

Gooch, P. (2012). BADREX: In situ expansion and coreference of biomedical abbreviations using dynamic regular expressions. London, UK: City University London.



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Original citation: Gooch, P. (2012). BADREX: In situ expansion and coreference of biomedical abbreviations using dynamic regular expressions. London, UK: City University London.

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BADREX: In situ expansion and coreference of biomedical abbreviations using dynamic regular expressions

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ABSTRACT

BADREX uses dynamically generated regular expressions to annotate term definition–term abbreviation pairs, and corefers unpaired acronyms and abbreviations back to their initial definition in the text. Against the Medstract corpus BADREX achieves precision and recall of 98% and 97%, and against a much larger corpus, 90% and 85%, respectively. BADREX yields improved performance over previous approaches, requires no training data and allows runtime customisation of its input parameters.

BADREX is freely available from <https://github.com/philgooch/BADREX-Biomedical-Abbreviation-Expander> as a plugin for the General Architecture for Text Engineering (GATE) framework and is licensed under the GPLv3.

1 INTRODUCTION

Identification of abbreviations and acronyms, or *short forms* (SF), for given term definitions, or *long forms* (LF), is a well researched topic in the biomedical natural language processing domain (see Torii *et al.* 2007 for a review). Existing tools such as Schwartz & Hearst (2003) and Ao & Takagi (2005) extract LF-SF pairs for dictionary creation, but do not provide automatic expansion of SFs within the text at the point at which they occur, which is a necessary precursor for semantic type assignment and coreference resolution. BADREX identifies, expands and annotates LF-SF pairs, and coreferences subsequent SF mentions back to their most recent definition in the text. This may facilitate disambiguation of unpaired abbreviations not possible with dictionary lookup alone (Stevenson *et al.* 2009).

2 METHODS

2.1 BADREX development

BADREX is implemented in Java as a plugin for the General Architecture for Text Engineering (GATE) framework (Cunningham *et al.* 2002). It takes a Set of sentences from GATE’s sentence splitter, over which it iterates once. For each sentence, five processing steps are performed, where Step 1 is similar to the first stage outlined in Schwartz & Hearst (2003) and Step 2 to the third phase of Ao & Takagi (2005):

- (1) Identification of candidate <LF, SF> pairs
- (2) Applying discard conditions to <LF, SF> candidates to filter unwanted pairs

- (3) Identifying the shortest substring in LF that best matches SF given the constraints of Steps 1 and 2
- (4) Matching characters in SF against characters in LF
- (5) Optional coreference of unpaired abbreviations/acronyms that match previously found short forms

In Step 1, we create two patterns: the ‘head’ regular expression (regex) identifies a string that contains {1, *maxOuterWords*} words followed by a string of {1, *maxInnerChars*} characters in parentheses or square brackets, and where the first character of the first group is an alphanumeric that matches the first character of the second group. The ‘tail’ regex consists of a similar pattern but where the first character of the *last* word of the first group is an alphanumeric that matches the *last* character of the second group. For each sentence in the input, if no match is made by the first pattern, then the second pattern may be executed. The ‘head’ pattern will identify candidate pairs such as:

the behaviour of confluent SV40 transformed rabbit corneal epithelial cells (TRCEC) (1)

and the ‘tail’ pattern identifies pairs such as

with two-dimensional proton nuclear magnetic resonance (2D 1H NMR) (2)

(matching characters underlined). In simplified form, the ‘head’ pattern can be expressed as:

```
\b((\w)\W{0,2}(\w+\W?){1,maxOuterWords})\s*\n((\2.{1,maxInnerChars})\(\p{Punct}\s*\w+\)?\)
```

and the ‘tail’ pattern as

```
\b(.{1,maxOuterChars}\b(\w)(\w+\W?))\s*\n((.{1,maxInnerChars}\2(\p{Punct}\s*\w+\)?\)
```

where *maxOuterWords* is the value of the user-defined parameter for the maximum number of words in the long form (default: 10, as per Ao & Takagi 2005), *maxInnerChars* is the maximum number of characters in the short form (default: 40, i.e. 10 words), and *maxOuterChars* = *maxOuterWords* * 4.

