
EHRSHOT: An EHR Benchmark for Few-Shot Evaluation of Foundation Models

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Abstract

While the general machine learning (ML) community has benefited from public datasets, tasks, and models, the progress of ML in healthcare has been hampered by a lack of such shared assets. The success of foundation models creates new challenges for healthcare ML by requiring access to shared pretrained models to validate performance benefits. We help address these challenges through three contributions. First, we publish a new dataset, EHRSHOT, which contains de-identified structured data from the electronic health records (EHRs) of 6,739 patients from Stanford Medicine. Unlike MIMIC-III/IV and other popular EHR datasets, EHRSHOT is longitudinal and not restricted to ICU/ED patients. Second, we publish the weights of CLMBR-T-base, a 141M parameter clinical foundation model pretrained on the structured EHR data of 2.57M patients. We are one of the first to fully release such a model for coded EHR data; in contrast, most prior models released for clinical data (e.g. GatorTron, ClinicalBERT) only work with unstructured text and cannot process the rich, structured data within an EHR. We provide an end-to-end pipeline for the community to validate and build upon its performance. Third, we define 15 few-shot clinical prediction tasks, enabling evaluation of foundation models on benefits such as sample efficiency and task adaptation. Our model and dataset are available via a research data use agreement from our website. Code to reproduce our results is available here.

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1 Introduction

Open datasets, code, and models have been essential in advancing machine learning (ML) over the past decade [34, 46, 19]. Though the benefits of open code and data are well known [40, 27], there is currently a dearth of publicly available datasets and pretrained models for electronic health records (EHRs), which makes conducting reproducible research challenging [38, 23].

This is especially problematic in the era of foundation models (FMs), which hold tremendous promise for clinical applications [24]. The ability of a shared FM to generalize across health systems would be highly valuable, as most hospitals lack the computational resources to train such models [36]. Yet many of the purported benefits of clinical FMs, such as sample efficiency and task adaptability, remain difficult to evaluate due to reproducibility and data access issues [38].

Unfortunately, most existing EHR datasets (e.g., MIMIC-III/IV [17, 16], eICU [28], AmsterdamUM-Cdb [45], and HiRID [6]) narrowly focus on the intensive care unit (ICU), which provides a limited snapshot of a patient’s overall health trajectory and limits what tasks can be evaluated [47]. Access to a patient’s complete medical timeline, referred to as “longitudinal” data, offers a more realistic representation of the breadth of information available to a health system. Longitudinal EHR data, however, remains scarce. The few public datasets that exist, such as the CPRD [11] and UK BioBank [2], lack consensus on shared evaluation tasks / data processing pipelines and require navigating a research protocol review process, which creates challenges when curating shared ML workflows [44].

While the limitations of prior benchmarks were less apparent when developing small-scale, task-specific models, their utility is limited for evaluating FMs on task adaptation, few-shot learning, and other properties of large-scale, self-supervised models [1, 31]. Clinical FMs surface new questions, and a dataset for evaluating such FMs should contain a diverse range of tasks in low-label settings with longitudinal data [22]. Most importantly, such a benchmark should also release the weights of its pretrained models so the community can reproduce and build upon its results. Unfortunately, few FMs trained on EHR data have had their model weights published [49].

Our work helps address both shortcomings – a lack of public EHR datasets and pretrained clinical FMs – as one of the first combined releases of a research dataset and FM trained on EHR data. We outline our three primary contributions towards more reproducible ML for healthcare below:

1. We release EHRSHOT, a longitudinal EHR benchmark for the few-shot evaluation of clinical FMs. EHRSHOT contains the **full coded medical timelines of 6,739 patients** from Stanford Medicine. Records include demographics, diagnoses, procedures, laboratory results, medications, and other structured data, for a total of 41.6 million clinical events across 921,499 encounters. EHRSHOT contains an average of **2.3x more clinical events and 95.2x more encounters per patient than MIMIC-IV [16]** and, unlike the majority of existing benchmarks, includes patients not seen in the ICU or emergency department (ED).
2. We publish the weights of a **141M parameter transformer-based foundation model** (CLMBR-T-base) pretrained on the deidentified structured data of **2.57M patients’ EHRs**. CLMBR-T-base was trained in a self-supervised manner to autoregressively predict the next code in a patient’s timeline given their previous codes [42]. We are among the first to publish the full weights of such a clinical FM [49] for the community to evaluate and build upon. Researchers who leverage our model can benefit from both improved downstream task accuracy and cost savings by shortcircuiting the model development process.
3. We define a new few-shot benchmark of **15 patient classification tasks**. Several tasks have naturally low prevalence, creating a realistic setting for few-shot experimentation. While our pretrained model offers significant AUROC/AUPRC gains in few-shot settings over a traditional supervised baseline, we demonstrate that there remains significant room for improvement on many of our tasks.

Our overall workflow is shown in Figure 1. We publish the full code to replicate our results here: <https://github.com/som-shahlab/ehrshot-benchmark>. We also publish the full weights of our pretrained

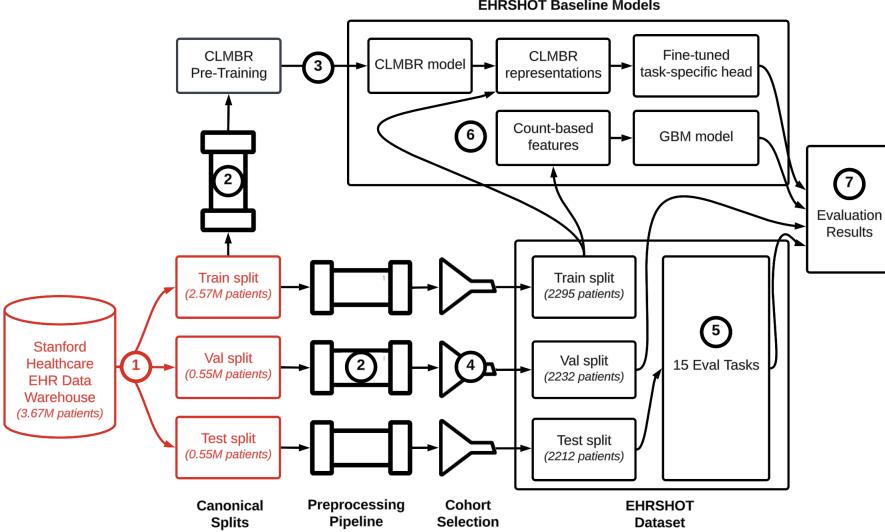


Figure 1: Overview of EHRSHOT. **Black boxes** represent open source code, data, and model weights. **Red boxes** are private data. (1) Starting with a source EHR database of 3.67M patients, we define a global train/val/test split across all patients. (2) We use an open source EHR preprocessing package called FEMR to transform our data. We keep all structured data (diagnoses, medications, labs, etc.) and discard images and clinical text. (3) We use the 2.57M patients in our global train split to pre-train a foundation model, CLMBR-T-base [42]. (4) We filter the source database down to a cohort of 6,739 patients, which we use for EHRSHOT. (5) We define 15 few-shot classification tasks and label each patient accordingly. (6) We test two baseline models for each task: our pretrained CLMBR-T-base and a count-based GBM model [32]. (7) We measure the AUROC and AUPRC of each model on each task, and share the results in Section 5.

clinical foundation model, as well as the EHRSHOT dataset and task labels, under a non-commercial data usage agreement here: <https://ehrshot.stanford.edu>.

2 Related Work

One of the most popular EHR datasets made accessible to researchers is MIMIC-III, which contains roughly 40,000 patients seen in the intensive care unit (ICU) of Beth Israel Deaconess Medical Center in Boston, Massachusetts, between 2001 and 2012 [17]. Other public datasets include eICU [28], HiRID [6], AmsterdamUMCdb [45], CPRD [11], MIMIC-IV [16], and the UK Biobank [2].

Most of the aforementioned datasets are narrowly scoped to a single department: the ICU [17, 28, 6, 45]. This makes it impossible to capture a patient’s full health trajectory to the extent that an academic medical center or health system would know of the patients it treats. Other datasets such as MIMIC-IV include data from multiple departments, but are still heavily anchored to the ICU, as only patients admitted for an ICU/ED visit are included [16]. In contrast, our work releases the full longitudinal EHR of patients across all departments of a major academic medical center, thus providing a more realistic setting for general prediction making.

Prior work has also typically relied on the creation of bespoke schemas to store their data. These custom schemas greatly increase the difficulty of transferring models across datasets and sites [44]. In contrast, the data preprocessing pipeline that we use is capable of ingesting both EHRSHOT as well as any dataset that follows the Observational Medical Outcomes Partnership Common Data Model (OMOP-CDM), an open community data standard for sharing EHRs used by over 100 health systems [35]. More details on our data preprocessing pipeline can be found in the Appendix in Section C.5.

Previously published EHR datasets typically only provide raw data. Thus, significant additional effort has been devoted to building standardized preprocessing pipelines, patient splits, and task definitions on top of these datasets [10, 30, 23]. These add-on benchmarks, however, are still limited by the narrow scope of their underlying data, and many recycle the same core set of tasks (e.g. in-patient mortality, long length-of-stay, ICU transfer, and ICD code prediction) [30, 10, 9]. Additionally, these benchmarks are typically not created with the purpose of measuring a pretrained model’s few-shot performance [22]. This limits their utility in assessing the key value propositions of foundation models, such as improved sample efficiency and adaptation to diverse tasks.

On the modeling side, substantial literature exists on training FMs for EHR data [29, 20, 33, 42, 25]. However, the vast majority of these FMs have never had their weights published [49]. This greatly hinders reproducibility and makes cross-model evaluations difficult. Worse, this lack of sharing undermines a primary advantage of FMs: transfer learning, i.e. the ability to use the pretrained weights of an existing FM to shortcut model development for other tasks [1].

EHRSHOT aims to fill several of these gaps by providing a longitudinal EHR benchmark specifically geared towards few-shot evaluation of pretrained FMs. EHRSHOT is built on top of a cross-site interoperable standard (OMOP-CDM), and leverages an open source data preprocessing pipeline to allow other researchers to reproduce our results end-to-end. Additionally, we release the weights of the clinical foundation model that we pretrain and evaluate, one of the first to do so. We provide additional points of comparison in Table 1.

Table 1: Comparison of our work to existing EHR benchmarks. Checkmark indicates full support, asterisk represents properties that are semi-supported.

