Interactive comment on "Factors controlling coccolithophore biogeography in the Southern Ocean" *by* Cara Nissen et al.

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Received and published: 8 July 2018

ï¿£Title: Factors controlling coccolithophore biogeography in the Southern Ocean

C. Nissen et al.

Submitted to BGD

I. General comments:

This work is a modelling exercise seeking to understand the potential mechanisms behind the simulated patterns of spatial and temporal variability for some major phytoplankton taxa over the Southern Ocean region (south of 30S). Particularly the authors main focus is on coccolithophores (coccos) and diatoms, with an emphasis on under-

standing coccos dynamics. The goal is to disentangle the several environmental factors (nutrients, solar radiation, temperature) affecting the growth of these phytoplankton groups as "bottom-up" effects, and compare them with the grazing "top-down" effects affecting their mortality. The work is quite original and goes beyond the simple description of the model results and seeks to dig into the mechanisms, so I really like the approach. The article is well written, the objectives are clear, and the results are well explained.

However I did find several technical and conceptual issues that I feel need to be addressed. Especifically the authors call i) "relative growth rate" what in reality is a "relative growth limitation" term, which is not the same thing; and ii) "relative grazing rate" what in reality is a "relative clearance rate", which is not the same thing either. Further, they make inferences on the relative effect of bottom-up versus top-down effects based on comparing these two concepts (i and ii) while they are not comparable – basically because they have different units (before making the log10 of their ratio for coccos : diatoms). What they need to compare is log10(x/y) where x has units of days-1 for coccos and y has units of days-1; BOTH for growth rate and grazing rate. At the moment for relative growth they are using x and y using non dimensional units (n.d), and for the relative grazing they are using x and y using clearance rate units (m3 * m-3 * d-1). To be consistent the growth limitation terms must be multiplied by maximum growth rate (mupmax; d-1) and the grazing clearance rate must be multiplied by zooplankton biomass (Z; mmol * m-3). This will make those processes (bottom-up vs. top-down) comparable because they will have the same units (d-1) before making the ratio and taking the log10. The two major things the author will notice are: 1) the specific growth rate (d-1) of diatoms is larger than coccos for most of the environmental conditions; only at very narrow window of small nutrient concentration will coccos outcompete diatmos; 2) the specific grazing rate (d-1) on diatoms is ALWAYS smaller than on coccos (for a constant zooplankton biomass).

I have performed myself an extensive analysis using MATLAB/OCTAVE of the niche

properties of these simulated phytoplankton taxa based on the model parameters provided. That is how I discovered these and other conceptual errors, which may affect the discussion of the manuscript. For example, the grazing equation eq(5) described in the text: G1 = gmax * Z * P1 / (K + P1) is incorrect to compute the grazing on P1. The correct equation should be G1 = gmax * Z * P1 / (K + P1 + P2) if we assume that there are two prey (P1 + P2) available for grazing (e.g. diatoms and coccos). This correction (adding P1 + P2 in the denominator of the grazing functional response) alters the results of the "relative clearance rates" (C:D) and the coccos are always grazed faster than diatoms. Therefore, given the parameter values provided by this model there is no surprise that diatoms will dominate coccos by a factor of x10 almost everywhere and at anytime. The idealized analyses of niche properties that I performed I think should be added as Supplementary Material in a revised form of this manuscript. A table with the model parameters is important for replication of this work but a figures showing the actual shapes of the nutrient uptake curves and grazing functional response are important for the reader because it provides a way of fast visual inspection and understanding. For example, just by visual inspection of the grazing functional responses one can predict a-priori that coccos are ALWAYS going to be grazed faster than diatoms.

Also the selection of uptake curves for nutrient uptake is quite puzzling to me. For DIN, NH4 and DIP, they are kind of similar where coccos are always losers to either diatom or small phyto; then for DOP the coccos appear to have small nutrient window where they can dominate. Then for iron coccos and small phyto are very similar in nutrient uptake strategy while diatoms dominates. Finally dizotrophs are clear losers for all nutrients against all other phytoplankton groups – no surprise they are almost zero biomass (less than 1%) in the model. I would suggest the authors to simplify the model parameters: define a single set of four values (one per phyto group) for the half saturation constant on Dissolved Organic Phosphorous (DOP) and then compute the half-sat for all other nutrients (DIN, NH4, DIP, Fe2, Silica) using constant redfield ratios. I did this myself and I feel that uptake curves obtained are nicer and more consistent across nutrient

types, and they also provide a slightly larger nutrient concentration niche window for coccos where they can dominate. There is "key switch" in my MATLAB/OCTAVE code (key_params = 'Original' or 'Redfield') to change from the original model parameters setup to the suggest parameter setup. The results of the simulation should not change qualitatively after this minor changes on parameter values, and if they do then there is an issue of model sensitivity to parameter values. Please see the resulting Figures in the attached PDF documents. I provide the MATLAB/OCTAVE code I wrote at the end of this review report. The authors are free to use it.

Regarding the Sensitivity Analysis (SA) performed by the authors, I am afraid to say that is not useful in the way it has been designed. Basically because 1) changing the selected parameters "from the values of coccos to the values of diamtoms" provides too little change of the parameter values; 2) the percentage of change for the selected parameters is different among them. That means that 1) the response of the model for the "sensitivity runs" will usually be quite small for most of the parameters; and 2) the responses of the model for the "sensitivity runs" will not be comparable accross parameters. For example, changing the Q10_coccos (1.45 n.d.) to Q10_diatoms (1.55 n.d.) is a meager 7% variation in the Q10 value of coccos; or changing the alpha_coccos (0.4) to alpha_diatoms (0.44) means a 10% variation in the alpha PI value of coccos. Then, changing mupmax_coccos (3.8 d-1) to mupmax_diatoms (4.6 d-1) implies a 20% variation in the mupmax of coccos; and changing the half sat kno3_coccos (0.3) to kno3_diatoms (0.5) implies a 66% variation. On the other hand, changing the half sat for grazing zgrz_coccos (1.05) to zgrz_diatoms (1.0) implies a 5% variation. Therefore, some parameters are changed less than 10% while others are changed more than 60%, and others are changed around 20%. This is too messy for a meaningful SA. The correct way to perform a proper (yet simple) SA is by changing a plus/minus 50% the selected parameter values, and then computing the Sensitivity Index (SI) as follows – and the plotted as shown in Figure 12 of Vallina et al. (2008) DMOS model, JGR:

SI = 100 * (X_pmax - X_pmin) / X_pcontrol ;

where:

