Benchmarking Bayesian Deep Learning on Diabetic Retinopathy Detection Tasks

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Abstract

Bayesian deep learning seeks to equip deep neural networks with the ability to precisely quantify their predictive uncertainty, and has promised to make deep learning more reliable for safety-critical real-world applications. Yet, existing Bayesian deep learning methods fall short of this promise; new methods continue to be evaluated on unrealistic test beds that do not reflect the complexities of the downstream real-world tasks that would benefit most from reliable uncertainty quantification. We propose a set of real-world tasks that accurately reflect such complexities and assess the reliability of predictive models in safety-critical scenarios. Specifically, we curate two publicly available datasets of high-resolution human retina images exhibiting varying degrees of diabetic retinopathy, a medical condition that can lead to blindness, and use them to design a suite of automated diagnosis tasks that require reliable predictive uncertainty quantification. We use these tasks to benchmark well-established and state-of-the-art Bayesian deep learning methods on task-specific evaluation metrics. We provide an easy-to-use codebase for fast and easy benchmarking following reproducibility and software design principles. We provide implementations of all methods included in the benchmark as well as results computed over 100 TPU days, 20 GPU days, 400 hyperparameter configurations, and evaluation on at least 6 random seeds each.

1 Introduction

Bayesian deep learning has been applied successfully to a wide range of real-world prediction problems such as *medical diagnosis* [9, 28, 37, 61], *computer vision* [29, 33], *scientific discovery* [38, 42], and *autonomous driving* [2, 17, 27, 30, 31, 33]. Despite the demonstrated usefulness of Bayesian deep learning for such practical applications and a growing literature on better inference methods [7, 14, 19, 21, 44, 45, 49, 57, 62], there exists no standardized benchmarking task that reflects the complexities and challenges of safety-critical real-world tasks while adequately evaluating the quality of models' predictive uncertainty estimates.

To make meaningful progress in the development and successful deployment of reliable Bayesian deep learning methods, we need easy-to-use benchmarking tasks that are legitimate litmus tests for practitioners aiming to deploy their models in safety-critical settings. Such tasks ought to be usable without the extensive domain expertise often necessary for appropriate experiment design and data preprocessing. Lastly, any such benchmarking task must include evaluation methods that test for predictive performance and assess different properties of models' predictive uncertainty estimates, while taking into account application-specific constraints.

In this paper, we propose a set of realistic safety-critical tasks that respect these desiderata and use them to benchmark well-established and state-of-the-art Bayesian deep learning methods. To do so, we consider the problem of using machine learning to *detect diabetic retinopathy*, a medical

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condition considered the leading cause of vision impairment and blindness [50]. Unlike in prior works on diabetic retinopathy detection, the benchmarking tasks presented in this paper are specifically designed to assess the reliability of machine learning models and the quality of their predictive uncertainty estimates using both aleatoric and epistemic uncertainty (Appendix E.2).

Medical diagnosis problems are particularly well-suited to assess reliability due to the severe harm caused by predictive models that make confident but poor predictions (for example, when a disease is not recognized). Good predictive uncertainty estimates can be a fail-safe against incorrect predictions: if a given data point is meaningfully different from data in the training set—for example, because it shows signs of the disease not captured there, exhibits visual artifacts, or was obtained using different measurement devices—a good predictive model will express a high level of predictive uncertainty and flag the example for further review by a medical expert. As a general desideratum for predictive models, we want a model's predictive uncertainty to increase the more distinct a given input datum is from the training data.

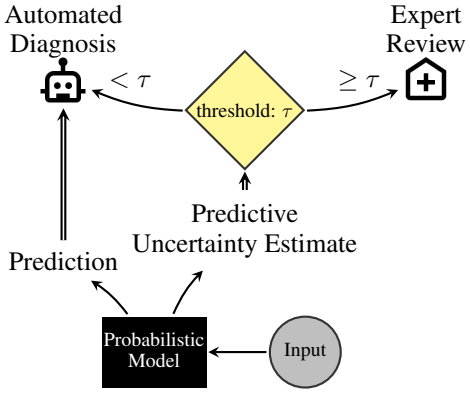


Figure 1: Automated Diagnosis Pipeline. For a given input, a model provides a prediction and a corresponding uncertainty estimate; if the estimate is below a referral rate τ (indicating low uncertainty) the diagnosis is processed without further review; otherwise, it is referred to an expert.

Contributions. We present an easy-to-use, expert-guided, open-source *suite of diabetic retinopathy detection benchmarking tasks* for Bayesian deep learning. We designed safety-critical downstream tasks from publicly available datasets and evaluated well-established and state-of-the-art Bayesian and non-Bayesian methods on a set of task-specific reliability and performance metrics. We will open-source code and pre-trained models obtained from an extensive hyperparameter optimization and evaluation over more than 400 total configurations, using over 100 TPU days and 20 GPU days of compute.[1]

2 Benchmarking Tasks for Diabetic Retinopathy Detection

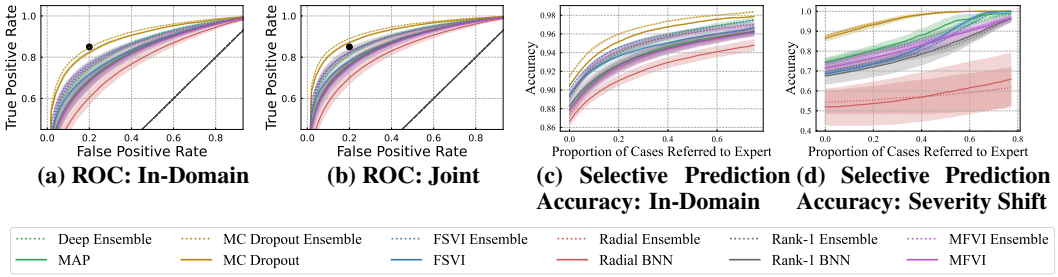
Below we present two real-world diabetic retinopathy detection problems and describe how we design corresponding prediction tasks. See Appendix D for details on task dataset construction.

Diabetic Retinopathy Detection under Severity Shift. Although diabetes is increasingly widespread, cases of sight-threatening diabetic retinopathy are still rare, and scans of retinas with no or mild retinopathy are more easily obtainable. As a result, predictive models for detecting diabetic retinopathy may be trained on only a very small number of retina images showing signs of severe or proliferative retinopathy. We design a prediction task to simulate this setting, by training models on retina images showing signs of at most moderate diabetic retinopathy, and evaluating them on a *Severity Shift* dataset composed of retina images showing signs of severe or proliferative diabetic retinopathy. Given that signs of moderate diabetic retinopathy are similar in appearance to signs of severe or proliferative retinopathy (just weaker), we expect a good predictive model to successfully detect the latter but exhibit increased predictive uncertainty.

Diabetic Retinopathy Detection under Country Shift. In countries without extensive screening, retina scans for training predictive models are scarce. Hence, models may be trained on images collected in other countries where many scans are performed—for example, the United States—and used to evaluate scans taken from patients in countries where scans are rarer and may be performed using different medical devices. We design a corresponding *Country Shift* task, in which we train models on retina images from the US-collected EyePACS dataset and evaluate them on images from the Indian APTOS dataset. This allows us to evaluate the reliability of predictive models for settings where training and evaluation data are not obtained from the same patient population or collected with the same medical equipment. See Appendix C for information on EyePACS and APTOS.

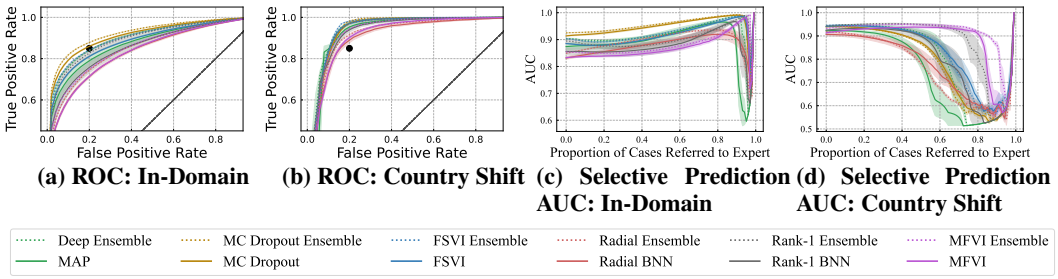
Downstream Tasks: Selective Prediction. In real-world settings where the evaluation data may be sampled from a shifted distribution, incorrect predictions may become increasingly likely. To account for that possibility, predictive uncertainty estimates can be used to identify input points for

[1] Code to reproduce results and benchmark new methods at `rebrand.ly/dr-distshift2021`.



(a) ROC: In-Domain **(b) ROC: Joint** **(c) Selective Prediction Accuracy: In-Domain** **(d) Selective Prediction Accuracy: Severity Shift**

Figure 2: Severity Shift. We jointly assess model predictive performance and uncertainty quantification on the in-domain test dataset composed only of cases with either no, mild, or moderate diabetic retinopathy, and the *Severity Shift* evaluation set composed only of severe and proliferate cases. **Left:** The receiver operating characteristic curve (ROC) for in-domain diagnosis (**a**) and for a joint dataset composed of examples from both the in-domain and *Severity Shift* evaluation sets (**b**). The dot in **black** denotes the NHS-recommended 85% sensitivity and 80% specificity ratios [59]. **Right:** Selective prediction on accuracy in the in-domain (**c**) and *Severity Shift* (**d**) settings. Shading denotes standard error computed over six random seeds. See Section 3.1.



(a) ROC: In-Domain **(b) ROC: Country Shift** **(c) Selective Prediction AUC: In-Domain** **(d) Selective Prediction AUC: Country Shift**

Figure 3: Country Shift. We jointly assess model predictive performance and uncertainty quantification on both in-domain and distributionally shifted data. **Left:** The *receiver operating characteristic curve (ROC)* for in-population diagnosis on the EyePACS [13] test set (**a**) and for changing medical equipment and patient populations on the APTOS [3] test set (**b**). The dot in **black** denotes the NHS-recommended 85% sensitivity and 80% specificity ratios [59]. **Right:** *selective prediction* on AUC in the EyePACS [13] (**c**) and the APTOS [3] (**d**) settings. Shading denotes standard error computed over six random seeds. See Section 3.2.

which the likelihood of an incorrect prediction is high and refer them to a human expert for further review (Figure 1). We consider a corresponding *selective prediction* metric, where the predictive performance of a given model is evaluated for varying expert referral rates. That is, for a given *referral rate* of $\tau \in [0, 1]$, we *refer* the τ proportion of evaluation images with the highest uncertainty estimates to a medical professional for further review. The model is assessed on the predictions for the remaining $(1 - \tau)$ proportion of images. For referral rates $\tau \in [0, 1]$ we obtain a *referral curve*. For each of the tasks above, we apply selective prediction on three evaluation settings: an evaluation dataset with in-domain distribution examples, shifted distribution examples, or both.

3 Benchmark

The aim of this benchmark is to adequately represent the challenges of real-world distributional shift, and to rigorously assess the reliability of Bayesian deep learning methods. To do so, we implement a suite of established and state-of-the-art methods, and evaluate them on selective prediction in the *Severity* and *Country Shift* settings.

We provide descriptions of each method in Appendix E.3 and uncertainty estimates are obtained as described in Appendix E.2. All experiments use a ResNet-50 architecture [22]. See Appendix G for details on the network architecture, as well as on hyperparameter tuning and evaluation. In Appendix I, we investigate other robustness and uncertainty metrics including *expected calibration error*, *out-of-distribution detection AUC*, and *predictive entropy histograms*, and report full results.

3.1 Severity Shift

On the *Severity Shift* task (Figure 2 and Table 2 in Appendix H), we find that models generalize well from cases with no worse than moderate diabetic retinopathy (in-domain, Figure 2(**a**)) to severe and proliferative cases (Figure 2(**b**)), improving their AUC under the distribution shift.

Practitioners Can Tune the Referral Rate τ With Selective Prediction. Good predictive uncertainty estimates correlate with predictive error, and therefore we would expect a model's performance (e.g., accuracy, AUC) to increase as more examples on which the model exhibits high uncertainty are referred to an expert. On both the in-domain and *Severity Shift* evaluation sets (Figures 2(**c**) and (**d**)), models demonstrate good uncertainty, with monotonically increasing accuracy as τ increases. This highlights two ways that practitioners may use selective prediction to prepare models for a real-world deployment in the presence of distribution shifts. First, given a performance target (e.g., $\geq 95\%$ accuracy) the referral curve can be used to determine the minimum τ achieving said performance, which estimates the specialist workload. Second, for a maximum acceptable referral rate (e.g., a clinic has specialist resources to handle referral of $\tau \leq 20\%$ of patients) the referral curve can be used to determine the optimal τ value and the corresponding model performance. For monotonically increasing referral curves, the optimal τ is uniquely the maximum acceptable referral rate.

Advantage of Epistemic Uncertainty Estimation. On the *Severity Shift* (Figure 2(**d**)) many models achieve near-perfect accuracy well before all examples have been referred. For example, MC DROPOUT, which incorporates both epistemic and aleatoric uncertainty (Appendix E.2), achieves 100% predictive accuracy near the 50% referral rate—nearly 20% lower than the deterministic neural network (MAP), which only represents aleatoric uncertainty. Other variational methods underperform MAP, underscoring the importance of continued work on uncertainty estimation.

3.2 Country Shift

The left two plots of Figure 3 presents the ROC curves of various methods evaluated on the in-domain (**a**) and *Country Shift* (**b**) evaluation datasets. The green dot in Figures 3(**a**) and (**b**) denotes the minimum sensitivity–specificity threshold set by the British National Health Service (NHS) for the deployment of automated diabetic retinopathy diagnosis systems [59]. Only the MC DROPOUT variants meet the NHS standard on the in-domain test dataset. On the APTOS dataset, essentially all methods surpass the standard; all methods appear to perform better on this shifted dataset than the in-domain dataset.[2] Hence, a practitioner using only the ROC curve and its AUC (Table 1, Appendix A) might conclude that models generalize well to the APTOS setting. However, the ROC curve does not provide information about the quality of a model's uncertainty estimates.

Uncertainty-Unaware Evaluation Can Be Misleading. Unlike the ROC curve, the selective prediction metric conveys how a model would perform in an automated diagnosis pipeline in which the quality of uncertainty estimates directly impacts performance (Figure 1). Recall that if a model has good uncertainty, AUC should increase as we refer more patients with uncertain predictions. We see this in the case of mean-field variational inference (MFVI) on the *Country Shift* (Figure 3(**d**) and Table 1), for which AUC improves from an initial 0.914 up to 0.938 when referring 50% of the patients, but then deteriorates as the model is forced to refer patients for whom predictions are both certain and correct. In contrast, other models trend downwards even at low referral rates τ, indicating that using uncertainty to refer patients actively *hurts* model performance on this shifted dataset.

Different Prediction Tasks Yield Different Method Rankings. In Figure 3(**c**), variational methods including MC DROPOUT, function-space variational inference (FSVI), and DEEP ENSEMBLE outperform MAP. This highlights that rankings are task-dependent, and hence the importance of generic evaluation frameworks like ours to enable rapid benchmarking of many tasks.

4 Conclusion

We introduced a set of prediction tasks to evaluate Bayesian deep learning methods on real-world clinical applications, including a *Country Shift* task on which existing methods fail to produce good uncertainty estimates (Section 3.2). The code for all inference methods, data processing, tuning, evaluation, and plotting, as well as model checkpoints will be open-sourced. We hope that this will significantly decrease the barrier to entry for researchers aiming to design and rigorously evaluate Bayesian deep learning methods on safety-critical medical diagnosis tasks.

[2] We investigate this in Appendix I and find that class proportions do not account for the improved predictive performance on shifted data, implying other factors such as patient population or collection devices.

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Checklist

1. For all authors...
   (a) Do the main claims made in the abstract and introduction accurately reflect the paper's contributions and scope? [Yes]
   (b) Did you describe the limitations of your work? [Yes] See Appendix B.
   (c) Did you discuss any potential negative societal impacts of your work? [Yes] We detail computational costs of the project and believe that our open-source contributions will mitigate these, as described in Appendix G.
   (d) Have you read the ethics review guidelines and ensured that your paper conforms to them? [Yes]
2. If you are including theoretical results...
   (a) Did you state the full set of assumptions of all theoretical results? [N/A] This was an empirical work.
   (b) Did you include complete proofs of all theoretical results? [N/A]
3. If you ran experiments...
   (a) Did you include the code, data, and instructions needed to reproduce the main experimental results (either in the supplemental material or as a URL)? [Yes] We provide a link to an anonymized folder where all code, documentation, and experimental scripts are provided, and will open-source these resources in the future.
   (b) Did you specify all the training details (e.g., data splits, hyperparameters, how they were chosen)? [Yes] Appendix C.1 describes the dataset splits and our contributed tasks, Appendix G.5 describes tuning details, and our code release contains tuning scripts.
   (c) Did you report error bars (e.g., with respect to the random seed after running experiments multiple times)? [Yes] We trained 6 random seeds for all selected hyperparameter configurations and reported standard error in all figures and tables.
   (d) Did you include the total amount of compute and the type of resources used (e.g., type of GPUs, internal cluster, or cloud provider)? [Yes] This is addressed in Appendix G.5.
4. If you are using existing assets (e.g., code, data, models) or curating/releasing new assets...
   (a) If your work uses existing assets, did you cite the creators? [Yes] We cite the creators of the Kaggle EyePACS [13] and APTOS 2019 [3] datasets, along with the major libraries used in our work in Appendix F.
   (b) Did you mention the license of the assets? [Yes] All Kaggle assets are fully available for public use and reproduction. Anyone with an account may access it.
   (c) Did you include any new assets either in the supplemental material or as a URL? [Yes] We include a link to our anonymized code release (which we will later open-source) in the main body and appendix.
   (d) Did you discuss whether and how consent was obtained from people whose data you're using/curating? [N/A] We are generating new tasks using fully available public datasets, e.g., provided as a public TensorFlow dataloader.
   (e) Did you discuss whether the data you are using/curating contains personally identifiable information or offensive content? [N/A] All of the data is from publicly available data sources which have been fully anonymized with respect to their clinical metadata.
5. If you used crowdsourcing or conducted research with human subjects...
   (a) Did you include the full text of instructions given to participants and screenshots, if applicable? [N/A] Does not apply – no crowdsourcing or research including human subjects.
   (b) Did you describe any potential participant risks, with links to Institutional Review Board (IRB) approvals, if applicable? [N/A] Does not apply – no crowdsourcing or research including human subjects.
   (c) Did you include the estimated hourly wage paid to participants and the total amount spent on participant compensation? [N/A] Does not apply – no crowdsourcing or research including human subjects.

Supplementary Material

Appendix A Country Shift Referral Results

Table 1: Country Shift. Prediction and uncertainty quality of baseline methods in terms of the area under the receiver-operating-characteristic curve (AUC) and classification accuracy, as a function of the proportion of data referred to a medical expert for further review. All methods are tuned on in-domain validation AUC, and ensembles have $K = 3$ constituent models (this is true for all subsequent tables unless specified otherwise). On in-domain data, MC DROPOUT performs best across all thresholds. On distributionally shifted data, no method achieves top performance across the board.