Benchmark	Source Dataset	EHR Properties			Evaluation		Reproducibility	
		ICU/ED Visits	Other Visits	# of Patients	# of Tasks	Few Shot	Dataset via DUA	Preprocessing Code
MIMIC-Extract [48]	MIMIC-III	✓	–	34k	5	–	✓	✓
Purushotham 2018 [30]	MIMIC-III	✓	–	35k	3	–	✓	✓
Harutyunyan 2019 [10]	MIMIC-III	✓	–	33k	4	–	✓	✓
Gupta 2022 [9]	MIMIC-IV	✓	*	257k	4	–	✓	✓
COP-E-CAT [21]	MIMIC-IV	✓	*	257k	4	–	✓	✓
Xie 2022 [50]	MIMIC-IV	✓	*	216k	3	–	✓	✓
eICU [37]	eICU	✓	–	73k	4	–	✓	✓
EHR PT [22]	MIMIC-III / eICU	✓	–	86k	11	✓	✓	✓
FIDDLE [44]	MIMIC-III / eICU	✓	–	157k	3	–	✓	✓
HiRID-ICU [51]	HiRID	✓	–	33k	6	–	✓	✓
Solares 2020 [39]	CPRD	✓	✓	4M	2	–	–	–
EHRSHOT	Stanford Medicine	✓	✓	7k	15	✓	✓	✓

3 Dataset

We are releasing EHRSHOT (pronounced "earshot"), an EHR benchmark for few-shot evaluation of foundation models. EHRSHOT is a collection of 6,739 unique patients with canonical train/validation/test splits and corresponding labels for 15 classification tasks. We also provide canonical k -shot samples for each few-shot evaluation task. Unlike prior EHR benchmarks focused on task-specific supervised models [22] for specific episodes of care, e.g. admission to the ICU [10, 28], our benchmark is designed for evaluating pretrained FMs on a broad range of tasks using the depth of information that a health system would typically possess for its patients. EHRSHOT is provided as a set of CSV files. It is essentially a lightweight serialization of the OMOP-CDM format. Please see Section C.4 in the Appendix for additional details on the dataset format.

EHRSHOT contains a total of 41.6 million coded observations (e.g. diagnoses, procedures, medications, lab results, etc.) and 921,499 unique visits across 6,739 patients. We exclude all patients less than 19 years of age or greater than 88 years of age. We also exclude patients with less than 10 total clinical events in their record. We include statistics of EHRSHOT’s cohort demographics in Table 2 and Appendix Table 4, and histograms of patient characteristics in Appendix Figure 4.

Table 2: Summary statistics on the number of events, visits, and length of patient timelines in EHRSHOT.

Attribute		Train	Val	Test	All Splits
Number of Events	Min	10	10	10	10
	Mean	5942	6758	5826	6174
	Max	113466	199913	129704	199913
Number of Visits	Min	0	0	0	0
	Mean	127	147	134	136
	Max	2099	2397	2023	2397
Timeline Length (yrs)	Min	19	19	19	19
	Mean	59	59	58	59
	Max	88	88	88	88

3.1 Data Source

We sourced the data for our benchmark from the Stanford Medicine Research Data Repository (STARR) [5], which contains EHR data from both Stanford Health Care (primarily adult care) and Lucile Packard Children’s Hospital (primarily pediatric care). The source dataset is structured according to the Observational Medical Outcomes Partnership Common Data Model (OMOP-CDM) [12] and comprises a total of 3.67M unique patients from 1990 to February 8th, 2023 [5]. Of these patients, 2.57M (70%) are used for training and 0.55M (15%) for validation of the foundation model that we release, CLMBR-T-base, the details of which we discuss in Section 4. All data that we work with is deidentified, and hence, our study did not require Institutional Review Board approval [5].

This source database contains demographics (e.g. age, sex, race), diagnoses, procedures, laboratory results, medication prescriptions, and other coded clinical observations, which we preserve. While the source database also contains clinical notes, we remove these in our released benchmark. We describe how we selected our patient cohort from this source dataset in the Appendix in Section C.6. We apply a few additional transformations on top of those described in [5] to prevent data leakage and fix timestamp issues, which are detailed in Section C.5 in the Appendix.

For our data preprocessing pipeline, we use the **Framework for Electronic Medical Records (FEMR)** library, which we developed in parallel to this work. FEMR is a Python library that supports the ingestion of multiple EHR data formats (e.g. OMOP, MIMIC, etc.) and provides a unified interface for building machine learning models on top of such data at scale. The full codebase is available on Github here: <https://github.com/som-shahlab/femr/>.

Additionally, all of the code used to generate the dataset for EHRSHOT can be found here: <https://github.com/som-shahlab/ehrshot-benchmark>.

3.2 Tasks

We define 15 tasks as part of our benchmark, as listed in Table 3. We selected these tasks based on clinician input as well as alignment with prior benchmarks [10, 8]. The tasks that we consider can be broadly grouped into the following 4 categories: (1) Operational Outcomes, (2) Anticipating Lab Test Values, (3) Assignment of New Diagnoses, (4) Anticipating Chest X-ray Findings.

All tasks are classification tasks. We include a total of nine binary classification tasks (*Operational Outcomes* and *Assignment of New Diagnoses*), five 5-way multiclass tasks (*Anticipating Lab Test Values*), and one 14-way multilabel task (*Anticipating Chest X-ray Findings*). The size of each task’s subcohort, as well as the prevalence of positive labels, is detailed in Table 3. For example, there are 552 positive labels within the test cohort for the Long Length of Stay task, while there are 2,195 total labels, meaning there are 1,643 negative labels. As there are only 1,238 unique patients in this task’s test cohort, some patients have multiple labels assigned to them.

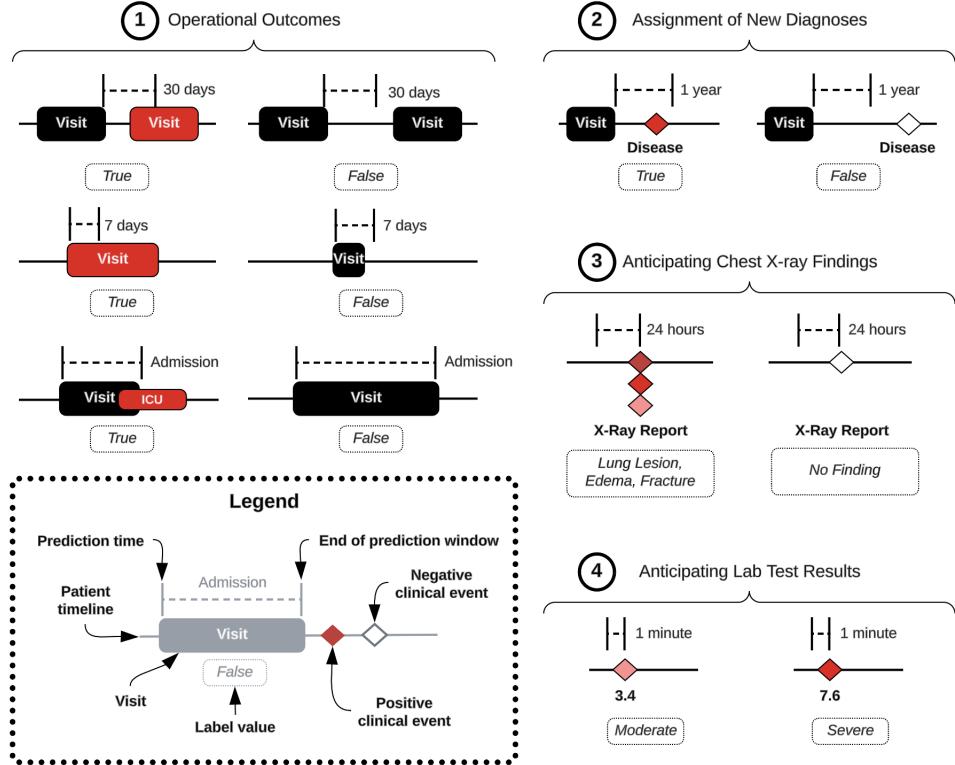


Figure 2: Summary of Benchmark Tasks. Each subfigure contains one of the 4 types of predictive classification tasks included in our benchmark: (1) *Operational Outcomes* (binary), (2) *Assignment of New Diagnoses* (binary), (3) *Anticipating Chest X-ray Findings* (multilabel), (4) *Anticipating Lab Test Results* (multiclass). Each **black line** represents a patient timeline. The **black boxes** represent how each timeline would be labeled for each task at a specific prediction time. The leftmost edge of the dotted lines above each timeline is the prediction time, and the rightmost edge is the end of the time horizon for that task. Note that each *Operational Outcome* task (1) has a different prediction window (30 days, 7 days, duration of admission), while the other three task categories (2, 3, 4) all have uniform prediction windows across their subtasks.

In the Appendix, we define the precise prediction windows for each task in Table 7 and the definition of each task in Section C.3. We also provide a visualization of our 4 task categories in Figure 2.

4 Baseline Models

We measure the performance of two baseline models on our dataset: (1) a gradient boosting machine (GBM) that uses count-based featurizations of patients to make predictions, (2) an autoregressive language model ("CLMBR-T-base") that ingests medical codes as tokens and was pretrained on the full longitudinal structured EHRs of 2.57M patients from our source institution [42, 8].

We chose these two models as our baselines for several reasons. First, language modeling has achieved state-of-the-art results on clinical prediction tasks [42, 33, 25, 29, 20], while count-based featurization remains a simple but competitive baseline [32, 33, 42]. Second, most prior FMs trained on structured EHR data have not had their model weights published, and were developed and tested exclusively on nonstandard data formats like MIMIC-III [49]. This makes it nearly impossible to conduct a fair comparison of prior models, which often requires re-implementation or significant modification to work across datasets [13]. This is one of the key challenges we are attempting to solve with EHRSHOT. We pre-train our own FM from scratch to have full control over its training, and publish its model weights so the community can reproduce and build upon our results.

Table 3: Task Demographics. The number of unique patients and total labels for each task. A single patient may have multiple labels for one task (e.g. a patient with multiple anemia lab results). We show the prevalence of positive patients/labels in parenthesis. For the multiclass lab test tasks, we define a positive label as any non-normal result. For the multilabel chest X-ray task, we define a positive label as a report with at least one finding.

Task Name	Train		Val		Test	
	# Patients (# Positive)	# Labels (# Positive)	# Patients (# Positive)	# Labels (# Positive)	# Patients (# Positive)	# Labels (# Positive)
Operational Outcomes						
Long Length of Stay	1377 (464)	2569 (681)	1240 (395)	2231 (534)	1238 (412)	2195 (552)
30-day Readmission	1337 (164)	2609 (370)	1192 (159)	2207 (281)	1190 (151)	2189 (260)
ICU Transfer	1306 (107)	2402 (113)	1157 (84)	2052 (92)	1154 (75)	2037 (85)
Anticipating Lab Test Results						
Thrombocytopenia	2084 (870)	68776 (9774)	1981 (774)	54504 (6962)	1998 (818)	56338 (7960)
Hyperkalemia	2038 (383)	76349 (1215)	1935 (348)	60168 (886)	1958 (339)	63653 (948)
Hypoglycemia	2054 (422)	122108 (1065)	1950 (362)	95488 (858)	1970 (356)	100568 (783)
Hyponatremia	2035 (1288)	81336 (20181)	1930 (1165)	64473 (14674)	1956 (1212)	67028 (16003)
Anemia	2092 (1251)	70501 (9544)	1992 (1122)	56224 (7445)	2002 (1151)	58155 (7636)
Assignment of New Diagnoses						
Hypertension	793 (130)	1260 (184)	784 (130)	1250 (177)	758 (130)	1261 (160)
Hyperlipidemia	923 (137)	1684 (205)	863 (140)	1441 (189)	864 (133)	1317 (172)
Pancreatic Cancer	1376 (128)	2576 (155)	1242 (46)	2215 (53)	1246 (40)	2220 (56)
Celiac	1392 (48)	2623 (62)	1252 (8)	2284 (11)	1255 (13)	2222 (21)
Lupus	1377 (79)	2570 (104)	1239 (24)	2226 (33)	1249 (19)	2243 (20)
Acute MI	1365 (130)	2534 (175)	1234 (112)	2177 (146)	1235 (115)	2127 (144)
Anticipating Chest X-ray Findings						
Chest X-Ray Findings	251 (237)	7481 (4771)	395 (378)	9366 (6032)	399 (381)	9428 (6400)

Count-based Features. Count-based featurization is a well-established baseline for EHR tasks, valued for its simplicity and effectiveness [32]. The fundamental idea involves converting each patient’s timeline into a count vector, where each element contains the number of occurrences of a specific medical concept prior to the prediction time of a task. These patient vectors are combined into a count matrix, which is high-dimensional and sparse. We use a technique called *ontology expansion* to increase the density of representation and improve the accuracy of code coverage by acknowledging the parent/child hierarchical relationships between medical concepts [4]. After generating our ontology-expanded count matrix, we train a gradient boosting machine (GBM) model on the EHRSHOT train split, and tune hyperparameters on the validation split. We use the LightGBM implementation [18]. We also evaluate a Logistic Regression and Random Forest model as baselines. Their results can be seen in Appendix in Figures 10 and 11. For clarity, we exclude them from the following analyses, as they perform roughly at par with the count-based GBM model.

