



CVPR
JUNE 3-7, 2026

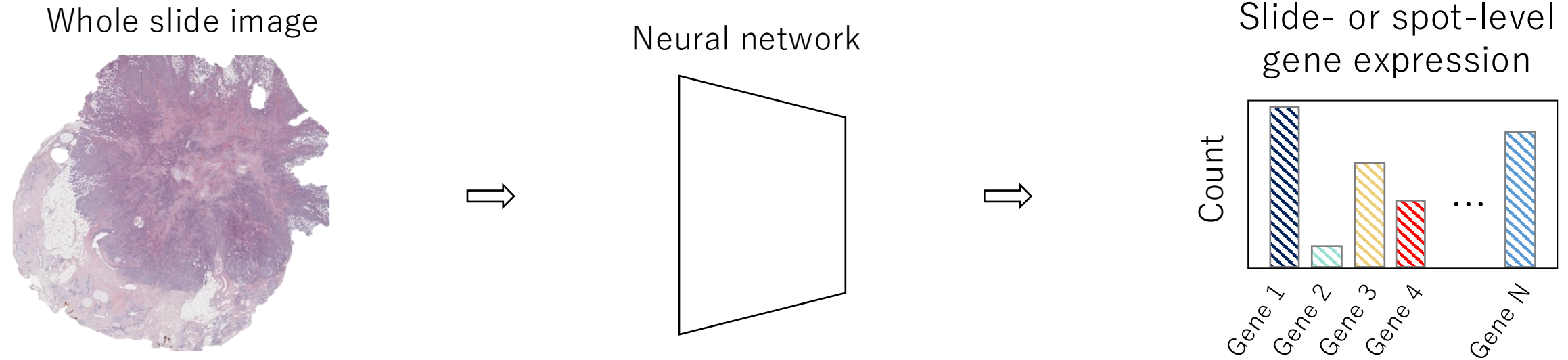


DENVER
COLORADO

Cell-Type Prototype-Informed Neural Network for Gene Expression Estimation from Pathology Images

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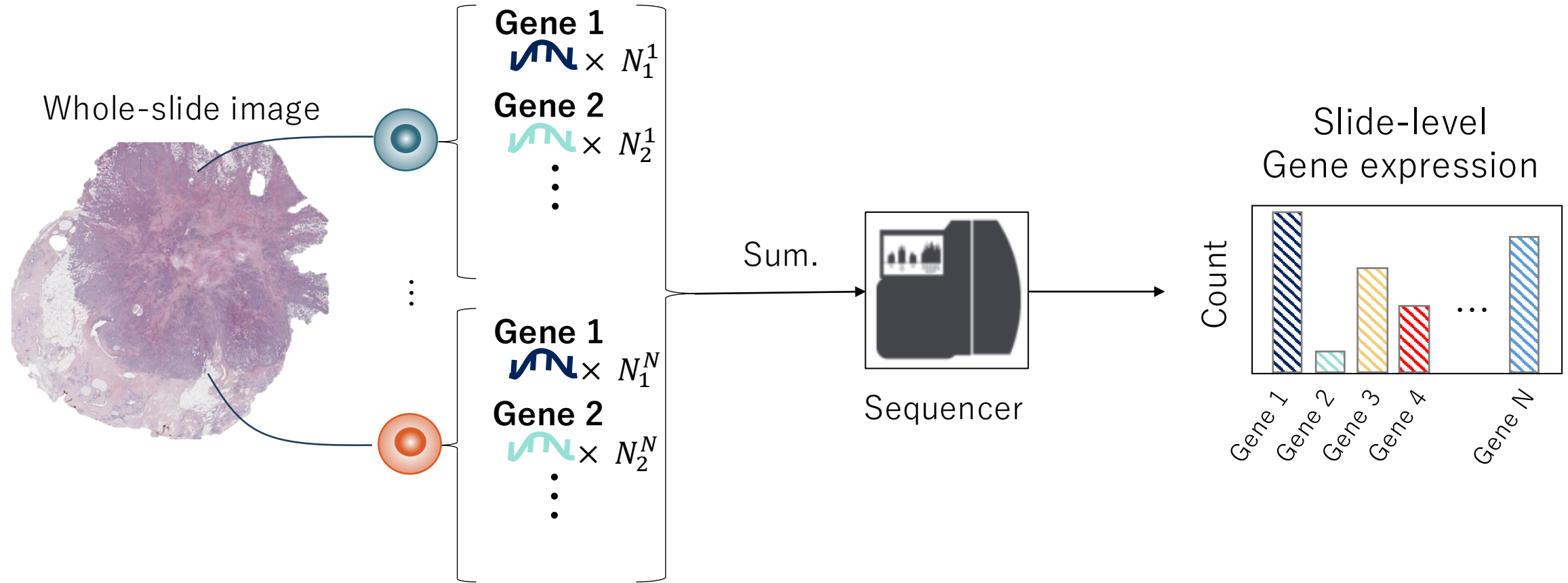
1: The University of Osaka, 2: Kyushu university,
3: National Cancer Center Japan