	No Referral		50% Data Referred		70% Data Referred	
Method	**AUC (%) ↑**	**Accuracy (%) ↑**	**AUC (%) ↑**	**Accuracy (%) ↑**	**AUC (%) ↑**	**Accuracy ↑**
EyePACS Dataset (In-Domain)						
MAP (Deterministic)	87.4±1.0	88.6±0.6	91.1±1.4	95.9±0.3	94.9±0.8	96.5±0.2
MFVI	83.3±0.1	85.7±0.1	85.5±0.5	94.5±0.1	88.2±0.5	95.9±0.1
RADIAL-MFVI	83.2±0.4	74.2±3.8	88.9±0.7	81.8±4.7	91.2±1.0	83.8±4.3
FSVI	88.5±0.1	89.8±0.0	91.0±0.3	96.4±0.0	94.3±0.2	97.2±0.0
MC DROPOUT	91.4±0.1	90.9±0.0	95.3±0.2	97.4±0.0	97.4±0.1	98.1±0.0
RANK-1	85.6±1.1	87.7±0.6	87.1±1.8	95.3±0.4	90.9±1.5	96.4±0.3
DEEP ENSEMBLE	90.3±0.1	90.3±0.2	91.7±0.5	97.2±0.0	95.0±0.4	97.9±0.0
MFVI ENSEMBLE	85.4±0.0	87.8±0.0	86.3±0.3	95.4±0.0	89.2±0.3	96.7±0.0
RADIAL-MFVI ENSEMBLE	85.1±0.0	77.8±1.7	91.6±0.3	87.9±1.7	94.0±0.3	90.5±1.6
FSVI ENSEMBLE	90.3±0.1	90.6±0.0	92.1±0.2	97.1±0.0	95.2±0.1	97.8±0.0
MC DROPOUT ENSEMBLE	**92.5±0.0**	**91.6±0.0**	**95.8±0.1**	**97.8±0.0**	**97.7±0.1**	**98.4±0.0**
RANK-1 ENSEMBLE	89.3±0.7	89.3±0.4	88.5±1.1	96.9±0.3	91.6±1.1	97.6±0.2
APTOS 2019 Dataset (Population Shift)						
MAP (Deterministic)	92.2±0.2	86.2±0.4	80.1±2.8	87.6±1.1	55.4±3.3	85.4±0.9
MFVI	91.4±0.2	84.1±0.3	93.8±0.3	92.1±0.4	93.0±0.5	92.7±0.4
RADIAL-MFVI	90.7±0.5	71.8±3.5	82.0±2.0	81.5±2.1	66.4±1.7	85.9±0.7
FSVI	94.1±0.1	87.6±0.4	90.6±0.7	90.7±0.6	77.2±3.6	89.8±0.2
MC DROPOUT	94.0±0.2	86.8±0.2	87.4±0.3	88.1±0.2	65.3±1.3	88.2±0.3
RANK-1	92.5±0.2	86.2±0.4	90.1±1.9	91.4±0.8	75.1±6.0	89.5±1.2
DEEP ENSEMBLE	94.2±0.2	87.5±0.1	91.2±1.4	92.4±0.7	67.4±5.6	90.1±0.9
MFVI ENSEMBLE	93.2±0.1	87.0±0.2	**94.9±0.3**	**93.7±0.3**	**94.2±0.2**	**94.0±0.3**
RADIAL-MFVI ENSEMBLE	91.8±0.2	71.7±1.9	81.8±1.5	82.7±1.3	65.9±3.1	87.6±0.5
FSVI ENSEMBLE	**94.6±0.0**	**88.9±0.1**	90.7±0.4	91.1±0.5	74.1±2.6	89.8±0.2
MC DROPOUT ENSEMBLE	94.1±0.1	87.6±0.1	86.8±0.2	88.0±0.1	62.3±0.3	87.7±0.2
RANK-1 ENSEMBLE	94.1±0.1	88.2±0.1	**94.8±0.3**	93.3±0.2	92.1±1.2	93.7±0.3

Appendix B Limitations and Further Discussion

We note two potential limitations of this benchmark. While the selective prediction task on the *Severity Shift* evaluation dataset sufficiently differentiates performance between the methods considered (Figure 2(**c**) and (**d**)), it is conceivable that as many factors across (Bayesian) deep learning continue to improve—e.g., network architectures, uncertainty quantification methods, and the feasibility of large-scale pretraining and ensembling—performance could be saturated (i.e., in Figure 2(**d**), models might achieve 100% accuracy at a very low τ). In addition, any individual prediction task is inherently limited in its ability to reflect the reliability of predictive models on other tasks.

We hope that this work will address these potential shortcomings by significantly decreasing the barrier to entry for researchers aiming to design and rigorously evaluate Bayesian deep learning methods on safety-critical medical diagnosis tasks. By following the best practices that we apply here, future uncertainty-aware benchmarking tasks would help ensure that new Bayesian deep learning methods are reliably safe across a wide array of safety-critical real-world settings.

Appendix C Source Datasets

C.1 Data and Preprocessing

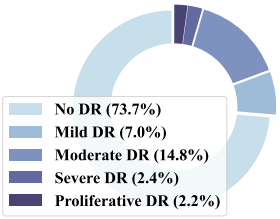
EyePACS Dataset. We construct training datasets for different tasks from the EyePACS dataset, previously used for the Kaggle Diabetic Retinopathy Detection Challenge [13]. It contains high-resolution labeled images of human retinas exhibiting varying degrees of diabetic retinopathy. The

dataset consists of 35,126 training, 10,906 validation, and 42,670 test images, each an RGB image of a human retina graded by a specialist on the following scale: 0 (no diabetic retinopathy), 1 (mild diabetic retinopathy), 2 (moderate diabetic retinopathy), 3 (severe diabetic retinopathy), and 4 (proliferative diabetic retinopathy).

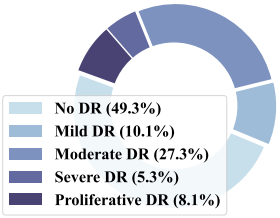
APTOS Dataset. To construct tasks that assess predictive models' performance under distribution shift, we use the APTOS 2019 Blindness Detection dataset [3]. The dataset also contains labeled images of human retinas exhibiting varying degrees of diabetic retinopathy, but was collected in India, from a different patient population, using different medical equipment. We use 80% of the images (2,929 images) as a test set and the other 20% (733 images) as a secondary validation set. Moreover, the images are significantly noisier than the images in the EyePACS dataset, with distinct visual artifacts. Each image was graded on the same 0-to-4 scale as the EyePACS dataset.

Prediction Targets. We follow Leibig et al. [37] and binarize the data by dividing the classes up into sight-threatening diabetic retinopathy—defined as moderate diabetic retinopathy or worse (classes $\{2, 3, 4\}$)—and non-sight-threatening diabetic retinopathy—defined as no or mild diabetic retinopathy (classes $\{0, 1\}$). This threshold corresponds to the point at which international guidelines recommend referral of a case to an ophthalmologist [60]. The data in both datasets is binarized in this way. Reflecting real-world challenges, the dataset is unbalanced, with only 19.6% of the training set and 19.2% of the test set having a positive label, and contains visual artifacts and noisy labels (i.e., some images are labeled incorrectly).

Data Preprocessing. Data preprocessing on both the EyePACS and APTOS datasets follows the winner of the Kaggle Challenge [13]: images are resized so that the radius of an eyeball is 300 pixels, are cropped to 90% of the radius, are encoded with 72 JPEG quality, and finally are resized to 512×512 pixels with all three color channels used. Examples of original images and corresponding processed images are provided in Figure 5.



(a) EyePACS [13].



(b) APTOS [3].

Figure 4: Data class labels.

Appendix D Task Datasets

D.1 Severity Shift

For this prediction task, we partition the EyePACS dataset into a subset containing all retina images labeled as no, mild, or moderate diabetic retinopathy (original classes $\{0, 1, 2\}$) and a subset of retina images labeled as exhibiting signs of severe or proliferative diabetic retinopathy (original classes $\{3, 4\}$).

Next, the samples in each subset are binarized as described in Appendix C.1: the subset of retina images showing signs of at most moderate diabetic retinopathy (subset "moderate") contains images of binarized classes $\{0, 1\}$; and the subset of retina images showing signs of severe or proliferative diabetic retinopathy (subset "severe") only contains the binarized class 1. This results in 33,545 images in the training set, and 40,727 and 3,524 images in the in-domain and distributionally shifted evaluation sets, respectively.

D.2 Country Shift

In the *Country Shift* task, we train on EyePACS data and use the APTOS data as a distributionally shifted evaluation dataset. We use the entire training and test data provided in the EyePACS dataset and convert the task into binary classification: we assign class labels 0 to images exhibiting 'no or mild signs of diabetic retinopathy' (original classes $\{0, 1\}$) and 1 to images exhibiting 'moderate or worse signs of diabetic retinopathy' (original classes $\{2, 3, 4\}$). This results in 35,126 images in the training set, and 42,670 and 2,929 images in the in-domain and distributionally shifted evaluation sets, respectively.

Appendix E Background

E.1 Related Work

This benchmark builds on prior works that demonstrated the usefulness of predictive uncertainty estimates in diabetic retinopathy detection and related downstream tasks [37]. We significantly extend the empirical evaluation in Leibig et al. [37] by designing new prediction problems and corresponding safety-critical downstream tasks for diabetic retinopathy detection, benchmarking a wide array of Bayesian deep learning methods, and providing a modular, extensible, and easy-to-use codebase. We also significantly extend Filos et al. [16], which does not consider severity shifts, only compares two variational inference methods, uses an outdated neural network architecture (with only $\approx$10% of the parameters of the ResNet-50 architecture used in this work), and considers only a small subset of the evaluation procedures included in this benchmark (see Appendix I for the full set of results).

Previous works have evaluated methods by predictive performance and quality of their predictive uncertainty estimates on curated datasets such as CIFAR-10 and FashionMNIST [45, 46, 24, 49]. Some prior works provide datasets and benchmarks for robustness and uncertainty quantification in real-world settings but have significant shortcomings. [36] considers object detection using a real-world dataset [20] but benchmarks only two methods, neither of which can quantify epistemic uncertainty (cf. Appendix E.2), and does not consider distributionally shifted evaluation data. [5, 15] use methods which quantify both epistemic and aleatoric uncertainty, and consider distribution shifts, but use performance metrics which do not sufficiently assess quality of uncertainty estimates, such as average precision and negative log-likelihood (cf. Section 3.2). Finally, [34] considers real-world datasets in domain adaptation, which restrictively assumes that the training data is composed of multiple training distributions with domain labels, and does not consider uncertainty quantification.

In contrast, our benchmark considers real-world safety-critical tasks and accompanying uncertainty-aware metrics in an important application domain, is composed of large amounts of high-dimensional data (>80 GB), compares a larger set of methods than prior works which notably can quantify both aleatoric and epistemic sources of uncertainty, and is implemented in adherence to software design best practices for easy future use and extension (see Appendix F), making it easier to benchmark other Bayesian deep learning methods not only on the tasks presented but also on a range of other datasets.

E.2 Uncertainty Estimation

Predictive models' total uncertainty can be decomposed into aleatoric and epistemic uncertainty. A model's aleatoric uncertainty is an estimate of the uncertainty inherent in the data (e.g., due to noisy inputs or targets), whereas a model's epistemic uncertainty is an estimate of the uncertainty due to constraints on the model (e.g., due to model misspecification) or the training process (e.g., due to convergence to a bad local optimum) [11]. For a model with stochastic parameters $\boldsymbol{\Theta}$, pre-likelihood outputs $f(\mathbf{X}; \boldsymbol{\theta})$, and a likelihood function $p(\mathbf{y} \mid f(\mathbf{X}; \boldsymbol{\theta}))$ and likelihood $p(\mathbf{y}_* \mid \mathbf{x}_*;\, \boldsymbol{\theta})$, its predictive uncertainty can be decomposed as

$$\underbrace{\mathcal{H}(\mathbb{E}[p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta}))])}_{\text{Total Uncertainty}} = \underbrace{\mathbb{E}[\mathcal{H}(p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta})))]}_{\text{Aleatoric Uncertainty}} + \underbrace{\mathcal{I}(\mathbf{y}_*;\, \boldsymbol{\Theta})}_{\text{Epistemic Uncertainty}}, \tag{E.1}$$

where the expectation is taken with respect to the model parameters, $\mathcal{H}(\cdot)$ is the entropy functional, and $\mathcal{I}(\mathbf{y}_*;\, \boldsymbol{\Theta})$ is the mutual information between the model parameters and its predictions [10, 51].

In binary classification settings with classes $\{0, 1\}$, the total predictive uncertainty is given by

$$\mathcal{H}(\mathbb{E}[p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta}))]) = -\sum_{c \in \{0,1\}} \mathbb{E}[p(\mathbf{y}_* = c \mid f(\mathbf{x}_*; \boldsymbol{\theta}))] \log \mathbb{E}[p(\mathbf{y}_* = c \mid f(\mathbf{x}_*; \boldsymbol{\theta}))], \tag{E.2}$$

where $f(\mathbf{x}_*; \boldsymbol{\theta})$ are logits and $p(\mathbf{y}_* = c \mid f(\mathbf{x}_*; \boldsymbol{\theta}))$ is a binary cross-entropy likelihood function. The total predictive uncertainty is high when either the aleatoric uncertainty is high (e.g., because the input is noisy), or when the epistemic uncertainty is high (e.g., because the model has many possible explanations for the input). In practice, the total predictive uncertainty $\mathcal{H}(\mathbb{E}[p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta}))])$ is computed with a Monte Carlo estimator $\mathbb{E}[p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta}))] \approx \frac{1}{S} \sum_i^S p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta}^{(i)}))$, where $\{\boldsymbol{\theta}^{(i)}\}_{i=1}^S$ are sampled from some distribution over the network parameters, and $p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta}^{(i)}))$ is a deterministic forward pass given parameter realization $\boldsymbol{\theta}^{(i)}$.

This Monte Carlo estimator of the total uncertainty is biased but consistent and commonly used in practice [7, 11, 19]. A model's aleatoric uncertainty, $\mathbb{E}[\mathcal{H}(p(\mathbf{y}_* \mid f(\mathbf{x}_*; \boldsymbol{\theta})))]$ is estimated analogously, and the epistemic uncertainty can then be computed as the difference between the total and the aleatoric predictive uncertainty estimates.

E.3 Bayesian Deep Learning Methods

Estimating a model's predictive uncertainty in terms of both aleatoric and epistemic uncertainty requires a *distribution over model predictions*. Such a distribution over model predictions can be obtained by treating the parameters of a neural network as random variables and inferring a posterior distribution $p(\boldsymbol{\theta} \mid \mathcal{D})$—a distribution over the network parameters conditioned on a set of training data $\mathcal{D} = (\mathbf{X}, \mathbf{y})$—according to the rules of Bayesian inference. Neural networks with such distributions over the network parameters—referred to as a Bayesian neural networks (BNN)—define distribution over predictions and are able to capture both aleatoric and epistemic uncertainty [18, 39, 43]. These models have been shown to be robust to over-fitting and to provide useful predictive uncertainty estimates for a variety of real-world problems [37, 27, 53]. Unfortunately, computing a posterior distribution over the parameters of a neural network according to the rule of Bayesian inference is analytically intractable and requires the use of approximate inference methods [18, 21, 25, 43, 48]. Below, we describe the baseline and state-of-the-art methods for which we implement standardized and optimized runscripts in the benchmark, which are readily extensible for experimentation and deployment in application settings.

E.3.1 Maximum A Posteriori Estimation in Bayesian Neural Networks

As an alternative to inferring a posterior distribution over neural network parameters, maximum a posteriori (MAP) estimation yields network parameter values equal to the mode of the exact posterior distribution. For a prior distribution over network parameters with zero mean and precision λ, the maximum a posteriori estimate is equal to the solution of the ℓ_2-regularized optimization problem $\arg\min_{\boldsymbol{\theta}}\{-\log p(\mathbf{y} \mid f(\mathbf{X}; \boldsymbol{\theta})) + \lambda ||\boldsymbol{\theta}||_2^2\}$, and as such is equivalent to parameter values obtained by training a neural network with weight decay. Since MAP estimation results in a deterministic neural network, MAP models are unable to capture any epistemic uncertainty. In classification tasks, they represent aleatoric uncertainty estimates via the predicted class probabilities [32]. We use neural networks with MAP estimation as a baseline for the benchmark.

E.3.2 Variational Inference in Bayesian Neural Networks

Variational inference is an approximate method that seeks to avoid the intractability of computing the exact posterior distribution over the network parameters by framing posterior inference as a variational optimization problem. This way, we can find an approximation to the posterior distribution over parameters by solving the optimization problem

$$\operatorname{argmax}_{q \in \mathcal{Q}}\{\mathbb{E}_q[\log p(\mathbf{y} \mid f(\mathbf{X}; \boldsymbol{\theta}))] - \mathbb{D}_{\mathrm{KL}}(q \,\|\, p)\}, \tag{E.3}$$

where $\mathcal{Q}$ is a variational family of distributions and p is a prior distribution.

Gaussian Mean-Field Variational Inference. If $p \doteq p(\boldsymbol{\theta})$ and $q \doteq q(\boldsymbol{\theta})$ are distributions over parameters, $\mathcal{Q}$ is the family of mean-field (that is, fully-factorized) Gaussian distributions, and the prior distribution over parameters $p(\boldsymbol{\theta})$ is also a diagonal Gaussian, the resulting variational objective is amenable to stochastic variational inference and can be optimized using stochastic gradient methods [6, 21, 25, 26, 56]. Henceforth, we will refer to BNN inference methods that make these variational assumptions as mean-field variational inference. To optimize this objective, the expectation is estimated using Monte Carlo sampling and the network parameters are reparameterized as $\boldsymbol{\Theta} \doteq \boldsymbol{\mu} + \boldsymbol{\sigma} \odot \boldsymbol{\epsilon}$ with $\boldsymbol{\epsilon} \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$. In our benchmark, we use the flipout estimator [57] to reduce the variance of the gradient estimates. Following Wenzel et al. [58], we temper the Kullback-Leibler divergence term in the variational objective.

Radial-Gaussian Mean-Field Variational Inference. Radial-Gaussian mean-field variational inference [14] uses the same variational objective, prior, and variational distribution as standard Gaussian mean-field variational inference, but uses an alternative gradient estimator to obtain an improved signal-to-noise ratio in the gradient estimates. Specifically, the network parameters are reparameterized as $\boldsymbol{\Theta} \doteq \boldsymbol{\mu} + \boldsymbol{\sigma} \odot \frac{\boldsymbol{\epsilon}}{||\boldsymbol{\epsilon}||_2} \cdot |r|$ with $\boldsymbol{\epsilon} \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$ and $r \sim \mathcal{N}(0, 1)$.

Function-Space Variational Inference. Rudner et al. [49] proposed a tractable function-space variational objective for Bayesian neural networks. If $p \doteq p(f(\mathbf{X}_\mathcal{I}; \boldsymbol{\theta}))$ and $q \doteq q(f(\mathbf{X}_\mathcal{I}; \boldsymbol{\theta}))$ are distributions over functions evaluated at a set of inducing inputs $\mathbf{X}_\mathcal{I}$, $\mathcal{Q}$ is the family of distributions over functions induced by some distribution over network parameters, and the Kullback-Leibler divergence between distributions over functions evaluated at $\mathbf{X}_\mathcal{I}$ is approximated by a linearization of the neural network mapping, then the resulting variational objective is amenable to stochastic variational inference. In our benchmark, we define a Gaussian mean-field distribution over the final layer of the neural network and reparameterize the parameters as $\boldsymbol{\Theta} \doteq \boldsymbol{\mu} + \boldsymbol{\sigma} \odot \boldsymbol{\epsilon}$ with $\boldsymbol{\epsilon} \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$.

