Optuna Documentation

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Optuna Contributors.

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CONTENTS:

Optuna is an automatic hyperparameter optimization software framework, particularly designed for machine learning. It features an imperative, *define-by-run* style user API. Thanks to our *define-by-run* API, the code written with Optuna enjoys high modularity, and the user of Optuna can dynamically construct the search spaces for the hyperparameters.

CHAPTER ONE

KEY FEATURES

Optuna has modern functionalities as follows:

- Lightweight, versatile, and platform agnostic architecture
  - Handle a wide variety of tasks with a simple installation that has few requirements.
- Pythonic search spaces
  - Define search spaces using familiar Python syntax including conditionals and loops.
- Efficient optimization algorithms
  - Adopt state-of-the-art algorithms for sampling hyperparameters and efficiently pruning unpromising trials.
- Easy parallelization
  - Scale studies to tens or hundreds of workers with little or no changes to the code.
- Quick visualization
  - Inspect optimization histories from a variety of plotting functions.

CHAPTER

TWO

BASIC CONCEPTS

We use the terms *study* and *trial* as follows:

- Study: optimization based on an objective function
- Trial: a single execution of the objective function

Please refer to sample code below. The goal of a *study* is to find out the optimal set of hyperparameter values (e.g., `classifier` and `svm_c`) through multiple *trials* (e.g., `n_trials=100`). Optuna is a framework designed for the automation and the acceleration of the optimization *studies*.

Open in Colab

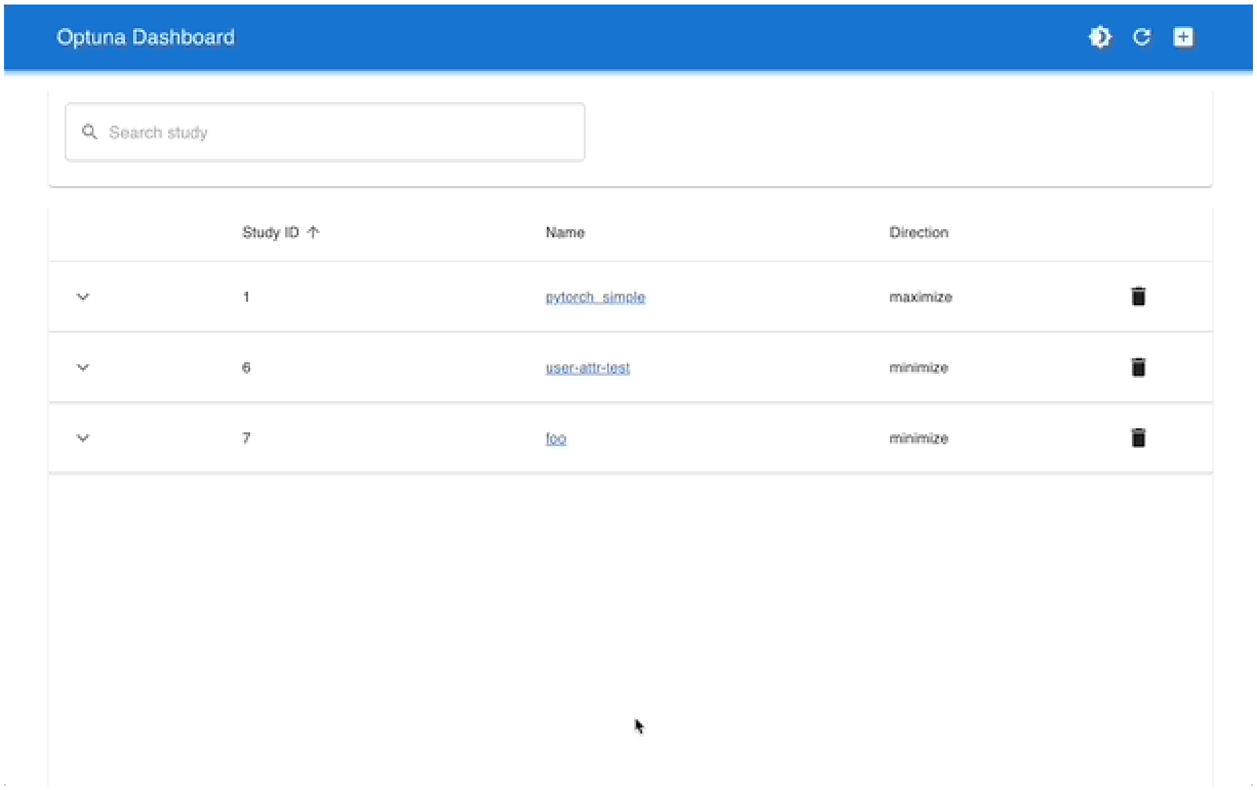
```
import ...

# Define an objective function to be minimized.
def objective(trial):

    # Invoke suggest methods of a Trial object to generate hyperparameters.
    regressor_name = trial.suggest_categorical('classifier', ['SVR', 'RandomForest'])
    if regressor_name == 'SVR':
        svr_c = trial.suggest_float('svr_c', 1e-10, 1e10, log=True)
        regressor_obj = sklearn.svm.SVR(C=svr_c)
    else:
        rf_max_depth = trial.suggest_int('rf_max_depth', 2, 32)
        regressor_obj = sklearn.ensemble.RandomForestRegressor(max_depth=rf_max_depth)

    X, y = sklearn.datasets.fetch_california_housing(return_X_y=True)
    X_train, X_val, y_train, y_val = sklearn.model_selection.train_test_split(X, y,␣
↪random_state=0)

    regressor_obj.fit(X_train, y_train)
    y_pred = regressor_obj.predict(X_val)

    error = sklearn.metrics.mean_squared_error(y_val, y_pred)

    return error  # An objective value linked with the Trial object.

study = optuna.create_study()  # Create a new study.
study.optimize(objective, n_trials=100)  # Invoke optimization of the objective function.
```

CHAPTER

THREE

WEB DASHBOARD

Optuna Dashboard is a real-time web dashboard for Optuna. You can check the optimization history, hyperparameter importance, etc. in graphs and tables. You don't need to create a Python script to call Optuna's visualization functions. Feature requests and bug reports are welcome!



Study ID ↑	Name	Direction
1	pytorch_simple	maximize
6	user-attr-test	minimize
7	foo	minimize

optuna-dashboard can be installed via pip:

```
$ pip install optuna-dashboard
```

Tip

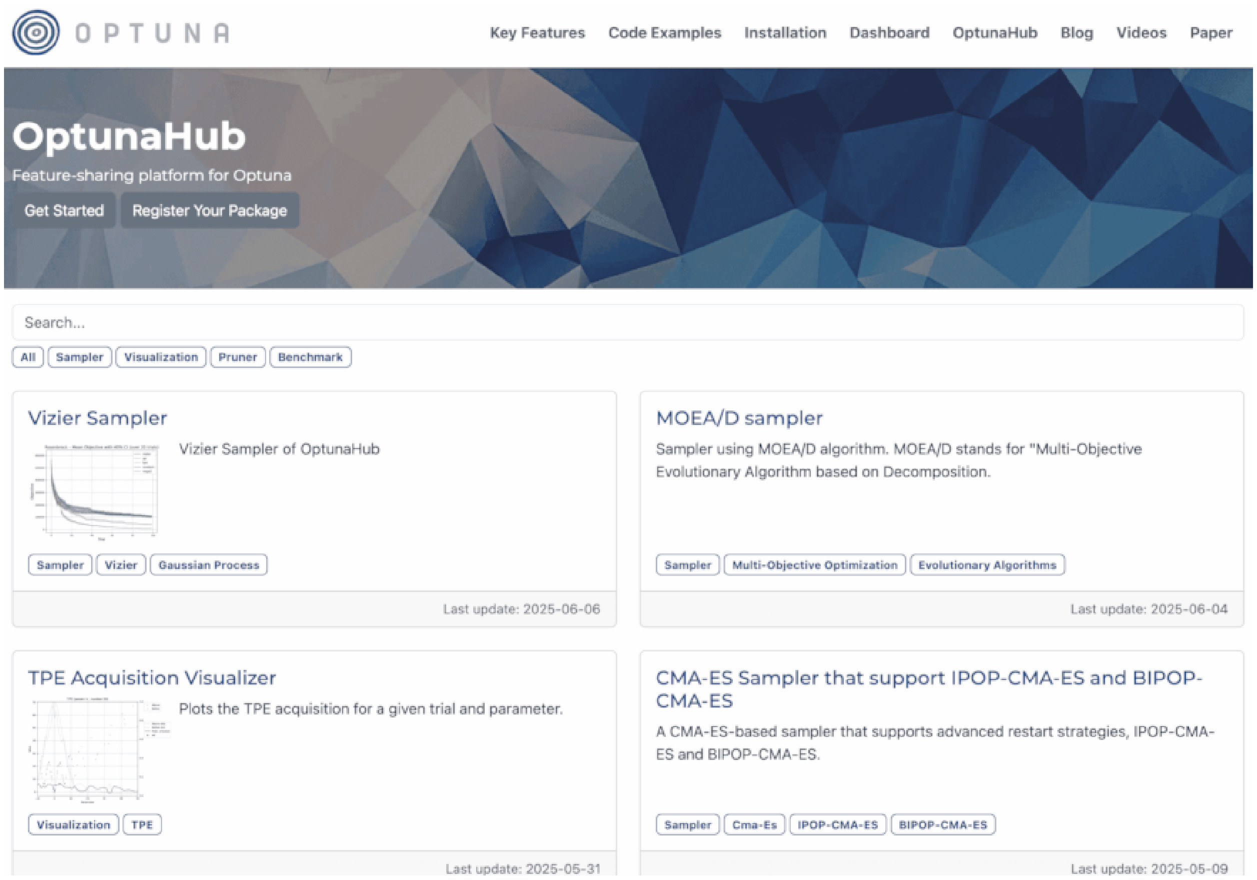
Please check out the getting started section of Optuna Dashboard's official documentation.

