Interpretable (not just posthoc-explainable) medical claims modeling for discharge placement to prevent avoidable all-cause readmissions or death

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Abstract

We developed an inherently interpretable multi-level Bayesian framework for representing variation in regression coefficients that mimics the piecewise linearity of ReLU-activated deep neural networks. We used the framework to formulate a survival model for using medical claims to predict hospital readmission and death that focuses on discharge placement, adjusting for confounding in estimating causal local average treatment effects. We trained the model on a 5% sample of Medicare beneficiaries from 2008 and 2011, based on their 2009–2011 inpatient episodes, and then tested the model on 2012 episodes. The model scored an AUROC of approximately 0.76 on predicting all-cause readmissions (defined using official CMS methodology) or death within 30-days of discharge, being competitive against XGBoost and a Bayesian deep neural network, demonstrating that one need-not sacrifice interpretability for accuracy. Crucially, we provide what blackboxes cannot – the exact gold-standard global interpretation of the model, identifying relative risk factors and quantifying the effect of discharge placement. We also show that the posthoc explainer SHAP fails to provide accurate explanations.

1 Introduction

Preventable readmission after hospital discharge is costly. In 2011, for adult 30-day all-cause hospital readmission in the United States, the cost was about $41.3 billion [Hines et al., 2014]. To improve outcomes, Medicare, through its Hospital Readmissions Reduction Program (HRRP) [McIlvennon et al., 2015], penalizes providers for readmissions that occur within the 30-days after discharge; penalties have spurred interest in interventions surrounding transitions of care including discharge planning services such as hand-offs to less-intensive healthcare institutions. Population-level medical claims data make it possible to assess the efficacy of these interventions retroactively. This manuscript focuses on the problem of deciding discharge placement for individuals in order to prevent readmission or death.

Readmission models: A recent review [Huang et al., 2021] surveyed properties of readmission models in the literature. By and large, they found no model type to perform consistently better than others, though several studies have reported marginal improvements using either XGBoost or neural networks over logistic regression [Shameer et al., 2016, Jamei et al., 2017, Allam et al., 2019, Liu et al., 2020, Min et al., 2019, Futoma et al., 2015, Larsson et al., 2021]. Generally, the literature has focused on 30-day readmissions, though nuances in how readmission is defined complicate direct performance comparisons. Models based on medical claims data typically achieved AUROC of approximately 0.70 for predicting their version of all cause 30-day readmission.

Another factor that complicates the direct comparison of modeling efforts is differences in datasets – and hence the underlying patient populations. We are aware of two readmission studies performed on datasets identical to ours. Lahlou et al. [2021] created an attention-based neural network for predicting admissions after discharge within 30-days and reported an AUROC value of 0.81, however, they did not distinguish between transfers, planned admissions, and acute admissions in their outcome label so they solve a different problem that is of less practical utility. More related to our work, MacKay et al. [2021] developed XGBoost models for predicting a set of adverse events, reporting an AUROC of 0.73 for all-cause readmission prediction.
Yet, having a high AUROC is insufficient for making a model useful. A model needs transparency in order to assess its validity. Most studies surveyed were aware of the importance of model interpretability, claiming their blackbox model to be interpretable. Yet, most studies that claim interpretability for their blackbox solutions only offer “posthoc explainability,” a catch-all phrase for narratives generated in order to promote a sense that a model is interpretable when it is not.

**Interpretability:** The goal of interpretable modeling is to produce predictions that an end-user can understand [Rudin, 2019, 2014], which is a prerequisite for making a prediction actionable. However an understandable explanation must always be true, which cannot be guaranteed in blackbox models. For this reason, a significant disconnect separates blackbox models from inherently interpretable models. Fig. 1 is a representation of the spectrum of interpretability focusing on structured data problems in healthcare.

There is also a distinction between computational interpretability and prediction comprehensibility. ReLU-activated neural networks, matrix composition methods like principle components analysis (PCA), and multiple regression models are computationally interpretable, whereas Deep Learning (DL) models in-general and ensemble trees methods like XGBoost are not.

However, knowing how a prediction is computed from individual features does not automatically make the prediction comprehensible – it may still difficult to understand how a model behaves as there is a limit to the capacity of information that humans can process simultaneously [Miller, 1956]. Sudjianto and Zhang [2021] note that additivity, sparsity, linearity, smoothness, monotonicity, and visualizability are some attributes of interpretable models that are also comprehensible.

The highest bar for interpretability is for a model to be mechanistically meaningful. These models often leverage domain knowledge and are capable of providing deep and robust insights. They also often justify causal interpretations [Peters et al., 2020]. Even if one can truly understand a model, one often cannot act on it. To be directly actionable, a model also needs to adjust for biases in the data so that its prediction of the effects of interventions can be interpreted causally [Pearl, 2009]. Yet, independent of causal understanding, model interpretability is still important because it allows practitioners to better understand the risks and biases of a given model.

