

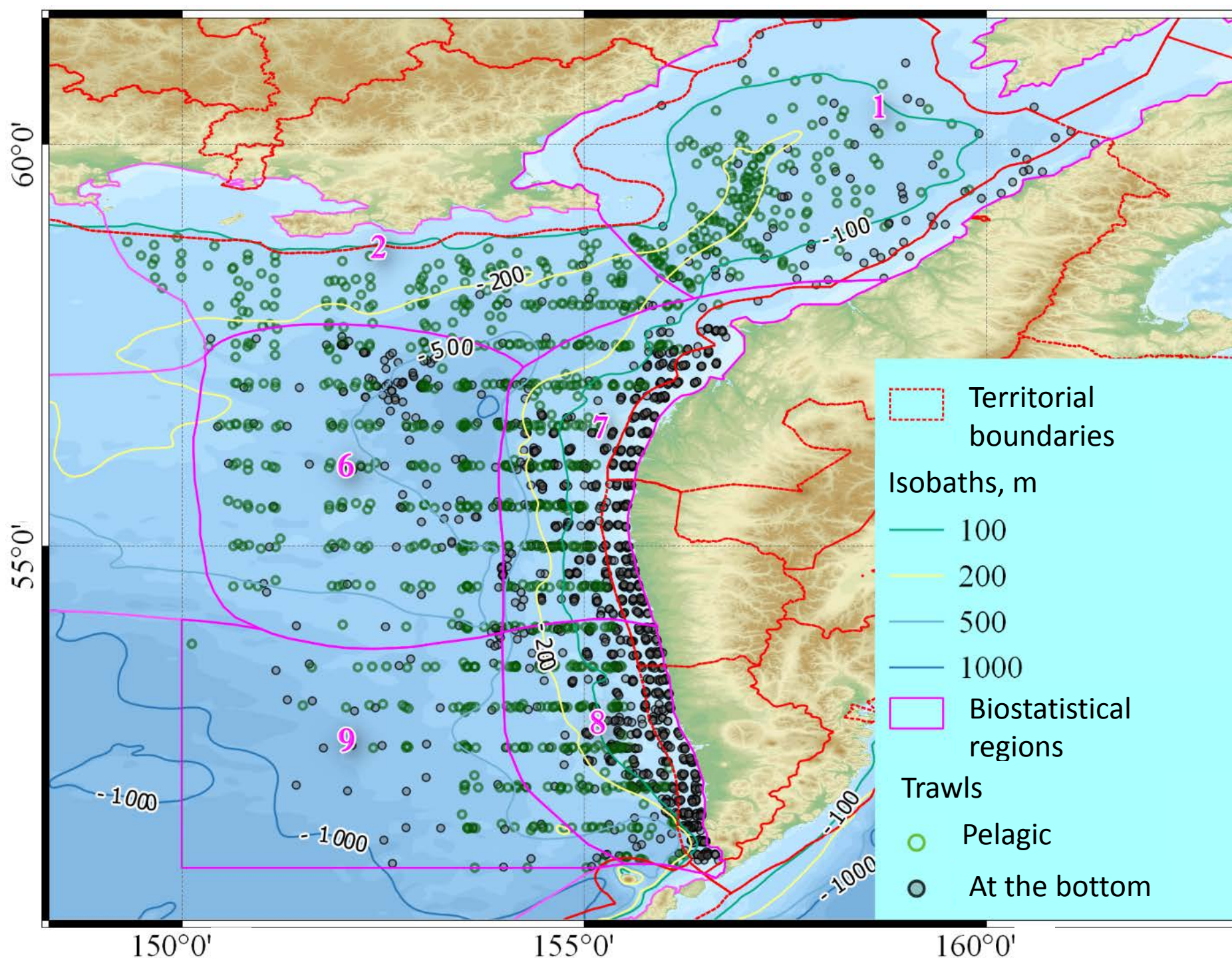


Carbon flows through
Gadidae species
in the ecosystem
of the Northeastern part
of the Sea of Okhotsk
estimated in a carbon flow
mass balance model

