



# The effects of fishing on ecosystem structure of the Northeastern part of the Okhotsk Sea

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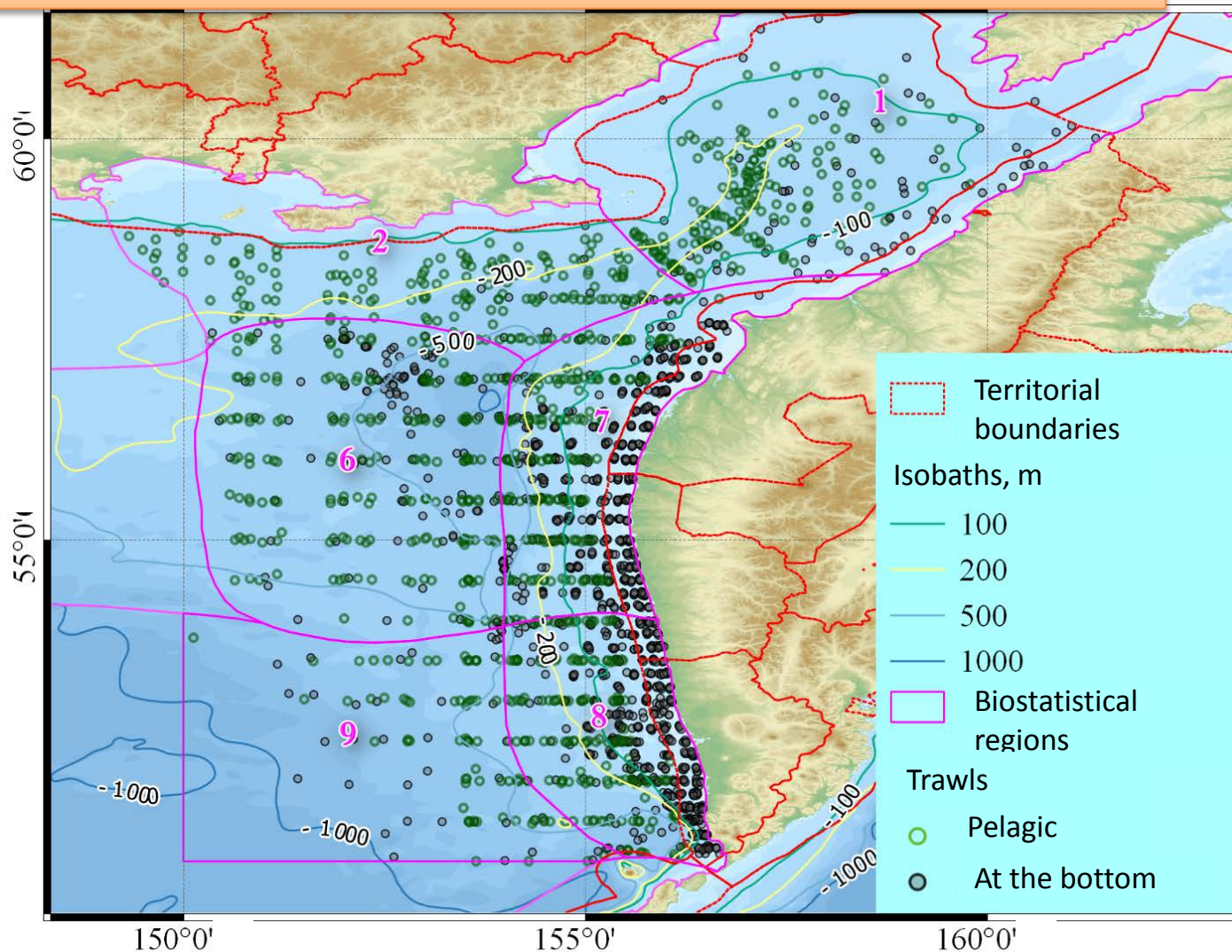
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The polygon of this research consists of the 1, 2, 6, 7, 8 and the part of the 9<sup>th</sup> biostatistical regions, used for aggregations of biomass estimates at TINRO-Center. Timeframe: 2000s years.

pros: we have the data about almost all TL, but cons: it is not a closed LME



Pollock (*Gadus chalcogrammus*, synonym – *Theragra chalcogramma*) is the most abundant commercial species in the Sea of Okhotsk

According to some experts, its catch reached 1.34 megatons in the northeastern part of the sea (1973) and 1.925 megatons in the entire northern part of the sea (1997). During the last 5 years, pollock catch in the area of its maximum concentrations (east of 150° E and north of 51° N) was reducing from 889 to 706 kilotons but its percentage in total walleye pollock catch in the entire northern part of the sea was remaining above 86%.

According to Company Statistical Reports data, 94 species **and their groups** are harvested in the northeastern part of the sea and, according to data of TINRO-Center fishery-independent surveys, 373 and 665 taxonomic units are registered in hauls in the pelagic zone and near the bottom respectively in this area.

Therefore, trawling fishing may affect several hundreds of aquatic species. It means that any assessment of trawling fishery impacts on the ecosystem is practically impossible without preliminary aggregation of species

The goals of this work are:

1. Tune the ecosystem linear inverse model (LIM)
2. Find out how the changes in fishery efforts can influence the trophic structure

Ecosystem model is overcomplicated even at the level of one size group for each of the most abundant species. Therefore, we joined several species into groups using optimal clustering by scaled  $\delta C^{13}$ ,  $\delta N^{15}$  and average individual weight (mg C)

## Fish

Species and sizes	cluster
<i>Aptocyclus ventricosus</i> $\leq 20$	Aptocyclus
<i>Aptocyclus ventricosus</i> $> 20$	Aptocyclus
<i>Berryteuthis magister</i> $4 < L \leq 8$	BerM0408
<i>Berryteuthis magister</i> $8 < L \leq 20$	LipOBerM
<i>Boreoteuthis borealis</i> $4 < L \leq 8$	BorB0408
<i>Boreoteuthis borealis</i> $8 < L \leq 20$	BorB0820
<i>Careproctus rastrinus</i> $10 < L \leq 20$	Careproct
<i>Careproctus rastrinus</i> $> 20$	Careproct
<i>Clupea pallasii</i> $5 < L \leq 14$	Clup0020
<i>Clupea pallasii</i> $14 < L \leq 20$	Clup0020
<i>Limanda sakhalinensis</i> $> 20$	Clup0020
<i>Clupea pallasii</i> $> 20$	Clup2040
<i>Eleginus gracilis</i> $L > 20$	EH2040
<i>Gadus macrocephalus</i> $40 < L \leq 60$	GadM4060
<i>Gadus macrocephalus</i> $> 60$	GadM60__
<i>Gonatus madokai</i> $> 20$	GonatMad
<i>Gymnacanthus detrisus</i> $> 20$	GymnDetr
<i>Hemilepidotus papilio</i> $> 20$	HemiPapi
<i>Hippoglossoides elassodon</i> $12.5 < L \leq 20$	Hipp1320
<i>Hippoglossoides elassodon</i> $> 20$	EH2040
<i>Leuroglossus schmidti</i>	LeuroShm
<i>Limanda aspera</i> $> 14$	LimAS
<i>Limanda sakhalinensis</i> $14 < L \leq 20$	LimAS
<i>Lipolagus ochotensis</i>	LipOBerM
<i>Mallotus villosus</i> $6 < L \leq 11$	Mallotus
<i>Mallotus villosus</i> $> 11$	Mallotus
<i>Osmerus mordax dentex</i> $\leq 20$	Osmerus
<i>Osmerus mordax dentex</i> $> 20$	Osmerus
<i>Reinhardtius hippoglossoides</i> $12 < L \leq 20$	RHip1220
<i>Reinhardtius hippoglossoides</i> $20 < L \leq 40$	Rther
<i>Theragra chalcogramma</i> $5 < L \leq 20$	TherC0520
<i>Theragra chalcogramma</i> $20 < L \leq 40$	Rther
<i>Theragra chalcogramma</i> $40 < L \leq 60$	TherC4060
<i>Theragra chalcogramma</i> $> 60$	TherC60__

## Plankton

Species	cluster
<i>Metridia okhotensis</i>	MetO
<i>Bradyidius pacificus</i>	Brad
<i>Aglantha digitale</i>	AgID
<i>Oikopleura</i>	Oiko
<i>Calanus glacialis</i>	CGlaNeoC
<i>Neocalanus plumchrus</i>	NeoP
<i>Limacina helicina</i>	LimH
<i>Eucalanus bungii</i>	EucB
<i>Pareuchaeta japonica</i>	ParJ
<i>Neocalanus cristatus</i>	CGlaNeoC
<i>Themisto pacifica</i>	TheP
<i>Beroe cucumis</i>	Bero
<i>Clione limacina</i>	CliL
<i>Parasagitta elegans</i>	SagE
<i>Mysidacea</i>	Mysid
<i>Thysanoessa raschii</i>	ThInRas
<i>Euphausia pacifica</i>	EupP
<i>Thysanoessa inermis</i>	ThInRas
<i>Thysanoessa longipes</i>	ThyL
<i>Themisto libellula</i>	TheL

Clusters shown had constraints from  $\delta C^{13}$ ,  $\delta N^{15}$   
Some other species were also included.

