

Supplementary information: Automated design of synthetic microbial communities

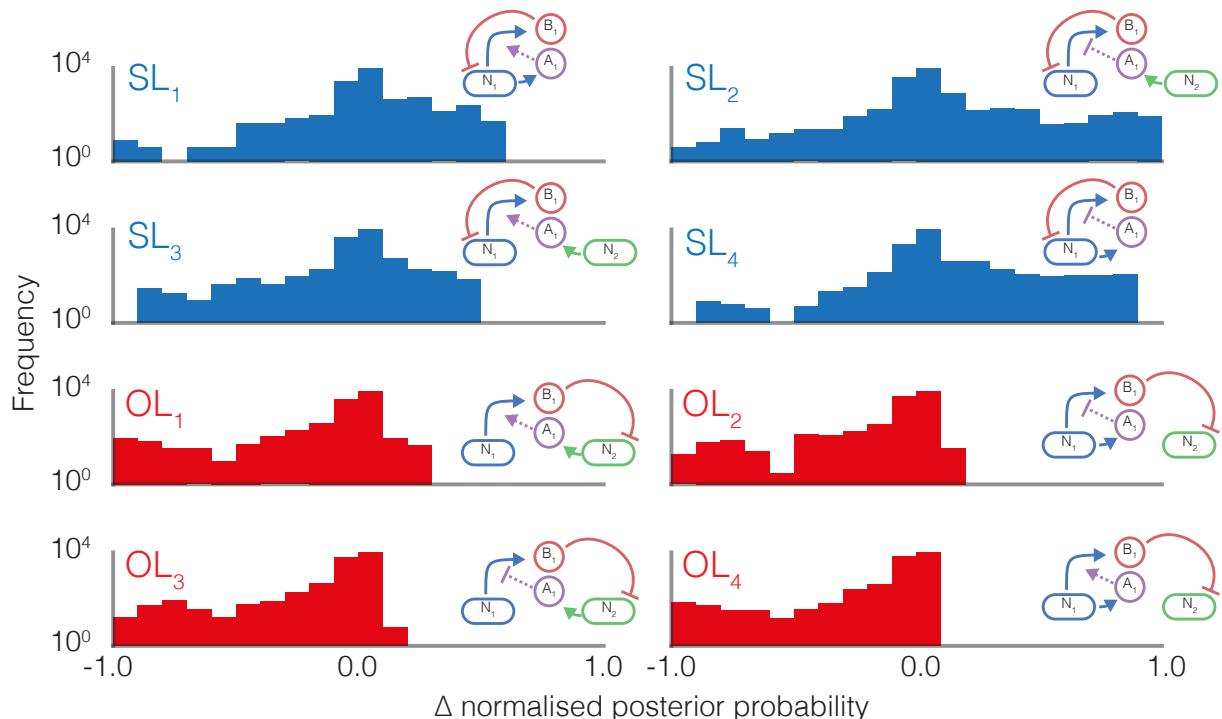
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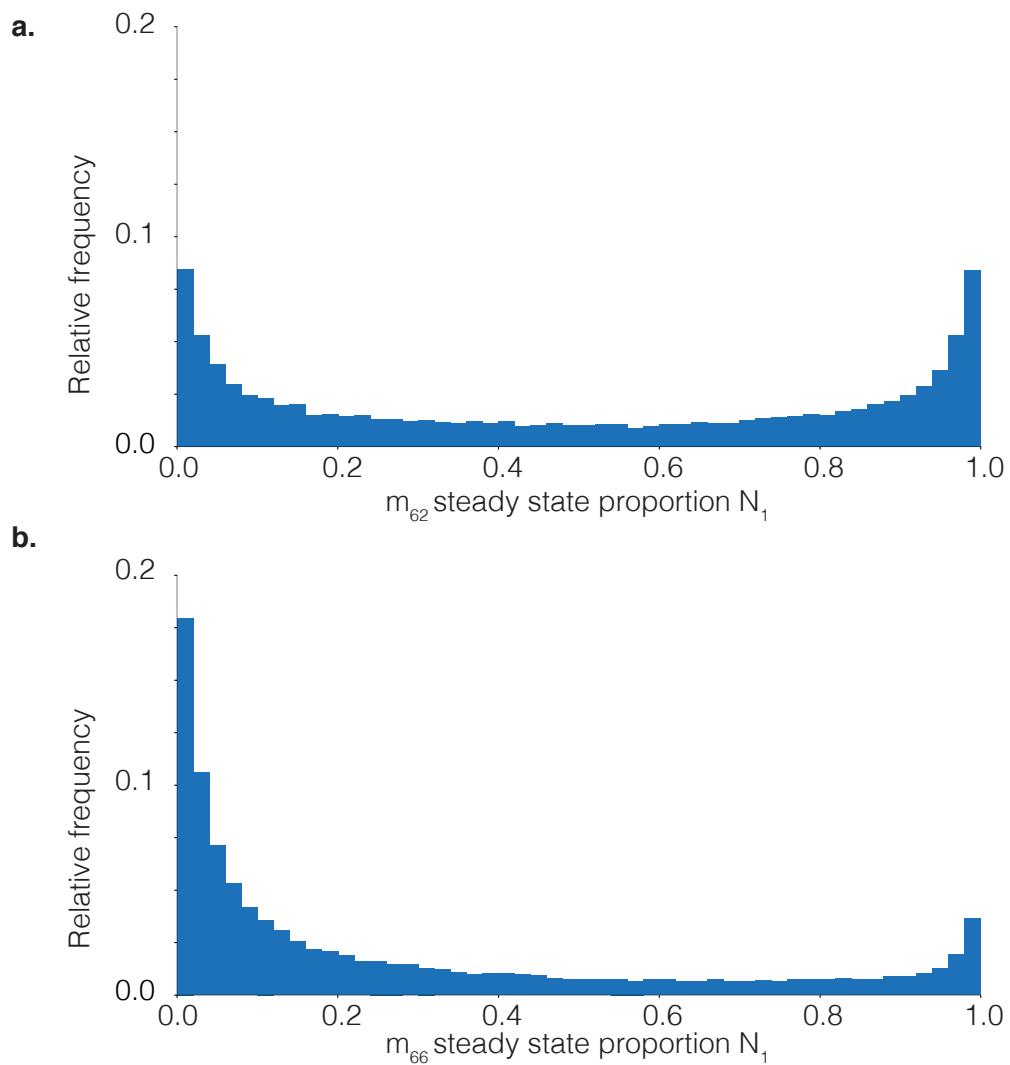
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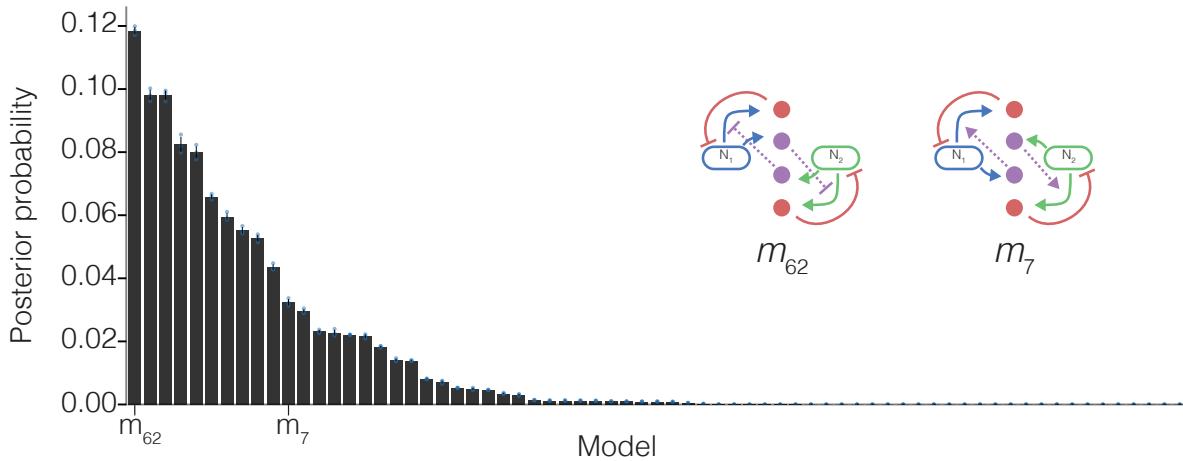
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Supplementary Figure 1: Motif impact analysis in three strain model space. Histograms show the change in posterior probability when adding each motif to a model in the three strain model space.



