

Biomedical Named Entity Recognition and Normalization Tools

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Overview

- 1. Background
 - BTM, NER, NEN
- 2. Challenges
- 3. Models and Corpora
- 4. Evaluation Method and Result
- 5. Discussion
- 6. Summary

PAPER

HunFlair2 in a cross-corpus evaluation of biomedical named entity recognition and normalization tools

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FOR PUBLISHER ONLY Received on Date Month Year; revised on Date Month Year; accepted on Date Month Year

Abstract



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1. Background

Biomedical Text Mining (BTM)

Extracts information from bio-literature

Key Processes

- NER (Named Entity Recognition)
 - Diseases, drugs, genes
- NEN (Named Entity Normalization)
 - Link entities to standard Knowledge base(KS) / dictionary
 - NCBI (National Center for Biotechnology Information)
 - CTD (Comparative Toxicogenomics Database)





Illuminating how chemicals affect human health.

Comparative Toxicogenomics Database

Challenges

- Ambiguity, complex terminology
- Al advancements, analytical integration

https://www.ncbi.nlm.nih.gov https://ctdbase.org



1. Background

BERN2 for example

Plain TextPubMed ID (PMID)

Autophagy maintains tumour growth through circulating arginine. Autophagy captures intracellular components and delivers them to lysosomes, where they are degraded and recycled to sustain metabolism and to enable survival during starvation1-5. Acute, whole-body deletion of the essential autophagy gene Atg7 in adult mice causes a systemic metabolic defect that manifests as starvation intolerance and gradual loss of white adipose tissue, liver glycogen and muscle mass1. Cancer cells also benefit from autophagy.

514/3000 characters



Disease

Annotation result in 581.84ms

Autopha Entity Aypei Gene/Protein rowth through circulating arginine. Autophagy captures intracellular components and delivers them to lysosomes, where they are degraded and recycled to sustain metabolism and to enable survival during starvation1-5. Acute, whole-body deletion of the essential autophagy gene Atg7 in adult mice causes a systemic metabolic defect that manifests as starvation intolerance and gradual loss of white adipose tissue, liver glycogen and muscle mass1. Cancer cells also benefit from autophagy.

Species Gene/Protein

DNA

Drug/Chemical

Cell type

http://bern2.korea.ac.kr



2. Challenges

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2. Challenge

Non-consecutive / Overlapping

"[...] is causing breast and ovarian cancer [...]"

- "breast" and "ovarian cancer"
- breast and ovarian cancer "
- "breast cancer" and "ovarian cancer

Synonyms

- **Diabetes**: Most commonly used term.
- Diabetes mellitus: The formal medical term
- DM: Abbreviation for "Diabetes Mellitus"
- Hyperglycemia:
 - Sometimes used in the context of describing prediabetes or complications, although it primarily describes a symptom.
- Type 1 Diabetes and Type 2 Diabetes:



2. Challenge

Example of BlueBERT handling NER:

"Patient with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is showing signs of improvement."

```
[CLS]: LABEL 1
patient: LABEL 1
with: LABEL 0
                            severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)
severe: LABEL 0
acute: LABEL 1
respiratory: LABEL 1
syndrome: LABEL 0
corona: LABEL 1
##virus: LABEL 1
2: LABEL 1
(: LABEL 1
sar: LABEL 1
##s: LABEL 1
-: LABEL 1
co: LABEL 0
##v: LABEL 1
-: LABEL 1
2: LABEL 1
): LABEL 1
is: LABEL 0
showing: LABEL 0
signs: LABEL 0
of: LABEL 0
improvement: LABEL 0
.: LABEL 0
[SEP]: LABEL 0
```



2. Challenge

Data Quality and Availability Status:

- BC2GM (2007): BioCreative II Gene Mention
- BC4CHEMD (2013)
- Linnaeus Dataset (2010)
- CRAFT (2012)
- BioNLP13 CG (2013)

Data Imbalance in Biomedical Research

- rare diseases with limited descriptions

Explainability

The "black box" nature of LLM technology

Existing Benchmark Limitations

- Focus: Only Recognition or Normalization
- Lacks: End-to-End NER and NEN Results

Technological Updates

Ignored: Latest Transformer-Based Models



3. Models and Corpora

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 $^{^\}dagger Authors$ contributed equally.

