NAS-Bench-360: Benchmarking Diverse Tasks for Neural Architecture Search

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Abstract

Most existing neural architecture search (NAS) benchmarks and algorithms priori-1 tize performance on well-studied tasks, focusing on computer vision datasets such 2 as CIFAR and ImageNet. However, the applicability of NAS approaches in other 3 areas is not adequately understood. In this paper, we present NAS-Bench-360, 4 a benchmark suite for evaluating state-of-the-art NAS methods on less-explored 5 datasets. To do this, we organize a diverse array of tasks, from classification of 6 simple deformations of natural images to predicting protein folding and partial 7 differential equation (PDE) solving. Our evaluation pipeline compares architecture 8 search spaces of different flavors, and reveals varying performance on different 9 tasks, providing baselines for further use. All data and reproducible evaluation 10 code are open-source and publicly available. The results of our evaluation show 11 that current state-of-the-art NAS methods often struggle to compete with sim-12 ple baselines and human-designed architectures on the majority of tasks in our 13 benchmark. At the same time, they can be quite effective on a few individual, 14 understudied tasks. This demonstrates the importance of evaluation on diverse 15 tasks to better understand the usefulness of different approaches to architecture 16 search and automation. 17

18 1 Introduction

Neural architecture search (NAS) aims to automate the design of deep neural networks, ensuring 19 performance on par with hand-crafted architectures while reducing human labor devoted to tedious 20 architecture tuning [8]. With the growing number of application areas of ML, and thus of use-cases 21 for automating it, NAS has experienced an intense amount of study, with significant progress in 22 search space design [3, 20, 33], search efficiency [22], and search algorithms [16, 28, 29]. While the 23 use of NAS techniques may be especially impactful in under-explored or under-resourced domains 24 25 where less expert help is available, the field has largely been dominated by methods designed for and evaluated on benchmarks in computer vision [6, 20, 30]. There have been a few recent efforts 26 to diversify these benchmarks to settings such as vision-based transfer learning [7] and speech and 27 language processing [13, 21]; however, evaluating NAS methods on such well-studied tasks using 28 traditional, domain-specific search spaces does not give a good indication of their utility on more 29 far-afield applications, which have often necessitated the design of custom neural operations [4, 19]. 30

We aim to rectify this issue by introducing a suite of diverse benchmark tasks drawn from various data domains that we collectively call **NAS-Bench-360**. This benchmark consists of an organized

Submitted to the 35th Conference on Neural Information Processing Systems (NeurIPS 2021) Track on Datasets and Benchmarks. Do not distribute.

33 setup of five suitable datasets that can both (a) be evaluated in a unified way using existing NAS

³⁴ approaches and (b) come from a variety of different application areas, including numerical analysis, ³⁵ organic chemistry, and medical imaging. We also include standard image classification evaluations as

organic chemistry, and medical imaging. We also include standard image classification evaluations as

³⁶ a point of comparison, as many new methods continue to be designed for such tasks.

Following our construction of this benchmark, we evaluate three different NAS approaches, each 37 characterized by an architecture (search space, search algorithm) pair, and compare the results to 38 expert-driven domain-specific architecture design. As a baseline comparator, the first approach 39 uses a singleton architecture, the Wide ResNet (WRN) [31], as the search space, paired with a 40 hyperparameter tuning algorithm to adjust the training procedure for each task. The other two search 41 spaces are well-studied in modern NAS: DARTS [20] and DenseNAS [9], and we pair them with 42 their respective best-performing search methods. We find that the modern NAS approaches struggle 43 to beat even the simple WRN comparator on the majority of tasks in the benchmark. On two of 44 the tasks—classifying electromyography signals and solving partial differential equations—NAS 45 methods do significantly worse. NAS lags even further behind when we include domain-specific 46 expert-designed architectures, where it lags far behind on even CIFAR-100 when disallowing extra 47 augmentation or pre-training on ImageNet [25]. On the other hand, DARTS cells perform relatively 48 well on two tasks that a priori seem more challenging: spherical image classification and protein-49 distance prediction. These observations and other empirical insights demonstrate the necessity of a 50 benchmark that provides a diverse array of data domains for evaluating NAS methods. Our evaluation 51 results also serve as a baseline for comparison in future development of NAS. 52

To ensure the availability and impact of this benchmark, the associated datasets and evaluation pipelines will remain open-source and accessible at https://rtu715.github.io/ NAS-Bench-360/. Reproducibility is assured from open-sourcing all relevant code for the end-toend procedure, including data processing, architecture search, model retraining, and hyper-parameter tuning frameworks.

