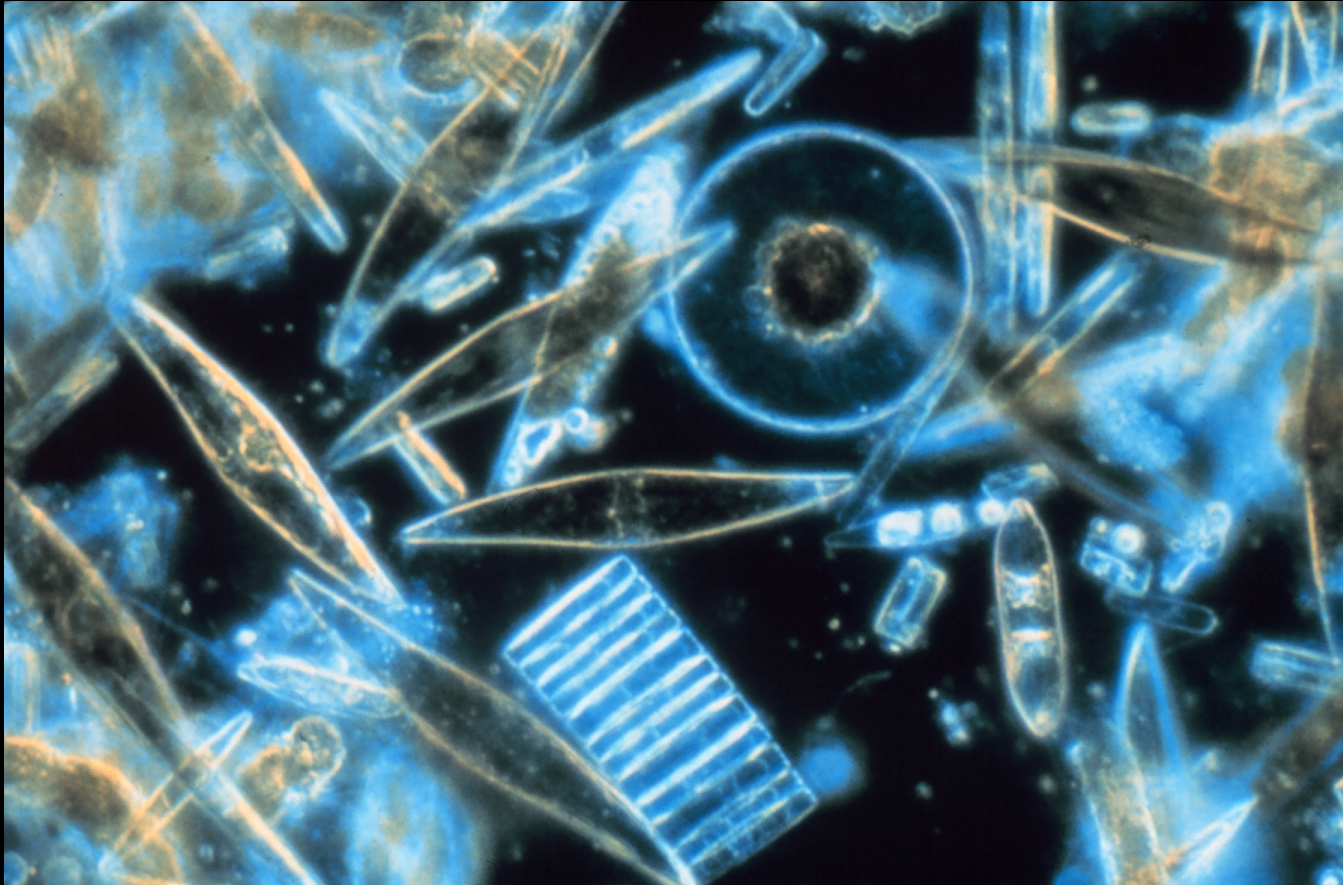


Hacking Ecology

a primer for data-driven ecology
in the Anthropocene

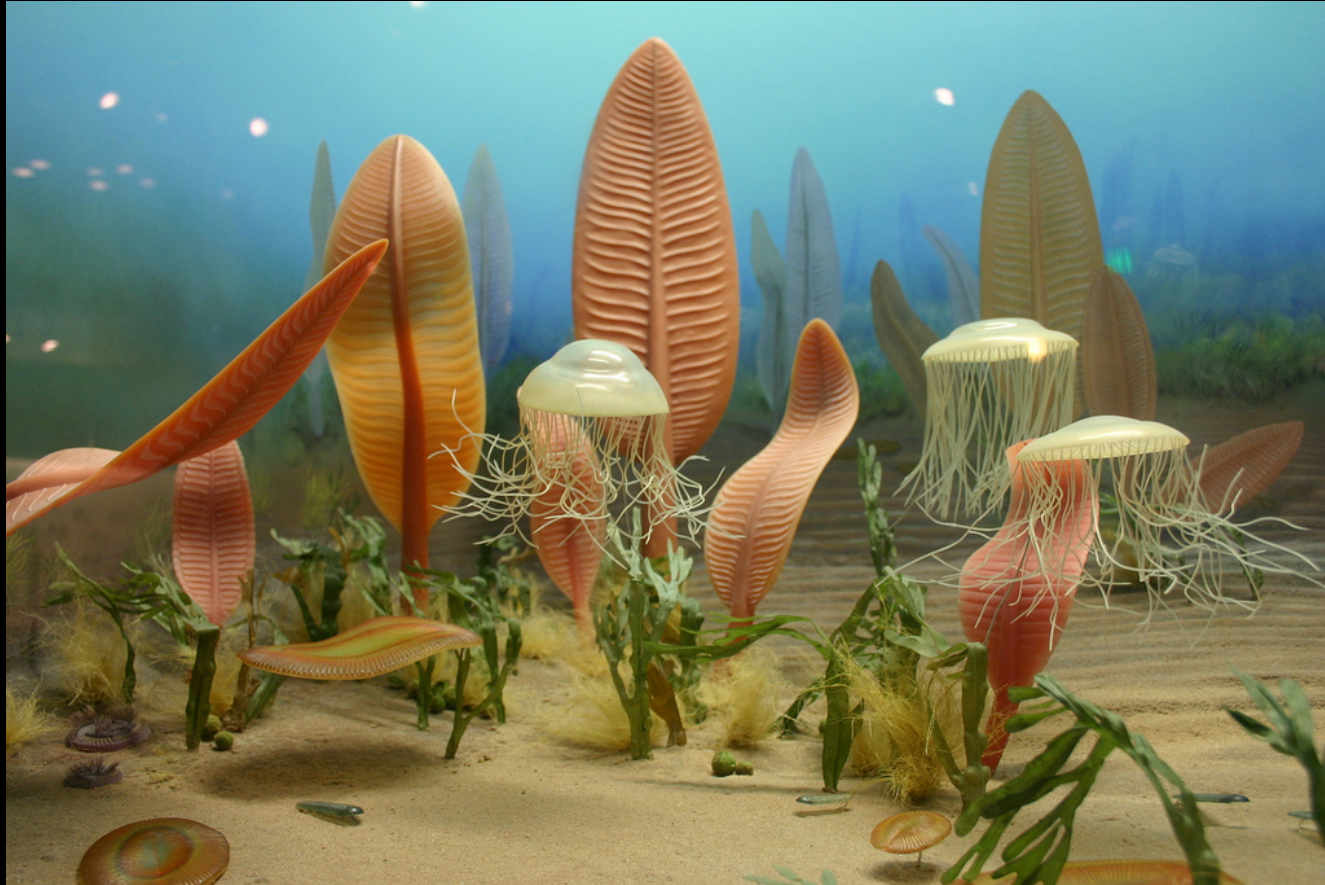
Theodor Sperlea
Uni Marburg, Bioinformatik
sperleath@posteo.net

In the Beginning...

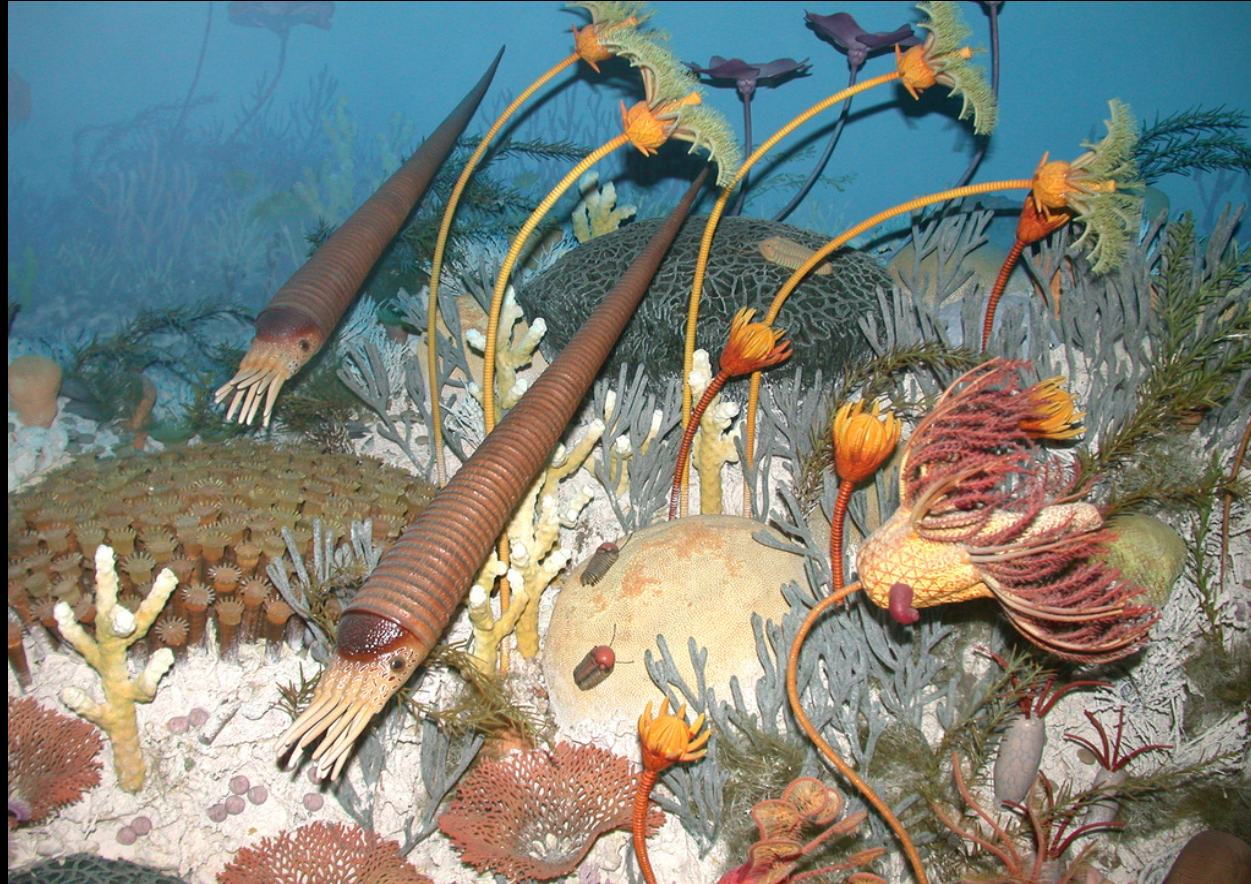


“Assorted diatoms found living between crystals of annual sea ice in Antarctica” (Public Domain)
by Prof. Gordon T. Taylor, Stony Brook University - corp2365, NOAA Corps Collection

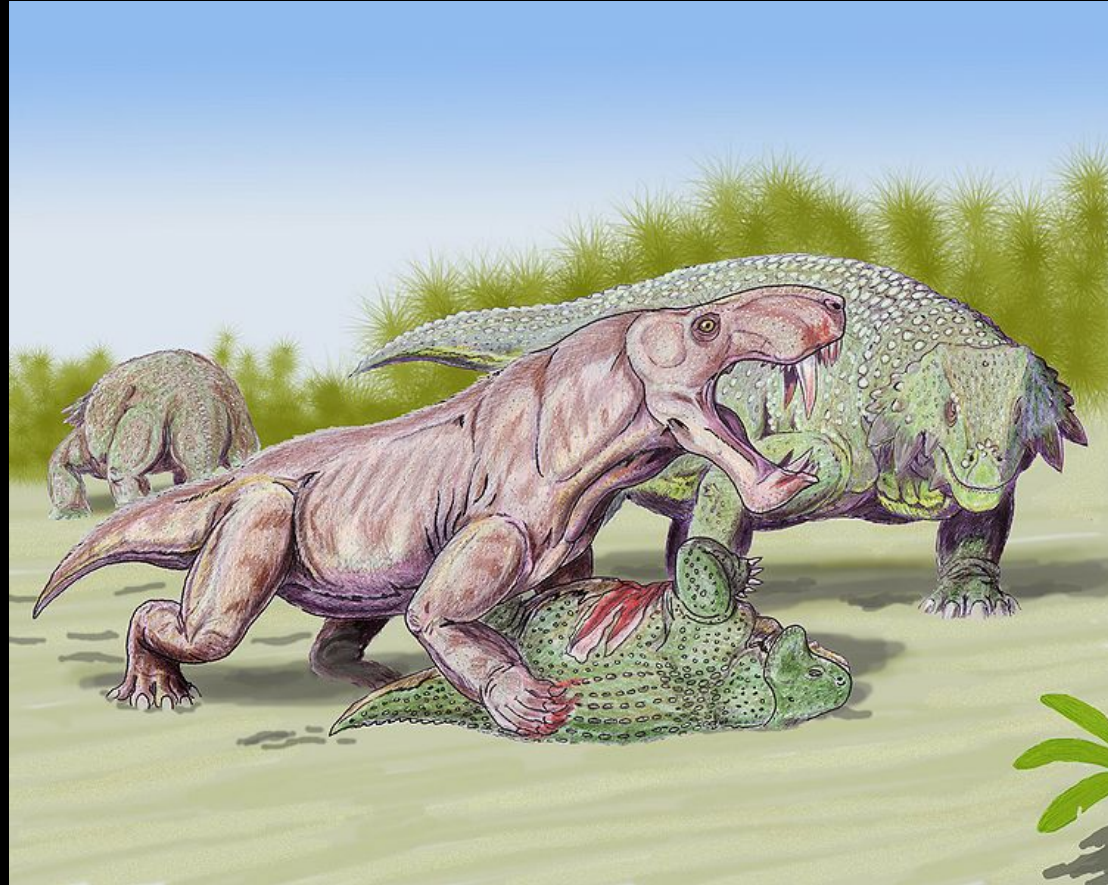
Diversification and Adaption



Diversification and Adaption



Diversification and Adaption



Extinction Events



The Age of the Mammals




The Anthropocene



The Anthropocene



More than 75 percent decline over 27 years in total flying insect biomass in protected areas

Caspar A. Hallmann , Martin Sorg, Eelke Jongejans, Henk Siepel, Nick Hofland, Heinz Schwan, Werner Stenmans, Andreas Müller, Hubert Sumser, Thomas Hörren, Dave Goulson, Hans de Kroon



Extinction rates rise...