**Post-hoc explainable-AI (xAI):** Posthoc xAI is a set of techniques to market blackbox models as interpretable (Fig. 1). The most popular xAI methods (LIME [Ribeiro et al., 2016] and SHAP [Lapovetsky and Conklin, 2001; Datta et al., 2016]), use approximations [Lundberg and Lee, 2017; Aas et al., 2021] to provide narratives of feature importance within a prediction. Other methods such as attention [Niu et al., 2021] build an explanation mechanism as a module within a blackbox model in order to more easily compute them. [Jain and Wallace, 2019; Zhou et al., 2022]. Narratives, convincing as they might seem, are not necessarily true. In fact, researchers have shown [Laugel et al., 2019; Kumar et al., 2020; Slack et al., 2020; Alvarez-Melis and Jaakkola, 2018; Zhou et al., 2022] that these methods provide imprecise and unreliable explanations of models, and often disagree. Aptly, Krishna et al. [2022] coined this the “disagreement problem” with posthoc interpretability and conducted a survey of real world data scientists finding no consistent or principled method to handle these inconsistencies. As Rudin [2019] notes, “an explanation model that is correct 90% of the time is wrong 10% of the time.” Despite marketing claims, xAI does not carry blackbox models across even a very minimal bar of requirements for interpretability. If an explanation is not true to one’s model, any sense that the model is comprehensible is based on faulty information.

**Blackbox models:** Methods such as Deep Learning (DL) and ensemble boosted trees (XGBoost, LightGBM, others) can model nonlinearities. When copious training data is available, these methods yield models that are more expressive than traditional generalized linear models. Most-generally, blackbox models like DL and ensemble trees are nonlinear kernel machines (function interpolations) [Domingos, 2020]. The convoluted nature of their interpolations makes these models uninterpretable.

Massive investment exists in these models because of their predictive performance and low effort. This existing investment, the challenge of creating truly interpretable models, and a myth that blackboxes perform better than interpretable models [Rudin, 2019], incentivize the marketing of posthoc-xAI as an alternative to interpretable modeling.

In finance, a similarly high-stakes domain, there has been wide resistance to blackbox modeling, formalized recently in model risk management guidelines published by The Office of the Comptroller of the Currency (OCC) [2021]. We should also reject the use of these models in healthcare, where the risk to patients requires truly trustworthy solutions.

**Deep learning (DL):** Blackboxes provide clues on how to extend traditional linear models. DL is the application of artificial neural networks (ANNs) to prediction problems. ANNs consist of sequences (or more generally of graphs) of successive affine matrix arithmetic operations, sandwiched between activation functions. In general, these methods are blackboxes, with the exception of ReLU-activated neural networks (ReLU-nets for short). Examining ReLU-nets elucidates the nature of how DL captures nonlinearities. ReLU-nets use the activation function

$$ReLU(x) = \begin{cases} 0 & \text{if } x \leq 0 \\ x & \text{otherwise} \end{cases}$$ (1)
In these models, Eq. (1) is independently applied to each matrix coordinate after each successive matrix operation. The output of the function is nonzero if and only if a linear combination of the elements computed by the prior layer are positive. Hence, ReLU defines an inequality over quantities within the model – applied to each coordinate within each layer, ReLU defines recursive sets of inequalities. These inequalities collectively segment the training data into disjoint regions. In sum, ReLU-nets are composed of regionally-disjoint generalized linear models – each of which is interpreted in the same manner as linear regression. Hence, ReLU-nets are computationally interpretable. The salient nonlinearity of these models is locality. To interpret a specific prediction given by these models, one needs to map the input to a particular linear submodel. Then, conditional on this mapping, a ReLU net can be interpreted as a tool for exactly interpreting trained ReLU neural networks, by unwrapping the cascades of inequalities. In this manuscript we mimic this property of ReLU-nets within a well-controlled multilevel Bayesian regression framework in order to gain expressiveness while prioritizing interpretability.

2 Methods

Figure 1: Model interpretability lies along a spectrum with a clear chasm existing between intrinsically interpretable models others. More-interpretable models are more trustworthy and insightful.

Figure 2: The wait time $T$ is the time (in days) between discharge of an index episode and the next unplanned acute inpatient admission.

We generalize the classic readmission problem of within 30 days of discharge, to the likelihood of readmission at any arbitrary day after discharge. To this end, our objective is to characterize the statistics of the inter-inpatient wait time $T_n$ (Fig. 2). Additionally, we focus on identifying the effects of discharge placement, representing the choices symbolically as $I_n$, ranked in terms of health acuity:

0. discharge home
1. discharge home with home health
2. discharge to skilled nursing
3. intermediate care/critical access
4. long term care
5. other less-acute inpatient.