Clinical Language-Model-Based Representations using Transformers (CLMBR-T-base). CLMBR-T-base is an autoregressive model designed to predict the next medical code in a patient’s timeline given previous codes. This objective enables it to learn robust global patterns for clinical prediction tasks. It is based on the CLMBR model originally developed in [42], but following [8] we substitute a transformer in place of a GRU as its base model. Our model employs causally masked local attention. This ensures forward-only flow of information which is vital for prediction tasks, and is in contrast to BERT-based models which are bidirectional in nature [42]. Note that our model does not process clinical text, only structured information. Our model has 141M trainable parameters, a hidden dimension of 768, and a next code prediction objective. This provides our version of CLMBR-T-base with minute-level resolution rather than the day-level aggregation of the original model formulation [42]. We leave training larger versions of CLMBR to future work.

More details about our baseline models can be found in the Appendix in Section D.

5 Results

We evaluate each baseline model in a few-shot setting. For each of the 15 benchmark tasks, we steadily increase the number of examples k that each model sees from $k = 1$ to the full training dataset, and record the model’s AUROC and AUPRC at each k .

More precisely, we define “ k -shot evaluation” of a model M on a specific task T as follows. We train M on k positive examples and k negative examples sampled from T ’s training split. We then select an additional k positive examples and k negative examples from T ’s validation split, and use these validation examples to select the best hyperparameters for M for task T . Finally, we evaluate the AUROC and AUPRC of the best performing version of M on T ’s entire held-out test split. For tasks where the total number of unique positive examples is less than k , we include all positive examples in our training set, and randomly resample positive examples until the total number of training examples seen by the model is k . We consider values of $k \in \{1, 2, 4, 8, 12, 16, 24, 32, 48, 64, 128\}$ for all tasks (with the exception of Celiac, for which we limit $k \leq 64$ as there are only 62 positive training labels).

For the count-based GBM, these few-shot examples are the only training examples seen by the model. For the pretrained CLMBR-T-base model, we use these few-shot examples to fine-tune a logistic regression head appended to the top of the model, while keeping the weights of the pretrained CLMBR-T-base model frozen. Pretraining the CLMBR-T-base model took roughly 4 days on a single Nvidia V100 hosted in an on-premise compute cluster.

The AUROC of each model across all 4 task categories is presented in Figure 3. In the Appendix, we show this grouping for AUPRC in Figure 5. We also break down each individual task’s AUROC in Figure 6 and AUPRC in Figure 7 of the Appendix. We also include results for additional baselines in the Appendix in Figures 10 and 11. The **bolded lines** are the Macro-AUC for each model within a task category, averaged across all subtasks at each k . We include the performance of each model trained on the entire EHRSHOT training split on the far right of every plot as *All*.

As shown in Figure 3, the pretrained foundation model CLMBR-T-base (blue) outperforms the count-based GBM (red) across all aggregated task categories for $k \leq 64$. This demonstrates the benefits of pretraining in few-shot settings, as the model can leverage patterns learned across millions of patients to derive more accurate representations out-of-the-box than a model trained from scratch. CLMBR-T-base outperforms the count-based GBM across all k on the *Operational Outcomes* and the majority of *Anticipating Lab Test Results* and *Anticipating Chest X-ray Findings* tasks. For these three task groups, the advantage of CLMBR-T-base seems most pronounced at intermediate levels of k between 8 and 128. At extremely low k (i.e. $k = 1$), both models struggle to learn anything, while as k increases the advantage of the pretrained model tends to shrink, a trend noted elsewhere [22]. This is most visible in the far-right of the plot at the *All* marker, which represents the performance of each model when trained on the full EHRSHOT training dataset.

In fact, the count-based GBM exceeds the performance of CLMBR-T-base on the *Assignment of New Diagnoses* tasks at $k > 64$. This suggests that the advantage of pretraining comes primarily from improved initialization of patient representations, and that the largest gains are achieved in the most data poor regimes.

There are several possible reasons for CLMBR-T-base’s underperformance at higher values of k for the *Assignment of New Diagnoses* tasks. First, the CLMBR-T-base model’s training objective is next code prediction, which makes it ill-suited for predictive tasks with long time horizons (which for these tasks is 1 year). Second, if a simple tree-based model exists for a task (i.e. a few medical concepts tightly correlate with a diagnosis), then it may be more difficult for a pretrained model to coerce patient representations learned over millions of patients to that specific task than training a model from scratch with enough data to learn those distinctive signals. We believe that this reversal in model rankings demonstrates a key strength of EHRSHOT – namely, the diversity of its predictive tasks can help identify opportunities for improving pretraining and few-shot strategies.

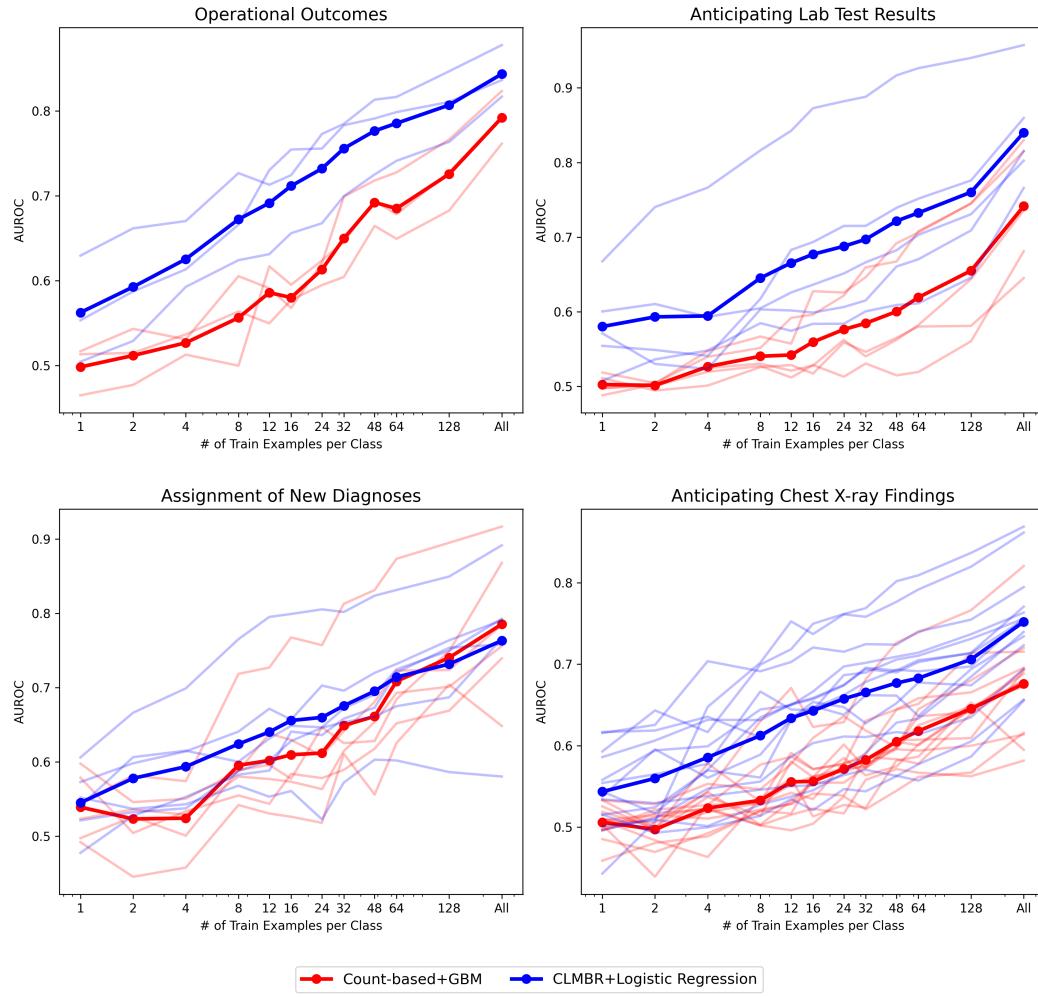


Figure 3: Aggregated AUROC across all subtasks within each of the 4 task categories for $k \in \{1, 2, 4, 8, 12, 16, 24, 32, 48, 64, 128\}$ shots. We show performance on the full training set as *All*. The **bolded lines** are the Macro-AUROC for each model, averaged across all subtasks within a task category for each value of k . The blurred lines are the average AUROC across 5 replicates for each subtask within a task category. CLMBR-T-base (blue) consistently outperforms the count-based GBM (red) at $k \leq 64$, but lags in higher label settings for the *Assignment of New Diagnoses* tasks.

We release all of our model weights, evaluation tasks, and data processing code to fully reproduce our results. To the best of our knowledge, the release of our pretrained CLMBR-T-base model is one of the first examples of such a clinical FM having its pretrained weights made publicly available [49].

6 Discussion

We believe that EHRSHOT represents a useful contribution to the ML community by enabling more reproducible healthcare ML research. The release of our pretrained CLMBR-T-base model’s weights will allow the community to replicate and build upon our work. Our results identify opportunities for improving pretrained models in few-shot settings.

Acquiring labeled EHR data is expensive and time-consuming. Additionally, certain rare conditions may only be present in a small cohort of patients out of millions within a health system [29]. Thus,

model performance in low-label settings is of paramount importance in healthcare. As our results in Section 5 demonstrate, pretrained FMs can yield large performance gains in few-shot settings. While we acknowledge that the tasks themselves may not be the most clinically meaningful, we believe that EHRSHOT offers a valuable contribution by providing a reproducible and rigorous point of comparison for different technical approaches to developing clinical FMs.

