(A) Double perturbation prediction error

Norman

CEBPE+KLF1
error: 5.2

TGFBR2+ETS2
error: 1.3
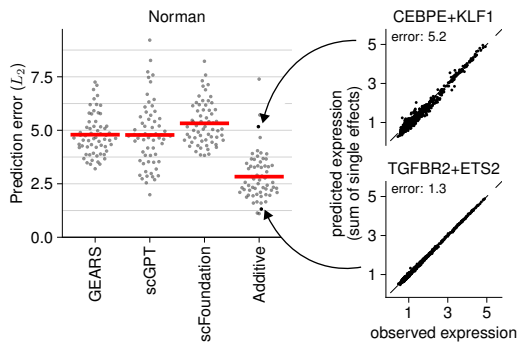
(B) Prediction error depending on number of considered genes

genes sorted by expression

genes sorted by differential expression

scFoundation

GEARS
scGPT

Additive

top n genes (log-scale)
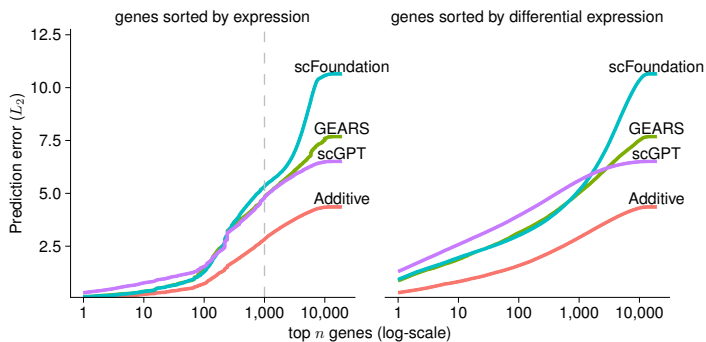
(C) Prediction of non-additive perturbation effects

GEARS

1,201	558
56,477	
397	3,367

scGPT

2,947	1,285
56,059	
261	1,448

scFoundation

612	679
53,793	
413	6,503

Deviation from additive model

density

Predicted deviation from additive model (predicted value − sum of single effects)

True deviation from additive model (observed value − sum of single effects)