



LGPMA: Complicated Table Structure Recognition with Local and Global Pyramid Mask Alignment

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CONTENT



1. Background

* Table Recognition

Targeted HTML code (output)

Table image (input)

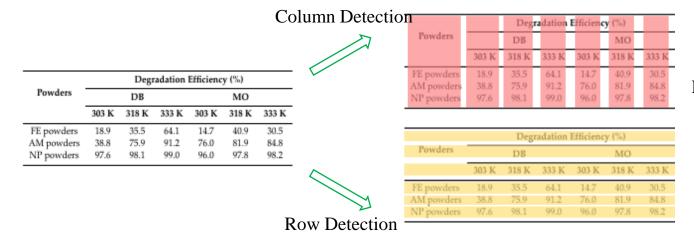
Do	\mathbf{g}	\mathbf{Cat}^a	
Woof	Arf	Meow	,

```
<html>
<body>
 <thead>
    <b>Dog</b>
    <b>Cat </b> <sup>a </sup> 
   </thead>
  Woof
    Arf
    Meow
   </body>
</html>
```

*** Table Structure Recognition**

- Global-object-based methods
- Local-object-based methods

* Previous Method——Global-object-based



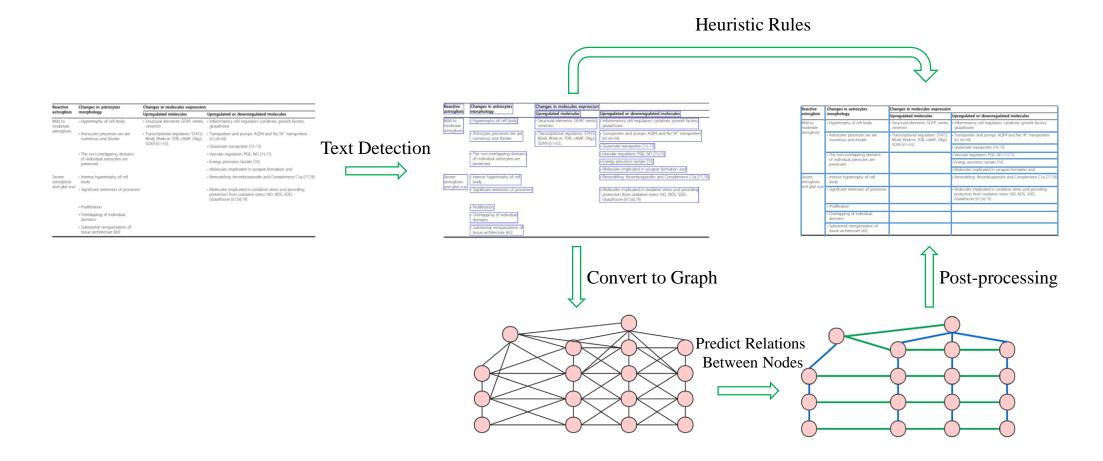
Heuristic Rules

		Degr	adation	Efficiency (%)				
Powders		DB		MO				
	303 K	318 K	333 K	303 K	318 K	333 K		
FE powders	18.9	35.5	64.1	14.7	40.9	30.5		
AM powders	38.8	75.9	91.2	76.0	81.9	84.8		
NP powders	97.6	98.1	99.0	96.0	97.8	98.2		

Problem of global-object-based methods:

- Lack of grid boundaries
- Cells spanning multiple rows/columns

*** Previous Method——Local-object-based**



Problem of local-object-based methods:

