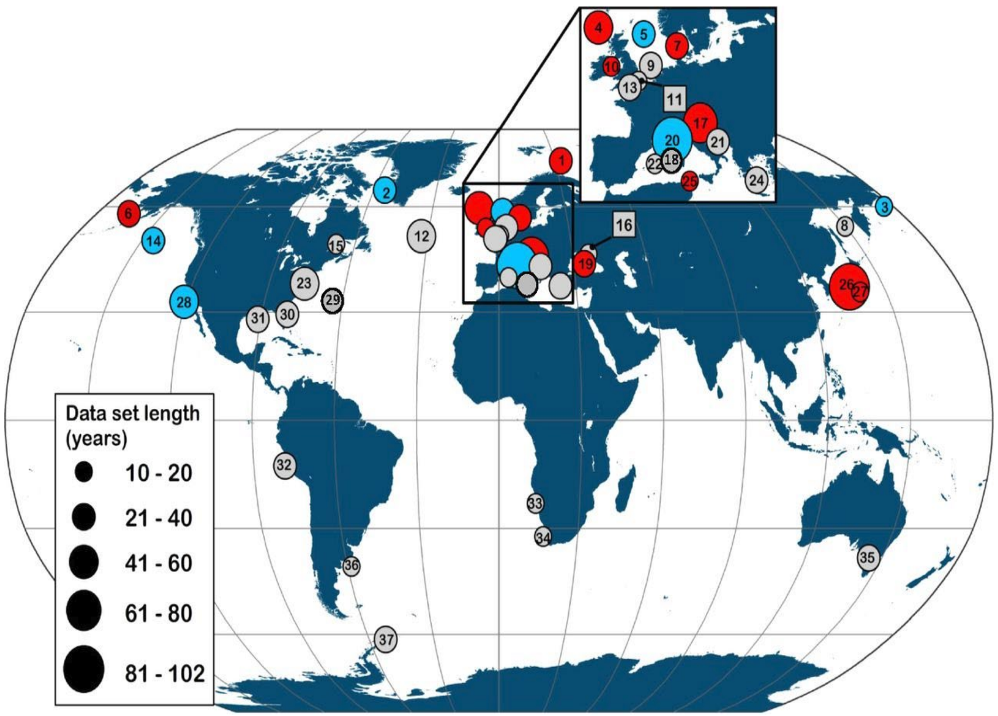
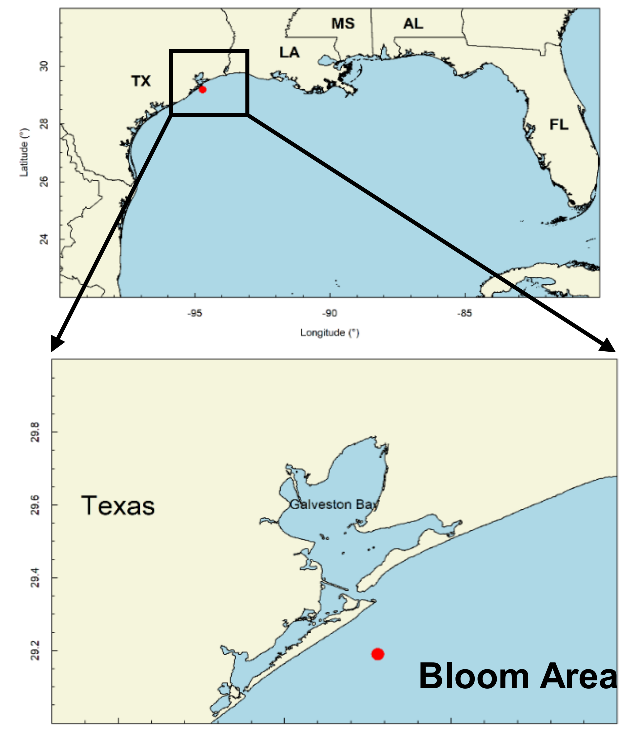
Worldwide Jellyfish Issues