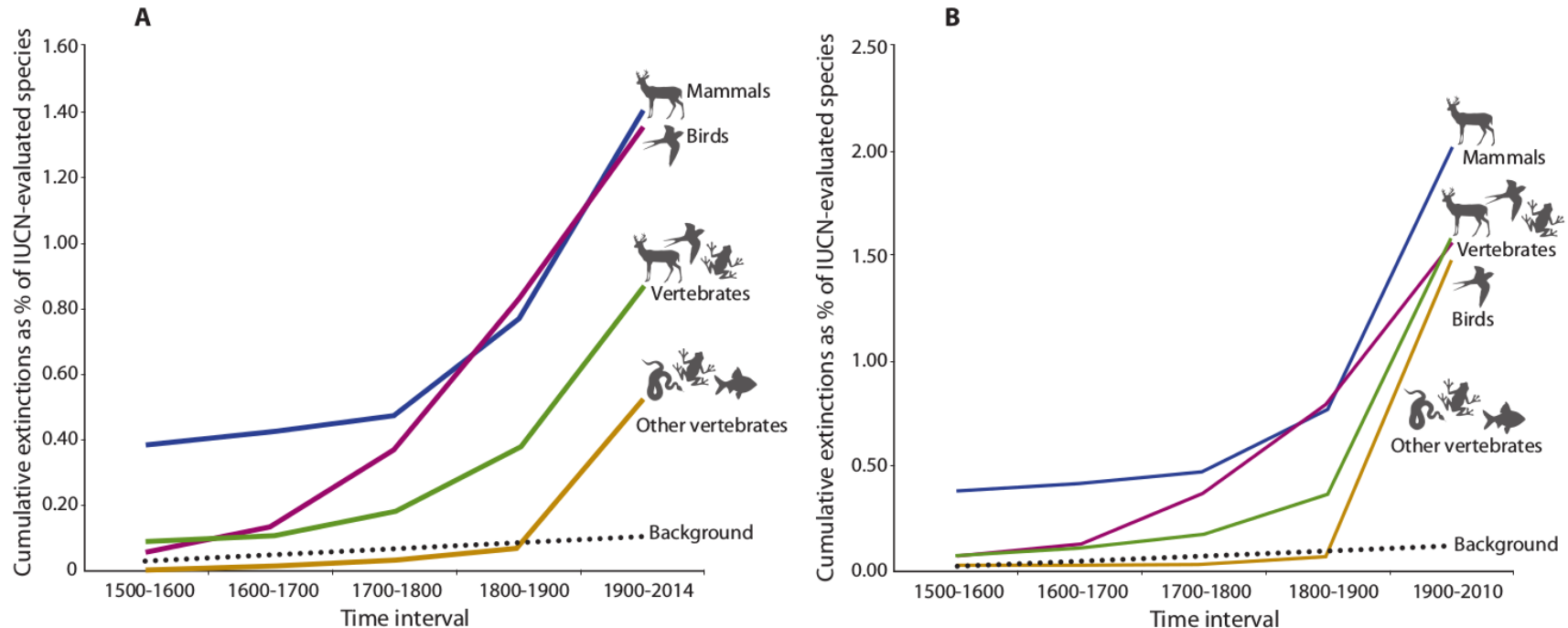
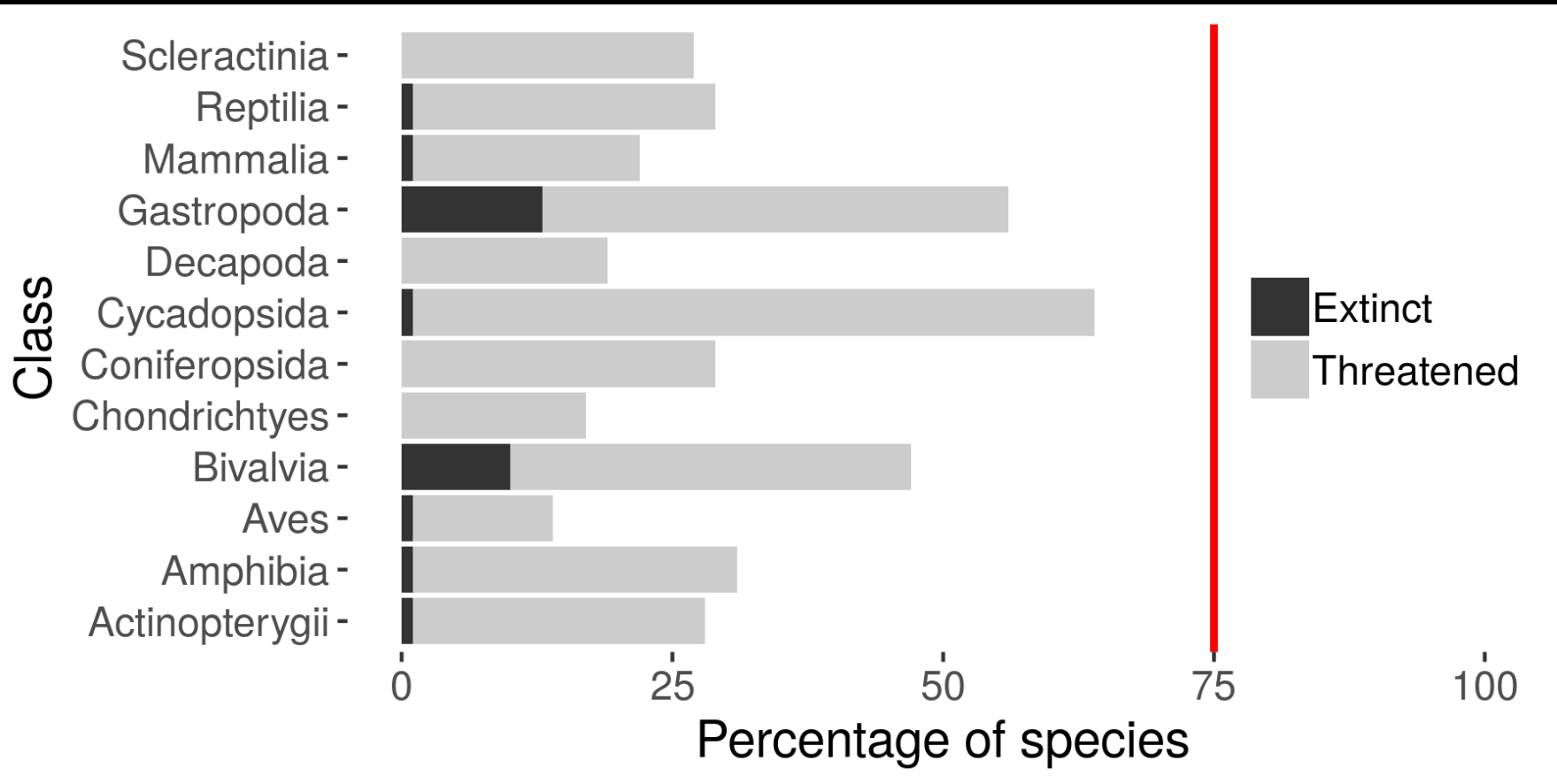


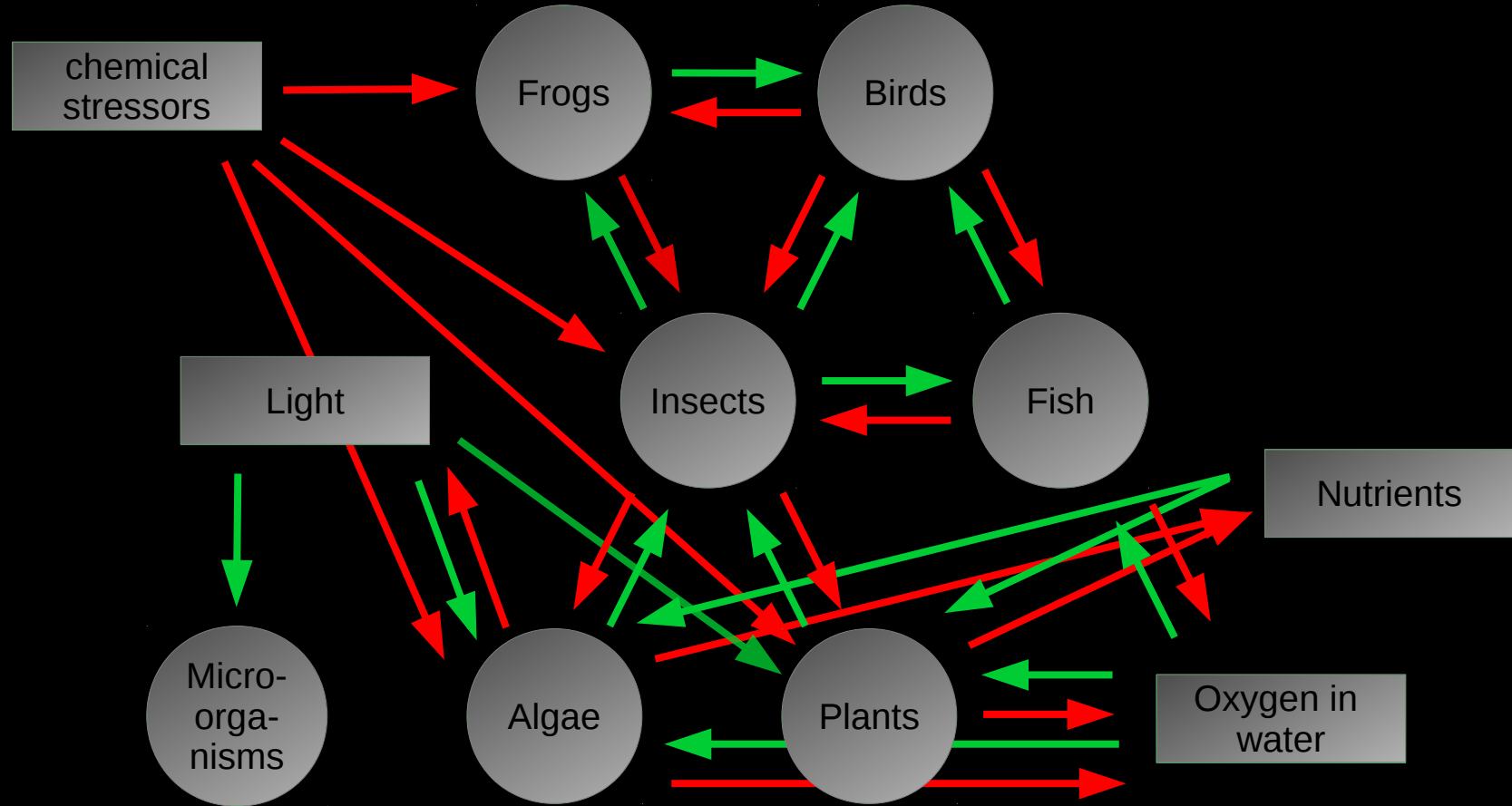
Fig. 1. Cumulative vertebrate species recorded as extinct or extinct in the wild by the IUCN (2012). Graphs show the percentage of the number of species evaluated among mammals (5513; 100% of those described), birds (10,425; 100%), reptiles (4414; 44%), amphibians (6414; 88%), fishes (12,457; 38%), and all vertebrates combined (39,223; 59%). Dashed black curve represents the number of extinctions expected under a constant standard background rate of 2 E/MSY. (A) Highly conservative estimate. (B) Conservative estimate.

Extinction rates rise...

