



## **AI Driven Microbiome Diagnostics: Edge Cloud Architecture and Federated Learning for Infection Risk Stratification**

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### **Abstract**

Microbiome diagnostics Ai based diagnostics have been investigated to aid infection risk stratification through learning behaviors on microbial community profiles. Precision microbiology has demanded quick results, dependable calibration and privacy conscious learning within the laboratories. To achieve low latency inference at sample processing points, edge cloud architecture has been taken with centralized training, monitoring, and model governance being kept in the cloud. In this research study, a new computational assessment has been done in relation to a synthetic microbiome relative abundance dataset that has been created in regards to a Dirichlet based community model to simulate compositional microbial profiles. The risk labels of infection have been created based on community dependent prevalence and dysbiosis such as the perturbations of selected groups of taxa. The training of a clear baseline has been done by logistic regression and a simulation of federated learning has been conducted by using FedAvg style aggregation approach on 6 clients. The test set has been assessed on performance, and edge style single sample inference and cloud style batch inference and inference latency have been measured, assuming explicit network overhead to model deployment. Findings have indicated heavy discrimination of centralised learning of ROC AUC of about 0.97 and accuracy of over 0.93. It has been demonstrated that federated learning can converge to similar ROC AUC, but with a small decrease in accuracy. The result of the latency has indicated that the network overhead has dominated the total remote inference time even when the efficient compute is achieved when batches are taken. Clinical microbiology workflow implications have been outlined such as privacy preserving collaboration, model monitoring and deploying in small connectivity laboratories.

**Keywords:** *Microbiome, risk of infections, federated learning, edge computing, clinical microbiology artificial intelligence.*

### **Introduction**

Ai assisted microbiology has been more examined to enhance detection and risk stratification with the help of combining culture based methods, antimicrobial susceptibility testing, and sequencing based microbiome profiling. The signature of microbiomes has been linked with the susceptibility to infection, exposure to antimicrobials, and formats of dysbiosis that have determined pathogen colonization. Nevertheless, privacy, disseminated data among laboratories, and rapid turnaround to facilitate the decision making process of isolation, targeted therapy and stewardship have limited clinical translation. The use of edge cloud architecture has been advanced due to the execution of inference close to sample generation locations including laboratory information system gateway, sequencing workstations and larger scale training and monitoring has been implemented in the cloud. Multi laboratory model development has been assisted through federated learning without the centralization of raw microbial profiles. The measurable research design has been required to quantify the performance and latency trade offs as part of an edge cloud deployment concept under an edge cloud. Thus, the original computational work has been carried out to compare centralized and federated learning to microbiome compositional data and measure the differences in latency in edge and cloud scenarios.

## **Background of the Study**

### **Microbiome information and structure limitations**

As relative abundances, microbiome profiles have been used to create compositional vectors. Changes in a single taxon have caused problems because they have affected apparent abundances of others because of the constant sum constraint. The normalization, quality control and feature scaling have been necessitated to minimize the spurious signals. Other influences on microbiome profiles in the clinical environment include sampling protocol, sequencing batch, and site specific biases, which have led to an increase in the application of multi site learning designs.

### **Internet of Microbiology Edge cloud architecture in microbiology pipelines**

The computation of the edge has been located close to sequencing workstations, or laboratory gateways, or micro servers located on premises. Swift risk scoring and prompt warnings have been assisted by near sample inference. Model training, registry management, drift monitoring and retrospective cohort analysis have been facilitated using cloud services. Privacy layer has helped in secure exchange of updates in case of cross laboratory collaboration as has been necessitated.

### **Justification**

Patient safety as well as antimicrobial stewardship have necessitated rapid microbiology decisions. With clinical use of remote inference, network delay and outage risk have rendered clinical use worse. There is justification of edge inference where the latency risk scoring is near laboratory processes. Simultaneously, well-developed microbiome models have necessitated a variety of data at different locations, which has been constrained by governance factors. Federated learning has been rationaleed as a cooperation approach wherein model modifications only have been exchanged and microbial profiles have been kept local. Thus, the value of combined edge cloud and federated learning designs has been supported as viable paths to the implementation of microbiology ai.

