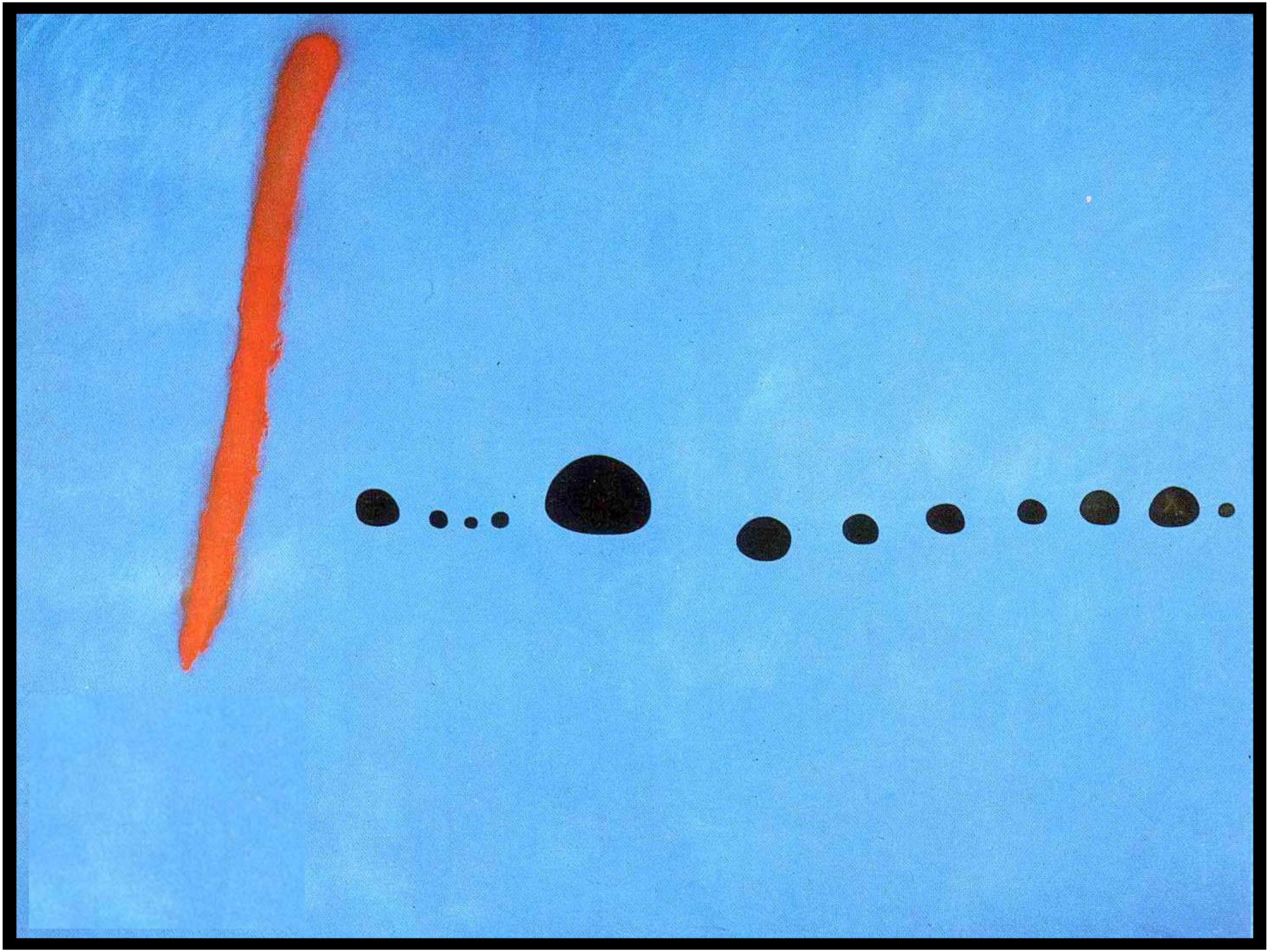
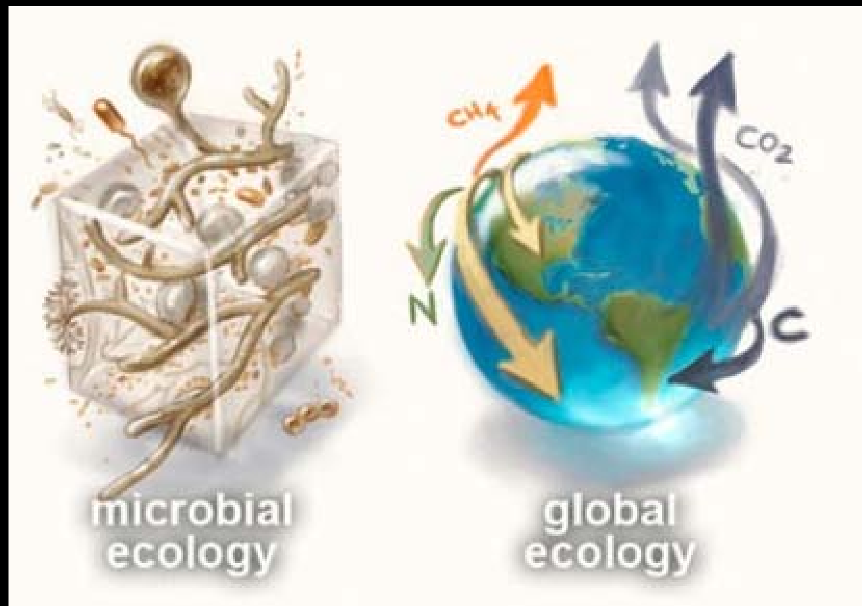


The microbial ecology of soil carbon across scales



Bruce Hungate, Rebecca Mau, Egbert Schwartz, Greg Caporaso, Paul Dijkstra, Natasja van Gestel, Benjamin J Koch, Cindy Liu, Theresa McHugh, Jane Marks, Ember Morrissey, Lance Price, Kees Jan van Groenigen

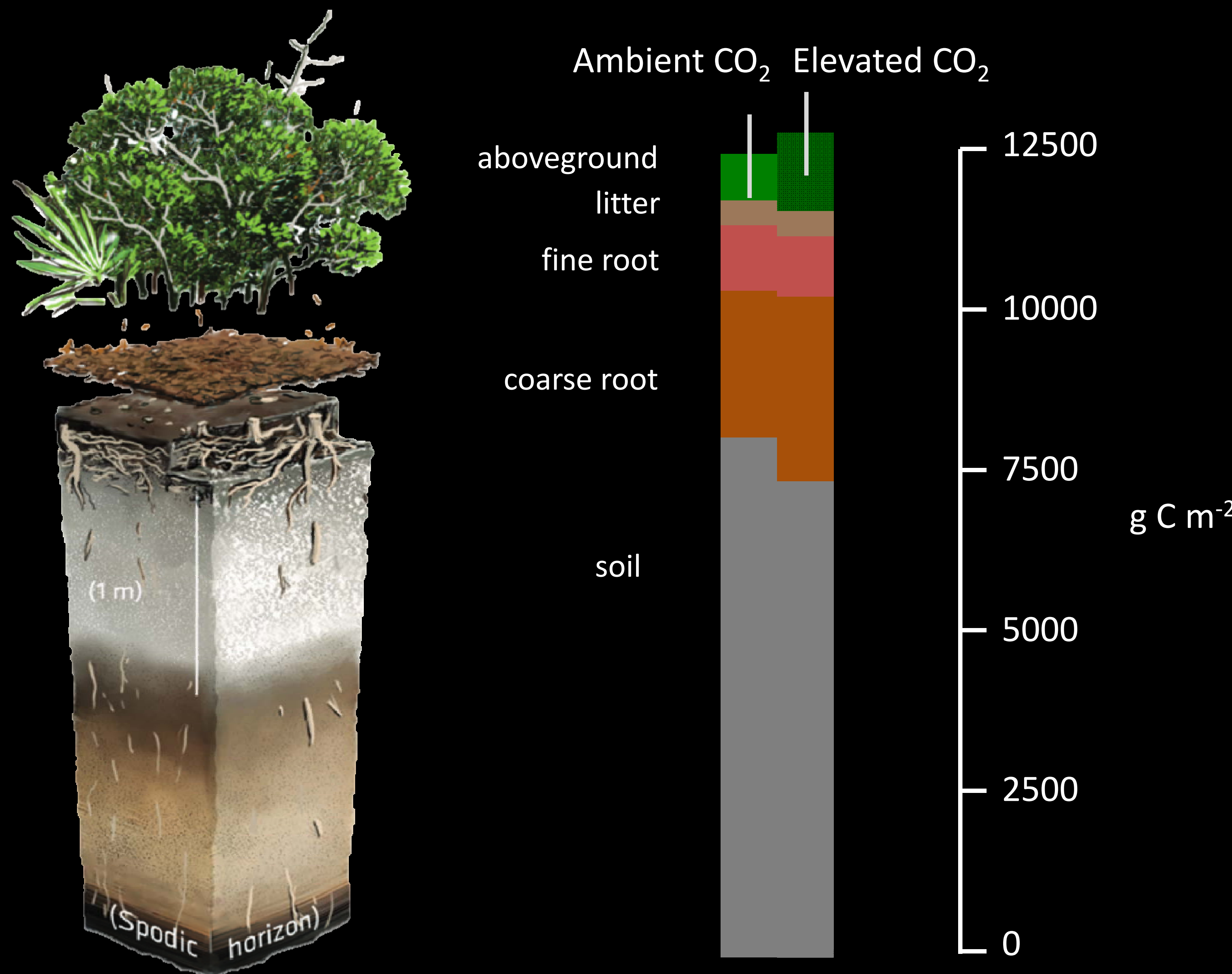
Northern Arizona University, Flagstaff AZ, USA

Funding from the US Department of Energy, Genomic Sciences, Regional and Climate Modeling, Terrestrial Ecosystem Sciences


(1 m)
(Spodic horizon)

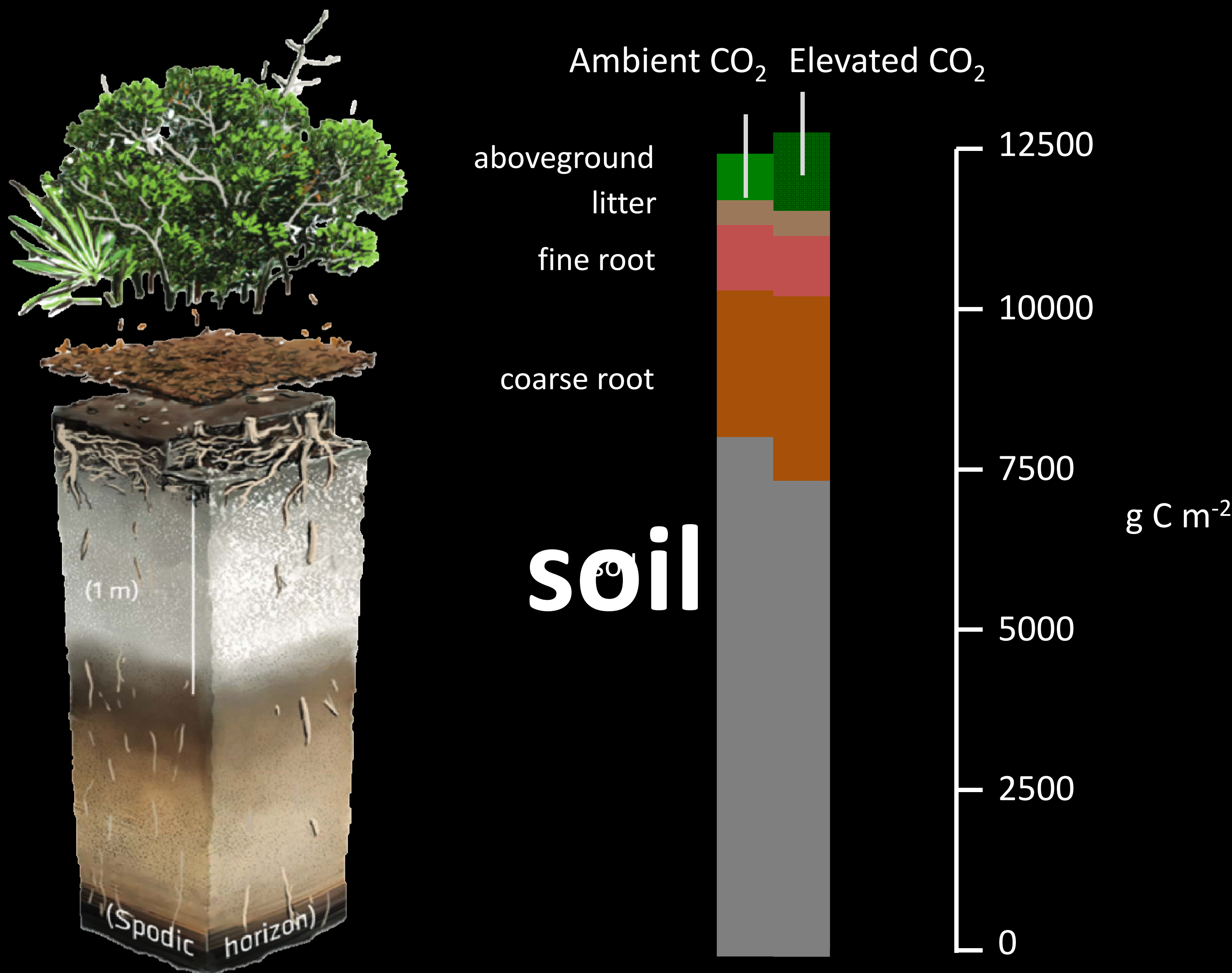
Florida CO_2 experiment

$\uparrow CO_2 \longrightarrow \uparrow$ C storage?



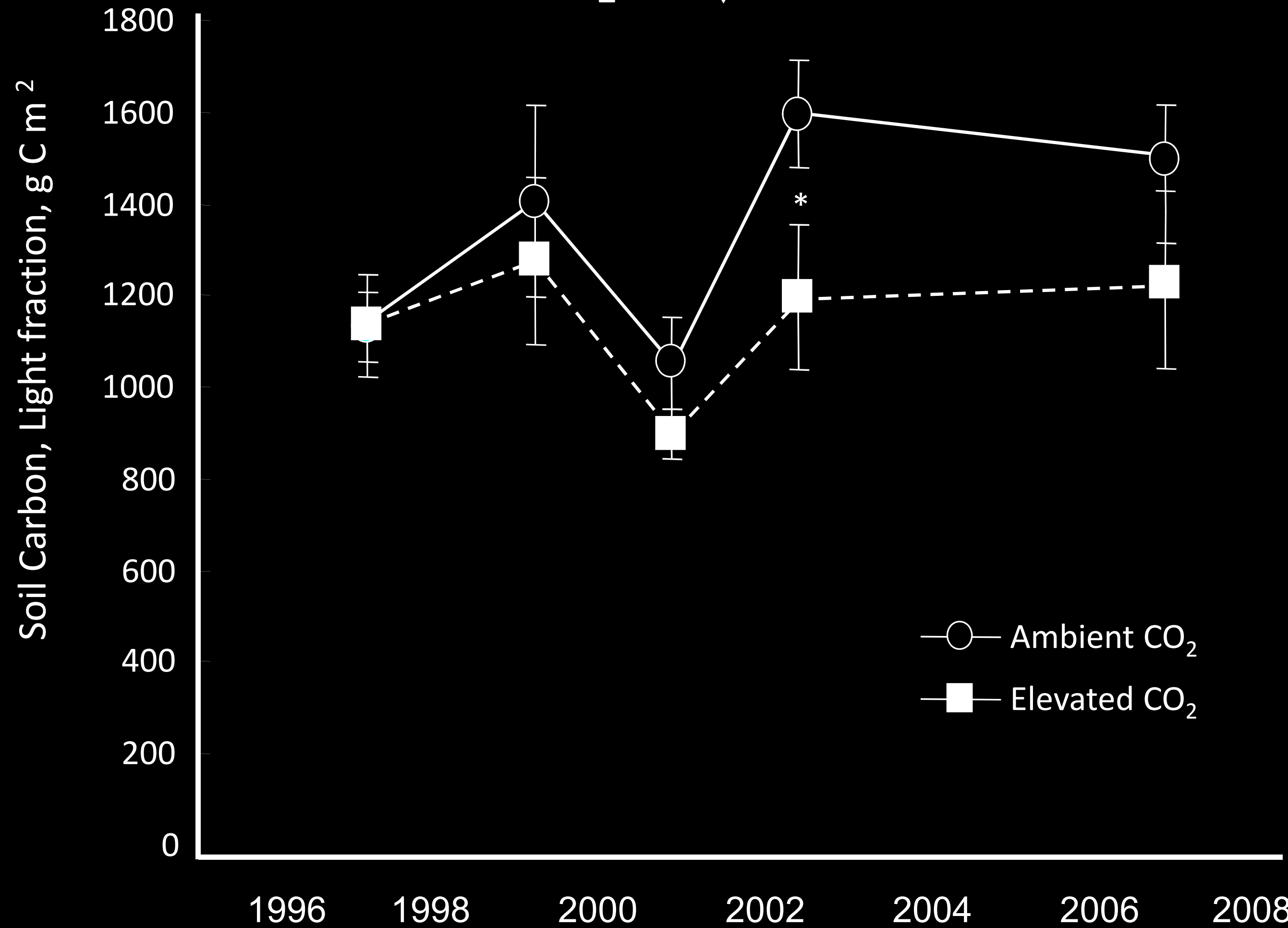
Hungate et al., New Phytologist, 2013

↑CO_2 → ↑C storage?



