**Supplementary material**

*Food web functions and interactions during spring and summer in the Arctic Water inflow region: Investigated through inverse modelling.*

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**Table S1.** Mass balance equations for the inverse analysis. Flow(A, B) denotes a food web flow from compartment A to B (g C m-2 d-1). Compartment abbreviations as in Table 2.

ΔPHY0/Δt = Flow(CO2, PHY0) - Flow(PHY0, DOC) - Flow(PHY0, CO2) - Flow(PHY0, DET) - Flow(PHY0, HNF) - Flow(PHY0, μZOO)

ΔPHY1/Δt = Flow(CO2, PHY1) - Flow(PHY1, DOC) - Flow(PHY1, CO2) - Flow(PHY1, DET) - Flow(PHY1, μZOO) - Flow(PHY1, ZOO1)

ΔPHY2/Δt = Flow(CO2, PHY2) - Flow(PHY2, DOC) - Flow(PHY2, CO2) - Flow(PHY2, DET) - Flow(PHY2, SED) - Flow(PHY2, μZOO) - Flow(PHY2, ZOO1) - Flow(PHY2, ZOO2)

ΔBAC/Δt = Flow(DOC, BAC) - Flow(BAC, CO2) - Flow(BAC, DET) - Flow(BAC, HNF) - Flow(BAC, μZOO)

ΔHNF/Δt = Flow(PHY0, HNF) + Flow(BAC, HNF) - Flow(HNF, CO2) - Flow(HNF, DOC) - Flow(HNF, DET) - Flow(HNF, μZOO) - Flow(HNF, ZOO1)

ΔμZOO/Δt = Flow(PHY0, μZOO) + Flow(PHY1, μZOO) + Flow(PHY2, μZOO) + Flow(HNF, μZOO) + Flow(BAC, μZOO) + Flow(DET, μZOO) - Flow(μZOO, CO2) - Flow(μZOO, DOC) - Flow(μZOO, DET) - Flow(μZOO, ZOO1) - Flow(μZOO, ZOO2)

ΔZOO1/Δt = Flow(PHY1, ZOO1) + Flow(PHY2, ZOO1) + Flow(μZOO, ZOO1) + Flow(HNF, ZOO1) + Flow(DET, ZOO1) - Flow(ZOO1, CO2) - Flow(ZOO1, DOC) - Flow(ZOO1, DET) - Flow(ZOO1, SED)

ΔZOO2/Δt = Flow(PHY2, ZOO2) + Flow(μZOO, ZOO2) + Flow(DET, ZOO2) - Flow(ZOO2, CO2) - Flow(ZOO2, DOC) - Flow(ZOO2, DET) - Flow(ZOO2, SED)

ΔDET/Δt = Flow(PHY0, DET) + Flow(PHY1, DET) + Flow(PHY2, DET) + Flow(BAC, DET) + Flow(HNF, DET) + Flow(μZOO, DET) - Flow(DET, μZOO) + Flow(ZOO1, DET) + Flow(ZOO2, DET) - Flow(DET, ZOO1) - Flow(DET, ZOO2) - Flow(DET, DOC) - Flow(DET, SED)

ΔDOC/Δt = Flow(PHY0, DOC) + Flow(PHY1, DOC) + Flow(PHY2, DOC) - Flow(DOC, BAC) + Flow(HNF, DOC) + Flow(μZOO, DOC) + Flow(ZOO1, DOC) + Flow(ZOO2, DOC) + Flow(DET, DOC)

**Table S2.** Inequalities constraints for the inverse analysis. Flow(A, B) denotes a food web flow from A to B (g C m-2 d-1), FlowTo(A) denotes the sum of flows to A (g C m-2 d-1), and A denotes the standing stock of A (g C m-2). Compartment abbreviations as in Table 2.

Detritus dissolution to DOC is between 1-10% of detritus mass.

[1] Flow(DET, DOC) < DET \* 0.1

[2] Flow(DET, DOC) > DET \* 0.01

Mass specific primary production for smaller autotrophs is larger than for the subsequent larger autotrophic compartment, but not more than two times larger.