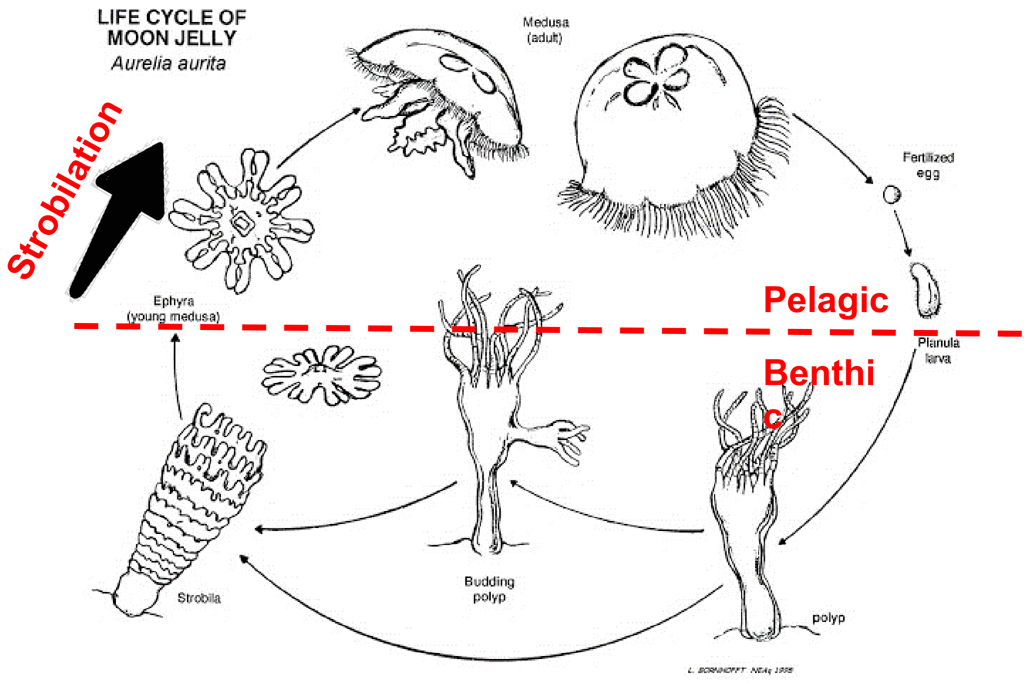
Condon et al. (2013)

Jellyfish blooms and climate-related changes in environmental conditions, overfishing, eutrophication, invasions, and coastal constructions (Graham, 2001; Purcell, 2005; Lynam et al., 2006; Attrill et al., 2007; Brodeur et al., 2008; Gibbons and Richardson, 2009; Miller and Graham, 2012; Condon et al., 2013).

Dense Jellyfish Observed Off Texas Coast



Modeling Complex Lifecycle of *Aurelia* spp.



- Strobilation is key for the dense aggregations of medusae in the water column.
- Environmental variables such as water temperature, salinity, and zooplankton density play an important role in regulating jellyfish life history.
- The complex interplay between these environmental factors limits our ability to understand the triggering mechanisms of jellyfish blooms.

Mechanistic Modeling (Individual-based Models)

- Better understanding the mechanisms driving population dynamics of zooplankton.
- Simulation and prediction of population dynamics in a changing climate.
- Contribute to understandings of fisheries production and ecosystem function.

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Effects of variability among individuals on zooplankton population dynamics under environmental conditions

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Exploring cosmopolitan jellyfish (*Aurelia* spp.) bloom dynamics and ecological implications in subtropical waters with mechanistic dynamic modeling

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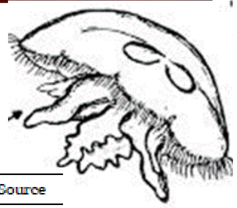
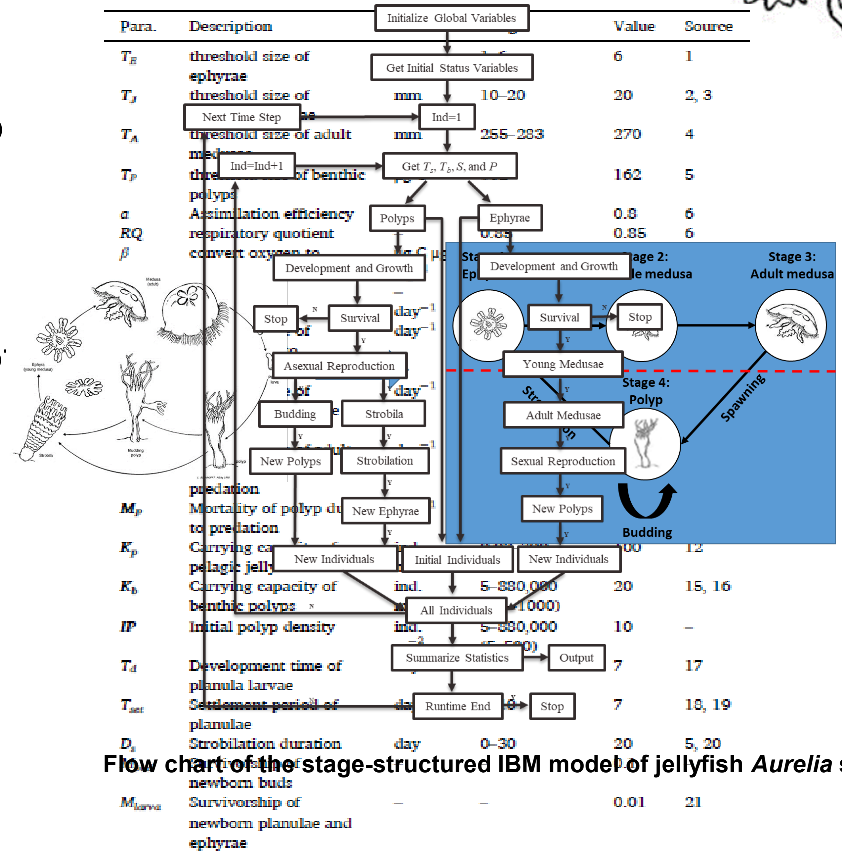