Monte Carlo Dropout. Gal and Ghahramani [19] showed that training a deterministic neural network with ℓ_2- and dropout regularization [54], that is, solving the optimization problem $\arg\min_{\boldsymbol{\theta}}\{-\mathbb{E}_q[\log p(\mathbf{y} \mid f(\mathbf{X}; \boldsymbol{\theta}))] + \lambda ||\boldsymbol{\theta}||_2^2\}$, where $q(\boldsymbol{\theta})$ is the distribution over parameters obtained by applying dropout with a given dropout rate, approximately corresponds to variational inference in a Bayesian neural network. To sample from the approximate posterior predictive distribution, dropout is applied to the deterministic network parameters. To optimize the objective above, the expectation is estimated using a single Monte Carlo sample (simply applying dropout at training).

Rank-1 Parameterization. Dusenberry et al. [12] propose a rank-1 parameterization of Bayesian neural networks, where each weight matrix involves only a distribution on a rank-1 subspace, that is, each stochastic weight matrix is defined as $\mathbf{W}'_k = \mathbf{W}_k \odot \mathbf{r}_k \mathbf{s}_k^\top$, where $\mathbf{W}_k$ is a deterministic set of weights, and $\mathbf{r}_k$ and $\mathbf{s}_k$ are random vectors of parameters. Variational distributions over $\mathbf{r}_k$ and $\mathbf{s}_k$ and a Dirac delta distribution over $\mathbf{W}_k$ for all layers k are obtained by optimizing a variational objective.

E.3.3 Model Ensembling

Deep Ensembles. A deep ensemble [35] is a mixture of multiple independently-trained deterministic neural networks. As such, unlike BNNs, deep ensembles do not explicitly infer a distribution over the parameters of a single neural network. Instead, deep ensembles marginalize over multiple deterministic models to obtain a predictive distribution that captures both aleatoric and epistemic uncertainty. In our benchmark, we construct deep ensembles from multiple neural network parameter MAP estimates obtained by training with different random seeds.

Ensembles of Bayesian Neural Networks. An ensemble of Bayesian neural networks [52] is a mixture of multiple independently-trained Bayesian neural networks. They can account for the possibility that any individual approximate posterior distribution obtained via variational inference may be a poor approximation to the exact posterior distribution and hence yield a poor predictive distribution. A common issue in Bayesian deep learning literature is that certain methods are compared with ensembling to others without, often due to computational constraints. In our benchmark, we provide a unified comparison and construct ensembles for all methods, including variational methods.

Appendix F Benchmark Software Design Principles

Reproducibility in machine learning is often hampered by the wide variety of experimental artifacts made available in papers. Perhaps the most common approach is a GitHub dump of experimental code lacking documentation and testing. This common practice fails to enforce a rigorous standard across works: for example, experiment protocol on cross-validation, access to distributionally shifted validation data, and various tweaks in optimization such as learning rate annealing.

The Diabetic Retinopathy Detection Benchmark conforms to explicit design principles intended to facilitate easy extension and reproduction of dataset loading utilities, metrics, and evaluation.

Extensibility. Each model baseline (e.g., MAP, MC DROPOUT, FSVI) is implemented in its own self-contained experiment pipeline. This minimizes external dependencies, and therefore provides researchers and practitioners an immediate starting point for experimenting with a particular model. Datasets are implemented as lightweight wrappers around TensorFlow Datasets [55]. Users that wish to extend our benchmark with new datasets (e.g., clinical practitioners that wish to apply our methods on their own diabetic retinopathy tasks) can follow our custom implementation of the APTOS [3] data loader, which constructs the dataset from raw images and a CSV containing metadata, and applies the preprocessing used by the winner of the EyePACS Kaggle competition [13]. Dataset implementation can be found in the code release.

Framework Agnosticity. The Diabetic Retinopathy Detection Benchmark is framework-agnostic. For example, FSVI is implemented in JAX, a variant of MC Dropout is in PyTorch [47] (though we use in this work a TensorFlow variant to simplify TPU tuning), and other models in raw TensorFlow [1]. This interoperability means that users can easily incorporate our datasets and evaluation utilities, including an arrangement of robustness and uncertainty metrics such as *selective prediction*, *out-of-distribution detection*, and *expected calibration error*.

Reproducibility. All models include testing, and all results are reported over multiple seeds. For each method (e.g., MC DROPOUT or MFVI), downstream task (*Country* and *Severity Shift*), and tuning assumption (whether or not distributionally shifted validation data is available for tuning), we test over at least 32 hyperparameter configurations. Instead of using a domain-specific and limiting tuning framework for this, we simply provide hyperparameters through Python flags, and implement for convenience of the user the ability to specify automatic logging to TensorBoard and Weights & Biases [4], an increasingly popular deep learning experiment management service.

Appendix G Training and Evaluation Details

G.1 Network Architecture

We use a ResNet-50 architecture for all experiments [22]. A sigmoid transformation is applied to the final linear layer of all networks to obtain class probabilities corresponding to the outcomes of the binary classification problems described in Section 2.

G.2 Access to Distributionally Shifted Validation Data

Reliable uncertainty estimation on data points from shifted distributions is the central challenge for Bayesian deep learning methods. In training and evaluating such methods, practitioners must decide how they should choose validation data: specifically, in which settings they would benefit from using "out-of-distribution" data points for hyperparameter tuning. We consider two real-world settings: **(i)** No distributionally shifted data is available during hyperparameter tuning, as when a practitioner does not know what data or distributional shift she might see at deployment and hence cannot make assumptions about it at training time. **(ii)** Shifted validation data *is* available for hyperparameter tuning. For example, if a practitioner intends to train a model on US data and deploy it in India, she may acquire a small number of Indian examples for use in tuning to improve generalization. Works in out-of-distribution detection [23] and Prior Networks [40] have considered **(ii)**, but have not provided a comparative analysis, which would inform practitioners on when they ought to collect shifted validation data for tuning. We rigorously investigate the two settings across downstream tasks in Appendix I. In the main paper, we report results for models tuned under **(i)**.

G.3 Adjusting for Class Imbalance

We compensate for the class imbalance discussed in Section 2 by reweighing the cross-entropy portion of each objective function, placing more weight on the minority class based on the relative class frequencies in each mini-batch of M samples, $p(k)_{\text{mini-batch}}$ [37]:

$$\mathcal{L} = -\frac{1}{KM} \sum_{i=1}^{M} \frac{\mathcal{L}_{\text{cross-entropy}}(i)}{p(k)_{\text{mini-batch}}}, \tag{G.4}$$

where k is the class of sample i. We also tried using constant class weights, but found that this resulted in lower overall performance.

G.4 Mean-Field Variational Inference Implementation Details

We employ a set of standard optimizations to improve training stability for the MFVI and RADIAL-MFVI methods. We fix the mean of the prior to that of the variational posterior, which causes the KL term to only penalize the standard deviation of the weight posterior, and not its mean. We use flipout for lower-variance gradients in convolutional layers and the final dense layer [57], and KL annealing using a cyclical schedule, following [8]. Finally, for RADIAL-MFVI, the prior's standard deviation is by default set to the He initializer standard deviation $\sqrt{2/\text{fan_in}}$ [43].

G.5 Hyperparameter Tuning

We provide full tuning details so that users of the benchmark will be able to reproduce our results.

All tuning scripts across all methods, tasks (*Country* and *Severity Shift*), and tuning procedures (on in-domain validation AUC and area under the selective prediction accuracy curve using the joint validation dataset, described in Appendix H) are provided in our code release[3] and will be open-sourced.

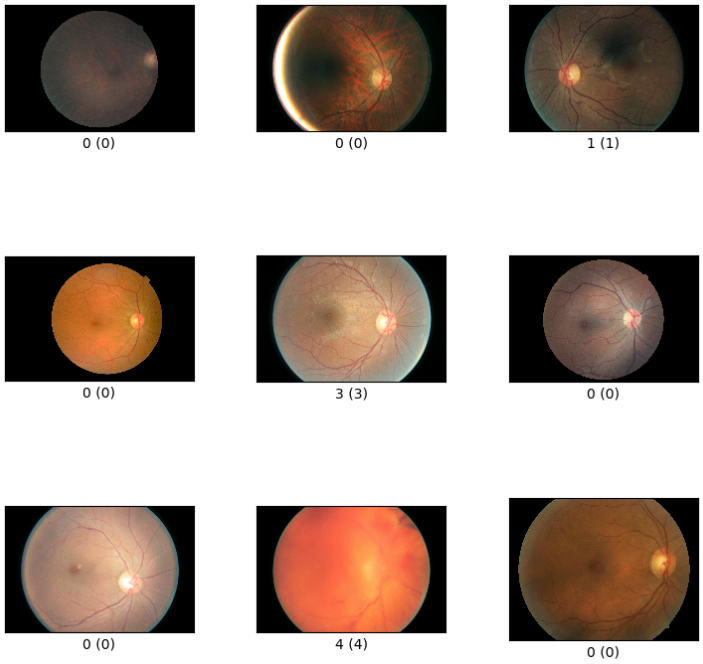
We tuned each model with a quasi-random search on several hyperparameters including learning rate, momentum, ℓ_2 regularization, and method-specific variables including dropout rate and variational posterior initializations. We used a minimum of 32 trials per model. Because of the large size of the input data and significant expense of multiple Monte Carlo samples at training time for some of the variational methods (in particular, MFVI, RANK-1, and RADIAL-MFVI), we were unable to achieve a large batch size with multiple variational samples at training time. With a single variational sample at training time, we were able to fit more reasonable batch sizes (≥ 64) and found this to significantly improve convergence and performance on validation metrics. We attribute this to the batch size increase and the usage of variance reduction techniques such as flipout layers [57], which mitigate the impact of only using a single variational sample.

We considered model selection for each of the models on each of the two tasks (*Country* and *Severity Shift*) using two different validation metrics: in-domain validation AUC, and area under the accuracy referral curve constructed using both in-domain and distributionally shifted validation data. We describe the reasoning behind the latter metric in Appendix H. We used this validation performance to select the best hyperparameter setting and retrained a configuration for each combination of model, task, and validation tuning metric for 6 random seeds. We evaluated single models by averaging performance over those seeds, and evaluated ensembles by randomly sampling ensembles of size 3 without replacement from the 6 available models, and averaging over 6 such ensemble constructions.

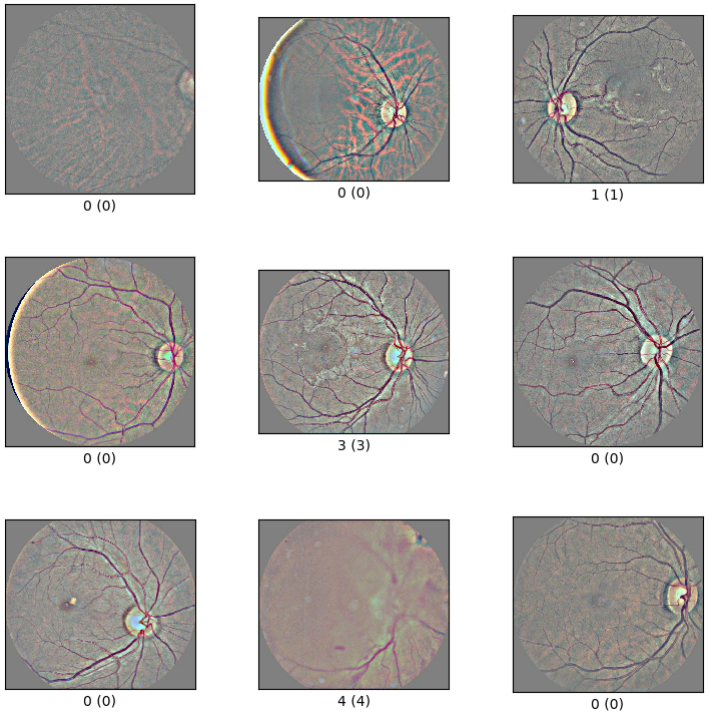
Compute Resources. The majority of methods were tuned on TPU v2-8 nodes. MFVI had particularly high memory requirements which required the use of TPU v3-8 nodes to achieve a reasonable batch size and stable training. Evaluation was performed on NVIDIA A100 GPUs with 40 GB memory, though GPUs with standard sizes (e.g., >6 GB) will be sufficient to run evaluation and inference with the models in the benchmark, e.g., using the model checkpoints. Approximately 100 TPU days and 20 GPU days were used collectively across the initial hyperparameter tuning, fine-tuning with selected configurations, and evaluation across the various tasks. Though a significant cost, we hope that our open-sourcing of all code along with hyperparameter sweep details and checkpoints will significantly decrease future consumption of researchers interested in designing deep models for diabetic retinopathy, along with Bayesian deep learning researchers using our configurations to inform their hyperparameter tuning, or our generally applicable evaluation utilities.

Receiver-Operating Characteristic Curves and Predictive Performance. The ROC curve (e.g., see Figure 3(**a**) and (**b**)) illustrates the diagnostic ability of a binary classification system as a function of the discrimination threshold. The curve is created by plotting the true positive rate (that is, the sensitivity) against the false positive rate (that is, $1 -$ specificity). The quality of the ROC curve can be summarized by the area under the curve, which ranges from 0.5 (chance level) to 1.0 (perfect classification).

[3] `rebrand.ly/dr-distshift2021`



(a) Original samples from the EyePACS Diabetic Retinopathy dataset [13].



(b) Processed and augmented samples from the EyePACS Diabetic Retinopathy dataset, following the procedure of the Kaggle competition winner [13].

Figure 5: Illustrative examples of retina images in the original EyePACS dataset (top) and after preprocessing (bottom).

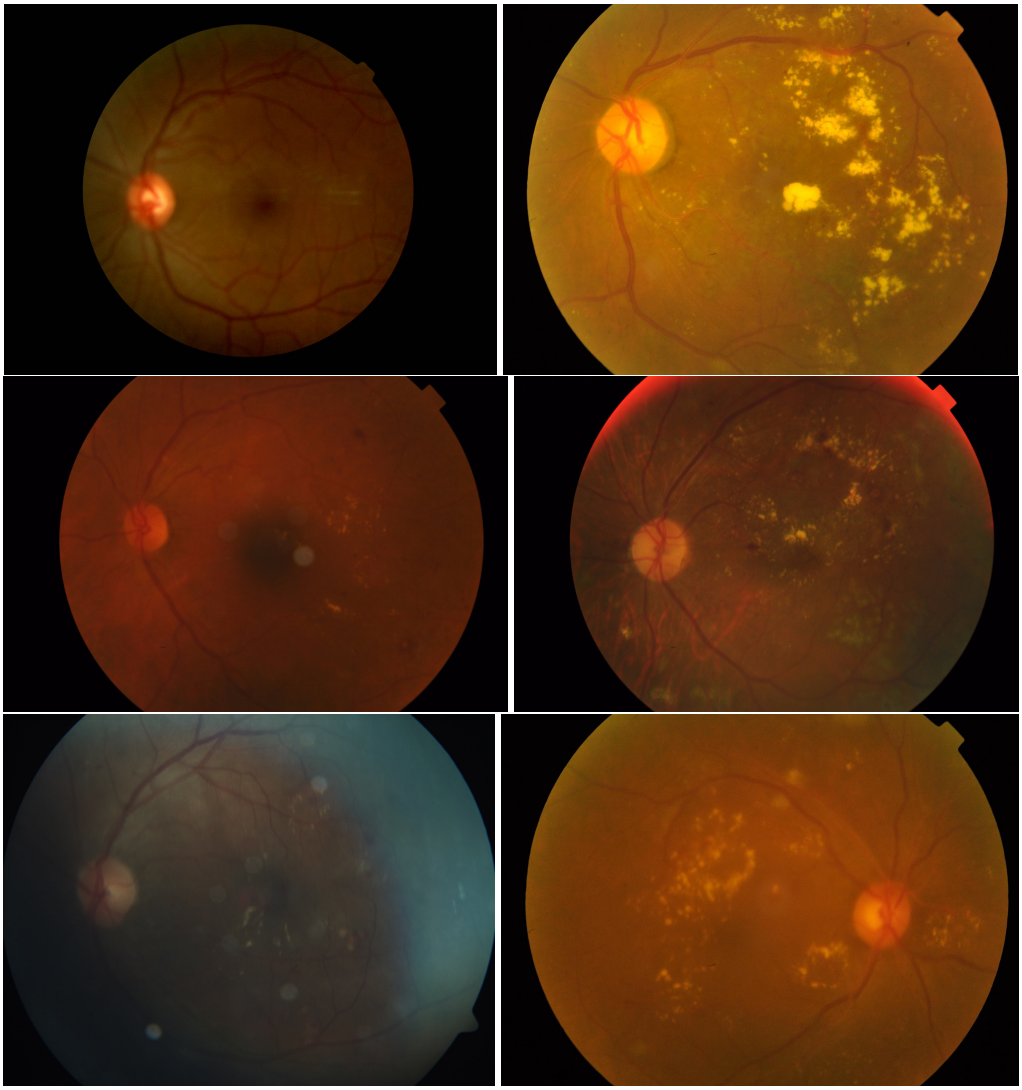


Figure 6: Illustrative examples of retina images in the APTOS dataset. The images are collected using different measurement devices than the EyePACS dataset. Note the artifacts present in the images including blur, low background lighting, and effects around the edges of the retina.

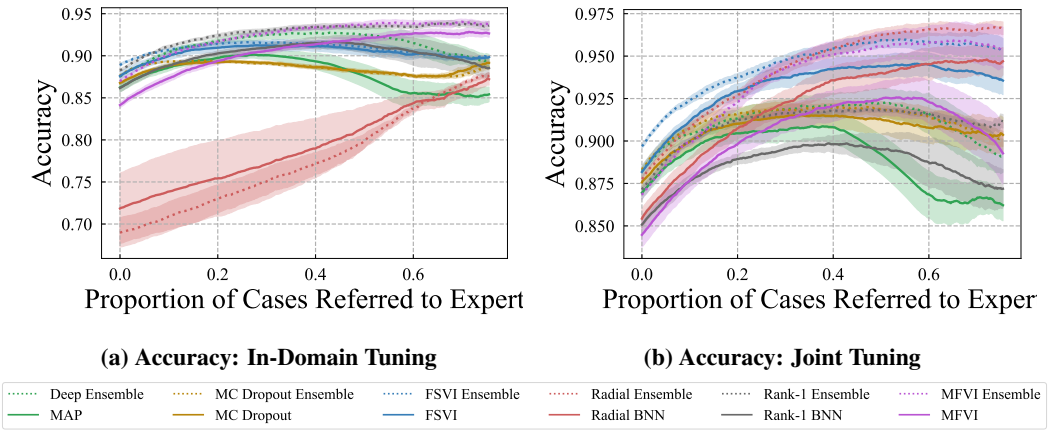
Appendix H Tuning in the Presence of Distributionally Shifted Data

In prior work in Bayesian deep learning, little emphasis has been placed on the standardization of a training and evaluation protocol; in particular, the assumption of whether a model has access to distributionally shifted validation data for hyperparameter tuning is often changed on an ad-hoc basis across studies.

This is a significant assumption, and researchers in Bayesian deep learning should be expected to outwardly declare their tuning procedure—in particular access to distributionally shifted data—as is done in works such as Prior Networks [40, 41]. This will permit researchers and practitioners to more fairly compare the performance of methods based on results reported in their respective papers.

