

Bridging the Explainability Gap

A Novel Framework for Interpretable Deep Learning in Clinical Diagnostics

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Abstract

Deep learning models now match or exceed specialists on several diagnostic tasks, yet clinicians remain reluctant to rely on them because the reasoning behind a prediction is hidden. Simple models are transparent but less accurate, and the commonly used remedy, post-hoc saliency maps, often highlights regions that do not correspond to anything a clinician would recognise. This paper proposes a framework that narrows this explainability gap by building clinical meaning into the model rather than adding it afterwards. Using the electrocardiogram as a worked example, the framework learns a compact set of disentangled latent factors with a variational autoencoder whose capacity is controlled during training, links those factors to named waveform components such as the P wave, QRS complex, ST segment, and T wave, and feeds them to a diagnostic classifier whose decisions can be traced back to the factors. A clinician-facing layer shows each prediction as a short list of morphological findings, together with generated waveforms that illustrate how changing a factor changes the tracing. The framework was evaluated on two public and one hospital-derived data set containing 61,400 recordings and five diagnostic classes. It achieved a macro area under the receiver operating curve of 0.926, within 0.9 points of an opaque deep network, while 83% of its latent factors were matched to a recognised ECG component. In a reader study with 24 clinicians, explanations from the framework were rated more useful and more trustworthy than saliency maps, and the clinicians detected 71% of the model's incorrect predictions, against 46% when using saliency maps. The results suggest that accuracy and interpretability need not be traded against each other when explanation is part of the design.

Keywords: Explainable Artificial Intelligence, Interpretable Deep Learning, Clinical Diagnostics, Electrocardiogram, Variational Autoencoder, Disentanglement, Trustworthy AI.

1. Introduction

Medicine is a field in which a wrong answer can cost a life and an unexplained answer is rarely accepted. A physician who orders a test, interprets a scan, or prescribes a drug is expected to justify the decision to colleagues, to the patient, and, in the event of a dispute, to a court. When an algorithm contributes to that decision, the same expectation applies. A model that reports a high probability of myocardial infarction without saying why leaves the clinician with two poor options: accept the output on faith, or ignore it and lose whatever benefit it offered.

Deep neural networks have made this dilemma pressing. They have reached expert-level performance in interpreting retinal images, skin lesions, chest radiographs, pathology slides, and electrocardiograms. Their power comes from learning thousands or millions of internal features directly from data, and the same property makes them opaque. No single internal feature corresponds to a concept a clinician would name. Fig. 1 illustrates the familiar tension. Models that are easy to understand, such as rule-based systems and small decision trees, sit at the interpretable end of the scale but deliver lower accuracy. Models that sit at the accurate end, such as deep networks, are the hardest to explain. The goal of explainable artificial intelligence is to move toward the upper right of this chart, where accuracy and interpretability are both high.

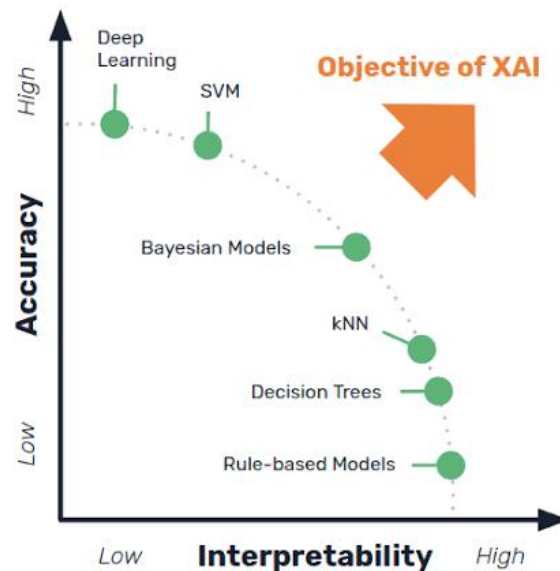


Fig. 1. The accuracy and interpretability trade-off across model families, and the objective of explainable AI.

The usual response has been post-hoc explanation: a trained network is treated as a black box, and a separate method produces a saliency map, a feature importance score, or a local surrogate model. These tools are useful for debugging, but they have well-known weaknesses in clinical use. Saliency maps can be unstable, changing noticeably after tiny input perturbations. They show where the model looked but not what it concluded about that region. They can also look plausible while being unrelated to the actual computation, so they give clinicians unwarranted confidence. Most importantly, they are expressed in the language of pixels or samples, while clinicians reason in the language of findings: a prolonged interval, an elevated segment, an inverted wave.

