Microbiology's N-body Problem:

interspecies metabolite transfer within spatially distributed populations

Robert Clegg, Rosemary Dyson, Jan Kreft

7th May 2014

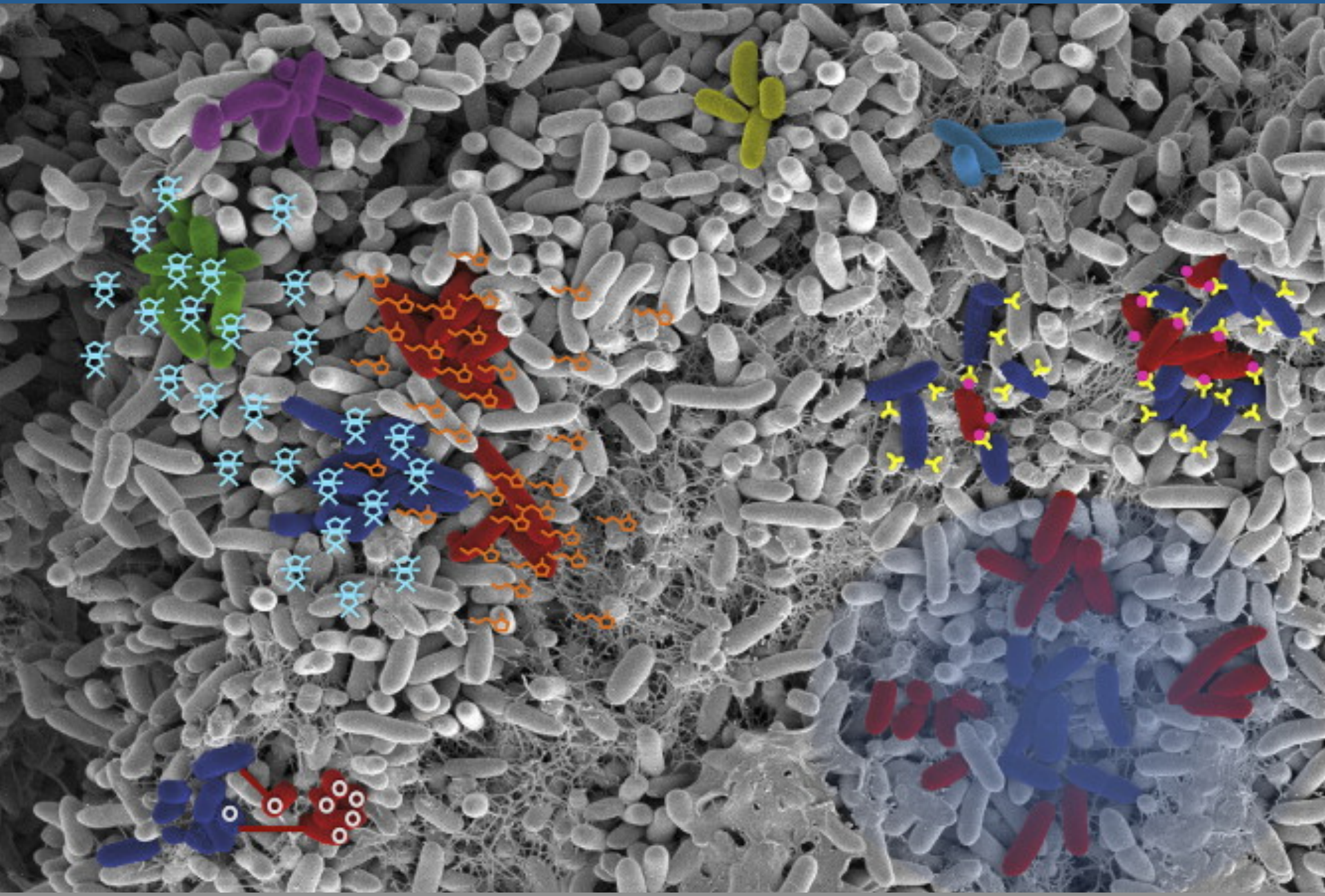