We investigate what impact this assumption—access to distributionally shifted validation data—has on downstream performance across all our tasks, and on held-out in-domain, distributionally shifted, and joint (in-domain combined with distributionally shifted) evaluation datasets. We find that it has a significant impact on metrics commonly used to assess robustness and uncertainty quantification, including area under referral curves (Figure 7) and expected calibration error (Appendix I).

Joint Validation Metric. To consider the performance of our baseline models under this assumption, we construct a metric that conveys both in-domain and distributionally shifted performance. In particular, we construct an accuracy referral curve on a combined set of in-domain and distributionally shifted validation examples. Because the in-domain validation dataset is significantly larger than the distributionally shifted dataset for both of the tasks, we upsample the shifted dataset to avoid the signal from the in-domain examples overwhelming that from the shifted examples. We construct an *upsampled shifted dataset* by first duplicating the shifted validation dataset as many times as possible without exceeding the size of the in-domain validation dataset, and then randomly sampling examples from the shifted validation dataset without replacement until the upsampled shifted dataset contains the same number of examples as the in-domain validation dataset. We construct the "balanced" joint validation dataset as the union of the in-domain validation and upsampled shifted datasets. We construct a "balanced" accuracy referral curve using this balanced joint validation dataset, sweeping over τ to obtain all possible partitions of the dataset into "referral" and "non-referral". We then tune on the area under this curve.



(a) Accuracy: In-Domain Tuning **(b) Accuracy: Joint Tuning**

Figure 7: Hyperparameter Tuning on Distributionally Shifted Data. Accuracy referral curve on the distributionally shifted APTOS dataset in the Country Shift task. **Left:** Performance of various methods when using the in-domain validation AUC for hyperparameter tuning. **Right:** The same methods when using the proposed balanced referral metric evaluated over a combination of in-domain and distributionally shifted validation data. Even without permitting a model to explicitly train on distributionally shifted data, the model selection process results in significantly improved predictive performance and quality of uncertainty estimates, as demonstrated by curves for respective methods shifted upwards, and steeper slopes in each curve as the first $\approx 50\%$ of cases are referred to an expert, respectively.

Appendix I Additional Experiments

I.1 Tabular Results

We report additional tabular results for standard predictive performance and robustness (expected calibration error), referral metrics, and out-of-distribution detection across the *Severity* and *Country* tasks, considering hyperparameter tuning on either in-domain validation AUC or the joint validation metric (see Appendix H), in Tables 2-11.

Table 2: Severity Shift. Prediction and uncertainty quality of baseline methods in terms of area under the receiver-operating-characteristic curve (AUC) and classification accuracy, as a function of the proportion of data referred to a medical expert for further review.

	No Referral		50% Data Referred		70% Data Referred	
Method	**AUC (%) ↑**	**Accuracy (%) ↑**	**AUC (%) ↑**	**Accuracy (%) ↑**	**AUC (%) ↑**	**Accuracy ↑**
In-Domain (No, Mild, or Moderate DR, Clinical Labels {0,1,2})						
MAP (Deterministic)	82.0±1.0	87.9±0.4	83.1±1.9	95.2±0.3	88.4±1.9	96.0±0.2
DEEP ENSEMBLE	85.1±0.7	89.3±0.2	82.0±0.9	96.3±0.2	85.3±0.9	97.3±0.2
MC DROPOUT	89.2±0.2	90.5±0.1	92.8±0.6	97.2±0.0	95.4±0.4	97.8±0.0
MC DROPOUT ENSEMBLE	**90.6±0.0**	**91.4±0.1**	**93.1±0.2**	**97.8±0.0**	**95.7±0.2**	**98.2±0.0**
FSVI	83.2±0.3	89.5±0.1	81.2±0.9	95.6±0.1	86.4±0.7	96.4±0.1
FSVI ENSEMBLE	86.2±0.1	90.0±0.0	81.2±0.3	96.4±0.0	86.1±0.3	97.3±0.0
RADIAL-MFVI	76.9±1.6	86.7±0.4	69.0±4.1	93.5±0.5	70.1±4.8	94.6±0.5
RADIAL-MFVI ENSEMBLE	81.3±1.2	87.4±0.3	66.3±2.3	95.1±0.4	66.2±3.0	96.1±0.4
RANK-1	81.6±1.5	88.3±0.5	79.4±2.9	95.1±0.4	82.9±2.9	96.0±0.4
RANK-1 ENSEMBLE	85.1±1.1	89.3±0.4	75.6±1.0	96.1±0.3	79.1±1.3	96.9±0.2
MFVI	81.3±1.4	87.8±0.6	79.5±2.4	95.0±0.4	82.6±2.6	95.9±0.3
MFVI ENSEMBLE	85.2±0.6	89.4±0.3	77.7±0.9	96.1±0.2	80.3±1.0	96.8±0.1
Severity Shift (Severe or Proliferate DR, Clinical Labels {3, 4})						
MAP (Deterministic)	–	74.4±1.9	–	93.2±2.6	–	98.6±1.1
DEEP ENSEMBLE	–	74.5±1.2	–	89.8±1.0	–	97.0±0.7
MC DROPOUT	–	86.4±1.3	–	**99.5±0.2**	–	**100.0±0.0**
MC DROPOUT ENSEMBLE	–	**87.4±0.3**	–	99.4±0.1	–	**100.0±0.0**
FSVI	–	68.6±1.0	–	88.5±1.0	–	99.6±0.2
FSVI ENSEMBLE	–	69.3±0.3	–	86.3±0.5	–	99.4±0.2
RADIAL-MFVI	–	52.0±7.6	–	59.3±10.8	–	63.9±11.1
RADIAL-MFVI ENSEMBLE	–	54.4±4.7	–	58.0±7.6	–	60.6±8.3
RANK-1	–	67.5±3.5	–	82.6±4.2	–	92.7±2.2
RANK-1 ENSEMBLE	–	69.7±1.9	–	81.6±1.6	–	92.0±1.3
MFVI	–	71.5±2.3	–	86.7±3.1	–	94.1±2.0
MFVI ENSEMBLE	–	73.5±1.2	–	87.4±0.7	–	94.2±0.7

Table 3: OOD Detection Metrics. We assess model uncertainty quantification across both shift tasks by using predictive entropy to detect out-of-distribution data.

	Country Shift		Severity Shift	
Method	**AUROC (%) ↑**	**AUPRC (%) ↑**	**AUROC (%) ↑**	**AUPRC (%) ↑**
MAP (Deterministic)	37.6±1.3	5.2±0.2	44.0±2.7	9.3±0.6
DEEP ENSEMBLE	41.7±1.0	5.6±0.1	56.8±0.9	12.4±0.3
MC DROPOUT	37.6±0.7	5.1±0.1	34.9±1.1	7.1±0.4
MC DROPOUT ENSEMBLE	39.5±0.2	5.3±0.0	38.3±0.9	7.7±0.2
FSVI	42.2±0.7	5.7±0.1	49.0±0.8	11.6±0.3
FSVI ENSEMBLE	43.8±0.4	5.9±0.1	54.5±0.4	14.5±0.2
RADIAL-MFVI	39.2±2.1	5.3±0.3	66.8±4.8	19.9±2.6
RADIAL-MFVI ENSEMBLE	36.5±0.6	4.9±0.1	**79.7±2.7**	**28.0±2.3**
RANK-1	44.3±1.9	6.0±0.3	54.5±3.4	12.8±1.1
RANK-1 ENSEMBLE	48.9±1.0	6.4±0.2	65.6±0.7	17.4±0.5
MFVI	51.2±0.7	6.7±0.1	51.3±2.8	10.4±0.7
MFVI ENSEMBLE	**52.4±0.3**	**6.9±0.1**	60.4±0.8	13.5±0.4

Table 4: Standard Metrics, Country Shift. We assess model predictive performance via standard metrics, and evaluate uncertainty quantification using expected calibration error on in-domain, shifted, and joint datasets (composed of the in-domain and shifted dataset, with no explicit balancing).

	NLL ↓			Accuracy (%) ↑			AUPRC (%) ↑		
Method	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**
MAP (Deterministic)	1.27±0.06	2.68±0.14	1.36±0.05	88.6±0.5	86.2±0.4	88.5±0.5	75.2±1.7	89.7±0.2	77.2±1.4
DEEP ENSEMBLE	0.60±0.00	1.60±0.12	0.67±0.01	90.3±0.2	87.5±0.1	90.1±0.2	79.9±0.4	**91.1±0.1**	81.0±0.3
MC DROPOUT	0.29±0.00	1.07±0.02	0.34±0.00	90.9±0.0	86.8±0.2	90.6±0.0	82.6±0.2	88.8±0.4	82.9±0.2
MC DROPOUT ENSEMBLE	**0.25±0.00**	0.92±0.02	**0.29±0.00**	**91.6±0.0**	87.6±0.0	**91.4±0.0**	**84.4±0.0**	88.3±0.3	**84.3±0.1**
FSVI	0.35±0.01	0.72±0.04	0.38±0.01	89.8±0.0	87.6±0.3	89.6±0.0	77.7±0.1	88.3±0.4	78.9±0.0
FSVI ENSEMBLE	0.28±0.01	**0.58±0.01**	0.30±0.01	90.6±0.0	**88.9±0.1**	90.5±0.0	80.7±0.1	88.9±0.2	81.3±0.0
RADIAL-MFVI	0.56±0.05	0.70±0.07	0.57±0.05	74.2±3.5	71.8±3.2	74.1±3.5	66.0±0.7	84.8±0.6	69.0±0.6
RADIAL-MFVI ENSEMBLE	0.55±0.01	0.65±0.03	0.56±0.01	74.2±1.1	69.0±1.3	73.8±1.1	68.9±0.3	86.1±0.1	71.6±0.2
RANK-1	0.99±0.05	1.85±0.15	1.05±0.04	87.7±0.5	86.2±0.4	87.6±0.5	71.6±1.9	88.8±0.4	74.1±1.6
RANK-1 ENSEMBLE	0.49±0.03	0.96±0.05	0.52±0.02	89.3±0.3	88.3±0.1	89.2±0.3	78.0±1.0	89.6±0.2	79.3±0.8
MFVI	0.91±0.01	1.26±0.05	0.93±0.01	85.7±0.1	84.1±0.2	85.6±0.1	66.7±0.2	85.9±0.2	69.7±0.2
MFVI ENSEMBLE	0.53±0.00	0.72±0.02	0.54±0.00	87.8±0.0	87.0±0.2	87.7±0.0	71.2±0.1	87.4±0.1	73.7±0.0
	AUROC (%) ↑			ECE ↓					
MAP (Deterministic)	87.4±0.9	92.2±0.2	88.3±0.8	0.10±0.00	0.13±0.00	0.10±0.00			
DEEP ENSEMBLE	90.3±0.1	94.2±0.1	90.9±0.1	0.06±0.00	0.08±0.00	0.06±0.00			
MC DROPOUT	91.4±0.1	94.0±0.1	91.9±0.1	0.03±0.00	0.09±0.00	0.03±0.00			
MC DROPOUT ENSEMBLE	**92.5±0.0**	94.1±0.1	**92.9±0.0**	**0.02±0.00**	0.09±0.00	**0.02±0.00**			
FSVI	88.5±0.1	94.1±0.1	89.4±0.0	0.05±0.01	0.08±0.00	0.06±0.01			
FSVI ENSEMBLE	90.3±0.1	**94.6±0.0**	90.9±0.0	0.03±0.00	0.07±0.00	0.03±0.00			
RADIAL-MFVI	83.2±0.4	90.7±0.5	84.3±0.3	0.09±0.02	0.14±0.03	0.09±0.02			
RADIAL-MFVI ENSEMBLE	84.9±0.1	91.8±0.1	85.9±0.1	0.06±0.01	0.10±0.01	0.05±0.01			
RANK-1	85.6±1.0	92.5±0.2	86.7±0.9	0.10±0.00	0.11±0.00	0.10±0.00			
RANK-1 ENSEMBLE	89.5±0.6	94.1±0.1	90.2±0.5	0.05±0.00	0.06±0.00	0.05±0.00			
MFVI	83.3±0.1	91.4±0.2	84.6±0.1	0.11±0.00	0.13±0.00	0.12±0.00			
MFVI ENSEMBLE	85.4±0.0	93.2±0.1	86.6±0.0	0.06±0.00	**0.06±0.00**	0.06±0.00			

Table 5: Standard Metrics, Severity Shift. We assess model predictive performance and expected calibration error on in-domain, shifted, and joint datasets (composed of the in-domain and shifted dataset, with no explicit balancing).

	NLL ↓			Accuracy (%) ↑			AUPRC (%) ↑		
Method	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**
MAP (Deterministic)	1.27±0.06	2.27±0.12	1.35±0.06	87.9±0.4	74.4±1.7	86.8±0.5	60.8±1.9	–	75.2±1.3
DEEP ENSEMBLE	0.62±0.02	1.03±0.05	0.65±0.02	89.3±0.2	74.5±1.1	88.1±0.3	65.6±1.2	–	79.2±0.8
MC DROPOUT	0.29±0.00	0.33±0.01	0.29±0.00	90.5±0.0	86.4±1.1	90.1±0.1	74.8±0.5	–	85.1±0.2
MC DROPOUT ENSEMBLE	**0.25±0.00**	**0.28±0.00**	**0.25±0.00**	**91.4±0.1**	**87.4±0.2**	**91.1±0.0**	**77.0±0.0**	–	**86.7±0.1**
FSVI	0.36±0.01	0.92±0.04	0.41±0.01	89.5±0.1	68.6±0.9	87.8±0.2	64.7±0.7	–	77.6±0.4
FSVI ENSEMBLE	0.31±0.00	0.76±0.01	0.34±0.00	90.0±0.0	69.3±0.2	88.4±0.1	70.0±0.1	–	81.6±0.1
RADIAL-MFVI	0.37±0.01	0.76±0.09	0.40±0.02	86.7±0.3	52.0±7.0	83.9±0.8	49.1±2.7	–	66.9±2.2
RADIAL-MFVI ENSEMBLE	0.35±0.01	0.73±0.05	0.38±0.01	87.4±0.3	54.4±4.3	84.8±0.6	56.2±2.0	–	73.5±1.5
RANK-1	0.56±0.05	1.14±0.12	0.61±0.05	88.3±0.5	67.5±3.2	86.6±0.7	59.4±2.8	–	74.1±1.9
RANK-1 ENSEMBLE	0.29±0.01	0.60±0.03	0.32±0.01	89.3±0.3	69.7±1.7	87.7±0.4	66.5±1.9	–	80.0±1.3
MFVI	0.66±0.08	1.26±0.16	0.71±0.09	87.8±0.5	71.5±2.1	86.5±0.6	59.0±2.5	–	73.7±1.8
MFVI ENSEMBLE	0.29±0.01	0.55±0.02	0.31±0.01	89.4±0.3	73.5±1.1	88.2±0.3	66.4±1.3	–	79.7±0.9
	AUROC (%) ↑			ECE ↓					
MAP (Deterministic)	82.0±0.9	–	86.3±0.7	0.11±0.00	0.23±0.01	0.12±0.00			
DEEP ENSEMBLE	85.1±0.6	–	88.9±0.5	0.06±0.00	0.15±0.01	0.07±0.00			
MC DROPOUT	89.2±0.2	–	92.0±0.1	0.02±0.00	0.06±0.00	0.02±0.00			
MC DROPOUT ENSEMBLE	**90.6±0.0**	–	**93.1±0.0**	**0.01±0.00**	**0.03±0.00**	**0.01±0.00**			
FSVI	83.2±0.3	–	86.9±0.2	0.06±0.00	0.23±0.01	0.07±0.00			
FSVI ENSEMBLE	86.2±0.1	–	89.4±0.0	0.04±0.00	0.19±0.00	0.06±0.00			
RADIAL-MFVI	76.9±1.4	–	82.2±1.2	0.05±0.01	0.23±0.06	0.04±0.01			
RADIAL-MFVI ENSEMBLE	81.3±1.1	–	86.2±0.9	0.07±0.01	0.15±0.03	0.06±0.01			
RANK-1	81.6±1.4	–	85.8±1.1	0.06±0.01	0.22±0.02	0.07±0.01			
RANK-1 ENSEMBLE	85.1±1.0	–	89.1±0.7	0.02±0.00	0.12±0.01	0.03±0.00			
MFVI	81.3±1.2	–	85.4±1.0	0.07±0.01	0.19±0.02	0.08±0.01			
MFVI ENSEMBLE	85.2±0.6	–	88.9±0.4	0.02±0.00	0.10±0.01	0.02±0.00			

Table 6: Expert Referral Metrics, Country Shift. We assess model predictive performance and uncertainty quantification in the context of expert referral. We construct referral curves on a variety of metrics—AUC, Accuracy, NLL and AUPRC—by sweeping over the referral thresholds τ, obtaining a point for each possible partition of the dataset into "referred" and "non-referred". We report the area under the referral curve for metric X as R-X AUC. All methods are tuned according to the area under the ROC curve on the in-domain dataset. The Balanced evaluation dataset is constructed using the procedure described in Appendix H.