## Decapoda

Species	cluster
<i>Paralithodes camtschatica</i>	Paralith
<i>Paralithodes platypus</i>	Paralith
<i>Eualus macilentus</i>	EuMacil
<i>Lithodes aequispina</i>	LAequis
<i>Chionoecetes angulatus</i>	ChAngul
<i>Pandalopsis longirostris</i>	Pandalop
<i>Pandalopsis ochotensis</i>	Pandalop
<i>Pandalus borealis</i>	PBorGon
<i>Pandalus goniurus</i>	PBorGon
<i>Chionoecetes bairdi</i>	ChionBO
<i>Chionoecetes opilio</i>	ChionBO
<i>Argis ochotensis</i>	PHypArO
<i>Pandalus hypsinotus</i>	PHypArO

Benthos species in many cases were already grouped in publications, so we had to assign  $\delta C^{13}$ ,  $\delta N^{15}$  and individual weight as mean weighted averages from the most abundant species

Taxon	Code
<i>Actiniaria</i>	Actin
<i>Gastropoda</i>	Gastro
<i>Echinoidea</i>	Echin
<i>Polychaeta</i>	Polych
<i>Cirripedia</i>	Cirrip
<i>Bivalvia</i>	Bivalv
<i>Holothuroidea</i>	Holot
<i>Isopoda</i>	Isopod
<i>Nemertea</i>	Nemer
<i>Ophiuroidea</i>	Ophiur
<i>Gammaridea</i>	Gamm
various benthos	varBenth

After several attempts to include marine mammals and birds at the level of species we came to the conclusion that it was not possible to optimize such complex system.

Finally, we included them only as a groups of:

1. Whales
2. Whale killer (WhKiller)
3. Seals
4. Fulmarus (Fulmar)
5. and other various birds (etcBirds)



# Why it was so important to define constraints on the flows of carbon?

flows  $\uparrow$

biomasses  $\nearrow$

$$\mathbf{Ax} \approx \mathbf{b}$$

parsimonious solution

$$\sum_i x_i^2 \longrightarrow 0$$

$$\mathbf{Gx} \geq \mathbf{h}$$

$$\sum_i x_{i \rightarrow j} (\delta N_i^{15} - \delta N_j^{15}) = -TEF_j \sum_i x_{i \rightarrow j}$$

2<sup>nd</sup> massbalance

$$Residual_{norm} = (\mathbf{Ax} - \mathbf{b})^T (\mathbf{Ax} - \mathbf{b}) + (\mathbf{Gx} - \mathbf{h})^T \Gamma (\mathbf{Gx} - \mathbf{h})$$

In other words any deviation from the point estimate increase the error. When we use limits then deviations increase error only when they occur after crossing the boundaries.

At the same time the wider limits are the lesser chance we have to find the solution (or we can find so many of them equal that the process of optimizing the parameters becomes useless)



Examples and basic theory are in:

Van Oevelen, D., Soetaert, K., Middelburg, J.J., Herman, P.M.J., Moodley, L., Hamels, I., Moens, T., Heip, C.H.R., **2006**.

*Carbon flows through a benthic food web: Integrating biomass, isotope and tracer data.*

// J. Mar. Res. 64, 453–482.

Kones, J.K., Soetaert, K., van Oevelen, D., Owino, J.O., Mavuti, K., **2006**.

*Gaining insight into food webs reconstructed by the inverse method.*

// J. Mar. Syst. 60, 153–166.

Van Oevelen, D., Meersche, K., Meysman, F.J.R., Soetaert, K., Middelburg, J.J., Vézina, A.F., **2009**.

*Quantifying Food Web Flows Using Linear Inverse Models.*

// Ecosystems 13, 32–45.

### 3 Peculiarities of this work consist of:

1) We allowed the **b** parameters to vary during the two-step minimization procedure

- 1) Started from the **b** parameters provided by TINRO experts (parsimonious solution was not found)
- 2) Generated parents and limits for **b** and started Genetic Optimization Using Derivatives to minimize residual normality, so only constraints on respiration, defecation, consumption, assimilation and shifts in trophic positions through fractionation of  $\delta N^{15}$  were fixed

The multi processor routine successfully finished using:

Walter, R.M.J., Sekhon, J.S., 2011. Genetic Optimization Using Derivatives: The **rgenoud** Package for R. J. Stat. Softw. 42, 1–26.

## LETTER

## Rescaling the trophic structure of marine food webs

## Abstract

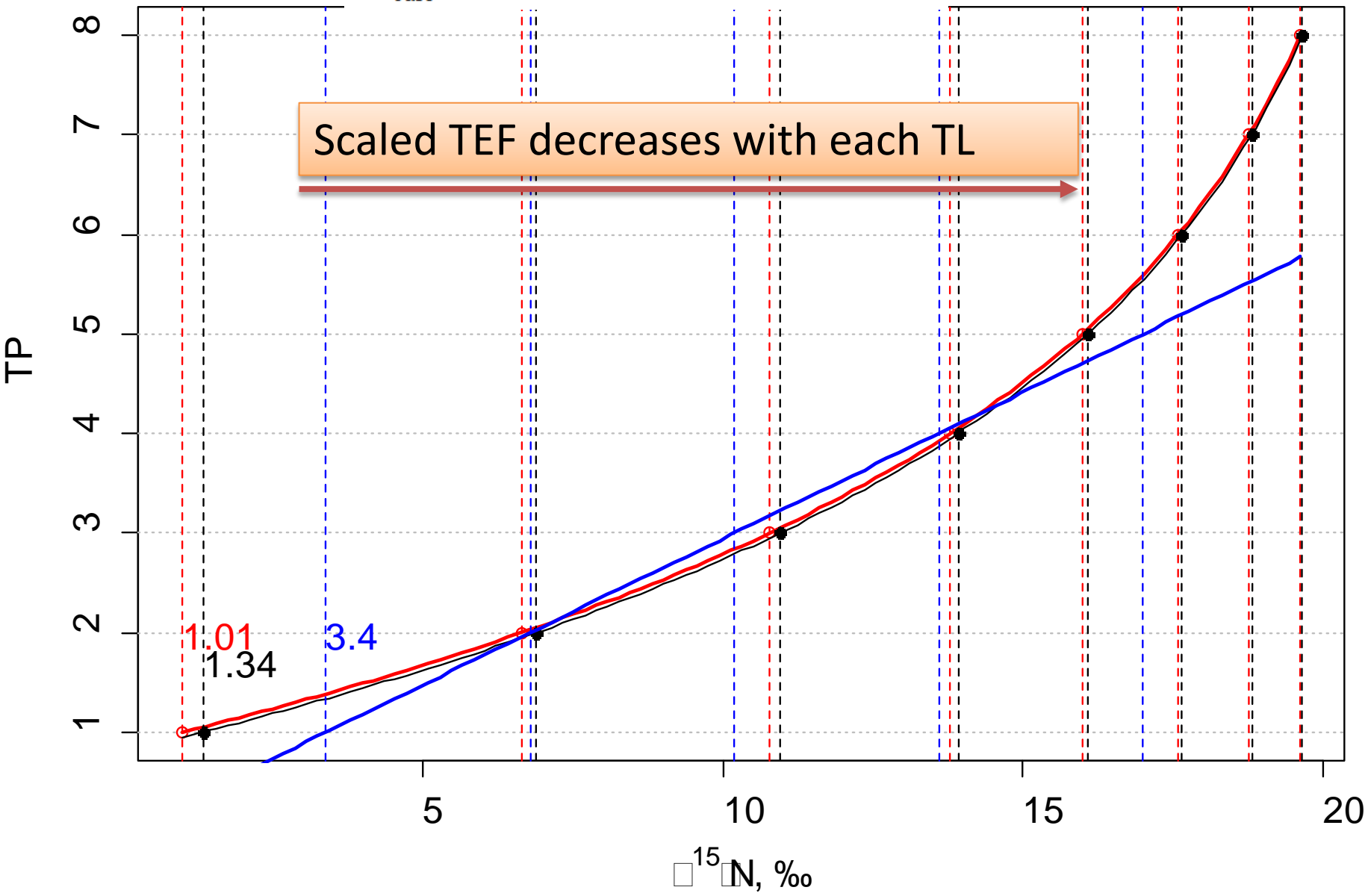
Measures of trophic position (TP) are critical for understanding food web interactions and human-mediated ecosystem disturbance. Nitrogen stable isotopes ( $\delta^{15}\text{N}$ ) provide a powerful tool to estimate TP but are limited by a pragmatic assumption that isotope discrimination is constant (change in  $\delta^{15}\text{N}$  between predator and prey,  $\Delta^{15}\text{N} = 3.4\text{‰}$ ), resulting in an additive framework that omits known  $\Delta^{15}\text{N}$  variation. Through meta-analysis, we determine narrowing discrimination from an empirical linear relationship between experimental  $\Delta^{15}\text{N}$  and  $\delta^{15}\text{N}$  values of prey consumed. The resulting scaled  $\Delta^{15}\text{N}$  framework estimated reliable TPs of zooplanktivores to tertiary piscivores congruent with known feeding relationships that radically alters the conventional structure of marine food webs. Apex predator TP estimates were markedly higher than currently assumed by whole-ecosystem models, indicating perceived food webs have been truncated and species-interactions over simplified. The scaled  $\Delta^{15}\text{N}$  framework will greatly improve the accuracy of trophic estimates widely used in ecosystem-based management.