CHAPTER

FOUR

OPTUNAHUB

OptunaHub is a feature-sharing platform for Optuna. You can use the registered features and publish your packages. For more details, please refer to the official documentation.



OptunaHub

Feature-sharing platform for Optuna

Vizier Sampler

Vizier Sampler of OptunaHub

Sampler | Vizier | Gaussian Process

Last update: 2025-06-06

MOEA/D sampler

Sampler using MOEA/D algorithm. MOEA/D stands for "Multi-Objective Evolutionary Algorithm based on Decomposition.

Sampler | Multi-Objective Optimization | Evolutionary Algorithms

Last update: 2025-06-04

TPE Acquisition Visualizer

Plots the TPE acquisition for a given trial and parameter.

Visualization | TPE

Last update: 2025-05-31

CMA-ES Sampler that support IPOP-CMA-ES and BIPOP-CMA-ES

A CMA-ES-based sampler that supports advanced restart strategies, IPOP-CMA-ES and BIPOP-CMA-ES.

Sampler | Cma-Es | IPOP-CMA-ES | BIPOP-CMA-ES

Last update: 2025-05-09

`optunahub` can be installed via pip:

```
$ pip install optunahub
```

CHAPTER

FIVE

COMMUNICATION

- GitHub Discussions for questions.
- GitHub Issues for bug reports and feature requests.

CHAPTER SIX

CONTRIBUTION

Any contributions to Optuna are welcome! When you send a pull request, please follow the contribution guide.

CHAPTER SEVEN

LICENSE

MIT License (see LICENSE).

Optuna uses the codes from SciPy and fdlibm projects (see Third-party License).

CHAPTER EIGHT

REFERENCE

Takuya Akiba, Shotaro Sano, Toshihiko Yanase, Takeru Ohta, and Masanori Koyama. 2019. Optuna: A Next-generation Hyperparameter Optimization Framework. In KDD (arXiv).

8.1 Installation

Optuna supports Python 3.8 or newer.

We recommend to install Optuna via pip:

```
$ pip install optuna
```

You can also install the development version of Optuna from master branch of Git repository:

```
$ pip install git+https://github.com/optuna/optuna.git
```

You can also install Optuna via conda:

```
$ conda install -c conda-forge optuna
```

8.2 Tutorial

If you are new to Optuna or want a general introduction, we highly recommend the below video.

8.2.1 Key Features

Showcases Optuna's Key Features.

1. 10_key_features/001_first
2. 10_key_features/002_configurations
3. 10_key_features/003_efficient_optimization_algorithms
4. 10_key_features/004_distributed
5. 10_key_features/005_visualization

8.2.2 Recipes

Showcases the recipes that might help you using Optuna with comfort.

- 20_recipes/001_rdb
- 20_recipes/002_multi_objective

- 20_recipes/003_attributes
- 20_recipes/004_cli
- 20_recipes/005_user_defined_sampler
- 20_recipes/006_user_defined_pruner
- 20_recipes/007_optuna_callback
- 20_recipes/008_specify_params
- 20_recipes/009_ask_and_tell
- 20_recipes/010_reuse_best_trial
- 20_recipes/011_journal_storage
- Human-in-the-loop Optimization with Optuna Dashboard
- 20_recipes/012_artifact_tutorial
- 20_recipes/013_wilcoxon_pruner

8.3 API Reference

8.3.1 optuna

The `optuna` module is primarily used as an alias for basic Optuna functionality coded in other modules. Currently, two modules are aliased: (1) from `optuna.study`, functions regarding the Study lifecycle, and (2) from `optuna.exceptions`, the TrialPruned Exception raised when a trial is pruned.

`create_study`	Create a new `Study`.
`load_study`	Load the existing `Study` that has the specified name.
`delete_study`	Delete a `Study` object.
`copy_study`	Copy study from one storage to another.
`get_all_study_names`	Get all study names stored in a specified storage.
`get_all_study_summaries`	Get all history of studies stored in a specified storage.
`TrialPruned`	Exception for pruned trials.

optuna.create_study

`optuna.create_study`(** (Keyword-only parameters separator (PEP 3102)), storage=None, sampler=None, pruner=None, study_name=None, direction=None, load_if_exists=False, directions=None*)

Create a new `Study`.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 10)
    return x**2

```

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```
study = optuna.create_study()
study.optimize(objective, n_trials=3)
```

Parameters

- **storage** (*str | storages.BaseStorage | None*) – Database URL. If this argument is set to None, *InMemoryStorage* is used, and the *Study* will not be persistent.

  Note

  When a database URL is passed, Optuna internally uses SQLAlchemy to handle the database. Please refer to SQLAlchemy's document for further details. If you want to specify non-default options to SQLAlchemy Engine, you can instantiate *RDBStorage* with your desired options and pass it to the `storage` argument instead of a URL.

- **sampler** (*'samplers.BaseSampler' | None*) – A sampler object that implements background algorithm for value suggestion. If `None` is specified, *TPESampler* is used during single-objective optimization and *NSGAIISampler* during multi-objective optimization. See also *samplers*.

- **pruner** (*pruners.BasePruner | None*) – A pruner object that decides early stopping of unpromising trials. If `None` is specified, *MedianPruner* is used as the default. See also *pruners*.

- **study_name** (*str | None*) – Study's name. If this argument is set to None, a unique name is generated automatically.

- **direction** (*str | StudyDirection | None*) – Direction of optimization. Set `minimize` for minimization and `maximize` for maximization. You can also pass the corresponding *StudyDirection* object. `direction` and `directions` must not be specified at the same time.

  Note

  If none of *direction* and *directions* are specified, the direction of the study is set to "minimize".

- **load_if_exists** (*bool*) – Flag to control the behavior to handle a conflict of study names. In the case where a study named `study_name` already exists in the `storage`, a *DuplicatedStudyError* is raised if `load_if_exists` is set to `False`. Otherwise, the creation of the study is skipped, and the existing one is returned.

- **directions** (*Sequence[str | StudyDirection] | None*) – A sequence of directions during multi-objective optimization. `direction` and `directions` must not be specified at the same time.

Returns

A *Study* object.

Return type

Study

See also

optuna.create_study() is an alias of *optuna.study.create_study()*.

See also

The rdb tutorial provides concrete examples to save and resume optimization using RDB.

optuna.load_study

optuna.**load_study**(**, study_name, storage, sampler=None, pruner=None*)

Load the existing *Study* that has the specified name.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 10)
    return x**2


study = optuna.create_study(storage="sqlite:///example.db", study_name="my_study")
study.optimize(objective, n_trials=3)

loaded_study = optuna.load_study(study_name="my_study", storage="sqlite:///example.
↪db")
assert len(loaded_study.trials) == len(study.trials)
```

Parameters

- **study_name** (*str | None*) – Study's name. Each study has a unique name as an identifier. If None, checks whether the storage contains a single study, and if so loads that study. study_name is required if there are multiple studies in the storage.
- **storage** (*str | storages.BaseStorage*) – Database URL such as sqlite:///example.db. Please see also the documentation of *create_study()* for further details.
- **sampler** (*'samplers.BaseSampler' | None*) – A sampler object that implements background algorithm for value suggestion. If None is specified, *TPESampler* is used as the default. See also *samplers*.
- **pruner** (pruners.BasePruner *| None*) – A pruner object that decides early stopping of unpromising trials. If None is specified, *MedianPruner* is used as the default. See also *pruners*.

Returns

A *Study* object.

Return type

Study

See also

optuna.load_study() is an alias of *optuna.study.load_study()*.

optuna.delete_study

optuna.**delete_study**(***, *study_name*, *storage*)

Delete a *Study* object.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2


study = optuna.create_study(study_name="example-study", storage="sqlite:///example.
↪db")
study.optimize(objective, n_trials=3)

optuna.delete_study(study_name="example-study", storage="sqlite:///example.db")
```

Parameters

- **study_name** (*str*) – Study's name.
- **storage** (*str | BaseStorage*) – Database URL such as `sqlite:///example.db`. Please see also the documentation of *create_study()* for further details.

Return type

None

See also

optuna.delete_study() is an alias of *optuna.study.delete_study()*.

optuna.copy_study

optuna.**copy_study**(***, *from_study_name*, *from_storage*, *to_storage*, *to_study_name=None*)

Copy study from one storage to another.

