Methods S1

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Resource partitioning model

Model description. In an attempt to explain the observed ratio between fermentative (F) and respirative bacteria (R) in our self-assembled glucose communities (**Fig. 1A**), we formulate a simple resource partitioning model. Generally, the biomass of F growing on a set of resources *i={1,N}* for a time *T* can be approximated by:

$$F = \sum_i \left(\sum_{S \in F} X_{Si} w_{Si} \right) = \sum_i r_i \qquad (1)$$

where w_{Si} is the yield efficiency of species *S* on resource *i*. *S* is summed over all members of the fermenter guild in the community. X_{Si} is the total amount of resource *i* metabolized by species *S* over the incubation time *T*. The parameter r_i represents the total biomass of fermentative bacteria that results from consumption of resource *i*. Similarly, the biomass accumulated by the respirative guild R over the incubation time *T* can be written as:

$$R = \sum_i \left(\sum_{S' \in R} X_{S'i} w_{Si} \right) = \sum_i \rho_i \qquad (2)$$

where *S'* runs over all respirative species. Our experiments show that acetate, lactate, and succinate, are the three primary by-products secreted by the members of the F guild when

grown on glucose (**Fig. S3**). Thus, considering that any other secreted resources are negligible, the biomass of F and biomass of R can be approximated by:

$$F \approx r_{glu} + r_{ace} + r_{lac} + r_{suc} \quad (3)$$

and

$$R \approx \rho_{glu} + \rho_{ace} + \rho_{lac} + \rho_{suc} \quad (4)$$

We make the further simplifying assumptions that glucose is only consumed by F, acetate is only consumed by R, and that succinate and lactate have negligible contributions on the R/F ratio. These assumptions are based on a few empirical observations. First, Enterobacteriaceae grow faster on glucose than Pseudomonadaceae whereas Pseudomonadaceae grow faster on the organic acids than Enterobacteriaceae (**Fig. 1B**). Second, Enterobacteriaceae have a growth advantage early on in the incubation period when glucose is abundant while Pseudomonadaceae have a growth advantage later in the incubation period when glucose is depleted and organic acids (OA) are abundant (**Fig. 1C**). Third, acetate is the dominant organic acid produced by single isolates of Enterobacteriaceae yet it is not consumed once the glucose is depleted, whereas lactate and succinate are almost fully depleted by the end of the 48h growth cycle (**Fig. 1B**), suggesting that when grown in coculture Pseudomonadaceae preferentially consume the acetate while succinate and lactate are used by both Enterobacteriaceae and Pseudomonadaceae. These assumptions can be formalized as:

$$r_{glu} >> \sum_{j=OA} r_j \quad (5)$$

and

$$\rho_{ace} >> \sum_{j \neq ace} \rho_j \quad (6)$$

thus

$$\frac{R}{F} = \frac{\rho_{ace}}{r_{glu}}. \quad (7)$$

The biomass of R on acetate and biomass of F on glucose can be re-written as

$$\rho_{ace} = \sum_{S' \in R} X^{S'}_{ace} w^{S'}_{ace} \quad (8)$$

and

$$r_{glu} = \sum_{S \in F} X^{S}_{glu} w^{S}_{glu} \quad (9)$$

Substituting in **Eq. 7**, R/F becomes

$$\frac{R}{F} = \frac{\sum_{S' \in R} X^{S'}_{ace} w^{S'}_{ace}}{\sum_{S \in F} X^{S}_{glu} w^{S}_{glu}} \quad (10)$$

Let us now consider that all acetate is produced by a single dominant F species (DF), the total amount of acetate in the environment can be approximated to:

$$X^{T}_{ace} = \sum_{S \in F} D^{S}_{ace,glu} X^{S}_{glu} \approx D^{DF}_{ace,glu} X^{DF}_{glu} \quad (11)$$

where $D^{DF}_{ace,glu}$ is the number of acetate molecules that the dominant member of the F guild DF secretes back to the environment per glucose molecule uptaken. And similarly, let us now consider that most acetate is consumed by a single dominant R species (DR), the R/F ratio can be approximated to:

$$\frac{R}{F} \approx \frac{X^{T}_{ace} w^{DR}_{ace}}{X^{DF}_{glu} w^{DF}_{glu}} = \frac{D^{DF}_{ace,glu} X^{DF}_{glu} w^{DR}_{ace}}{X^{DF}_{glu} w^{DF}_{glu}} \quad (12)$$

which becomes

$$\frac{R}{F} \approx \frac{D^{DF}_{ace,glu} w^{DR}_{ace}}{w^{DF}_{glu}} = \frac{D^{F}_{ace,glu} w^{R}_{ace}}{w^{F}_{glu}}. \quad (13)$$

Model calibration. We next validated our model both empirically and using Flux Balance Analysis (FBA) simulations. The table below describes how the three parameters were calculated empirically and using FBA.