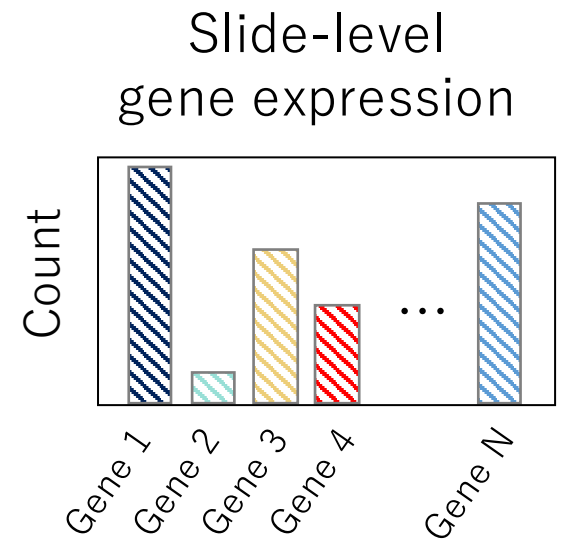
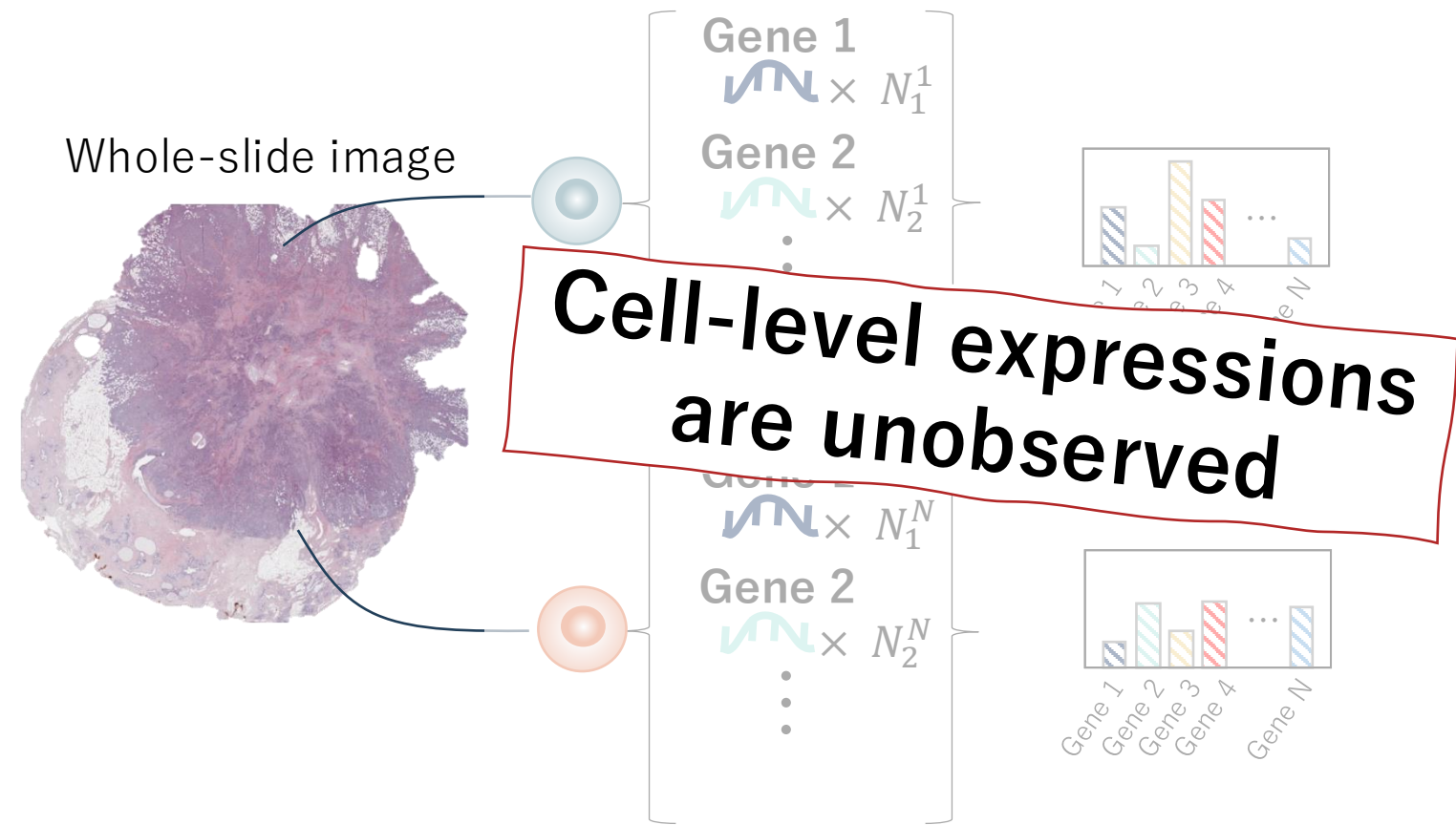