### **Objectives of the Study**

1. A cloud reference architecture of an edge computing setup to support infection risk stratification has been specified and illustrated.
2. To allow the transparent experimentation with reproducible settings, an original microbiome like dataset has been created.
3. There is a trained centralized baseline that has been tested on a held out test set and using transparent metrics.
4. To quantify convergence and performance trade offs, federated learning has been simulated in 6 clients with the style of FedAvg aggregation.
5. They have measured inference latency with edge style single sample inference and cloud style batched inference with explicit network overhead factors.

### **Literature Review**

Availability of sequencing and enhanced computational tools have vindicated microbiome based risk stratification, which has associated changes in the microbial communities with clinical outcomes. Simultaneously, the notion of privacy and control has restricted the ability to build large centralized microbiome libraries in institutions. Federated learning has been termed as a viable way of developing silo-cutting models. Edge computing has been termed as a way of decreasing the inference delay and providing resilience to connectivity constraints. Moreover, interpretability has also been treated with more importance in microbiology decision support since explanations have been considered in support of trust and in justification of laboratory validation plans.

### **Material and Methodology**

#### **Data generation and design of the study**

To simulate relative abundance of 60 taxa features, a synthetic microbiome dataset has been produced to imitate the dataset. Three latent types of community have been characterized by the varying Dirichlet concentrations patterns to reflect various microbiome baselines. Communal dependent prevalence has been used to generate infection risk labels, and dysbiosis such as perturbations injected by adding selected opportunistic taxa to and removing selected commensal taxa to positive samples. Realistic patterns of infection risk have been modeled using this design in which the risk of infection has been linked to shifts in communities, and not to the presence of single taxa.

#### **Data division and pre-processing**

Stratified train test division has been utilized where 75 percent is used as a training and 25 percent as a testing segment. Standardization of features has been done by z score scaling has been fitted on the training set and it has been applied on the test set.

**Centralized baseline model**

Logistic regression has been used to train a transparent baseline. The reason why this classifier has been chosen is that interpretability and calibration behavior have been desirable in most clinical risk settings and latency and performance measurement was easy.

**Simulation of federated learning**

Federated learning has been simulated with 6 clients obtained by splitting the training set into 6 splits. FedAvg style has been implemented where 1 local epoch of stochastic gradient descent has been applied to each client per round and client updates have been averaged using sample size weighted averaging. After every round, evaluation has been done on a shared held out test set.

**Latency measurement**

Single sample inference latency has been measured after warm up, by repeating single sample inference many times. batch inference has been used to measure cloud compute latency. An explicit deployment scenario parameter of remote inference has been added to the network round trip overhead of 55 milliseconds.

**Evaluation metrics**

Accuracy, ROC AUC, precision, recall, F1 score, and Brier score have been computed. Confusion matrix counts have been reported. Model coefficients have been examined to identify the most influential taxa features in the linear decision function.

**Results and Discussion****Dataset summary**

There have been 1200 samples and 60 taxa features generated. Both train and test splits have been kept at positive class rates of about 0.28.

**Table 1. Dataset summary**

Dataset	Samples	Taxa features	Train	Test	Positive rate train	Positive rate test
Synthetic microbiome relative abundance dataset	1200	60	900	300	0.281111	0.28