Parameters	**Empirically calibrated**	**FBA simulations**
$D_{ace,\,glu}$	X_{ace}/X_{glu}	N_{ace} / 1 molecule glucose
w^{R}_{ace}	ρ^{R}/X_{ace}	Biomass(P)/1 molecule acetate

w_{glu}^{F}	r^{F}/X_{glu}	Biomass (F)/1 molecule of glucose

where r^{F} is the biomass of F after 16h of growth on X_{glu} amount of glucose, X_{ace} is the median acetate amount secreted by Enterobacteriaceae after the 16h of growth (shown in **Fig. 1B**), and ρ^{R} is the biomass of R after 32h growth on X_{ace} (see below). The calculated R/F ratios are shown in **Fig. 1D**.

Growth of Pseudomonas isolates on acetate and empirical calibration of our resource-partitioning model. *Pseudomonas* isolates were streaked from glycerol stock into chromogenic agar plates, and incubated for 48h at 30C. Prior to growth on acetate, single colonies were picked and passaged twice for 48h each in 500ul of fresh glucose minimal media (0.2%) at 30C. Cultures were passaged a third time in glucose minimal media for 16h, and the OD620 was measured. 4ul of each culture was transferred to 500ul of fresh acetate minimal media (8.5 mM) (3 replicates each). Cultures were incubated for 32h at 30C, after which OD620 was measured. The change in biomass of each isolate for growth on acetate was calculated as Biomass(P, ace) = Biomass(*P*, *ace*)$_f$- Biomass(*P*, *ace*)$_i$ where Biomass(*P*, *ace*)$_f$ is the OD620 of the Pseudomonas culture after 32h growth on acetate and Biomass(*P*, *ace*)$_i$= Biomass(*P*, *glu*)/125 is the biomass after 16h growth on glucose divided by the dilution factor (125x). Isolates with Biomass(P, ace) <=0.001 were discarded from the analysis. The R/F ratio was calculated as R/F = Biomass(P, ace)/Biomass(E, glu) where Biomass(E, glu) is the change in biomass (OD620) of Enterobacteriaceae isolates after 16h growth on glucose (see Methods, section entitled '48h growth assay of single strains').

To estimate w_{ace}^{R} for the dominant R isolates shown in **Fig. 2** (*Alcaligenes* and *Pseudomonas*), *Alcaligenes* and *Pseudomonas* were acclimated in fresh acetate minimal medium (7.8mM) (4 replicates each) instead of glucose as done above because *Alcaligenes* cannot grow on glucose minimal medium alone. We chose an acetate concentration of 7.8mM because it is the amount of acetate present in the supernatant of the dominant F strain (Kp) after 16h growth on 0.2% glucose minimal medium.

FBA and constraint-based modeling

***Summary*.** To examine whether the conserved R/F ratio may reflect optimal growth strategies in glucose and acetate, we carried out Flux Balance Analysis (FBA) simulations (which assume optimal growth) using a recently developed extension that naturally exhibits overflow metabolism (Mori et al. 2016). In our simulations, we first used a well-curated genome-scale metabolic model of a representative Enterobacteriaceae, the *E. coli* model (iJO1366, (Orth et al. 2011)), and a well-curated genome-scale metabolic model of Pseudomonadaceae, the *P. putida* model (iJN1463, (Nogales et al. 2020)). To predict the

amount of *E. coli* biomass generated, we simulate growth on excess glucose using constrained allocation flux balance analysis (CAFBA) (Mori et al. 2016). We use CAFBA because it includes a proteome-allocation constraint that results in the secretion of organic acids such as acetate in aerobic environments. The CAFBA predicted secretions are then used to set the environment for the *P. putida* model. To predict the amount of *P. putida* biomass, we simulate growth on the constructed environment using Flux Balance Analysis.

