

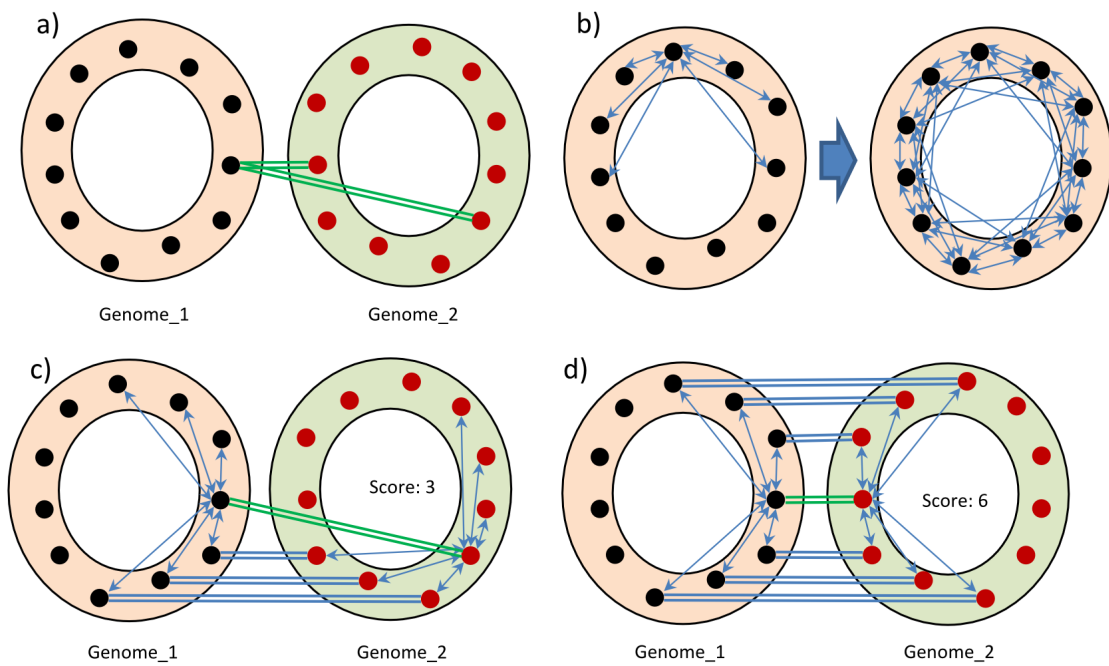


Figure S1: Synteny ortholog detection (SynOrF). The red and black dots represent genes located on two different bacterial genomes. The double lines indicate homology between genes. The arrows are edges in a graph. **a)** The query gene of Genome_1 has two homologs in Genome_2. **b)** The detailed construction of a graph is shown. The edges of the graph are the connections for each gene and its genomic neighbors up to the third degree. To evaluate the synteny, a score is calculated based on the number of neighbors of a homolog that are also homolog to the neighbors of the query gene (**c, d**). Homologs with the highest score (≥ 2) are selected as synteny orthologs.