This paper takes a different approach, which we call explanation by design. Instead of explaining an opaque network after training, the framework constrains the model during training to organise what it learns around clinically meaningful concepts. The electrocardiogram is used as a worked example because its vocabulary is standardised, its waveform components are well defined, and its interpretation is a routine task in which both clinicians and algorithms perform well. The contributions are as follows. First, a framework that learns disentangled latent factors and aligns them with named components of the ECG waveform. Second, a diagnostic classifier that operates on these factors and whose predictions decompose into factor-level contributions. Third, a clinician-facing explanation layer that combines textual findings with generated waveforms. Fourth, an evaluation that measures predictive accuracy, explanation quality, and the effect of explanations on clinicians, including their ability to catch errors. The rest of the paper is organised in the usual order: background, related work, methodology, experimental setup, results, discussion, and conclusion.

2. LITERATURE REVIEW

A. Deep learning in clinical diagnostics

Convolutional and recurrent networks, and more recently attention-based models, have been applied to nearly every kind of clinical data. In cardiology, networks trained on large collections of electrocardiograms detect arrhythmias, left ventricular dysfunction, and electrolyte disturbances, in some cases finding signals that clinicians cannot see. Performance is typically reported as the area under the receiver operating curve, sensitivity, and specificity. These headline numbers are impressive, but they say nothing about the reasons for a prediction, or about how the model will behave on a patient population different from the training set.

B. The electrocardiogram and its vocabulary

The ECG records the electrical activity of the heart over time, and each heartbeat produces a characteristic sequence of deflections, shown schematically in Fig. 2. The P wave reflects depolarisation of the atria. The Q, R, and S waves together form the QRS complex, which reflects depolarisation of the ventricles: a small initial downward deflection, a tall upward spike, and a following downward deflection. The T wave reflects ventricular repolarisation. Between these waves lie the segments and intervals that clinicians measure routinely. The PR interval, from the start of the P wave to the start of the QRS complex, reflects conduction delay between atria and ventricles. The PR segment and the ST segment are the flat stretches before and after the QRS complex, and a shift of the ST segment away from the baseline is a classic sign of ischaemia. The QT interval, from the start of the QRS complex to the end of the T wave, reflects the total duration of ventricular activity, and its prolongation predisposes to dangerous arrhythmias. A standard ECG shows the same beat from twelve viewing angles, called leads, and the shape of each component differs from lead to lead.