58 2 Related Work

Benchmarks have been very important to the development of NAS in recent years. This includes 59 standard evaluation datasets and protocols, of which the most popular are the CIFAR-10 and ImageNet 60 routines used by DARTS [20]. Another important type of benchmark has been tabular benchmarks 61 such as NAS-Bench-101 [30], NAS-Bench-201 [6], and NAS-Bench-1Shot1 [32]; these benchmarks 62 exhaustively evaluate all architectures in their search spaces, which is made computationally feasible 63 by defining simple searched cells. Consequently, these benchmark cells are less expressive than the 64 65 DARTS cell [20], often regarded as the most powerful search space in the cell-based regime. Notably, our benchmark is *not* a tabular benchmark, i.e. we do *not* evaluate every architecture from a fixed 66 search space: rather, the focus is on the organization of a suite of tasks to evaluate both NAS methods 67 and search spaces, which would necessarily be restricted if we first fixed a search space to construct a 68 tabular benchmark from. 69

70 While NAS methods and benchmarks have generally been focused on computer vision, recent work such as AutoML-Zero [23] and XD operations [24] has started moving towards a more generically 71 applicable set of tools for AutoML. However, even more recent benchmarks that do go beyond the 72 73 most popular vision datasets have continued to focus on well-studied tasks, including vision-based transfer learning [7], speech recognition [21], and natural language processing [13]. Our aim is to 74 go beyond such areas in order to evaluate the potential of NAS to automate the application of ML 75 in truly under-explored domains. One analogous work to ours in the field of meta-learning is the 76 Meta-Dataset benchmark of few-shot tasks [27], which similarly aimed to establish a wide-ranging 77 set of evaluations for that field. 78

79 **3** NAS-Bench-360: A Suite of Diverse and Practical Tasks

In this section, we introduce the NAS setting being targeted by our benchmark, our motivation for organizing a new set of diverse tasks as a NAS evaluation suite, and our task-selection methodology.

We report evaluations of specific algorithms on this new benchmark in the next section.

3.1 Neural Architecture Search: Problem Formulation and Baselines

For completeness and clarity, we first formally discuss the architecture search problem itself, starting 84 with the extended hypothesis class formulation [16]. Here the goal is to use a dataset of points $x \in \mathcal{X}$ 85 to find parameters $\mathbf{w} \in \mathcal{W}$ and $a \in \mathcal{A}$ of a parameterized function $f_{\mathbf{w},a} : \mathcal{X} \mapsto \mathbb{R}_{\geq 0}$ that minimize 86 the expectation $\mathbb{E}_{x\sim\mathcal{D}}f_{\mathbf{w},a}(x)$ for some test distribution \mathcal{D} over \mathcal{X} ; here \mathcal{X} is the input space, \mathcal{W} is 87 the space of model weights, and A is the set of architectures. For generality, we do not require the 88 training points to be drawn from \mathcal{D} to allow for domain adaptation, as is the case for one of our tasks, 89 and we do not require the loss to be supervised. Note also that the goal here does not depend on the 90 issue of computational or memory efficiency, which we do not focus on in our evaluations; there our 91 restriction is only that the entire pipeline can be run on an NVIDIA V100 GPU. 92 Notably, this formulation makes no distinction between the model weights \mathbf{w} and architectures a, 93

treating both as parameters of a larger model. Indeed, the goal of NAS may be seen as similar to 94 model design, except now we include the design of an (often-discrete) architecture space A such that 95 it is easy to find an architecture $a \in A$ and model weights $\mathbf{w} \in W$ whose test loss $\mathbb{E}_{\mathcal{D}} f_{\mathbf{w},a}$ is low 96 using a search algorithm. This can be done in a one-shot manner—simultaneously optimizing a and 97 \mathbf{w} —or using the standard approach of first finding an architecture a and then keeping it fixed while 98 training model weights w for it using a pre-specified algorithm such as tuned stochastic gradient 99 descent (SGD). 100 This formulation also includes non-NAS methods by allowing the architecture search space to be a 101

rins formulation also includes for 1016 includes by anowing the architecture search space to be a
 singleton. When the sole architecture is a standard and common network such as WRN [31], this yields
 a natural baseline with an algorithm searching for training hyperparameters, not architectures. On the
 other hand, when A contains a single domain-specific architecture, such as a spherical convolutional
 neural network (CNN) [4], it yields the "human baseline" competitor approach without search. For
 our empirical investigation, we compare the performance of state-of-the-art NAS approaches against
 that of the two singleton baselines.