Usually, the short form will appear in parentheses following the long form, but they may appear in reverse order. We allow for this by setting the maximum number of characters as the same by default in both LF and SF. If the matched short form is longer than the candidate long form text preceding it, the values of LF and SF are swapped, so that SF always points to the abbreviation/acronym, and LF always to the definition.

In Step 2 we make use of a simplified subset of the discard conditions for short forms given in Appendix 1 of Ao & Takagi (2005). For example, short forms starting with a preposition, or starting and ending with a digit, are discarded. These conditions are implemented as regular expressions loaded from external configuration files, allowing this behaviour to be easily customised.

In Step 3, we use dynamically generated regular expressions to find the shortest substring of LF following a preposition (if present) and where either the first character matches the first character of SF, or the first character of the last word matches the last character of SF, depending on whether the ‘head’ or ‘tail’ pattern was executed in Step 1. In example (1) above, ‘the behaviour of confluent SV40 transformed rabbit corneal epithelial cells’ would be shortened to ‘transformed rabbit corneal epithelial cells’.

In Step 4, we strip non-alpha characters from LF and SF, split LF into a character array, and iterate over SF to match adjacent characters, in the same order, in the LF array. If the proportion of matches in relation to the total alpha characters in SF \geq threshold (default: 0.80), then the <LF, SF> pair is accepted and added to a Map of <SF, LF> key/value pairs.

The accepted pair are converted to inline annotations in the text by making use of the start() and end() methods of the regex Matcher, adjusted for term truncation in Step 3 and for the start offset of each sentence. The value of LF is stored as a feature on

SF, and vice versa. If the term definition has already been annotated with one of a configurable set of known annotations, this annotation is used. For example, if ‘transformed rabbit corneal epithelial cells’ was previously annotated as AnatomicalSite, then ‘rRCEC’ would also be annotated with this semantic type.

In Step 5, we generate regex Matchers over the Map of pairs populated up to that point, and use these to locate and annotate unpaired, candidate SFs in sentences forward of the point at which the corresponding LF-SF pair was first introduced.

Figures 1 and 2 show sample BADREX output in the GATE Developer application for two abstracts from the evaluation corpora. Figure 1 shows semantic type assignment (DiseaseOrSyndrome and Protein) copied from the long form to subsequent short form mentions, and coreference and expansion of unpaired short forms. In coreference mode, short forms occurring within subsequent long forms are also expanded: here, the ‘WAS protein’ term contains an inner ‘WAS’ abbreviation that has been expanded to ‘Wiskott-Aldrich syndrome’.

Figure 2 shows how BADREX allows for whitespace variations in subsequent mentions of the earlier-introduced short form. Future versions of BADREX may incorporate configurable string distance metrics for greater control of coreference resolution of unpaired short forms.