X – is the model state variable of interest (e.g. Diatom concentration) # pcontrol – is the selected parameter value for the control run (e.g. mupmax of coccos) # pmax = 1.5 x pcontrol – is the run for the plus(+) 50% increase in the parameter value # pmax = 1.5 x pcontrol – is the run for the minus(-) 50% decrease in the parameter value # SI – is the Sensitivity Index in percentage of change (can be positive or negative %)

II. DETAILED COMMENTS:

- Page 1, Line 01: Change "controls not only the local biogeo but also" to "controls the local biogeo and" – Avoid unnecessary negatives in affirmative sentences. - Page 3, Line 03: "interaction" is very generic term – Would be better to specify "competitive interaction" (for light and nutrients) or just "competition". - Page 4, Table 1: The parameter values for mupmax at 30C are quite large (3.6, 4.6 d-1) and in my view quite beyond the reality of these values in nature. - Page 4, Table 1: The parameter values for Q10 are almost the same for all phyto – why dont you just use 1.5 for all of them? - Page 4, Table 1: The parameter values for knh4 are a factor of x 10 smaller (i.e. 0.10) than kno3 for all C, D and SP; but 0.15 for diazotrophs – why dont you just use time 0.10 for all of them? - Page 4, Table 1: The parameter values for kpo4 are the same value than for kno3 for C, D, and SP (even if the Redfiled ratio N:P is 16:1 – why?) but for diazos is ten times smaller – why? - Page 4, Table 1: The parameter values for alpha PI curve are between 0.38 and 0.44 for all phyto groups (very narrow variability) – why dont you just use 0.4 for all of them? - Page 4, Table 1: The parameter values for zgrz half sat grazing are between 1.0 and 1.2 for all phyto groups (very narrow variability) – why dont you just use 1.0 for all of them? - Page 4, Table 1: - Page 4, Table 1: Basically I find that the selection of parameter values can be simplified a lot given the similarity among many of the values. I would suggest selecting one nutrient (e.g. DOP) and define the half-sat values for it, then compute the half-sat for all other

nutrients (DIN, NH4, DIP) using Redfield ratios and constant factors. This will make the list of parameter values much smaller without compromising the simulations. Also this will simplify the Sensitivity Analysis because it reduces the degrees of freemdom in the parameter space. - Page 4, Line 5: "coccos have a higher nutrient affinity (smaller half-sat) and a smaller max growth rate than diatoms" – the half sat parameter is in fact a composite of two primary parameters (ksat = mupmax / affinity) therefor lower half sat does not necessarily mean higher affinity, it also depends on the mupmax value. Also, the smaller size of coccos cannot be the reason of their smaller mupmax because mupmax usually decreases with increasing cell size. - Page 6, Table 2: Run name 10 and 11; Holling Type III and Active Switching – I dont understand... Very confusing. Please double check and make it clearer. - Page 6: Table 2: Run name 12; TEMP; Reduce temperature by 1C – This seems a pretty low decrease in temperature for a SA. What percentage is this? - Page 6, Line 04: "We then add an active prey switching term to the original Holling Type II" – The Holling Type III has already "active prey switching" dynamics so I dont really know what this addition to Holling Type II means. - Page 7, Line 15: "Ideal env conditions ... at every location" – The nutrient concentration window where coccos reach a higher specific growth rate than diatoms is very narrow and happens at very low nutrient concentrations; for all other conditions the diatom are superior competitors regardless of light and temperature levels. Therefore what dominates the competition between coccos and diatoms is basically nutrients only (in your model setup). - Page 7, Line 19: The equation for grazing rate on Pj is wrong: it should be – gamma_j = gammax_j * f(T) * Z * (P_j / (zgrz_j + sum[P_i])) NOTE: The sum[P_i] - Page 7, Line 23: Why do you use the notation "P_j prime" (P') instead of just P (without the prime)? - Page 7, Line 20: "loss threshold below which no losses occur (eq B11)" – This is called imposed "prey refuge" and helps prevent competitive exclusion of the less dominant prey types (in a similar way as active prey switching). - Page 8, Line 03: The ratio (gamma_j / P_j) will only have units of clearance rate (m3 * mmol-1 * d-1) if divided by zooplankton biomass. Otherwise it will have units of specific grazing rate (d-1) – please double check units and concepts. - Page 8, Line 03: Neverthe-

less, if (gamma_j / P_j) is called a "clearance rate", you should call "log10((gamma_C / P_D)/(gamma_C / P_D))" as "Relative clearance rate" (instead of "Relative grazing rate"). - Page 8, Line 04: "the specific grazing (clearance) rate on diatoms is larger" – as far as I can tell, using the correct gamma_j functional response (with the zgrz + sum[P_i]; see above) the specific grazing (clearance) rate on diatoms will ALWAYS be smaller than on coccos. Plase double check. See my MATLAB/OCTAVE analyses and figures. - Page 8, Line 25: "caused either by too much uptake by phytoplankton" – Given the too high mupmax selected for this model I am not surprised about this; why dont you tune down mupmax accordingly to prevent this bias? - Page 9, Table 3: "(global)" – what that this means? confusing. - Page 9, Table 3: The contribution of coccos is: 15%, 10% and 1% for the three regions – isnt it this too low? - Page 9, Table 3: I dont really see how coccos can even survive based on the uptake curves (nutrient niches) defined in the model set up. The coccos uptake curves seem to be always below those of either diatoms (at high nutrients) and small phyto (at small nutrients). The temperature dependence is almost the same for all phyto groups so it does not play a role. The light dependence is also quite similar for the three dominant groups (C,D,SP). Thus it is mostly down to nutrients competition and if the coccos uptake curve is never above those of their competitors, with a Type II grazing functional response they should be competitively excluded. Only the imposed prey refuge will keep them persisting in the model. - Page 9, Line 17: "within the globally estimated" – what do you mean? how can you compare a regional estimate to a whole ocean estimate? - Page 9, Figure 1: The model simulates chla fairly well spatially despite some biases – How well does the model reproduce the seasonal dynamics of chla? Please provide a figure in Supplementary Material. - Page 9, Figure 1, f) Personally I find that the model does a poor job with coccos in terms of spatial distribution, only the absolute values seem to be the correct but clearly not the patterns. The deviation from the data values especially between 60S and 75S is too large, up to an order of magnitude even. Can you say that the model simulations for coccos have been validated really? - Page 10, Line 7: The model NPP estimates are between [0.23 - 0.69] (PgC * y-1) and the real data NPP