[3] Flow(CO2, PHY1) \* PHY2 < Flow(CO2, PHY2) \* PHY1 \* 2

[4] Flow(CO2, PHY1) \* PHY2 > Flow(CO2, PHY2) \* PHY1 \* 1

[5] Flow(CO2, PHY0) \* PHY1 < Flow(CO2, PHY1) \* PHY0 \* 2

[6] Flow(CO2, PHY0) \* PHY1 > Flow(CO2, PHY1) \* PHY0 \* 1

Autotrophic respiration is between 1 and 55% of the gross primary production

[7] Flow(PO, CO2) < Flow(CO2, PHY0) \* 0.55

[8] Flow(PO, CO2) > Flow(CO2, PHY0) \* 0.01

[9] Flow(PHY1, CO2) < Flow(CO2, PHY1) \* 0.55

[10] Flow(PHY1, CO2) > Flow(CO2, PHY1) \* 0.01

[11] Flow(PHY2, CO2) < Flow(CO2, PHY2) \* 0.55

[12] Flow(PHY2, CO2) > Flow(CO2, PHY2) \* 0.01

Phytoplankton mortality is at least 1% of the biomass per day.

[13] Flow(PO, DET) < PHY0 \* 1

[14] Flow(PO, DET) > PHY0 \* 0.01

[15] Flow(PHY1, DET) < PHY1 \* 1

[16] Flow(PHY1, DET) > PHY1 \* 0.01

[17] Flow(PHY2, DET) < PHY2 \* 1

[18] Flow(PHY2, DET) > PHY2 \* 0.01

Mesozooplankton assimilation is between 40-80% of the food intake.

FlowTo(ZOO1) – Flow(ZOO1, DET) – Flow(ZOO1, DOC) – Flow(ZOO1, SED) < 0.8 \* FlowTo(ZOO1)

FlowTo(ZOO1) – Flow(ZOO1, DET) – Flow(ZOO1, DOC) – Flow(ZOO1, SED) > 0.4 \* FlowTo(ZOO1)

FlowTo(ZOO2) – Flow(ZOO2, DET) – Flow(ZOO2, DOC) – Flow(ZOO2, SED) < 0.8 \* FlowTo(ZOO2)

FlowTo(ZOO2) – Flow(ZOO2, DET) – Flow(ZOO2, DOC) – Flow(ZOO2, SED) > 0.4 \* FlowTo(ZOO2)

Mesozooplankton respiration is partitioned into basal respiration, 1-10% of respective biomass, plus respiration associated with growth, which is at least 40% of assimilated food.

Flow(ZOO1, CO2) < ZOO1 \* 0.1 + (FlowTo(ZOO1) – Flow(ZOO1, DET) – Flow(ZOO1, DOC) – Flow(ZOO1, SED))\*1.0

Flow(ZOO1, CO2) > ZOO1 \* 0.01 + (FlowTo(ZOO1) – Flow(ZOO1, DET) – Flow(ZOO1, DOC) – Flow(ZOO1, SED)) \* 0.4

Flow(ZOO2, CO2) < ZOO2\*0.1 + (FlowTo(ZOO2) – Flow(ZOO2, DET) – Flow(ZOO2, DOC) – Flow(ZOO2, SED)) \* 1.0

Flow(ZOO2, CO2) > ZOO2 \* 0.01 + (FlowTo(ZOO2) – Flow(ZOO2, DET) – Flow(ZOO2, DOC) – Flow(ZOO2, SED)) \*0.4

Mesozooplankton DOC release (sloppy feeding, other processes) is constrained to be between 1-50% of the food intake.

Flow(ZOO1, DOC) < FlowTo(ZOO1) \* 0.5

Flow(ZOO1, DOC) > FlowTo(ZOO1) \* 0.01

Flow(ZOO2, DOC) < FlowTo(ZOO2) \* 0.5

Flow(ZOO2, DOC) > FlowTo(ZOO2) \* 0.01

Mesozooplankton defaecation is between 10-60% of food intake.