Individual-based Modeling (IBM)

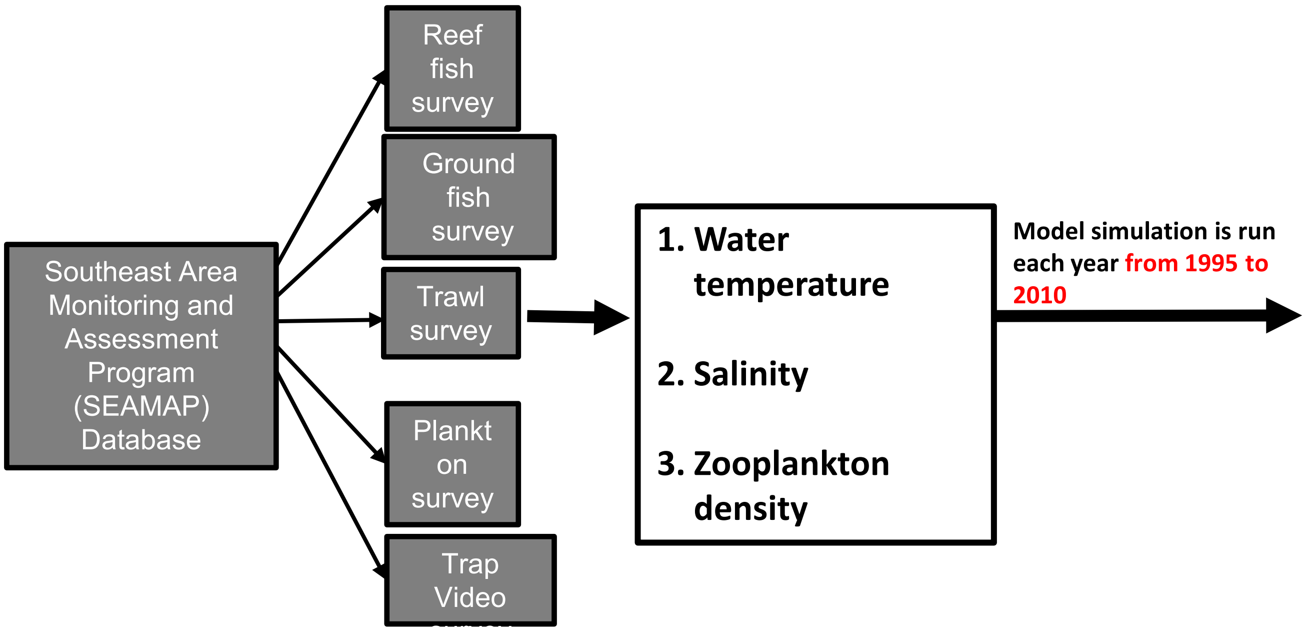
- It incorporates species life history details to track population dynamics in response to biotic and abiotic environmental factors (Bi and Liu 2017).
- It considers the main biological processes o jellyfish including growth, development, sexual reproduction, asexual reproduction (budding and strobilation), and mortality.
- Environmental variables (surface water temperature, bottom water temperature, bottom salinity, zooplankton density) included as drivers controlling the bioenergetics of jellyfish.



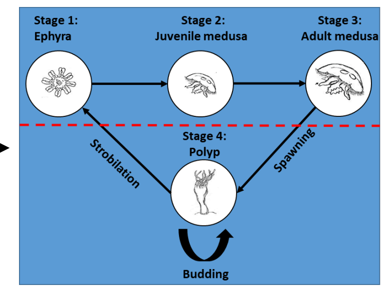
Flow chart of the stage-structured IBM model of jellyfish *Aurelia* spp.