The issue that complicates the estimation of discharge placement effects is unobserved confounding – providers use the patient’s health status in order to decide placement. To resolve the treatment assignment bias, we model the joint outcomes

\[
I_n \sim g(I_n | x_n, \nu_n, \xi_n),
\]

\[
T_n \sim f(T_n | x_n, I_n, \alpha_n, \beta_n, \gamma_n)
\]

where $x_n \in \mathbb{R}^p$ is a covariate vector and we explicitly adjust for assignment bias. Note that we distinguish between the scalar-valued $I_n$, which corresponds to the list of interventions above, and the vector valued $I_n$ which we will explain later in this manuscript.

For the sake of interpretability, we formulate $f$ and $g$ in Eq. 2 as hierarchical multilevel Bayesian generalized linear regression models. However, to increase expressivity by introducing the type of nonlinearity seen in ReLU-nets, we allow all of the model parameters $\alpha_n, \beta_n, \gamma_n, \nu_n, \xi_n$ to vary locally across regions defined by $x_n$, in ways that comport with domain knowledge.

2.1 Data Preprocessing

The available dataset, the CMS Limited Dataset (CMS LDS), consists of a national 5% beneficiary sample of Medicare FFS Part A and B claims from 2008 to 2012. The 2008 claims had only quarter date specificity so we used them solely to fill out the medical history for 2009 inpatient stays, by assuming that each 2008 claim fell in the middle of its given quarter. We trained the readmission models on 2009 – 2011 admissions, and evaluated the models on 2012 admissions.

After grouping claims into coherent episodes, based on date, provider, and patient overlap, we filtered for inpatient-specific episodes with certain characteristics to use as index admissions. We retained only episodes where the
patient had a continuous prior year of Part A/B enrollment. We also excluded episodes from consideration as index episodes if they did not correspond to discharges to less-intensive care (excluding death and most inpatient-to-inpatient transfers). Additionally, we used the official CMS methodology for determining whether each episode is a planned admission, acute admission, or potentially planned admission [201]. For each episode we then computed the waiting time to either the next unplanned acute episode or death, or until censorship due to the end of the observation window. In the end, the training dataset consisted of approximately 1.2 million inpatient episodes, of which approximately 17% were followed by an unplanned acute inpatient episode or death within 30 days. The histogram of the wait times is presented in Fig. 3.

Figure 3: Histogram of the wait time after discharge to the next acute admission or death.

For each episode, we collected all billing codes, creating lists of concurrent procedure and diagnostic codes. Additionally, we collected the preceding four quarters of his history for each episode, aggregating billing codes on a lagged quarterly basis.

**Feature engineering:** Medical claims data consists of series of billing codes in several dialects (ICD9/10, HCPCS, RUG, HIPPS, etc). We down-sampled diagnostic (Dx) and procedure (Tx) codes, from their original dialects to multilevel Clinical Classification Software (CCS) codes [HCU]. CCS codes are clinically curated hierarchical categories that are more tractable for analysis and interpretation. Mapping to CCS drastically decreases the dimensionality of the dataset and helps to extract the health-specific information in billing codes buried noisy reimbursement-specific details.

We used AHRQ Healthcare Cost and Utilization Project (HCUP) databases in order to tag codes for comorbidities, chronic conditions, surgical flags, utilization flags, and procedure flags. Included within skilled nursing facility (SNF) and home health (HH) claim codes are also activities of daily living (ADL) assessments. We converted these codes to ADL scores, where higher scores correspond to lower functional ability. We also incorporated CMS’s risk adjustment methodology, hierarchical condition categories (HCC), as model predictors.

The CMS LDS contains beneficiary county codes that we used to incorporate the urban rural index and social economic scale as model features. Together with beneficiary race information and Medicaid state buy-in, these variables allowed for some measure of social determinants of health.

We encoded CCS and other code mappings into numerical vectors by counting the incidences of each permissible code. In the case of CCS, which is multilevel, we truncated codes at each of the first two levels and counted at each level. Altogether, the numerically encoded derived features constituted a vector of size $p = 1072$, which encompassed both concurrent episode codes and the past four quarters of history, where CCS was truncated to the first level for history.

**Feature quantization:** To improve model interpretability, we made an effort to place all model parameters (log hazard ratios) on the same scale so that the magnitudes of the parameters are directly comparable. In examining our derived data features, we came to find that they were predominantly sparse and heavy tailed. This finding, and our desire to optimize model interpretability, led us to quantize all numerical variables so that the input variables into the model are entirely binary. To this end, we first computed the percentiles for each feature across the entire dataset. Then we re-coded each quantity into a series of binary variables corresponding to inequalities, where the cutoffs were determined by examining the computed percentiles and eliminating duplicate values. Generally, we retained only the quantized features in specifying the models except when otherwise specified. The total size of the feature vector after dropping all original non-quantized numerical features and all constant features expanded to $p = 3143$.