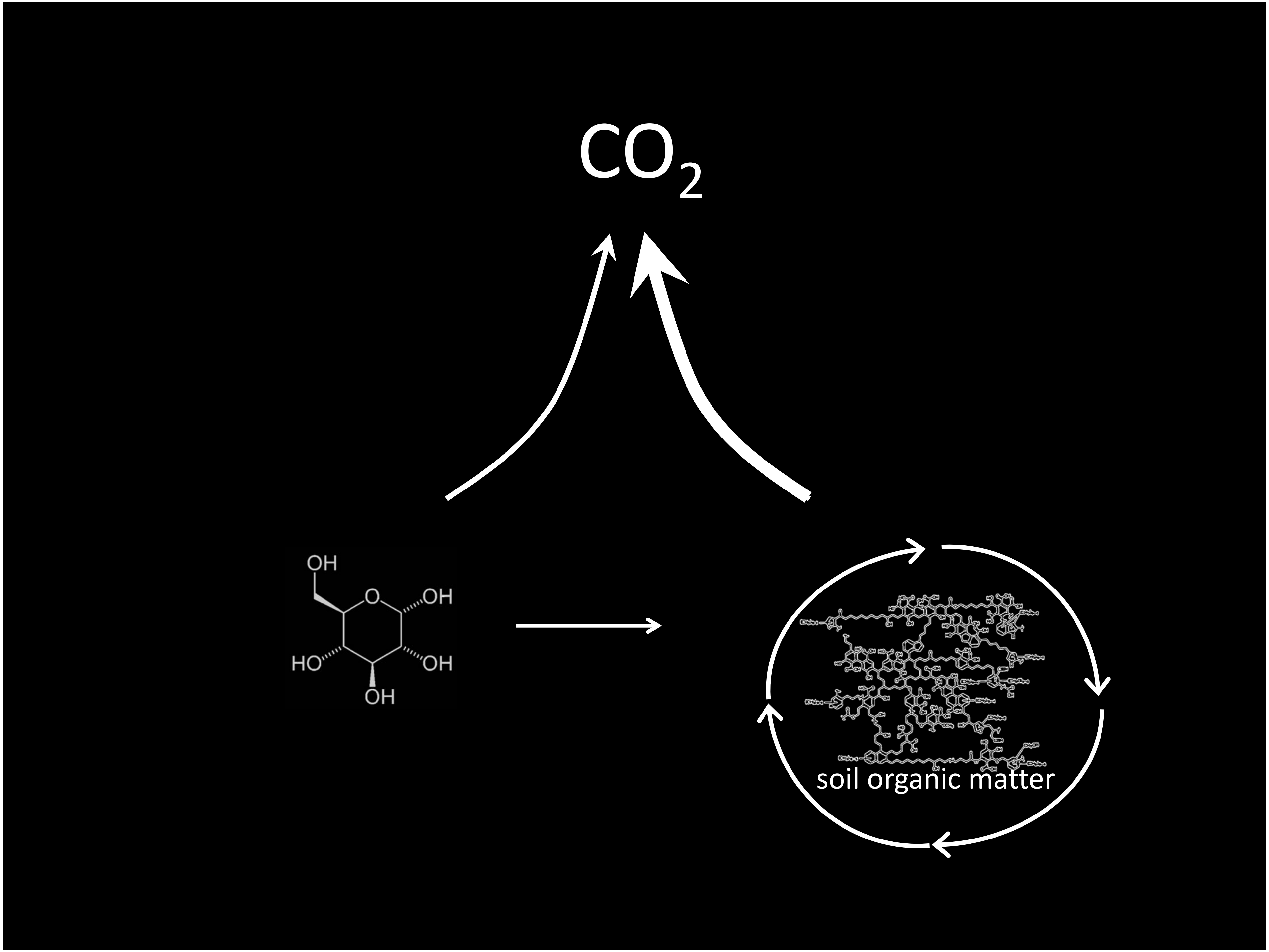
Hungate et al., New Phytologist, 2013

↑CO_2 → ↓soil carbon

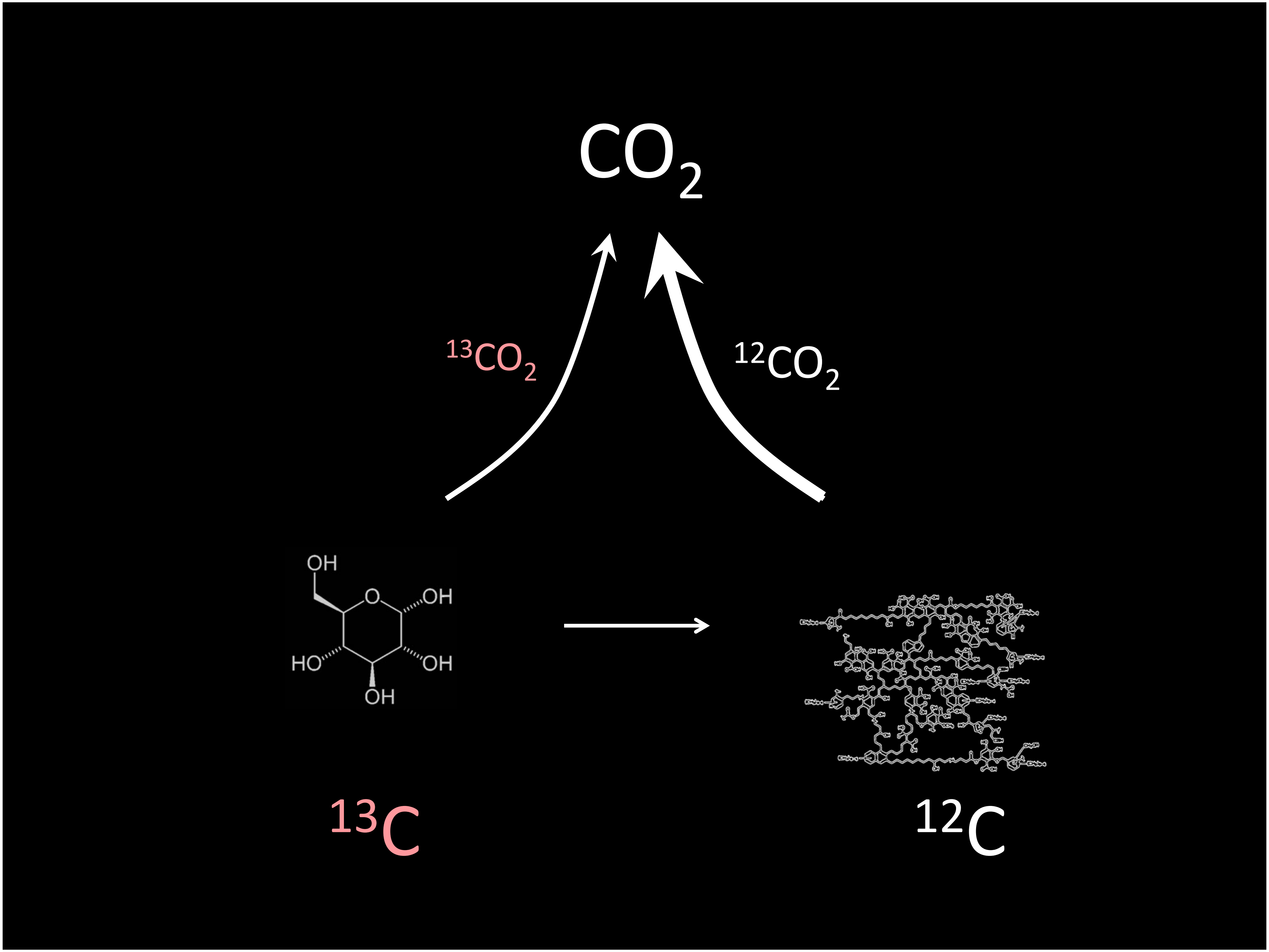


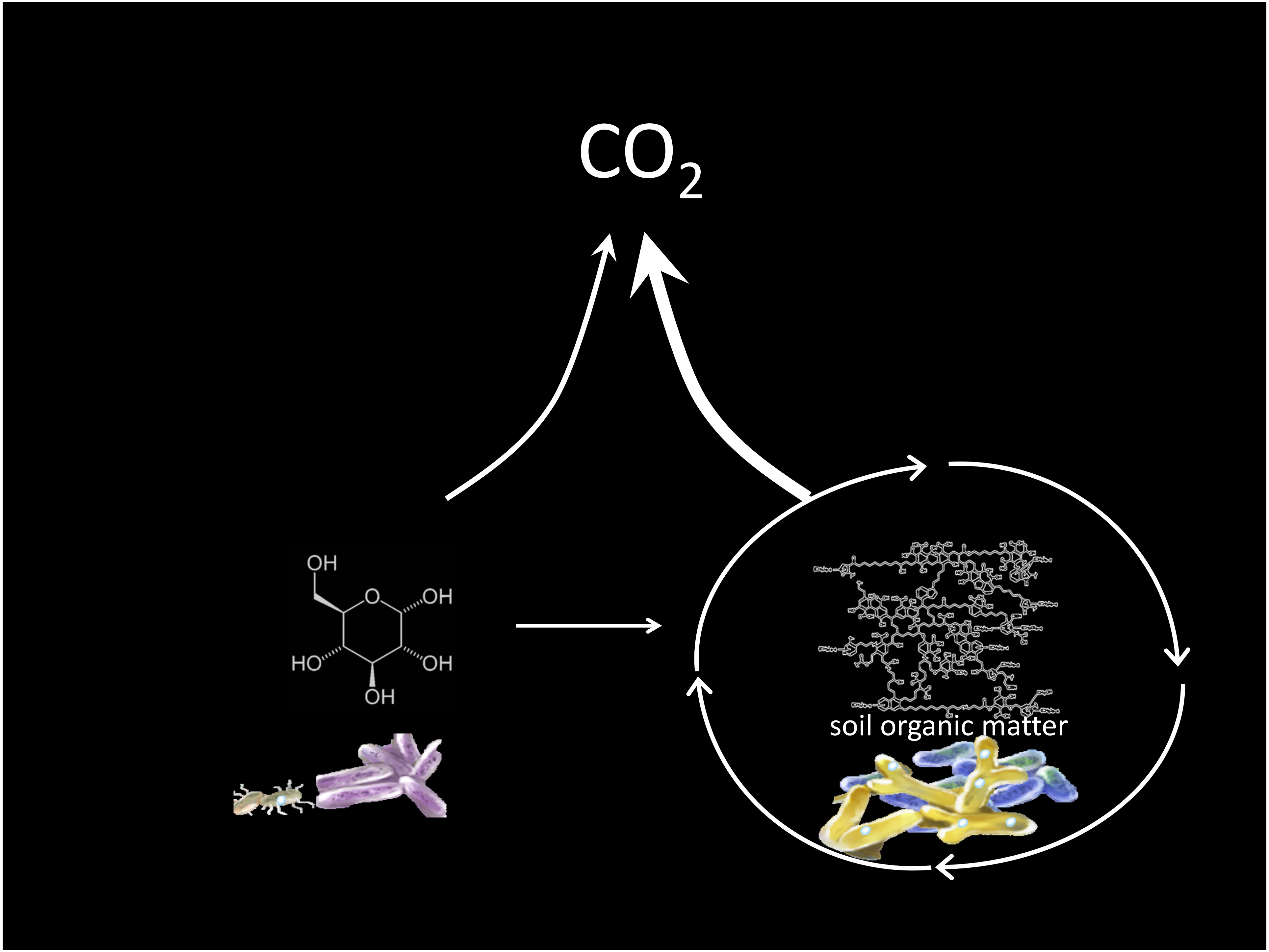
Why?

Carney, Hungate, Drake & Megonigal, PNAS, 2007; Hungate et al. New Phytologist, 2013b



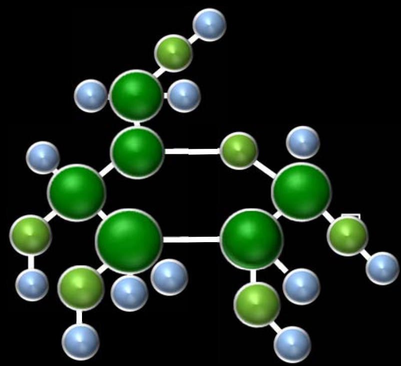
CO_2
OH
O
OH
HO
OH
OH
soil organic matter

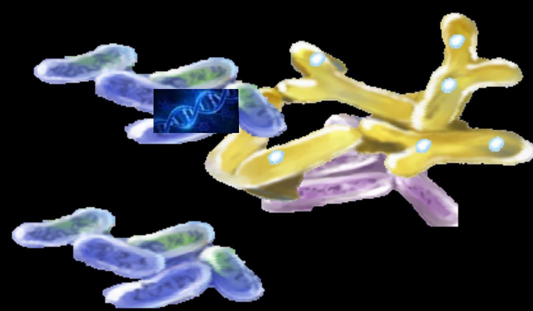

CO_2
$^{13}CO_2$
$^{12}CO_2$
OH
O
OH
HO
OH
OH
^{13}C
^{12}C

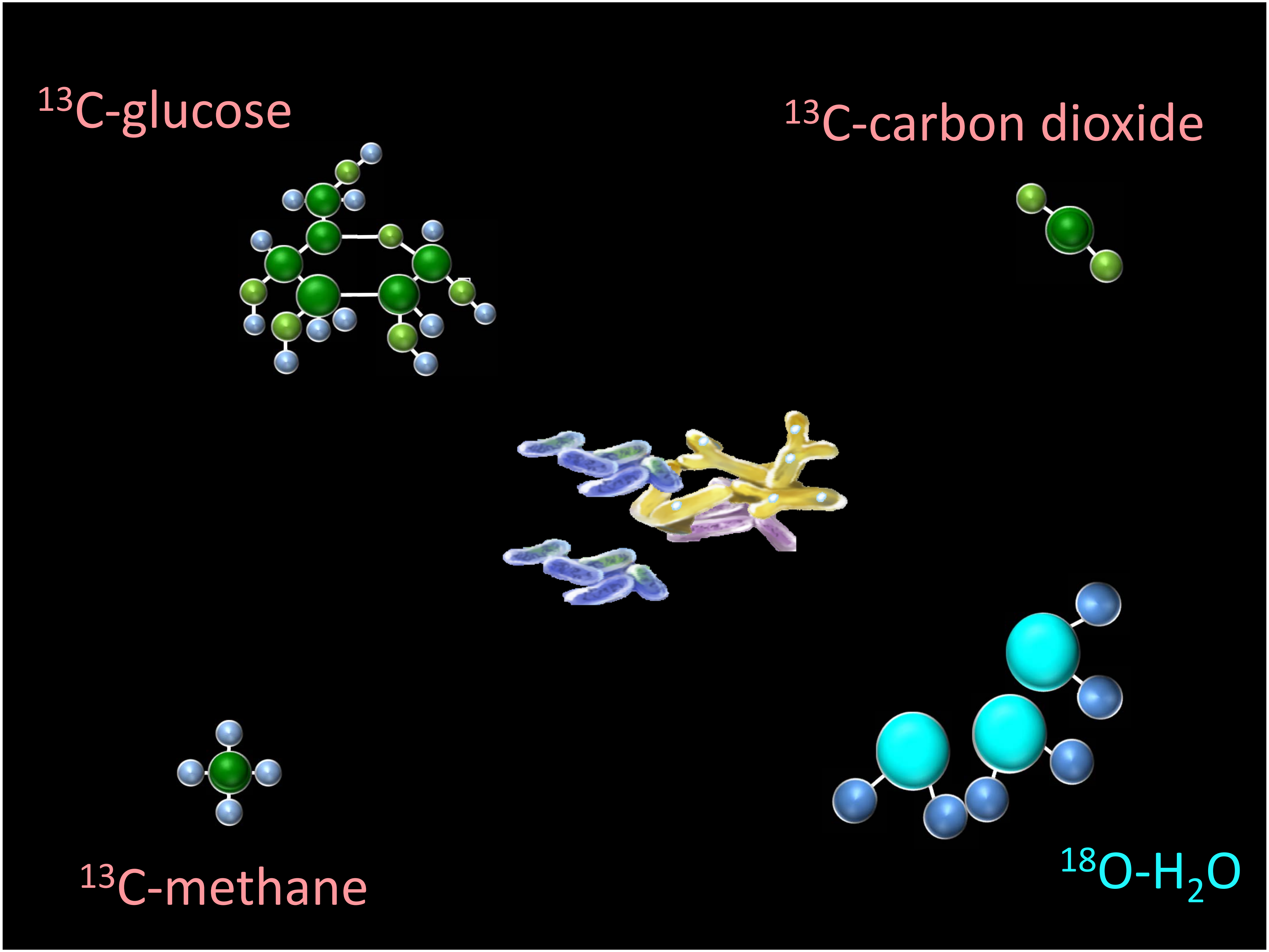


CO2
OH
OH
HO
OH
OH
soil organic matter

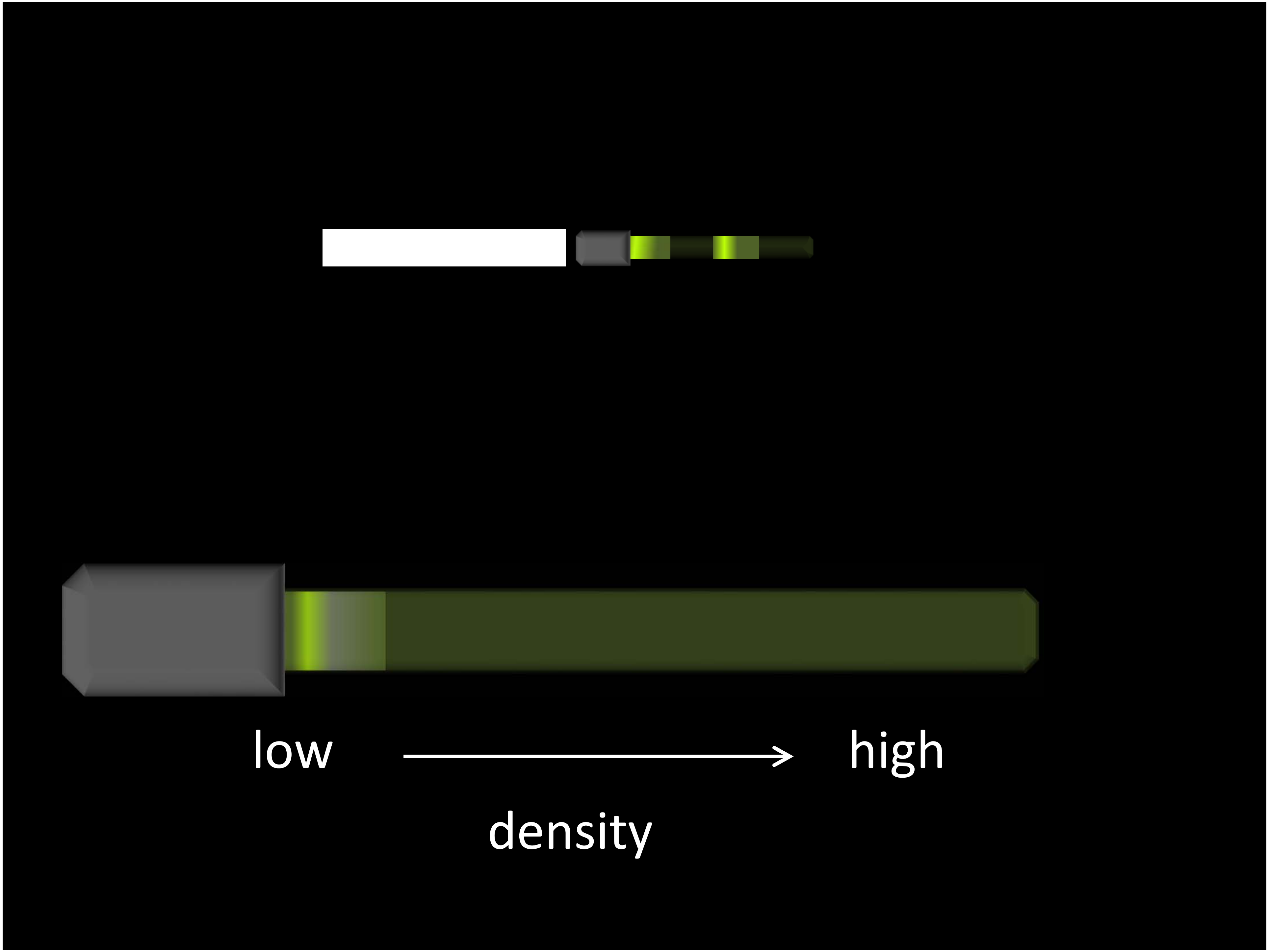
^{13}C-glucose

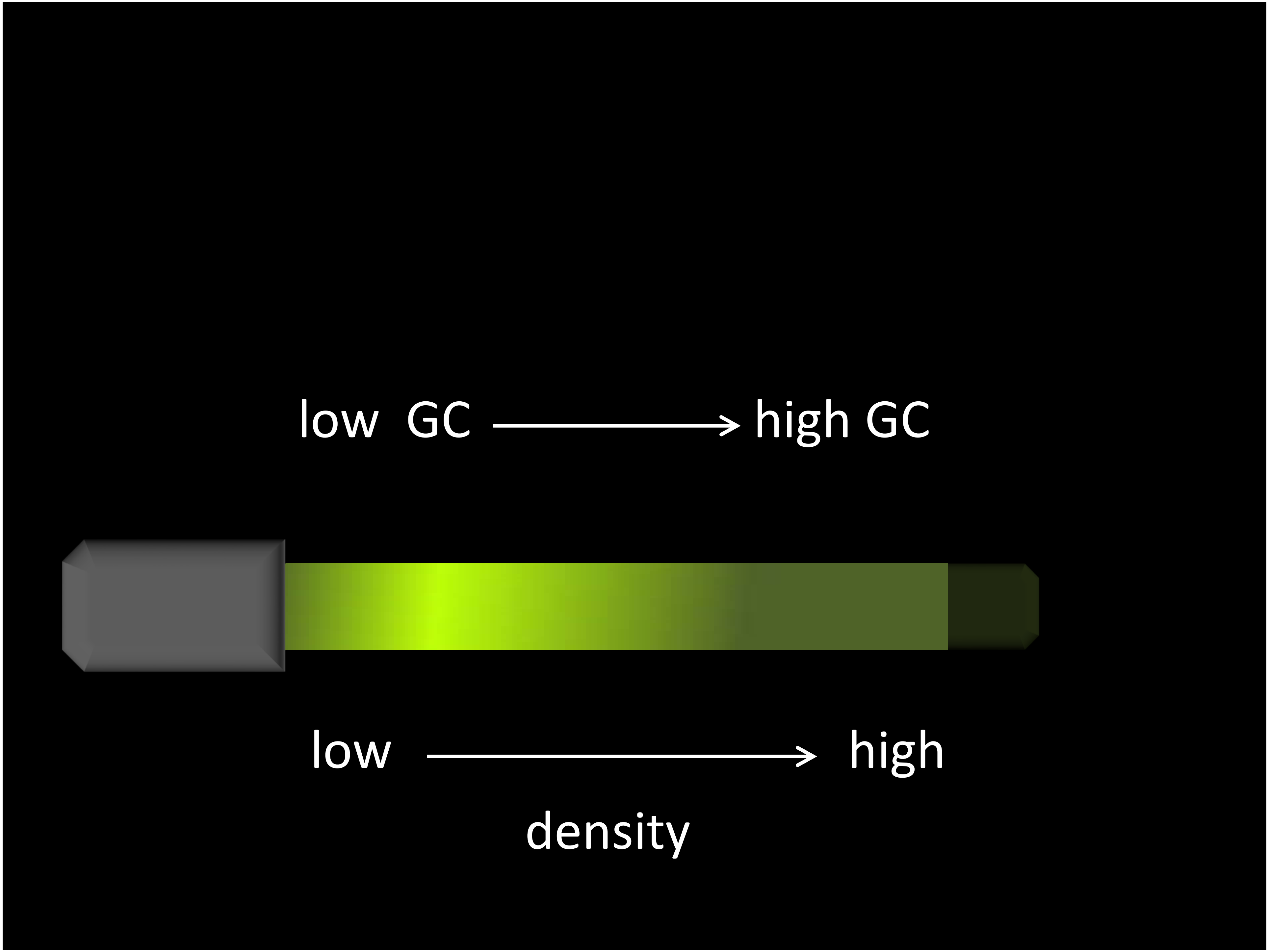




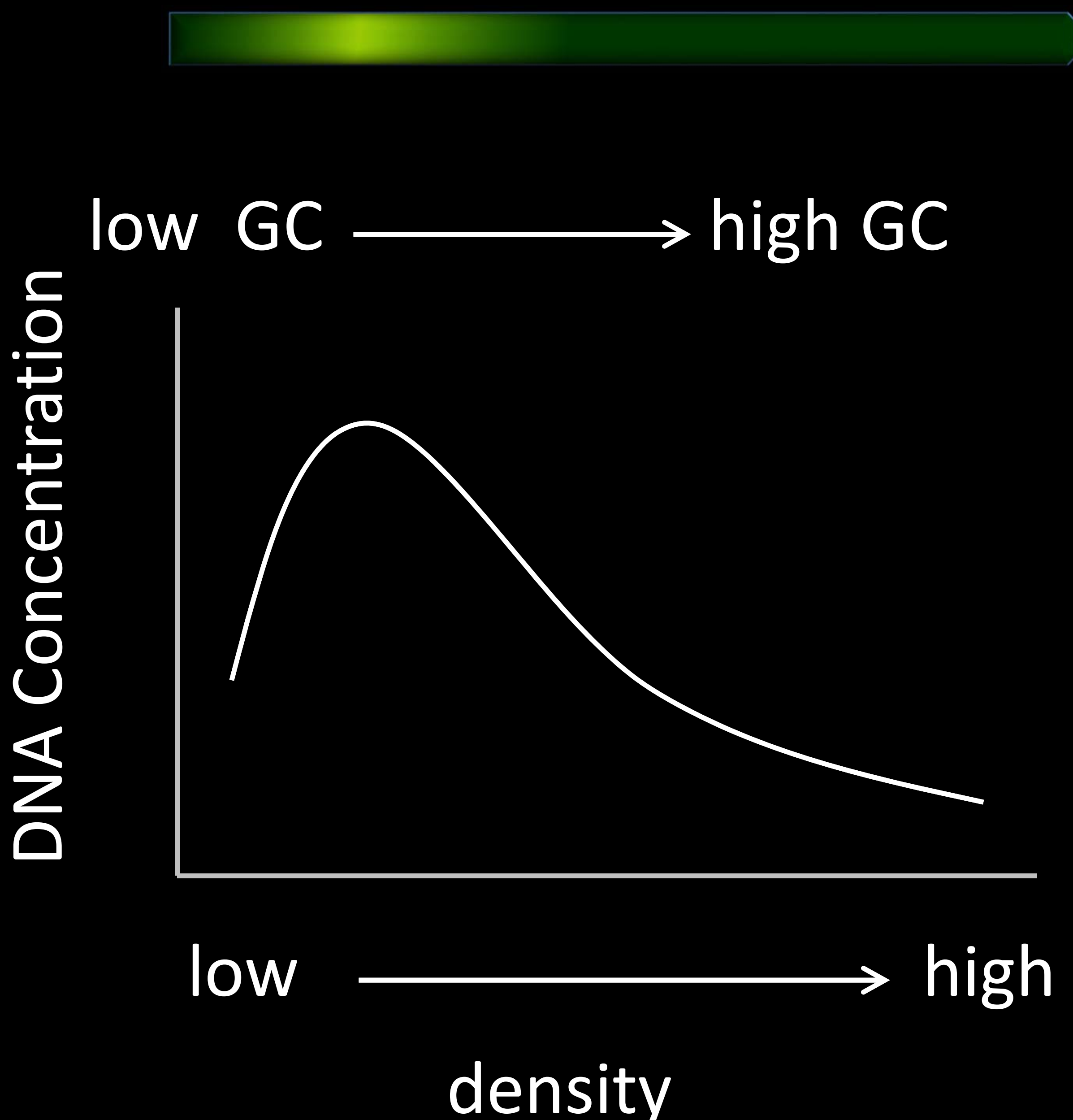


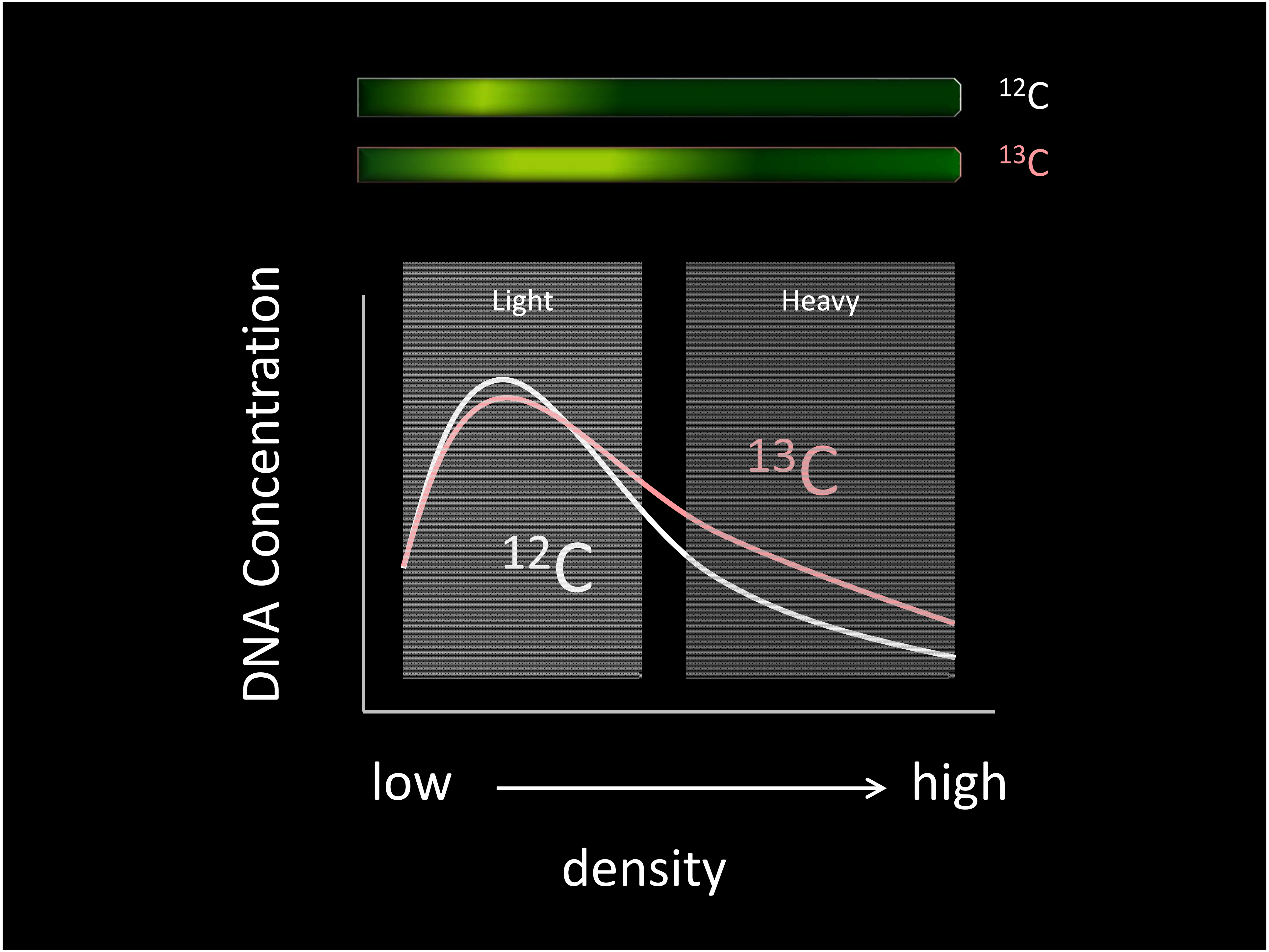
^{13}C-glucose
^{13}C-carbon dioxide
^{13}C-methane
^{18}O-H_2O


