A Survey of MWE Identification Experiments: The Devil is in the Details

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MWE 2023 Workshop

Outline

Introduction and scope

Corpus constitution and selection

Pre- and post-processing

Evaluation metrics

Significance

Error analysis

Conclusions and open issues

Introduction

Full-text multiword expression identification – sequence annotation

→ Focus of recurrent shared tasks (ST): DiMSUM & PARSEME

Survey's goal

- Analyses MWE identification papers with experiments on data
- Look at methodological issues often seen as minor or omitted
- Hypothesis: these issues influence results and conclusions

Scope

Selection criteria:

- Available on the ACL Anthology
- Focus on MWE identification (Constant et al. 2017)
- Report experimental results
  - DiMSUM or PARSEME shared task or system description

    OR
  - report experiments on DiMSUM or PARSEME corpora

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Paper stats

- 40 papers

  → 4 overall ST papers

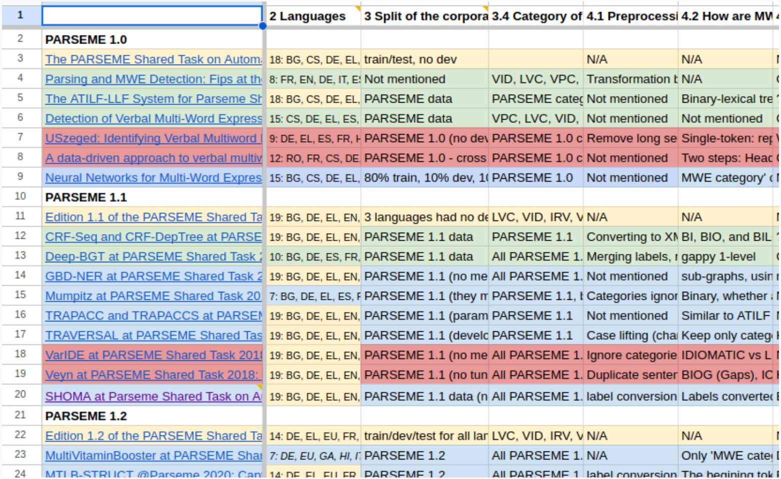
  → 27 ST system descriptions

  → 9 non-ST system descriptions

Questions

- Data
  - → Corpora
  - → Pre- and post-processing
  - → Sequence label encoding and decoding
- Evaluation
  - → Metrics
  - → Significance of comparisons
  - → Error analysis

Working table



1		2 Languages	3 Split of the corpora	3.4 Category of	4.1 Preprocessi	4.2 How are MW
2	**PARSEME 1.0**					
3	The PARSEME Shared Task on Autom	18: BG, CS, DE, EL,	train/test, no dev		N/A	N/A
4	Parsing and MWE Detection: Fips at th	8: FR, EN, DE, IT, E	Not mentioned	VID, LVC, VPC,	Transformation t	N/A
5	The ATILF-LLF System for Parseme Sh	18: BG, CS, DE, EL,	PARSEME data	PARSEME categ	Not mentioned	Binary-lexical tre
6	Detection of Verbal Multi-Word Express	15: CS, DE, EL, ES,	PARSEME data	VPC, LVC, VID,	Not mentioned	Not mentioned
7	USzeged: Identifying Verbal Multiword	9: DE, EL, ES, FR, H	PARSEME 1.0 (no dev	PARSEME 1.0 c	Remove long se	Single-token: rep
8	A data-driven approach to verbal multiv	12: RO, FR, CS, DE,	PARSEME 1.0 - cross	PARSEME 1.0 c	Not mentioned	Two steps: Head
9	Neural Networks for Multi-Word Expres	15: BG, CS, DE, EL,	80% train, 10% dev, 1(	PARSEME 1.0	Not mentioned	MWE category' c
10	**PARSEME 1.1**					
11	Edition 1.1 of the PARSEME Shared Ta	19: BG, DE, EL, EN,	3 languages had no de	LVC, VID, IRV, V	N/A	N/A
12	CRF-Seq and CRF-DepTree at PARSE	19: BG, DE, EL, EN,	PARSEME 1.1 data	PARSEME 1.1	Converting to XM	BI, BIO, and BIL
13	Deep-BGT at PARSEME Shared Task 2	10: BG, DE, ES, FR,	PARSEME 1.1 data	All PARSEME 1.	Merging labels, r	gappy 1-level
14	GBD-NER at PARSEME Shared Task 2	19: BG, DE, EL, EN,	PARSEME 1.1 (no me	All PARSEME 1.	Not mentioned	sub-graphs, usin
15	Mumpitz at PARSEME Shared Task 20	7: BG, DE, EL, ES, F	PARSEME 1.1 (they m	PARSEME 1.1, t	Categories ignor	Binary, whether a
16	TRAPACC and TRAPACCS at PARSEM	19: BG, DE, EL, EN,	PARSEME 1.1 (param	PARSEME 1.1	Not mentioned	Similar to ATILF
17	TRAVERSAL at PARSEME Shared Tas	19: BG, DE, EL, EN,	PARSEME 1.1 (develo	PARSEME 1.1	Case lifting (cha	Keep only categ
18	VarIDE at PARSEME Shared Task 201	19: BG, DE, EL, EN,	PARSEME 1.1 (no me	All PARSEME 1.	Ignore categorie	IDIOMATIC vs L
19	Veyn at PARSEME Shared Task 2018:	19: BG, DE, EL, EN,	PARSEME 1.1 (no tun	All PARSEME 1.	Duplicate senter	BIOG (Gaps), IC
20	SHOMA at Parseme Shared Task on A	19: BG, DE, EL, EN,	PARSEME 1.1 data (n	All PARSEME 1.	label conversion	Labels convertec
21	**PARSEME 1.2**					
22	Edition 1.2 of the PARSEME Shared Ta	14: DE, EL, EU, FR,	train/dev/test for all lar	LVC, VID, IRV, V	N/A	N/A
23	MultiVitaminBooster at PARSEME Shar	*7: DE, EU, GA, HI, I*	PARSEME 1.2	All PARSEME 1.	N/A	Only 'MWE cate
24	MTLB-STRUCT @Parseme 2020: Can	14: DE, EL, EU, FR,	PARSEME 1.2	All PARSEME 1.	label conversion	The begining tok