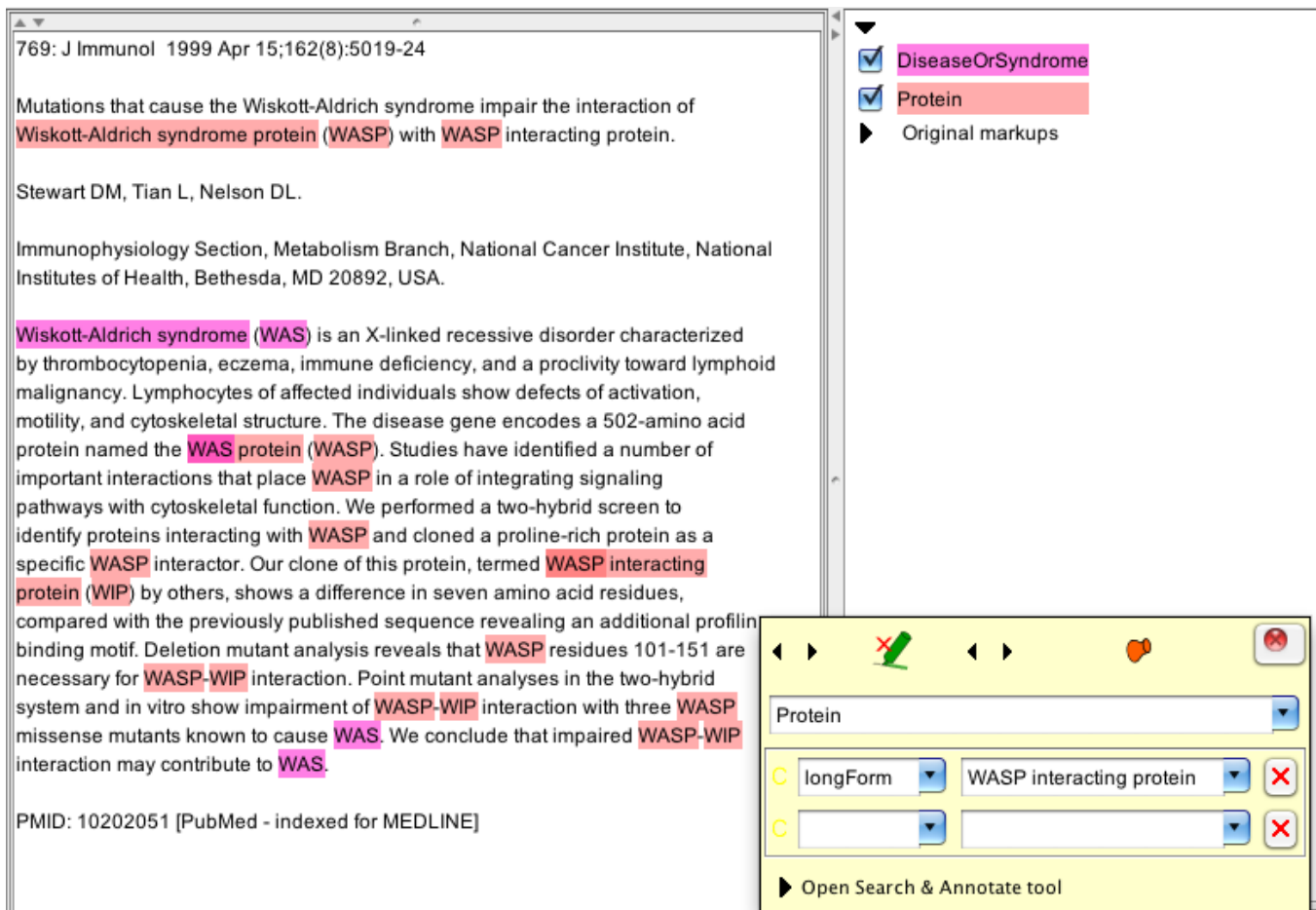


Fig. 1. Visualisation of BADREX output in GATE, showing automatically annotated and coreferenced short forms.