We first determined the biomass ratio of *P. putida* to *E. coli* in the limit scenario where *E. coli* metabolizes all of the glucose, secreting acetate as the predominant byproduct, and *P. putida* subsequently respires all of the secreted acetate to CO_2. The model predicts a *P. putida*/*E. coli* ratio of 0.36. This estimate is robust to fluctuations in the parameters used in the model (**Table S2**). To test how representative this ratio is for interactions between Enterobacteriaceae and Pseudomonadaceae, we compiled a library of 59 Enterobacteriaceae and 74 *Pseudomonas* previously published metabolic models and repeated the above simulation to predict the R/F ratio for every pair of Enterobacteriaceae and *Pseudomonas* (**Fig. S10**). Our simulations predict a median R/F ratio of 0.303 (Q1=0.302, Q3=0.356, N=4366) which is strongly aligned with the experimentally observed median R/F ratio of 0.27 (Q1=0.15, Q3=0.70, N=92) in our glucose communities and the empirically calculated R/F ratio of 0.31 (Q1=0.22, Q3=0.43, N=846) (**Fig. 1D**).

To further understand such a strong alignment between theory and experiments, we used Flux Balance Analysis to calculate the amount of acetate secreted per molecule of glucose uptaken for all of the 59 Enterobacteriaceae genome-scale models. We find that the FBA calculation (median=0.81, Q1 = 0.81, Q3=0.92) predicts well the empirically measured ratio of acetate secreted per glucose consumed in our 47 Enterobacteriaceae isolates (median =0.74, Q1=0.65, Q3=0.84) (**Fig. S9**). In sum, given the theoretically predicted amount of acetate produced per molecule of glucose consumed, and the biomass yields of acetate and glucose, the R/F ratio (in a scenario where both R and F obtain all of their biomass from their preferred substrates) is predicted to be very close to what we observe experimentally.

***Constraint-Based Modelling*.** CAFBA and FBA simulations were performed using the COBRApy package. CAFBA is an extension of FBA which explicitly incorporates a global constraint on proteome allocation (Mori et al. 2016). Unlike FBA, CAFBA correctly predicts the secretion of acetate at high growth rates (Basan et al. 2015). The exact notation of the constraint is as follows:

$$\max_{v \in F} \mu \quad \text{subj. to} \quad w_C J_C + w_R \mu + \sum_{i \in E} w_i |v_i| = \Phi_{max} \ .$$

To simulate *E. coli* growth on excess glucose we follow the approach taken by (Mori et al. 2016). We set $\phi_{\max}$ and w_R to their *E. coli*-specific empirical values of 0.484 and 0.169/h. The cost w_i of all reactions in the E-sector is set to some constant w_E so that a maximum

achievable growth rate on glucose ($w_C \rightarrow 0$) is 1/h. Because glucose is in excess, w_C =0.0 and the lower bound on the glucose exchange flux is effectively unbounded by setting to an arbitrarily large negative value (-1000 mmol/g_{DW}h). The following inorganic compounds are set to be unbounded using the same approach: ca2_e, cbl1_e, cl_e, co2_e, cobalt2_e, cu2_e, fe2_e, fe3_e, h_e, h2o_e, k_e, mg2_e, mn2_e, mobd_e, na1_e, nh4_e, ni2_e, pi_e, sel_e, slnt_e, so4_e, tungs_e, zn2_e, o2_e. By unbounding these nutrients we are assuming that all inorganic compounds (including oxygen) are in excess and we are allowing the uptake rates to be chosen by CAFBA based on the proteome allocation constraint. As in (Mori et al. 2016), we silence the glucose dehydrogenase reactions (GLCDe and GLCDpp). Growth is optimized using cobrapy's optimize function and we record the flux through the objective function (BIOMASS_Ec_iJO1366_core_53p95M) as well as the fluxes through the exchange reactions.

