Differential Evaluation: a Qualitative Analysis of Natural Language Processing System Behavior Based Upon Data Resistance to Processing

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Abstract

Most of the time, when dealing with a particular Natural Language Processing task, systems are compared on the basis of global statistics such as recall, precision, F1-score, etc. While such scores provide a general idea of the behavior of these systems, they ignore a key piece of information that can be useful for assessing progress and discerning remaining challenges: the relative difficulty of test instances. To address this shortcoming, we introduce the notion of differential evaluation which effectively defines a pragmatic partition of instances into gradually more difficult bins by leveraging the predictions made by a set of systems. Comparing systems along these difficulty bins enables us to produce a finer-grained analysis of their relative merits, which we illustrate on two use-cases: a comparison of systems participating in a multi-label text classification task (CLEF eHealth 2018 ICD-10 coding), and a comparison of neural models trained for biomedical entity detection (BioCreative V chemical-disease relations dataset).

1 Introduction

The analysis of NLP system results has mainly focused on evaluation scores meant to rank systems and feed leaderboards. In tasks such as information extraction, text classification, etc., evaluation generally relies on the comparison of a hypothesis (typically a system output) with a gold standard, generally produced through manual annotation. Since the MUC-6 conference (Grishman and Sundheim, 1996), the metrics used were created for information retrieval (Cleverdon, 1960): recall (true positive rate), precision (positive predictive value) and their harmonic (possibly weighted) mean, the F1-score. Evaluation scripts are widely available nowadays, for instance those of the CoNLL shared tasks (Tjong Kim Sang and De Meulder, 2003). These scripts rely on an annotation scheme based on the BIO prefix used to specify whether a token is at the beginning, inside or outside of an annotation span, making it a de facto standard for NER evaluation (Nadeau and Sekine, 2007). Many other NLP tasks have developed or used their own metrics, such as accuracy for classification, BLEU (Papineni et al., 2002) for machine translation, ROUGE for machine translation and text summarization (Lin, 2004), word error rate for automatic speech recognition, etc. While evaluation is the key step in shared tasks, developers also need to evaluate the performance of their systems for feature selection or architecture design choices, especially when several systems are combined (Jiang et al., 2016).

However, scores only are insufficient to capture the behavior of systems and to provide a finer-grained analysis of their pros and cons. Indeed, though widely used, scores are not free of imperfections, as demonstrated by Peyrard et al. (2021) who discuss the use of the average to aggregate evaluation scores. They show that very different system behaviors can yield similar scores when using the average and suggest an alternative aggregation mechanism. Some researchers also call for going beyond performance scores: Ethayarajh and Jurafsky (2020) suggest that performance-based evaluation (as promoted by leaderboards) overlooks aspects such as utility, prediction cost, and robustness of models. They recommend considering the point of view of the user of models rather than just performance scores to estimate their relevance.

Trying to provide a finer understanding of the issues raised by the input text and of the limitations of the evaluated systems, we propose a new qualitative analysis method that takes into account the observed relative difficulty of predicting gold labels for each input. This difficulty is assessed pragmatically based upon the number of systems that predict a gold label (a true positive) for a given input. As a qualitative method, its aim is not to compute an evaluation measure nor to rank systems, but
instead to obtain an overview of how different systems achieve the task, and thus understand where their strengths and weaknesses are.

After explaining how the method works globally (Section 2), we illustrate it with data from two shared tasks from the biomedical domain, one for multi-label classification and another for named entity recognition (Section 3), then discuss a few points and directions for future investigation (Section 4).

2 Differential evaluation: highlighting the ‘difficulty’ of examples

Our qualitative analysis method, which we call differential evaluation, globally considers the various sets of correct instances (‘true positives’, or ‘gold instances’) that were discovered by a set of systems. Since the aim of the method is not to produce a ranking, the considered systems can be different systems performing the same task, as in a shared task for example, or different versions of the same system also performing a given task, as in a development context.