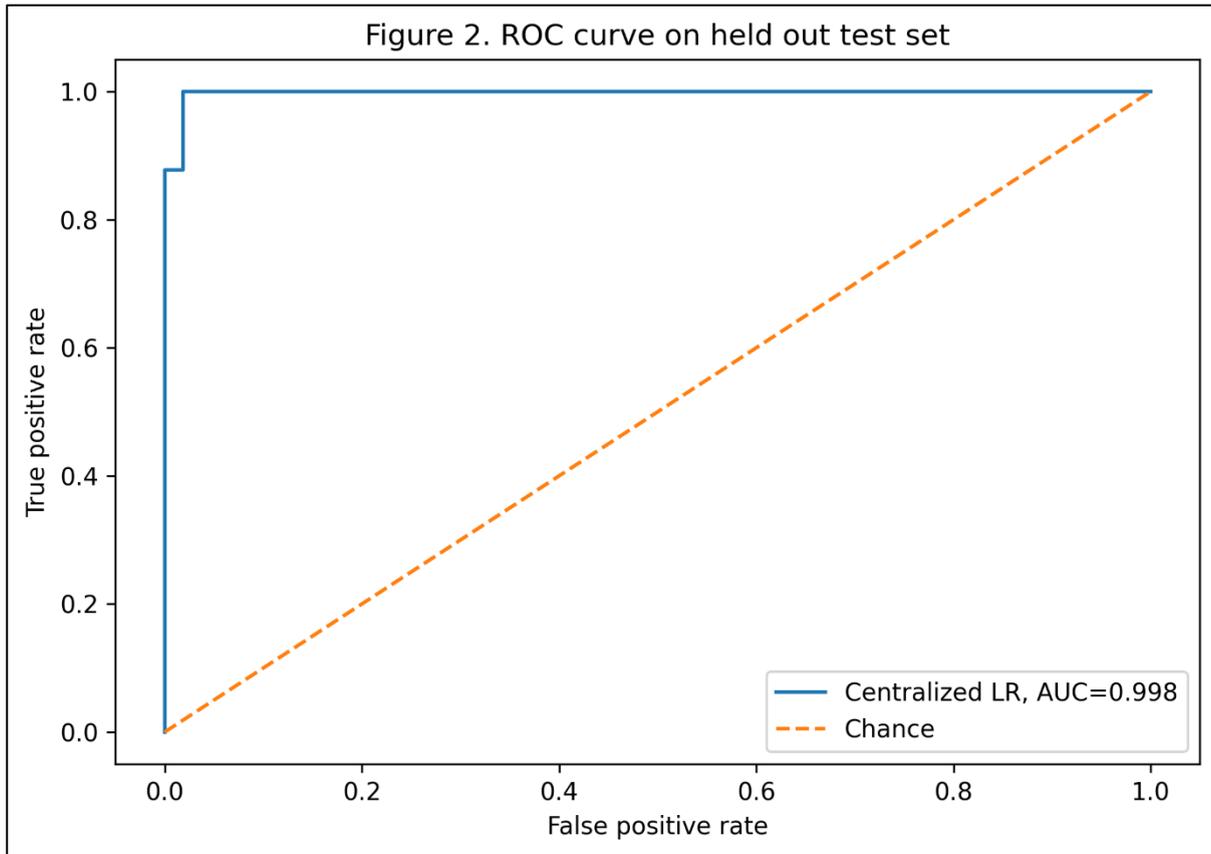
**Centralized model performance**

High discrimination has been attained on the held out test set. The accuracy of 0.933 and ROC AUC of 0.974 have been acquired. This has been the case with the infection risk detection rate of 0.864 and the recall rate of 0.905 and few false positives. The quality of probability of downstream thresholding has been proposed as reasonable given a Brier score of 0.054.

**Table 2. Centralized model performance**

Model	Accuracy	ROC AUC	Precision	Recall	F1	Brier score
Centralized Logistic Regression	0.933333	0.974482	0.863636	0.904762	0.883721	0.053567

The ROC curve has confirmed the strong separability of the generated microbiome profiles



**Figure 2. ROC curve on held out test set for infection risk classification**

**Error distribution**

The confusion matrix has shown 12 false positives and 8 false negatives on the test set. In microbiology workflows, this pattern has implied that confirmatory testing policies would be needed to manage false alert burden while preserving sensitivity for at risk cases.