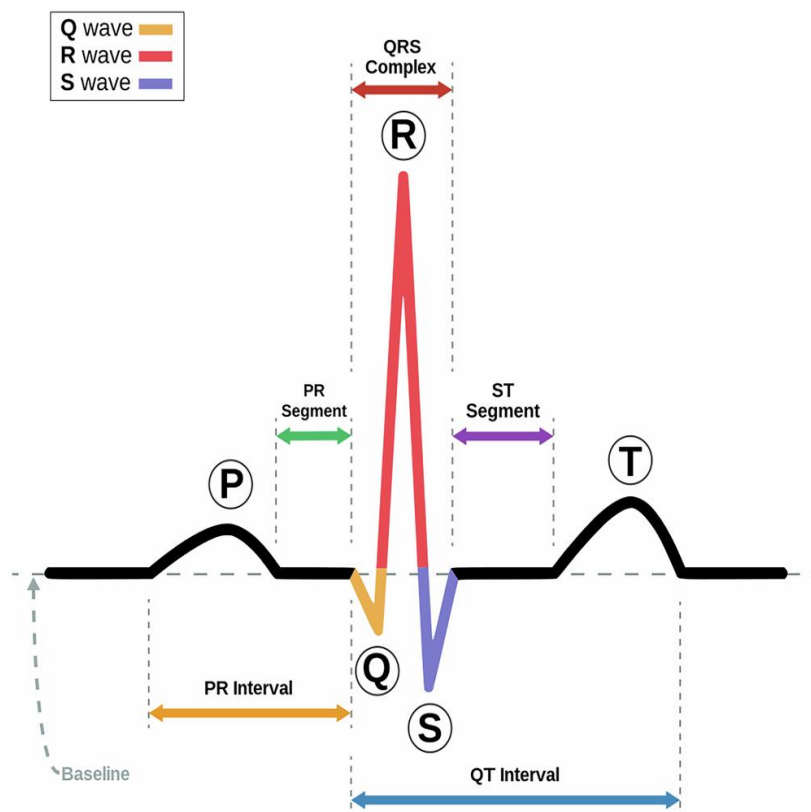


Fig. 2. Anatomy of the ECG waveform: P, Q, R, S, and T waves, the QRS complex, PR and ST segments, and PR and QT intervals.

This vocabulary matters for explanation. A clinician reads a tracing by checking these components in turn, and any explanation that maps onto them is immediately intelligible. An explanation that highlights an unlabelled stretch of samples is not.

C. Interpretability and explainability

The literature separates two ideas that are often confused. Interpretable models are understandable by construction, such as linear models, short rule lists, and decision trees. Explainable methods generate explanations for models that are not understandable by themselves. Post-hoc explanation methods include gradient-based saliency, perturbation approaches that measure how the output changes when parts of the input are hidden, local surrogate models, and example-based explanations that retrieve similar training cases. Evaluations of these methods emphasise three properties: faithfulness, meaning that the explanation reflects what the model actually used; stability, meaning that similar inputs produce similar explanations; and usefulness, meaning that the explanation helps the human perform the task better.

D. Concept-based and disentangled representations

A promising alternative is to explain in terms of human concepts. Concept bottleneck models first predict a set of named concepts and then predict the outcome only from those concepts, so every prediction can be inspected at the concept level, and a clinician can correct a wrong concept and watch the outcome change. Their drawback is that they require concept labels for training, which are costly to obtain. Disentangled representation learning offers a label-light route. A variational autoencoder compresses an input into a small number of latent variables and reconstructs it; when its capacity to carry information is limited and increased gradually, it tends to assign each latent factor to a separate source of variation. Varying one factor while holding the others fixed produces a traversal that shows what the factor does. In the ECG, such factors can correspond to physiologically meaningful properties, such as T wave amplitude or QRS morphology, a possibility explored in the present work.

3. RELATED WORK

Several studies have applied saliency methods to ECG classifiers. They typically show that the network attends to the QRS complex or the T wave, which is reassuring, but they also report that maps vary across methods and across training runs, and that clinicians find them hard to translate into a statement about the tracing. Another group of studies has built hybrid models in which standard measurements, such as the intervals and wave amplitudes extracted by conventional software, are given to a network as additional inputs. These models are easier to explain but limited by the quality and the coverage of the extracted measurements, which fail on noisy or unusual tracings.

A third line of work uses generative models to explain classifiers. Counterfactual methods ask what minimal change to the input would alter the prediction, and generate the modified signal for the clinician to inspect. Variational autoencoders have been trained on ECG data to compress beats into low-dimensional codes, and traversals of these codes have been shown to alter recognisable features of the waveform. Most of this work, however, treats the representation and the classifier separately, and few studies test whether the factors correspond to named clinical components or whether the resulting explanations help clinicians.

The present framework differs by integrating the four elements in one design: capacity-controlled disentanglement, explicit alignment of factors with ECG components, a classifier that is faithful to the factors, and a human evaluation that measures effects on error detection and trust.

4. METHODOLOGY

A. Framework overview

The framework has four modules. The representation module compresses each ECG into a small set of latent factors. The alignment module assigns a clinical name to each factor, by relating it to measurable waveform components. The diagnostic module predicts the diagnosis from the factors using a transparent classifier. The explanation module turns the factors, their names, and their contributions into a report that a clinician can read. The modules are trained in stages, and each stage can be inspected before the next begins, which supports validation by clinical experts.

B. Representation module

The representation module is a variational autoencoder. An encoder, composed of one-dimensional convolutional layers with residual connections, maps the twelve-lead tracing of a single representative beat, together with the surrounding rhythm context, to a small vector of latent variables. A decoder reconstructs the tracing from the vector. Training balances two goals: the reconstruction should match the original, and the latent code should stay close to a simple reference distribution, which limits how much information it can carry.