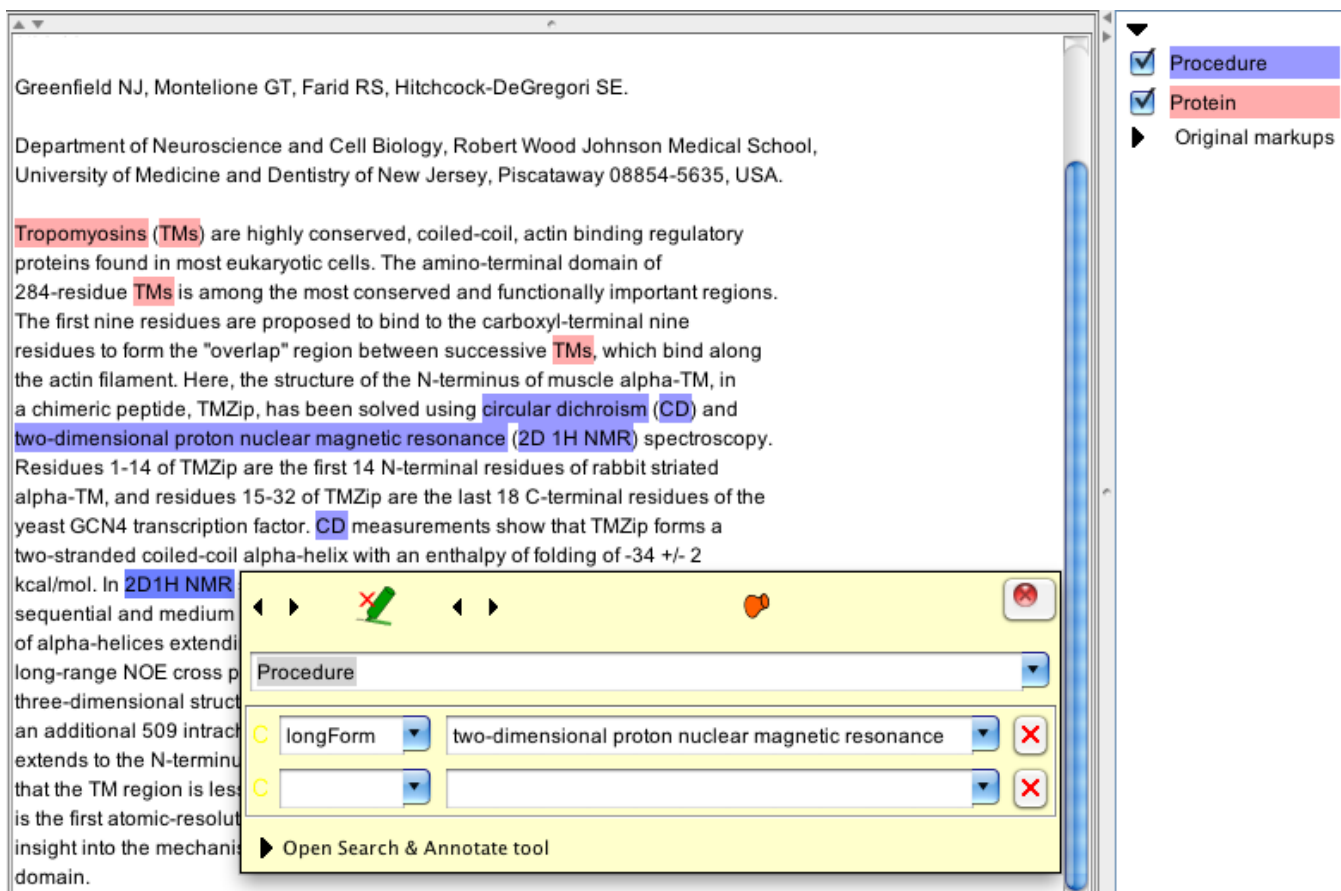


Fig. 2S. Example showing how BADREX's abbreviation coreference allows for white-space variations in subsequent mentions of the initially introduced short form. Here, '2D1H NMR' is coreferenced with '2D 1H NMR' and annotated with the original long form text as a feature.

2.2 Correction of BioText and Medstract data

The labelled, gold standard BioText 'yeast' data (<http://biotext.berkeley.edu/data.html>; Schwartz & Hearst 2003) comprises 1000 MedLine abstracts in a plain text file containing 954 LF-SF pairs annotated with XML-like tags, e.g.

```
<Long id=1>endoplasmic reticulum</Long>
(<Short id=1>ER</Short>)
```

where the 'id' attribute on the <Long> element matches that in the corresponding <Short> element. Using a standard XML parser, we identified and corrected errors in malformed 'id' attributes and mismatched or malformed <Long> and <Start> tags. Correction iterations continued until the file parsed.

