### **Biomedical Named Entity Recognition** With Multiple Segment Representations Han-Cheol Cho and Jun'ichi Tsujii, Tsujii Lab., The University of Tokyo **4. Hierarchical Segment Representations 1. What is Named Entity Recognition ? Named Entity Recognition (NER)** is a task to recognize and To use conventional CRFs framework, we define a classify target entities in text deterministic mapping from a fine-grained SR to a coarsegrained SR **E.g. Gene names in biomedical text** IOSegment Non-segment ... does not affect proinflammatory cytokine ( interleukin - 6 B I O O B I I Coarse-grained BIES В В S S **IOB2** *IOE*2 tumor necrosis factor - alpha and interferon - gamma ) IOBES В S Ο Ο Ο Ο E IOBES 0 0 1 **O** 1 IOB2 В В Ο Ο Fine-grained release from ... BIES ю Ο Ο Ο ...

When the IOB2 segment ••• representation is used

# 2. Segment Representation

Various segment representations (SRs) for NLP tasks

Task	SR
NER	IOB2, IOBES,
SP	IOB1, IOB2, IOE1, IOE2,
WS	BI, BIS, BIES, $B_1B_2IES$ , $B_1B_2B_3IES$ ,

SP for shallow parsing and WS for word segmentation

- **Designing a proper SR primarily depends on**
- the size of training data and
- the characteristics of segments (e.g. words, NEs, ...) 2.
- However, using a single SR may not be enough to capture the characteristics of diverse segment instances

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## **5. Experiment Results**

**Experiment results on the BioCreative 2 task** 

Model	Prec.	Rec.	<b>F1</b>	AFI	# feat
IO	86.92	81.44	84.09	7.36	8.68
IOB2	88.48	82.39	85.33	7.25	13.02
IOE2	87.12	81.11	84.01	7.27	13.02
BI	88.80	81.52	85.00	7.00	17.36
IE	88.48	82.37	85.32	7.01	17.36
IOBES	89.24	82.78	85.89	7.14	21.70
BIES	89.37	82.23	85.65	6.67	34.79
IOB2+	88.52	82.83	85.58	7.30	21.70
IOBES+	88.98	83.54	86.18	7.24	56.43
BIES+	89.58	83.51	86.44	7.09	125.87
BIES & IO	89.74	83.04	86.26	7.00	43.41

### F1 Rank Prec. Recall 88.48 85.97 87.21 89.30 84.49 86.83 2 86.57 3 84.93 88.28 **BIES+** 89.58 83.51 86.44 87.27 85.41 86.33 **BIES&IO** 89.74 86.26 83.04 85.77 86.28 86.80 5 IOBES 89.24 82.78 85.89 82.71 89.32 85.89 6 82.39 85.33 IOB2 88.48 **BANNER** 87.18 82.78 84.93 84.70 86.97 82.55 7

## **Statistical significance test** 2.

	IOB2+	IOBES+	BIES&IO	BIES+
IOB2	0.02	<< 0.01	<< 0.01	<< 0.01
IOB2+	Х	<< 0.01	0.01	<< 0.01
BIES	Х	0.05†	<< 0.01	<< 0.01
IOBES	Х	0.04	0.10 <mark>†</mark>	0.02
IOBES+	Х	Х	0.39	0.18
BIES&IO	Х	Х	Х	0.16

## **Error analysis** 3.

to BIES to BIES&IO Ο

The BIES+ model outperforms all conventional models using a single SR

Model	Prec.	Recall	F1-score
IOB2	88.48%	82.39%	85.33%
IOBES	89.24%	82.78%	85.89%

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From (IOB2)	To (IOBES)	# of instances	
ТР	ТР	5077	
	FN	139 (-)	<
FN	FN	951	
	ТР	164 (+)	<
TN	TN	•••	
	FP	131 (-)	<
FP	FP	501	
	TN	178 (+)	<

Preliminary experiment results on the BioCreative 2 gene mention recognition task

- Although the IOBES SR seems better the IOB2 SR in standard performance measures, the IOB2 SR still makes correct predictions for many NE instances whereas the IOBES SR don't
- 1.



- 1. Changing a SR from the IO to the BIES causes a lot of difference in labeling results
- 2. However, the positive changes (FN to TP and FP to tN) is undermined by the negative changes
- 3. By using the proposed method, the BIES&IO model recovered 24~26% negative changes while minimizing the opposite changes 8~12%
- The effect of training data size 4.



