

Illustration of the assessment of similarity in terms of the Hamming distance between two phenotypes.

|     |                    |                    |                                                               |
|-----|--------------------|--------------------|---------------------------------------------------------------|
| (a) | <b>Phenotype 1</b> | <b>Phenotype 2</b> |                                                               |
|     | - + + + + -        | - + + - - +        | $H(P1,P2) = 3/6 = 0.5$ $S(P1,P2) = 1 - 0.5 = 0.5$             |
| (b) | <b>Phenotype 1</b> | <b>Phenotype 2</b> |                                                               |
|     | - + + + + -        | - + + + + -        | $H(P1,P2,1) = 0/6 = 0$                                        |
|     |                    | + - - + + -        | $H(P1,P2,2) = 3/6 = 0.5$                                      |
|     |                    |                    | $S(P1,P2) = 1 - \text{mean}\{H(P1,P2,1), H(P1,P2,2)\} = 0.75$ |

Plus and minus signs refer to the activity state, active or inactive respectively, that the structural genes have at the end of a network's dynamics. Different corresponding activity states in the two phenotypes appear in red. Phenotypes can be fixed points ( $\kappa = 1$ ) or  $\kappa$ -period limit cycles ( $\kappa > 1$ ). In (a) both phenotypes are fixed points.  $H(P1,P2)$  refers to the normalized Hamming distance between two phenotypes, P1 and P2. Namely, it is the fraction of different activity states in the two phenotypes. Similarity,  $S(P1,P2)$ , equals 1 minus the normalized Hamming distance. In (b) P2 is a two-step limit cycle. We obtain the Hamming distance between P1 and each row in P2. Thus,  $S(P1,P2)$  equals 1 minus the average of the normalized Hamming distance between P1 and each row in P2.