Expected:

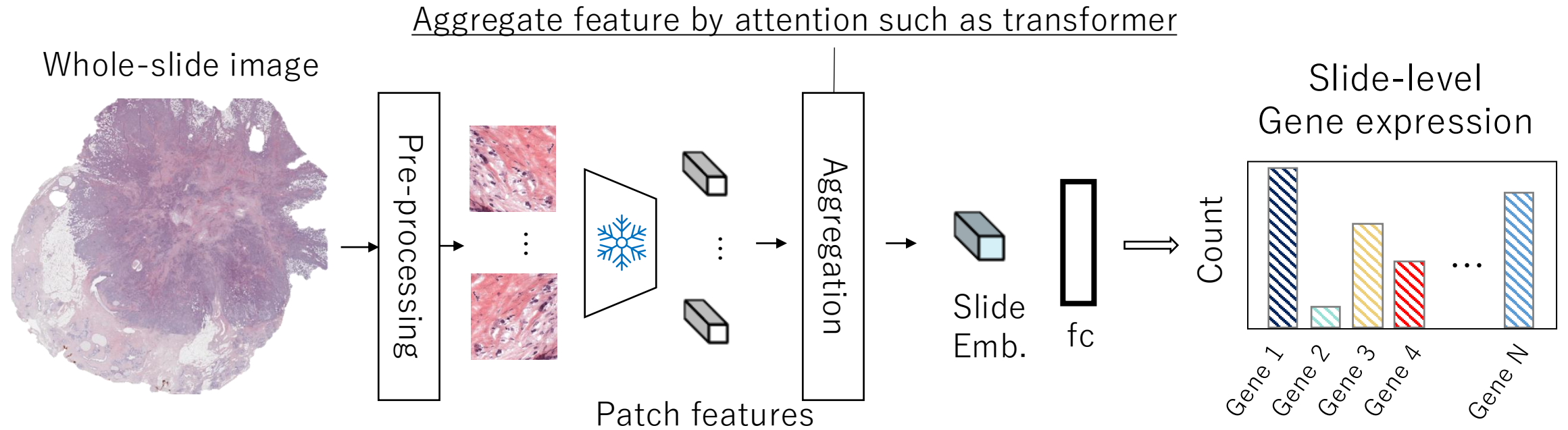
- ✓ Reduce sequencing cost of gene expression
- ✓ Improve subtype classification performance
- ✓ Morphological understanding