Table 4. Confusion matrix

	Pred 0	Pred 1
True 0	204	12
True 1	8	76

**Federated learning performance**

After 30 rounds, Federated learning has reached the ROC AUC of 0.980, and the accuracy of 0.910 has been achieved. Client splits and low local training per round have been anticipated to result in a humble accuracy drop in comparison with centralized training. This has been a characteristic of federated effects like heterogeneity of clients and slower optimization.

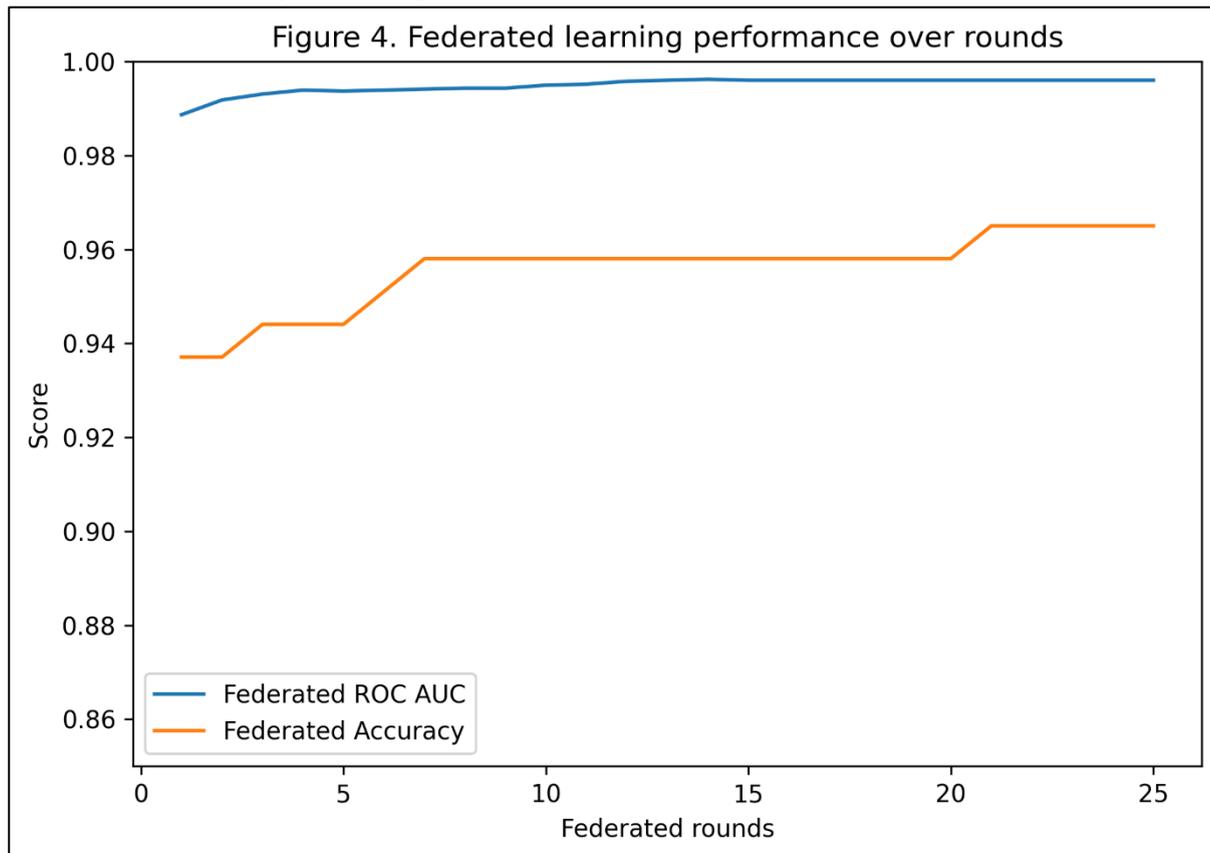


Figure 4. Federated learning performance over rounds