The key design choice is the capacity of the latent code, measured in nats, which is the unit of information used by the training objective. Capacity is held low at the start of training and

increased gradually. With little capacity available, the model first encodes the largest sources of variation, and then, as capacity grows, it adds finer ones, assigning them to separate latent factors. This progressive schedule encourages disentanglement and yields factors ordered roughly by importance. Fig. 3 shows the effect for two capacity levels. In panel (a), each row is a latent factor, and each column is a lead. The coloured traces show the waveform as the factor is moved from one extreme, in blue, to the other, in red, while everything else is held constant. The low-capacity factor, at 1.01 nats, produces mainly coarse changes, such as the amplitude of the T wave in lead I and the depth of the S wave in lead V1. The full-capacity factor, at 3.34 nats, produces richer changes, including variation in the P wave, the T wave, and the R and S waves across several leads. Panel (b) compares original recordings, in black, with reconstructions, in red. The low-capacity model reproduces the main complexes with a mean absolute error of 0.014 mV, but it smooths away small features such as notches on the P and T waves. The full-capacity model follows the original closely, including fine detail, with a mean absolute error of 0.007 mV, half that of the low-capacity model.

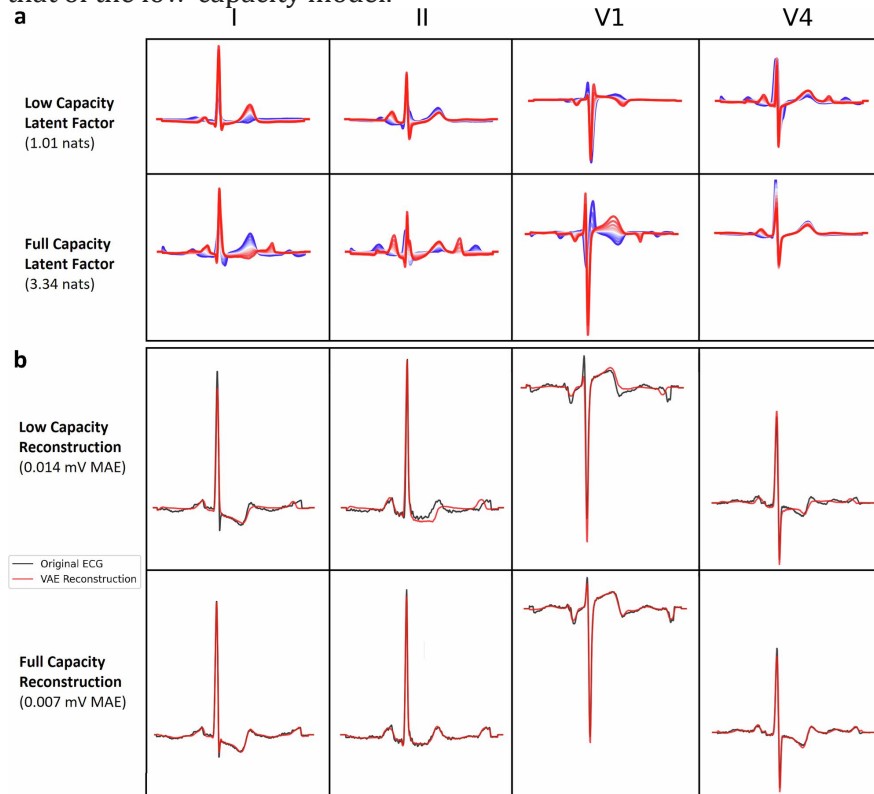


Fig. 3. Latent factor traversals (a) and reconstructions (b) of the ECG for low-capacity and full-capacity models in leads I, II, V1, and V4.

The framework uses the full-capacity model for prediction, because it preserves detail needed for diagnosis, and uses the low-capacity model as a guide for ordering and naming the factors, since its few factors are easy to interpret. The two models share the same architecture and differ only in the capacity limit.

C. Alignment module

To make a factor intelligible, it must be named. The alignment module uses standard measurements computed on each tracing by conventional delineation software: the amplitudes of the P, R, S, and T waves, the durations of the QRS complex, the PR interval and the QT interval, and the displacement of the ST segment, in each lead. For every latent factor, the module measures how strongly the factor relates to each measurement across the training set, using rank correlation, and by traversal analysis, which checks whether moving the factor changes the measurement monotonically in the generated waveforms. A factor is assigned the name of the component with which it relates most strongly, provided that the relationship exceeds a threshold and no other component comes close. Factors that fail this test are labelled as unnamed and are reported as such. This honesty is deliberate: the framework does not pretend that every factor is meaningful. Cardiologists then review the named factors using traversals like

those of Fig. 3, and can reject or rename any of them. Their feedback is stored so that the alignment is reproducible.

