

ALCF Computational Performance Workshop, May 2020





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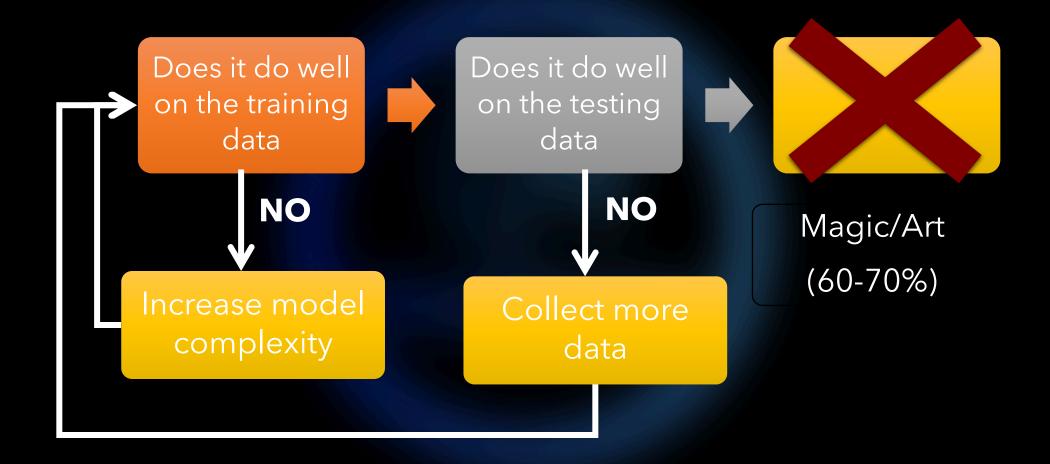
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The way of Deep neural networks