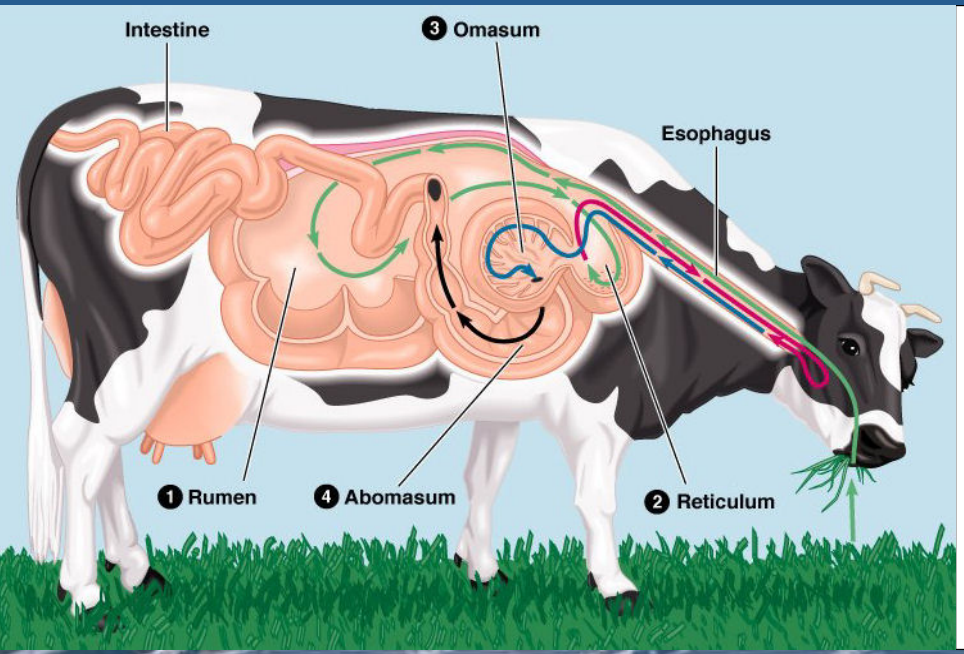
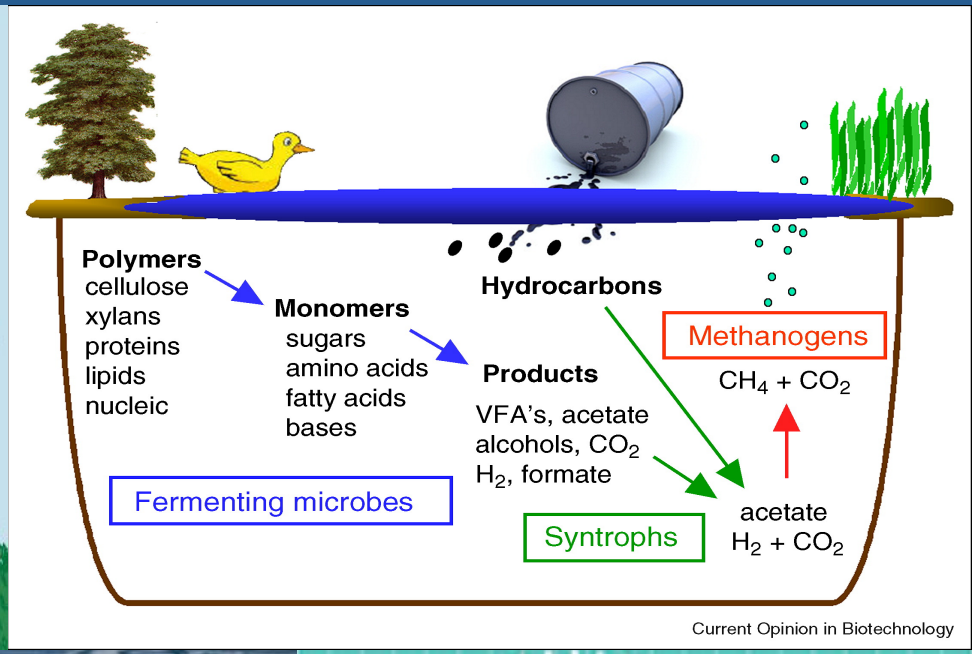
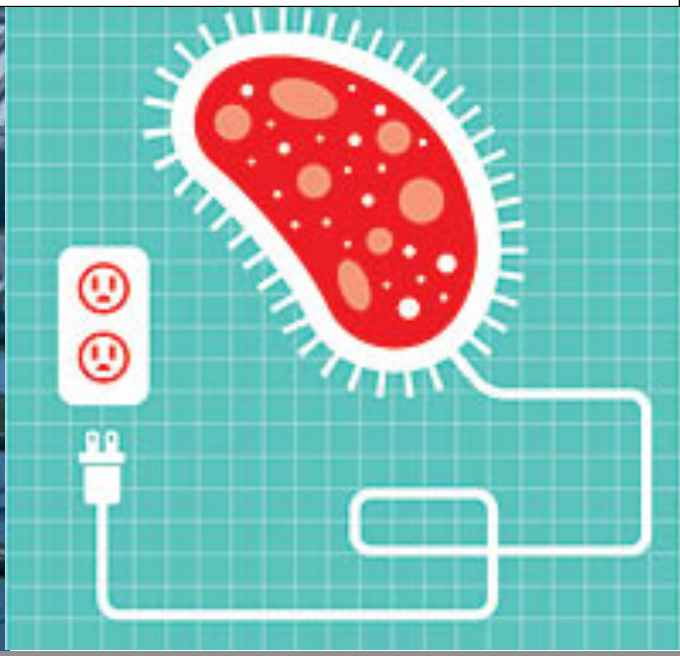
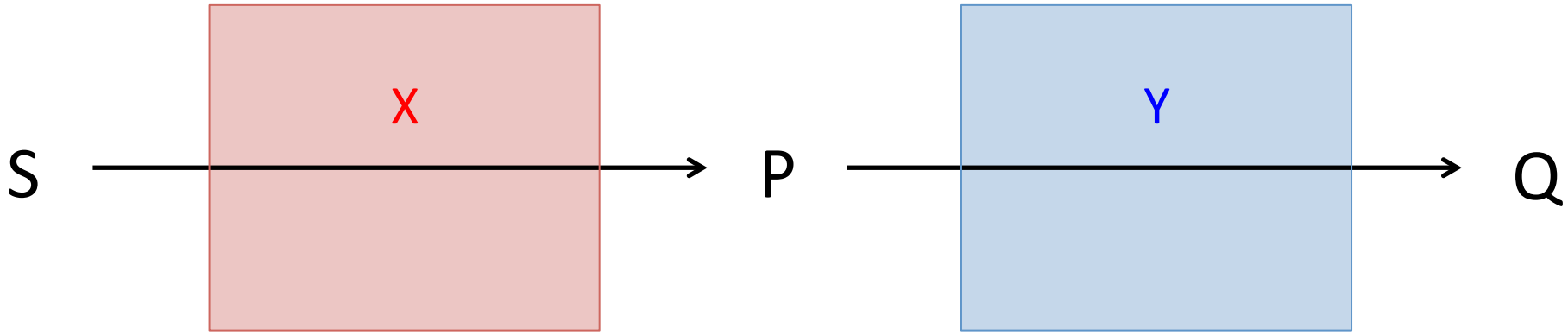