$$TP = \frac{\log(\delta N_{\text{lim}}^{15} - \delta N_{\text{base}}^{15}) - \log(\delta N_{\text{lim}}^{15} - \delta N_{TP}^{15})}{k} + TP_{\text{base}}$$

where  $\delta N_{\text{lim}}^{15}$  and  $k$  are factors derived by meta-analysis results (Hussey et al., 2014) and equal to 21.9 and 0.315 respectively,  $\delta N_{\text{base}}^{15} - \delta N^{15}$  ratio for the species taken as the base of the food chain,  $TP_{\text{base}}$  – trophic level of the species taken as the base of the food chain,  $\delta N_{TP}^{15} - \delta N^{15}$  ratio for the species whose trophic position ( $TP$ ) is being determined.

2) We used different TEF for each component

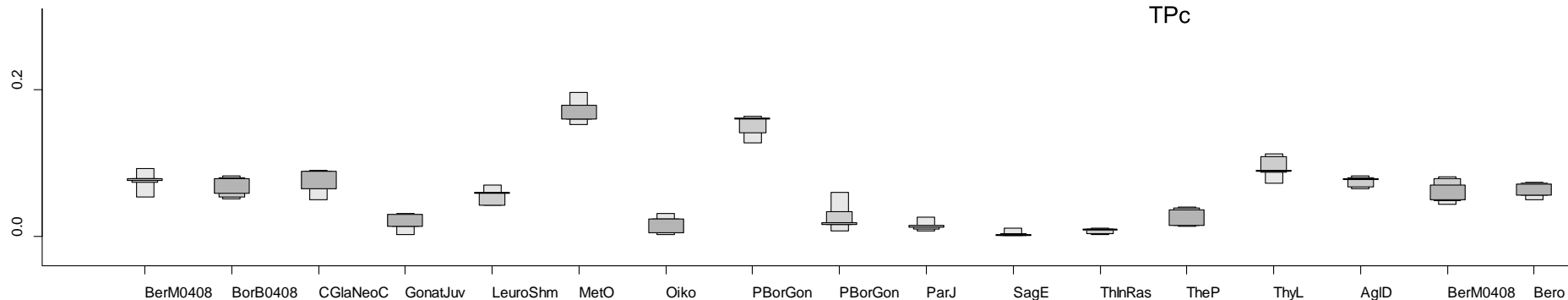
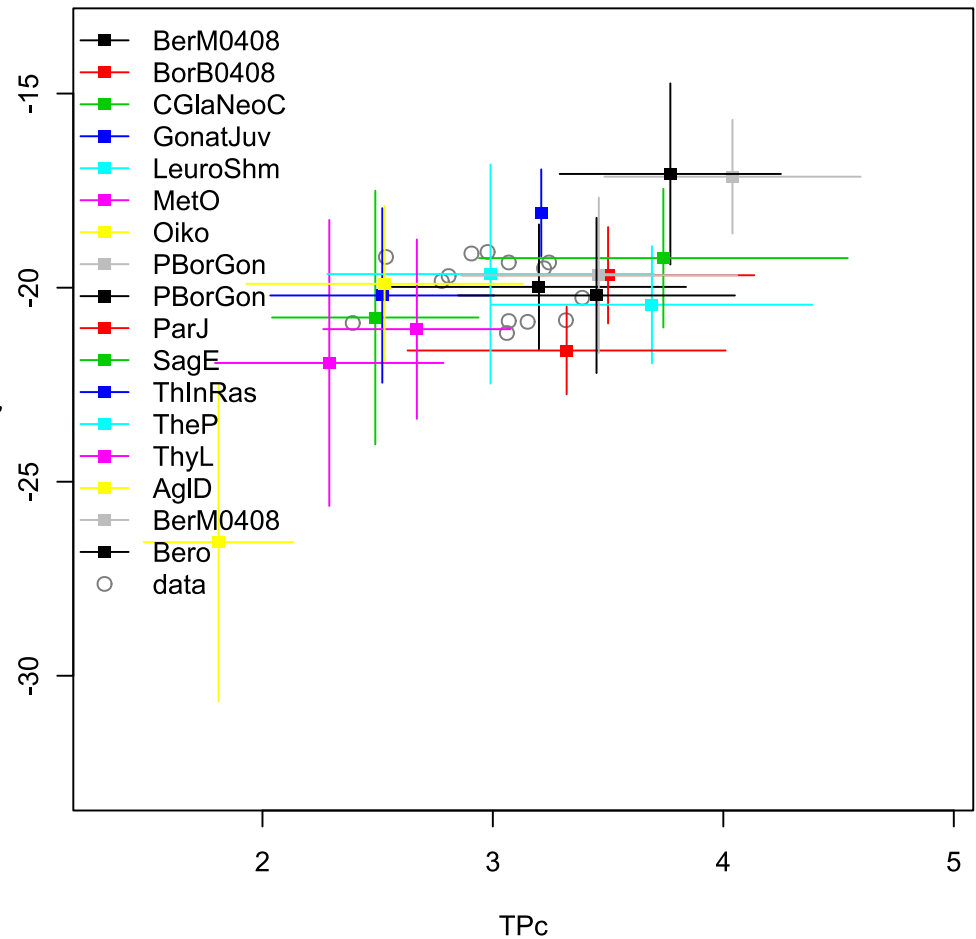
Scaled trophic positions starting from benthos (red lines)  
and plankton (black lines)  
relative to constant  $TEF = 3.4\text{‰}$  (blue lines)  
with an average base  $\delta N_{base}^{15} = 6.8\text{‰}$  for second level of  $TP$



2) We used food ratios not as point estimates, but as limits (IQR) defined from SIAR

**Parnell, A.C., Inger, R., Bearhop, S., Jackson, A.L., 2010.**  
*Source partitioning using stable isotopes: coping with too much variation.*  
 // PLoS One V.5, No3, 1-5.