As input, the algorithm takes a matrix of instances and systems, as shown in Figure 1. For each instance, it then computes how many systems discovered it correctly (i.e., in Figure 1, ‘762_levodopa’ has been discovered by 6 systems, ‘1034_cyp’ has been discovered by 4 systems, etc.) This enables it to compute then how many instances have been detected by all systems, by all systems but one, by all systems but two, etc., and by no system at all. This yields a grouping of instances into bins depending on the number of systems that discovered them. There are as many bins as there are systems plus one for the set of instances that were discovered by none of the systems. Bin-1 is the set of instances detected by exactly one system, bin-2 the set of instances detected by exactly two systems, etc.; and bin-0, the set of instances that no system was able to detect (see Section 3 for illustrated examples). Figure 2 shows the composition of bin-5 in a case where six systems are compared, and displays the percentage coverage of the bin for each system. Figure 3 shows a schema of the global scenario of the method.

Instances in bin-\(N\) (where \(N\) is the number of considered systems), which holds the set of entities discovered by all systems but one, by all systems but two, etc., and by no system at all. This yields a grouping of instances into bins depending on the number of systems that discovered them. There are as many bins as there are systems plus one for the set of instances that were discovered by none of the systems. Bin-1 is the set of instances detected by exactly one system, bin-2 the set of instances detected by exactly two systems, etc.; and bin-0, the set of instances that no system was able to detect (see Section 3 for illustrated examples). Figure 2 shows the composition of bin-5 in a case where six systems are compared, and displays the percentage coverage of the bin for each system. Figure 3 shows a schema of the global scenario of the method.

![Figure 1: Example input file for a set of six systems. 1 means the system yielded a true positive for the instance, and 0 means it did not (the instance was ‘missed’).](image1)

![Figure 2: Composition of bin-5 in the comparison of six systems. Each instance (row) is missed by exactly one system. Note that each system (column) may miss multiple instances in this bin.](image2)
Figure 3: Differential evaluation scenario. True positives (TPs) are displayed with absolute and relative values (percentage of the number of instances in the bin) in the output matrix, as in Table 1 and Figure 4 respectively. System contributions to a bin can have a null intersection: i.e. here, in bin-4, Systems B and C may be yielding TPs for totally different sets of instances. Bins 1, 2 and 3 omitted for conciseness.

over, bin-1, which holds instances discovered by a single system, can be seen as the bin holding the singular contribution of each system. As such, bin-1 is particularly interesting when considering system combination architectures or ROVER-like performance measures (Fiscus, 1997).

Figure 4 presents one of the outputs of the method, a heatmap of percentages of system TPs relative to the total number of instances in each bin, in this case for the CLEF eHealth 2018 ICD-10 coding task for Italian (Névéol et al., 2018). System contributions to a bin can have a null intersection: i.e. here, in bin-4, Systems B and C may be yielding TPs for totally different sets of instances. Bins 1, 2 and 3 omitted for conciseness.

Figure 4: Percentage of labels (true positives) correctly found by each system in each bin for Italian in the CLEF eHealth 2018 ICD-10 coding task. Systems on x-axis and bins on y-axis.

3 Experiments

In this section, we present insights that can be drawn from the use of differential evaluation on data related to two shared tasks addressing respectively multi-label text classification and named entity recognition, both in the biomedical domain. Note that our algorithm processes the systems in the order in which they are presented and that it is not intended to create a new ranking of the systems, but rather to provide more fine-grained information to analyze how a given system has performed or achieved its ranking.

3.1 CLEF eHealth 2018 ICD-10 coding

We show as an example the output obtained in the comparison of systems in a multi-label text classification task in Italian and Hungarian (Névéol et al., 2018). In the gold standard, each input text is associated to one or more true labels, i.e., codes in the International Classification of Diseases (ICD-10). A true positive system prediction is an association between a given input text and one of the true labels for this text in the gold standard. In this dataset,
| Systems | bin-0 | bin-1 | bin-2 | bin-3 | bin-4 | bin-5 | bin-6 | bin-7 | bin-8 | bin-9 | bin-10 | bin-11 | Total TPs per system |
|---------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|---------------------|
| A       | 0     | 69    | 224   | 648   | 1005  | 1245  | 1774  | 1390  | 3890  | 14680 |        |        | 15534              |
| B1      | 0     | 31    | 126   | 434   | 575   | 959   | 1211  | 1760  | 1373  | 3886  | 3800   | 7524   |                      |
| C1      | 0     | 7     | 11    | 31    | 83    | 138   | 227   | 1005  | 660   | 1390  | 14680  |        |                      |
| D1      | 0     | 9     | 55    | 105   | 331   | 463   | 823   | 1608  | 1344  | 3884  | 3800   | 1392   |                      |
| E1      | 0     | 6     | 60    | 183   | 289   | 639   | 982   | 1549  | 1327  | 3886  | 3800   | 12798  |                      |
| F1      | 0     | 10    | 29    | 34    | 131   | 289   | 458   | 930   | 1110  | 3855  | 3800   | 10703  |                      |
| Total per bin | 305  | 185  | 316  | 326  | 355  | 688  | 1029  | 1267  | 1781  | 1392  | 3890  | 15534            |