Parameters with ranges and default values used in the IBM.

Compilation of Environmental Data

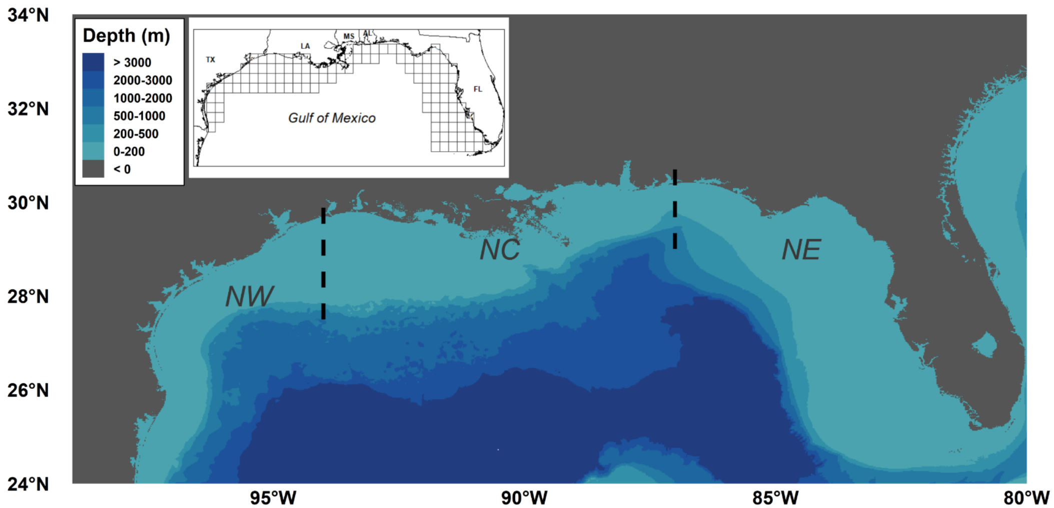


Stage-structured IBM

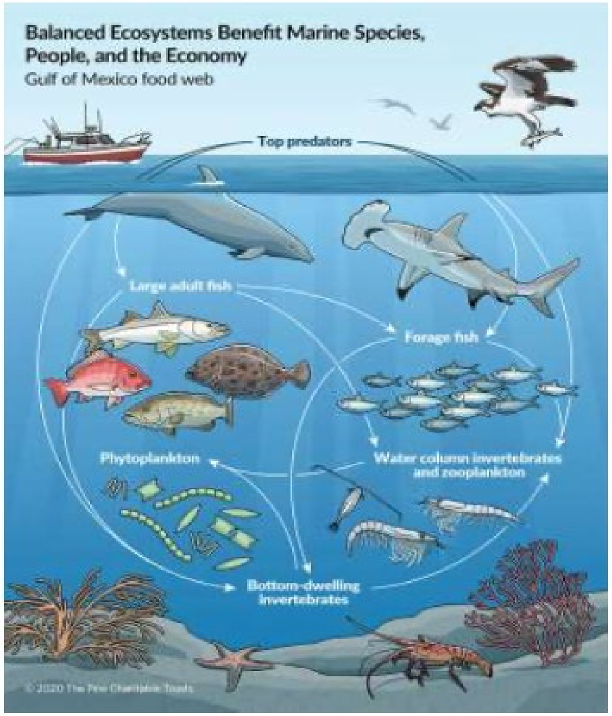


Data Source: Southeast Area Monitoring and Assessment Program (SEAMAP)