Epoch

001,644

Learning rate

Activation

Regularization

Regularization rate

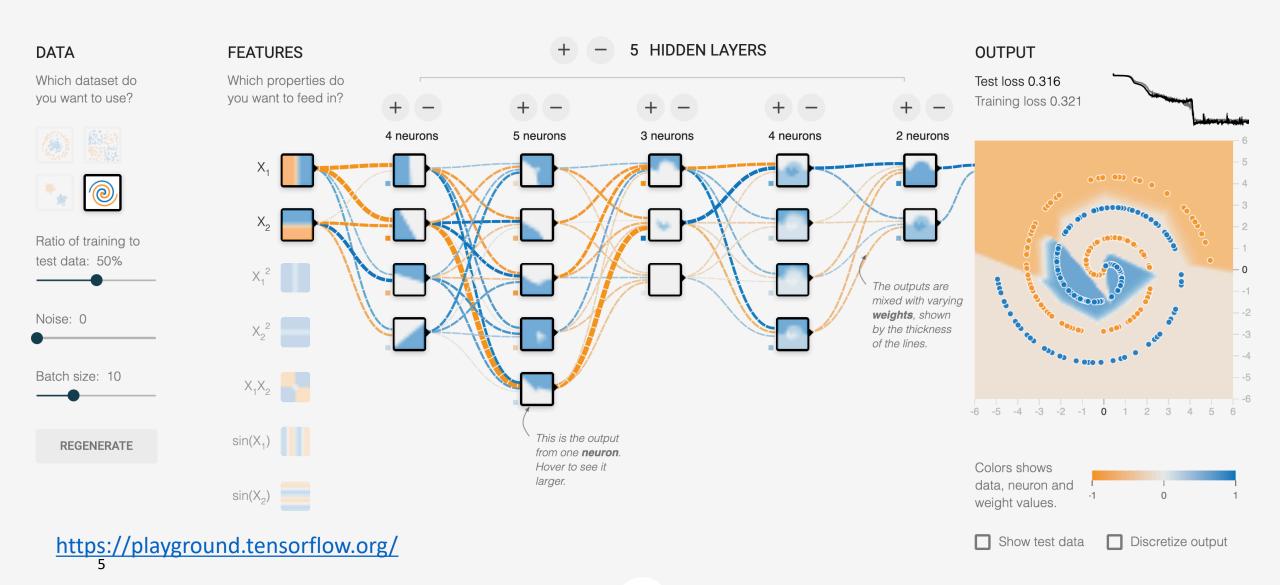
Problem type

0.03

ReLU

None

Classification



Epoch

001,142

Learning rate

0.03

Activation

Regularization

Regularization rate

Show test data

Problem type

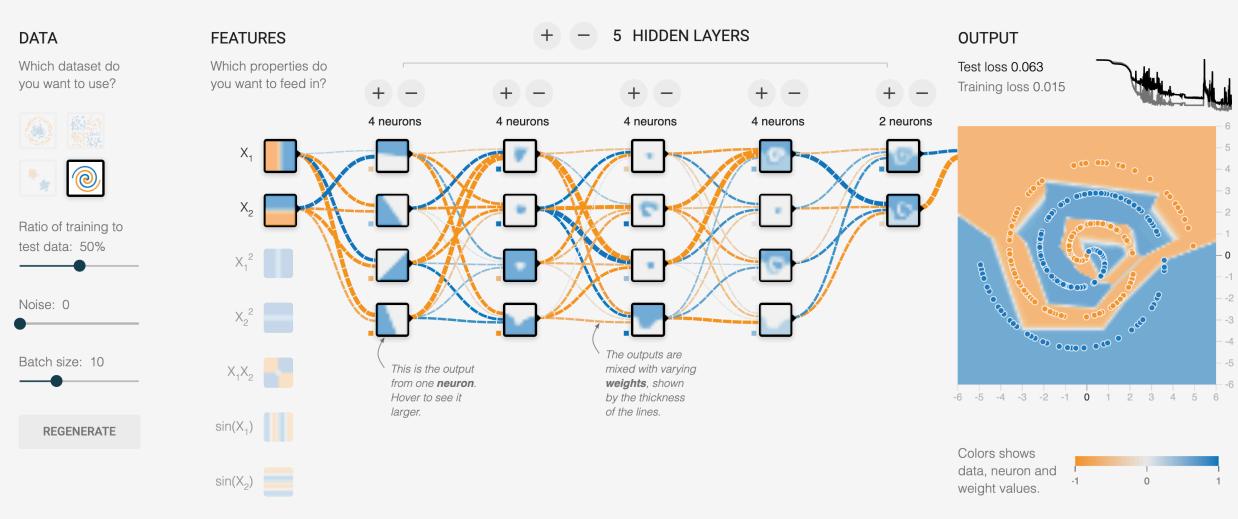
Discretize output





None

Classification





Epoch

Learning rate

Activation

Regularization

Regularization rate

Problem type

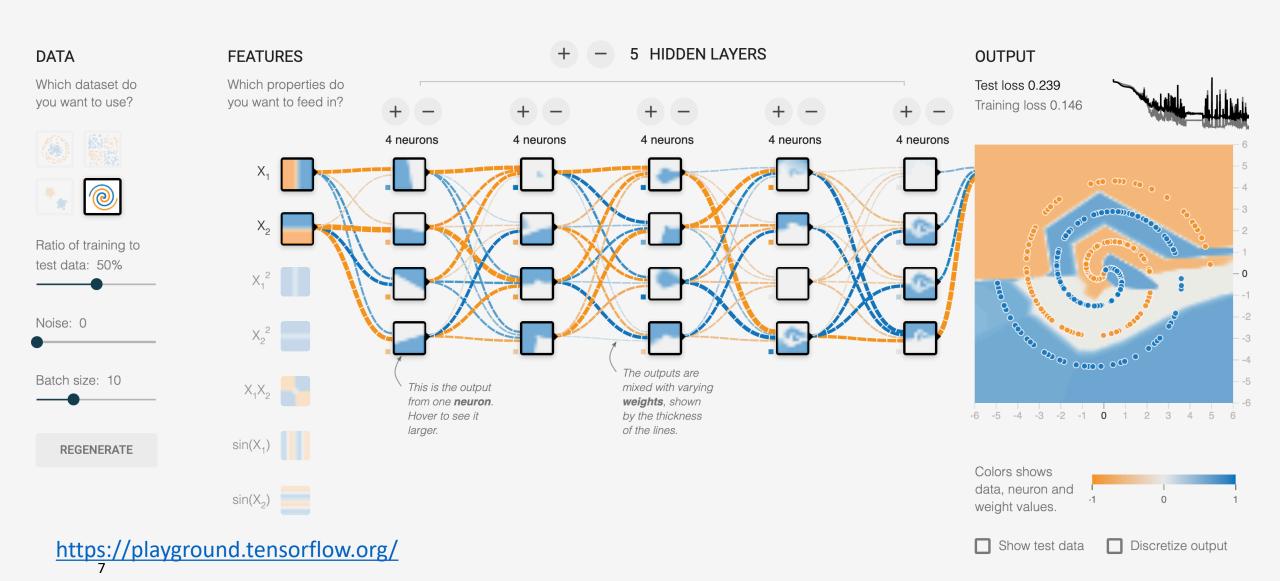
Classification



0.03

ReLU

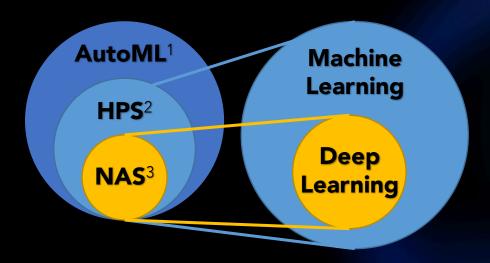
None



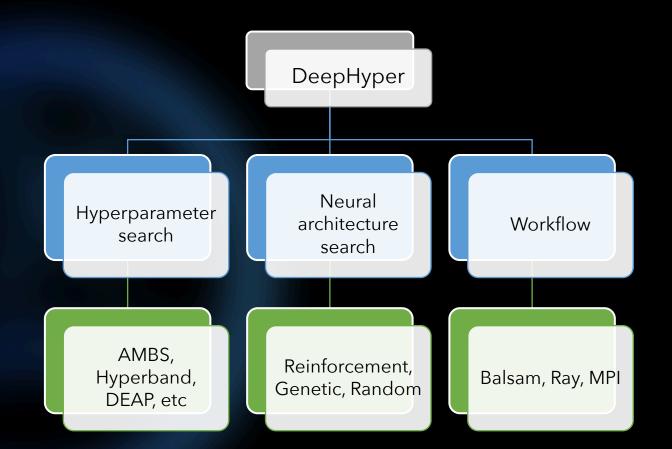
A scalable automated machine learning (AutoML) package for developing deep neural networks