Supplementary Figure 2: Stable steady state population distribution in two strain models. **a** A histogram of the proportion of population occupied by strain N_1 at stable steady for m_{62} . **b** A histogram of the proportion of population occupied by strain N_1 at stable steady for m_{66} .

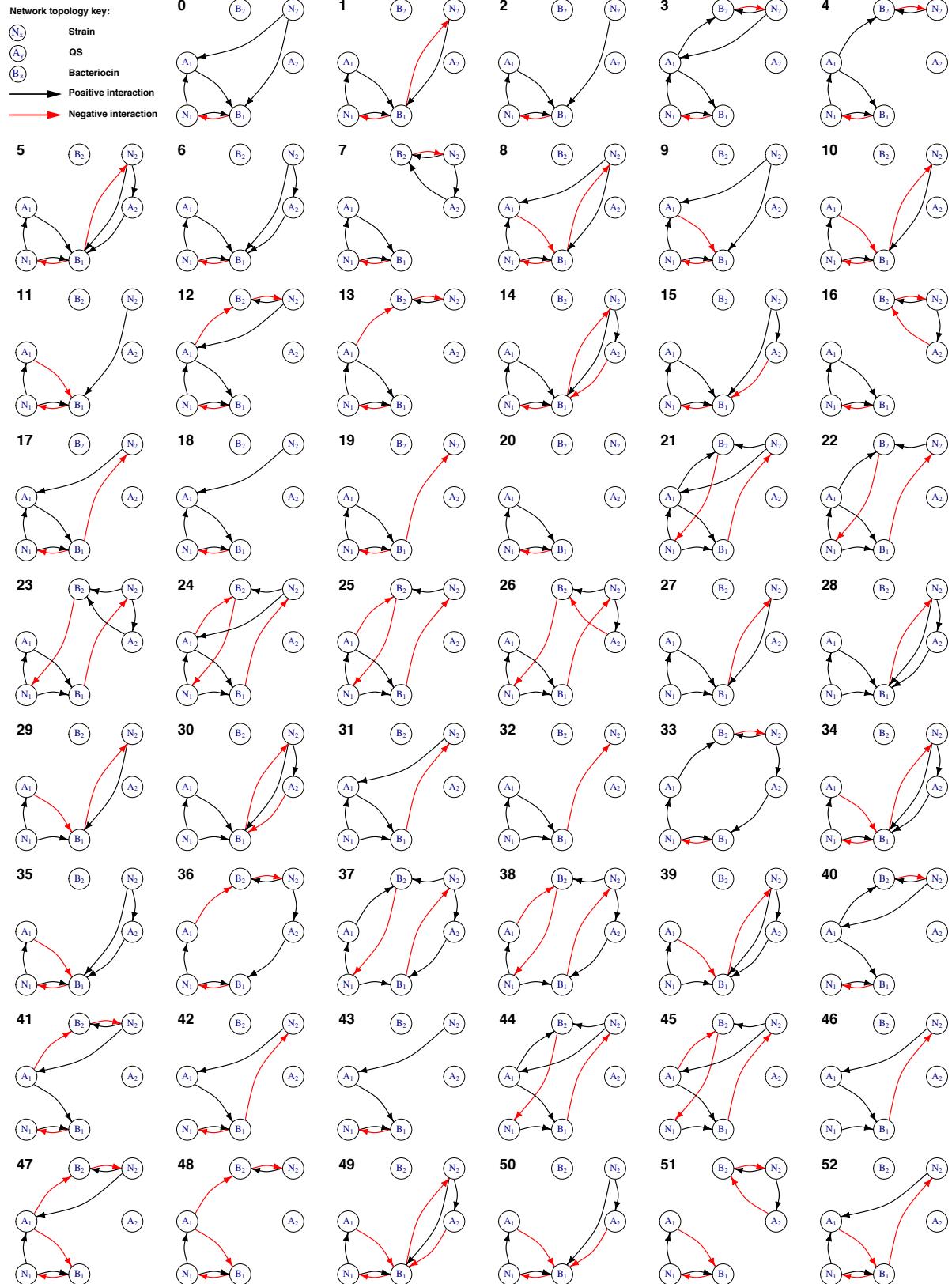


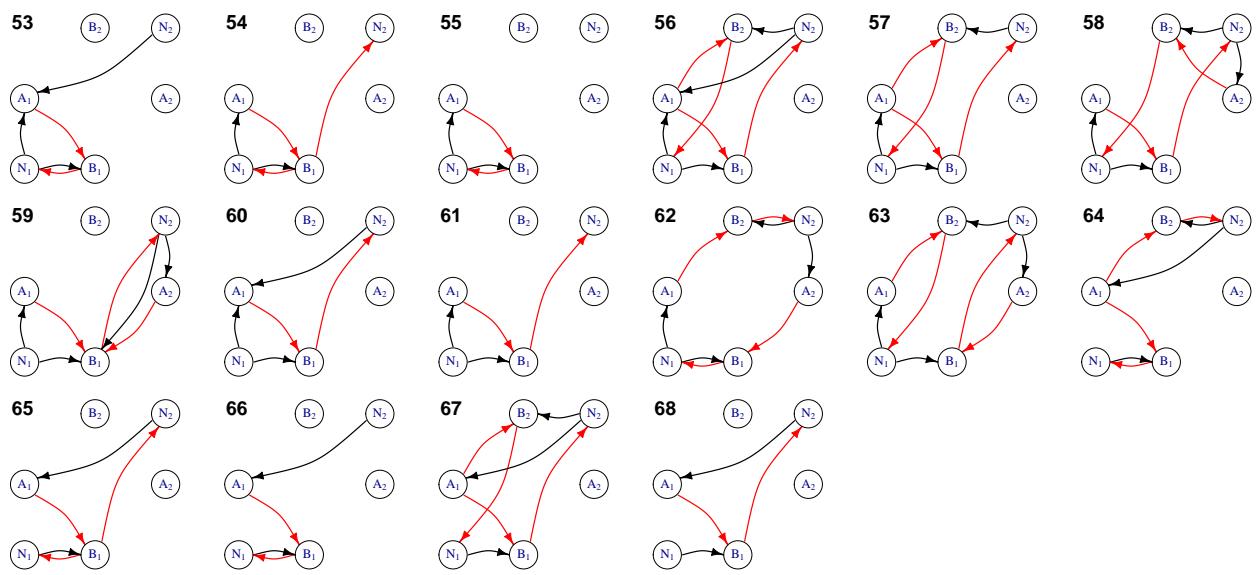
Supplementary Figure 3: Posterior probability of two strain model space in order of descending posterior probability. m_{62} and m_7 are highlighted, drawing attention to two models with and without interdependence between strains. The configuration of these parts is what differentiates the robustness of these two models for the stable steady state objective.

Supplementary Algorithm 1: Algorithm for model selection with ABC SMC

- 1 Set population indicator, $t = 0$
- 2 Set initial epsilon, $\epsilon_t = \inf$
- 3 Set final epsilon, $\epsilon_F = [x, y, z]$
- 4 Set particle indicator, $i = 0$
- 5 **if** $t = 0$ **then**
 - 6 Sample m^* from $\pi(m)$
 - 7 Sample θ^{**} from $\pi(\theta(m^*))$
