

a Evals framework

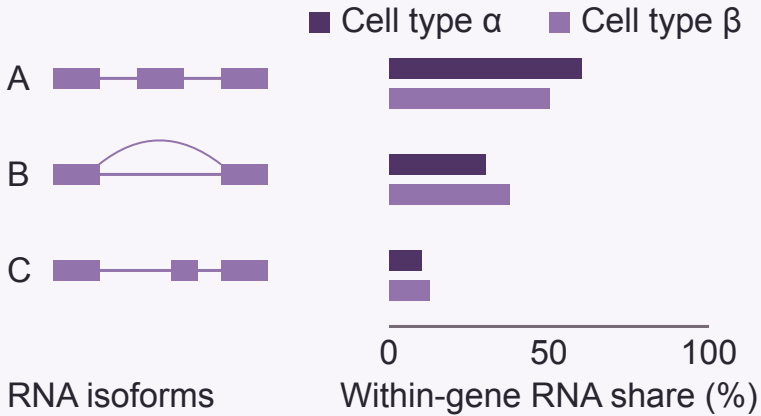


b Cell and gene-level evals

 **SnISOR-Seq2**

1. What RNA isoforms are used?
Cell type-specific RNA isoform prediction

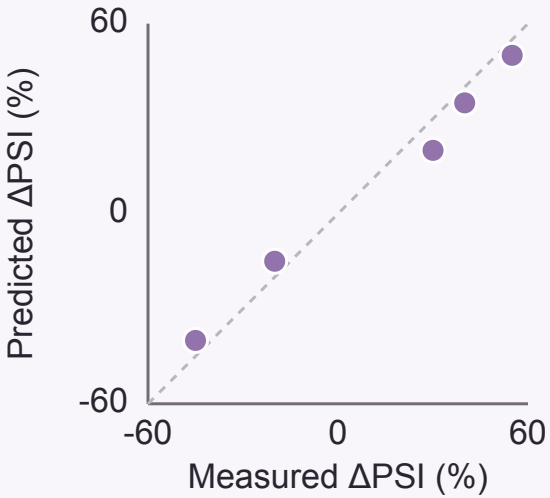
- **Input:** Short-read counts matrix + cell type
- **Task:** Compositional regression
- **Metrics:** JSD, MAE, dominant-isoform accuracy



RNA isoforms	Cell type α (%)	Cell type β (%)
A	~60	~50
B	~30	~40
C	~10	~15

2. Which exons change in disease?
Disease differential exon usage prediction

- **Input:** Gene + exon IDs; cell type; FTD contrast
- **Task:** Signed regression
- **Metrics:** ρ , RMSE, r , R^2 , direction accuracy



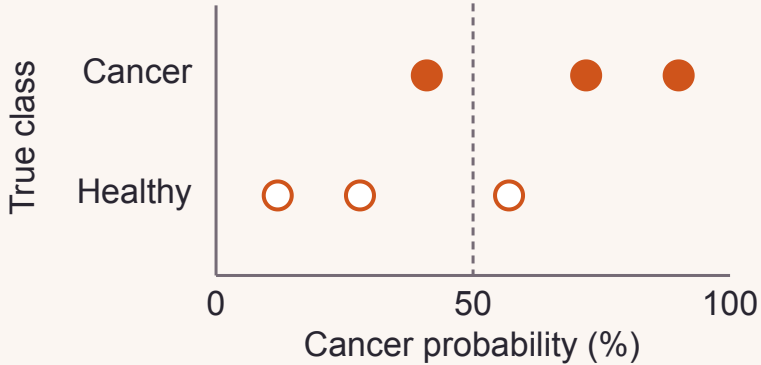
Measured Δ PSI (%)	Predicted Δ PSI (%)
-45	-45
-10	-10
10	10
25	25
40	40
55	55

