

## Abstract

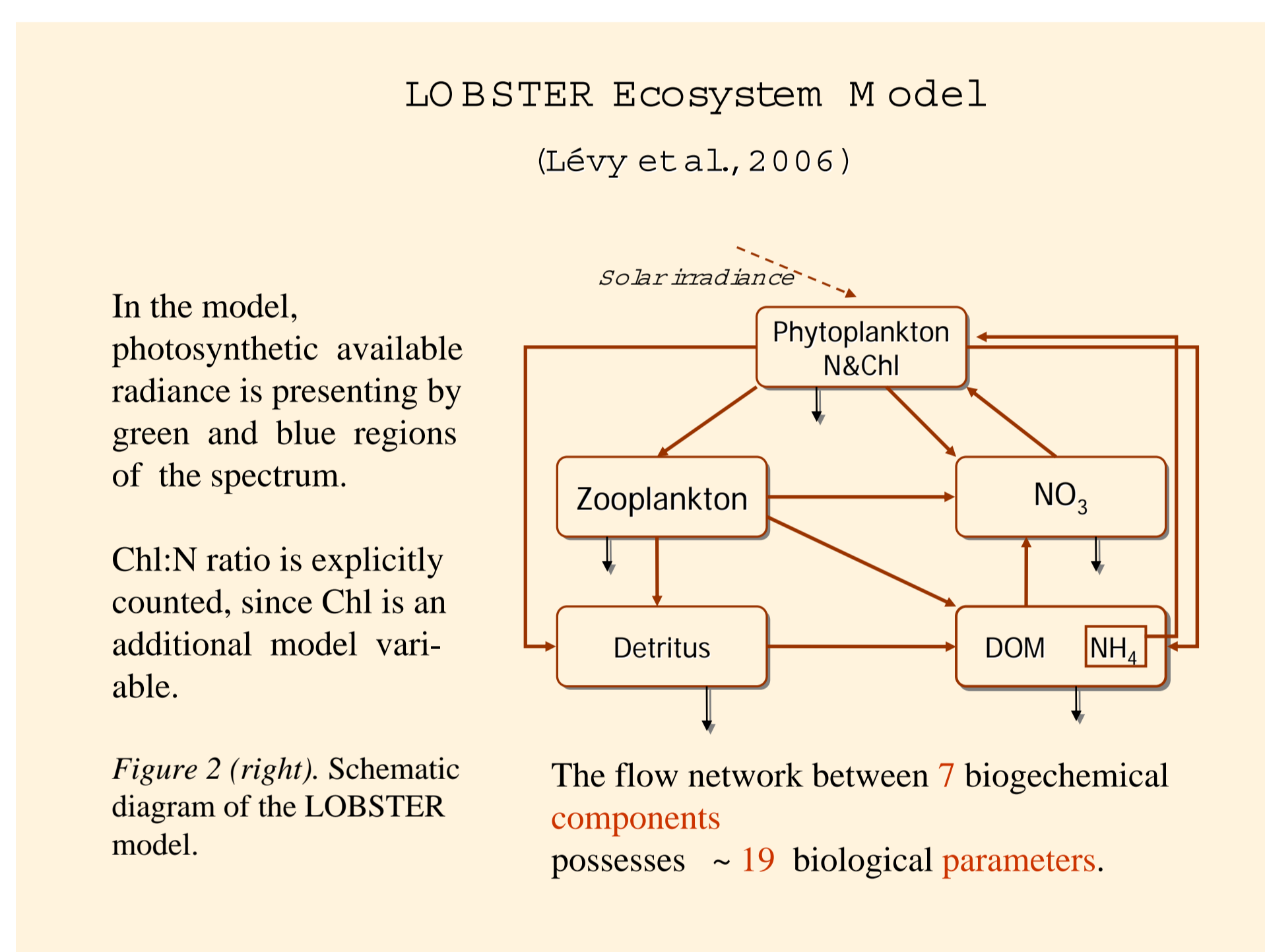
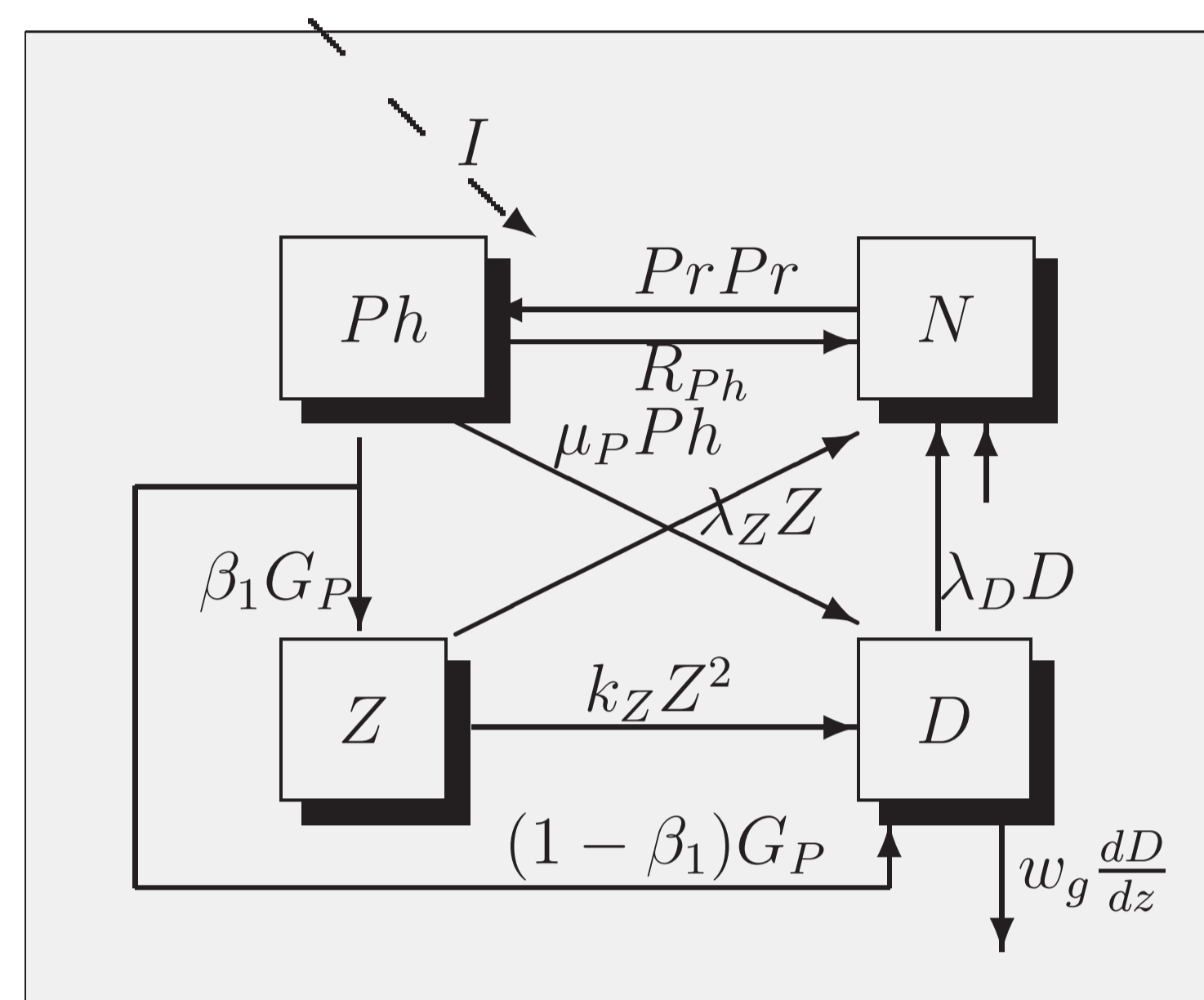
All the versions of the MERSEA biogeochemical model developed within WP7 for simulating the North Atlantic ecosystem dynamics are of a different mathematical and biological complexity and possess a number of poorly known biological parameters which have been adjusted via a data assimilation procedure. We compare the ecosystem models in particular, LOBSTER and size dependent NPZD model- and validate them against existing biogeochemical data.