Limitations. There are several limitations to this work. First, we only release structured data – i.e. we do not publish any of the clinical text or images associated with our patients. While many datasets for medical images exist [3], publishing clinical text remains a challenge [41]. Second, we only consider one type of foundation model (CLMBR-T-base) for our experiments [42]. We look forward to seeing the additional foundation models that the community applies to our benchmark. Third, we release a very small cohort of patients (<1%) from our source EHR database, and specifically select these patients for the tasks that we define. Releasing our full pretraining dataset would be infeasible from a governance and effort perspective. Thus, while necessary in order to publish our EHR dataset and still broader than existing ICU-specific datasets, our cohort selection process limits the types of questions we can answer and does not reflect the full diversity of medical data. Fourth, as we only were able to evaluate our pretrained FM on Stanford Medicine data, it is unclear how well our pretrained model will perform at other institutions. We anticipate there will be some drop in performance, but the extent is unclear. Fifth, several of our tasks are "low label" in the most extreme sense – for example, the Celiac task only has 13 positive patients in its test set. This makes obtaining low variance estimates of model performance difficult. We aim to mitigate this by adding additional patients to our benchmark in future releases.

Societal Implications. We believe that the release of this dataset can help spur positive innovations for improving clinical care with ML. However, we recognize that there are patient privacy concerns anytime EHR data is released. We believe we sufficiently mitigate this risk through the rigorous deidentification process on which our data is subjected [5]. Additionally, we gate access to the dataset through a research data use agreement. Another concern is that models trained on biased data will reflect those biases [7]. Thus, the pretrained FM that we release may propagate biases in care delivery or outcomes present in our source EHR database [7]. However, we hope that by encouraging the full release of models, we can help the community better identify and mitigate these issues [26].

7 Conclusion

We publish EHRSHOT, a benchmark containing the structured data of 6,739 patients' full longitudinal medical timelines specifically geared towards few-shot evaluation of foundation models for clinical data. Unlike most prior work, EHRSHOT contains longitudinal health data rather than a single department (e.g. ICU). We define a set of 15 tasks ranging from well-studied outcomes like 30-day readmission to lesser explored settings such as anticipating abnormal lab values. Finally, we release the weights of a foundation model pretrained on over 2.57M patient timelines and publish the code needed to replicate our results. We hope that this work represents a first step towards moving the field of ML for healthcare towards more reproducible and open model development.

Acknowledgments and Disclosure of Funding

We thank the Stanford AIMI Center and Stanford Medicine Research IT for their assistance in publishing this dataset. This work was supported in part by the Mark and Debra Leslie Endowment for AI in Healthcare, the Clinical Excellence Research Center at Stanford Medicine, and Technology and Digital Solutions at Stanford Healthcare. MW is supported by an NSF Graduate Research Fellowship. JF was supported in part by a Stanford AIMI-HAI Partnership Grant.

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Supplementary Material

A Author Responsibility Statement

The authors confirm that they bear all responsibility in case of violation of rights or licenses.

B Public Accessibility + Licenses

B.1 Dataset

We release EHRSHOT under a research data use agreement. The dataset is available here: <https://ehrshot.stanford.edu/>. Access is gated by a researcher data use agreement due to the sensitive nature of the dataset. We do not upload our dataset to another data repository due to these concerns.

In order to ensure we do not reveal Protected Health Information (PHI) in our dataset, we take several precautions. First, we only release deidentified data. The deidentification process has been previously described in [5]. Second, on top of this deidentification process, we also apply additional privacy-protecting transformations following the best practices of the MIMIC-III dataset [17], which are detailed in Section C.5. Third, we do not publish any clinical notes. Fourth, we release our dataset under a data usage agreement that requires researchers to register with their identity and gain approval before accessing the dataset.

License: The license for the dataset is the standard Stanford University Dataset Research Use Agreement, and is reproduced below:

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B.2 Pretrained Foundation Model (CLMBR-T-base)

We release CLMBR-T-base, a foundation model pre-trained on the structured EHR data of roughly 2.5 million patients at Stanford Medicine [42]. The model's weights can be found at our website here: <https://ehrshot.stanford.edu/>. Access is gated by a researcher data use agreement due to the sensitive nature of the training dataset.

A concern with the release of such a model is the lack of solid theoretical privacy assurances, thus creating the possibility of the model revealing medical data. To mitigate these concerns, we implement several additional precautions. First, the model is trained exclusively on deidentified data to eliminate the chance of any Protected Health Information (PHI) seeping into the model. Second, all unique

text strings released as part of our CLMBR-T-base model’s dictionary (e.g. terms such as "Yes" or "No" that serve as categorical variables) were manually reviewed to ensure they do not reveal any PHI. Third, we make our model available under a data usage agreement that requires researchers to register with their identity and gain approval before accessing the model.

License: The license for the code for the model is here: <https://github.com/somshahlab/femr/blob/main/LICENSE>. The license for the model weights is here: <https://huggingface.co/StanfordShahLab/clmbr-t-base>.

C Dataset Details

C.1 EHRSHOT Cohort

Demographics of the EHRSHOT cohort are included below.

Table 4: EHRSHOT: Patient demographics in the train, validation, and test splits.

	Attribute	Train	Val	Test	All Splits
Gender	Male	1122	1090	1086	3298
	Female	1173	1142	1126	3441
	19-20	8	3	2	13
Age	21-40	412	457	431	1300
	41-60	648	597	576	1821
	61-80	916	892	905	2713
Race	81-88	311	283	298	892
	American Indian	14	7	4	25
	Asian	356	347	340	1043
	Black	98	105	95	298
	Pacific Islander	23	21	30	74
	White	1286	1222	1228	3736
Ethnicity	Unknown	518	530	515	1563
	Hispanic	374	342	322	1038
Total		2295	2232	2212	6739

C.2 Pretraining Dataset

The pretraining dataset for CLMBR-T-base contains a total of 3.67 million patient records, of which 2.57 million are used to train the model. We include summary statistics of these patients’ demographics in Table 5 and Table 6.

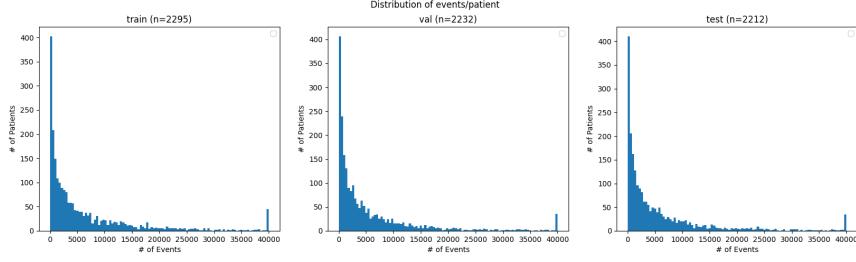
C.3 Task Definitions

Here, we detail the precise definitions for each of the 15 tasks for which we provide labels in our benchmark dataset.

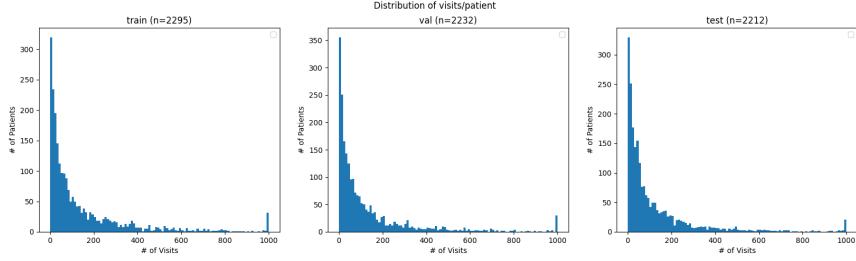
Operational Outcomes. These tasks are related to hospital operations. They are all binary classification tasks, and are defined as follows:

- **Long Length of Stay:** Predict whether a patient’s total length of stay during a visit to the hospital will be at least 7 days. The prediction time is at 11:59pm on the day of admission, and visits that last less than one day (i.e. discharge occurs on the same day of admission) are ignored.
- **30-day Readmission:** Predict whether a patient will be re-admitted to the hospital within 30 days after being discharged from a visit. The prediction time is at 11:59pm on the day of

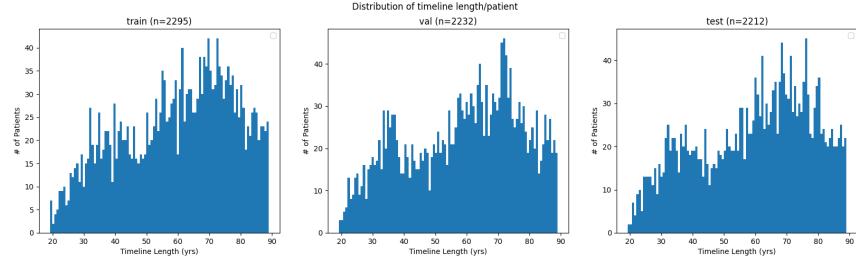
Figure 4: Histograms of EHRSHOT patient timeline characteristics



(a) Total number of events per patient, broken down by train/val/test split. Note that the x-axis is clamped at 40000 for clarity (i.e. along the x-axis we plot $\min(x, 40000)$)



(b) Total number of visits per patient, broken down by train/val/test split. Note that the x-axis is clamped at 1000 for clarity (i.e. along the x-axis we plot $\min(x, 1000)$)



(c) Total length of each patient timeline (i.e. difference in time between birth date and last recorded event), broken down by train/val/test split.

admission, and admissions where a readmission occurs on the same day as the corresponding discharge are ignored.

- **ICU Transfer:** Predict whether a patient will be transferred to the ICU during a visit to the hospital. The prediction time is at 11:59pm on the day of admission, and ICU transfers that occur on the same day as admission are ignored.

Anticipating Lab Test Results. These tasks are related to lab value prediction. They are all multiclass classification tasks. The prediction time is immediately before the lab result is recorded. They are defined as follows:

- **Thrombocytopenia:** Predict whether a thrombocytopenia lab comes back as normal ($\geq 150 \text{ } 10^9/\text{L}$), mild ($\geq 100 \text{ and } < 150 \text{ } 10^9/\text{L}$), moderate ($\geq 50 \text{ and } < 100 \text{ } 10^9/\text{L}$), or severe ($< 50 \text{ } 10^9/\text{L}$). We consider all lab results coded as LOINC/LP393218-5, LOINC/LG32892-8, or LOINC/777-3.
- **Hyperkalemia:** Predict whether a hyperkalemia lab comes back as normal ($\leq 5.5 \text{ mmol/L}$), mild ($> 5.5 \text{ and } \leq 6 \text{ mmol/L}$), moderate ($> 6 \text{ and } \leq 7 \text{ mmol/L}$), or severe ($> 7 \text{ mmol/L}$). We consider all lab results coded as LOINC/LG7931-1, LOINC/LP386618-5, LOINC/LG10990-6, LOINC/6298-4, or LOINC/2823-3.

Table 5: Pretraining Dataset: Patient demographics in the train, validation, and test splits.