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- **Konstantin M. Gorbatenko** 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.
- **Vladimir V. Kulik** corrected the estimates of zooplankton made by **Anatoly F. Volkov** for the epipelagic layer (0-200 m) to include deeper layers down to the bottom, calculated the average annual abundance of macrofauna species and tuned LIM.
- **Artem E. Lazshentsev** calculated mean ratios of food items by different size groups of every species (which then were used as the starting points to make the possible limits),
- **Alexander V. Zavolokin** calculated the average abundance of salmon and jellyfish species
- **Victor A. Nadtochy** provided estimates of abundance of benthos species as taxon groups
- **Valeriy N. Koblikov** Calculated the average abundance of big decapoda species

Position
of trawling
stations



Dominant species or higher taxons included in the foodweb:

Euphausiacea: *Euphausia pacifica*, *Thysanoessa inermis*, *Thysanoessa longipes* and *Thysanoessa raschii* ;

Mysidacea ;

Amphipoda: *Themisto libellula* and *Themisto pacifica* ;

Copepoda: *Calanus glacialis*, *Eucalanus bungii*, *Metridia okhotensis*, *Neocalanus cristatus*, *Neocalanus plumchrus*, *Bradyidius pacificus* and *Pareuchaeta japonica* ;

Chaetognatha: *Sagitta elegans* ;

Pteropoda: *Clione limacine* and *Limacina helicina* ;

Oikopleura ;

Coelenterata: *11 species* ;

+ 1 macrophyte component (from 8 sps.) ;

+ 26 benthic taxon groups ;

+ 13 decapoda species ;

+ 46 fish species and their size groups ;

+ 4 groups of birds ;

+ 5 seal species ;

+ 7 whale species ;

+ 2 fisheries blocks + 1 block to represent wastes from processing of the catches

+ base blocks, export block etc.

Initial total sum of components with seasonal differentiation was equal to 166.

Methods

For each fish and squid species and its size group abundance was estimated as follows
(below is the part of a loop in R language with loaded `mgcv` library)

```
# At First the GAM model was optimized for each member of the collection in the "sp" data.frame:

if (length(unique(sp$years)) > 4) {
  formula1 <- kgkm2 ~ s(X, Y, k=50) + s(Ln_Htr, k=4) + s(Y2k, k=4)
  selpred <- dtpred}

if (length(unique(sp$years)) %in% 2:4){
  formula1 <- kgkm2 ~ s(X, Y, k=50) + s(Ln_Htr, k=4) + charyears
  selpred <- droplevels(subset(dtpred, charyears %in% levels(sp$charyears))) }

if (length(unique(sp$years)) == 1) {
  formula1 <- kgkm2 ~ s(X, Y, k=20) + s(Ln_Htr, k=4)
  selpred <- droplevels(subset(dtpred, charyears %in% levels(sp$charyears))) }

sp.tw1 <- gam(formula1, family = tw(theta = -1.5, a=1.1, b=1.9), data = sp)

# Then each model was used to predict abundance on the grid with centers on 10km*10km mesh,
# from 25 m depth down the bottom with 25m step for 10 years. Finally those values were
# averaged and converted into mmol C per square m.
```

All the rest of the methods of estimating abundance were traditional for our specialists (at TINRO-Centre) and thus many times published (basically its arithmetic mean of kg per sq. km multiplied on the area of the bioregion, except Decapoda sps.)

It was useful to solve not only the default mass balance, but also an additional mass balances based e.g. on stable isotope data.

See e.g. where isotope mixing model succeeded in reducing the uncertainty of the food web model solution:

van Oevelen, D., Soetaert, K., Middelburg, J., Herman, P., Moodley, L., Hamels, I., Moens, T., Heip, C.,

“Carbon flows through a benthic food web: integrating biomass, isotope and tracer data”

2006. Journal of Marine Research 64, 453–482

Basic form of carbon flow.

$$\frac{dC_i}{dt} = \sum_{j=1}^n F_{j \rightarrow i} - \sum_{j=1}^n F_{i \rightarrow j} - \text{Feces}_i - \text{Resp}_i$$

Verbally, a **linear mixing model** (used by van Oevelen et. al.) assumes that the isotope value of a consumer is a flow-weighted average of its resources.

Mathematically this is represented by:

$$X_j = \frac{\sum_i F_{i \rightarrow j} (X_i + \Delta_j)}{\sum_i F_{i \rightarrow j}} \quad (9)$$

in which X_j is the isotope composition of the consumer, $F_{i \rightarrow j}$ is the flow from resource i to consumer j and Δ_j is trophic fractionation (e.g. ^{15}N fractionates with **3.4‰** per trophic level).