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estimates are between [0.64 - 0.94] (PgC * y-1). This implies that the model's NPP is basically half of the real data NPP estimates – why do you say then that if "falls with the range estimated by satellite"? Just say that the models underestimates NPP by 50%. - Page 12, Figure 3: Dizatrophs are basically extinct in this model simulations. This is because the selected uptake curves for them (see my MATLAB/OCTAVE figures) that makes them very poor nutrient competitors. Why do you even bother in having them as a phytoplankton group? I dont understand this. - Page 12, Lines 15-20: Basically this means that you dont know why? Is not it any way to explore the reasons beyond verbal speculation? - Page 13, Line 1: "this PFT (Phaeocystis) is not included in our simulations" – Honestly I dont think this is a valid excuse. Given that diazotrophs are irrelevant in this model simulations, why dont you use that tracer to model Phaeocystis instead? - Page 13, Line 4: "simulated gradient ... coccos contribution" – This is a misleading statement: diatoms clearly dominate everywhere in the model by about a factor of x10, so talking about mixed community, south-north increase in coccos contribution, etc. is verbally misleading. - Page 13, Line 13: "whereas diatom biomass peaks south of 60S where they dominate the community" – again, this is misleading; diatoms dominate the community *everywhere* in your domain, not just south of 60S. - Page 15, Line 10: "the specific growth rate of coccos is on average 10% larger than of diatoms" – IMPORTANT: This statement is wrong due to a conceptual misunderstanding. Doing log(x/y) where x = DIN / (kdin + DIN) for diatoms and y is the equivalent thing for coccos does *not* measure the "relative growth rate" of diatoms versus coccos but the "relative growth limitation", which is not the same thing. If you want to evaluate "relative growth rate" you have to do: Rel growth = log(umax_D/umax_C) + log(x/y) – Please change this in the analysis and the text accordingly. - Page 15, Line 18: "The 21% larger umax of diatoms ... all year round in the whole model domain" – This is a main result of the model simulations. Thus it must be at the beginning of section 4.5 not buried here. - Page 15, Line 21: "coccos being less temperature limited" – Misleading, the differences of Q10 are marginal (7% is basically nothing) - Page 15, Line 24: "are less nutrient limited" – This is the right wording. One thing is being less nutrient limited

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and another thing is having a faster nutrient uptake curve, the difference lies on the umax. - Page 15, Line 35: "differences in the sensitivity to increases of PAR at low irradiance (alfa PI) and diffs in photoaclim" – Misleading, the differences of alfa_PI are marginal (9% is basically nothing) - Page 16, Figure 5: The different terms that are being plotted here as "relative growth ratio" for nutrients, temperature, light, and total are not really "growth rate" ratios" but "growth limitation" ratios. This leads to wrong interpretation of the results. The right way should be to plot the following curves:

Qdin = DIN / (Kdin + DIN); Nutrients limitation [0 - 1] n.d. Qpar = f(PAR); Irradiance limitation [0 - 1] n.d. Qsst = f(SST); Temperature limitation [0 - 1] n.d.

Rel_umax = log(umax_D/umax_C); Rel_Qdin = log(Qdin_D/Qdin_C); – Relative nutrient growth "limitation" Rel_Qpar = log(Qpar_D/Qpar_C); – Relative irradiance growth "limitation" Rel_Qsst = log(Qsst_D/Qsst_C); – Relative temperature growth "limitation"

Rel_din = Rel_umax + Rel_Qdin; – Relative nutrient growth "rate" Rel_par = Rel_umax + Rel_Qpar; – Relative irradiance growth "rate" Rel_sst = Rel_umax + Rel_Qsst; – Relative temperature growth "rate"

Rel_Qlim = Rel_Qdin + Rel_Qpar + Rel_Qsst; – Relative total growth "limitation" Rel_growth = Rel_mupmax + Rel_Qlim; – Relative total growth "rate"

- Page 17, Figure 6b) – "Relative grazing ratio higher on diatoms" – This is very weird, I think this computation of grazing ratio is wrong. When I did on my MATLAB/OCTAVE analyses I find that the "grazing ratio" (in fact it should be called "clearance rate" ratio) is ALWAYS higher on coccos. And if we look at the grazing functional response we can se that it is higher than those for coccos at any prey concentration. I think the reason is the lack of the (zgrz + sum[Pi]) at the denominator of the grazing computation. If you are using (zgrz + P1), instead of (zgrz + P1 + P2), that will be wrong. Please double-check. - Page 17, Line 1: "coccos have a lower alfa PI" – Only 9% lower, please explicitly say so. - Page 17, Line 2: "a generally lower chla-to-carbon" ratio (not shown) – How much lower in percentage? Why it is not shown? - Page 17, Line 4: "coccos

are on average 2% - 3% more light limited than diatom" – This is basically nothing from a competitive exclusion point of view at ecological (seasonal) time scales. - Page 17, Line 11: "coccos and diatom together contribute on average 87% and 95%" – Misleading statement because diatoms clearly dominate (90% diatoms vs 10% coccos); dont plug them together. - Page 17, Line 13: "They are thus not only competing for resources between each other but with SP as well" – This statement is obvious; of course all phytoplankton PFT compete among them for nutrients. - Page 18, Line 5: "advantage in specific growth" – LIMITATION not RATE. This must be clear. - Page 18, Line 6: "greater importance" – Misleading, coccos are always poor competitors in this model simulations. - Page 18, Line 10: "higher specific growth rate" – WRONG: this should say "higher specific growth limitation"; it is *not* the same thing. - Page 18, Line 11: "We calculated whether the length of the growing season is long enough" – Good try, but wrong answer. Coccos may grow faster (in days-1) than diatoms over a very narrow band of nutrient concentration which I dont think is even hapening on your models simulations. I suspect that diatoms grow faster (in days-1) than coccos everywhere in your domain and everytime in the year. Plase double-check. - Page 18, Line 25: If grazing pressure were able to explain the mismatch between the expected results for coccos vs diatoms (from the model) and observed ones (from the model), this could be easily confirmed by performing a run where maximum grazing rate (gamma max) and half saturation constant for grazing (zgrz) are the same for both coccos and diatoms. Please do it and report the results in Supp. Material. - Page 18, Line 28: "specific grazing rate on coccos" – it is not clear to me if this is measuring relative "specific grazing rates" (d-1 vs d-1) or relative "specific clearance rates" (m3 * mol-1 * d-1) vs. (m3 * mol-1 * d-1). Ideally it should measure (d-1 vs d-1) to be correct and consistent. - Page 18, Line 34: "differences in specific grazing rates between diatoms and coccos are of similar magnitude as differences in specific growth rates" – WRONG: You cannot compare differences in specific clearance rates (I am not sure about the units yet; maybe [d-1] or maybe [m3 * mol-1 * d-1]) with specific LIMITATION rates (in non dimensional [n.d.] units), even when having them log transformed so that

