AGMDT: Virtual Staining of Renal Histology Images with Adjacency-Guided Multi-Domain Transfer

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Problem Definition and Contribution

Goal: Generating multi-stained histological images utilizing correlations across adjacent slices on the basis of existing unpaired virtual staining methods.

Key Contributions:
- A novel **adjacency-guided multi-domain transfer framework (AGMDT)** to transfer renal histology images into multiple staining types.
- **Adaptive Pairing Module** and **Adjacency-guided Encoder** which can avoids pixel-level alignment and meanwhile utilize the correlations among adjacent tissue slices.
- **A renal histological dataset** where each case possesses all the four staining types: H&E, Masson, PASM, PAS that applied on serial slices of the same tissue.

Dataset

After the processing of the adaptive pairing module, we have successfully created a comprehensive renal histological dataset.
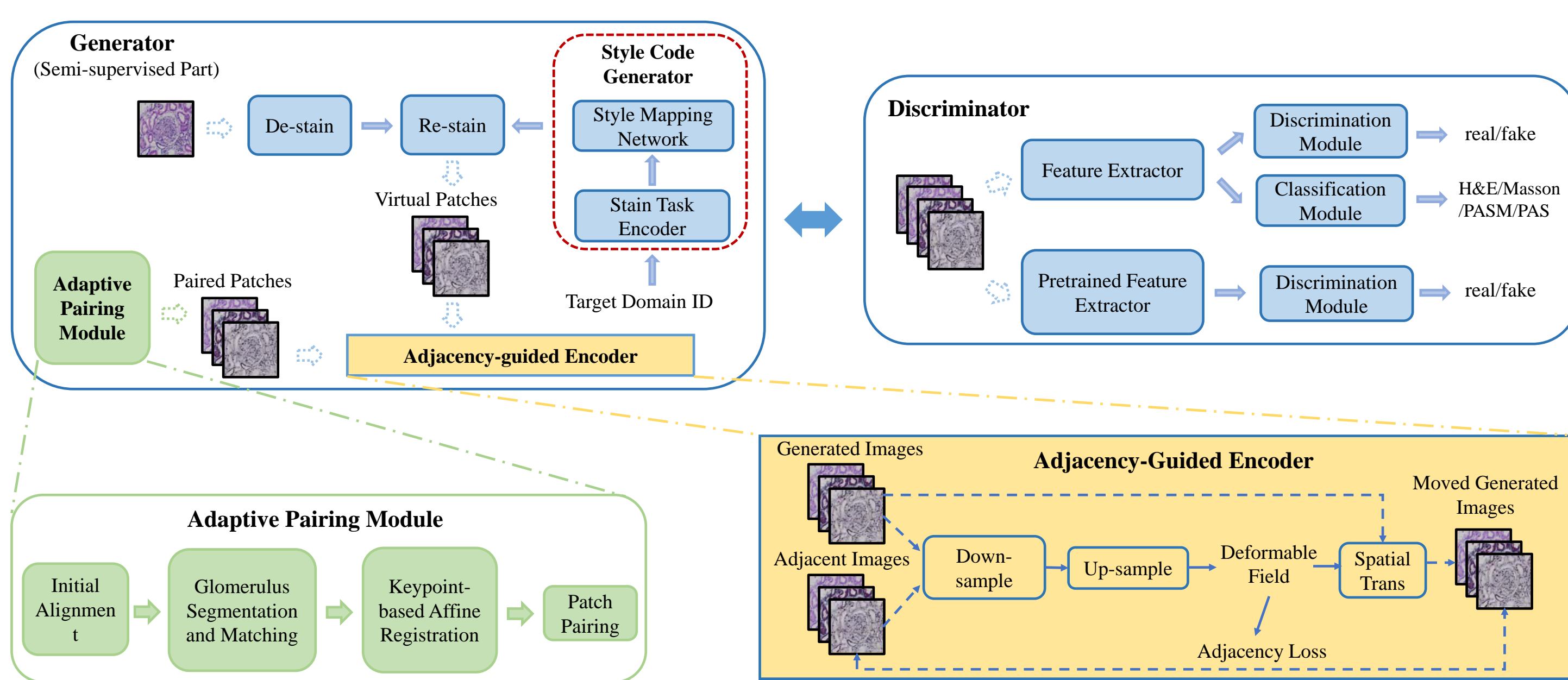
Details
- Obtained from serial slices stained with H&E, PAS, PASM, and Masson.
- 188 whole slide images from 22 patients with pathologists' WSI-level diagnoses.
- 32,413 pairs of patch-level aligned glomeruli.

Method

Overall Structure of AGMDT:

Adjacency-Guided Multi-Domain Transfer Framework

- AGMDT has two key components, respectively an adaptive pairing module and an adjacency-guided encoder.