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Corpus splits

Shared tasks

- DiMSUM: 3 domains, 1 lang, train + test
- PARSEME 1.0: news, 18 lang, train + test
- PARSEME 1.1: news, 19 lang, train + test + dev (16 lang)
- PARSEME 1.2: news, 14 lang, train + test + dev

  → Biased split: focus on unseen MWEs

Corpus use

- Training corpus unused: 4/36 papers
  - → External resources (2 papers), other corpora (2 papers)
- Development corpus not provided:
  - → Custom train-dev set: 6/36 papers
  - → Cross-validation: 3/36 papers
  - → Dev on another language: 2/36 papers
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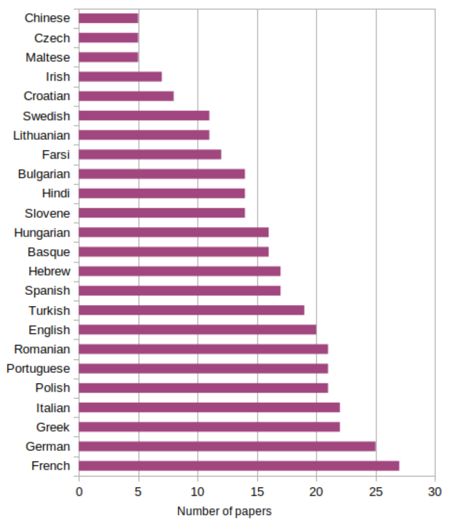
Recommendation
Always mention development data

Languages


Chinese
Czech
Maltese
Irish
Croatian
Swedish
Lithuanian
Farsi
Bulgarian
Hindi
Slovene
Hungarian
Basque
Hebrew
Spanish
Turkish
English
Romanian
Portuguese
Polish
Italian
Greek
German
French
0
5
10
15
20
25
30
Number of papers

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Pre-processing

Variants of BIO-style encoding: 12/36 papers

DiMSUM	The	staff	leaves	a	lot	to	be	desired	.
	O	O	B	b	i_	I_	I_	I_	O
PARSEME	I	did	a	lot	of	study	and	research	.
	*	1:LVC;2:LVC	*	*	*	1	*	2	*

- Gaps: 12/36 papers account for gaps
- Nesting and overlaps

→ Ignored, handled by modifying BIO-style

→ Kept the tags as they are, dependency graphs

→ No mention (most papers)

