U-Compare Named Entity Recognition Service

1. BASIC INFORMATION

Service name

U-Compare Named Entity Recognition Service

Overview and purpose of the tool

This is a web service that identifies biomedical named entities (genes and proteins) in English text. Also identifies sentences.

A short description of the algorithm

This web service is based on a UIMA-based workflow, created using the U-Compare text mining system[1]. The workflow was exported from U-Compare as a web service using the built in functionality (Kontonastsios et al., In Press). The workflow was created as part of the work to increase the number of interoperable tools operating on different European languages (Ananiadou et al, 2011).

The workflow consists of the following UIMA-compliant tools

1) Cafetiere Sentence Splitter (University of Manchester)
2) NEMine (University of Manchester) (Sasaki et al., 2008).

2. TECHNICAL INFORMATION

Software dependencies and system requirements

This is a web service that can be run from a browser or accessed programmatically. The only basic requirement is an Internet connection.

Installation

There is no installation. The web service can be accessed at the following URL:

http://nactem001.mib.man.ac.uk:8080/UCompareWebServices/NER_CafetiereSentSplitter_NeMine

[1] http://nactem.ac.uk/ucompare/

The web form available at this URL is shown in Figure 1, with some English text entered into the text box.

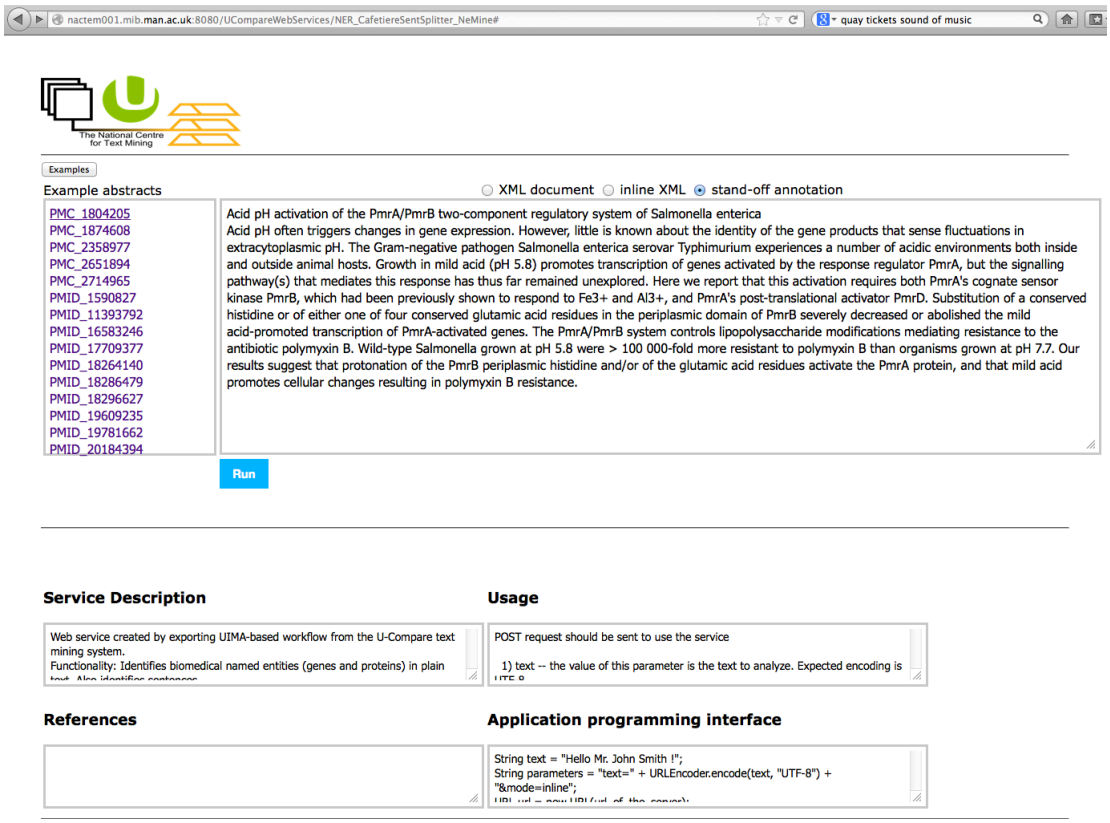


Figure 1: Web form for the web service

Execution instructions

The web service can be executed by typing or pasting text into the online form and clicking on the "Run" button.