- Rules have limitations
- Empty cell ambiguity

2. Method

※ Insight

Reactive	Changes in astrocytes	Changes in molecules expression		
astrogliois	morphology	Upregulated molecules	Upregulated or downregulated molecules	
noderate	· Hypertrophy of cell body	 Structural elements: GFAP, nestin, vimentin 	 Inflammatory cell regulators: cytokines, growth factors, glutathione 	
	 Astrocytes processes are are numerous and thicker 	NFxB, Rheb-m TOR, cAMP, Olig2,	 Transporters and pumps: AQP4 and Na*/K* transporters [61,06-66] 	
		S2X9 [61-65].	Glutamate transporter [70-73]	
	The non-overlapping domains		Vascular regulators: PGE, NO [74,75]	
	of individual astrocytes are preserved		Energy provision: lactate [76]	
	proteins		Molecules implicated in synapse formation and	 Detection Algori
estroglosis	Intense hypertrophy of cell body		Remodeling: thrombospondin and Complement C1q [77,71]	Detection Algori
and glial scar	Significant extension of processes		 Molecules implicated in oxidative stress and providing protection from oxidative stress: NO, NOS, SOO, Gutathione [67,68,79] 	
	- Proliferation			
	 Overlapping of individual domains 			
	Substantial reorganization of tissue architecture [60]			

Image of Table

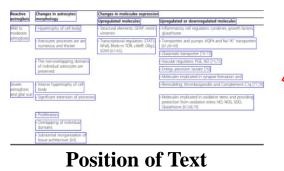
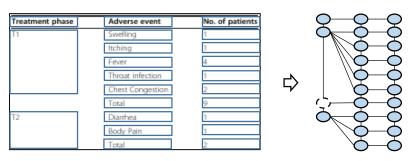


Table Structure

Reactive	Changes in astrocytes	Changes in molecules expression						
astrogliois	morphology	Upregulated molecules	Upregulated or downregulated molecules					
Mild to moderate	Hypertrophy of cell body	 Structural elements: GFAP, nestin, vimentin 	 Inflammatory cell regulators: cytokines, growth factors, glutathione 					
astrogliosis	 Astrocytes processes are are numerous and thicker 	 Transcriptional regulators: STAT3, NFx8, Rheb-m TOR, cAMP, Olig2, 	 Transporters and pumps: AQP4 and Na*/K* transporters [61,66-69] 					
		SOX9 [61-65].	Glutamate transporter [70-73]					
	The non-overlapping domains		Vascular regulators: PGE, NO [74,75]					
	of individual astrocytes are preserved		Energy provision: lactate [76]					
			Molecules implicated in synapse formation and					
Severe astrogliosis	Intense hypertrophy of cell body		- Remodeling: thrombospondin and Complement C1q [77,78]					
and glial scar	Significant extension of processes		Molecules implicated in oxidative stress and providing protection from oxidative stress: NO, NOS, SOO, Glutathione [67,68,79]					
	- Proliferation							
	Overlapping of individual domains							
	Substantial reorganization of tissue architecture [60]							

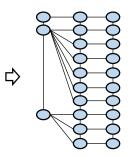
Position of Aligned Cell





Treatment phase	Adverse event	No. of patients
T1	Swelling	1
	Itching	1
	Fever	4
	Throat infection	1
	Chest Congestion	2
	Total	9
T2	Diarrhea	1
	Body Pain	1
	Total	2

(b)



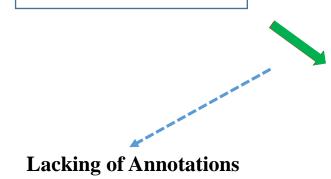
(a)