Study Area and Model Domain

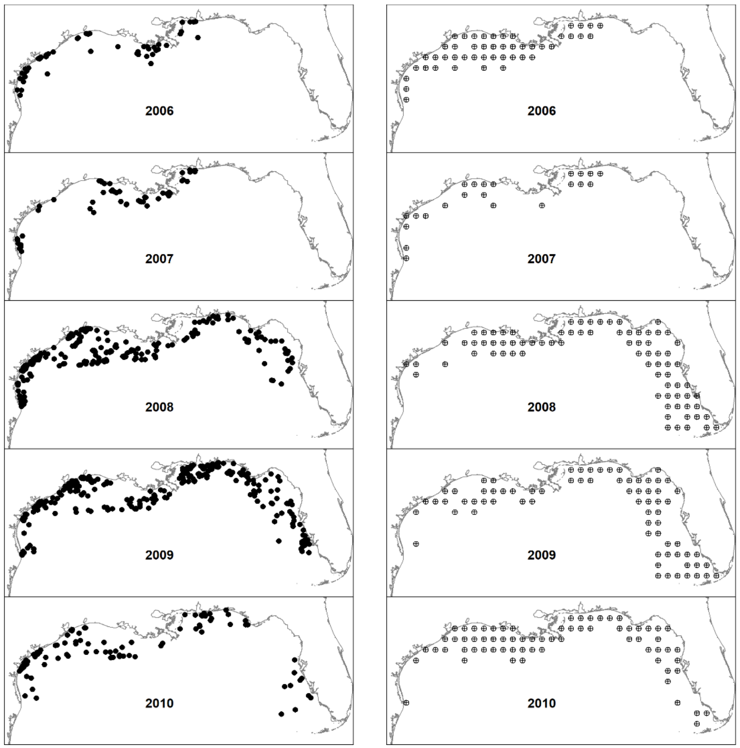


- Spatial domain: areas with depth < 200 m.
- Spatial resolution: 1/2° latitude/longitude
- Number of grids: 117
- Three sub-regions: NW GoM (Texas), NC GoM (Louisiana-Alabama), NE GoM (Florida)

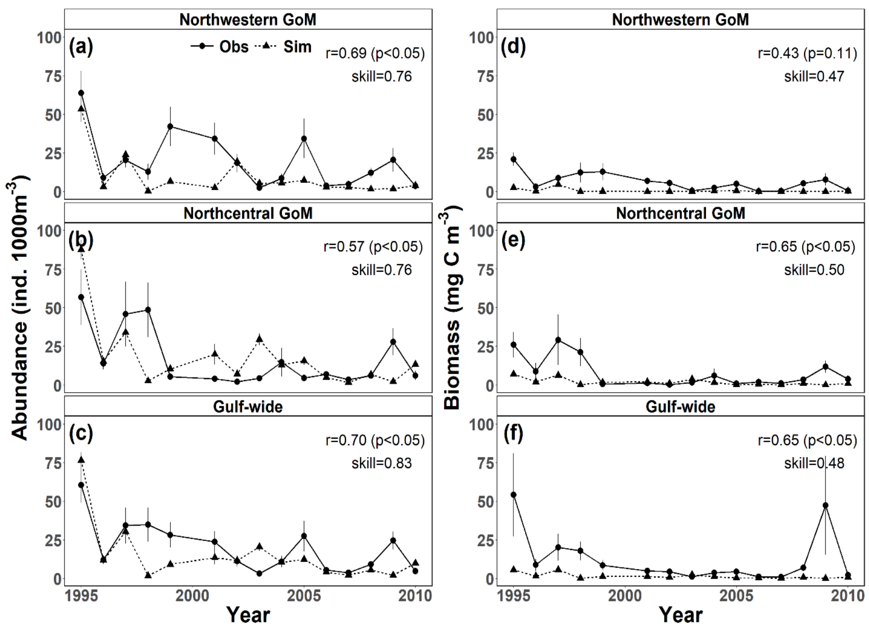


Source: Pew Charitable Trusts, 2020

Model Validation



Comparisons of observations (left-black dots) and simulations (right-circle plus) for the appearance and distribution of *Aurelia* medusae from 2006 to 2010.



Field observations of *Aurelia* medusa abundance (left) and biomass (right) compared with the simulations from 1995 to 2010. The error bar presents the standard error (SE).