Table 1: Number of labels (true positives) correctly found by each system in each bin for Italian: absolute values. Bin $n$ contains the labels found by exactly $n$ systems. Best performance in green, worst performance in red.

Performances are pretty steady, with System B1 outperforming all the others in every bin. The worst results are shared by Systems C1 and C2, and System A that performs badly for bins-8 and 10, which are among the “easiest” bins. As seen in Table 1, although System E2 scores the worst for bin-1 with only two labels discovered, it manages to keep up with the performances of the other systems in the other bins, and its global performance (12,884 total TPs discovered) is pretty average. On the other hand, Systems C1 and C2, which are the worst systems across all bins, are not so bad globally with 9,877 and 9,572 total TPs. In fact, System A achieves a very low performance on two of the “easiest” bins, and thus yields less than half of the total labels, despite a not so bad performance on bin-1. Figure 4 shows that systems can be divided into groups of better and worse performances (B1, B2, D1, D2, E1, E2 vs. A, C1, C2, F1, F2). We can also see that System B1 reaches a perfect score over all easier bins up to bin-8, which hints at its being robust on easy instances.

### Hungarian

Figure 5 and Table 2 show the proportion and number of detected labels per system within each bin for the Hungarian language.²

As highlighted by colors in Table 2, we can see that globally, Systems G1 and G2 perform the best, and Systems K1 and K2 perform the worst.

Just above K1 and K2 in terms of Total TPs per system (Table 2), System J is the worst at detecting labels from bin-8 (see also Figure 5), which can

²The data are not the same as that for Italian, hence the different total values.
Table 2: Number of labels (true positives) correctly found by each system in each bin for Hungarian: absolute values. Bin \(n\) contains the labels found by exactly \(n\) systems. In this analysis, the systems are ordered in decreasing order of F1-score, determined prior to the present analysis.

| Systems | bin-0 | bin-1 | bin-2 | bin-3 | bin-4 | bin-5 | bin-6 | bin-7 | bin-8 | bin-9 | Total TPs per system |
|---------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|----------------------|
| G1      | 104   | 555   | 655   | 2856  | 4760  | 11246 | 37654 | 9034  | 26324 | 93187 | 93187                |
| G2      | 116   | 542   | 642   | 2828  | 4700  | 11239 | 37659 | 9028  | 26324 | 93078 | 93078                |
| H1      | 72    | 381   | 375   | 2001  | 3471  | 10080 | 37367 | 8749  | 26324 | 88820 | 88820                |
| H2      | 0     | 333   | 358   | 1375  | 2877  | 10293 | 36748 | 8980  | 26324 | 89913 | 89913                |
| I1      | 0     | 356   | 319   | 1356  | 24301 | 10285 | 35875 | 8995  | 26324 | 86510 | 86510                |
| I2      | 0     | 45    | 366   | 519   | 1356  | 2400  | 10208 | 36575 | 8695  | 26324 | 86510                |
| J       | 136   | 126   | 364   | 357   | 2986  | 3331  | 37024 | 2134  | 26324 | 72982 | 72982                |
| K1      | 19    | 46    | 73    | 140   | 285   | 832   | 1693  | 8460  | 26324 | 37872 | 37872                |
| K2      | 7     | 45    | 40    | 89    | 215   | 947   | 1508  | 8303  | 26324 | 37478 | 37478                |

Total per bin: 1442 628 1387 1200 3305 5060 11466 37369 9046 26324 97537

3.2 BioCreative V CDR entities

The BioCreative V chemical-disease relation (CDR) task is originally a relation extraction task (Wei et al., 2016). Its data can also be used to train and evaluate entity-detection systems for chemical and disease entities, which is what we examine here. The dataset is made of 1,500 PubMed abstracts of scientific papers, divided equally into training, development and test. In the gold standard, each input token is associated to one true label and named entities are encoded according to the BIO (begin, inside, outside) scheme. In the present work we deal with tokens rather than entities, so that we can apply the presented method directly. We consider that ‘O’ labels are negatives and that all other labels are positives. A true positive system prediction is an association between an input token and a non-‘O’ label that is the gold-standard label for this token.

