NLP-BASED CLASSIFICATION OF SOFTWARE TOOLS FOR METAGENOMICS SEQUENCING DATA ANALYSIS INTO EDAM SEMANTIC ANNOTATION

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ABSTRACT

Motivation: The rapid growth of metagenomics sequencing data makes metagenomics increasingly dependent on computational and statistical methods for fast and efficient analysis. Consequently, novel analysis tools for big-data metagenomics are constantly emerging. One of the biggest challenges for researchers occurs in the analysis planning stage: selecting the most suitable metagenomics software tool to gain valuable insights from sequencing data. The building process of data analysis pipelines is often laborious and time-consuming since it requires a deep and critical understanding of how to apply a particular tool to complete a specified metagenomics task.

Results: We have addressed this challenge by using machine learning methods to develop a classification system of metagenomics software tools into 13 classes (11 semantic annotations of EDAM and two virus-specific classes) based on the descriptions of the tools. We trained three classifiers (Naive Bayes, Logistic Regression, and Random Forest) using 15 text feature extraction techniques (TF-IDF, GloVe, BERT-based models, and others). The manually curated dataset includes 224 software tools and contains text from the abstract and the methods section of the tools’ publications. The best classification performance, with an Area Under the Precision-Recall Curve score of 0.85, is achieved using Logistic regression, BioBERT for text embedding, and text from abstracts only. The proposed system provides accurate and unified identification of metagenomics data analysis tools and tasks, which is a crucial step in the construction of metagenomics data analysis pipelines.

Keywords  natural language processing, software tool classification, information retrieval, language models, metagenomics, EDAM ontology

1 Introduction

Metagenomics aims to provide insight into the genetic material present in various environmental samples. Viral metagenomics, for example, studies viral communities in water, soil, animals, and plants. The most common approach in metagenomics is to use high-throughput sequencing (HTS) of DNA or RNA, which generates millions of short-read nucleotide sequences. HTS data are used to detect and quantify genomes and transcriptomes in a biological sample. The
widespread adoption of HTS techniques in biological studies caused a rapid increase in the volume of metagenomics data that needs to be analyzed as efficiently and rapidly as possible. These metagenomics big data make the field increasingly dependent on computational and statistical methods that lead to discovering new knowledge from such data. Consequently, new analysis tools for big-data metagenomics are constantly emerging \[1\]. \textit{e.g.} 2500 new tools were produced in 2016. HTS data analysis tools are computer programs that assist users with computational analyses of DNA and RNA sequences to understand their features and functionality using different analytical methods. Interest in such analysis may be motivated by different research questions, ranging from pathogen monitoring and identification to identifying all organisms in a sequenced biological sample. The standard approach to achieve this is to apply a combination of trimming, assembly, alignment and mapping, annotation, and other complex pipelines of software algorithms to HTS data.

HTS data analysis tools play an essential role in the pipeline construction process. Helping scientists select and use the appropriate tools facilitates the development of analysis-specific efficient pipelines and updating of existing ones. Individual institutions with various project constraints increasingly use metagenomics tools and gradually improve their knowledge and tool use. Under these circumstances, selecting the most suitable metagenomics software tool to gain valuable data insights can be complex and confusing for people involved in the pipeline-building process.

Before adding a tool to a pipeline, it is essential to know certain details about it. What are the required inputs? Which input and output file formats are supported? Most importantly, which data analysis task does the tool perform? \“Task\” refers to the function of the metagenomics tool or the analysis it performs. Having an overview of all the available tools for a given task is also crucial. The results provided by search engines are too unstructured to allow for a swift differentiation and comparison of similar tools. Furthermore, selecting a suitable tool for each data analysis step based on official publications and websites is not straightforward. Therefore, several benchmark studies tried to address \“the best tool for the task\” challenge, considering different perspectives, \textit{e.g.} plant-associated metagenome analysis tools \[2-4\], machine learning-based approaches for metagenome analysis \[3,5\], task-specific tools for mapping \[2,6\] and assembly \[4\], and complete pipelines for virus classification \[7,9\] and taxonomic classification \[10-12\].

Other fields face a similar challenge with the abundance of software to classify. Machine learning approaches for software classification have been widely used in the cybersecurity domain \[13,14\]. Examples include data protection by developing misuse-based systems that detect malicious code and classify malware into different known families, \textit{e.g.} Worm, Trojan, Backdoor, Ransomware, and others. Another active area is anomaly-detection-based systems, which cluster binaries that behave similarly to identify new categories.

There is a plethora of metagenomics tool functions available. Understanding the functions of a given tool and comparing it with similar tools are complicated tasks. Different benchmark efforts for metagenomics tools are published regularly. Still, they are often incomplete, covering only a specific research question, including a limited set of tools, focusing extensively on technical metrics, or lacking transparency and continuity.

The Galaxy platform \[15\] provides a recommendation-based solution \[16\] to help users create workflows. The recommendations are based on data from more than 18000 workflows and thousands of available tools for various scientific analyses. The deep learning-based recommendation system uses the tool sequences, the workflow quality, and the pattern analysis of tool usage to suggest highly relevant tools to the users for their specific data analysis. A set of tool sequences is extracted from each workflow created by the platform users. This approach is not fully personalized, as it only considers one metric, \textit{i.e.}, the similarity between tool sequences in workflows. The system will recommend the same next-step set of tools to all the users with the same built sequence. Furthermore, it limits the system to the workflow data available on the platform’s internal database, where a certain type of analysis can predominate at a specific point in time. These constraints directly influence the quality of the recommendations, especially for minority user profiles, who will receive low-quality or unsuitable tool recommendations more frequently.

Machine learning-based classification systems of research papers were developed to help users find the appropriate paper. The search can be directed towards differentiating the topics \[17,18\] or be focused on specific domains, \textit{e.g.} computer science \[19,20\] or bioinformatics \[21\].

Classification systems use different algorithms and combinations of paper sections. In some works \[19,22\] they rely on established ontologies such as CSO - the computer science ontology \[23\], EDAM - the ontology of bio-scientific data analysis and data management \[24\], and SWO - the software ontology \[25\].

We propose a machine learning-based system that uses curated and peer-reviewed abstract text descriptions to classify metagenomics tools into classes representing their main task. The classification system facilitates users to investigate tools quicker, decide where a tool fits in the metagenomics pipeline construction process, and quickly and efficiently select tools from 13 different classes.
2 Methods

Our main goal was to be able to infer the main task of metagenomics tools from their description in natural text. We explored different combinations of the classification algorithm, its set of hyperparameters, the textual description, and the text embedding method to identify the best model for the task.

2.1 Data sources

The information contained in most scientific papers is typically divided into the title, abstract, introduction, methods, results, and discussion sections. We manually gathered descriptions from the paper publications of 224 metagenomics tools. We collected the abstract sections in the “abstracts only” dataset and the methods section in the “methods only” dataset. We also prepared tool descriptions that include both the abstracts and methods sections in the “abstracts+methods” dataset (Supplementary Datasets S1, S2, and S3 and see Supplementary Section S1). All datasets include the title of the paper as the first sentence in the description of each tool. Each record in the collected datasets represents a single tool and contains the tool’s name, description, and task (class) as represented in Table 1.

Table 1: Excerpt of raw “abstracts only” dataset for five tools belonging to different categories.

| Tool name   | Tool description                                      | Tool task (Class)   |
|-------------|-------------------------------------------------------|---------------------|
| KrakenUniq  | KrakenUniq: confident and fast metagenomics cl.       | Classification      |
| ViruDetect  | ViruDetect: An automated pipeline or efficie.          | Virus identification|
| ALLPATHS    | ALLPATHS: de novo assembly of whole-genome sho.        | Assembly            |
| Bambino     | Bambino: a variant detector and alignment view.        | Visualisation       |
| imGLAD      | imGLAD: accurate detection and quantification         | Abundance estimation|

2.2 Task ontology

The diverse and complex operations in bio-scientific data analysis lead us to rely on the well-established and comprehensive EDAM ontology [24] to categorize the tools from a functional perspective. The 11 classes comprise bioinformatics operations and processes from the EDAM ontology: “(Sequence) alignment”, “(Taxonomic) classification”, “Mapping”, “(Sequence) assembly”, “(Sequence) trimming”, “(Sequencing) quality control”, “(Sequence) annotation”, “(Sequence) assembly validation”, “(RNA-seq quantification for) abundance estimation”, “SNP-Discovery”, “Visualization”.