	R-AUROC AUC ↑				R-Accuracy AUC ↑			
Method	**In-Domain**	**Shifted**	**Joint**	**Balanced**	**In-Domain**	**Shifted**	**Joint**	**Balanced**
MAP (Deterministic)	94.7±0.5	91.4±0.6	95.1±0.4	95.1±0.4	97.0±0.2	94.1±0.2	96.8±0.2	95.4±0.1
DEEP ENSEMBLE	95.5±0.1	94.3±0.5	96.1±0.1	96.1±0.1	97.7±0.0	95.6±0.2	97.6±0.0	96.6±0.1
MC DROPOUT	96.9±0.1	93.6±0.1	97.1±0.1	97.1±0.1	97.9±0.0	94.3±0.1	97.6±0.0	95.9±0.0
MC DROPOUT ENSEMBLE	**97.2±0.0**	93.4±0.1	**97.4±0.0**	**97.4±0.0**	**98.2±0.0**	94.4±0.0	**97.9±0.0**	96.1±0.0
FSVI	94.9±0.1	94.9±0.2	95.6±0.1	95.6±0.1	97.4±0.0	95.2±0.2	97.2±0.0	96.2±0.1
FSVI ENSEMBLE	95.5±0.1	94.9±0.1	96.1±0.0	96.1±0.0	97.8±0.0	95.4±0.1	97.6±0.0	96.5±0.1
RADIAL-MFVI	93.4±0.3	91.9±0.5	93.8±0.3	93.8±0.3	89.8±2.0	89.1±1.3	89.8±1.9	89.3±1.6
RADIAL-MFVI ENSEMBLE	94.4±0.1	91.4±0.1	94.7±0.1	94.7±0.1	90.2±0.6	88.2±0.5	90.0±0.6	88.9±0.5
RANK-1	93.3±0.6	94.1±0.6	94.1±0.5	94.1±0.5	96.7±0.2	94.9±0.2	96.5±0.2	95.7±0.0
RANK-1 ENSEMBLE	94.4±0.4	96.6±0.2	95.3±0.3	95.3±0.3	97.5±0.1	**96.2±0.1**	97.4±0.1	**96.8±0.1**
MFVI	92.5±0.2	96.1±0.1	93.4±0.1	93.4±0.1	96.0±0.0	94.9±0.1	95.9±0.0	95.4±0.1
MFVI ENSEMBLE	93.1±0.1	**97.0±0.1**	94.0±0.1	94.0±0.1	96.7±0.0	96.0±0.1	96.6±0.0	96.3±0.0
	R-NLL AUC ↓				R-AUPRC AUC ↑			
MAP (Deterministic)	60.5±3.6	179.5±11.4	69.4±2.5	126.0±5.2	90.9±0.9	95.8±0.1	91.9±0.7	91.9±0.7
DEEP ENSEMBLE	28.7±0.2	110.5±9.7	34.7±0.8	73.0±5.5	91.7±0.3	**96.6±0.1**	92.8±0.2	92.8±0.2
MC DROPOUT	10.5±0.2	74.4±2.0	15.2±0.3	44.9±1.1	94.5±0.1	95.1±0.2	94.4±0.1	94.4±0.1
MC DROPOUT ENSEMBLE	**8.2±0.1**	63.6±1.4	12.2±0.2	38.0±0.8	**94.9±0.1**	94.8±0.1	**94.7±0.0**	**94.7±0.0**
FSVI	13.4±0.5	45.1±3.1	15.6±0.6	30.2±1.8	91.1±0.2	94.9±0.2	91.9±0.1	91.9±0.1
FSVI ENSEMBLE	9.8±0.3	35.5±0.8	**11.6±0.3**	**23.5±0.5**	91.9±0.1	95.2±0.1	92.5±0.1	92.5±0.1
RADIAL-MFVI	26.2±3.7	34.6±4.0	26.9±3.8	30.9±3.9	87.5±0.4	93.5±0.3	88.6±0.4	88.6±0.4
RADIAL-MFVI ENSEMBLE	24.4±0.8	**31.1±1.6**	24.9±0.9	28.3±1.3	88.9±0.1	93.9±0.1	89.8±0.1	89.8±0.1
RANK-1	48.0±3.0	123.5±12.0	53.6±1.9	89.2±5.5	88.1±1.2	95.8±0.1	89.6±1.0	89.6±1.0
RANK-1 ENSEMBLE	22.2±1.7	64.3±3.7	25.1±1.4	44.2±1.8	89.3±0.7	96.1±0.1	90.8±0.6	90.8±0.6
MFVI	42.5±0.6	76.4±3.9	44.7±0.8	59.8±2.2	86.3±0.3	94.6±0.1	87.9±0.2	87.9±0.2
MFVI ENSEMBLE	24.9±0.2	44.6±1.8	26.2±0.3	34.9±1.0	87.3±0.2	94.9±0.0	88.9±0.1	88.9±0.1

Table 7: Expert Referral Metrics, Severity Shift. We assess model predictive performance and uncertainty quantification in the context of expert referral. We construct referral curves on a variety of metrics—AUC, Accuracy, NLL and AUPRC—by sweeping over the referral thresholds τ, obtaining a point for each possible partition of the dataset into "referred" and "non-referred". We report the area under the referral curve for metric X as R-X AUC. All methods are tuned according to the area under the ROC curve on the in-domain dataset. The Balanced evaluation dataset is constructed using the procedure described in Appendix H.

	R-AUROC AUC ↑				R-Accuracy AUC ↑			
Method	**In-Domain**	**Shifted**	**Joint**	**Balanced**	**In-Domain**	**Shifted**	**Joint**	**Balanced**
MAP (Deterministic)	91.5±0.7	–	94.0±0.5	94.0±0.5	96.6±0.2	92.7±0.9	96.4±0.2	94.9±0.4
DEEP ENSEMBLE	91.5±0.4	–	94.5±0.3	94.5±0.3	97.3±0.1	92.2±0.5	97.0±0.1	95.2±0.2
MC DROPOUT	95.7±0.2	–	97.2±0.1	97.2±0.1	97.8±0.0	97.5±0.3	97.8±0.0	97.7±0.1
MC DROPOUT ENSEMBLE	**96.1±0.1**	–	**97.5±0.0**	**97.5±0.0**	**98.1±0.0**	**97.7±0.1**	**98.1±0.0**	**98.0±0.0**
FSVI	90.7±0.3	–	93.6±0.2	93.6±0.2	97.0±0.1	90.3±0.4	96.7±0.1	94.2±0.2
FSVI ENSEMBLE	91.0±0.1	–	94.2±0.1	94.2±0.1	97.5±0.0	90.0±0.1	97.1±0.0	94.5±0.1
RADIAL-MFVI	85.6±1.5	–	88.5±1.5	88.5±1.5	95.9±0.2	78.4±4.4	95.2±0.3	89.5±1.6
RADIAL-MFVI ENSEMBLE	85.3±1.0	–	88.4±1.1	88.4±1.1	96.5±0.2	78.5±3.0	95.9±0.3	90.2±1.1
RANK-1	90.0±1.1	–	92.9±0.8	92.9±0.8	96.7±0.2	88.7±1.7	96.3±0.3	93.5±0.7
RANK-1 ENSEMBLE	89.3±0.4	–	93.1±0.4	93.1±0.4	97.3±0.2	89.4±0.8	96.9±0.2	94.3±0.4
MFVI	90.1±0.9	–	93.1±0.7	93.1±0.7	96.5±0.2	90.6±1.2	96.2±0.3	94.0±0.6
MFVI ENSEMBLE	90.0±0.3	–	93.6±0.2	93.6±0.2	97.3±0.1	91.4±0.4	97.0±0.1	94.9±0.2
	R-NLL AUC ↓				R-AUPRC AUC ↑			
MAP (Deterministic)	61.6±3.3	89.5±7.7	63.2±3.4	73.3±4.7	83.1±1.3	–	90.2±0.9	90.2±0.9
DEEP ENSEMBLE	29.7±1.1	49.2±2.9	30.7±1.2	37.5±1.8	82.0±0.7	–	90.2±0.5	90.2±0.5
MC DROPOUT	10.3±0.2	7.8±0.5	10.0±0.2	8.9±0.1	91.2±0.5	–	95.4±0.3	95.4±0.3
MC DROPOUT ENSEMBLE	**7.8±0.2**	**6.6±0.1**	**7.7±0.2**	**7.0±0.1**	**91.6±0.2**	–	**95.8±0.1**	**95.8±0.1**
FSVI	14.2±0.5	36.0±2.1	15.6±0.6	24.0±1.1	81.8±0.6	–	89.6±0.4	89.6±0.4
FSVI ENSEMBLE	11.0±0.1	30.9±0.4	12.1±0.1	19.3±0.2	81.3±0.3	–	89.8±0.2	89.8±0.2
RADIAL-MFVI	14.4±0.7	37.5±6.7	15.3±0.9	22.9±2.8	69.8±3.1	–	78.1±3.2	78.1±3.2
RADIAL-MFVI ENSEMBLE	13.3±0.4	36.9±4.0	14.2±0.5	21.9±1.6	66.1±2.1	–	75.1±2.5	75.1±2.5
RANK-1	25.1±2.8	50.4±7.7	26.4±3.0	35.5±4.5	79.7±2.2	–	87.7±1.5	87.7±1.5
RANK-1 ENSEMBLE	10.1±0.5	25.2±1.7	10.8±0.6	15.9±0.9	77.5±0.9	–	87.3±0.7	87.3±0.7
MFVI	30.0±4.5	52.8±8.0	31.4±4.6	39.9±5.7	80.4±1.8	–	88.4±1.2	88.4±1.2
MFVI ENSEMBLE	10.3±0.3	22.3±1.0	11.0±0.3	15.3±0.6	79.6±0.6	–	88.8±0.4	88.8±0.4

Table 8: Standard Metrics, Country Shift, Tuned on Joint Dataset. Here all methods are tuned according to the joint validation metric (Appendix H): area under the retention–accuracy curve constructed on the balanced joint validation dataset (composed of the in-domain and upsampled shifted validation datasets). Ensembles have $K = 3$ constituent models. We assess model predictive performance and expected calibration error on in-domain, shifted, and joint (union of in-domain and shifted, without explicit balancing) evaluation datasets.

	NLL ↓			Accuracy (%) ↑			AUPRC (%) ↑		
Method	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**
MAP (Deterministic)	1.02±0.07	2.41±0.14	1.11±0.05	89.3±0.2	87.0±0.3	89.2±0.2	77.5±0.9	90.5±0.2	79.2±0.7
DEEP ENSEMBLE	0.54±0.00	1.65±0.13	0.61±0.01	90.8±0.0	88.3±0.1	90.7±0.0	81.1±0.1	**91.3±0.2**	82.0±0.1
MC DROPOUT	0.31±0.01	0.77±0.06	0.34±0.01	90.0±0.2	87.6±0.3	89.9±0.2	81.1±0.3	87.7±0.4	82.0±0.2
MC DROPOUT ENSEMBLE	**0.25±0.00**	0.58±0.03	**0.28±0.00**	**91.2±0.0**	88.3±0.1	**91.0±0.0**	**83.3±0.1**	87.7±0.3	**83.7±0.1**
FSVI	0.52±0.04	0.67±0.05	0.53±0.04	88.7±0.4	88.2±0.3	88.7±0.3	75.8±0.6	88.1±0.8	77.5±0.5
FSVI ENSEMBLE	0.39±0.02	0.42±0.02	0.39±0.01	89.2±0.2	**89.7±0.1**	89.3±0.2	79.5±0.3	88.9±0.4	80.5±0.2
RADIAL-MFVI	0.60±0.08	0.72±0.16	0.61±0.08	85.9±0.2	85.4±0.4	85.9±0.2	66.2±0.6	87.9±0.4	69.6±0.4
RADIAL-MFVI ENSEMBLE	0.38±0.00	**0.34±0.01**	0.38±0.00	87.2±0.2	87.8±0.1	87.2±0.2	69.7±0.3	89.3±0.2	72.6±0.2
RANK-1	0.88±0.06	1.95±0.21	0.95±0.07	87.0±0.6	85.1±0.4	86.9±0.6	71.3±1.9	88.4±0.3	73.8±1.6
RANK-1 ENSEMBLE	0.40±0.01	1.02±0.09	0.44±0.02	89.1±0.3	87.1±0.2	89.0±0.3	77.2±1.0	89.4±0.1	78.7±0.8
MFVI	1.09±0.10	1.69±0.20	1.12±0.11	85.9±0.4	84.5±0.6	85.8±0.4	67.1±1.5	87.6±0.7	70.3±1.2
MFVI ENSEMBLE	0.46±0.03	0.71±0.12	0.48±0.04	88.4±0.1	86.8±0.2	88.3±0.1	73.5±0.7	89.6±0.4	75.7±0.6
	AUROC (%) ↑			ECE ↓					
MAP (Deterministic)	88.6±0.5	93.2±0.2	89.5±0.4	0.09±0.00	0.12±0.00	0.09±0.00			
DEEP ENSEMBLE	90.6±0.0	94.5±0.2	91.3±0.0	0.05±0.00	0.09±0.00	0.05±0.00			
MC DROPOUT	90.7±0.2	93.9±0.2	91.4±0.1	0.03±0.00	0.08±0.00	0.04±0.00			
MC DROPOUT ENSEMBLE	**91.9±0.0**	94.2±0.1	**92.5±0.0**	**0.02±0.00**	0.06±0.00	**0.02±0.00**			
FSVI	87.4±0.3	94.0±0.3	88.5±0.3	0.08±0.01	0.08±0.00	0.08±0.01			
FSVI ENSEMBLE	89.6±0.2	**94.6±0.1**	90.4±0.1	0.06±0.00	0.05±0.00	0.06±0.00			
RADIAL-MFVI	83.0±0.3	92.7±0.3	84.3±0.2	0.09±0.01	0.07±0.01	0.09±0.01			
RADIAL-MFVI ENSEMBLE	84.8±0.2	94.1±0.1	86.0±0.1	0.05±0.00	**0.03±0.00**	0.05±0.00			
RANK-1	85.4±1.0	92.0±0.2	86.5±0.9	0.10±0.01	0.12±0.00	0.10±0.00			
RANK-1 ENSEMBLE	89.0±0.6	94.0±0.1	89.8±0.5	0.05±0.00	0.07±0.00	0.05±0.00			
MFVI	83.4±0.7	91.7±0.5	84.7±0.6	0.11±0.01	0.12±0.01	0.11±0.01			
MFVI ENSEMBLE	86.8±0.4	94.0±0.3	87.9±0.3	0.05±0.00	0.06±0.01	0.05±0.00			

Table 9: Standard Metrics, Severity Shift, Tuned on Joint Dataset. Here all methods are tuned according to the joint validation metric (Appendix H): area under the retention–accuracy curve constructed on the balanced joint validation dataset (composed of the in-domain and upsampled shifted validation datasets). Ensembles have $K = 3$ constituent models. We assess model predictive performance and expected calibration error on in-domain, shifted, and joint (union of in-domain and shifted, without explicit balancing) evaluation datasets.

	NLL ↓			Accuracy (%) ↑			AUPRC (%) ↑		
Method	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**	**In-Domain**	**Shifted**	**Joint**
MAP (Deterministic)	1.05±0.11	1.48±0.20	1.09±0.12	87.6±0.6	81.5±0.9	87.1±0.6	63.6±2.0	–	77.5±1.3
DEEP ENSEMBLE	0.39±0.04	0.49±0.07	0.40±0.04	89.6±0.3	83.1±0.4	89.1±0.3	68.1±1.1	–	81.3±0.6
MC DROPOUT	0.32±0.02	0.31±0.03	0.32±0.02	89.0±0.6	87.5±0.9	88.9±0.6	72.6±1.7	–	83.5±1.2
MC DROPOUT ENSEMBLE	**0.26±0.00**	**0.24±0.00**	**0.26±0.00**	**90.9±0.1**	**89.2±0.1**	**90.8±0.0**	**76.9±0.1**	–	**86.6±0.1**
FSVI	0.40±0.02	0.57±0.03	0.41±0.02	87.8±0.6	79.8±0.8	87.1±0.5	63.3±1.6	–	77.1±1.1
FSVI ENSEMBLE	0.29±0.00	0.41±0.01	0.30±0.00	90.0±0.1	81.5±0.4	89.4±0.1	68.7±0.6	–	81.4±0.3
RADIAL-MFVI	0.37±0.01	0.76±0.09	0.40±0.02	86.7±0.3	52.0±7.0	83.9±0.8	49.1±2.7	–	66.9±2.2
RADIAL-MFVI ENSEMBLE	0.35±0.01	0.73±0.05	0.38±0.01	87.4±0.3	54.4±4.3	84.8±0.6	56.2±2.0	–	73.5±1.5
RANK-1	0.56±0.05	1.14±0.12	0.61±0.05	88.3±0.5	67.5±3.2	86.6±0.7	59.4±2.8	–	74.1±1.9
RANK-1 ENSEMBLE	0.29±0.01	0.60±0.03	0.32±0.01	89.3±0.3	69.7±1.7	87.7±0.4	66.5±1.9	–	80.0±1.3
MFVI	0.56±0.06	0.75±0.16	0.57±0.07	83.7±0.2	79.8±1.8	83.4±0.1	55.2±0.4	–	71.0±0.6
MFVI ENSEMBLE	0.35±0.00	0.37±0.01	0.36±0.00	86.2±0.3	81.6±0.6	85.8±0.2	59.9±0.2	–	75.3±0.1
	AUROC (%) ↑			ECE ↓					
MAP (Deterministic)	83.7±0.9	–	87.8±0.7	0.09±0.01	0.15±0.02	0.09±0.01			
DEEP ENSEMBLE	86.3±0.4	–	90.0±0.3	0.03±0.01	0.07±0.01	0.03±0.01			
MC DROPOUT	88.2±0.8	–	91.1±0.7	0.02±0.00	0.06±0.01	0.02±0.00			
MC DROPOUT ENSEMBLE	**90.6±0.1**	–	**93.1±0.0**	0.02±0.00	**0.02±0.00**	0.02±0.00			
FSVI	82.8±0.7	–	86.8±0.6	0.06±0.00	0.14±0.01	0.06±0.00			
FSVI ENSEMBLE	86.1±0.2	–	89.7±0.1	0.03±0.00	0.08±0.00	0.03±0.00			
RADIAL-MFVI	76.9±1.4	–	82.2±1.2	0.05±0.01	0.23±0.06	0.04±0.01			
RADIAL-MFVI ENSEMBLE	81.3±1.1	–	86.2±0.9	0.07±0.01	0.15±0.03	0.06±0.01			
RANK-1	81.6±1.4	–	85.8±1.1	0.06±0.01	0.22±0.02	0.07±0.01			
RANK-1 ENSEMBLE	85.1±1.0	–	89.1±0.7	**0.02±0.00**	0.12±0.01	0.03±0.00			
MFVI	79.8±0.4	–	84.3±0.4	0.07±0.01	0.12±0.03	0.07±0.01			
MFVI ENSEMBLE	82.3±0.1	–	86.8±0.1	0.02±0.00	0.05±0.01	**0.02±0.00**			

Table 10: Expert Referral Metrics, Country Shift, Tuned on Joint Dataset. We assess model predictive performance and uncertainty quantification in the context of expert referral. Here all methods are tuned according to the joint validation metric (Appendix H): area under the retention–accuracy curve constructed on the balanced joint validation dataset (composed of the in-domain and upsampled shifted validation datasets). We construct referral curves on a variety of metrics—AUC, Accuracy, NLL and AUPRC—by sweeping over the referral thresholds τ, obtaining a point for each possible partition of the dataset into "referred" and "non-referred". The Balanced evaluation dataset is constructed using the procedure described in Appendix H.