No Visible Boundaries

Table Structure



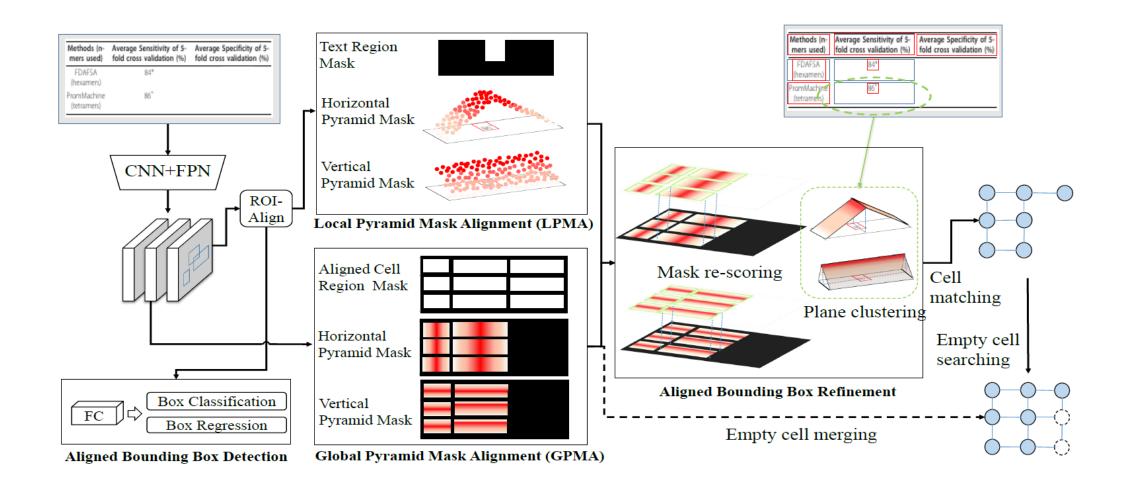
Image of Table



LGPMA

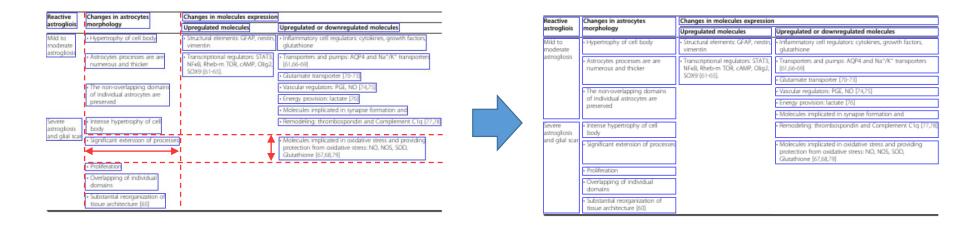
Position of Aligned Cell

※ Workflow of LGPMA



* Aligned Bounding Box Detection

• Ground Truth of aligned bounding boxes for non-empty cell



Method to approximate real cell regions

* Local Pyramid Mask Alignment

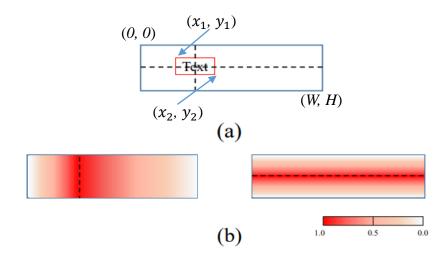
- Binary mask of text region
- Pyramid mask in horizontal
- Pyramid mask in vertical

For pixel (h, w), pyramid masks formed as

$$t_h^{(w,h)} = \begin{cases} w/x_1 & w \le x_{mid} \\ \frac{W-w}{W-x_2} & w > x_{mid} \end{cases}, \quad t_v^{(w,h)} = \begin{cases} h/y_1 & h \le y_{mid} \\ \frac{H-h}{H-y_2} & h > y_{mid} \end{cases},$$

※ Global Pyramid Mask Alignment

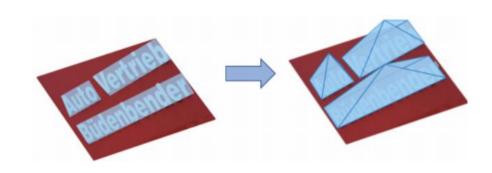
- Binary mask of all aligned cells (including empty cell)
- Pyramid mask of all non-empty cells in horizontal
- Pyramid mask of all non-empty cells in vertical



(a) aligned cell box (blue) and text region box (red).

(b) pyramid mask labels in horizontal and vertical

(1)



PMTD: Pyramid Mask Text Detector, 2019

Aligned Bounding Box Refine

Re-scoring strategy to compromise local and global pyramid mask

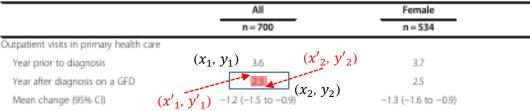
Female n = 534

Local pyramid masks

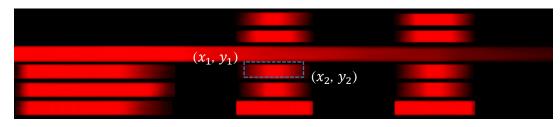
Final pyramid mask of (x, y) can be re-scored as:

$$F(x) = \begin{cases} \frac{x - x_1}{x_{mid} - x_1} F_{hor}^{(L)}(x, y) + \frac{x_{mid} - x_1}{x_{mid} - x_1} F_{hor}^{(G)}(x, y) & x_1 \le x \le x_{mid} \\ \frac{x - x_2}{x_{mid} - x_2} F_{hor}^{(L)}(x, y) + \frac{x_{mid} - x_2}{x_{mid} - x_2} F_{hor}^{(G)}(x, y) & x_{mid} < x \le x_2 \end{cases},$$

$$F(y) = \begin{cases} \frac{y - y_1}{y_{mid} - y_1} F_{ver}^{(L)}(x, y) + \frac{y_{mid} - y}{y_{mid} - y_1} F_{ver}^{(G)}(x, y) & y_1 \le y \le y_{mid} \\ \frac{y - y_2}{y_{mid} - y_2} F_{ver}^{(L)}(x, y) + \frac{y_{mid} - y}{y_{mid} - y_2} F_{ver}^{(G)}(x, y) & y_{mid} < y \le y_2 \end{cases},$$



Original bounding box of cell and mask of text

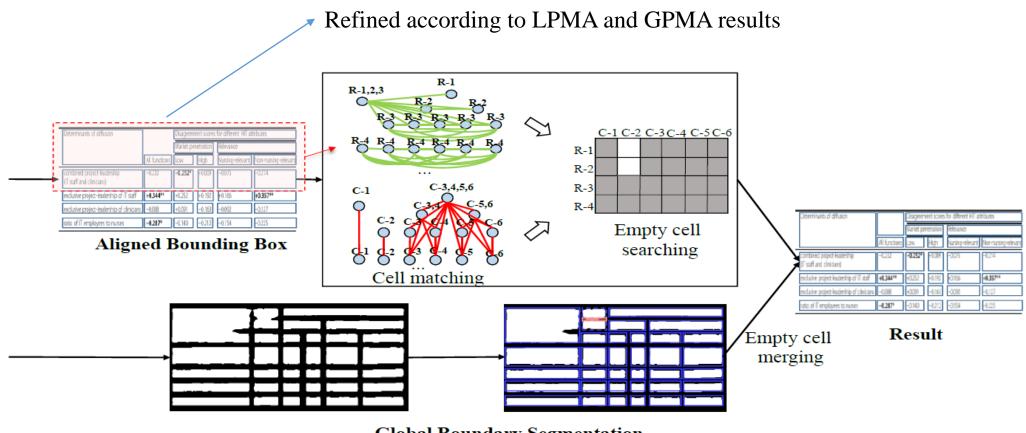


Global pyramid masks

• Final horizontal and vertical pyramid mask can fit two planes respectively.

The four planes' intersection lines with the zero plane are the refined boundaries

Table Structure Recovery Pipeline



Global Boundary Segmentation

3. Experiment

*** Implement Details:**

- Backbone: ResNet-50 + FPN
- 4 x feature map
- Pre-trained model of ImageNet
- Anchor ratios: 1/20, 1/10, 1/5, 1/2, 1, 2
- Pytorch, 8 32GB-Tesla-V100 GPUs
- Data augmentations: mutli-scale training
- Single scale testing

