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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☒	☐	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Each site used different software in order to mine their medical records or data repositories for the required data. We do not have any visibility into what software they used to extract/prepare their data.
Data analysis	We used Client-server based federated learning (FL) using the FederatedAveraging algorithm (add number) as implemented in NVIDIA Clara Train v3.1 SDK. This code is freely available for use through NVIDIA Clara Imaging. https://developer.nvidia.com/clara-medical-imaging . For the model pipeline, we used the following: FL training software: Clara Train SDK v3.1.01 Model: clara_train_covid19_exam_ehr_xray v1 Preprocessing: pydicom==2.0.0 missingpy==0.2.0 (which includes the referenced 'MissForest' function) sklearn==0.0 imageio==2.9.0 numpy==1.19.1 scipy==1.5.2 Pillow==7.2.0 pandas==1.1.1 matplotlib==3.3.1

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The dataset from the 20 institutes that participated in this study remains under their custody. This data was used for training at each of the local sites and was not shared with any of the other participant institutions or with the Federated Server, and it is not publicly available. The dataset from the 3 independent test sites is maintained by Massachusetts General Brigham (MGB), and can be requested for access following appropriate procedures according to MGB IRB and policy (contact: Dr. Quanzheng Li).

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	The 20 client-sites prepared 16,148 cases (both positive and negative) for the purpose of training, validating, and testing the model. Each case included one CXR and the requisite data inputs taken from the patient's medical record. Based on our experience with training CORISK (the MGH local model that inspired the EXAM federated model), we expected that over 5,000 cases (roughly) should bring a model to performance, and additional data diversity would contribute to model robustness. We did not have a way to assess the amount nor diversity of the data needed to achieve robustness as there is no benchmark nor reliable methods to determine that in a non-empiric way.
Data exclusions	No data was excluded from the model training. In Fig. 3, Federated Learning vs. local training performance, we show the performance for 18 of 20 clients here as client 12 had only outcomes for 72 hours (see Extended Data Fig. 7) and client 14 only cases with room air treatment, resulting in the evaluation metric (avg. AUC) being not applicable (see Methods). This decision was established preemptively.
Replication	Each experiment was replicated 3 times, apart from the experiment evaluating efficacy of differential privacy. All attempts were successful.
Randomization	Data was randomized at the sites into train, validation and testing data.
Blinding	The main motivation for conducting federated learning is that the training of a deep learning model can occur without participants sharing or transferring data. This means that everyone was blinded to the data collection/allocation. The analysis took place after all training was complete, and incorporated all of the available information.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	Patient data inclusion criteria were: 1. patient presented to the hospital's ED or equivalent, 2. patient had a RT-PCR test done anytime between presentation to the ED and discharge from the hospital, 3. patient had a CXR in the ED, 4. Patient's record had at least 5 of the EMR values detailed in Extended Data Table 1, all obtained in the ED, and the relevant outcomes captured during the hospitalization. Of note, The CXR, lab values, and vitals used were the first available captured during the visit to the ED. The model did not incorporate any CXR, lab values, or vitals acquired after leaving the ED.
Recruitment	This was a retrospective data study. Each institute completed their own review process in order to include their retrospective data in the study.
Ethics oversight	All procedures were conducted in accordance with principles for human experimentation as defined in the Declaration of Helsinki and International Conference on Harmonization Good Clinical Practice guidelines and approved by the relevant institutional review boards at the following validation sites: Cooley Dickinson Hospital (CDH), Martha's Vineyard Hospital (MVH), Nantucket Cottage Hospital (NCH), and at the following training sites: Mass Gen Brigham (MGB), Mass General Hospital (MGH), Brigham and Women's Hospital, Newton-Wellesley Hospital, North Shore Medical Center, Faulkner Hospital (all eight of these hospitals were covered under MGB's ethics board reference # 2020P002673 and informed consent was waived by the IRB). Similarly, the participation of the remaining sites was approved by their respective relevant institutional review processes: Children's National Hospital in Washington, D.C. (00014310, IRB Certified Exempt), NIHR Cambridge Biomedical Research Centre (20/SW/0140, Informed consent waived), The Self-Defense Forces Central Hospital in Tokyo (02-014, Informed consent waived), National Taiwan University MeDA Lab and MAHC and Taiwan National Health Insurance Administration (202108026W, Informed consent waived), Tri-Service General Hospital in Taiwan (B202105136, Informed consent waived); Kyungpook National University Hospital in South Korea (KNUH 2020-05-022, Informed consent waived), Faculty of Medicine, Chulalongkorn University in Thailand (490/63, 291/63, Informed consent waived), Diagnosticos da America SA in Brazil (26118819.3.0000.5505, Informed consent waived), University of California, San Francisco (20-30447, Informed consent waived), VA San Diego (H200086, IRB Certified Exempt), University of Toronto (20-0162-C, Informed consent waived), National Institutes of Health in Bethesda, Maryland (12-CC-0075, Informed consent waived), University of Wisconsin-Madison School of Medicine and Public Health (2016-0418, Informed consent waived), Memorial Sloan Kettering Cancer Center in New York (20-194, Informed consent waived), and Mount Sinai Health System in New York (IRB-20-03271, Informed consent waived).

Note that full information on the approval of the study protocol must also be provided in the manuscript.