Flow(ZOO1, DET) + Flow(ZOO1, SED) > FlowTo(ZOO1) \* 0.1

Flow(ZOO1, DET) + Flow(ZOO1, SED) < FlowTo(ZOO1) \* 0.6

Flow(ZOO2, DET) + Flow(ZOO2, SED) > FlowTo(ZOO2) \* 0.1

Flow(ZOO2, DET) + Flow(ZOO2, SED) < FlowTo(ZOO2) \* 0.6

Mesozooplankton food intake at least 5% of mesozooplankton biomass

FlowTo(ZOO1) > 0.05 \* ZOO1

FlowTo(ZOO2) > 0.05 \* ZOO2

The fraction of sinking fecal pellets is smaller than the fraction of fecal pellets disintegrating in the water column and forming detritus.

Flow(ZOO1, DET) > Flow(ZOO1, SED)

Flow(ZOO2, DET) > Flow(ZOO2, SED

Microzooplankton respiration is partitioned into basal respiration, 1-10% of respective biomass, plus respiration associated with growth, which is at least 40% of food intake

Flow(μZOO, CO2) < μZOO \* 0.1 + FlowTo(μZOO) \* 1.0

Flow(μZOO, CO2) > μZOO \* 0.01 + FlowTo(μZOO) \* 0.4

Microzooplankton exudation to DOC pools is between 1-10% of food intake.

Flow(μZOO, DOC) < FlowTo(μZOO) \* 0.1

Flow(μZOO, DOC) > FlowTo(μZOO) \* 0.01

Flow from microzooplankton to detritus is partitioned between mortality, 1-10% of respective biomass, plus 10-20% of food intake, corresponding to assimilation efficiency of 80-90%

Flow(μZOO, DET) < μZOO \* 0.1 + FlowTo(μZOO) \* 0.2

Flow(μZOO, DET) > μZOO \* 0.01 + FlowTo(μZOO) \* 0.1

Heterotrophic nanoflagellate respiration is partitioned into basal respiration, 1-10% of respective biomass, plus respiration associated with growth, which is at least 40% of food intake

Flow(HNF, CO2) < HNF \* 0.1 + FlowTo(HNF) \* 1.0

Flow(HNF, CO2) > HNF \* 0.01 + FlowTo(HNF) \* 0.4

Heterotrophic nanoflagellate exudation to DOC pool is between 1-10% of food intake

Flow(HNF, DOC) < FlowTo(HNF) \* 0.1

Flow(HNF, DOC) > FlowTo(HNF) \* 0.01

Flow from heterotrophic nanoflagellates to detritus is partitioned between mortality, 1-10% of respective biomass, plus 10-20% of food intake, corresponding to assimilation efficiency of 80-90%.

Flow(HNF, DET) < HNF \* 0.1 + FlowTo(HNF) \* 0.2

Flow(HNF, DET) > HNF \* 0.01 + FlowTo(HNF) \* 0.1

Bacterial respiration is partitioned into basal respiration, 1-10% of respective biomass, plus respiration associated with growth, which is at least 40% of assimilation.

Flow(BAC, CO2) < BAC \* 0.1 + FlowTo(BAC) \* 1.0

Flow(BAC, CO2) > BAC \* 0.01 + FlowTo(BAC) \* 0.4

Bacterial daily mortality is between 1-10% of the biomass.

Flow(BAC, DET) < BAC \* 0.1

Flow(BAC, DET) > BAC \* 0.01

Preferential grazing of alternative prey sources, but not more than 0.5-2 times the respective prey biomass ratios.