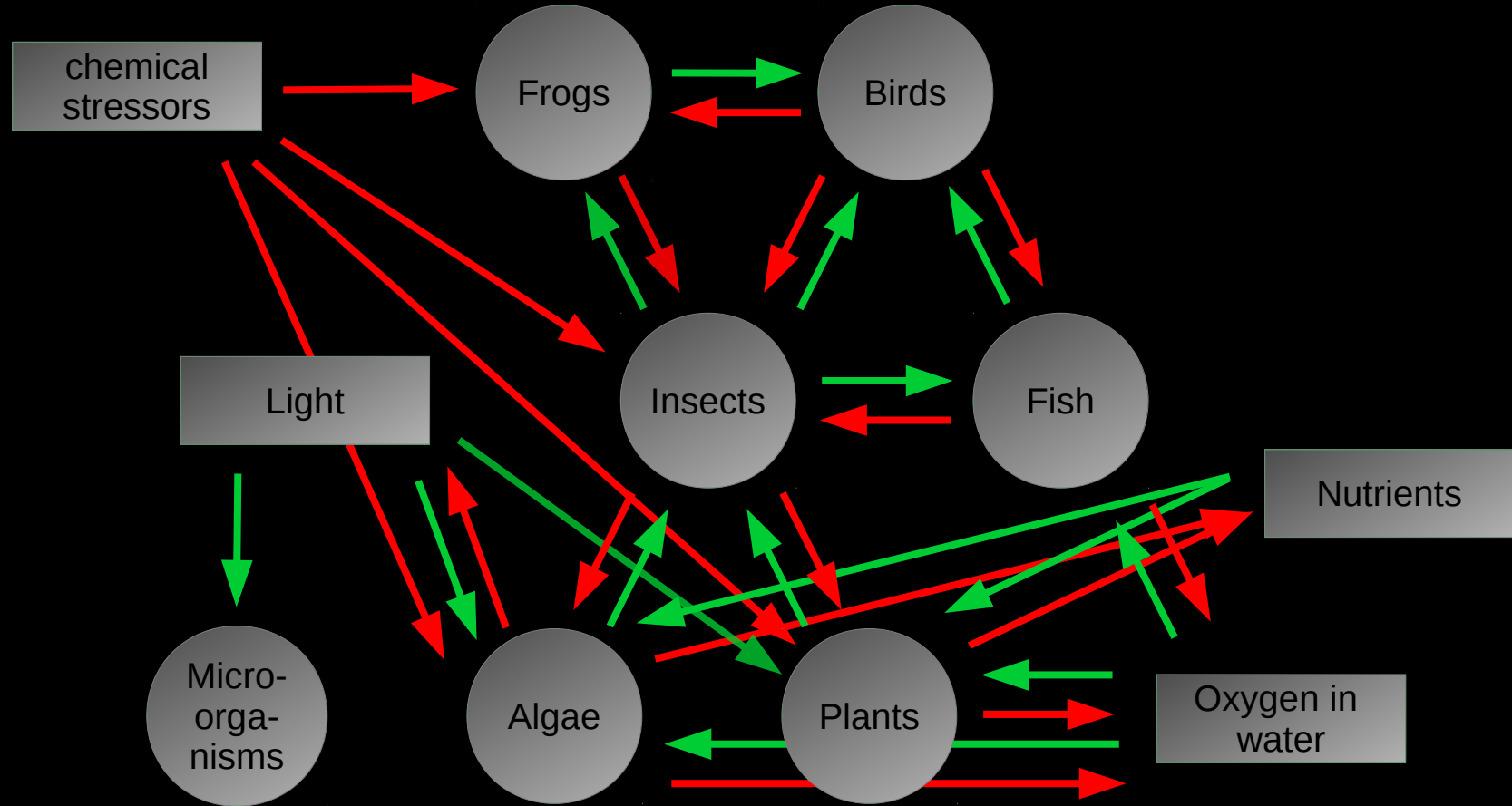


And everyone knows it

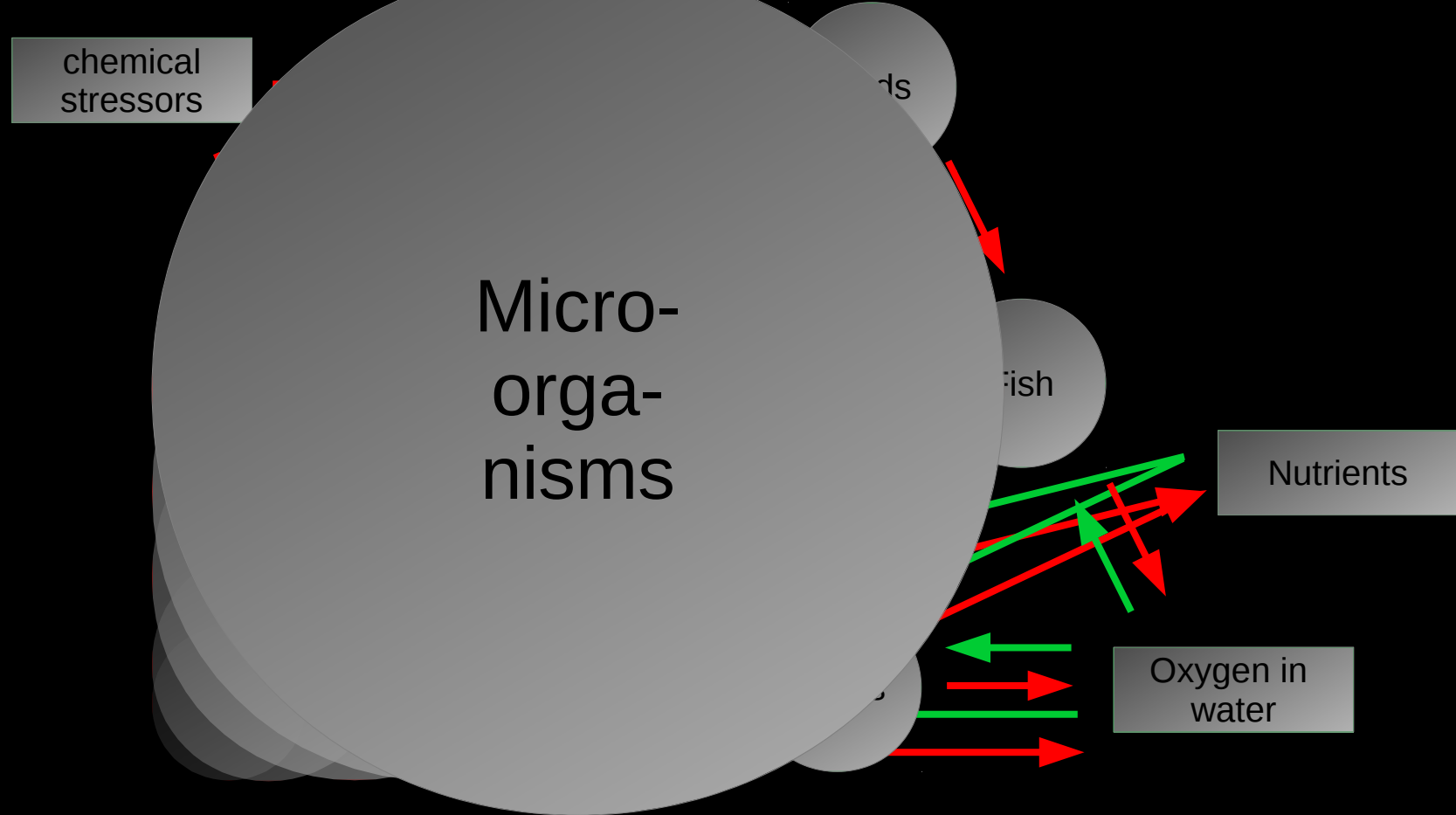
What is an ecosystem, anyway?



