A Appendix Overview

This section summarizes the elements required by NeurIPS for inclusion in supplementary materials.

1. **Dataset documentation and intended uses. Recommended documentation frameworks include datasheets for datasets, dataset nutrition labels, data statements for NLP, and accountability frameworks.** We have provided datasheets for all datasets (see §M) in BIGBIO as well as a datasheet for the meta-dataset itself (see §N). The intended use of BIGBIO is to enable research on (biomedical) Natural Language Processing. Any usage for direct diagnostic use or medical decision making without review and supervision by medical professionals is out of scope.
2. **URL to website/platform where the dataset/benchmark can be viewed and downloaded by the reviewers.** All code required to download datasets and run machine learning experiments outlined in this manuscript is available on the BIGBIO GitHub code repository `https://github.com/bigscience-workshop/biomedical`. We are in the process of creating a website that summarizes the aims and contributions of BIGBIO.
3. **Author statement that they bear all responsibility in case of violation of rights, etc., and confirmation of the data license.** The authors of this manuscript bear all responsibility for any violation of rights caused by the development and release of BIGBIO. All code for BIGBIO is released under Apache License 2.0. All dataset licensing remains the same as the source.
4. **Hosting, licensing, and maintenance plan. The choice of hosting platform is yours, as long as you ensure access to the data (possibly through a curated interface) and will provide the necessary maintenance.** All code is hosted on GitHub at the repository linked above. We have released all dataset-related software under an Apache License 2.0. BIGBIO is an active open source project that is maintained by an international community of volunteers and 4+ code administrators associated with the BigScience biomedical working group. See §E and §B for protocols for new dataset contributions and unit testing to ensure ongoing quality checks. Datasets are hosted by their original owners. In cases where the original license permits redistribution, we will mirror dataset releases on our community hub `https://huggingface.co/bigscience-biomedical`.
5. **Links to access the dataset and its metadata.** See our project GitHub for all dataset code and metadata.
6. **The dataset itself should ideally use an open and widely used data format. Provide a detailed explanation on how the dataset can be read. For simulation environments, use existing frameworks or explain how they can be used.** BIGBIO is implemented using Hugging Face's datasets library to support easy integration into existing machine learning workflows. See §C for details on standardized schema to permit easier reuse.
7. **Long-term preservation** For the subset of public datasets that can be redistributed, we intend to create regular snapshots on BIGBIO on a data archiving website such as `https://zenodo.org/`.
8. **Explicit license** All code for BIGBIO is released under Apache License 2.0. All dataset licensing remains the same as the source. See §D and §N for complete licensing information for all datasets in BIGBIO.
9. **For benchmarks, the supplementary materials must ensure that all results are easily reproducible.** All machine learning experiments include instructions and code for reproducing results. See §J for zero-shot biomedical benchmarking and §K for multi-task learning experiments.

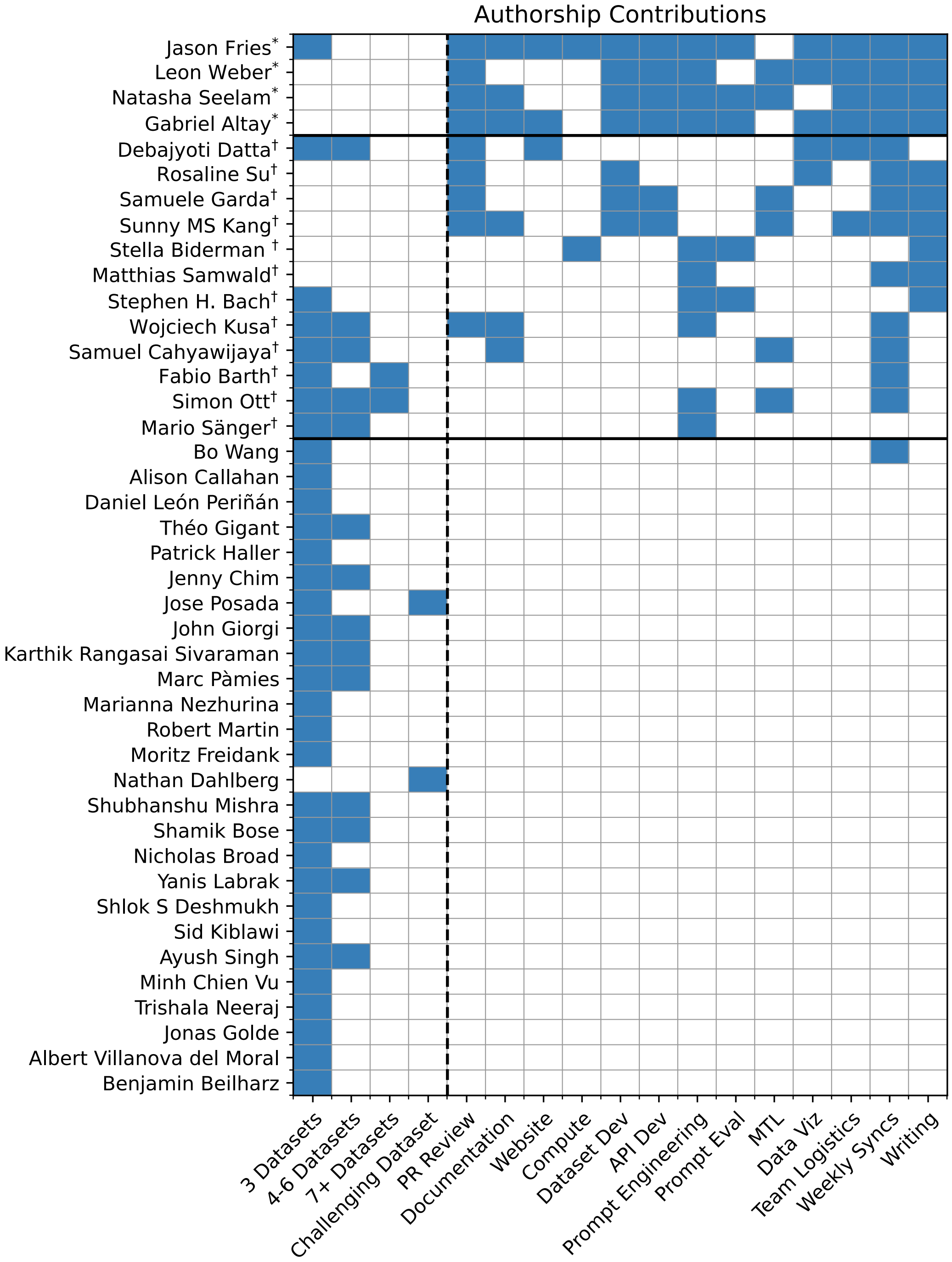
B Author Contributions

The core idea behind this manuscript emerged from discussions in the BigScience biomedical working group. We formalized the following criteria for determining authorship. Joint first authorship required significant intellectual contribution shaping this project, including organization, contributing/reviewing code, writing documentation, and writing this manuscript. Co-authorship required 3+ submitted dataset implementations that passed all unit tests and other quality control measures. Co-second authorship required one or more significant contributions to the project beyond participation in the hackathon.

We also thank Giyaseddin Bayrak, Gully Burns, Antonio Miranda-Escalada, Abhinav Ramesh Kashyap and Tanmay Laud (tlaud@ucsd.edu) for their dataset contributions.

Specific contribution categories are listed below and visualized by author in Figure 4.

- **3 Datasets, 4-6 Datasets, 7+ Datasets**: Number of dataset loaders coded during the hackathon.
- **Challenging Dataset**: Implemented a difficult dataset loader (e.g., many label errors, poor documentation on structure).
- **PR Review**: Managed PR process during hackathon, including code review, debugging, and other quality control measures. This includes llive QA sessions during hackathon office hours on the team Discord server.
- **Documentation**: Wrote instructional material for participants on designing data loaders, coding tutorials, and logistics material for hackathon participation
- **Website**: Contributed to the creation of the BigBIO hackathon website.
- **Compute**: Provided computational resources for running machine learning experiments.
- **Dataset Dev**: Contributed to the design and implementation of task schema design, designing dataset loaders, data unit tests, and other dataset loader infrastructure.
- **API Dev**: Contributed to the design and development of the BIGBIO API, including querying of metadata, programmatic access across datasets, and other infrastructure.
- **Prompt Engineering**: Designed biomedical dataset prompts in PromptSource
- **Prompt Eval**: Contributed to the infrastructure of connecting BIGBIO data loaders with the language model evaluation harness and/or ran prompt evaluation experiments.
- **MTL**: Contributed to the multi-task learning experiments
- **Data Viz**: Designed data visualizations
- **Team Logistics**: Organizational tracking of team goals and action items.
- **Weekly Syncs**: Attended and contributed to weekly team meetings
- **Writing**: Contributed text or edited content within this manuscript



	3 Datasets	4-6 Datasets	7+ Datasets	Challenging Dataset	PR Review	Documentation	Website	Compute	Dataset Dev	API Dev	Prompt Engineering	Prompt Eval	MTL	Data Viz	Team Logistics	Weekly Syncs	Writing
Jason Fries*	■				■	■	■	■	■	■	■	■		■	■	■	■
Leon Weber*					■				■	■	■		■	■	■	■	■
Natasha Seelam*					■	■			■	■	■	■	■		■	■	■
Gabriel Altay*					■	■	■		■	■	■	■		■	■	■	■
Debajyoti Datta†	■	■			■		■							■	■	■	
Rosaline Su†					■				■					■		■	■
Samuele Garda†					■				■	■			■			■	■
Sunny MS Kang†					■	■			■	■			■		■	■	■
Stella Biderman †								■			■	■					■
Matthias Samwald†											■					■	■
Stephen H. Bach†	■										■	■					■
Wojciech Kusa†	■	■			■	■					■					■	
Samuel Cahyawijaya†	■	■				■							■			■	
Fabio Barth†	■		■													■	
Simon Ott†	■	■	■								■		■			■	
Mario Sänger†	■	■									■						
Bo Wang	■															■	
Alison Callahan	■																
Daniel León Periñán	■																
Théo Gigant	■	■															
Patrick Haller	■																
Jenny Chim	■	■															
Jose Posada	■			■													
John Giorgi	■	■															
Karthik Rangasai Sivaraman	■	■															
Marc Pàmies	■	■															
Marianna Nezhurina	■																
Robert Martin	■																
Moritz Freidank	■																
Nathan Dahlberg				■													
Shubhanshu Mishra	■	■															
Shamik Bose	■	■															
Nicholas Broad	■																
Yanis Labrak	■	■															
Shlok S Deshmukh	■																
Sid Kiblawi	■																
Ayush Singh	■	■															
Minh Chien Vu	■																
Trishala Neeraj	■																
Jonas Golde	■																
Albert Villanova del Moral	■																
Benjamin Beilharz	■																

Figure 4: Authorship contribution matrix. Cells to the left of the dotted black vertical line are hackathon dataset contributions, while the right are other paper contributions as part of the BigScience biomedical working group. For each author, $*$ denotes co-first author and † denotes co-second author, with equal contributions within category.

Table 5: Author Affiliations

Name	Affiliation
Jason Fries	Stanford University
Leon Weber	Humboldt-Universität zu Berlin & Max Delbrück Center for Molecular Medicine
Natasha Seelam	Sherlock Biosciences
Gabriel Altay	Tempus Labs Inc.
Debajyoti Datta	University of Virginia
Rosaline Su	Independent researcher
Samuele Garda	Humboldt-Universität zu Berlin
Sunny MS Kang	Immuneering
Stella Biderman	EleutherAI, Booz Allen Hamilton
Matthias Samwald	Institute of Artificial Intelligence, Medical University of Vienna
Stephen H. Bach	Brown University
Wojciech Kusa	TU Wien
Samuel Cahyawijaya	The Hong Kong University of Science and Technology
Fabio Barth	Humboldt-Universität zu Berlin
Simon Ott	Institute of Artificial Intelligence, Medical University of Vienna
Mario Sänger	Humboldt-Universität zu Berlin
Bo Wang	Massachusetts General Hospital
Alison Callahan	Stanford University
Daniel León Periñán	TU Dresden
Théo Gigant	Independent researcher
Patrick Haller	Humboldt-Universität zu Berlin
Jenny Chim	Queen Mary University of London
Jose Posada	Universidad del Norte
John Giorgi	University of Toronto
Karthik Rangasai Sivaraman	BITS Pilani
Marc Pàmies	Barcelona Supercomputing Center
Marianna Nezhurina	Kuban State University Of Technology
Robert Martin	Humboldt-Universität zu Berlin
Michael Cullan	Independent researcher
Moritz Freidank	Visium SA
Nathan Dahlberg	Independent researcher
Shubhanshu Mishra	shubhanshu.com
Shamik Bose	Independent researcher
Nicholas Broad	Hugging Face
Yanis Labrak	Avignon University
Shlok S Deshmukh	Elucidata, Inc.
Sid Kiblawi	Microsoft
Ayush Singh	Independent researcher
Minh Chien Vu	Detomo Inc.
Trishala Neeraj	Cornell University
Jonas Golde	Humboldt-Universität zu Berlin
Albert Villanova del Moral	Hugging Face
Benjamin Beilharz	TU Darmstadt

C Task Schema and Harmonization

We have defined a set of lightweight, task-specific schema to help simplify programmatic access to common biomedical datasets.

Each dataset loader implemented in BIGBIO provides at least one `source` view of the dataset and at least one `bigbio` view of the dataset. The `source` view attempts to capture the original form of the dataset with as little change as possible. The `bigbio` view attempts to normalize the dataset into one of our BIGBIO task-specific schemas. All schemas are defined by creating an instance of the `datasets.Features` class from the Hugging Face datasets package.

Every element of the BIGBIO schemas has an `id` attribute that is unique across the dataset. In some datasets, entities are represented as discontiguous spans. For example, the string "estrogen and progesterone receptor positive" could be labeled with two entities and two lists of character offsets,

```
    ["estrogen", "receptor"]; [(0,8), (26,34)]
    ["progesterone receptor"]; [(13, 34)]
```

To support these types of annotations and maintain consistency, we represent all text-offset combinations this way.

C.1 Schema Definitions

Knowledge Base (KB) The knowledge base schema covers entity based tasks and includes named entity recognition (NER), named entity disambiguation/normalization (NED), event extraction (EE), relation extraction (RE), and coreference resolution (COREF). The schema is loosely based on the XML BioC format [10] and the brat annotation format [43]. The top level features are,

```
{
    "id": datasets.Value("string"),
    "document_id": datasets.Value("string"),
    "passages": [],
    "entities": [],
    "events": [],
    "coreferences": [],
    "relations": [],
}
```

The `id` attribute can be set to anything that makes it unique and the `document_id` attribute represents any identifying value included in the original dataset. Passages capture the text content of a sample. A single sample can have one passage (such as a single abstract) or multiple elements (such as abstract and title). The character offsets in the rest of the KB schema elements index into the string that would be created by joining all the passage texts.

```
"passages": [
    {
        "id": datasets.Value("string"),
        "type": datasets.Value("string"),
        "text": datasets.Sequence(datasets.Value("string")),
        "offsets": datasets.Sequence([datasets.Value("int32")]),
    }
]
```

Entities can be associated with a type as well as multiple database entries.

```
"entities": [
    {
        "id": datasets.Value("string"),
        "type": datasets.Value("string"),
        "text": datasets.Sequence(datasets.Value("string")),
        "offsets": datasets.Sequence([datasets.Value("int32")]),
        "normalized": [
            {
                "db_name": datasets.Value("string"),
                "db_id": datasets.Value("string"),
            }
        ],
    }
]
```

Events are modeled in BigBio as they are in the brat annotation tool.

```
"events": [
    {
        "id": datasets.Value("string"),
        "type": datasets.Value("string"),
        "trigger": {
            "text": datasets.Sequence(datasets.Value("string")),
            "offsets": datasets.Sequence([datasets.Value("int32")]),
        },
        "arguments": [
            {
                "role": datasets.Value("string"),
                "ref_id": datasets.Value("string"),
            }
        ],
    }
]
```

Coreference annotations can be specified using a sequence of entity IDs.

```
"coreferences": [
    {
        "id": datasets.Value("string"),
        "entity_ids": datasets.Sequence(datasets.Value("string")),
    }
]
```

Binary typed relations with multiple database normalizations are also supported.

```
"relations": [
    {
        "id": datasets.Value("string"),
        "type": datasets.Value("string"),
        "arg1_id": datasets.Value("string"),
        "arg2_id": datasets.Value("string"),
        "normalized": [
            {
                "db_name": datasets.Value("string"),
                "db_id": datasets.Value("string"),
            }
        ],
    }
]
```

Question Answering (QA) The QA schema supports several question answering tasks. The `type` attribute is not constrained but takes the values "factoid", "how", "list", "multiple_choice", "summary", "why", and "yesno" in the current BigBio datasets. For "multiple_choice" and "yesno" questions, the `choices` attribute is populated with valid answers. The `context` attribute is used for closed-domain QA.

```
{
    "id": datasets.Value("string"),
    "question_id": datasets.Value("string"),
    "document_id": datasets.Value("string"),
    "question": datasets.Value("string"),
    "type": datasets.Value("string"),
    "choices": [datasets.Value("string")],
    "context": datasets.Value("string"),
    "answer": datasets.Sequence(datasets.Value("string")),
}
```

Textual Entailment (TE) The TE schema supports tasks in which two text spans can be mapped onto the triplet of entailment labels ("entailment", "neutral", "contradict").

```
{
    "id": datasets.Value("string"),
    "premise": datasets.Value("string"),
    "hypothesis": datasets.Value("string"),
    "label": datasets.Value("string"),
}
```

Text (TEXT) The TEXT schema supports tasks with a single text span and one or more associated labels (TXTCLASS).

```
{
    "id": datasets.Value("string"),
    "document_id": datasets.Value("string"),
    "text": datasets.Value("string"),
    "labels": [datasets.Value("string")],
}
```

Text Pairs (PAIRS) The PAIRS schema supports tasks with two text spans and one label. In this initial release, the only task using this schema is semantic similarity (STS).

```
{
    "id": datasets.Value("string"),
    "document_id": datasets.Value("string"),
    "text_1": datasets.Value("string"),
    "text_2": datasets.Value("string"),
    "label": datasets.Value("string"),
}
```

Text to Text (T2T) The T2T schema supports sequence to sequence tasks such as paraphasing (PARA), translation (TRANSL), and summarization (SUM).

```
{
    "id": datasets.Value("string"),
    "document_id": datasets.Value("string"),
    "text_1": datasets.Value("string"),
    "text_2": datasets.Value("string"),
    "text_1_name": datasets.Value("string"),
    "text_2_name": datasets.Value("string"),
}
```

C.2 Harmonization

Harmonization efforts aimed for the simplest schema, per task, that was able to flexibly cover the majority of relevant features. We found in the majority of cases, the schema provided suited the task of the original dataset. Toward that end, we found that only 22% (29/129 datasets submitted) of the datasets required major refactors (defined by significant changes or fixes to the dataloader post submission). While the schema satisfied most cases, we noted some areas of improvement below:

Extension of question answering Question-answering supports multiple choice, binary choice, or span-based answers, but does not enable 'long-form' responses that may provide greater context to the question asked. This particular issue arose in PubMedQA, of which the source schema has a context key that provides framing for the answer.