low
high
density

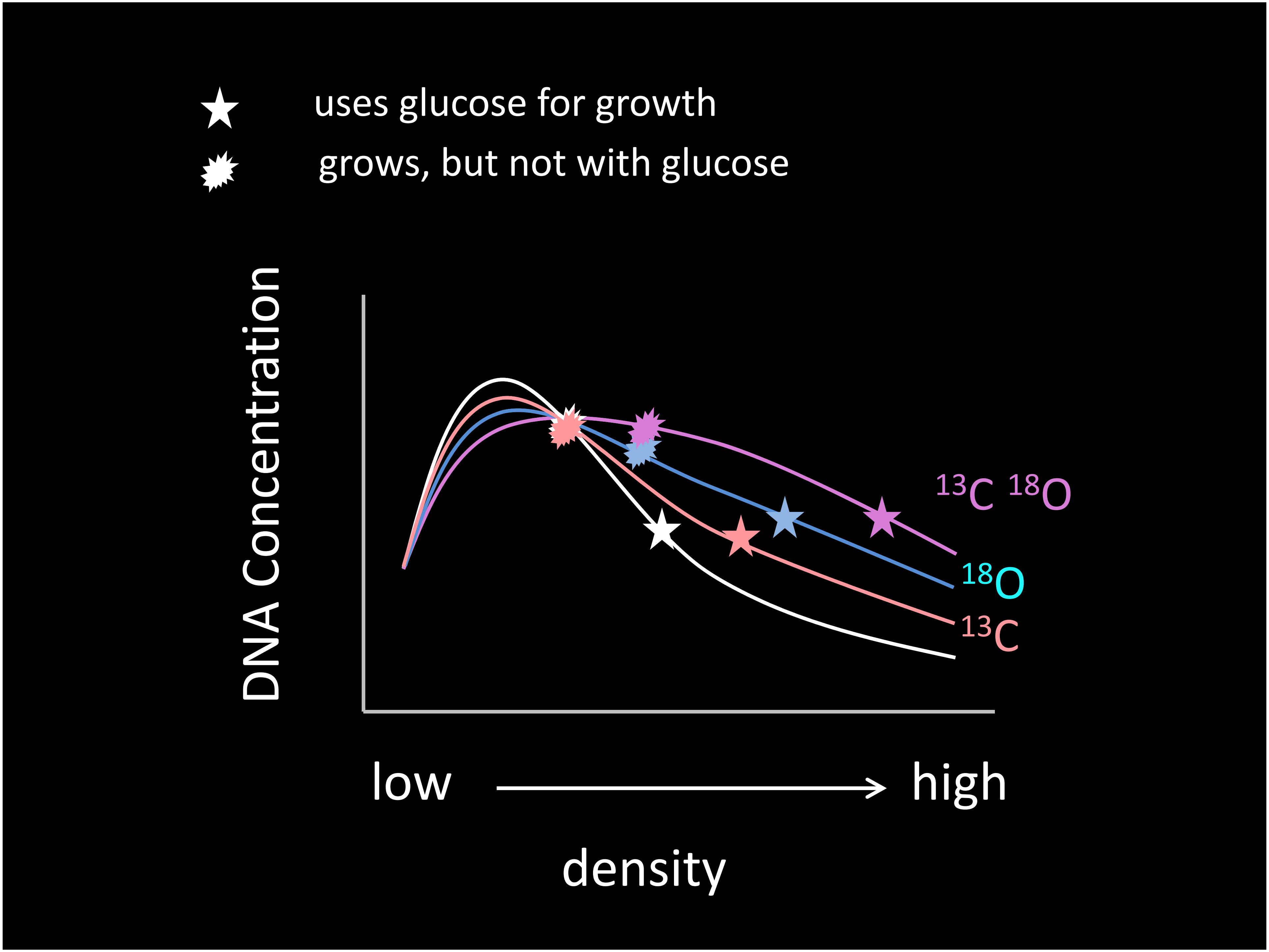


low GC
high GC
low
high
density

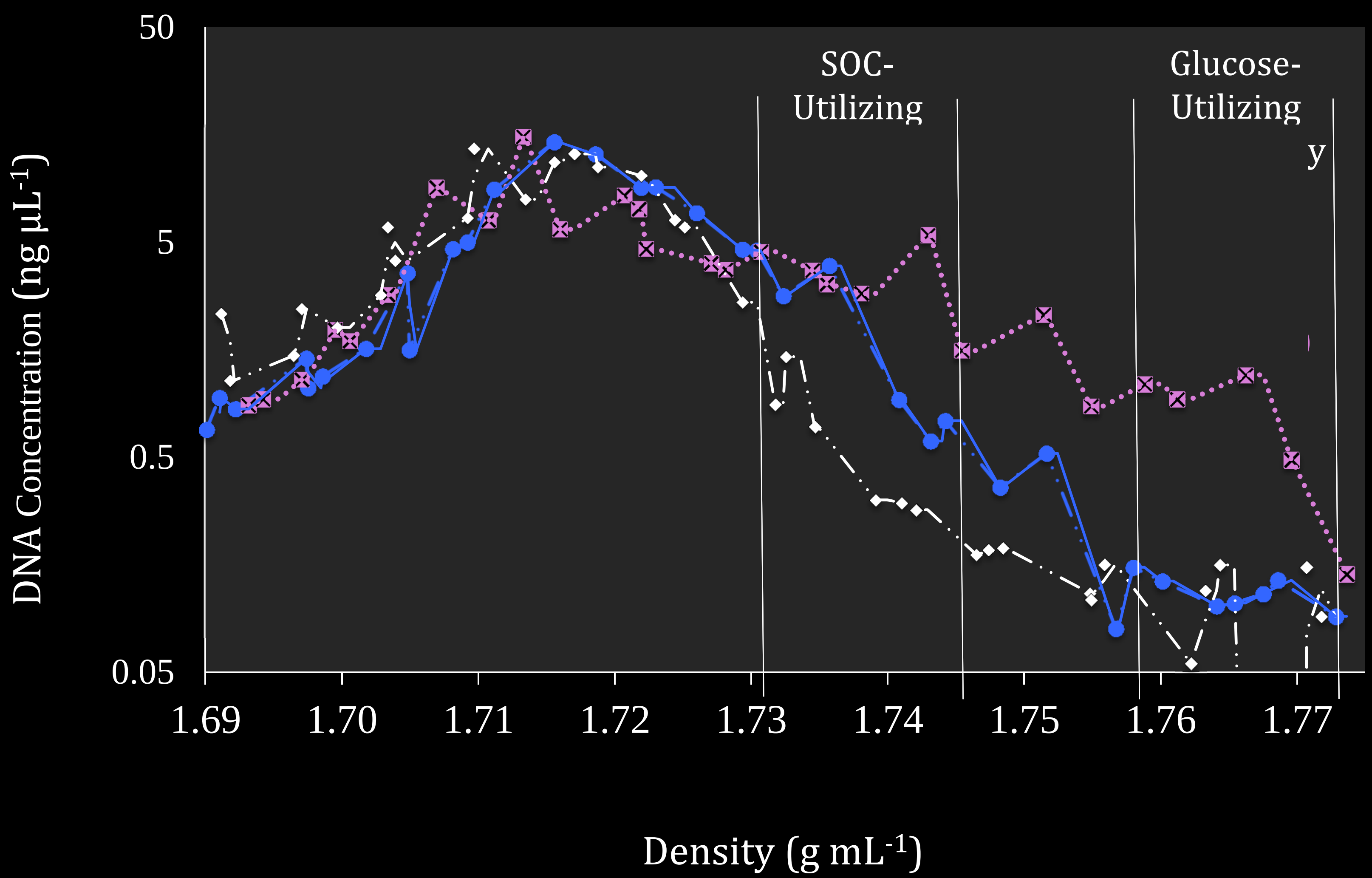

low GC
high GC
DNA Concentration
low
high
density



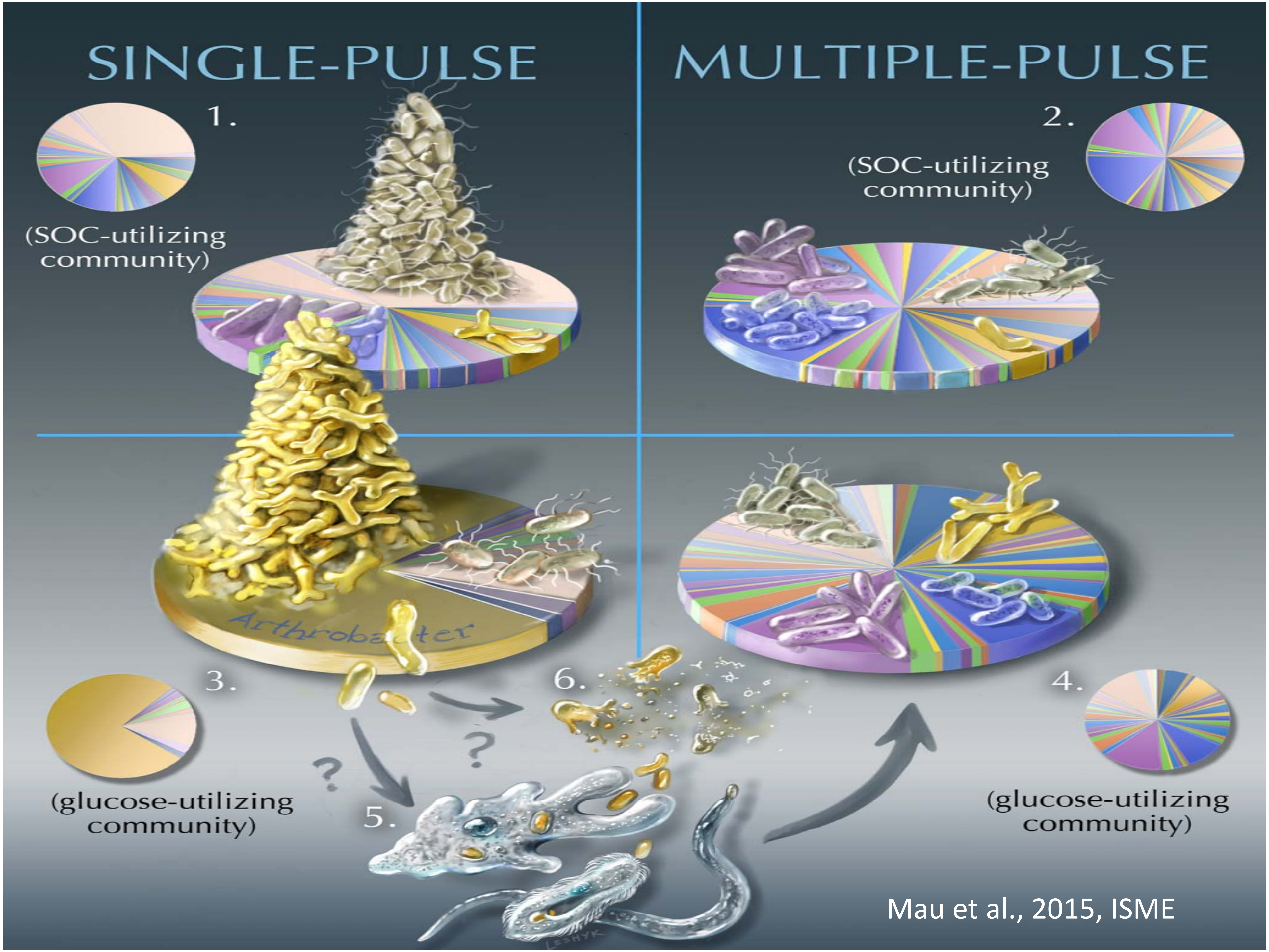
12C
13C
DNA Concentration
Light
Heavy
13C
12C
low
high
density



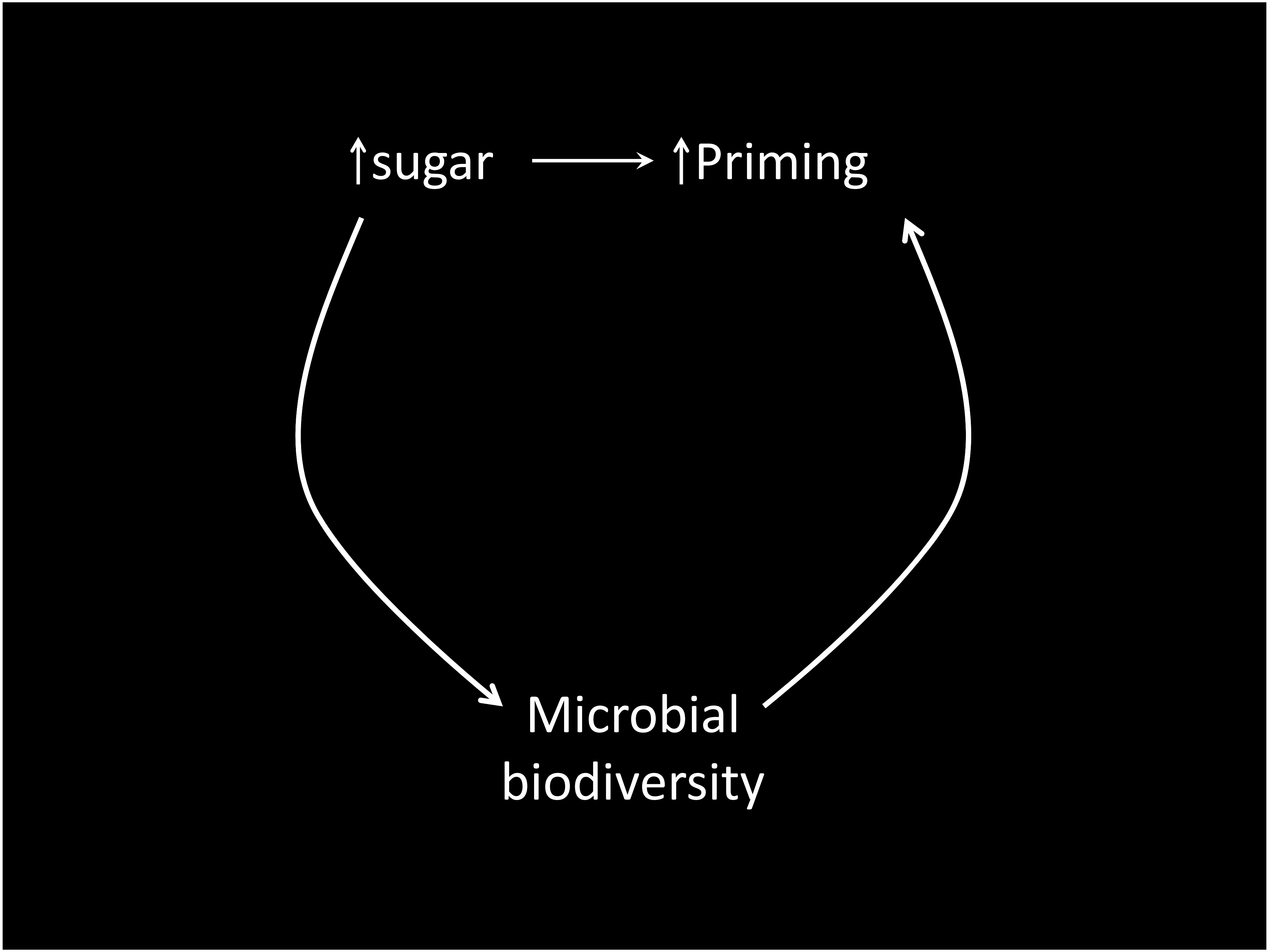
uses glucose for growth
grows, but not with glucose
DNA Concentration
13C 18O
18O
13C
low
high
density

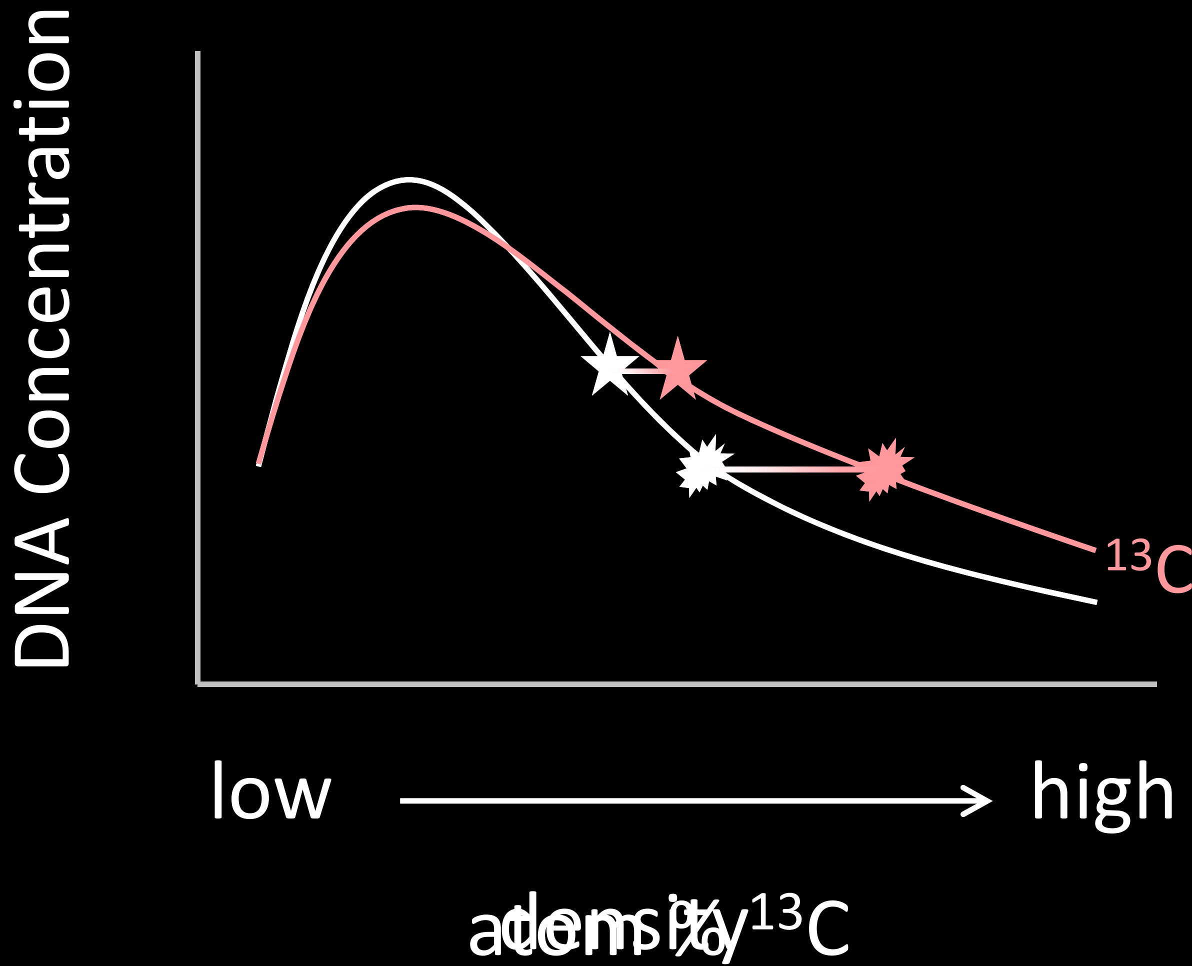


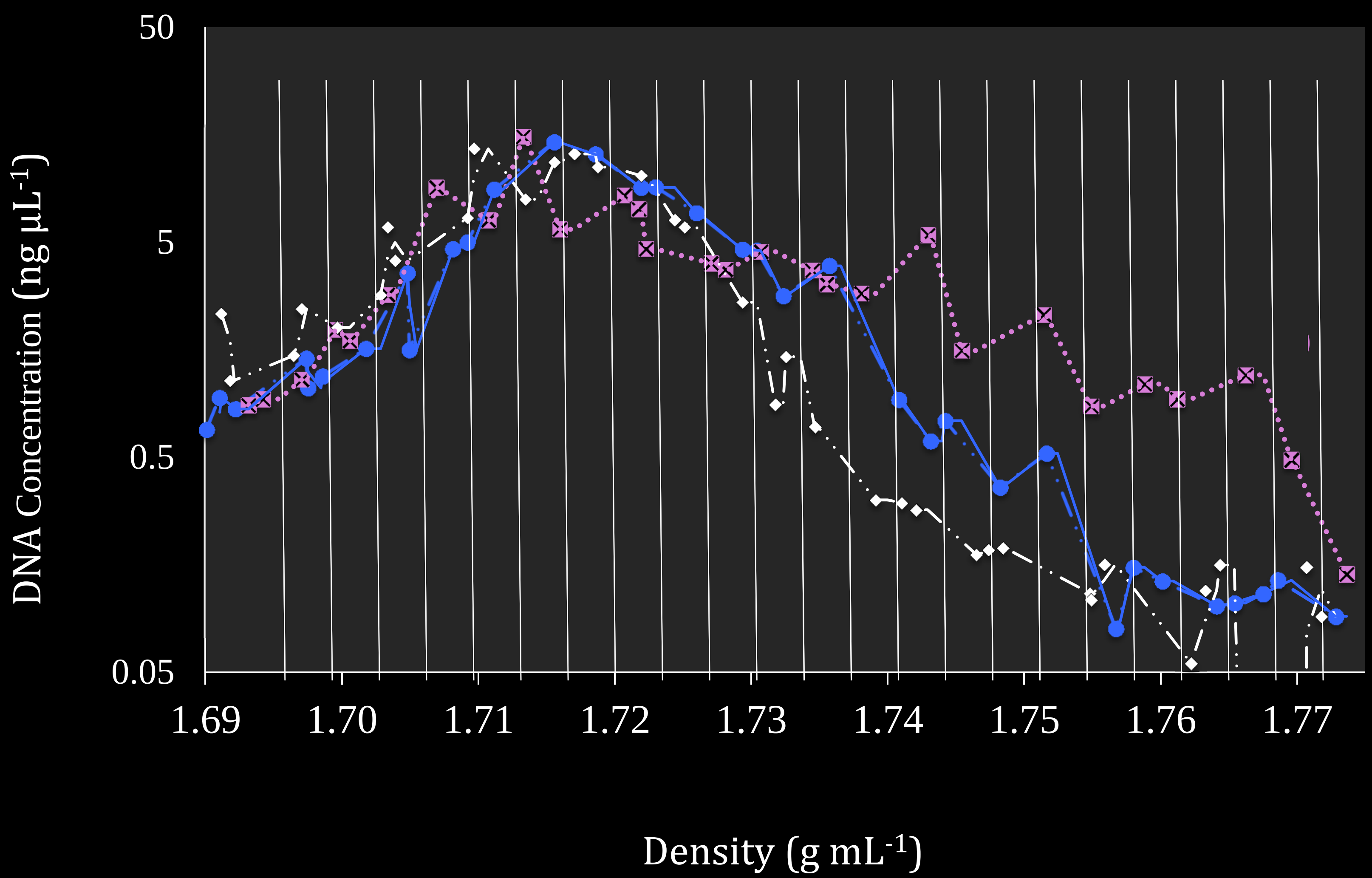
Mau et al., 2015, ISME



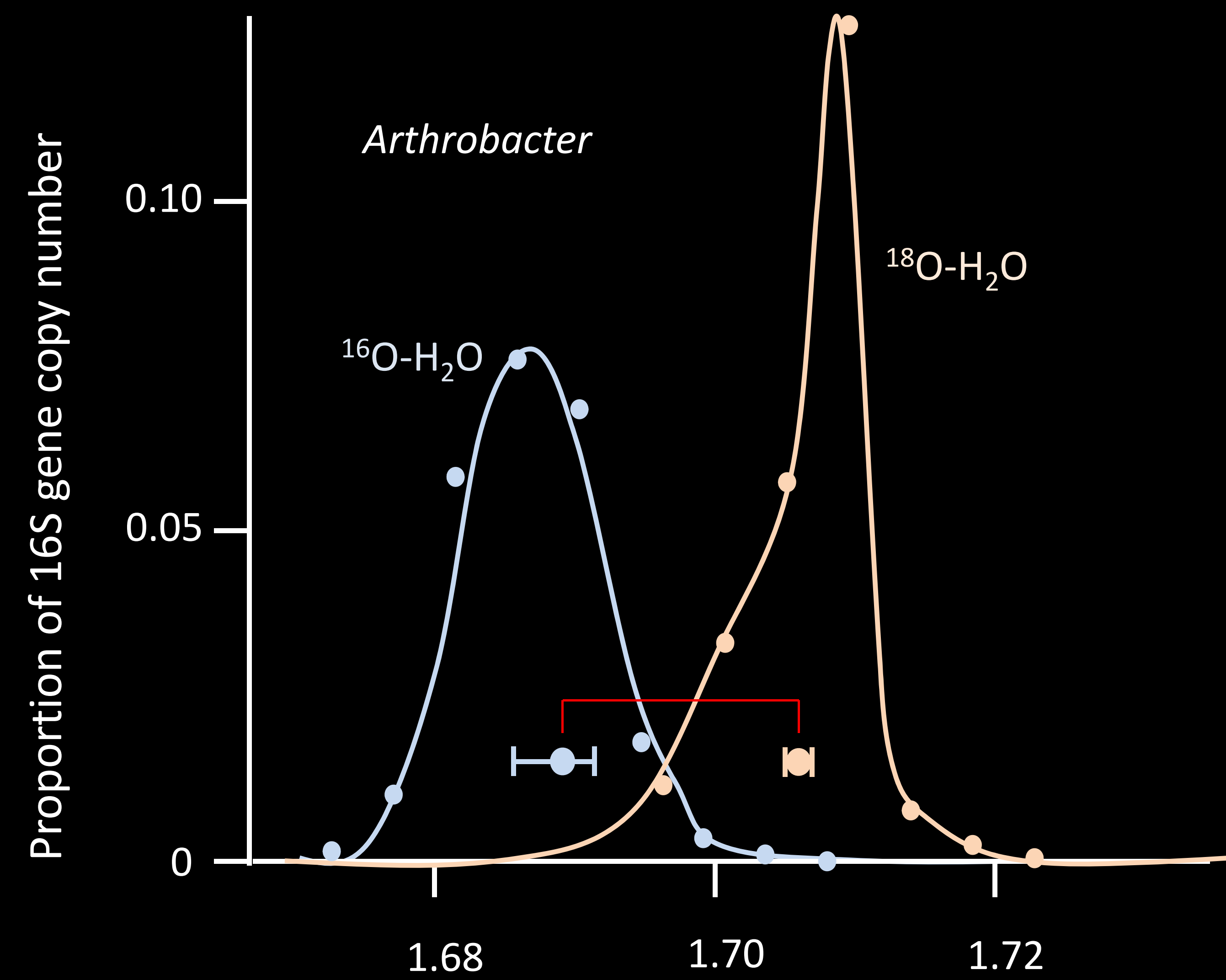
Mau et al., 2015, ISME


↑sugar
↑Priming
Microbial biodiversity


DNA Concentration
13C
low
high
density
atom % 13C



Mau et al., in review, ISME



Arthrobacter
Proportion of 16S gene copy number
0.10
0.05
0
$^{16}O-H_2O$
$^{18}O-H_2O$
1.68
1.70
1.72