- 8 **else if** $t > 0$ **then**
 - 9 Sample particle θ^* from previous population $\{\theta(m^*)_{t-1}^i\}$ with weights $w(m^*)_{t-1}$
 - 10 Perturb θ^* to obtain $\theta^{**} \sim K_t(\theta|\theta^*)$
 - 11 **if** $\pi(\theta^{**}) = 0$ **then**
 - 12 **go to** 5
 - 13
 - 14 Simulate, $x^* \sim f(x|\theta^{**}, m^*)$
 - 15 **if** $d(x^*, x_0) > \epsilon_t$ **then**
 - 16 **go to** 5
 - 17
 - 18 Set $m_t^i = m^*$
 - 19 Set $\theta_t^i = \theta^{**}$
 - 20 Calculate particle weight, w_t^i
 - 21 **if** $t = 0$ **then**
 - 22 $w_t^i = 1$
 - 23 **else**
 - 24 $w_t^i = \frac{\pi(\theta^{**})}{\sum_{j=1}^N w_{t-1}^j K_t(\theta_{t-1}^j | \theta^{**})}$
 - 25 **if** $i < N$ **then**
 - 26 Set $i = i + 1$
 - 27 **go to** 5
 - 28
 - 29 Normalise weights for every m .
 - 30 **if** $\epsilon_t \neq \epsilon_T$ **then**
 - 31 Update population number, $t = t + 1$
 - 32 Update ϵ according to accepted particle distances, $\epsilon_t = f_\epsilon()$
 - 33 **go to** 5

Supplementary Figure 4: Two strain model space topologies





Supplementary Figure 5: Three strain model space topologies