	R-AUROC AUC ↑				R-Accuracy AUC ↑			
Method	**In-Domain**	**Shifted**	**Joint**	**Balanced**	**In-Domain**	**Shifted**	**Joint**	**Balanced**
MAP (Deterministic)	95.1±0.5	92.1±0.5	95.6±0.3	95.6±0.3	97.3±0.1	94.6±0.3	97.1±0.1	95.8±0.1
DEEP ENSEMBLE	95.6±0.2	94.3±0.5	96.2±0.1	96.2±0.1	97.8±0.0	95.5±0.2	97.6±0.0	96.5±0.1
MC DROPOUT	96.5±0.2	95.4±0.4	96.9±0.2	96.9±0.2	97.7±0.0	95.3±0.3	97.5±0.1	96.4±0.1
MC DROPOUT ENSEMBLE	**96.9±0.1**	95.8±0.2	**97.2±0.0**	**97.2±0.0**	**98.1±0.0**	95.6±0.1	**97.9±0.0**	96.7±0.1
FSVI	93.0±0.4	97.0±0.3	94.0±0.3	94.0±0.3	97.1±0.1	96.4±0.2	97.0±0.1	96.7±0.1
FSVI ENSEMBLE	93.2±0.3	97.9±0.2	94.3±0.3	94.3±0.3	97.4±0.1	**97.0±0.1**	97.4±0.0	**97.2±0.0**
RADIAL-MFVI	90.0±0.7	96.9±0.3	91.3±0.6	91.3±0.6	96.0±0.1	95.8±0.3	96.0±0.1	95.8±0.1
RADIAL-MFVI ENSEMBLE	89.6±0.4	**98.0±0.1**	91.1±0.4	91.1±0.4	96.4±0.1	96.8±0.1	96.4±0.0	96.5±0.0
RANK-1	93.9±0.5	93.3±0.5	94.5±0.4	94.5±0.4	96.4±0.2	94.2±0.2	96.2±0.2	95.2±0.1
RANK-1 ENSEMBLE	95.1±0.3	95.5±0.1	95.8±0.2	95.8±0.2	97.4±0.1	95.4±0.1	97.3±0.1	96.4±0.1
MFVI	92.1±0.8	95.0±0.6	93.1±0.6	93.1±0.6	96.0±0.2	94.9±0.3	96.0±0.1	95.5±0.1
MFVI ENSEMBLE	91.8±0.8	97.4±0.4	93.3±0.6	93.3±0.6	96.9±0.1	96.5±0.2	96.9±0.1	96.7±0.1
	R-NLL AUC ↓				R-AUPRC AUC ↑			
MAP (Deterministic)	46.3±2.8	161.5±10.9	54.8±1.9	109.5±5.1	91.4±1.0	96.1±0.1	92.4±0.7	92.4±0.7
DEEP ENSEMBLE	25.0±0.2	113.0±9.8	31.4±0.9	72.4±5.6	92.0±0.5	**96.6±0.1**	93.0±0.3	93.0±0.3
MC DROPOUT	11.3±0.3	48.6±5.2	13.9±0.6	31.1±2.9	93.6±0.4	94.6±0.2	93.8±0.3	93.8±0.3
MC DROPOUT ENSEMBLE	**8.3±0.1**	34.9±2.5	**10.2±0.3**	22.4±1.4	**94.3±0.2**	94.5±0.2	**94.4±0.1**	**94.4±0.1**
FSVI	20.7±1.4	39.1±4.1	22.0±1.3	30.3±2.1	86.9±1.1	95.0±0.5	88.8±0.7	88.8±0.7
FSVI ENSEMBLE	14.6±0.7	21.2±1.7	15.1±0.6	18.1±0.7	86.3±0.9	95.4±0.3	88.5±0.6	88.5±0.6
RADIAL-MFVI	25.8±4.2	38.7±11.0	26.8±4.7	32.8±7.6	80.5±1.7	95.3±0.1	83.4±1.4	83.4±1.4
RADIAL-MFVI ENSEMBLE	14.9±0.2	**13.0±1.0**	14.8±0.2	**14.3±0.5**	79.0±1.0	95.9±0.1	82.4±0.9	82.4±0.9
RANK-1	42.8±3.6	132.7±15.8	49.2±3.8	91.1±9.4	89.4±0.9	95.5±0.0	90.6±0.7	90.6±0.7
RANK-1 ENSEMBLE	17.0±0.9	69.9±7.2	20.6±1.2	44.7±4.1	91.1±0.4	95.8±0.1	92.0±0.3	92.0±0.3
MFVI	51.7±5.4	106.8±14.6	55.5±5.9	80.6±9.8	85.2±1.9	95.5±0.3	87.4±1.4	87.4±1.4
MFVI ENSEMBLE	20.5±2.1	42.4±10.3	22.0±2.6	31.8±6.3	84.0±1.7	96.3±0.2	87.2±1.2	87.2±1.2

Table 11: Expert Referral Metrics, Severity Shift, Tuned on Joint Dataset. We assess model predictive performance and uncertainty quantification in the context of expert referral. Here all methods are tuned according to the joint validation metric (Appendix H): area under the retention–accuracy curve constructed on the balanced joint validation dataset (composed of the in-domain and upsampled shifted validation datasets). We construct referral curves on a variety of metrics—AUC, Accuracy, NLL and AUPRC—by sweeping over the referral thresholds τ, obtaining a point for each possible partition of the dataset into "referred" and "non-referred". The Balanced evaluation dataset is constructed using the procedure described in Appendix H.

	R-AUROC AUC ↑				R-Accuracy AUC ↑			
Method	**In-Domain**	**Shifted**	**Joint**	**Balanced**	**In-Domain**	**Shifted**	**Joint**	**Balanced**
MAP (Deterministic)	93.0±0.4	–	95.2±0.3	95.2±0.3	96.6±0.2	95.9±0.4	96.6±0.2	96.3±0.2
DEEP ENSEMBLE	93.4±0.2	–	95.9±0.1	95.9±0.1	97.4±0.1	96.4±0.1	97.3±0.1	97.0±0.1
MC DROPOUT	95.7±0.4	–	97.0±0.3	97.0±0.3	97.3±0.2	97.9±0.3	97.3±0.2	97.6±0.3
MC DROPOUT ENSEMBLE	**96.5±0.1**	–	**97.7±0.0**	**97.7±0.0**	**98.0±0.0**	**98.3±0.1**	**98.0±0.0**	**98.2±0.0**
FSVI	92.7±0.4	–	94.9±0.2	94.9±0.2	96.5±0.2	95.7±0.3	96.4±0.2	96.0±0.2
FSVI ENSEMBLE	93.4±0.1	–	95.8±0.1	95.8±0.1	97.4±0.0	95.8±0.1	97.3±0.0	96.7±0.1
RADIAL-MFVI	85.6±1.5	–	88.5±1.5	88.5±1.5	95.9±0.2	78.4±4.4	95.2±0.3	89.5±1.6
RADIAL-MFVI ENSEMBLE	85.3±1.0	–	88.4±1.1	88.4±1.1	96.5±0.2	78.5±3.0	95.9±0.3	90.2±1.1
RANK-1	90.0±1.1	–	92.9±0.8	92.9±0.8	96.7±0.2	88.7±1.7	96.3±0.3	93.5±0.7
RANK-1 ENSEMBLE	89.3±0.4	–	93.1±0.4	93.1±0.4	97.3±0.2	89.4±0.8	96.9±0.2	94.3±0.4
MFVI	91.5±0.3	–	94.1±0.3	94.1±0.3	95.3±0.0	94.4±0.8	95.2±0.0	94.9±0.4
MFVI ENSEMBLE	92.7±0.0	–	95.2±0.0	95.2±0.0	96.2±0.1	95.9±0.2	96.2±0.1	96.1±0.1
	R-NLL AUC ↓				R-AUPRC AUC ↑			
MAP (Deterministic)	50.2±6.2	49.0±8.0	49.9±6.3	48.8±6.9	85.9±0.9	–	92.2±0.5	92.2±0.5
DEEP ENSEMBLE	16.2±2.5	14.8±2.7	15.9±2.5	15.1±2.6	86.5±0.6	–	93.2±0.3	93.2±0.3
MC DROPOUT	11.9±0.8	7.1±1.3	11.4±0.9	9.4±1.1	91.0±0.7	–	95.2±0.5	95.2±0.5
MC DROPOUT ENSEMBLE	**8.3±0.1**	**4.7±0.2**	**8.0±0.1**	**6.3±0.1**	**92.4±0.2**	–	**96.2±0.1**	**96.2±0.1**
FSVI	16.8±1.1	15.6±1.4	16.8±1.1	16.4±1.1	85.9±0.8	–	92.2±0.5	92.2±0.5
FSVI ENSEMBLE	10.4±0.1	11.6±0.3	10.5±0.1	10.8±0.2	86.6±0.4	–	93.1±0.2	93.1±0.2
RADIAL-MFVI	14.4±0.7	37.5±6.7	15.3±0.9	22.9±2.8	69.8±3.1	–	78.1±3.2	78.1±3.2
RADIAL-MFVI ENSEMBLE	13.3±0.4	36.9±4.0	14.2±0.5	21.9±1.6	66.1±2.1	–	75.1±2.5	75.1±2.5
RANK-1	25.1±2.8	50.4±7.7	26.4±3.0	35.5±4.5	79.7±2.2	–	87.7±1.5	87.7±1.5
RANK-1 ENSEMBLE	10.1±0.5	25.2±1.7	10.8±0.6	15.9±0.9	77.5±0.9	–	87.3±0.7	87.3±0.7
MFVI	24.4±3.4	30.7±8.4	24.9±3.8	27.4±5.9	82.3±0.5	–	89.8±0.4	89.8±0.4
MFVI ENSEMBLE	12.9±0.1	10.3±0.4	12.6±0.1	11.4±0.1	84.6±0.0	–	91.7±0.0	91.7±0.0

I.2 Selective Prediction

We below show additional experiments on selective prediction.

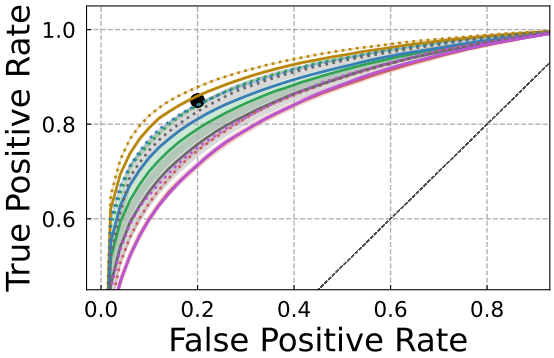
Class Balancing the APTOS Dataset (Figure 8 and 9). We additionally investigated to what extent the change in class distribution—in terms of the underlying clinical labels ranging from 0 (No DR) to 4 (Proliferative DR)—contributed to the higher performance of models in AUC, and weaker performance of models in selective prediction on the APTOS dataset (the distributionally shifted dataset in the *Country Shift* task) than the in-domain test dataset.

In order to normalize for the change in class distribution, we constructed a variant of the APTOS dataset with the same clinical class proportions as the in-domain EyePACS dataset. This was done by randomly sampling APTOS examples from each class, weighted by the empirical class probability of the EyePACS dataset, until reaching 10,000 samples.

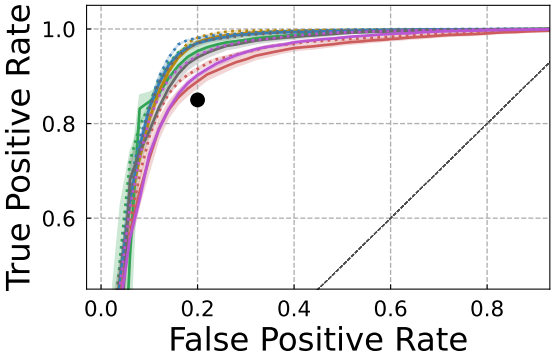
In Figure 8, we see that the ROC curves of models on the rebalanced APTOS dataset is shifted further towards the upper left as compared to the original APTOS dataset. This suggests that the class proportions of the original APTOS dataset were not the reason why models obtained stronger ROC performance on APTOS than the in-domain test set—on the contrary, introducing the in-domain class proportions in the class-balanced dataset improves model performance.

In Figure 9, we observe that the selective prediction performance of models on this rebalanced APTOS dataset is slightly better than on the original APTOS dataset, but the ordering of models does not notably change, and performance is still significantly worse at high referral thresholds than on the in-domain data.

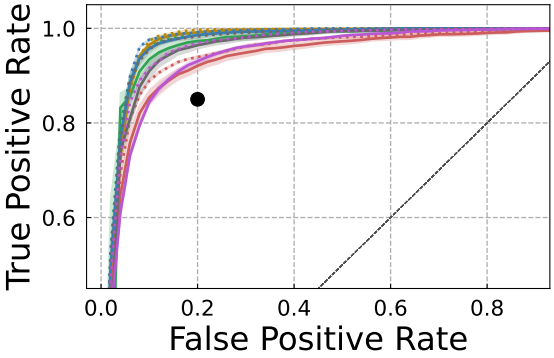
This supports the claim that factors other than simply a changed class distribution, such as meaningful shifts in equipment or patient demographics, result in both stronger predictive performance at 0% of data referred and poorly calibrated uncertainty in the shifted setting.



(a) ROC: In-Domain

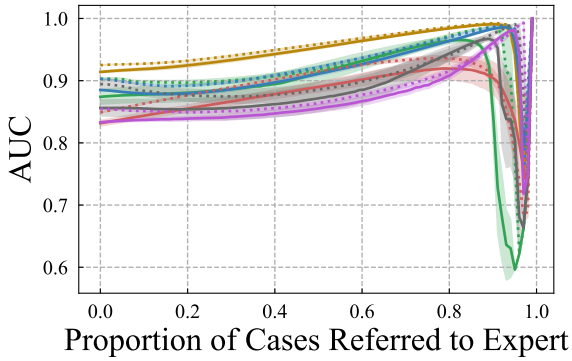


(b) ROC: Country Shift

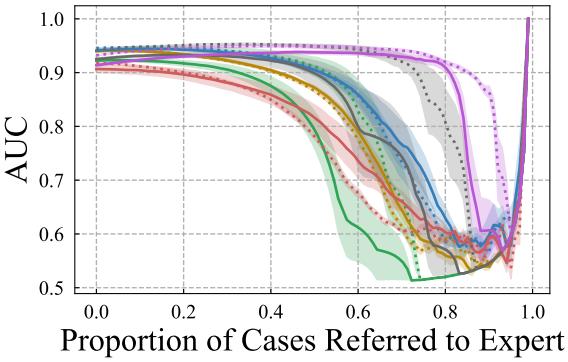


(c) ROC: Class-Balanced Country Shift

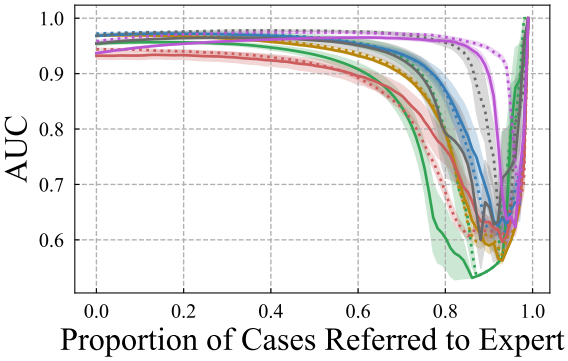
Figure 8: Class Balancing the Country Shift Dataset (ROC Curves). We consider how balancing the proportions of the underlying clinical class labels—ranging from 0 (No DR) to 4 (Proliferative DR)—affects performance on the *Country Shift* receiver-operating characteristic (ROC) curve. (**a**): ROC curve on in-domain test data. (**b**): ROC curve for changing medical equipment and patient populations on the shifted APTOS [3] test set. (**c**): ROC curve on the class rebalanced APTOS dataset. Shading denotes one standard error.



(a) Selective Prediction AUC: In-Domain



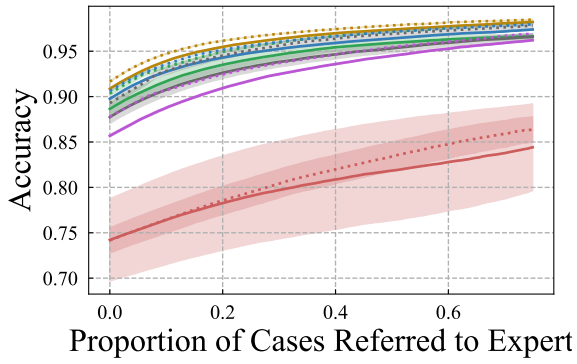
(b) Selective Prediction AUC: Country Shift



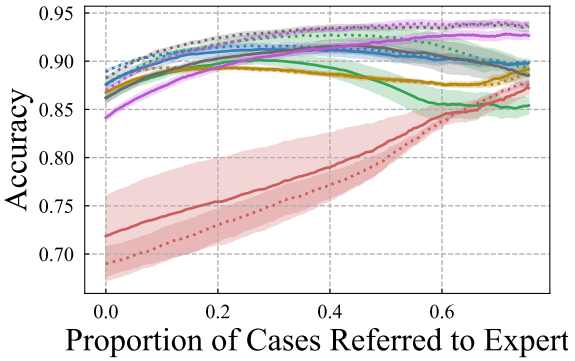
(c) Selective Prediction AUC: Class-Balanced Country Shift

Figure 9: Class Balancing the Country Shift Dataset (Selective Prediction). We consider how balancing the proportions of the underlying clinical class labels—ranging from 0 (No DR) to 4 (Proliferative DR)—affects performance on the *Country Shift* selective prediction over AUC. (**a**): selective prediction AUC on in-domain test data. (**b**): selective prediction AUC for changing medical equipment and patient populations on the shifted APTOS [3] test set. (**c**): selective prediction AUC on the class rebalanced APTOS dataset. Shading denotes one standard error.

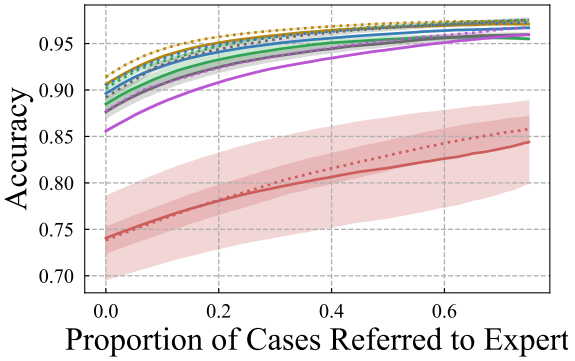
Country Shift: Accuracy (Figure 10). We provide referral curves on accuracy for *Country Shift* with in-domain validation tuning in Figure 10.



(a) Selective Prediction Accuracy: In-Domain



(b) Selective Prediction Accuracy: Country Shift



(c) Selective Prediction Accuracy: Joint

Figure 10: Selective Prediction: Country Shift (Accuracy). We use the binary accuracy for in-domain diagnosis on the EyePACS [13] test set (**a**), for changing medical equipment and patient populations on the shifted APTOS [3] evaluation set (**b**), and on a joint dataset composed of both the in-domain and APTOS datasets (**c**). Shading denotes one standard error.

I.3 The Effect of Preprocessing on Downstream Tasks

Preprocessing played an important role in the EyePACS Kaggle challenge [13]. Here, we investigate how changes in preprocessing affect downstream predictive performance and uncertainty quantification.

In the above experiments, we used the preprocessing procedure of the Kaggle competition winner which consisted of the following steps:

1. Rescaling the images such that the retinas have a radius of 300 pixels,
2. Subtracting the local average color, computed using Gaussian blur, and finally,
3. Clipping the images to 90% size to remove "boundary effects".

While (1) and (3) are (somewhat) standard techniques used to make the data more amenable for use in non-convex optimization, the standard deviation hyperparameter of the Gaussian blur kernel in (2) presupposes some amount of expert knowledge as the size of the standard deviation governs how visible certain visual artifacts are. As such, varying it has a dramatic visual effect on the preprocessed image, and likely required significant tuning.

In the preprocessing procedure, the standard deviation of the kernel is computed as $\sigma = (\texttt{target_radius}/\texttt{blur_constant})$, where by default, $\texttt{target_radius} = 300$ and $\texttt{blur_constant} = 30$.

Decreasing the `blur_constant` results in a larger kernel standard deviation, and hence the local average color at each pixel location is computed using a larger window. This ultimately results in the preservation of more signal as well as more noise in the input image (because lower-frequency patterns are subtracted). See Figure 11 for examples of unprocessed retina images along with processed images with various blur constants.

We test the downstream performance of MAP estimation (a deterministic model), a DEEP ENSEMBLE, MC DROPOUT, and an MC DROPOUT ENSEMBLE on the Country and Severity Shift prediction tasks, varying the $\texttt{blur_constant} \in \{5, 10, 20, 30\}$.

Severity Shift: Varying Blur Constant (Figure 12, Table 12). On the in-domain evaluation dataset, higher `blur_constant` (corresponding to stronger smoothing) tends to perform better across MAP and MC DROPOUT, single and ensembled models, and the various referral thresholds. However, on the Severity Shift (distributionally shifted evaluation dataset), the MC DROPOUT variants perform better with *lower* `blur_constant`. This highlights the importance for practitioners to test changes in experimental settings, including preprocessing, across a variety of uncertainty quantification methods.