108 3.2 Motivation and Task Selection Methodology

Curating a diverse, practical set of tasks for the study of NAS is our primary motivation behind this 109 work. We observe that past NAS benchmarks focused on the creation of larger search spaces and 110 more sophisticated search methods for neural networks. However, the utility of these search spaces 111 and methods are only evaluated on canonical computer vision datasets. Whether these new methods 112 can improve upon non-NAS baselines remains an open question. This calls for the introduction of 113 new datasets lest NAS research overfits to the biases of CIFAR-10 and ImageNet. By identifying 114 these possible biases, future directions in NAS research can be better primed to suit the needs of 115 practitioners, thereby incentivizing the deployment of NAS techniques on real applications. 116

NAS-Bench-360 comprises tasks from existing datasets their variants as summarized in Table 1. This 117 118 work focuses exclusively on datasets with 2d input data including images, wave spectra, differential 119 equations, and protein sequence features. Although in practice neural networks are employed to analyze different data modalities, the most well-studied NAS approaches only accept 2d inputs 120 and therefore we study tasks within this scope. During the selection of tasks, breadth is our main 121 consideration. First, we formalize the categorization of tasks into **point prediction** (point) and 122 dense prediction (dense) [26], respectively referring to tasks with scalar outputs and 2d matrix 123 outputs. In other words, point prediction tasks are classification tasks, and dense prediction tasks are 124 element-wise prediction tasks, which is a specific form of regression. The heavy bias of previous 125 NAS research towards point prediction tasks motivates the inclusion of dense prediction tasks in our 126 benchmark. Second, breadth is achieved by selecting tasks from various subjects and applications of 127 deep learning, where introducing NAS could improve upon the performance of handcrafted neural 128 networks. 129

130 3.3 List of Tasks from Diverse Data Sources

In lieu of providing raw data, we perform data pre-processing locally and store the processed data on a public Amazon Web Service's S3 data bucket with download links available on our website. Our data treatment largely follows the procedure defined by the researchers who provided them. This would enhance the reproducibility of results by ensuring the uniformity of input data for different pipelines. Specific pre-processing and augmentation steps are described below.

Task name	Dataset size	Туре	Learning objective	New to NAS
CIFAR-100	60K	Point	Classify natural images into 100 classes	
Spherical	60K	Point	Classify spherically projected images into 100 classes	\checkmark
NinaPro	3956	Point	Classify sEMG signals into 18 classes corresponding to hand gestures	\checkmark
Darcy Flow	1100	Dense	Predict the final state of a fluid from its initial conditions	\checkmark
PSICOV	3606	Dense	Predict pairwise distances between resi- duals from 2d protein sequence features	\checkmark

Table 1: Information of tasks in NAS-Bench-360

136 3.3.1 CIFAR-100: Standard Image Classification

As a starting point of comparison to existing benchmarks, we include the CIFAR-100 task [14], which
 contains RGB images from natural settings to be classified into 100 fine-grained categories. CIFAR 100 is preferred over CIFAR-10 because it is more challenging and suffers less from over-fitting in
 previous research.

Data pre-processing: while the 10,000 testing images are kept aside only for evaluating architectures, the 50,000 training images are randomly partitioned into 40,000 for architecture search and 10,000 for validation. On all of the 50,000 training images, we apply standard CIFAR augmentations including random crops and horizontal flipping, and finally normalize them using a pre-calculated mean and standard deviation of this set. On the 10,000 testing images, we only apply normalization with the same constants.

147 3.3.2 Spherical: Classifying Spherically Projected CIFAR-100 Images

To test NAS methods applied to natural-image-like data, we consider the task of classifying spherical 148 projections of the CIFAR-100 images, which we call the Spherical task. In addition to scientific 149 interest, spherical image data is also present in a variety of applications, such as omnidirectional 150 vision in robotics and weather modeling in meteorology, as sensors usually produce distorted image 151 signals in real-life settings. To create a spherical variant of CIFAR, we project the planar signals of 152 the CIFAR images to the northern hemisphere and add a random rotation to produce spherical signals 153 for each individual channel following the procedure specified in [4]. The resulting images are 60*60 154 pixels with RGB channels. 155

Data pre-processing: with the same split ratios CIFAR-100, the generated spherical image data is directly used for training and evaluation without data augmentation and pre-processing.