$$y_{ijk} = p_{ijk} \cdot f_{jk}$$

For each density fraction, *k*, estimate abundance of taxon, *i*, for each sample, *j*, as the product of relative abundance of *i* in total assemblage, *f*

$$y_{ij} = \sum_{k=1}^{K} y_{ijk}$$

Sum across density fractions for each taxon, *i*

$$W_{ij} = \sum_{k=1}^{K} x_{jk} \cdot \left(\frac{y_{ijk}}{y_{ij}} \right)$$

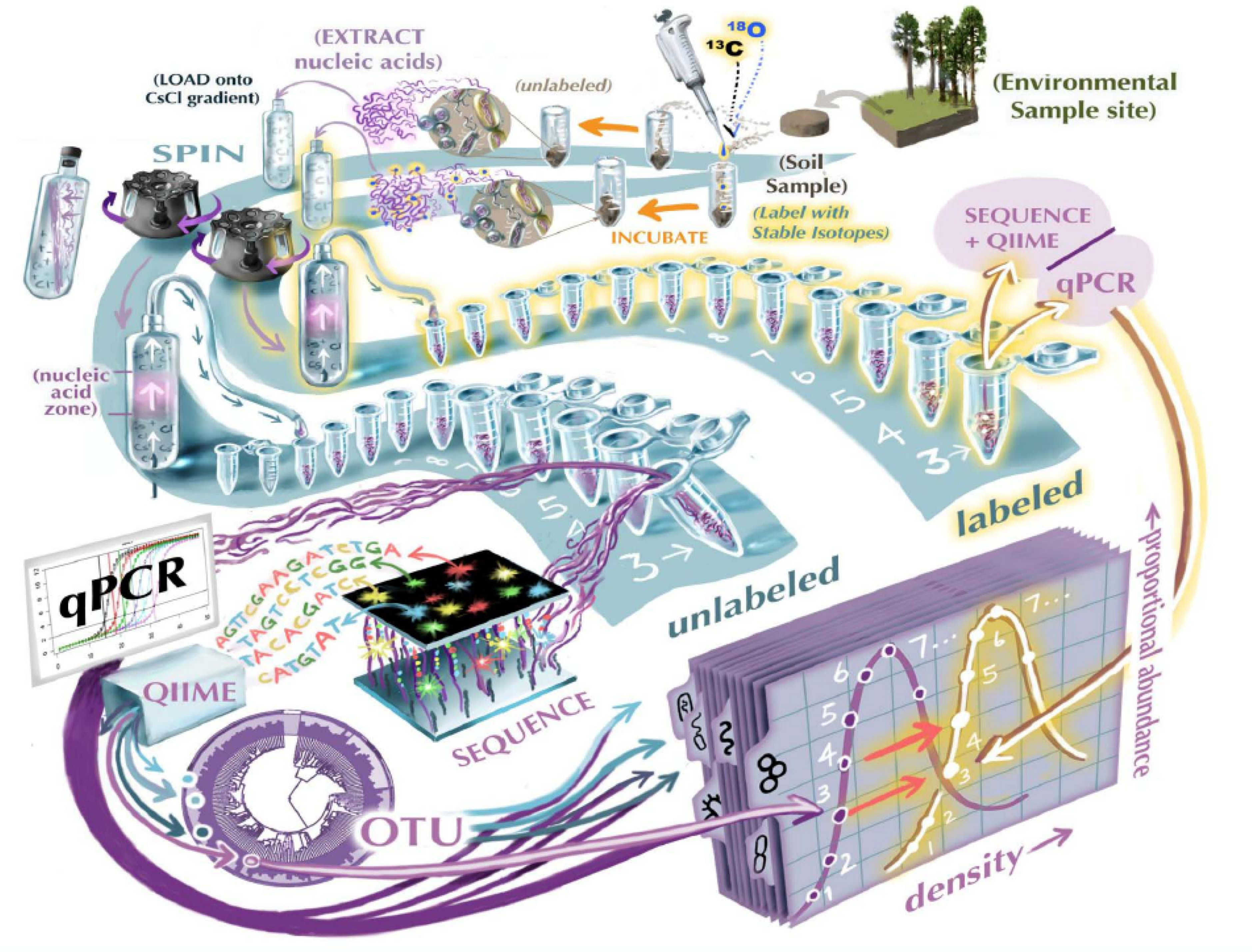
Calculate the weighted average density for each taxon

$$M_{\mathrm{LAB}i} = \left(\frac{Z_i}{W_{\mathrm{LIGHT}i}} + 1 \right) \cdot M_{\mathrm{LIGHT}i}$$

Increase in weighted average density with isotope uptake ~ increase in molecular weight of the labeled DNA (M_{LABi})

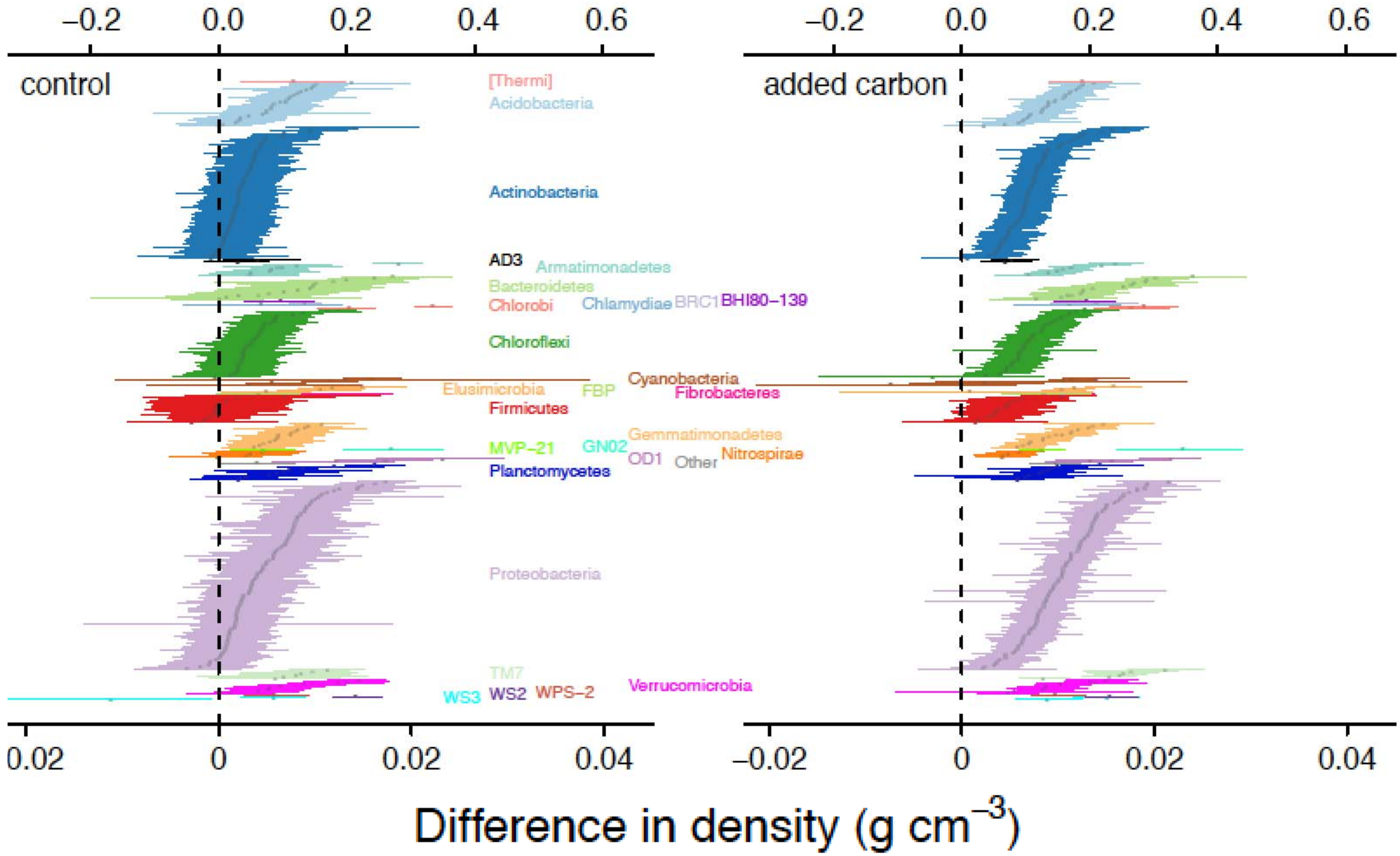
$$A_{\mathrm{OXYGEN}i} = \frac{M_{\mathrm{LAB}i} - M_{\mathrm{LIGHT}i}}{M_{\mathrm{HEAVYMAX}i} - M_{\mathrm{LIGHT}i}} \cdot (1 - 0.002000429)$$

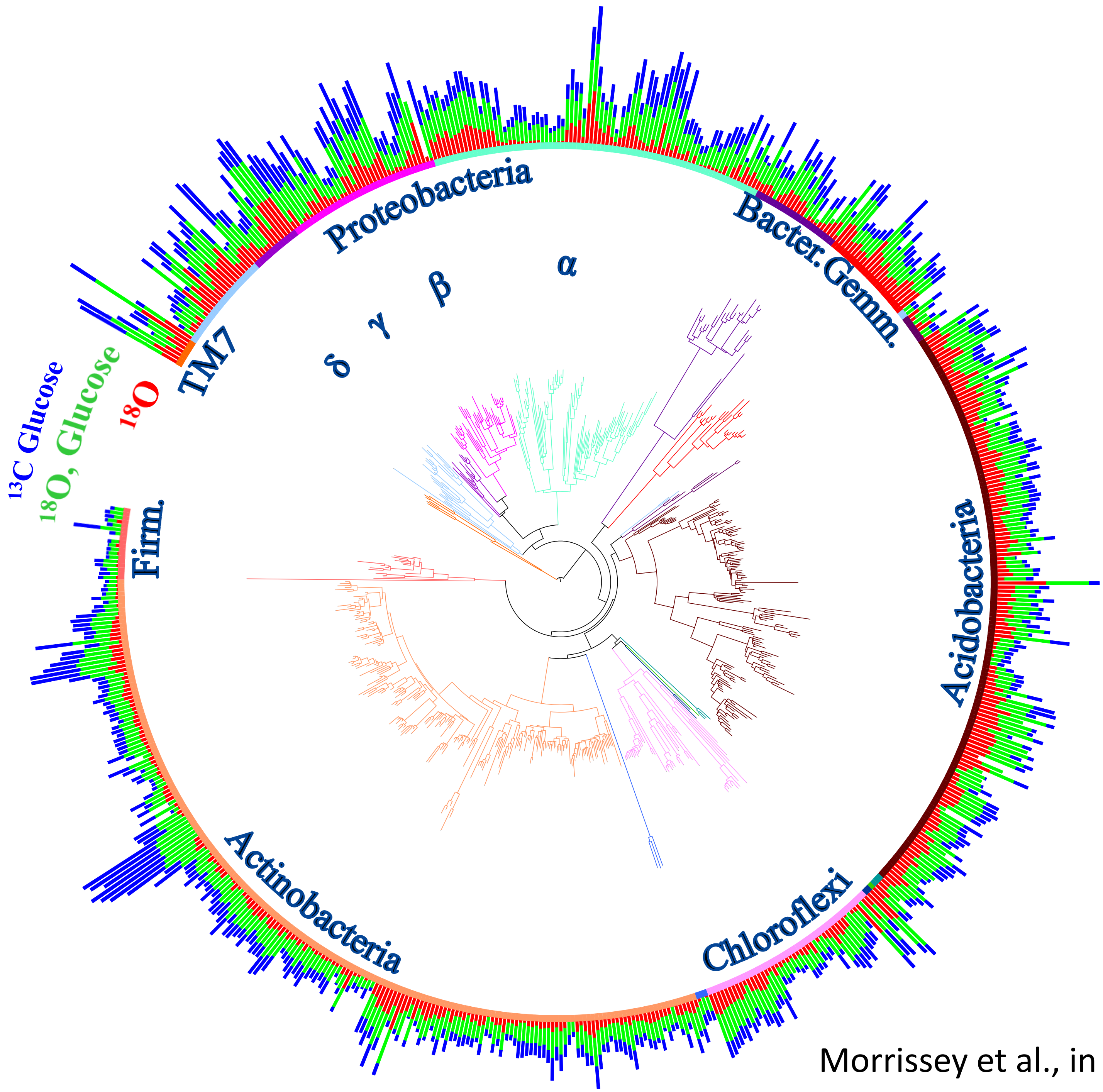
Calculate atom fraction excess isotope composition, *A*, for each taxon, *i*



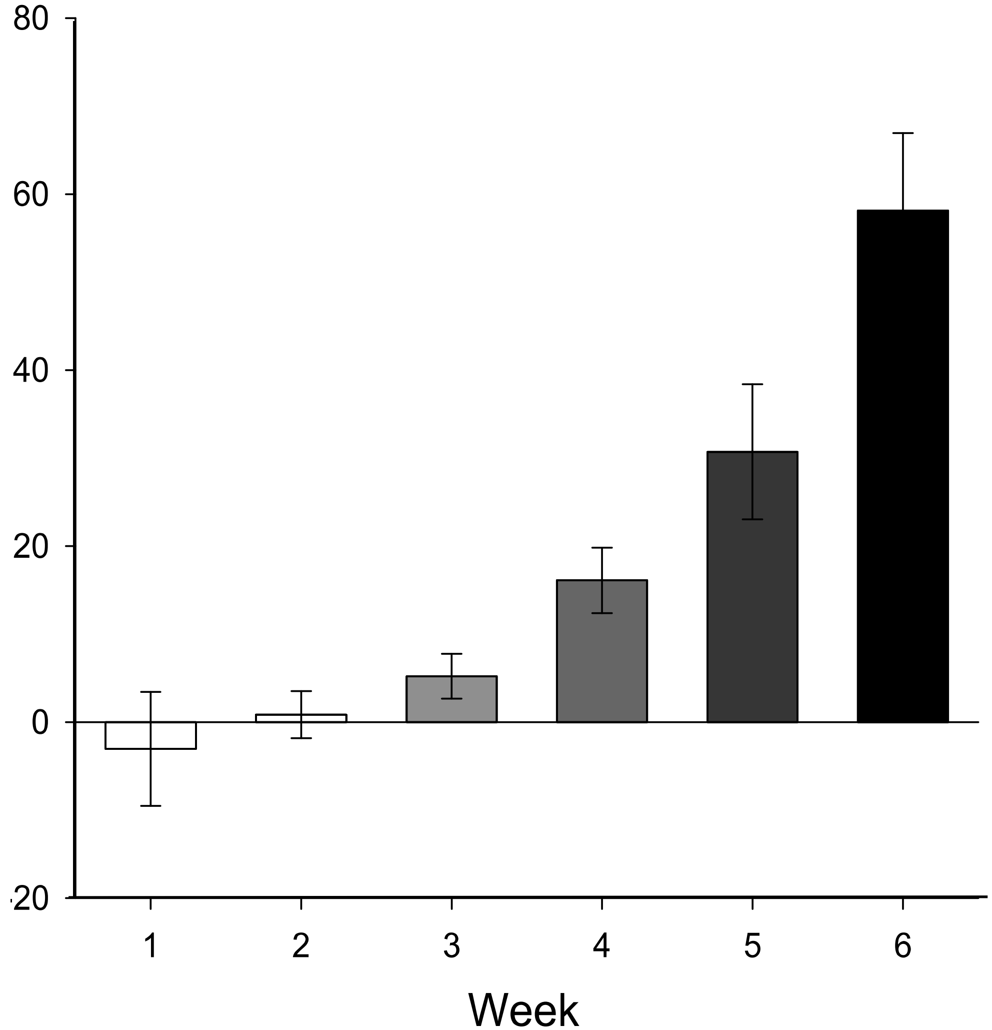
(EXTRACT nucleic acids)
(LOAD onto CsCl gradient)
(unlabeled)
^{13}C
^{18}O
(Environmental Sample site)
SPIN
(Soil Sample)
(Label with Stable Isotopes)
INCUBATE
SEQUENCE + QIIME
qPCR
(nucleic acid zone)
labeled
unlabeled
qPCR
QIIME
SEQUENCE
OTU
density
proportional abundance

Atom fraction excess ^{18}O

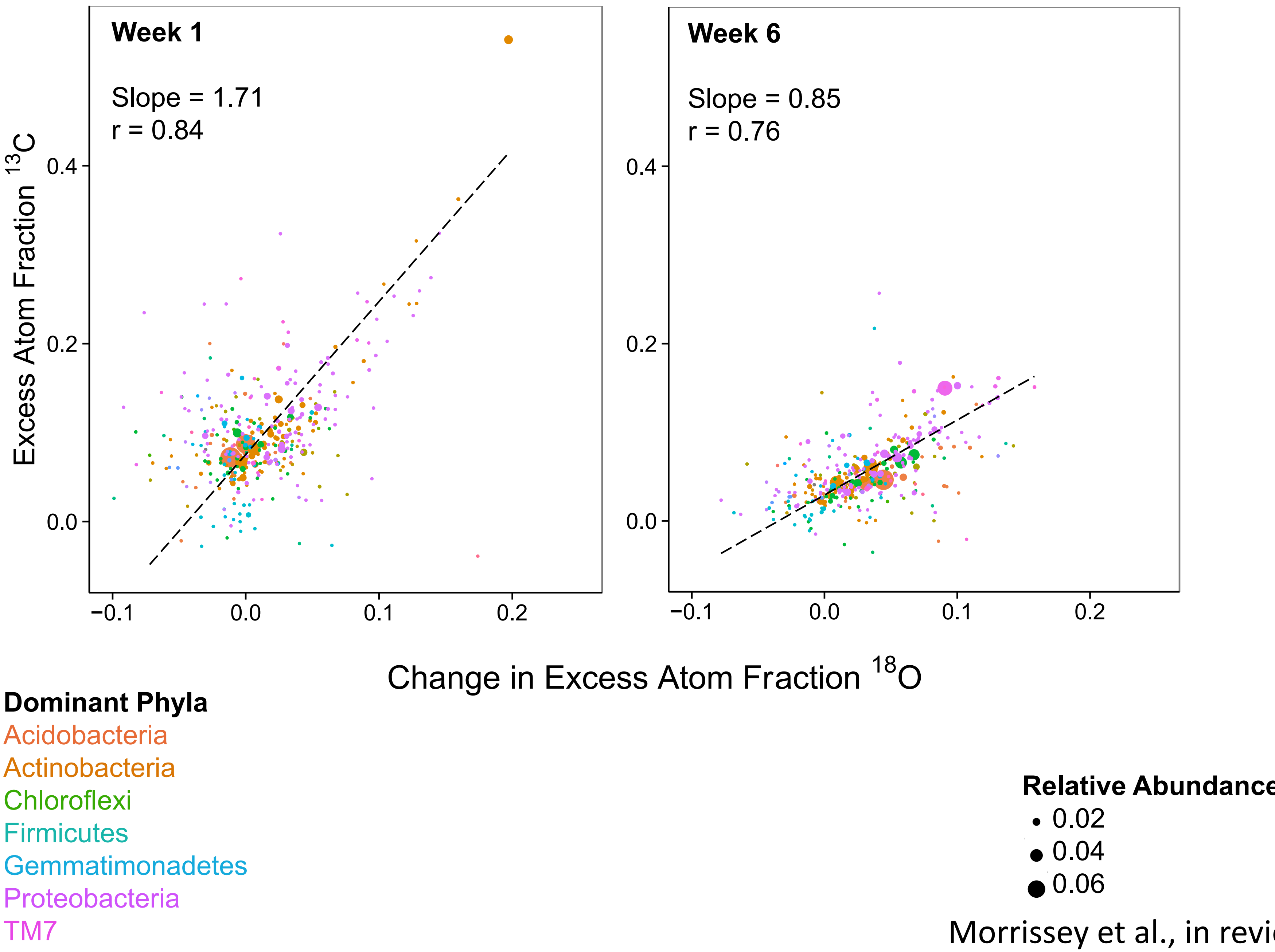




Morrissey et al., in press, ISME



Morrissey et al., in review



Morrissey et al., in review

Extending model to estimate vital rates

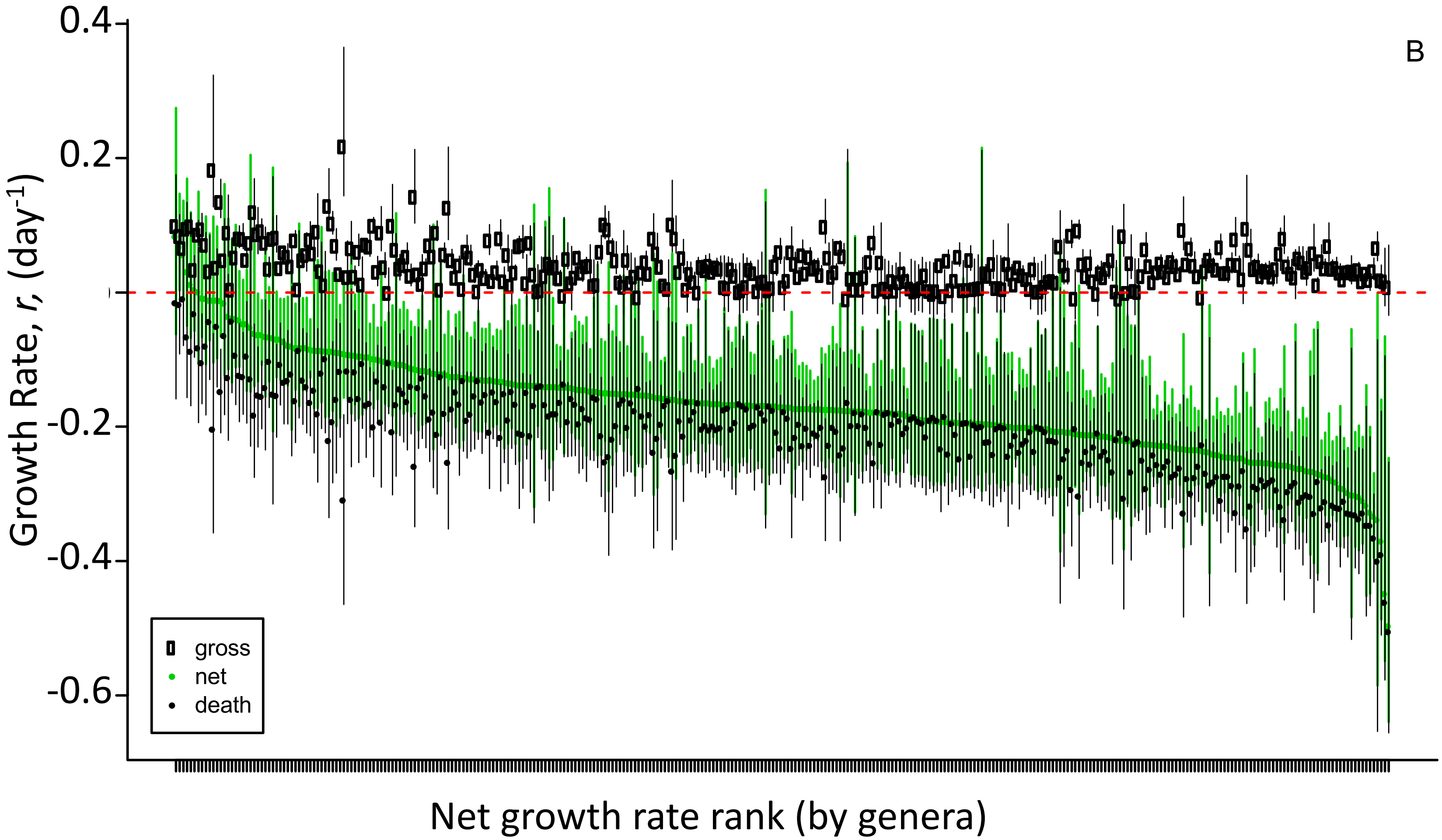
equation	*translation*
$N_{\mathrm{TOTAL}it} = N_{\mathrm{LIGHT}it} + N_{\mathrm{HEAVY}it}$	Total organisms = labeled organisms plus unlabeled organisms
$N_{\mathrm{LIGHT}it} = N_{\mathrm{TOTAL}it} \cdot \left(\frac{M_{\mathrm{HEAVY}i} - M_{\mathrm{LAB}i}}{M_{\mathrm{HEAVY}i} - M_{\mathrm{LIGHT}i}} \right)$	Unlabeled organisms = total organisms x proportion unlabeled

...