Express gene for the activity



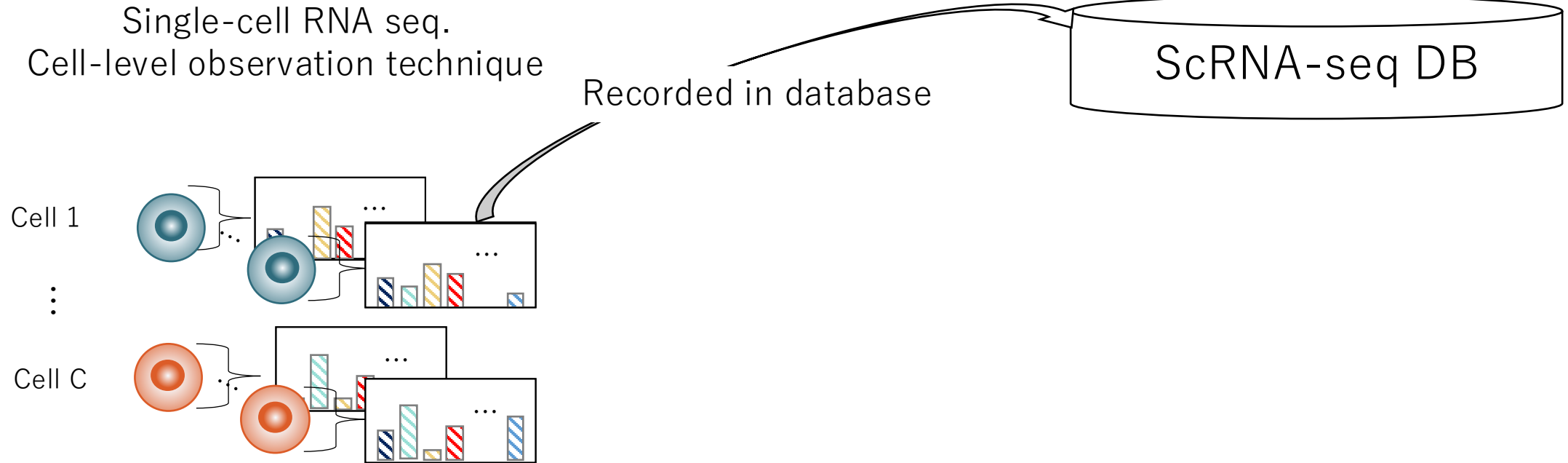


Gene expression estimation based on MIL



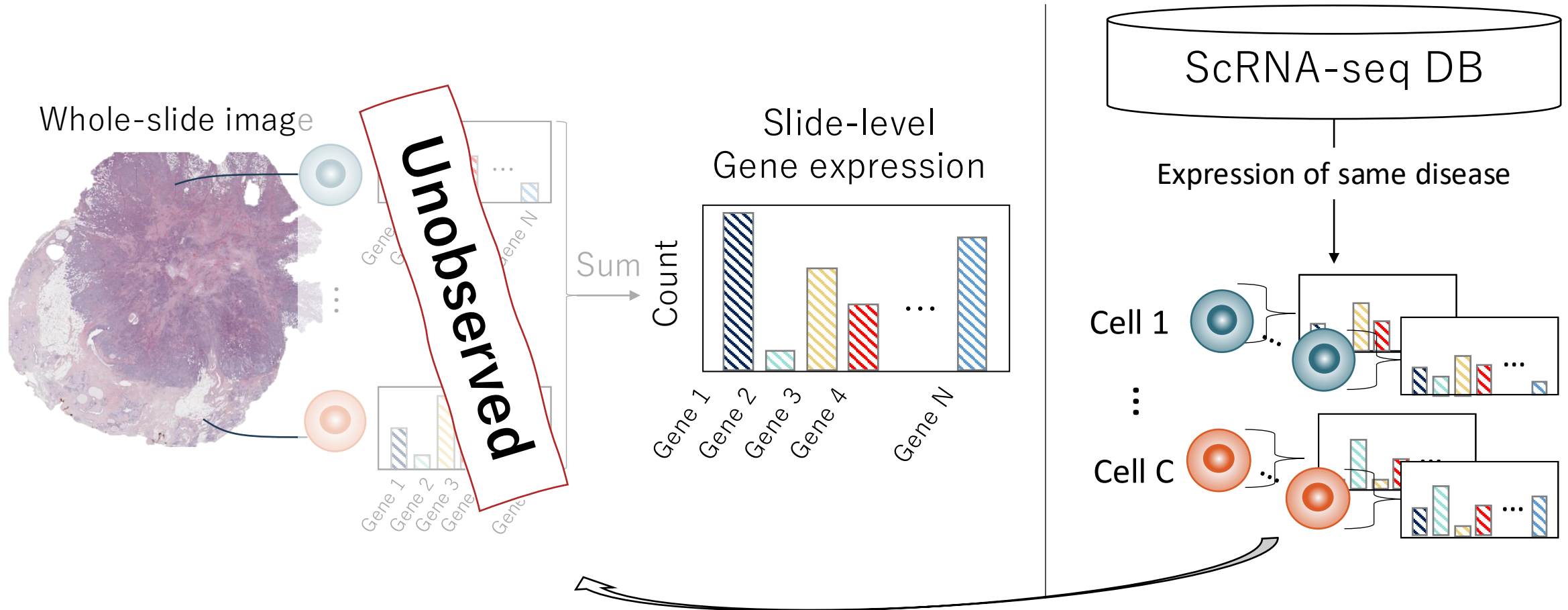