The Medstract corpus (Pustejovsky *et al.* 2002; <http://www.medstract.org/index.php?f=gold-standard>) comprises

400 MedLine abstracts in a plain text file, where 414 gold standard LF-SF pairs have been extracted into a separate text file (<http://www.medstract.org/index.php?f=gold-result>; the 'markables'). We analysed the markables file for offset errors, and following correction of these, we compared the abstracts file against the markables to identify any missing pairs.

We evaluated the performance of BADREX against the corrected BioText and Medstract corpora, and compared the performance alongside that of three published systems: Schwartz & Hearst (S-H, 2003), ALICE (Ao & Takagi 2005) and MBA (Xu *et al.* 2009) against the same data. For S-H and ALICE, executable code was available to evaluate on the corrected corpora; for MBA, code was not available so we report the Medstract figures provided by Xu *et al.*

Table 1. Missing and corrected short-form-long-form pairs in the Medstract gold standard markables

Short form	Long form	
<i>Missing pairs</i>		
hCG	human chorionic gonadotrophin	
eNOS	endothelial type of NO synthase	
3beta-HSD II	3beta-hydroxysteroid dehydrogenase type II	
tTGase	tissue transglutaminase	
hMG	human menopausal gonadotrophin	
IVF ET	in vitro fertilization/embryo transfer	
hMG	human menopausal gonadotrophin	
hCG	human chorionic gonadotrophin	
ds	double-stranded	
frag	fragmentation	
3-D	3-dimensional	
22K hGH	22 kDa growth hormone	
alpha-DB	alpha-dystrobrevin	
bHLH	basic helix-loop-helix	
b FGF	basic fibroblast growth factor	
CI	confidence interval	
oc	Osteosclerosis	
topo II	topoisomerase II	
ALP	alkaline phosphatase levels	
BMD	bone mineral density	
CI	confidence interval	
micro-CT	micro-computed tomography	
PrE	primitive endoderm	
hHb1	Human hair keratin basic 1	
bp	base pair	
mtDNA	mitochondrial genome	
beta 2M	beta 2-microglobulin	
pb	peripheral blood	
AT	Ataxia teleangiectasia	
I.L.S.G.	International Lymphoma Study Group	
R.E.A.L.	Revised European-American Classification of Lymphoid Neoplasms	
tHcy	total homocysteine	
iNOS	inducible nitric oxide synthase	
5-FU	5-fluorouracil	
rAAV	recombinant adeno-associated virus	
oriP	origin of latent viral DNA replication	
HVJ	hemagglutinating virus of Japan	
E0'	equilibrium reduction potential	
O2-	superoxide	
eNOS	endothelial NO synthase	
GIOx	glutamate oxidase	
beta-END	beta endorphin	
tRCEC	transformed rabbit corneal epithelial cells	
<i>Corrected pairs</i>		
Short form	Corrected long form	Original long form
RAR	RA receptor	regulation of tissue transglutaminase
IAA	indoleacetic acid	in the presence of 10(-6) m 3-indoleacetic acid
EXACCT	exonuclease-amplification coupled capture technique	e exonuclease-amplification coupled capture technique
GlyRalpha2 E3A	glycine alpha2 exon 3A	glycine alpha2 exon 3a (glylalpha2 e3a) and gaba(a) exon gamma
EGFr	EGF receptor	eration through binding to egf receptor
VIN	vulval intraepithelial neoplasia	val intraepithelial neoplasia

