



**Fig. 4.** This higher-order singular value decomposition (HOSVD) is a transformation of the data tensor from the space of  $K$ -genes  $\times$   $L$ - $x$ -settings  $\times$   $M$ - $y$ -settings to the reduced space of  $LM < K$ -eigenarrays  $\times$   $L$ - $x$ -eigengenes  $\times$   $M$ - $y$ -eigengenes. Raster display of Eq. 1,  $\mathcal{T} = \mathcal{R} \times_a U \times_b V_x \times_c V_y$ , with overexpression (red), no change in expression (black), and underexpression (green). The expression of each array and eigenarray is centered at its gene-invariant level. The expression of each gene and  $x$ - and  $y$ -eigen gene is centered at its  $x$ - and  $y$ -setting-invariant levels, respectively. The genes are sorted by the “angular distance”  $\theta_i = \arctan(U_{:,8+2}/U_{:,3+7})$  between the two superpositions of eigenarrays  $U_{:,8+2}$  and  $U_{:,3+7}$ , which define the expression variation across the genes in the ninth and tenth subtensors, respectively.