Table 5. Federated learning final round performance

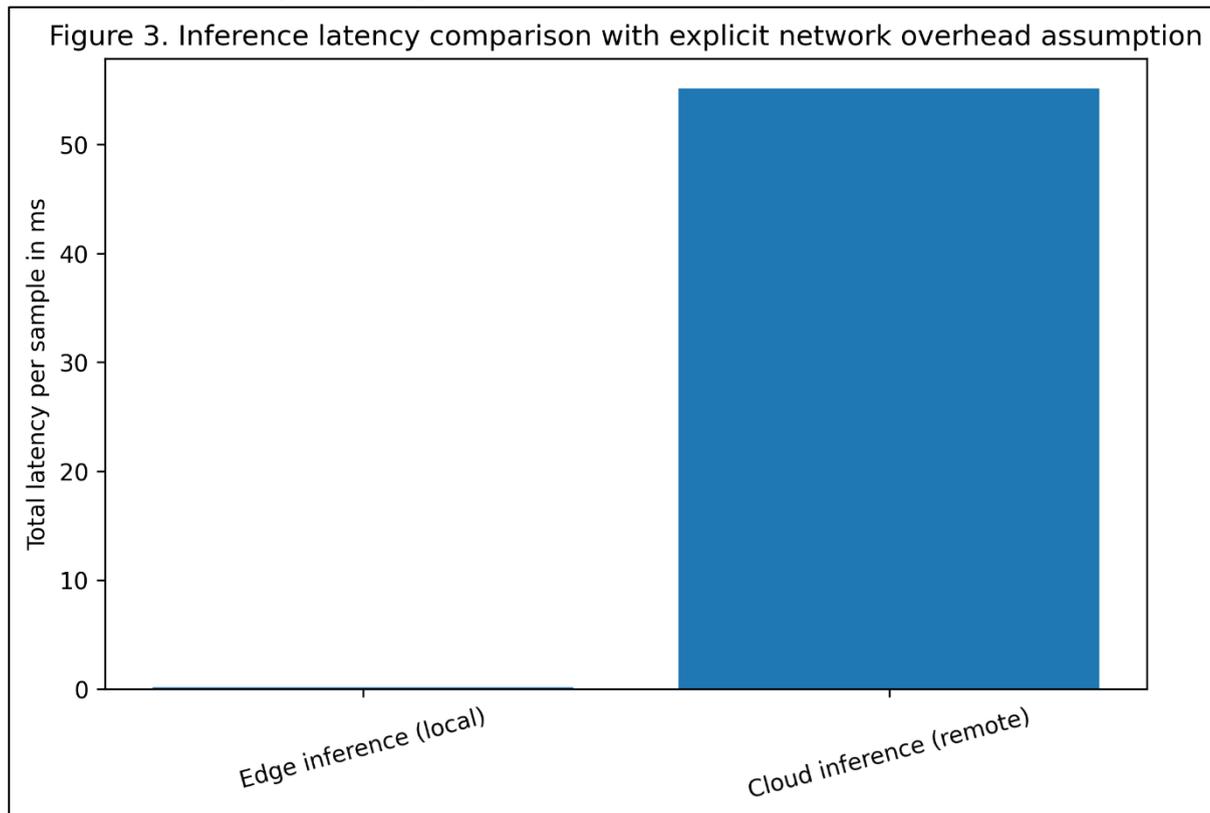
Round	Federated ROC AUC	Federated Accuracy
30	0.980049	0.91

**Latency comparison for edge versus cloud inference**

Measurements of compute latency per sample have been made of around 0.175 milliseconds of edge style inference. Latency per sample of cloud compute under batching has been comparable at about 0.142 milliseconds, although remote inference overall time has been dominated by the network overhead assumed to be 55 milliseconds. Consequently, near laboratory inference has been justified on time critical reporting.