*** Visualization Results:**

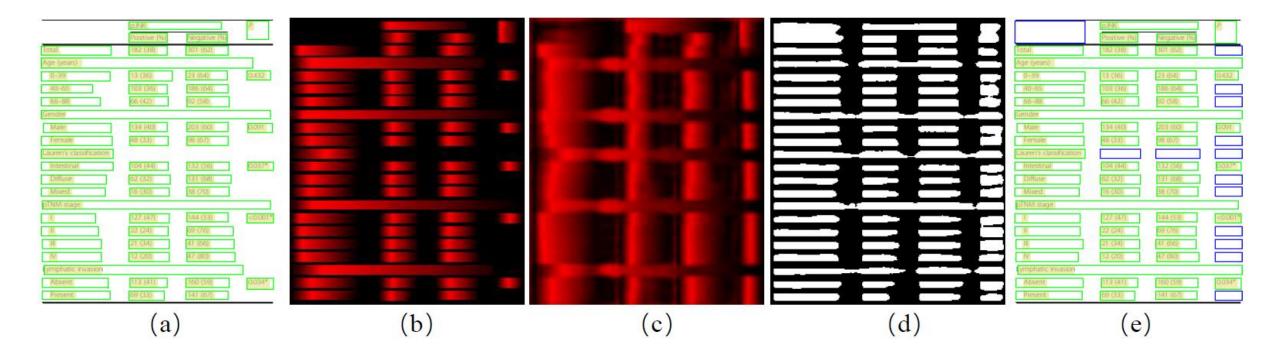
	THRESHOLD FOR RELEASES
	to air to water to land kg/year kg/year
1,2,3,4,5,6- hexachlorocyclohexane (HCH)	10 1 1
Alachlor	1 1
Aldrin	1 1 1
Atrazine	1 1
Chlordane	1 1 1
Chlordecone	1 1 1
Chlorfervinghos	1 1
Chlorpyrifos	1 1
DDT	1 1
Diuron	1 1
Endosulphan	1 1
Endrin	1 1
Heptachlor	
Isodrin	
Isoproturon	1 1
Lindane	
Mirex	
Simazine	
Toxaphene	
Tributylin and compounds	1 1
Trifluralin	1 1
Triphenyltin and compounds	1 1

Senmatic labels \rightarrow Cityscapes imags									
	PSNR(dB)	SSIM	UQI	VIE					
pix2pix-cGAN	15.74	0.4275	0.07315	0.05208					
PAN	16.06	0.4820	0.1116	0.06581					
	Edge	$s \rightarrow Shoes$							
PSNR(dB) SSIM UQI VIF									
ID-cGAN	20.07	0.7504	0.2724	0.2268					
PAN	19.51	0.7816	0.3442	0.2393					
	Edges -	→ Handbags							
	PSNR(dB)	SSIM	UQI	VIE					
ID-cGAN	16.50	0.6307	0.3978	0.1723					
PAN	15.90	0.6570	0.4042	0.1841					
Ci	tyscapes imag	es o Seman	tic labels						
	PSNR(dB)	SSIM	UQI	VIE					
ID-cGAN	19.46	0.7270	0.1555	□0.1180□					
PAN	20.67	0.7725	0.1732	0.1638					
	Aerial ph	iotos $ ightarrow$ Maj	ps						
	PSNR(dB)	SSIM	UQI	VIE					
ID-cGAN	26.10	0.6465	0.09125	0.02913					
PAN	28.32	0.7520	0.3372	0.1617					

	CM	SC.	P value
	(n=18)	(n=156)	
Operation time (min)			
Mean	129±34	108±48	0.084
Range	63-190	50-375	
Amount of bleeding (mL)			
Mean	146.7±185.2	79.7±236.4	0.247
Range	0-675	0-1970	
Success rate of			< 0 001
intraoperative cholangiography			
Possible	9	145	
Not possible	9		
Site of proximal bile duct stump			< 0 001
Cystic duct	11:	148	
Neck of gallbladder	7	8	
Methodology of treatment		П	
for bile duct stump			
Clip	6	131	< 0.001
Endoloop	1	2	
Ligation	4	7	
Suture	3	6	
Bastic yam (for transcystic drainage)	2	10	
None	2	0	
Conversion rate (%)	6/17(35.3)	7/146(4.8)	< 0.001