The direction(s) of the objective(s) in the study, trials, user attributes and system attributes are copied.

Note

copy_study() copies a study even if the optimization is working on. It means users will get a copied study that contains a trial that is not finished.

Example

```python
import optuna


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2


study = optuna.create_study(
    study_name="example-study",
    storage="sqlite:///example.db",
)
study.optimize(objective, n_trials=3)

optuna.copy_study(
    from_study_name="example-study",
    from_storage="sqlite:///example.db",
    to_storage="sqlite:///example_copy.db",
)

study = optuna.load_study(
    study_name=None,
    storage="sqlite:///example_copy.db",
)
```

Parameters

- **from_study_name** (*str*) – Name of study.
- **from_storage** (*str | BaseStorage*) – Source database URL such as `sqlite:///example.db`. Please see also the documentation of *create_study()* for further details.
- **to_storage** (*str | BaseStorage*) – Destination database URL.
- **to_study_name** (*str | None*) – Name of the created study. If omitted, `from_study_name` is used.

Raises

DuplicatedStudyError – If a study with a conflicting name already exists in the destination storage.

Return type

None

optuna.get_all_study_names

optuna.**get_all_study_names**(*storage*)

Get all study names stored in a specified storage.

Example

```python
import optuna
```

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```
def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2


study = optuna.create_study(study_name="example-study", storage="sqlite:///example.
↪db")
study.optimize(objective, n_trials=3)

study_names = optuna.study.get_all_study_names(storage="sqlite:///example.db")
assert len(study_names) == 1

assert study_names[0] == "example-study"
```

Parameters
: `storage` (*str | BaseStorage*) – Database URL such as `sqlite:///example.db`. Please see also the documentation of *create_study()* for further details.

Returns
: List of all study names in the storage.

Return type
: list[str]

See also

optuna.get_all_study_names() is an alias of *optuna.study.get_all_study_names()*.

optuna.get_all_study_summaries

`optuna.`**`get_all_study_summaries`**`(`*storage*, *include_best_trial=True*`)`

Get all history of studies stored in a specified storage.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2


study = optuna.create_study(study_name="example-study", storage="sqlite:///example.
↪db")
study.optimize(objective, n_trials=3)

study_summaries = optuna.study.get_all_study_summaries(storage="sqlite:///example.db
↪")
assert len(study_summaries) == 1
```

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```
study_summary = study_summaries[0]
assert study_summary.study_name == "example-study"
```

Parameters

- **storage** (*str | BaseStorage*) – Database URL such as `sqlite:///example.db`. Please see also the documentation of *create_study()* for further details.
- **include_best_trial** (*bool*) – Include the best trials if exist. It potentially increases the number of queries and may take longer to fetch summaries depending on the storage.

Returns

List of study history summarized as *StudySummary* objects.

Return type

list[StudySummary]

See also

optuna.get_all_study_summaries() is an alias of *optuna.study.get_all_study_summaries()*.

optuna.TrialPruned

exception optuna.**TrialPruned**

Exception for pruned trials.

This error tells a trainer that the current *Trial* was pruned. It is supposed to be raised after *optuna.trial.Trial.should_prune()* as shown in the following example.

See also

optuna.TrialPruned is an alias of *optuna.exceptions.TrialPruned*.

Example

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
    clf = SGDClassifier(alpha=alpha)
    n_train_iter = 100
```

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```
    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step)

        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=20)
```

add_note()

Exception.add_note(note) – add a note to the exception

8.3.2 optuna.artifacts

The *artifacts* module provides the way to manage artifacts (output files) in Optuna. Please also check artifact_tutorial and our article. The storages covered by *artifacts* are the following:

Class Name	Supported Storage
FileSystemArtifactStore	Local File System, Network File System
Boto3ArtifactStore	Amazon S3 Compatible Object Storage
GCSArtifactStore	Google Cloud Storage

Note

The methods defined in each `ArtifactStore` are not intended to be directly accessed by library users.

Note

As `ArtifactStore` does not officially provide user API for artifact removal, please refer to *How can I delete all the artifacts uploaded to a study?* for the hack.

class optuna.artifacts.**FileSystemArtifactStore**(*base_path*)

An artifact store for file systems.

Parameters

base_path (*str | Path*) – The base path to a directory to store artifacts.

Example

```python
import os

import optuna
from optuna.artifacts import FileSystemArtifactStore
from optuna.artifacts import upload_artifact


base_path = "./artifacts"
os.makedirs(base_path, exist_ok=True)
artifact_store = FileSystemArtifactStore(base_path=base_path)


def objective(trial: optuna.Trial) -> float:
    ... = trial.suggest_float("x", -10, 10)
    file_path = generate_example(...)
    upload_artifact(
        artifact_store=artifact_store,
        file_path=file_path,
        study_or_trial=trial,
    )
    return ...
```

`class optuna.artifacts.`**`Boto3ArtifactStore`**(*bucket_name*, *client=None*, ***, *avoid_buf_copy=False*)

An artifact backend for Boto3.

Parameters

- **`bucket_name`** (*`str`*) – The name of the bucket to store artifacts.
- **`client`** (*`S3Client | None`*) – A Boto3 client to use for storage operations. If not specified, a new client will be created.
- **`avoid_buf_copy`** (*`bool`*) – If True, skip procedure to copy the content of the source file object to a buffer before uploading it to S3 ins. This is default to False because using `upload_fileobj()` method of Boto3 client might close the source file object.

Example

```python
import optuna
from optuna.artifacts import upload_artifact
from optuna.artifacts import Boto3ArtifactStore


artifact_store = Boto3ArtifactStore("my-bucket")


def objective(trial: optuna.Trial) -> float:
    ... = trial.suggest_float("x", -10, 10)
    file_path = generate_example(...)
    upload_artifact(
        artifact_store=artifact_store,
        file_path=file_path,
        study_or_trial=trial,
```

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```
    )
    return ...
```

class optuna.artifacts.**GCSArtifactStore**(*bucket_name*, *client=None*)

An artifact backend for Google Cloud Storage (GCS).

Parameters

- **bucket_name** (*str*) – The name of the bucket to store artifacts.
- **client** (*google.cloud.storage.Client | None*) – A google-cloud-storage `Client` to use for storage operations. If not specified, a new client will be created with default settings.

Example

```
import optuna
from optuna.artifacts import GCSArtifactStore, upload_artifact


artifact_backend = GCSArtifactStore("my-bucket")


def objective(trial: optuna.Trial) -> float:
    ... = trial.suggest_float("x", -10, 10)
    file_path = generate_example(...)
    upload_artifact(
        artifact_store=artifact_store,
        file_path=file_path,
        study_or_trial=trial,
    )
    return ...
```

Before running this code, you will have to install `gcloud` and run

```
gcloud auth application-default login
```

so that the Cloud Storage library can automatically find the credential.

Note

Added in v3.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.4.0.

class optuna.artifacts.**Backoff**(*backend*, ***, *max_retries=10*, *multiplier=2*, *min_delay=0.1*, *max_delay=30*)

An artifact store's middleware for exponential backoff.

Example

```
import optuna
from optuna.artifacts import upload_artifact
from optuna.artifacts import Boto3ArtifactStore
from optuna.artifacts import Backoff
```

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```
artifact_store = Backoff(Boto3ArtifactStore("my-bucket"))


def objective(trial: optuna.Trial) -> float:
    ... = trial.suggest_float("x", -10, 10)
    file_path = generate_example(...)
    upload_artifact(
        artifact_store=artifact_store,
        file_path=file_path,
        study_or_trial=trial,
    )
    return ...
```

Parameters

- **backend** (*ArtifactStore*)
- **max_retries** (*int*)
- **multiplier** (*float*)
- **min_delay** (*float*)
- **max_delay** (*float*)

class optuna.artifacts.**ArtifactMeta**(*artifact_id*, *filename*, *mimetype*, *encoding*)

Meta information for an artifact.

Note

All the artifact meta linked to a study or trial can be listed by *get_all_artifact_meta()*. The artifact meta can be used for *download_artifact()*.

Parameters

- **artifact_id** (*str*) – The identifier of the artifact.
- **filename** (*str*) – The artifact file name used for the upload.
- **mimetype** (*str*) – A MIME type of the artifact. If not specified, the MIME type is guessed from the file extension.
- **encoding** (*str | None*) – An encoding of the artifact, which is suitable for use as a Content-Encoding header, e.g., gzip. If not specified, the encoding is guessed from the file extension.

optuna.artifacts.**upload_artifact**(**, artifact_store, file_path, study_or_trial, storage=None, mimetype=None, encoding=None*)

Upload an artifact to the artifact store.

Parameters

- **artifact_store** (*ArtifactStore*) – An artifact store.
- **file_path** (*str*) – A path to the file to be uploaded.

- **study_or_trial** (Trial | FrozenTrial | Study) – A *Trial* object, a *FrozenTrial*, or a *Study* object.
- **storage** (*BaseStorage | None*) – A storage object. This argument is required only if study_or_trial is *FrozenTrial*.
- **mimetype** (*str | None*) – A MIME type of the artifact. If not specified, the MIME type is guessed from the file extension.
- **encoding** (*str | None*) – An encoding of the artifact, which is suitable for use as a Content-Encoding header (e.g. gzip). If not specified, the encoding is guessed from the file extension.

Returns
An artifact ID.

Return type
str

optuna.artifacts.**get_all_artifact_meta**(*study_or_trial*, *, *storage=None*)

List the associated artifact information of the provided trial or study.

Parameters

- **study_or_trial** (Trial | FrozenTrial | Study) – A *Trial* object, a *FrozenTrial*, or a *Study* object.
- **storage** (*BaseStorage | None*) – A storage object. This argument is required only if study_or_trial is *FrozenTrial*.

Return type
list[*ArtifactMeta*]

Example

An example where this function is useful:

```
import os

import optuna


# Get the storage that contains the study of interest.
storage = optuna.storages.get_storage(storage=...)

# Instantiate the artifact store used for the study.
# Optuna does not provide the API that stores the used artifact store information,␣
↪so
# please manage the information in the user side.
artifact_store = ...