Country Shift: Varying Blur Constant (Figure 13, Table 13). Similarly to the Severity Shift results, higher `blur_constant` tends to perform better on the in-domain evaluation data across methods and referral rates. Notably, on the distributionally shifted APTOS data, DEEP ENSEMBLE outperforms MC DROPOUT ENSEMBLE, and $\texttt{blur_constant} = 20$ significantly improves performance from the default $\texttt{blur_constant} = 30$ for DEEP ENSEMBLE between referral rates 0.4 and 0.7. For example, for DEEP ENSEMBLE at $\tau = 0.7$, we observe 82.2 ± 2.5 AUC with $\texttt{blur_constant} = 20$ versus 67.4 ± 5.6 AUC with $\texttt{blur_constant} = 30$.

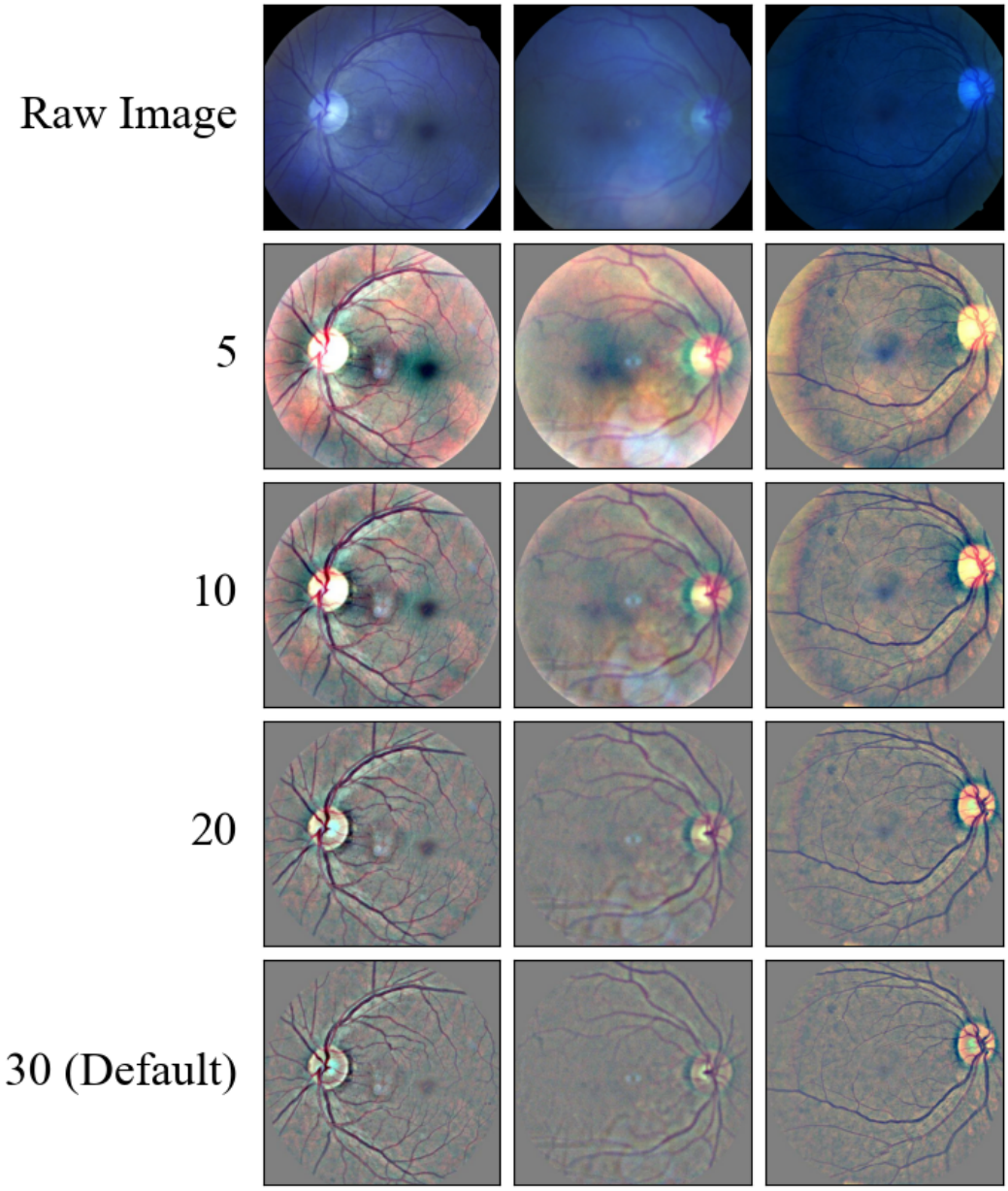


Figure 11: Preprocessing Examples. Input unprocessed EyePACS images (top row), and images processed with varying `blur_constant` (labeled on left side of grid). Higher `blur_constant` corresponds to stronger smoothing.

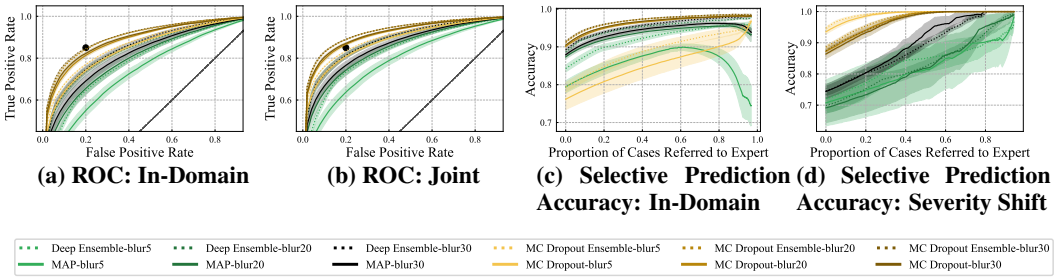


Figure 12: Severity Shift, Varying Blur Constant. We consider how preprocessing affects model predictive performance and uncertainty quantification on the in-domain test dataset composed only of cases with either no, mild, or moderate diabetic retinopathy, and the *Severity Shift* evaluation set composed only of severe and proliferate cases. **Left:** The receiver operating characteristic curve (ROC) for in-domain diagnosis (**a**) and for a joint dataset composed of examples from both the in-domain and *Severity Shift* evaluation sets (**b**). The dot in **black** denotes the NHS-recommended 85% sensitivity and 80% specificity ratios [59]. **Right:** Selective prediction on accuracy in the in-domain (**c**) and *Severity Shift* (**d**) settings. Shading denotes standard error computed over six random seeds. We vary the standard deviation hyperparameter of the Gaussian blur kernel through a `blur_constant` (e.g., blur5 below corresponds to `blur_constant` $= 5$). A higher `blur_constant` results in a stronger smoothing of the image as per the preprocessing procedure outlined in Appendix I. The default `blur_constant` used in other experiments throughout this work is 30.

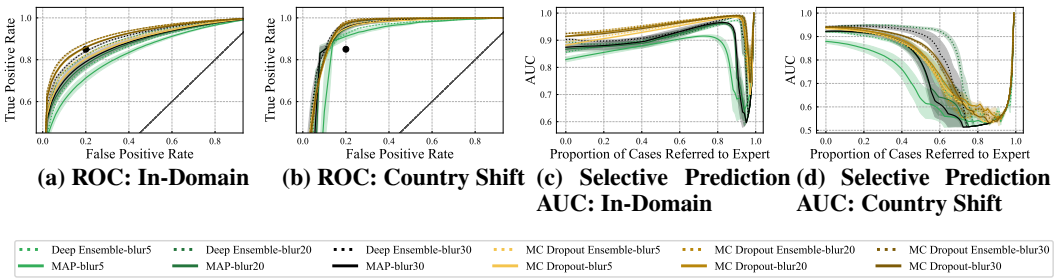


Figure 13: Country Shift, Varying Blur Constant. We consider how preprocessing affects model predictive performance and uncertainty quantification on both in-domain and distributionally shifted data. **Left:** The *receiver operating characteristic curve (ROC)* for in-population diagnosis on the EyePACS [13] test set (**a**) and for changing medical equipment and patient populations on the APTOS [3] test set (**b**). The dot in **black** denotes the NHS-recommended 85% sensitivity and 80% specificity ratios [59]. **Right:** *selective prediction* on AUC in the EyePACS [13] (**c**) and the APTOS [3] (**d**) settings. Shading denotes standard error computed over six random seeds. We vary the standard deviation hyperparameter of the Gaussian blur kernel through a `blur_constant` (e.g., blur5 below corresponds to `blur_constant` $= 5$). A higher `blur_constant` results in a stronger smoothing of the image as per the preprocessing procedure outlined in Appendix I. The default `blur_constant` used in other experiments throughout this work is 30.

Table 12: Severity Shift, Varying Blur Constant We consider how preprocessing affects downstream prediction and uncertainty quality of baseline methods in terms of the area under the receiver-operating-characteristic curve (AUC) and classification accuracy, as a function of the proportion of data referred to a medical expert for further review. All methods are tuned on in-domain validation AUC, and ensembles have $K = 3$ constituent models. We vary the standard deviation hyperparameter of the Gaussian blur kernel through a `blur_constant` (e.g., blur5 below corresponds to `blur_constant` $= 5$). A higher `blur_constant` results in a stronger smoothing of the image as per the preprocessing procedure outlined in Appendix I. The default `blur_constant` used in other experiments is 30.

	No Referral		50% Data Referred		70% Data Referred	
Method	**AUC (%)** ↑	**Accuracy (%)** ↑	**AUC (%)** ↑	**Accuracy (%)** ↑	**AUC (%)** ↑	**Accuracy** ↑
In-Domain (No, Mild, or Moderate DR, Clinical Labels {0,1,2})						
MAP (Deterministic)-blur5	73.7±1.3	79.4±1.4	75.5±3.1	89.0±0.9	79.1±3.4	89.3±1.0
MAP (Deterministic)-blur10	78.7±1.1	84.6±0.6	80.0±2.3	93.4±0.3	84.5±2.2	94.1±0.4
MAP (Deterministic)-blur20	79.9±1.3	87.3±0.5	77.2±3.4	94.5±0.4	80.9±4.1	95.3±0.3
MAP (Deterministic)-blur30	82.0±1.0	87.9±0.4	83.1±1.9	95.2±0.3	88.4±1.9	96.0±0.2
MC DROPOUT-blur5	84.8±0.4	76.1±2.3	91.4±0.3	86.0±2.4	94.1±0.4	88.6±2.2
MC DROPOUT-blur10	86.3±0.1	84.2±1.3	92.4±0.4	93.5±0.8	95.2±0.2	95.1±0.6
MC DROPOUT-blur20	88.7±0.3	90.1±0.2	92.5±0.5	97.0±0.1	95.3±0.3	97.7±0.1
MC DROPOUT-blur30	89.2±0.2	90.5±0.1	92.8±0.6	97.2±0.0	95.4±0.4	97.8±0.0
DEEP ENSEMBLE-blur5	78.6±0.6	84.3±0.8	75.0±2.6	93.3±0.5	75.9±3.3	94.8±0.3
DEEP ENSEMBLE-blur10	82.4±0.3	87.7±0.1	80.9±1.3	95.1±0.1	84.1±1.3	96.1±0.1
DEEP ENSEMBLE-blur20	84.2±0.8	88.6±0.3	70.9±1.1	95.8±0.2	71.4±1.4	96.7±0.2
DEEP ENSEMBLE-blur30	85.1±0.7	89.3±0.2	82.0±0.9	96.3±0.2	85.3±0.9	97.3±0.2
MC DROPOUT ENSEMBLE-blur5	86.5±0.1	79.4±1.0	93.2±0.1	90.2±1.1	95.7±0.2	92.5±0.9
MC DROPOUT ENSEMBLE-blur10	87.5±0.0	86.7±0.6	**93.4±0.2**	95.4±0.3	**96.0±0.2**	96.5±0.3
MC DROPOUT ENSEMBLE-blur20	90.3±0.0	91.1±0.1	**93.5±0.2**	97.6±0.0	**96.0±0.1**	**98.2±0.0**
MC DROPOUT ENSEMBLE-blur30	**90.6±0.0**	**91.4±0.1**	93.1±0.2	**97.8±0.0**	95.7±0.2	**98.2±0.0**
Severity Shift (Severe or Proliferate DR, Clinical Labels {3, 4})						
MAP (Deterministic)-blur5	–	70.8±6.2	–	81.4±7.9	–	87.7±7.9
MAP (Deterministic)-blur10	–	77.3±2.2	–	91.9±2.8	–	97.2±1.5
MAP (Deterministic)-blur20	–	69.1±4.0	–	81.8±5.3	–	88.8±4.4
MAP (Deterministic)-blur30	–	74.4±1.9	–	93.2±2.6	–	98.6±1.1
MC DROPOUT-blur5	–	93.5±0.6	–	**100.0±0.0**	–	**100.0±0.0**
MC DROPOUT-blur10	–	91.0±1.3	–	99.9±0.0	–	**100.0±0.0**
MC DROPOUT-blur20	–	87.2±0.9	–	99.7±0.1	–	**100.0±0.0**
MC DROPOUT-blur30	–	86.4±1.3	–	99.5±0.2	–	**100.0±0.0**
DEEP ENSEMBLE-blur5	–	72.0±3.9	–	85.1±3.7	–	87.5±3.3
DEEP ENSEMBLE-blur10	–	80.0±1.2	–	94.0±1.0	–	97.8±0.5
DEEP ENSEMBLE-blur20	–	69.8±2.1	–	82.4±1.5	–	89.1±1.5
DEEP ENSEMBLE-blur30	–	74.5±1.2	–	89.8±1.0	–	97.0±0.7
MC DROPOUT ENSEMBLE-blur5	–	**94.7±0.3**	–	**100.0±0.0**	–	**100.0±0.0**
MC DROPOUT ENSEMBLE-blur10	–	91.9±0.7	–	**100.0±0.0**	–	**100.0±0.0**
MC DROPOUT ENSEMBLE-blur20	–	88.6±0.4	–	99.8±0.0	–	**100.0±0.0**
MC DROPOUT ENSEMBLE-blur30	–	87.4±0.3	–	99.4±0.1	–	**100.0±0.0**

Table 13: Country Shift, Varying Blur Constant. We consider how preprocessing affects downstream prediction and uncertainty quality of baseline methods in terms of the area under the receiver-operating-characteristic curve (AUC) and classification accuracy, as a function of the proportion of data referred to a medical expert for further review. All methods are tuned on in-domain validation AUC, and ensembles have $K = 3$ constituent models. We vary the standard deviation hyperparameter of the Gaussian blur kernel through a `blur_constant` (e.g., blur5 below corresponds to `blur_constant` $= 5$). A higher `blur_constant` results in a stronger smoothing of the image as per the preprocessing procedure outlined in Appendix I. The default `blur_constant` used in other experiments is 30.

	No Referral		50% Data Referred		70% Data Referred	
Method	**AUC (%)** ↑	**Accuracy (%)** ↑	**AUC (%)** ↑	**Accuracy (%)** ↑	**AUC (%)** ↑	**Accuracy** ↑
EyePACS Dataset (In-Domain)						
MAP (Deterministic)-blur5	82.9±0.7	80.3±0.8	89.1±0.6	91.0±0.7	91.4±0.3	91.6±0.6
MAP (Deterministic)-blur10	87.1±0.1	85.6±0.3	92.6±0.1	95.0±0.2	95.0±0.2	94.9±0.3
MAP (Deterministic)-blur20	86.7±1.0	88.0±0.5	90.5±1.4	95.6±0.3	94.4±0.9	96.3±0.2
MAP (Deterministic)-blur30	87.4±1.0	88.6±0.6	91.1±1.4	95.9±0.3	94.9±0.8	96.5±0.2
MC DROPOUT-blur5	88.1±0.2	85.9±0.4	94.0±0.1	95.0±0.2	96.5±0.1	96.4±0.1
MC DROPOUT-blur10	89.0±0.2	85.5±0.5	94.7±0.2	94.9±0.3	96.9±0.1	96.3±0.2
MC DROPOUT-blur20	91.4±0.1	90.2±0.2	95.7±0.2	97.3±0.1	97.5±0.1	98.0±0.1
MC DROPOUT-blur30	91.4±0.1	90.9±0.0	95.3±0.2	97.4±0.0	97.4±0.1	98.1±0.0
DEEP ENSEMBLE-blur5	85.6±0.2	84.6±0.1	90.9±0.3	94.3±0.0	93.6±0.3	95.8±0.2
DEEP ENSEMBLE-blur10	88.8±0.0	88.0±0.1	94.2±0.1	96.2±0.0	96.4±0.1	97.3±0.0
DEEP ENSEMBLE-blur20	89.2±0.2	89.5±0.2	90.5±0.3	96.9±0.1	93.8±0.3	97.7±0.0
DEEP ENSEMBLE-blur30	90.3±0.1	90.3±0.2	91.7±0.5	97.2±0.0	95.0±0.4	97.9±0.0
MC DROPOUT ENSEMBLE-blur5	89.3±0.0	87.3±0.1	94.7±0.0	95.7±0.1	97.1±0.0	96.9±0.0
MC DROPOUT ENSEMBLE-blur10	90.1±0.0	87.4±0.1	95.4±0.0	96.0±0.0	97.3±0.0	97.0±0.1
MC DROPOUT ENSEMBLE-blur20	92.4±0.0	91.2±0.0	**96.2±0.1**	97.7±0.0	**97.9±0.0**	98.3±0.0
MC DROPOUT ENSEMBLE-blur30	**92.5±0.0**	**91.6±0.0**	95.8±0.1	**97.8±0.0**	97.7±0.1	**98.4±0.0**
APTOS 2019 Dataset (Population Shift)						
MAP (Deterministic)-blur5	87.9±0.7	69.9±1.4	64.0±5.3	78.6±1.7	55.3±3.2	78.9±1.9
MAP (Deterministic)-blur10	90.2±0.2	77.0±0.7	63.1±2.0	81.1±0.6	51.1±0.0	80.0±0.6
MAP (Deterministic)-blur20	92.1±0.2	85.2±0.3	79.8±3.8	87.9±1.5	60.0±4.6	86.0±1.2
MAP (Deterministic)-blur30	92.2±0.2	86.2±0.4	80.1±2.8	87.6±1.1	55.4±3.3	85.4±0.9
MC DROPOUT-blur5	93.4±0.2	78.4±0.7	82.2±0.4	84.6±0.1	62.5±0.6	88.0±0.5
MC DROPOUT-blur10	93.3±0.2	77.3±0.9	79.7±0.3	83.3±0.3	59.6±1.0	87.2±0.4
MC DROPOUT-blur20	93.9±0.1	84.9±0.4	83.8±1.2	86.2±0.6	63.8±2.4	87.9±0.2
MC DROPOUT-blur30	94.0±0.2	86.8±0.2	87.4±0.3	88.1±0.2	65.3±1.3	88.2±0.3
DEEP ENSEMBLE-blur5	92.1±0.1	70.8±0.6	82.5±1.7	85.0±0.3	63.2±4.2	87.1±0.6
DEEP ENSEMBLE-blur10	91.8±0.0	78.8±0.3	73.5±0.3	84.5±0.1	51.1±0.0	82.0±0.1
DEEP ENSEMBLE-blur20	**94.1±0.0**	87.0±0.1	**93.7±0.4**	**93.6±0.3**	**82.2±2.5**	**91.7±0.5**
DEEP ENSEMBLE-blur30	94.2±0.2	87.5±0.1	91.2±1.4	92.4±0.7	67.4±5.6	90.1±0.9
MC DROPOUT ENSEMBLE-blur5	93.7±0.1	80.1±0.3	81.9±0.2	84.7±0.1	63.2±0.4	87.2±0.2
MC DROPOUT ENSEMBLE-blur10	93.6±0.1	78.7±0.4	79.1±0.1	83.4±0.1	59.6±0.2	87.3±0.3
MC DROPOUT ENSEMBLE-blur20	94.0±0.0	86.4±0.3	83.3±0.7	85.7±0.3	58.3±0.9	87.6±0.1
MC DROPOUT ENSEMBLE-blur30	94.1±0.1	**87.6±0.1**	86.8±0.2	88.0±0.1	62.3±0.3	87.7±0.2

I.4 Quality of Uncertainty Estimates at Each Clinical Label 0-to-4

We aim to investigate how model predictive uncertainty estimates vary with respect to the underlying clinical label ranging from 0 to 4, where 0 is No Diabetic Retinopathy and 4 is Proliferative Diabetic Retinopathy.