Alternatively, the web service can executed from within program code, as explained in the "Usage" and "Application programming interface" boxes of the web form.

A POST request should be used to call the service. The following parameters may be used in the request:

- **text** - the value of this parameter is the text to analyze. Expected encoding is UTF-8. This parameter is obligatory.
- **lang** - This parameter sets the language of the text. If this parameter is not provided, then the value"en" will be used
- **mode** - This parameter sets the format of the annotated information returned by the service. If this parameter is not set, XML output will be produced. The two possible types of output are as follows:
    - **inline** – annotations are encoded as inline XML.

- **xml** – results are output as an XML document containing the annotations added

The following code example shows how the web service can be called from Java code:

```
//Set the input text
String text = " <Text_to_be_analysed>";
//Set the parameter string
String parameters = "text=" + URLEncoder.encode(text,
"UTF-8") + "&mode=inline";
//Create the URL connection
URL url = new
URL("http://nactem001.mib.man.ac.uk:8080/UCompareWebServi
ces/NER_CafetiereSentSplitter_NeMine");
URLConnection connection = url.openConnection();
connection.setDoOutput(true);
//Create Output stream
OutputStreamWriter writer = new
OutputStreamWriter(connection.getOutputStream());
//write parameters to output stream
writer.write(parameters);
writer.flush();

//Read the results returned by the service
BufferedReader reader = new BufferedReader(new
InputStreamReader(connection.getInputStream(), "UTF-8"));
String line;
while ((line = reader.readLine()) != null) {
    System.out.println(line);

}
```

Input/Output data formats

Input data formats

The input is plain text, UTF-encoded.

Output data format

If the service is run from the web interface, then the output is visualized in the interface using colored highlights in the text to show the individual annotations, and one or more tables of information below, each corresponding to a particular type of annotation.

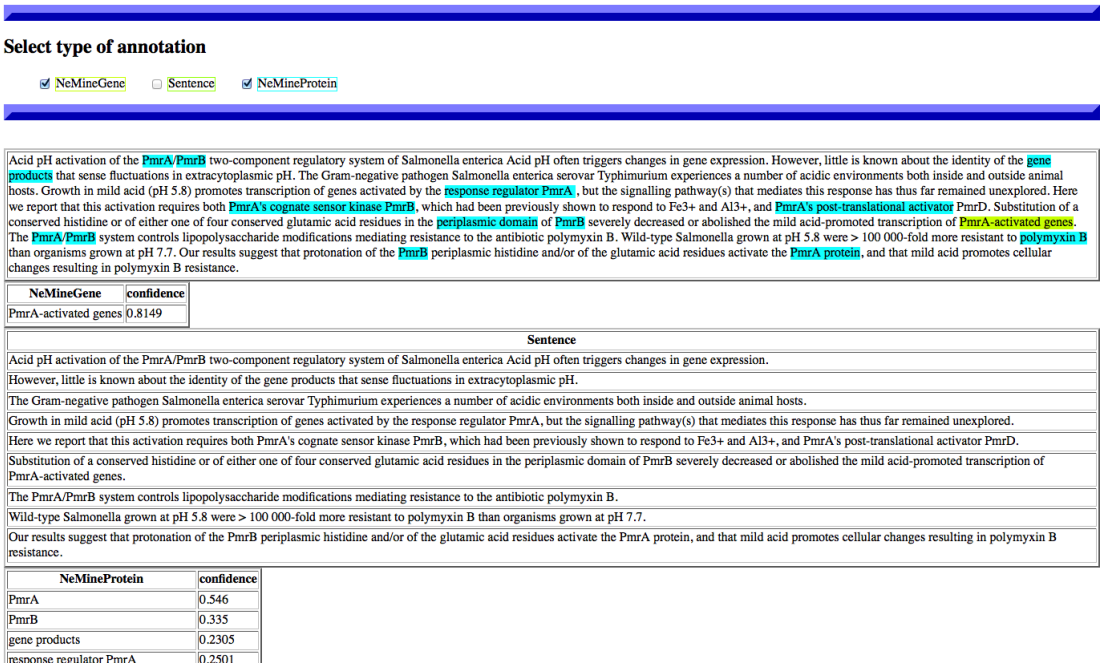
If the service is run programmatically, then the output is provided in XML format. See section 3 for an example.

