10-fold cross-validation

All knowledge genes

Split as training and validation gene sets

Split training gene set as learning set and test set

Cluster whole gene population into $n$ clusters $n = 1, 2, 3...$

ICA on each gene cluster

Calculate weights and rank genes based on learning gene set

Predict test gene set

Determine optimal cluster number $n_{opt}$

Cluster whole gene population into $n_{opt}$ clusters, implement ICA on each cluster

Calculate weights and rank genes based on training gene set

Predict validation gene set