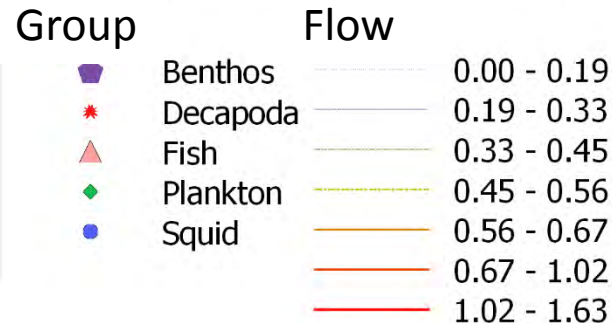
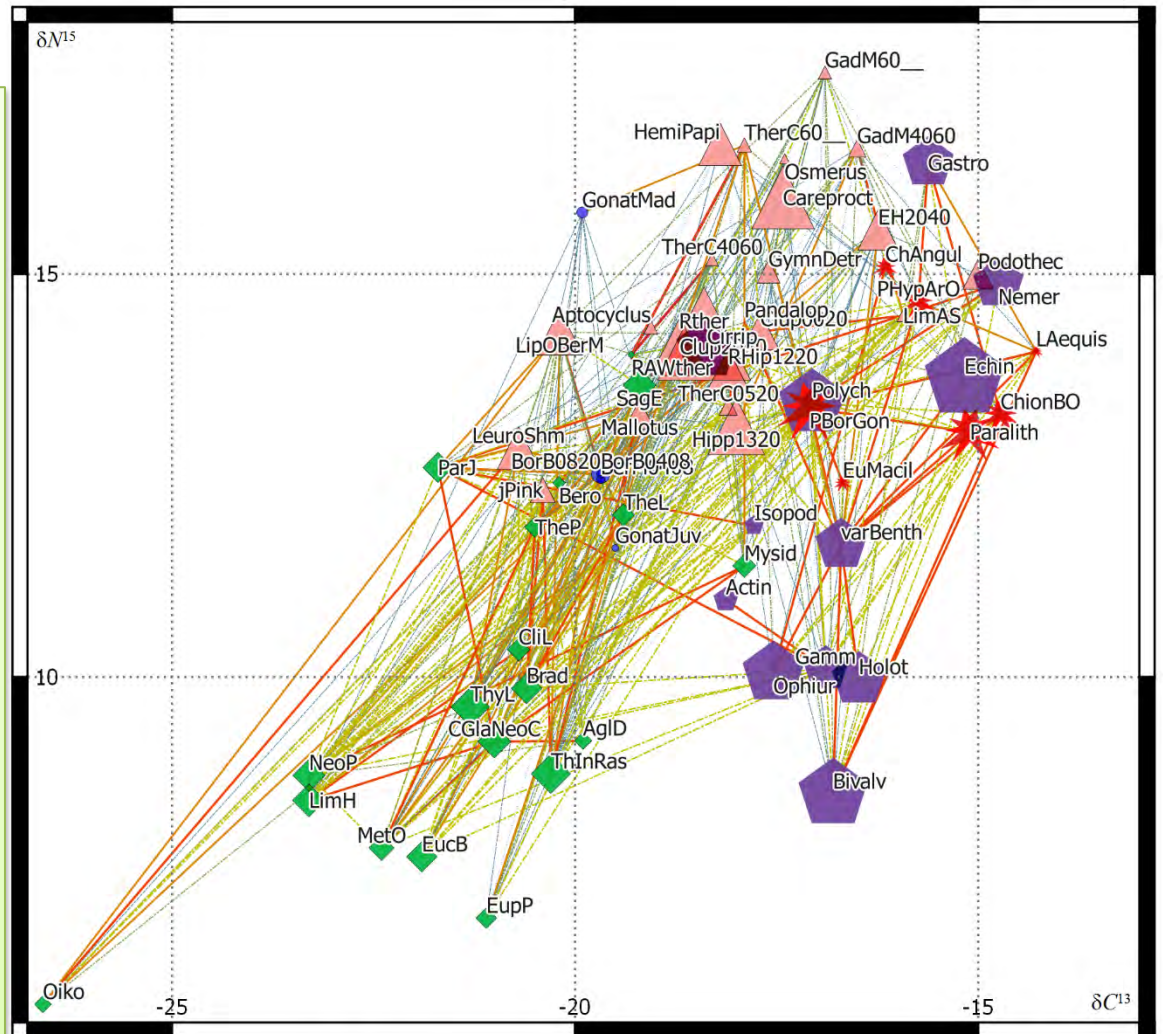
Example of calculating ratio constraints from isotopic composition of food items and consumer (LipOBerM)



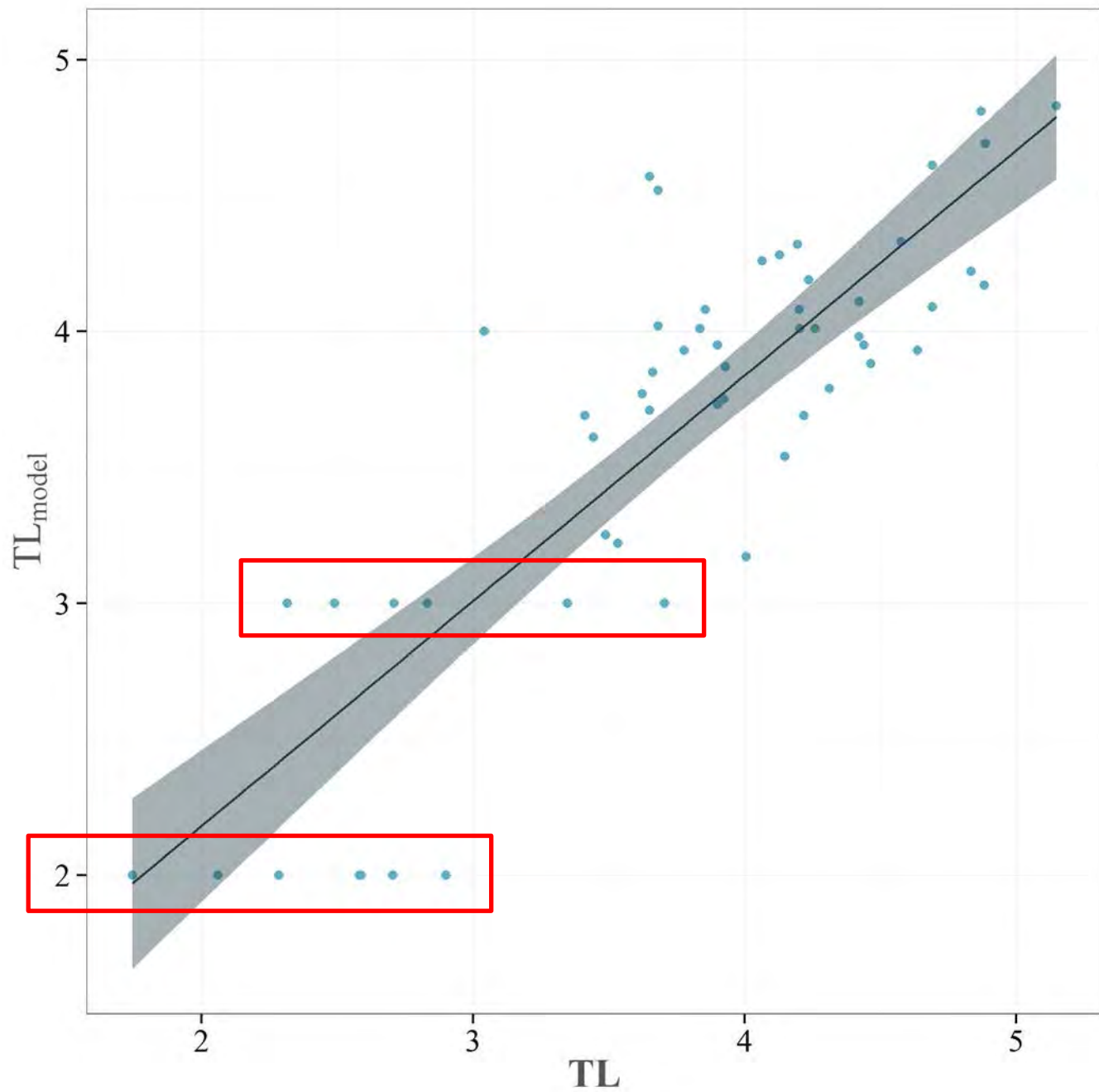
The solution at minimum of residual normality for the selected components, which were solved **exactly**, but the total balance was far from 0.