Integration with external tools

The API allows the functionality of the web service to be embedded in any application.

3. CONTENT INFORMATION

Using the web interface, the output of the service is visualised as shown in Figure 2.



Select type of annotation

☑ NeMineGene ☐ Sentence ☑ NeMineProtein

Acid pH activation of the PmrA/PmrB two-component regulatory system of Salmonella enterica Acid pH often triggers changes in gene expression. However, little is known about the identity of the gene products that sense fluctuations in extracytoplasmic pH. The Gram-negative pathogen Salmonella enterica serovar Typhimurium experiences a number of acidic environments both inside and outside animal hosts. Growth in mild acid (pH 5.8) promotes transcription of genes activated by the response regulator PmrA , but the signalling pathway(s) that mediates this response has thus far remained unexplored. Here we report that this activation requires both PmrA's cognate sensor kinase PmrB , which had been previously shown to respond to Fe3+ and Al3+, and PmrA's post-translational activator PmrD. Substitution of a conserved histidine or of either one of four conserved glutamic acid residues in the periplasmic domain of PmrB severely decreased or abolished the mild acid-promoted transcription of PmrA-activated genes. The PmrA/PmrB system controls lipopolysaccharide modifications mediating resistance to the antibiotic polymyxin B. Wild-type Salmonella grown at pH 5.8 were > 100 000-fold more resistant to polymyxin B than organisms grown at pH 7.7. Our results suggest that protonation of the PmrB periplasmic histidine and/or of the glutamic acid residues activate the PmrA protein , and that mild acid promotes cellular changes resulting in polymyxin B resistance.

NeMineGene	confidence
PmrA-activated genes	0.8149

Sentence
Acid pH activation of the PmrA/PmrB two-component regulatory system of Salmonella enterica Acid pH often triggers changes in gene expression.
However, little is known about the identity of the gene products that sense fluctuations in extracytoplasmic pH.
The Gram-negative pathogen Salmonella enterica serovar Typhimurium experiences a number of acidic environments both inside and outside animal hosts.
Growth in mild acid (pH 5.8) promotes transcription of genes activated by the response regulator PmrA, but the signalling pathway(s) that mediates this response has thus far remained unexplored.
Here we report that this activation requires both PmrA's cognate sensor kinase PmrB, which had been previously shown to respond to Fe3+ and Al3+, and PmrA's post-translational activator PmrD.
Substitution of a conserved histidine or of either one of four conserved glutamic acid residues in the periplasmic domain of PmrB severely decreased or abolished the mild acid-promoted transcription of PmrA-activated genes.
The PmrA/PmrB system controls lipopolysaccharide modifications mediating resistance to the antibiotic polymyxin B.
Wild-type Salmonella grown at pH 5.8 were > 100 000-fold more resistant to polymyxin B than organisms grown at pH 7.7.
Our results suggest that protonation of the PmrB periplasmic histidine and/or of the glutamic acid residues activate the PmrA protein, and that mild acid promotes cellular changes resulting in polymyxin B resistance.