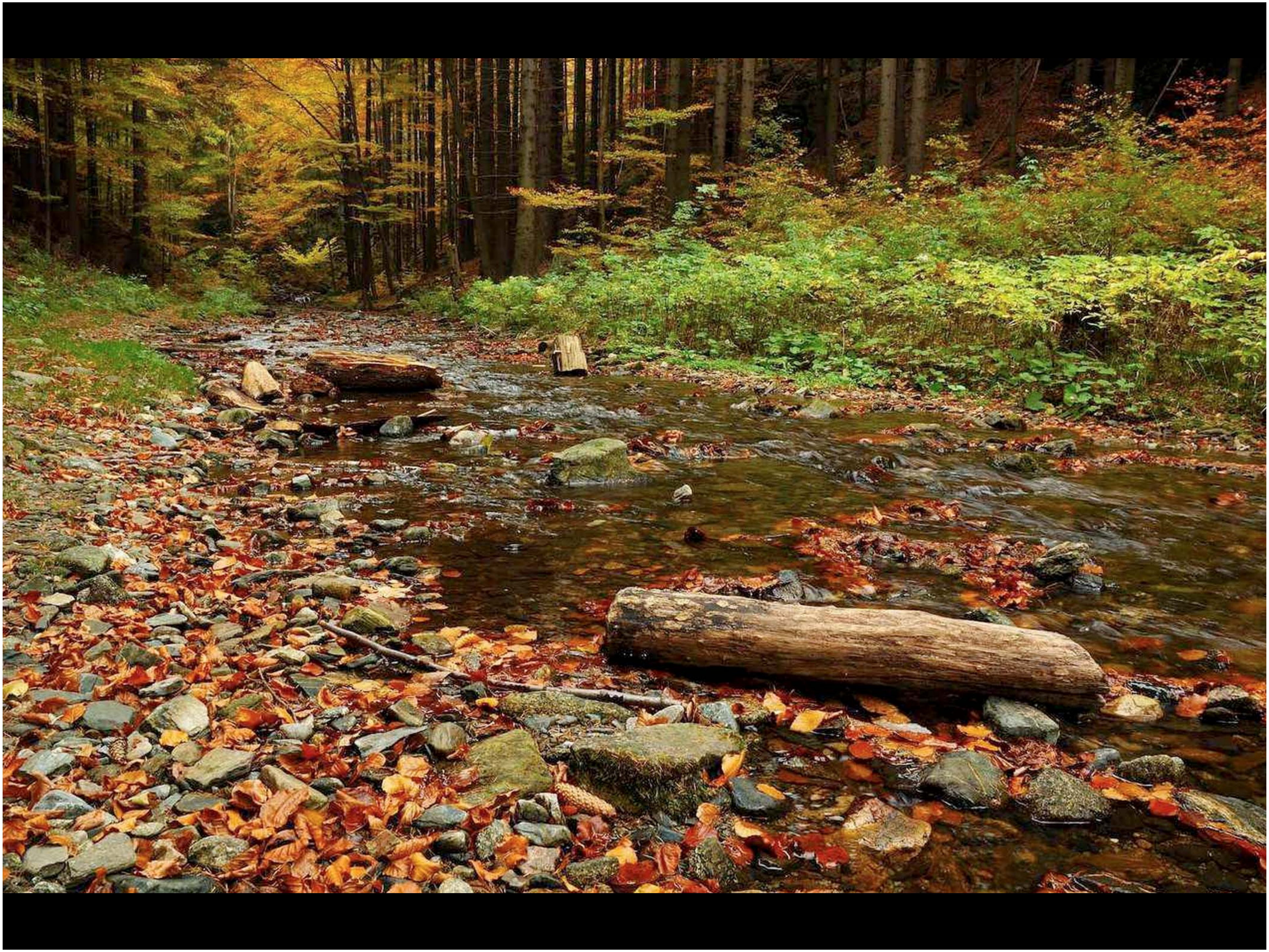
$d_i = \ln\left(\frac{N_{\mathrm{LIGHT}it}}{N_{\mathrm{LIGHT}i0}} \right) \cdot \frac{1}{t}$	Mortality is how fast unlabeled organisms disappear
$b_i = \ln\left(\frac{N_{\mathrm{TOTAL}it}}{N_{\mathrm{LIGHT}it}} \right) \cdot \frac{1}{t}$	Birth or reproduction is is how fast new labeled organisms appear
$d_i + b_i = r_i$	birth + death = net growth (r)

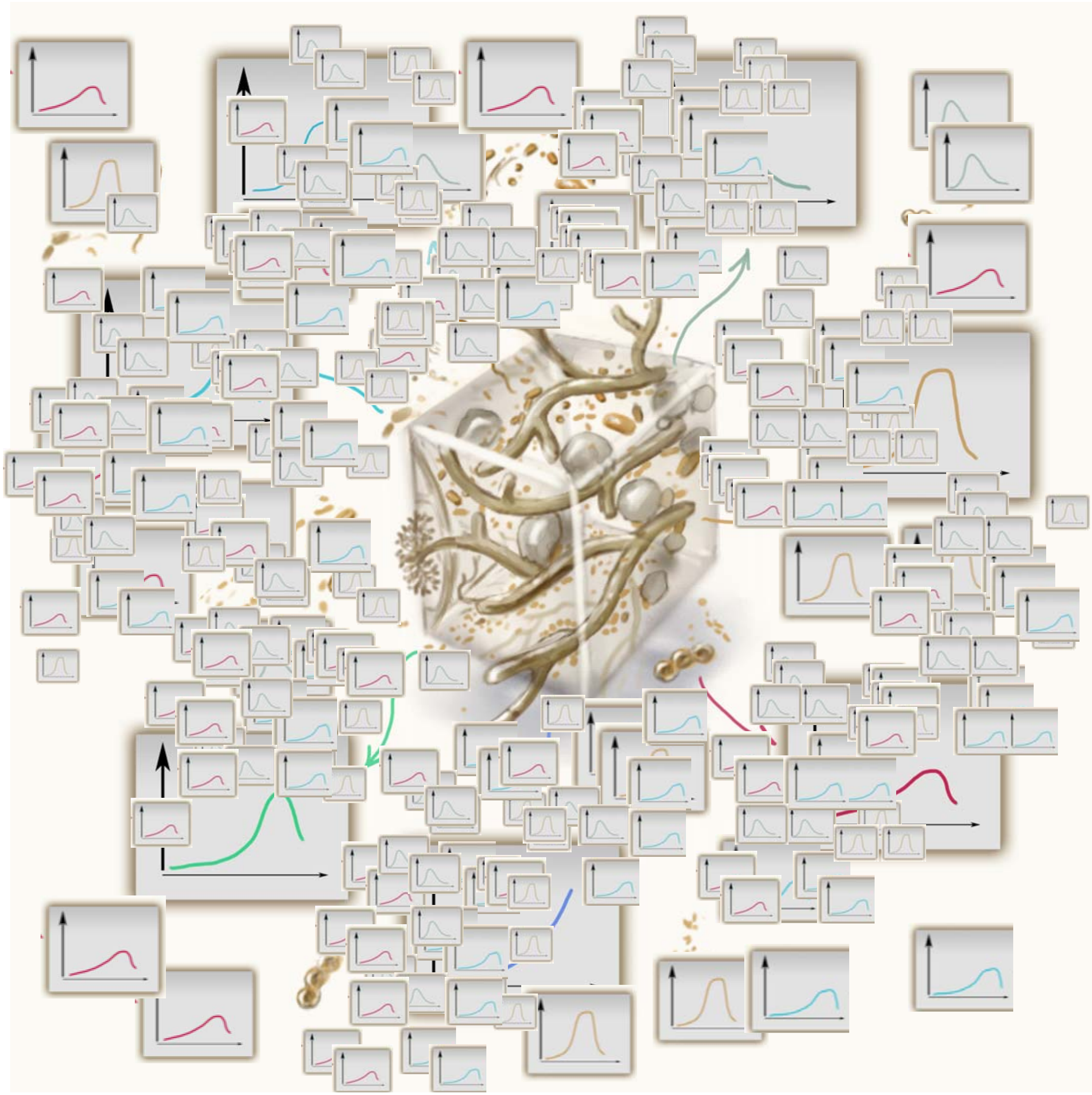
Ben Koch et al., in prep

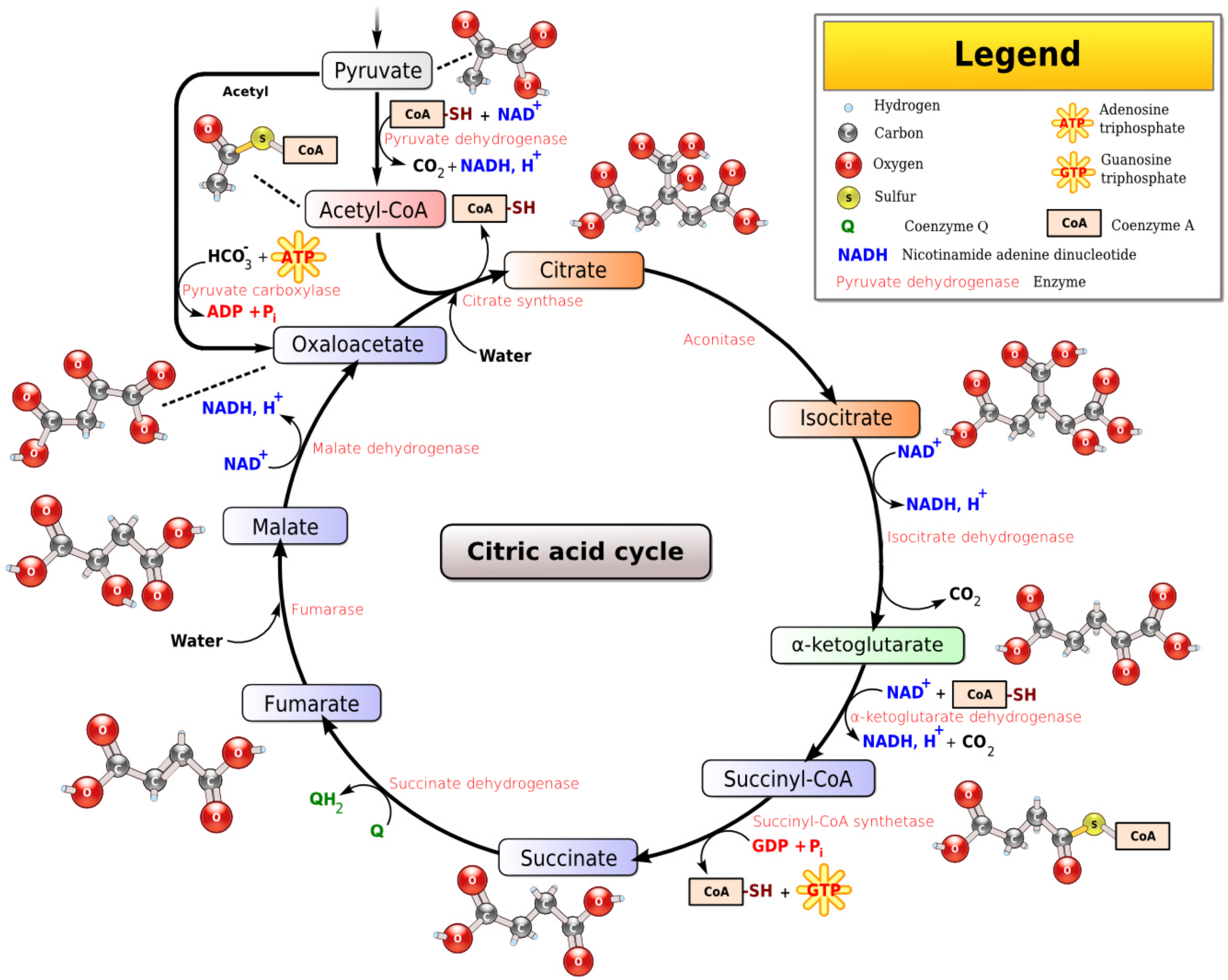
Normal distribution of growth rate



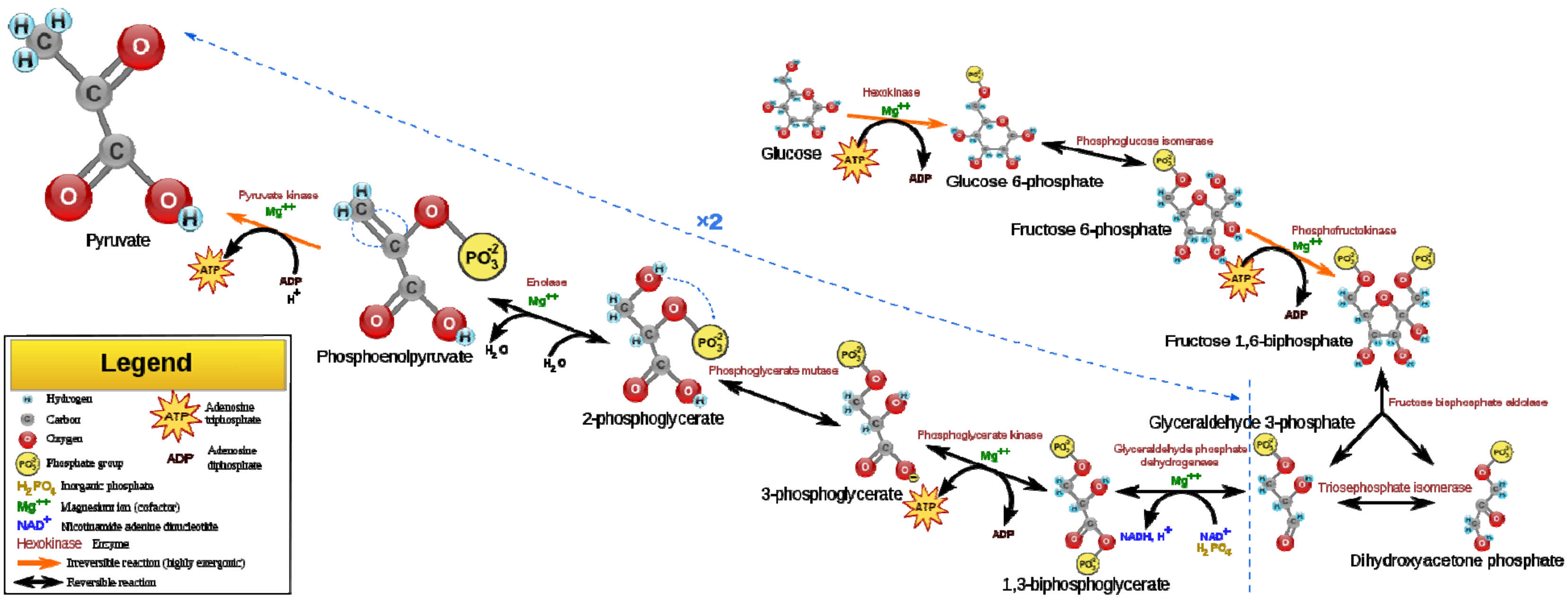
Ben Koch et al. in prep



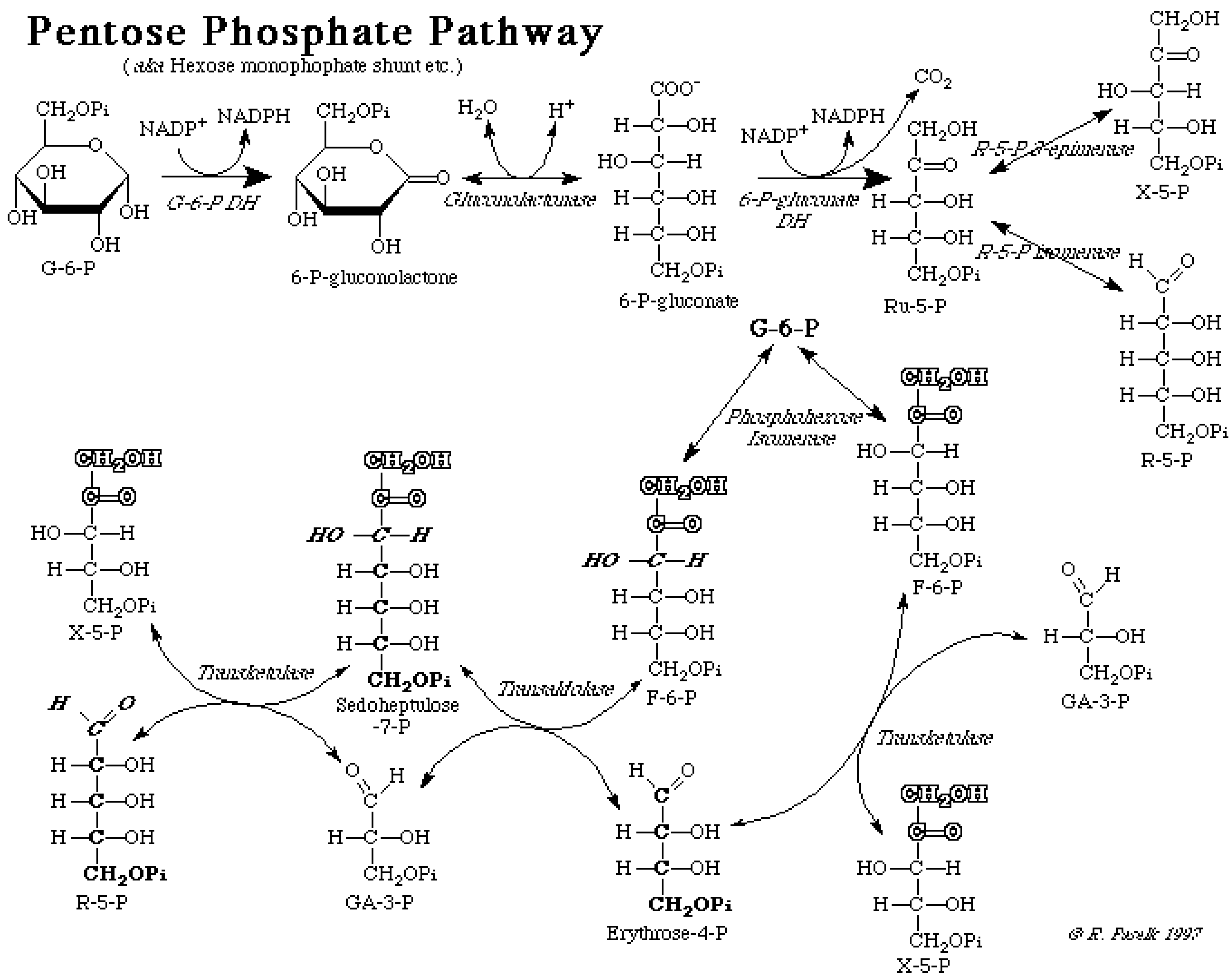




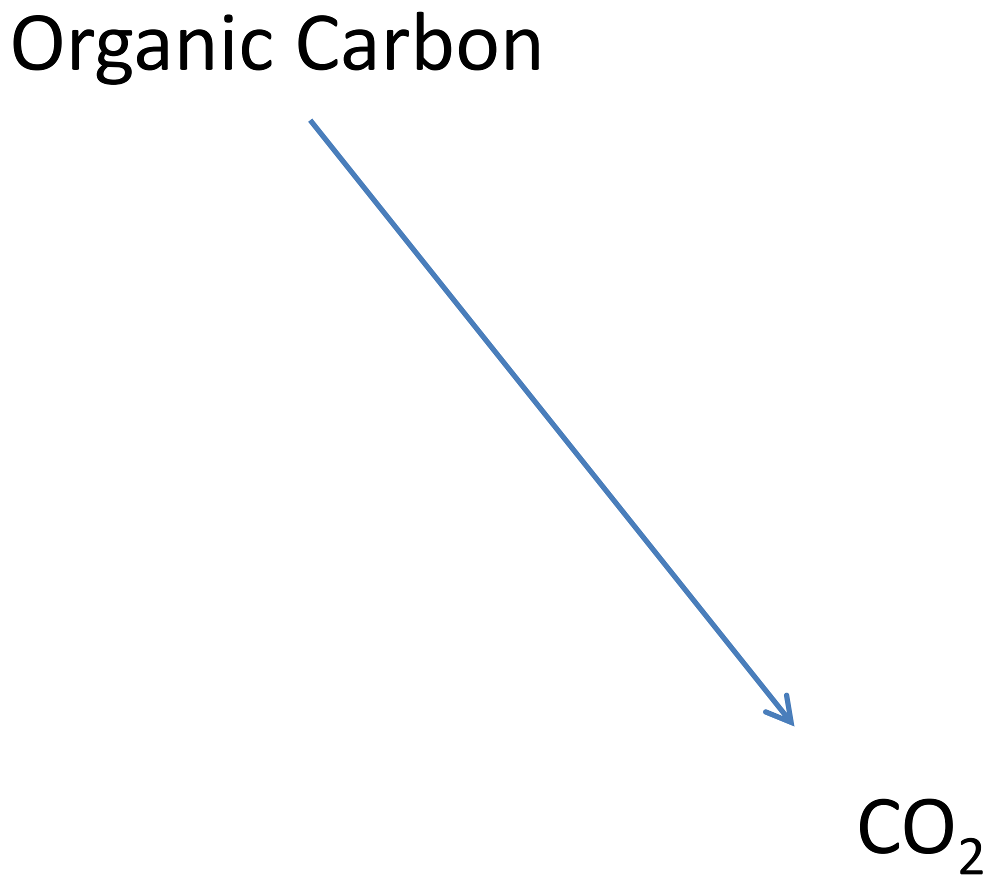
http://en.wikipedia.org/wiki/File:Krebs.svg

