

Application of Artificial Intelligent in Healthcare

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Abstract

This short example shows a contrived example on how to format the authors' information for *IJCAI-19 Proceedings* using L^AT_EX.

1 Introduction

This short example shows a contrived example on how to format the authors' information for *IJCAI-19 Proceedings*.

2 History of AI in Healthcare

2.1 Recent Developments in Healthcare AI

Ever since the age of big data, there has been a surge in AI developments. This acceleration originates from several factors, including the wealth of data collected by big tech, the decreased cost of computational power, developments of more efficient machine learning techniques, and the availability of open-source machine learning packages. The healthcare and medical fields are no exclusion from this wave of AI developments. In fact, AI and ML application is an active field of research, receiving attention from researchers, medical stakeholders, and policy makers. The immersion of the technology in the medical field is evident in the growth of FDA-approved AI/ML-enabled medical devices in Figure 1

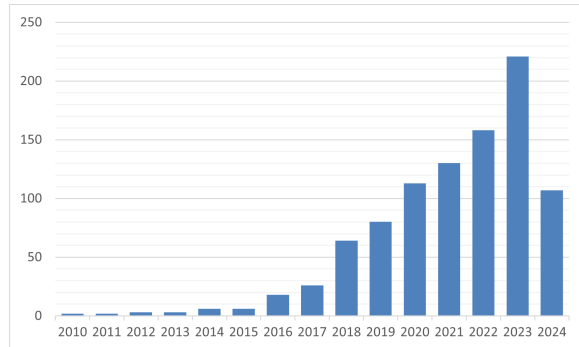


Figure 1: Number of FDA-approved AI/ML-enabled medical devices since 2010

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In **radiology**, machine learning is a powerful tool that can help physicians with CT scan and MRI scan to diagnose diseases and extract latent insights from the scans. Some example work include

- Classification of triple negative breast cancer using ultrasound images [Wu *et al.*, 2019]
- Detection of pulmonary lung nodules from CT scans by convolutional neural network [van Ginneken *et al.*, 2015]
- Pneumonia detection from chest X-rays using modern deep learning [Rajpurkar *et al.*, 2017]
- Detection of breast mass from mammography scans using convolutional neural networks [Arevalo *et al.*, 2015]

In **dermatology** diagnosis, visual inspection is still the main method for determining the severity of a skin abnormalities or lesions. Machine learning emerges as an effective method for automating this process as they can learn the latent features that differentiate between benign and malignant lesions in skin melanoma. In [Esteva *et al.*, 2017], a convolutional neural network was trained on 100,000 clinical images of skin cancer and achieved an accuracy similar to that of a dermatologist. Once these models have been trained extensively on computationally efficient hardware, they can be packaged and deployed on mobile devices to make inferences on skin lesions. This can further increase the accessibility of machine learning functionalities to the wider population.

In the case of **haematological** diseases, early prediction can help prevent progression and complication of blood disorders such as leukemia and lymphoma. However, [Walter *et al.*, 2023] suggests that diagnostic ambiguity often occurs in the manual process depending on the operator skills and experience. This leads to a desire for an automated process for reduced reliance on expert knowledge and increased consistency in data interpretation. Given its predictive power, machine learning implementation in disease diagnosis from blood samples is an active research topic. In [Gunčar *et al.*, 2018], two ML models were developed to predict haematologic disease. One of them was trained on all available blood test parameters and the other trained on a reduced set of parameters usually obtained from patient admittance. When this input is paired with the knowledge of the five most likely diseases, the models achieve predictive performance on par with haematology specialists

Ophthalmology

Oncology

3 Challenges

3.1 Trust

3.2 Accountability

3.3 Data privacy and protection

AI technologies depend on a vast amount of patient data and record to make accurate predictions when subjected to unseen data. However, in the event of a database violation or data breach, confidential patient information can be exploited for malicious intentions (identity theft, social stigma, discrimination,...). This can put a mental burden on the patient susceptible to the violation and other relevant stakeholders. Therefore, adequate law and guidelines are crucial to regulate the application of AI in medical and prevent misuse of data

The data gathering and handling of health data in the US is controversial, raising legal and ethical privacy questions [Price and Cohen, 2019]. Although the data can originate from various sources, such as healthcare providers, insurance claim, and wearable devices, US privacy law operates in different extents depending on the data source. This law also depends on the custodian of the data. Under the Health Insurance Portability and Accountability Act (HIPAA), the federal Privacy Rule only governs data handling between the conventional entities, such as healthcare providers, health insurance provides, patients, and intermediaries. However, [Price and Cohen, 2019] pointed out existing gap in HIPAA regulation. Although, HIPAA protect patient privacy from health data breach via a deidentifying process, patient data can be reidentified through data triangulation from other datasets.

Furthermore, a more fundamental problem is the amount of health related data not regulated under HIPAA [Price and Cohen, 2019]. Originally enacted to regulate data privacy in health records and between covered entities, HIPAA does not account for health data generate outside the confinement of these covered entities. In the big data world, tech companies are displacing covered entities in the collection of health information and personal data from online searches, application logs, and smart wearable devices.

4 Conclusion

5 Template notes

5.1 Author names

Each author name must be followed by:

- A newline `\\` command for the last author.
- An `\\And` command for the second to last author.
- An `\\and` command for the other authors.

5.2 Affiliations

After all authors, start the affiliations section by using the `\\affiliations` command. Each affiliation must be terminated by a newline `\\` command. Make sure that you include the newline on the last affiliation too.

5.3 Mapping authors to affiliations

If some scenarios, the affiliation of each author is clear without any further indication (e.g., all authors share the same affiliation, all authors have a single and different affiliation). In these situations you don't need to do anything special.

In more complex scenarios you will have to clearly indicate the affiliation(s) for each author. This is done by using numeric math superscripts $\{^i, ^j, \dots\}$. You must use numbers, not symbols, because those are reserved for footnotes in this section (should you need them). Check the authors definition in this example for reference.

5.4 Emails

This section is optional, and can be omitted entirely if you prefer. If you want to include e-mails, you should either include all authors' e-mails or just the contact author(s)' ones.

Start the e-mails section with the `\\emails` command. After that, write all emails you want to include separated by a comma and a space, following the same order used for the authors (i.e., the first e-mail should correspond to the first author, the second e-mail to the second author and so on).

You may "contract" consecutive e-mails on the same domain as shown in this example (write the users' part within curly brackets, followed by the domain name). Only e-mails of the exact same domain may be contracted. For instance, contracting "person@example.com" and "other@test.example.com" is not allowed because the domains are different.

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