We defined two additional classes: “Virus detection” and “Virus identification”. We assign to these two classes viral analysis tools classified as machine learning tools in EDAM ontology, e.g. DeepVirFinder [26] and VirNet [27]. We assign other viral analysis pipelines to the two classes even if the pipelines include several tools belonging to other EDAM classes, such as K-mer counting, assembly, mapping, and others. Examples of such tools are Kodoja [28], VirFind [29] and VirusFinder [30], which are all developed for virus detection and identification.

We assigned 224 tools into 13 tasks (classes). Some tools can be used for several tasks and thus belong to several classes. However, we only assigned them to one of the 13 classes, i.e., to the main task for which they were designed, see Supplementary Section S2. The obtained class distribution is shown in Figure 1.

2.3 Data pre-processing

Before a classifier can use the available data, the appropriate pre-processing steps are required. The steps involved in extracting data from a tool description are summarized in Figure 2. To create features from the raw text, train the classifiers and infer machine learning models, we performed the following steps: text cleaning and preparation, label coding, and vector representation of text (Supplementary Datasets S4, S5, and S6). For text cleaning and preparation, we use downcasing, lemmatization, removal of stop words, possessive pronouns, words composed of one or two letters, words starting with digits, special characters, punctuation signs, numbers, and links. We represent the class variable as a nominal discrete variable with 13 different values. We then generated text vector representations, which are discussed in the following subsection.
2.4 Vector representation of text

To train the different classifiers, we represented the text description of the tools as a vector of numbers using language models, prediction-based and frequency-based techniques (Supplementary Datasets S7-S42).

2.4.1 Word embedding methods

We used and evaluated the 12 most commonly used approaches to extract features from the text. We describe them in the following paragraphs.

TF-IDF for a word in a document is calculated by multiplying the frequency of the term (term frequency) \[31\] of a word in a document with the inverse document frequency of a word \[32\] in a set of documents. If the word is very common and appears in many documents, this number will approach 0. Otherwise, the TF-IDF will approach 1.

GloVe Embeddings \[33\], which stands for global vectors, capture the semantic context of words using both local statistics (local word context) and global statistics (word co-occurrences) to generate a word vector. This regression neural network, trained on five combinations of general domain corpora (English Wikipedia and Gigaword), combines the advantages of global matrix factorization and local context window methods. It uses a gradient descent optimization algorithm and a decreasing weighting function where distant word pairs are expected to have less information about their relationship.

ELMO \[34\], deep contextualized word representation, represents each token based on the complete input sentence. The word representations combine the internal states of a pre-trained bidirectional language model (biLM) in a linear function learned by the end task model.

BERT \[35\], which stands for Bidirectional Encoder Representations from Transformers, improves the fine-tuning-based strategies for applying pre-trained language representations to downstream tasks. It uses two unsupervised tasks during pre-training: binarized Next Sentence Prediction (NSP) and Masked Language Model (MLM). Given a set of input tokens, the Masked Language Model randomly masks 15% of the tokens. The goal is to predict the masked words based on their bidirectional context. To understand the relationship between sentences, which is crucial for many downstream tasks, BERT pre-trains on NSP tasks which can be generated from the monolingual vocabulary. The final hidden state corresponding to the [CLS] token (the first token of every sequence) is used as the aggregate sequence representation.
for classification tasks. In this work, we refer to L as the number of layers (transformer blocks), H as the number of hidden states, and A as the number of self-attention heads, and we report results on BERTBASE: L=12, H=768, A=12.

In addition to using the [CLS] token to represent a text sequence, we investigated three additional pooling strategies for BERTBASE, representing different choices of vectors from different layers:

- **BERTS2L**: Summing the vector embeddings generated from the Second to the Last Layer.
- **BERTSL4**: Summing the vector embeddings generated from the Last Four Layers.
- **BERTCL4**: Concatenation of the vector embeddings generated from the Last Four Layers.

**BioBERT** [36] is a domain-specific language representation model based on the adaptation of BERT to the biomedical domain. With the same architecture, weights, and Wordpiece vocabulary as BERT, BioBERT is pre-trained on corpora from the biomedical domain (PubMed abstracts and PMC full-text articles). BioBERT achieved a new state-of-the-art performance on three biomedical tasks: Biomedical named entity recognition (in terms of F1 score), biomedical relation extraction (in terms of F1 score), and biomedical question answering (in terms of mean reciprocal rank).

**XLNET** [37] is a generalized AutoRegressive pre-training method that combines the best of AutoEncoding and Autoregressive language modeling while overcoming their limitations. XLNet is not based on a data corruption mechanism such as BERT. Consequently, special symbols used in pre-training are not missed in fine-tuning step. XLNet also improves the pre-training design architecture by (1) increasing the performance of long text-related tasks by including the segment recurrence mechanism and the relative encoding scheme of Transformer-XL in the training step, and (2) reparameterizing the Transformer-XL network to apply its architecture to permutation-based language modeling.

**RoBERTA** [38] is an optimized method of pre-training BERT-based models that demonstrate the benefits of bigger datasets, batches, and sequences to enhance model performance. The improved strategy also recommends training the models for a longer period, dynamically modifying the masking pattern used on the training data, and removing the next-sentence prediction objective.

**ELECTRA** [39] BERT is pre-trained using the masked language modeling approach to learn bidirectional word representations. ELECTRA (Efficiently Learning an Encoder that Classifies Token Replacements Accurately) proposes an alternative pre-training task (replaced token detection). The tokens are replaced with proposed alternatives produced by a generator network. Then the discriminator network predicts which token is original and which is a replacement.

**ELECTRAMed** [40], based on ELECTRA, is a pre-trained domain-specific language model for the biomedical domain, inheriting the general-domain ELECTRA architecture learning framework and computational benefits.

### 2.4.2 Short vs. long text

The complexity of the attention layer is quadratic to the length of the sequence [35], therefore longer sequences are more expensive for BERT and BERT-based language models. The length of the text sequences cannot exceed 510 tokens, excluding special tokens ([CLS] and [SEP]). When analyzing the “abstracts only” dataset, we were not faced with this limitation. To extend the analysis to longer texts, we explored libraries **NLU** [41], **sentence transformers** by UKP lab [42] and **transformers** by Hugging Face [43], depending on the availability of the models. We applied the long-text approach to all studied datasets, where we mapped input text into a fixed-length embedding based on the pre-trained model used. We also compared the performances of the direct, short-text and long-text approaches on the “abstracts only” dataset.

As shown in the Supplementary Table S2, the resulting word or token embeddings have different sizes, ranging from 100 to 3072 elements, depending on the algorithm we used to generate the vectors. Except for TF-IDF, all embedding methods were subjected to the following two steps to obtain the final sentence vector. First, for each row in the dataset, we constructed an embedding matrix with n rows and m columns consisting of a list of words or tokens in the text and their corresponding numeric vector representations, as shown in Figure 3, where n is the number of words/tokens in the text description, and m is the number of elements in the generated word embedding vectors. Second, we calculated the average of the elements in each column of the resulting embedding matrix. Thus, we obtained sentence embeddings of the same size regardless of the length of the original text description.

### 2.5 Learning algorithms

To find which learning algorithm performed best on our data, we investigated three machine learning classification models with different parameter settings (Supplementary Data Table S44): Logistic Regression (LR), Random Forest (RF), and Naive Bayes (NB). We assembled a pipeline for the TF-IDF vectorizer and the classifiers so that they can be
Figure 3: Method of generating the input text vector representation with the same length as the tokens/words vectors generated by a given embedding method.

cross-validated together while setting different parameters. The feature extraction step was performed separately for text embedding models, and then we trained the classifiers on the resulting datasets.

2.6 Model cross-validation on independent test set

Firstly, we randomly split the dataset into a stratified train set and a test set, which we refer to as the independent test set. We then used repeated nested cross-validation on the training set with five outer folds and three inner folds. For hyperparameter tuning, we used scikit-learn’s `GridSearchCV` function. The function was performed in the inner cross-validation on each inner training set and evaluated on the inner test set to select the best hyperparameter values. The model with the best hyperparameter setting was then trained on the outer train set and evaluated on the outer test set. For a list of hyperparameter values, see Supplementary Table S1. Finally, the performance of the final model was estimated on the independent test set. The methodology used to train each model was as follows:

- Assemble the pipeline.
- Decide which hyperparameters we want to tune.
- Build a grid containing the set of possible values of hyperparameters of the pipeline.
- Define the metric to measure the performance of a model in a specific parameter setting. In our case, we use balanced accuracy.
- Use a grid search cross-validation process to find the best combination of hyperparameters exhaustively, as described in the previous paragraph.
- Obtain the model’s performance with the best parameter settings using the Area Under the Receiver Operating Characteristic Curve.
- Select the final model with the highest AUPRC score in the five nested cross-validation rounds.
- Obtain the final performance of the model on the independent test set using the different metrics described in the next section.