https://github.com/deephyper/deephyper





¹Automated Machine Learning ²Hyperparameter Search ³Neural Architecture Search

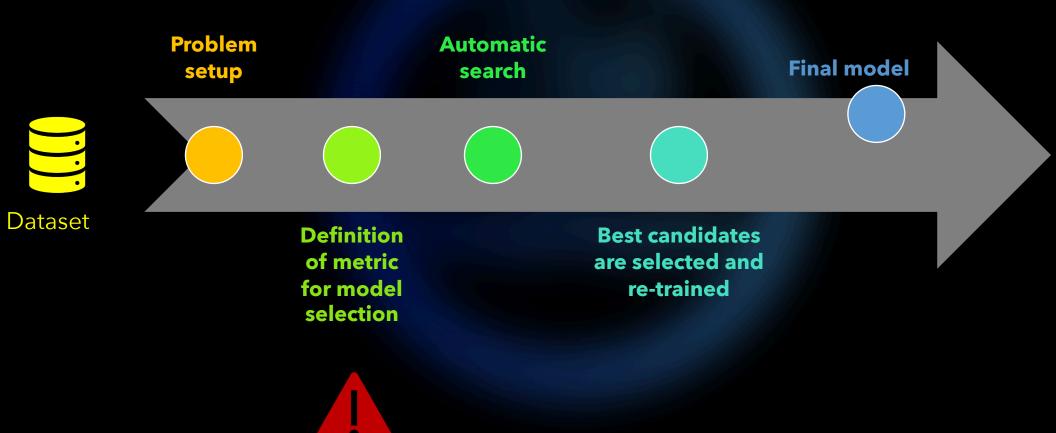




The DeepHyper workflow

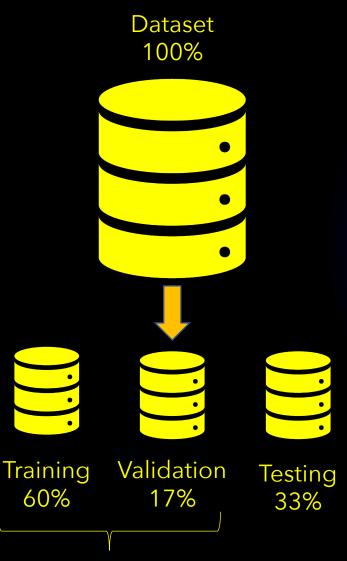


The DeepHyper workflow





Problem setup



load_data.py

def load_data():

•••

Return Training, Validation

problem.py

Problem = HpProblem(seed=42)

Problem.add_hyperparameter(alpha, (0.0, 1.0))

Problem.add_starting_point(alpha=0.01)



Definition of metric for model selection

```
run.py
def run(configuration):
   set_random_state(seed)
   training, validation = load_data()
   model = create_model(configuration)
   model.fit(training)
   score = model.evaluate(validation, metric)
   objective = compute_objective(score)
   return objective
```



Automatic search

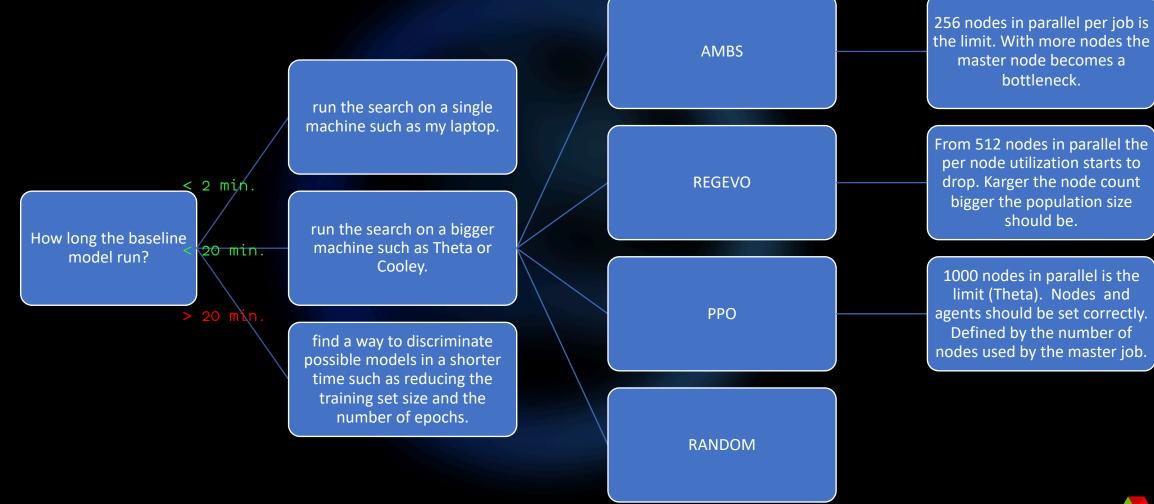
How to choose my search?

if you have a reasonable baseline model (NN or **HPS** scikit-learn based models) if you do not reasonable baseline scikit-learn AutoML for scikit-learn model (such as random forest, xgboost etc) If you do not have a reasonable NN model NAS (make sure it is NAS compatible)



Automatic Search

How to scale or run my search?



