Fused 3-Stage Image Segmentation for Pleural Effusion Cell Clusters

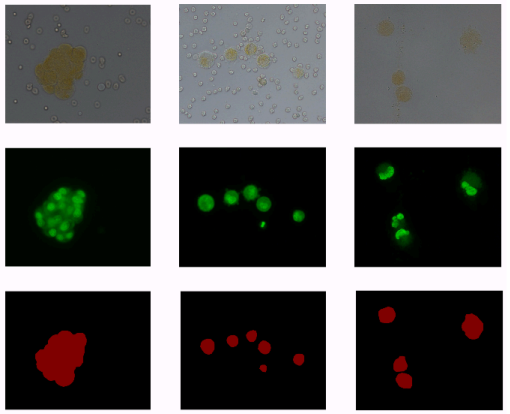
Sike Ma, Meng Zhao, Hao Wang, Fan Shi, Xuguo Sun, Shengyong Chen, Hong-Ning Dai
sike_ma@126.com,zh_m@tju.edu.cn, hawa@ntnu.no,
shifan@email.tjut.edu.cn,sunxuguo@tmu.edu.cn,sy@ieee.org,hndai@ieee.or

Problem

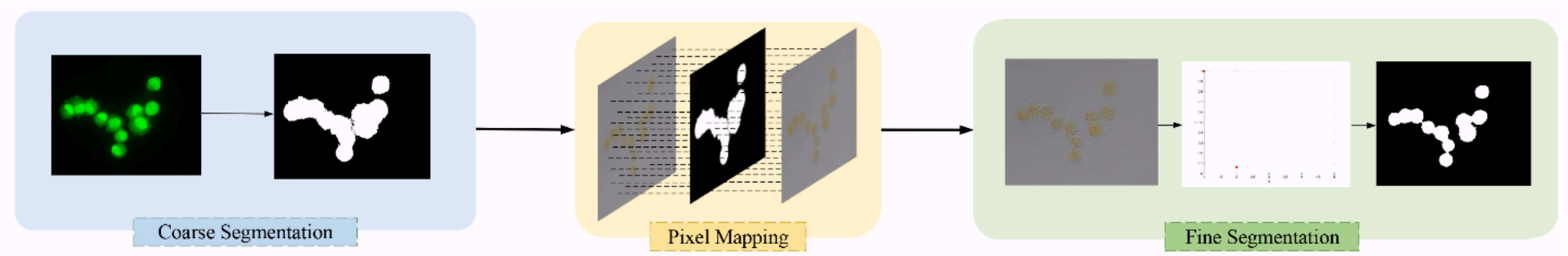
- A variety of cells in pleural effusion are easy to adhere together to form cell clusters.
- Cell segmentation is the basis of cell recognition and classification.
- Because of the uneven staining and fuzzy boundary, the segmentation of cell clusters becomes a difficult problem.

Contributions

- **Point 1** : The data acquisition and labelling of tumor cell clusters in pleural effusion are difficult.
  - We establish a dataset of cell clusters with ground truth, by collaborating with health professionals.



- **Point 2** : Existing cell recognition algorithms usually focus on the characteristics of individual cells, and tumor cell metastasis is more efficient than tumor cells when pleural effusion tumor cell clusters fall off into the blood. Tumor cell clusters suggest a worse prognosis.
  - We propose a fused segmentation algorithm CMF for cell clusters to obtain accurate segmentation boundaries.



Datasets

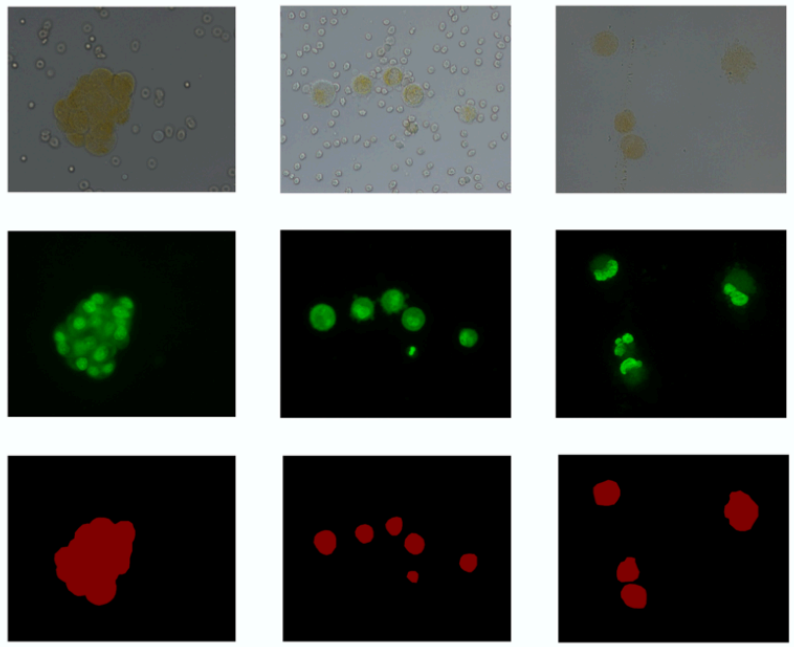


Fig 1. Tumor cell clusters pathology image samples and their corresponding fluorescent staining images and the ground-truth images.