Extension of text pairs classification The text-pairs schema enables a relationship between two input texts and their corresponding labels. However, in at least one dataset (Scielo), a three-language translation was provided. This can be handled be implementing the dataset twice, one for each translation, or omitting this feature altogether.

Multi-label entities Several datasets had multiple labels associated to a single entity. While we have adapted the schema to associate multiple labels to a single entity. To resolve this concern, we duplicate the feature but change the label and provide a new unique id. This concern was particularly noted in the `MedMentions` dataset.

Diverse label representations For classification problems, the labels associated to a feature may be a string answer, or a numerical score. To maintain a consistent format across all datasets, label keys across schemas in the BIGBIO-view are always `str` types. This limitation affected at least 4 datasets (UMNSRS, MayoSRS, BioSimVerb), particulary in the context of semantic similarity scores across text. For the user to appropriately cast the score type, they would need familiarity of the dataset. We opted to enable the source view to represent label information for scores as floats when present.

Unsupported task types In certain cases, tasks may extend beyond the descriptive capacity of the provided BIGBIO-schemas. For example, tasks that explicitly required contextualization were unable to fit into a pre-existing schema. For example, speech-based tasks, such as MedDialogue require a text, label, and potential context; the BIGBIO-text classification schema does not enable a context key. Additionally, Ask-a-Patient required a tuple-like structure to represent a text, a social media response, and a medical concept to be relevant to the task. In addition to tasks that require context, part-of-speech tagging or annotations on a per-token basis was not easily represented in our pre-existing schema.

During the initiative, common themes of recurring problems in biomedical NLP processing occurred. We denote them as follows:

Issues with offsets One of the unit-tests specifically monitored whether reported features matched offsets provided from the original dataset. We found a several datasets with slight offset errors, or inconsistencies. In several cases, offset errors included off-by-one or whitespacing considerations, discontiguous spans, and one case, entirely omitted from the original dataset.

Large datasets Several datasets possessed corpora that were large in size (upwards of 20 GB). In at least one instance, the initial implementation of the dataset yielded examples exceedingly slow. While we standardized information content, we did not explicitly optimize for efficiency.

D Dataset Metadata

We collected the structured metadata outlined in Table 6 for all datasets in the BIGBIO catalog. Required elements are written as code in the data loader. Figures 5 and 6 show treemap visualizations of all datasets based on their license and language respectively.

Table 6: Metadata collected for all datasets.

Field	Required	Description
Name	✓	Dataset name
Task Types	✓	NER, question answering, coreference resolution, etc.
Domain	✓	Corpora domain: biomedical or clinical/health-related
PubMed/PMC	✓	Corpora are from PubMed/PubMed Central (PMC)
Splits	✓	Canonical definitions for training/validation/testing splits
Publication	✓	Manuscript describing dataset
Year		Publication year
Homepage	✓	Website describing dataset
Public URL	✓	Open URL (no authentication)
Private	✓	Requires authentication/credentialing
License	✓	Provided license type
Languages	✓	Included languages
Multilingual		Parallel corpora
Annotation Source		Expert label provenance (e.g., hand labeled, silver labels)

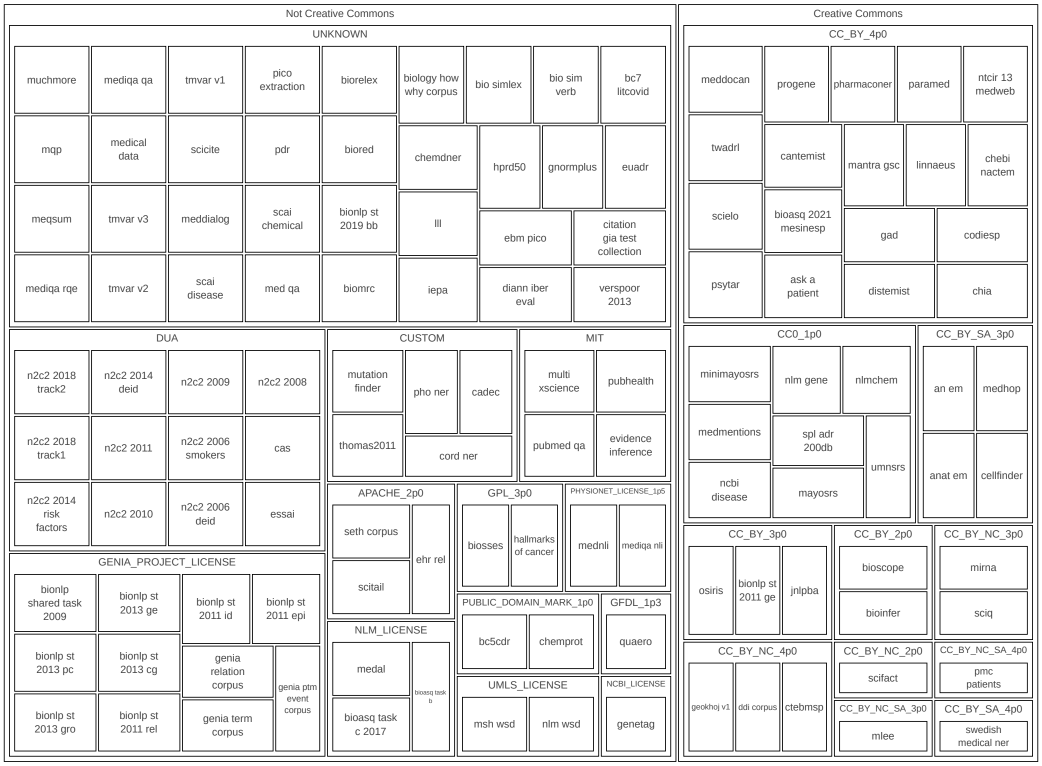


Figure 5: Treemap visualization of datasets by license.

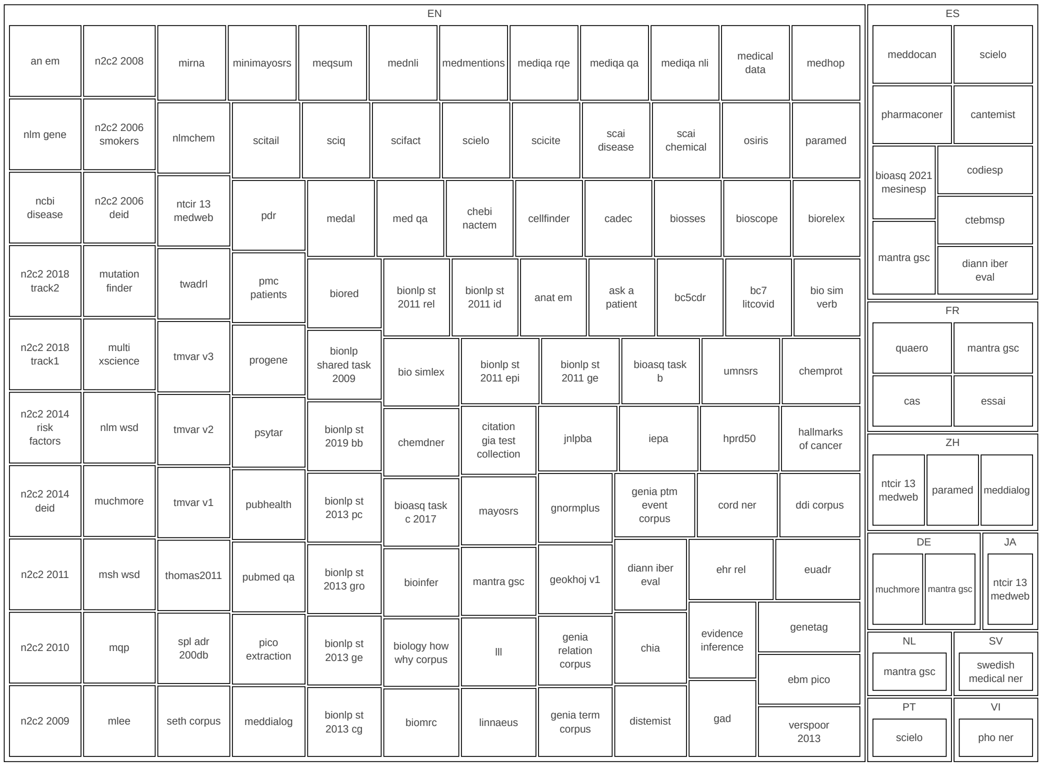


Figure 6: Treemap visualization of datasets by language.

E Unit Tests

We developed 11 unit tests to check the BIGBIOversions of all implemented data loaders. Unit tests run on all BIGBIO *configurations* (i.e., a schema view of the dataset) found within a dataset, whether they represent different dataset subsets or different tasks.

Among all implemented unit tests, we differentiate between **global** and **task-specific** tests. For datasets that support configurations with multiple schemas (each supporting different tasks), we run the task-specific tests using only the configuration supporting the task.

Below, we describe each unit test found in BIGBIO:

E.1 Global Tests

1. **Metadata** Checks if the dataloader module provides relevant metadata attributes. Supported attributes include `LANGUAGE` (language of the dataset), `LOCAL` (whether the dataset is publicly accessible or requires local files), `PUBMED` (is part of Pubmed), and `LICENSE` (type of license). The `LANGUAGE` and `LICENSE` are standardized to common labels across datasets, whereas `LOCAL` and `PUBMED` are boolean.
2. **Unique Global IDs** Each element within a dataset is assigned a string ID that is unique across the dataset split (such as train, validation or test). For example, all passages, entities, relations, questions, labels, and other attributes will be assigned a unique string. This ID can be used to reference a given element if it is being used in a new context without considering explicit text overlap or other heuristics. This unit-test confirms that a every element has an ID that is unique across the full dataset split.
3. **Schema** This test checks whether the populated fields in the examples are consistent with the tasks supported by the dataset. For instance, if a dataset is annotated to support NER but there is not a single entity field populated across a full dataset split, the test will fail. Additionally, the test will provide a warning if fields are populated that would support a task missing from the annotated supported tasks. The loading procedure in Hugging Face's datasets fails if a dataloader does not adhere to its defined schema. Thus, we implicitly check for consistency between data and schema by loading the dataset.
4. **Feature Statistics** This test prints statistics of populated fields in the dataset to allow the user to manually check their plausibility. For each data split, it collects the number of elements (e.g. number of entities, relations, text pairs, etc.). We use these statistics for quality control by manually comparing to the dataset statistics reported in the publication describing the respective dataset.

E.2 Task-specific Tests: Knowledge Base

1. **Referenced ids** Certain fields may be referenced by other elements (for example, a relation usually references two entities). References in the BIGBIO-schema will use the unique ID assigned to them. This unit test checks if all referenced IDs exist, and have an appropriate type. For instance, it makes sure that the arguments of a relation are indeed entities (and not relations or events).
2. **Passage Offsets** This test checks whether the start and end indices of all passages are correct. This is achieved by comparing the text span defined by the indices to the text field assigned to the passage. Additionally, the unit test will make sure that each passage is contiguous and does not overlap.
3. **Entity Offsets** This test makes sure that the start and end indices of entities are correct. Analogous to the *Passage Offsets* test, we compare the reported feature text for entities versus the extracted text from the start/ending index provided from the data. This test does not provide an explicit failure, but instead warns the user of all entities that do not explicitly match their offset-extracted text. We chose a warning over failure because some datasets contain faulty offsets in the original formats due to annotation errors.
4. **Event Offsets** Similar to the passage-offsets and entities-offset check, we compare the reported event text feature to the extracted text from provided offsets. We warn the user of any instances of discordance between the reported and extracted text.

5. **Multi-label Entities** The current BIGBIO schema does not support multiple types for entities. This test flags instances where an entity is assigned multiple types by concatenating the types with common connector symbols (such as '|' or ';').
6. **Multi-label Types** This unit-test performs the same check as `Multi-label Entities` for other features with the `type` attribute (passages, relations, events). This test is distinct from the multi-label entities test, because the envisioned BIGBIO schema revision to support multiple labels is different in this case.

E.3 Task-specific Tests: Question Answering

1. **Multiple Choice** This test checks whether the answers of a question-answering schema are either multiple choice or binary (yes/no). It verifies that the answer provided exists in the choices available for each example.

All accepted data-loading scripts must pass code review, unit-tests, and implement explicit fixes for warnings that indicated destructive transformations of the original dataset (such as introducing faulty offsets).

In general, participants who implemented data-loading scripts were asked to refrain from resolving dataset issues in the dataloader for the original dataset but were free to fix the issues for the BIGBIO versions. Any data quality changes were explicitly annotated within the review process, and the data loading script itself.

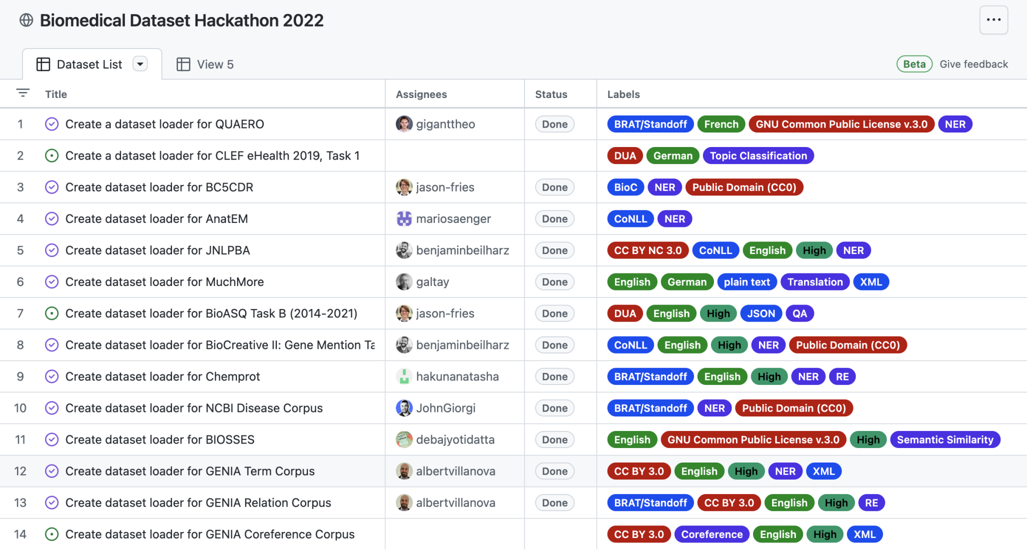
Certain datasets may require specific keys to be ignored. We implemented functions that allow a user to bypass a specific key (e.g., skip all events), a data split (e.g., skip the validation set), or a specific key within a dataset (e.g., skip relation labels in the test set). These functions were used to check the `BioNLP shared task` datasets, as the test splits of these datasets omitted annotations for some supported tasks. These bypass functions allow a user to test if all other aspects of the dataset implementation work as intended.

F Dataset Submission Checklist

- □ Confirm that this PR is linked to the dataset issue.
- □ Create the dataloader script `biodatasets/my_dataset/my_dataset.py` (please use only lowercase and underscore for dataset naming).
- □ Provide values for
  - □ `_CITATION`
  - □ `_DATASETNAME`
  - □ `_DESCRIPTION`
  - □ `_HOMEPAGE`
  - □ `_LICENSE`
  - □ `_URLs`
  - □ `_SUPPORTED_TASKS`
  - □ `_SOURCE_VERSION`
  - □ `_BIGBIO_VERSION`
- □ Data loader implementations for
  - □ `_info()`
  - □ `_split_generators()`
  - □ `_generate_examples()`
- □ Make sure that the `BUILDER_CONFIGS` class attribute is a list with at least one 'BigBioConfig' for the source schema and one for a bigbio schema.
- □ Confirm dataloader script works with `datasets.load_dataset` function.
- □ Confirm that your dataloader script passes the test suite run with `python -m tests.test_bigbio biodatasets/my_dataset/my_dataset.py`.
- □ If my dataset is local, I have provided an output of the unit-tests in the PR (please copy paste). This is OPTIONAL for public datasets, as we can test these without access to the data files.

G BigScience Biomedical Hackathon

We catalogued an initial set of 174 datasets and prior to launching the hackathon, we provided users with a project board that tagged each dataset as a new issue within our GitHub repository. For all datasets, we provided meta-data tags such as language, license, and associated task (e.g., NER, question answering). Participants could assign themselves to a dataset via issues and status would be reflected in the project board (see Figure 7). Admins could change the status of the issue based on progress of the data loading script.