158 3.3.3 NinaPro: Classifying Electromyography Signals

Our final classification task, **NinaPro**, moves away from the image domain to classify hand gestures indicated by electromyography signals. For this, we use a subset of the NinaPro DB5 dataset [2] in which two thalmic Myo armbands collect EMG signals from 10 test individuals who hold 18 different hand gestures to be classified. These armbands leverage data from muscle movement, which is collected using electrodes in the form of wave signals. Each wave signal is then sampled using a wavelength and frequency prescribed in [5] to produce 2d signals.

Data pre-processing: Containing less than 4,000 samples, the data is comprised of single-channel signals with an irregular shape of 16*52 pixels. This task also differs from CIFAR for its class imbalance, as over 65% of all gestures are the neutral position. We split the data using the same ratio as CIFAR, resulting in 2638 samples for training, and 659 samples for validation and testing each. No additional pre-processing is performed.

170 **3.3.4 Darcy Flow: Solving Partial Differential Equations (PDEs)**

Our first regression task, **Darcy Flow**, focuses on learning a map from the initial conditions of a PDE to the solution at a later timestep. This application aims to replaced traditional solvers with learned neural networks, which can output a result in a single forward pass. The input is a 2d grid specifying the initial conditions of a fluid and the output is a 2d grid specifying the fluid state at a later time, with the ground truth being the result computed by a traditional solver.

Data pre-processing: we use scripts provided by [19] to generate the PDEs and their solutions, for a total of 900 data points for training, 100 for validation, and 100 for testing. All input data is normalized with constants calculated on the training set before fed into the neural network and de-normalized following an encode-decode scheme. The solutions, or labels, for the training set are also encoded and decoded this way. The test labels are not processed. We report the mean square error (MSE or ℓ_2).

182 3.3.5 PSICOV: Protein Distance Prediction

Our final task, **PSICOV**, studies the use of neural networks in the protein folding prediction pipeline, which has recently received significant attention to the success of methods like AlphaFold [12]. While the dataset and method they use are too large-scale for our purposes, we consider a smaller set of protein structures to tackle the specific problem of inter-residual distance predictions outlined in [1]. 2d large-scale features are extracted from protein sequences, resulting in input feature maps with a massive number of channels. Correspondingly, the labels are pairwise-distance matrices with the same spatial dimension.

Data pre-processing: we adopt the chosen subset of DeepCov proteins in [1], consisting of 3,456 proteins each with 128*128 feature maps across 57 channels. 100 proteins from this set are used for validation and the rest for training. Test data for final evaluation is gathered from another set of 150 proteins, PSICOV. Since these produce feature maps that are larger (512*512), we run the prediction network over all of its non-overlapping 128*128 patches. The evaluation metric is mean absolute error (MAE or ℓ_1) computed on distances below 8 Å, referred to as MAE₈.

196 **3.4 Ethics and Responsible Use**

Within our array of tasks, the only dataset containing human-derived data is NinaPro. Our chosen 197 subset of NinaPro contains only muscle movement data from 10 healthy individuals, without any 198 exposure of personal information from clinical data. The original experiments to acquire NinaPro 199 data are approved by the ethics commission of the state of Valais, Switzerland [2]. For other datasets, 200 we have listed the data licenses in the appendix for responsible usages of data. While we do not 201 202 view the specific datasets we use in this benchmark as potential candidates for misuse, the broader 203 goal of applying NAS to new domains comes with inherent risks that may require mitigation on an application-by-application basis. 204

205 4 Using NAS-Bench-360 to Study Architecture Search Methods

Having detailed our construction of NAS-Bench-360, we now demonstrate its usefulness on (a)
comparing and evaluating state-of-the-art architecture search methods on powerful search spaces and
(b) discovering new insights on their performance on under-explored domains. In this section, we
first specify the different NAS algorithms and baselines we compare, followed by the experimental
and reproducibility setup we follow. Finally, we report our main comparisons and analyze the results.