Attribute		Train	Val	Test	All Splits
Gender	Male	1186614	255179	254733	1696526
	Female	1380836	295126	296127	1972089
Age	0-20	625949	135045	134684	895678
	21-40	671018	143607	144045	958670
	41-60	617519	131996	132432	881947
	61-80	502842	107299	107746	717887
	81-88	150122	32358	31953	214433
Race	American Indian	7229	1509	1516	10254
	Asian	371065	79638	80418	531121
	Black	83624	17895	17919	119438
	Pacific Islander	20959	4350	4435	29744
	White	987676	211262	211429	1410367
	Unknown	1096897	235651	235143	1567691
Ethnicity	Hispanic	325037	69912	69689	464638
	Non-Hispanic	2242413	480393	481171	3203977
Total		2567450	550305	550860	3668615

Table 6: Pretraining Dataset: Summary statistics on the number of events, visits, and length of patient timelines.

Attribute		Train	Val	Test	All Splits
Number of Events	Min	1	1	1	1
	Mean	707	706	704	706
	Max	191369	213133	214400	214400
Number of Visits	Min	0	0	0	0
	Mean	28	28	28	28
	Max	3701	4305	3109	4305
Timeline Length (yrs)	Min	0	0	0	0
	Mean	40	40	40	40
	Max	92	90	90	92

- **Hypoglycemia:** Predict whether a hypoglycemia lab comes back as normal (≥ 3.9 mmol/L), mild (≥ 3.5 and < 3.9 mmol/L), moderate (≥ 3 and < 3.5 mmol/L), or severe (< 3 mmol/L). We consider all lab results coded as SNOMED/33747003, LOINC/LP416145-3, or LOINC/14749-6.
- **Hyponatremia:** Predict whether a hyponatremia lab comes back as normal (≥ 135 mmol/L), mild (≥ 130 and < 135 mmol/L), moderate (≥ 125 and < 130 mmol/L), or severe (< 125 mmol/L). We consider all lab results coded as LOINC/LG11363-5, LOINC/2951-2, or LOINC/2947-0.
- **Anemia:** Predict whether an anemia lab comes back as normal (≥ 120 g/L), mild (≥ 110 and < 120 g/L), moderate (≥ 70 and < 110 g/L), or severe (< 70 g/L). We consider all lab results coded as LOINC/LP392452-1.

Please note that for the results of our baseline experiments in Section 5, we reframe these lab value tasks as binary classification tasks, where a label is "negative" if the result is normal and "positive" otherwise.

Table 7: Task Prediction Windows. *Prediction Time* is the precise time point (up to minute precision) in a patient's timeline when the prediction is made. *Time Horizon* is the length of time considered after the prediction time to determine whether an event occurs, i.e. we only consider a patient "positive" for a new diagnosis of pancreatic cancer if she receives that diagnosis within a year of being discharged.

Task Name	Task Type	Prediction Time	Time Horizon
Operational Outcomes			
Long Length of Stay	Binary	11:59pm on day of admission	Admission duration
30-day Readmission	Binary	11:59pm on day of discharge	30 days post-discharge
ICU Transfer	Binary	11:59pm on day of admission	Admission duration
Anticipating Lab Test Results			
Thrombocytopenia	4-way multiclass	Immediately before result	Next result
Hyperkalemia	4-way multiclass	Immediately before result	Next result
Hypoglycemia	4-way multiclass	Immediately before result	Next result
Hyponatremia	4-way multiclass	Immediately before result	Next result
Anemia	4-way multiclass	Immediately before result	Next result
Assignment of New Diagnoses			
Hypertension	Binary	11:59pm on day of discharge	1 year post-discharge
Hyperlipidemia	Binary	11:59pm on day of discharge	1 year post-discharge
Pancreatic Cancer	Binary	11:59pm on day of discharge	1 year post-discharge
Celiac	Binary	11:59pm on day of discharge	1 year post-discharge
Lupus	Binary	11:59pm on day of discharge	1 year post-discharge
Acute MI	Binary	11:59pm on day of discharge	1 year post-discharge
Anticipating Chest X-ray Findings			
Chest X-Ray Findings	14-way multilabel	24hrs before report is recorded	Next report

Assignment of New Diagnoses. These tasks are related to predicting the first diagnosis of a disease. They are all binary classification tasks. The prediction time is at 11:59pm on the day of discharge from an inpatient visit, and we count any diagnosis that occurs within 365 days post-discharge as a positive outcome. We ignore all discharges in which the patient already has an existing diagnosis of a disease. The tasks are defined as follows:

- **Hypertension:** Predict whether the patient will have her first diagnosis of essential hypertension within the next year. We define hypertension as an occurrence of the code SNOMED/59621000, as well as its children codes in our ontology.
- **Hyperlipidemia:** Predict whether the patient will have her first diagnosis of hyperlipidemia within the next year. We define hyperlipidemia as an occurrence of the code SNOMED/55822004, as well as its children codes in our ontology.
- **Pancreatic Cancer:** Predict whether the patient will have her first diagnosis of pancreatic cancer within the next year. We define pancreatic cancer as an occurrence of the code SNOMED/372003004, as well as its children codes in our ontology.
- **Celiac:** Predict whether the patient will have her first diagnosis of celiac disease within the next year. We define celiac disease as an occurrence of the code SNOMED/396331005, as well as its children codes in our ontology.
- **Lupus:** Predict whether the patient will have her first diagnosis of lupus within the next year. We define lupus as an occurrence of the code SNOMED/55464009, as well as its children codes in our ontology.

- **Acute MI:** Predict whether the patient will have her first diagnosis of an acute myocardial infarction within the next year. We define myocardial infarction as an occurrence of the code SNOMED/57054005, as well as its children codes in our ontology.

Anticipating Chest X-ray Findings. The chest X-ray findings task is a multilabel classification task to identify which of 14 possible findings were included in a chest X-ray report. The prediction time is 24 hours before the radiology report is recorded. The labels are derived by running the CheXpert NLP labeler on the unstructured text of the corresponding radiology report [14]. We do not release this unstructured text as part of our dataset due to patient privacy concerns.

The possible findings are as follows: "No Finding", "Enlarged Cardiomediastinum", "Cardiomegaly", "Lung Lesion", "Lung Opacity", "Edema", "Consolidation", "Pneumonia", "Atelectasis", "Pneumothorax", "Pleural Effusion", "Pleural Other", "Fracture", "Support Devices".

C.4 Dataset Format

Our dataset is comprised of two main sets of tabular files: **(A) Events** files which contain all of the clinical events associated with every patient in our dataset, and **(B) Labels** files which contain the labels associated with all of our benchmark tasks for every patient in our dataset.

(A) Events is as a set of CSV files containing every clinical event that happened to the patients in our dataset. Every row is a unique clinical event. Each CSV file shares the same column schema, which is as follows:

- **Patient ID** - Integer - Unique identifier for patient
- **Start** - Datetime - Start time of event
- **End** - Datetime (optional) - End time of event
- **Code** - String - Name of the clinical event (e.g. "SNOMED/3950001" or "ICD10/I25.110")
- **Value** - Float/String (optional) - Either a numerical value associated with an event (e.g. a lab test result) or a string associated with a categorical variable (e.g. "Yes/No" questions)
- **Unit** - String (optional) - Unit of measurement for **Value**
- **Visit ID** - Integer (optional) - Unique identifier for the visit during which this event occurred
- **OMOP-CDM Table** - String - Name of the source OMOP-CDM table where this event was recorded

Every event is associated with the OMOP-CDM table in the source STARR database from which it was taken (**OMOP-CDM Table**) [35]. Researchers unfamiliar with the OMOP-CDM can simply ignore this column.

(B) Labels is a set of CSV files containing the labels for every task for every patient. Every row is a unique label associated with a specific patient, task, and time point. Each CSV file shares the same column schema, which is as follows:

- **Patient ID** - Integer - Unique identifier for patient
- **Prediction Time** - Datetime - Time at which the prediction for this label is made
- **Value** - Boolean / Integer - Value for this label. Boolean if task is binary classification. Integer if task is multiclass or multilabel classification.
- **Label Type** - String - Type of task associated with this label. Can be "boolean" (binary classification), "numeric" (regression), "survival" (time-to-event), or "categorical" (multilabel or multiclass classification).

C.5 Data Preprocessing

The source dataset we use, the Stanford STARR research database [5], is an Observational Medical Outcomes Partnership Common Data Model (OMOP-CDM) [12] compliant transformation of data extracted from Stanford’s production EHR system (Epic). We do not alter any of the transformations or deidentification steps in the ETL used to generate this OMOP-CDM extract described in [5].

Following the best practices of the MIMIC-III dataset, we apply several additional custom transformations to prevent data leakage and add an additional layer of patient privacy protections [17]. First, we jitter all dates within each patient timeline by the same random amount (to a random year between 2100 and 2200). Second, we remove all patients ≤ 18 or ≥ 89 years of age. Third, we remove all instances of free form text (i.e., notes and narratives). For the clinical events which take on categorical values specified as strings (e.g. a questionnaire which can be answered "Yes" or "No"), we select the top-100 most representative such categorical text strings, manually verify that they do not contain any PHI, and remove the rest of the text strings from our model release by replacing them with blank strings. This preserves roughly 65% of all categorical values in our dataset. Fourth, we remove any patients with less than 10 clinical events in their record. Fifth, we adjust the timing of certain events to more realistically reflect the chronology of care delivery. Specifically, we move any events recorded before a patient’s birth to after their time of birth; we set the start times of visits equal to the start time of the first event in each visit; we move billing codes recorded during a visit to the end of the visit; we move any event coded at midnight to 11:59pm of that day; we remove all duplicate codes that occur sequentially on the same day; and we remove all codes with ‘None’ values that occur on the same day as an identical code with a non-‘None’ value associated with it. These transformations are all specified in code in our Github repo.

C.6 Cohort Selection Process

We selected a cohort of 6,739 patients for EHRSHOT from the larger STARR source dataset of 3.67M patients. Per the motivation of this project, we were primarily interested in few-shot evaluation of models across diverse tasks. Several of the tasks that would be of interest to a health system, however, have fairly low prevalence within the general patient population. Thus, we needed to construct our cohort in a way that preserved sufficient positive labels to enable downstream models to conduct few-shot learning. We aimed to have at least $k = 128$ positive and negative examples in each of the train/val/test splits for every task that we considered in order to allow for a broad range of few-shot learning scenarios, and at least $k = 128$ positive examples for each label within a multiclass or multilabel classification task. Where this was not possible (e.g. the Celiac task), we included as many positive labels in each split as possible.

We began with our set of 15 tasks of interest. For each task, we labeled all patients within our source database per that task’s definition. For tasks that have a low prevalence (which we consider as a 1:5 ratio of positive to negative labels), we subsample negative labels to bring the prevalence of positive labels up to that ratio. We then subsample further for few-shot evaluation, selecting 128 unique patients for each split who have at least one positive label for the task. We then sample sufficient negative labels to maintain the chosen prevalence. We repeat this process for all tasks to arrive at our final cohort of patients. For each successive task, we prioritize selecting patients that have already been sampled into our cohort to reduce the total number of patients added to our cohort (since some patients have positive labels for multiple tasks).

D Results Details

In order to fully reproduce our results, please follow the instructions at our Github repo here: <https://github.com/som-shahlab/ehrshot-benchmark>.