Other components are not shown. Because their exact solution was not required.

Though we got the solution with the tolerance of  $10^{-6}$  for the whole system without requirement of exact solution for plankton, fish, squid and some benthos. But in that case there were several unrealistic inverted flows (like fish eaten by plankton)

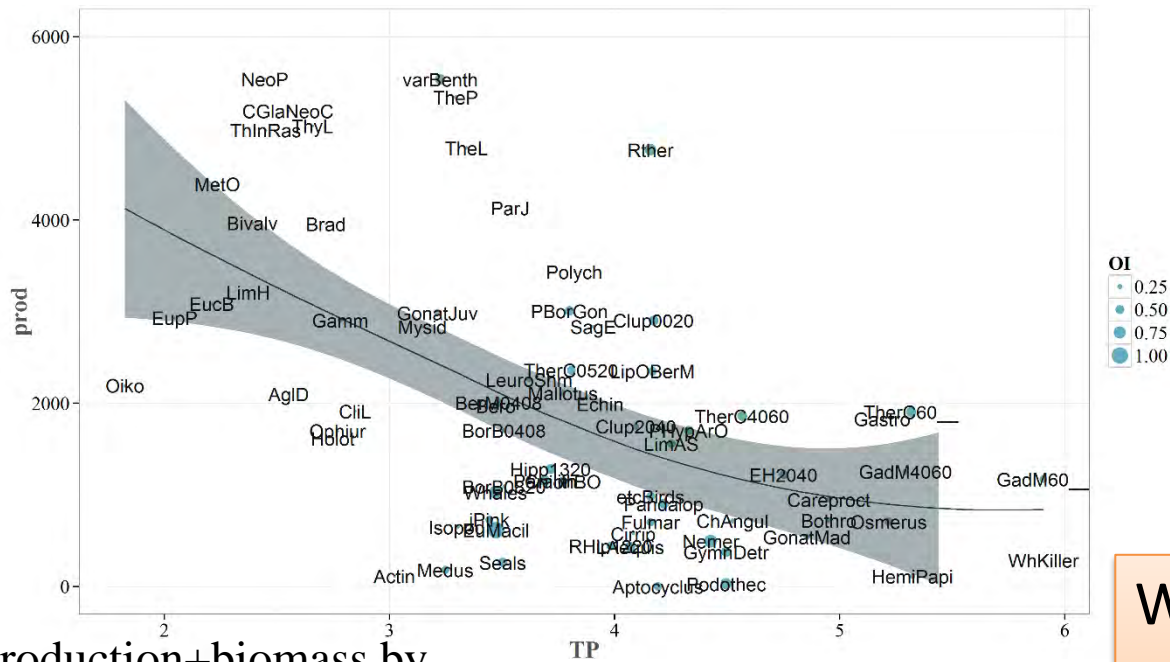




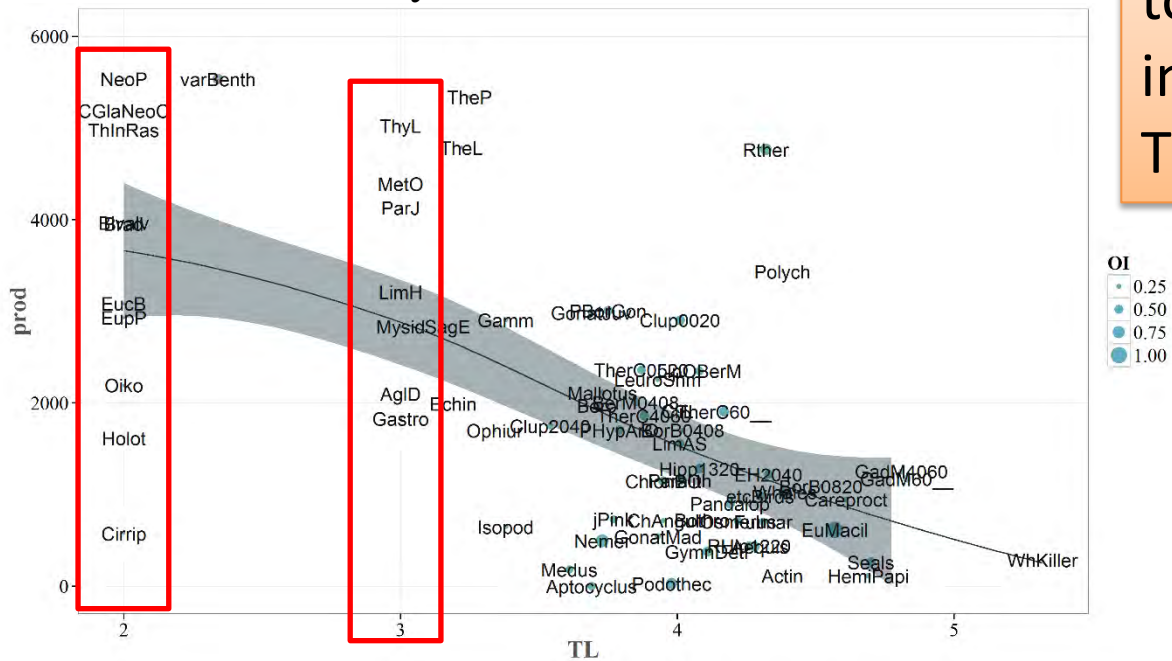


Estimates obtained instrumentally (TL) vs. Obtained from LIM (TL<sub>model</sub>)





Distribution of production+biomass by



We preferred to use TP instead of TLmodel

EcoTroph uses trophic spectra to represent marine ecosystems, leaving aside the notion of species and modelling the functioning of marine ecosystems as flows of biomass from low to high trophic levels. The model can be used as a standalone application, especially in data poor environments, or, taking as input the outputs of other models such as Ecopath with Ecosim.

# ICES Journal of Marine Science



ICES International Council for  
the Exploration of the Sea  
CIEM Comisión Internacional para  
l'Exploración de la Mar

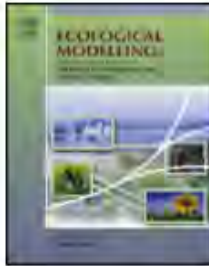
ICES Journal of Marine Science (2013), 70(3), 498–510. doi:10.1093/icesjms/fst016

## **EcoTroph: a simple model to assess fishery interactions and their impacts on ecosystems**

Loïc Gasche<sup>1</sup> and Didier Gascuel<sup>2\*</sup>

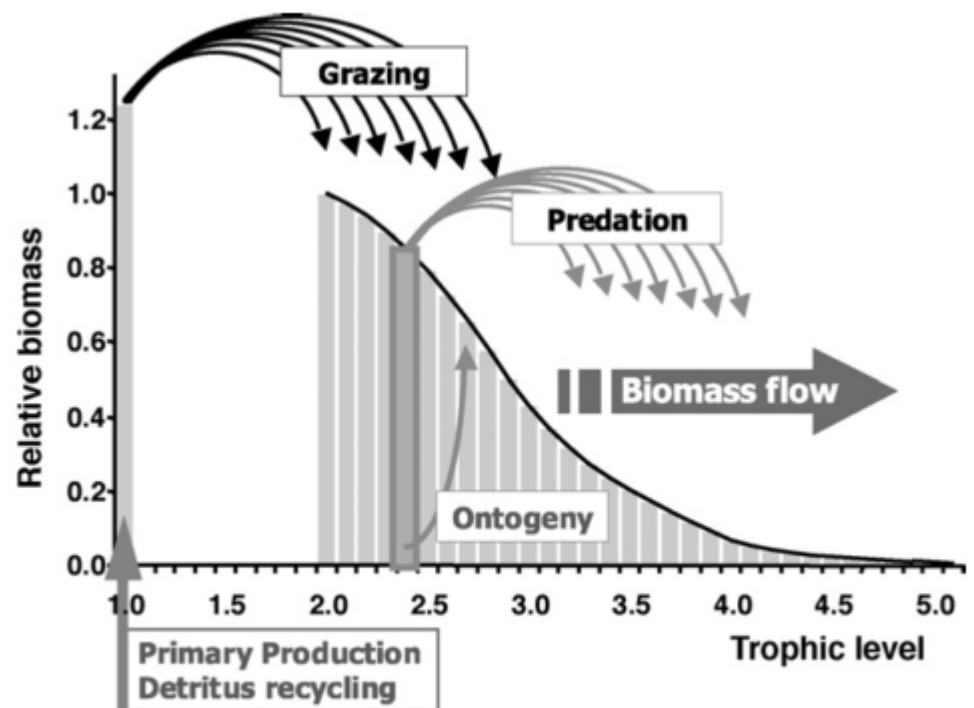
<sup>1</sup>IFREMER centre Atlantique, Unité EMH, rue de l'île d'Yeu, BP 21105, 44311 Nantes cedex 03, France