## 1 Models

### Model of Krist and Oschlies (2006)

The version of a nitrogen based four-compartment (NPZD) model has been developed by *I. Krist* and *A. Oschlies* (WP 7.2.1). In the new model, phytoplankton is implicitly presented by a spectrum of different sizes. Thus, some of the described biogeochemical processes are size-dependent. (We will refer to the model as SD NPZD)

Figure 1. NPZD model schematic diagram.



## 2 Parameter optimization method (WP 7.3.1.2, in collaboration with P.J. van Leeuwen, Universiteit Utrecht)

Sequential Importance Resampling Filter (Smoother).

## 3 Data

The model is constrained by monthly mean data of

the Bermuda Atlantic Time-series Study (BATS 32°N, 65°W), Ocean Weather station PAPA (50°N, 145°W), the North Atlantic Bloom Experiment (NABE, 47°N, 20°W), the Arabian Sea C station (AS-C, 10°N, 65°E), Equatorial Pacific Ocean (EqPac, 0°S, 140°W), the Ross Sea (63.2°S, 170°W)

particularly, by measurements of dissolved inorganic nitrogen and chlorophyll concentrations.

## 4 Model validation

Nonparametrical (distribution free) rank statistics (based on "rank order") is used as criteria of "goodness" of model-to-data fit. See Table 1 and Table 2 to compare the quality of Lobster ecosystem model performance against a similar experiment carried out with the phytoplankton size structure SD NPZD model version. (Light brown color indicates better agreement with the data).

Table 1. Agreement between model (Lobster and SD versions) and observed chlorophyll "a"

Stat. criteria	PAPA		NABE		BATS		AS-C		EqPac.		Ross Sea	
	Lobster	SD	Lobster	SD	Lobster	SD	Lobster	SD	Lobster	SD	Lobster	SD
$r_{Sp}$	0.22	0.41	0.63	0.38	0.16	0.45	0.55	0.74	0.91	0.78	0.71	-0.07
MW	-4.31	-0.68	-6.06	-5.91	-8.72	-1.05	-0.02	-1.29	-1.11	-2.16	-2.2	-0.84
W	4.46	0.10	4.77	4.75	13.06	3.17	0.19	2.4	2.12	4.14	0.91	1.19

Table 2. Agreement between model (simple and SD versions) and observed DIN concentrations

Stat. criteria	PAPA		NABE		BATS		AS-C		EqPac.		Ross Sea	
	Lobster	SD	Lobster	SD	Lobster	SD	Lobster	SD	Lobster	SD	Lobster	SD
$r_{Sp}$	0.67	0.67	0.1	0.027	0.61	0.77	0.20	0.095	0.52	0.57	0.83	-0.90
MW	-6.70	-4.47	-7.2	-7.30	-22.8	-10.7	-1.51	-2.95	-6.80	-1.40	-1.10	-3.57
W	7.71	5.25	5.22	5.22	16.19	14.85	0.74	2.04	9.00	2.45	1.06	2.60