211 4.1 Baselines and Search Procedures

From the discussion in Section 3, the two non-NAS baseline methods we consider—applying a tuned WRN to all tasks and using a fixed, domain-specific architecture—can be viewed via the NAS setup as having a singleton architecture search space. As for NAS algorithms themselves, we focus on two well-known paradigms for search: cell-based NAS (using DARTS [20]) and macro NAS (using DenseNAS [9]). We detail these four approaches below.

Wide ResNet with Hyperparameter Tuning The residual network (ResNet) and its derivative 217 architectures are canonical for classic computer vision, and we investigate their ability to generalize to 218 our selection of tasks. A more powerful adaptation of ResNet, the Wide ResNet [31] is chosen as the 219 backbone architecture. For automated training, we wrap the training procedure with a hyperparameter 220 tuning algorithm, ASHA [15], an asynchonous version of Hyperband [18]. Given a range for each 221 hyperparameter, either discrete or continuous, ASHA uniformly samples configurations and uses 222 brackets of elimination: at each round, each configuration is trained for some epochs, before the 223 algorithm selects the best-performing portion based on validation metrics. Since we use the Wide 224 ResNet backbone for all tasks, our tuning budget is fixed and uniform. 225

Expert-Designed Networks We also include expert-driven design of architectures in specific domains as a more rigorous comparator for NAS methods on our tasks. Frequently this includes not only hand-designed topologies and operation patterns but custom neural operations themselves, which are often crucial for success on domains beyond computer vision. Below we briefly summarize the architectures chosen for each task.

- **CIFAR-100**: While this task is very heavily studied and one can achieve very high accuracies using optimization tricks and transfer from ImageNet, we restrict our selection to existing results that use only the simple (standard) data augmentation we allow for the evaluation phase. Here the best result found is using DenseNet-BC [10].
- **Spherical**: This task is often regarded as a canonical example where a specific neural operation, specifically spherical convolutions, are the "right" operation to substitute for the convolution due to data-specific properties. Our result is from a wide variation of the spherical CNN in [4], with a max width of 256 channels from 64.
- **NinaPro**: As the original paper studying NinaPro used fairly weak networks that achieve a much higher error, here we simply report the performance of our tuned WRN baseline.
- Darcy Flow: Here we report the performance of a four-layer network that replaces convolutions with Fourier Neural Operators (FNOs) [19], which were specially designed solving partial differential equations. Note that our reproduced result attains slightly better MSE than the numbers reported by the authors.
- **PSICOV**: We report the reproduced performance of the ResNet-256 network used by the PDNET, a deeper, narrow, and dilated version of the standard ResNet used for ImageNet; note our reproduction attains much better MAE₈ than the authors report [1].

Cell-based Search Using DARTS The first state-of-the-art NAS paradigm within our consideration 248 is cell-based NAS. Cell-based methods first search for a genotype, which is a cell containing neural 249 operations such as convolution and pooling. During evaluation, a neural network is constructed by 250 replicating the searched cell and stacking them together. The most popular search space for this 251 approach is the one used by the DARTS space [20], consisting of assigning one of eight operations to 252 six edges in two types of cells: "normal" cells preserve the shape of the input representation while 253 "reduction" cells downsample it. Note that for the dense tasks we do not use the reduction cell so as 254 to not introduce a bottleneck. 255

Finally, to adhere to standard ML practices we do *not* adapt the standard DARTS pipeline, which
uses test performance to select from multiple random seeds. This, in addition to not using other
evaluation-time enhancements such—specifically auxiliary towers and the cutout data augmentation—
leads to lower performance on CIFAR-100 than is reported in the literature. As this search space has
been heavily studied since its introduction, we use as a search routine a recent approach—GAEA
PC-DARTS—that achieves some of the best-known results on CIFAR-10 and ImageNet for this
benchmark [16].

Macro NAS Using DenseNAS The second NAS paradigm we consider is macro NAS. Instead of building from a fixed cell, macro NAS requires the specification of a super network with different inter-connected network blocks. These blocks and connections are then pruned during the search phase to construct the output neural net for evaluation. For this benchmark, we also choose a recent search space in this NAS paradigm, DenseNAS [9], which similarly to the DARTS space has near state-of-the-art results on ImageNet.

Table 2: Comparing NAS methods with baseline and expert-designed methods on NAS-Bench-360.
All automated results (WRN, DenseNAS, and GAEA PC-DARTS) are averages of three random
seeds. See Appendix for standard deviations.