<sup>2</sup>Université Européenne de Bretagne, UMR 985 Agrocampus Ouest/INRA Ecologie et Santé des Ecosystèmes, 65 rue de Saint-Brieuc, CS 84215, 35042 Rennes cedex, France

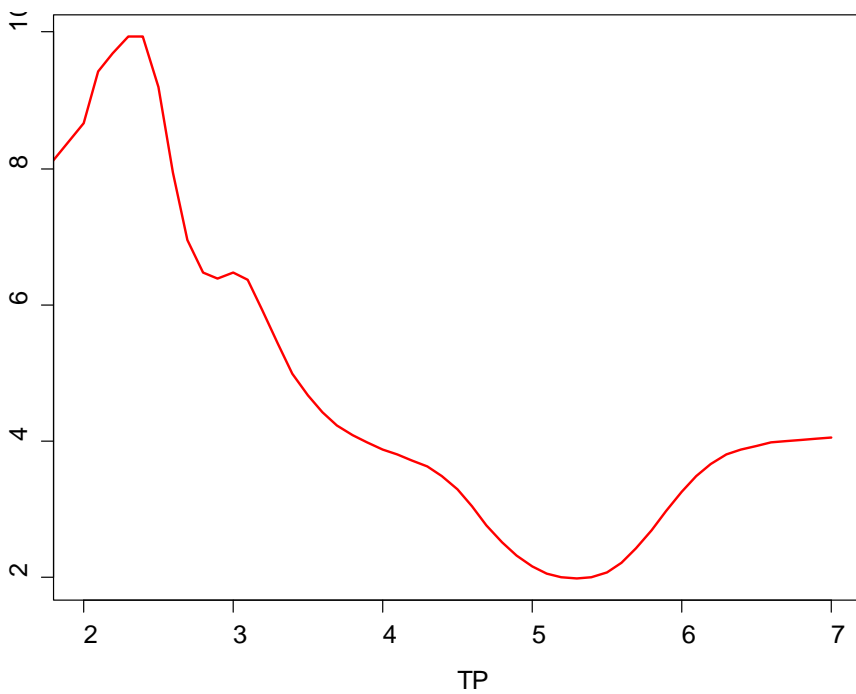
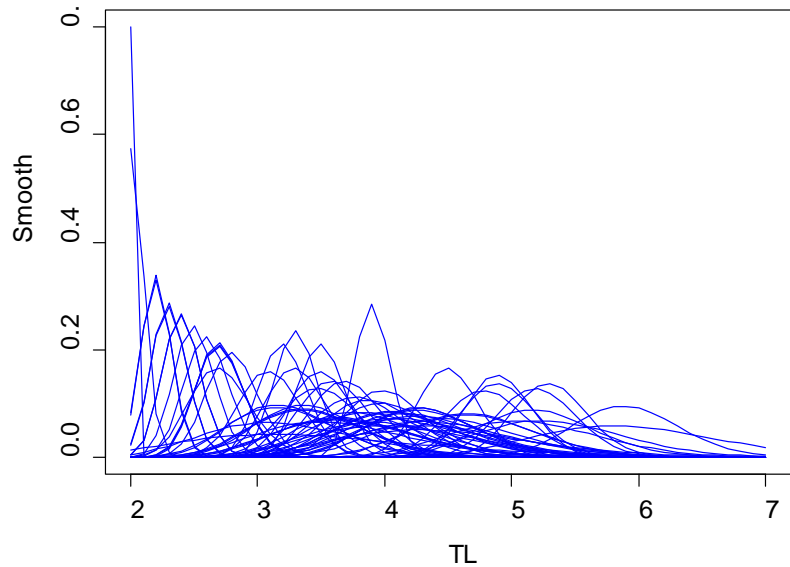


## EcoTroph: Modelling marine ecosystem functioning and impact of fishing

Didier Gascuel<sup>a,\*</sup>, Daniel Pauly<sup>b</sup>



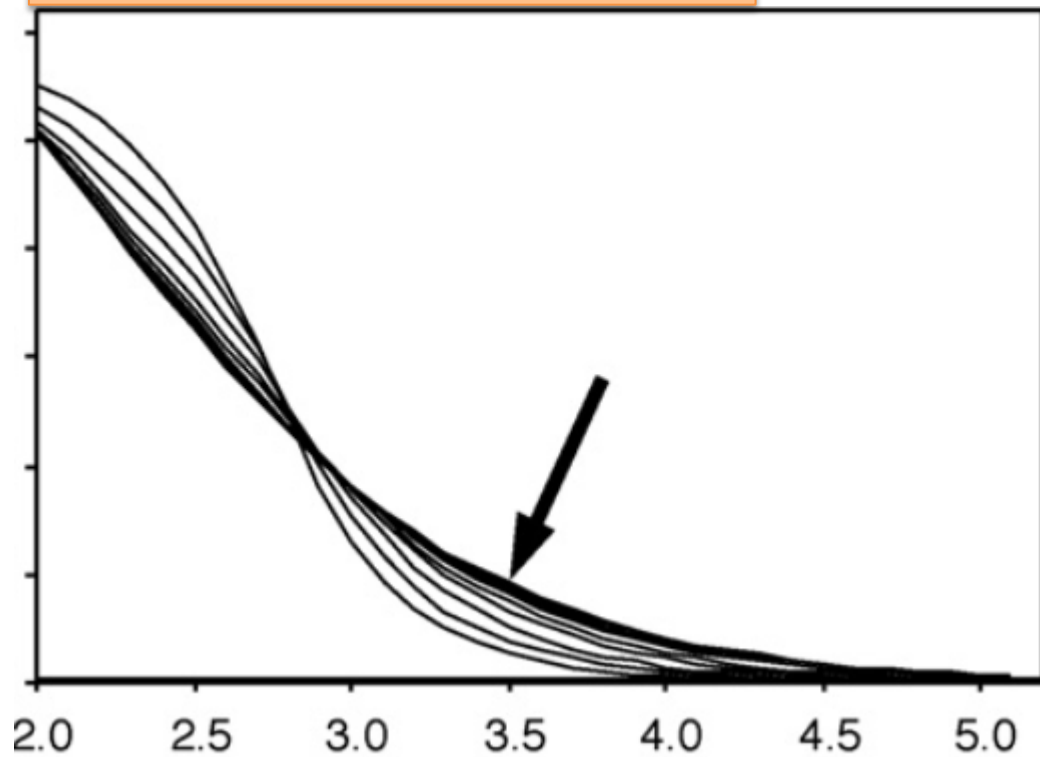
**Fig. 1.** Diagram of the trophic functioning of an ecosystem: theoretical distribution of the biomass by trophic level and trophic transfers processes, given an arbitrary input of biomass (fixed equal to 1 for TL = 2).



