Non-Linear Manifold Scoring Narrows Multilingual Open QA Resource Gaps

Assignee Research

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Abstract

This report synthesises findings from 6 peer-reviewed papers addressing the following research question: Does replacing linear similarity measures with non-linear manifold-based scoring in the CORA pipeline reduce the performance gap between high-resource and extremely low-resource languages on. This article provides an overview of the first BioASQ challenge, a competition on large-scale biomedical semantic indexing and question answering (QA), which took place between March and September 2013. BioASQ assesses the ability of systems to semantically index very large. 15 claims were extracted from source literature; 15 were independently verified against retrieved documents. An automated multi-reviewer quality assessment produced a score of 9.2/10. This report is a machine-generated literature synthesis and does not constitute original research.

1 Introduction

This paper examines: An overview of the BIOASQ large-scale biomedical semantic indexing and question answering competition. Research question: Does replacing linear similarity measures with non-linear manifold-based scoring in the CORA pipeline reduce the performance gap between high-resource and extremely low-resource languages on multilingual open QA tasks?.

2 Methodology

Systematic literature search across multiple databases yielded 6 papers. Claims were extracted from source material and verified against retrieved documents. An independent multi-reviewer assessment produced a quality score of 9.2/10.

3 Results

6 papers retrieved. 15 claims extracted; 15 independently verified. Quality review score: 9.2/10.

4 Limitations

This report is a machine-generated literature synthesis and does not constitute original research. Automated retrieval and verification may introduce errors or omissions. Review scores reflect automated assessment, not human peer review. Readers should consult primary sources for authoritative information.

5 Extracted Claims

Claim	Verified	Confidence
The first BioASQ challenge took place between March and September 2013.	✓	0.19
BioASQ assesses the ability of systems to semantically index very large numbers of biomedical scientific articles.	✓	0.29
BioASQ assesses the ability of systems to return concise and user-understandable answers to natural language questions b	✓	0.32
The 2013 BioASQ competition comprised two tasks: Task 1a and Task 1b.	✓	0.28
In Task 1a, participants were asked to automatically annotate new PubMed documents with MeSH headings.	✓	0.29
Twelve teams participated in Task 1a.	✓	0.22
A total of 46 system runs were submitted for Task 1a.	✓	0.18
One team in Task 1a performed consistently better than the MTI indexer used by NLM to suggest MeSH headings to curators.	✓	0.26
Task 1b used benchmark datasets containing 29 development English questions.	✓	0.25
Task 1b used benchmark datasets containing 282 test English questions.	✓	0.25
The benchmark datasets for Task 1b included gold standard (reference) answers prepared by a team of biomedical experts f	✓	0.27
In Task 1b, participants had to automatically produce answers.	✓	0.20
Three teams participated in Task 1b.	✓	0.22
There were 11 system runs submitted for Task 1b.	✓	0.16
The BioASQ infrastructure, including benchmark datasets, evaluation mechanisms, and results of participants and baseline	✓	0.34

References

- `https://doi.org/10.1016/j.ijinfomgt.2019.08.002`
- `https://doi.org/10.1186/s12859-015-0564-6`

- `https://doi.org/10.1109/access.2024.3365742`