Flow(BAC, HNF) \* PHY0 < 2 \* Flow(PHY0, HNF) \* BAC

Flow(BAC, HNF) \* PHY0 > 0.5 \* Flow(PHY0, HNF) \*BAC

Flow(PHY1, μZOO) \* PHY0 < 2 \* Flow(PHY0, μZOO) \* PHY1

Flow(PHY1, μZOO) \* PHY0 > 0.5 \* Flow(PHY0, μZOO) \* PHY1

Flow(HNF, μZOO) \* PHY0 < 2 \* Flow(PHY0, μZOO) \* HNF

Flow(HNF, μZOO) \* PHY0 > 0.5 \* Flow(PHY0, μZOO) \* HNF

Flow(BAC, μZOO) \* PHY0 < 2 \* Flow(PHY0, μZOO) \* BAC

Flow(BAC, μZOO) \* PHY0 > 0.5 \* Flow(PHY0, μZOO) \* BAC

Flow(HNF, μZOO) \* PHY1 < 2 \* Flow(PHY1, μZOO) \* HNF

Flow(HNF, μZOO) \* PHY1 > 0.5 \* Flow(PHY1, μZOO) \* HNF

Flow(BAC, μZOO) \* PHY1 < 2 \* Flow(PHY1, μZOO) \* BAC

Flow(BAC, μZOO) \* PHY1 > 0.5 \* Flow(PHY1, μZOO) \* BAC

Flow(BAC, μZOO) \* HNF < 2 \* Flow(HNF, μZOO) \* BAC

Flow(BAC, μZOO) \* HNF > 0.5 \* Flow(HNF, μZOO) \* BAC

Zooplankton grazers (µZOO, ZOO1, ZOO2) feed on detritus and living compartments, but prefer live food. The grazing rates on detritus divided by the grazing rates on live compartments was set lower than the biomass ratio of detritus to live prey compartments

-Flow(DET, μZOO) \* PHY0 - Flow(DET, μZOO) \* PHY1 - Flow(DET, μZOO) \* HNF -Flow(DET, μZOO) \* BAC + Flow(PHY0, μZOO) \* DET + Flow(PHY1, μZOO) \* DET + Flow(HNF, μZOO) \* DET + Flow(BAC, μZOO) \* DET > 0

-Flow(DET, ZOO1) \* PHY1 - Flow(DET, ZOO1) \* PHY2 - Flow(DET, ZOO1) \* μZOO -Flow(DET,ZOO1) \* HNF + Flow(PHY1, ZOO1) \* Det + Flow(PHY2, ZOO1) \* DET + Flow(μZOO, ZOO1) \* DET + Flow(HNF, ZOO1) \* DET > 0

-Flow(DET, ZOO2) \* PHY2 - Flow(DET, ZOO2) \* μZOO + Flow(PHY2, ZOO2) \* DET + Flow(μZOO, ZOO2) \* DET > 0