3. Models

Model Selection Criteria

- C1: Supports both NER and NEN
- C2: Utilizes machine-learning-based models for NER
 - Machine-learning NER as state-of-the-art
- C3: Extracts genes, diseases, chemicals, species
 - Important for downstream applications
- C4: No additional licenses required (e.g., commercial, UMLS)
 - Usability in research pipelines without licensing constraints

Qualified Tools

- BERN2
- PubTator
- SciSpacy
- bent
- HunFlair2



3. Models

Table 1. Overview of the tools selected for our evaluation. We distinguish rule-based ("RB"), machine learning-based ("ML") and neural-network based ("NN") approaches for NER and NEN. Moreover, for each tool we illustrate the support of the following entity types: genes (Ge), species (Sp), disease (Di), chemical (Ch), cell line (Cl) and variant (Va). For each entity type we illustrate whether the tool supports NER and NEN of the type by marking the column with \checkmark , if only NER is supported we use (\checkmark). Last update highlights the last update of the code repository of the respective tool. Citations counts are taken from Google Scholar on 01/10/2024.

| Tool | API | Ge | \mathbf{Sp} | Di | Ch | Cl | Va | NER | NEN | Pub. Year | Last Update | Citations |
|------------------------|-----------------|-------------|---------------|----|----|----|-------------|---------|---------|-----------|-------------|-----------|
| PubTator Central [116] | REST/ Tools | ✓ | ✓ | ✓ | ✓ | 1 | ✓ | ML / NN | RB | 2019 | - | 315 |
| BERN2 [78] | REST/ Python | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | NN | RB / NN | 2022 | 11/2023 | 46 |
| SciSpacy [79] | Python | (✓) | ✓ | ✓ | ✓ | ✓ | (✓) | NN | RB | 2019 | 10/2023 | 635 |
| bent [88, 89] | Python | ✓ | ✓ | ✓ | ✓ | ✓ | (✓) | NN | RB | 2020 | 12/2023 | 13 |
| HunFlair2 [114] | Python | ✓ | ✓ | ✓ | ✓ | 1 | | NN | RB / NN | 2021 | 01/2024 | 83 |

Sänger, Mario, et al. "HunFlair2 in a cross-corpus evaluation of named entity recognition and normalization tools." arXiv preprint arXiv:2402.12372 (2024).



3.1 BERN2

NER (Named Entity Recognition)

- Transformer-Based: RoBERTa
 - Multi-Task Training

NEN (Named Entity Normalization)

- Hybrid System:
 - Rule-Based + Neural-Based
- Neural-Based Model: BioSyn

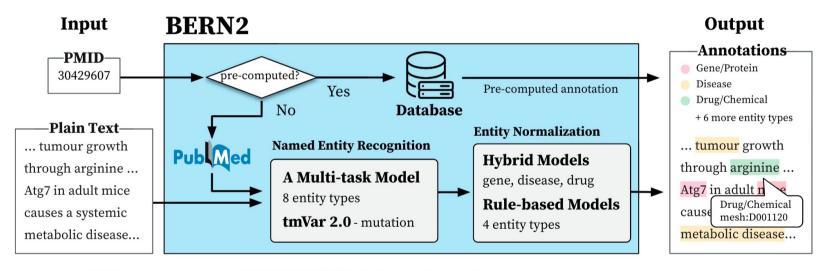


Fig. 1. An overview of BERN2. Given plain text or a PubMed ID (PMID), BERN2 recognizes nine biomedical entity types and normalizes each concept

Sung, Mujeen, et al. "BERN2: an advanced neural biomedical named entity recognition and normalization tool." Bioinformatics 38.20 (2022): 4837-4839.



3.1 BERN2

| Entity Type | NER Model | NER Training Corpus | NEN Model | NEN Training Corpus |
|-------------|-----------|---------------------|-------------------------------------|---------------------------|
| Genes | RoBERTa | BC2GM | GNormPlus, BioSyn(NN) | BC2GN |
| Diseases | | NCBI Disease | sieve-based approach, BioSyn(NN) | BC5CDR, NCBI Disease |
| Chemicals | | BC4CHEMD | tmChem4, BioSyn(NN) | BC5CDR |
| Species | | Linnaeus | dictionary lookup | Not specified for species |



3.2 PubTator

| Entity Type | NER Model | NER Training Corpus | NEN Model | NEN Training Corpus |
|-------------|------------------------------|---------------------------------|---|---------------------------------|
| Genes | BlueBERT | GNormPlus, NLM-Gene | TF-IDF frequencies | Not specifically stated |
| Species | SR4GN (Rule-based system) | Not specifically stated | SR4GN (Rule-based system) | Not specifically stated |
| Chemicals | BlueBERT | BC5CDR, NLM-Chem | Multi-terminology candidate resolution (MTCR) | Not specifically stated |
| Disease | TaggerOne | NCBI Disease, BC5CDR corpora | TaggerOne | NCBI Disease, BC5CDR corpora |