D.1 Problem Formulation

Our dataset and models can be formulated as follows. Our dataset $\mathcal{D} = (\{\mathbf{X}_p, \mathbf{Y}_p\})_{p=1}^{|\mathcal{P}|}$ contains the full coded medical timeline (\mathbf{X}_p) and task-specific set of labels (\mathbf{Y}_p) for each patient $p \in \mathcal{P}$, for a total of $|\mathcal{P}|$ patients. Each patient p is defined by a sequence of clinical events $\mathbf{X}_p = \{x_{p1}, x_{p2}, \dots, x_{pn}\}$, where x_{pi} denotes the i th code in the timeline of patient p . Note that a code x_{pi} can be any form of structured data taken from the patient's EHR, including a diagnosis, procedure, medication prescription, lab test, etc. We define $\mathbf{X}_p^{(t)}$ to be the patient timeline up to time t – i.e. if event x_{pj} occurs before or at t but $x_{p(j+1)}$ occurs after t , then if $\mathbf{X}_p = \{x_{p1}, \dots, x_{pj}, x_{p(j+1)}, \dots, x_{pn}\}$ we have that $\mathbf{X}_p^{(t)} = \{x_{p1}, \dots, x_{pj}\}$.

In addition to the timeline of each patient, our dataset also contains labels for each task and patient. We define benchmark tasks $b \in \mathcal{B}$, where $|\mathcal{B}| = 15$ for our dataset. Each patient has a set of labels $\mathbf{Y}_p = \{y_{pb_1}^{(t_1)}, y_{pb_1}^{(t_2)}, \dots, y_{pb_1}^{(t_L)}\}$, where L is the total number of labels for patient p , and the expression $y_{pb_i}^{(t_j)}$ represents the label for patient p for task b_i at time point t_j .

We are interested in making predictions of the following format: Given a patient p 's entire medical history up to and including time point t (i.e. $\mathbf{X}_p^{(t)}$), predict the value of $y_{pb}^{(t)}$ for each corresponding benchmark task $b \in \mathcal{B}$ where such a label exists.

Please note that this prediction task is at the level of individual clinical events rather than visits/encounters.

D.2 Count-Based GBM

We train a LightGBM model as one of our baseline models. In order to train such a model on a patient's timeline, we must first featurize the timeline into a vector. We follow best practices for competitive baseline models by using count-based featurization, in which a patient is transformed into a vector containing the counts of how many times each clinical event has occurred in that patient's timeline prior to the prediction time point [32, 42].

Let \mathcal{C} be the set of all unique medical codes in our dataset. Let us consider making a prediction for patient p at time t . Then the count-based featurization for p at time t is given by the vector $\mathbf{p}^{(t)} \in \mathbb{N}^{|\mathcal{C}|}$, where each element is defined as $\mathbf{p}_i^{(t)} = \sum_{x_j \in \mathbf{X}_p^{(t)}} I(x_j = i)$, i.e. the count of medical code i recorded for patient p before the prediction time t . Stacking these patient vectors results in a count matrix $\mathbf{M} \in \mathbb{N}^{|\mathbf{Y}| \times |\mathcal{C}|}$. As there are hundreds of thousands of unique codes, most of which occur infrequently among patients, this results in a very high-dimensional and sparse matrix.

To help address the sparseness of \mathbf{M} , we use a technique called *ontology expansion* [4], in which we count each occurrence of a code once for the code itself, and once for every parent node of that code in the OMOP ontology up to the root node of our ontology. Consider the ICD10 code E10.1 (Type 1 diabetes mellitus). Any occurrence of this code in a patient's timeline should also give the patient "credit" for having the parent codes of E10.1 – E10 (Type 1 diabetes mellitus) and E08–E13 (Diabetes mellitus). This is because having E10.1 implies that the patient has E10 and E08-E13. We leverage existing OMOP ontology tools for ontology expansion and map codes to their ancestors. Then, when constructing our count matrix \mathbf{M} , we count each occurrence of a code for both that code and all of its parent codes. We refer to this ontology-expanded version of our count matrix as \mathbf{M}' .

Once the ontology-expanded count matrix \mathbf{M}' is generated, a LightGBM model is trained on this input to predict the target label for each task [18]. Hyperparameter tuning is performed on a validation set following the schedule described in Table 9.

D.3 CLMBR-T-base

For CLMBR-T-base, each unique medical code $c \in \mathcal{C}$ is associated with a d -dimensional embedding $e^c \in \mathbb{R}^d$. Each medical code $x_{pi} = c$ in patient p 's timeline is associated with both a code embedding

e^c and a position embedding e^s which is defined using rotary positions embeddings [43]. Thus, the input to the model for x_{pi} is given by the concatenation of these vectors, i.e. $e^c \parallel e^s$. For our model, the code embeddings e^c are generated using a standard embedding layer with a vocabulary size of $|\mathcal{C}| = 65,536$. Though there are more unique codes in our dataset, we only keep the top 65,536 codes with the highest contribution to the overall entropy of the dataset – the rest of the codes occurring in our dataset are discarded in order to keep the size of our model’s dictionary tractable.

Lab values were discretized by computing decile statistics over the entire dataset and then creating tokens for each lab / decile pair. For example, if the 40th percentile of weight is 180 pounds and the 50th percentile is 190 pounds, we would create one token for “Weight/180-190” which would represent all events with values in that range.

Given this fixed dictionary, a classification task is defined to predict the next code in a patient’s timeline given their preceding codes. We use a transformer as our classification model. Our transformer uses a local attention mechanism with a fixed context window of 496 tokens (i.e. clinical events) per layer. As our CLMBR model contains 12 stacked layers, this gives our model an effective context window of $496 * 12 = 5,952$ clinical events, on which it conditions to generate its output at each step i . Sequences longer than that were truncated.

The output at step i is a d -dimensional vector representation of the cumulative information up to and including event x_{pi} . We stack these representations for patient p into a matrix $\mathbf{R}_p \in \mathbb{R}^{|\mathbf{X}_p| \times d}$ such that $\mathbf{R}_{p,i}$ is the cumulative d -dimensional representation of all events up to and including event i for patient p . We then take the dot product of each row in this matrix with every code embedding e^j for all $j \in \mathcal{C}$ in order to calculate a logit for each code j at each event i , thus yielding: $\text{logit}_{pij} = \mathbf{R}_{p,i} \cdot e^j$. The model is then trained end-to-end using standard cross-entropy classification log-likelihood loss, employing an indicator variable I_{pij} to mark if the next event for patient p after event i is an event with code j .

The overall loss function, $L(I|\text{logit})$, is computed as:

$$L(I|\text{logit}) = \prod_{p,i,j} I_{pij} \cdot \text{softmax}(\text{logit}_{pi})_j$$

For training our model, we use the best hyperparameters identified in [8] and perform a limited hyperparameter search as defined in 8.

Table 8: CLMBR-T-base Hyperparameters

Name	Values	Best Value
Learning Rate	0.0001, 0.00001	0.00001
Context Window Size	496	496
Internal Dropout	0, 0.2, 0.4	0
# of Layers	6, 12	12
LR Head Learning Rate	1e-6, 1e-5, ..., 1e5, 1e6	Task dependent
Hidden dimension	768	768

Table 9: GBM Hyperparameters

Name	Values	Best Value
Learning Rate	0.02, 0.1, 0.5	Task-dependent
Max Depth	3, 6, -1	Task-dependent
Number of Leaves	10, 25, 100	Task-dependent

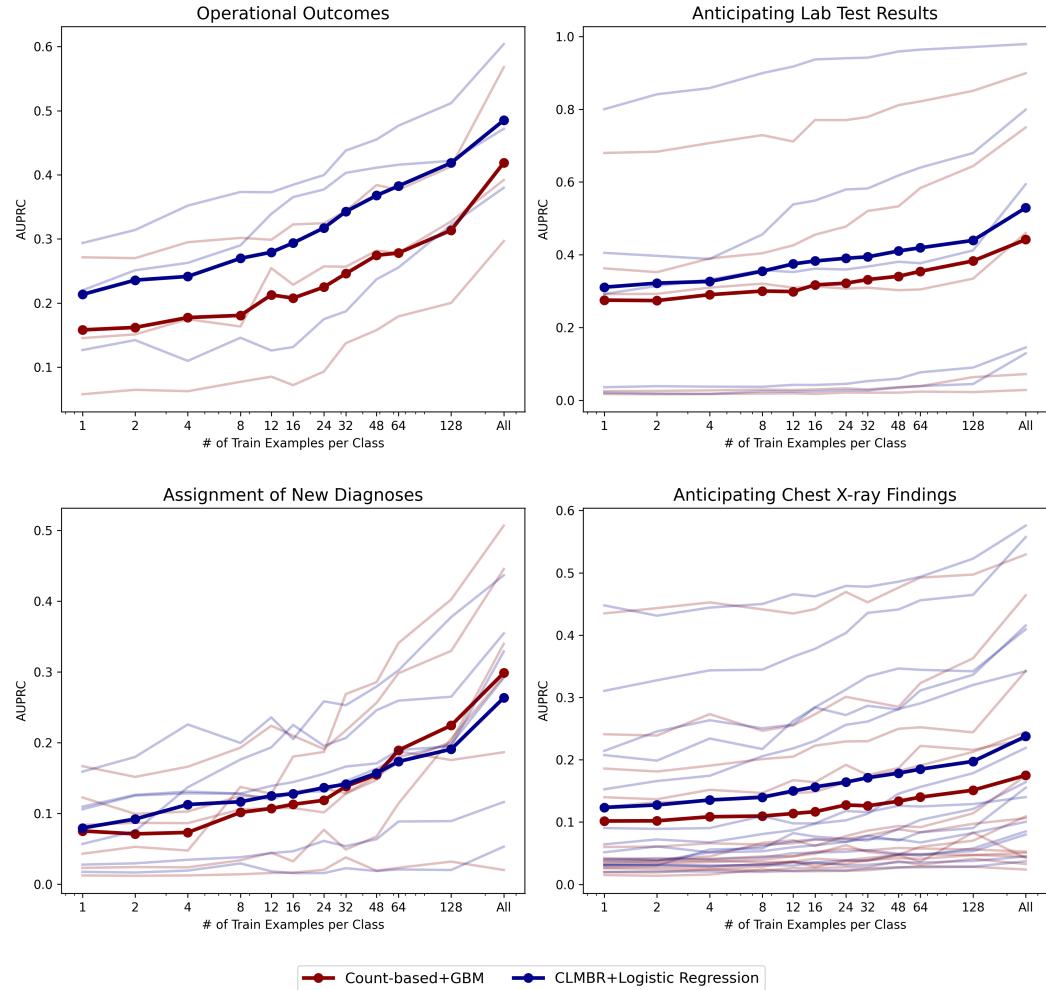


Figure 5: Aggregated AUPRC across all subtasks within each of the 4 task categories for $k \in \{1, 2, 4, 8, 12, 16, 24, 32, 48, 64, 128\}$ shots. We also show performance on the full training set as *All*. The **bolded lines** are the Macro-AUPRC for each model, averaged across all subtasks within a task category for each value of k . The blurred lines are the average AUPRC across 5 replicates for each subtask within a task category. Similar to the case with AUROC, the pretrained foundation model CLMBR-T-base (blue) performs better across all k on the *Operational Outcomes*, *Anticipating Lab Test Results*, and *Anticipating Chest X-ray Findings* tasks, while the count-based GBM model (red) performs slightly better at higher k on the *Assignment of New Diagnoses* tasks.