Search space	Search method	CIFAR-100 (0-1 err.)	Spherical (0-1 err.)	NinaPro (0-1 err.)	Darcy Flow MSE	PSICOV MAE ₈
WRN baseline	ASHA	24.89	88.45	6.88	0.041	5.71
expert design*	hand-tuning	17.17	64.42	6.88	0.0096	3.50
DenseNAS-R1	DenseNAS	27.44	72.99	10.17	0.10	3.84
DARTS Cell	GAEA PC-DARTS	24.19	52.90	11.43	0.056	2.80

^{*} Chosen according to best-effort literature search and implementation; c.f. Section 4.1.

DenseNAS searches for architectures with densely-connected, customizable routing blocks to emulate 269 DenseNet [10]. In our experiments, we use the ResNet-based search space, DenseNAS-R1, with all of 270 WRN's neural operations for better comparison with the baseline backbone. For point tasks and dense 271 tasks, we adapt two super networks from the one used for ImageNet as inputs to the search algorithm. 272 The super network for dense tasks maintains the same spatial dimensions without downsampling to 273 avoid bottlenecks, and we use a lower learning rate for evaluating architectures on dense tasks to 274 prevent divergence. Other training and evaluation procedures are identical to those in the original 275 paper and uniform across all tasks. 276

277 4.2 Experimental Setup

Our main experiments consist of 3 evaluation trials for every combination of method and task, fixing one random seed for each trial. We present these results in Table 2 and discuss the specific procedure, reproducibility, and extension experiments in the following subsections.

Using validation data For best practices in NAS, we argue for the separation of the final testing set and the validation set, which is specifically for selecting neural architectures and hyperparameters. After this process, we combine training and validation data to perform retraining and evaluation on the test set. This result is reported as final and is not used in any way to further optimize the model.

Hyperparameter tuning In experiments with hyperparameter tuning, we consistently use the same hyperparameter ranges and fix the tuning budget, in terms of the number of configurations and maximum training epochs, across all tasks. The tuning budget is selected to be 2.5 to 3 times the backbone training time. This is to eliminate inductive biases for specific tasks. Details on the tuning procedure are in the appendix.

Software and hardware We adopt the free, open-source software *Determined*¹ for experiment management, hyperparameter tuning, AWS cloud deployment with docker containers. All experiments are performed on a single p3.2xlarge instance with one Nvidia V100 GPU. The computation cost in GPU hours of individual experiments using this setup can be found in the appendix.

Reproducibility The following measures in our experimental pipeline are taken to ensure the reproducibility of our results:

- We perform most data pre-processing steps beforehand and store the processed data in the cloud for download. A data splitting scheme, once randomly selected, is then fixed for all experiments on that task, i.e. the same training, validation, and testing sets fed into the dataloader are always the same.
- Experimentation code is always executed in a fixed docker container using a pre-built docker image on Docker Hub. This guarantees a uniform execution environment and saves users from the manual labor of configuring dependencies.

¹GitHub repository: https://github.com/determined-ai/determined

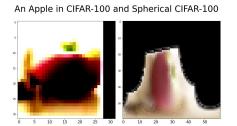


Figure 1: Comparison of the same CIFAR-100 image before and after the spherical transformation.

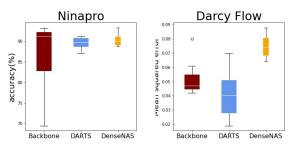


Figure 2: Distribution of random architectures and hyperparameters' performance on NinaPro and Darcy Flow.

Task	GAEA PC-DARTS	DenseNAS	WRN
CIFAR-100	33	2	8
Spherical CIFAR-100	39	2.5	8.5
NinaPro	2	0.5	1
Darcy Flow	15	0.5	2
PSICOV	59.5	23	61

Table 3: Experiment runtimes of NAS-Bench-360 (GPU hours)

3. Via the specification of a random seed, *Determined* controls several important sources of
 randomness during code execution, including hyperparameter sampling and training data
 shuffling.

4. During training, we always validate on the full validation set, not on a mini-batch, to avoid stochasticity in the results.