To simulate *P. putida* growth on secreted metabolites, we use Flux Balance Analysis (FBA). We first set all metabolites to be unavailable (lower bound of 0) excluding the same set of inorganic compounds as before. We set the lower bound on *P. putida*'s uptake of acetate to match the predicted secretion of acetate by *E.coli*. Growth is then optimized using cobrapy's *optimize* function and we record the flux through the biomass reaction (BIOMASS_KT2440_WT3). The predicted R/F ratio is the flux through biomass reaction of the *P. putida* metabolic model divided by the flux through the biomass reaction of the *E. coli* metabolic model. For iJO1366 and iJN1463 we get a R/F ratio of 0.356. We find that this value is extremely robust to the exact CAFBA parameters used. The parameters w_E, $\phi_{\max}$, and w_r can all be halved or doubled without substantially changing the predicted R/F ratio (**Table S2**). Furthermore, whilst we simulated *P. putida* using conventional FBA, we note that if we do impose the CAFBA constraints on the *P. putida* metabolic model using the same parameters as for *E. coli* (modeling *P. putida* as growing on *E. coli* secretions as though they were in excess), we obtain a R/F ratio of 0.355 which is extremely close to the value reported in the main text. We repeated the above analysis for every pair of Enterobacteriaceae and Pseudomonadaceae metabolic models in a manually compiled collection of published metabolic models (see below). This was used to obtain a distribution of predicted R/F ratios. For all simulations we set lower bound on ATPM maintenance to the default value in the published model (3.15 for iJO1366 and 0.92 for iJN1463). Because we are considering scenarios where resources are in excess, the simulations throughout this paper are robust to the removal of a lower bound on ATP maintenance.

We make note of a minor technical difference between our simulations and those of (Mori et al. 2016) in how we determined which reactions belong to the E-sector. Here the E-sector is defined as including all enzyme catalyzed reactions except for transporters and exchanges. Unlike in (Mori et al. 2016), where E-sector identity was determined using SBML subsystem assignment (which are not available for all metabolic models), we define transporters using reaction stoichiometry and metabolite compartments which are available for all metabolic

models and can be inferred from metabolite IDs or compartment assignments. Ignoring sodium and hydrogen ions, a transporter is defined as any reaction that consumes at most one metabolite in one compartment and produces at most one metabolite in another compartment (cytoplasm, periplasm and extracellular). This includes all common transporter types (symporters, diffusion reaction etcs) whilst excluding membrane associated reactions such as those involved in oxidative phosphorylation (which are part of the E-sector). For the iJR904 model used by (Mori et al. 2016), this approach gives us w_E for all reactions in the E-sector of 0.00084 which is extremely similar to the 0.00083 they obtained. For the iJO1366 model, this approach gives us a w_E of 0.000885.

Published Metabolic Model Dataset. To compile a collection of Enterobacteriaceae metabolic models we downloaded every available metabolic model from the BIGG database (version 1.6). We used every Enterobacteriaceae model, except for those that could not grow on minimal glucose. This gave us 59 metabolic models (55 *Escherichia*, 1 *Klebsiella*, 2 *Salmonella*, and 1 *Shigella*). In the iECIAI1_1343 model, we knocked out the Hydroxyacylglutathione hydrolase reaction (GLYOX_2) as this was a stoichiometrically unbalanced reaction that led to growth in the absence of any supplied carbon source.

Because only 2 *Pseudomonas* metabolic models are available in the BIGG database (and iJN746 is merely an older version of the iJN1463 metabolic model), we instead compiled a library of 74 *Pseudomonas* metabolic models from the literature. Including iJN1643, 69 out of the 74 metabolic models were for different strains of *P. putida* and corresponded to 69 of the strain-specific models used in (Nogales et al. 2020). To ensure compatibility with COBRApy version 0.17.1, we reconstructed these models in-house using the methodology and gene orthology matrix (Table S5) in Nogales et al. For each of the strains of *P. putida*, we started with the iJN1463 metabolic model and removed genes and reactions that were missing. As in (Nogales et al. 2020), genes with less than 80% percentage identity were considered to be missing and we excluded strains with >300 genes missing. This gave us 69 strain-specific models. Gapfilling was then performed using Cobrapy's *gapfilling* module to identify the reaction from iJN1463 that would enable growth on minimal acetate. Reactions identified using gap filling were added back to the strain-specific models to create the final models used in our simulations. To confirm that our results would apply to Pseudomonads other than *P. putida*, we also included three *P. aeruginosa* metabolic models (iMO1056, iPAE1146, iPAU1129) and as well as a *P. stutzeri* metabolic model (iPB890) and a *P. fluorescens* metabolic model (iSB1139). **Fig. 1D** shows the full distribution of predicted R/F values whilst in **Fig. S10** we break down the results by Enterobacteriaceae genus and *Pseudomonas* species.

Calculating the R/F Ratio using metabolic models constructed from whole-genome sequences. In addition to the large dataset of published metabolic models described in the previous section, we also analyzed 5 genome-scale metabolic models which we built using

whole genome-sequences. These 5 sequences correspond to isolates from communities previously stabilized in minimal glucose (**Fig. 1B**) (Goldford et al. 2018). They include a single isolate of *Pseudomonas* and 4 Enterobacteriaceae isolates each belonging to a different genus (*Klebsiella*, *Enterobacter*, *Citrobacter* and *Raoultella*).