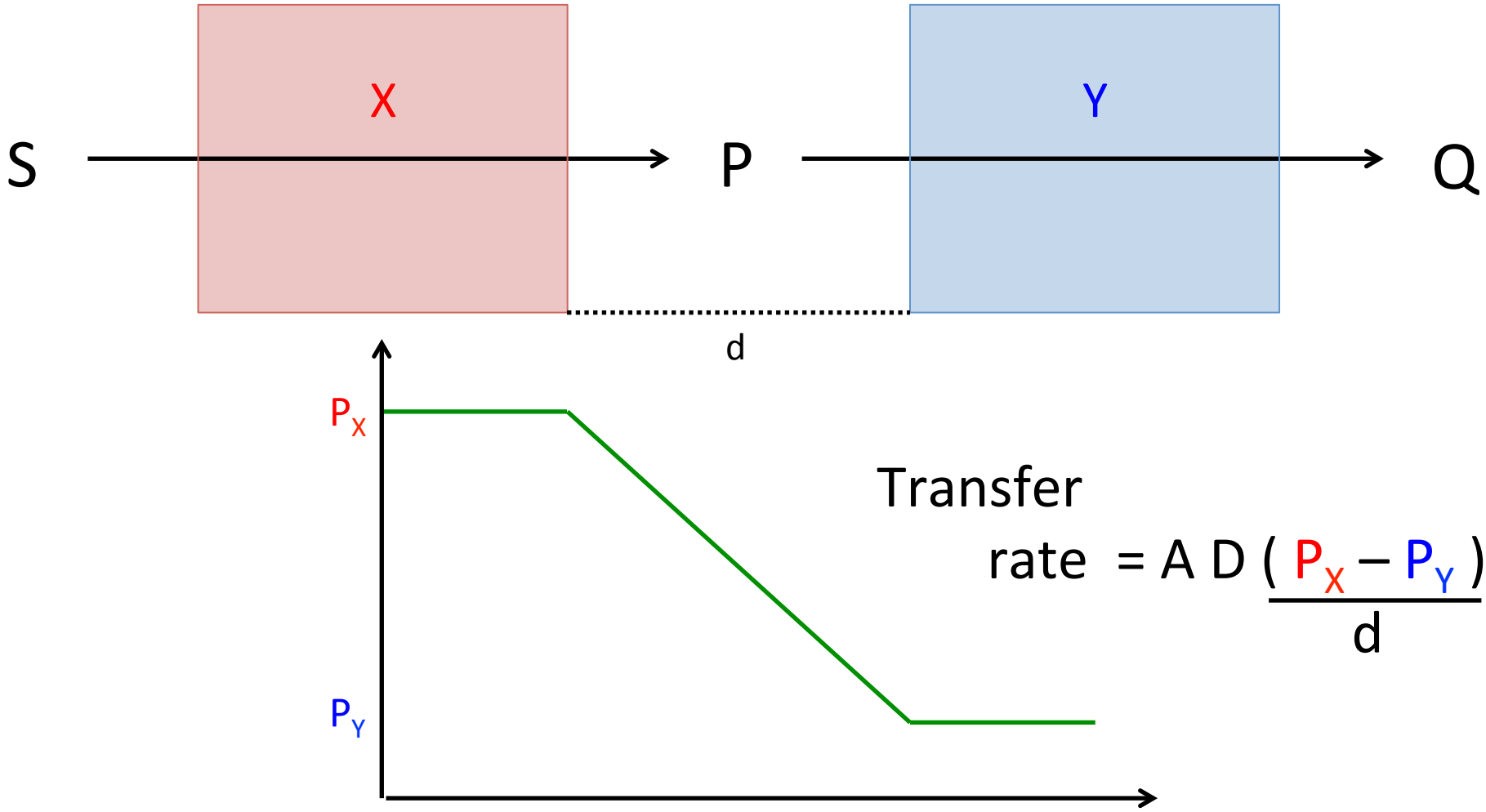
Image: Burmølle *et al* (2014) *Trends in Microbiology*