Flow(PHY2, ZOO1) \* PHY1 < 2 \* Flow(PHY1, ZOO1) \* PHY2

Flow (PHY2, ZOO1) \* PHY1 > 0.5 \* Flow(PHY1, ZOO1) \* PHY2

Flow(HNF, ZOO1) \* PHY1 < 2 \* Flow(PHY1, ZOO1) \* HNF

Flow(HNF, ZOO1) \* PHY1 > 0.5 \* Flow(PHY1, ZOO1) \* HNF

Flow(μZOO, ZOO1) \* PHY1 < 2 \* Flow(PHY1, ZOO1) \* μZOO

Flow(μZOO, ZOO1) \* PHY1 > 0.5 \* Flow(PHY1, ZOO1) \* μZOO

Flow(HNF, ZOO1) \* PHY2 < 2 \* Flow(PHY2, ZOO1) \* HNF

Flow(HNF, ZOO1) \* PHY2 > 0.5 \* Flow(PHY2, ZOO1) \* HNF

Flow(μZOO, ZOO1) \* PHY2 < 2 \* Flow(PHY2, ZOO1) \* μZOO

Flow(μZOO, ZOO1) \* PHY2 > 0.5 \* Flow(PHY2, ZOO1) \* μZOO

Flow(μZOO, ZOO1) \* HNF < 2 \* Flow(HNF, ZOO1) \* μZOO

Flow(μZOO, ZOO1) \* HNF > 0.5 \* Flow(HNF, ZOO1) \* μZOO

Flow(μZOO, ZOO2) \* PHY2 < 2 \* Flow(PHY2, ZOO2) \* μZOO

Flow(μZOO, ZOO2) \* PHY2 > 0.5 \* Flow(PHY2, ZOO2) \* μZOO

**Table S3.** Mean carbon flows (mg C m-2 d-1; ± standard deviation) in the food webs of stations P1 to P7.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Flow | Stations | | | | | |
|  | P1 | P3 | P4 | P5 | P6 | P7 |
| Flow(CO2, PHY2) | 1620±189 | 649±92 | 369±32 | 138±22 | 94±15 | 284±38 |
| Flow(CO2, PHY1) | 316±39 | 138±17 | 168±19 | 139±13 | 54±6.3 | 158±13 |
| Flow(CO2, PHY0) | 910±176 | 539±90 | 117±22 | 722±29 | 143±17 | 418±38 |
| Flow(PHY0, DOC) | 493±191 | 261±112 | 52±32 | 61±30 | 24±17 | 35±18 |
| Flow(PHY1, DOC) | 227±83 | 87±39 | 63±38 | 36±25 | 26±18 | 17±13 |
| Flow(PHY2, DOC) | 844±205 | 273±114 | 91±45 | 22±18 | 24±17 | 21±16 |
| Flow(PHY0, CO2) | 21±11 | 44±37 | 24±18 | 97±72 | 33±22 | 5±0.95 |
| Flow(PHY1, CO2) | 15±10 | 25±19 | 32±24 | 24±18 | 14±8.6 | 2±0.85 |
| Flow(PHY2, CO2) | 28±11 | 51±43 | 63±50 | 20±16 | 22±15 | 4±0.93 |
| Flow(PHY0, DET) | 113±81 | 108±68 | 47±31 | 317±97 | 69±43 | 193±38 |
| Flow(PHY1, DET) | 94±74 | 52±33 | 67±40 | 41±26 | 62±29 | 26±15 |
| Flow(PHY2, DET) | 140±73 | 127±45 | 124±61 | 25±18 | 69±45 | 45±31 |
| Flow(PHY2, SED) | 133±101 | 54±48 | 78±59 | 24±22 | 53±40 | 52±37 |
| Flow(BAC, CO2) | 504±12 | 380±78 | 279±80 | 200±85 | 382±89 | 58±0.87 |
| Flow(BAC, DET) | 5±0.58 | 12±3.0 | 28±15 | 9±2.7 | 24±13 | 11±1.7 |
| Flow(DOC, BAC) | 535±12 | 406±78 | 330±80 | 256±85 | 439±89 | 123±0.87 |
| Flow(HNF, CO2) | 42±3.4 | 42±21 | 79±38 | 51±12 | 168±92 | 14±1.3 |
| Flow(HNF, DOC) | 3±1.7 | 3±2.0 | 4±2.7 | 5±2.9 | 10±7.1 | 1±0.65 |
| Flow(HNF, DET) | 13±2.2 | 26±11.4 | 46±18 | 21±8.1 | 45±19 | 6±0.97 |
| Flow(PHY0, HNF) | 84±4.9 | 41±21 | 33±19 | 80±16 | 80±49 | 15±2.6 |
| Flow(BAC, HNF) | 14±0.83 | 8±3.6 | 40±17 | 21±3.6 | 89±40 | 14±1.7 |
| Flow(μZOO, CO2) | 73±13 | 174±71 | 339±96 | 127±46 | 566±147 | 28±1.8 |
| Flow(μZOO, DOC) | 7±4.1 | 12±7.6 | 21±12 | 11±7.2 | 33±19 | 2±0.94 |
| Flow(μZOO, DET) | 31±12 | 60±22 | 75±27 | 57±26 | 147±53 | 15±1.3 |
| Flow(PHY0, μZOO) | 13±5.0 | 61±26 | 32±14 | 60±18 | 94±42 | 5±2.1 |
| Flow(PHY1, μZOO) | 6±2.5 | 22±9.3 | 66±25.9 | 12±3.9 | 51±23 | 2±0.93 |
| Flow(PHY2, μZOO) | 136±26 | 80±68 | 74±61 | 33±25 | 53±42 | 18±10 |
| Flow(HNF, μZOO) | 1±0.35 | 7±3.0 | 34±14 | 12±3.7 | 84±33 | 2±0.61 |
| Flow(BAC, μZOO) | 3±0.86 | 13±3.9 | 42±15 | 18±3.7 | 112±40 | 6±1.8 |
| Flow(DET, ZOO1) | 1±0.69 | 44±32 | 133±91 | 101±50 | 231±144 | 12±7.5 |
| Flow(ZOO1, CO2) | 24±1.0 | 9±0.26 | 2±0 | 12±0.56 | 4±0 | 32±1.6 |
| Flow(ZOO1, DOC) | 11±8.6 | 7±4.7 | 1±0.69 | 10±6.9 | 2±1.4 | 8±5.7 |
| Flow(ZOO1, DET) | 36±13 | 11±4.6 | 2±0.65 | 16±6.7 | 3±1.2 | 17±8.5 |
| Flow(ZOO1, SED) | 12±8.0 | 4±2.6 | 1±0.37 | 5±3.8 | 1±0.74 | 6±4.4 |
| Flow(ZOO2, CO2) | 28±1.0 | 14±0.26 | 15±0 | 12±0.56 | 11±0 | 34±1.6 |
| Flow(ZOO2, DOC) | 11±8.4 | 7±5.0 | 8±5.3 | 7±5.2 | 6±3.8 | 9±6.4 |
| Flow(ZOO2, DET) | 36±14 | 12±4.7 | 13±4.8 | 12±5.2 | 9±3.4 | 19±10 |
| Flow(ZOO2, SED) | 12±8.3 | 4±2.7 | 4±2.9 | 4±2.9 | 3±2.1 | 6±4.9 |
| Flow(PHY1, ZOO1) | 13±4.0 | 5±1.4 | 1±0.30 | 7±2.5 | 1±0.32 | 6±1.4 |
| Flow(PHY2, ZOO1) | 86±12 | 26±4.0 | 3±0.60 | 8±2.9 | 2±0.66 | 15±2.7 |
| Flow(μZOO, ZOO1) | 5±1.6 | 2±0.55 | 0.2±0.06 | 18±5.7 | 4±0.94 | 14±1.9 |
| Flow(HNF, ZOO1) | 2±0.62 | 2±0.47 | 0.5±0.16 | 7±2.6 | 2±0.47 | 4±0.89 |
| Flow(DET , ZOO1) | 2±1.1 | 5±3.6 | 1±0.74 | 16±10 | 2±1.7 | 58±7.4 |
| Flow(PHY2, ZOO2) | 103±14 | 32±5.0 | 29±6.7 | 8±3.8 | 8±3.0 | 17±3.0 |
| Flow(μZOO, ZOO2) | 6±2.3 | 2±0.80 | 2±0.81 | 18±7.0 | 13±4.2 | 15±2.1 |
| Flow(DET , ZOO2) | 2±1.3 | 7±4.3 | 11±7.1 | 17±9.4 | 9±6.1 | 63±9.6 |
| Flow(DET, DOC) | 10±5.5 | 156±81 | 169±83 | 165±87 | 163±92 | 51±8.0 |
| Flow(DET, SED) | 372±101 | 207±48 | 168±59 | 190±22 | 147±40 | 81±37 |