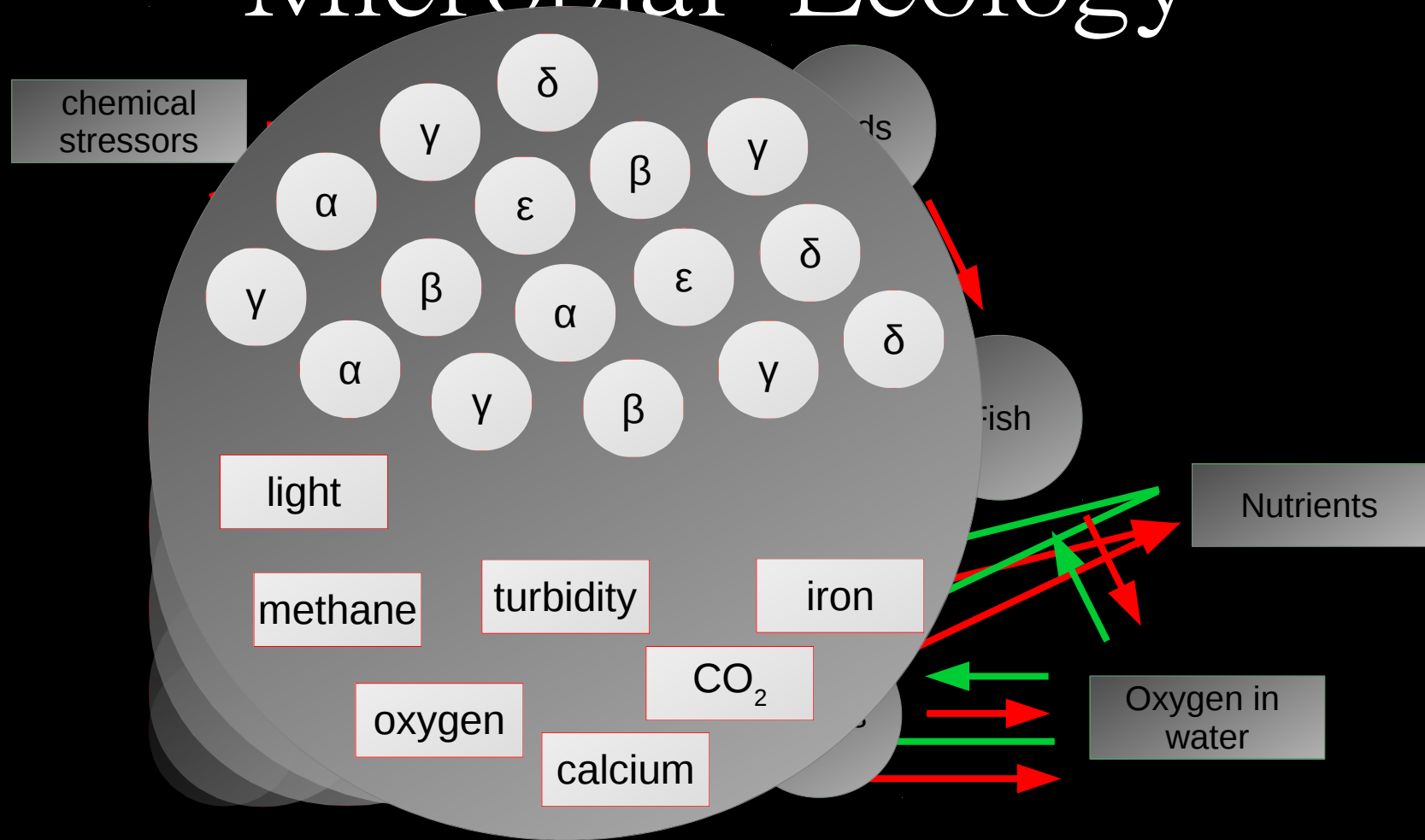
Microbial Ecology



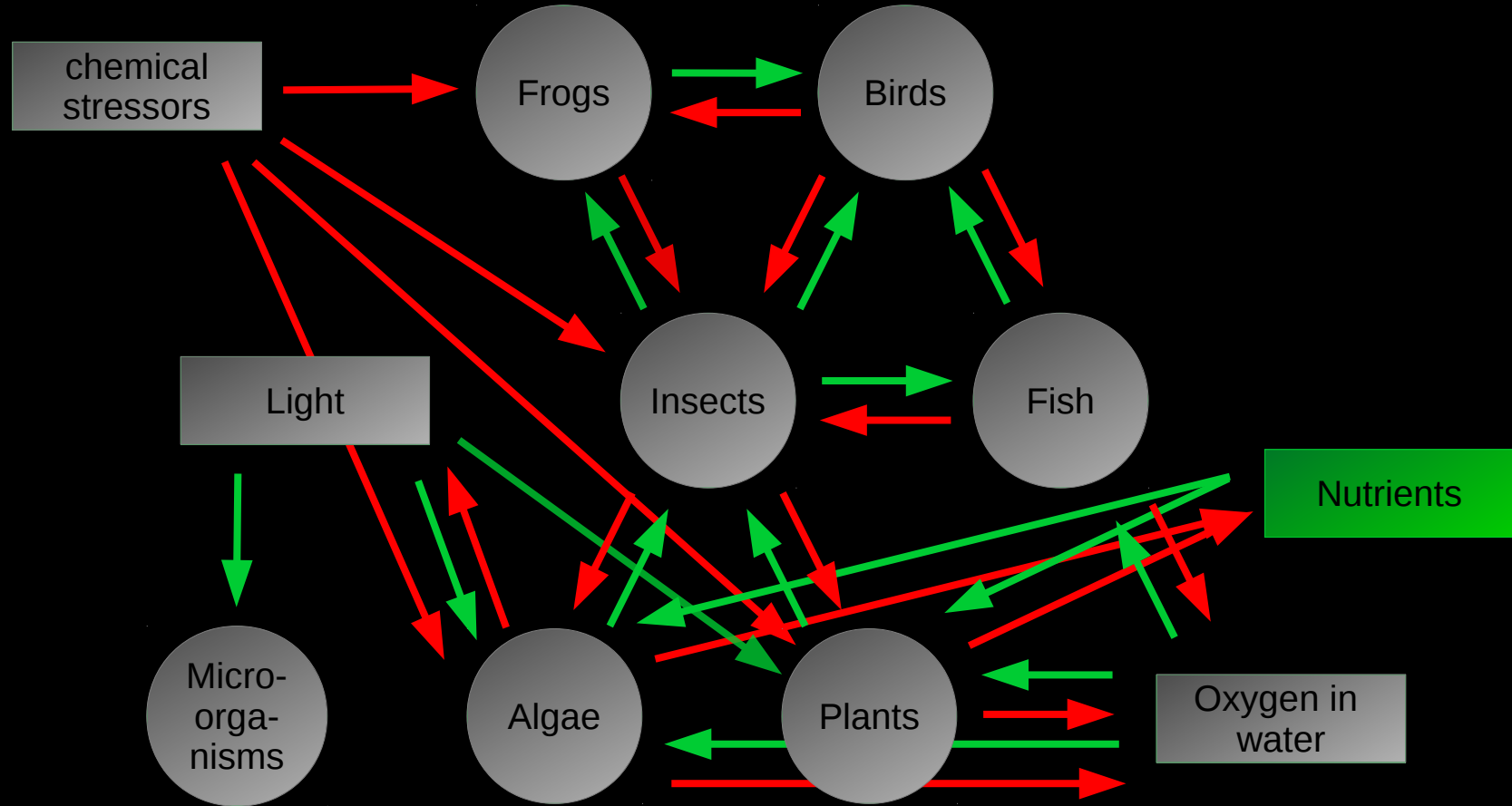
Microbial Ecology



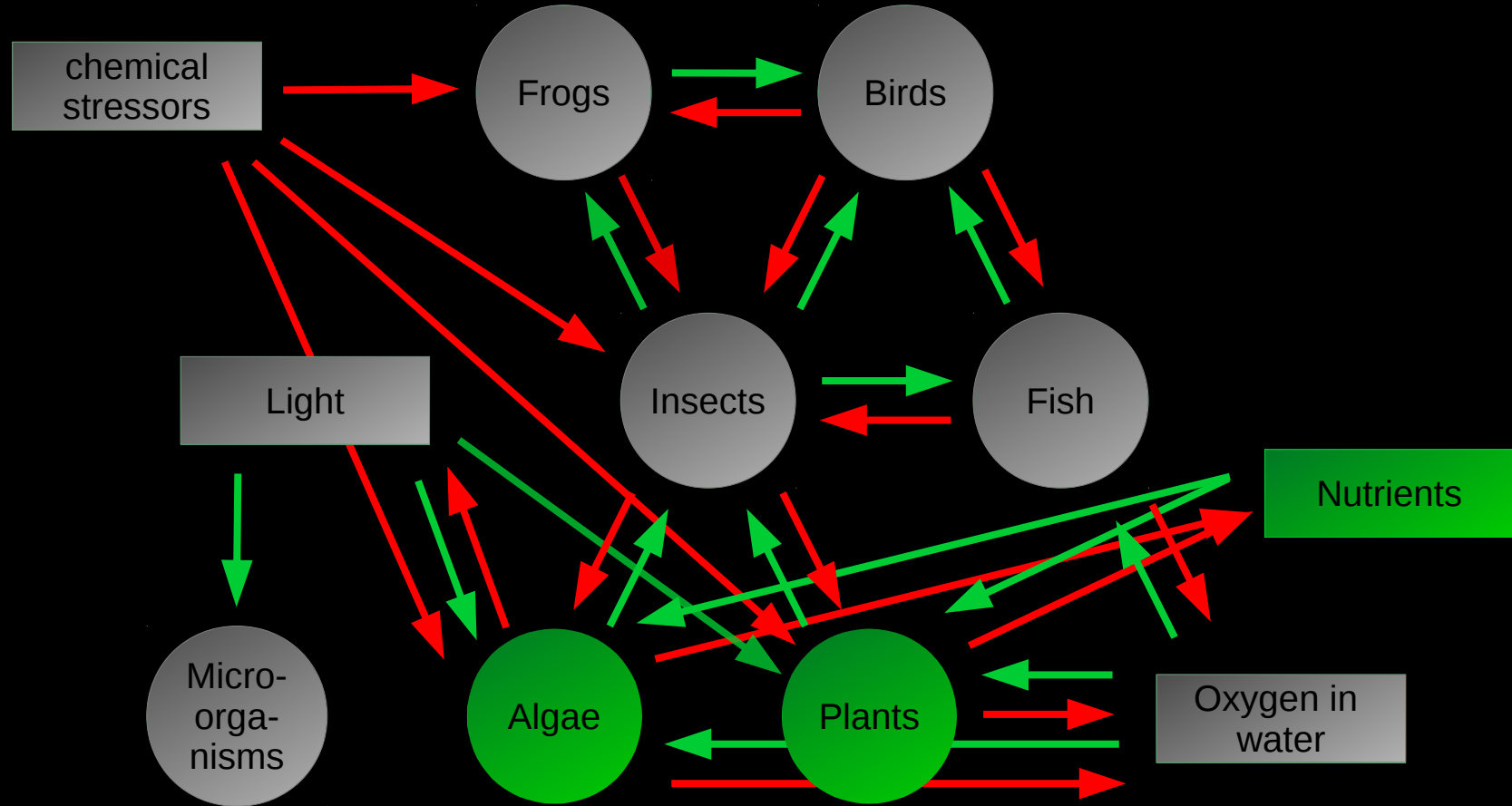
Microbial Ecology



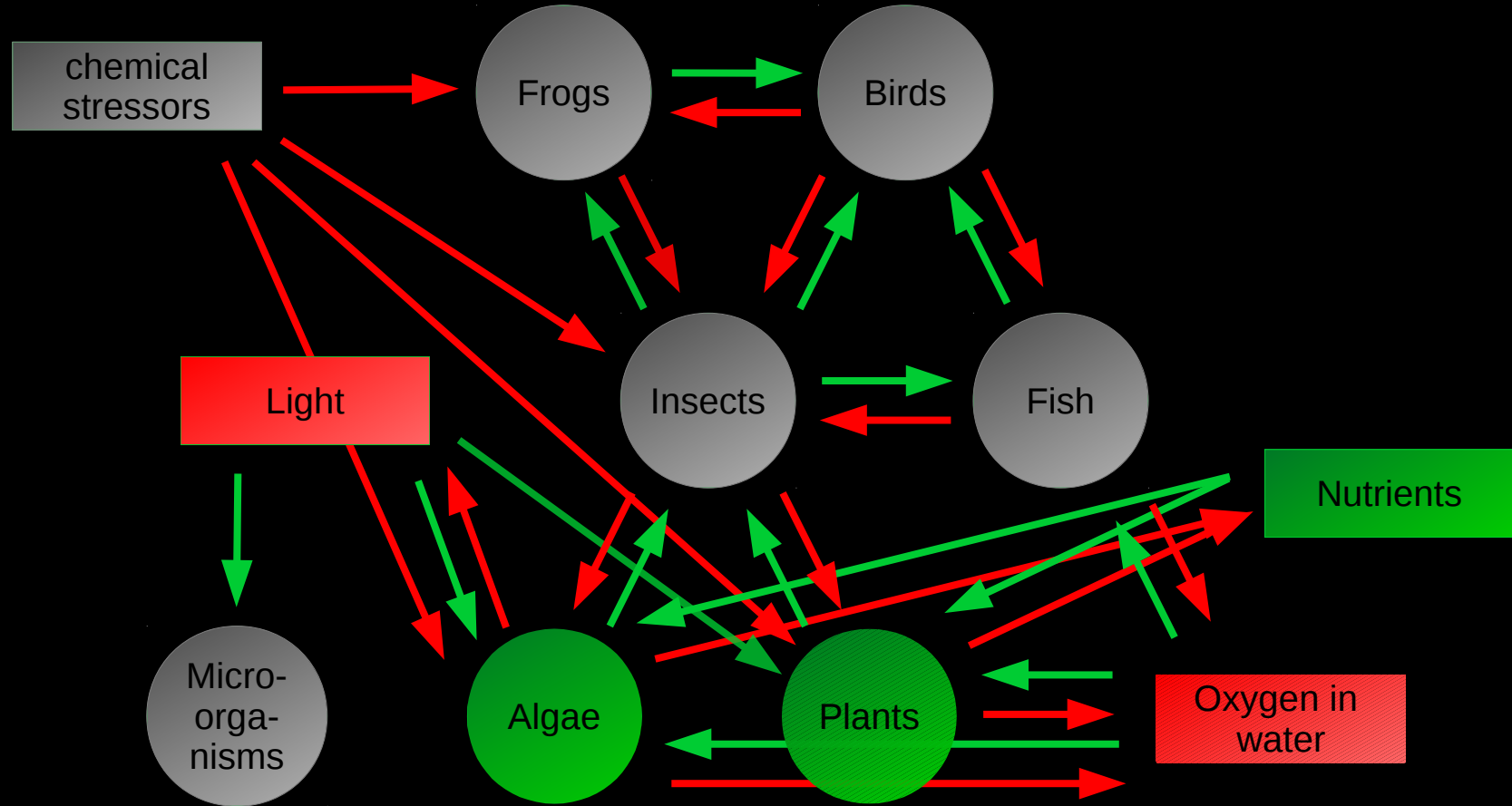
Disruption I: Nutrient excess



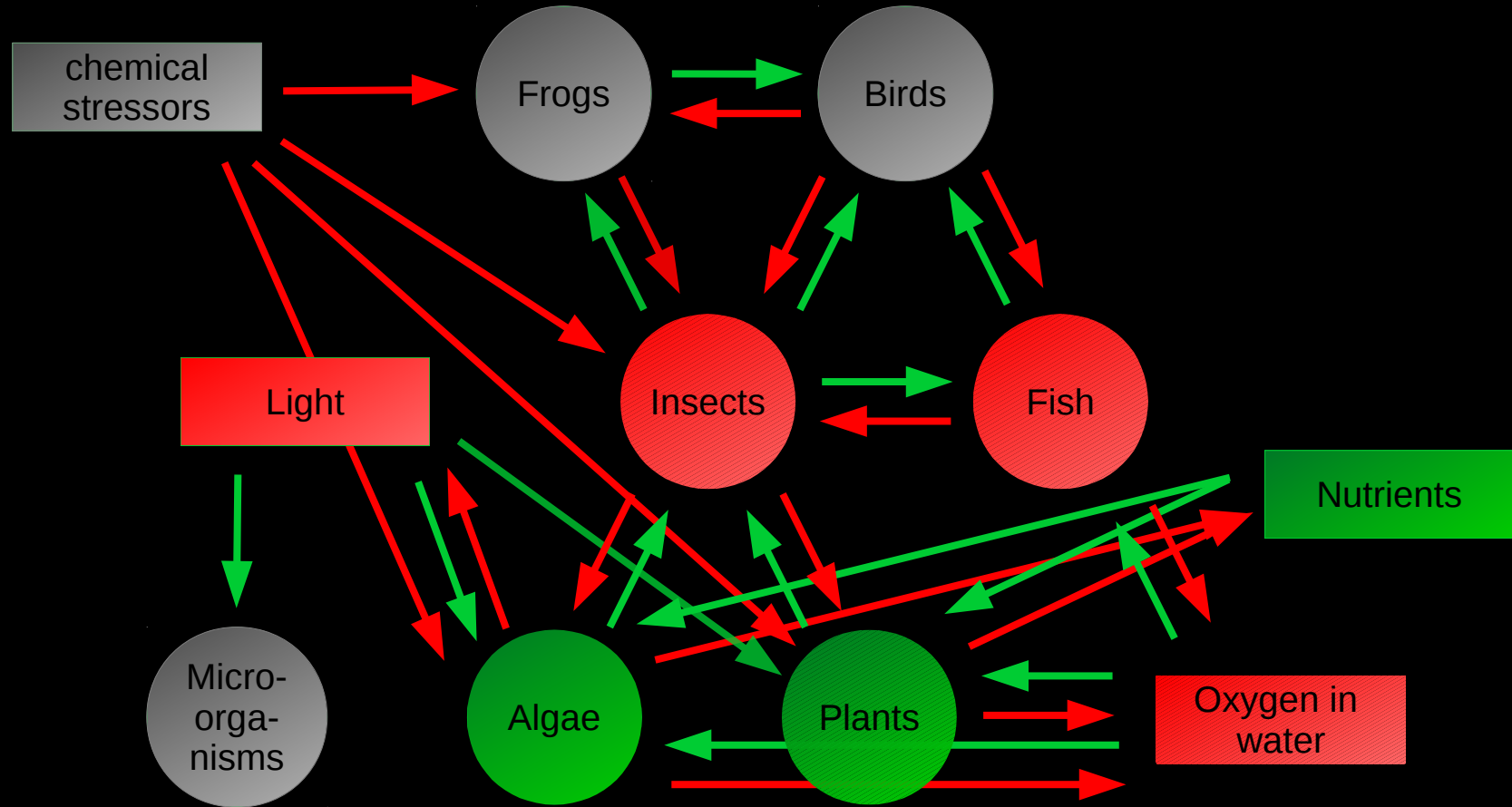
Disruption I: Nutrient excess



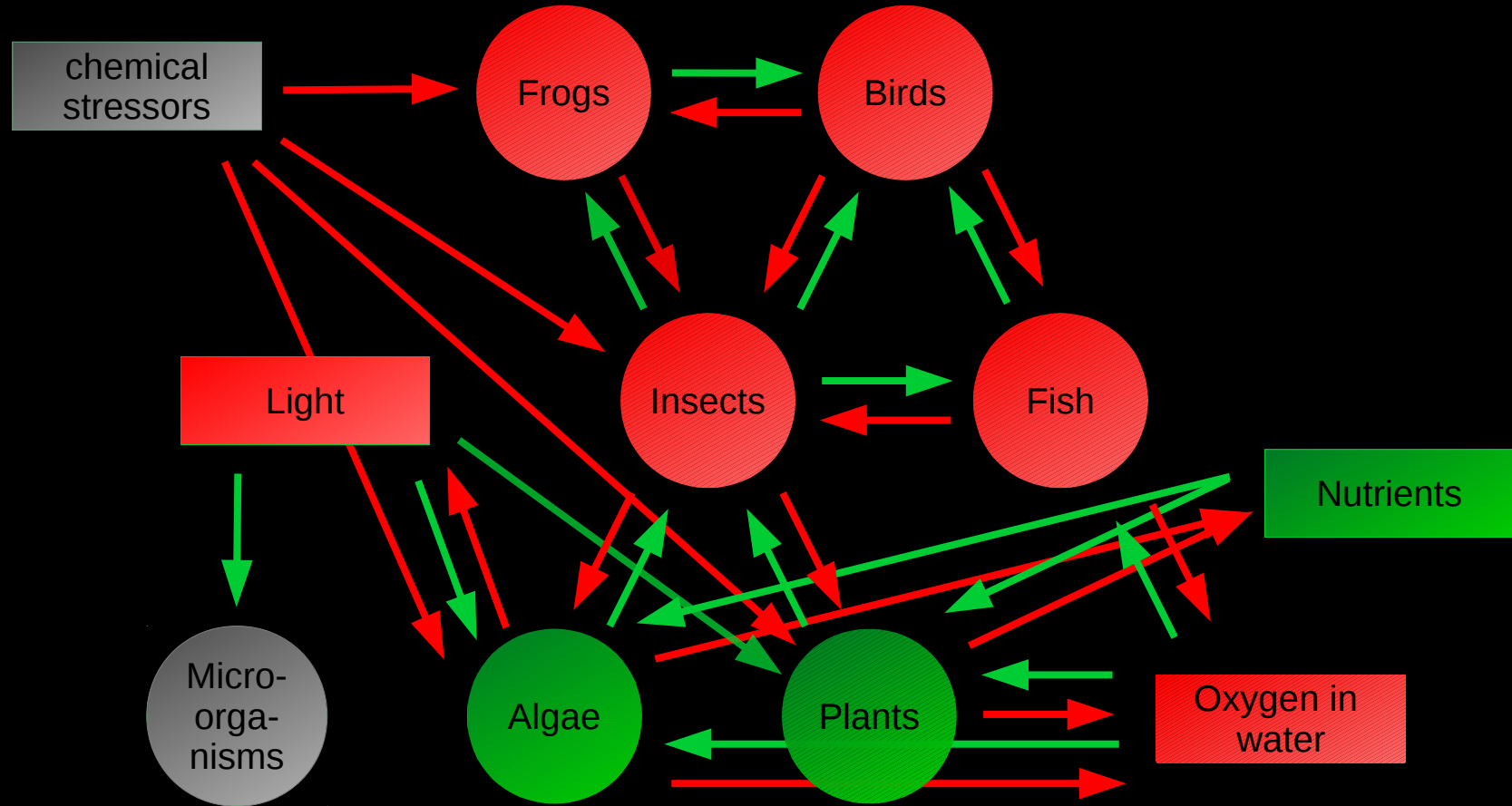
Disruption I: Nutrient excess