	URS+	URS-	P-value
	Mean±SD/ (N,96) 3,079 (\$3.9)	Mean±SD/ (N,%) 2,634 (46.1)	_
Conde	3/07/3 (33/9)	2(034 (40.1)	
Gender Male (N, 96)	1,346 (43.72%)	1,126 (42.75%)	0.462
Fernale (N, %)	1,733 (56.28%)	1,508 (57.25%)	COMEC
Age (Wean±SD)	67.79 (±10.68)	67.63 (±11.15)	Professional Control
	OV.79 (±10.08)	07.03 (±11.15)	0.599
Age (N,%)	1,092 (35.47%)	000 000 000	0.401
<65 years	1,150 (37.35%)	952 (36.14%) 944 (35.84%)	0.491
65-74 years			<u> </u>
>74 years	837 (27.18%)	738 (28.02%)	
CCI score (N,96)		Name of the Owner, which is not a second	0.000.0000
gi .	272 (8.83%)	341 (12.95%)	<0.00
1	217 (7.05%)	245 (9.30%)	
≦2	2,590 (84.12%)	2,048 (77.75%)	
Comorbidity			_
Hypertension			_
No	1,443 (46.87%)	1,300 (49.35%)	0.061
Yes	1,636 (53.13%)	1,334 (50.65%)	
Hyperlipidemia			
No	2,371 (77.01%)	2,138 (81.17%)	< 0.001
Yes	708 (22.99%)	496 (18.83%)	
Diabetes			4
No	2,345 (76.16%)	2,054 (77.98%)	0.103
Yes	734 (23.84%)	580 (22.02%)	\vdash
ESRD			
No	2,490 (80.87%)	2,072 (78.66%)	0.038
Yes	589 (19.13%)	562 (21.34%)	

※ Visualization Results:



*** Performance Evaluation:**

Methods	Training	ICI	DAR 2	013		SciTSR	L	SciT	SR-CO	OMP
Methods	Dataset	P	R	F1	P	R	F1	P	R	F1
DeepDeSRT 30	-	0.959	0.874	0.914	0.906	0.887	0.890	0.863	0.831	0.846
Split [33]	Private	0.869	0.866	0.868	-	-	-	-	-	-
DeepTabStR 31	ICDAR 2013	0.931	0.930	0.930	-	-	-	-	-	-
Siddiqui et al. [32]	Synthetic 500k	0.934	0.934	0.934	-	-	-	-	-	-
ReS2TIM [36]	ICDAR 2013†	0.734	0.747	0.740	-	-	-	-	-	-
GTE [38]	ICDAR 2013†	0.944	0.927	0.935	-	-	-	-	-	-
GraphTSR 2	SciTSR	0.885	0.860	0.872	0.959	0.948	0.953	0.964	0.945	0.955
TabStruct-Net [26]	SciTSR	0.915	0.897	0.906	0.927	0.913	0.920	0.909	0.882	0.895
LGPMA	SciTSR	0.930	0.977	0.953	0.982	0.993	0.988	0.973	0.987	0.980
LGPMA	ICDAR 2013†	0.967	0.991	0.979	-	-	-	-	-	-

Table 1: Results on ICDAR 2013, SciTSR, SciTSR-COMP datasets

Methods	Training	Tesing	TEDS	TEDS-Struc.
	Dataset		· /	(All)
EDD [39]	PTN-train	PTN-val	88.3	-
TabStruct-Net [26]	SciTSR	PTN-val	90.1	-
GTE [38]	PTN-train	PTN-val	93.0	-
LGPMA (ours)	PTN-train	PTN-val	94.6	96.7

Table 2: Results on PubTabNet

ℜ Ablation Summary:

Table 3: Ablation experiments on modules effect the aligned bounding box detection

Models		Modules	S	Det of	text re	gions	Det of aligned b	f non-en oounding		TEDS- Struc.
	LPMA	GPMA	AL[26]	Precision	Recall	Hmean	Precision	Rrecall	Hmean	Struc.
Faster R-CNN				-	-	-	81.32	81.31	81.31	94.63
				91.71	91.53	91.62	81.83	81.82	81.83	94.65
Mask R-CNN	✓			91.92	91.66	91.79	84.29	84.10	84.20	95.22
Wiask It-Civiv		\checkmark		91.98	91.50	91.74	83.48	83.18	83.33	95.04
	✓	\checkmark		92.27	91.86	92.06	85.14	84.77	84.95	95.53
Mask R-CNN			✓	92.11	91.85	91.98	81.91	81.79	81.85	94.94
Wask n-CIVIV	✓	✓	✓	92.05	91.65	91.85	84.87	84.50	84.68	95.31

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More works from Davar-Lab: https://davar-lab.github.io/



Thank you