- **The clinical group**：cases of pathological images obtained from the pleural effusion of lung cancer patients.
- **The simulation group**： mixing A549 cells and blood cells into a cell suspension to simulate the pleural effusion of clinical lung cancer patients.
- **The cancer cell group**：the sample that contains only A549 tumor cells.

CMF Algorithm

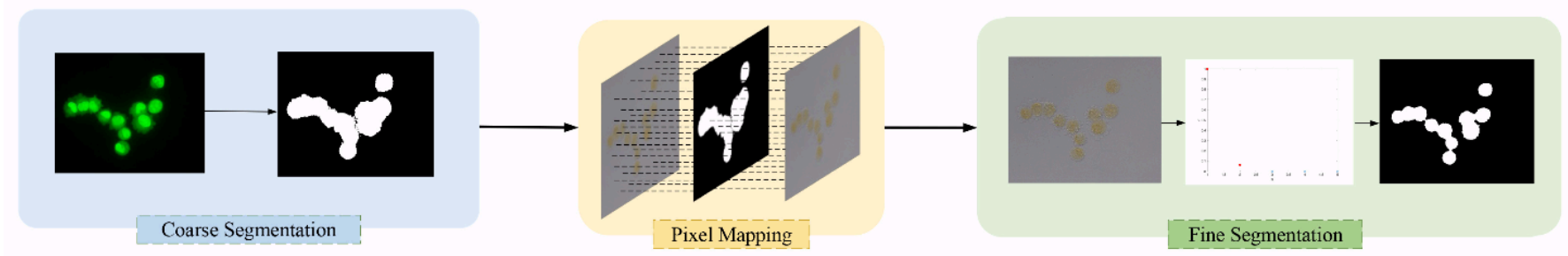


Fig. 2: Schematic overview of the proposed algorithm

- Coarse Segmentation — Threshold segmentation
- Pixel Mapping

$$O_{p(x,y)} = \begin{cases} 1 & p(x,y) \in F_r \\ 0 & p(x,y) \notin F_r \end{cases}$$

- Fine Segmentation
  - Multiscale morphological gradient reconstructio (MMGR-WT)
  - The density peak algorithm (DP)
  - A priori entropy-based fuzzy clustering algorithm (PEFC)