308 4.3 Comparing NAS Approaches Using NAS-Bench-360

Generalization of NAS to other domains Our experiments demonstrate that state-of-the-art NAS 309 approaches in classic vision are unable to outperform human-designed neural networks on 3 out 310 of 5 tasks in NAS-Bench-360. They do especially poorly on the Darcy Flow task and fall short 311 of matching both non-NAS comparators by a large margin. Perhaps most surprisingly, neither the 312 DARTS space nor DenseNAS, both very recent search spaces with strong results on ImageNet 313 (and CIFAR-10 for the former) are able to outperform the reported performance of a fairly basic 314 architecture (DenseNet) on CIFAR-100; this is especially interesting as DenseNAS was built around 315 this architecture. Overall, our results suggest that modern NAS, despite its promise to automate deep 316 learning, is not yet well-equipped to handle its various domains of applications studied in this paper. 317 These empirical results also serve as new baselines for comparison in future research to extend NAS 318 approaches to generalize to new areas. 319

Computational cost In some time-sensitive applications of NAS, both efficiency and perfor-320 mance are criteria for NAS method selection. Our choice of methods exemplifies a tradeoff 321 between these two factors. As a more computationally heavy method, GAEA PC-DARTS 322 beats the more lightweight DenseNAS on most of the tasks except for NinaPro, where they 323 achieve similar accuracies. On certain tasks, such as NinaPro and PSICOV, DenseNAS would 324 be the more cost-effective option than GAEA PC-DARTS to have decent performance on par 325 with handcrafted neural architectures. Note that the computation cost of the WRN baseline can 326 vary due to randomness inherent in ASHA's asynchrony. We report all experiment runtimes in Table 3. 327 328

CIFAR-100 vs. Spherical The Spherical task can be directly compared to CIFAR-100 to assess how well NAS methods could handle image distortions. With the same setup across tasks, both

Table 4: ℓ_1 error of supernet and searched architectures (discretized) on grid tasks

	DARTS		DenseNAS		
Task	Supernet	Discretized	Supernet	Discretized	
Darcy Flow PSICOV	$\begin{array}{c} 0.031 \pm 0.001 \\ 3.87 \pm 0.12 \end{array}$	$\begin{array}{c} 0.057 \pm 0.012 \\ 2.80 \pm 0.057 \end{array}$	$\begin{array}{c} 0.041 \pm 0.002 \\ 7.96 \pm 0.20 \end{array}$	$\begin{array}{c} 0.10 \pm 0.010 \\ 3.84 \pm 0.15 \end{array}$	

the DARTS space and DenseNAS have reasonably good numbers on CIFAR-100, but their results 331 significantly deteriorate on the spherical variant. Both obtain much worse error when the images 332 are spherically projected, but a much larger gap emerges between the two methods, with DenseNAS 333 performing quite badly. On the other hand, the searched DARTS Cell not only performs 20-36% better 334 than the other convolutional approaches but even beats our best-effort adaptation of the spherical 335 CNN approach to this task [4], in which we expanded the size of that network. This is surprising 336 because spherical convolutions were designed specifically for such data. We believe these results 337 indicate that the spherical dataset may be a useful but simple way for distinguishing NAS approaches 338 when they are overfitting to standard computer vision domains; Figure 1 provides an example of the 339 distortion. 340

WRN as a baseline Viewing the WRN baseline as a singleton architecture search space, we 341 compare this baseline to more sophisticated NAS search spaces. On our set of new tasks, NAS does 342 not perform better than Wide ResNet with hyperparameter tuning on CIFAR-100, NinaPro, and 343 Darcy Flow but excels on the rest. Hyperparameter optimization can boost the backbone performance 344 considerably to rival the performance of NAS methods. Most non-Bayesian hyperparameter tuning 345 algorithms, such as random search [17], population-based training [11], and Hyperband [18], are 346 also straightforward to apply with any neural network backbone. Therefore, we argue for the use of 347 hyperparameter-tuned backbones to assess the effectiveness of NAS approaches and encourage their 348 inclusion in NAS benchmarks. 349

350 4.4 In-Depth Studies Using NAS-Bench-360

Supernet performance on grid tasks During architecture search, our NAS methods on the DARTS 351 and DenseNAS search spaces train the supernets to find optimal neural operations on the validation 352 set. Surprisingly, the validation error of the supernet is sometimes lower than that of the final searched, 353 discretized neural network. Therefore, we evaluate the supernet of DARTS and DenseNAS on the 354 testing set, and we compare its performance with that of the final neural network in Table 4. The 355 supernet outperforms the final network on Darcy Flow for both methods, but the reverse is true for 356 the PSICOV task and all point tasks. The supernet is not in the search space and so we report the 357 discretized result; nevertheless, this fact suggests that performance on a task like Darcy Flow might 358 benefit from a better search space. 359