### 2.2 Survival Modeling

For flexibly modeling the wait time distribution $f$, we use the piecewise exponential survival regression model (PEM) [Friedman 1952]. PEMs are defined by specifying the time-dependent hazard $\lambda(t)$: $\mathbb{R}^+ \to \mathbb{R}^+$ using a piecewise constant function, where the hazard changes across breakpoints that define disjoint time intervals. The probability density function for the PEM follows

$$f(t) = \lambda(t)e^{-\int_0^t \lambda(u)du}.$$  \hspace{1cm} (3)

In this manuscript we set the breakpoints between time intervals at 1 week, 4 weeks, and 9 weeks after discharge. For each episode $ni$, we can estimate a wait time distribution by estimating the log-hazard within each time interval $i$,

$$\log \lambda_{ni} = \alpha_{ni} + \beta'_{ni} x_n + \gamma'_{ni} I_n,$$  \hspace{1cm} (4)

where we allow the model parameters to vary across the data regionally, in a manner that emulates the type of non-linearity seen in ReLU-nets. In Eq. 4 we separate out the discharge placement effects ($\gamma_{ni}$) from other effects ($\beta_{ni}$). Doing so makes it easier to structure the model for causally
interpreting the discharge assignment effects. We incorporate domain knowledge by acuity-ordering the interventions, enforcing monotonicity of intervention effect by constraining the last five coefficients of $\xi_n$ to non-positivity.

**Causal inference:** We model the discharge placement process $g$ using an ordinal logistic regression model, where

$$I_n|p_n \sim \text{Categorical}(p_{n0}, \ldots, p_{n5})$$

$$p_{nk}|x_n, \nu_n, \xi_n = \Pr(I_n \geq k|x_n, \nu_n, \xi_n)$$

$$\Pr(I_n \geq k|x_n, \nu_n, \xi_n) = \logit^{-1}(\nu_{nk} + \xi_n x_n),$$

(5)

where $\xi_n$ are slopes corresponding to episode $n$ and $\nu_n = [\nu_{n1}, \ldots, \nu_{n5}]$ are intercepts under the constraints $\nu_{nk} < \nu_{n,k+1}$, $\forall k, n$. The predictions given by this model then feed back into the prediction of the wait time through a slope term for each of the covariate vector $I_n = [\Pr(I_n \geq 1), \ldots, \Pr(I_n \geq 5)]$. Utilizing the discharge placement probabilities as model covariates allows for the confounding bias caused by the selection process, in a manner analogous to incorporating the local treatment probability as a covariate [Bafumi and Gelman 2007]. Additionally, directly modeling the treatment effects within a multilevel model allows us to infer locally-varying treatment effects, partially pooled for stable inference in regions where the data is sparse [Gelman 2006; Feller and Gelman 2015].

**Parameter decomposition:** The piecewise linear nature of ReLU-nets, and the observation that neural networks produce learned data representations [Goodfellow et al. 2016], suggest that an approach to mimicking their expressivity within regression models is to allow slopes (and intercepts) to vary across regions of the data. We do so by expressing each of these regionally-varying parameters using an additive decomposition.

First, for delineating regions in data space (corresponding to cohorts), we project portions of the input data to lower dimensions through unsupervised methods. In Chang et al. [2020], the authors make a connection between sparse probabilistic matrix factorization and probabilistic autoencoders. We use this approach to develop a low-dimensional representation of the portions of the input covariate vector that pertain to the lagged quarterly history. Then, we compute the statistics of the learned representation in the training data and develop for each dimension a set of cut-offs to use for bucketization. This procedure puts each inpatient episode into a specific cohort, represented by a location within a multidimensional lattice, based on medical history. Specifically, we used a single cut-off (the median) for each of five dimensions (Fig. 3), creating a set of $2^5 = 32$ groups based on history. By design, the rules governing the group assignment can be easily converted to a set of inequalities over sparse subsets of the original data features. Additionally, we included interactions between the history groups with other discrete attributes such as the major diagnostic category (MDC), complication or comorbidity (CC) or a major complication or comorbidity (MCC), and race, to create high dimensional discrete lattices where the cells define coarse interaction cohorts in the data.

