Table iA. An overview of the fuzzy k-means clustering process.

1. Seed k centroids with the eigen vectors identified by PCA of Dataset B

2. Assign each gene to the centroid to which it is most similar and remove eigen vectors to which no gene is assigned.

3. Calculate the gene memberships to each centroid, recalculate each centroid, and iterate until convergence or when stop criterion is met.

4. To perform additional clustering rounds:
    a. Calculate the pearson correlation between each gene and each centroid and remove genes that are correlated to any centroid with a pearson correlation >0.7
    c. Recalculate the gene and array weights as described in Materials and Methods
    d. Perform another round of fuzzy k-means clustering (steps 1-3)

5. Combine the identified centroids from each cycle into one set
    a. Calculate the pairwise pearson correlation of the centroids, and average centroids that are correlated >0.9. This is unique set of centroids is outputted by the method.

    b. Calculate the membership of each gene in Dataset A to the unique centroids. This is the final list of gene memberships outputted by the method.