Intestine
3 Omasum
Esophagus
1 Rumen
4 Abomasum
2 Reticulum


Polymers
cellulose
xylans
proteins
lipids
nucleic
Monomers
sugars
amino acids
fatty acids
bases
Products
VFA's, acetate
alcohols, CO_2
H_2, formate
Hydrocarbons
Methanogens
$CH_4 + CO_2$
Fermenting microbes
Syntrophs
acetate
$H_2 + CO_2$
Current Opinion in Biotechnology




X
Y
S
P
Q



$$\text{Transfer rate} = A\,D\,\frac{(P_X - P_Y)}{d}$$

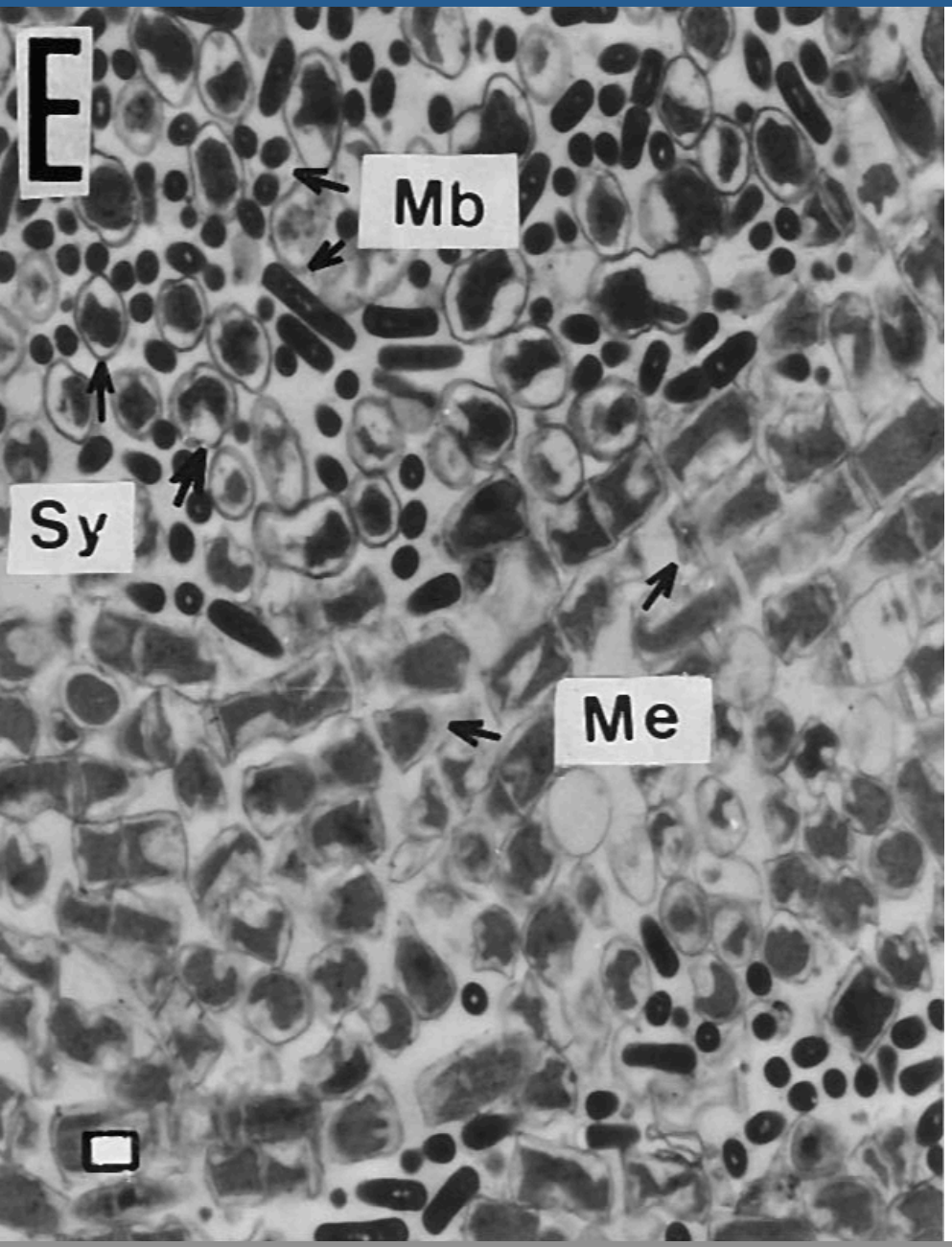
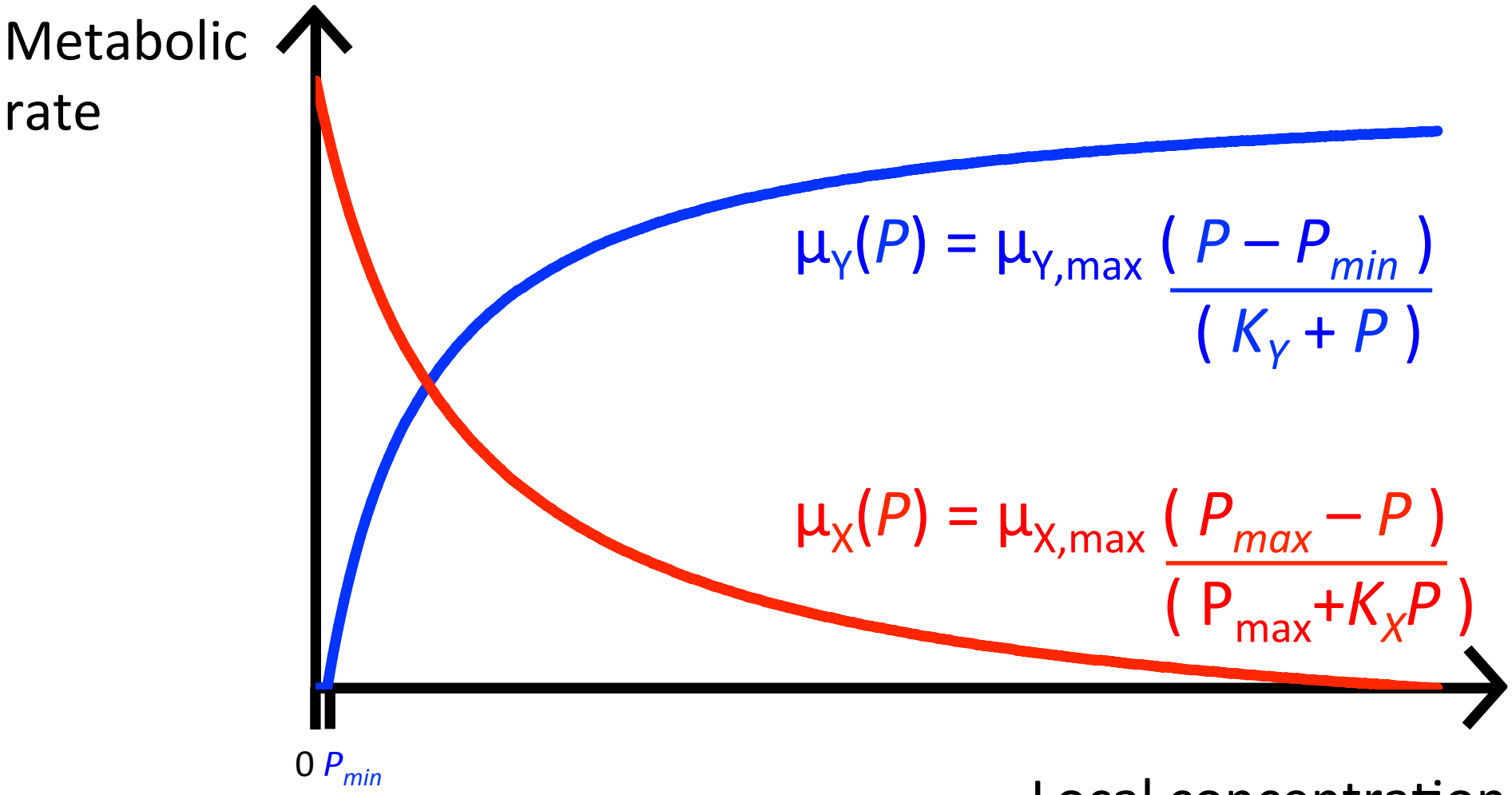
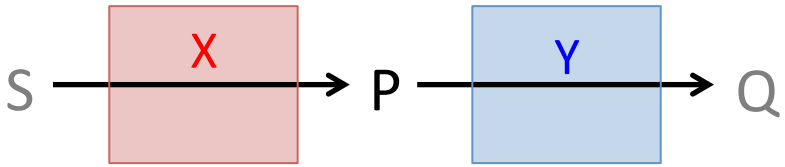