For TF-IDF, we fine-tuned its parameters in the inner loop (Supplementary Data Table S45).

Our datasets have unbalanced classes, making the classification task inherently more challenging, see Figure 1. As we wanted to detect the correct class for each tool, all target classes were equally important. The traditional classification algorithms we used in this study tend to favor majority over minority class elements due to their incorrect implicit assumption of an equal class representation during learning. To properly investigate the ability of our models to correctly detect each class, we used the F-score, the Area Under the Receiver Operating Characteristics curve (AUC-ROC) score, and class-specific Precision, Recall and Accuracy, as well as the Area Under the Precision-Recall Curve (AUC-PR) score as a ranking metric, which is more suitable to assess the performance of the classifiers on unbalanced datasets. To directly compare the models (classifier + embedding method) and select the best classification model while taking into account the class unbalance of the datasets, we measured Precision, Recall, and used the (AUC-PR) score.
Table 2: \((\text{AUC-PR})\) scores of machine learning models by dataset. The embedding methods in bold were evaluated only on the “abstracts only” dataset. Rows are sorted in descending order of the best classifier (LR) performance on the “abstracts only” dataset. The highest scores in each column are in bold. Starred scores refer to the best-performing classifier for each dataset and embedding method pair.

| embedding methods | abstracts only | methods only | abstracts+methods |
|-------------------|---------------|--------------|-------------------|
|                  | LR RF NB      | LR RF NB     | LR RF NB          |
| BioBert-hf        | **0.85** 0.61 0.56 | - - - | - - - |
| BERTS2L           | 0.83 0.47 0.53 | 0.44 0.31 0.27 | **0.84** 0.54 0.53 |
| BERTSL4           | 0.81 0.5 0.47 | 0.4 0.37 0.27 | **0.83** 0.52 0.49 |
| BERTCL4           | 0.79 0.52 0.49 | 0.41 0.33 0.24 | **0.82** 0.55 0.54 |
| BERT-st           | 0.75 0.54 0.53 | 0.48 0.35 0.3 | **0.73** 0.58 0.54 |
| BioBERT-nlu       | 0.73 0.63 0.49 | 0.46 0.33 0.28 | **0.77** 0.57 0.48 |
| TFIDF             | 0.7 0.8 0.71 | **0.62** 0.66 0.61 | 0.73 **0.74** 0.71 |
| ELECTRA-hf        | 0.64 0.5 0.51 | - - - | - - - |
| ELECTRAmed-hf     | 0.64 0.49 0.41 | - - - | - - - |
| RoBERTa-st        | 0.61 0.5 0.43 | 0.38 0.36 0.31 | **0.59** 0.46 0.4 |
| ELMO              | 0.5 0.46 0.31 | 0.48 0.38 0.19 | **0.51** 0.48 0.17 |
| XLNET-nlu         | 0.46 0.33 0.33 | 0.4 0.32 0.34 | 0.43 0.3 0.44 |
| GLOVE-nlu         | 0.33 0.44 0.36 | 0.2 0.36 0.29 | 0.22 0.35 0.33 |
| ELECTRAmed-st     | 0.24 0.21 0.15 | 0.17 0.2 0.13 | 0.22 0.27 0.16 |
| ELECTRA-nlu       | 0.2 0.17 0.14 | 0.12 0.18 0.14 | 0.2 0.22 0.14 |

3 Results and Discussion

We are reporting the results of the developed models. Each model consists of two steps: an embedding step and a classifier step, and these steps are performed using various methods and algorithms. Firstly, we discuss the efficacy of various embedding and classification methods. Next, we identify the combination with the best predictive performance. Finally, we report and comment on the best model’s typical misclassifications.

3.1 BioBERT yields the best embedding representation

When generated from the “methods only” dataset, TF-IDF embedding was by far the most informative embedding method for all three classifiers, with Random Forest classifier achieving the highest \((\text{AUC-PR})\) score of 0.66, see Table 2, Supplementary Figures S6 and S3. On the “abstracts only” and “abstracts+methods” datasets, TF-IDF was among the top five.

ELECTRA’s implementation of the NLU library was the least informative embedding in all datasets, see Supplementary Figure S11. On one hand, the model is pre-trained on a general corpus, which produced the reverse effect of BioBERT embeddings on the classifiers’ performance by reducing the informativeness of the model on a metagenomics-specific text (the tools’ text descriptions). The slight increase in the classifiers’ performance when trained on ELECTRA-hf embeddings instead of ELECTRAmed-hf also highlights the substantial effect of the pre-training corpus on the results. We deduce that a medical pre-training corpus does not improve the informativeness of the embeddings for metagenomics text, see the comparison of ELECTRA-hf and ELECTRAmed-hf in Supplementary Figure S5. However, the most important factor influencing the low informativeness of ELECTRA-nlu embeddings is the pre-built pipelines used by the NLU library. We can see a significant increase in the performance of the classifiers when the ELECTRA embeddings were generated without resorting to the NLU library on the “abstracts only” dataset, see the comparison of ELECTRA-nlu and ELECTRA-hf in Supplementary Figure S5.

On the “abstracts only” and “abstracts+methods” datasets, the set of BERT variations (BERTS2L, BERTSL4 and BERTCL4) which use different pooling strategies, in addition to the BERT-based methods such as BioBERT, built by pre-training BERT on the medical corpus, and the hugging face implementation of ELECTRA which adapts the pre-training approach of BERT, consistently helped the classifiers yield better results.

3.2 Logistic Regression outperforms Naive Bayes

We evaluated the three classifiers (Logistic Regression, Random Forests, and Naive Bayes) with a statistical comparison using the Nemenyi test, as proposed by [46], to reflect the overall performance of each classifier using their average
ranks across the datasets. With \( N \) classifiers, the method that performs the best has a rank of 1, while the method that performs the worst has a rank of \( N \).

On the “abstract only” descriptions, the Logistic Regression classifier was significantly better than Random Forests and Naive Bayes. Logistic Regression outperformed the other two classifiers in every dataset, see Figure 4 and Supplementary Figure S2. The mean (AUC-PR) scores of Logistic Regression, Random Forest and Naive Bayes on “abstracts only” embeddings datasets are 0.60, 0.47 and 0.42 respectively; 0.37, 0.34 and 0.28 on “methods only” embeddings datasets; and 0.57, 0.46 and 0.41 on “abstracts+methods” embeddings datasets. It is worth noticing that Logistic Regression consistently performed better than Random Forests and Naive Bayes on the “abstracts only”-based embedding datasets, even if one among Naive Bayes or Random Forests was performing the worse.

The Logistic Regression significantly outperformed the other classifiers when trained on the language models-based embeddings of the three datasets. At the same time, the Naive Bayes always performed the worse through all the datasets and embedding strategies.

3.3 Abstracts are crucial for good predictive performance

All models showed lower performance when trained on the “methods only” dataset, compared to their performance on the “abstracts only” and the “abstracts+methods” datasets, see Supplementary Figure S6 and Supplementary Figures S5 and S7. The significant drop in (AUC-PR) scores across all classifiers and embedding methods indicates that the text description of the tools covering only the methods section has poor informativeness. We note that the text informativeness of the methods sections in the scientific articles improved when we added the abstract section text, as shown in Figure S5.

Our findings are consistent with previous studies where abstracts proved to be effective in capturing the context, e.g. in bioinformatics research [21] and computer science research papers [17].
3.4 Evaluation of the best model

The Logistic Regression classifier with BioBERT-hf embedding strategy on the “abstracts only” dataset was the best model with an (AUC-PR) score of 0.85, see Table 2. As shown in Figure 5, the model achieved perfect classification accuracy for the classes “Classification”, “Virus detection”, “Virus Identification”, “Abundance estimation”, “Trimming” and “Quality control”, without completely missing any other class. Most of the other models had difficulty distinguishing “Virus detection” from “Virus identification” instances and “classification” from “Abundance estimation” or “Assembly”, as shown in Supplementary Figures S8, S9, and S10, which can be explained with the significant similarity between the three classes. Supplementary Figure S4 also highlights the improvement in the performance of the top models compared to the baseline (Supplementary Section S3.1) and to the worst trained model (Logistic Regression classifier with ELECTRA-nlu embedding strategy on the “methods only” dataset).

The correct class of misclassified instances (Supplementary Table S2) was usually in the top three classification probabilities predicted by the model (Supplementary Data Table S46) for predicted probabilities. This pattern excluded two instances, “Tagdb” and “DeepVariant”, where the correct class probabilities were ranked 7 and 8 out of 13 consecutively. In addition, our model produced few seeming misclassifications when the tools in question performed more than one task:

- “Savant” [47] was misclassified as an “Annotation” tool instead of a “Visualisation” tool since it is a sequence annotation, visualization, and analysis framework, see Supplementary Figure S12.
- “Kart” [48] was misclassified as a “Trimming” tool instead of an “Alignment” tool, as it performs a trimming step first by dividing long reads into shorter bits to align them independently, see Supplementary Figure S13.
- “dnAQET” [49] was misclassified as a “Quality Control” tool instead of an “Assembly validation” tool, as it requires calculating the contigs individual quality scores, see Supplementary Figure S14.

This behavior highlights that the classifiers will always struggle to detect the correct class of a given metagenomics tool in this particular evaluation scheme where we assume a multi-class classification problem.

4 Conclusion

According to our results, the model composed of the Logistic Regression classifier trained on text representation of the “abstracts only” dataset generated using the Hugging Face implementation of BioBERT has the best ability to distinguish between the different classes (Supplementary Data Table S46). The considerable number of tools belonging to more than one class explains a subset of the misclassifications of the models as we picked only one class for each tool during manual data curation. A multi-label classification problem setting would address this issue.

Another reason for the misclassifications of the models is the absence of a controlled vocabulary or unified terminology in the metagenomics domain. We can see the interchangeable use of terms that refer to different processes for different people, e.g. terms “mapping” and “alignment” have been generating a lot of confusion recently. In reality, both terms pertain to aligning sequences; however, whereas “mapping” aligns short sequences against a reference genome, “alignment” aligns short sequences against one another. The readers become confused when such terms are used as synonyms. Wider adoption of a unified vocabulary e.g. EDAM, would reduce inconsistencies in word usage and improve machine and human comprehension.

In our study, the abstract section was the most informative for classifying tools, as it summarizes the research paper well. In the case of the “methods only” dataset, the performance drop and inexplicable misclassifications on our independent test set may be caused by the noise introduced in the text descriptions and our manual text extraction process.

The low informativeness of the methods section was previously reported for computer science research [17] and some other research fields, e.g. astrophysics research, where the Discussion section captures the most context. Identifying the most informative part of the paper, which describes a tool in detail, can be challenging. The description depends on the author’s writing style and journal structuring methods, even if one looks at papers in the same research field. Developing a novel text segmentation approach that can automatically detect and extract specific topics and sentences, depending on the query, might help improve information retrieval from metagenomics-specific text content.

We also note the significant influence of the text corpus used during the training phase of the embedding models, mainly when applied to domain-specific text data. The metagenomics field can primarily benefit from a language model, such as BERT, pre-trained on the metagenomics corpus.

Different embedding-pooling strategies also influence the performance of classifiers. Embedding models are pre-trained on a few specific Natural Language Processing (NLP) tasks; with each transitioning step from one layer to another,
the encoded information about a given word and its context becomes more relevant to these specific tasks. Therefore, the efficiency of such contextualized vector representations is application-specific. It also depends on the downstream task [50], the linguistic properties of the datasets, and inference tools (Bi-LSTM, CNN or other).

We developed and tested several (NLP)-based classification models on a dataset of 224 manually collected tool papers, categorized into 13 different EDAM classes (tasks). The Galaxy platform database, for instance, contains more than 7800 tools corresponding to more than 40 classes (EDAM operations). This fact highlights the need for a more generalized and human-independent system that can automatically look for newly published tools, scan their papers, cluster them to identify new categories and label them according to their classes. We propose a classifier system that uses Logistic Regression trained on the BioBERT embeddings of the tools’ publications abstracts to map the tools’ descriptions to a space of EDAM classes/tasks. Oriented toward learning the “essentials” (the correct task a given tool can perform), it avoids its users’ misidentification of tools characteristics and function. This system can be easily scaled by training on larger datasets with more classes simply by collecting scientific articles from online sources. It can also be integrated into platforms such Galaxy to accelerate the integration of new tools to its internal database.

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Availability

Supporting data and code are available on Github [https://github.com/kaoutarDaoudHiri/NLP-based-classification-of-metagenomics-tools](https://github.com/kaoutarDaoudHiri/NLP-based-classification-of-metagenomics-tools) and on Figshare [https://doi.org/10.6084/m9.figshare.21350583](https://doi.org/10.6084/m9.figshare.21350583).

References

[1] Levin Clément, Dynomant Emeric, Gonzalez Bruno J, Mouchard Laurent, Landsman David, Hovig Eivind, and Vlahovicke Kristian. A data-supported history of bioinformatics tools, 2018.

[2] Hanna Marie Schilbert, Andreas Rempel, and Boas Pucker. Comparison of read mapping and variant calling tools for the analysis of plant NGS data. Plants, 9(4), 2020.

[3] Edna Chebet Too, Li Yujian, Sam Njuki, and Liu Yingchun. A comparative study of fine-tuning deep learning models for plant disease identification. Computers and Electronics in Agriculture, 161:272–279, jun 2019.

[4] Sairam Behera, Adam Voshall, and Etsuko N. Moriyama. Plant Transcriptome Assembly: Review and Benchmarking. Exon Publications, Brisbane, Australia, 2021.

[5] Almas Jabeen, Nadeem Ahmad, and Khalid Raza. Machine learning-based state-of-the-art methods for the classification of RNA-Seq data. In Lecture Notes in Computational Vision and Biomechanics, pages 133–172. Springer, 2018.

[6] Ayat Hatem, Doruk Bozdağ, Amanda E. Toland, and Ümit V. Çatalyürek. Benchmarking short sequence mapping tools. BMC Bioinformatics, 2013.

[7] Sam Nooij, Dennis Schmitz, Harry Vennema, Annelies Kroneman, and Marion P. G. Koopmans. Overview of virus metagenomic classification methods and their biological applications. Frontiers in Microbiology, 9(APR), apr 2018.

[8] Susan Jones, Amanda Baizan-Edge, Stuart MacFarlane, and Lesley Torrance. Viral diagnostics in plants using next generation sequencing: Computational analysis in practice, 2017.

[9] Peter Simmonds and Pakorn Aiewsakun. Virus classification – where do you draw the line? Archives of Virology, 163(8):2037–2046, aug 2018.

[10] Simon H. Ye, Katherine J. Siddle, Daniel J. Park, and Pardis C. Sabeti. Benchmarking metagenomics tools for taxonomic classification, 2019.

[11] Mette V. Larsen, Salvatore Cosentino, Oksana Lukjancenko, Dhany Saputra, Simon Rasmussen, Henrik Hasman, Thomas Sicheritz-Pontén, Frank M. Aarestrup, David W. Ussery, and Ole Lund. Benchmarking of methods for genomic taxonomy. Journal of Clinical Microbiology, 52(5):1529–1539, 2014.
[12] Alejandra Escobar-Zepeda, Elizabeth Ernestina Godoy-Lozano, Luciana Raggi, Lorenzo Segovia, Enrique Merino, Rosa María Gutiérrez-Rios, Katy Juarez, Alexei F. Licea-Navarro, Liliana Pardo-Lopez, and Alejandro Sanchez-Flores. Analysis of sequencing strategies and tools for taxonomic annotation: Defining standards for progressive metagenomics. *Scientific Reports*, 2018.

[13] Sanket Agarkar and Soma Ghosh. Malware detection and classification using machine learning. In *Proceedings - 2020 IEEE International Symposium on Sustainable Energy, Signal Processing and Cyber Security, iSSSC 2020*, 2020.

[14] Asmaa Halbouni, Teddy Surya Gunawan, Mohamed Hadi Habaebi, Murad Halbouni, Mira Kartiwi, and Robiah Ahmad. Machine learning and deep learning approaches for cybersecurity: A review. *IEEE Access*, 10:19572–19855, 2022.

[15] Enis Afgan, Dannon Baker, Bérénice Batut, Marius Van Den Beek, Dave Bouvier, Martin Ech, John Chilton, Dave Clements, Nate Coraor, Björn A. Grüning, Aysam Guerler, Jennifer Hillman-Jackson, Saskia Hiltemann, Vahid Jalili, Helena Rasche, Nicola Soranzo, Jeremy Goecks, James Taylor, Anton Nekrutenko, and Daniel Blankenberg. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. *Nucleic Acids Research*, 46(W1), 2018.

[16] Anup Kumar, Helena Rasche, Björn Grüning, and Rolf Backofen. Tool recommender system in galaxy using deep learning. *GigaScience*, 10(1), 2021.

[17] K. M. Anil Kumar, S. G. Gagan, N. Rajasimha, B. Anil, and U. Rajath Kumar. Scoring based unsupervised approach to classify research papers. In *Proceedings of the 2016 2nd International Conference on Contemporary Computing and Informatics, IC3I 2016*, 2016.

[18] E. A. Calvillo, R. Mendoza, J. Muñoz, J. C. Martínez, M. Vargas, and L. C. Rodríguez. Automatic algorithm to classify and locate research papers using natural language. *IEEE Latin America Transactions*, 14(3), 2016.

[19] Ghalam Mustafa, Muhammad Usman, Muhammad Tanvir Afzal, Abdul Shahid, and Anis Koubaa. A comprehensive evaluation of metadata-based features to classify research paper’s topics. *IEEE Access*, 9:133500–133509, 2021.

[20] Er. Rajvir Kaur and Er. Nishi. Automated classification of research papers using hybrid algorithm. *International Journal of Hybrid Information Technology*, 8(6), 2015.

[21] Hisham Al-Mubaid and Andrew Nash. A feature learning based technique to classify Medline disease abstracts. In *Proceedings of the International Joint Conference on Neural Networks*, 2020.

[22] Alexandros Kyriakakis, Lefteris Koumakis, Alexandros Kanterakis, Galateia Iatraki, Manolis Tsiknakis, and George Potamias. Enabling ontology-based search: A case study in the bioinformatics domain. In *Proceedings - 2019 IEEE 19th International Conference on Bioinformatics and Bioengineering, BIBE 2019*, 2019.

[23] Angelo A. Salatino, Thiviyan Thanapalasingam, Andrea Mannocci, Francesco Osborne, and Enrico Motta. The computer science ontology: A large-scale taxonomy of research areas. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 11137 LNCS, 2018.

[24] Jon Ison, Matiš Kalaš, Inge Jonassen, Dan Bolser, Mahmut Uludag, Hamish McWilliam, James Malone, Rodrigo Lopez, Steve Pettifer, and Peter Rice. EDAM: An ontology of bioinformatics operations, types of data and identifiers, topics and formats. *Bioinformatics*, 29(10), 2013.

[25] James Malone, Andy Brown, Allyson L. Lister, Jon Ison, Duncan Hull, Helen Parkinson, and Robert Stevens. The Software Ontology (SWO): A resource for reproducibility in biomedical data analysis, curation and digital preservation. *Journal of Biomedical Semantics*, 5(1), 2014.

[26] Jie Ren, Kai Song, Chao Deng, Nathan A. Ahlgren, Jed A. Fuhrman, Yi Li, Xiaohui Xie, Ryan Poplin, and Fengzhu Sun. Identifying viruses from metagenomic data using deep learning. *Quantitative Biology*, 8(1), 2020.

[27] Aly O. Abdelkareem, Mahmoud I. Khalil, Mostafa Elaraby, Hazem Abbas, and Ali H.A. Elbehery. VirNet: Deep attention model for viral reads identification. In *Proceedings - 2018 13th International Conference on Computer Engineering and Systems, ICCES 2018*, 2019.

[28] Amanda Baizan-Edge, Peter Cock, Stuart MacFarlane, Wendy McGavin, Lesley Torrance, and Susan Jones. Kodoja: A workflow for virus detection in plants using k-mer analysis of RNA-sequencing data. *Journal of General Virology*, 100(3), 2019.

[29] Thien Ho and Ioannis E. Tzanetakis. Development of a virus detection and discovery pipeline using next generation sequencing. *Virology*, 471–473, 2014.
[30] Qingguo Wang, Peilin Jia, and Zhongming Zhao. VirusFinder: Software for efficient and accurate detection of viruses and their integration sites in host genomes through next generation sequencing data. PLoS ONE, 8(5), 2013.

[31] H. P. Luhn. A statistical approach to mechanized encoding and searching of literary information. IBM Journal of Research and Development, 1(4):309–317, 1957.

[32] Karen Spärck Jones. A statistical interpretation of term specificity and its application in retrieval. Journal of Documentation, 28:11–21, 1972.

[33] Jeffrey Pennington, Richard Socher, and Christopher Manning. GloVe: Global vectors for word representation. In Proceedings of the 2014 Conference on Empirical Methods in Natural Language Processing (EMNLP), pages 1532–1543, Stroudsburg, PA, USA, 2014. Association for Computational Linguistics.

[34] Matthew E. Peters, Mark Neumann, Mohit Iyyer, Matt Gardner, Christopher Clark, Kenton Lee, and Luke Zettlemoyer. Deep contextualized word representations, 2018.

[35] Jacob Devlin, Ming-Wei Chang, Kenton Lee, and Kristina Toutanova. BERT: Pre-training of deep bidirectional transformers for language understanding. In Jill Burstein, Christy Doran, and Thamar Solorio, editors, Proceedings of the 2019 Conference of the North American Chapter of the Association for Computational Linguistics: Human Language Technologies, NAACL-HLT 2019, Minneapolis, MN, USA, June 2-7, 2019, Volume 1 (Long and Short Papers), pages 4171–4186, Minneapolis, Minnesota, 2019. Association for Computational Linguistics.

[36] Jinhyuk Lee, Wonjin Yoon, Sungdong Kim, Donghyeon Kim, Sunkyu Kim, Chan Ho So, and Jaewoo Kang. BioBERT: a pre-trained biomedical language representation model for biomedical text mining. Bioinformatics, sep 2019.

[37] Zhilin Yang, Zihang Dai, Yiming Yang, Jaime Carbonell, Ruslan Salakhutdinov, and Quoc V. Le. XLNet: Generalized autoregressive pretraining for language understanding. Advances in Neural Information Processing Systems, 32, jun 2019.

[38] Yinhan Liu, Myle Ott, Naman Goyal, Jingfei Du, Mandar Joshi, Danqi Chen, Omer Levy, Mike Lewis, Luke Zettlemoyer, and Veselin Stoyanov. RoBERTa: A robustly optimized BERT pretraining approach, 2019.

[39] Kevin Clark, Minh-Thang Luong, Quoc V. Le, and Christopher D. Manning. ELECTRA: Pre-training text encoders as discriminators rather than generators. In 8th International Conference on Learning Representations, ICLR 2020, Addis Ababa, Ethiopia, April 26-30, 2020, 2020.

[40] Giacomo Miolo, Giulio Mantoan, and Carlotta Orsenigo. ELECTRAMed: a new pre-trained language representation model for biomedical NLP. CoRR, 2021.

[41] Veysel Kocaman and David Talby. Spark NLP: Natural language understanding at scale. Software Impacts, page 100058, 2021.

[42] Nils Reimers and Iryna Gurevych. Sentence-bert: Sentence embeddings using siamese bert-networks. In Proceedings of the 2019 Conference on Empirical Methods in Natural Language Processing, Association for Computational Linguistics, 11 2019.

[43] Thomas Wolf, Lysandre Debut, Victor Sanh, Julien Chaumond, Clement Delangue, Anthony Moi, Pierric Cistac, Tim Rault, Rémi Louf, Morgan Funtowicz, Joe Davison, Sam Shleifer, Patrick von Platen, Clara Ma, Yacine Jernite, Julien Plu, Canwen Xu, Teven Le Scao, Sylvain Gugger, Mariama Drame, Quentin Lhoest, and Alexander M. Rush. HuggingFace’s transformers: State-of-the-art natural language processing, 2020.

[44] F. Pedregosa, G. Varoquaux, A. Gramfort, V. Michel, B. Thirion, O. Grisel, M. Blondel, P. Prettenhofer, R. Weiss, V. Dubourg, J. Vanderplas, A. Passos, D. Cournapeau, M. Brucher, M. Perrot, and E. Duchesnay. Scikit-learn: Machine learning in Python. Journal of Machine Learning Research, 12:2825–2830, 2011.

[45] Jean Gabriel Gaudreault, Paula Branco, and João Gama. An analysis of performance metrics for imbalanced classification. In Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics), volume 12986 LNAI, pages 67–77. Springer Science and Business Media Deutschland GmbH, 2021.

[46] Janez Demšar. Statistical comparisons of classifiers over multiple data sets. The Journal of Machine Learning Research, 7:1–30, 2006.

[47] Marc Fiume, Vanessa Williams, Andrew Brook, and Michael Brudno. Savant: Genome browser for high-throughput sequencing data. Bioinformatics, 26(16), 2010.

[48] Hsin Nan Lin and Wen Lian Hsu. Kart: A divide-and-conquer algorithm for NGS read alignment. Bioinformatics, 33(15), 2017.
[49] Gokhan Yavas, Huixiao Hong, and Wenming Xiao. dnAQET: A framework to compute a consolidated metric for benchmarking quality of de novo assemblies. *BMC Genomics*, 20(1), 2019.