From the **LIM** documentation:

We can rewrite equation 9 as

$$\sum_i F_{i \rightarrow j} (X_i - X_j) = -\Delta_j \sum_i F_{i \rightarrow j} \quad (10)$$

in which the left-hand side of the equation is the mass balance of the isotope and the right-hand side accounts for trophic fractionation processes.

The **LIM** package (for **R** language) offers a simplification for the input file (with the help of `### MARKER` section and `Massbalance` function).

Thus instead of writing many lines of code for only one equation you can use e.g.:

```
Massbalance(TherC60___) = -flowto(TherC60___)*FracN
```


The heading of the input file for the setup of LIM

```
Units      :      Fluxes:      mmol C/m2/d
              Standing stocks:  mmol C/m2
#####
```

```
## PARAMETERS
```

```
! Minagawa and Wada 1988, trophic fractionation
FracN          = 3.4      ! {%}
! Altabet, pg 168 in Particle Flux in the Ocean
FracBACT       = 1.35    ! {%} ! Bacteria
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

```
!-- General
minAE          = 0.10
maxAE          = 0.90
minPE          = 0.10
maxPE          = 0.80
!-- Bacteria
minBGE         = 0.20
maxBGE         = 0.45
```

Respiration constraints were calculated from the mean individual weight of each size group of each species.

To reduce the uncertainty of unknowns flows were also constrained by the limits, based on diet studies.

The results from the first run were disappointing

180 components for 166 equations with 3994 inequalities to find 2034 flows

names	first run
residuals	107
solution	3759
GPP	57.08
flows to gadidae	1.198
% GPP	2.1%
<i>flows to gadidae without undefined plankton sps.</i>	0.936
<i>%GPP</i>	1.6%

the sum of residuals of equalities and violated inequalities
the value of the minimised quadratic function
at the solution

The most unrealistic values were in seasonal divisions and various groups of minor plankton species aggregated together.

So, we decided to redistribute total plankton biomasses between major dominant species as if they represented 100% and not 90% and also we removed seasonal division.

Thus we decreased the number of components (parameters) and consequently the number of unknowns (flows)

Basically the foodweb with higher level of aggregation of nodes should be solvable and there are publications by the first author based on different method, where flows are calculated from the mean of food intake ratios.

Therefore, we compared what we would loose if we chose e.g. families of plankton species instead of species.

We found out that we were loosing the accuracy of trophic level determination.

Correlation between estimated trophic levels from the LIM (**without** additional massbalance on stable **isotope** of nitrogen ratios and plankton nodes at the level of species) with trophic levels from stable isotope ratios of nitrogen

correlation	std.err	t.value	p.value
0.42	0.084	5	2e-06

Correlation between estimated trophic levels from the LIM (**with** additional massbalance on stable **isotope** of nitrogen ratios and plankton nodes at the level of species) with trophic levels from stable isotope ratios of nitrogen

correlation	std.err	t.value	p.value
0.68	0.068	10	2.5e-17

Correlation between estimated trophic levels from the LIM (with additional massbalance on stable isotope of nitrogen ratios and plankton nodes at the level of **Families**) with trophic levels from stable isotope ratios of nitrogen

correlation	std.err	t.value	p.value
-0.1	0.11	-0.95	0.34

That is why we decided to work further with nodes of plankton at the level of species

New structure has less components, but the level of complexity became higher as well as solution and residuals

158 components for 131 equations with 4664 inequalities to find 2214 flows

The sum of estimated flows to Gadidae spp. stays the same even in the situation of random parameters of fish and squid biomasses. We suppose, that ratios of stable isotope of nitrogen, which constrain every 20 cm group of every fish species and every plankton species, play a very big role in determination of flows.

3 best by residuals from runif (min,max,80) biomasses.