For each task (Country or Severity Shift) and each method, we bin examples by their ground-truth clinical label. Then, for each (model, clinical label) pair, we plot the distribution of predictive uncertainty for correctly and incorrectly predicted examples (in blue and red, respectively). See Figures 14-19 below.

A model that has good uncertainty estimates should successfully assign low predictive uncertainty to examples that it correctly classifies (the blue distribution should have most of its mass near 0) and a high predictive uncertainty to incorrect examples (the red distribution should have its mass concentrated at a higher x-value).

Below, we describe highlights of the clinical label–binned predictive entropy results. We focus the discussion on single models on the shifted datasets, though we also include evaluation of ensembles and in-domain datasets below. In each figure, all histograms are normalized and are displayed with the same range on the x- and y-axis. Some bars of the histograms are cut off because the plots are zoomed-in along the y-axis, in order to improve visibility of the important portion.

Severity Shift – Single Models (Figure 14). On the Severity Shift, we find that MAP (the deterministic model), RANK-1, and MFVI have poor uncertainty estimates on the labels which constitute the distributionally shifted data (labels 3 and 4, with labels appearing on the right of the figure); this can be seen by many of the incorrect predictions also being assigned low predictive uncertainty, i.e., the red distribution having much of its mass near 0. This corresponds to a particularly dangerous situation in a real-world deployment: many false negatives with low uncertainty, meaning a specialist might not be able to correct the model's misdiagnosis. MC DROPOUT, function-space variational inference (FSVI), and radial mean-field variational inference (RADIAL-MFVI) have better uncertainty estimates at most severity labels. However, all methods other than MC DROPOUT perform poorly on label 2 (moderate diabetic retinopathy), either assigning low uncertainty to many incorrect predictions or high uncertainty to many correct predictions.

Country Shift – Single Models (Figure 15). On the Country Shift, MAP, RANK-1, and MFVI have poor predictive uncertainty at all severity levels. MC DROPOUT and FSVI exhibit decent predictive uncertainty estimates at all levels except severity 1, where surprisingly, examples that are correctly classified have consistently higher predictive uncertainty than incorrect examples for both methods.

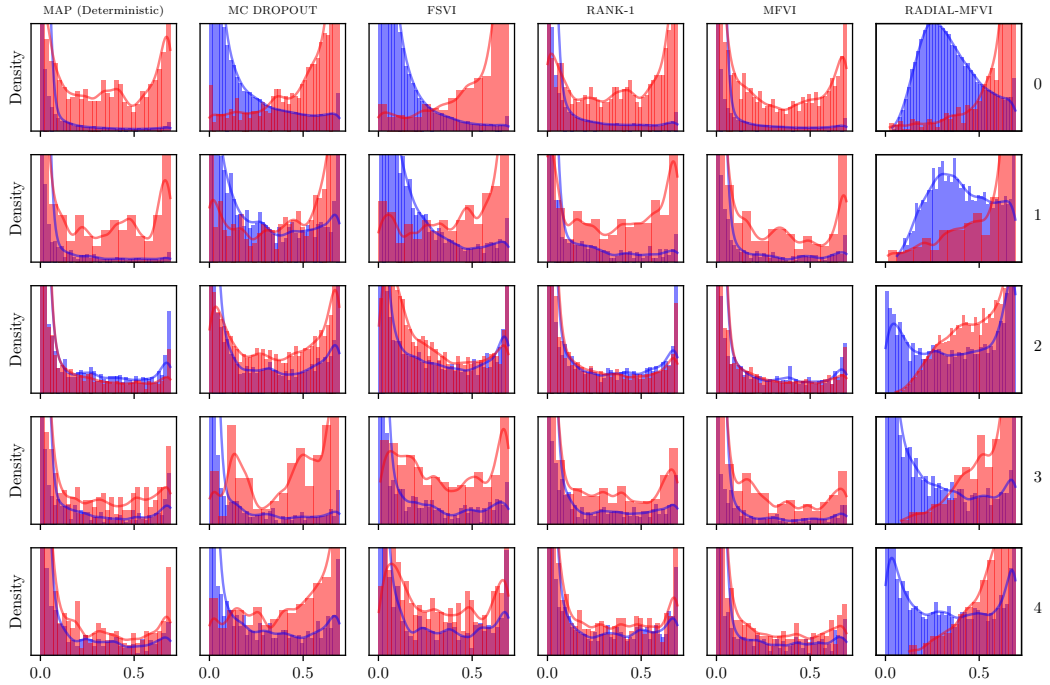


Figure 14: Clinical Label Binning – Severity Shift, Single Models. We analyze predictive uncertainty for each underlying clinical severity label (rows, label on right) and each uncertainty quantification method (columns). Here, we consider the distributionally shifted Severity Shift evaluation dataset, and single models ($K = 1$). Predictive uncertainty, as measured by predictive entropy (cf. Appendix E.2), is displayed as a normalized density for correct (blue) and incorrect (red) predictions.

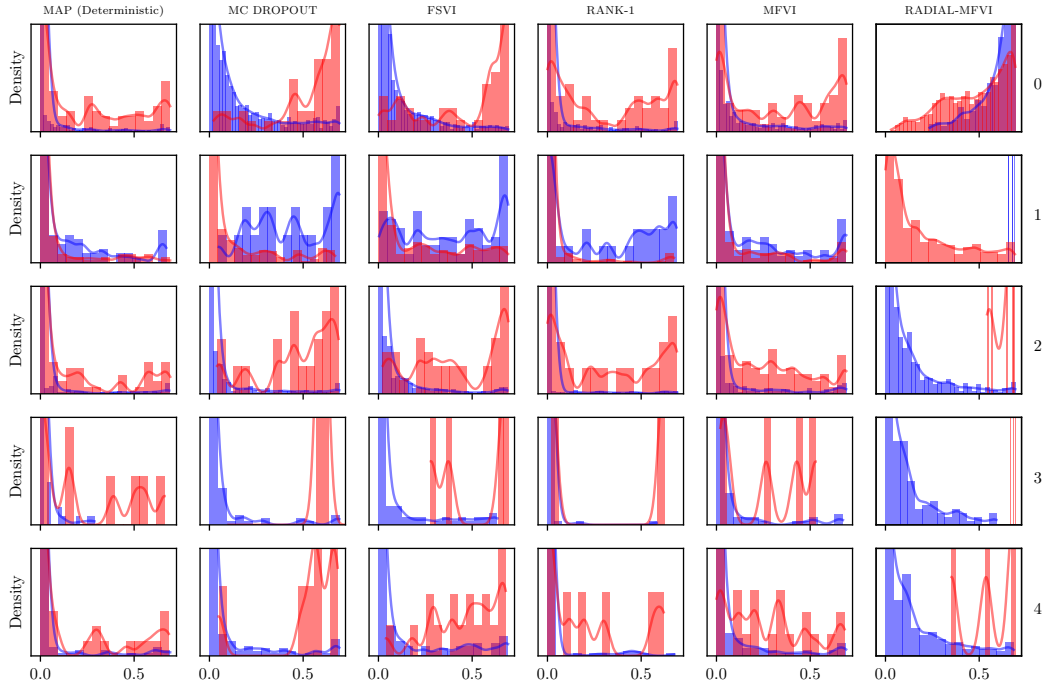


Figure 15: Clinical Label Binning – Country Shift, Single Models. We analyze predictive uncertainty for each underlying clinical severity label (rows, label on right) and each uncertainty quantification method (columns). Here, we consider the distributionally shifted Country Shift evaluation dataset (APTOS), and single models ($K = 1$). Predictive uncertainty, as measured by predictive entropy (cf. Appendix E.2), is displayed as a normalized density for correct (blue) and incorrect (red) predictions.

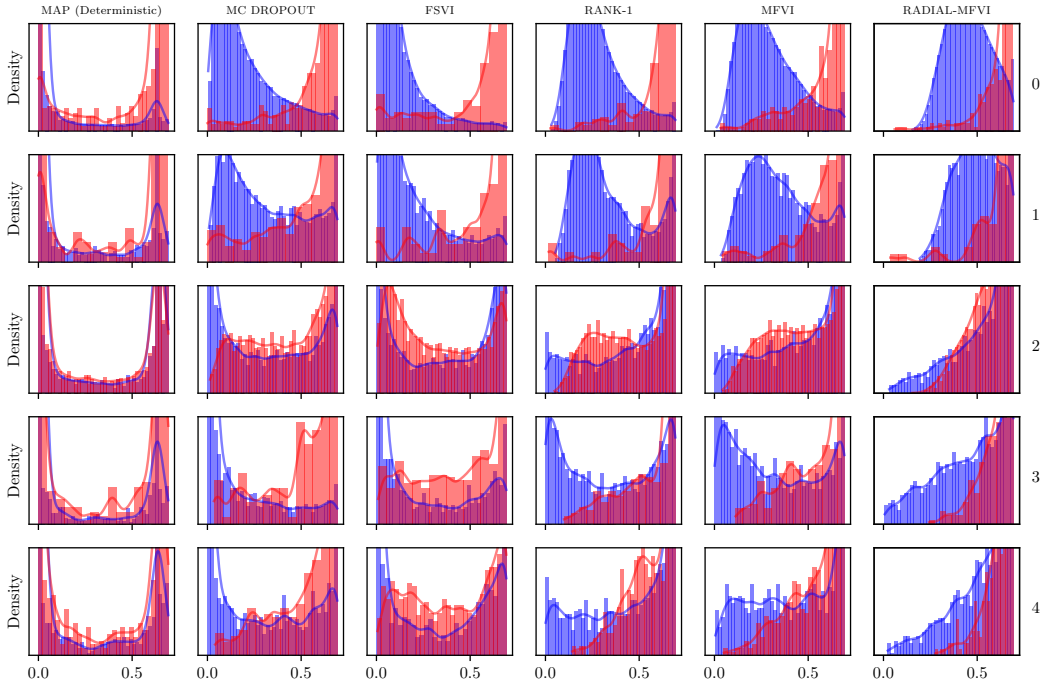


Figure 16: Clinical Label Binning – Severity Shift, Ensembles. We analyze predictive uncertainty for each underlying clinical severity label (rows, label on right) and each uncertainty quantification method (columns). Here, we consider the distributionally shifted Severity Shift evaluation dataset, and ensembles ($K = 3$). Predictive uncertainty, as measured by predictive entropy (cf. Appendix E.2), is displayed as a normalized density for correct (blue) and incorrect (red) predictions.

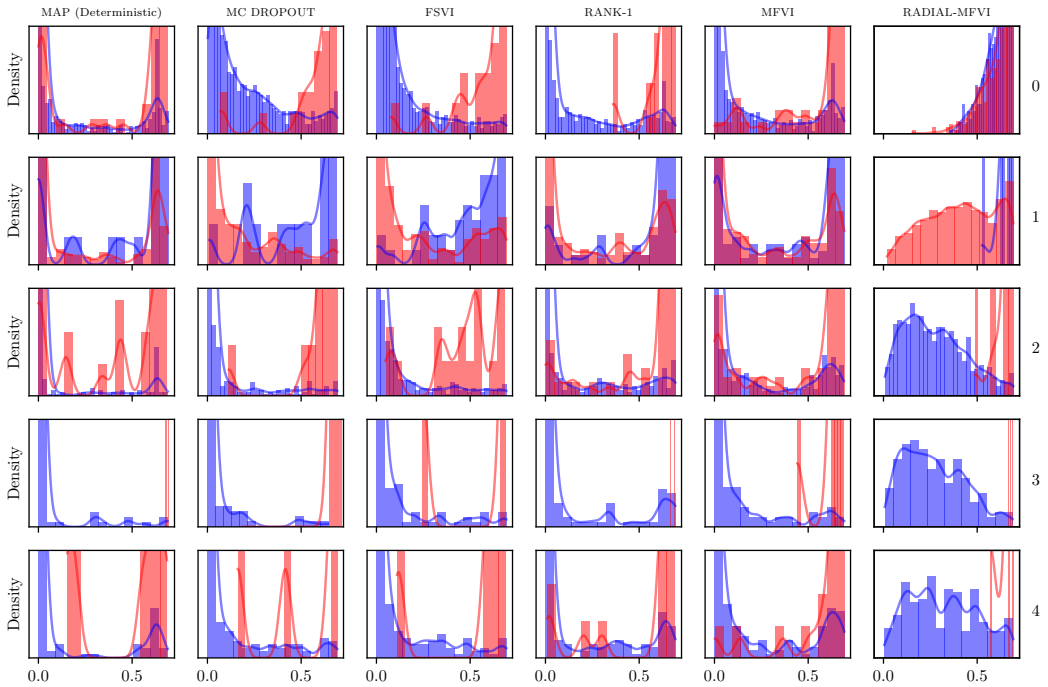


Figure 17: Clinical Label Binning – Country Shift, Ensembles. We analyze predictive uncertainty for each underlying clinical severity label (rows, label on right) and each uncertainty quantification method (columns). Here, we consider the distributionally shifted Country Shift evaluation dataset (APTOS), and ensembles ($K = 3$). Predictive uncertainty, as measured by predictive entropy (cf. Appendix E.2), is displayed as a normalized density for correct (blue) and incorrect (red) predictions.

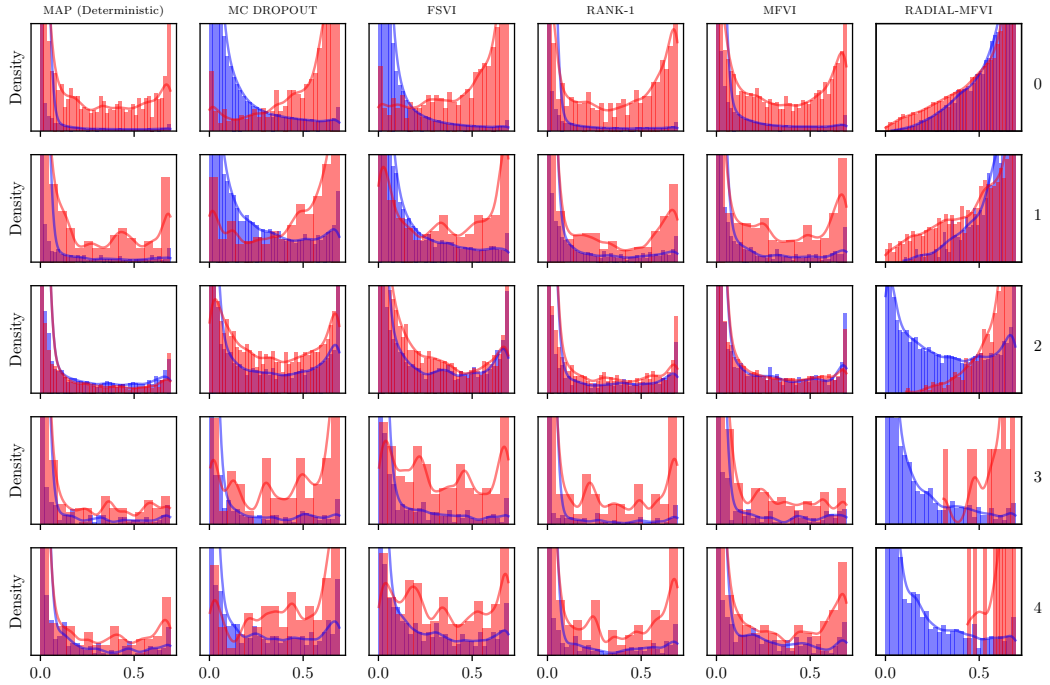


Figure 18: Clinical Label Binning – Country Shift (In-Domain), Single Models. We analyze predictive uncertainty for each underlying clinical severity label (rows) and each uncertainty quantification method (columns). Here, we consider the in-domain Country Shift evaluation dataset, and single models ($K = 1$). Predictive uncertainty, as measured by predictive entropy (cf. Appendix E.2), is displayed as a normalized density for correct (blue) and incorrect (red) predictions.

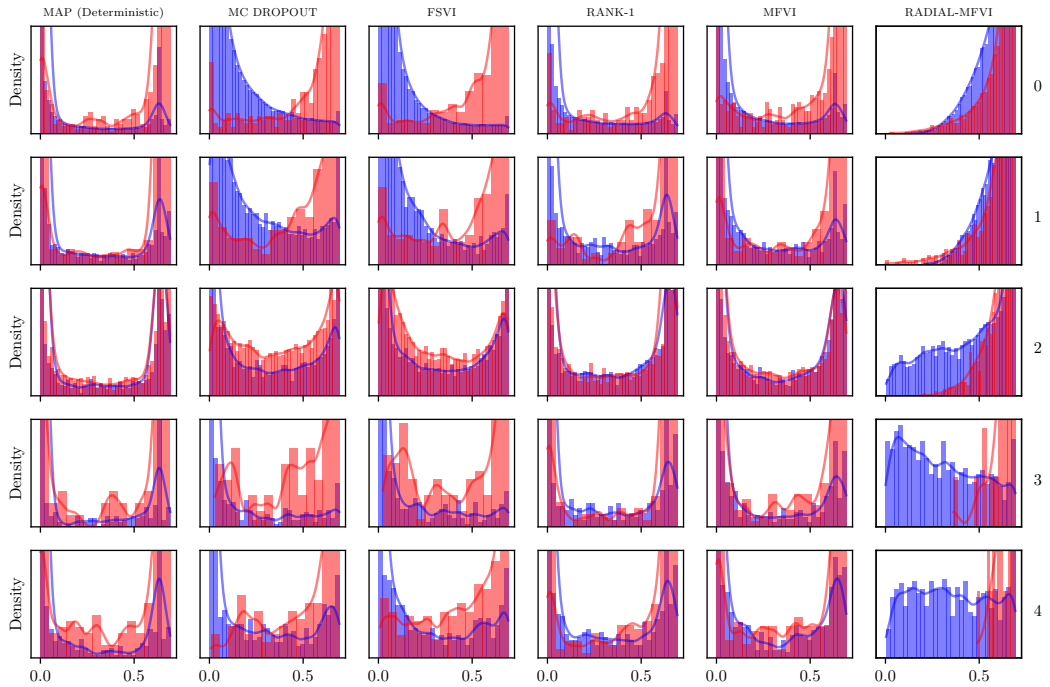


Figure 19: Clinical Label Binning – Country Shift, Ensembles. We analyze predictive uncertainty for each underlying clinical severity label (rows, label on right) and each uncertainty quantification method (columns). Here, we consider the in-domain Country Shift evaluation dataset (APTOS), and ensembles ($K = 3$). Predictive uncertainty, as measured by predictive entropy (cf. Appendix E.2), is displayed as a normalized density for correct (blue) and incorrect (red) predictions.