When partitioning data by a high-order interaction, a big data problem quickly becomes many small data problems – divide-and-conquer approaches can suffer from overfitting. To combat this issue, we developed a multiscale modeling approach where higher-order interactions are regularized by partially pooling their effects into related lower-order interactions. Specifically, given a multidimensional lattice that represents all cohorts for which the parameter will vary, we assign for each parameter a value within the lattice by decomposing the value into the form

$$\theta(\kappa) = \theta^{(0)}(\kappa) + \theta^{(1)}(\kappa_1, \kappa_2, \ldots) + \theta^{(2)}(\kappa_1, \kappa_2, \kappa_3, \ldots) + \ldots + \text{H.O.T.},$$

(6)

where $\kappa = (\kappa_1, \kappa_2, \ldots, \kappa_D)$ is a $D$ dimensional multi-index. In practice, we truncate the maximum order of terms in this decomposition due to memory constraints. More details on the exact decompositions that we used for our model parameters can be found in the Supplemental Materials.

![Figure 4: History encoding weights for inpatient episodes](image)
sitions in order to encourage shrinkage at higher orders. For the regression coefficients, we utilized the horseshoe prior for local-global shrinkage [Ghosh and Doshi-Velez, 2017, Bhadra et al., 2019, Polson and Scott, 2011, van Erp et al., 2019]. Please see the Supplemental Materials for more details on the model specification.

**Implementation and computation:** We implemented our model using Tensorflow Probability (TFP) [Dillon et al., 2017], developing a set of libraries for managing the parameter decompositions that is publicly available at github:xxxx/xxxx. The probabilistic matrix factorization method that we use for dimensionality reduction is publicly available at github:xxxx/xxxx.

We trained our model using minibatch mean-field stochastic ADVI, using batch sizes of $10^4$, and a parameter sample size of 8 for approximating the variational loss function. We utilized the Adam optimizer with a starting learning rate of 0.0015, embedded within a lookahead optimizer [Zhang et al., 2019] for stability. Each epoch where the mean batch loss did not decrease, we set the learning rate to decay by 10%. Training was set to conclude if there was no improvement for 5 epochs, or if we reached 100 epochs, whichever came sooner. More information on the training is present in the Supplemental Materials.

For data preprocessing, we developed a pipeline using Apache Spark 3.2.1 via the pyspark API. We used scikit-learn 1.1.1 for fitting baseline logistic regression models, and XGBoost 1.6.1 for fitting a reference blackbox model for comparison. We implemented a horseshoe Bayesian convolution neural network with ReLU activation using TFP, where we used a single hidden layer of size one-fifth the input layer. For computing global SHAP values, we used regression-based KernelSHAP [Covert and Lee, 2021].

All computation was performed using the Pittsburgh Supercomputing Center’s Bridges2 resources. We utilized extreme memory (EM) nodes for preprocessing, and Bridges2-GPU-AI for training.

### 3 Results

#### 3.1 Prediction Accuracy

| Model       | Interpretability | AUROC | AUPRC |
|-------------|------------------|-------|-------|
| XGBoost     | None             | 0.758 | 0.497 |
| ReLU-BNN    | Computationally  | 0.757 | 0.500 |
| LR w/o quantization | Comprehensibly | 0.731 | 0.381 |
| LR          | Comprehensibly   | 0.755 | 0.481 |
| PEM         | Mechanistically  | 0.757 | 0.497 |

Table 1: 30-day unplanned readmission or death classification metrics for evaluated models: XGBoost, Sparse logistic regression (LR), Bayesian neural network (BNN), our Piecewise exponential model (PEM). Quantization refers to the histogram-based bucketization of real-valued features. Area under the receiver operator curve (AUROC) and area under the precision-recall curve (AUPRC) computed on held-out 2012 inpatient episodes. Models trained on 2009-2011 episodes. Interpretability judged according to Fig. 1.

Figure 5: Mean baseline log-hazards by week for each episode interaction cohort defined within the model. Larger log-hazards corresponds to more readmission risk. Personalized values of $\alpha_n$ specific to each episode are found by mapping an episode into its cohort grouping.

#### 3.2 Interpretation

In addition to being competitive with blackbox methods in terms of prediction accuracy, our model is easily interpretable. Our model is exactly a generalized linear survival model where the coefficients vary. Here, we provide select portions of the ground-truth global interpretation of the model. Please see the Supplemental Materials for a more-complete accounting of the model. This type of exposition is impossible with blackbox models without relying on unreliable approximations.

**Time-dependent risk factors:** The model segments the
The 40 predictors with the largest absolute coefficients in the first week (through day 7) after readmission. All predictors are binary and all parameters are additive log hazard ratios. Higher (red) corresponds to larger hazards and greater readmission risk.