 Fish and squid limits were between
 (trimmed mean-mad) and (mean+mad*3)
 from predicted by GAMs grids

	min	vf33	vf48	vf18	avg	max
residuals	166	163	163	163	164	175
solution	6133	6133	6133	6133	6133	6133
GPP	19.027	57.08	57.08	57.08	57.08	570.8
flows to gadidae	1.627	1.627	1.627	1.627	1.627	1.627
%GPP	8.6%	2.9%	2.9%	2.9%	2.9%	0.3%

# best trial	Va53	Va26	Va55
residuals	401.219	389.465	353.052
solution	2000	3201	3367
GPP	32.5006	41.2334	42.0708
flows to gadidae	0.88	1.175	1.116
%GPP	2.7%	2.8%	2.7%

80 **Va** trials varied biomass parameters uniformly random between Mean/3.3 and Mean*10 EXCEPT fish and squid, which limits were between (trimmed mean-mad) and (mean+mad*3) from predicted by GAMs grids

# best trial	V79	V221	V124
residuals	1034	721	690
solution	211	428	2320
GPP	10.3007	14.445	34.2919
flows to gadidae	0.245	0.326	0.829
%GPP	2.4%	2.3%	2.4%

240 **V** trials varied biomass parameters uniformly random between the same minimums as in **Va** but twice less and the same maximums as in **Va** but twice bigger.

Looking through the biomass parameters which had relatively lowest residuals (which include deviations from the constraint boundaries) we discovered that many of them have biological sense: e.g. compared to the first configuration highly underestimated was Sagitta elegans and the least changes were in Pteropoda species. This fact let us suppose that the reason was in the catchability coefficients used in the process of estimating biomasses. So, we decided to look into possible biomasses leading to decrease of residuals with the goal of diagnosing possible errors in the mean estimates of biomasses.

Therefore, we started double fitting procedure: genopt on biomass parameters and limSolve on flows.

Minimum, the best from random search

(V79, V124, V221, Va26, Va53, Va55),

mean and maximum biomass parameters were used as collection of parents

for genetic and simulated annealing optimizer

(Burns Statistics (2012). BurStMisc: Burns Statistics miscellaneous.

R package version 1.00. <http://CRAN.R-project.org/package=BurStMisc>)

This optimization procedure let us understand that seasonal differentiation was not a very good idea.

Finally, we averaged seasonally different groups upto the annual basis and their values of stable isotope ratios also.

Again we started genopt with parents from minimum, maximum and mean values of biomasses.

This time some minimum was found very quickly (after 70 births), but, unfortunately,

the foodweb stayed with the solution much bigger than 0.

After 100 of births with several dozens of random hopes we got that new flows were more than 2 times less, comparing to the average biomasses in the following edges:

fname	name	perc
MICRO->LIMH	LimHMicro	6%
POC->EXPORT	POCout	15%
THEP->RHIP1220	RHip1220TheP	19%
FORAM->PANOCH	PanOchForam	19%
THEL->HEMIPAPI	HemiPapiTheL	29%
THEP->CARR1020	CarR1020TheP	31%
LEUROSHM->SEALRING	SealRingLeuroShm	39%
GONATJUV->EUMSOLD	EumSoldGonatJuv	43%
CLUP1420->GADM60__	GadM60__Clup1420	46%
MALL0611->CARR2040	CarR2040Mall0611	47%

And we got that new flows were more than 2 times higher, comparing to the average biomasses in the following edges:

fname	name	perc
PARPLAT->FISHERIES	FisheriesParPlat	204%
POLYCH->PANOCH	PanOchPolych	209%
LIMH->JPINK	jPinkLimH	212%
LIMH->ETCBIRDS	etcBirdsLimH	302%
ISOPOD->PANLON	PanLonIsopod	361%
BORB0408->SFFULMAR	sfFulmarBorB0408	362%
ASTER->BOTN2040	BotN2040Aster	386%
GONATJUV->SFFULMAR	sfFulmarGonatJuv	616%
LAEQUIS->GADM4060	GadM4060LAequis	1676%

The conclusion

The proposed foodweb model is not operational, yet (because it did not converge to 0), but it is useful for diagnostic purposes.

It can help us to highlight possible errors in estimates of mean biomasses and due to the use of stable isotope ratio constraints it is useful for diet studies.

The first run showed that the sum of flows from defined plankton species to Gadidae species was around 1.6% from PP or 2.1% with undefined plankton species, but during optimization of biomass parameters the share was even higher.

Further work is planned to include additional constraints from stable isotope ratios of carbon.