Biomedical Dataset Hackathon 2022

	Title	Assignees	Status	Labels
1	Create a dataset loader for QUAERO	giganttheo	Done	BRAT/Standoff French GNU Common Public License v.3.0 NER
2	Create a dataset loader for CLEF eHealth 2019, Task 1			DUA German Topic Classification
3	Create dataset loader for BC5CDR	jason-fries	Done	BioC NER Public Domain (CC0)
4	Create dataset loader for AnatEM	mariosaenger	Done	CoNLL NER
5	Create dataset loader for JNLPBA	benjaminbeilharz	Done	CC BY NC 3.0 CoNLL English High NER
6	Create dataset loader for MuchMore	galtay	Done	English German plain text Translation XML
7	Create dataset loader for BioASQ Task B (2014-2021)	jason-fries	Done	DUA English High JSON QA
8	Create dataset loader for BioCreative II: Gene Mention Ta	benjaminbeilharz	Done	CoNLL English High NER Public Domain (CC0)
9	Create dataset loader for Chemprot	hakunanatasha	Done	BRAT/Standoff English High NER RE
10	Create dataset loader for NCBI Disease Corpus	JohnGiorgi	Done	BRAT/Standoff NER Public Domain (CC0)
11	Create dataset loader for BIOSSES	debajyotidatta	Done	English GNU Common Public License v.3.0 High Semantic Similarity
12	Create dataset loader for GENIA Term Corpus	albertvillanova	Done	CC BY 3.0 English High NER XML
13	Create dataset loader for GENIA Relation Corpus	albertvillanova	Done	BRAT/Standoff CC BY 3.0 English High RE
14	Create dataset loader for GENIA Coreference Corpus			CC BY 3.0 Coreference English High XML

Figure 7: Participants volunteered to implement dataset loaders using GitHub project tracking tools.

Participants were asked to create a fork of the repository, and implement their data-loading script. We provided a template of a dataloading script, where explicit comments were left to indicate key functions and attributes the participant must complete. For datasets in common formats like BRAT or BioC, we provided utility functions to improve standardization across formats. At minimum, participants implemented an `_info_` function that instantiated the `source` and `bigbio` configs. A `_split_generators` function that identified how to access each data split in the dataset, and the `_generate_examples` that extracted relevant information from each data split according to the specifications of the configs.

Dataloader scripts were submitted through pull-requests (PRs) on GitHub. Prior to submitting code for review, we asked participants to check if the code passed unit-tests and style guidelines. Accepted PRs required at least 1 admin approval to merge to the library. To respect data governance, we did not accept any submissions that provided explicit dataset files. Dataloading scripts must access datasets via URLs, or expect a filepath to the local dataset.

If a dataset had multiple tasks, we asked the participant to implement tasks based on the number of unique schemas, if possible. Some datasets possess different views based on the different tasks that can be performed on them. Participants were told to handle multiple annotations/harmonization per the original dataset's recommendations. If none were given, participants were asked to choose what seemed reasonable, and iterate with an admin.

All contribution instructions may be found here.

Of the 174 datasets identified, 126 datasets satisfied the acceptance criteria, including the checklist in §F, code-review, and passing unit-tests. Exceptions were made on a case-by-case basis for datasets with unique challenges that extended beyond the scope of the schema provided.

G.1 Frequently Asked Questions (FAQ)

During the hackthon, we developed the following list of frequently asked questions (FAQ).

How can I find the appropriate license for my dataset? The license for a dataset is not always obvious. Here are some strategies to try in your search:

1. Check the Experiment A: Annotated Datasets sheet of the we used while planning the hackathon
2. Check for files such as README or LICENSE that may be distributed with the dataset itself
3. Check the dataset webpage
4. Check publications that announce the release of the dataset
5. Check the website of the organization providing the dataset

If no official license is listed anywhere, but you find a webpage that describes general data usage policies for the dataset, you can fall back to providing that URL in the `_LICENSE` variable. If you can't find any license information, please make a note in your PR and put `_LICENSE = "Unknown"` in your dataset script.

What if my dataset is not publicly available? We understand that some biomedical datasets are not publicly available due to data usage agreements or licensing. For these datasets, we recommend implementing a dataloader script that references a local directory containing the dataset. You can find examples in the `n2c2_2011` and `bioasq` implementations. There are also local dataset specific instructions in template.

What types of libraries can we import? Eventually, your dataloader script will need to run using only the packages supplied by the datasets package. If you find a well supported package that makes your implementation easier (e.g. bioc), then feel free to use it.

We will address the specifics during review of your PR to the BigScience biomedical repo and find a way to make it usable in the final submission to huggingface bigscience-biomedical

Can I upload my dataset anywhere? No. Please don't upload the dataset you're working on to the huggingface hub or anywhere else. This is not the goal of the hackathon and some datasets have licensing agreements that prevent redistribution. If the dataset is public, include a downloading component in your dataset loader script. Otherwise, include only an "extraction from local files" component in your dataset loader script. If you have a custom dataset you would like to submit, please make an issue and an admin will get back to you.

My dataset supports multiple tasks with different bigbio schemas. What should I do? In some cases, a single dataset will support multiple tasks with different bigbio schemas. For example, the muchmore dataset can be used for a translation task (supported by the Text to Text (T2T) schema) and a named entity recognition task (supported by the Knowledge Base (KB) schema). In this case, please implement one config for each supported schema and name the config `<datasetname>_bigbio_<schema>`. In the muchmore example, this would mean one config called `muchmore_bigbio_t2t` and one config called `muchmore_bigbio_kb`.

My dataset comes with multiple annotations per text and no/multiple harmonizations. How should I proceed? Please implement all different annotations and harmonizations as source versions (see `examples/bioasq.py` for an example). If the authors suggest a preferred harmonization, use that for the bigbio version. Otherwise use the harmonization that you think is best.

How should I handle offsets and text in the bigbio schema? Full details on how to handle offsets and text in the bigbio kb schema can be found in the schema documentation.

My dataset is complicated, can you help me? Yes! Please feel free to leave a question in questions or ping the admins directly with @admins. We will be hosting office hours round the clock to be able to answer you in a timely manner!

My dataset is too complicated, can I switch? Yes! Some datasets are easier to write dataloader scripts for than others. If you find yourself working on a dataset that you can not make progress on, please make a comment in the associated issue, asked to be un-assigned from the issue, and start the search for a new unclaimed dataset. You are also welcome to ping the admins - we are happy to help you!

Can I change the Big-Bio schema? No, please do not modify the Big-Bio Schema. The goal of this hackathon is to enable simple, programmatic access to a large variety of biomedical datasets. Part of this requires having a dependable interface. We developed our schema to address the most salient types of questions to ask of the datasets. We would be more than happy to discuss your suggestions, and you are welcome to implement it as a new config.

My dataset has multiple labels to a span of text - what do I do? In many of our schemas, we have a 1:1 mapping between a key and its label (i.e. in KB, entity and label). In some datasets, we've noticed that there are multiple labels assigned to a text entity. Generally speaking, if a big-bio key has multiple labels associated with it, please populate the list with multiple instances of (key, label) according to each label that correspond to it.

So for instance if the dataset has an entity "copper" with the types "Pharmacologic Substance" and "Biologically Active", please create one entity with type "Pharmacologic Substance" and an associated unique id and another entity with type "Biologically Active" with a different unique id. The rest of the inputs (text, offsets, and normalization) of both entities will be identical.

What happens after I claim a dataset? In order to keep turnaround time reasonable, and ensure datasets are being completed, we propose a few notes on claiming a dataset:

1. Please claim a dataset only if you intend to work on it. We'll try to check in within 3 days to ensure you have the help you need. Don't hesitate to contact the admins! We are ready to help!
2. If you have already claimed a dataset prior to (2022/04/05), we will check in on Friday (2022/04/08). If we do not hear back via GitHub issues OR a message to the Discord admins on general, we will make the dataset open for other participants by Saturday (2022/04/09).
3. If things are taking longer than expected - that is totally ok! Please let us know via GitHub issues (preferred) or by pinging the @admins channel on Discord.

H Assessing Dataset Overlap for De-Duplication

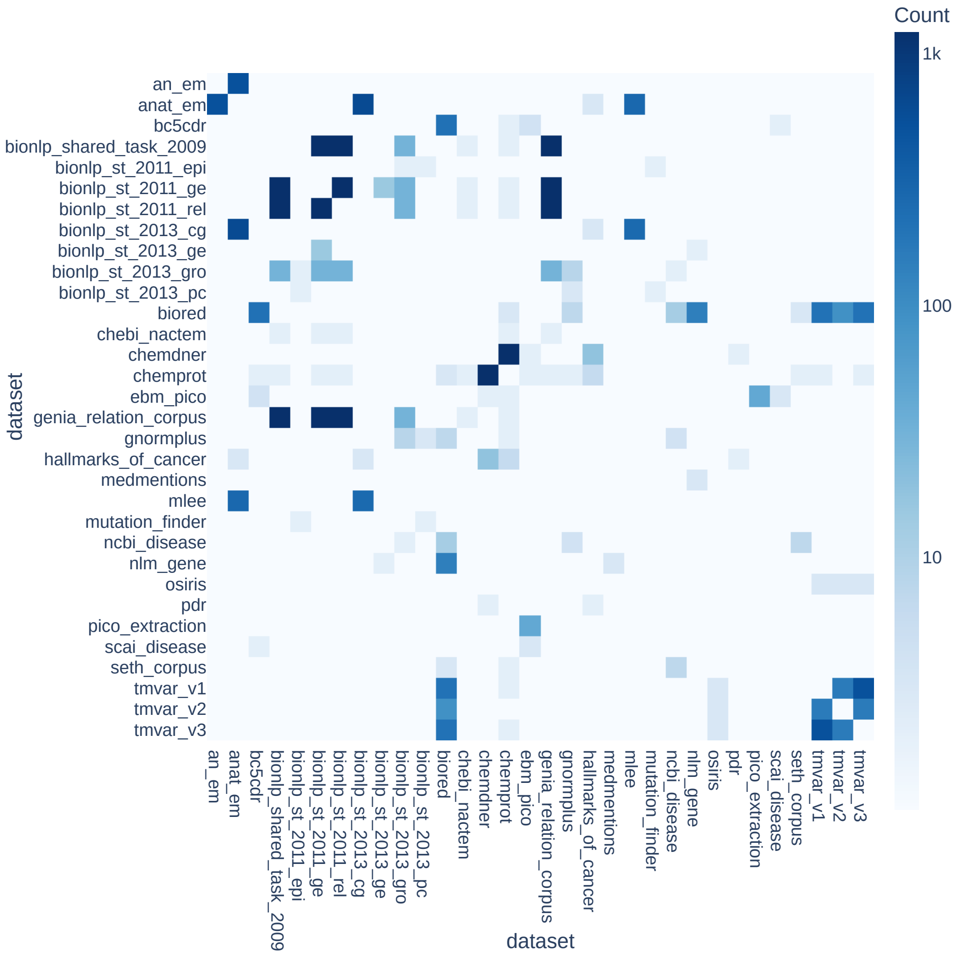


Figure 8: A heatmap representation of PubMed overlap between public datasets in BigBio. Each cell is shaded using the log count of PMIDs shared by the pair of datasets it represents.

Table 7: Example document IDs as they appear in the original source datasets and their corresponding BigBio normalization to PubMed PMIDs, Pubmed Central PMCIDs, and journal titles.

Original Document ID	PMID	PMCID	Journal
PMID-12604762	12604762	PMC1497507	Public Health Rep
BB-kb+ner-F-25496341-000	25496341	PMC4320590	BMC Genomics
17389645_04_discussion	17389645	PMC1885650	Nucleic Acids Res
pmcA2538543	2538543	PMC2189270	J Exp Med
10747015-3	10747015	PMC310216	EMBO J
6421395:4	6421395	PMC1444356	Br Med J (Clin Res Ed)
PMC2885601-03-RESULTS-01	20556207	PMC2885601	Open Microbiol J
PMC-2626671-01-INTRODUCTION	19139168	PMC2626671	J Exp Med

As biomedical models are trained and evaluated on ever larger meta-datasets, it is important to characterize duplication within and between datasets. This can take the form of direct train/test leakage [13] or more subtle issues of near-duplicates and repeated substrings which can negatively impact performance and training time of language models [25]. In biomedical NLP, annotation efforts often build upon existing datasets meaning meta-dataset curation needs to take additional steps to mitigate possible train/test leakage. To assess the magnitude of this phenomena across the

Table 8: Dataset clusters of document (PMID) overlap.

Dataset Names	Count	PMID Overlap
BioRED, NCBI Disease	2	11
MLEE, AnatEM	2	12
Hallmarks of Cancer, CHEMDNER	2	12
BioNLP ST 2013 GE, BioNLP ST 2011 GE	2	14
BioNLP ST 2011 REL, BioNLP ST 2013 GRO, GENIA Relation Corpus, BioNLP Shared Task 2009, BioNLP ST 2011 GE	5	29
PICO Extraction, EBM PICO	2	41
tmVar v1, tmVar v2, tmVar v3	3	69
BioRED, tmVar v1, tmVar v2, tmVar v3	4	87
BioRED, tmVar v1, tmVar v3	3	109
NLM Gene, BioRED	2	140
BC5CDR, BioRED	2	203
tmVar v1, tmVar v3	2	232
MLEE, BioNLP ST 2013 CG, AnatEM	3	250
BioNLP ST 2013 CG, AnatEM	2	348
AnatEM, AnEM	2	492
GENIA Relation Corpus, BioNLP Shared Task 2009, BioNLP ST 2011 REL, BioNLP ST 2011 GE	4	1179
ChemProt, CHEMDNER	2	1199

BIGBIO corpus, we conducted a preliminary analysis counting the number of shared documents across all annotated datasets sourced from PubMed or PubMed Central (PMC).

PubMed Document ID Normalization PubMed/PMC provides uniform identifiers for documents: PubMed PMID and PubMed Central PMCID. However, many datasets encode this document information using inconsistent formats as shown in Table 7. We wrote a normalization function to standardize all document identifiers to facilitate joins with other PubMed/PMC datsets. We then joined this data with the `PMC-ids.csv.gz` file available from the National Library of Medicine[1].

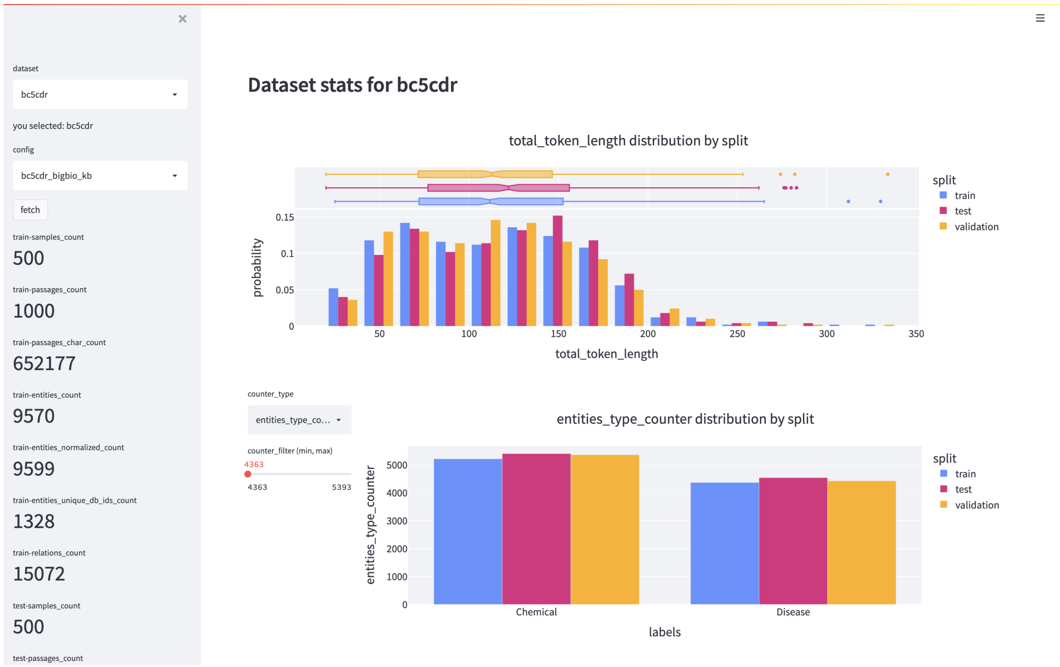
PubMed Dataset Overlap Analysis Our normalizations of PMIDs allowed us to calculate which PubMed articles were used in multiple datasets. In Table 8 we show the largest PMID clusters, i.e., sets of datasets that contain the same documents. In Figure 8 we visualize this overlap as a heatmap. We observe several cases of clear dataset iteration (e.g., tmVar v1-v3, AnEM to AnatEM) and NLP challenges building on the same source datasets (BioNLP shared tasks 2009 and 2011 build on the GENIA Relation Corpus). BioRED illustrates another common pattern, where documents were sampled from 5 existing biomedical datasets before annotating [121].

[1] `https://ftp.ncbi.nlm.nih.gov/pub/pmc` accessed May 29, 2022

I Data Visualization and Exploration

To highlight the efficiency of using consistent schema across datasets, we created a Streamlit[2] web application to allow anyone to browse through any schema-specific details and visualization for all supported datasets. The web application enables task sorting at the level of task schema (e.g., NER), which supports downstream approaches to use groups of datasets with minimal effort. Such as prompt based methods or multi-task learning (MTL).