# Load study that contains the artifacts of interest.
study = optuna.load_study(study_name=..., storage=storage)

# Fetch the best trial.
best_trial = study.best_trial

# Fetch all the artifact meta connected to the best trial.
```

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```
artifact_metas = optuna.artifacts.get_all_artifact_meta(best_trial, storage=storage)

download_dir_path = "./best_trial_artifacts/"
os.makedirs(download_dir_path, exist_ok=True)

for artifact_meta in artifact_metas:
    download_file_path = os.path.join(download_dir_path, artifact_meta.filename)
    # Download the artifacts to ``download_file_path``.
    optuna.artifacts.download_artifact(
        artifact_store=artifact_store,
        artifact_id=artifact_meta.artifact_id,
        file_path=download_file_path,
    )
```

Returns
The list of artifact meta in the trial or study. Each artifact meta includes `artifact_id`, `filename`, `mimetype`, and `encoding`. Note that if *Study* is provided, we return the information of the artifacts uploaded to `study`, but not to all the trials in the study.

Parameters

- **study_or_trial** (`Trial | FrozenTrial | Study`)
- **storage** (*BaseStorage | None*)

Return type
list[*ArtifactMeta*]

`optuna.artifacts.`**`download_artifact`**`(*, artifact_store, file_path, artifact_id)`

Download an artifact from the artifact store.

Parameters

- **artifact_store** (*ArtifactStore*) – An artifact store.
- **file_path** (*str*) – A path to save the downloaded artifact.
- **artifact_id** (*str*) – The identifier of the artifact to download.

Return type
None

8.3.3 optuna.cli

The *cli* module implements Optuna's command-line functionality.

For detail, please see the result of

```
$ optuna --help
```

See also

The cli tutorial provides use-cases with examples.

8.3.4 optuna.distributions

The *distributions* module defines various classes representing probability distributions, mainly used to suggest initial hyperparameter values for an optimization trial. Distribution classes inherit from a library-internal `BaseDistribution`, and is initialized with specific parameters, such as the `low` and `high` endpoints for a *IntDistribution*.

Optuna users should not use distribution classes directly, but instead use utility functions provided by *Trial* such as *suggest_int()*.

FloatDistribution	A distribution on floats.
IntDistribution	A distribution on integers.
CategoricalDistribution	A categorical distribution.
distribution_to_json	Serialize a distribution to JSON format.
json_to_distribution	Deserialize a distribution in JSON format.
check_distribution_compatibility	A function to check compatibility of two distributions.

optuna.distributions.FloatDistribution

class optuna.distributions.**FloatDistribution**(*low*, *high*, *log=False*, *step=None*)

A distribution on floats.

This object is instantiated by *suggest_float()*, and passed to *samplers* in general.

Note

When `step` is not `None`, if the range $[\mathrm{low}, \mathrm{high}]$ is not divisible by step, high will be replaced with the maximum of $k \times \mathrm{step} + \mathrm{low} < \mathrm{high}$, where k is an integer.

Parameters

- **low** (*float*)
- **high** (*float*)
- **log** (*bool*)
- **step** (*None | float*)

low

Lower endpoint of the range of the distribution. `low` is included in the range. `low` must be less than or equal to `high`. If `log` is `True`, `low` must be larger than 0.

high

Upper endpoint of the range of the distribution. `high` is included in the range. `high` must be greater than or equal to `low`.

log

If `log` is `True`, this distribution is in log-scaled domain. In this case, all parameters enqueued to the distribution must be positive values. This parameter must be `False` when the parameter `step` is not `None`.

step

A discretization step. `step` must be larger than 0. This parameter must be `None` when the parameter `log` is `True`.

Methods

single()	Test whether the range of this distribution contains just a single value.
to_external_repr(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
to_internal_repr(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

single()

Test whether the range of this distribution contains just a single value.

Returns
`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type
bool

to_external_repr(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters
param_value_in_internal_repr (*float*) – Optuna's internal representation of a parameter value.

Returns
Optuna's external representation of a parameter value.

Return type
Any

to_internal_repr(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters
param_value_in_external_repr (*float*) – Optuna's external representation of a parameter value.

Returns
Optuna's internal representation of a parameter value.

Return type
float

optuna.distributions.IntDistribution

class optuna.distributions.**IntDistribution**(*low*, *high*, *log=False*, *step=1*)

A distribution on integers.

This object is instantiated by *suggest_int()*, and passed to *samplers* in general.

Note

When `step` is not `None`, if the range $[\mathsf{low}, \mathsf{high}]$ is not divisible by step, high will be replaced with the maximum of $k \times \mathsf{step} + \mathsf{low} < \mathsf{high}$, where k is an integer.

Parameters

- **low** (*int*)
- **high** (*int*)
- **log** (*bool*)
- **step** (*int*)

low

Lower endpoint of the range of the distribution. `low` is included in the range. `low` must be less than or equal to `high`. If `log` is `True`, `low` must be larger than or equal to 1.

high

Upper endpoint of the range of the distribution. `high` is included in the range. `high` must be greater than or equal to `low`.

log

If `log` is `True`, this distribution is in log-scaled domain. In this case, all parameters enqueued to the distribution must be positive values. This parameter must be `False` when the parameter `step` is not 1.

step

A discretization step. `step` must be a positive integer. This parameter must be 1 when the parameter `log` is `True`.

Methods

single()	Test whether the range of this distribution contains just a single value.
to_external_repr(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
to_internal_repr(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

single()

Test whether the range of this distribution contains just a single value.

Returns
`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type
bool

to_external_repr(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters
param_value_in_internal_repr (*float*) – Optuna's internal representation of a parameter value.

Returns
Optuna's external representation of a parameter value.

Return type
int

to_internal_repr(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters
param_value_in_external_repr (*int*) – Optuna's external representation of a parameter value.

Returns
Optuna's internal representation of a parameter value.

Return type
float

optuna.distributions.CategoricalDistribution

class optuna.distributions.**CategoricalDistribution**(*choices*)

A categorical distribution.

This object is instantiated by *suggest_categorical()*, and passed to *samplers* in general.

Parameters
choices (*Sequence[CategoricalChoiceType]*) – Parameter value candidates. `choices` must have one element at least.

Note

Not all types are guaranteed to be compatible with all storages. It is recommended to restrict the types of the choices to `None`, `bool`, `int`, `float` and `str`.

choices

Parameter value candidates.

Methods

single()	Test whether the range of this distribution contains just a single value.
to_external_repr(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
to_internal_repr(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

single()

Test whether the range of this distribution contains just a single value.

Returns
`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type
bool

to_external_repr(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters
param_value_in_internal_repr (*float*) – Optuna's internal representation of a parameter value.

Returns
Optuna's external representation of a parameter value.

Return type
None | bool | int | float | str

`to_internal_repr`(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters
param_value_in_external_repr (*None | bool | int | float | str*) – Optuna's external representation of a parameter value.

Returns
Optuna's internal representation of a parameter value.

Return type
float

optuna.distributions.distribution_to_json

`optuna.distributions.distribution_to_json`(*dist*)

Serialize a distribution to JSON format.

Parameters
dist (*BaseDistribution*) – A distribution to be serialized.

Returns
A JSON string of a given distribution.

Return type
str

optuna.distributions.json_to_distribution

`optuna.distributions.json_to_distribution`(*json_str*)

Deserialize a distribution in JSON format.

Parameters
json_str (*str*) – A JSON-serialized distribution.

Returns
A deserialized distribution.

Return type
BaseDistribution

optuna.distributions.check_distribution_compatibility

`optuna.distributions.check_distribution_compatibility`(*dist_old*, *dist_new*)

A function to check compatibility of two distributions.

It checks whether `dist_old` and `dist_new` are the same kind of distributions. If `dist_old` is *CategoricalDistribution*, it further checks `choices` are the same between `dist_old` and `dist_new`. Note that this method is not supposed to be called by library users.

Parameters

- **dist_old** (*BaseDistribution*) – A distribution previously recorded in storage.
- **dist_new** (*BaseDistribution*) – A distribution newly added to storage.

Return type
None

The following classes are deprecated and will be removed in the future.

UniformDistribution	A uniform distribution in the linear domain.
LogUniformDistribution	A uniform distribution in the log domain.
DiscreteUniformDistribution	A discretized uniform distribution in the linear domain.
IntUniformDistribution	A uniform distribution on integers.
IntLogUniformDistribution	A uniform distribution on integers in the log domain.

optuna.distributions.UniformDistribution

class optuna.distributions.**UniformDistribution**(*low*, *high*)

A uniform distribution in the linear domain.

This object is instantiated by *suggest_float()*, and passed to *samplers* in general.

Parameters

- **low** (*float*)
- **high** (*float*)

low

Lower endpoint of the range of the distribution. `low` is included in the range. `low` must be less than or equal to `high`.

high

Upper endpoint of the range of the distribution. `high` is included in the range. `high` must be greater than or equal to `low`.

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use *FloatDistribution* instead.

Methods

single()	Test whether the range of this distribution contains just a single value.
to_external_repr(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
to_internal_repr(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

single()

Test whether the range of this distribution contains just a single value.

Returns

`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type

bool

to_external_repr(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters

param_value_in_internal_repr (*float*) – Optuna's internal representation of a parameter value.

Returns

Optuna's external representation of a parameter value.

Return type

Any

to_internal_repr(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters

param_value_in_external_repr (*float*) – Optuna's external representation of a parameter value.

Returns

Optuna's internal representation of a parameter value.

Return type

float

optuna.distributions.LogUniformDistribution

class optuna.distributions.**LogUniformDistribution**(*low*, *high*)

A uniform distribution in the log domain.

This object is instantiated by *suggest_float()* with `log=True`, and passed to *samplers* in general.

Parameters

- **low** (*float*)
- **high** (*float*)

low

Lower endpoint of the range of the distribution. `low` is included in the range. `low` must be larger than 0. `low` must be less than or equal to `high`.

high

Upper endpoint of the range of the distribution. `high` is included in the range. `high` must be greater than or equal to `low`.

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use *FloatDistribution* instead.

Methods

single()	Test whether the range of this distribution contains just a single value.
to_external_repr(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
to_internal_repr(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

single()

Test whether the range of this distribution contains just a single value.

Returns
`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type
bool

to_external_repr(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters
param_value_in_internal_repr (*float*) – Optuna's internal representation of a parameter value.

Returns
Optuna's external representation of a parameter value.

Return type
Any

to_internal_repr(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters
param_value_in_external_repr (*float*) – Optuna's external representation of a parameter value.

Returns
Optuna's internal representation of a parameter value.

Return type
float

optuna.distributions.DiscreteUniformDistribution

class optuna.distributions.**DiscreteUniformDistribution**(*low*, *high*, *q*)

A discretized uniform distribution in the linear domain.

This object is instantiated by *suggest_float()* with `step` argument, and passed to *samplers* in general.

Note

If the range $[\text{low}, \text{high}]$ is not divisible by q, high will be replaced with the maximum of $kq + \text{low} < \text{high}$, where k is an integer.

Parameters

- **low** (*float*) – Lower endpoint of the range of the distribution. `low` is included in the range. `low` must be less than or equal to `high`.
- **high** (*float*) – Upper endpoint of the range of the distribution. `high` is included in the range. `high` must be greater than or equal to `low`.
- **q** (*float*) – A discretization step. `q` must be larger than 0.

low

Lower endpoint of the range of the distribution. `low` is included in the range.

high

Upper endpoint of the range of the distribution. `high` is included in the range.

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use *FloatDistribution* instead.

Methods

single()	Test whether the range of this distribution contains just a single value.
to_external_repr(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
to_internal_repr(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

Attributes

q	Discretization step.

property q: float

Discretization step.

DiscreteUniformDistribution is a subtype of *FloatDistribution*. This property is a proxy for its `step` attribute.

single()

Test whether the range of this distribution contains just a single value.

Returns
`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type
bool

to_external_repr(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters
`param_value_in_internal_repr` (*float*) – Optuna's internal representation of a parameter value.

Returns
Optuna's external representation of a parameter value.

Return type
Any

`to_internal_repr`(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters
`param_value_in_external_repr` (*float*) – Optuna's external representation of a parameter value.

Returns
Optuna's internal representation of a parameter value.

Return type
float

optuna.distributions.IntUniformDistribution

`class optuna.distributions.IntUniformDistribution`(*low*, *high*, *step=1*)

A uniform distribution on integers.

This object is instantiated by *suggest_int()*, and passed to *samplers* in general.

Note

If the range $[\mathsf{low}, \mathsf{high}]$ is not divisible by step, high will be replaced with the maximum of $k \times \mathsf{step} + \mathsf{low} < \mathsf{high}$, where k is an integer.

Parameters

- **low** (*int*)
- **high** (*int*)
- **step** (*int*)

`low`

Lower endpoint of the range of the distribution. `low` is included in the range. `low` must be less than or equal to `high`.

`high`

Upper endpoint of the range of the distribution. `high` is included in the range. `high` must be greater than or equal to `low`.

`step`

A discretization step. `step` must be a positive integer.

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use `IntDistribution` instead.

Methods

`single`()	Test whether the range of this distribution contains just a single value.
`to_external_repr`(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
`to_internal_repr`(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

`single()`

Test whether the range of this distribution contains just a single value.

Returns
`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type
bool

`to_external_repr`(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters
`param_value_in_internal_repr` (*float*) – Optuna's internal representation of a parameter value.

Returns
Optuna's external representation of a parameter value.

Return type
int

`to_internal_repr`(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters
`param_value_in_external_repr` (*int*) – Optuna's external representation of a parameter value.

Returns
Optuna's internal representation of a parameter value.

Return type
float

optuna.distributions.IntLogUniformDistribution

class optuna.distributions.**IntLogUniformDistribution**(*low*, *high*, *step=1*)

A uniform distribution on integers in the log domain.

This object is instantiated by `suggest_int()`, and passed to `samplers` in general.

Parameters

- **low** (*int*)
- **high** (*int*)
- **step** (*int*)

low

Lower endpoint of the range of the distribution. `low` is included in the range and must be larger than or equal to 1. `low` must be less than or equal to `high`.

high

Upper endpoint of the range of the distribution. `high` is included in the range. `high` must be greater than or equal to `low`.

step

A discretization step. `step` must be a positive integer.

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use `IntDistribution` instead.

Methods

single()	Test whether the range of this distribution contains just a single value.
to_external_repr(param_value_in_internal_repr)	Convert internal representation of a parameter value into external representation.
to_internal_repr(param_value_in_external_repr)	Convert external representation of a parameter value into internal representation.

single()

Test whether the range of this distribution contains just a single value.

Returns

`True` if the range of this distribution contains just a single value, otherwise `False`.

Return type

bool

to_external_repr(*param_value_in_internal_repr*)

Convert internal representation of a parameter value into external representation.

Parameters

param_value_in_internal_repr (*float*) – Optuna's internal representation of a parameter value.

Returns
Optuna's external representation of a parameter value.

Return type
int

to_internal_repr(*param_value_in_external_repr*)

Convert external representation of a parameter value into internal representation.

Parameters
param_value_in_external_repr (*int*) – Optuna's external representation of a parameter value.

Returns
Optuna's internal representation of a parameter value.

Return type
float

8.3.5 optuna.exceptions

The *exceptions* module defines Optuna-specific exceptions deriving from a base *OptunaError* class. Of special importance for library users is the *TrialPruned* exception to be raised if *optuna.trial.Trial.should_prune()* returns `True` for a trial that should be pruned.

OptunaError	Base class for Optuna specific errors.
TrialPruned	Exception for pruned trials.
CLIUsageError	Exception for CLI.
StorageInternalError	Exception for storage operation.
DuplicatedStudyError	Exception for a duplicated study name.
UpdateFinishedTrialError	Exception for updating a finished trial.

optuna.exceptions.OptunaError

exception optuna.exceptions.**OptunaError**

Base class for Optuna specific errors.

add_note()

Exception.add_note(note) – add a note to the exception

optuna.exceptions.TrialPruned

exception optuna.exceptions.**TrialPruned**

Exception for pruned trials.

This error tells a trainer that the current *Trial* was pruned. It is supposed to be raised after *optuna.trial.Trial.should_prune()* as shown in the following example.

See also

optuna.TrialPruned is an alias of *optuna.exceptions.TrialPruned*.

Example

```python
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
    clf = SGDClassifier(alpha=alpha)
    n_train_iter = 100

    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step)

        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=20)
```

add_note()

Exception.add_note(note) – add a note to the exception

optuna.exceptions.CLIUsageError

exception optuna.exceptions.**CLIUsageError**

Exception for CLI.

CLI raises this exception when it receives invalid configuration.

add_note()

Exception.add_note(note) – add a note to the exception

optuna.exceptions.StorageInternalError

exception optuna.exceptions.**StorageInternalError**

Exception for storage operation.

This error is raised when an operation failed in backend DB of storage.

add_note()

Exception.add_note(note) – add a note to the exception

optuna.exceptions.DuplicatedStudyError

exception optuna.exceptions.**DuplicatedStudyError**

Exception for a duplicated study name.

This error is raised when a specified study name already exists in the storage.

add_note()

Exception.add_note(note) – add a note to the exception

optuna.exceptions.UpdateFinishedTrialError

exception optuna.exceptions.**UpdateFinishedTrialError**

Exception for updating a finished trial.

This error is raised when attempting to update a finished trial.

add_note()

Exception.add_note(note) – add a note to the exception

8.3.6 optuna.importance

The *importance* module provides functionality for evaluating hyperparameter importances based on completed trials in a given study. The utility function *get_param_importances()* takes a *Study* and optional evaluator as two of its inputs. The evaluator must derive from `BaseImportanceEvaluator`, and is initialized as a *FanovaImportanceEvaluator* by default when not passed in. Users implementing custom evaluators should refer to either *FanovaImportanceEvaluator*, *MeanDecreaseImpurityImportanceEvaluator*, or *PedAnovaImportanceEvaluator* as a guide, paying close attention to the format of the return value from the Evaluator's `evaluate` function.

get_param_importances	Evaluate parameter importances based on completed trials in the given study.
FanovaImportanceEvaluator	fANOVA importance evaluator.
MeanDecreaseImpurityImportanceEvaluator	Mean Decrease Impurity (MDI) parameter importance evaluator.
PedAnovaImportanceEvaluator	PED-ANOVA importance evaluator.

optuna.importance.get_param_importances

optuna.importance.**get_param_importances**(*study*, ***, *evaluator=None*, *params=None*, *target=None*, *normalize=True*)

Evaluate parameter importances based on completed trials in the given study.

The parameter importances are returned as a dictionary where the keys consist of parameter names and their values importances. The importances are represented by non-negative floating point numbers, where higher values mean that the parameters are more important. The returned dictionary is ordered by its values in a descending order. By default, the sum of the importance values are normalized to 1.0.

If `params` is `None`, all parameter that are present in all of the completed trials are assessed. This implies that conditional parameters will be excluded from the evaluation. To assess the importances of conditional parameters, a `list` of parameter names can be specified via `params`. If specified, only completed trials that contain all of the parameters will be considered. If no such trials are found, an error will be raised.

If the given study does not contain completed trials, an error will be raised.

Note

If `params` is specified as an empty list, an empty dictionary is returned.

See also

See *`plot_param_importances()`* to plot importances.

Parameters

- **`study`** (`Study`) – An optimized study.
- **`evaluator`** (*`BaseImportanceEvaluator | None`*) – An importance evaluator object that specifies which algorithm to base the importance assessment on. Defaults to *`FanovaImportanceEvaluator`*.
- **`params`** (*`list[str] | None`*) – A list of names of parameters to assess. If `None`, all parameters that are present in all of the completed trials are assessed.
- **`target`** (*`Callable[[FrozenTrial], float] | None`*) – A function to specify the value to evaluate importances. If it is `None` and `study` is being used for single-objective optimization, the objective values are used. `target` must be specified if `study` is being used for multi-objective optimization.

  Note

  Specify this argument if `study` is being used for multi-objective optimization. For example, to get the hyperparameter importance of the first objective, use `target=lambda t: t.values[0]` for the target parameter.

- **`normalize`** (*`bool`*) – A boolean option to specify whether the sum of the importance values should be normalized to 1.0. Defaults to `True`.

  Note

  Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Returns

A `dict` where the keys are parameter names and the values are assessed importances.

Return type

dict[str, float]

optuna.importance.FanovaImportanceEvaluator

`class optuna.importance.`**`FanovaImportanceEvaluator`**`(*, n_trees=64, max_depth=64, seed=None)`

fANOVA importance evaluator.

Implements the fANOVA hyperparameter importance evaluation algorithm in An Efficient Approach for Assessing Hyperparameter Importance.

fANOVA fits a random forest regression model that predicts the objective values of *COMPLETE* trials given their parameter configurations. The more accurate this model is, the more reliable the importances assessed by this class are.

Note

Requires the sklearn Python package.

Note

The performance of fANOVA depends on the prediction performance of the underlying random forest model. In order to obtain high prediction performance, it is necessary to cover a wide range of the hyperparameter search space. It is recommended to use an exploration-oriented sampler such as *RandomSampler*.

Note

For how to cite the original work, please refer to https://automl.github.io/fanova/cite.html.

Parameters

- **n_trees** (*int*) – The number of trees in the forest.
- **max_depth** (*int*) – The maximum depth of the trees in the forest.
- **seed** (*int | None*) – Controls the randomness of the forest. For deterministic behavior, specify a value other than None.

Methods

evaluate(study[, params, target])	Evaluate parameter importances based on completed trials in the given study.

evaluate(*study*, *params=None*, ***, *target=None*)

Evaluate parameter importances based on completed trials in the given study.

Note

This method is not meant to be called by library users.

See also

Please refer to *get_param_importances()* for how a concrete evaluator should implement this method.

Parameters

- **study** (Study) – An optimized study.

- **params** (*list[str] | None*) – A list of names of parameters to assess. If None, all parameters that are present in all of the completed trials are assessed.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to evaluate importances. If it is None and `study` is being used for single-objective optimization, the objective values are used. Can also be used for other trial attributes, such as the duration, like `target=lambda t: t.duration.total_seconds()`.

  Note

  Specify this argument if `study` is being used for multi-objective optimization. For example, to get the hyperparameter importance of the first objective, use `target=lambda t: t.values[0]` for the target parameter.

Returns
A `dict` where the keys are parameter names and the values are assessed importances.

Return type
dict[str, float]

optuna.importance.MeanDecreaseImpurityImportanceEvaluator

`class optuna.importance.`**`MeanDecreaseImpurityImportanceEvaluator`**`(*, n_trees=64, max_depth=64, seed=None)`

Mean Decrease Impurity (MDI) parameter importance evaluator.

This evaluator fits fits a random forest regression model that predicts the objective values of *COMPLETE* trials given their parameter configurations. Feature importances are then computed using MDI.

Note

This evaluator requires the sklearn Python package and is based on sklearn.ensemble.RandomForestClassifier.feature_importances_.

Parameters

- **n_trees** (*int*) – Number of trees in the random forest.
- **max_depth** (*int*) – The maximum depth of each tree in the random forest.
- **seed** (*int | None*) – Seed for the random forest.

Methods

evaluate(study[, params, target])	Evaluate parameter importances based on completed trials in the given study.

evaluate(*study*, *params=None*, ***, *target=None*)

Evaluate parameter importances based on completed trials in the given study.

Note

This method is not meant to be called by library users.

See also

Please refer to *get_param_importances()* for how a concrete evaluator should implement this method.

Parameters

- **study** (Study) – An optimized study.
- **params** (*list[str] | None*) – A list of names of parameters to assess. If None, all parameters that are present in all of the completed trials are assessed.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to evaluate importances. If it is None and `study` is being used for single-objective optimization, the objective values are used. Can also be used for other trial attributes, such as the duration, like `target=lambda t: t.duration.total_seconds()`.

Note

Specify this argument if `study` is being used for multi-objective optimization. For example, to get the hyperparameter importance of the first objective, use `target=lambda t: t.values[0]` for the target parameter.

Returns

A `dict` where the keys are parameter names and the values are assessed importances.

Return type

dict[str, float]

optuna.importance.PedAnovaImportanceEvaluator

`class optuna.importance.PedAnovaImportanceEvaluator(*, baseline_quantile=0.1, evaluate_on_local=True)`

PED-ANOVA importance evaluator.

Implements the PED-ANOVA hyperparameter importance evaluation algorithm.

PED-ANOVA fits Parzen estimators of *COMPLETE* trials better than a user-specified baseline. Users can specify the baseline by a quantile. The importance can be interpreted as how important each hyperparameter is to get the performance better than baseline.

For further information about PED-ANOVA algorithm, please refer to the following paper:

- PED-ANOVA: Efficiently Quantifying Hyperparameter Importance in Arbitrary Subspaces

Note

The performance of PED-ANOVA depends on how many trials to consider above baseline. To stabilize the analysis, it is preferable to include at least 5 trials above baseline.

Note

Please refer to the original work.

Parameters

- **baseline_quantile** (*float*) – Compute the importance of achieving top-baseline_quantile quantile objective value. For example, baseline_quantile=0.1 means that the importances give the information of which parameters were important to achieve the top-10% performance during optimization.
- **evaluate_on_local** (*bool*) – Whether we measure the importance in the local or global space. If True, the importances imply how importance each parameter is during optimization. Meanwhile, evaluate_on_local=False gives the importances in the specified search_space. evaluate_on_local=True is especially useful when users modify search space during optimization.

Example

An example of using PED-ANOVA is as follows:

```
import optuna
from optuna.importance import PedAnovaImportanceEvaluator


def objective(trial):
    x1 = trial.suggest_float("x1", -10, 10)
    x2 = trial.suggest_float("x2", -10, 10)
    return x1 + x2 / 1000


study = optuna.create_study()
study.optimize(objective, n_trials=100)
evaluator = PedAnovaImportanceEvaluator()
importance = optuna.importance.get_param_importances(study, evaluator=evaluator)
```

Note

Added in v3.6.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.6.0.

Methods

evaluate(study[, params, target])	Evaluate parameter importances based on completed trials in the given study.

evaluate(*study*, *params=None*, ***, *target=None*)

Evaluate parameter importances based on completed trials in the given study.

Note

This method is not meant to be called by library users.

See also

Please refer to *get_param_importances()* for how a concrete evaluator should implement this method.

Parameters

- **study** (Study) – An optimized study.
- **params** (*list[str] | None*) – A list of names of parameters to assess. If None, all parameters that are present in all of the completed trials are assessed.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to evaluate importances. If it is None and study is being used for single-objective optimization, the objective values are used. Can also be used for other trial attributes, such as the duration, like `target=lambda t: t.duration.total_seconds()`.

Note

Specify this argument if `study` is being used for multi-objective optimization. For example, to get the hyperparameter importance of the first objective, use `target=lambda t: t.values[0]` for the target parameter.

Returns

A dict where the keys are parameter names and the values are assessed importances.

Return type

dict[str, float]

8.3.7 optuna.integration

The *integration* module contains classes used to integrate Optuna with external machine learning frameworks.

Note

Optuna's integration modules for third-party libraries have started migrating from Optuna itself to a package called *optuna-integration*. Please check the repository and the documentation.

For most of the ML frameworks supported by Optuna, the corresponding Optuna integration class serves only to implement a callback object and functions, compliant with the framework's specific callback API, to be called with each intermediate step in the model training. The functionality implemented in these callbacks across the different ML frameworks includes:

(1) Reporting intermediate model scores back to the Optuna trial using *optuna.trial.Trial.report()*,

(2) According to the results of *optuna.trial.Trial.should_prune()*, pruning the current model by raising *optuna.TrialPruned()*, and

(3) Reporting intermediate Optuna data such as the current trial number back to the framework, as done in `MLflowCallback`.

For scikit-learn, an integrated `OptunaSearchCV` estimator is available that combines scikit-learn BaseEstimator functionality with access to a class-level `Study` object.

Dependencies of each integration

We summarize the necessary dependencies for each integration.

Integration	Dependencies
AllenNLP	allennlp, torch, psutil, jsonnet
BoTorch	botorch, gpytorch, torch
CatBoost	catboost
ChainerMN	chainermn
Chainer	chainer
pycma	cma
Dask	distributed
FastAI	fastai
Keras	keras
LightGBMTuner	lightgbm, scikit-learn
LightGBMPruningCallback	lightgbm
MLflow	mlflow
MXNet	mxnet
PyTorch Distributed	torch
PyTorch (Ignite)	pytorch-ignite
PyTorch (Lightning)	pytorch-lightning
SHAP	scikit-learn, shap
Scikit-learn	pandas, scipy, scikit-learn
SKorch	skorch
TensorBoard	tensorboard, tensorflow
TensorFlow	tensorflow, tensorflow-estimator
TensorFlow + Keras	tensorflow
Weights & Biases	wandb
XGBoost	xgboost

8.3.8 optuna.logging

The *logging* module implements logging using the Python `logging` package. Library users may be especially interested in setting verbosity levels using *set_verbosity()* to one of `optuna.logging.CRITICAL` (aka `optuna.logging.FATAL`), `optuna.logging.ERROR`, `optuna.logging.WARNING` (aka `optuna.logging.WARN`), `optuna.logging.INFO`, or `optuna.logging.DEBUG`.

get_verbosity	Return the current level for the Optuna's root logger.
set_verbosity	Set the level for the Optuna's root logger.
disable_default_handler	Disable the default handler of the Optuna's root logger.
enable_default_handler	Enable the default handler of the Optuna's root logger.
disable_propagation	Disable propagation of the library log outputs.
enable_propagation	Enable propagation of the library log outputs.

optuna.logging.get_verbosity

`optuna.logging.`**`get_verbosity`**`()`

Return the current level for the Optuna's root logger.

Example

Get the default verbosity level.

```
import optuna

# The default verbosity level of Optuna is `optuna.logging.INFO`.
print(optuna.logging.get_verbosity())
# 20
print(optuna.logging.INFO)
# 20

# There are logs of the INFO level.
study = optuna.create_study()
study.optimize(objective, n_trials=5)
# [I 2021-10-31 05:35:17,232] A new study created ...
# [I 2021-10-31 05:35:17,238] Trial 0 finished with value: ...
# [I 2021-10-31 05:35:17,245] Trial 1 finished with value: ...
# ...
```

Returns
Logging level, e.g., `optuna.logging.DEBUG` and `optuna.logging.INFO`.

Return type
int

Note

Optuna has following logging levels:

- `optuna.logging.CRITICAL`, `optuna.logging.FATAL`
- `optuna.logging.ERROR`
- `optuna.logging.WARNING`, `optuna.logging.WARN`
- `optuna.logging.INFO`
- `optuna.logging.DEBUG`

optuna.logging.set_verbosity

`optuna.logging.`**`set_verbosity`**(*verbosity*)

Set the level for the Optuna's root logger.

Example

Set the logging level `optuna.logging.WARNING`.

```
import optuna

# There are INFO level logs.
study = optuna.create_study()
study.optimize(objective, n_trials=10)
# [I 2021-10-31 02:59:35,088] Trial 0 finished with value: 16.0 ...
```

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```
# [I 2021-10-31 02:59:35,091] Trial 1 finished with value: 1.0 ...
# [I 2021-10-31 02:59:35,096] Trial 2 finished with value: 1.0 ...

# Setting the logging level WARNING, the INFO logs are suppressed.
optuna.logging.set_verbosity(optuna.logging.WARNING)
study.optimize(objective, n_trials=10)
```

Parameters
verbosity (*int*) – Logging level, e.g., `optuna.logging.DEBUG` and `optuna.logging.INFO`.

Return type
None

Note

Optuna has following logging levels:

- `optuna.logging.CRITICAL`, `optuna.logging.FATAL`
- `optuna.logging.ERROR`
- `optuna.logging.WARNING`, `optuna.logging.WARN`
- `optuna.logging.INFO`
- `optuna.logging.DEBUG`

optuna.logging.disable_default_handler

`optuna.logging.`**`disable_default_handler`**`()`

Disable the default handler of the Optuna's root logger.

Example

Stop and then resume logging to `sys.stderr`.

```
import optuna

study = optuna.create_study()

# There are no logs in sys.stderr.
optuna.logging.disable_default_handler()
study.optimize(objective, n_trials=10)

# There are logs in sys.stderr.
optuna.logging.enable_default_handler()
study.optimize(objective, n_trials=10)
# [I 2020-02-23 17:00:54,314] Trial 10 finished with value: ...
# [I 2020-02-23 17:00:54,356] Trial 11 finished with value: ...
# ...
```

Return type
None

optuna.logging.enable_default_handler

`optuna.logging.enable_default_handler()`

Enable the default handler of the Optuna's root logger.

Please refer to the example shown in *disable_default_handler()*.

Return type
None

optuna.logging.disable_propagation

`optuna.logging.disable_propagation()`

Disable propagation of the library log outputs.

Note that log propagation is disabled by default. You only need to use this function to stop log propagation when you use *enable_propagation()*.

Example

Stop propagating logs to the root logger on the second optimize call.

```
import optuna
import logging

optuna.logging.disable_default_handler()  # Disable the default handler.
logger = logging.getLogger()

logger.setLevel(logging.INFO)  # Setup the root logger.
logger.addHandler(logging.FileHandler("foo.log", mode="w"))

optuna.logging.enable_propagation()  # Propagate logs to the root logger.

study = optuna.create_study()

logger.info("Logs from first optimize call")  # The logs are saved in the logs file.
study.optimize(objective, n_trials=10)

optuna.logging.disable_propagation()  # Stop propogating logs to the root logger.

logger.info("Logs from second optimize call")
# The new logs for second optimize call are not saved.
study.optimize(objective, n_trials=10)

with open("foo.log") as f:
    assert f.readline().startswith("A new study created")
    assert f.readline() == "Logs from first optimize call\n"
    # Check for logs after second optimize call.
    assert f.read().split("Logs from second optimize call\n")[-1] == ""
```

Return type
None

optuna.logging.enable_propagation

optuna.logging.**enable_propagation**()

Enable propagation of the library log outputs.

Please disable the Optuna's default handler to prevent double logging if the root logger has been configured.

Example

Propagate all log output to the root logger in order to save them to the file.