Best candidates selection and retraining

With the « deephyper-analytics » commande line you can analyze the results of your search. See if the outcome is meaningful then rank the evaluated models and select the top-k. In the case of neural networks you can launch a post-training procedure to train the top-k models to their limits with a greater number of epochs for instance.



Final model

You should not have used the « testing dataset » yet. Evaluate the best model you have on it and you will have its final performance.



Good Practices (alias Zen of DeepHyper)

- 1. Always have a baseline model before starting using DeepHyper (see "deephyper.baseline")
- 2. Always try it on your local machine before running experiments at scale
- 3. Always try it in debug queue before running experiments at scale



I - General Hyperparameter Search (HPS)

II - Hyperparameter Search for AutoML

III - Neural Architecture Search (NAS)



General Hyperparameter Search (HPS)



A bilevel optimization framework

Lower-level problem: Training data

solve
$$\min_{w} \operatorname{inimize} \operatorname{err}_{T} \left(\left[\mathcal{X}_{\mathcal{A}}, \mathcal{X}_{\mathcal{P}} \right]; \mathcal{T}; w \right)$$

Upper-level problem: Validation data

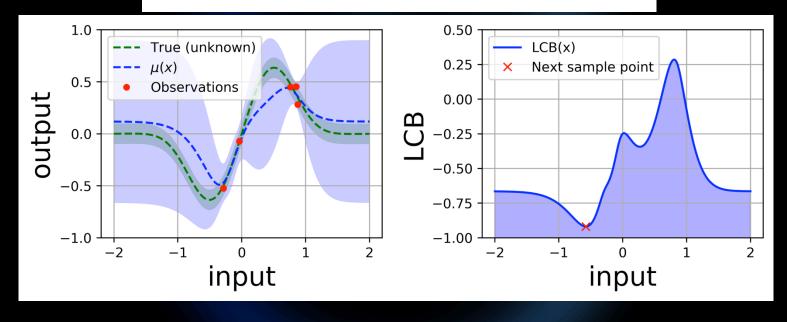
solve minimize
$$\operatorname{err}_V([\mathcal{X}_{\mathcal{A}}, \mathcal{X}_{\mathcal{P}}]; \mathcal{V}; w^* [\mathcal{X}_{\mathcal{A}}, \mathcal{X}_{\mathcal{P}}])$$

Architecture space Hyperparameter space



Bayesian optimization

$$LCB(x,\beta) = \mu(x) - \beta \times \sigma(x)$$





Problem example

```
from deephyper.problem import HpProblem

Problem = HpProblem()
Problem.add_dim("epochs", (5, 500))
Problem.add_dim("nunits_l1", (1, 1000))
Problem.add_dim("nunits_l2", (1, 1000))
Problem.add_dim("activation_l1", ["relu", "elu", "selu", "tanh"])
Problem.add_dim("activation_l2", ["relu", "elu", "selu", "tanh"])
Problem.add_dim("batch_size", (8, 1024))
Problem.add_dim("dropout_l1", (0.0, 1.0))
Problem.add_dim("dropout_l2", (0.0, 1.0))
```



П

Hyperparameter Search for AutoML



Problem example

```
import numpy as np
from deephyper.search.hps.automl.classifier import autosklearn1
def load_data():
    from sklearn.datasets import load_breast_cancer
    X, y = load_breast_cancer(return_X_y=True)
    print(np.shape(X))
    print(np.shape(y))
    return X, y
def run(config):
    return autosklearn1.run(config, load_data)
```



Custom auto-sklearn?

```
import ConfigSpace as cs
from deephyper.problem import HpProblem
Problem = HpProblem(seed=45)
classifier = Problem.add_hyperparameter(
    name="classifier",
   value=["RandomForest", "Logistic", "AdaBoost", "KNeighbors", "MLP", "SVC", "XGBoost"],
# n estimators
n_estimators = Problem.add_hyperparameter(
    name="n_estimators", value=(1, 2000, "log-uniform")
cond_n_estimators = cs.OrConjunction(
    cs.EqualsCondition(n_estimators, classifier, "RandomForest"),
    cs.EqualsCondition(n_estimators, classifier, "AdaBoost"),
Problem.add_condition(cond_n_estimators)
```

Model selection advice

```
from sklearn.model_selection import Kfold
from deephyper.search.nas.model.preprocessing import minmaxstdscaler
kf = KFold(n_splits=10, random_state=42, shuffle=True)
cross_score = []
for train_index, valid_index in kf.split(X):
    X_train, X_valid = X[train_index], X[valid_index]
    y_train, y_valid = y[train_index], y[valid_index]
     sm = SMOTE(random_state=seed, k_neighbors=smote_k_neighbors, n_jobs=4)
    X_train, y_train = sm.fit_resample(X_train, y_train)
     scaler = minmaxstdscaler()
    X_train = scaler.fit_transform(X_train)
     X_valid = scaler.transform(X_valid)
     score = model.evaluate(X_valid, metric)
     cross_scores.append(score)
     return mean(cross_scores)
```