NeMineProtein	confidence
PmrA	0.546
PmrB	0.335
gene products	0.2305
response regulator PmrA	0.2501

Figure 2: Visualisation of web service output

In Figure 2, the top of the screen has check boxes corresponding to each type of annotation produced by the workflow – in this case "Sentence", "NeMineGene" and "NeMineProtein" (the latter two corresponding to named entity types). Checking one or more of the boxes will cause the annotations to become highlighted in the view of the text below. In Figure 2, the "NeMineGene" and "NeMineProtein" annotations are highlighted, each in a different colour.

Below the text, the different types of annotations added by the workflow are shown in tabular format, with each type of annotation in a separate table. In Figure 2, shows the

tables of sentences, NeMineGenes and NeMineProteins. The named entity annotations have a confidence value assigned to them.

An example of the XML output format, which is more suited to programmatic use, is shown in Figure 3. In the XML, the start and end offsets of each annotation in the text are encoded in the "begin" and "end" attributes. For the "NeMineGene" and "NeMineProtein" annotation types, a "confidence" attribute is also present.

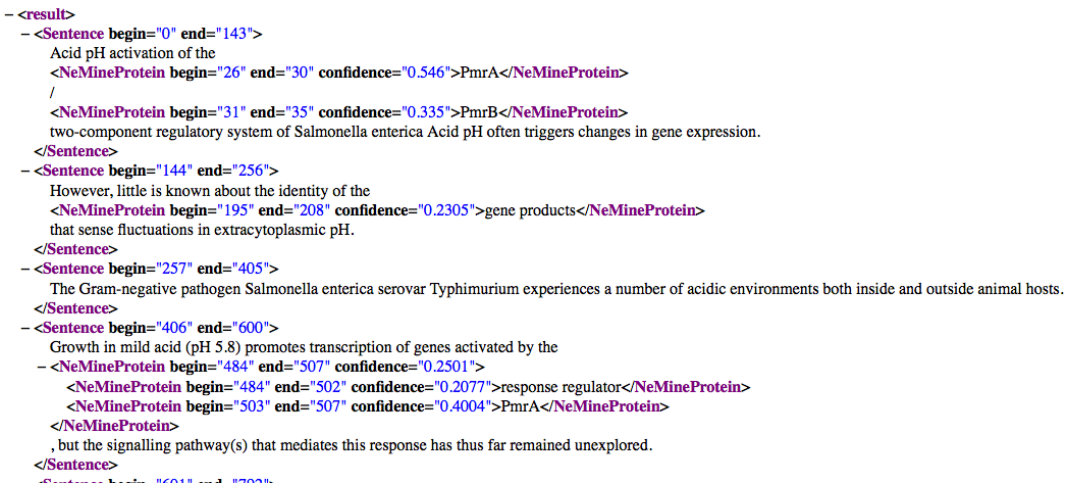


Figure 3: XML output example

3. LICENCE

a) The web service only is licenced NaCTeM Web Service Licence Agreement (standard non-commercial use) – see "U-Compare-Named-Entity-Recognition-Service-Licence.pdf" in the "licences" directory. Please contact us using the details below if you require a commercial licence.

b) The tools used in the workflow on which the web service is based may have their own licences. The NaCTeM Web Service Licence Agreement does NOT apply to these tools.

4. ADMINISTRATIVE INFORMATION

Contact

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5. REFERENCES

Ananiadou, S., Thompson, P., Kano, Y., McNaught, J., Attwood, T. K., Day, P. J. R., Keane, J., Jackson, D. and Pettifer, S.. (2011). Towards Interoperability of European Language Resources. *Ariadne,* 67.

Kontonatsios, G., Korkontzelos, I., Kolluru, B., Thompson, P. and Ananiadou, S. (In Press). Deploying and Sharing U-Compare Workflows as Web Services. *Journal of Biomedical Semantics.*

Sasaki, Y., Tsuruoka, Y., McNaught, J. and Ananiadou, S. (2008). How to make the most of NE dictionaries in statistical NER. *BMC Bioinformatics* 9(Suppl 11):S5.