SR4GN (Species Recognition for Gene Normalization)



3.3 SciSpacy

| Entity Type | NER Model | NER Training Corpus | NEN Model |
|-------------|-----------------|-------------------------------|--|
| Genes | Stack LSTMs(NN) | CRAFT, BioNLP13 CG | |
| Diseases | Stack LSTMs(NN) | BC5CDR, BioNLP13 CG | |
| Chemicals | Stack LSTMs(NN) | BC5CDR, CRAFT, BioNLP13 CG | string-matching approach based on characters 3-grams |
| Species | Stack LSTMs(NN) | CRAFT, BioNLP13 CG | |

Stack LSTMs (Stacked Long Short-Term Memory networks)



3.4 bent

| Entity Type | NER Model | NER Training Corpus | NEN Model |
|-------------|------------|-------------------------|-----------|
| Genes | PubMedBERT | BC2GM, CRAFT | |
| Diseases | PubMedBERT | BC5CDR, NCBI-disease | PageRank |
| Chemicals | PubMedBERT | BC5CDR, NLMChem | |
| Species | PubMedBERT | Linnaeus, CRAFT | |



3.5 HunFlair2

NER (Named Entity Recognition)

- Entity Extraction:
 - BioLink-BERT
 - Joint Extraction, the end-to-end entity extraction

Indicate the entity types to extract

- Examples:
 - [Tag genes] <input-example>
 - [Tag diseases] <input-example>
 - [Tag chemicals, diseases, genes, species] <input-example>
- Output Labels: IOB Scheme (B-<entity type>, I-<entity type>)

NEN (Named Entity Normalization)

- Models Employed:
 - BioSyn
 - SapBERT

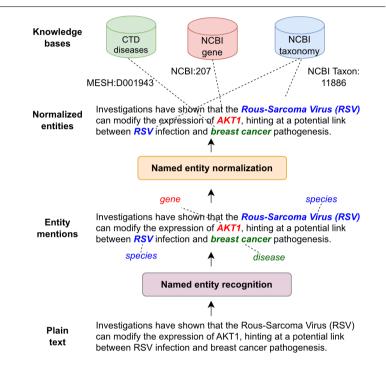


Fig. 1. Illustration of the named entity extraction process. First entity mentions in plain will be identified using named entity recognition (NER) tools. Afterwards named entity normalization (NEN) approaches map the found mentions to standard identifiers in a knowledge base.

Sänger, Mario, et al. "HunFlair2 in a cross-corpus evaluation of named entity recognition and normalization tools." arXiv preprint arXiv:2402.12372 (2024).



3.5 HunFlair2

| Entity Type | NER Model | NER Training Corpus | NEN Model | NEN Training Corpus |
|-------------|--------------|--|-----------|--|
| Genes | | BioRED, NLM Gene, GNormPlus | | BC2GN, NCBI Gene (human subset) |
| Diseases | BioLink-BERT | BioRED, NCBI Disease, SCAI Disease | BioSyn | Not explicitly mentioned for diseases |
| Chemicals | | BioRED, NLM Chem, SCAI Chemical | | Not explicitly mentioned for chemicals |
| Species | | BioRED, Linneaus, S800 | SapBERT | UMLS |



3. Models and Corpora

| Model Name | NER Technique Details | NEN Technique Details |
|------------|-------------------------|-----------------------------------|
| BERN2 | RoBERTa | Rule-based, Neural Networks |
| bent | PubMedBERT | PageRank algorithm |
| PubTator | BlueBERT, rule-based | TF-IDF frequencies mixed methods |
| SciSpacy | Stack LSTMs | Character 3-grams string matching |
| HunFlair2 | BioLink-BERT | Neural Networks, SapBERT |



3. Models and Corpora

| Models | Genes | Chemicals | Diseases | Species |
|-----------|-------------------------|----------------------------|-------------------------------|-----------------------|
| BERN2 | BC2GM | BC4CHEMD | NCBI Disease | Linnaeus |
| bent | BC2GM, CRAFT | BC5CDR, NLM-Chem | BC5CDR, NCBI-disease | Linnaeus, CRAFT |
| PubTator | GnormPlus, NLM- Gene | BC5CDR, NLM-Chem | NCBI-Disease, BC5CDR | - |
| SciSpacy | CRAFT | BC5CDR, BioNLP13 CG | BC5CDR | CRAFT, BioNLP13 CG |
| HunFlair2 | NLM Gene, GNormPlus | NLM Chem, SCAI Chemical | NCBI Disease, SCAI disease | Linnaeus, S800 |