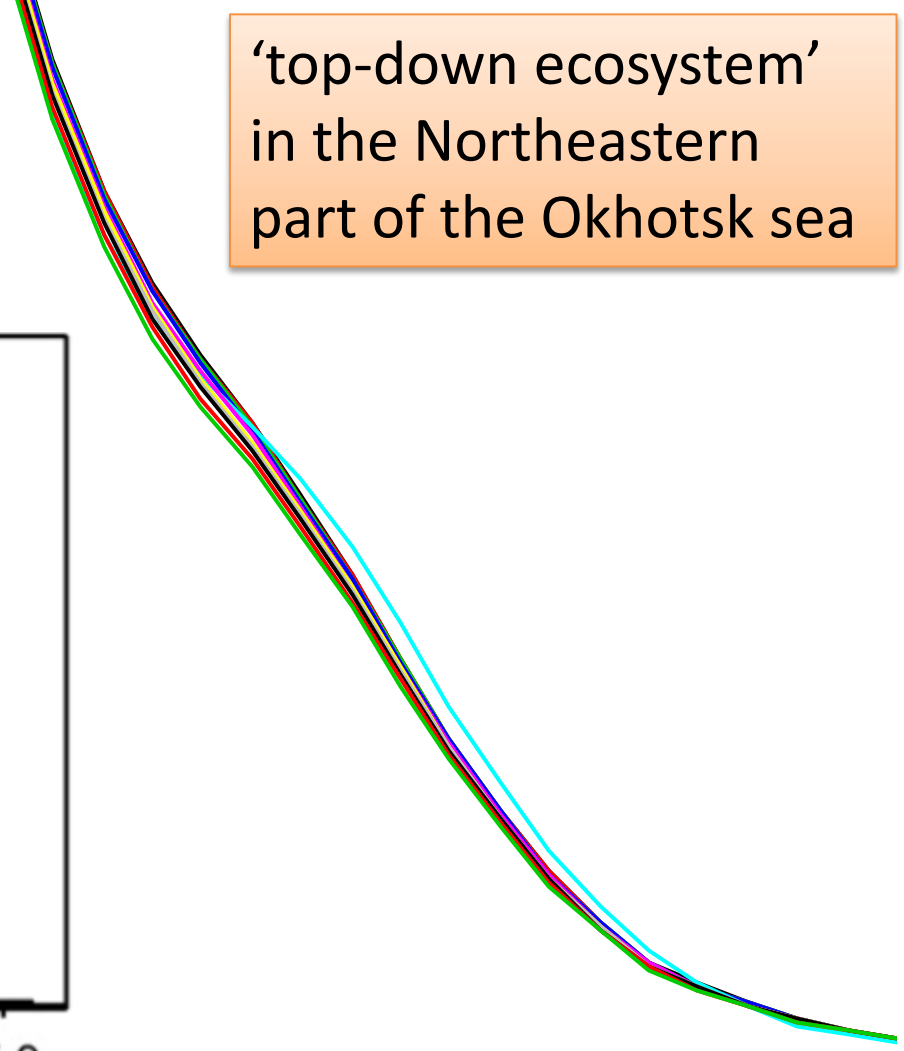
An unexpected rise in the biomass turnover dynamic is observed at the highest trophic levels which may be explained only by summer migrations to the Sea of Okhotsk of large numbers of killer whales who continue building up their biomass in the cold season in areas other than the Sea of Okhotsk. Therefore, this accelerated flow of biomass at levels 6 and 7 during a quarter of period is explained by biomass inflow from outside rather than its high production rates.



More clear example of  
'top-down ecosystem'



'top-down ecosystem'  
in the Northeastern  
part of the Okhotsk sea



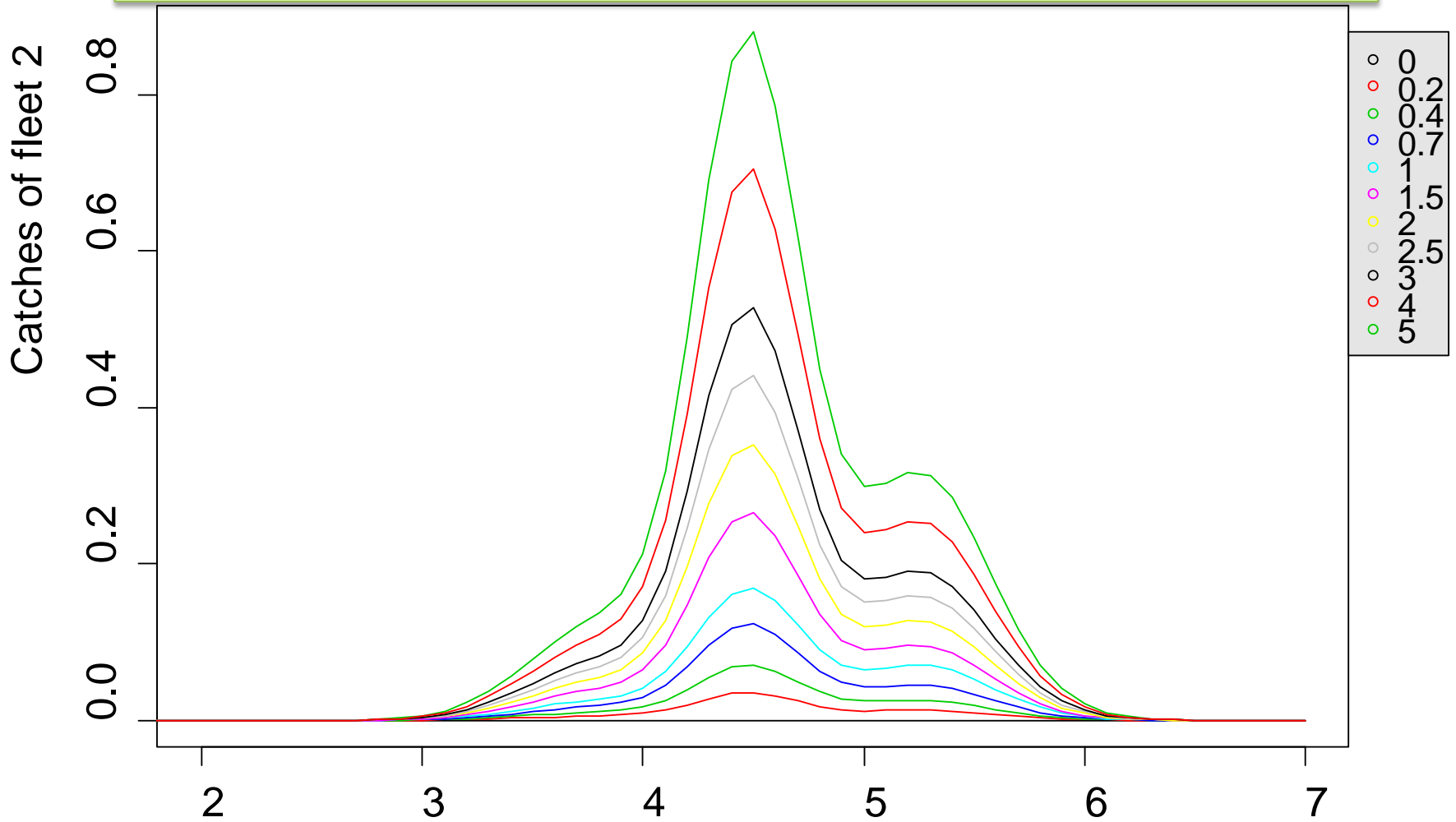
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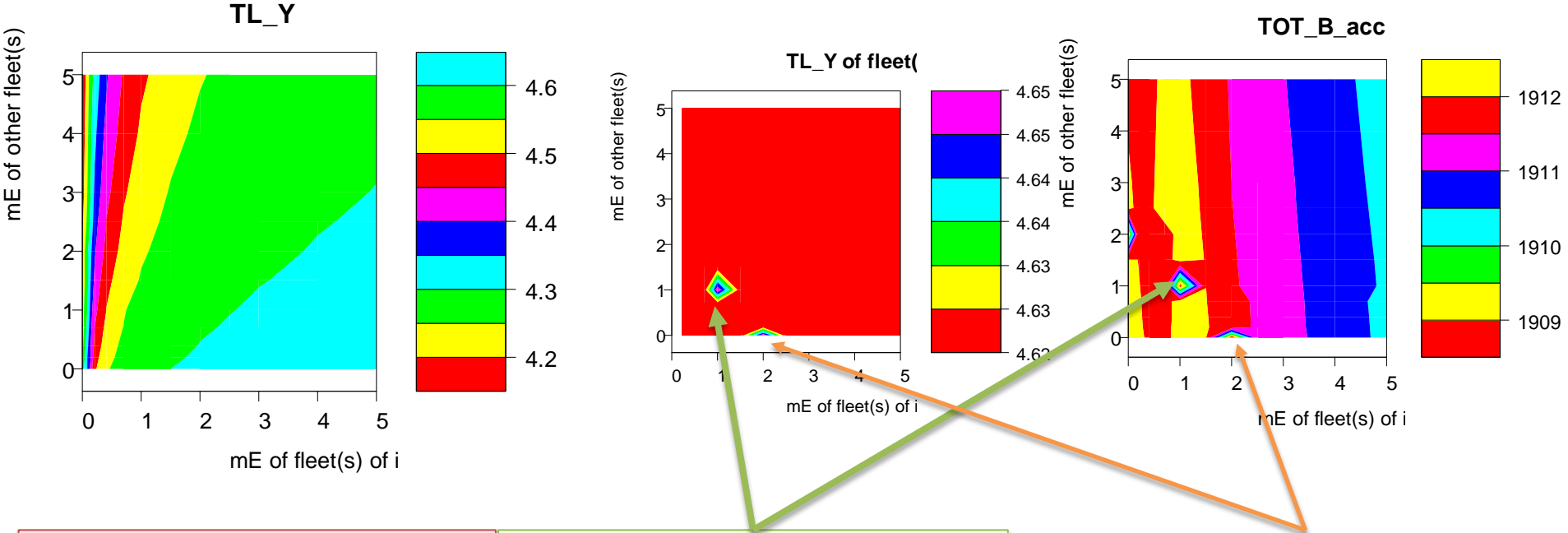
TL