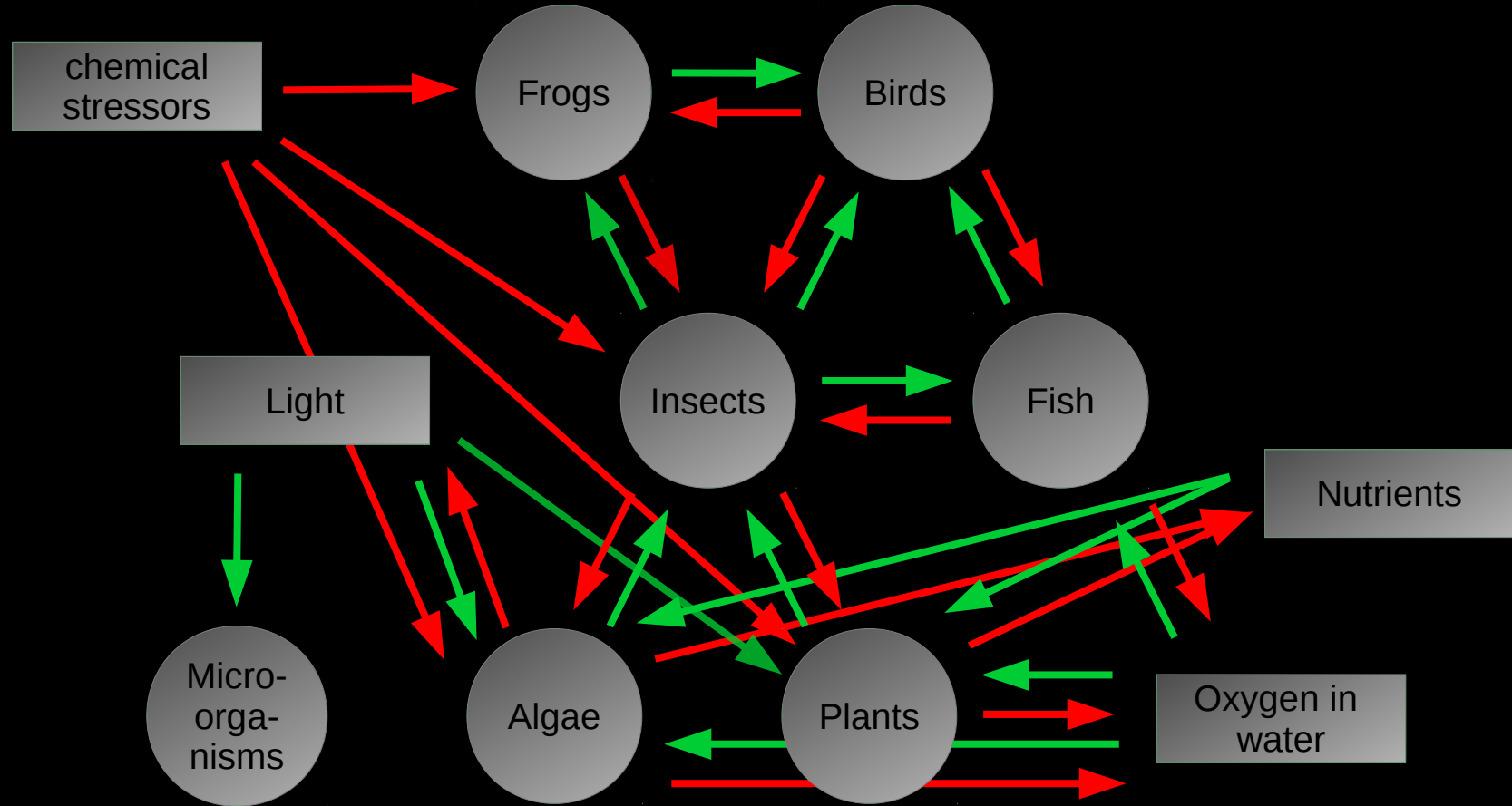
Disruption I: Nutrient excess



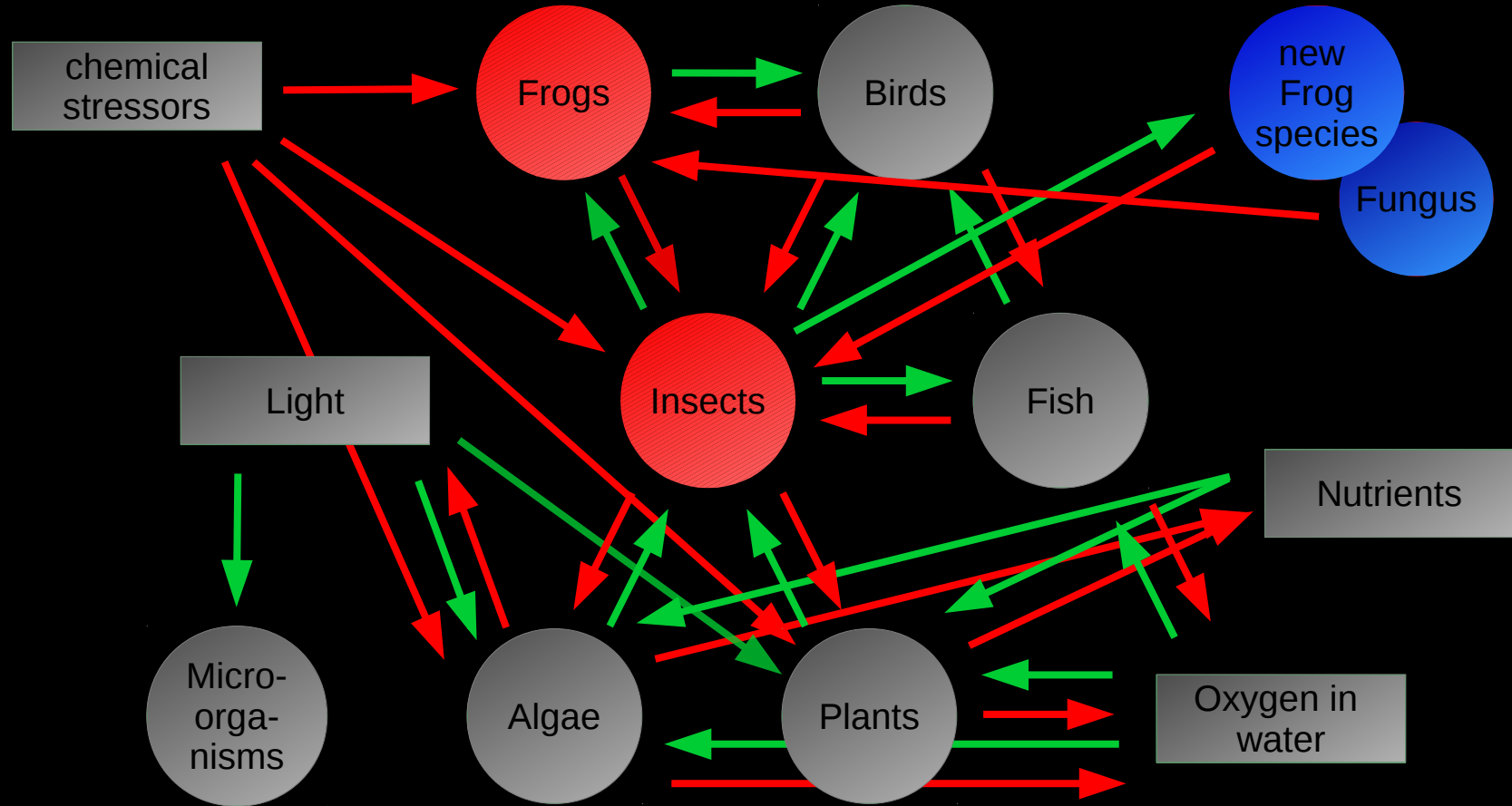
Disruption I: Nutrient excess



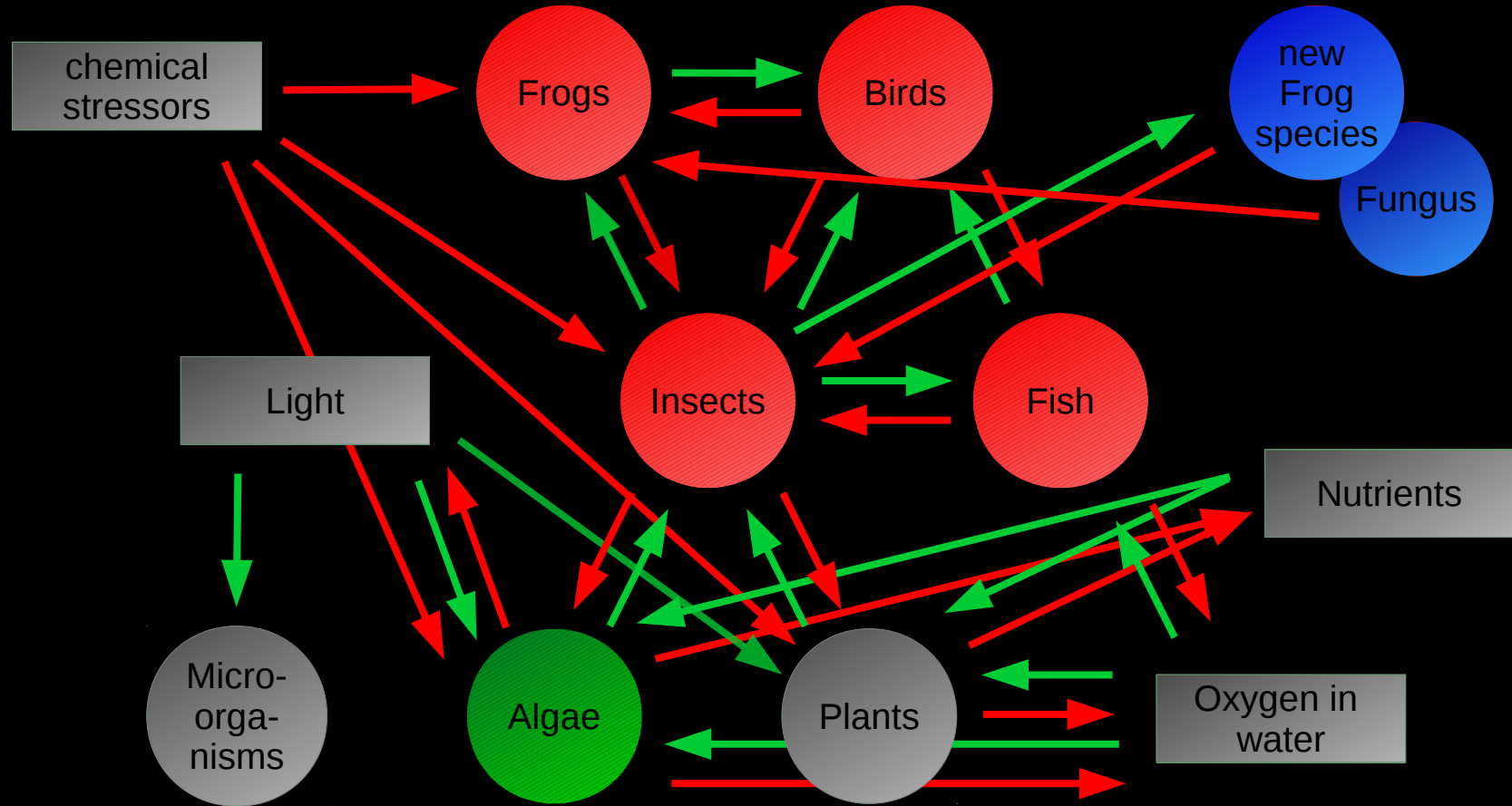
Disruption II: Alien species



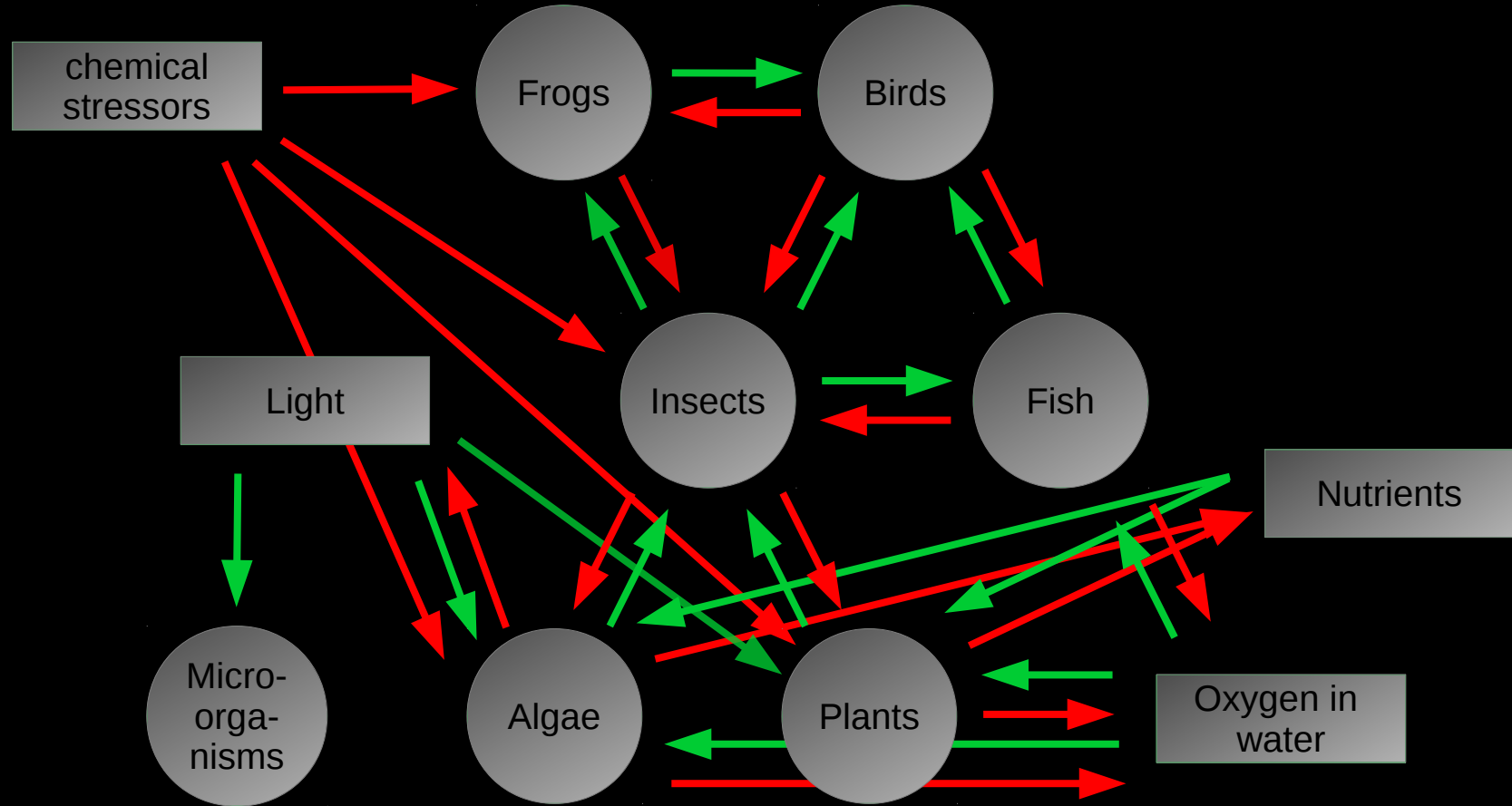
Disruption II: Alien species



Disruption II: Alien species



Disruption III: A Dam



Solution I: Leave Earth alone.



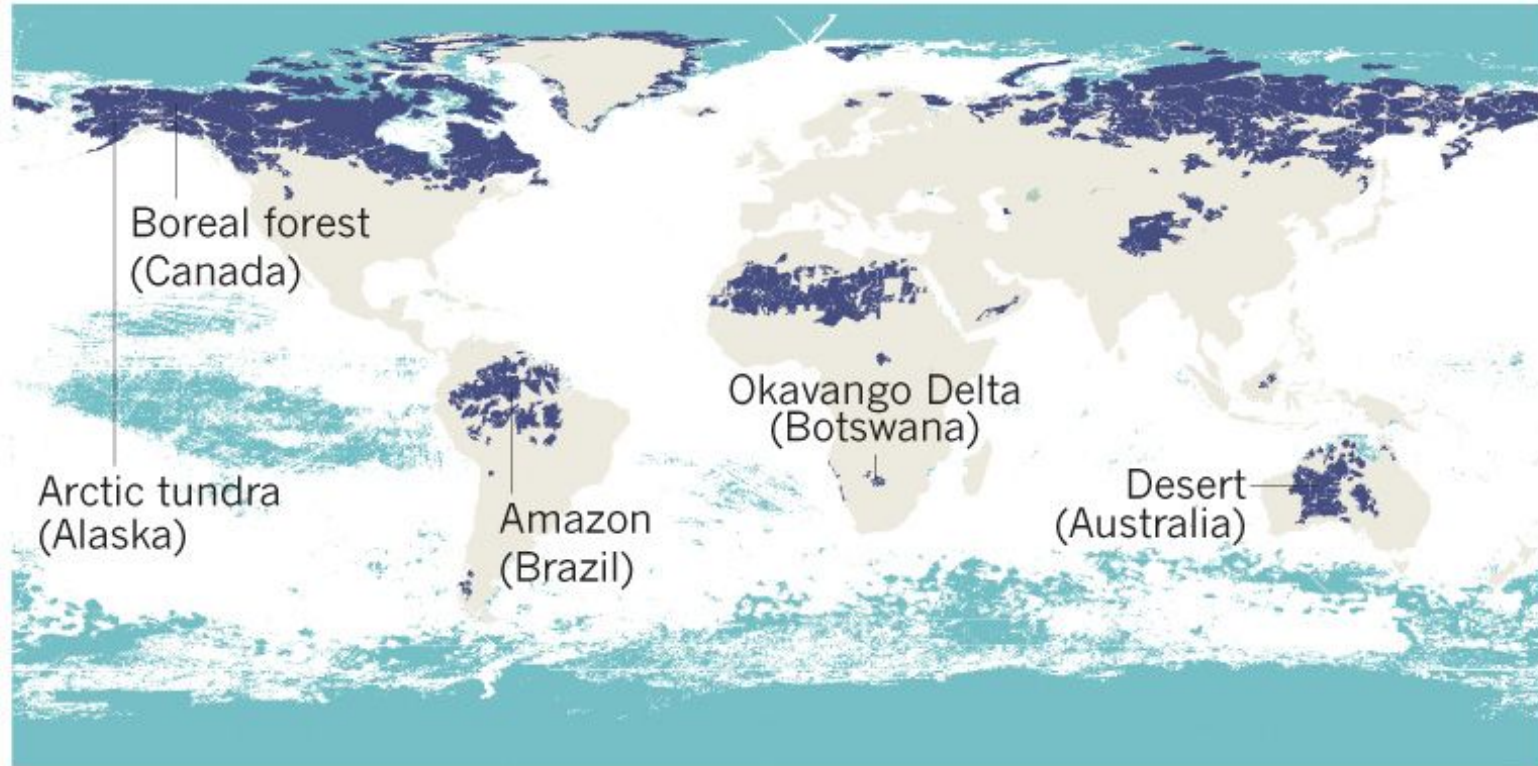