Never considered cell-level expression

Leverage cell-level gene expression database



No corresponds image
Noisy and biased

Retrieve cell-level expression from DB



- 1. No corresponds image
- 2. noisy and biased



Focus on the relation between slide and cell

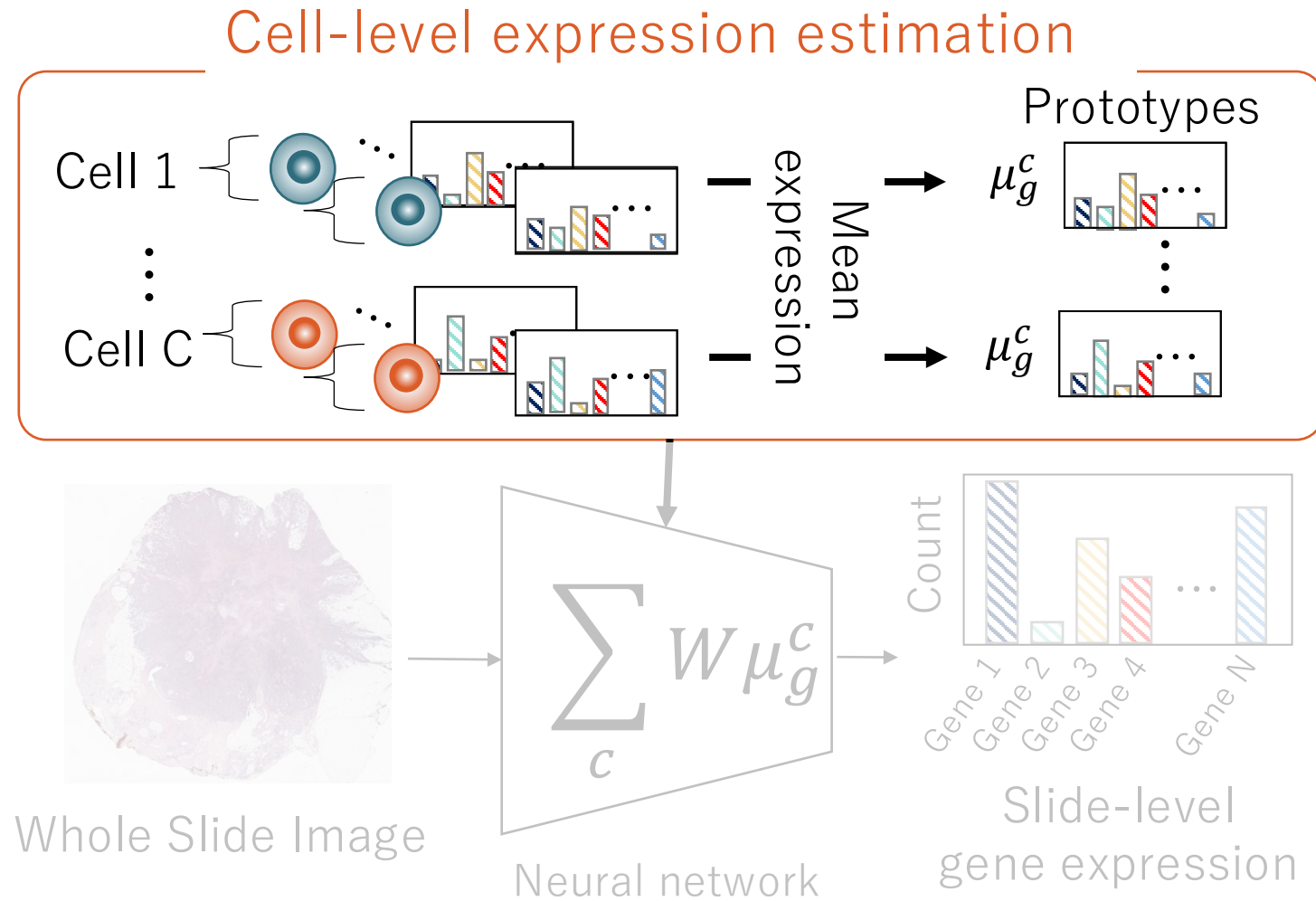
[Kleshchevnikov+, 2022]