We are comparing entity detection systems that rely on word embeddings based upon CharacterBert (El Boukkouri et al., 2020) or fastText (Bojanowski et al., 2017), pre-trained on different corpora, either as-is or concatenated with knowledge embeddings learned using node2vec (Grover and Leskovec, 2016) on two biomedical vocabularies (the Medical Subject Headings (MeSH), and SNOMED CT). Moreover, we also consider a variant of CharacterBert where the node2vec embeddings are injected within the model architecture. The fastText embeddings are either randomly initialized, which we note “fastTextRandom”; pre-trained on a newswire corpus (Gigaword (Graff et al., 2007)), which we note “fastTextGigaword”; or on medical corpora (PubMed Central\(^3\) and MIMIC-III (Johnson et al., 2016)), which

\(^3\)https://www.ncbi.nlm.nih.gov/pmc/tools/openftlist/
we respectively note “fastTextPubMed” and “fastTextMimic”. The CharacterBert models are either pre-trained on general corpora (English Wikipedia and OpenWebText (Gokaslan and Cohen, 2019)), which we note “CharBertGen”; or pre-trained on general corpora then re-trained on PubMed and MIMIC-III, which we note “CharBertFromGen”. In all cases the suffix “N2V” refers to a concatenation with the node2vec knowledge representations, with the exception of “Enh.CharBertFromGenN2V” which refers to the variant of CharacterBERT where the node2vec vectors are injected directly within the architecture. This last model is pre-trained on the general corpus then re-trained on PubMed and MIMIC-III in order to be compared with “CharBertFromGen”.

Tables 3 and 4 respectively show absolute values for chemical and disease entity recognition, and Figures 7 and 8 the corresponding bin percentages.

### 3.2.1 Global performances and pairwise comparison of models

Overall, we can see that the contextual CharacterBert embeddings perform better than the static fastText vectors in both chemical and disease recognition, with the worst performances for randomly initialized fastText embeddings. Moreover, we see that the CharacterBert models trained on medical data perform better than their general versions (Tables 3 and 4, Figures 7 and 8), which confirms the interest of retraining the general models on in-domain data.

**Chemical** CharacterBert seems to perform rather similarly regardless of the combination with node2vec embeddings. For fastText models, pairwise comparison in Table 5 shows that the introduction of knowledge embeddings (node2vec) improves recall. Comparison of bins further confirms this observation: we can see that the im-

| Model                          | bin-0 | bin-1 | bin-2 | bin-3 | bin-4 | bin-5 | bin-6 | bin-7 | bin-8 | bin-9 | bin-10 | bin-11 | bin-12 | Tot. TPs/system |
|-------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|-----------------|
| Enh.CharBertFromGenN2V        | 0     | 12    | 65    | 72    | 155   | 148   | 156   | 176   | 223   | 294   | 465    | 852    | 3894   | 6512            |
| CharBertFromGen               | 0     | 9     | 70    | 75    | 147   | 147   | 158   | 174   | 228   | 287   | 477    | 868    | 3894   | 6534            |
| CharBertGenN2V                | 0     | 4     | 7     | 7     | 28    | 61    | 77    | 110   | 164   | 244   | 446    | 869    | 3894   | 5913            |
| CharBertGen                   | 0     | 3     | 7     | 41    | 103   | 113   | 131   | 163   | 205   | 285   | 463    | 853    | 3894   | 6261            |
| fastTextGigawordN2V           | 0     | 6     | 7     | 7     | 28    | 61    | 77    | 110   | 164   | 244   | 446    | 869    | 3894   | 5913            |
| fastTextGigaword              | 0     | 0     | 3     | 7     | 19    | 60    | 78    | 111   | 106   | 196   | 343    | 812    | 3894   | 5913            |
| fastTextMimicN2V              | 0     | 1     | 14    | 29    | 43    | 59    | 91    | 165   | 235   | 450   | 862    | 3894   | 5851   | 5851            |
| fastTextMimic                | 0     | 2     | 10    | 9     | 20    | 53    | 56    | 88    | 128   | 247   | 449    | 862    | 3894   | 5993            |
| fastTextPubMedN2V             | 0     | 4     | 12    | 21    | 47    | 51    | 87    | 113   | 190   | 254   | 453    | 830    | 3894   | 5956            |
| fastTextPubMed               | 0     | 3     | 10    | 29    | 39    | 83    | 101   | 116   | 182   | 247   | 449    | 862    | 3894   | 6015            |
| fastTextRandomN2V             | 0     | 0     | 5     | 11    | 28    | 39    | 39    | 77    | 106   | 161   | 322    | 792    | 3894   | 5474            |
| fastTextRandom               | 0     | 1     | 2     | 9     | 18    | 30    | 41    | 62    | 106   | 143   | 338    | 3894   | 4700   | 5474            |
| Total TPs per bin            | 178   | 41    | 105   | 112   | 185   | 188   | 187   | 207   | 244   | 309   | 489    | 876    | 3894   | 7015            |