Evaluating random architectures and hyperparameters The power of an architecture or hyper-360 parameter space can also be characterized by the performance of its random elements. We assess both 361 the average and variance of the results. To do this, we randomly sample 8 network architectures each 362 from the search spaces of DARTS and DenseNAS, and we test their performance on the NinaPro 363 and Darcy Flow tasks, one for classification and the other for regression. For comparison, we also 364 randomly sample 8 hyperparameter configurations to train the backbone Wide-ResNet in Figure 2. 365 While rather successful on NinaPro, the random architectures have a high average error and vary in 366 367 performance on the Darcy Flow task. Random hyperparameters are more unstable on NinaPro, but its median performance is better than NAS. 368

Utility of hyperparameter tuning The final experiment examines whether hyperparameter tuning improves the performance of WRN on various tasks. During hyperparameter search, we compare the validation metrics of training using default hyperparameters and using tuned ones from ASHA to select final hyperparameters for retraining. Despite the small tuning budget allocated to ASHA, tuned hyperparameters could outperform the default setting on all tasks except for CIFAR-100. Our results suggest that wide ResNet's standard set of hyperparameters are only optimized for conventional image classification. On other tasks, hyperparameter optimization is helpful for boosting performance.

376 5 Conclusion

NAS-Bench-360 is a benchmarking suite with a novel, diverse set of tasks. The tasks are derived from 377 378 various fields of academic research, leading to different potential applications. Our selection of NAS approaches achieves state-of-the-art performances on most tasks, which points to new possibilities 379 of incorporating NAS into new research domains. All datasets and reproducible experiment code 380 are open-sourced, and we welcome researchers to use these tasks and further iterate on them with 381 new NAS methods. Finally, a possible extension to generalize this set of tasks is datasets with 1d or 382 3d inputs, such as audio. We hope our work can encourage the NAS community to move towards 383 384 tackling more diverse problems in the real world.

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488 Checklist

489	1. For all authors
490 491	 (a) Do the main claims made in the abstract and introduction accurately reflect the paper's contributions and scope? [Yes]
492	(b) Did you describe the limitations of your work? [Yes] . See conclusion (section 5).
493	(c) Did you discuss any potential negative societal impacts of your work? [Yes], in section
494	3.4.
495	(d) Have you read the ethics review guidelines and ensured that your paper conforms to
496	them? [Yes]
497	2. If you are including theoretical results
498	(a) Did you state the full set of assumptions of all theoretical results? [N/A]
499	(b) Did you include complete proofs of all theoretical results? [N/A]
500	3. If you ran experiments
501	(a) Did you include the code, data, and instructions needed to reproduce the main experi-
502	mental results (either in the supplemental material or as a URL)? [Yes]. Instructions
503	are described in the paper; code and data are available on our dedicated website.
504	(b) Did you specify all the training details (e.g., data splits, hyperparameters, how they
505	were chosen)? [Yes], in both section 3 and appendix section A.
506	(c) Did you report error bars (e.g., with respect to the random seed after running experi-
507	ments multiple times)? [Yes], in the main results table and the appendix table.
508	(d) Did you include the total amount of compute and the type of resources used (e.g., type
509	of GPUs, internal cluster, or cloud provider)? [Yes], in section 4.2.
510	4. If you are using existing assets (e.g., code, data, models) or curating/releasing new assets
511	(a) If your work uses existing assets, did you cite the creators? [Yes]
512	(b) Did you mention the license of the assets? [Yes], in appendix section B.
513	(c) Did you include any new assets either in the supplemental material or as a URL? [Yes]
514	. New assets are on our website.
515	(d) Did you discuss whether and how consent was obtained from people whose data you're
516	using/curating? [N/A]
517	(e) Did you discuss whether the data you are using/curating contains personally identifiable
518	information or offensive content? [Yes], in section 3.4.

519	5. If you used crowdsourcing or conducted research with human subjects
520 521	(a) Did you include the full text of instructions given to participants and screenshots, if applicable? [N/A]
522 523 524	 (b) Did you describe any potential participant risks, with links to Institutional Review Board (IRB) approvals, if applicable? [N/A] (c) Did you include the estimated hourly wage paid to participants and the total amount
525	spent on participant compensation? [N/A]