Avoid lucky findings

For unbalanced classes

Distributed computation on CPU



Visualize your results #1

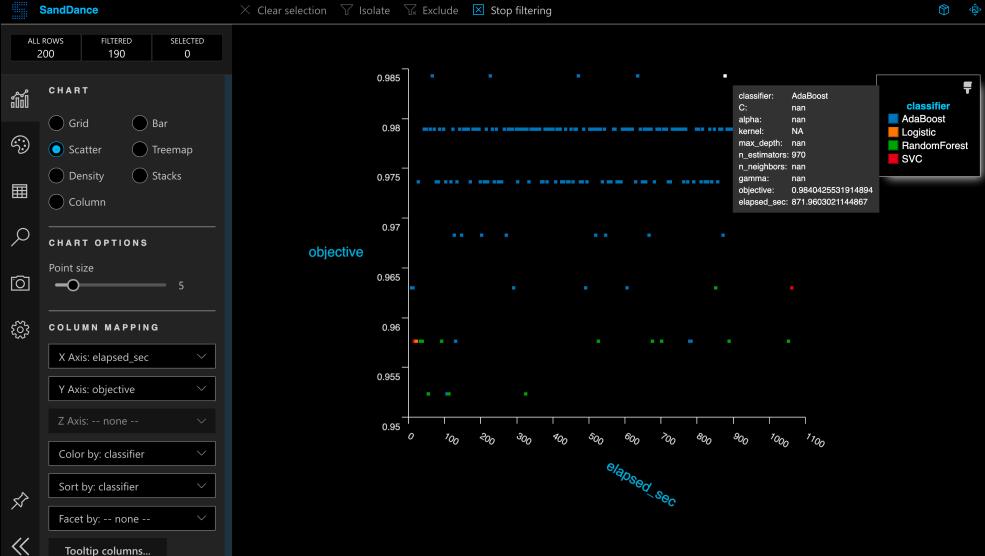
Visual Studio Code + Rainbow CSV

```
classifier, C, alpha, kernel, max_depth, n_estimators, n_neighbors, gamma, objective, elapsed_sec
AdaBoost, nan, nan, NA, nan, 187, nan, nan, 0.9627659574468085, 3.8781380653381348
AdaBoost, nan, nan, NA, nan, 19, nan, nan, 0.9627659574468085, 7.370249271392822
SVC, 0.910144037187624, nan, linear, nan, nan, nan, nan, 0.9574468085106383, 11.247097969055176
Logistic, 0.056704414597599125, nan, NA, nan, nan, nan, nan, 0.9574468085106383, 15.790768146514893
AdaBoost, nan, nan, NA, nan, 1662, nan, nan, 0.973404255319149, 22.461848974227905
RandomForest, nan, nan, NA, 64, 561, nan, nan, 0.9574468085106383, 26.977345943450928
RandomForest, nan, nan, NA, 15, 1812, nan, nan, 0.9574468085106383, 33.18859791755676
```