For each split, we provide basic dataset details (like number of training samples, character counts, word counts, number of unique labels, etc.). Further, we also present distributions of token lengths and labels (or sub-component types) within each dataset to compare across splits. We used periods and new lines to break the text block into sentences, and tokenized each sentence by white space to count the token lengths. For datasets of tasks that do not have labels, which is the case for most common knowledge base construction and information extraction tasks, we analyze the data distribution across the sub-component types. For instance, our task schema for the BioCreative V Chemical Disease Relation (CDR) dataset [112] provides an efficient way to compare the distribution of chemical and disease entities across splits (See Figure 9).



dataset: bc5cdr

you selected: bc5cdr

config: bc5cdr_bigbio_kb

fetch

train-samples_count: 500

train-passages_count: 1000

train-passages_char_count: 652177

train-entities_count: 9570

train-entities_normalized_count: 9599

train-entities_unique_db_ids_count: 1328

train-relations_count: 15072

test-samples_count: 500

test-passages_count

Dataset stats for bc5cdr

counter_type: entities_type_co...

counter_filter (min, max): 4363 (4363–5393)

Figure 9: Streamlit web application for visualizing dataset-specific details and textual analysis at the span-level. Here we show plots for the BioCreative V Chemical Disease Relation (CDR) dataset.

[2] https://streamlit.io/

J Zero-shot Language Model Evaluation

J.1 Expanded Results

Table 9 summarizes key properties of the language models used in our zero-shot experiments.

Table 9: Language model parameter counts and pretraining datasets.

Language Model	Parameters	PubMed/PMC	Pretraining Dataset(s)
SciFive-Base	220M	✓	C4, PubMed Abstracts, PubMed Central (PMC)
SciFive-Large	770M	✓	C4, PubMed Abstracts, PubMed Central (PMC)
GPT-Neo-1.3B	1.3B	✓	The Pile
GPT-2	1.5B		WebText
GPT-J-6B	6B	✓	The Pile
T0_3B	3B		C4, P3 (Public Pool of Prompts)
T5 v1.1-xxl	11B		C4
T0	11B		C4, P3 (Public Pool of Prompts)
T0+	11B		C4, P3 (Public Pool of Prompts)
T0++	11B		C4, P3 (Public Pool of Prompts)
GPT-NeoX-20B	20B	✓	The Pile
OPT-66B	66B		RoBERTa (subsets: BookCorpus, Stories, CC-News v2), The Pile (subsets: CommonCrawl, DM Mathematics, Project Gutenberg, HackerNews, OpenSubtitles, OpenWebText2, USPTO and Wikipedia), PushShift.io Reddit
GPT-3	175B		WebText, ???
BLOOM	176B		Roots Corpus

Tables 10 and 11 and contains complete zero-shot language model results pooled across all prompts by dataset.

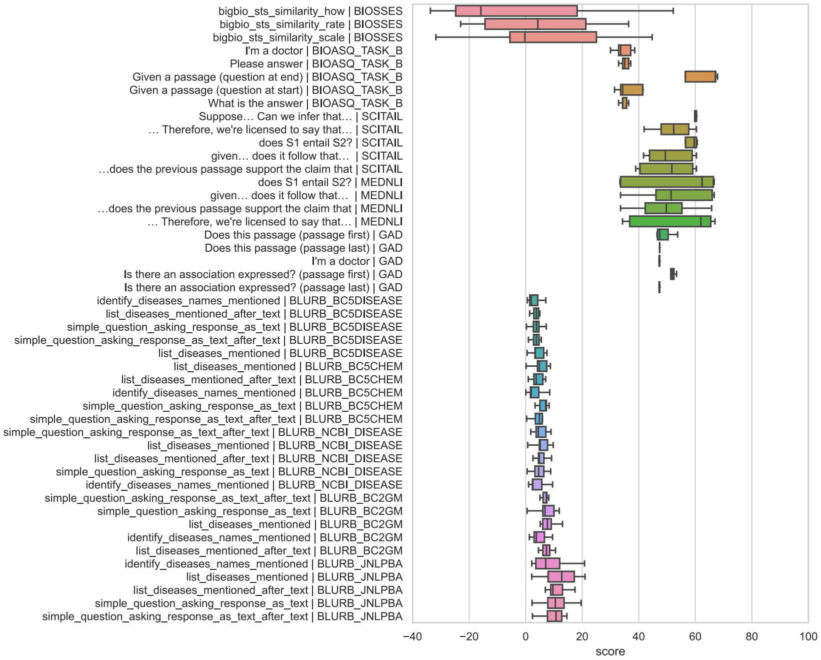


Figure 10: Per-prompt scores (x-axis) for all non-instruction tuned language models (SciFive, GPT-Neo-1.3B, GPT-2, GPT-J-6B, T5 v1.1-xxl, OPT-66B, BLOOM). Prompt template and dataset names are on the y-axis.

Table 10: Summary results across all non-NER tasks.

Model	Dataset	Metric	Mean	SE	Min	Max
SciFive-Base	bigbio_biosses	pearson	17.9	17.4	-4.7	52.2
SciFive-Base	bigbio_bioasq_task_b	accuracy	35.9	1.5	32.9	41.4
SciFive-Base	bigbio_scitail	accuracy	60.1	0.3	59.1	60.4
SciFive-Base	bigbio_mednli	accuracy	63.7	2.8	55.3	66.8
SciFive-Base	bigbio_gad	accuracy	51.9	1.3	46.8	53.7
SciFive-Large	bigbio_biosses	pearson	15.3	29.5	-14.2	44.7
SciFive-Large	bigbio_bioasq_task_b	accuracy	30.7	0.6	29.3	32.9
SciFive-Large	bigbio_scitail	accuracy	59.8	0.5	57.7	60.4
SciFive-Large	bigbio_mednli	accuracy	61.6	4.8	47.3	66.7
SciFive-Large	bigbio_gad	accuracy	47.4	0.0	47.4	47.4
GPT-Neo-1.3B	bigbio_biosses	pearson	36.4	NaN	36.4	36.4
GPT-Neo-1.3B	bigbio_bioasq_task_b	accuracy	43.9	5.9	35.7	67.1
GPT-Neo-1.3B	bigbio_scitail	accuracy	50.7	4.1	38.9	60.4
GPT-Neo-1.3B	bigbio_mednli	accuracy	43.0	7.1	33.5	64.0
GPT-Neo-1.3B	bigbio_gad	accuracy	47.9	0.9	46.4	51.3
GPT-2	bigbio_biosses	pearson	10.9	8.6	2.4	19.5
GPT-2	bigbio_bioasq_task_b	accuracy	38.4	5.4	32.9	60.0
GPT-2	bigbio_scitail	accuracy	50.4	4.3	39.6	60.4
GPT-2	bigbio_mednli	accuracy	54.1	7.3	33.4	66.0
GPT-2	bigbio_gad	accuracy	47.4	0.0	47.4	47.6
GPT-J-6B	bigbio_biosses	pearson	0.2	31.9	-31.8	32.1
GPT-J-6B	bigbio_bioasq_task_b	accuracy	40.6	6.6	33.6	67.1
GPT-J-6B	bigbio_scitail	accuracy	51.6	4.4	40.4	60.3
GPT-J-6B	bigbio_mednli	accuracy	46.3	6.0	34.2	62.8
GPT-J-6B	bigbio_gad	accuracy	48.2	1.0	46.6	52.1
T0_3B	bigbio_biosses	pearson	0.9	NaN	0.9	0.9
T0_3B	bigbio_bioasq_task_b	accuracy	63.9	2.4	58.6	72.9
T0_3B	bigbio_scitail	accuracy	69.9	7.4	46.0	84.5
T0_3B	bigbio_mednli	accuracy	64.6	7.9	41.4	76.2
T0_3B	bigbio_gad	accuracy	47.7	0.3	47.4	48.7
T5 v1.1-xxl	bigbio_biosses	pearson	-6.1	19.1	-33.7	30.5
T5 v1.1-xxl	bigbio_bioasq_task_b	accuracy	64.9	2.1	56.4	67.9
T5 v1.1-xxl	bigbio_scitail	accuracy	54.1	4.2	39.6	60.7
T5 v1.1-xxl	bigbio_mednli	accuracy	52.4	6.9	33.5	65.5
T5 v1.1-xxl	bigbio_gad	accuracy	52.1	0.5	50.2	52.6
T0	bigbio_biosses	pearson	27.2	4.8	17.7	32.0
T0	bigbio_bioasq_task_b	accuracy	86.4	0.9	84.3	89.3
T0	bigbio_scitail	accuracy	72.3	7.5	49.0	88.6
T0	bigbio_mednli	accuracy	68.8	7.6	46.1	78.4
T0	bigbio_gad	accuracy	55.1	0.7	52.6	56.6
T0+	bigbio_biosses	pearson	35.2	5.5	29.7	40.7
T0+	bigbio_bioasq_task_b	accuracy	84.3	1.8	80.7	90.7
T0+	bigbio_scitail	accuracy	71.0	7.6	46.8	87.9
T0+	bigbio_mednli	accuracy	68.9	8.4	44.0	79.7
T0+	bigbio_gad	accuracy	52.4	0.9	49.3	53.9
T0++	bigbio_biosses	pearson	26.9	NaN	26.9	26.9
T0++	bigbio_bioasq_task_b	accuracy	94.1	0.1	93.6	94.3
T0++	bigbio_scitail	accuracy	71.6	5.6	57.0	87.0
T0++	bigbio_mednli	accuracy	74.2	3.9	63.8	81.4
T0++	bigbio_gad	accuracy	53.5	0.7	51.7	55.4
GPT-NeoX-20B	bigbio_biosses	pearson	-14.8	8.3	-23.0	-6.5
GPT-NeoX-20B	bigbio_bioasq_task_b	accuracy	41.3	6.5	34.3	67.1
GPT-NeoX-20B	bigbio_scitail	accuracy	50.5	3.6	41.9	59.8
GPT-NeoX-20B	bigbio_mednli	accuracy	48.6	5.7	34.7	62.4
GPT-NeoX-20B	bigbio_gad	accuracy	47.9	0.9	46.4	51.3
OPT-66B	bigbio_bioasq_task_b	accuracy	43.0	6.2	35.7	67.9
OPT-66B	bigbio_scitail	accuracy	44.7	2.4	39.6	52.3
OPT-66B	bigbio_mednli	accuracy	38.1	3.6	33.3	48.6
OPT-66B	bigbio_gad	accuracy	48.3	1.1	46.6	52.4
GPT-3	bigbio_biosses	pearson	47.3	9.4	32.0	64.5
GPT-3	bigbio_bioasq_task_b	accuracy	73.0	5.8	55.7	92.1
GPT-3	bigbio_scitail	accuracy	52.0	4.0	39.7	61.4
GPT-3	bigbio_gad	accuracy	48.4	0.8	46.1	50.9
BLOOM	bigbio_biosses	pearson	0.5	9.7	-15.8	17.7
BLOOM	bigbio_bioasq_task_b	accuracy	40.9	6.6	33.6	67.1
BLOOM	bigbio_scitail	accuracy	52.4	3.6	39.6	59.6
BLOOM	bigbio_mednli	accuracy	64.0	1.8	59.6	66.9
BLOOM	bigbio_gad	accuracy	48.8	1.0	47.2	51.9

Table 11: Summary results across all NER tasks.

Model	Dataset	Metric	Mean	SE	Min	Max
SciFive-Base	bigbio_blurb_bc5chem	rouge1_fmeasure	2.6	1.6	0.0	7.1
SciFive-Base	bigbio_blurb_bc5disease	rouge1_fmeasure	1.9	0.9	0.2	4.6
SciFive-Base	bigbio_blurb_ncbi_disease	rouge1_fmeasure	2.1	0.9	0.5	4.8
SciFive-Base	bigbio_blurb_bc2gm	rouge1_fmeasure	4.1	2.0	0.5	9.6
SciFive-Base	bigbio_blurb_jnlpba	rouge1_fmeasure	7.9	3.1	2.2	16.1
SciFive-Large	bigbio_blurb_bc5chem	rouge1_fmeasure	5.4	1.7	0.3	8.7
SciFive-Large	bigbio_blurb_bc5disease	rouge1_fmeasure	5.1	1.4	1.0	7.5
SciFive-Large	bigbio_blurb_ncbi_disease	rouge1_fmeasure	7.0	1.5	1.8	9.7
SciFive-Large	bigbio_blurb_bc2gm	rouge1_fmeasure	9.4	2.1	2.6	13.1
SciFive-Large	bigbio_blurb_jnlpba	rouge1_fmeasure	14.7	3.7	2.4	21.0
GPT-Neo-1.3B	bigbio_blurb_bc5chem	rouge1_fmeasure	5.6	1.0	1.9	7.2
GPT-Neo-1.3B	bigbio_blurb_bc5disease	rouge1_fmeasure	4.0	0.8	1.6	6.1
GPT-Neo-1.3B	bigbio_blurb_ncbi_disease	rouge1_fmeasure	6.0	1.3	2.3	8.6
GPT-Neo-1.3B	bigbio_blurb_bc2gm	rouge1_fmeasure	6.5	0.7	3.7	7.7
GPT-Neo-1.3B	bigbio_blurb_jnlpba	rouge1_fmeasure	11.4	1.6	7.6	16.9
GPT-2	bigbio_blurb_bc5chem	rouge1_fmeasure	5.2	1.3	0.9	7.7
GPT-2	bigbio_blurb_bc5disease	rouge1_fmeasure	4.4	1.1	1.4	6.6
GPT-2	bigbio_blurb_ncbi_disease	rouge1_fmeasure	5.7	1.0	2.6	7.5
GPT-2	bigbio_blurb_bc2gm	rouge1_fmeasure	8.3	1.1	4.5	10.3
GPT-2	bigbio_blurb_jnlpba	rouge1_fmeasure	12.7	2.5	6.0	17.4
GPT-J-6B	bigbio_blurb_bc5chem	rouge1_fmeasure	4.9	0.9	1.9	7.3
GPT-J-6B	bigbio_blurb_bc5disease	rouge1_fmeasure	3.4	0.6	1.9	5.0
GPT-J-6B	bigbio_blurb_ncbi_disease	rouge1_fmeasure	5.0	1.2	2.5	9.1
GPT-J-6B	bigbio_blurb_bc2gm	rouge1_fmeasure	7.1	1.1	3.8	10.5
GPT-J-6B	bigbio_blurb_jnlpba	rouge1_fmeasure	10.9	2.0	6.7	17.4
T0_3B	bigbio_blurb_bc5chem	rouge1_fmeasure	38.6	1.0	36.1	41.2
T0_3B	bigbio_blurb_bc5disease	rouge1_fmeasure	23.1	1.4	19.3	26.5
T0_3B	bigbio_blurb_ncbi_disease	rouge1_fmeasure	28.5	1.7	25.4	34.0
T0_3B	bigbio_blurb_bc2gm	rouge1_fmeasure	22.0	0.4	21.3	23.4
T0_3B	bigbio_blurb_jnlpba	rouge1_fmeasure	16.7	3.3	7.7	23.7
T5 v1.1-xxl	bigbio_blurb_bc5chem	rouge1_fmeasure	3.3	0.3	2.0	3.7
T5 v1.1-xxl	bigbio_blurb_bc5disease	rouge1_fmeasure	3.1	0.5	1.3	3.8
T5 v1.1-xxl	bigbio_blurb_ncbi_disease	rouge1_fmeasure	4.3	0.5	2.4	5.6
T5 v1.1-xxl	bigbio_blurb_bc2gm	rouge1_fmeasure	5.0	0.5	3.3	5.9
T5 v1.1-xxl	bigbio_blurb_jnlpba	rouge1_fmeasure	7.2	1.5	2.1	10.0
T0	bigbio_blurb_bc5chem	rouge1_fmeasure	46.5	3.1	42.6	58.8
T0	bigbio_blurb_bc5disease	rouge1_fmeasure	30.8	4.5	22.5	43.9
T0	bigbio_blurb_ncbi_disease	rouge1_fmeasure	38.6	4.9	29.9	56.0
T0	bigbio_blurb_bc2gm	rouge1_fmeasure	24.0	1.5	21.1	29.5
T0	bigbio_blurb_jnlpba	rouge1_fmeasure	16.2	3.4	7.7	23.5
T0+	bigbio_blurb_bc5chem	rouge1_fmeasure	44.4	2.5	38.9	54.0
T0+	bigbio_blurb_bc5disease	rouge1_fmeasure	29.4	3.2	24.3	40.7
T0+	bigbio_blurb_ncbi_disease	rouge1_fmeasure	36.3	3.7	31.0	50.1
T0+	bigbio_blurb_bc2gm	rouge1_fmeasure	25.0	0.6	23.9	27.1
T0+	bigbio_blurb_jnlpba	rouge1_fmeasure	11.1	4.0	3.2	25.2
T0++	bigbio_blurb_bc5chem	rouge1_fmeasure	43.1	1.7	39.0	49.1
T0++	bigbio_blurb_bc5disease	rouge1_fmeasure	28.6	2.2	24.7	35.2
T0++	bigbio_blurb_ncbi_disease	rouge1_fmeasure	36.2	3.0	31.4	47.7
T0++	bigbio_blurb_bc2gm	rouge1_fmeasure	25.1	0.2	24.8	25.7
T0++	bigbio_blurb_jnlpba	rouge1_fmeasure	13.3	2.3	7.5	19.7
GPT-NeoX-20B	bigbio_blurb_bc5chem	rouge1_fmeasure	5.7	1.6	1.5	10.3
GPT-NeoX-20B	bigbio_blurb_bc5disease	rouge1_fmeasure	3.5	0.6	2.1	5.5
GPT-NeoX-20B	bigbio_blurb_ncbi_disease	rouge1_fmeasure	5.5	0.9	4.2	8.9
GPT-NeoX-20B	bigbio_blurb_bc2gm	rouge1_fmeasure	7.0	1.2	2.6	9.9
GPT-NeoX-20B	bigbio_blurb_jnlpba	rouge1_fmeasure	8.9	1.7	2.7	13.0
GPT-3	bigbio_blurb_bc5chem	rouge1_fmeasure	40.5	9.9	13.3	63.3
GPT-3	bigbio_blurb_bc5disease	rouge1_fmeasure	36.9	9.8	12.8	60.8
GPT-3	bigbio_blurb_ncbi_disease	rouge1_fmeasure	40.4	10.5	14.9	66.7
GPT-3	bigbio_blurb_bc2gm	rouge1_fmeasure	39.1	10.7	14.7	64.5
GPT-3	bigbio_blurb_jnlpba	rouge1_fmeasure	37.7	4.4	23.8	48.6