Loss function:

$$\ell^G = \lambda_1 \times (\ell^G_{adv} + \ell^G_{cls} + \ell_{cyc} + \ell_{idt})$$
$$+ \lambda_2 \times (\ell^G_{\eta adv} + \ell^G_{\eta cls}) + \lambda_3 \times \ell_{adj} \qquad (1)$$

The generator's loss function consists of six components, including:
- adversarial loss ℓ^G_{adv}
- classification ℓ^G_{cls}
- auxiliary loss $\ell^G_{\eta adv}$, $\ell^G_{\eta cls}$
- cycle loss ℓ_{cyc}
- identity loss ℓ_{idt}
- adjacency-guided loss ℓ_{adj}, which measures the discrepancy between the generated data and its corresponding adjacency data.
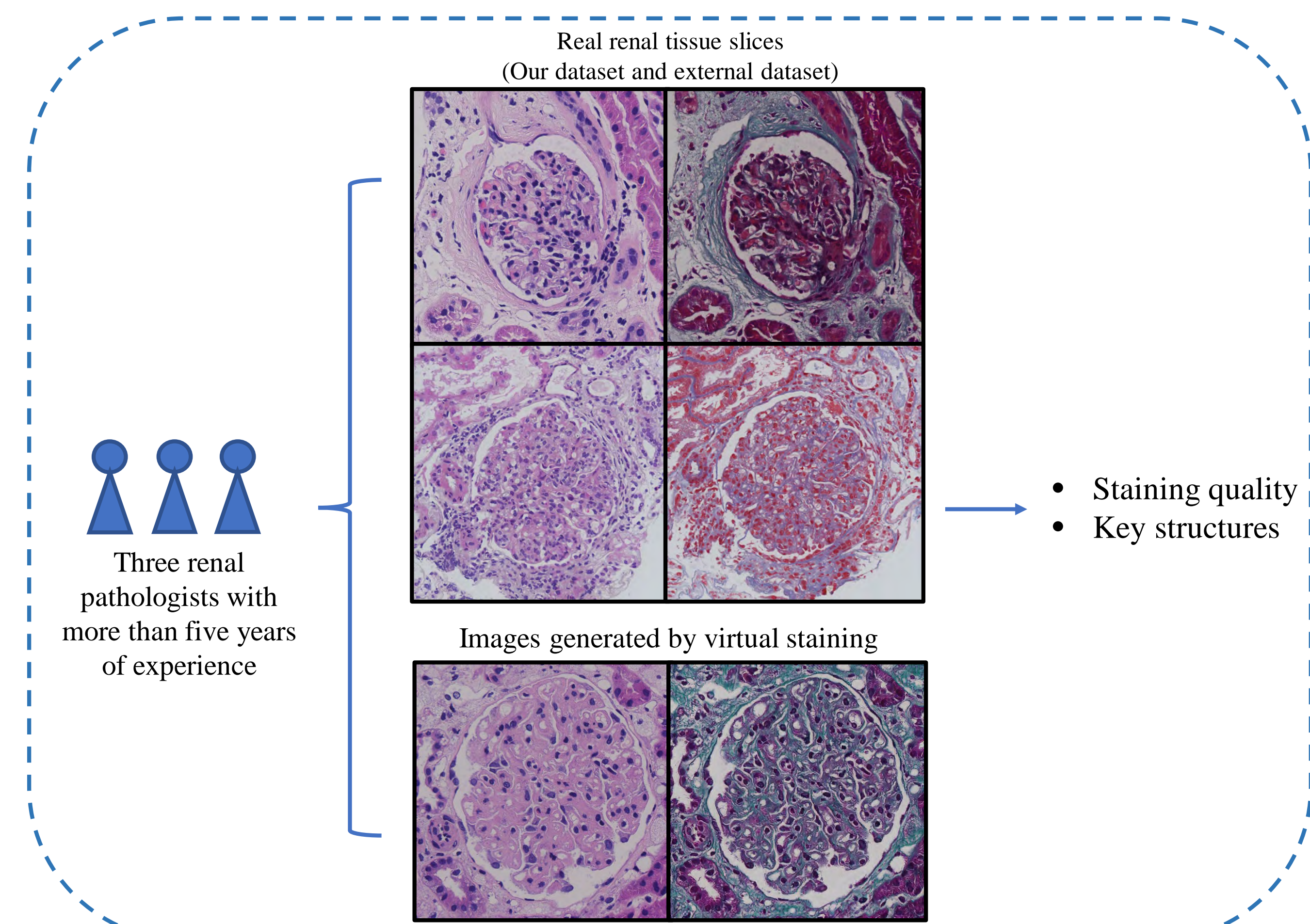
Experiments & Results

Blind Evaluation:

Real renal tissue slices (Our dataset and external dataset)

Images generated by virtual staining

Three renal pathologists with more than five years of experience

- Staining quality
- Key structures

Table 1: Comparison of different methods

Methods	H&E2MASS DISTS↓	H&E2MASS DBCNN↑	H&E2PASM DISTS↓	H&E2PASM DBCNN↑	H&E2PAS DISTS↓	H&E2PAS DBCNN↑
FUNIT[4]	0.2452	56.52	0.2496	54.01	0.2259	53.17
MUNIT[1]	0.3207	29.76	0.3037	32.67	0.2764	36.02
UGATIT[2]	0.2374	57.18	0.2467	55.64	0.2166	51.91
UMDST[3]	0.2064	53.44	0.2770	54.02	0.2162	51.90
Ours(w/o Adj)	0.2143	58.75	0.2468	60.61	0.1917	55.74
Ours (w Adj)	**0.2020**	**64.49**	**0.2453**	**66.23**	**0.1909**	**59.85**

Table 2: Blind Evaluation of staining results

	Masson	PASM	PAS
Real(our part)	4.25	**4.92**	4.33
Real(external part)	3.48	4.77	**4.46**
FUNIT[4]	0.69	1.42	2.25
MUNIT[1]	2.67	0.75	2.42
UGATIT[2]	2.67	3.67	3.08
UMDST[3]	4.10	4.09	4.17
AGMDT	**4.59**	4.17	4.25

The virtual staining results of AGMDT and baseline methods:

Ablation of Adjacency-guided Encoder: