

RESEARCH

A sample article title

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available at the end of the article**Abstract****First part title:** Text for this section.**Second part title:** Text for this section.**Keywords:** sample; article; author

Introduction

Data and Information modeling in the healthcare domain have witnessed significant improvements in the last decade owing to advances in the development of state-of-the-art information and communication technologies (ICT) and formalization of storage and messaging standards. Subsequently, the scope of Healthcare Management Information Systems (HMIS), medical ontologies, and Clinical Decision Support Systems (CDSS) has broadened, beyond the operational capabilities of traditional rule based systems.

Related Work

Althubait et al. [1] proposed an ontology expansion methodology that identifies and extracts new class from text articles using word embedding and machine learning techniques. The authors identified the similarity of tokens and phrases of the text articles with the exiting classes of the ontology. The target ontology is expanded with classes from text articles having greater similarity with that of already added classes. A similar word embedding technique was also used by Nozaki et al. [2], where the authors used instance based schema matching technique to identify the semantic similarity between two instances. The results of the study showed the possibility of detecting similar string attributes of different schemas. Yousfi et al. [3] also utilized semantic base techniques and proposed xMatcher XML schemas matching approach. xMatcher transforms schemas into a set of words, followed by measuring words context, and relatedness score using WordNet. The terms from different schemas having similarities greater or equal to 0.8 are considered similar. Bylygin et al. [4] devised an ontology and schema matching approach by combined lexical and semantic similarity with machine learning approaches. The authors used lexical and semantic measure as features and trained various machine learning algorithms including Naive Bayes, logistic regression, and gradient boosted tree. The result achieved showed that the combination of algorithms outperformed the single modal.

Kersloot et al. [5] performed a comprehensive systematic review to evaluate natural language processing (NLP) algorithms used for clinical text mapping onto ontological concepts. The findings of the studies were evaluated with respect to five categories; use of NLP algorithms, data used, validation and evaluation performed,

result presentation, and generalization of results. The authors revealed that over one-fourth of the NLP algorithms used were not evaluated and have no validation. The systems that claimed generalization, were self evaluated and having no external validation.

Content

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Section title

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In this section we examine the growth rate of the mean of Z_0 , Z_1 and Z_2 . In addition, we examine a common modeling assumption and note the importance of considering the tails of the extinction time T_x in studies of escape dynamics. We will first consider the expected resistant population at vT_x for some $v > 0$, (and temporarily assume $\alpha = 0$)

$$E[Z_1(vT_x)] = \int_0^{v \wedge 1} Z_0(uT_x) \exp(\lambda_1) du.$$

If we assume that sensitive cells follow a deterministic decay $Z_0(t) = xe^{\lambda_0 t}$ and approximate their extinction time as $T_x \approx -\frac{1}{\lambda_0} \log x$, then we can heuristically estimate the expected value as

$$\begin{aligned} E[Z_1(vT_x)] \\ = \frac{\mu}{r} \log x \int_0^{v \wedge 1} x^{1-u} x^{(\lambda_1/r)(v-u)} du. \end{aligned} \quad (1)$$

Thus we observe that this expected value is finite for all $v > 0$ (also see [6, 7, 8, 9, 10, 11]).

Appendix

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Abbreviations

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Availability of data and materials

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Ethics approval and consent to participate

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Competing interests

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Consent for publication

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References

1. Althubaiti, S., Kafkas, Ş., Abdelhakim, M., Hoehndorf, R.: Combining lexical and context features for automatic ontology extension. *Journal of biomedical semantics* **11**(1), 1–13 (2020)
2. Nozaki, K., Hochin, T., Nomiya, H.: Semantic schema matching for string attribute with word vectors. In: 2019 6th International Conference on Computational Science/Intelligence and Applied Informatics (CSII), pp. 25–30 (2019). IEEE
3. Yousfi, A., El Yazidi, M.H., Zellou, A.: xmatcher: Matching extensible markup language schemas using semantic-based techniques. *International Journal of Advanced Computer Science and Applications* **11**(8), 655–665 (2020)
4. Bulygin, L.: Combining lexical and semantic similarity measures with machine learning approach for ontology and schema matching problem. In: Proceedings of the XX International Conference "Data Analytics and Management in Data Intensive Domains" (DAMDID/RCDL'2018), pp. 245–249 (2018)
5. Kersloot, M.G., van Putten, F.J., Abu-Hanna, A., Cornet, R., Arts, D.L.: Natural language processing algorithms for mapping clinical text fragments onto ontology concepts: a systematic review and recommendations for future studies. *Journal of biomedical semantics* **11**(1), 1–21 (2020)
6. Koonin, E.V., Altschul, S.F., Bork, P.: Brca1 protein products: functional motifs. *Nat. Genet.* **13**, 266–267 (1996)
7. Jones, X.: Zeolites and synthetic mechanisms. In: Smith, Y. (ed.) Proceedings of the First National Conference on Porous Sieves: 27–30 June 1996; Baltimore, pp. 16–27 (1996)
8. Margulis, L.: Origin of Eukaryotic Cells. Yale University Press, New Haven (1970)
9. Schnepf, E.: From prey via endosymbiont to plastids: comparative studies in dinoflagellates. In: Lewin, R.A. (ed.) Origins of Plastids, 2nd edn., pp. 53–76. Chapman and Hall, New York (1993)
10. Kohavi, R.: Wrappers for performance enhancement and obvious decision graphs. PhD thesis, Stanford University, Computer Science Department (1995)
11. ISSN International Centre: The ISSN register (2006). <http://www.issn.org> Accessed Accessed 20 Feb 2007

Figures

Figure 1 Sample figure title

Figure 2 Sample figure title

Tables

Table 1 Sample table title. This is where the description of the table should go

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