J.2 Evaluation

All language models summary statistics are calculated using n=5 samples (1 score per prompt). Standard error is calculated using the sample standard deviation. Pearson's Correlation was calculated using SciPy v1.7.3. All other metrics are calculated calculated using Scikit-learn v1.0.2. All models less than 11B in size are evaluated using fp32 precision on a single 8x A40 compute node

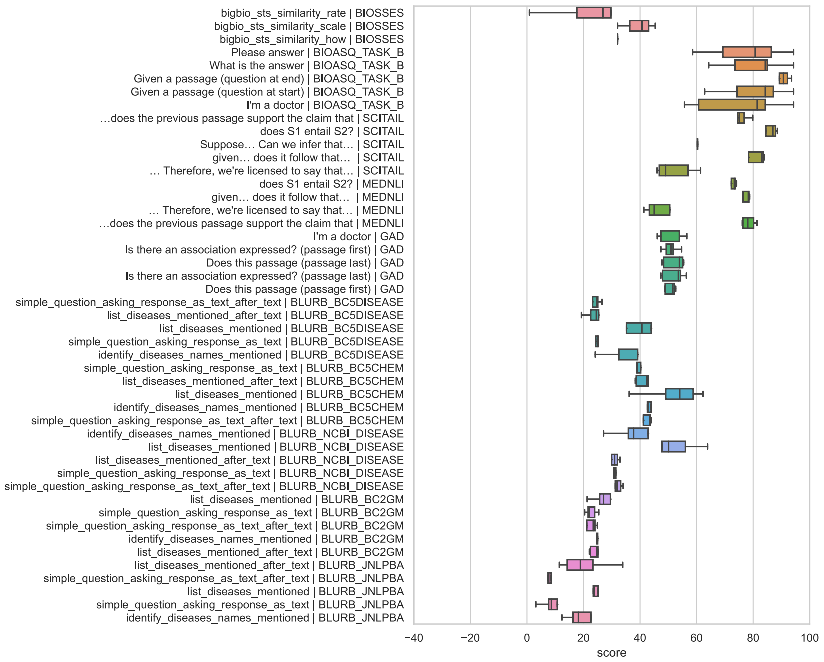


Figure 11: Per-prompt scores (x-axis) for all instruction-tuned language models (T0_3B, T0, T0+, T0++, GPT-3 (text-davinci-0002). Prompt template names are on the y-axis. Performance for non semantic similarity tasks is more varied and higher performing compared to current GPT-2 style pretrained models or T5 models with standard pretraining.

running CUDA 11.2. GPT-NeoX-20B, OPT-66B, and BLOOM were run on an 4xA100 80GB using LLM.int8() for inference. GPT-3 results were queried from OpenAI on 10/3/2022.

J.3 Code

All experiment were run using the most up-to-date version of BIGBIO before paper submssion. `https://github.com/bigscience-workshop/biomedical` commit `0ff295b25bb1be813e64f13246090bff6168cb5a`

Complete language model evaluation harness code and instructions for running BIGBIO experiments: `https://github.com/bigscience-workshop/lm-evaluation-harness/tree/bigbio`

For these experiments, we used a modified version of PromptSource: `https://github.com/bigscience-workshop/promptsource/tree/eval-hackathon` Prompt templates are available at `https://github.com/OpenBioLink/promptsource` and are outlined below.

All pretrained language models were downloaded from Hugging Face's datasets hub.

J.4 Prompt Templates

The following prompt templates were developed using PromptSource. A prompt consists of a set of answer choices, an input template, and an output template.

J.4.1 BIOSSES

Prompt 1: “bigbio_sts_similarity_scale"

Answer Choices:

```
0.0 ||| 0.1 ||| 0.2 ||| 0.3 ||| 0.4 ||| 0.5 ||| 0.6 ||| 0.7 ||| 0.8 ||| 0.9
||| 1.0 ||| 1.1 ||| 1.2 ||| 1.3 ||| 1.4 ||| 1.5 ||| 1.6 ||| 1.7 ||| 1.8
```

Table 12: BIOSSES example instance.

Key	Value
id	6
document_id	7
text_1	`Recently, it was reported that expression of IDH1R132H su...`
text_2	`the mechanism was clarified by yet another genomic survey...`
label	`1.6`

```
||| 1.9 ||| 2.0 ||| 2.1 ||| 2.2 ||| 2.3 ||| 2.4 ||| 2.5 ||| 2.6 ||| 2.7
||| 2.8 ||| 2.9 ||| 3.0 ||| 3.1 ||| 3.2 ||| 3.3 ||| 3.4 ||| 3.5 ||| 3.6
||| 3.7 ||| 3.8 ||| 3.9 ||| 4.0
```

Input Template:

```
from {{"0"}} to {{"4"}}, how similar are "{{text_1}}" and "{{text_2}}"?
```

Output Template:

```
{{label}}
```

Prompt 2: “bigbio_sts_similarity_how"

Answer Choices:

```
0.0 ||| 0.1 ||| 0.2 ||| 0.3 ||| 0.4 ||| 0.5 ||| 0.6 ||| 0.7 ||| 0.8 ||| 0.9
||| 1.0 ||| 1.1 ||| 1.2 ||| 1.3 ||| 1.4 ||| 1.5 ||| 1.6 ||| 1.7 ||| 1.8
||| 1.9 ||| 2.0 ||| 2.1 ||| 2.2 ||| 2.3 ||| 2.4 ||| 2.5 ||| 2.6 ||| 2.7
||| 2.8 ||| 2.9 ||| 3.0 ||| 3.1 ||| 3.2 ||| 3.3 ||| 3.4 ||| 3.5 ||| 3.6
||| 3.7 ||| 3.8 ||| 3.9 ||| 4.0
```

Input Template:

```
How similar are "{{text_1}}" and "{{text_2}}"? Give a score \
between {{"0"}} and {{"4"}}.
```

Output Template:

```
{{label}}
```

Prompt 3: “bigbio_sts_similarity_rate"

Answer Choices:

```
0.0 ||| 0.1 ||| 0.2 ||| 0.3 ||| 0.4 ||| 0.5 ||| 0.6 ||| 0.7 ||| 0.8 ||| 0.9
||| 1.0 ||| 1.1 ||| 1.2 ||| 1.3 ||| 1.4 ||| 1.5 ||| 1.6 ||| 1.7 ||| 1.8
||| 1.9 ||| 2.0 ||| 2.1 ||| 2.2 ||| 2.3 ||| 2.4 ||| 2.5 ||| 2.6 ||| 2.7
||| 2.8 ||| 2.9 ||| 3.0 ||| 3.1 ||| 3.2 ||| 3.3 ||| 3.4 ||| 3.5 ||| 3.6
||| 3.7 ||| 3.8 ||| 3.9 ||| 4.0
```

Input Template:

```
Rate the similarity of these two sentences ({{"0"}} being the lowest \
and {{"4"}} the highest):
"{{text_1}}" and "{{text_2}}"
```

Output Template:

```
{{label}}
```

Prompt 4: “bigbio_sts_similarity_on_a_scale"

Answer Choices:

```
0.0 ||| 0.1 ||| 0.2 ||| 0.3 ||| 0.4 ||| 0.5 ||| 0.6 ||| 0.7 ||| 0.8 ||| 0.9
||| 1.0 ||| 1.1 ||| 1.2 ||| 1.3 ||| 1.4 ||| 1.5 ||| 1.6 ||| 1.7 ||| 1.8
||| 1.9 ||| 2.0 ||| 2.1 ||| 2.2 ||| 2.3 ||| 2.4 ||| 2.5 ||| 2.6 ||| 2.7
||| 2.8 ||| 2.9 ||| 3.0 ||| 3.1 ||| 3.2 ||| 3.3 ||| 3.4 ||| 3.5 ||| 3.6
||| 3.7 ||| 3.8 ||| 3.9 ||| 4.0
```

Input Template:

```
On a scale of {{"0"}} (completely unrelated) to {{"4"}} (exactly same) \
score these sentences:
"{{text_1}}" and "{{text_2}}"
```

Output Template:

```
{{label}}
```

Prompt 5: “bigbio_sts_similarity_what_is"

Answer Choices:

```
0.0 ||| 0.1 ||| 0.2 ||| 0.3 ||| 0.4 ||| 0.5 ||| 0.6 ||| 0.7 ||| 0.8 ||| 0.9
||| 1.0 ||| 1.1 ||| 1.2 ||| 1.3 ||| 1.4 ||| 1.5 ||| 1.6 ||| 1.7 ||| 1.8
||| 1.9 ||| 2.0 ||| 2.1 ||| 2.2 ||| 2.3 ||| 2.4 ||| 2.5 ||| 2.6 ||| 2.7
||| 2.8 ||| 2.9 ||| 3.0 ||| 3.1 ||| 3.2 ||| 3.3 ||| 3.4 ||| 3.5 ||| 3.6
||| 3.7 ||| 3.8 ||| 3.9 ||| 4.0
```

Input Template:

```
What is the similarity of these two sentences on a scale of {{"0"}} (low) \
to {{"4"}} (high): "{{text_1}}" and "{{text_2}}"
```

Output Template:

```
{{label}}
```

Table 13: BioASQ example instance.

Key	Value
id	5c58a74e86df2b917400000d_0
question_id	5c58a74e86df2b917400000d
document_id	http://www.ncbi.nlm.nih.gov/pubmed/29623652
question	Is Baloxavir effective for influenza?
type	yesno
choices	[]
context	Baloxavir marboxil (Xofluza™; baloxavir) is an oral cap-d...
answer	[‘yes’]

J.4.2 BioASQ

Prompt 1: “Given a passage (question at end)"

Answer Choices:

```
no ||| yes
```

Input Template:

```
Given a passage: {{ context }}

Answer the question: "{{question}}"
```

Output Template:

```

{{answer[0]}}
```

Prompt 2: “I’m a doctor"

Answer Choices:

```
no ||| yes
```

Input Template:

```
I’m a doctor and I need to answer the question "{{ question }}" using \
the following passage:

{{ context }}
```

Output Template:

```

{{answer[0]}}
```

Prompt 3: “What is the answer"

Answer Choices:

```
no ||| yes
```

Input Template:

```
What is the answer to the question "{{ question }}" based on \
the following passage:

{{ context }}
```

Output Template:

```

{{answer[0]}}
```

Prompt 4: “Please answer"

Answer Choices:

```
no ||| yes
```

Input Template:

```
Please answer the question "{{ question }}" using \
the following passage:

{{ context }}
```

Output Template:

```

{{answer[0]}}
```

Prompt 5: “Given a passage (question at start)"

Answer Choices:

```
no ||| yes
```

Input Template:

```
Given the following passage, answer the question: "{{question}}"

Passage: {{ context }}
```

Output Template:

```

{{answer[0]}}
```

J.4.3 SciTail

Table 14: SciTail example instance.

Key	Value
id	`0`
premise	`Based on the list provided of the uses of substances 1-7,...`
hypothesis	`If a substance has a ph value greater than 7,that indicat...`
label	`neutral`

Prompt 1: “... Therefore, we’re licensed to say that..."

Answer Choices:

```
true ||| false
```

Input Template:

```
{{premise}} Therefore, we are licensed to say that {{hypothesis}}
{{ answer_choices | join(’ or ’) }}
```

Output Template:

```


{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

Prompt 2: “Suppose... Can we infer that..."

Answer Choices:

```
neutral ||| entailment
```

Input Template:

```
Suppose {{premise}} Can we infer that {{hypothesis}}?
```

Output Template:

```
 {{label}}
```

Prompt 3: “...does the previous passage support the claim that"

Answer Choices:

```
yes ||| no
```

Input Template:

```
{{premise}} Does the previous passage support the claim that {{hypothesis}}?
```

Output Template:

```
{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

Prompt 4: “given... does it follow that..."

Answer Choices:

```
yes ||| no
```

Input Template:

```
Given that {{premise}} Does it follow that {{hypothesis}}
{{ answer_choices | join(’ or ’) }}
```

Output Template:

```

{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

Prompt 5: “does S1 entail S2?"

Answer Choices:

```
yes ||| no
```

Input Template:

```
Sentence 1: {{premise}}

Sentence 2: {{hypothesis}}

Question: Does Sentence 1 entail Sentence 2? \
{{ answer_choices | join(’ or ’) }}
```

Output Template:

```

{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

J.4.4 MedNLI

Table 15: MedNLI example instance.

Key	Value
id	`1f2a8146-66c7-11e7-b4f2-f45c89b91419`
premise	`In the ED, initial VS revealed T 98.9, HR 73, BP 121/90, ...`
hypothesis	`The patient is hemodynamically stable`
label	`entailment`

Prompt 1: “... Therefore, we’re licensed to say that..."

Answer Choices:

```
yes ||| no
```

Input Template:

```
{{premise}} Therefore, we are licensed to say that {{hypothesis}}
{{ answer_choices | join(’ or ’) }}
```

Output Template:

```

{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

Prompt 2: “Suppose... Can we infer that..."

Answer Choices:

```
yes ||| no
```

Input Template:

```
Suppose {{premise}} Can we infer that {{hypothesis}}?
```

Output Template:

```

{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

Prompt 3: “...does the previous passage support the claim that"

Answer Choices:

```
yes ||| no
```

Input Template:

```
{{premise}} Does the previous passage support the claim that {{hypothesis}}?
```

Output Template:

```
{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

Prompt 4: “given... does it follow that..."

Answer Choices:

```
yes ||| no
```

Input Template:

```
Given that {{premise}} Does it follow that {{hypothesis}} \
{{ answer_choices | join(’ or ’) }}
```

Output Template:

```

{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

Prompt 5: “does S1 entail S2?"

Answer Choices:

```
yes ||| no
```

Input Template:

```
Sentence 1: {{premise}}

Sentence 2: {{hypothesis}}

Question: Does Sentence 1 entail Sentence 2? \
{{ answer_choices | join(’ or ’) }}
```

Output Template:

```

{% if label == "entailment" %}
{{answer_choices[0]}}
{% else %}
{{answer_choices[1]}}
{% endif %}
```

J.4.5 GAD

Table 16: GAD example instance.

Key	Value
id	0
document_id	0
text	`These results suggest that the C1772T polymorphism in @GE...`
labels	`[‘1’]`

Prompt 1: “Does this passage (passage last)"

Answer Choices:

```
No ||| Yes
```

Input Template:

```
Does the following passage indicate that there is an association \
between the gene @GENE$ and the disease @DISEASE$ ?

{{ text }}
```

Output Template:

```
{{ answer_choices[labels[0] | int] }}
```

Prompt 2: “Does this passage (passage first)"

Answer Choices:

```
No ||| Yes
```

Input Template:

```
{{ text }}

Does this passage indicate that there is an association between the \
gene @GENE$ and the disease @DISEASE$ ?
```

Output Template:

```
{{ answer_choices[labels[0] | int] }}
```

Prompt 3: “Is there an association expressed? (passage last)"

Answer Choices:

```
No ||| Yes
```

Input Template:

```
Is there an association between the gene @GENE$ and the disease \
@DISEASE$ expressed in this passage?

{{ text }}
```

Output Template:

```
{{ answer_choices[labels[0] | int] }}
```

Prompt 4: “I’m a doctor"

Answer Choices:

```
No ||| Yes
```

Input Template:

```
I’m a doctor. Can you tell me, is there an association between the \
gene @GENE$ and the disease @DISEASE$ expressed in this passage?

{{ text }}
```

Output Template:

```

{{ answer_choices[labels[0] | int] }}
```

Prompt 5: “Is there an association expressed? (passage first)"

Answer Choices:

```
No ||| Yes
```

Input Template:

```
{{ text }}

Is there an association between the gene @GENE\$ and the disease \
@DISEASE$ expressed in this passage?
```

Output Template:

```

{{ answer_choices[labels[0] | int] }}
```

K Large-scale Multi-Task Learning

We make the MTL model available at https://huggingface.co/bigscience-biomedical/bigbio-mtl. Code and instructions to reproduce our results can be found in https://github.com/leonweber/biomuppet.

Table 17: MTL dataset statistics

Task	Abbrev.	# Train Examples	# Valid Examples	# Datasets
Relation Extraction	RE	656,171	106,519	14
Coreference Resolution	COREF	113,137	35,030	9
Event Argument Extraction	EAE	294,129	119,033	10
Text Classification	CLASS	30,743	3,416	2
Semantic Textual Similarity	STS	7,215	804	6
Question Answering	QA	6,490	561	2
Named Entity Recognition	NER	287,582	89,135	53
Event Detection	ED	28,388	9,883	10
Total		1,423,855	364,381	106

K.1 Conversion to MaChAmp

We generated training and evaluation data for 106 datasets that were available when we started to develop the MTL project source code (BigBio version found here). If a dataset within this collective set did not have a predefined validation split, we reserved 10% of its training data as the validation set. Each dataset also had one BigBio-to-MaChAmp transformation script per BigBio task. The purpose of this transformation script is to convert the data represented in the BigBio-schema in a MaChAmp-compatible input for simple extension to the ML library. For statistics of the resulting data set Table 17 and for examples of the transformed task data see Tables 18 and 19.

We model **Relation Extraction** (RE) as relation classification. Each sentence in an input passage is split; subsequently, we construct on example per entity-pair by introducing special marker tokens to mark the start and end of each head and tail entity. We consider each example as a text classification problem in MaChAmp, where the goal is to predict the type of relation between the marked head/ail entities, including a 'None' type relation. We follow the BLURB preprocessing strategy for RE and replace the strings of the marked head and tail entity with their respective entity type. For multi-label datasets where an entity or relation may possess multiple labels, we transform such cases to a multiclass dataset by concatenating all labels. We use this multilabel-to-multiclass transformation for all task types, if required.