Isolates were grown in glucose M9 minimal media, and genomic DNA was isolated using the DNeasy Blood & Tissue Kit from Qiagen. Genomic libraries were constructed at the BioMicro Center at MIT with the Nextera XT DNA Library Prep Kit. 150 base-pair Paired-end sequences were generated using an Illumina NextSeq 500 at a sequencing depth of >100x per genome, and demultiplexed using a custom analytical pipeline at BioMicro Center. Sequences were investigated with FASTQC, and revealed a high frequency of poly-G repeats, which were subsequently trimmed using AfterQC (v0.9.6) with default parameters (Chen et al. 2017). The trimmed sequences were then assembled into contigs using the IDBA assembler (v1.1.3) (Peng et al. 2012) on the KBase platform (Arkin et al. 2018), and CheckM (v1.0.18) (Parks et al. 2015) was used to assess genome completeness and contamination. Each genome was annotated using Prokka (v1.14.5) (Seemann 2014).

A metabolic model for each isolate was built using the '*Compare Two Proteomes*' and '*Propagate Model to New Genome*' apps in the KBase platform, using the default parameters (Arkin et al. 2018). For the 4 Enterobacteriaceae isolates we used the iJO1366 (*E. coli MG1655*) model as a template. For the *Pseudomonas* isolate we used the iJN1463 (*P. putida KT2440*) model as a template. The corresponding reference genomes were used in the '*Compare Two Proteomes*' App (*NC_000913* and *NC_002947* respectively). The iJO1366 and iJN1463 metabolic models were downloaded from the Biggs Database and loaded into KBase using '*Import TSV/XLS/SBML File as an FBAModel from Staging Area*'. The constructed metabolics models for each isolate were downloaded from KBASE as SBML files and analyzed as described in the ***Constraint-Based Modelling*** section. As before, we calculated $D_{ace,\,glu}$, w_{ace}^{R}/w_{glu}^{F}, and the R/F ratio for all possible Enterobacteriaceae-*Pseudomonas* pairs (N=4) (**Fig. S18**).

Effect of Non-Acetate Secretions on the R/F ratio

Summary. It is important to emphasize that, while glucose is primarily metabolized by F specialists and acetate is primarily metabolized by R specialists, R specialists may still grow within the first phase of the incubation where glucose is the only carbon source but less than F specialists do (**Fig. S6**). Likewise, F specialists grow too after the glucose has been exhausted, indicating that they do too consume organic acids (**Fig. S6**). Indeed, when grown in monoculture, F isolates switch to consume the organic acids they had previously secreted after they exhaust the glucose (**Fig. 1B**). Among these, they generically exhibit a strong preference for lactate and succinate over acetate, which they leave largely untouched (**Fig. 1B**). This observation, together with the fact that acetate is the most abundant secreted

byproduct by all of the F isolates in our collection, justified the assumptions we made in the resource partitioning model in **Eq. 1**. Although we do not know precisely what fractions of the succinate, lactate, and all of the other lower-concentration byproducts are uptaken by F, here we explore scenarios where these additional byproducts are either (i) evenly consumed by F and R alike; (ii) uptaken entirely by R; or (iii) uptaken entirely by F (**Fig. S16**). Although the expected R/F ratio is of course sensitive to these choices, it remains within the bounds of the R/F ratios observed in our experimental communities, even for the two extreme scenarios (ii) and (iii). We also note that overflow glucose metabolism in Enterobacteriaceae produces additional byproducts at lower concentrations, in addition to those three organic acids (Paczia et al. 2012). These additional carbon sources likely mediate the coexistence of multiple members of the same ecological guild.

Model. A major limitation of our genome-scale models is that they fail to predict the secretion of lactate, succinate, and other byproducts (Mori et al. 2016). This is because CAFBA simulations predict secretion of acetate as the principal product of overflow metabolism. Other carbon organic compounds such as methanol, dihydroxyacetone and glycolate are secreted by some models, though this is in negligible amounts. 58 out of the 59 Enterobacteriaceae metabolic models secrete more than 99.99% of secreted carbon (asides from CO_2) in the form of acetate.