Data based on covariability and assigns for each predictor a cohort-level effect within each time interval. The effects within the model are hazard ratios, which describe the instantaneous relative risk associated with a predictor relative to a baseline. In most cases, the baseline refers to a typical or normal value of a variable. Membership to cohorts also itself is associated with a baseline risk – baseline or death. Patients who received skilled nursing care in the quarter preceding an inpatient episode, who had a Resource Utilization Group (RUG) Activities of Daily Living (ADL) score of at least 6.125 tended to have a lower risk of readmission in the first week than otherwise, however, the risk increased for quarter-lagged ADL scores of at least 13.5.

Discharge placement effects: In Fig. 7 we show the cohort-wise causally-adjusted mean local average treatment effects of discharge to each of the given care settings as well as the local standard deviation in the effect. Focusing on the effect of discharging to skilled nursing care, the effects were greatest for episodes graded by DRG code as having either a complication or comorbidity (CC) or a major complication or comorbidity (MCC). In particular, CC/MCC episodes with a major diagnostic code of 2 (Diseases and Disorders of the Eye), 14 (Pregnancy, Childbirth And Puerperium), and 22 (Burns) have the greatest inferred effect for discharging to care at least as intensive as skilled nursing.

Posthoc-xAI (SHAP) misleads Now that we know what the model is doing in exact terms, let us see how posthoc-xAI (SHAP) misleads.
In this manuscript, we developed a method for mimicking the nonlinear ReLU-nets within inherently interpretable multilevel Bayesian models. While not our focus, the method also automatically quantifies uncertainty. We applied this methodology to the prediction of hospital readmissions or death after discharge, and to the causal inference of the effects of discharge assignments.

**Accuracy without blackboxes:** We demonstrated how we were able to perform like blackboxes, without sacrificing interpretability. We accomplished this feat through two classes of methods: First, our novel modeling framework allowed us some fine-grain resolution in looking at the differential effects of the predictors in data subgroups. Additionally, it helped regularize the inference of local average treatment effects for choosing discharge placement. Second, we performed layers of feature engineering. The first layer was an extraction of medically-relevant information from the raw billing that gave us attributes such as chronic diseases, comorbidities, and ADL function. Second, we reduced noise in the raw coding by mapping to the clinically-relevant CCS system. These two steps were sufficient for our logistic regression model to match the performance of an XGBoost model in the literature based on the same dataset [MacKay et al., 2021]. Finally, we performed feature quantization based on the per-feature statistics. Quantization led to a big performance increase in logistic regression and also in the neural network for a given model size. We took these lessons and used them in defining our interpretable survival model.

**Posthoc xAI is inherently untrustworthy:** Our model, being inherently interpretable, admits an unequivocal ground-truth explanation. Hence, it is a good test case for testing the accuracy of posthoc explainers. We tested SHAP on our model; it failed in coming close to the ground-truth. This finding is consistent with other literature that has looked critically at SHAP and other xAI tools.

While posthoc-xAI does not make blackboxes interpretable, interpretability is not always unnecessary. Quantifying sample average treatment effects and making predictions does not require interpretable modeling [Hill, 2011], or even necessarily models at all [Ding and Mrratrix, 2017]. Blackbox methods offer good performance with minimal thoughtfulness. For these reasons, blackbox methods remain inherently useful – so long as one does not whitewash them with false explainability.

**Limitations:** Our modeling approach has downsides. Numerical stability generally requires the use of double precision floating point. The lattice-based parameter decomposition is memory-intensive which in some applications may...
severely limit expressivity.

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A Supplementary Methods

A.1 Medicare data preprocessing

Here we describe some details on the choices we made in preprocessing that will help make our work reproducible. Kyle Barron’s Medicare Documentation repository of Medicare data documentation is an excellent resource for acquainting oneself with this standardized dataset. Our first steps in processing the CMS LDS were to merge the files, originally organized by year, into long tables for each claim type. In the process, we renamed pre-2011 columns in the dataset to match 2011+ plus columns where-ever they differed. We will refer to the dataset using 2011 and beyond column names.

A.1.1 Episode Grouping

The CMS LDS consists of records organized into claims. Multiple claims can constitute a single period or episode of service. We determined episodes of the following types:

1. inpatient (inp)
2. skilled nursing facility (snf)
3. hospice (hosp)
4. outpatient (out, car)

For determining episodes, we grouped claims of each of the given types by person, and sorted by either the admission date (for inp, snf, hosp), or the claim through-date for (out, car).

Then for inp, snf, hosp, we merged successive claims into running episodes if they overlapped temporally, if the provider was the same and the intermediate discharge code indicates that the individual was not otherwise discharged home in between (we allow for distinct episodes with zero days of wait if a patient is discharged home and returns on the same day).

For out and car, we did the same merging with all claim types together, relaxing the need for the provider to match in an episode. Then we filtered for out/car episodes that did not overlap with inp, snf, hosp episodes – we determined these to be true outpatient episodes.