Image: Harmsen *et al* (1996) Applied & Environmental Microbiology

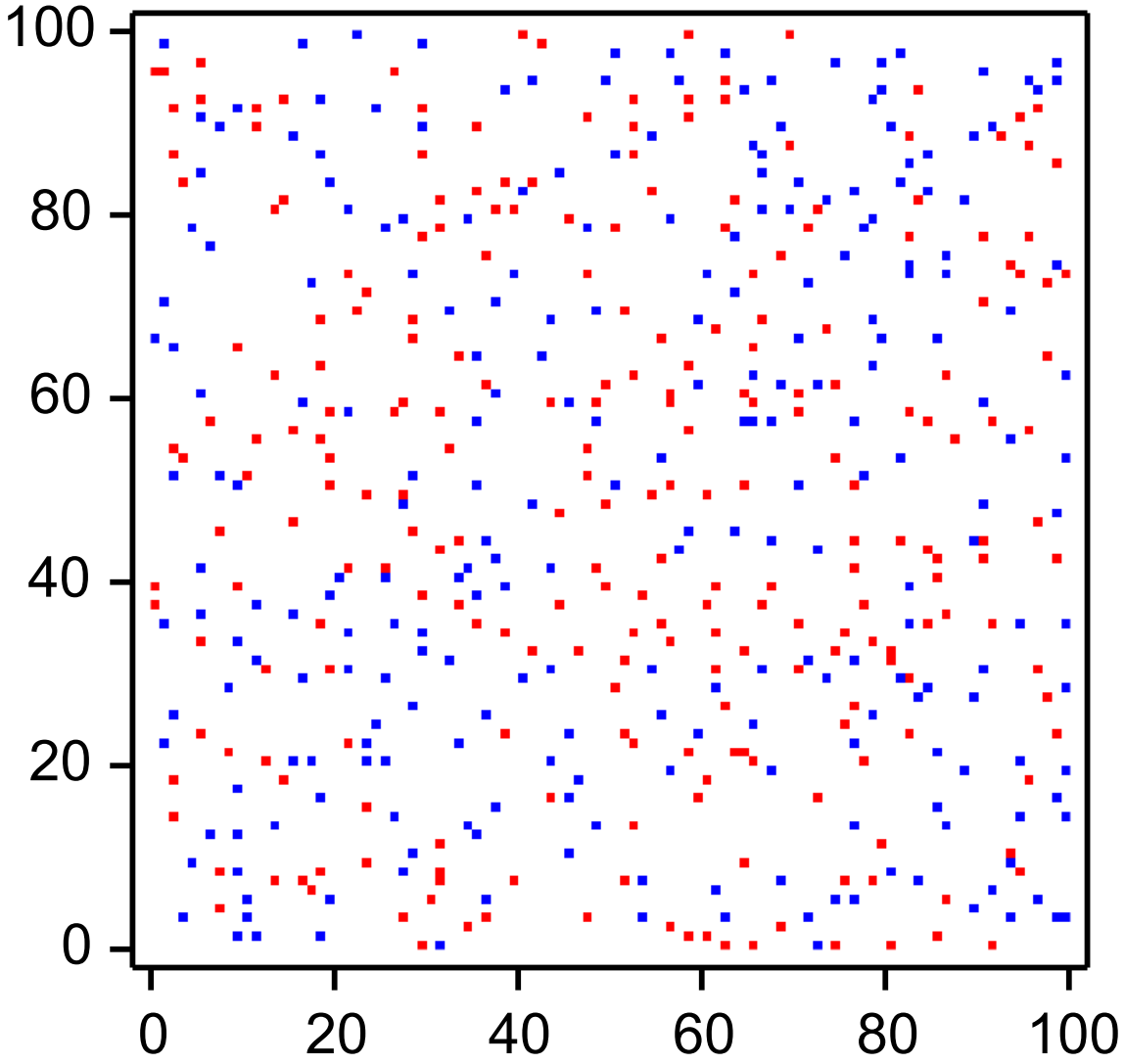
Blank slide


Metabolic rate
$\mu_Y(P) = \mu_{Y,max} \frac{(P - P_{min})}{(K_Y + P)}$
$\mu_X(P) = \mu_{X,max} \frac{(P_{max} - P)}{(P_{max} + K_X P)}$
0 P_{min}
Local concentration of product P


S
X
P
Y
Q

Density 0.05 ➡ 500 cells total

X 1 : 1 Y

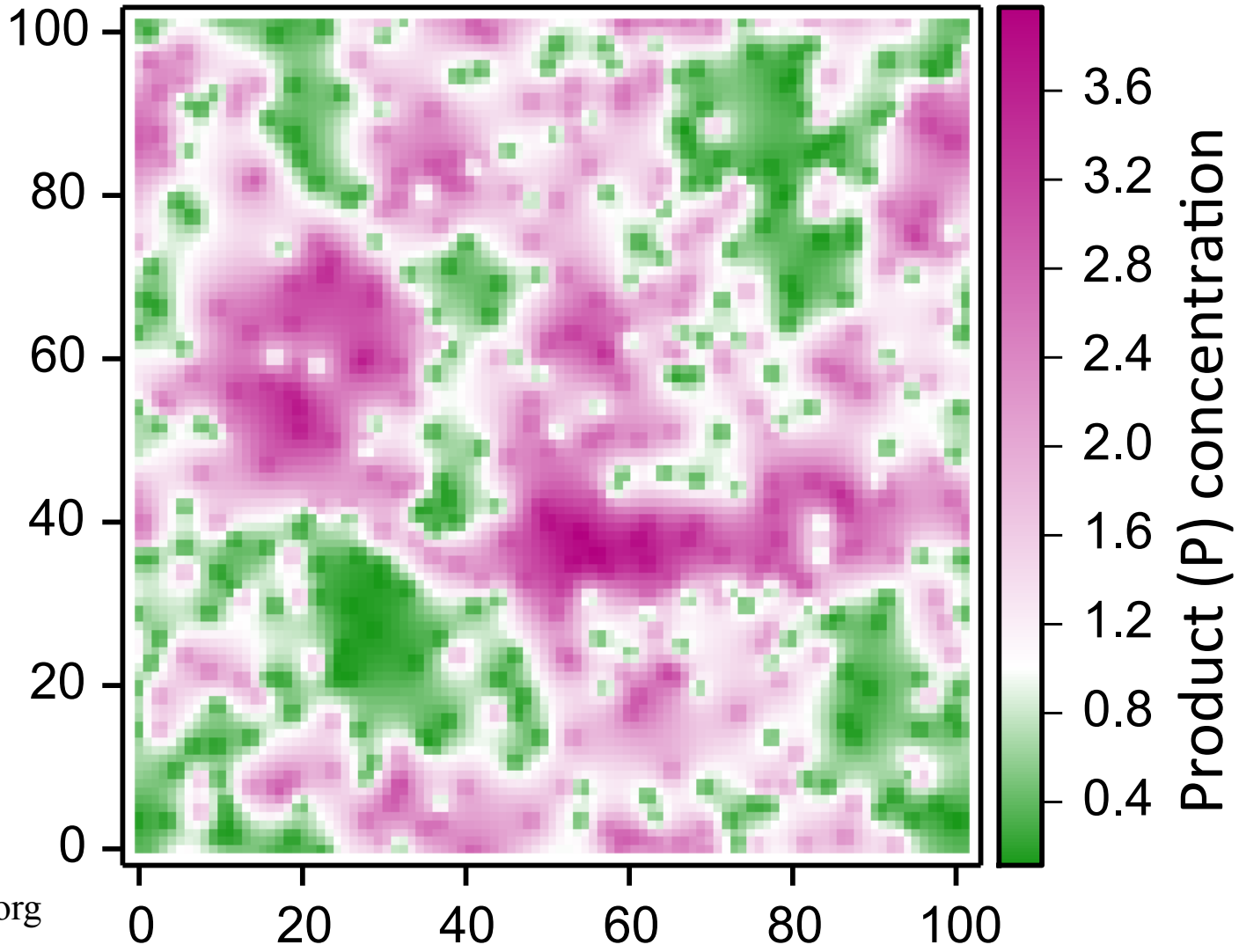


$\mu_{X,max} = 1$, $P_{max} = 10$, $K_X = 8$

$\mu_{Y,max} = 1$, $P_{min} = 0.1$, $K_Y = 0.8$

Density 0.05 ➡ 500 cells total

X 1 : 1 Y



Elmer
www.elmerfem.org

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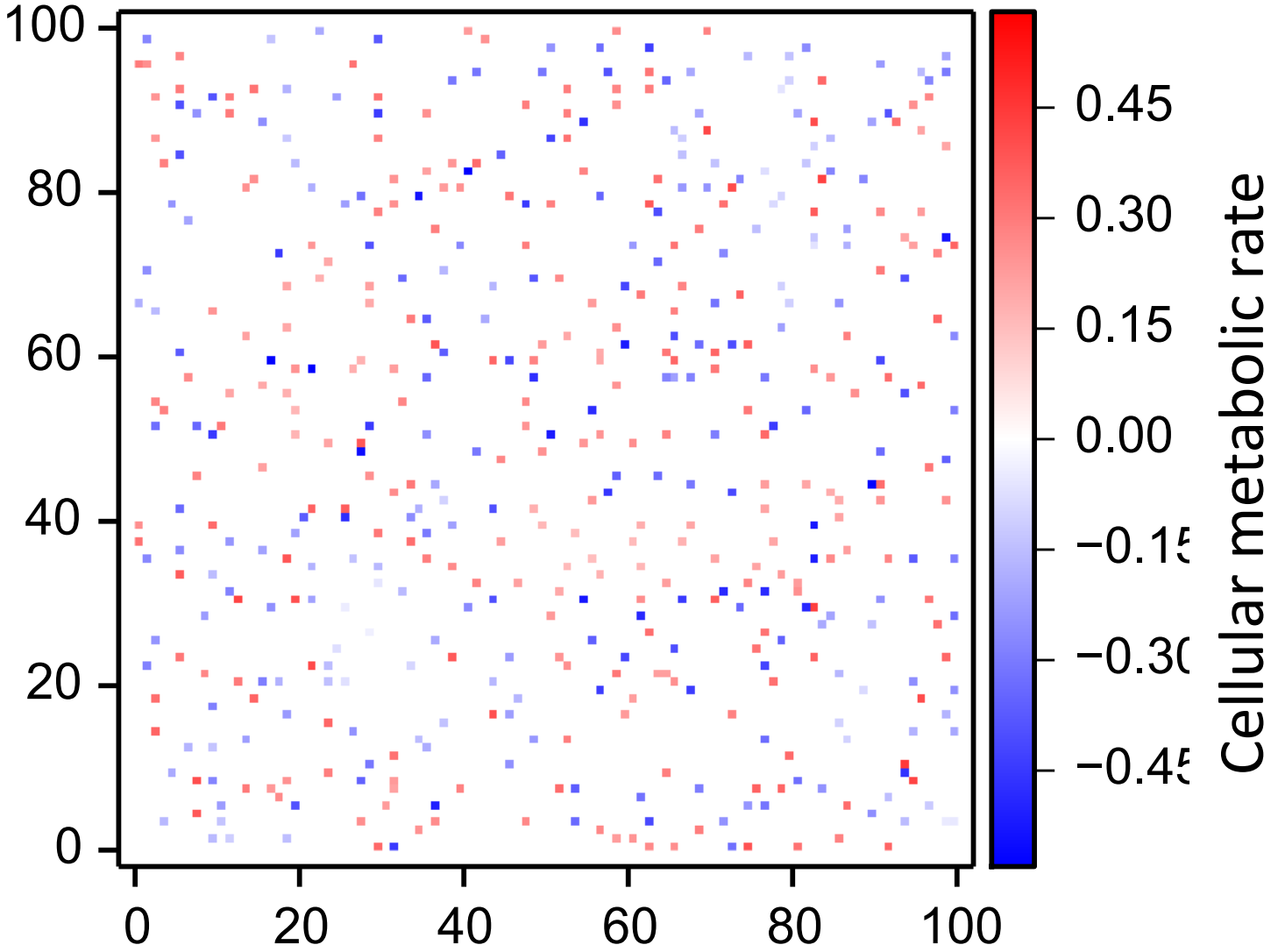
$\mu_{Y,max} = 1$, $P_{min} = 0.1$, $K_Y = 0.8$

