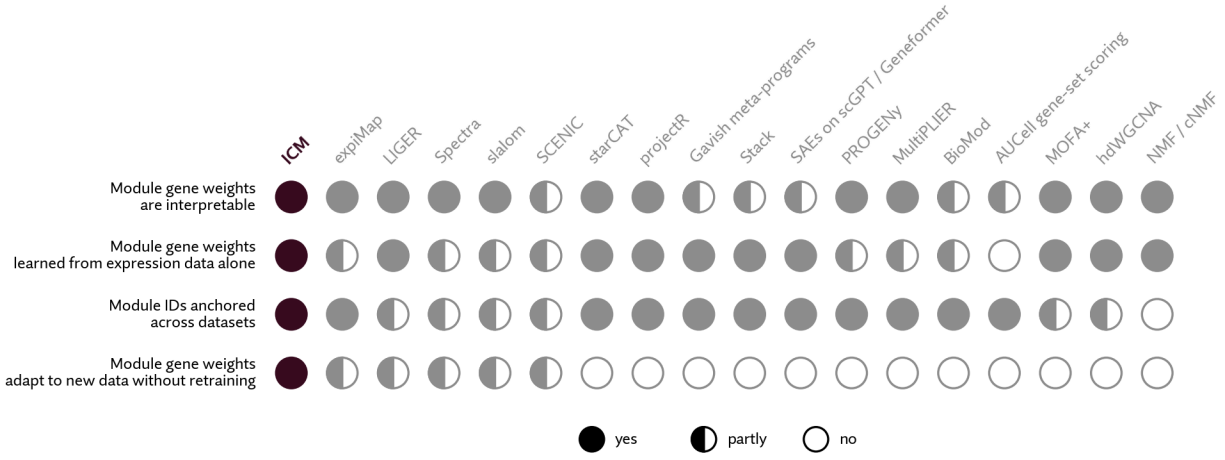

ICM
expiMap
LIGER
Spectra
slalom
SCENIC
starCAT
projectR
Gavish meta-programs
Stack
SAEs on scGPT / Geneformer
PROGENy
MultiPLIER
BioMod
AUCell gene-set scoring
MOFA+
hdWGCNA
NMF / cNMF
Module gene weights are interpretable
Module gene weights learned from expression data alone
Module IDs anchored across datasets
Module gene weights adapt to new data without retraining
yes
partly
no
Last row: partly = gene weights adapt only by refitting the model