their both lose their original units. Make sure that "relative grazing rate" and "relative growth rate" is based on process with units of days-1 in both cases. Otherwise they are not comparable. - Page 19, Line 7: "During this times coccos experience a larger per biomass grazing pressure" – in fact coccos experience a larger per biomass grazing pressure at ALL TIMES. Please double check and correct the text accordingly (e.g. line 10) - Page 19, Line 17: "Parameter Sensitivity Simulations" – Change to "Parameter Sensitivity Analysis" and perform the SA suggested in my General Comments. The current SA is not meaningful. - Page 20, Line 18: "coccos are a non-negligible" – Change to "coccos are a minor but non-negligible" - Page 21, Line 20: "The net sign of ... future research" – Why future research? I think this may actually be the most important point to be addressed by this work. Why cannot be done now? - Page 21, Line 26: "succession" – Margalef's Mandala concept of succession implies a temporal dominance. However coccos do never get anywhere close to dominate the biomass since diatoms are always above 80%. Therefore the term "succession" does not apply here. - Page 21, Line 24: "specific growth rate" – Change to "specific growth limitation" or compute the correct "specific growth rate" after multiplying by umax. Currently what is higher is the nutrient limitation "Qdim = DIN / (kdin + DIN)" term (n.d.) but not the growth rate "umax * Qdim" term (d-1) - Page 23, Figure 8: This figure is pretty but to complex – Too many info (colors, shades, arrows, shapes, letters, low high); I honestly dont understand anything. - Page 25, Line 1: "pressure on less abundant" – Change to "pressure on relatively less abundant". - Page 26, Line 9: "coccos biomass is high when diatoms" – Change to "coccos biomass is higher"; their biomass is never high. - Page 26, Line 11: "never exceeds that of" – Change to "never gets even close to" that of diatoms.

— # MATLAB / OCTAVE:

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%SWITCHING KEYS: key_params = 'Original'; %%key_params = 'Redfield';

cmap_redblue(01,:) = [0.00000 0.15959 0.35490]; cmap_redblue(02,:) = [0.13721 0.37159 0.56690]; cmap_redblue(03,:) = [0.34921 0.58359 0.77890]; cmap_redblue(04,:) = [0.56121 0.79559 0.99090]; cmap_redblue(05,:) = [0.77321 1.00000 1.00000]; cmap_redblue(06,:) = [0.98521 1.00000 1.00000]; cmap_redblue(07,:) = [1.00000 1.00000 0.97950]; cmap_redblue(08,:) = [1.00000 0.95243 0.68290]; cmap_redblue(09,:) = [1.00000 0.65583 0.38630]; cmap_redblue(10,:) = [1.00000 0.35923 0.08970]; cmap_redblue(11,:) = [0.79310 0.06263 0.00000]; cmap_redblue(12,:) = [0.49650 0.00000 0.00000]; cmap = [cmap_redblue(01:05,:);cmap_redblue(08:12,:)];

%REDFIELD RATIOS: R_FeP = (0.10/1.00); %[molFe* molP-1] R_NP = (16.00/1.00); %[molN * molP-1] R_CN = (106.00/16.00); %[molC * molN-1]

%MODEL PARAMS: Q10(1) = 1.45; Q10(2) = 1.55; Q10(3) = 1.50; Q10(4) = 1.50;

alfa(1) = 0.40; alfa(2) = 0.44; alfa(3) = 0.44; alfa(4) = 0.38;

teta(1) = 0.01; %[mgChla * mgC-1] teta(2) = 0.01; teta(3) = 0.01; teta(4) = 0.01;

kpar = (1./alfa) .* (1./teta)*(1/4); %[W * m-2] gammax(1) = 4.40; %Coccos gammax(2) = 3.80; %Diatom gammax(3) = 4.40; %SamllP gammax(4) = 2.00; %Diazos

zgrz(1) = 1.05; %Coccos zgrz(2) = 1.00; %Diatom zgrz(3) = 1.05; %SamllP zgrz(4) = 1.20; %Diazos

mupmax(1) = 3.8; %Coccos mupmax(2) = 4.6; %Diatom mupmax(3) = 3.6; %SamllP mupmax(4) = 0.9; %Diazos

kdin = ones(1,4)*nan; %Nitrate (NO3) kdip = ones(1,4)*nan; %Phosphate (PO4) kdop = ones(1,4)*nan; %Diss. Org. Phos. (DOP) knh4 = ones(1,4)*nan; %Ammonium (NH4) kfe2 = ones(1,4)*nan; %Iron (Fe2) ksio = ones(1,4)*inf; %Silica (SiO3)

kdop(1) = 0.30; %Coccos kdop(2) = 0.90; %Diatom kdop(3) = 0.26; %SamllP kdop(4) = 0.09; %Diazos

if strcmp(key_params,'Original')

%ORIGINAL VALUES: kdin(1) = 0.3; kdin(2) = 0.5; kdin(3) = 0.1; kdin(4) = 1.0; kfe2(1) = 0.10; kfe2(2) = 0.12; kfe2(3) = 0.08; kfe2(4) = 0.08; ksio(2) = 1.00;

kdip = kdin/10; knh4 = kdin/10; kdip(4) = kdin(4)/50; knh4(4) = kdin(4)*(3/20);

elseif strcmp(key_params,'Redfield')

%REDFIELD VALUES:

mupmax(3) = mupmax(3)*0.90; %SmallP (my modification) kdop(3) = kdop(3)*(1/4); %SmallP (my modification)

kfe2 = kdop*(R_FeP)*2.00; kdin = kdop*(R_NP)*1/20; kdip = kdin*(1/R_NP); knh4 = kdin/10; ksio(2) = 1.0; %Diatom

end %endif

figure(5) subplot(2,2,1) plot(kdin,knh4,'b-',kdin,knh4,'r*') set(gca,'Xlim',[0 1.20 + eps]) set(gca,'Ylim',[0 0.20 + eps]) xlabel('ksat (DIN)') ylabel('ksat (NH4)') title('ksat (NH4 vs. DIN)') grid on subplot(2,2,2) plot(kdin,kdip,'b-',kdin,kdip,'r*') set(gca,'Xlim',[0 1.20 + eps]) set(gca,'Ylim',[0 0.12 + eps]) xlabel('ksat (DIN)') ylabel('ksat (DIP)') title('ksat (DIP vs. DIN)') grid on subplot(2,2,3) plot(kdin,kdop,'b-',kdin,kdop,'r*') set(gca,'Xlim',[0 1.20 + eps]) set(gca,'Ylim',[0 1.40 + eps]) xlabel('ksat (DIN)') ylabel('ksat (DOP)') title('ksat (DOP vs. DIN)') grid on subplot(2,2,4) plot(kdin,kfe2,'b-',kdin,kfe2,'r*') set(gca,'Xlim',[0 1.20 + eps]) set(gca,'Ylim',[0 0.30 + eps]) xlabel('ksat (DIN)') ylabel('ksat (Fe2)') title('ksat (Fe2 vs. DIN)') grid on print('-dpng ','-r100','nissen_bg_KSAT.png') print('-depsc','-r100','nissen_bg_KSAT.eps')