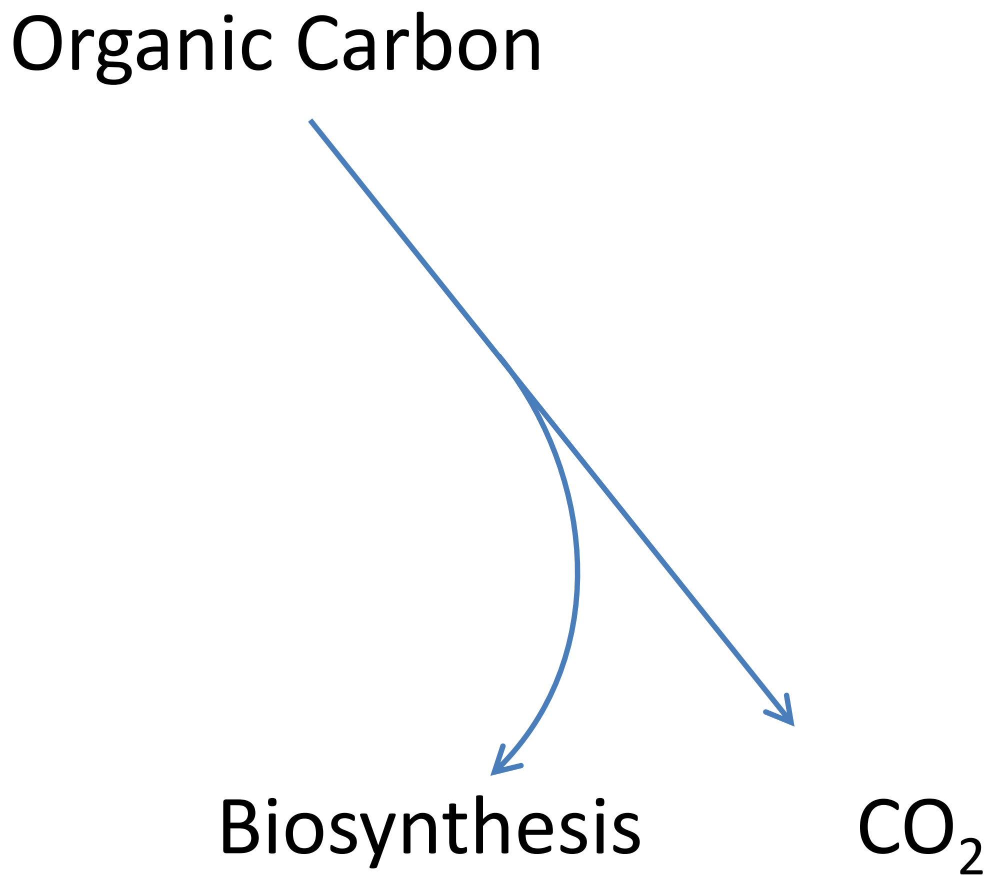


http://en.wikipedia.org/wiki/File:Glycolysis.svg

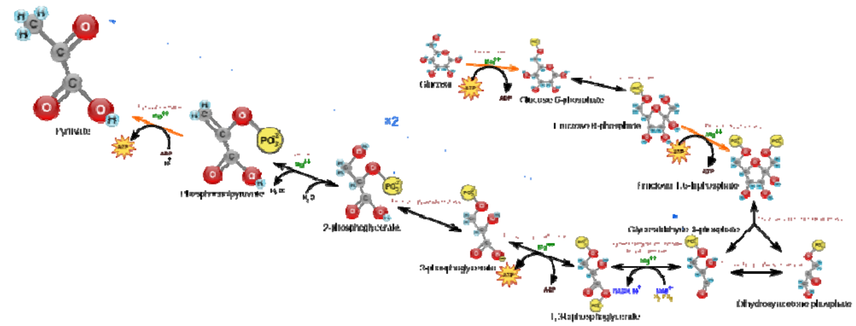


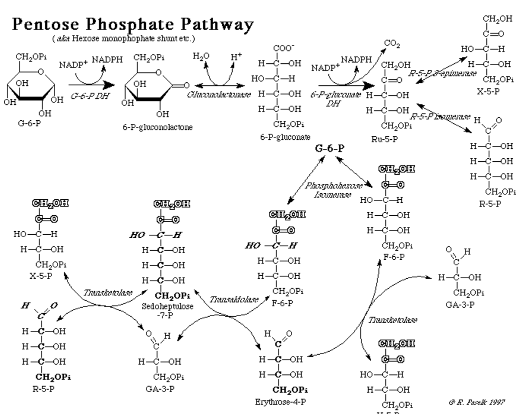
http://users.humboldt.edu/rpaselk/C431.F01/PathwayDiagrams/PentPhosPath.gif&imgrefurl

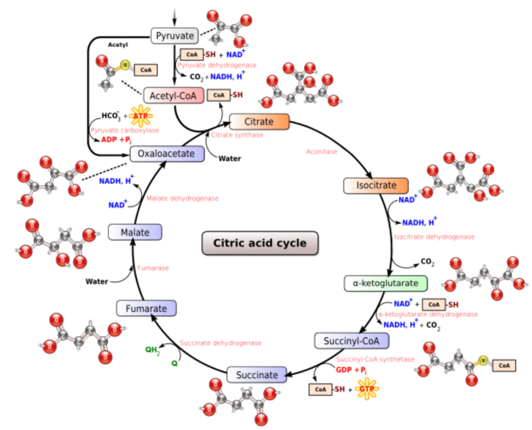

Organic Carbon
CO_2


Organic Carbon
Biosynthesis
CO_2

Organic Carbon

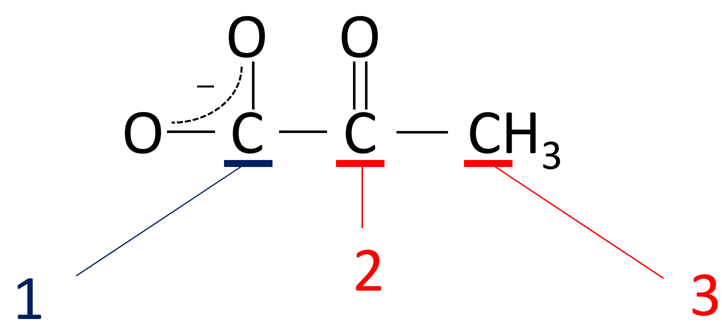






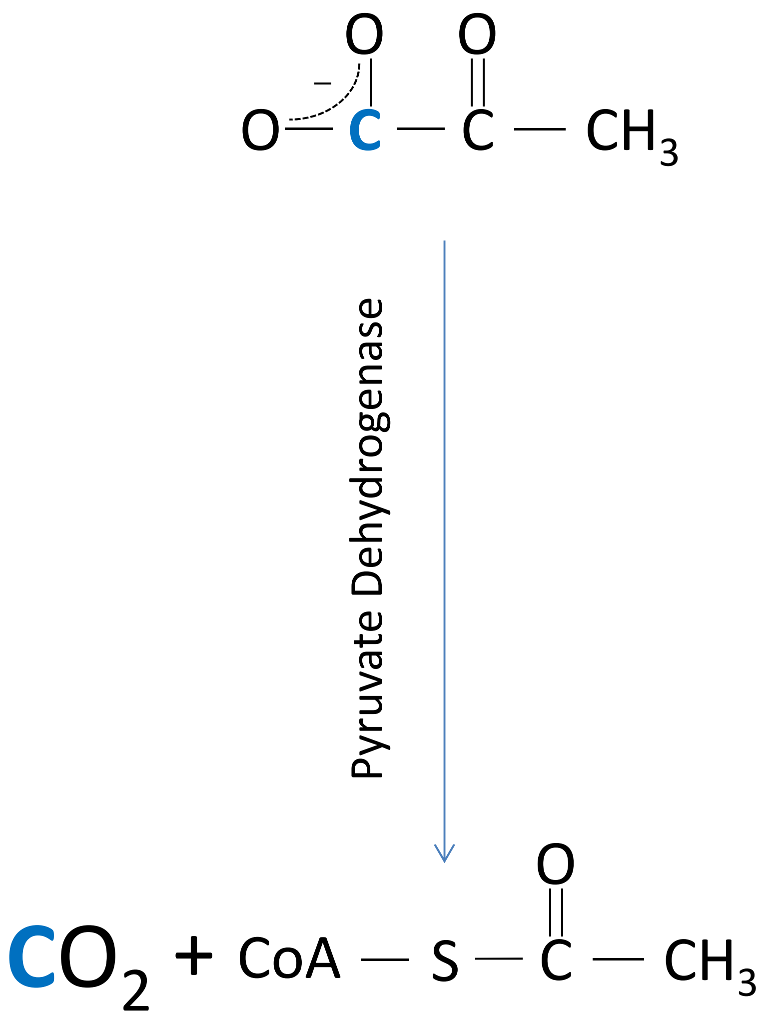
Biosynthesis

CO_2

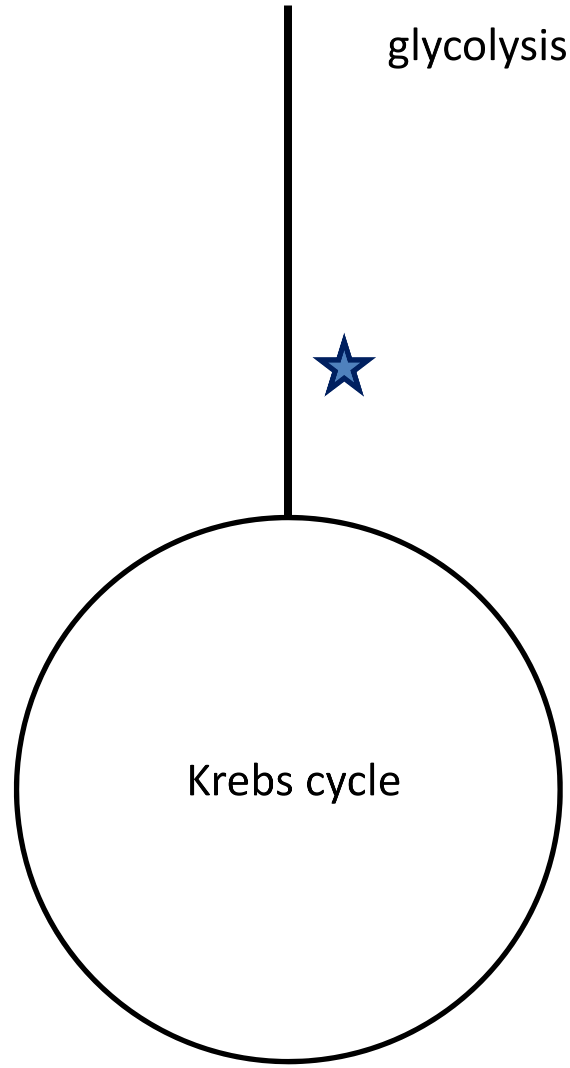


pyruvate

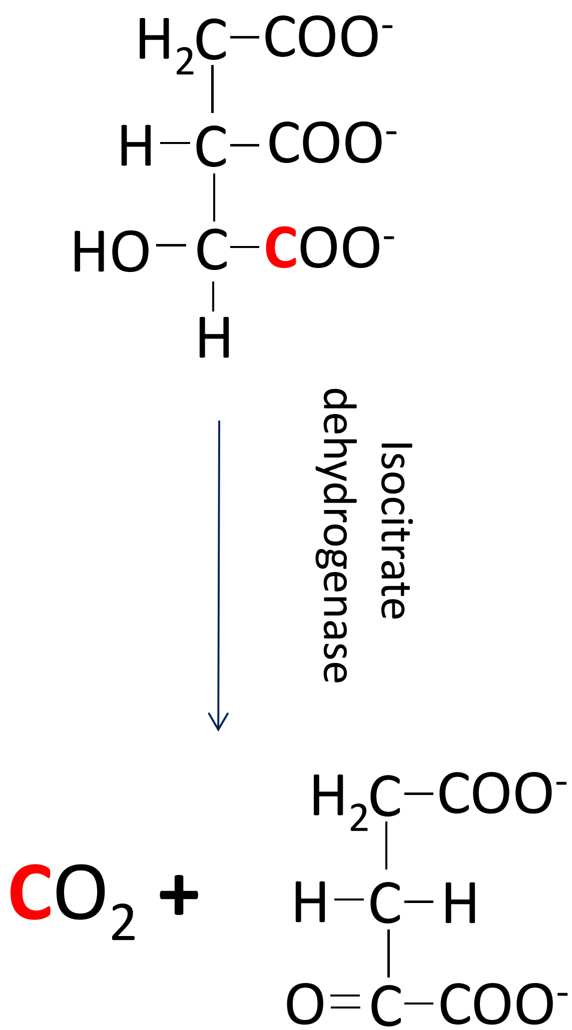
Pyruvate



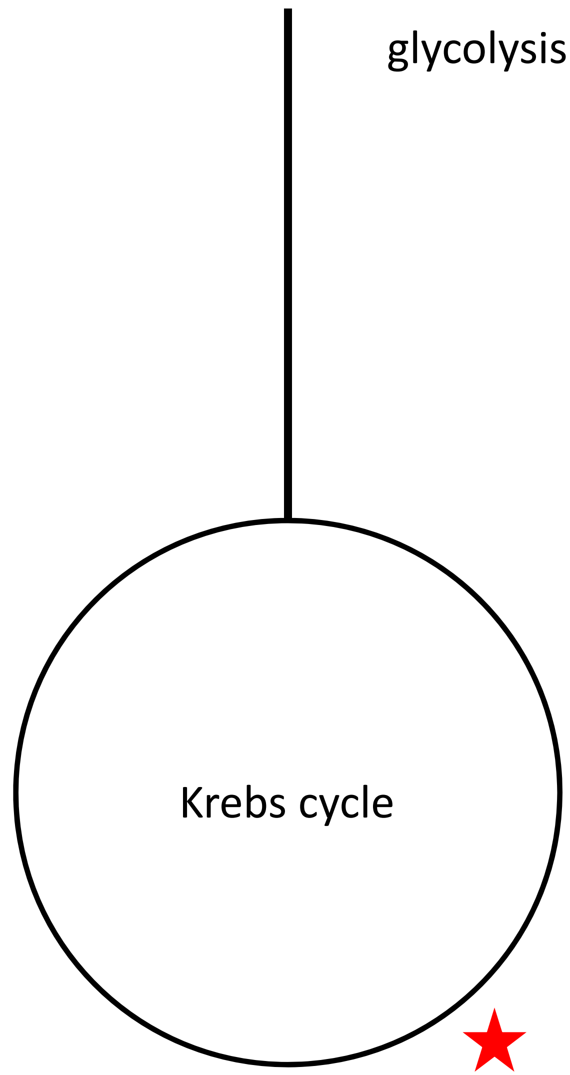
Acetyl coenzyme A



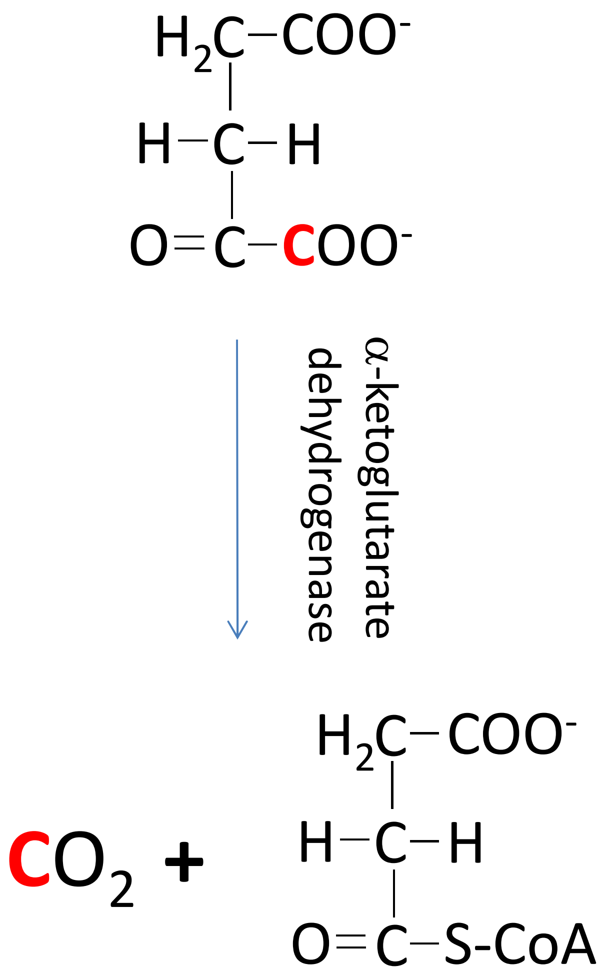
isocitrate



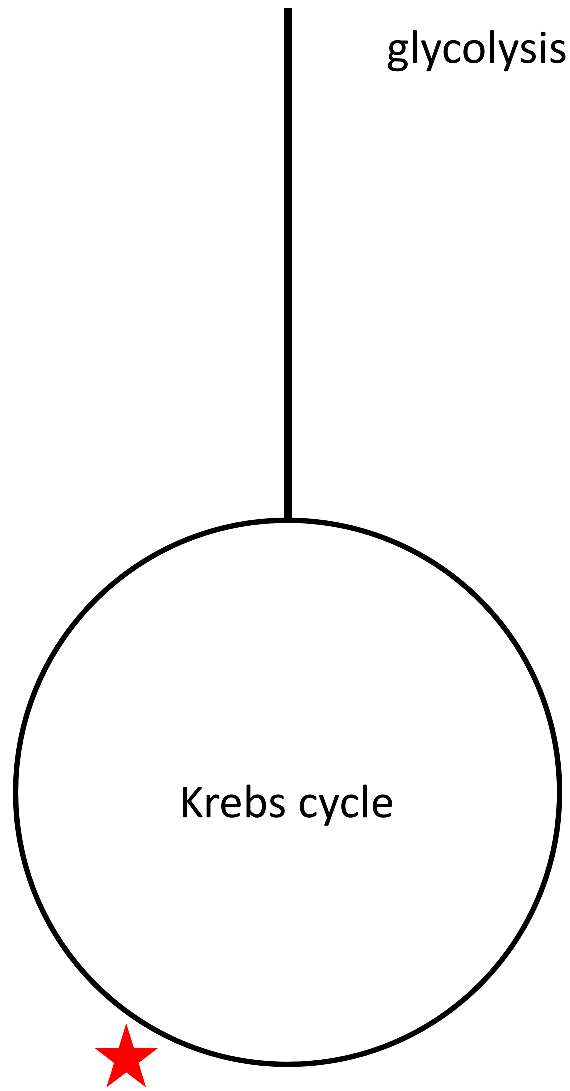
α-ketoglutarate



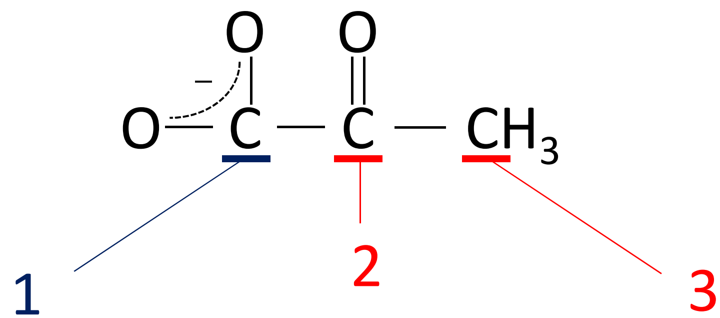
α-ketoglutarate



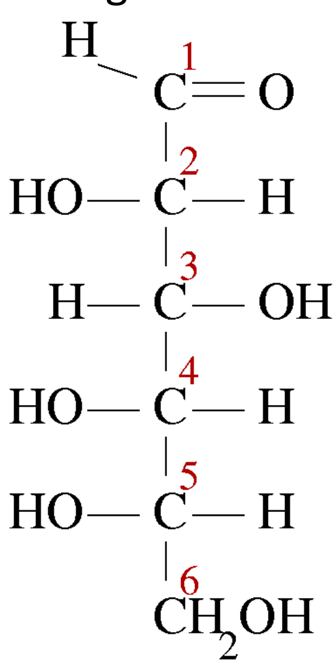
succinyl coenzyme-A

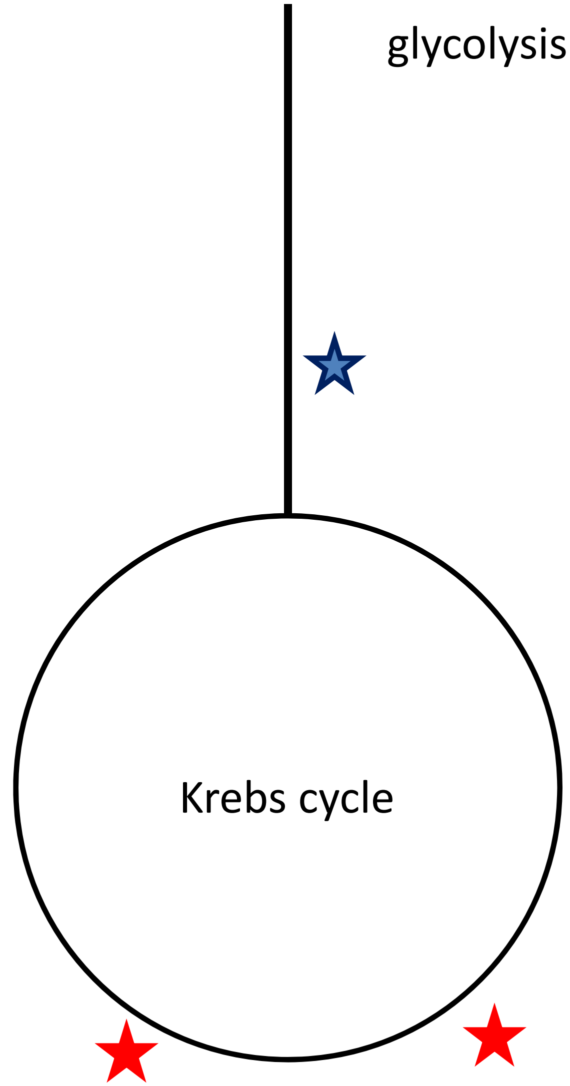


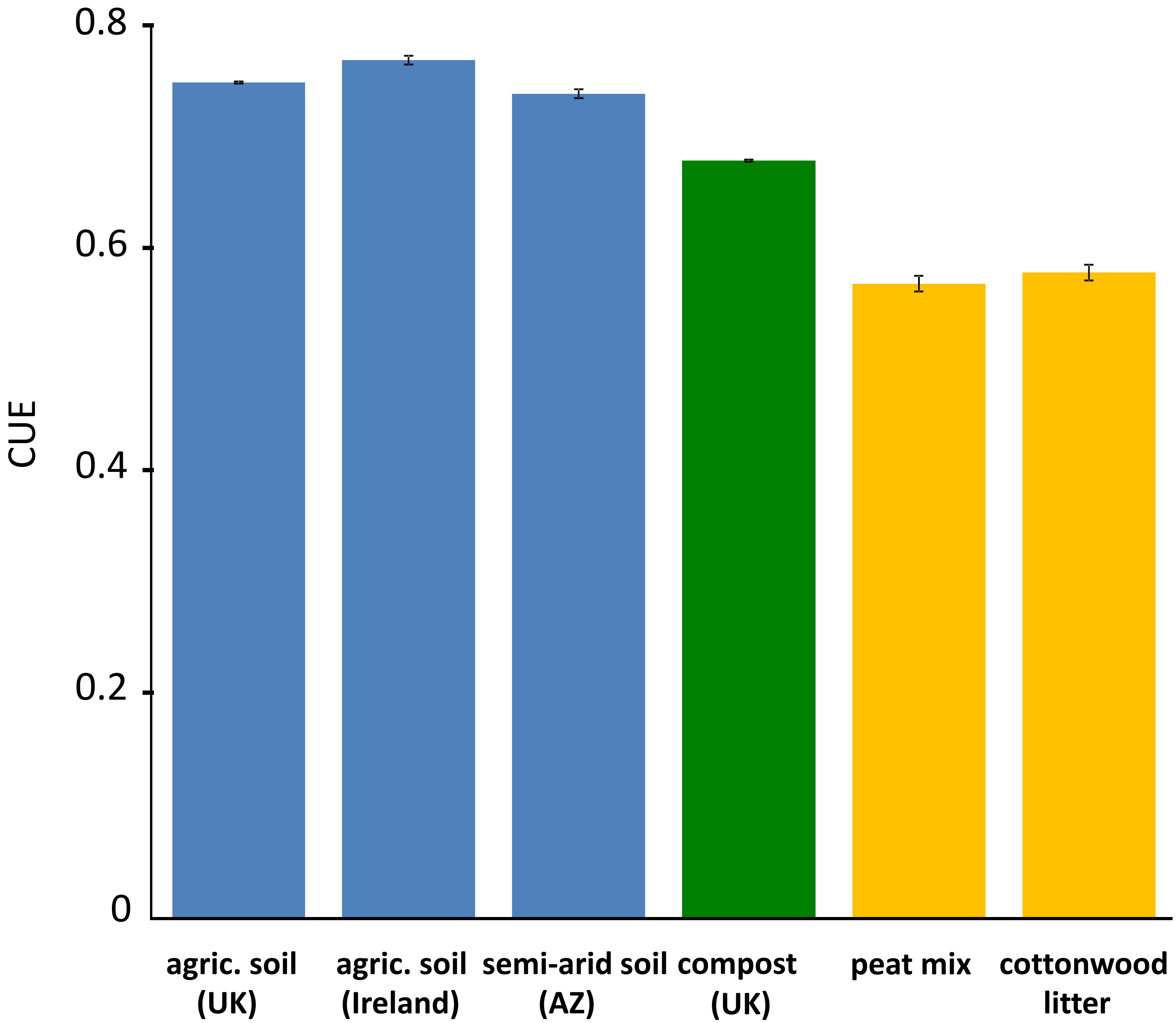
pyruvate



glucose






CUE
0.8
0.6
0.4
0.2
0
agric. soil (UK)
agric. soil (Ireland)
semi-arid soil (AZ)
compost (UK)
peat mix
cottonwood litter

