1. Motivation

Less semantic-aware tasks such as relation extraction has been developed in Japanese medical domain natural language processing. In this work, we target two types of reports for annotating:

- novel annotation of medical and temporal relations in Japanese.
- an open-access toolkit for accurately recognizing entities, modalities and relations from medical texts.

2. Japanese medical relation annotation

We conduct novel relation annotation over an existing Japanese medical corpus (Yada+, 2020) with following entity and modality information annotated:

- Disease
- Anatomical
- Feature
- Change
- Time
- Test
- Medicine
- Remedy
- Clinical Context

On the top of the entity and modality annotation, we designed medical relations and temporal relations between two entities.

Medical Relation

- Change
  "<A>intrahepatic bile ducts</A> are <C>dilated</C>"
- Compare
  "<C>not changed</C> since <TIMEX3> Sep. 2003</TIMEX3>"
- Feature
  "<F>pathologically significant</F> <D>lymph node enlargement</D>"
- Region
  "There are no <D>abnormalities</D> in the <A>liver</A>"
- Value
  "<T-key> Smoking</T-key>: <T-val>20 cigarettes</T-val>"

3. Japanese temporal relation annotation

Temporal Relation

- On
  "<TIMEX3>3 Sep. 2003</TIMEX3>, diagnosed as <D>podagra</D>"
- Before
  "<TIMEX3>April 11th</TIMEX3>"
- After
  "since <TIMEX3>11 Aug</TIMEX3>, PSL was <C>normalized</C>"
- Start
  "<TIMEX3>23 April</TIMEX3>"
- Finish
  "<TIMEX3>17 Nov</TIMEX3>, quitting <R>HOT</R>"

4. Pipeline System of JaMIE

JaMIE: A Pipeline Japanese Medical Information Extraction System

5. The statistics of the relation annotation

In this work, we target two types of reports for annotating:

- RIRLC denotes 1,000 Radiography Interpretation Reports of Lung Cancer.
- MRIPF denotes 156 Medical Reports of Idiopathic Pulmonary Fibrosis.

<table>
<thead>
<tr>
<th>Medical</th>
<th># RIRLC</th>
<th># MRIPF</th>
<th>Temporal</th>
<th># RIRLC</th>
<th># MRIPF</th>
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<tbody>
<tr>
<td>Change</td>
<td>689</td>
<td>465</td>
<td>On</td>
<td>696</td>
<td>1,583</td>
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<tr>
<td>Compare</td>
<td>615</td>
<td>229</td>
<td>Before</td>
<td>1</td>
<td>14</td>
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<tr>
<td>Feature</td>
<td>5,077</td>
<td>294</td>
<td>After</td>
<td>3</td>
<td>22</td>
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<tr>
<td>Region</td>
<td>6,794</td>
<td>631</td>
<td>Start</td>
<td>5</td>
<td>219</td>
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<tr>
<td>Value</td>
<td>2</td>
<td>1,932</td>
<td>Finish</td>
<td>2</td>
<td>43</td>
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</tbody>
</table>

6. Main results

Our BERT-based model achieves accurate analyzing performance, especially in the RIRLC data.

<table>
<thead>
<tr>
<th>Report type</th>
<th>Encoder</th>
<th>MER</th>
<th>MC</th>
<th>RE</th>
</tr>
</thead>
<tbody>
<tr>
<td>RIRLC</td>
<td>LSTM</td>
<td>93.63</td>
<td>93.01</td>
<td>66.88</td>
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<td></td>
<td>BERT</td>
<td>95.65</td>
<td>94.10</td>
<td>86.53</td>
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<td></td>
<td>Yada+ 2020</td>
<td>95.30</td>
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<td></td>
</tr>
<tr>
<td>MRIPF</td>
<td>LSTM</td>
<td>82.73</td>
<td>75.26</td>
<td>60.42</td>
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<tr>
<td></td>
<td>BERT</td>
<td>85.49</td>
<td>78.06</td>
<td>71.04</td>
</tr>
</tbody>
</table>

7. Additional comparison with comparable training data

<table>
<thead>
<tr>
<th>Report type</th>
<th>Training data</th>
<th>RE</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRIPF</td>
<td>100%</td>
<td>71.04</td>
</tr>
<tr>
<td>RIRLC</td>
<td>Comparable</td>
<td>82.33</td>
</tr>
</tbody>
</table>

8. User Interface

JaMIE provides an easy-to-use Command-Line Interface (CLI), which is similar to PyTorch Transformers. We demonstrate how to train/test a relation model with following scripts:

- # Training
  - $ python clinical_pipeline_rel.py
  - $ --pretrained_model $PRETRAINED_JAPANESE_BERT
  - $ --saved_model $FINETUNED_MODEL
  - $ --train_file $TRAIN_FILE
  - $ --dev_file $DEV_FILE
  - $ --batch_size 16
  - $ --do_train
- # Testing
  - $ python clinical_pipeline_rel.py
  - $ --saved_model $FINETUNED_MODEL
  - $ --test_file $TEST_FILE
  - $ --test_out $TEST_OUTPUT