Results

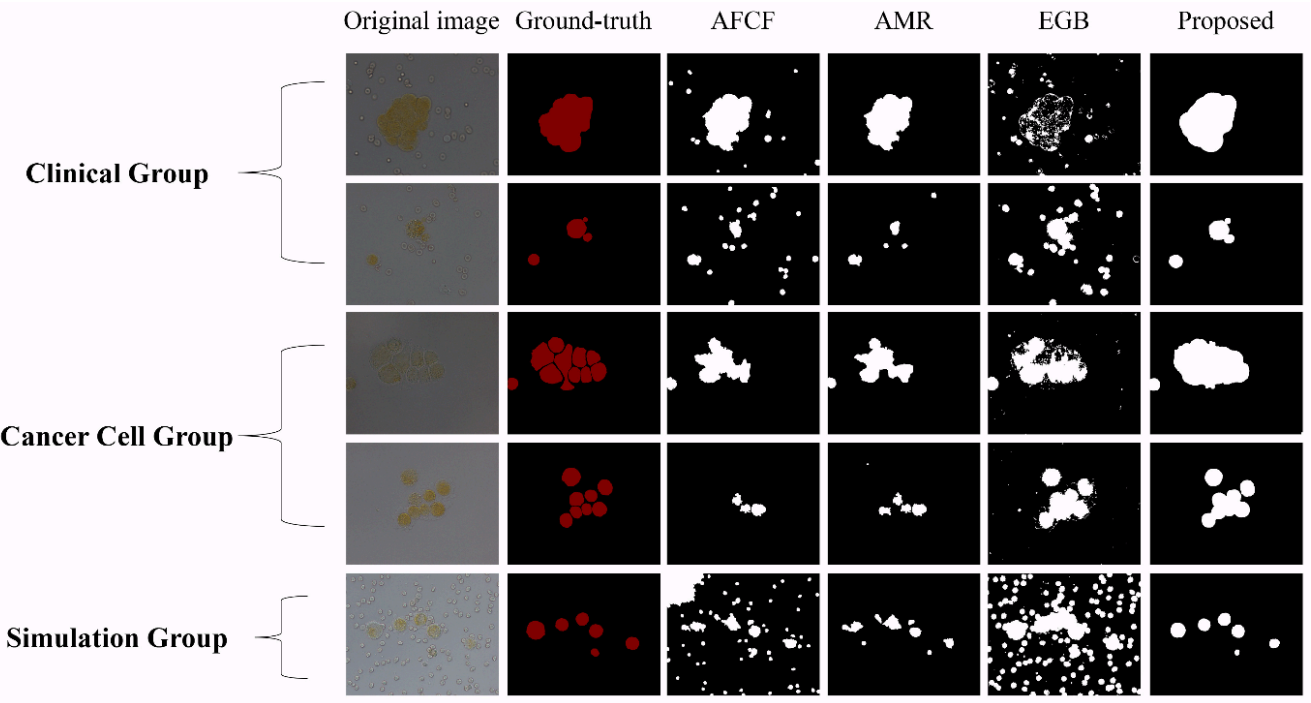


Fig. 3: Sample results obtained by applying AMR, EGB, AFCF and CMF algorithm to an image from the dataset

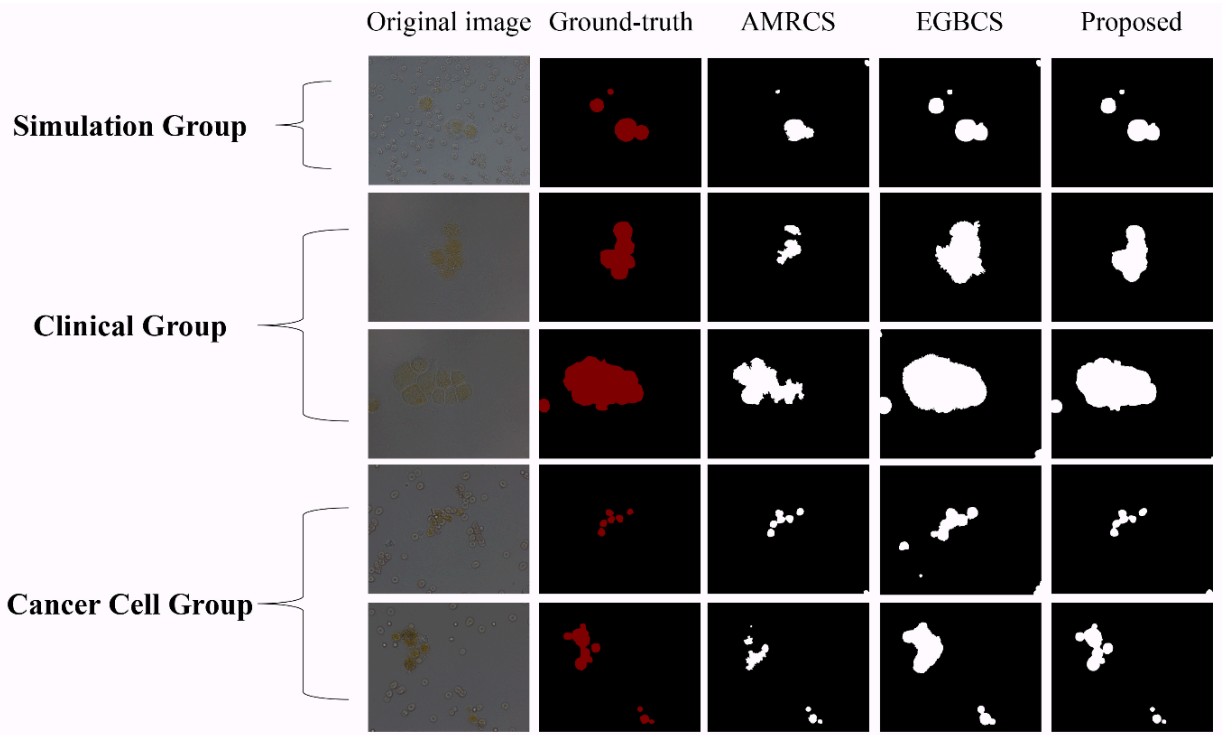


Fig. 4: Sample results obtained by applying AMRCS, EGBCS and CMF algorithm to an image from the dataset