%ENVIRONMENTAL LIMITATIONS (DIN, PAR, SST): dinmin = 0.05; dinmax = 6.4; parmin = 4.0; %[W * m-2] parmax = 256; %[W * m-2] sstmin = 0; sstmax = 30; sstref = 30; sst = [sstmin:0.50:sstmax]; par = [parmin:4.00:parmax]; %[W * m-2] din = [dinmin:0.05:dinmax]; dip = din*(1.00/16.00); nh4 = din/10; dop = dip*20; fe2 =

dop*R_FeP*2.0; sio = din; par(1) = par(2)/1d2; %to avoid +inf when divided by zero. sst(1) = sst(2)/1d2; %to avoid +inf when divided by zero.

%GRAZING LIMITATION (PHY): phy_chla = [0.02:0.02:2.56]*2; %(mgChla * m-3) cf1 = 1/teta(1); %(mgC * mgChla-1) cf2 = 1/(12.00*R_CN); %(mmolN * mgC-1) phy = phy_chla * cf1 * cf2; %(mmolN * m-3) pc = phy; %(mmolN * m-3) %%pd = phy; %(mmolN * m-3) pd = phy([1:2:end])*2; %(mmolN * m-3)

for i = 1:4 Qsst(:,i) = Q10(i) * exp((sst - sstref) / 10.0); Qphy(:,i) = phy ./ (zgrz(i) + phy); Qdin(:,i) = din ./ (kdin(i) + din); Qdip(:,i) = dip ./ (kdip(i) + dip); Qnh4(:,i) = nh4 ./ (knh4(i) + nh4); Qdop(:,i) = dop ./ (kdop(i) + dop); Qfe2(:,i) = fe2 ./ (kfe2(i) + fe2); Qsio(:,i) = sio ./ (ksio(i) + sio); %%Qpar(:,i) = par ./ (kpar(i) + par); %Simpler function.

dinAve = median(kdin); sstAve = median(sst); QdinAve = dinAve ./ (kdin(i) + dinAve); QsstAve = Q10(i) * exp((sstAve - sstref) / 10.0); % $$$ QdinAve = mean(Qdin(:,i)); % $$$ QsstAve = mean(Qsst(:,i)); Qpar(:,i) = 1.0 - exp(-1.0 * (alfa(i)*teta(i)*par)./(mupmax(i)*QdinAve*QsstAve)); %Original function.

grz_phy(:,i) = Qphy(:,i)*gammax(i); mup_din(:,i) = Qdin(:,i)*mupmax(i); mup_dip(:,i) = Qdip(:,i)*mupmax(i); mup_nh4(:,i) = Qnh4(:,i)*mupmax(i); mup_dop(:,i) = Qdop(:,i)*mupmax(i); mup_fe2(:,i) = Qfe2(:,i)*mupmax(i); mup_sio(:,i) = Qsio(:,i)*mupmax(i); end

figure(10) subplot(2,3,1) hp = plot(din,mup_din,'-'); set(hp,'linewidth',[2]); set(gca,'Xlim',[0 max(din) + eps]) set(gca,'Ylim',[0 5.00 + eps]) axis square xlabel('DIN') ylabel('DIN growth [d-1]') title('DIN') grid on subplot(2,3,1+3) hp = plot(dip,mup_dip,'-'); set(gca,'Xlim',[0 max(dip) + eps]) set(gca,'Ylim',[0 5.00 + eps]) set(hp,'linewidth',[2]); axis square xlabel('DIP') ylabel('DIP growth [d-1]') title('DIP') grid on subplot(2,3,2) hp = plot(nh4,mup_nh4,'-'); set(gca,'Xlim',[0 max(nh4) + eps]) set(gca,'Ylim',[0 5.00 + eps]) set(hp,'linewidth',[2]); axis square xlabel('NH4') ylabel('NH4 growth [d-1]') title('NH4') grid on subplot(2,3,2+3) hp = plot(dop,mup_dop,'-'); set(gca,'Xlim',[0 max(dop) + eps]) set(gca,'Ylim',[0 5.00 + eps]) set(hp,'linewidth',[2]); axis square

xlabel('DOP') ylabel('DOP growth [d-1]') title('DOP') grid on subplot(2,3,3) hp = plot(sio,mup_sio,'-'); set(gca,'Xlim',[0 max(sio) + eps]) set(gca,'Ylim',[0 5.00 + eps]) set(hp,'linewidth',[2]); axis square xlabel('SiO') ylabel('SiO growth [d-1]') title('SiO') legend('coccos','diatom','smallP','diazos','location','east') grid on subplot(2,3,3+3) hp = plot(fe2,mup_fe2,'-'); set(gca,'Xlim',[0 max(fe2) + eps]) set(gca,'Ylim',[0 5.00 + eps]) set(hp,'linewidth',[2]); axis square xlabel('Fe2') ylabel('Fe2 growth [d-1]') title('Fe2') grid on print('-dpng ','-r100','nissen_bg_DIN.png') print('-depsc','-r100','nissen_bg_DIN.eps')

figure(15) subplot(2,2,1) hp = plot(par,Qpar,'-'); set(gca,'Xlim',[0 max(par)]); set(gca,'Ylim',[0 1]) set(hp,'linewidth',[2]); axis square xlabel('PAR') ylabel('PAR limit [n.d.]') title('PAR limit') grid on subplot(2,2,2) hp = plot(sst,Qsst,'-'); set(hp,'linewidth',[2]); axis square xlabel('SST') ylabel('SST limit [n.d.]') title('SST limit') legend('coccos','diatom','smallP','diazos','location','north') grid on subplot(2,2,3) hp = plot(phy,Qphy,'-'); set(gca,'Xlim',[0 max(phy)]); set(gca,'Ylim',[0 1.0]); set(hp,'linewidth',[2]); axis square xlabel('PHY') ylabel('Graze limit [n.d.]') title('Grazing limit') grid on subplot(2,2,4) hp = plot(phy,grz_phy,'-'); set(gca,'Xlim',[0 max(phy)]); set(gca,'Ylim',[0 floor(max(gammax))]); set(hp(1),'linewidth',[2.0],'linestyle','-'); set(hp(2),'linewidth',[2.0],'linestyle','-'); set(hp(3),'linewidth',[2.0],'linestyle',':'); set(hp(4),'linewidth',[2.0],'linestyle','-'); axis square xlabel('PHY') ylabel('Graze rate [d-1]') title('Grazing rate') grid on print('-dpng ','-r100','nissen_bg_PAR.png') print('-depsc','-r100','nissen_bg_PAR.eps')