We treat **Coreference Resolution** (COREF) in a similar fashion as RE, with the only difference that we have only two relation types: 'coref' denoting a coreference relation between two token spans and 'None'.

We transform the **Event Argument Extraction** (EAE) data in exactly the same way as RE, with the trigger span acting as the head entity and all possible event arguments (entities and triggers) acting as tail entities.

For **Text Classification** (CLASS), we adapt the BigBio version to the MaChAmp format without any further modification apart from the multilabel-to-multiclass transformation.

We transform the **Semantic Textual Similarity** (STS) task from a regression task to classification by replacing the STS score with the decantile into which it falls. We use the template 'Text1 [SEP] Text2' where 'Text1' and 'Text2' are either words, sentences or paragraphs depending on the dataset.

We model **Named Entity Recognition** (NER) and Event Detection (ED) as sequence labelling tasks using an IOB-tagging scheme after sentence splitting.

For **Question Answering** (QA), we experimented with two formulations. In the classification formulation, we construct one example per answer candidate by using the template 'Context [SEP] Question [SEP] AnswerCandidate' and the two labels 'True' (if 'AnswerCandidate' is the correct answer) and 'False' (if 'AnswerCandidate' is the wrong answer). In the sequence labelling setting, we use the template ‘Context. Question‘ and mark all tokens in occurrences of the answer in ‘Context’ with ‘answer’ and the rest with ‘O’.

We use Flair’s [59] ‘SegtokSentenceSplitter‘ for sentence splitting and ‘SpaceTokenizer‘ for tokenization.

Table 18: Examples for the classification task formulation

Task Type	Input	Label
RE	Taken together, these results make it clear that @chemical$-bound forms of ORC and @protein$ are likely to be required for productive interactions and pre-RC formation.	`bind`
COREF	We investigated the potential of the @aryl hydrocarbon receptor$ (@AHR$) to suppress NF-kappaB regulated-gene expression, especially acute-phase genes, such as serum amyloid A (Saa).	`coref`
EAE	v-erbA @Gene_expression$ is required to @Negative_regulation$ c-erbA function in erythroid cell differentiation and regulation of the erbA target gene CAII.	cause
CLASS	These results are in contrast with the findings of Santos et al.(16), who reported a significant association between low sedentary time and healthy CVF among Portuguese	`result&supportive`
STS	Renal failure [SEP] Kidney failure	`8`
QA (class)	Cytokeratin 7/20 staining has been reported to be helpful [...] [SEP] Is cytokeratin immunoreactivity useful in the diagnosis of short-segment Barrett’s oesophagus in Korea?	`True`

K.2 Hyperparameters

For hyperparameter choices, we use a mixture of the MaChAmp default hyperparameters and the suggestions from [1]. We use AdamW [119] with a polynomial decay learning rate schedule with 50,000 warmup steps with a maximum learning rate of 1e-4. We set weight decay to 0.01, dropout to 0.1 and the maximum length of the transformer to 512. We use an effective batch size of 32 tasks and 16 examples per task, train the model with Automated Mixed Precision set to fp16 using apex (`https://github.com/NVIDIA/apex`) and clip the gradient norm to 5. Finally, we downsample large datasets by using MaChAmp’s multinomial sampling with alpha set to 0.5.

For model selection we evaluate the model after each epoch on all validation sets and select the model with the highest average accuracy.

K.3 Results on Validation Sets

We evaluate our MTL model on all validation sets and deliberately refrain from evaluating on the test sets, because we did not rule out train/test overlap. The validation results can be found in Figure 12. Results vary strongly across task types, with the model performing well on COREF (mean 86.9% F1), CLASS (mean 85.4 acc), and NER (mean 72.2% F1). Performance on STS (mean 28.1 Pearson’s r) and QA (mean 42.8 acc) is surprisingly low. We attribute the weak performance on both STS and QA

Table 19: Examples for the sequence labeling task formulation

Task Type	Input	Label
NER	Tricuspid valve regurgitation and lithium carbonate toxicity in a newborn infant.	`B-Disease I-Disease I-Disease O B-Chemical I-Chemical B-Disease O O O O`
ED	Coexpression of NF-kappa B/Rel and Sp1 transcription factors in human immunodeficiency virus 1-induced, dendritic cell-T-cell syncytia.	`B-Gene_expression O O O O O O O O O O O O O O O`
QA (seq)	a frameshift mutation is a deletion or insertion of one or more nucleotides [...] a frameshift mutation is a deletion or insertion of one or more of what that changes the reading frame of the base sequence ?	`O O O O O [...] answer [...] O`

to the small amount of data per task (7,215 and 6,490 training examples respectively), which might prevent the model from allocating parameters for these tasks.

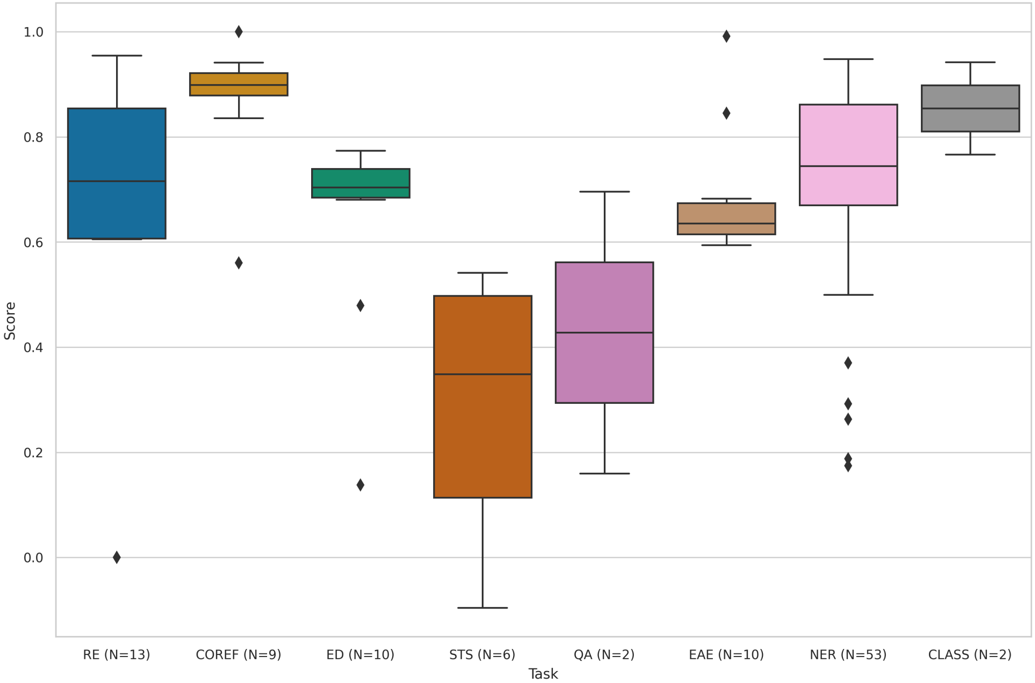


Figure 12: Validation set results of the MTL model by task. ‘RE’ denotes Relation Extraction, ‘COREF’ Coreference Resolution, ‘ED’ event detection, ‘STS’ Semantic Textual Similarity, ‘QA’ Question Answering, ‘EAE’ Event Argument Extraction, ‘NER’ Named Entity Recognition, and ‘CLASS‘ Text Classification. Score is accuracy for QA and CLASS, Pearson’s r for STS and F1 for the rest.

K.4 Resources Used for Training

We trained the MTL model on a local machine on four RTX 3090 GPUs. Training for 50 epochs allowed the model to converge in all tested configurations and took roughly 33 hours.

L BigBio vs. Existing Benchmarks

Biomedical Meta-dataset Benchmarks Table 20 compares BigBio against attributes of other popular English language biomedical meta-dataset benchmarks. To-date, our framework is the only one that supports API-based dataset access, providing access to 4x more datasets than the largest comparable meta-dataset. BLUE and BLURB do not provide dataset access via an API and require manual downloading and preprocessing. Depending on the dataset, these preprocessing choices may not be easily reproducible. For example, in 4/5 NER tasks BLURB uses the IOB transformed datasets generated by Crichton et al. [75]. These datasets rely on regular expression-based tokenization and sentence boundary detection methods developed by Crichton et al. and can vary by dataset, making it difficult to systemically the impact of different tokenization and sentence splitting choices.

End-to-end few and zero-shot evaluation of datasets, prompts, and pretrained language models is emerging as a standardized way to measure the performance of pretrained language models. BLUE and BLURB do not directly support prompt evaluation. BoX provides prompts for 32 biomedical datasets and Python tools for evaluating BART [116]-based language models, however BoX does not provide any access to the original datasets themselves. BigBio integrates with the prompt engineering framework PromptSource to support users more easily designing prompts and running evaluations using the EleutherAI Language Model Evaluation Harness [17]. We currently support several seq2seq and causal language models (e.g., T5, T0, GPT families) available in Hugging Face's model hub. Currently BigBio implements 25 prompts (5 datasets, 5 prompts), with future work focusing on constructing a library of task and dataset-specific biomedical prompts.

Table 20: Attributes of existing English biomedical meta-dataset benchmarks

Name	Datasets	Tasks	Langs	Data API	Reproducible Preprocessing	Prompts	Evaluation Harness
BigBio	127	12	10	✓	✓	*partial*	✓
BLUE [34]	10	5	1		*partial*		
BLURB [19]	13	7	1		*partial*		
BoX [32]	32	9	1			✓	✓

Dataset Coverage Table 21 enumerates the list of datasets currently used by BigBio , BLUE, BLURB, and BoX. Abbreviations are as follows: Named Entity Recognition (NER); Relation Extraction (RE); Question Answering (QA); Part-of-Speech Tagging (POS); Sentiment Analysis (SA) ; Natural Language Inference (NLI); and Systematic Review (SR). For the 32 public datasets BigBio provides data loaders for the majority (28/32), while the remaining 4 are still being implemented by volunteers as of 06/16/2022. Note that *private* indicates that datasets are not available publicly or via DUA and thus cannot currently be included in BigBio.

Table 21: BigBio support of datasets used in popular meta-dataset benchmarks.

Task Type	Dataset	BigBio	BLUE	BLURB	BoX	DUA
NER	BC2GM	✓		✓	✓	
NER	BC5-chem	✓	✓	✓	✓	
NER	BC5-disease	✓	✓	✓	✓	
NER	EBM PICO	✓		✓		
NER	JNLPBA	✓		✓	✓	
NER	NCBI-disease	✓		✓	✓	
RE	ChemProt	✓	✓	✓	✓	
RE	DDI	✓	✓	✓	✓	
RE	GAD	✓		✓		
QA	PubMedQA	✓		✓	✓	
QA	BioASQ	✓		✓	✓	✓
DC	HoC	✓	✓	✓	✓	
STS	BIOSSES	✓	✓	✓		
STS	MedSTS	*	✓			✓
NER	n2c2 2010	✓	✓		✓	✓
NER	ShARe/CLEF 2013	*	✓			✓
NLI	MedNLI	✓	✓			✓
NER	n2c2 deid 2006	✓			✓	✓
DC	n2c2 RFHD 2014	✓			✓	✓
NER	AnatEM	✓			✓	
NER	BC4CHEMD	✓			✓	
NER	BioNLP09	✓			✓	
NER	BioNLP11EPI	✓			✓	
NER	BioNLP11ID	✓			✓	
NER	BioNLP13CG	✓			✓	
NER	BioNLP13GE	✓			✓	
NER	BioNLP13PC	✓			✓	
NER	CRAFT	*			✓	
NER	Ex-PTM	✓			✓	
NER	Linnaeus	✓			✓	
POS	GENIA	*			✓	
SA	Medical Drugs	✓			✓	
SR	COVID				*private*	
SR	Cooking				*private*	
SR	HRT				*private*	
SR	Accelerometer				*private*	
SR	Acromegaly				*private*	

* denotes dataset implementation in-progress

M Example Data Card

We generated data cards for all BIGBIO datasets. We include an example dataset from each schema type to illustrate data cards for different tasks. A PDF of all content is available on our project homepage.

Cantemist Data Card

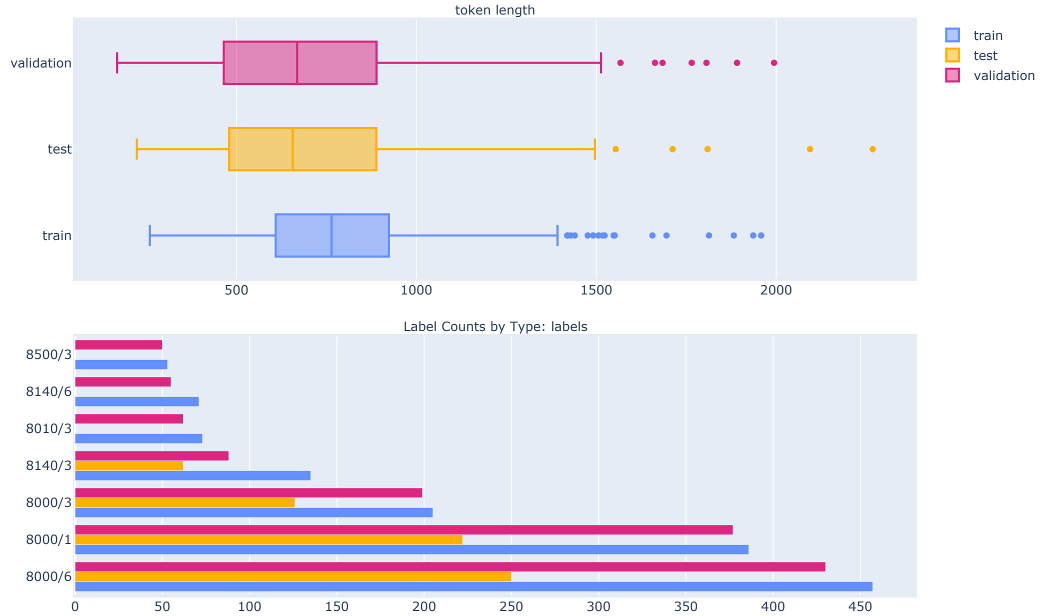


Figure 13: Token frequency distribution by split (top) and frequency of different kind of instances (bottom).

Dataset Description: Collection of 1301 oncological clinical case reports written in Spanish, with tumor morphology mentions manually annotated and mapped by clinical experts to a controlled terminology. Every tumor morphology mention is linked to an eCIE-O code (the Spanish equivalent of ICD-O). The original dataset is distributed in BRAT format, and was randomly sampled into 3 subsets. The training, development and test sets contain 501, 500 and 300 documents each, respectively. This dataset was designed for the CANcer TExt Mining Shared Task, sponsored by Plan-TL. The task is divided in 3 subtasks: CANTEMIST-NER, CANTEMIST-NORM and CANTEMIST-CODING.

CANTEMIST-NER track: requires finding automatically tumor morphology mentions. All tumor morphology mentions are defined by their corresponding character offsets in UTF-8 plain text medical documents.

CANTEMIST-NORM track: clinical concept normalization or named entity normalization task that requires to return all tumor morphology entity mentions together with their corresponding eCIE-O-3.1 codes i.e. finding and normalizing tumor morphology mentions.

CANTEMIST-CODING track: requires returning for each of document a ranked list of its corresponding ICD-O-3 codes. This it is essentially a sort of indexing or multi-label classification task or oncology clinical coding.

For further information, please visit `https://temu.bsc.es/cantemist` or send an email to encargo-pln-life@bsc.es

Homepage: `https://temu.bsc.es/cantemist/?p=4338`

URL: `https://zenodo.org/record/3978041/files/cantemist.zip?download=1`

Licensing: Creative Commons Attribution 4.0 International

Languages: Spanish

Tasks: NER, NED, Text Classification

Schemas: `TEXT`, `KB`, `source`

Splits: train, validation, test

MEDIQA Data Card

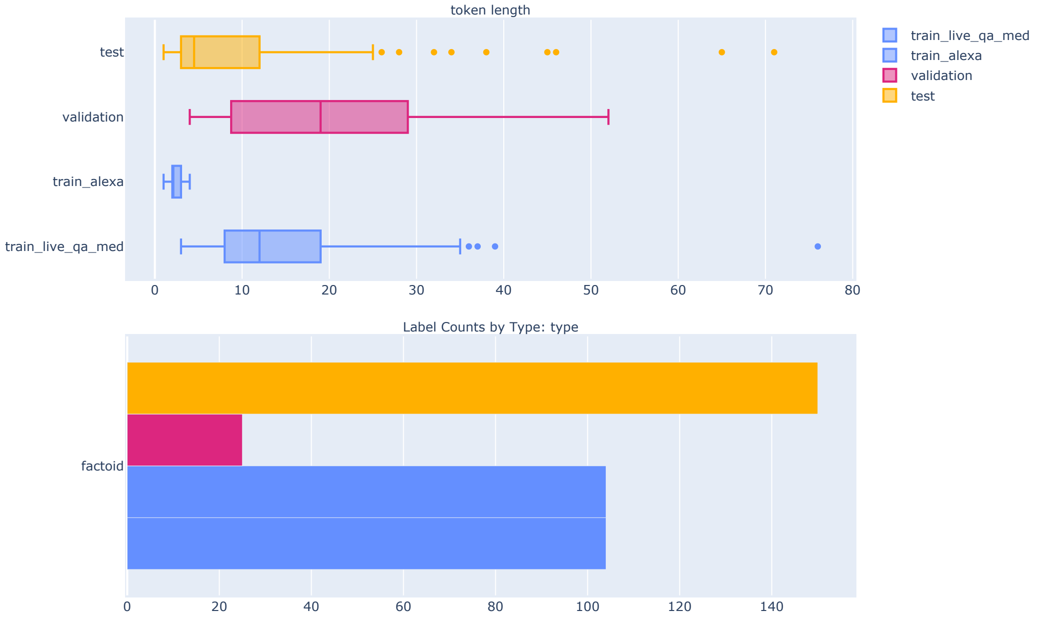


Figure 14: Token frequency distribution by split (top) and frequency of different kind of instances (bottom).