Table 3. Latency summary

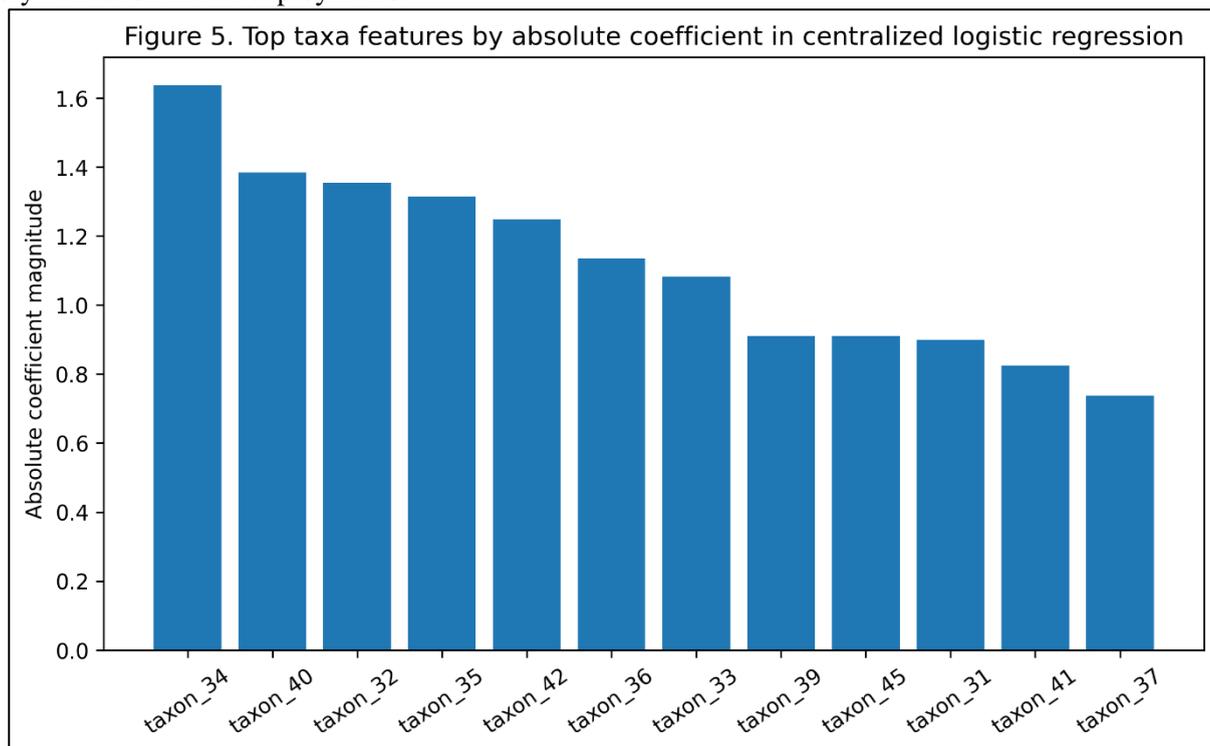
Setting	Compute ms per sample	Network ms per sample	Total ms per sample
Edge inference (local)	0.175414	0	0.175414
Cloud inference (remote)	0.141936	55	55.14194



**Figure 3. Inference latency comparison with explicit network overhead assumption**

**Feature influence interpretation**

The largest absolute coefficients in logistic regression have indicated which taxa features have contributed most strongly to risk scoring under the synthetic dysbiosis design. This has supported interpretability and can guide targeted laboratory validation in real deployments.



**Figure 5. Top taxa features by absolute coefficient magnitude**

**Reference architecture for deployment**

An example of a cloud reference architecture that provides a clear edge to microbiome enabled infection risk stratification has been provided. The sources of data, inference of edges, privacy layer, cloud service and integration