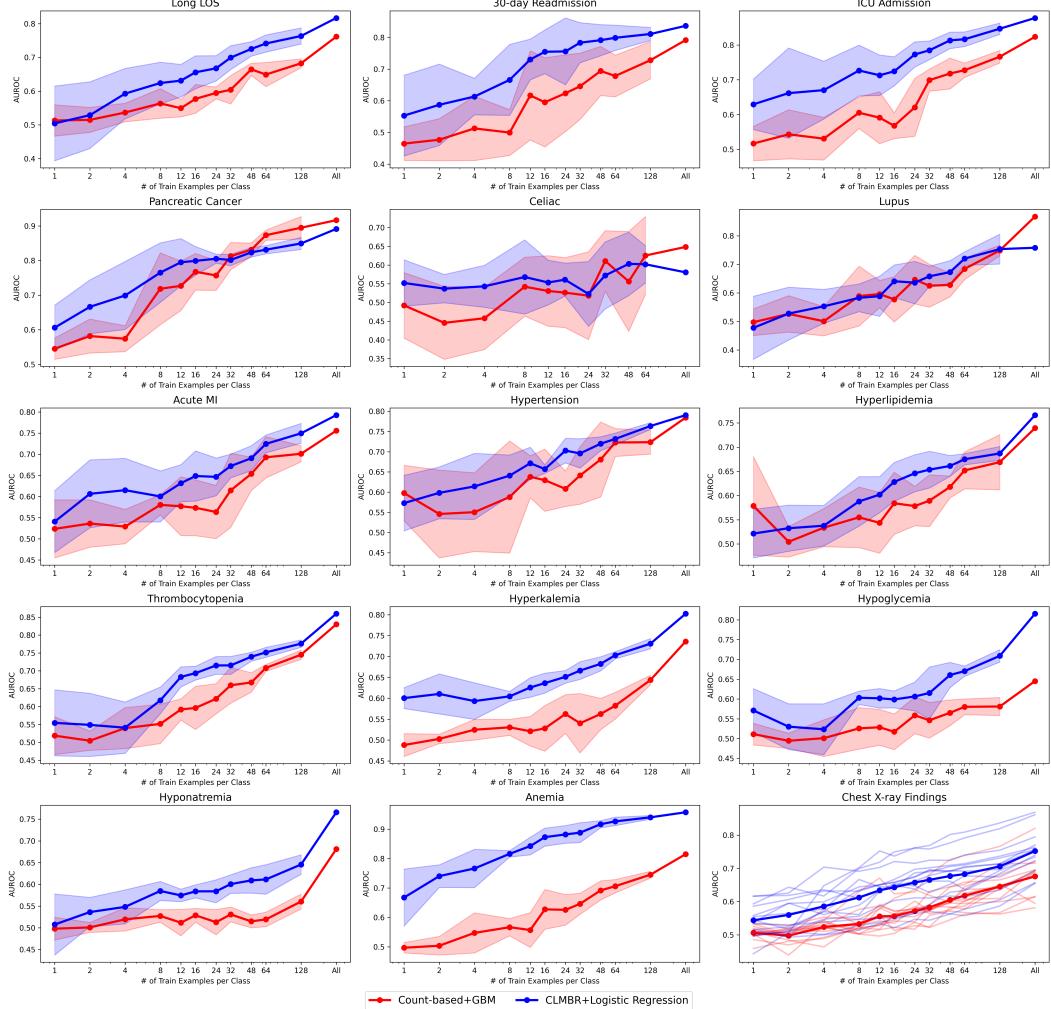


Figure 6: AUROC scores for each model across $k \in \{1, 2, 4, 8, 12, 16, 24, 32, 48, 64, 128\}$ shots. We also show performance on the full training set as *All*. The pretrained foundation model CLMBR-T-base (**blue**) shows stronger performance on *Operational Outcomes* and *Anticipating Lab Test Results* tasks, while the count-based GBM model (**red**) exhibits competitive performance at higher values of k for the *Assignment of New Diagnoses* tasks. For *Chest X-ray Findings*, each blurred line represents one of the 14 individual labels, and the bolded line is macro-AUROC across all labels.

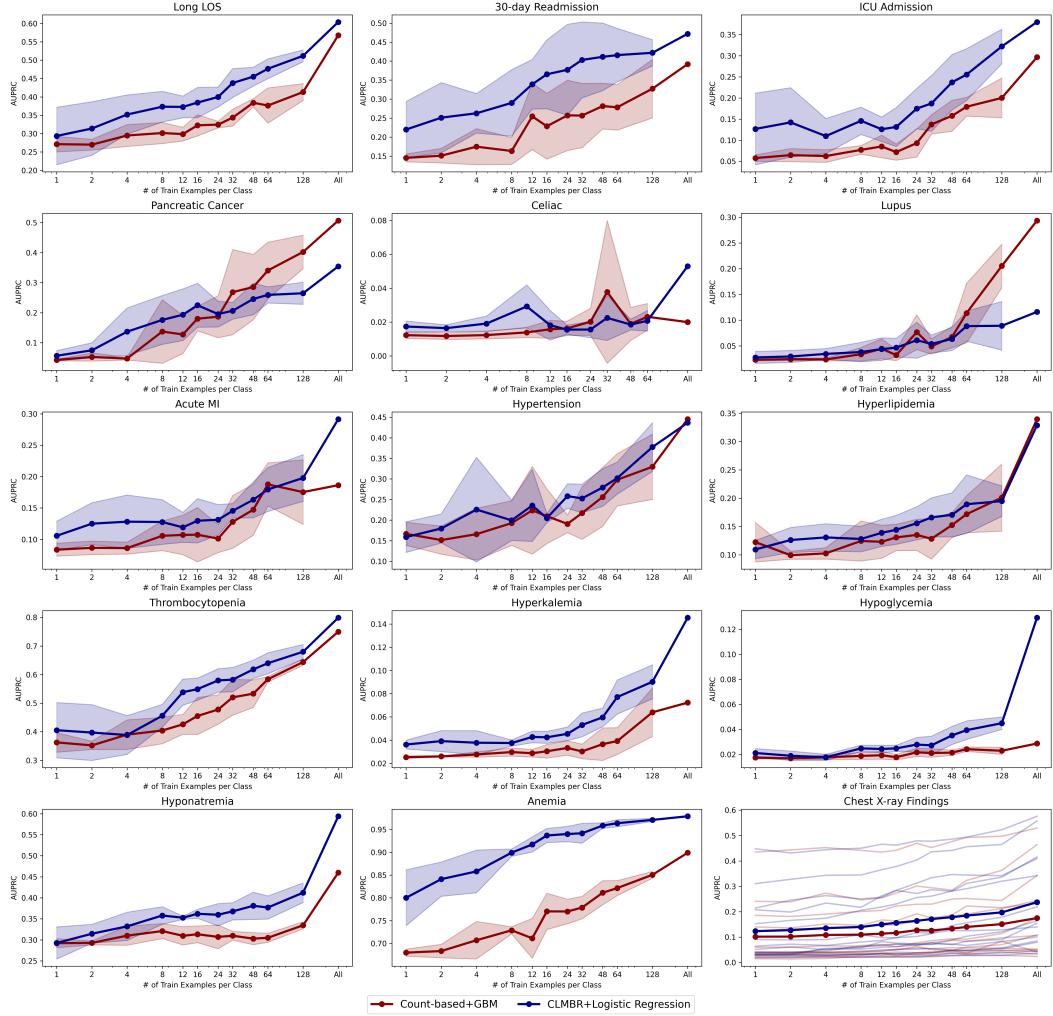


Figure 7: AUPRC scores for each model across $k \in \{1, 2, 4, 8, 12, 16, 24, 32, 48, 64, 128\}$ shots. We also show performance on the full training set as *All*. CLMBR-T-base is in **blue**, count-based GBM model is in **red**. For *Chest X-ray Findings*, each blurred line represents one of the 14 individual labels, and the bold line is macro-AUPRC across all labels.

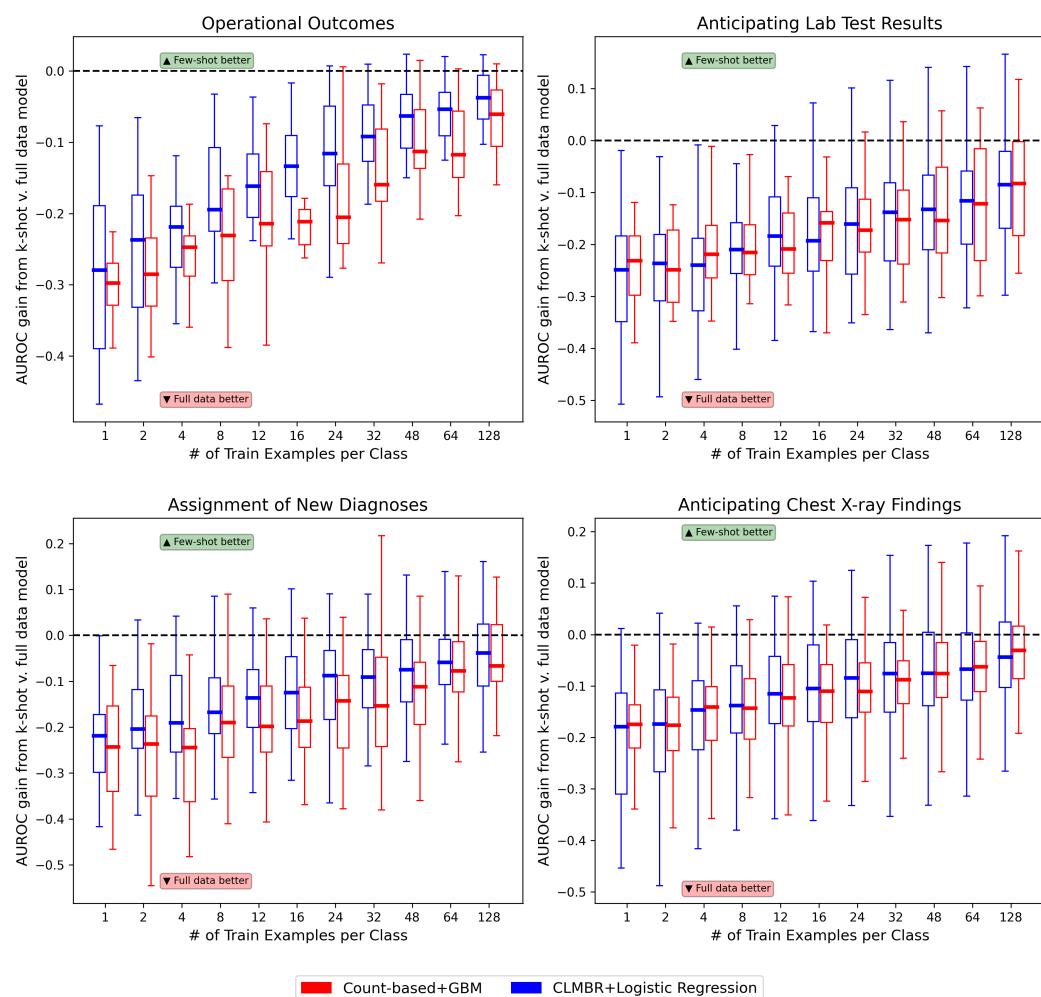


Figure 8: Difference in AUROC between each k -shot model replicate and a model trained on the full dataset. The pretrained foundation model CLMBR-T-base (blue) closes the gap with the full data model faster than does the count-based GBM model (red).