To estimate the effect of these missing secretions on the expected R/F Ratio, we performed standard FBA using the *E.coli* iJO1366 and *P. putida* iJN1463 metabolic models, constraining the *E.coli* model to secrete the empirically observed amounts of acetate, succinate and lactate produced by one specific isolate after 16h of growth in glucose minimal media (**Fig 1B**). We repeated this step for each of the 48 fermenter isolates. We use 16h because glucose has generally been fully depleted by this time point. We model three scenarios (**Fig. S16**). Below we outline the precise procedure taken for scenario 2. A similar approach is taken for scenarios 1 and 3.

Suppose that after 16h a given isolate has produced X mM of acetate, Y mM of lactate and Z mM of succinate.

Step 1. Take the *E. coli* model. The initial glucose concentration of 0.07 moles of carbon per litre corresponds to 11.66 mM. Glucose uptake is thus constrained to a lower bound of 11.66. Acetate, lactate and succinate secretion are constrained to a lower bound of X, Y and Z respectively. FBA is used to quantify the biomass obtained from this amount of glucose, whilst secreting the corresponding amount of metabolic by-products (F_glc).

Step 2. Take the *P. putida* model. Acetate uptake is constrained to X. Lactate and succinate uptake are constrained to Y/2 and Z/2 respectively. FBA is used to quantify the biomass obtained from these secretions (R_sec).

Step 3. Take the *E. coli* model. Lactate and succinate uptake are constrained to Y/2 and Z/2 respectively. FBA is used to quantify the biomass obtained from the secretions (F_sec).

Step 4. The final predicted R/F ratio is R/F = R_Sec/(F_glc+F_sec).

The results (**Fig. S16**) suggest that the less abundant metabolites such as succinate or lactate have a relatively small effect on the R/F ratio, which provides an explanation for the success of the models, despite the fact that they failed to capture these secretions.

Oxygen is necessary for growth on acetate, succinate and lactate

Summary. Our communities were grown on a single limiting carbon source under static conditions. Our experimental methods do not allow us to track the oxygen dynamics over a single incubation time at different depths of our habitats. However, it is likely that oxygen may be significantly depleted at the bottom portion of our wells towards the end of our incubations, after the initially available dissolved oxygen has been exhausted. For our purposes, though, the relevant question is not whether an oxygen gradient is established, but whether it should quantitatively impact the ability of **Eq. 1** to capture the R/F ratio. In this equation, $D_{ace,glu}$ represents the average number of acetate molecules secreted per glucose molecule over the entire incubation period by the F specialists. In turn, w_{glu}^{F} and w_{ace}^{R} reflect the average amount of biomass that can be obtained by F and R specialists per molecule of glucose and acetate, respectively. We obtained these parameters empirically by averaging acetate production and cell growth over the entire incubation period. Therefore, any oxygen dynamics within the incubation period are already incorporated in the empirical parameters. It is worth noting that when we estimated those same three parameters using Flux Balance Analysis under unlimited oxygen availability, the values we obtained were very similar to our empirical estimates (**Fig. S9**). This further suggests that the oxygen dynamics within an incubation do not fundamentally alter our results. Consistent with this idea, we had previously found that when a limited number of communities were assembled under vigorous shaking (a process that should stimulate oxygen introduction into the system), communities converged to an R/F ratio that was comparable to those found under static conditions (see Fig. S15 in (Goldford et al. 2018)). Perhaps most importantly, the acetate that accumulates in mixed communities due to glucose metabolism in the first half of our incubation is generally fully depleted in the second half, and so were lactate and succinate in Enterobacteriaceae monocultures. Using FBA, here we show that oxygen is required for growth on acetate, lactate, and succinate (**Fig. S17**), thus suggesting that enough oxygen must be present in our habitats to fully respire these primary byproducts.

Model. We use flux balance analysis to illustrate that oxygen is generically required for growth on the three primary by-products of glucose metabolism, acetate, lactate and succinate (**Fig. S17**). We followed the same procedures as above, setting all inorganic ions to be unbounded (-1000 mmol/g_{DW}h). When oxygen is in excess (lower bound = -1000

mmol/g_{DW}h), the vast majority of our 59 *Enterobacteriaceae* metabolic models and 74 *Pseudomonas* metabolic models can grow on glucose and any one of the three secreted by-products as the sole carbon source (lower bound = -10 mmol/g_{DW}h). In contrast, when oxygen is not available (lower bound =0.0mmol/g_{DW}h), none of our models can grow on acetate, lactate or succinate, and all *Enterobacteriaceae* but only one *Pseudomonas* metabolic model can grow on glucose.