**Supplementary Text S3:** Pseudo-code of attractor metagene finding algorithm

1. Start from a seed gene .
2. Calculate the associations between each gene and
3. Create a metagene using the weighted average of all the genes, with the weights being a function of , i.e.,
4. Given metagene , calculate the associations between metagene and each gene
5. Create metagene using
6. Repeat iteration until , or until a preset maximum iteration number is reached.
7. The converged is the attractor metagene given by