Dataset Description: The MEDIQA challenge is an ACL-BioNLP 2019 shared task aiming to attract further research efforts in Natural Language Inference (NLI), Recognizing Question Entailment (RQE), and their applications in medical Question Answering (QA). Mailing List: `https://groups.google.com/forum/#!forum/bionlp-mediqa`

In the QA task, participants are tasked to:- filter/classify the provided answers (1: correct, 0: incorrect).- re-rank the answers.

Homepage: `https://sites.google.com/view/mediqa2019`

URL: `https://github.com/abachaa/MEDIQA2019/archive/refs/heads/master.zip`

Licensing: License information unavailable

Languages: English

Tasks: Question Answering

Schemas: `QA`, `source`

Splits: train-1-liveQAMed, train-2-Alexa, validation, test

AnEM Data Card

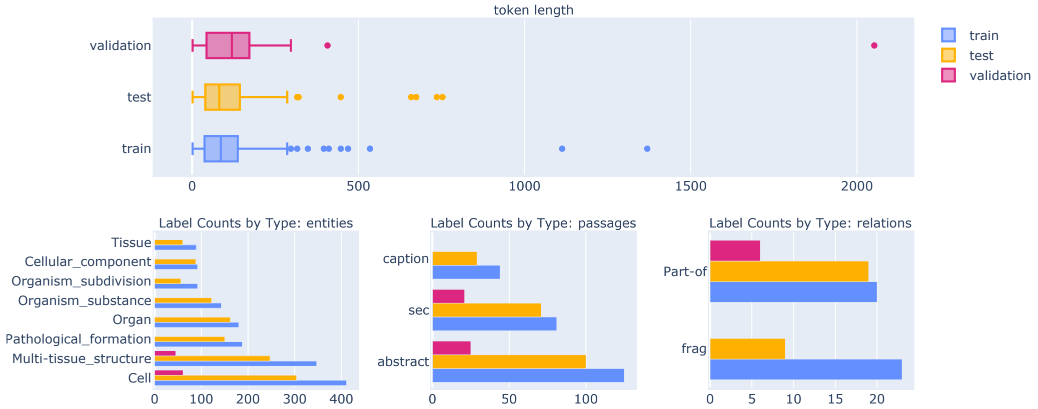


Figure 15: Token frequency distribution by split (top) and frequency of different kind of instances (bottom).

Dataset Description AnEM corpus is a domain- and species-independent resource manually annotated for anatomical entity mentions using a fine-grained classification system. The corpus consists of 500 documents (over 90,000 words) selected randomly from citation abstracts and full-text papers with the aim of making the corpus representative of the entire available biomedical scientific literature. The corpus annotation covers mentions of both healthy and pathological anatomical entities and contains over 3,000 annotated mentions.

Homepage: `http://www.nactem.ac.uk/anatomy/`

URL: `http://www.nactem.ac.uk/anatomy/data/AnEM-1.0.4.tar.gz`

Licensing: Creative Commons Attribution Share Alike 3.0 Unported

Languages: English

Tasks: NER, Coreference Resolution, Relation Extraction

Schemas: `KB`, `source`

Splits: train, validation, test

ParaMed Data Card

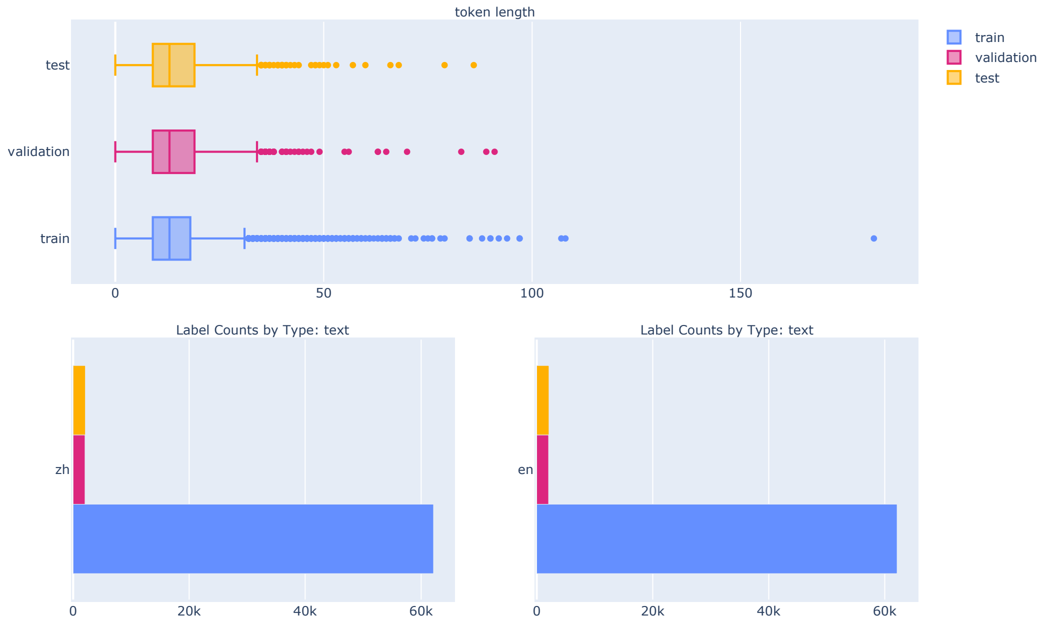


Figure 16: Token frequency distribution by split (top) and frequency of different kind of instances (bottom).

Dataset Description: NEJM is a Chinese-English parallel corpus crawled from the New England Journal of Medicine website. English articles are distributed through https://www.nejm.org/ and Chinese articles are distributed through http://nejmqianyan.cn/. The corpus contains all article pairs (around 2000 pairs) since 2011.

Homepage: `https://github.com/boxiangliu/ParaMed`

URL: `https://github.com/boxiangliu/ParaMed/blob/master/data/nejm-open-access.tar.gz?raw=true`

Licensing: Creative Commons Attribution 4.0 International

Languages: English, Chinese

Tasks Translation

Schemas: `t2t`, `source`

Splits: train, validation, test

SciTail Data Card

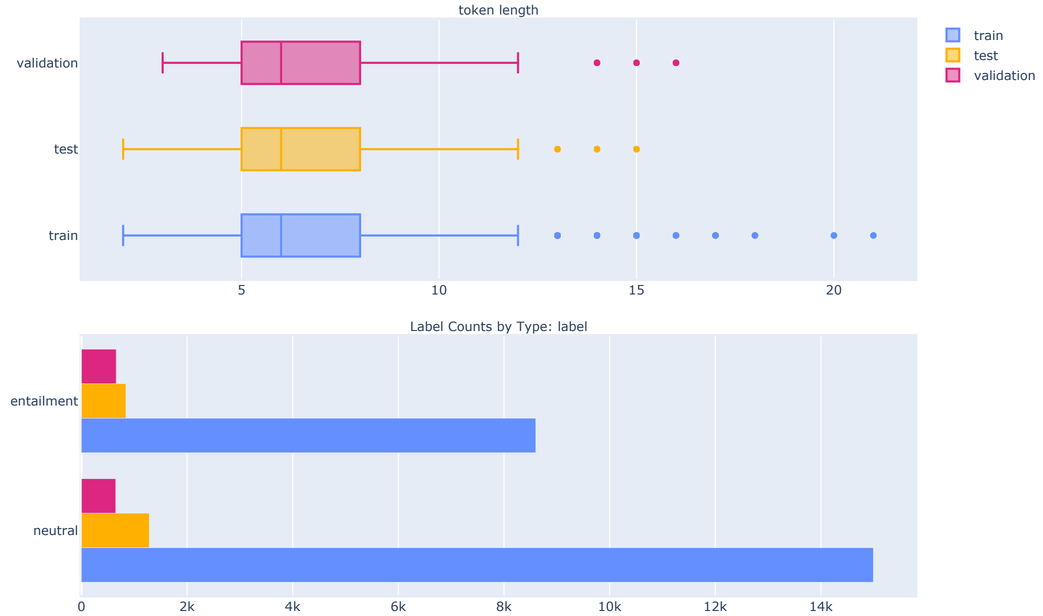


Figure 17: Token frequency distribution by split (top) and frequency of different kind of instances (bottom).

Dataset Description The SciTail dataset is an entailment dataset created from multiple-choice science exams and web sentences. Each question and the correct answer choice are converted into an assertive statement to form the hypothesis. We use information retrieval to obtain relevant text from a large text corpus of web sentences, and use these sentences as a premise P. We crowdsource the annotation of such premise-hypothesis pair as supports (entails) or not (neutral), in order to create the SciTail dataset. The dataset contains 27,026 examples with 10,101 examples with entails label and 16,925 examples with neutral label.

Homepage: `https://allenai.org/data/scitail`

URL: `https://ai2-public-datasets.s3.amazonaws.com/scitail/SciTailV1.1.zip`

Licensing: Apache License 2.0

Languages: English

Tasks: Textual Entailment

Schemas: `te`, `source`

Splits: train, validation, test

MQP Data Card

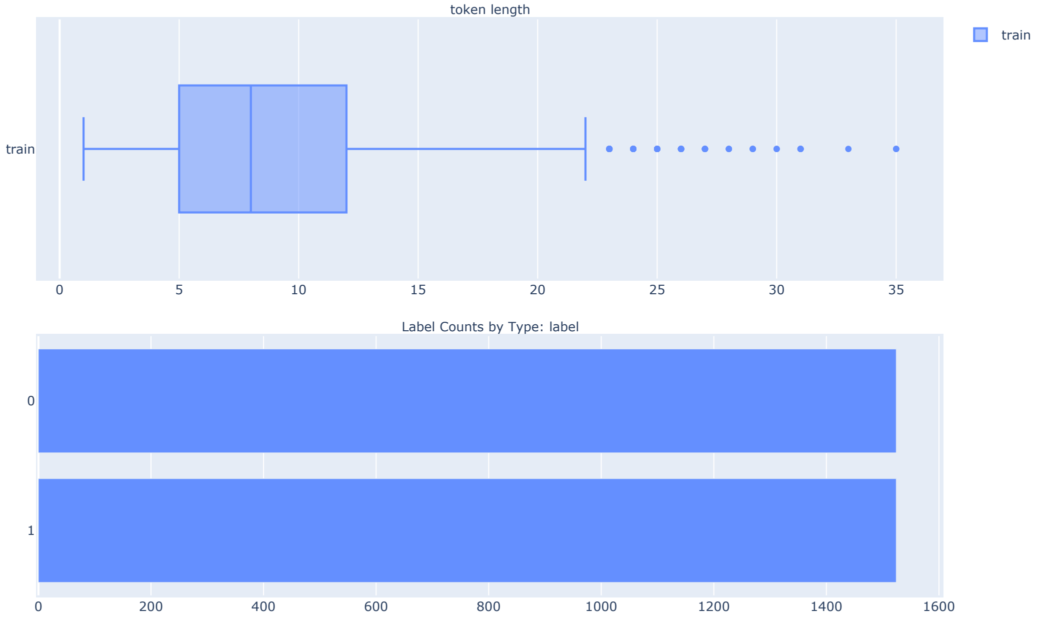


Figure 18: Token frequency distribution by split (top) and frequency of different kind of instances (bottom).

Dataset Description: Medical Question Pairs dataset by McCreery et al (2020) contains pairs of medical questions and paraphrased versions of the question prepared by medical professional. Paraphrased versions were labelled as similar (syntactically dissimilar but contextually similar) or dissimilar (syntactically may look similar but contextually dissimilar). Labels 1: similar, 0: dissimilar

Homepage: `https://github.com/curai/medical-question-pair-dataset`

URL: `https://raw.githubusercontent.com/curai/medical-question-pair-dataset/master/mqp.csv`

Licensing: License information unavailable

Languages: English

Tasks: Semantic Similarity

Schemas: `pairs`, `source`

Splits: train

N BigBio Data Card

Dataset Description: BigBio is a community project and meta-dataset consisting of 126+ dataset loader scripts providing programmatic access to expertly annotated biomedical natural language processing datasets. The constituent datasets support 12 tasks grouped into 6 schema types. 105 of these datasets are publicly available and can be automatically downloaded using the BigBio Python package. The remaining 21 require some level of manual action ranging from simple web forms to credentialed access and training on how to handle protected health information.

Homepage: `https://github.com/bigscience-workshop/biomedical`

URL: `https://github.com/bigscience-workshop/biomedical`

Licensing: `https://choosealicense.com/licenses/apache-2.0/`

Languages: English, Spanish, French, Chinese, German, Japanese, Dutch, Portuguese, Swedish, and Vietnamese

Tasks: named entity recognition (`NER`), named entity disambiguation/normalization (`NED`), event extraction (`EE`), relation extraction (`RE`), coreference resolution (`COREF`), question answering (`QA`), textual entailment (`TE`), text classification (`TXTCLASS`), semantic similarity (`STS`), paraphrasing (`PARA`), translation (`TRANSL`), summarization (`SUM`).

Schemas: Knowledge Base (`KB`), Question Answering (`QA`), Textual Entailment (`TE`), Text (`TEXT`), Text Pairs (`PAIRS`), Text to Text (`T2T`), source (`source`).

Splits: train, validation, test, sample

Table 22: Summary statistics for all datasets included in BigBio. Token counts (# Toks) assumes white space tokenziation and example instances (# N) correspond to the unit of text emitted by the dataloader iterable, usually a document, sentence, or text pair. Some datasets include k-folds or multiple training splits, which are noted by $k = *$. See each dataset's data card for more specific details, such as label counts by task.

Dataset Name	BigBio Name	Split	# Chars	# Toks	# N	License	Tasks	Schema	Langs	Access
AnEM [134]	`an_em`	train	300k	44.3k	250	CC BY SA 3.0	RE, NER, COREF	KB	EN	Public
		valid	85.6k	11k	50					
		test	242k	36.2k	200					
AnatEM [140]	`anat_em`	train	840k	122k	606	CC BY SA 3.0	NER	KB	EN	Public
		valid	319k	44.7k	202					
		test	547k	79.2k	404					
AskAPatient [117]	`ask_a_patient`	train k=10	31.3k	202k	15665	CC BY 4.0	NER, NED	KB	EN	Public
		validation k=10	1.74k	10.6k	792					
		test k=10	1.92k	11.7k	866					
BC5CDR [112]	`bc5cdr`	train	653k	93k	500	Public Domain Mark 1.0	RE, NER, NED	KB	EN	Public
		valid	647k	92.3k	500					
		test	677k	96.5k	500					
BC7-LitCovid [70]	`bc7_litcovid`	train	34.4M	4.97M	24960	*Unknown*	TXTCLASS	TEXT	EN	Public
		valid	3.69M	532k	2489					
		test	8.68M	1.26M	6239					
Bio-SimVerb [72]	`bio_sim_verb`	train	14.9k	2k	1000	*Unknown*	STS	PAIRS	EN	Public
Bio-SimLex [72]	`bio_simlex`	train	16.1k	1.98k	988	*Unknown*	STS	PAIRS	EN	Public
MESINESP 2021 [86]	`bioasq_2021_mesinesp`	valid	256k	38.6k	109	CC BY 4.0	TXTCLASS	TEXT	ES	Public
		test	59.4k	9.06k	119					
BioASQ Task B [161]	`bioasq_task_b`	train	5.21M	2.26M	9955	NLM	QA	QA	EN	DUA
		valid	573k	249k	1029					
		test	581k	253k	1041					
BioASQ Task C 2017 [127]	`bioasq_task_c_2017`	train	2.59B	346M	62952	NLM	TXTCLASS	TEXT	EN	DUA
		test	895M	120M	22610					
BioInfer [141]	`bioinfer`	train	164k	23.7k	894	CC BY 2.0	RE, NER	KB	EN	Public
		test	40.8k	5.93k	206					
BiologyHowWhy-Corpus [95]	`biology_how_why_corpus`	train	2.33M	985k	1269	*Unknown*	QA	QA	EN	Public
BIOMRC [137]	`biomrc`	train	114k	48.6k	30	*Unknown*	QA	QA	EN	Public
BioNLP 2009 [104]	`bionlp_shared_task_2009`	train	1.21M	176k	800	GENIA Project	EE, NER, COREF	KB	EN	Public
		valid	234k	33.8k	150					
		test	397k	57.3k	260					
BioNLP 2011 EPI [133]	`bionlp_st_2011_epi`	train	901k	127k	600	GENIA Project	EE, NER, COREF	KB	EN	Public
		valid	310k	43.5k	200					
		test	653k	91.9k	440					
BioNLP 2011 GE [105]	`bionlp_st_2011_ge`	train	1.41M	206k	908	CC BY 3.0	EE, NER, COREF	KB	EN	Public
		valid	435k	64.1k	259					
		test	541k	79k	347					
BioNLP 2011 ID [145]	`bionlp_st_2011_id`	train	438k	64.7k	152	GENIA Project	EE, NER, COREF	KB	EN	Public
		valid	119k	18.4k	46					
		test	335k	50k	118					
BioNLP 2011 REL [146]	`bionlp_st_2011_rel`	train	1.21M	176k	800	GENIA Project	RE, NER, COREF	KB	EN	Public
		valid	234k	33.8k	150					
		test	397k	57.3k	260					
BioNLP 2013 CG [142]	`bionlp_st_2013_cg`	train	467k	66.1k	300	GENIA Project	EE, NER, COREF	KB	EN	Public
		valid	153k	21.7k	100					
		test	297k	42.1k	200					
BioNLP 2013 GE [106]	`bionlp_st_2013_ge`	train	371k	54.9k	222	GENIA Project	RE, EE, NER, COREF	KB	EN	Public
		valid	391k	57.9k	249					
		test	506k	75.1k	305					
BioNLP 2013 GRO [107]	`bionlp_st_2013_gro`	train	200k	29.4k	150	GENIA Project	RE, EE, NER	KB	EN	Public
		valid	59.8k	8.7k	50					
		test	132k	19k	100					
BioNLP 2013 PC [132]	`bionlp_st_2013_pc`	train	378k	53.8k	260	GENIA Project	EE, NER, COREF	KB	EN	Public