<https://www.half-earthproject.org/>

"Apollo 13 - View of Earth.jpg"
(Public Domain) by NASA

THE HUMAN FOOTPRINT

77% of land (excluding Antarctica) and 87% of the ocean has been modified by the direct effects of human activities.

REMAINING WILDERNESS: ■ Terrestrial ■ Marine



Solution II: Hack Ecosystems.

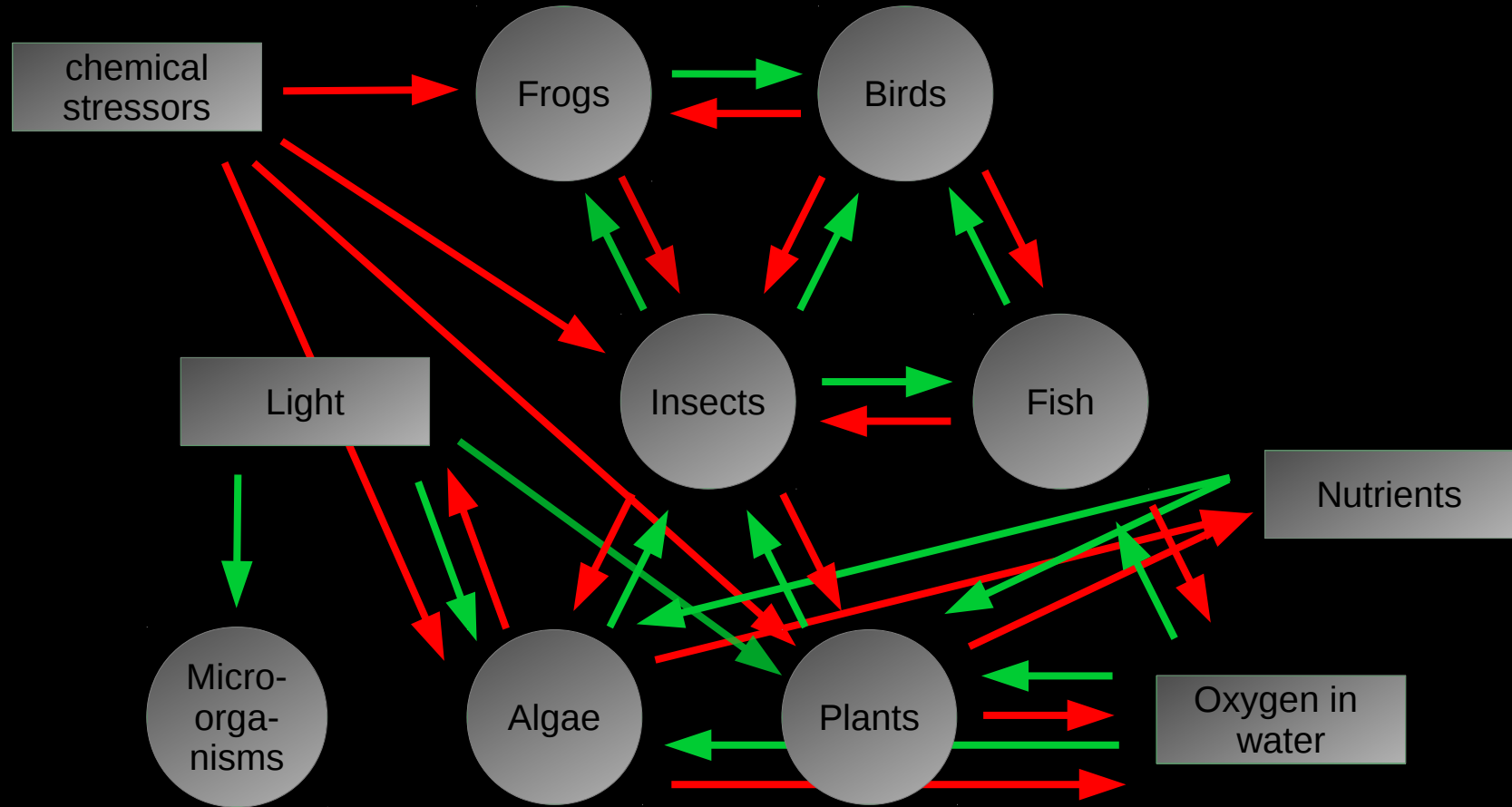


Solution II: Hack Ecosystems.