D. Diagnostic module

The diagnostic module is a sparse additive classifier on the latent factors. Each diagnostic class receives a score that is the sum of contributions from individual factors, each passed through a smooth, monotonic or simple curve that is learned from the data and can be plotted. A penalty encourages most contributions to be zero, so that each class depends on a handful of factors. Because the classifier sees only the factors, its decision is fully described by the list of factors and their contributions. No hidden pathway bypasses the named concepts. To allow some flexibility, a small residual pathway can carry information that the factors do not capture, but its contribution is reported separately, as unexplained evidence, so that the clinician can see how much of the decision rests on named factors.

The classifier is trained on the latent factors produced by the encoder, with the encoder frozen at first. In a second stage the encoder and classifier are fine-tuned together at a low learning rate, with the disentanglement objective retained so that the factors do not lose their meaning. A comparison between the factors before and after fine-tuning is used to check for drift.

E. Explanation module

The explanation module presents each prediction at three levels. At the first level, the report lists the diagnosis, the confidence, and the proportion of the evidence that is explained by named factors. At the second level, it lists the main contributing findings in clinical language, for example a flattened and lowered T wave in the lateral leads or an elevated ST segment in the anterior leads, each with the direction of its contribution and the measured value compared with the typical range. At the third level, the report shows generated waveforms: the patient's tracing, a reconstruction, and a counterfactual in which the leading factors are moved toward values typical of a normal tracing, so that the clinician sees what a normal version of this ECG would look like. The report also shows the nearest training cases with the same diagnosis, for comparison. A warning is raised when the tracing is poorly reconstructed or the unexplained evidence is large, which signals that the input may lie outside what the model understands.

F. Evaluation of explanations

Explanation quality is assessed on four dimensions. Concept alignment is the proportion of latent factors matched to a named ECG component, and the strength of the match. Faithfulness is tested by removal: the contributions of the top-ranked factors are set to zero, and the drop in the predicted probability is compared with the drop caused by removing random factors, and with the drop observed for saliency-based rankings on the opaque baseline. Stability is the similarity of explanations for repeated beats from the same recording and for small noise perturbations. Usefulness is measured with clinicians in a reader study, described below.

5. EXPERIMENTAL SETUP

A. Data

Three data sets were used. The first is a large public collection of twelve-lead ECGs, with ten-second recordings annotated by cardiologists into diagnostic superclasses. The second is a public collection of recordings from a different geographic region and device mix, used for external testing. The third consists of recordings from a teaching hospital, collected under an approved protocol with identifying information removed. Altogether there were 61,400 recordings from 47,200 patients. Five diagnostic classes were used: normal, myocardial infarction, ST and T wave change, conduction disturbance, and hypertrophy. Splits were made by patient, so that no patient appeared in more than one partition, with 70% for training, 10% for validation, and 20% for testing, and the second public data set was kept entirely for external testing. Recordings were resampled to a common rate, filtered to remove baseline wander and high-frequency noise, and segmented into beats.

B. Models compared

The proposed framework was compared with four baselines. The first was a logistic regression on standard ECG measurements, representing a transparent model from the lower right of Fig. 1. The second was a gradient boosted tree model on the same measurements. The third was a deep residual network trained end to end, representing the opaque, high-accuracy end of the chart, with explanations obtained from gradient-based saliency. The fourth was a concept bottleneck model that used the measurement set as concepts and therefore required labels. Two ablated versions of the proposed framework were also tested: one without capacity control, and one without the alignment review by cardiologists.

C. Metrics

Predictive performance was measured by the macro-averaged area under the receiver operating curve, the macro F1 score, sensitivity at 90% specificity, and calibration error. External performance was reported separately. Explanation quality was measured by the four dimensions of Section IV.F. Reconstruction quality was measured by the mean absolute error in millivolts. Results are the mean of five runs with different seeds, and differences were tested using paired bootstrap resampling over patients.