Post-processing

Conversion from BIO-style

- Combination heuristics (7/36 papers)
  - → B-labelled and I-labelled words matched
  - → Standalone I-labelled ignored
- Greedy-matching algorithm (1/36 paper)
- Viterbi decoding (1/36 paper)
- Conditional random fields (8/36 papers)
- Dependency trees (2/36 papers)
  - → Elements of MWE assumed to be nodes in the same subtree

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Recommendation
Explicitly report all pre- and post-processing + MWE encoding

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Evaluation metrics

DIMSUM exact match and linked-based P, R and F1

PARSEME MWE-based and token-based P, R and F1

PARSEME focused measures:

- Seen/Unseen: focus of 9 papers
- Diversity: 2 PARSEME papers
- Discontinuity: focus of 5 papers

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Recommendation
Focused measures help highlight system strengths and limitations

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Compare systems A and B

- Test set
  - $x = x^{(1)} \dots x^{(m)}$ – m input sentences
  - $y = y^{(1)} \dots y^{(m)}$ – m reference MWE annotations
- Method :
  1. Apply A to x to obtain $\hat{y}_A$, compare to y
  2. Calculate evaluation metric $M(A, x, y)$ (e.g. MWE-based F1)
  3. Do the same for B, obtain $M(B, x, y)$
  4. Calculate difference (effect)

$$\delta_{A-B}(x, y) = M(A, x, y) - M(B, x, y)$$

- $\delta_{A-B}(x, y) > 0 \implies A$ better than B?

Hypothesis testing

- $H_0 : \delta(X, Y) \leq 0 \implies$ if true, then A not better than B
- $H_1 : \delta(X, Y) > 0$
- $X, Y \rightarrow$ random variables, all possible test sets
  - Of which x, y is an m-sized sample
- Reject $H_0 \implies$ significant difference between the systems
- **P-value**: probability of observing $\delta_{A-B}(x, y)$ while H_0 is true:
  - $p - value = P[\delta(X, Y) \geq \delta_{A-B}(x, y) | H_0]$
  - probability to reject H_0 when it is true

Bootstrap p-value (Berg-Kirkpatrick et al. 2012)

Input

- Test set $x = x^{(1)} \dots x^{(m)}, y = y^{(1)} \dots y^{(m)}$,
- Predictions $\hat{y}_A^{(i)}$ and $\hat{y}_B^{(i)}$ of systems A and B
- Evaluation metric $M(\cdot)$

```
deltaobs = M(A,x,y) - M(B,x,y)  # observed difference
for i in range(R) :             # R constant 10k
  xsample, ysample = sample(x,y,m)  # m with repetition
  deltasample = M(A,xsample,ysample) - M(B,xsample,ysample)
  if deltasample > 2 * deltaobs :
        r = r + 1
pvalue = r/R                    # % of surprising results
return pvalue
```

Significance analysis

- Only 2/40 papers report significance
- Our tool estimates p-values for two CUPT predictions
  - → `https://gitlab.com/parseme/significance`
- We compare all system pairs and metrics of PARSEME 1.2
  - → 2,728 p-values in total
  - → 783 above the $\alpha = 0.05$ threshold (29%)

P-values for MWE-based F1 in Swedish

Systems		TRAVIS-multi	Seen2Unseen	TRAVIS-mono
	F1	**0.6911**	**0.6892**	**0.6709**
MTLB-STRUCT	**0.7158**	0.025	0.038	0.0
TRAVIS-multi	**0.6911**		0.464	0.081
Seen2Unseen	**0.6892**			0.103

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Recommendation
Systematically calculate/report p-values for model comparison

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Error Analysis

- 33/36 papers report some error analysis
- 11/36 report MWE category or cross-language analyses
- Heterogeneous analyses
    - → Discontinuities, seen/unseen
    - → POS sequences, syntactic structure
    - → Ablation, role of external lexicons
    - → Pre-trained embeddings, tagging schemes

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Recommendation
Error analyses uncover interesting phenomena for future work

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Recommendations

We advocate reporting on experimental choices:

- corpus constitutions and selections
- pre- and post-processing
- evaluation metrics and significance testing of performance
- error analysis

We encourage focused measures that facilitate error analysis

We propose a tool to predict p-values from 2 CUPT predictions

Open issues

- Hyper-parameter tuning
  - → Selection of the data
  - → Strategy (e.g. grid search, random, etc.)
- Should manual evaluation of detected MWEs be performed?
- New evaluation protocols
  - → e.g. are some MWE categories more important than others?

Thanks! Questions?

Acknowledgments

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