## Supplementary Material

Xu Zhang<sup>1</sup>, Bo Ni<sup>2</sup>, Yang Yang<sup>3</sup> ( $\boxtimes$ ), and Lefei Zhang<sup>1</sup> ( $\boxtimes$ )

## 1 Detailed Description of the Dataset

For lung infection segmentation, text annotations primarily convey the presence of infection in both lungs, the number of lesion regions, and the approximate localization of infected areas. For example, a statement like "Bilateral pulmonary infection, two infected areas, upper left lung and upper right lung." indicates infection in both lungs with two distinct areas of infection in the upper left lung and upper right lung, respectively. Similarly, annotations in the MosMedData+ dataset provide comparable information to the QaTa-COV19 dataset, exhibiting a similar text structure. For instance, "Unilateral pulmonary infection, two infected areas, middle lower left lung." Detailed dataset information is presented in Table 1. For the polyp segmentation

Table 1. The division of QaTa-COV19 and MosMedData+

	QaTa-COV19	MosMedData+
Train set	5716	2183
		273
Test set	2113	273
Total	9258	2729

task, the datasets' detailed information is shown in Table 2. The annotations for it are relatively more complex. Some examples include: "One large, irregular, partially smooth polyp on the bottom center." "Two polyps. One small, elliptical, smooth polyp on the bottom right. One small, elliptical, smooth polyp on the top center."

## 2 Supplementary Ablation Study

We studied the effect of the number of MAdapters. Table 3 shows the results of using different numbers of MAdapter. The results indicate that selecting an appropriate number of MAdapters is beneficial for improving the outcomes.

<sup>&</sup>lt;sup>1</sup> School of Computer Science, Wuhan University, Wuhan, China zhanglefei@whu.edu.cn

<sup>&</sup>lt;sup>2</sup> Computer School, Hubei Polytechnic University, Huangshi, China Renmin Hospital, Wuhan University, Wuhan, China carlayangyang@whu.edu.cn

Table 2. The division of five polyp datasets

	ClinicDB	Kvasir	ColonDB	CVC-300	ETIS
Training	550	900	-	-	-
Testing	62	100	380	60	196
Total	612	1000	380	60	196

**Table 3.** Ablation studies of the number of MAdapters. We used different numbers (1–3) of MAdapters

			MosMedData+		ClinicDB	
	Dice	mIoU	Dice	mIoU	Dice	mIoU
1	89.04	80.24	77.14	62.78	94.13	88.91
2	89.28	80.63	77.80		94.85	
3	90.22	82.16	<b>78.62</b>	64.78	95.46	91.32

## 3 Evaluation Metrics

In this paper, two authoritative evaluation metrics for medical image segmentation are used to evaluate our method, including the dice coefficient (mDice), and the mean intersection over union (mIoU):

$$Dice = \frac{2 \times TP}{2 \times TP + FP + FN}$$
 
$$mIoU = \frac{TP}{TP + FP + FN}$$
 (1)

where TP represents true-positive, FP false-positive, and FN false-negative.