Density 0.05 ➡ 500 cells total

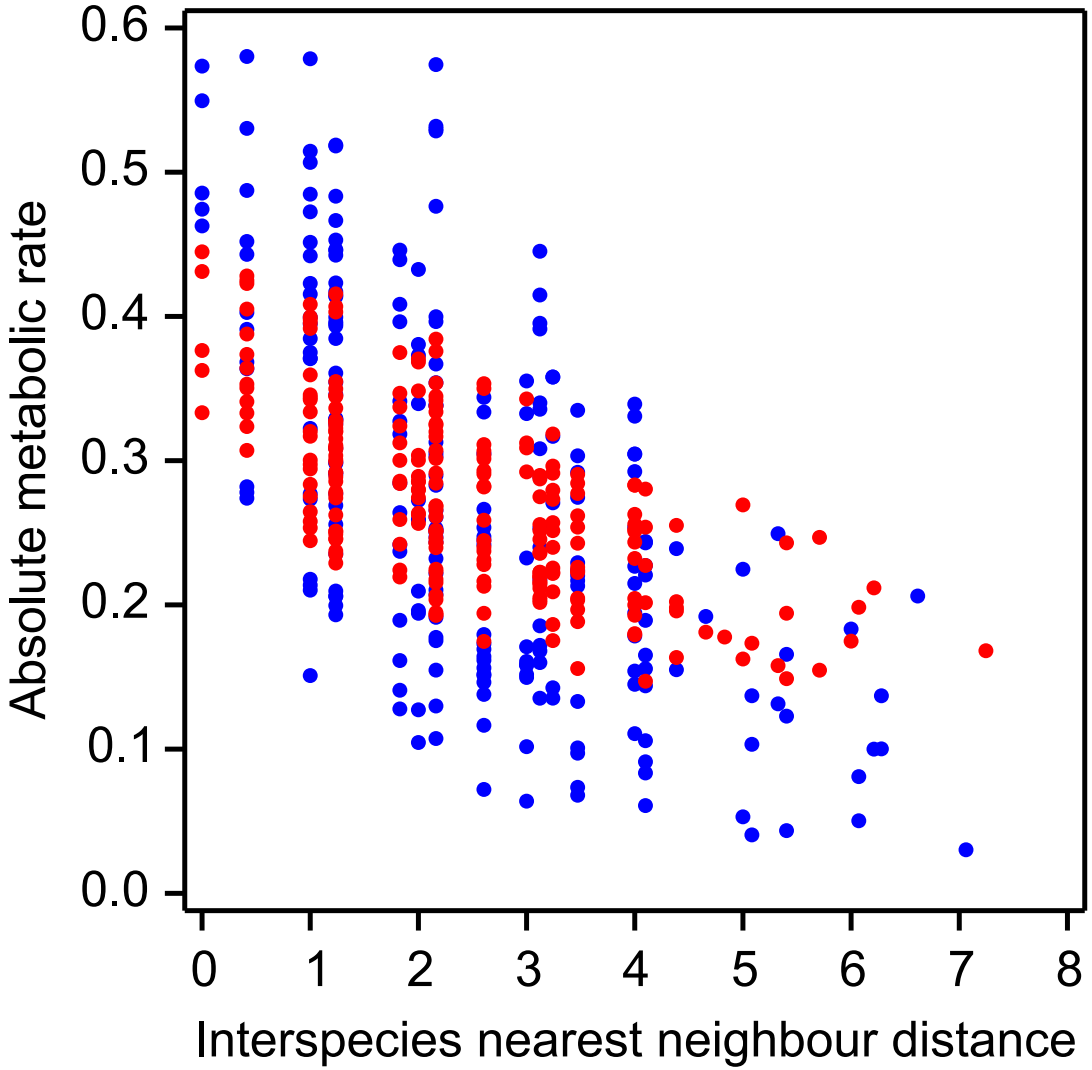
X 1 : 1 Y

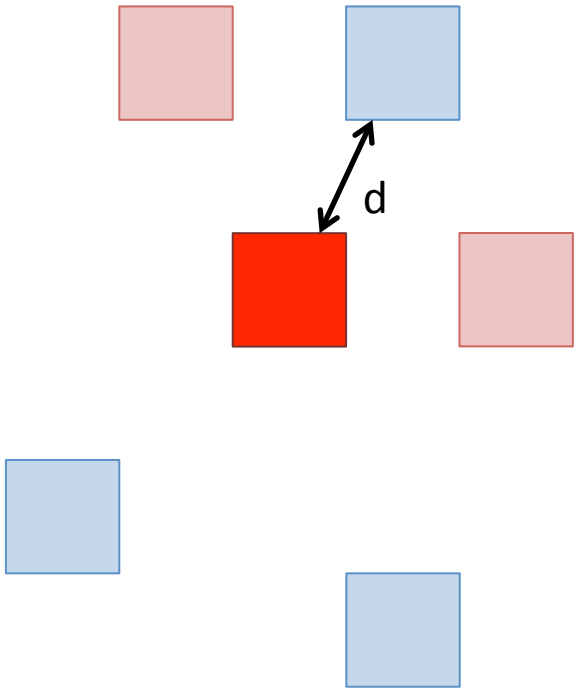


$\mu_{X,max} = 1$, $P_{max} = 10$, $K_X = 8$ $\mu_{Y,max} = 1$, $P_{min} = 0.1$, $K_Y = 0.8$