[50] Bin Wang, Angela Wang, Fenxiao Chen, Yuncheng Wang, and C. C.Jay Kuo. Evaluating word embedding models: Methods and experimental results, 2019.

[51] Joseph F. Ryan. Baa.pl: A tool to evaluate de novo genome assemblies with RNA transcripts, 2013.
Supplementary material

S1 Preparation of datasets

In this section, we list the datasets used in the study. We prepared the following datasets by manually extracting sections from the tools’ published articles:

- abstracts stored as “abstracts only” dataset,
- methods stored as “methods only” dataset, and
- both sections stored as “abstracts+methods” dataset.

We describe a collection of six datasets:

- three datasets of the tools’ descriptions in their unprocessed raw form and
- three pre-processed tool descriptions datasets.

The text processing steps reduced the number of characters in the documents, but the influence on the number of words was negligible. Text processing did not alter the distribution of the three datasets, see Supplementary Figures S1, S2, S4, S5, and S6.

S1.1 Raw tool description datasets

Supplementary data files

Dataset S1. Raw Tool Description Abstracts Only.
Dataset S2. Raw Tool Description Methods Only.
Dataset S3. Raw Tool Description Abstracts+Methods.

Description

Throughout the manual curation process of the “methods only” dataset, we attempted to standardize the information contained in this description as much as possible, reducing the effect of different journals’ writing requirements and authors’ writing styles. We searched for natural language text chunks in a given tool publication that describe the tool in great detail: techniques, algorithms, approaches, and processes. We focused on the methods section and other comparable parts of the publication. We omitted details that involved mathematical explanations and formulae from the tool descriptions. We removed any remaining mathematical symbols or equations during the text pre-processing stage.

For example, consider the description of the “cuBLASTP” tool from the “methods only” dataset. The journal publication of this tool has the following sections: (1) Introduction, (2) Background, (3) Related Work, (4) Design of Fine-Grained Blastp, (5) Performance Evaluation, and (6) Conclusion and Future Work. Therefore, we extracted the text description of this tool from the different sub-sections of the “Design of a Fine-Grained Blastp” section. The same approach was taken in 56 out of the 224 tool publications in our dataset, where the section explicitly titled “Methods” or similar (e.g. “Online methods”, “Materials and methods”, “Methods and implementation”, “Systems and methods”, “Methods and technologies”, “Methodology”, etc.) was absent.

In some publications, the “Methods” section is not a part of the main document; it appears in the supplementary materials. Sometimes the “Methods” section is present; however, it includes only technical details about the implementation of the tools (see Supplementary Figure S3 taken from [S1]). In this case, we also collected the tool’s description from other sections. In other cases, where the “Methods” section was present in the publication and contained an explanation of how the tool works with only a few technical details, the entire section was considered a tool description. We decided case-by-case how much technical detail was acceptable and what was excessive.

All of the datasets include the title of the tool publication. We stored the title as the first sentence of the tool description. For the “abstracts only” dataset, we did not perform any manual selection of text parts from the publications’ abstracts as this section was consistent throughout the publications. We categorized the tools into the 13 classes of tools’ tasks based on the authors’ claims on the tool’s primary use (11 EDAM operations and 2 additional classes: “Virus detection” and “Virus identification”).
Supplementary Figures

(a)

(b)

Supplementary Figure S1: Distribution of the tool descriptions length in terms of the number of words by dataset, on the (a) unprocessed text and (b) pre-processed text.

(a)

(b)

Supplementary Figure S2: Distribution of the tool descriptions length in terms of the number of characters by dataset, on the (a) unprocessed text and (b) pre-processed text.

Materials and Methods

I downloaded chromosome 22 and 42 mRNA products of this chromosome from NCBI on August 14, 2013. I developed a Perl script to introduce random permutations to the genomic sequence of chromosome 22 at various frequencies. I aligned the 42 transcripts to chromosome 22 and to its random permutations using default parameters in BLAT (version 35x1). I then ran baa.pl (version 0.20) with default parameters using the output of each BLAT run. All scripts and random datasets used in these analyses are available as supplemental material.

Supplementary Figure S3: Example of technical content of the “Materials and Methods” section, taken from [51] titled “Baa.pl: A tool to evaluate de novo genome assemblies with RNA transcripts sets”. The tool is assigned to the “Assembly evaluation” task class.
S1.2 Pre-processed tool description datasets

Supplementary data files

Dataset S4. Pre-processed Tool Description Abstracts Only.
Dataset S5. Pre-processed Tool Description Methods Only.
Dataset S6. Pre-processed Tool Description Abstracts+Methods.

Description

Pre-processed datasets contain raw tool descriptions pre-processed in the following way:

- down-casing,
- removing special characters,
- punctuation signs,
- possessive pronouns,
- numbers,
- links,
- words composed of one or two letters,
- words starting with digits,
- stop words removal,
- and lemmatization.

We assigned a numerical ID to each of the 13 classes.

Supplementary Figures

Supplementary Figure S4: Distribution of the tool descriptions length in terms of the number of characters by task/category, (a) unprocessed text, (b) pre-processed text - "abstracts only" dataset.
Supplementary Figure S5: Distribution of the tool descriptions length in terms of the number of characters by task/category, (a) unprocessed text, (b) pre-processed text - “methods only” dataset.

Supplementary Figure S6: Distribution of the tool descriptions length in terms of the number of characters by task/category, (a) unprocessed text, (b) pre-processed text - “abstracts+methods” dataset.
S2 Methods

In this section, we explain the methods used to build the models, including the hyperparameters values tested during cross-validation and the different pooling strategies evaluated on BERT. We also list the text embedding datasets generated by the different embedding strategies.

S2.1 Model hyperparameters

Description

During the repeated nested cross-validation process, we optimized the parameters of the classifiers (Logistic Regression, Random Forest, Naive Bayes) on the datasets generated by each embedding method. The embedding methods were not fine-tuned, except for TF-IDF. We report on the scikit-learn’s `GridSearchCV` hyperparameters names and corresponding settings tested in Supplementary Table S1.

Tables

Supplementary Table S1: Hyperparameter settings tested during the cross-validation step for the TF-IDF embedding and the classification algorithms.

| Algorithm      | Hyperparameter     | Value set                  |
|----------------|--------------------|----------------------------|
| TF-IDF         | max_features       | [40, 140, 180, 220]        |
|                | ngram_range        | [(1, 1), (1, 2), (2, 2)]  |
|                | min_df             | [0.001, 0.01, 0.1]         |
|                | max_df             | [0.5, 0.6, 0.7, 0.8, 0.9]  |
|                | stop_words         | [None, 'english']          |
| Logistic Regression | C                | [0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0] |
|                | solver             | ['newton-cg', 'sag', 'saga', 'lbfgs'] |
|                | class_weight       | ['balanced', None]        |
| Random Forest  | max_depth          | [100]                      |
|                | min_samples_split  | [2, 5, 10]                 |
|                | min_samples_leaf   | [1, 2, 4]                  |
| Naive Bayes    | max_leaf_nodes     | [None]                     |
|                | max_features       | ['auto', 'sqrt']           |
|                | bootstrap          | [True, False]              |
|                | var_smoothing      | [0.000000001, 0.000000001, 0.000000001] |

S2.2 BERT pooling strategies

Description

In this study, we used the feature-based approach with all the embedding methods we tested to extract fixed features based on pre-trained methods. In addition to the different BERT-based models, which use different training corpora, architectures, and training methodologies, we also tested the “best layer to use” of the BERT model by extracting the activations from different layers. We deduced that the sum (BERTSL4) and concatenation (BERTCL4) of the last four layers work better than the last layer (BERT-st). However, the sum of the second to last layer (BERTS2L) is the best pooling strategy. For details, see Supplementary Figure S5. Although these results are specific to the problem of classifying bioinformatics text based on the abstract descriptions of tools that we address in our study, they are still similar to the results of the original BERT paper [35]. Some specific choices of layers outperform the last layer, which can be explained by the bias introduced by the proximity of the last layer to the target functions, e.g., next sentence prediction pre-training task. Due to the high noise in the text data from the “methods only” dataset, we did not consider its results.