## 5 Results of

simultaneous tuning the SD NPZD and Lobster models for all the noted locations

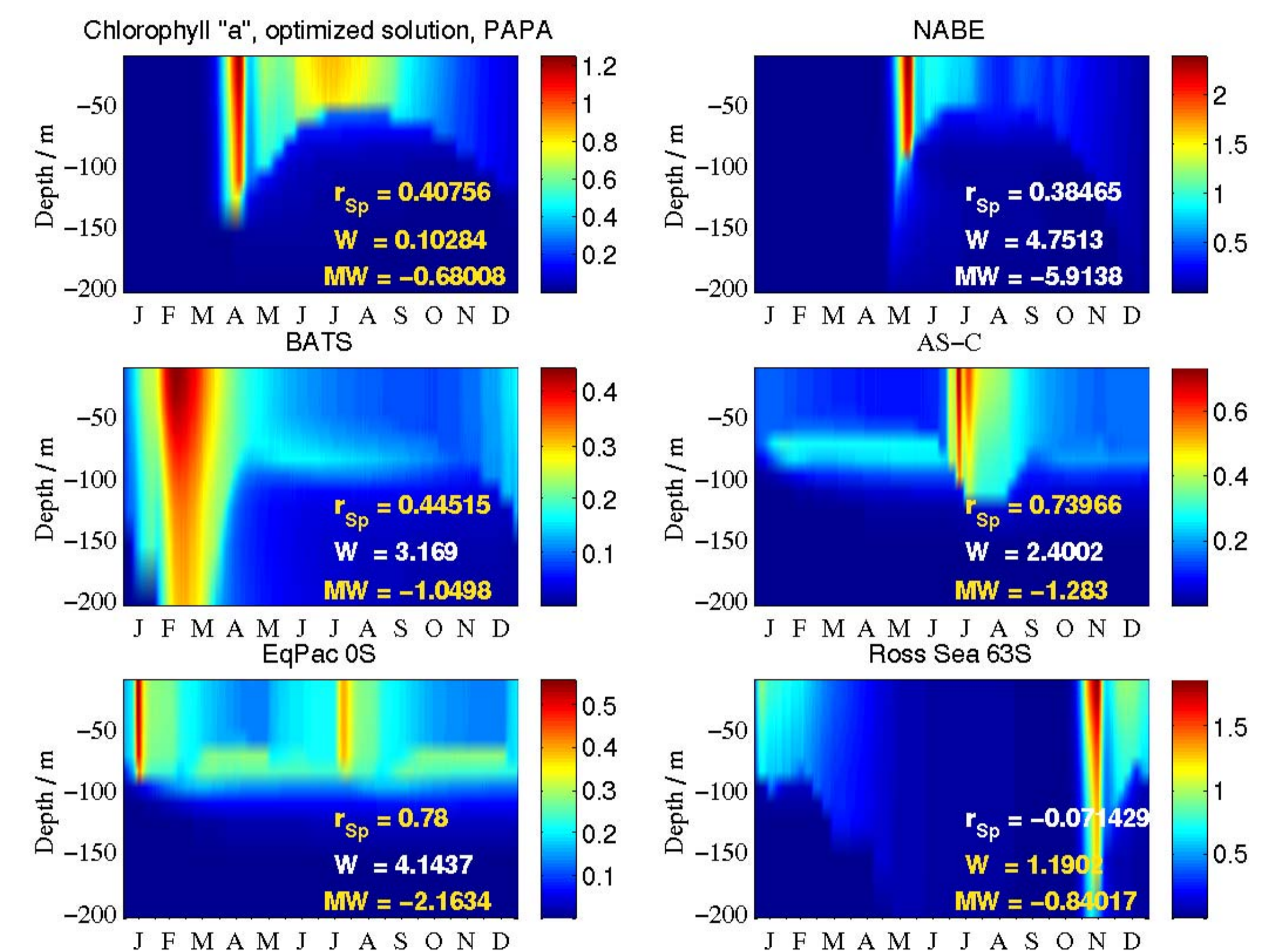


Figure 1: Chlorophyll "a" simulated by the size-dependent NPZD eco model at 6 sites. The statistics criteria values of yellow color indicate sufficient agreement between model and observed chlorophyll, with respect to a certain criterion.