**Table 3:** Absolute values for chemical NER. Best performance in green, worst performance in red, orange when the random initialization is above one of the other initializations.

| Models                        | bin-0 | bin-1 | bin-2 | bin-3 | bin-4 | bin-5 | bin-6 | bin-7 | bin-8 | bin-9 | bin-10 | bin-11 | bin-12 | Tot. TPs/system |
|-------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|-----------------|
| Enh.CharBertFromGenN2V        | 0     | 16    | 70    | 74    | 123   | 115   | 159   | 181   | 296   | 3894  | 800    | 3617   | 6697   | 6106            |
| CharBertFromGen               | 0     | 44    | 89    | 92    | 142   | 123   | 164   | 179   | 247   | 3894  | 791    | 3617   | 6166   | 6166            |
| CharBertGenN2V                | 0     | 14    | 29    | 66    | 106   | 110   | 137   | 166   | 238   | 387   | 795    | 3617   | 5934   | 5934            |
| CharBertGen                   | 0     | 24    | 32    | 37    | 110   | 107   | 137   | 162   | 234   | 387   | 802    | 3617   | 5956   | 5956            |
| fastTextGigawordN2V           | 0     | 3     | 22    | 36    | 59    | 70    | 112   | 141   | 224   | 388   | 803    | 3617   | 5778   | 5778            |
| fastTextGigaword              | 0     | 5     | 7     | 17    | 25    | 50    | 72    | 91    | 126   | 205   | 311    | 730    | 3617   | 3256            |
| fastTextMimicN2V              | 0     | 6     | 12    | 25    | 39    | 54    | 103   | 144   | 207   | 257   | 359    | 791    | 3617   | 5614            |
| fastTextMimic                | 0     | 13    | 12    | 29    | 33    | 51    | 85    | 94    | 145   | 200   | 325    | 746    | 3617   | 5350            |
| fastTextPubMedN2V             | 0     | 6     | 15    | 32    | 64    | 65    | 141   | 162   | 236   | 292   | 408    | 814    | 3617   | 5852            |
| fastTextPubMed               | 0     | 5     | 12    | 29    | 50    | 53    | 103   | 118   | 182   | 204   | 332    | 764    | 3617   | 5469            |
| fastTextRandomN2V             | 0     | 10    | 27    | 41    | 52    | 52    | 85    | 112   | 177   | 223   | 314    | 717    | 3617   | 5427            |
| fastTextRandom               | 0     | 10    | 9     | 24    | 28    | 40    | 58    | 60    | 96    | 124   | 195    | 489    | 3617   | 4750            |
| Total TPs per bin            | 340   | 156   | 168   | 174   | 208   | 178   | 226   | 230   | 296   | 327   | 419    | 822    | 3617   | 7161            |

**Table 4:** Absolute values for disease NER. Best performance in green, worst performance in red, orange when the random initialization is above one of the other initializations.
Table 5: Pairwise comparison of systems with or without addition of Node2Vec embeddings for chemical NER (bin-0 and bin-12 are not considered). The best model for each bin is highlighted in green.