%RELATIVE GROWTH RATIO (Diatoms / Coccos) 1D:

Rel_mupmax = log(mupmax(2)./mupmax(1)); Rel_Qdin = log(Qdin(:,2)./Qdin(:,1)); Rel_Qpar = log(Qpar(:,2)./Qpar(:,1)); Rel_Qsst = log(Qsst(:,2)./Qsst(:,1));

Rel_din = Rel_mupmax + Rel_Qdin; Rel_par = Rel_mupmax + Rel_Qpar; Rel_sst = Rel_mupmax + Rel_Qsst;

figure(20) subplot(3,3,1) hp = plot(din,Rel_Qdin,'-'); set(gca,'Xlim',[0 max(din) +

eps]) set(gca,'Ylim',[-1.0 +1.0]) set(hp,'linewidth',[2]); xlabel('DIN') ylabel('Rel limit − DIN [n.d.]') title('DIN limitation') grid on subplot(3,3,2) hp = plot(par,Rel_Qpar,'-'); set(gca,'Xlim',[0 max(par) + eps]) set(gca,'Ylim',[-1.0 +1.0]) set(hp,'linewidth',[2]); xlabel('PAR') ylabel('Rel limit − PAR [n.d.]') title('PAR limitation') grid on subplot(3,3,3) hp = plot(sst,Rel_Qsst,'-'); set(gca,'Xlim',[0 max(sst) + eps]) set(gca,'Ylim',[-1.0 +1.0]) set(hp,'linewidth',[2]); xlabel('SST') ylabel('Rel limit − SST [n.d.]') title('SST limitation') grid on subplot(3,3,4) hp = plot(din,Rel_din,'-'); set(gca,'Xlim',[0 max(din) + eps]) set(gca,'Ylim',[-1.0 +1.0]) set(hp,'linewidth',[2]); xlabel('DIN') ylabel('Rel growth − DIN [n.d.]') title('DIN growth') grid on subplot(3,3,5) hp = plot(par,Rel_par,'-'); set(gca,'Xlim',[0 max(par) + eps]) set(gca,'Ylim',[-1.0 +1.0]) set(hp,'linewidth',[2]); xlabel('PAR') ylabel('Rel growth − PAR [n.d.]') title('PAR growth') grid on subplot(3,3,6) hp = plot(sst,Rel_sst,'-'); set(gca,'Xlim',[0 max(sst) + eps]) set(gca,'Ylim',[-1.0 +1.0]) set(hp,'linewidth',[2]); xlabel('SST') ylabel('Rel growth − SST [n.d.]') title('SST growth') grid on print('-dpng ','-r100','nissen_bg_RelMup_1D.png') print('-depsc','-r100','nissen_bg_RelMup_1D.eps')

%ENVIRONMENTAL NICHE 3D:

[DIN,PAR,SST] = ndgrid(din,par,sst); [DIP,PAR,SST] = ndgrid(dip,par,sst);

for i = 1:4

[QDIN_i,QPAR_i,QSST_i]   =   ndgrid(Qdin(:,i),Qpar(:,i),Qsst(:,i)); [QDIP_i,QPAR_i,QSST_i] = ndgrid(Qdip(:,i),Qpar(:,i),Qsst(:,i));

QDIN(:,:,:,i) = QDIN_i; QDIP(:,:,:,i) = QDIP_i; QPAR(:,:,:,i) = QPAR_i; QSST(:,:,:,i) = QSST_i;

end

for i = 1:4 QDIN_bis(:,:,:,i) = DIN ./ (kdin(i) + DIN); QDIP_bis(:,:,:,i) = DIP ./ (kdip(i) + DIP); QPAR_bis(:,:,:,i) = PAR ./ (kpar(i) + PAR); QSST_bis(:,:,:,i) = Q10(i) * exp((SST - sstref) / 10.0); end

QLIM = QDIN .* QPAR .* QSST; for i = 1:4

QLIM_dinpar(:,:,i) = squeeze(QDIN(:,:,1,i) .* QPAR(:,:,1,i)); %QDIN-QPAR ONLY
QLIM_dinsst(:,:,i) = squeeze(QDIN(:,1,:,i) .* QSST(:,1,:,i)); %QDIN-QSST ONLY
QLIM_parsst(:,:,i) = squeeze(QPAR(1,:,:,i) .* QSST(1,:,:,i)); %QPAR-QSST ONLY

MUP(:,:,:,i) = QLIM(:,:,:,i) * mupmax(i); end

%RELATIVE GROWTH RATIO 3D:

%—

Rel_QDIN = log(QDIN(:,:,:,2)./QDIN(:,:,:,1)); Rel_QDIP = log(QDIP(:,:,:,2)./QDIP(:,:,:,1)); Rel_QPAR = log(QPAR(:,:,:,2)./QPAR(:,:,:,1)); Rel_QSST = log(QSST(:,:,:,2)./QSST(:,:,:,1)); Rel_QLIM = Rel_QDIN + Rel_QPAR + Rel_QSST;

Rel_QLIM_dinpar = squeeze(Rel_QDIN(:,:,1) + Rel_QPAR(:,:,1)); %QDIN-QPAR ONLY Rel_QLIM_dinsst = squeeze(Rel_QDIN(:,1,:) + Rel_QSST(:,1,:)); %QDIN-QSST ONLY Rel_QLIM_parsst = squeeze(Rel_QPAR(1,:,:) + Rel_QSST(1,:,:)); %QPAR-QSST ONLY

%—

Rel_MUP_din = Rel_mupmax + Rel_QDIN; Rel_MUP_par = Rel_mupmax + Rel_QPAR; Rel_MUP_sst = Rel_mupmax + Rel_QSST; Rel_MUP_tot = Rel_mupmax + Rel_QLIM;

Rel_MUP_dinpar = Rel_mupmax + Rel_QLIM_dinpar; Rel_MUP_dinsst = Rel_mupmax + Rel_QLIM_dinsst; Rel_MUP_parsst = Rel_mupmax + Rel_QLIM_parsst;

%—

%RELATIVE GRAZING RATIO ON COCCOS AND DIATOMS (ONLY) – 2D: CLRmax =

max(gammax) / min(zgrz); %Maximum clearance rate (m3 * mmolN-1 * d-1) gammaxC = gammax(1); %Coccos gammaxD = gammax(2); %Diatom zgrzC = zgrz(1); %Coccos zgrzD = zgrz(2); %Diatom

[PC,PD] = ndgrid(pc,pd);

GRZ_COCO = gammaxC * (PC ./ (zgrzC + PC + PD)); %OK GRZ_DIAT = gammaxD * (PD ./ (zgrzD + PC + PD)); %OK

GRZ_COCO_WRONG = gammaxC * (PC ./ (zgrzC + PC)); %WRONG! GRZ_DIAT_WRONG = gammaxD * (PD ./ (zgrzD + PD)); %WRONG!

