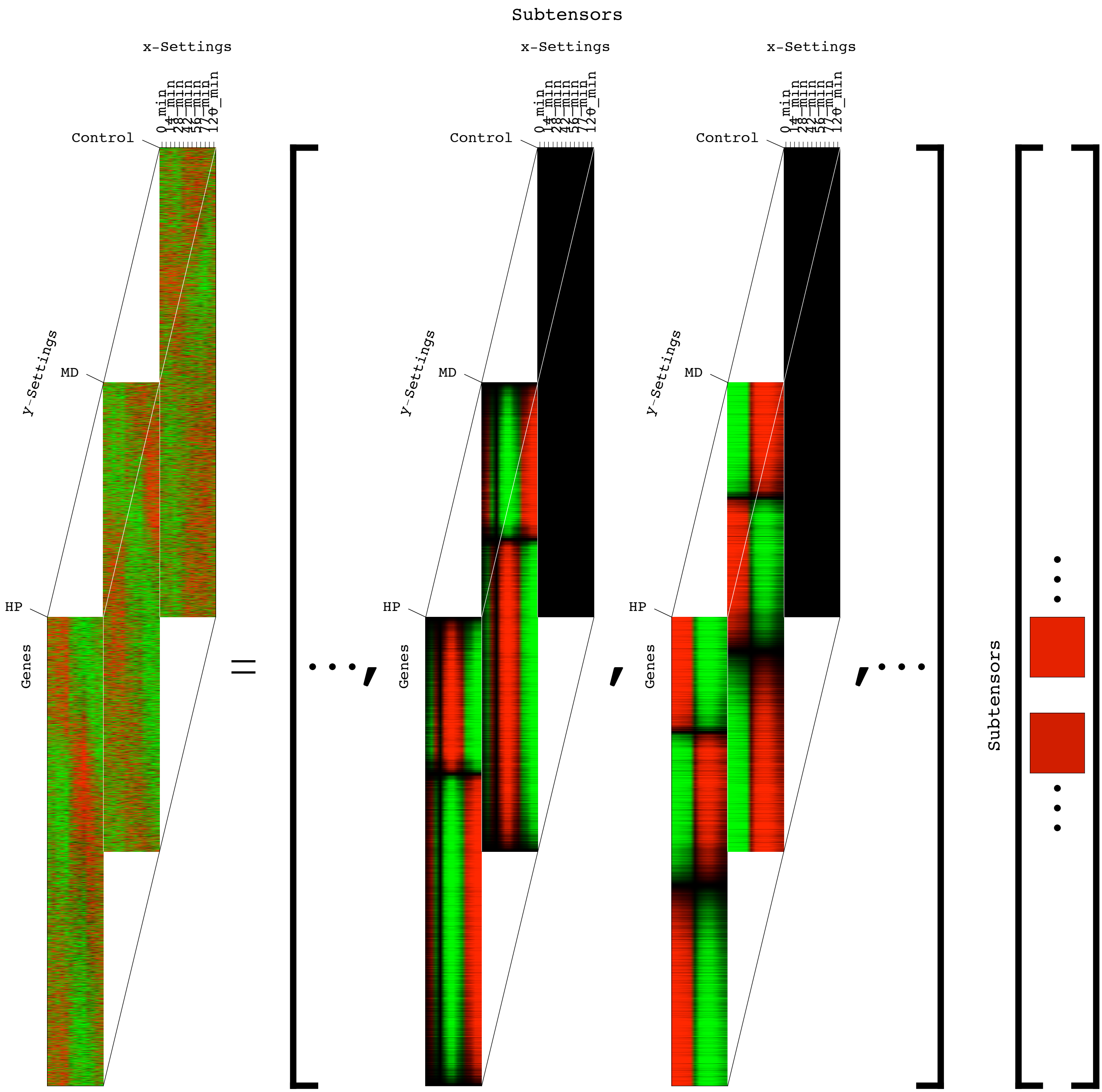
Subtensors
x-Settings
y-Settings
Control
MD
HP
Genes
0_min
14_min
28_min
42_min
56_min
77_min
120_min
=
Subtensors

Fig. 5. This multilinear HOSVD is reformulated such that it decomposes a data tensor into a linear superposition of all outer products of an eigenarray, an x- and a y-eigengene, that is, rank-1 subtensors. Raster display of Eq. **2**, $\mathcal{T} = \sum_{a=1}^{LM} \sum_{b=1}^{L} \sum_{c=1}^{M} \mathcal{R}_{abc} U_{:a} \otimes V_{x,b:}^T \otimes V_{y,c:}^T \equiv \sum_{a=1}^{LM} \sum_{b=1}^{L} \sum_{c=1}^{M} \mathcal{R}_{abc} \mathcal{S}(a,b,c)$, with overexpression (red), no change in expression (black), and underexpression (green). Explicitly shown are the ninth and tenth subtensors, $\mathcal{S}(8+2,4,3)$ and $\mathcal{S}(3+7,2,3)$, with the corresponding superposition coefficients, that is, higher-order singular values, $\mathcal{R}_{8+2,4,3}$ and $\mathcal{R}_{3+7,2,3}$. The expression of each array and eigenarray is centered at its gene-invariant level. The expression of each gene and x- and y-eigengene is centered at its x- and y-setting-invariant levels, respectively. The genes are sorted by the angular distance $\theta_{:} = \arctan(U_{:,8+2}/U_{:,3+7})$ 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.