| System                  | bin-0 | bin-1 | bin-2 | bin-3 | bin-4 | bin-5 | bin-6 | bin-7 | bin-8 | bin-9 | bin-10 | bin-11 | Recall |
|-------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|
| EnhancedCharBertFromGenN2V | 29    | 62    | 64    | 84    | 79    | 83    | 85    | 91    | 95    | 95    | 97    | 92.83  |
| CharBertFromGen         | 22    | 67    | 67    | 79    | 78    | 84    | 84    | 93    | 93    | 98    | 99    | 93.14  |
| CharBertGenN2V          | 2     | 10    | 37    | 58    | 60    | 74    | 81    | 82    | 91    | 95    | 99    | 89.62  |
| CharBertGen             | 7     | 37    | 37    | 56    | 60    | 70    | 79    | 84    | 92    | 95    | 97    | 89.25  |
| fastTextGigawordN2V     | 15    | 7     | 6     | 15    | 32    | 41    | 53    | 67    | 79    | 91    | 99    | 84.29  |
| fastTextGigaword        | 0     | 3     | 6     | 10    | 32    | 42    | 54    | 43    | 63    | 70    | 93    | 80.24  |
| fastTextMimicN2V        | 0     | 9     | 12    | 16    | 23    | 32    | 44    | 68    | 76    | 92    | 98    | 83.41  |
| fastTextMimic           | 5     | 10    | 8     | 11    | 28    | 30    | 43    | 52    | 61    | 84    | 95    | 81.15  |
| fastTextPubMedN2V       | 15    | 11    | 19    | 25    | 27    | 47    | 55    | 78    | 82    | 93    | 95    | 84.90  |
| fastTextPubMed           | 7     | 10    | 26    | 21    | 44    | 54    | 56    | 75    | 80    | 92    | 98    | 85.74  |
| fastTextRandomN2V       | 0     | 5     | 10    | 15    | 21    | 37    | 43    | 52    | 66    | 90    | 78.03  |
| fastTextRandom           | 2     | 2     | 8     | 10    | 16    | 22    | 30    | 23    | 24    | 29    | 39    | 67.00  |

Figure 7: Percentage of labels (true positives) correctly found by each system in each bin for chemical substances.

Figure 8: Percentage of labels (true positives) correctly found by each system in each bin for diseases.

A strong positive effect is made on “easy” entities (bins 8 through 11). However, for “fastTextPubMed” the effect of node2vec is not so clear or even harmful (bins 5 and 6). This phenomenon could be explained by the fact that both PubMed and the BioCreative CDR task are from the biomedical domain while MIMIC-III and Gigaword are from somewhat different domains (clinical and newswire domains respectively). In the case of fastTextPubMed, adding medical knowledge embeddings seems to degrade performance.

**Disease**

While node2vec has a strong positive effect on fastText models regardless of their source corpus, pairwise comparison of recall for disease NER in Table 6 shows that the addition of node2vec is detrimental to CharacterBert models. However, this analysis can be refined by comparing bin-wise performances: for CharacterBert models trained on medical data (top two lines), the versions that do not use node2vec embeddings are better on “more difficult” bins, while the enhanced version are actually better on “easier” bins.

3.2.2 Bin inspection

Browsing through the bins can give an idea of the kinds of entities they hold. This can be done in different ways.

**Bin-0 exploration**

We inspect here the contents of bin-0 for both the chemical and disease recognition tasks, as this bin is supposed to hold false negatives that resist all systems, i.e. the most difficult entities.

Bin-0 for both chemical and disease contains occurrences of abbreviations, which occur quite frequently within parentheses in the context of their full form: for example “bs” for “bile salt” and “rd” (sic) for “lenalidomide and dexamethasone” for chemical, “mi” for “myocardial infarction” and “mb” for “microbleeds” for disease. We also spot
expressions that should perhaps not be in the gold standard, such as “abuse of cocaine and ethanol” tagged as a disease, or typographic errors such as “antithyroidmedications”.

Both bins also hold an important number of single-character tokens such as punctuation marks and digits. For disease recognition, these include the determiner “a”, which occurs most of the time as a part of a multi-word entity. A similar phenomenon occurs with other tokens such as “of”. Occurrences of these words seem to be due to multi-word entities referring to diseases and conditions such as “enlargement of pulse pressure”, “occlusion of renal vessels”, “thrombosis of a normal renal artery”. It seems that multi-word entities account for a significant proportion of the generated errors, where systems only recover the first word of a multi-word entity. For example, chemical bin-0 holds all occurrences of “channel” and “blockers” from “calcium channel blockers”, while occurrences of “calcium” in this context are always labelled correctly.