c Sample-level evals

 **cfRNA**

3. Is cancer present?
Cancer detection from plasma cfRNA profiles

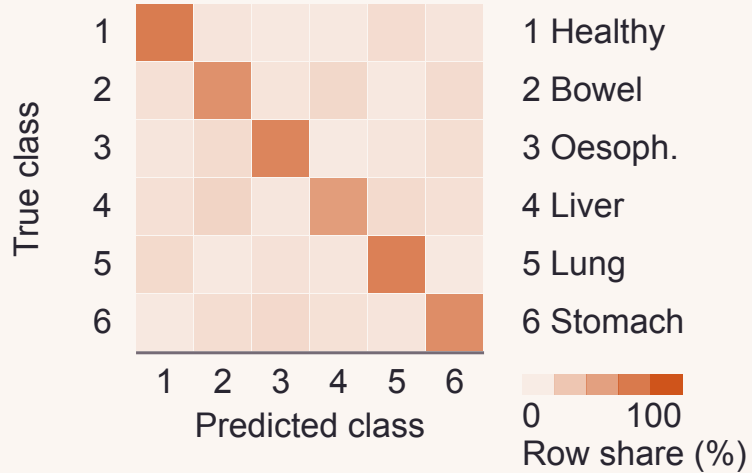
- **Input:** Plasma cfRNA counts matrix or read bag
- **Task:** Binary classification
- **Metrics:** AUROC, AUPRC, TPR, TNR, MCC, balanced accuracy



True class	Cancer probability (%)
Cancer	~45, ~75, ~85
Healthy	~10, ~25, ~55

4. Which cancer is present, if any?
Cancer type detection from plasma cfRNA profiles

- **Input:** Plasma cfRNA counts matrix or read bag
- **Task:** Multiclass classification
- **Metrics:** Macro F1, recall, AUROC, AUPRC; per-class recall



True class	1	2	3	4	5	6
1 Healthy	High	Low	Low	Low	Low	Low
2 Bowel	Low	High	Low	Low	Low	Low
3 Oesoph.	Low	Low	High	Low	Low	Low
4 Liver	Low	Low	Low	High	Low	Low
5 Lung	Low	Low	Low	Low	High	Low
6 Stomach	Low	Low	Low	Low	Low	High

d Sequence-level evals

 **qDA-seq**

5. How much chromatin became accessible?
Cumulative chromatin accessibility prediction

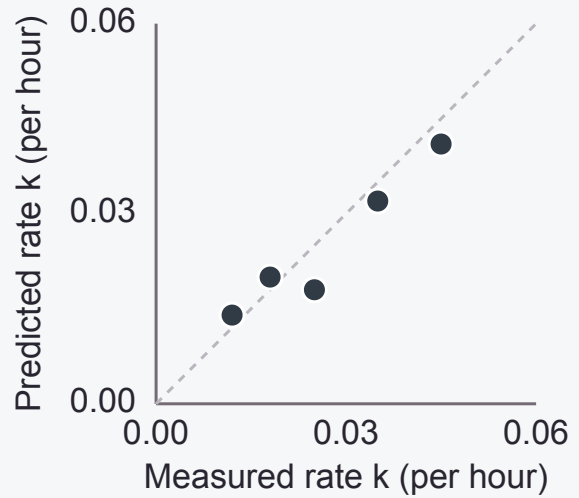
- **Input:** 100 bp GATC-centred DNA + exposure time
- **Task:** Bounded regression
- **Metrics:** RMSE, ρ , r , R^2



DNA site	Cumulative marked fraction (%)
Site 1	~25
Site 2	~45
Site 3	~70

6. How fast does marking build up?
Apparent chromatin marking rate prediction

- **Input:** 100 bp GATC-centred DNA; fixed cell line
- **Task:** Positive regression
- **Metrics:** ρ , RMSE, r , R^2



Measured rate k (per hour)	Predicted rate k (per hour)
0.01	0.01
0.02	0.02
0.03	0.03
0.04	0.04
0.05	0.05