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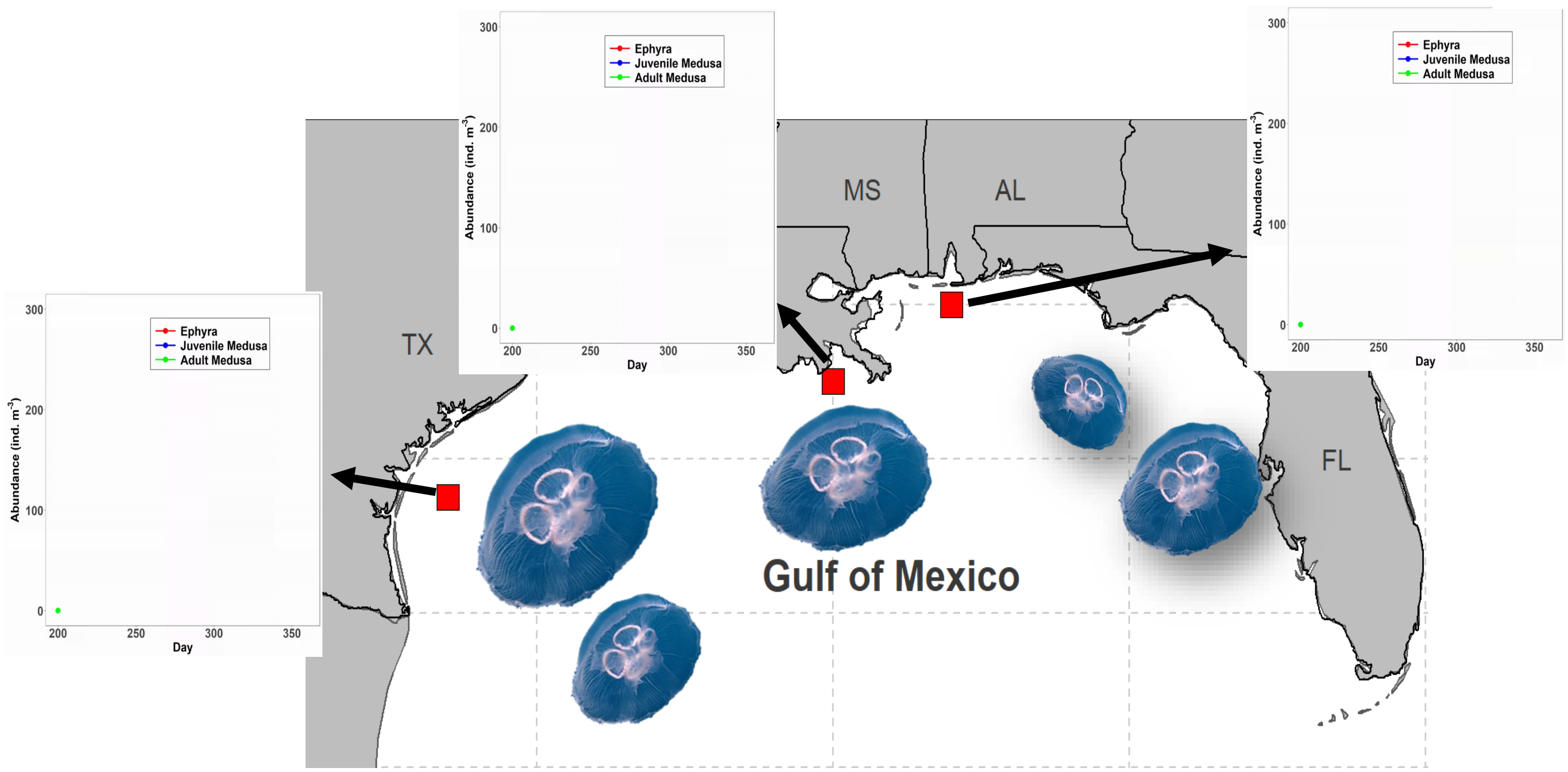
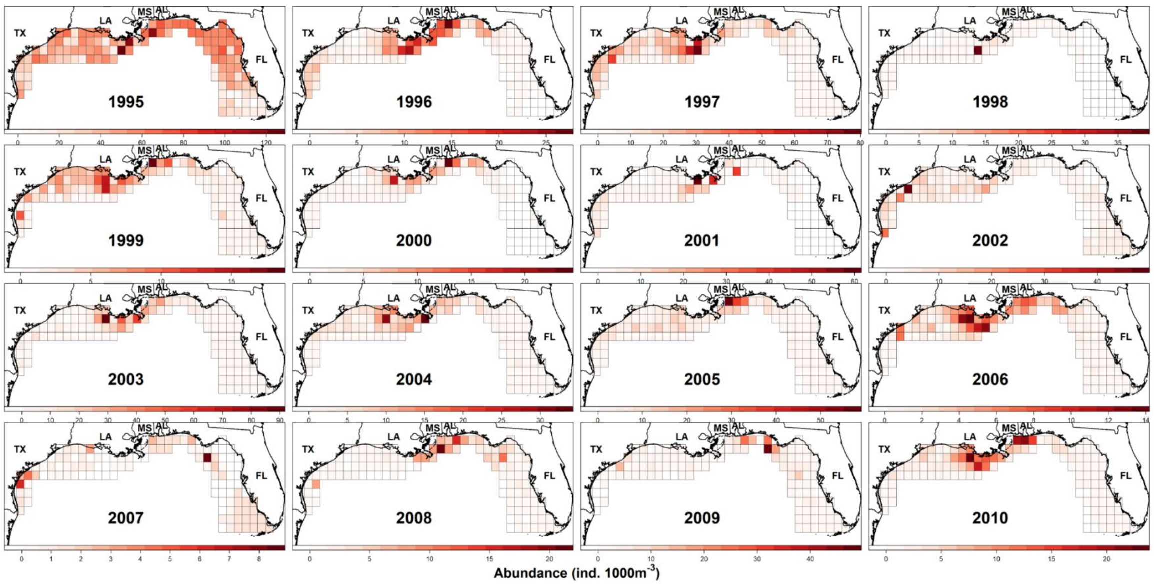
Simulated Bloom Spots