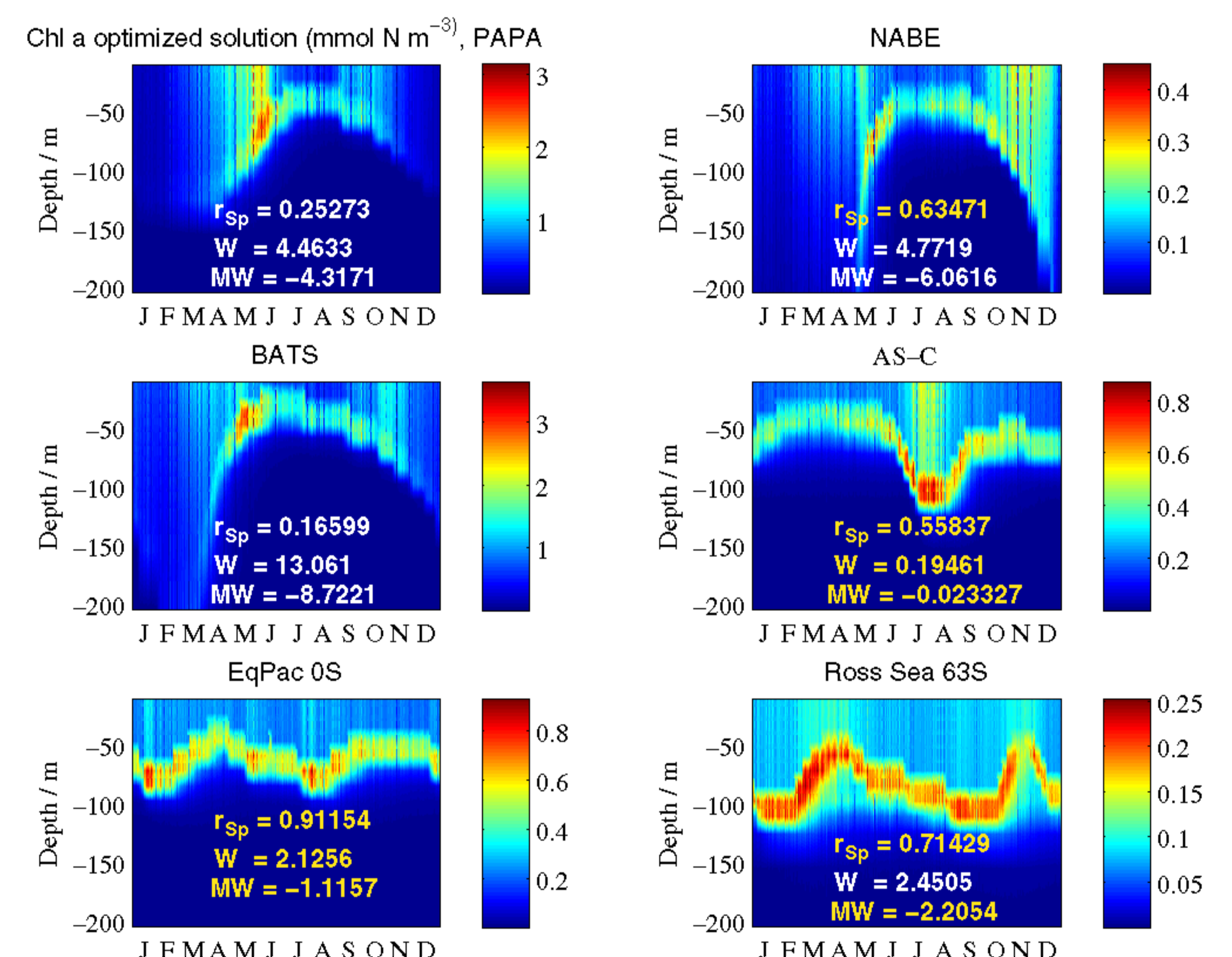


Figure 2: The time evolution of Chlorophyll "a" simulated by the Lobster eco model at 6 sites. The statistics criteria values of yellow color indicate sufficient agreement between model and observed concentrations, with respect to a certain criterion.

## 6 Conclusions

Does it make any sense different approaches for parameterizing biogeochemical processes (use a models hybrid)?

Nevertheless the results make us concluding that with the present versions of the ecosystem model it is not possible to reproduce the dynamics under different environmental conditions given one biological parameter set.

## References

- [1] Krist, I. and Oschlies, A., 2006. Towards a new implicitly size-structured marine ecosystem model. Part I: Evaluating cell size-dependent nutrient uptake and exudation (submitted).
- [2] Lévy, M., Gavart, M., Mémery, L., Caniaux, G. and A. Paci, 2005. A four-dimensional mesoscale map of the spring bloom in the northeast Atlantic (POMME experiment): Results of a prognostic model. J. of Geoph. Res., 110, C07S21.

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