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Spotlight

When blockchain meets artificial intelligence: An application to cancer histopathology

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A recent study by Saldanha et al. demonstrates that blockchain-based models outcompeted local models and performed similarly with merged models to predict molecular features from cancer histopathology images. The results reveal the capability of decentralized models in molecular diagnosis of cancer.

In the past decade, we have seen that artificial intelligence (AI) has revolutionized many fields, including precision medicine. In particular, deep-learning models, which consist of artificial neural networks, showed their capabilities in not only the advancement of autopilot, machine translation, and biometry but also in the prognosis and diagnosis of cancer with H&E-stained digital histopathology images. In the past few years, a number of studies reported that deep-learning-based computer vision models successfully predict molecular characteristics, such as gene mutation status, molecular subtypes, and microsatellite instability (MSI), with H&E-stained whole-slide images (WSIs) across various cancer types and even at pan-cancer level.[1–5] Moreover, many of these studies also claimed that their models are generalizable on external H&E image datasets, further illustrating the robustness and potential clinical applicability.

One critical issue of the aforementioned models is that their high predictive performance relies on large and diversified training datasets, which oftentimes involves gathering and sharing clinical data to make the training possible on a single server.[6] This process could lead to data access barriers, especially when datasets are located in different institutions and countries where regulations covering patient health information vary. One solution to circumvent this issue is federated learning (FL), where individual models are trained locally, and only the learned weights are shared to a central coordinator that governs the process and incorporates the weights into a final model.[7,8] However, the centralized design of FL models has the intrinsic weakness of monopoly and potential exploitation, which is against the data democracy idea and poses a different yet crucial data access issue. An alternative option is swarm learning (SL), which uses blockchain-based coordination between each locally trained models, eliminating the central coordinator of FL.[9] When training multicentric models on medical data, SL has its advantages over FL, because it centralizes neither the data nor the models (Figure 1). Prior to the recent study by Saldanha et al.,[10] there was no application of SL to cancer histopathology data, making the study a pioneer in the field of computational histopathology.

Saldanha's study offers a substantial proof of concept of applying SL models to H&E WSI to predict two molecular features, BRAF mutational status and MSI, in colorectal cancer. They compared the performance of three individually trained local models by using three datasets located on physically separated computer servers: a merged model trained on the combined dataset and three SL models with different terminating checkpoints (b-chkpt1, b-chkpt2, w-chkpt) on external independent clinical test sets. In the BRAF mutation prediction task, the AUROCs (area under the receiver operating characteristic curve) of all three SL models outcompeted the three local models, and the w-chkpt model (AUROC of 0.7736 ± 0.0057) also achieved significantly better performance than did the merged model (AUROC of 0.7567 ± 0.0139), whereas the other two SL models were on par with the merged model. For the MSI prediction task, two clinical test sets (QUASAR and YCR BCIP) were used for evaluation. In QUASAR, the SL models significantly outperformed two of the three local models, and the w-chkpt model (AUROC of 0.8326 ± 0.0089) performed similarly with the merged model (AUROC of 0.8308 ± 0.0190). Similar results were obtained from the YCR BCIP test set. In addition, by reducing the size of training sets, Saldanha et al. found that SL models were generally more data efficient than were all three local models. When compared with the merged model, the SL models maintained similar performance as the merged model with training set size down to 100 patients on the BRAF mutation prediction task. By visualizing the WSI prediction, Saldanha et al. qualitatively and quantitatively examined the histopathological features on the top predicted BRAF mutated and MSI tiles. They demonstrated that SL models generally captured more relevant structures and patterns, although not all of these observations were statistically significant.

This study by Saldanha et al. is a major contribution to the field of computation histopathology, where they attempted to integrate the blockchain technology into imaging-based cancer molecular diagnosis in order to tackle the current limitation of large data size requirement and the data access barriers through a decentralized multicentric model training approach. Their results illustrate that the proposed SL models generally outperformed local models and achieved

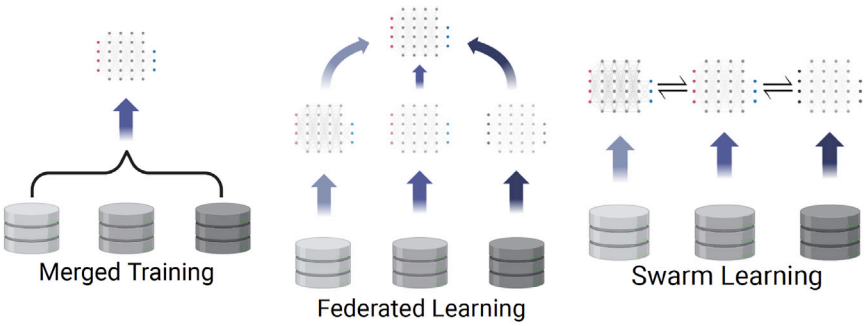

Figure 1. Different model training strategies
Conventional merged data training involves data sharing and aggregation (left). FL allows only the weights of the locally trained models to be shared to a centralized coordinator (middle). SL adopts decentralized blockchain-based communication during the training process that shares neither the data nor the models (right). Created with biorender.com.

similar predictive power as did the merged models. More importantly, Saldanha et al. demonstrated that SL models are data efficient and might capture more plausible and human interpretable histopathological features. Nevertheless, the study by Saldanha et al. could still be merely a pilot study of applying decentralized blockchain technology to cancer histopathology. Specifically, the two benchmark tasks that they showcased in the paper, BRAF mutational status and MSI, have been proved to be predictable with high accuracy in previous publications, and the SL models did not significantly improve the precision and accuracy for these two tasks. In addition, the differences between the performance of SL models on BRAF mutation and MSI predictions lead to the question as to whether the SL models' advantages over the local models might be task dependent. With testing AUROCs in the 0.7 to 0.8 range, the SL models, as well as other deep-learning-based cancer histopathology models, still have to go through more improvements and scrutiny before their actual deployment in clinical settings. Therefore, more future studies are necessary to ensure that the integration of blockchain and AI could tangibly benefit the prognosis and molecular diagnosis of cancer.

DECLARATION OF INTERESTS

The authors declare no competing interests.

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