The maximum likelihood carbon flow estimates are mean values of 10 000 Monte Carlo runs of respective food webs (*xsample()* function in the *limSolve* library of the R software).



**Figure S1.** Vertical biomass profiles (mg C m-3) of particulate organic carbon (POC, solid lines) and total phytoplankton carbon (dotted line) in stations P1 to P7. Phytoplankton carbon is calculated from chlorophyll a concentration, by using a Chl:C conversion factor of 27. POC error bars represent standard deviation between replicate subsamples (sampling uncertainty). Note the 2x difference in x-scale between P1-P4 and P5-P7.



**Figure S2.** Vertical profiles of production rates (mg C m-3 d-1) in stations P1 to P7. Solid line – total primary production; dashed line – dissolved primary production, which represents the exudation by phytoplankton; dotted line – bacterial production multiplied with 100 to fit the scale. Note the 2x difference in x-scale between P1-P4 and P5-P7.



**Figure S3.** Vertical profiles of the biomass (mg C m-3) of microbial loop compartments in stations P1 to P7. Solid line – microzooplankton; dashed line – heterotrophic nanoflagellates; dotted line – heterotrophic bacteria.



**Figure S4.** Vertical profiles of mesozooplankton carbon (mg C m-3) in stations P1 to P7. Mesozooplankton was sampled with stratified sampling (see methods). Solid line – large mesozooplankton (> 4 mm); thin line – small mesozooplankton (< 4 mm).



**Figure S5.** Vertical flux profiles of POC (mg C m-2 d-1) in stations P1 to P7. Vertical flux was measured with sediment traps at discrete depths from 20 m to 200 m; only the upper 90 m is shown here.