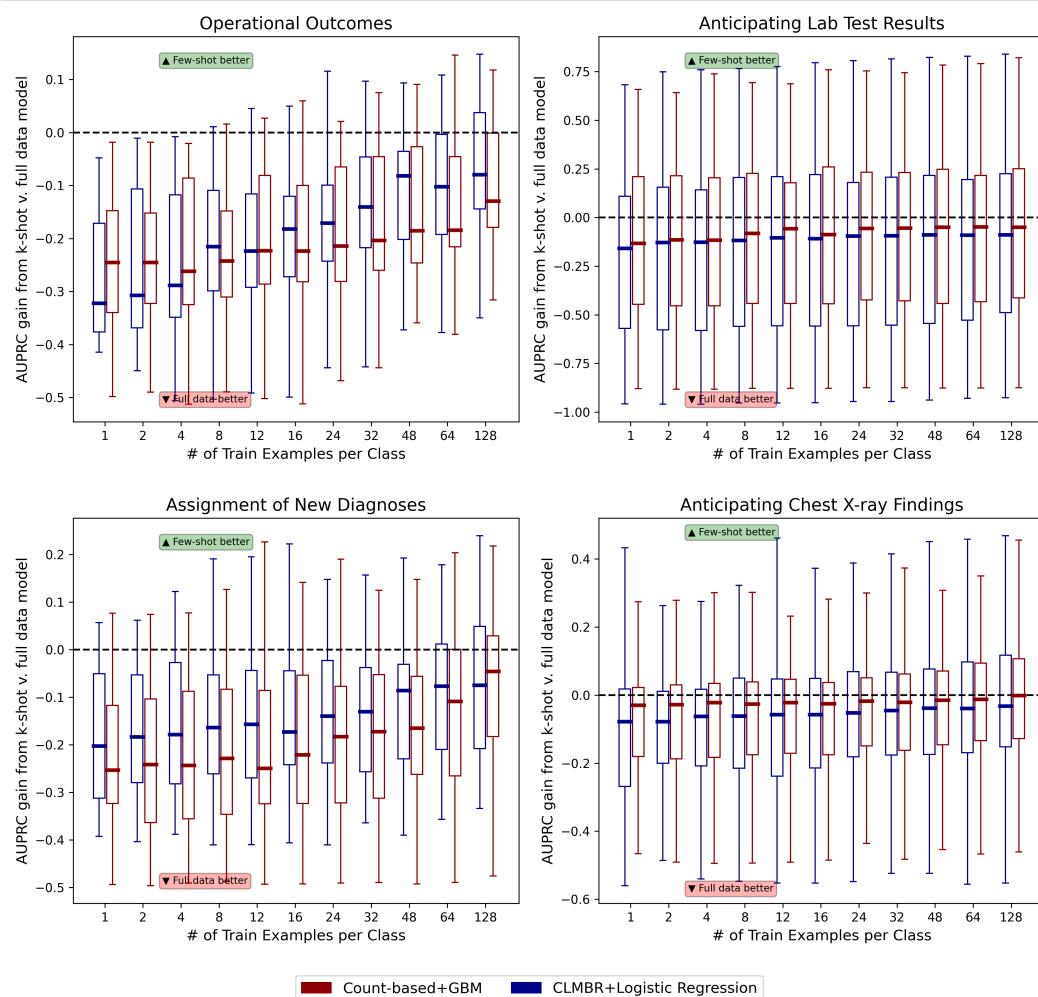


Figure 9: Difference in AURPC between each k -shot model replicate and a model trained on the full dataset. The pretrained foundation model CLMBR-T-base (blue) closes the gap with the full data model faster than does the count-based GBM model (red).

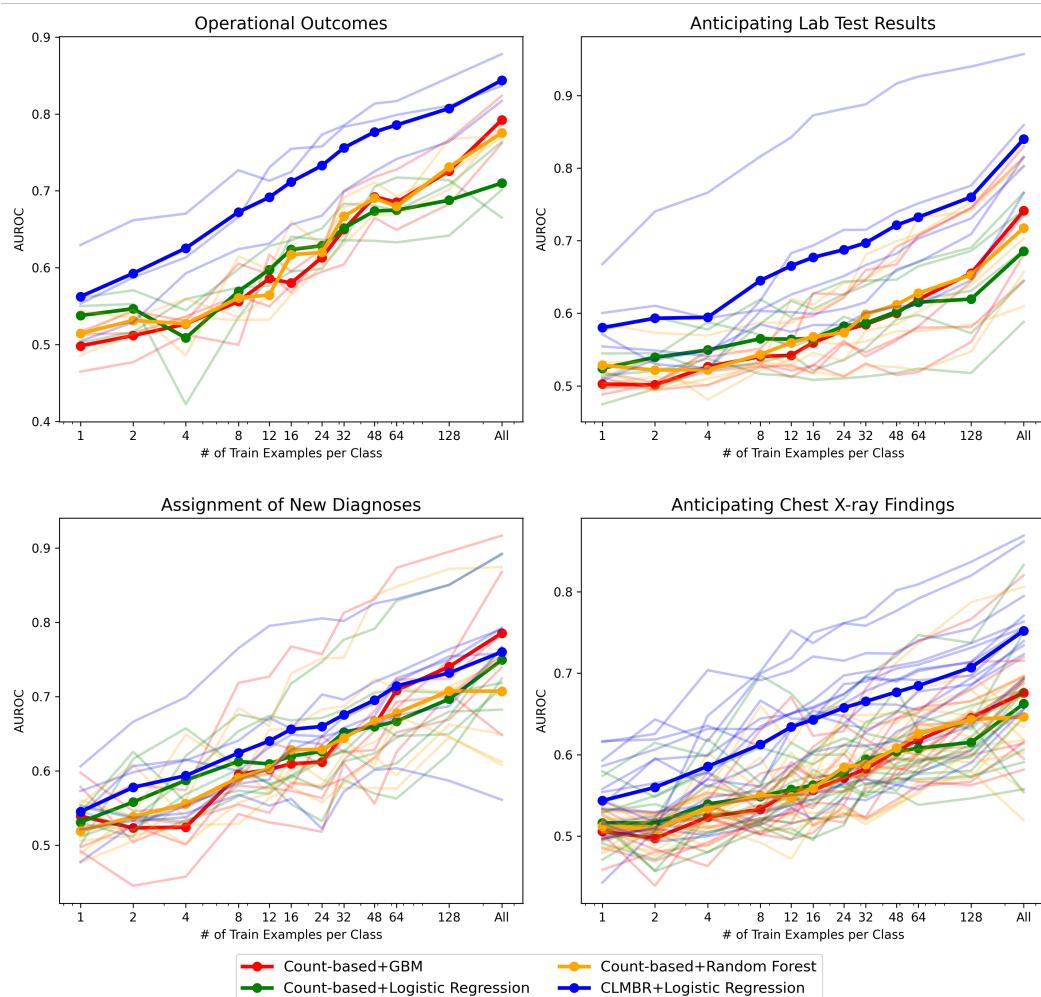


Figure 10: Replication of Figure 3 for aggregated AUROC, but including the following baseline models: CLMBR-T-base (blue), GBM (red), Random Forest (yellow), and Logistic Regression (green).

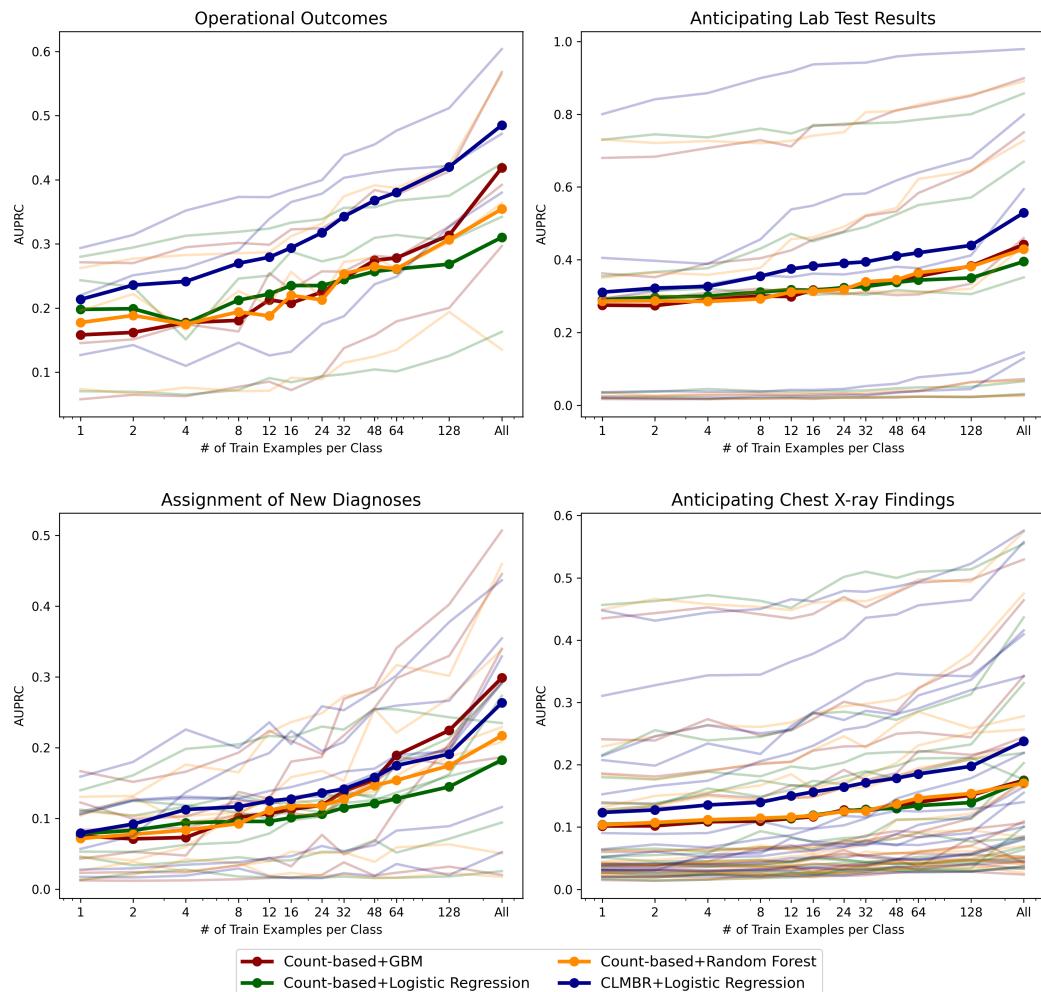


Figure 11: Replication of Figure 5 for aggregated AUPRC, but including the following baseline models: CLMBR-T-base (blue), GBM (red), Random Forest (yellow), and Logistic Regression (green)