Predicating Hotspots of Jellyfish Abundance and Biomass



- **<u>East Louisiana</u>**

1. Nutrients from the Mississippi-Atchafalaya River system (Rabalais et al. 2002)

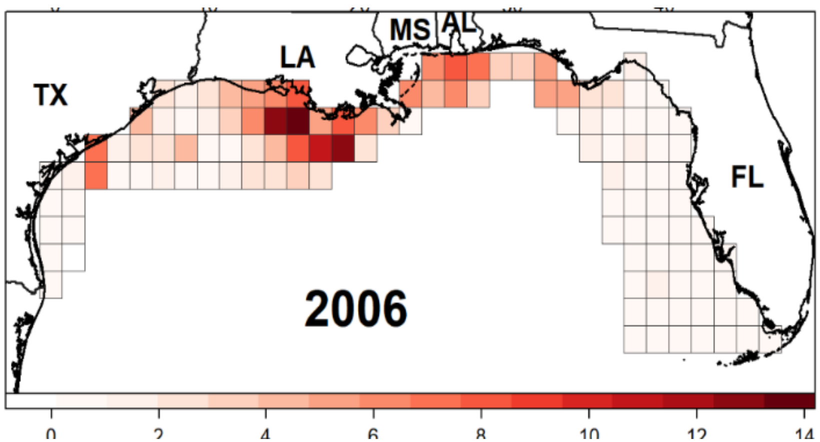
- **<u>Mississippi Bight</u>**

1. Nutrients from the Mobile Bay system (Lehrter, 2008), and the wind-driven eastward dispersal of the Mississippi River discharge (Biggs et al. 2008; O'Connor et al. 2016)

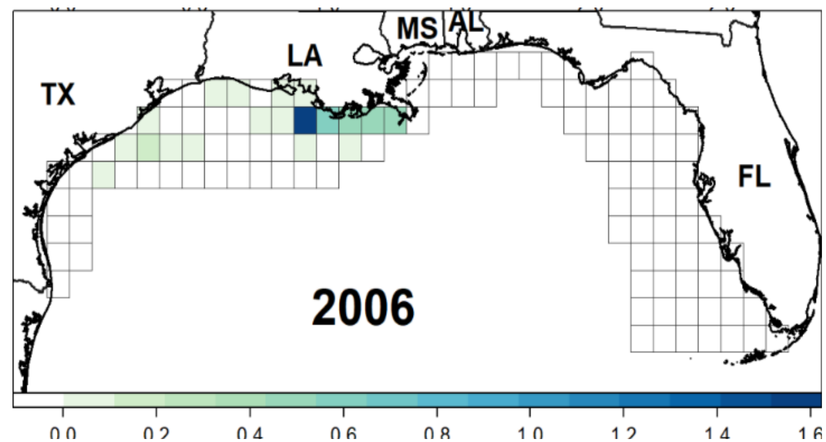
- **<u>South Texas</u>**

1. Nutrients from seasonal downcoast transport of the Mississippi-Atchafalaya River discharge (Nowlin et al. 2005)
2. Nutrients from seasonal wind-driven upwelling (Cochrane and Kelly, 1986; Zavala-Hidalgo et al. 2006; Hetland and Campbell, 2007)

