

Parameter	Unit	Default value	Literature	MCMC (Q1)	MCMC (Q2)	MCMC (Q3)	MCMC (95% CI)
$V_{1,g}$	mmol/h	5.52×10^{-13}	2.99×10^{-14} (Ref. [1])	3.92×10^{-13}	4.64×10^{-13}	5.48×10^{-13}	$[4.808, 4.825] \times 10^{-13}$
$V_{3,g}$	mmol/h	6.28×10^{-13}	4.43×10^{-14} (Ref. [1])	4.42×10^{-13}	5.24×10^{-13}	6.17×10^{-13}	$[5.427, 5.445] \times 10^{-13}$
K_g	mM	1.00×10^{-2}	1.00×10^{-2} (Ref. [1] *)				
$I_{1,a}$	mM	2.63×10^1	4.00×10^1 (Ref. [2])	3.31×10^1	3.91×10^1	4.84×10^1	$[4.263, 4.281] \times 10^1$
$I_{3,a}$	mM	1.13×10^2	1.00×10^2 (Ref. [2])	1.39×10^2	1.98×10^2	3.57×10^2	$[4.642, 4.772] \times 10^2$
$C_{1,g}$	mM	8.70×10^{-1}	1.18×10^1 (Ref. [3])	3.17×10^{-1}	1.23	4.78	$[1.261, 1.319] \times 10^1$
$V_{1,a}$	mmol/h	4.26×10^{-13}	1.26×10^{-13} (Ref. [1])	2.51×10^{-13}	3.45×10^{-13}	5.23×10^{-13}	$[4.266, 4.299] \times 10^{-13}$
$K_{1,a}$	mM	2.00×10^{-1}	2.00×10^{-1} (Ref. [1] *)				
γ_a	1/mmol	2.00×10^{11}	$[0.67, 1.00] \times 10^{11}$ (Ref. [4])	1.90×10^{11}	2.31×10^{11}	2.92×10^{11}	$[2.454, 2.463] \times 10^{11}$
φ_a		3.30×10^{-1}		2.98×10^{-1}	3.67×10^{-1}	4.46×10^{-1}	$[3.749, 3.763] \times 10^{-1}$
δ_a		3.00	Constant (*)				

Supplementary Table 1: Estimated parameter values for the simplified unilateral cross-feeding model. The column "Default value" are the parameter values obtained through manual fitting and used in all simulations. The column "Literature" lists values reported in literature. A literature value is marked with "*" if the corresponding parameter is constrained to be equal to this value during parameter fitting processes. The columns "MCMC (Q1)", "MCMC (Q2)", "MCMC (Q3)" and "MCMC (95% CI)" are the 25% percentile, 50% percentile (median), 75% percentile and 95% confidence interval of their posterior distributions sampled by Markov-Chain-Monte-Carlo algorithm. To convert units of $V_{1,g}$, $V_{3,g}$, $V_{1,a}$, and γ_a from their original data, we assume 3×10^{-13} g dry mass per cell. We chose $\delta_a = 3$, which conserves carbon in the production of acetate from glucose. The "carbon conservation" choice may not reflect the actual stoichiometry in cells: one molecule of glucose can also be fermented to produce 2 molecules of acetate and 2 molecules of carbon dioxide (in this case, $\delta_a = 2$). But most importantly, the different choices of δ_a would not alter model behavior because it can be absorbed into $V_{1,g}$ and $V_{3,g}$ as a scaling factor.

References

- [1] R Frank Rosenzweig, RR Sharp, David S Treves, and Julian Adams. Microbial evolution in a simple unstructured environment: genetic differentiation in *Escherichia coli*. *Genetics*, 137(4):903–917, 1994.
- [2] Ivana Gudelj, Margie Kinnersley, Peter Rashkov, Karen Schmidt, and Frank Rosenzweig. Stability of cross-feeding polymorphisms in microbial communities. *PLoS computational biology*, 12(12):e1005269, 2016.
- [3] Emmanuel Anane, Peter Neubauer, M Nicolas Cruz Bournazou, et al. Modelling overflow metabolism in *Escherichia coli* by acetate cycling. *Biochemical Engineering Journal*, 125:23–30, 2017.
- [4] Brice Enjalbert, Pierre Millard, Mickael Dinclaux, Jean-Charles Portais, and Fabien Létisse. Acetate fluxes in *Escherichia coli* are determined by the thermodynamic control of the Pta-AckA pathway. *Scientific Reports*, 7:42135, 2017.