Visualize your results #2

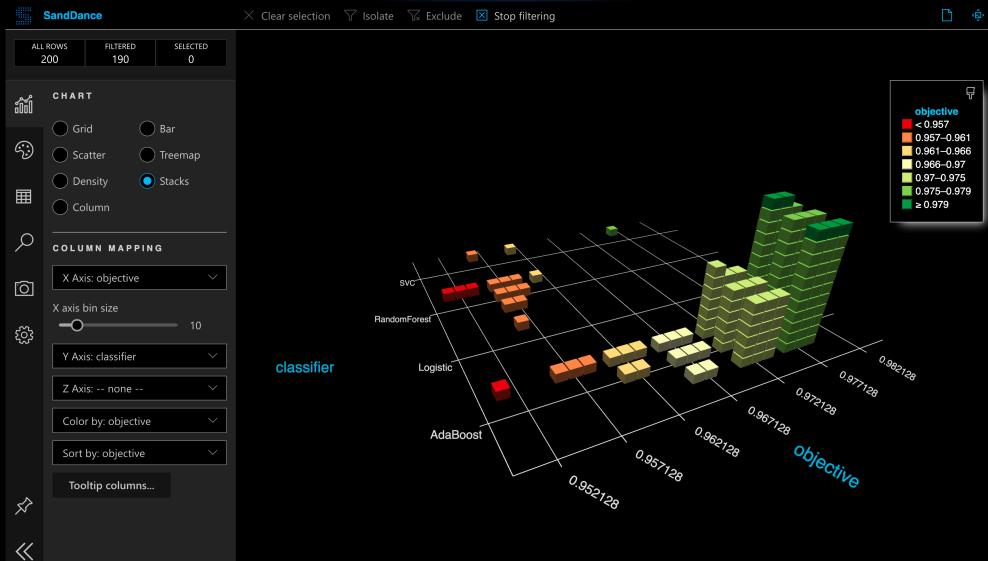
Visual Studio Code + SandDance





Visualize your results #3

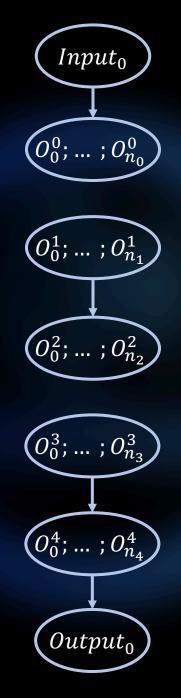
Visual Studio Code + SandDance



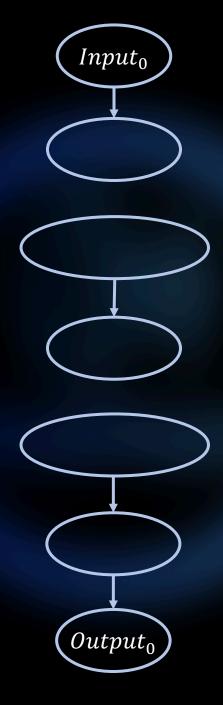
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Neural Architecture Search (NAS)

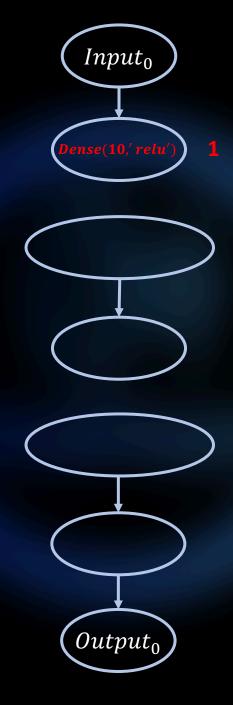




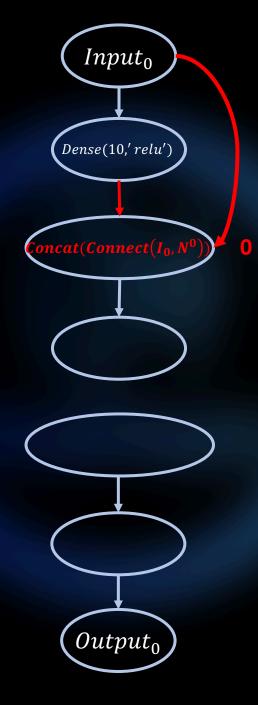




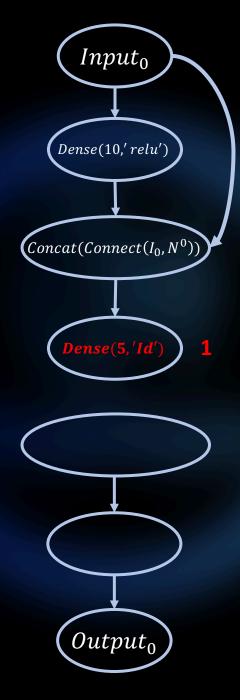








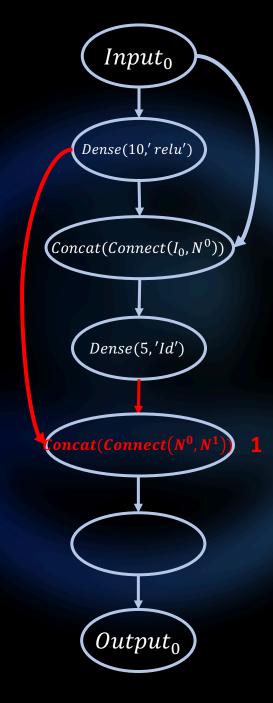






The NAS Search Space

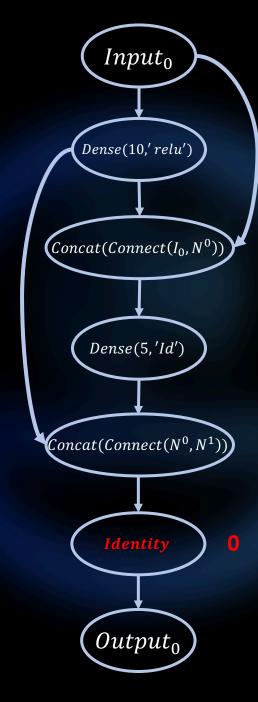
A discrete space embedded as a directed graph where each nodes represents a choice between differents operations.





The NAS Search Space

A discrete space embedded as a directed graph where each nodes represents a choice between differents operations.

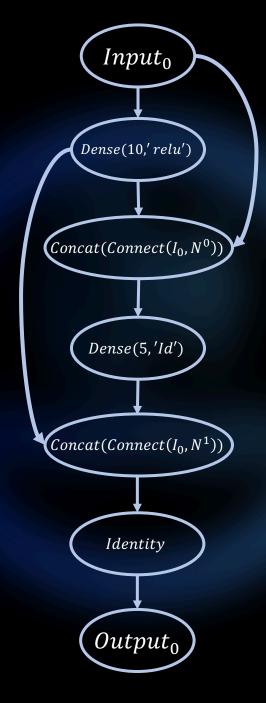




The NAS Search Space

A discrete space embedded as a directed graph where each nodes represents a choice between differents operations.