CLR_COCO = GRZ_COCO./PC; %clearance rate on coccos (m3 * mmolN-1 * d-1) CLR_DIAT = GRZ_DIAT./PD; %clearance rate on diatom (m3 * mmolN-1 * d-1) Rel_CLR = log(CLR_COCO./CLR_DIAT);

CLR_COCO_WRONG = GRZ_COCO_WRONG./PC; %clearance rate on coccos (m3 * mmolN-1 * d-1) CLR_DIAT_WRONG = GRZ_DIAT_WRONG./PD; %clearance rate on diatom (m3 * mmolN-1 * d-1) Rel_CLR_WRONG = log(CLR_COCO_WRONG./CLR_DIAT_WRONG);

%»> DY = diff(GRZ_COCO_WRONG,[],1); DX = diff(PC,[],1); SLOPE = DY./DX; CLR_COCO_ALONE = [SLOPE;SLOPE(end,:)];

DY = diff(GRZ_DIAT_WRONG,[],2); DX = diff(PD,[],2); SLOPE = DY./DX; CLR_DIAT_ALONE = [SLOPE,SLOPE(:,end)];

figure(1) %just checking things. subplot(2,2,1) plot(CLR_COCO_WRONG(:),CLR_COCO_AL set(gca,'Xlim',[0 4]) set(gca,'Ylim',[0 4]) grid on subplot(2,2,2) plot(CLR_DIAT_WRONG(:),CLR_DIAT_ALONE(:),'*') set(gca,'Xlim',[0 4]) set(gca,'Ylim',[0 4]) grid on %«<

%ALTERNATIVE METHOD: PHY(:,:,1) = PC; PHY(:,:,2) = PD; PHYTOT = sum(PHY,3); for i = 1:2 %Coccos and Diatoms (only) QPHY(:,:,i) = PHY(:,:,i) ./ (zgrz(i) + PHYTOT);

GRZ(:,:,i) = QPHY(:,:,i)*gammax(i); end

Rel_gammax = log(gammax(1)./gammax(2)); Rel_QPHY = log(QPHY(:,:,1)./QPHY(:,:,2)); Rel_GRZ = Rel_gammax + Rel_QPHY;

CLR = GRZ ./ PHY; %clearance rate (m3 * mmolN-1 * d-1) GRZ_COCO_bis = GRZ(:,:,1); %specific grazing rate on coccos (d-1) GRZ_DIAT_bis = GRZ(:,:,2); %specific grazing rate on diatom (d-1) CLR_COCO_bis = CLR(:,:,1); %clearance rate on coccos (m3 * mmolN-1 * d-1) CLR_DIAT_bis = CLR(:,:,2); %clearance rate on diatom (m3 * mmolN-1 * d-1) Rel_GRZ_bis = log(GRZ_COCO_bis./GRZ_DIAT_bis); Rel_CLR_bis = log(CLR_COCO_bis./CLR_DIAT_bis);

QPHY_TOT = sum(QPHY,3); GRZ_TOT = sum(GRZ,3); CLR_TOT = sum(CLR,3);

figure(100) subplot(2,2,1) imagesc(din,par,QLIM_dinpar(:,:,1)') set(gca,'YDir','normal') caxis([0.0 1.0]) xlabel('DIN') ylabel('PAR') title('Coccos Limit (DIN + PAR)') colormap(cmap) colorbar grid on subplot(2,2,2) imagesc(din,par,QLIM_dinpar(:,:,2)') set(gca,'YDir','normal') caxis([0.0 1.0]) xlabel('DIN') ylabel('PAR') title('Diatom Limit (DIN + PAR)') colormap(cmap) colorbar grid on subplot(2,2,3) imagesc(din,par,Rel_QLIM_dinpar') set(gca,'YDir','normal') caxis([-0.4 +0.4]) xlabel('DIN') ylabel('PAR') title('Rel Limit (DIN + PAR)') colormap(cmap) colorbar grid on subplot(2,2,4) imagesc(din,par,Rel_MUP_dinpar') set(gca,'YDir','normal') caxis([-0.4 +0.4]) xlabel('DIN') ylabel('PAR') title('Rel Growth (DIN + PAR)') colormap(cmap) colorbar grid on print('-dpng ','-r100','nissen_bg_RelMup_Limit-vs-Rate_2D.png') print('-depsc','-r100','nissen_bg_RelMup_Limit-vs-Rate_2D.eps')

figure(110) subplot(3,3,1) imagesc(pc,pd,QPHY(:,:,1)') set(gca,'YDir','normal') caxis([0.0 1.0]) xlabel('PC') ylabel('PD') title('Grazing Limit (PC)') colormap(cmap) colorbar grid on subplot(3,3,2) imagesc(pc,pd,QPHY(:,:,2)') set(gca,'YDir','normal') caxis([0.0 1.0]) xlabel('PC') ylabel('PD') title('Grazing Limit (PD)') colormap(cmap) colorbar grid on subplot(3,3,3) imagesc(pc,pd,QPHY_TOT') set(gca,'YDir','normal') caxis([0.0 1.0]) xlabel('PC') ylabel('PD') title('Grazing Limit (PC + PD)') col-

ormap(cmap) colorbar grid on subplot(3,3,1+3) imagesc(pc,pd,GRZ(:,:,1)') set(gca,'YDir','normal') caxis([0.0 floor(max(gammax))]) xlabel('PC') ylabel('PD') title('Grazing Rate (PC)') colormap(cmap) colorbar grid on subplot(3,3,2+3) imagesc(pc,pd,GRZ(:,:,2)') set(gca,'YDir','normal') caxis([0.0 floor(max(gammax))]) xlabel('PC') ylabel('PD') title('Grazing Rate (PD)') colormap(cmap) colorbar grid on subplot(3,3,3+3) imagesc(pc,pd,GRZ_TOT') set(gca,'YDir','normal') caxis([0.0 floor(max(gammax))]) xlabel('PC') ylabel('PD') title('Grazing Rate (PC + PD)') colormap(cmap) colorbar grid on subplot(3,3,1+6) imagesc(pc,pd,CLR(:,:,1)') set(gca,'YDir','normal') caxis([0.0 CLRmax/2]) xlabel('PC') ylabel('PD') title('Clearance Rate (PC)') colormap(cmap) colorbar grid on subplot(3,3,2+6) imagesc(pc,pd,CLR(:,:,2)') set(gca,'YDir','normal') caxis([0.0 CLRmax/2]) xlabel('PC') ylabel('PD') title('Clearance Rate (PD)') colormap(cmap) colorbar grid on subplot(3,3,3+6) imagesc(pc,pd,CLR_TOT') set(gca,'YDir','normal') caxis([0.0 CLRmax/2]) xlabel('PC') ylabel('PD') title('Clearance Rate (PC + PD)') colormap(cmap) colorbar grid on print('-dpng ','-r100','nissen_bg_RelGrz_Limit-vs-Rate_2D.png') print('-depsc','-r100','nissen_bg_RelGrz_Limit-vs-Rate_2D.eps')