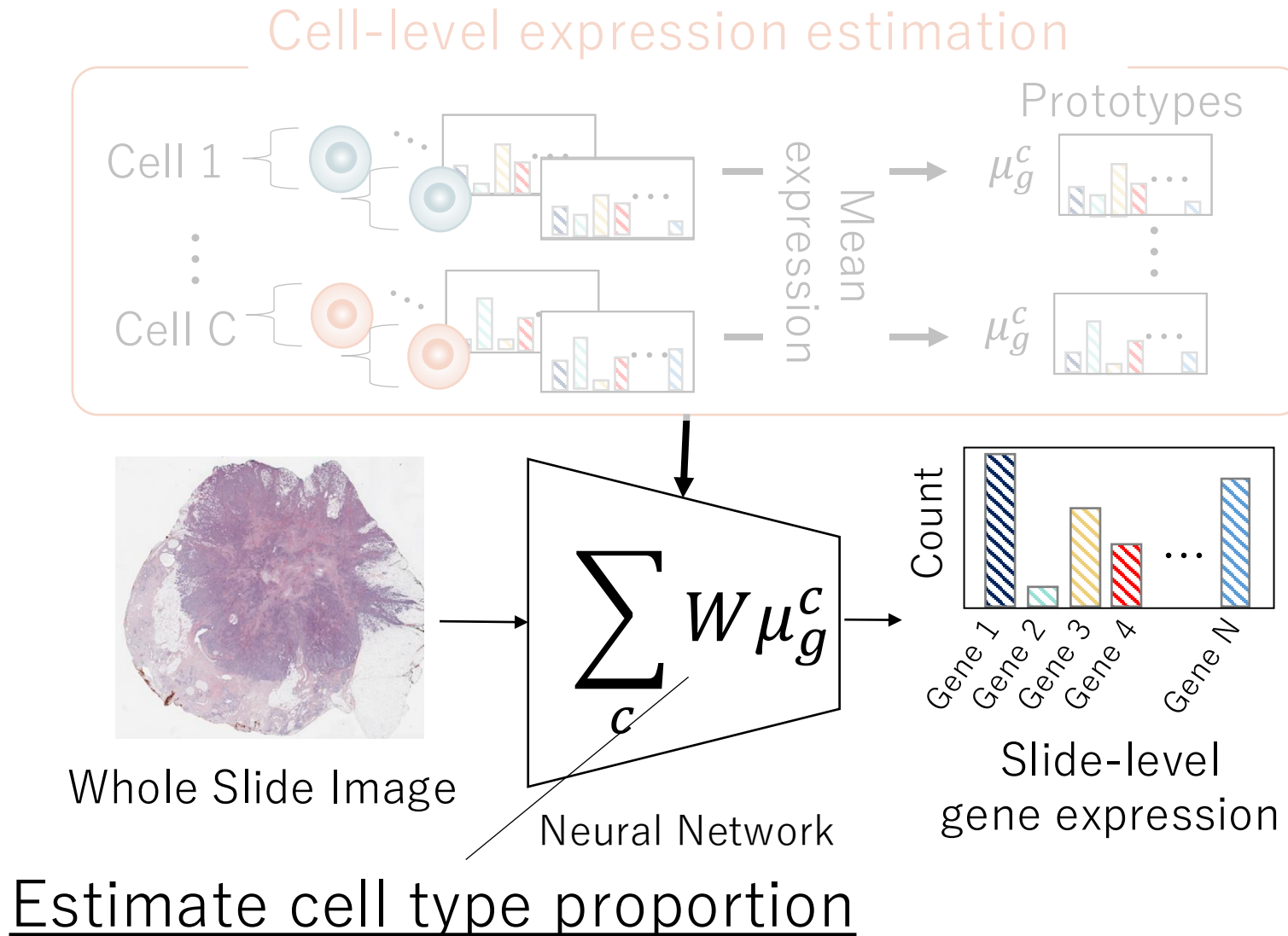
Target gene expression

Cell-level average expression

$$\mu_g^s = \sum_c W \mu_g^c$$

Cell proportion







Comparison with previous methods

		BRCA		KIRC		LUAD	
		PCC	SCC	PCC	SCC	PCC	SCC
MIL	Max [Wang+ 2018]	0.149	0.15	0.09	0.094	0.106	0.109
	Mean [Wang+ 2018]	0.216	0.22	0.191	0.201	0.239	0.247
	AbMIL [ILSE+ 2018]	0.306	0.308	0.233	0.234	0.251	0.261
	CLAM [Lu+ 2021]	0.278	0.280	0.192	0.200	0.172	0.180
	ILRA [Xiang+ 2023]	0.261	0.264	0.171	0.176	0.247	0.257
MIR	HE2RNA [Schmauch+ 2020]	0.274	0.271	0.212	0.228	0.278	0.29
	AbReg [Graziani+ 2022]	0.240	0.238	0.180	0.182	0.230	0.237
	tRNAformer [Alsaafin+ 2022]	0.299	0.299	0.269	0.264	0.305	0.317
	MOSBY [Senbabaoglu+ 2024]	0.304	0.302	0.188	0.196	0.250	0.253
	SEQUOIA [Pizurica+ 2024]	0.287	0.287	0.244	0.24	0.241	0.247
	Ours	0.315	0.324	0.297	0.296	0.302	0.334