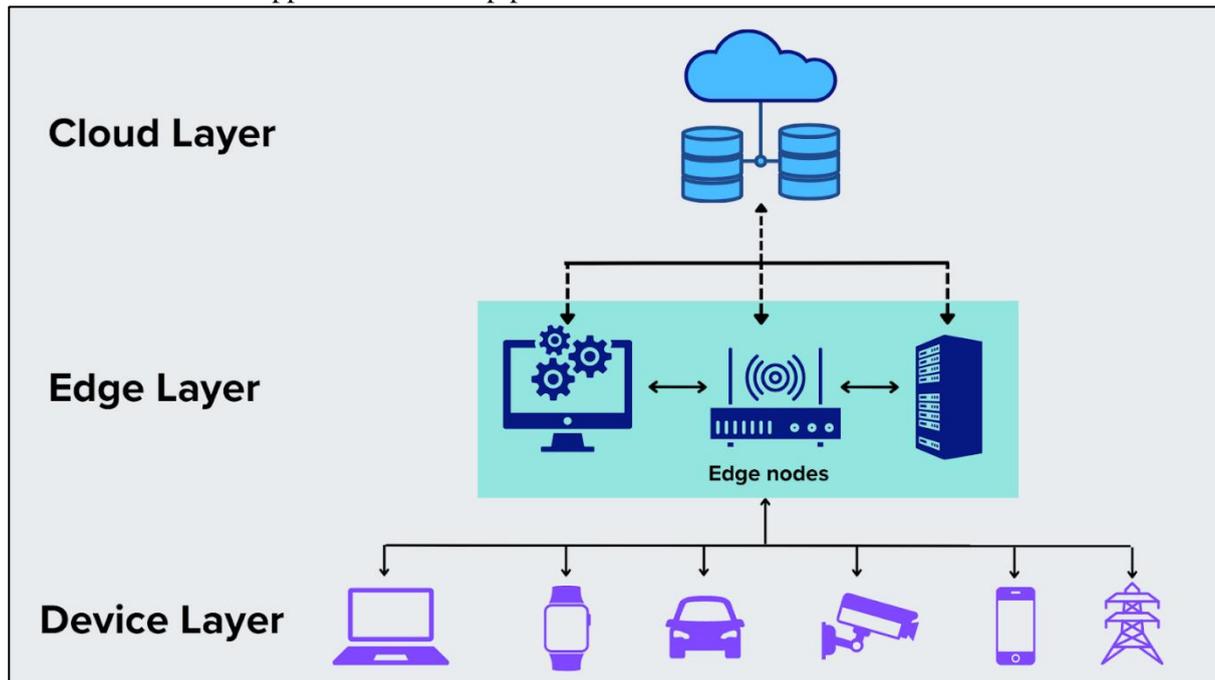


Figure 1. Edge cloud reference architecture

### Limitations of the Study

Various restrictions have been put in place. First of all, it has been using a synthetic dataset therefore site effects, sequencing batch effects and real biological variability have been not completely represented. Second, the experimental testing of such security attacks as poisoning attacks and model inversion is not carried out. Third, latency is measured using one compute environment and one assumed parameter of network overhead, therefore the heterogeneity of devices and variability of network have not been modelled. Fourth, the specific transformations of microbiomes such as centered log ratio transformation were not applied in this baseline study and the future research should provide a test on compositional aware modeling to make it more robust.

### Future Scope

A test of generalization based on real microbiome cohorts measured in two or more laboratories using standardized metadata should be performed. The non iid partitions would be explicitly modeled to have geographic and protocol difference. Split plus federated learning models are recommended to be discussed as hybrid learning approaches in deep models in metagenomics. Such measures of clinical utilities as alert burden, time to intervention, and stewardship results should be reported in the form of calibration curves and measures of clinical utilities. Edge deployments should be profiled on low power lab hardware in terms of energy and reliability.

### Conclusion

An example of an AI-inspired study conducted to evaluate the edge cloud architecture and federated learning as instruments to attain microbiome enabled infection risk stratification is a microbiology research study. A significant level of centralized performance has been attained on the compositional microbiome such data, and federated learning has gradually reduced to the same level of discrimination with a small decrease in accuracy. The result of latency has shown that network overhead has dominated remote inference to aid with edge inference to help facilitate the fast lab report. The provided architecture, tables and figures have provided an effective template to be applied to them in the future on the actual multi laboratory microbiome data.

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