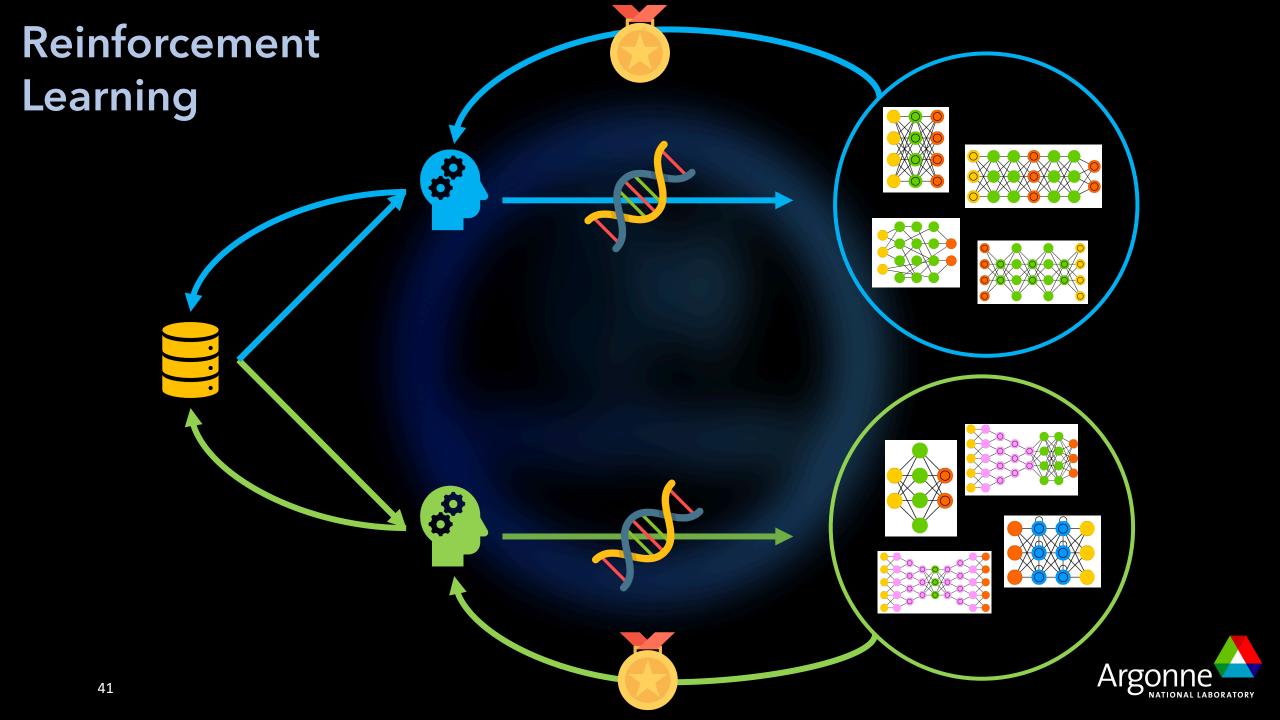
Decisions Summary



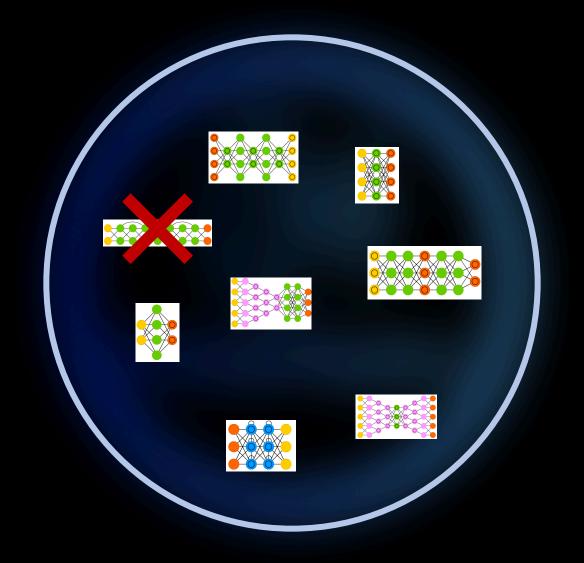


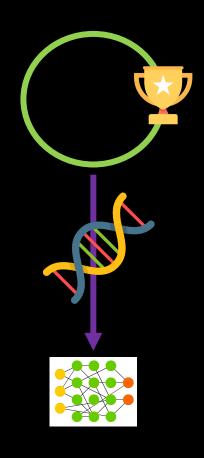
NAS Workflow $Input_0$ $Input_0$ Dense(10,' relu') Decisions $Concat(Connect(I_0, N^0))$ Feedback **Model Loading** Dense(5,'Id') $Concat(Connect(N^0, N^1))$ Identity **Model Evaluation** Data Loading • feature engineering Training pre-processing $Output_0$ $Output_0$





Aging Evolution







CANcer Distributed Learning Environment (CANDLE)

Combo

Given combination drug screening results on NCI60 cell lines predict the growth percentage from the cell line molecular features and the descriptors of both drugs.

Uno

Predict tumor dose response across multiple data sources.

NT3

Classify RNA-seq gene expression profiles into normal or tumor tissue categories.