Short form	Long form	
<i>Corrected pairs – continued</i>		
SSSS	staphylococcal scalded skin syndrome	scalded skin syndrome
EBER	EBV-encoded small nuclear RNA	ed ebv-encoded small nuclear rna
HD	Hodgkin's disease	15 with Hodgkin's disease (HD †
GluR	glutamate receptor	g chemical selectivity of agonists for the nmda subtype of glutamate receptor
TUNEL	terminal deoxynucleotidyl transferase mediated deoxyuridine triphosphate biotin nick end labelling	ted deoxyuridine triphosphate biotin nick end labelling
LC/ESI/MS/MS	HPLC/electrospray ionization tandem mass spectrometric	lective hplc/electrospray ionization tandem mass spectrometric
CYSP	cysteine peptide	conformations of the polypeptides beta endorphin
ESI/MS	electrospray ionization mass spectrometry	ectrospray ionization mass spectrometry
Lid	Lidocaine	lidated for the quantitation of lidocaine
DEX-MPS	dextran-methylprednisolone succinate	DEX-MPS) and its degradation products methylpr †
UV	Ultraviolet	60:40 v/v) and ultraviolet (UV) detection at †

† Incorrect short form

3 RESULTS

In the BioText corpus, we found 13 incorrectly matching or malformed ‘id’ attributes and 21 mismatched or malformed <Long> and <Start> tags. The corrected labelled corpus is available from <http://soi.city.ac.uk/~abdy181/software/#badrex> (reproduced with permission).

Table 1 shows the results of analysis of the Medstract corpus; against the Medstract gold standard markables: we added an additional 43 markables that we judged to be correct short-form–long-form pairs and amended 17 pairs that we judged to have incorrect spans. The corrected markables file is also available from the above URL.

Evaluation of BADREX performance against both corpora in comparison to that of S-H, ALICE and MBA are shown in Table 2.

Table 2. Evaluation results against corrected gold standard data sets

System	Corpus	Precision	Recall	F_1
BADREX ^a	Medstract	98%	97%	0.97
	BioText†	90%	85%	0.88
S-H	Medstract	90%	97%	0.93
	BioText	91%	79%	0.85
ALICE	Medstract	98%	94%	0.96
	BioText	92%	68%	0.78
MBA*	Medstract	91%	88%	0.89
	BioText	-	-	-

^a Coreference mode disabled in BADREX for this evaluation

† Corrected BioText corpus available in XML format from the author.

* Results reported by authors; software unavailable to evaluate on BioText corpus.

4 DISCUSSION

Our goal was to develop a customisable tool for identifying, expanding and annotating *in situ* biomedical abbreviations in free text, while matching or exceeding the performance of existing approaches. Running both ‘head’ and ‘tail’ candidate matches, allowing a variable threshold and only considering alpha characters when matching allows us to identify pairs such as ‘topoisomerase I

(Top1p)’ and ‘two-dimensional polyacrylamide gel electrophoresis (2D-PAGE)’ missed by the other approaches, yet without unduly compromising precision.

By using regular expressions in steps 1 and 3, we simplify the creation of the finite state machine hard-coded in Schwartz & Hearst (2003) and allow it to be easily parameterised, so that optimal parameter values for a given corpus can be identified. While we used default values for these (detailed above) in this evaluation, iterative regression techniques could be used to find minimum values for the `maxOuterWords`, `maxInnerChars`, and `threshold` parameters that maximise precision and/or recall for other corpora.

We have not evaluated the coreferencing features of BADREX here. In addition, BADREX can be configured to annotate common medical abbreviations extracted from Wikipedia (Wikipedia 2012). Future work will evaluate the contribution of these features as components in the disambiguation of unpaired abbreviations. BADREX is currently coupled to GATE but a standalone version is planned.

5 CONCLUSION

The use of regular expressions dynamically generated from document content yields modestly improved performance over previous approaches to identifying term definition–term abbreviation pairs, with the benefit of providing in-place annotation, expansion and coreference in a single pass. BADREX requires no training data and allows runtime customisation of its input parameters. The GATE plugin is freely available from <https://github.com/philgooch/BADREX-Biomedical-Abbreviation-Expander> and is licensed under the GPLv3.

ACKNOWLEDGEMENTS

We thank Prof. Marti Hearst for permission to make available the corrected BioText yeast corpus in XML format. The author acknowledges funding and support from the Engineering and Physical Sciences Research Council (EPSRC) in carrying out this research as part of PhD studentship EP/P504872/1.

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