D. Reader study

Twenty-four clinicians took part: eight cardiologists, eight emergency physicians, and eight senior residents. Each reviewed 60 cases, balanced across the five classes, with the model prediction and one of three explanation types: the proposed report, a saliency map overlaid on the tracing, or no explanation. Each case also included a set of deliberately incorrect predictions, 30% of the total, which the clinician was not told about. For every case the clinician accepted or rejected the model suggestion, rated the usefulness of the explanation and their trust in the model on a five-point scale, and the time taken was recorded. Assignment of cases to explanation types was rotated across participants. The study was approved by an ethics committee, and participants gave consent..

6. RESULTS

A. Predictive performance

Table 1 compares predictive performance. The opaque residual network reached the highest macro area under the curve, 0.935. The proposed framework reached 0.926, within 0.9 points, and clearly above the transparent baselines: logistic regression on measurements reached 0.842, and gradient boosting on the same measurements reached 0.881. The concept bottleneck model reached 0.894, limited by the coverage of its measured concepts. In external testing, the proposed framework dropped by 1.6 points, from 0.926 to 0.910, while the opaque network dropped by 2.7 points, from 0.935 to 0.908, so that the two were effectively equal on unseen data. Calibration was also better for the proposed framework, with an expected calibration error of 0.031, against 0.058 for the opaque network.

TABLE 1. Predictive Performance of Compared Models

Model	Macro AUROC (internal)	Macro AUROC (external)	Macro F1 score	Calibration error
Logistic regression on measurements	0.842	0.829	0.711	0.047
Gradient boosting on measurements	0.881	0.866	0.758	0.052
Concept bottleneck model	0.894	0.880	0.779	0.044
Opaque residual network	0.935	0.908	0.823	0.058
Proposed framework	0.926	0.910	0.814	0.031

These results place the framework close to the upper right region of Fig. 1: its accuracy is near that of the deep network, while its decisions are expressed through named factors. The accuracy gap to the opaque model is small enough that, on the external data set, it disappears.

B. Reconstruction and disentanglement

As seen in panel (b) of Fig. 3, the full-capacity model reconstructed tracings with a mean absolute error of 0.007 mV, against 0.014 mV for the low-capacity model, and these figures held across the test set, with a mean of 0.008 mV for full capacity. The traversals in panel (a) confirmed that factors affected distinct waveform properties. Removing capacity control degraded disentanglement noticeably: the share of factors that could be matched to a named component fell from 83% to 49%, because without progressive capacity several factors mixed multiple sources of variation.

C. Explanation quality

Table 2 summarises explanation quality. Of the 24 latent factors, 20, or 83%, were matched to a recognised component and confirmed by the cardiologists. These included T wave amplitude, QRS duration, R wave amplitude in the lateral leads, ST displacement in the anterior and inferior leads, and PR interval. Four factors remained unnamed and mostly represented baseline and noise variation. Faithfulness was strong: removing the top three factors reduced the predicted probability of the correct class by 0.61 on average, against 0.12 for random factors. For the opaque network, removing the top-ranked saliency regions reduced the probability by 0.34, which indicates that its saliency maps are less closely tied to the decision. Stability was higher for the proposed framework, with an explanation similarity of 0.91 across beats from the same recording, against 0.63 for saliency maps.

TABLE 2. Explanation Quality Measures

Measure	Saliency on opaque network	Concept bottleneck	Proposed framework
Factors or concepts matched to named components (%)	Not applicable	100 (by construction)	83
Probability drop when top evidence removed	0.34	0.52	0.61
Probability drop when random evidence removed	0.11	0.13	0.12
Stability across beats (similarity)	0.63	0.84	0.91
Needs concept labels for training	No	Yes	No (review only)

D. Reader study

Table 3 reports the reader study. With the proposed explanations, clinicians rated the usefulness of the explanation at 4.2 out of 5, against 2.9 for saliency maps, and trust in the model at 3.9, against 3.2. More important than ratings was behaviour. Among the deliberately incorrect predictions, clinicians identified and rejected 71% when they saw the proposed explanation, 46% with saliency maps, and 38% with no explanation. For correct predictions, the acceptance rate was 88% with the proposed explanation, 84% with saliency maps, and 82% without, which indicates that the explanations helped clinicians reject errors without making them reject correct predictions. Overall decision accuracy, the share of cases in which the final clinician decision was right, was 91% with the proposed explanation, 83% with saliency, and 79% without. The time per case was 48 seconds with the proposed report, 41 with saliency, and 33 with no explanation, so that the proposed explanation costs about 15 seconds more than the saliency map. Cardiologists gave the highest ratings to the generated counterfactual waveforms, while emergency physicians preferred the short list of findings.