ECOLOGY LETTERS

Ecology Letters, (2013) **16**: 930–939 doi: 10.1111/ele.12113

REVIEW AND SYNTHESIS

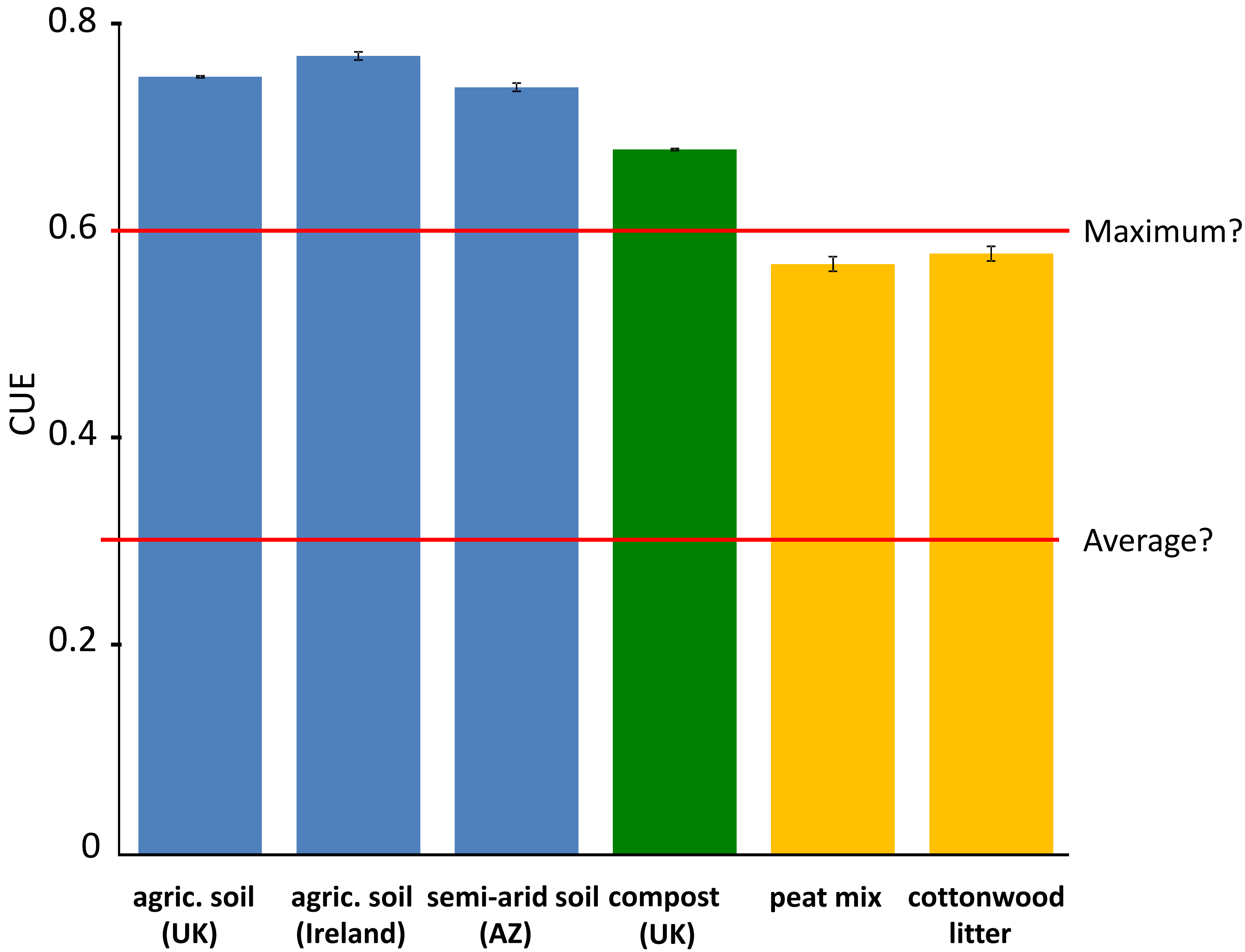
Carbon use efficiency of microbial communities: stoichiometry, methodology and modelling

Robert L. Sinsabaugh,[1]* Stefano Manzoni,[2] Daryl L. Moorhead[3] and Andreas Richter[4]

Abstract

Carbon use efficiency (CUE) is a fundamental parameter for ecological models based on the physiology of microorganisms. CUE determines energy and material flows to higher trophic levels, conversion of plant-produced carbon into microbial products and rates of ecosystem carbon storage. Thermodynamic calculations support a maximum CUE value of ~ 0.60 (CUE_{max}). Kinetic and stoichiometric constraints on microbial growth suggest that CUE in multi-resource limited natural systems should approach ~ 0.3

maximum CUE 0.6 actual CUE ~ 0.3



0.8
0.6
0.4
0.2
0
CUE
Maximum?
Average?
agric. soil (UK)
agric. soil (Ireland)
semi-arid soil (AZ)
compost (UK)
peat mix
cottonwood litter

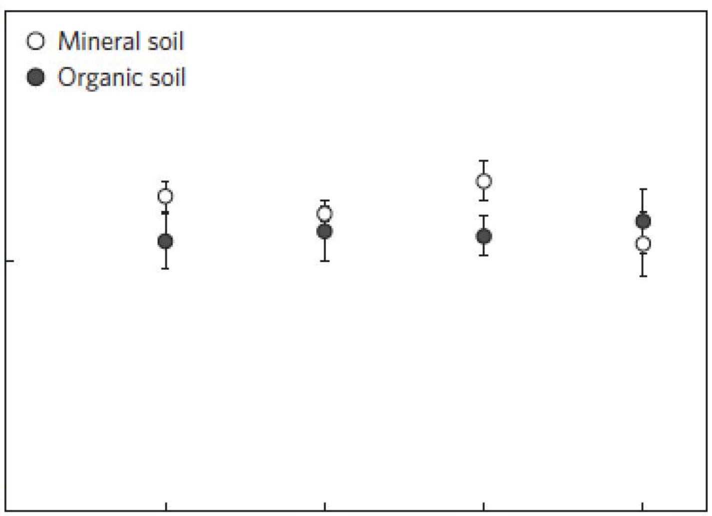
nature climate change

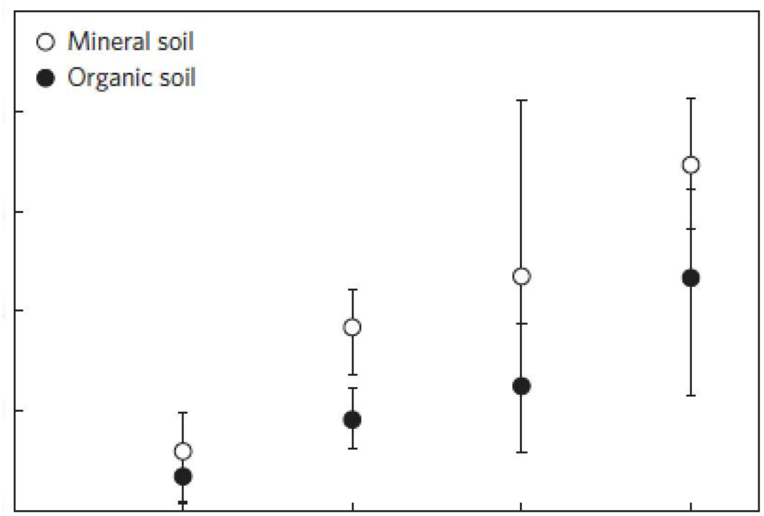
LETTERS

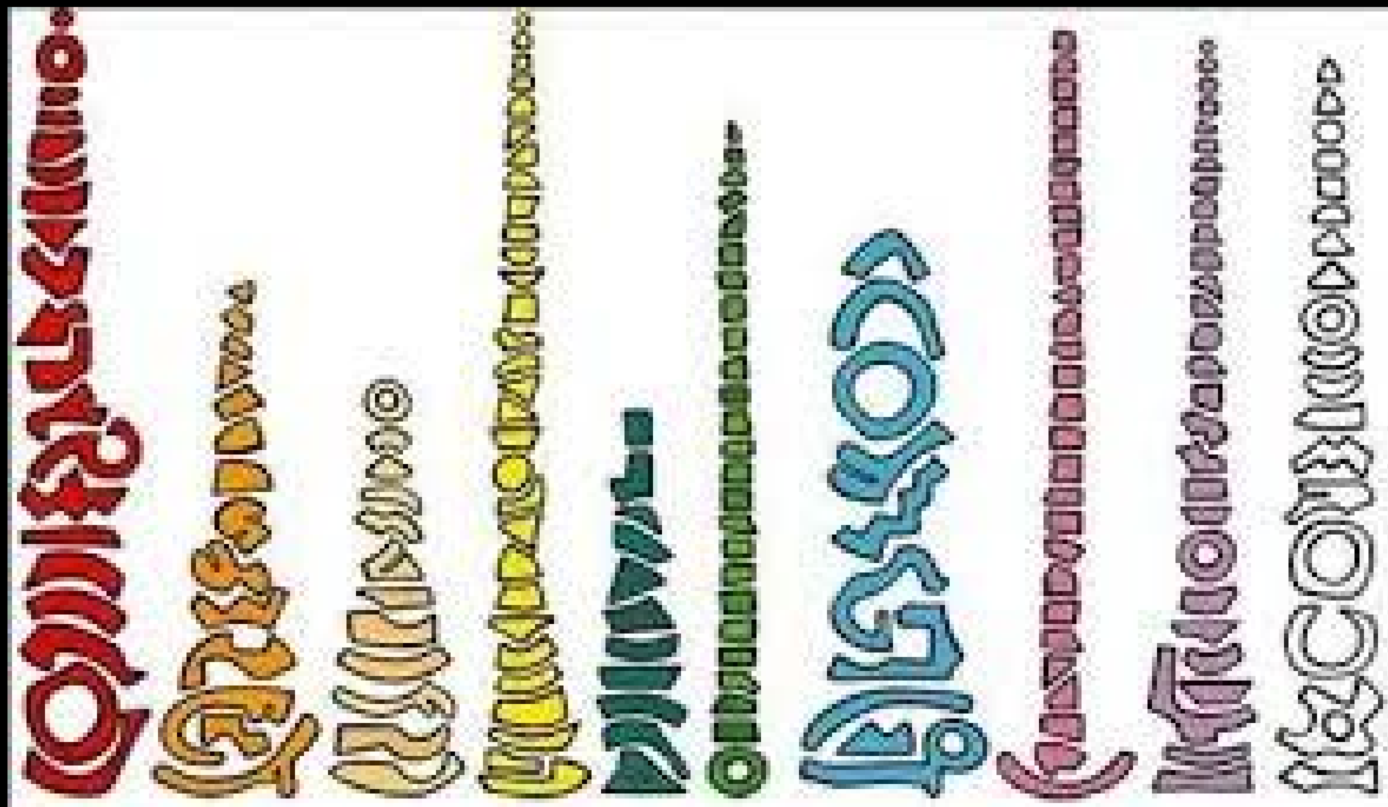
PUBLISHED ONLINE: 7 SEPTEMBER 2014 | DOI: 10.1038/NCLIMATE2361

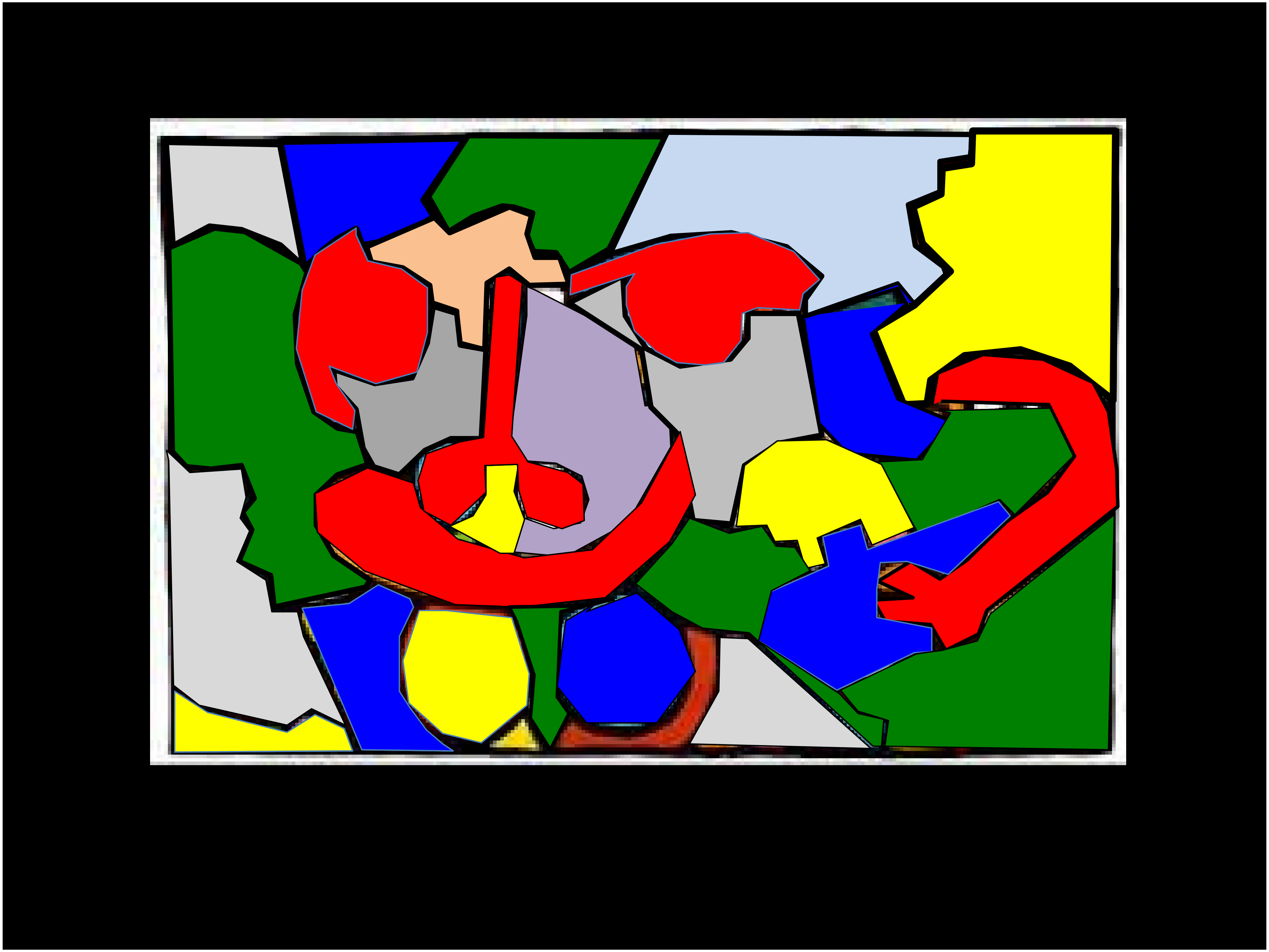
Accelerated microbial turnover but constant growth efficiency with warming in soil

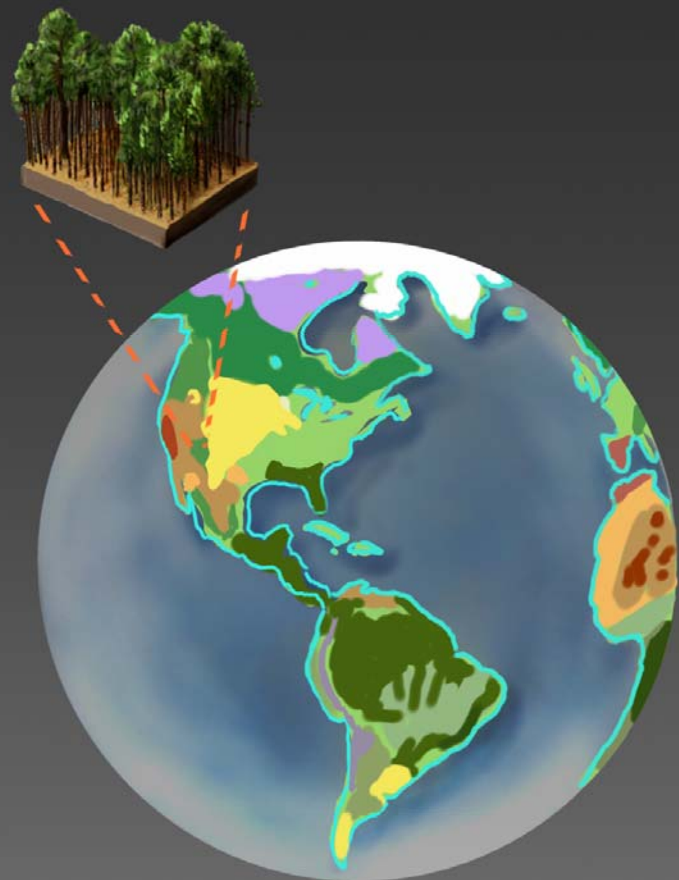
Shannon B. Hagerty[1], Kees Jan van Groenigen[1,2], Steven D. Allison[3], Bruce A. Hungate[1,2], Egbert Schwartz[1], George W. Koch[1,2], Randall K. Kolka[4] and Paul Dijkstra[1,2]*









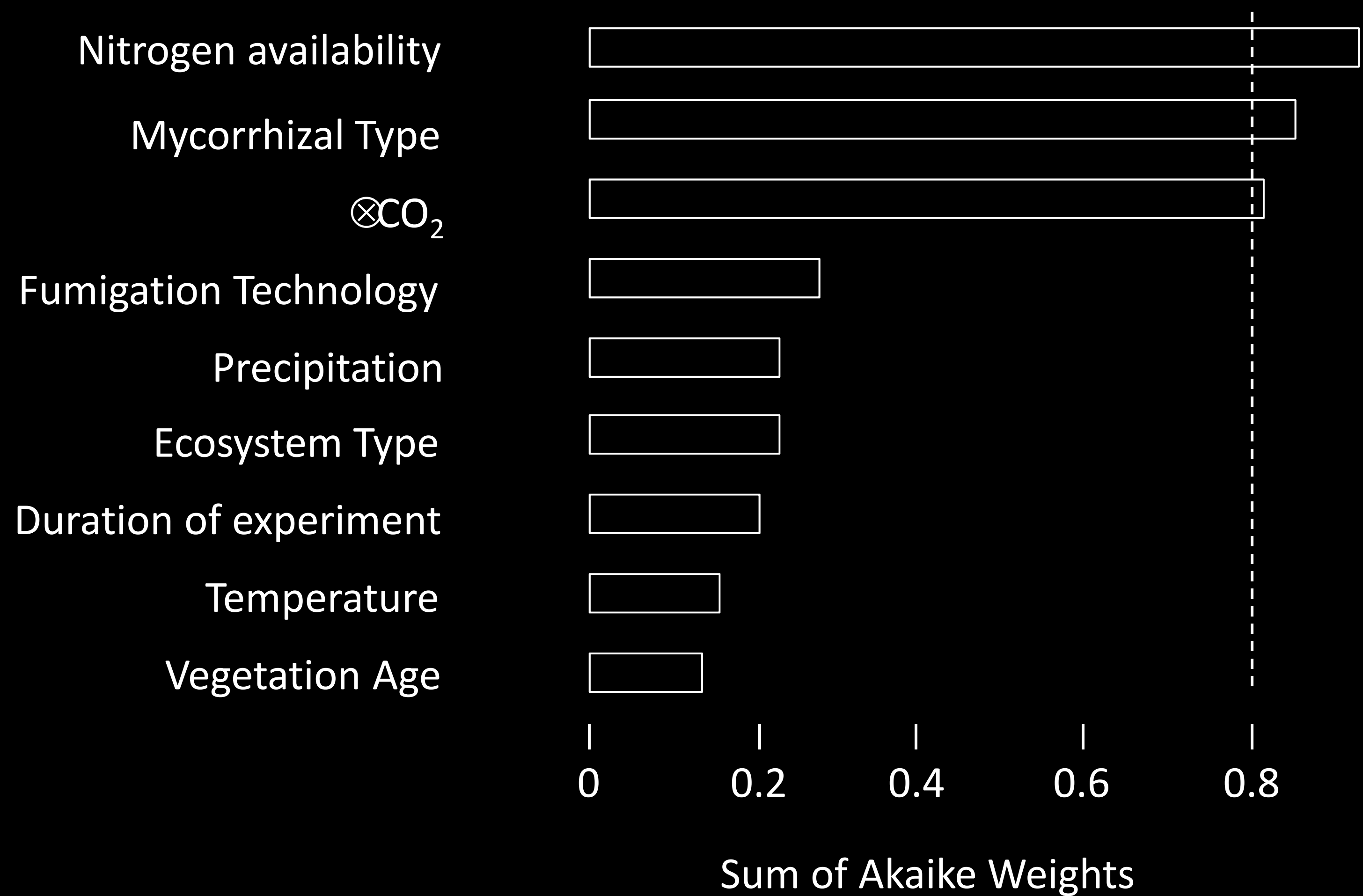


RESEARCH | REPORTS

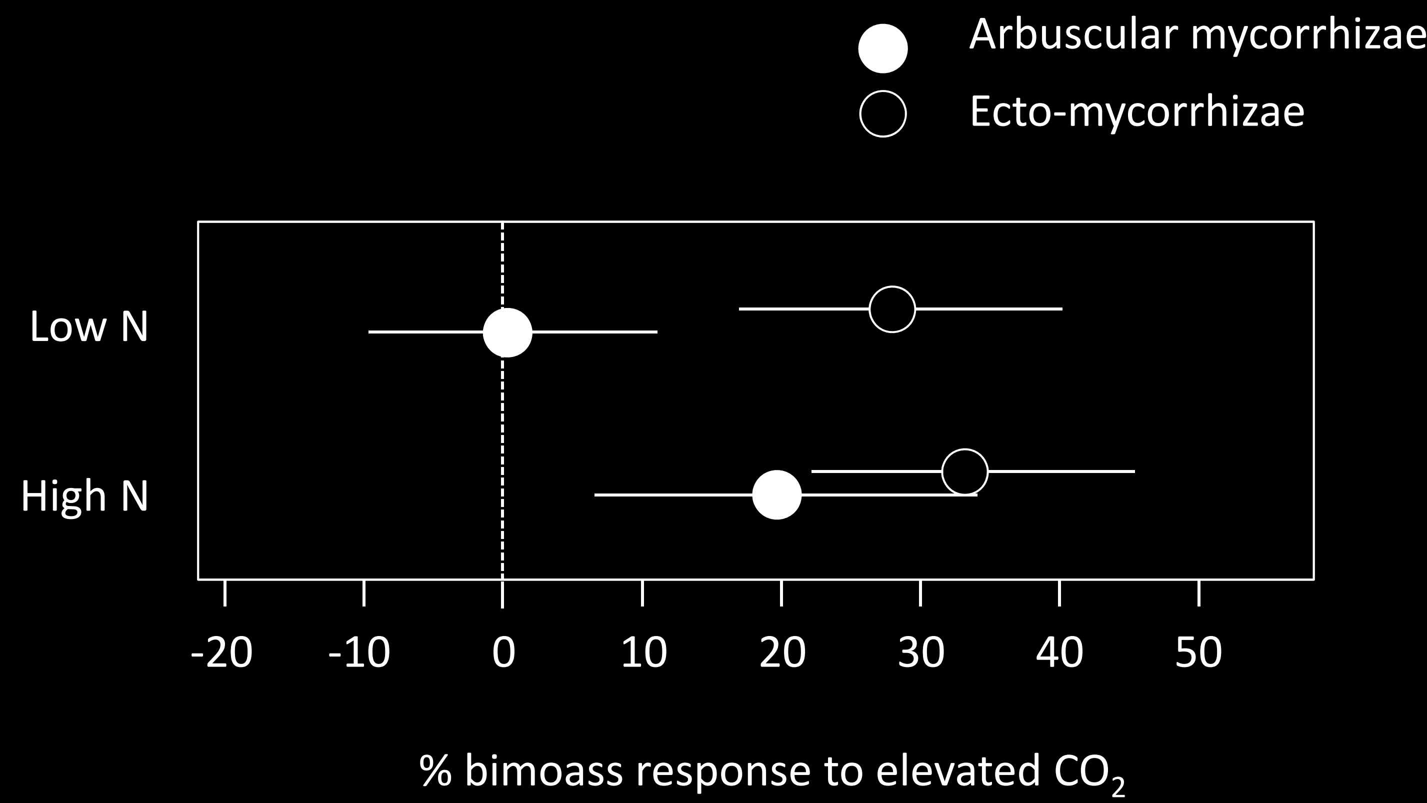
CARBON CYCLE

Mycorrhizal association as a primary control of the CO_2 fertilization effect

César Terrer,[1*] Sara Vicca,[2] Bruce A. Hungate,[3,4] Richard P. Phillips,[5] I. Colin Prentice[1,6]