Then, for out and inp episodes, we determined if they corresponded to emergency department visits by looking for corresponding revenue center codes.

A.2 Model Specification

The specific decompositions that we used for each of the model terms are displayed in Fig. 2. For the missing parameter $\xi$, the results in this manuscript are all determined using $\xi = 0$.

| Parameter | Decomposition | Max order |
|-----------|---------------|-----------|
| $\alpha$  | MDC $\times$ Hx $\times$ CC/MCC | 2         |
| $\beta$   | race          | 1         |
| $\gamma$  | MDC $\times$ Hx $\times$ CC/MCC | 2         |
| $\nu$     | MDC $\times$ Hx $\times$ CC/MCC | 2         |

Table 2: Specific decompositions used per parameter to define cohorts, where major diagnostic category (MDC) is of size 26, history (Hx) is of size $2^5$, corresponding to low/high in each of the five dimensions, CC/MCC is of size 3, and race is of size 5.

The python package bayesianquilts, with demonstration available at [github:xxxxx/bayesianquilts](https://github.com/xxxxx/bayesianquilts) contains utilities for managing decompositions such as these.

We used a regularized horseshoe prior in order to encourage $\beta$ to be sparse. Specifically, we applied an independent horseshoe prior to this parameter within every model cohort.

The individual components of each of the parameter decompositions were all modeled using Gaussian weakly-informative priors (with a default scale of 5 for the zero-order terms in the expansion). We helped encourage shrinkage by having the scale of these priors decay for higher order terms in the decomposition. For the results in the paper, we used a decay factor of 0.1 per each order.

A.2.1 Training

We utilize TFP’s ADVI routines, which utilize stochastic sampling in computation of the ELBO. For this reason, it is not uncommon for specific parameter combinations to be in highly improbable locations – which can trigger underflows. To avoid instabilities, re adjust the likelihood on a per-observation level, first computing the minimum finite value of the log likelihood and then setting any divergent values to the minimum finite value minus a fixed offset of 100. We use the soft-plus function as a default bijector for any parameters that are supposed to be non-negative.

A.2.2 SHAP

KernelSHAP, the general all-purpose model-agnostic implementation of SHAP, is very resource intensive, so we had to tune it in order to run it. First, we used the regression-based version of KernelSHAP, found in the python package [shapreg](https://github.com/marcobartolozzi/shapreg) [Covert and Lee, 2021], which is not as resource intensive.

Second, although we had a very powerful computational resource at our disposal (Pittsburgh Supercomputer Center Bridges 2-AI with 512GB RAM), we had to restrict the input data size to 5k random training examples. Otherwise, we found that the system would run out of memory, causing the application to segmentation fault.
Finally, in order to get around an error involving a singular matrix, we regularized the linear algebra problem embedded within the algorithm, adding a fixed small constant of $10^{-8}$ to the diagonal of the linear transformation matrix (see [github:xxxxxx/shapley-regression]) for the exact modification made.

We were able to run \texttt{shapref} with \texttt{n_samples=2400} and \texttt{batch_size=24} on our resource in approximately 5 hours. Due to the memory requirement issues with our large dataset, we are not able to scale this result to more data. SHAP is known to be computationally expensive, particularly for large datasets and a large number of features (see [github issues 1053 1495]), and its very computation is inherently based on approximations. We believe that our computation of SHAP for our model is a reasonable representation of how well-approximated it is in practice, on a real problem and on a real dataset with a large number of predictors.

Our main point in the main text is a reiteration of the well-known fact that SHAP feature importance is not guaranteed to match what a model is doing in practice when the features in the training data are correlated – as would be true in most real-world problems. Examining Fig. 8 in the context of Fig. S8 one sees that the most-important SHAP features are not themselves very important in the model.

### B Supplementary Results

Here are results omitted from the main text for space constraints.

#### B.1 History representation

We utilized sparse probabilistic matrix factorization in order to obtain a low-dimension representation of personal medical history for the year prior to each episode. The encodings given by the model (Fig. S1) is an expanded version of Fig. 4 from the main text) specify linear combinations of the original data features that define a representation of an episode’s history. The representations then can be constituted into a predictive distribution for the original features by transformation against a decoding matrix (Fig. S2). Note that this method finds a subset of the input features that can be used to predict the value of all features.

##### B.1.1 Random slopes

Although we do not use this terminology in the main text, in the language of hierarchical mixed effects models the parameters $\beta$, $\xi$ in the model are random slopes. In the main text we presented the week 1 slopes in Fig. 6. In Fig. S3 we present the components of $\beta$ of the largest magnitudes, across all time intervals. As we noted in the main text, length of stay being at least 1 day, or conversely, being at least 0.5 days, across all time intervals. As we noted in the main text, length of stay being at least 1 day, or conversely, being at least 0.5 days, across all time intervals.
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B.1.2 Random intercepts

The parameter \( \alpha \) from Eq. 4 is specific to each cohort in the model – it is a random intercept in hierarchical mixed effects modeling terminology. We presented the posterior mean for this parameter in Fig. S5, interpreting this quantity as a cohort-specific baseline survival.