4. Evaluation Method and Result

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4.1 Evaluation

- End-to-End Approach: Direct entity and relation identification for efficiency
 - Normal benchmarks have limitations too, either recognizing entities or normalizing
 - End-to-End: start and end offset of the mention boundary and KB identifier. triplets (start, end, KBID)

Data Selection Criteria:

- a: Corpora unused in tool training (training/development split)
- b: Corpora with NER and NEN annotations
- c: Entity types normalized to universally supported KBs

Knowledge Bases (KBs) Selected:

- Genes: NCBI Gene

Diseases: CTD DiseasesChemicals: CTD ChemicalsSpecies: NCBI Taxonomy

Corpora Selected for Benchmark:

- BioID
- MedMentions
- tmVar (v3)



4.2 Result

| Tool | In-corpus | Cross-corpus |
|----------|------------------------------|--------------------------|
| BERN2 | | |
| Chemical | 96.60† (BC5CDR) | $41.68 \; (MedMentions)$ |
| Disease | 93.90† (BC5CDR) | $47.31 \; (MedMentions)$ |
| Gene | $95.90\dagger$ (BC2GM) | $43.81 \ (tmVar \ v3)$ |
| PubTator | | |
| Chemical | $77.20 \; (NLM-Chem)$ | $31.26 \; (MedMentions)$ |
| Disease | 80.70 (NCBI-Disease) | $40.76 \; (MedMentions)$ |
| Gene | $72.70 \; (NLM\text{-}Gene)$ | $85.92 \ (tmVar \ v3)$ |

Sänger, Mario, et al. "HunFlair2 in a cross-corpus evaluation of named entity recognition and normalization tools." arXiv preprint arXiv:2402.12372 (2024).



4.2 Result

| | BERN2 | HunFlair2 | PubTator | SciSpacy | bent |
|---|----------------|--------------|---------------|----------|-------|
| $\begin{array}{c} \hline Chemical \\ {\rm MedMentions} \\ \hline \end{array}$ | 41.79 (33.42†) | 51.17 | 31.28 | 34.95 | 40.90 |
| Disease MedMentions | 47.33 | 57.57 | 41.11 | 40.78 | 45.94 |
| Gene tmVar (v3) | 43.96 | 76.75 | 86.02 | - | 0.54 |
| Species BioID | 14.35 | 49.66 | 58. 90 | 37.14 | 10.35 |
| Avg | 36.86 (34.72†) | 58.79 | 54.33 | 37.61 | 24.43 |

Sänger, Mario, et al. "HunFlair2 in a cross-corpus evaluation of named entity recognition and normalization tools." arXiv preprint arXiv:2402.12372 (2024).



5. Discussion

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5. Discussion

In-Corpus Evaluations:

Consistency, high scores, limited real-world applicability.

Cross-Corpus Evaluations:

- Unfamiliar datasets, realistic generalization assessment.
- Lower performance, generalization challenges.

Annotation Consistency:

- Varying guidelines and definitions, evaluation impact.

Evaluation Settings:

- excluding non-consecutive entities,
- Method choices, potential tool bias.



5. Discussion

Multi-task LLM in BERN2

- Reduce Parameters
- Enhanced Generalization
- Increased Efficiency

Simplified LLM, DistilBERT

- Reduced Parameters
- Faster Training
- Performance Retention
- Resource Optimization
- Scalability
- Biomedical Adaptability



6. Summary

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5. Summary

Study Focus:

- Biomedical NER and NEN tool evaluation
- Cross-corpus performance analysis

Tools Evaluated:

- HunFlair2, BERN2, bent, PubTator, SciSpacy

Evaluation Metrics:

- Precision, Recall, F1 Score
- End-to-End Approach

Main Findings:

- High performance in training-corpus
- Notable decline in cross-corpus settings
- Best performers: HunFlair2, BERN2

Challenges Identified:

- Generalization across different corpora
- Performance degradation in new contexts

Future Directions:

- Development of adaptive machine learning models
- Creation of diverse and comprehensive datasets
- Collaborative research efforts
- Simplified LLM
- Multi-task LLM in BERN2
- KB Enhancement

Conclusion:

- Need for innovations in model generalization
- Enhancement of biomedical text mining tools



References

- Sänger, Mario, et al. "HunFlair2 in a cross-corpus evaluation of named entity recognition and normalization tools." arXiv preprint arXiv:2402.12372 (2024).
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Thank you for your attention!