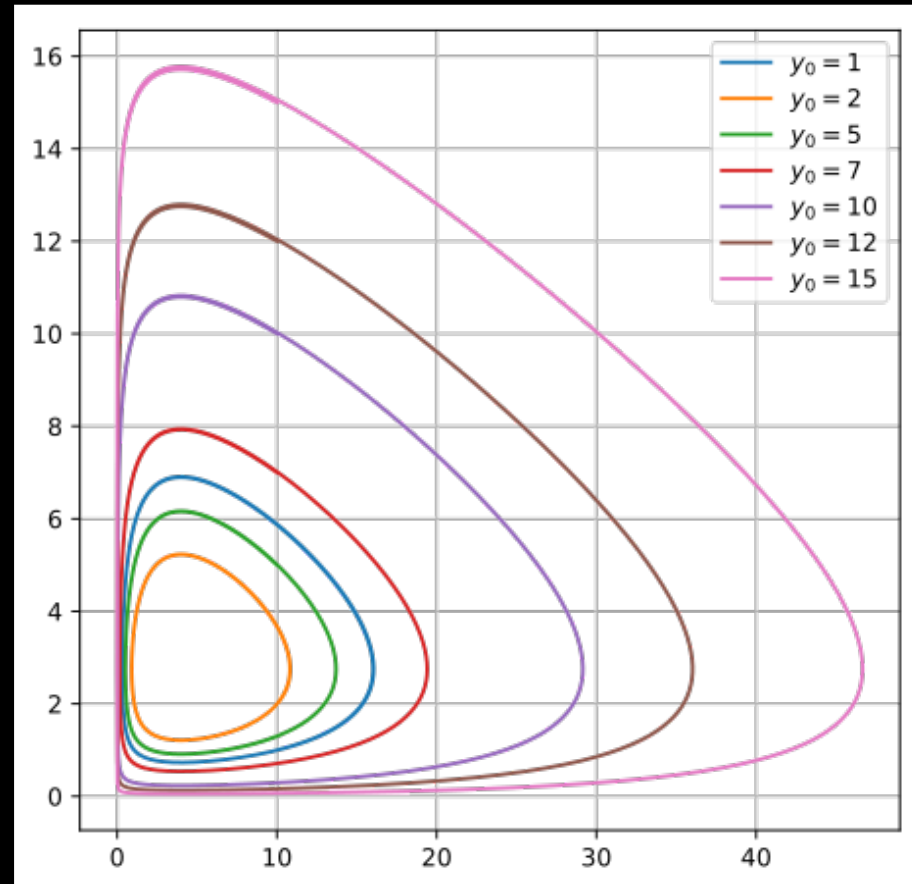


“The Earth seen from Apollo 17.jpg” (Public Domain) by [NASA](#), [Hacking-cyber-blackandwhite-crime-2903156](#) (CC0) by [iAmMrRob](#)

Data-driven ecology



Data-driven ecology: Modeling



$$\frac{dx}{dt} = \alpha x - \beta x y$$

$$\frac{dy}{dt} = \delta x y - \gamma y$$

Data-driven ecology: Modeling

The physical model is mathematically transposed by the balance equation of phytoplankton biomass (A), herbivore zooplankton biomass (Z), total phosphorus (P), ammonia (NH_4) and nitrate (NO_3) [5]:

$$\frac{\partial A}{\partial t} = k_{max} f_{nutri} A - c_{za} AZ, \quad (1)$$

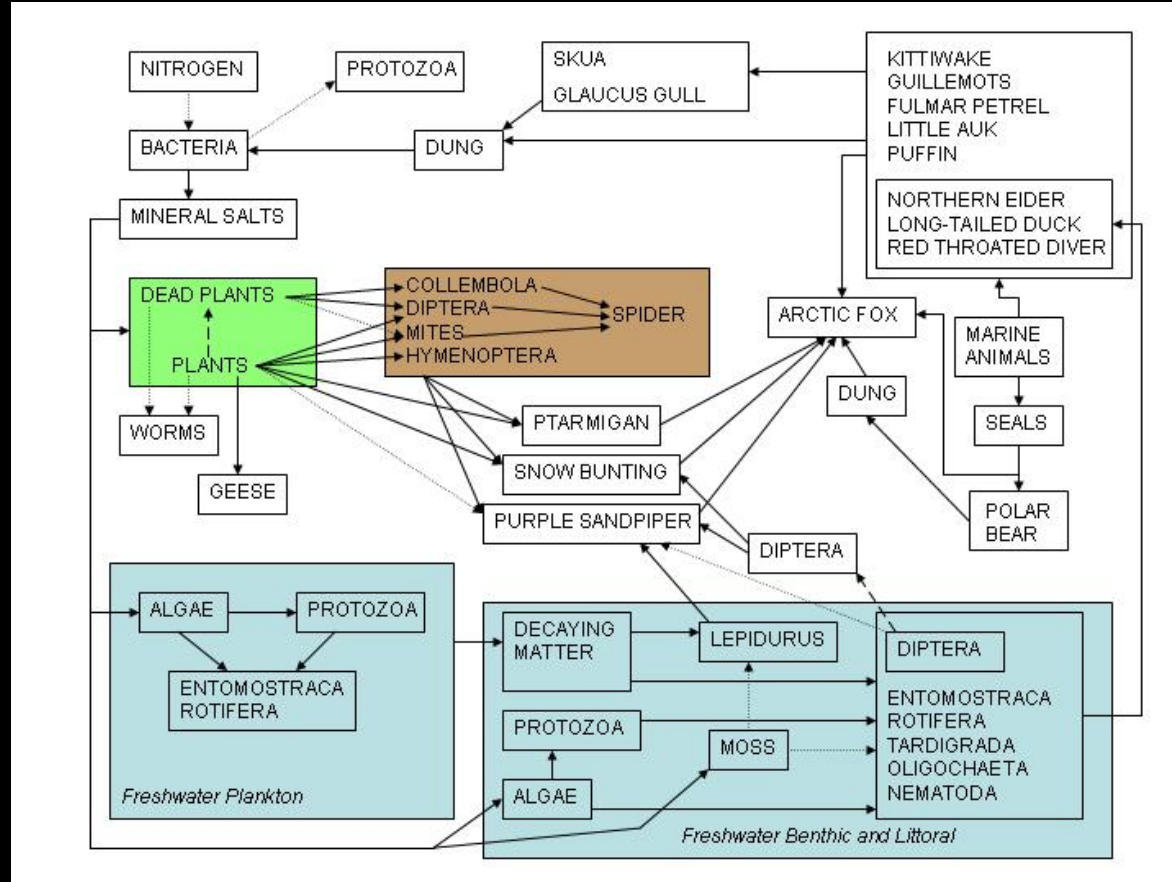
$$\frac{\partial Z}{\partial t} = a_{ca} \varepsilon c_{za} AZ - k_{dz} Z, \quad (2)$$

$$\frac{\partial P}{\partial t} = a_{pa} (1 - \varepsilon) c_{za} AZ + a_{pc} k_{dz} Z - a_{pa} k_{max} f_{nutri} A, \quad (3)$$

$$\frac{\partial NH_4}{\partial t} = a_{na} (1 - \varepsilon) c_{za} AZ + a_{nc} k_{dz} Z - F_{am} a_{na} k_{max} f_{nutri} A - k_{nt} NH_4, \quad (4)$$

$$\frac{\partial NO_3}{\partial t} = k_{nt} NH_4 - a_{na} (1 - F_{am}) k_{max} f_{nutri} A. \quad (5)$$

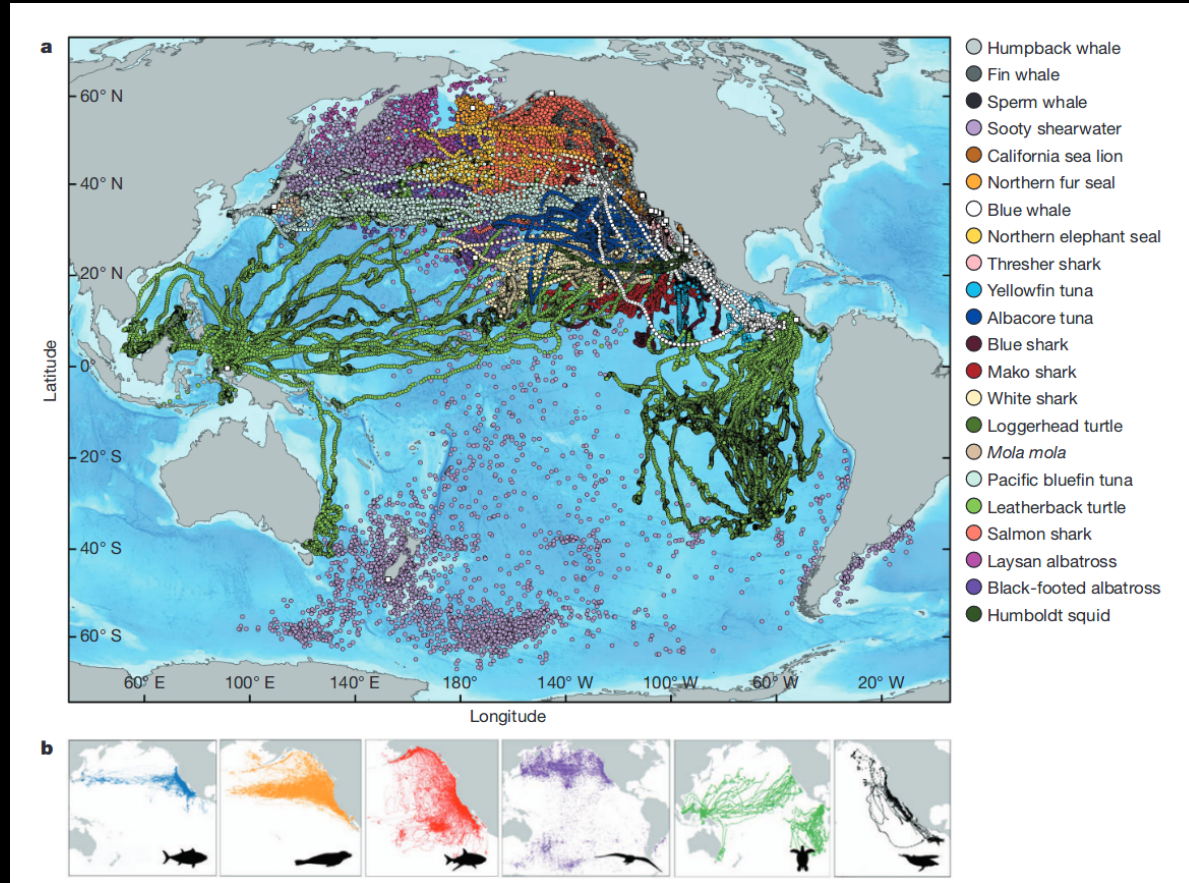
Data-driven ecology: Interactions



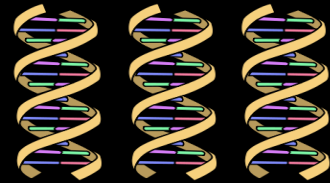
Data-driven ecology: Interactions



Data-driven ecology: Movement



Data-driven ecology: DNA sequencing



Sequencing

```
>GXP_210035 loc=GXL_175098|sym=FAM149A|taxid=9606|spec=Homo  
#aplens|chr=4|ctg=NC_000004|str=(+)|start=187065495|end=187066181|len=687|comm=Promoter  
Region  
GGACGGGCGTGGAAAGGTCACGTCCTTAGTATGCAATGCTTATGATCTAGCGTCCCTGTTGATGGGTAATGGTCTCGCA  
TTGACCAATCCGGGGTTCATTTTAAACCTCATTGTCACCTCCACCCAGCCTGTGTGCCACCCCTTGAATGG  
GGCGGGGATAGCGGAGATGCTCTGGGTTCTCTGGCTCTTCTGGTAAATAAATCCGATTTGGAGAGAGAAAGGCA  
GCCAGCACAGTATGCACAGCCCCCGGCCCCAGAGACCAGGAAAGGATAGGAGCCCGGACCTGCGCGGAGGATGGC  
CGCTGGGTTGAAACCCGGCCCGGAGGAGCCGGGAAAGCCGCTTCCCGAGGTCGGCCGGGGCCGGGGCCGGGGC  
CGGGCCCGGAGCGGGATGGCGGGCCCGCGGATAGCTGGCCGAGCCGACCGGAGGGAGGGAGGGGGAG  
GGGGCCCGGCGGGCGGGCGGAGGATCTGGAGAGGGAAGGGGCTGCGAGCCCCCGGACCCCGGGCCCGCCCGGGC  
CGCTGAGCTGGCCAGCCCGCGGGCCCGGCGCGGGCCCGGGCCGGGGCGGGGCGGGGCGGGGAGCCCGAGCCCG  
GGGGCCCGGGGCGCGTGAACGGCTGTCTGCTGGGGCCCGCGC
```

RNA
Sequencing

```
>GXP_210035 loc=GXL_175098|sym=FAM149A|taxid=9606|spec=Homo  
#aplens|chr=4|ctg=NC_000004|str=(+)|start=187065495|end=187066181|len=687|comm=Promoter  
Region  
GGACGGGCGTGGAAAGGTCACGTCCTTAGTATGCAATGCTTATGATCTAGCGTCCCTGTTGATGGGTAATGGTCTCGCA  
TTGACCAATCCGGGGTTCATTTTAAACCTCATTGTCACCTCCACCCAGCCTGTGTGCCACCCCTTGAATGG  
GGCGGGGATAGCGGAGATGCTCTGGGTTCTCTGGCTCTTCTGGTAAATAAATCCGATTTGGAGAGAGAAAGGCA  
GCCAGCACAGTATGCACAGCCCCCGGCCCCAGAGACCAGGAAAGGATAGGAGCCCGGACCTGCGCGGAGGATGGC  
CGCTGGGTTGAAACCCGGCCCGGAGGAGCCGGGAAAGCCGCTTCCCGAGGTCGGCCGGGGCCGGGGCCGGGGC  
CGGGCCCGGAGCGGGATGGCGGGCCCGCGGATAGCTGGCCGAGCCGACCGGAGGGAGGGAGGGGGAG  
GGGGCCCGGCGGGCGGGCGGAGGATCTGGAGAGGGAAGGGGCTGCGAGCCCCCGGACCCCGGGCCCGCCCGGGC  
CGCTGAGCTGGCCAGCCCGCGGGCCCGGCGCGGGCCCGGGCCGGGGCGGGGCGGGGAGCCCGAGCCCG  
GGGGCCCGGGGCGCGTGAACGGCTGTCTGCTGGGGCCCGCGC
```