Results

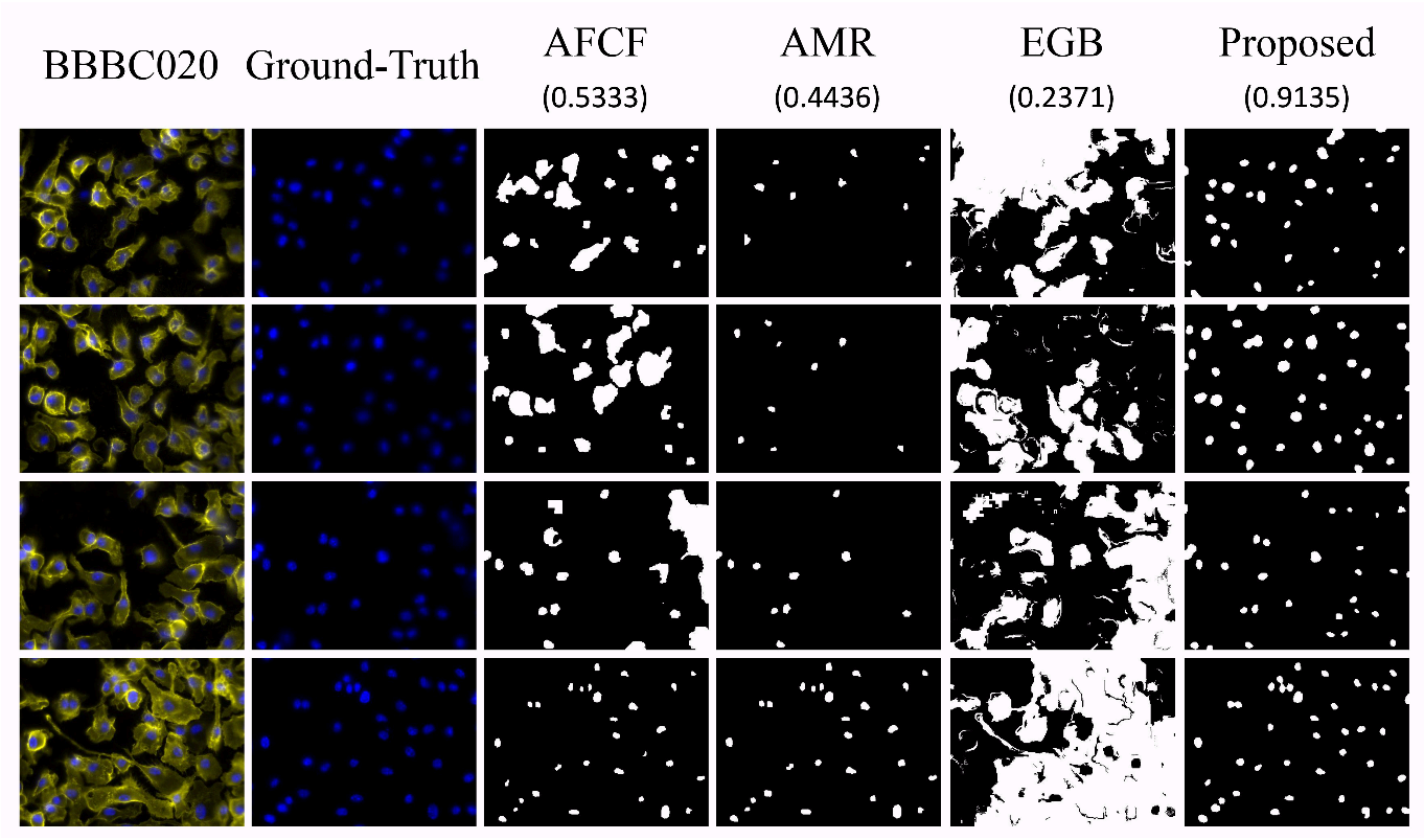


Fig. 5: Sample results obtained by applying AMRCS, EGBCS and CMF algorithm to an image from BBBC020. The Dice coefficient is shown in brackets

Results

TABLE I: Comparison of all algorithms in the segmentation performance on cell cluster dataset

Group	Method	Dice	Jaccard	F1-score
The Simulation Group (50 sets)	AMR	0.4613	0.3057	0.4691
	EGB	0.5352	0.4028	0.6271
	AFCF	0.4478	0.3308	0.4642
	AMRCS	0.6388	0.4845	0.6693
	EGBCS	0.8175	0.7082	0.8385
	CMF	**0.8845**	**0.7957**	**0.8886**
The Cancer Cell Group (35 sets)	AMR	0.5015	0.3480	0.5081
	EGB	0.6140	0.4871	0.6958
	AFCF	0.5163	0.3688	0.5558
	AMRCS	0.6079	0.4568	0.6281
	EGBCS	0.8169	0.6918	0.8179
	CMF	**0.9250**	**0.8611**	**0.9263**
The Clinical Group (22 sets)	AMR	0.5394	0.3918	0.5503
	EGB	0.5494	0.4155	0.6338
	AFCF	0.6383	0.5154	0.6458
	AMRCS	0.7227	0.5952	0.7296
	EGBCS	0.7848	0.6689	0.8020
	CMF	**0.8961**	**0.8148**	**0.8972**

Plans

- Combine deep learning methods such as U-net to separate the overlapping cells from the unstained pleural effusion cell clusters.
- Identify the normal cells and tumour cells, so as to determine the cancer severity of the patient.

Thanks for watching！