B.1.3 Causal inference

In our model we adjust for treatment selection bias by incorporating estimates of the treatment probabilities as covariates. The ordinal logistic regression intercepts are provided in Fig. S4.

The first five components in the parameter \( \gamma \) adjust for the selection bias present in claims. We present our cohort-specific estimates of \( \gamma \) in Fig. S5. We present the full time-course of discharge placement effects in Fig. S6. Largely, the discharge placement affects appear to strengthen from week 1 to weeks 2/3 before weakening from week four onwards. The discharge placement bias effects have more cohort-level variability after the first week. In Fig. S7 we zoom in on the effects for the cohorts that benefit the most from the discharge placement interventions. A key advantage of this form of modeling against even the computationally interpretable ReLU-nets is the ability to perform mesoscopic cohort-level inference and interpretation. Cohort-level information facilitates making a model actionable since actions can be applied to subgroups all at once.

B.2 Understanding the correlations implied by the decomposition

Let

\[
\theta(\kappa) = \sum_{o=0}^{O} \theta_o(\kappa),
\]

where \( E(\theta_o(\kappa)) = \mu_{\theta_o}^{(\kappa)}, \forall o \leq O \). Suppose that for two multi-indices \( \kappa_1, \kappa_2 \), that

- \( \theta_o(\kappa_1) = \theta_o(\kappa_2), \forall o \leq U < O \)
- \( \text{Cov}\left( \theta_j^{(\kappa_1)}, \theta_k^{(\kappa_2)} \right) = 0 \) if \( j \neq k \)
- \( \text{Var}(\theta_o^{\kappa}) = \sigma_o^2 \)

Figure S2: Decoding matrix corresponding to the encoding model of Fig. S1 showing up 25 features per dimension

ing less than a full day, was the most impact predictor of early readmission. However, the effect disappears after one week. Long length of stay (greater than 30 days) appeared to follow the same trend, with those having a length of stay of at least a month having a lower readmission risk in the first week after discharge, but not reduced risk after the first week. Generally, the magnitude of the slopes tended to increase over time, with a few exceptions.
Figure S3: **The 50 most influential regressors** $\beta$ (posterior mean, standard deviation) tracked through all time intervals. A more-comprehensive version of this figure can be found in our other supplemental file.
Then,

\[
\text{Cov}\left(\theta^{(\kappa_1)}, \theta^{(\kappa_2)}\right) = \sum_j \sum_k \text{Cov}\left(\theta^{(\kappa_1)}_j, \theta^{(\kappa_2)}_k\right)
\]

\[
= \left(\sum_{j=0}^{U} \sum_{k=0}^{U} O \sum_{j=U+1}^{U} \sum_{k=0}^{U} O \sum_{j=0}^{U+1} \sum_{k=0}^{U+1} \right) \text{Cov}\left(\theta^{(\kappa_1)}, \theta^{(\kappa_2)}\right)
\]

\[
= \sum_{\omega=0}^{U} \sigma^2_\omega + \sum_{\omega=U+1} O \text{Cov}\left(\theta^{(\kappa_1)}_\omega, \theta^{(\kappa_2)}_\omega\right). \quad (8)
\]

So,

\[
\rho(\theta^{(\kappa_1)}, \theta^{(\kappa_2)}) = \frac{\sum_{\omega=0}^{U} \sigma^2_\omega + \sum_{\omega=U+1} O \text{Cov}\left(\theta^{(\kappa_1)}_\omega, \theta^{(\kappa_2)}_\omega\right)}{\sum_{\omega=0}^{U} \sigma^2_\omega}
\]

\[
= \frac{\sum_{\omega=0}^{U} \sigma^2_\omega + \sum_{\omega=U+1} O \rho_\omega \sigma^2_\omega}{\sum_{\omega=0}^{U} \sigma^2_\omega}. \quad (9)
\]

Figure S4: **Cohort-wise ordinal intercept terms** \(\nu\) for the prediction of the distribution of discharge assignments.
Figure S5: Discharge assignment adjustment terms corresponding to first five terms of $\gamma$ (posterior mean, standard deviation) in terms of log hazard ratio under the log-additive effects model of Eq. [4]
Figure S6: Discharge placement effects $\gamma$ (posterior mean, standard deviation) in terms of log hazard ratio under the log-additive effects model of Eq. 4.
Figure S7: Discharge placement effects for select cohorts with the largest mean discharge placement effects.