Assembly,
mapping

List of (micro-)
organisms

Correlation
analyses

Assembly,
mapping

List of active
genes

Correlation
analyses

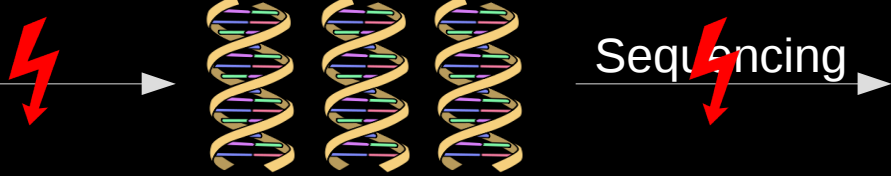
Co-occurrence
network

The good news

01010100 01101000 01100101 00100000 01110001 01110101
01101001 01100011 01101011 00100000 01100010 01110010
01101111 01110111 01101110 00100000 01100110 01101111
01111000 00100000 01101010 01110101 01101101 01110000
01110011 00100000 01101111 01110110 01100101 01110010
00100000 00110001 00110011 00100000 01101100 01100001
01111010 01111001 00100000 01100100 01101111 01100111
01010100 01101000 01100101 00100000 01110001 01110101
01101001 01100011 01101011 00100000 01100010 01110010
01101111 01110111 01101110 00100000 01100110 01101111
01111000 00100000 01101010 01110101 01101101 01110000
01110011 00100000 01101111 01110110 01100101 01110010
00100000 00110001 00110011 00100000 01101100 01100001
01111010 01111001 00100000 01100100 01101111 01100111
01010100 01101000 01100101 00100000 01110001 01110101
01101001 01100011 01101011 00100000 01100010 01110010
01101111 01110111 01101110 00100000 01100110 01101111
01111000 00100000 01101010 01110101 01101101 01110000
01110011 00100000 01101111 01110110 01100101 01110010
00100000 00110001 00110011 00100000 01101100 01100001
01111010 01111001 00100000 01100100 01101111 01100111

data

The bad news: Batch effects



```
>GXP_210035 loc=GXL_175098|sym=FAM149A|taxid=9606|spec=Homo
sapiens|chr=4|ctg=NC_000004|str=(+)|start=187065495|end=187066181|len=687|comm=Promoter
Region
GGACGGGCGTGGAAAGGTCACGTCCTTAGTATGCATGCTTAGATCAGCGTCCCTGTGATGGAGTAATGGTCTCGCA
TTGACCAGATCCGGGGTTCATTTTAAACCTCATTGTCACCTCCACCACCAGCCCTGATGCGCACCCCTTGAATGG
GGCCGGGATGGCCGAGTGGTCTCGGGTCTCTGCGCTTCTCTGGTGAATTAATCCGATTTGGAGAGAGAAAGGCA
GCCAGCCAGTATGCACAGCCCGGCCCCAGAGACCAGGAAAGAGTAGGAGAGCCCGGCGCTGCGCGAGGAGTGGC
CGCTGGGTTGAAACCAGCCCGGCGAGGAGCCGGGAAAGCCGCTTCCCGAGGATCGCGCGGGCCGGGGCCGGGCG
CGGGCCCGGCGGGGATGGCGGGCCCGCGGATCTGGAGAGGAGAGGCGCTCGAGCCCGCAGACCAGGAGAGGGAG
GGGCGCCCGGCGGGCGGGGCGAGGATCTGGAGAGGAGAGGGCGTGCAGACCCCGGAGCCCGGCGCCCGCGGGC
CGCTGAGCTGGCCAGCCCGCGCGGGCCCGCGCGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGC
GGGCGCGGGCGCGCGTGAACGGCTGTCTGCTGTGGGCGCCCGCGC
```

RNA Sequencing

```
>GXP_210035 loc=GXL_175098|sym=FAM149A|taxid=9606|spec=Homo
sapiens|chr=4|ctg=NC_000004|str=(+)|start=187065495|end=187066181|len=687|comm=Promoter
Region
GGACGGGCGTGGAAAGGTCACGTCCTTAGTATGCATGCTTAGATCAGCGTCCCTGTGATGGAGTAATGGTCTCGCA
TTGACCAGATCCGGGGTTCATTTTAAACCTCATTGTCACCTCCACCACCAGCCCTGATGCGCACCCCTTGAATGG
GGCCGGGATGGCCGAGTGGTCTCGGGTCTCTGCGCTTCTCTGGTGAATTAATCCGATTTGGAGAGAGAAAGGCA
GCCAGCCAGTATGCACAGCCCGGCCCCAGAGACCAGGAAAGAGTAGGAGAGCCCGGCGCTGCGCGAGGAGTGGC
CGCTGGGTTGAAACCAGCCCGGCGAGGAGCCGGGAAAGCCGCTTCCCGAGGATCGCGCGGGCCGGGGCCGGGCG
CGGGCCCGGCGGGGATGGCGGGCCCGCGGATCTGGAGAGGAGAGGGCGTGCAGACCCCGGAGCCCGGCGCCCGCGGGC
GGGCGCCCGGCGGGCGGGGCGAGGATCTGGAGAGGAGAGGGCGTGCAGACCCCGGAGCCCGGCGCCCGCGGGC
CGCTGAGCTGGCCAGCCCGCGCGGGCCCGCGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGC
GGGCGCGGGCGCGCGTGAACGGCTGTCTGCTGTGGGCGCCCGCGC
```

Assembly, mapping

List of (micro-) organisms

Assembly, mapping

List of active genes

Correlation analyses

Correlation analyses

Co-occurrence network

Lightning_Symbol.svg (Public Domain) by LuluBee, FAM149A_Promotor_region_(FASTA_format) (CC BY-SA 3.0) by LarsonGCD, DNA_simple.svg (Public Domain) by Forluvof, Ben_test_tube.svg (Public Domain) by ben

Summary

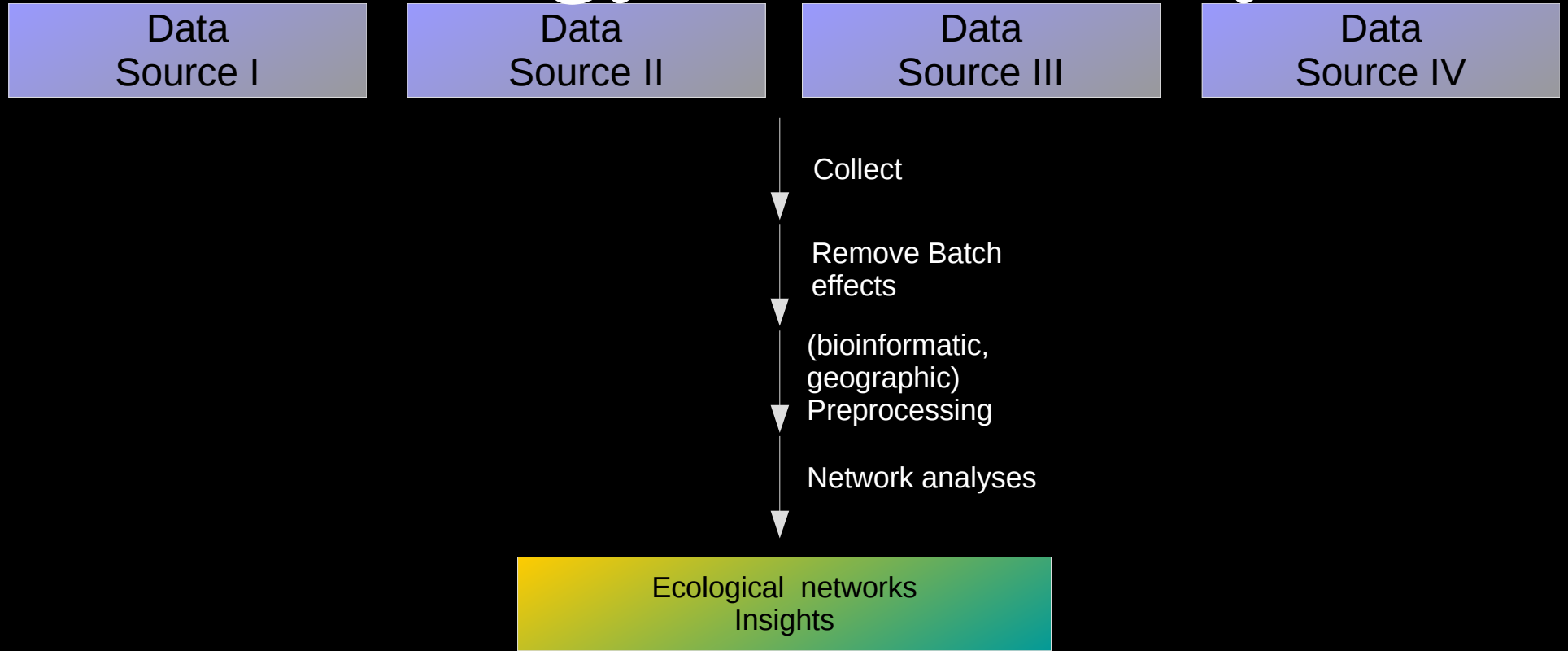
My invitation: Open Digital Ecology Community

- Open as in “Open Source”
- Digital as in “Data Science”
- Community as in “Citizen Science”

My invitation: Open Digital Ecology Community

- Open as in “Open Source”
- Digital as in “Data Science”
- Community as in “Citizen Science”
- The name is provisional

My invitation: Open Digital Ecology Community



Thank you!

sperleath@posteo.net

Twitter: @TSperlea

... or meet me around!

Further reading

- Berry, David, and Stefanie Widder. 2014. “*Deciphering Microbial Interactions and Detecting Keystone Species with Co-Occurrence Networks.*” *Frontiers in Microbiology* 5 (May). <https://doi.org/10.3389/fmicb.2014.00219>.
- Ceballos, Gerardo, Paul R. Ehrlich, Anthony D. Barnosky, Andrés García, Robert M. Pringle, and Todd M. Palmer. 2015. “*Accelerated Modern Human-induced Species Losses: Entering the Sixth Mass Extinction.*” *Science Advances* 1 (5): e1400253. <https://doi.org/10.1126/sciadv.1400253>.
- Clark, Michael, and David Tilman. 2017. “*Comparative Analysis of Environmental Impacts of Agricultural Production Systems, Agricultural Input Efficiency, and Food Choice.*” *Environmental Research Letters* 12 (6): 64016. <https://doi.org/10.1088/1748-9326/aa6cd5>.
- Gonze, Didier, Katharine Z Coyte, Leo Lahti, and Karoline Faust. 2018. “*Microbial Communities as Dynamical Systems.*” *Current Opinion in Microbiology* 44 (August): 41–49. <https://doi.org/10.1016/j.mib.2018.07.004>.
- Hallmann, Caspar A., Martin Sorg, Eelke Jongejans, Henk Siepel, Nick Hofland, Heinz Schwan, Werner Stenmans, et al. 2017. “*More than 75 Percent Decline over 27 Years in Total Flying Insect Biomass in Protected Areas.*” Edited by Eric Gordon Lamb. *PLOS ONE* 12 (10): e0185809. <https://doi.org/10.1371/journal.pone.0185809>.
- Lister, Bradford C., and Andres Garcia. 2018. “*Climate-Driven Declines in Arthropod Abundance Restructure a Rainforest Food Web.*” *Proceedings of the National Academy of Sciences* 115 (44): E10397–406. <https://doi.org/10.1073/pnas.1722477115>.
- Prosser, James I., Brendan J. M. Bohannan, Tom P. Curtis, Richard J. Ellis, Mary K. Firestone, Rob P. Freckleton, Jessica L. Green, et al. 2007. “*The Role of Ecological Theory in Microbial Ecology.*” *Nature Reviews Microbiology* 5 (5): 384–92. <https://doi.org/10.1038/nrmicro1643>.
- Ramirez, Kelly S., Christopher G. Knight, Mattias de Hollander, Francis Q. Brearley, Bede Constantinides, Anne Cotton, Si Creer, et al. 2017. “*Detecting Macroecological Patterns in Bacterial Communities across Independent Studies of Global Soils.*” *Nature Microbiology* 3 (2): 189–96. <https://doi.org/10.1038/s41564-017-0062-x>.
- Rubin, Melissa A., and Laura G. Leff. 2007. “*Nutrients and Other Abiotic Factors Affecting Bacterial Communities in an Ohio River (USA).*” *Microbial Ecology* 54 (2): 374–83. <https://doi.org/10.1007/s00248-007-9209-2>.
- Sinclair, Lucas, Omneya Ahmed Osman, Stefan Bertilsson, and Alexander Eiler. 2015. “*Microbial Community Composition and Diversity via 16S rRNA Gene Amplicons: Evaluating the Illumina Platform.*” Edited by Ludovic Orlando. *PLOS ONE* 10 (2): e0116955. <https://doi.org/10.1371/journal.pone.0116955>.
- Sperlea, Theodor, Stefan Fuser, Jens Boenigk, and Dominik Heider. 2018. “*SEDE-GPS: Socio-Economic Data Enrichment Based on GPS Information*” *BMC Bioinformatics* 19 (S15). <https://doi.org/10.1186/s12859-018-2419-4>