		valid	131k	18.6k	90					
		test	253k	36k	175					
BioNLP 2019 BB [65]	bionlp_st_2019_bb	train	129k	19k	133	*Unknown*	RE, NER, NED	KB	EN	Public
		valid	66.5k	9.71k	66					
		test	110k	16.2k	96					
BioRED [122]	biored	train	660k	94.2k	400	*Unknown*	RE, NER	KB	EN	Public
		valid	173k	24.9k	100					
		test	168k	24.1k	100					
BioRelEx [100]	biorelex	train	237k	37.8k	1405	*Unknown*	RE, NER, NED, COREF	KB	EN	Public
		valid	33.1k	5.29k	201					
BioScope [170]	bioscope	train	171k	42k	6383	CC BY 2.0	NER	KB	EN	Public
BIOSSES [154]	biosses	train	20.1k	2.94k	64	GPL 3.0	STS	PAIRS	EN	Public
		valid	5.09k	733	16					
		test	6.44k	925	20					
CADEC [99]	cadec	train	575k	104k	1250	Custom	NER, NED	KB	EN	Public
CANTEMIST [124]	cantemist	train	2.6M	382k	501	CC BY 4.0	NER, NED, TXTCLASS	KB, TEXT	ES	Public
		valid	2.33M	341k	500					
		test	1.41M	206k	300					
CAS [89]	cas	train	972k	175k	7580	DUA	TXTCLASS	TEXT, KB	FR	DUA
CellFinder [129]	cellfinder	train	171k	25.2k	26	CC BY SA 3.0	NER	KB	EN	Public
		test	205k	30.3k	27					
CHEBI Corpus [149]	chebi_nactem	train	1.95M	306k	100	CC BY 4.0	RE, NER	KB	EN	Public
CHEMDNER [111]	chemdner	train	4.88M	687k	3500	*Unknown*	NER, TXTCLASS	KB, TEXT	EN	Public
		valid	4.86M	683k	3500					
		test	4.19M	591k	3000					
ChemProt [112]	chemprot	train	1.64M	230k	1020	Public Domain Mark 1.0	RE, NER	KB	EN	Public
		valid	990k	139k	612					
		test	1.3M	182k	800					
CHIA [114]	chia	train	1.04M	151k	2000	CC BY 4.0	RE, NER	KB	EN	Public
Citation GIA Test Collection [177]	citation_gia_ test_collection	test	230k	33.4k	151	*Unknown*	NER, NED	KB	EN	Public
CodiEsp [125]	codiesp	train	193M	29.1M	176294	CC BY 4.0	TXTCLASS	TEXT	ES	Public
		train	0	0	500					
		valid	0	0	250					
		test	0	0	250					
CORD-NER [172]	cord_ner	train	407M	62.5M	29500	Custom	NER	KB	EN	Public
CT-EBM-SP [68]	ctebmsp	train	625k	90.3k	420	CC BY NC 4.0	NER	KB	ES	Public
		valid	212k	30.7k	140					
		test	206k	29.9k	140					
DDI Corpus [93]	ddi_corpus	train	928k	128k	714	CC BY NC 4.0	RE, NER	KB	EN	Public
		test	281k	38.7k	303					
DIANN [147]	diann_iber_eval	train	548k	81.8k	400	*Unknown*	NER	KB	EN, ES	Public
		test	144k	21.5k	100					
		train	1.06M	156k	400					
		test	275k	40.9k	100					
DisTEMIST [85]	distemist	train	1.76M	264k	750	CC BY 4.0	NER	KB	EN	Public
EBM NLP [130]	ebm_pico	train	7.68M	1.29M	4746	*Unknown*	NER	KB	EN	Public
		test	306k	50.9k	187					
EHR-Rel [148]	ehr_rel	train	174k	23.4k	3741	Apache 2.0	STS	PAIRS	EN	Public
ESSAI [76]	essai	train	1.83M	314k	13848	DUA	TXTCLASS	TEXT, KB	FR	DUA
EU-ADR [168]	euadr	train	452k	64.3k	300	*Unknown*	RE, NER	KB	EN	Public
Evidence Inference 2.0 [78]	evidence_inference	train	2.91M	446k	10150	MIT	TE	TE	EN	Public
		valid	352k	53.6k	1238					
		test	358k	54.9k	1228					
GAD [66]	gad	train	740k	113k	4261	CC BY 4.0	TXTCLASS	TEXT	EN	Public
		valid	91k	13.9k	535					
		test	98.6k	14.9k	534					
GENETAG [157]	genetag	train	1.16M	197k	7500	NCBI	NER	KB	EN	Public
		valid	783k	133k	5000					
		test	387k	65.5k	2500					

PTM Events [131]	genia_ptm_event_corpus	train	145k	20.8k	112	GENIA Project	EE, NER, COREF	KB	EN	Public
GENIA Relation Corpus [143]	genia_relation_corpus	train	1.21M	176k	800	GENIA Project	RE	KB	EN	Public
		valid	234k	33.8k	150					
		test	397k	57.3k	260					
GENIA Term Corpus [135]	genia_term_corpus	train	2.99M	435k	2000	GENIA Project	NER	KB	EN	Public
GEOkhoj v1 [81]	geokhoj_v1	train	4.25M	554k	25000	CC BY NC 4.0	TXTCLASS	TEXT	EN	Public
		test	848k	111k	5000					
GNormPlus [177]	gnormplus	train	379k	55.7k	281	*Unknown*	NER, NED	KB	EN	Public
		test	359k	52.5k	262					
Hallmarks of Cancer [62]	hallmarks_of_cancer	train	1.96M	312k	12119	GPL 3.0	TXTCLASS	TEXT	EN	Public
		valid	296k	47.1k	1798					
		test	573k	91.8k	3547					
HPRD50 [83]	hprd50	train	18.1k	2.67k	34	*Unknown*	RE, NER	KB	EN	Public
		test	4.94k	710	9					
IEPA [79]	iepa	train	75.1k	10.9k	160	*Unknown*	RE	KB	EN	Public
		test	18.6k	2.68k	40					
JNLPBA [74]	jnlpba	train	0	0	37094	CC BY 3.0	NER	KB	EN	Public
		valid	0	0	7714					
LINNAEUS [87]	linnaeus	train	2.46M	373k	84	CC BY 4.0	NER, NED	KB	EN	Public
LLL05 [72]	lll	train	13.2k	1.99k	77	*Unknown*	RE	KB	EN	Public
		test	13.1k	2.07k	87					
Mantra GSC [109]	mantra_gsc	train	16k	2.12k	50	CC BY 4.0	NER, NED	KB	EN, FR, DE, NL, ES	Public
MayoSRS [139]	mayosrs	train	2.69k	314	101	CC0 1.0	STS	PAIRS	EN	Public
MedQA [97]	med_qa	train	1.84M	890k	11298	*Unknown*	QA	QA	EN	Public
		valid	229k	111k	1412					
		test	234k	114k	1413					
MedDialog [71]	meddialog	train	290k	51k	981	*Unknown*	TXTCLASS	TEXT	EN, ZH	Public
		valid	41.8k	7.35k	126					
		test	35.5k	6.31k	122					
MEDDOCAN [123]	meddocan	train	1.42M	208k	500	CC BY 4.0	NER	KB	ES	Public
		valid	755k	111k	250					
		test	711k	105k	250					
MedHop [180]	medhop	train	187M	78.7M	1620	CC BY SA 3.0	QA	QA	EN	Public
		valid	32.8M	13.8M	342					
Medical Data [101]	medical_data	train	11M	1.81M	5279	*Unknown*	TE	TE	EN	DUA
		test	7.12M	1.16M	2924					
MEDIQA NLI [151]	mediqa_nli	test	49.6k	8.37k	405	PhysioNet 1.5	TE	TE	EN	DUA
MEDIQA QA [64]	mediqa_qa	train k=2	1.91M	4.56M	104	*Unknown*	QA	QA	EN	Public
		valid	1.24M	519k	25					
		test	5.78M	2.42M	150					
MEDIQA RQE [64]	mediqa_rqe	train	1.69M	262k	8588	*Unknown*	TE	TE	EN	Public
		valid	86.5k	15.6k	302					
		test	68.1k	12.1k	230					
MedMentions [126]	medmentions	train	4.16M	606k	2635	CC0 1.0	NER, NED	KB	EN	Public
		valid	1.4M	204k	878					
		test	1.39M	203k	879					
MedNLI [150]	mednli	train	1.51M	240k	11232	PhysioNet 1.5	TE	TE	EN	DUA
		valid	196k	31.1k	1395					
		test	187k	29.6k	1422					
MeQSum [63]	meqsum	train	405k	70.8k	1000	*Unknown*	SUM	T2T	EN	Public
MiniMayoSRS [139]	minimayosrs	train	803	92	29	CC0 1.0	STS	PAIRS	EN	Public
miRNA [61]	mirna	train	272k	38.2k	201	CC BY NC 3.0	NER, NED	KB	EN	Public
		test	115k	16k	100					
MLEE [144]	mlee	train	199k	27.9k	131	CC BY NC SA 3.0	RE, EE, NER, COREF	KB	EN	Public
		valid	68.1k	9.61k	44					

		test	135k	19.1k	87					
MQP [112]	`mqp`	train	644k	120k	3048	*Unknown*	STS	PAIRS	EN	Public
MSH WSD [96]	`msh_wsd`	train	52.8M	7.59M	37888	UMLS	NED	KB	EN	DUA
MuchMore [67]	`muchmore`	train train	8.43M 12.7M	1.11M 1.69M	7808 6374	*Unknown*	NER	KB	EN, DE	Public
Multi-XScience [120]	`multi_xscience`	train valid test	143M 23.9M 23.6M	21.3M 3.54M 3.51M	30369 5066 5093	MIT	SUM, PARA	T2T	EN	Public
MutationFinder [69]	`mutation_finder`	valid test	416k 726k	61.4k 107k	305 508	Custom	NER	KB	EN	Public
n2c2 2006 De-identification [165]	`n2c2_2006_deid`	train test	2.25M 952k	340k 146k	669 220	DUA	NER	KB	EN	DUA
n2c2 2006 Smoking Status [164]	`n2c2_2006_smokers`	train test	1.72M 479k	304k 85.1k	398 104	DUA	TXTCLASS	TEXT	EN	DUA
n2c2 2008 Obesity [162]	`n2c2_2008`	train test	5M 3.5M	852k 595k	730 507	DUA	TXTCLASS	TEXT	EN	DUA
n2c2 2009 Medication [166]	`n2c2_2009`	train test	4.86M 3.75M	824k 637k	696 553	DUA	NER	KB	EN	DUA
n2c2 2010 Relations [167]	`n2c2_2010`	train test	827k 1.48M	150k 267k	170 256	DUA	RE, NER	KB	EN	DUA
n2c2 2011 Coreference [163]	`n2c2_2011`	train test	1.37M 916k	247k 167k	251 173	DUA	COREF	KB	EN	DUA
n2c2 2014 De-identification [156]	`n2c2_2014_deid`	train test	3.4M 2.19M	489k 316k	790 514	DUA	NER	KB	EN	DUA
n2c2 2014 Cardiac Risk Factors [113]	`n2c2_2014_risk_factors`	train test	3.4M 2.19M	489k 316k	790 514	DUA	TXTCLASS	TEXT	EN	DUA
n2c2 2018 Selection Criteria [155]	`n2c2_2018_track1`	train test	3.91M 1.64M	550k 231k	202 86	DUA	TXTCLASS	TEXT	EN	DUA
n2c2 2018 ADE [92]	`n2c2_2018_track2`	train test	3.84M 2.54M	574k 377k	303 202	DUA	RE, NER	KB	EN	DUA
NCBI Disease [80]	`ncbi_disease`	train valid test	747k 133k 135k	113k 20.1k 20.4k	592 100 100	CC0 1.0	NER, NED	KB	EN	Public
NLM-Gene [94]	`nlm_gene`	train test	812k 180k	114k 25.2k	450 100	CC0 1.0	NER, NED	KB	EN	Public
NLM WSD [173]	`nlm_wsd`	train	8.37M	1.22M	5000	UMLS	NED	KB	EN	DUA
NLM-Chem [94]	`nlmchem`	train valid test	2.69M 663k 1.52M	408k 100k 229k	80 20 50	CC0 1.0	NER, NED, TXTCLASS	KB, TEXT	EN	Public
NTCIR-13 MedWeb [152]	`ntcir_13_medweb`	train test train test	79.4M 8.38M 163k 50.7k	3.71M 412k 27.2k 8.47k	1920 640 1920 640	CC BY 4.0	TXTCLASS	TEXT	EN, ZH, JA	DUA
OSIRIS [84]	`osiris`	train	172k	25.7k	105	CC BY 3.0	NER, NED	KB	EN	Public
ParaMed [118]	`paramed`	train valid test	16.2M 552k 564k	3.74M 128k 130k	62127 2036 2102	CC BY 4.0	TRANSL	T2T	EN, ZH	Public
PDR [103]	`pdr`	train	274k	40.5k	179	*Unknown*	EE, NER, COREF	KB	EN	Public
PharmaCoNER [88]	`pharmaconer`	train valid test	1.18M 567k 587k	177k 85.1k 88.2k	500 250 250	CC BY 4.0	NER, TXTCLASS	KB, TEXT	ES	Public
PhoNER_COVID19 [160]	`pho_ner`	train valid test	671k 286k 433k	168k 71.3k 108k	5027 2000 3000	Custom	NER	KB	VI	Public
PICO Annotation [182]	`pico_extraction`	train	60.4k	10.2k	421	*Unknown*	NER	KB	EN	Public
PMC-Patients [181]	`pmc_patients`	train valid test	1.22B 6.72M 7.67M	184M 1.02M 1.17M	257366 2144 2366	CC BY NC SA 4.0	STS	PAIRS	EN	Public
ProGene [82]	`progene`	split k=10	821k	4.76M	30926	CC BY 4.0	NER	KB	EN	Public

		split k=10 split k=10	43.3k 96.1k	251k 557k	1676 3623					
PsyTAR [183]	`psytar`	train train	319k 57k	56.4k 7.56k	3398 6003	CC BY 4.0	NER	KB	EN	DUA
PUBHEALTH [110]	`pubhealth`	train valid test	5.61M 683k 692k	899k 110k 111k	9804 1223 1231	MIT	TXTCLASS	PAIRS	EN	Public
PubMedQA [98]	`pubmed_qa`	train valid test	1.28M 141k 1.45M	549k 60.3k 618k	450 50 500	MIT	QA	QA	EN	Public
PubTator Central [174]	`pubtator_central`	train	19.5k	2.91k	4	NCBI	NER, NED	KB	EN	Public
QUAERO [128]	`quaero`	train valid test	67.7k 68.2k 70k	10.6k 10.5k 10.9k	833 832 832	GFDL 1.3	NER	KB	FR	Public
SCAI Chemical [108]	`scai_chemical`	train	155k	20.9k	100	*Unknown*	NER	KB	EN	Public
SCAI Disease [91]	`scai_disease`	train	630k	90.4k	400	*Unknown*	NER	KB	EN	Public
SciCite [73]	`scicite`	train valid test	1.82M 203k 413k	280k 31.3k 63.4k	8243 916 1861	*Unknown*	TXTCLASS	TEXT	EN	Public
SciELO [153]	`scielo`	train	995M	153M	2828917	CC BY 4.0	TRANSL	T2T	EN, ES, PT	Public
SciFact [171]	`scifact`	train valid test	787k 280k 26.4k	112k 39.6k 3.62k	919 339 300	CC BY NC 2.0	TE	TE	EN	Public
SciQ [179]	`sciq`	train valid test	11.8M 993k 1.02M	4.96M 418k 428k	11679 1000 1000	CC BY NC 3.0	QA	QA	EN	Public
SciTail [102]	`scitail`	train valid test	4.19M 237k 372k	681k 38.8k 62.3k	23596 1304 2126	Apache 2.0	TE	TE	EN	Public
SETH Corpus [159]	`seth_corpus`	train	760k	111k	630	Apache 2.0	RE, NER	KB	EN	Public
SPL ADR [77]	`spl_adr_200db`	train	29M	3.46M	2208	CC0 1.0	RE, NER, NED	KB	EN	Public
Swedish Medical NER [60]	`swedish_medical_ner`	train	85k	14.1k	926	CC BY SA 4.0	NER	KB	SV	Public
SNP Corpus [158]	`thomas2011`	test	0	0	296	Custom	NER, NED	KB	EN	Public
tmVar v1 [176]	`tmvar_v1`	train test	547k 265k	80.2k 38.8k	334 166	*Unknown*	NER	KB	EN	Public
tmVar v2 [178]	`tmvar_v2`	train	259k	38k	158	*Unknown*	NER, NED	KB	EN	Public
tmVar v3 [175]	`tmvar_v3`	test	812k	119k	500	*Unknown*	NER, NED	KB	EN	Public
TwADR-L [117]	`twadrl`	train k=10 validation k=10 test k=10	10k 327 361	76.1k 1.84k 2.03k	4805 125 142	CC BY 4.0	NER, NED	KB	EN	Public
UMNSRS [136]	`umnsrs`	train	11.3k	1.2k	587	CC0 1.0	STS	PAIRS	EN	Public
Verspoor 2013 [169]	`verspoor_2013`	train	279k	42.9k	120	*Unknown*	RE, NER	KB	EN	Public

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