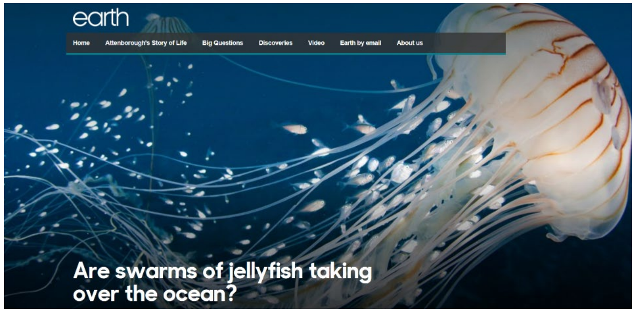
Blooms in Abundance ≠ Blooms in Biomass



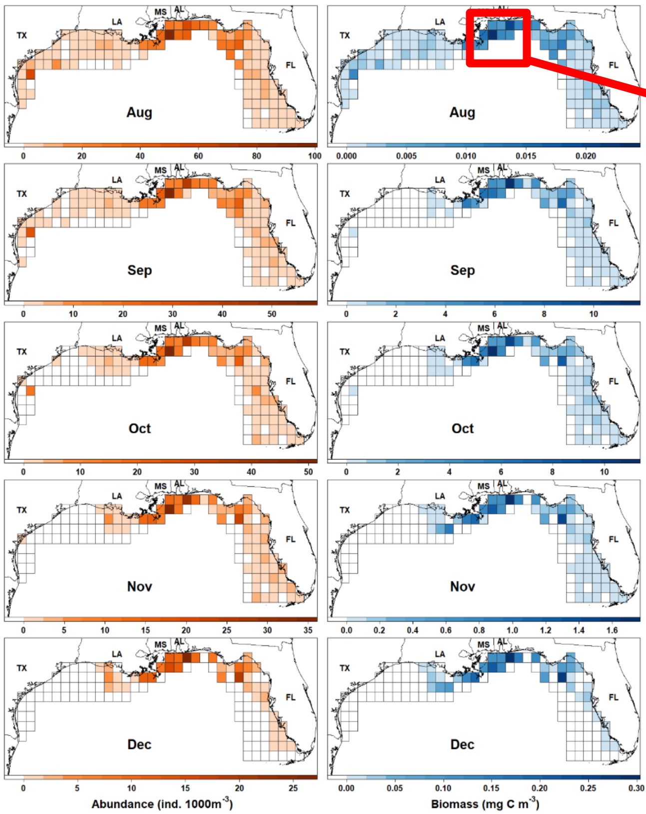
Abundance (ind. 1000m^-3)



Biomass (μg C m^-3)

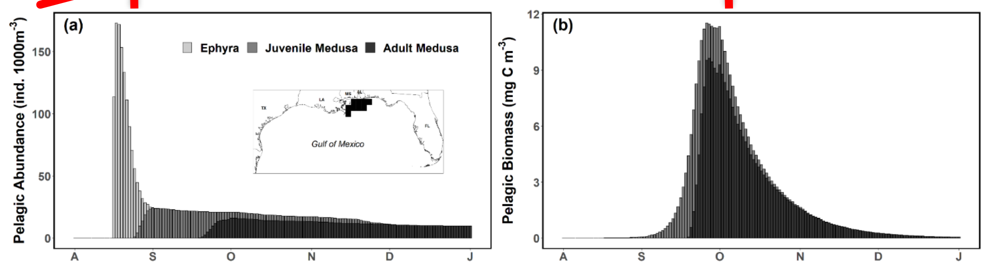


Case Scenario in 2008



Peak abundance in August

Peak biomass in October



Mismatch in the bloom timing between the peak of abundance in mid-August and the peak of biomass in early October.

This raised an interesting question to further understand the ecological relevance of jellyfish blooms in pelagic food-web dynamics and in biogeochemical cycling.

Detecting Triggers of GoM Jellyfish Blooms

Table 5. Coefficients of multiple linear regression models for abundance and biomass of *Aurelia* spp. Relative contribution of each predictor was estimated by dominance analysis.

Dependent Variable	Independent Variables	Estimated Coef.	Standard Error	P-value	Contribution
Abundance (ind. 1000 m^3)	Zooplankton biomass	1.979	0.063	< 0.001 ***	0.359
	Surface water temperature	-1.849	0.584	< 0.001 **	0.030
	Bottom water temperature	-0.555	0.301	0.066	0.018
	Salinity	1.577	0.361	< 0.001 ***	0.006
Biomass (mg C m^3)	Zooplankton biomass	0.109	0.005	< 0.001 ***	0.216
	Surface water temperature	-0.147	0.047	< 0.01 **	0.025
	Bottom water temperature	-0.093	0.024	< 0.001 ***	0.012
	Salinity	0.062	0.029	< 0.05 *	0.005

Note: Subscripts represent statistically significant differences: * = p < 0. 05, ** = p <0 .01, *** = p <0 .001

Bottom-up control is the main driver triggering jellyfish blooms in the GoM.

Water temperature has negative effects because

- summer heat stress in subtropical regions suppresses the growth of medusae.
- winter warm temperatures cause mortality of benthic polyps and limit ephyra production.

Summary

1. Jellyfish population dynamics show large interannual variations from 1995 to 2010.
2. Coastal waters off South Texas, East Louisiana, and Mississippi Bight appear to be potential bloom hotspots with distinctive driving processes.
3. Bloom timings defined in abundance and biomass are worthy of further consideration.
4. Jellyfish blooms in the GoM seem to be triggered by the bottom-up control.