S2.3 Text embedding datasets

Supplementary data files

Dataset S7. BioBERT Hugging Face Abstracts Only.
Dataset S8. BERTSL4 Abstracts Only.
Dataset S9. BERTCL4 Abstracts Only.
Dataset S10. BERTS2L Abstracts Only.
Dataset S11. BERT Sentence Transformer Abstracts Only.
Dataset S12. BioBERT NLU Abstracts Only.
Dataset S13. ELECTRA Hugging Face Abstracts Only.
Dataset S14. ELECTRAm ed Hugging Face Abstracts Only.
Dataset S15. RoBERTa Sentence Transformer Abstracts Only.
Dataset S16. ELMO Abstracts Only.
Dataset S17. XLNET NLU Abstracts Only.
Dataset S18. GLOVE NLU Abstracts Only.
Dataset S19. ELECTRAm ed Sentence Transformer Abstracts Only.
Dataset S20. ELECTRA NLU Abstracts Only.
Dataset S21. BERTSL4 Methods Only.
Dataset S22. BERTCL4 Methods Only.
Dataset S23. BERTS2L Methods Only.
Dataset S24. BERT Sentence Transformer Methods Only.
Dataset S25. BioBERT NLU Methods Only.
Dataset S26. RoBERTa Sentence Transformer Methods Only.
Dataset S27. ELMO Methods Only.
Dataset S28. XLNET NLU Methods Only.
Dataset S29. GLOVE NLU Methods Only.
Dataset S30. ELECTRAm ed Sentence Transformer Methods Only.
Dataset S31. ELECTRA NLU Methods Only.
Dataset S32. BERTSL4 Abstracts+Methods.
Dataset S33. BERTCL4 Abstracts+Methods.
Dataset S34. BERTS2L Abstracts+Methods.
Dataset S35. BERT Sentence Transformer Abstracts+Methods.
Dataset S36. BioBERT NLU Abstracts+Methods.
Dataset S37. RoBERTa Sentence Transformer Abstracts+Methods.
Dataset S38. ELMO Abstracts+Methods.
Dataset S39. XLNET NLU Abstracts+Methods.
Dataset S40. GLOVE NLU Abstracts+Methods.
Dataset S41. ELECTRAm ed Sentence Transformer Abstracts+Methods.
Dataset S42. ELECTRA NLU Abstracts+Methods.

Description

This supplement section contains text vector representations generated by different Embedding strategies for the three pre-processed tool description datasets: “abstracts only”, “methods only” and “abstracts+methods”.

Tables

Supplementary Table S2: Overview of the vector size generated by each embedding technique. The size of the TF-IDF vector varies according to the hyperparameter tuning results.

| Embedding Method | Embedding size |
|------------------|----------------|
| TF-IDF           | -              |
| GLOVE            | 100            |
| ELMO             | 1024           |
| BERT             | 768            |
| BERT S2L         | 768            |
| BERT SL4         | 768            |
| BERT CL4         | 3072           |
| BioBERT          | 768            |
| RoBERTa          | 768            |
| XLNET            | 768            |
| ELECTRA          | 256            |

S3 Results

In this section, we report on the models’ best hyperparameters setting, the performance metrics of all models, including the baseline model, the classification probabilities produced by the best models, and a detailed table of the best model misclassifications. We also examined the results of the top three models and the worst model.
S3.1 Baseline model - Majority classifier

Description

The baseline model classifies all the tools as Assembly tools, the majority class, which represents 19.6% of the examples in our datasets, see Supplementary Table S1 and Figure S1.

Tables

Supplementary Table S1: Majority Classifier metrics - independent of dataset and embedding method.

| Evaluation metric          | Score |
|---------------------------|-------|
| Training set Accuracy     | 0.19  |
| Test set Accuracy         | 0.20  |
| AUC-ROC                   | 0.50  |
| AUC-PR                    | 0.10  |
| Precision                 | 0.04  |
| Recall                    | 0.20  |
| Fscore                    | 0.06  |

Supplementary Figures

Supplementary Figure S1: Majority classifier test set confusion matrix - similar for all datasets.

S3.2 Model performance

Supplementary data files

Data Table S43. Performance of tested models.

Description

For each dataset (“abstracts only”, “methods only”, and “abstracts+methods”), we report the following scores of all trained models on the independent test set, ordered by the Area Under the Receiver Operating Characteristic Curve (AUC-ROC) score:

- training set Accuracy,
- independent test set Accuracy,
• \((\text{AUC-ROC})\) score,
• \text{Precision},
• \text{Recall}, and
• \text{F1-score}.

The results are discussed in Supplementary Section S3.5.

S3.3 Models’ best hyperparameters

Supplementary data files

Data Table S44. Hyperparameters set.
Data Table S45. Model best hyperparameters.

Description

For each dataset (“abstracts only”, “methods only”, and “abstracts+methods”), we report the set of tested values for each hyperparameter as well as the best hyperparameter values of the three classifiers (Logistic Regression, Random Forest, and Naive Bayes) when trained on different text vector representations.

S3.4 Best models’ class probabilities

Supplementary data files

Data Table S46. Best models predicted class probabilities.

Description

In this supplementary data, we report the classification probabilities of each class on the independent test set composed of 45 examples for the models that achieved the best \((\text{AUC-PR})\). The datasets are as follows:

1. Logistic Regression on BioBERT-hf embeddings of “abstracts only” dataset.
2. Logistic Regression on BERTS2L embeddings of “abstracts+methods” dataset.
3. Logistic Regression on BERTS2L embeddings of “abstracts only” dataset, and Logistic Regression on BERTSL4 of “abstracts+methods” dataset.

S3.5 Model comparison

Description

All trained models were evaluated as described in Supplementary Subsection S3.2, see Supplementary Figures S8-S11. We determined that Logistic Regression on NLU library implementation of ELECTRA embeddings of the “methods only” dataset performed the worst with an \((\text{AUC-PR})\) score of 0.13. The model missed 8 out of 13 classes: “(Sequence) alignment”, “(Taxonomic) classification”, “Virus identification”, “Mapping”, “(Sequence) trimming”, “SNP-Discovery”, “(Sequence) annotation” and “(Sequence) assembly validation”; thus, it partially learned five categories only. Logistic Regression on BERTS2L embeddings of the “abstracts+methods” dataset was the second-best model with \((\text{AUC-PR})\) score of 0.84. It completely missed the instances of the “(Sequence) annotation”, “(Sequence) assembly”, and “Visualization” classes. The model also had problems distinguishing between instances from “Virus detection” and “Virus identification” classes. Oppositely, the model achieved a 100% accuracy in classifying instances of four classes: “Mapping”, “(RNA-seq quantification for) abundance estimation”, “(Sequencing) quality control” and “(Sequence) assembly validation” classes. Logistic Regression on BERTS2L embeddings of the “abstracts only” dataset, and the Logistic Regression on BERTSL4 embeddings of the “abstracts+methods” dataset, third-best models with a 0.83 \((\text{AUC-PR})\) score both, achieved similar results to the second-best model.

In addition, models were compared using the Critical Distance diagram method proposed by Demšar [46]. A comparison of the best three models and the worst model against our baseline is shown in Supplementary Figure S4.

For an easier comparison of the performance of the various methods and data sources, we present the results from “Data Table S43. Performance of tested models” as graphs in Supplementary Figures S5, S6 and S7.
Supplementary Figures

Supplementary Figure S2: Critical distance (CD) diagram for LR, RF, an NB classifiers tested on 12 embeddings. Groups of classifiers that are not significantly different are connected on the (a) “abstracts only”, (b) “methods only”, and (c) “abstracts+methods” dataset.

Supplementary Figure S3: Comparison of embedding methods, ranked by $\textit{AUC-PR}$, using the Nemenyi test. Tested on three classifiers and three datasets. Groups of embeddings that are not significantly different are connected.
Supplementary Figure S4: Average precision scores, micro-averaged over all classes. The majority classifier, the worst model (LR ELECTRA-NLU) and the top four models (third and fourth have the same performance) are shown.

Supplementary Figure S5: Classifiers’ AUC-PR scores grouped by embedding method on “abstracts only” dataset.

Supplementary Figure S6: Classifiers’ AUC-PR scores grouped by embedding method on “methods only” dataset.
Supplementary Figure S7: Classifiers’ AUC-PR scores grouped by embedding method on “abstracts+methods” dataset.

Supplementary Figure S8: Logistic Regression on BERTS2L - test set confusion matrix - “abstracts+methods” dataset.

Supplementary Figure S9: Logistic Regression on BERTS2L - test set confusion matrix - “abstracts only” dataset.

Supplementary Figure S10: Logistic Regression on BERTSL4 - test set confusion matrix - “abstracts+methods” dataset.

Supplementary Figure S11: Logistic Regression on the ELECTRA implementation of the NLU library - test set confusion matrix - “methods only” dataset.
S3.6 Misclassifications done by the best model

Description

In Supplementary Table S2, we report the eight misclassified tools by the best model (Logistic Regression on “abstracts only” BioBERT-hf Embeddings) from a test set of 45 examples.