figure(40) subplot(3,3,1) himg = imagesc(din,par,Rel_QLIM_dinpar); %QDIN-QPAR ONLY. set(gca,'YDir','normal') %%axis square caxis([-0.4 +0.4]) xlabel('DIN') ylabel('PAR') title('Rel Limit (DIN + PAR)') %%colormap(redbluecmap) colormap(cmap) colorbar grid on subplot(3,3,2) himg = imagesc(din,sst,Rel_QLIM_dinsst); %QDIN-QSST ONLY. set(gca,'YDir','normal') %%axis square caxis([-0.4 +0.4]) xlabel('DIN') ylabel('SST') title('Rel Limit (DIN + SST)') colormap(cmap) colorbar grid on subplot(3,3,3) himg = imagesc(par,sst,Rel_QLIM_parsst); %QPAR-QSST ONLY. set(gca,'YDir','normal') %%axis square caxis([-0.4 +0.4]) xlabel('PAR') ylabel('SST') title('Rel Limit (PAR + SST)') colormap(cmap) colorbar grid on subplot(3,3,4) himg = imagesc(din,par,Rel_MUP_dinpar); %QDIN-QPAR ONLY. set(gca,'YDir','normal') %%axis square caxis([-0.4 +0.4]) xlabel('DIN') ylabel('PAR') title('Rel Growth (DIN + PAR)') %%colormap(redbluecmap) colormap(cmap) colorbar grid on subplot(3,3,5) himg = imagesc(din,sst,Rel_MUP_dinsst); %QDIN-QSST ONLY.

set(gca,'YDir','normal') %%axis square caxis([-0.4 +0.4]) xlabel('DIN') ylabel('SST') title('Rel Growth (DIN + SST)') colormap(cmap) colorbar grid on subplot(3,3,6) himg = imagesc(par,sst,Rel_MUP_parsst); %QPAR-QSST ONLY. set(gca,'YDir','normal') %%axis square caxis([-0.4 +0.4]) xlabel('PAR') ylabel('SST') title('Rel Growth (PAR + SST)') colormap(cmap) colorbar grid on %»> % $$$ subplot(2,2,4) % $$$ caxis([-0.4 +0.4]) % $$$ text(0.4,0.8,'Diatom win (red)') % $$$ text(0.4,0.2,'Coccos win (blue)') % $$$ set(gca,'Xtick',[],'Xticklabel',[]) % $$$ set(gca,'Ytick',[],'Yticklabel',[]) % $$$ colormap(cmap) % $$$ colorbar % $$$ axis off %«< print('-dpng ','-r100','nissen_bg_RelMup_2D.png') print('-depsc','-r100','nissen_bg_RelMup_2D.eps')

figure(70) subplot(3,3,1) himg = imagesc(pc,pd,CLR_COCO_WRONG'); set(gca,'YDir','normal') caxis([0.0 CLRmax/2]) %%axis square xlabel('PC – WRONG!') ylabel('PD') title('Clearance rate – PC') colormap(cmap) colorbar grid on subplot(3,3,2) himg = imagesc(pc,pd,CLR_DIAT_WRONG'); set(gca,'YDir','normal') caxis([0.0 CLRmax/2]) %%axis square xlabel('PC – WRONG!') ylabel('PD') title('Clearance rate – PD') colormap(cmap) colorbar grid on subplot(3,3,3) himg = imagesc(pc,pd,Rel_CLR_WRONG'); %if Rel_CLR is positive, then PC is being grazed faster than PD. set(gca,'YDir','normal') caxis([-0.4 +0.4]) %%axis square xlabel('PC – WRONG!') ylabel('PD') title('Rel Clearance (C:D)') colormap(cmap) colorbar grid on subplot(3,3,1+3) himg = imagesc(pc,pd,CLR_COCO'); set(gca,'YDir','normal') caxis([0.0 CLRmax/2]) %%axis square xlabel('PC') ylabel('PD') title('Clearance rate – PC') colormap(cmap) colorbar grid on subplot(3,3,2+3) himg = imagesc(pc,pd,CLR_DIAT'); set(gca,'YDir','normal') caxis([0.0 CLRmax/2]) %%axis square xlabel('PC') ylabel('PD') title('Clearance rate – PD') colormap(cmap) colorbar grid on subplot(3,3,3+3) himg = imagesc(pc,pd,Rel_CLR'); %if Rel_CLR is positive, then PC is being grazed faster than PD. set(gca,'YDir','normal') caxis([-0.4 +0.4]) %%axis square xlabel('PC') ylabel('PD') title('Rel Clearance (C:D)') colormap(cmap) colorbar grid on subplot(3,3,1+6) imagesc(pc,pd,Rel_QPHY') set(gca,'YDir','normal') caxis([-0.4 +0.4]) axis square xlabel('PC') ylabel('PD') title('Rel Limit (PC:PD)') colormap(cmap) colorbar grid on subplot(3,3,2+6) im-

agesc(pc,pd,Rel_GRZ') set(gca,'YDir','normal') caxis([-0.4 +0.4]) axis square xlabel('PC') ylabel('PD') title('Rel Grazing (PC:PD)') colormap(cmap) colorbar grid on subplot(3,3,3+6) imagesc(pc,pd,Rel_CLR') set(gca,'YDir','normal') caxis([-0.4 +0.4]) axis square xlabel('PC') ylabel('PD') title('Rel Clearance (PC:PD)') colormap(cmap) colorbar grid on print('-dpng ','-r100','nissen_bg_RelGrz.png') print('-depsc','-r100','nissen_bg_RelGrz.eps')

return

publish('nissen_bg_myreview','pdf')

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Please also note the supplement to this comment:
https://www.biogeosciences-discuss.net/bg-2018-157/bg-2018-157-RC2-supplement.pdf