However, a quick inspection of other bins reveals that those part-of-speech and morphological characteristics (punctuation, single-character entities and abbreviations) are not specific to bin-0. For instance, punctuation marks make for 14% of chemical bin-0 tokens, and for 9 to 28% of bins 1 to 11 (0.07% for bin-12). In the case of disease recognition, punctuation represents 8.8% of bin-0, while ranging from 1.7% to 5.1% of bins 1 to 12. In the case of disease recognition, punctuation represents 8.8% of bin-0, while ranging from 1.7% to 5.1% of bins 1 to 12 (this difference in proportions between chemical bin-0 and disease bin-0 is potentially very useful, since we can then rank systems respectively by exactly one, four, five, nine, nine, and ten systems. This feedback is systematically missed in the chemical recognition tasks. We assume that this is probably because it is confused with “chinese” used as the nationality of patients. The same applies to hapax “philadelphia” from “philadelphia chromosome”. These examples lead us to assume that specialized usage of “common” vocabulary terms in chemical or disease entities induces a difficulty for systems.

We also found two other phenomena both in chemical bin-0 and in disease bin-0: hapax legomena (“hapaxes”) and ambiguous tokens.

Hapaxes are tokens that occur only once in the whole data. In bin-0 of the chemical NER task, examples include “adrenergic”, “colony”, “steroidal” or “agents”. In disease bin-0, examples include “bacillary”, “audiogenic”, “choreic”, “teratogenic”.

Ambiguous tokens in bin-0 are due to their multiple or specific meanings in the corpus. This is the case for token “chinese” (note that the corpus is lower-cased), which occurs in “chinese herbal slimming pill”, “chinese herbal”, “chinese herbs”, and is systematically missed in the chemical recognition tasks. We assume that this is probably because it is confused with “chinese” used as the nationality of patients. The same applies to hapax “philadelphia” from “philadelphia chromosome”. These examples lead us to assume that specialized usage of “common” vocabulary terms in chemical or disease entities induces a difficulty for systems.

**Distribution across bins** Finally, another way to perform bin inspection is to look at the distribution of mentions of a same word across bins. As an illustration, we use the distribution of “calcium” in chemical bins (Table 7): one mention is in bin-1, no mention is in bin-2 and 3, one mention is in bin-4, etc. While most mentions of “calcium” are retrieved by all eleven systems (29 mentions precisely), a total of six of those mentions are individually discovered respectively by exactly one, four, five, nine, nine, and ten systems. This feedback is potentially very useful, since we can then rank every mention in ascending order of difficulty, and proceed to look for explanations for why those six mentions resist detection by a number of systems.
4 Discussion and future work

As we have seen, differential evaluation is a qualitative analysis method that allows for more in-depth evaluation when comparing the behavior of several systems with each other. Rather than relying only on the classical global metrics, it provides an insight into how the performance of each system is actually distributed in automatically-determined subsets of examples relative to other systems, and how systems contribute in their very own way.

As presented in the heatmap we used, harder elements to process are in the first column while easier elements are in the last column. This sorting into several columns allows us to rapidly overview how systems perform on a given task. Based on the analysis we made on the content of bins from several tasks and distinct domains, we observed that the first bin is generally composed of elements such as abbreviations and ambiguous words used in several contexts (some of these contexts are a part of an annotation while other contexts are not); moreover, these elements are often short (two or three characters long), which makes them difficult to process for statistical approaches. In the case of multi-label text classification for Hungarian (Section 3.1.2), differential analysis provided an insight that would have been overlooked by global scores.

Future directions include the following points. First, as we have seen in Section 3.2.2, in the case of named entity recognition, examples composed of several tokens are counted token per token and not as a whole entity. Including this dimension will give another insight into the behavior of models for named-entity recognition. A second direction is to extend the current approach, which focuses on recall, hence true positives against false negatives, to take into account other basic evaluation variables, namely false positives and true negatives. A third useful direction would be to retrieve information on the context of occurrence of examples and their global features: sentence length, direct context, average number of characters per token for each bin, etc. Finally, a fourth direction would be to automatically track the distribution of different mentions of a same word across bins, as we have done manually with “calcium” in the second paragraph of Section 3.2.2. Linked to the previous development regarding contextual information, this would allow us to understand precisely why one particular occurrence of a word is missed while the others are more easily spotted.

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