CANcer Distributed Learning Environment (CANDLE)

Combo Uno

NT3

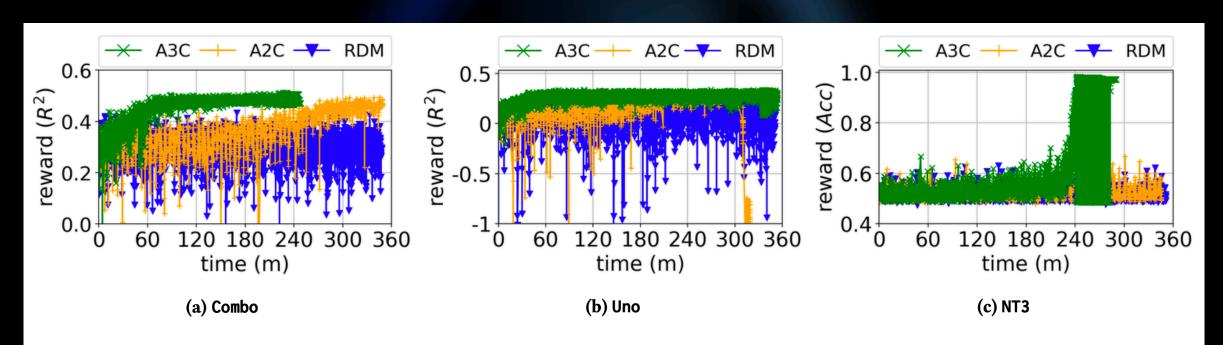


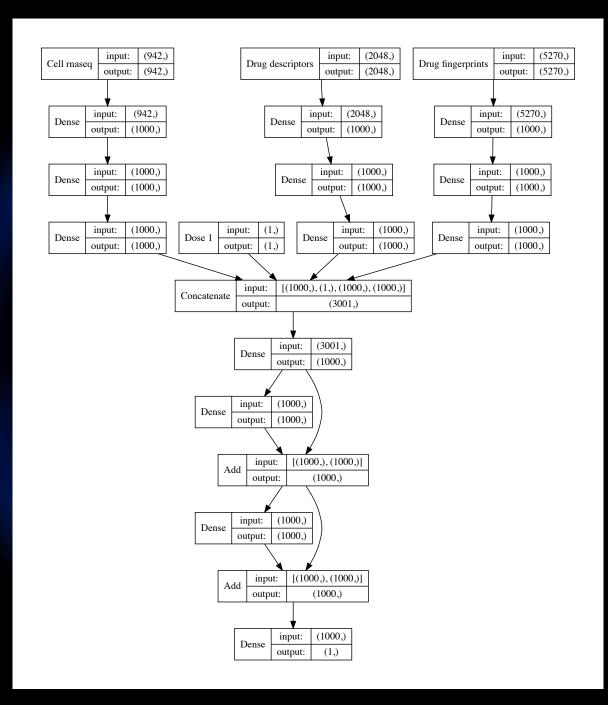
Figure 4: Search trajectory showing reward over time for A3C, A2C, and RDM on the small search space



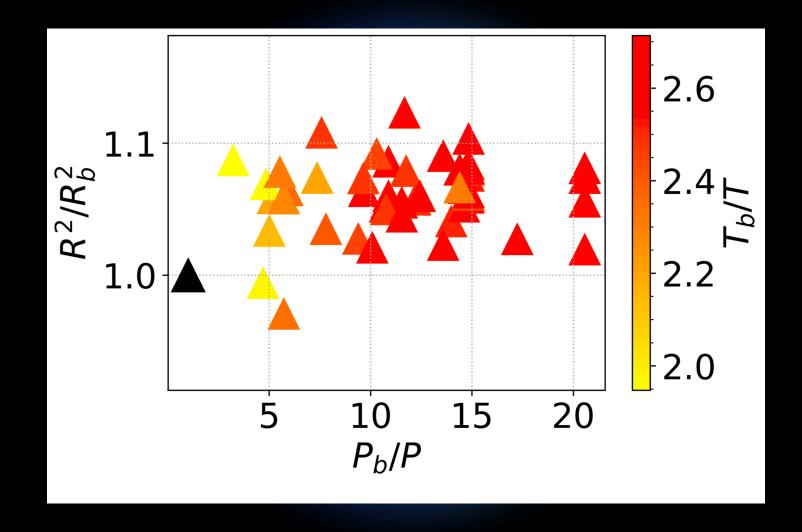
Uno

Prédire la réponse de la tumeur au dosage d'une molécule/médicament (eng: drug) à partir de plusieurs données:

- Séquence ARN
- Dosage de la molécule
- Descripteur de la molécule
- Empreinte de la molécule









Best models found

	Trainable	Training	
	Parameters	Time (s)	R^2 or ACC
Combo			
manually designed	13,772,001	705.26	0.926
A3C-best	1,883,301	283.00	0.93
	Uno		
manually designed	19,274,001	164.94	0.649
A3C-best	1,670,401	63.53	0.729
	NT3		
manually designed	96,777,878	247.63	0.986
A3C-best	120,968	16.65	0.989



281474976710656 possibilities

6.541611696775362e-09% explored

18413 unique models

256 nodes

6 hours

~50 selected



Acknowledgements



DOE Early Career Research Program, ASCR

Argonne Leadership Computing Facility



Laboratory Directed Research and Development (LDRD)



Thank you!



https://deephyper.readthedocs.io