Density 0.05 ➡ 500 cells total

X 1 : 1 Y





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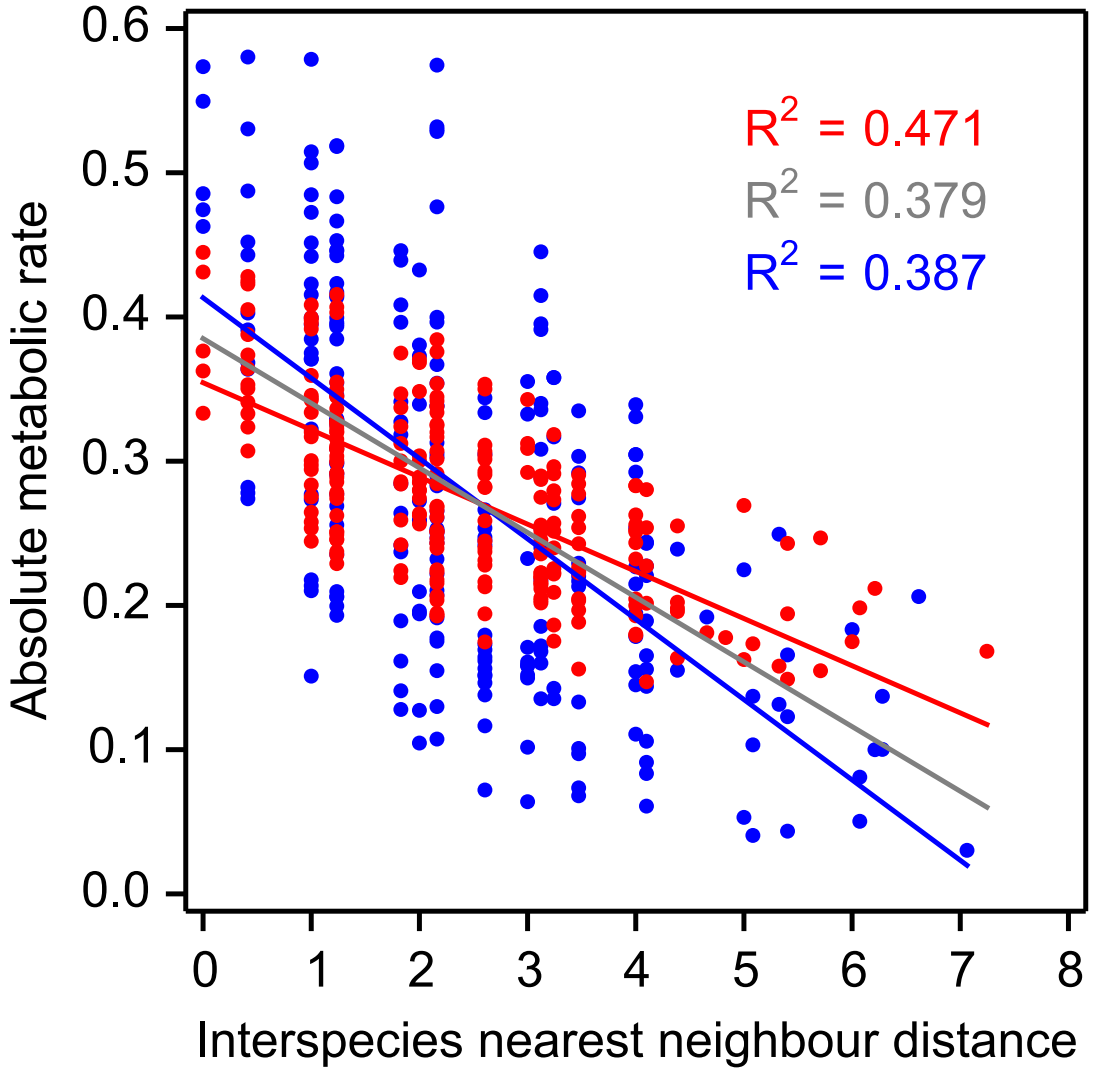
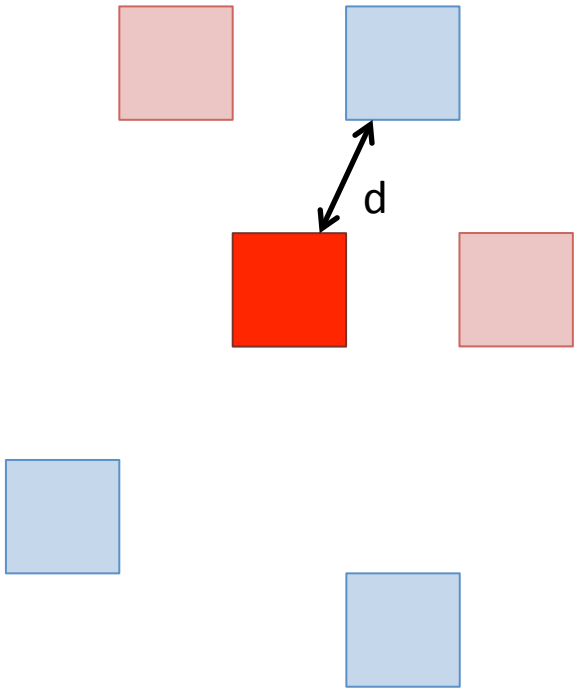
Density 0.05 ➡ 500 cells total

X 1 : 1 Y



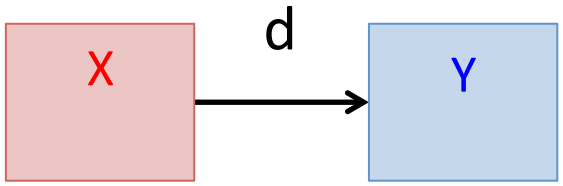


$\mu_{X,max} = 1$, $P_{max} = 10$, $K_X = 8$

$\mu_{Y,max} = 1$, $P_{min} = 0.1$, $K_Y = 0.8$

Transfer

$$\text{rate} = A\,D\,\frac{(P_X - P_Y)}{d}$$



Estimator for P_X	Estimator for P_Y	Estimator for d	Log_2(Estimate/Actual)
P_{max}	P_{min}	**h**mean (NN dist X-> Y)	+2.33
P_{max}	amean (Y surf concn)	**h**mean (NN dist X-> Y)	+2.29
P_{max}	P_{min}	**a**mean (NN dist X-> Y)	+1.44
P_{max}	amean (Y surf concn)	**a**mean (NN dist X-> Y)	+1.39
amean (X surf concn)	P_{min}	**h**mean (NN dist X-> Y)	+0.35
amean (X surf concn)	amean (Y surf concn)	**h**mean (NN dist X-> Y)	+0.15
amean (X surf concn)	P_{min}	**a**mean (NN dist X-> Y)	-0.42
amean (X surf concn)	amean (Y surf concn)	**a**mean (NN dist X-> Y)	-0.55
amean (global P)	P_{min}	**h**mean (NN dist X-> Y)	-0.75
amean (global P)	amean (Y surf concn)	**h**mean (NN dist X-> Y)	-0.78
amean (global P)	P_{min}	**a**mean (NN dist X-> Y)	-1.31
amean (global P)	amean (Y surf concn)	**a**mean (NN dist X-> Y)	-1.68

'amean' = arithmetic mean 'hmean' = harmonic mean

Future directions:

- Replicates
- Parameter sweep
- 3D
- Spatial bias
- Different kinetic models

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