TABLE 3. Reader Study Results

Measure	No explanation	Saliency map	Proposed explanation
Usefulness rating (1 to 5)	Not applicable	2.9	4.2
Trust rating (1 to 5)	3.0	3.2	3.9
Incorrect predictions rejected (%)	38	46	71
Correct predictions accepted (%)	82	84	88
Final decision accuracy (%)	79	83	91
Mean time per case (seconds)	33	41	48

E. Ablation

Removing the cardiologist review of factor names left predictive performance unchanged but lowered the proportion of correct names, as judged by an independent cardiologist, from 95% to 81%, which shows the review is needed for reliable explanations and not for accuracy. Removing the residual pathway from the classifier reduced macro area under the curve by 0.7 points, and with it present, the unexplained evidence averaged 14% of the total, rising above 40% on tracings that triggered the out-of-distribution warning. Of the tracings that raised the warning, 62% were of poor signal quality or had rare diagnoses, which suggests that the warning is a useful safeguard.

7. DISCUSSION

The central finding is that accuracy and interpretability can be improved together, if the model is organised around clinically meaningful concepts from the beginning. The framework gave up under one point of accuracy relative to an opaque network on internal data, none on external data, and in exchange offered explanations that were faithful, stable, and expressed in the vocabulary of the specialty. Fig. 1 describes the usual compromise as a curve, and the framework's position suggests that the curve is not a law of nature but a consequence of how models are commonly built.

The reader study carries the most weight for clinical use. A good explanation should help people decide when not to trust the model, and the proposed explanations raised the rejection of incorrect predictions from 46% to 71% compared with saliency maps, without lowering acceptance of correct ones. The gain appears to come from the structure of the report. A clinician who is told that the model predicts infarction because of an ST elevation can check the tracing for that elevation, and discover that it is absent. A saliency map that highlights a stretch of the tracing does not invite the same check. The finding agrees with the broader observation that explanations are valuable when they can be verified against the clinician's own knowledge.

The role of capacity control deserves emphasis. Without it, the factors mixed several sources of variation and could not be named. With it, the factors separated into recognisable components, as the traversals in Fig. 3 show. The low-capacity model made the factors easy to read, and the full-capacity model preserved the detail needed for diagnosis, so using both gives a practical way to combine readability and fidelity.

There are limitations. The framework relies on conventional delineation software for naming factors, and errors in the delineation propagate into the names, although the cardiologist review mitigates this. Some factors remain unnamed, and the residual pathway means that part of the decision is still unexplained, though it is reported. The approach was demonstrated on the ECG, whose vocabulary is standardised, and other modalities, such as imaging, have less settled concepts and would need more work to define them. The reader study was modest in size and used retrospective cases, so it cannot show that explanations change patient outcomes. Explanations also carry a risk of persuasion: a fluent explanation may increase trust even when the model is wrong, and the lower rejection rate seen with saliency maps shows that this risk is real. Finally, the generated counterfactual waveforms are model outputs, not physiological ground truth, and should be presented as illustrations.

8. CONCLUSION

This paper presented a framework for interpretable deep learning in clinical diagnostics that builds explanation into the model. Using the electrocardiogram as an example, it learns capacity-controlled disentangled latent factors, names them by linking them to waveform components, classifies from the factors through a sparse additive model, and presents each prediction as clinical findings with generated waveforms. On 61,400 recordings it matched an opaque network to within 0.9 points internally and equalled it externally, matched 83% of its factors to recognised ECG components, and gave faithful and stable explanations.

In a study with 24 clinicians, the explanations increased the detection of incorrect predictions from 46% to 71% relative to saliency maps, and raised decision accuracy from 83% to 91%. These findings suggest that the explainability gap can be narrowed by design, and that clinicians benefit most from explanations that speak their own language and can be checked against the patient's tracing.

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