Tables

Supplementary Table S2: Logistic Regression on “abstracts only” BioBERT-hf Embeddings. Independent test set instance classifications. Misclassified examples are highlighted.

| Tool          | True class (TC)          | TC probability - rank | Predicted class (PC)          | PC probability |
|---------------|--------------------------|-----------------------|-------------------------------|----------------|
| GASiC         | AbundanceEstimation      | 0.75 - 1              | AbundanceEstimation           | 0.75           |
| thAQET        | AssemblyEvaluation       | 0.31 - 2              | QualityControl                | 0.32           |
| cutPrimers    | Trimming                 | 0.71 - 1              | Trimming                      | 0.71           |
| GAAS          | AbundanceEstimation      | 0.49 - 1              | AbundanceEstimation           | 0.49           |
| Taxonomer     | Classification           | 0.27 - 1              | Classification                | 0.27           |
| Kall           | Alignment                | 0.24 - 3              | Trimming                      | 0.3            |
| SKESA         | Assembly                 | 0.78 - 1              | Assembly                      | 0.78           |
| Vipie         | VirusIdentification      | 0.32 - 1              | VirusIdentification           | 0.32           |
| Bambino       | Visualisation            | 0.29 - 1              | Visualisation                 | 0.29           |
| EasyQC        | QualityControl           | 0.59 - 1              | QualityControl                | 0.59           |
| VirSorter     | VirusIdentification      | 0.25 - 1              | VirusIdentification           | 0.25           |
| Sailfish      | AbundanceEstimation      | 0.63 - 1              | AbundanceEstimation           | 0.63           |
| AlienTrimmer  | Trimming                 | 0.41 - 1              | Trimming                      | 0.41           |
| Bowie         | Alignment                | 0.62 - 1              | Alignment                     | 0.62           |
| ATLAS-SNP2    | SNPDiscovery             | 0.29 - 1              | SNPDiscovery                  | 0.29           |
| Minimus       | Assembly                 | 0.66 - 1              | Assembly                      | 0.66           |
| Centrifuge    | Classification           | 0.43 - 1              | Classification                | 0.43           |
| Kraken        | Classification           | 0.43 - 1              | Classification                | 0.43           |
| ALLPATHS      | Assembly                 | 0.81 - 1              | Assembly                      | 0.81           |
| Savant        | Annotation               | 0.16 - 2              | Visualisation                 | 0.42           |
| cuBLASTp      | Alignment                | 0.35 - 1              | Alignment                     | 0.55           |
| PhageFinder   | VirusDetection           | 0.37 - 1              | VirusDetection                | 0.37           |
| SOAP2         | Mapping                  | 0.33 - 1              | Mapping                       | 0.33           |
| Remotator     | Assembly                 | 0.20 - 1              | Assembly                      | 0.2            |
| consed        | Visualisation            | 0.17 - 2              | QualityControl                | 0.23           |
| VoorU       | VirusIdentification      | 0.51 - 1              | VirusDetection                | 0.51           |
| MePIC        | VirusIdentification      | 0.33 - 1              | VirusIdentification           | 0.33           |
| Minimap2      | Alignment                | 0.38 - 1              | Alignment                     | 0.38           |
| SPADES        | Assembly                 | 0.57 - 1              | Assembly                      | 0.57           |
| Bosot         | Assembly                 | 0.30 - 2              | Classification                | 0.32           |
| VERS         | VirusDetection           | 0.61 - 1              | VirusDetection                | 0.61           |
| SSPACE        | Assembly                 | 0.66 - 1              | Assembly                      | 0.66           |
| PyroBayes     | SNPDiscovery             | 0.18 - 3              | Mapping                       | 0.36           |
| VCJAK         | Assembly                 | 0.37 - 1              | Assembly                      | 0.37           |
| TACdb         | Mapping                  | 0.05 - 7              | Assembly                      | 0.37           |
| VirusDetect   | VirusIdentification      | 0.40 - 1              | VirusIdentification           | 0.4            |
| Baa pl        | AssemblyEvaluation       | 0.19 - 1              | AssemblyEvaluation            | 0.19           |
| H-BLAST       | Alignment                | 0.70 - 0.7            | Alignment                     | 0.7            |
| VirusMiner    | VirusIdentification      | 0.32 - 1              | VirusIdentification           | 0.32           |
| MetaShot      | Classification           | 0.42 - 1              | Classification                | 0.42           |
| SSPACE-LongRead| Assembly               | 0.60 - 1              | Assembly                      | 0.6            |
| CSN           | Annotation               | 0.23 - 1              | Annotation                    | 0.23           |
| FQC           | QualityControl           | 0.68 - 1              | QualityControl                | 0.68           |
| PhiSpy        | VirusDetection           | 0.57 - 1              | VirusDetection                | 0.57           |
| DeepVariant   | SNPDiscovery             | 0.04 - 7              | Alignment                     | 0.35           |
Supplementary Figures

Savant: genome browser for high
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ABSTRACT
Motivation: The advent of high-throughput sequencing (HTS) technologies has made it affordable to sequence many individuals' genomes. Simultaneously the computational analysis of the large volumes of data generated by the new sequencing machines remains a challenge. While a plethora of tools are available to map the resulting reads to a reference genome, and to conduct primary analysis of the mappings, it is often necessary to visually examine the results and underlying data to confirm predictions and understand the functional effects, especially in the context of other datasets.
Results: We introduce Savant, the Sequence Annotation, Visualization and Analysis Tool, a desktop visualization and analysis browser for genomic data. Savant was developed for visualizing and analyzing HTS data, with special care taken to enable dynamic visualization in the presence of gigabases of genomic reads and references the size of the human genome. Savant supports the visualization of genome-based sequence, point, interval and continuous datasets, and multiple visualization modes that enable easy identification of genomic variants (including single nucleotide polymorphisms, structural and copy number variants), and functional genomic information (e.g. peaks in Chip-seq data) in the context of genomic annotations.

Supplementary Figure S12: Savant abstract section.

Kart: a divide-and-conquer algorithm for NGS read alignment
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Abstract
Motivation: Next-generation sequencing (NGS) provides a great opportunity to investigate genome-wide variation at nucleotide resolution. Due to the huge amount of data, NGS applications require very fast and accurate alignment algorithms. Most existing algorithms for read mapping basically adopt seed-and-extend strategy, which is sequential in nature and takes much longer time on longer reads.
Results: We develop a divide-and-conquer algorithm, called Kart, which can process long reads as fast as short reads by dividing a read into small fragments that can be aligned independently. Our experiment result indicates that the average size of fragments requiring the more time-consuming gapped alignment is around 50% regardless of the original read length. Furthermore, it can tolerate much higher error rates. The experiments show that Kart spends much less time on longer reads than other aligners and still produce reliable alignments even when the error rate is as high as 15%.

Supplementary Figure S13: Kart abstract section.

dnAQET: a framework to compute a consolidated metric for benchmarking quality of de novo assemblies
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Abstract
Background: Accurate de novo genome assembly has become reality with the advancements in sequencing technology. With the ever-increasing number of de novo genome assembly tools, assessing the quality of assemblies has become of great importance in genome research. Although many quality metrics have been proposed and software tools for calculating those metrics have been developed, the existing tools do not provide a unified measure to reflect the overall quality of an assembly.
Results: To address this issue, we developed de novo Assembly Quality Evaluation Tool (dnAQET) that generates a unified metric for benchmarking the quality assessment of assemblies. Our framework first calculates individual quality scores for the scaffolds/contigs of an assembly by aligning them to a reference genome. Next, it computes a quality score for the assembly using its overall reference genome coverage, the quality score distribution of its scaffolds and the redundancy identified in it. Using synthetic assemblies randomly generated from the latest human genome build, various builds of the reference genome for five organisms and six de novo assemblies for simpler NAGATS, we tested dnAQET to assess its capability for benchmarking quality evaluation of genome assemblies. For synthetic data, our quality score increased with decreasing number of mismatches and redundancy and increasing average length and coverage, as expected. For genome builds, dnAQET quality score calculated for a more recent reference genome was better than the score for an older version. To compare with some of the most frequently used measures, 11 other quality measures were calculated. The quality score from dnAQET was found to be better than all other measures in terms of consistency with the known quality of the reference genomes, indicating that dnAQET is reliable for benchmarking quality assessment of de novo genome assemblies.

Conclusions: The dnAQET is a scalable framework designed to evaluate a de novo genome assembly based on the aggregated quality of its scaffolds (or contigs). Our results demonstrate that dnAQET quality score is reliable for benchmarking quality assessment of genome assemblies. dnAQET can help researchers to identify the most suitable assembly tools and to select high-quality assemblies generated.

Keywords: de novo genome assembly, Assembly quality assessment, Next Generation Sequencing, Massively

Supplementary Figure S14: dnAQET abstract section.