# If catches of Fleet 2 included walleye pollock only



If efforts become increased for the second fleet specialized in pollock fishing, we can see that growth of large-size pollock catches (at higher trophic positions) noticeably lags behind growth of small pollock catches

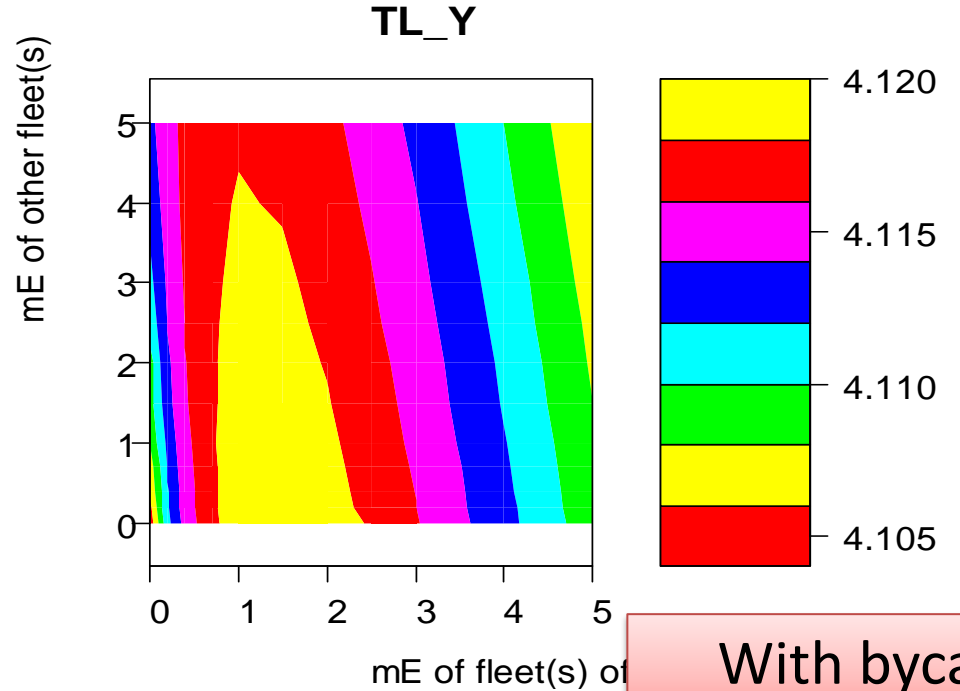




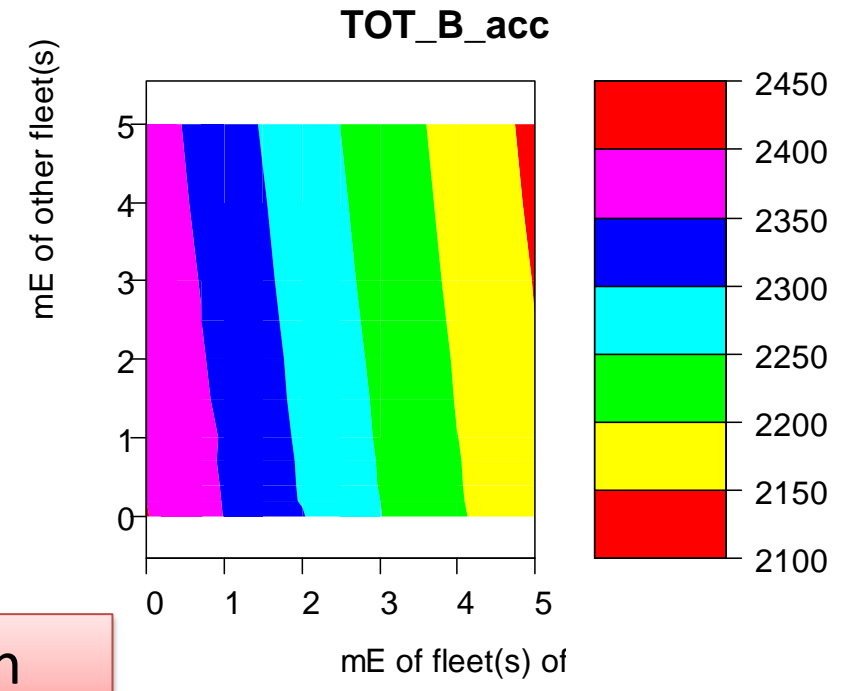
Synergistic effects of two fleets on the TL: fleet 1 (Y axis) – all other catches, fleet 2 (X axis) – fishery of walleye pollock

Pollock catches based on multi-year means (641 kilotons) without effort variation are optimal for biomass accumulation.

Another optimum is found in case of a double increase of pollock catches but with other fisheries completely stopped.



With bycatch



In general, TL variation due to pollock catches was found in very narrow limits – from 4.625 to 4.655 without bycatch, and with unofficial bycatch in fleet 2, the range of TL in the second fleet’s catches becomes lower and narrower (from 4.105 to 4.120).

After inclusion of species by-caught in the course of the target pollock fishery, we could not single out any (other than 0 efforts) points of biomass accumulation optimum because drop of total biomass is almost linearly inversely related to efforts.

In general, efficiency of biomass accumulation **and TP** in catches declines already after 2- or 3-fold increase of pollock catch regardless of catches of other species but only 5-fold increase of pollock catch can influence biomass distribution at all considered trophic levels. This conclusion is confirmed both by results of EcoTroph analysis based on expert judgments of biomass and production and by modeling results computed in LIM.

Therefore the goal of maximizing biomass and TP of walleye pollock catches is more strict and sensitive than the goal of keeping the mean TP of the observed levels of ecosystem from significant decreasing.

It should be noted that various commercial capture scenarios were tested in conditions of a climax mean multi-year ecosystem of the northeastern part of the Sea of Okhotsk in 2000s.

However, even during such short interval of time, considerable differences were observed both in indices and structure of the communities which were most likely related to changes in habitat conditions rather than to pollock catches.

## Special thanks to experts from TINRO-Center

- **Konstantin M. Gorbatenko** who managed the collection of stable isotope ratios of nitrogen, share of bio-carbon in the dry weight and share of water in the wet weight,
- **Anatoly F. Volkov** who made the estimates of zooplankton for the epipelagic layer (0-200 m) which were used further for the proportional estimation of the total zooplankton abundance (to include deeper layers down to the bottom) accordingly to the ratios obtained by Gorbatenko in the plankton surveys (down to 1 km depth),
- **Artem E. Lazshentsev** who calculated the mean ratios of food items by different size groups of every species (which then were used as the a priori points for SIAR),
- **Alexander V. Zavolokin** who calculated the average abundance of salmon and jellyfish species during the whole year in the area of research,
- **Victor A. Nadtochy** who provided estimates of abundance of benthos species as taxon groups,
- **Valeriy N. Koblikov** who Calculated the average abundance of big decapoda species,
- **Vyacheslav P. Shuntov** who made invaluable advice on the role of birds and marine mammals in the Northeastern part of the Okhotsk Sea

**Thank you for the attention!**



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