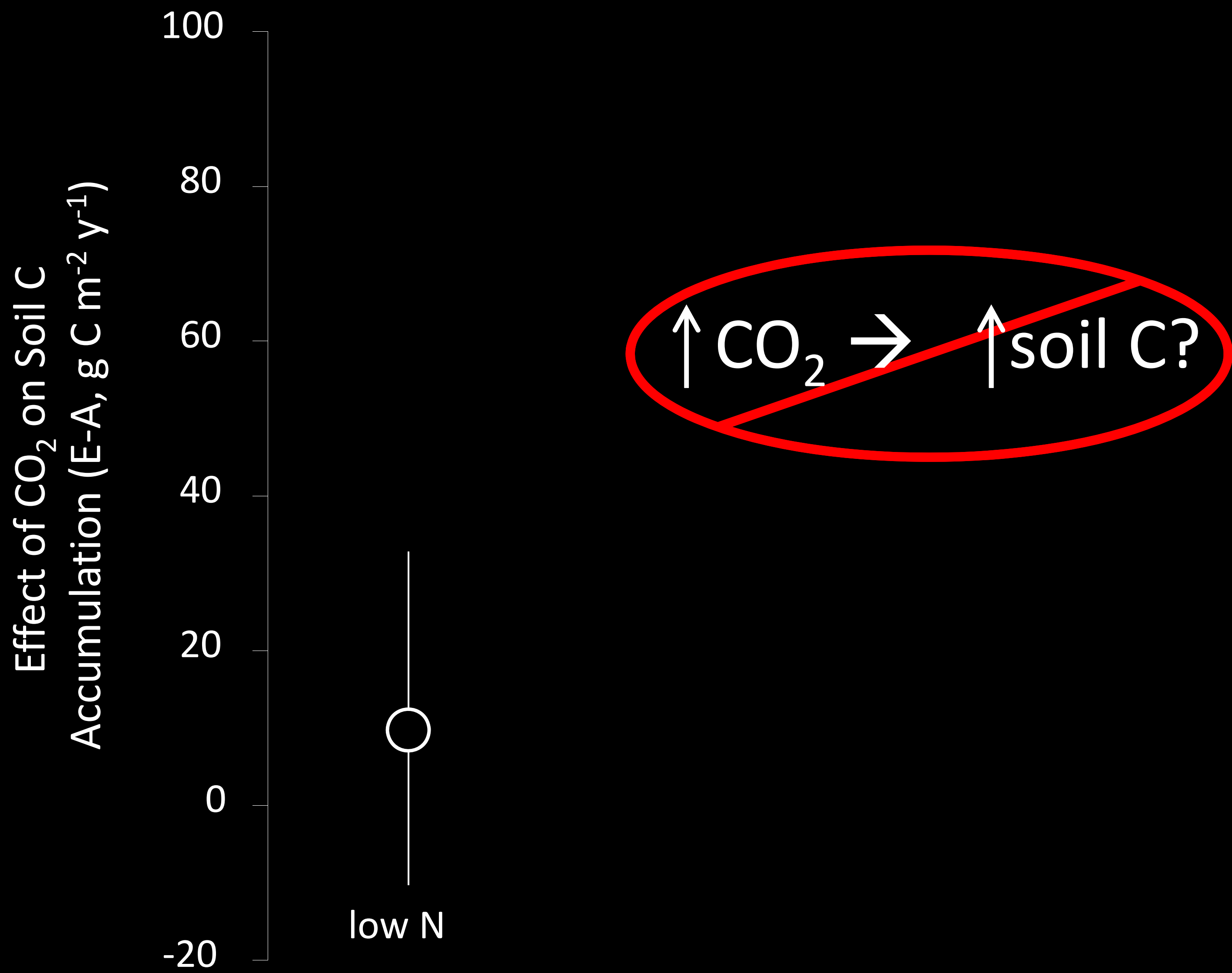


Terrer et al., 2016, *Science*



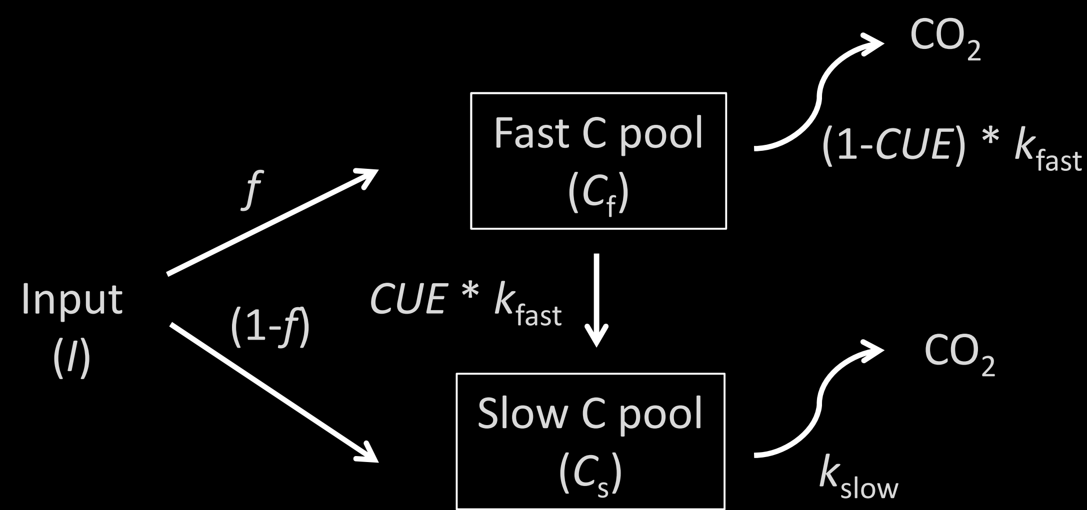
Terrer et al., 2016, *Science*


N



Hungate *et al.*, Global Change Biology 2009

2-pool model of soil C over time



Van Gestel et al., in review

$$C_t = C_0 e^{-kt} + \frac{I}{k}(1 - e^{-kt})$$

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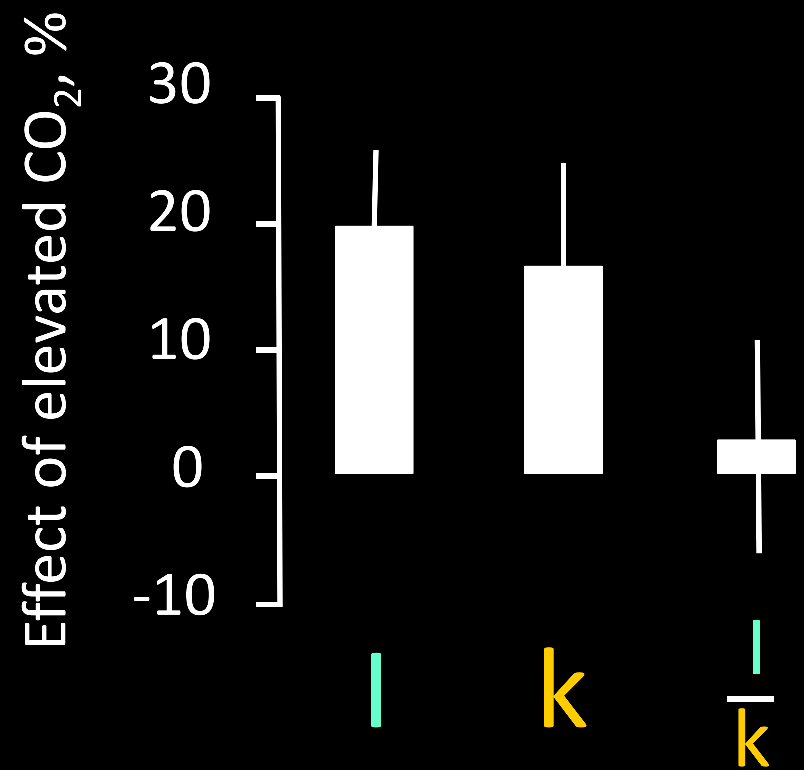
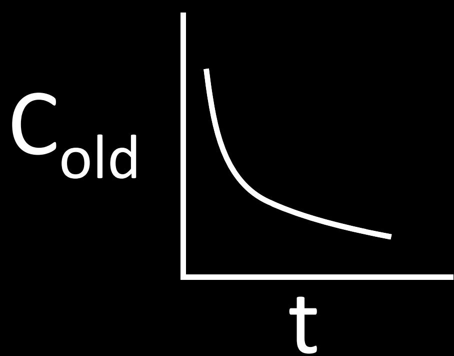
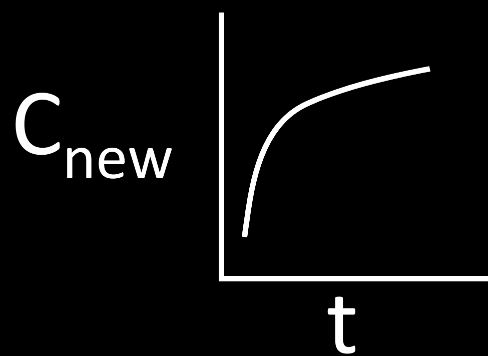


van Groenigen, et al., 2014, ***Science***

$$C_t = C_0 e^{-kt} + \frac{I}{k}(1 - e^{-kt})$$





$$C_t = C_0 e^{-k_{old} t} + \frac{I}{k_{new}}(1 - e^{-k_{new} t})$$

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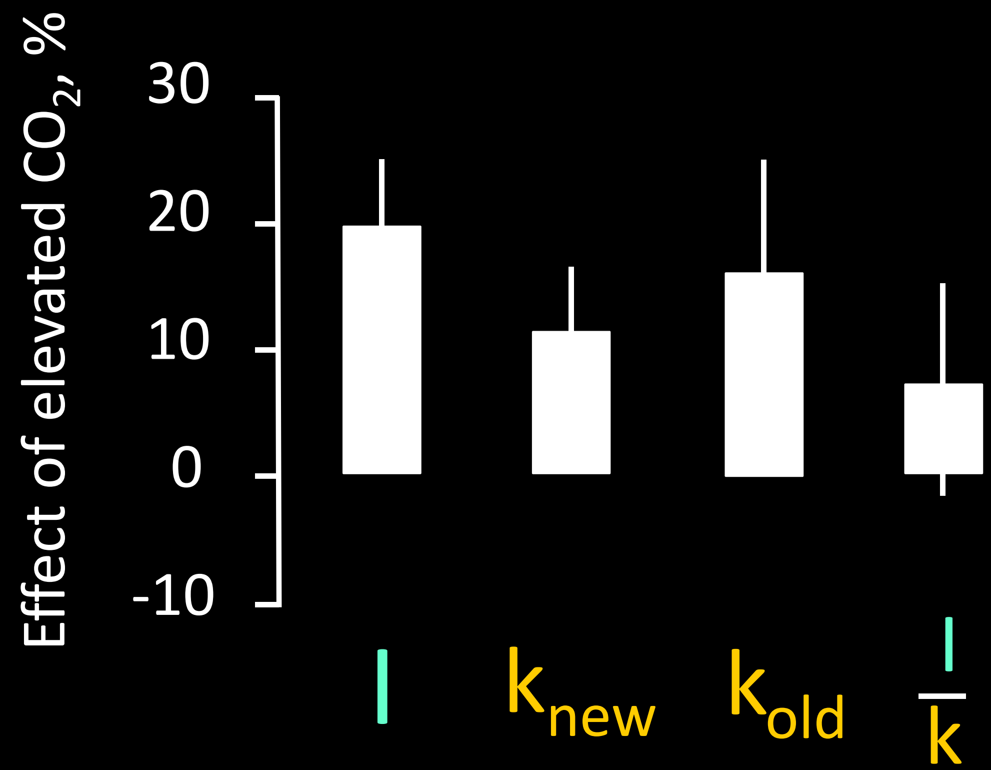
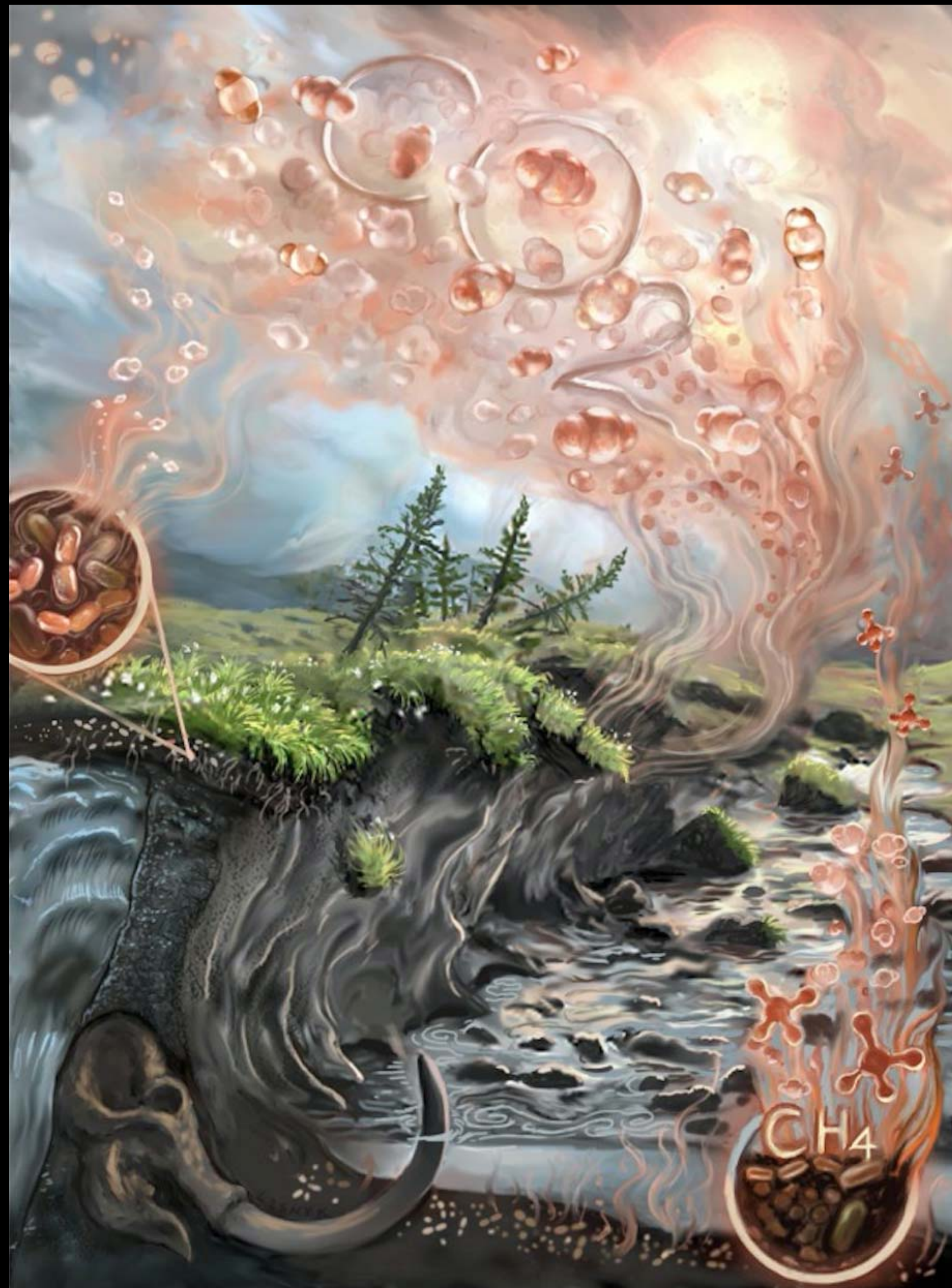


van Groenigen, et al., 2014, ***Science***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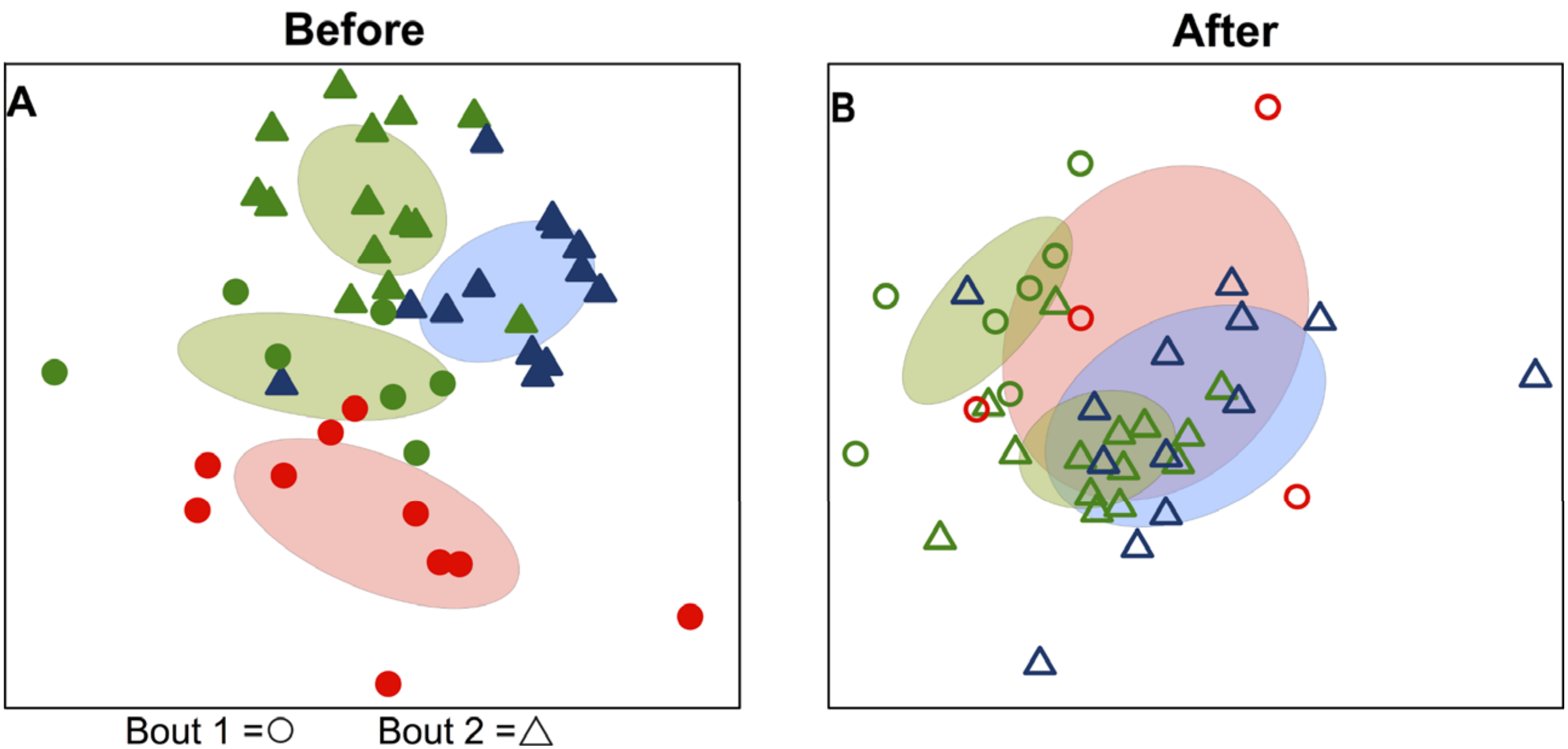
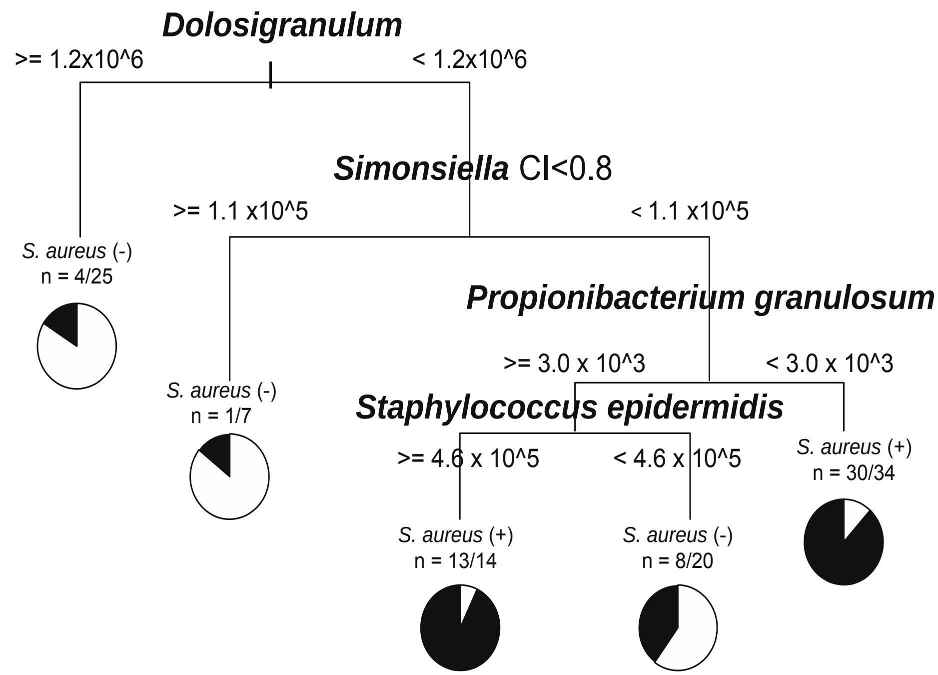


Significant changes in the skin microbiome mediated by the sport of roller derby

James F. Meadow[1], Ashley C. Bateman[1], Keith M. Herkert[1,2], Timothy K. O'Connor[1,3], Jessica L. Green[1,4]

PeerJ 1:e53 https://dx.doi.org/10.7717/peerj.53



Colonization of the human nose by *Staphylococcus aureus*: community predictors

Threshold densities predict *S. aureus* carriage

Liu et al., in review

Male Circumcision Significantly Reduces Prevalence and Load of Genital Anaerobic Bacteria

Cindy M. Liu, Bruce A. Hungate, Aaron A. R. Tobian, et al. 2013. Male Circumcision Significantly Reduces Prevalence and Load of Genital Anaerobic Bacteria . mBio 4(2): . doi:10.1128/mBio.00076-13.

Circumcision → lower bacterial abundance, especially anaerobes