```
import optuna
import logging

logger = logging.getLogger()

logger.setLevel(logging.INFO)  # Setup the root logger.
logger.addHandler(logging.FileHandler("foo.log", mode="w"))

optuna.logging.enable_propagation()  # Propagate logs to the root logger.
optuna.logging.disable_default_handler()  # Stop showing logs in sys.stderr.

study = optuna.create_study()

logger.info("Start optimization.")
study.optimize(objective, n_trials=10)

with open("foo.log") as f:
    assert f.readline().startswith("A new study created")
    assert f.readline() == "Start optimization.\n"
```

Return type

None

8.3.9 optuna.pruners

The *pruners* module defines a *BasePruner* class characterized by an abstract *prune()* method, which, for a given trial and its associated study, returns a boolean value representing whether the trial should be pruned. This determination is made based on stored intermediate values of the objective function, as previously reported for the trial using *optuna.trial.Trial.report()*. The remaining classes in this module represent child classes, inheriting from *BasePruner*, which implement different pruning strategies.

Warning

Currently *pruners* module is expected to be used only for single-objective optimization.

See also

pruning tutorial explains the concept of the pruner classes and a minimal example.

See also

user_defined_pruner tutorial could be helpful if you want to implement your own pruner classes.

BasePruner	Base class for pruners.
MedianPruner	Pruner using the median stopping rule.
NopPruner	Pruner which never prunes trials.
PatientPruner	Pruner which wraps another pruner with tolerance.
PercentilePruner	Pruner to keep the specified percentile of the trials.
SuccessiveHalvingPruner	Pruner using Asynchronous Successive Halving Algorithm.
HyperbandPruner	Pruner using Hyperband.
ThresholdPruner	Pruner to detect outlying metrics of the trials.
WilcoxonPruner	Pruner based on the Wilcoxon signed-rank test.

optuna.pruners.BasePruner

class optuna.pruners.**BasePruner**

Base class for pruners.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

abstractmethod prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns

A boolean value representing whether the trial should be pruned.

Return type

bool

optuna.pruners.MedianPruner

class optuna.pruners.**MedianPruner**(*n_startup_trials=5*, *n_warmup_steps=0*, *interval_steps=1*, ***, *n_min_trials=1*)

Pruner using the median stopping rule.

Prune if the trial's best intermediate result is worse than median of intermediate results of previous trials at the same step. It stops unpromising trials early based on the intermediate results compared against the median of previous completed trials.

The pruner handles NaN values in the following manner:

1. If all intermediate values of the current trial are NaN, the trial will be pruned.
2. During the median calculation across completed trials, NaN values are ignored. Only valid numeric values are considered.

Example

We minimize an objective function with the median stopping rule.

```python
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
    clf = SGDClassifier(alpha=alpha)
    n_train_iter = 100

    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step)

        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(
    direction="maximize",
    pruner=optuna.pruners.MedianPruner(
        n_startup_trials=5, n_warmup_steps=30, interval_steps=10
    ),
)
study.optimize(objective, n_trials=20)
```

Parameters

- **n_startup_trials** (*int*) – Pruning is disabled until the given number of trials finish in the same study.
- **n_warmup_steps** (*int*) – Pruning is disabled until the trial exceeds the given number of step. Note that this feature assumes that `step` starts at zero.

- **interval_steps** (*int*) – Interval in number of steps between the pruning checks, offset by the warmup steps. If no value has been reported at the time of a pruning check, that particular check will be postponed until a value is reported.
- **n_min_trials** (*int*) – Minimum number of reported trial results at a step to judge whether to prune. If the number of reported intermediate values from all trials at the current step is less than `n_min_trials`, the trial will not be pruned. This can be used to ensure that a minimum number of trials are run to completion without being pruned.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns

A boolean value representing whether the trial should be pruned.

Return type

bool

optuna.pruners.NopPruner

class optuna.pruners.**NopPruner**

Pruner which never prunes trials.

Example

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
```

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```
    clf = SGDClassifier(alpha=alpha)
    n_train_iter = 100

    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step)

        if trial.should_prune():
            assert False, "should_prune() should always return False with this␣
↪pruner."
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize", pruner=optuna.pruners.NopPruner())
study.optimize(objective, n_trials=20)
```

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns
A boolean value representing whether the trial should be pruned.

Return type
bool

optuna.pruners.PatientPruner

class optuna.pruners.**PatientPruner**(*wrapped_pruner*, *patience*, *min_delta=0.0*)

Pruner which wraps another pruner with tolerance.

This pruner monitors intermediate values in a trial and prunes the trial if the improvement in the intermediate values after a patience period is less than a threshold.

The pruner handles NaN values in the following manner:

1. If all intermediate values before or during the patient period are NaN, the trial will not be pruned 2. During the pruning calculations, NaN values are ignored. Only valid numeric values are considered.

Example

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
    clf = SGDClassifier(alpha=alpha)
    n_train_iter = 100

    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step)

        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(
    direction="maximize",
    pruner=optuna.pruners.PatientPruner(optuna.pruners.MedianPruner(), patience=1),
)
study.optimize(objective, n_trials=20)
```

Parameters

- **wrapped_pruner** (BasePruner | *None*) – Wrapped pruner to perform pruning when *PatientPruner* allows a trial to be pruned. If it is None, this pruner is equivalent to early-stopping taken the intermediate values in the individual trial.
- **patience** (*int*) – Pruning is disabled until the objective doesn't improve for patience consecutive steps.
- **min_delta** (*float*) – Tolerance value to check whether or not the objective improves. This value should be non-negative.

Note

Added in v2.8.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.8.0.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns

A boolean value representing whether the trial should be pruned.

Return type

bool

optuna.pruners.PercentilePruner

class optuna.pruners.**PercentilePruner**(*percentile*, *n_startup_trials=5*, *n_warmup_steps=0*, *interval_steps=1*, ***, *n_min_trials=1*)

Pruner to keep the specified percentile of the trials.

Prune if the best intermediate value is in the bottom percentile among trials at the same step.

Example

```python
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
```

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```python
    clf = SGDClassifier(alpha=alpha)
    n_train_iter = 100

    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step)

        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(
    direction="maximize",
    pruner=optuna.pruners.PercentilePruner(
        25.0, n_startup_trials=5, n_warmup_steps=30, interval_steps=10
    ),
)
study.optimize(objective, n_trials=20)
```

Parameters

- **percentile** (*float*) – Percentile which must be between 0 and 100 inclusive (e.g., When given 25.0, top of 25th percentile trials are kept).
- **n_startup_trials** (*int*) – Pruning is disabled until the given number of trials finish in the same study.
- **n_warmup_steps** (*int*) – Pruning is disabled until the trial exceeds the given number of step. Note that this feature assumes that `step` starts at zero.
- **interval_steps** (*int*) – Interval in number of steps between the pruning checks, offset by the warmup steps. If no value has been reported at the time of a pruning check, that particular check will be postponed until a value is reported. Value must be at least 1.
- **n_min_trials** (*int*) – Minimum number of reported trial results at a step to judge whether to prune. If the number of reported intermediate values from all trials at the current step is less than `n_min_trials`, the trial will not be pruned. This can be used to ensure that a minimum number of trials are run to completion without being pruned.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns
A boolean value representing whether the trial should be pruned.

Return type
bool

optuna.pruners.SuccessiveHalvingPruner

class optuna.pruners.**SuccessiveHalvingPruner**(*min_resource='auto'*, *reduction_factor=4*, *min_early_stopping_rate=0*, *bootstrap_count=0*)

Pruner using Asynchronous Successive Halving Algorithm.

Successive Halving is a bandit-based algorithm to identify the best one among multiple configurations. This class implements an asynchronous version of Successive Halving. Please refer to the paper of Asynchronous Successive Halving for detailed descriptions.

Note that, this class does not take care of the parameter for the maximum resource, referred to as R in the paper. The maximum resource allocated to a trial is typically limited inside the objective function (e.g., `step` number in simple_pruning.py, `EPOCH` number in chainer_integration.py).

See also

Please refer to *report()*.

Example

We minimize an objective function with `SuccessiveHalvingPruner`.

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
    clf = SGDClassifier(alpha=alpha)
    n_train_iter = 100

    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
```

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```
        trial.report(intermediate_value, step)

        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(
    direction="maximize", pruner=optuna.pruners.SuccessiveHalvingPruner()
)
study.optimize(objective, n_trials=20)
```

Parameters

- **min_resource** (*str* | *int*) – A parameter for specifying the minimum resource allocated to a trial (in the paper this parameter is referred to as r). This parameter defaults to 'auto' where the value is determined based on a heuristic that looks at the number of required steps for the first trial to complete.

  A trial is never pruned until it executes $\mathsf{min\_resource} \times \mathsf{reduction\_factor}^{\mathsf{min\_early\_stopping\_rate}}$ steps (i.e., the completion point of the first rung). When the trial completes the first rung, it will be promoted to the next rung only if the value of the trial is placed in the top $\frac{1}{\mathsf{reduction\_factor}}$ fraction of the all trials that already have reached the point (otherwise it will be pruned there). If the trial won the competition, it runs until the next completion point (i.e., $\mathsf{min\_resource} \times \mathsf{reduction\_factor}^{(\mathsf{min\_early\_stopping\_rate}+\mathsf{rung})}$ steps) and repeats the same procedure.

  Note

  If the step of the last intermediate value may change with each trial, please manually specify the minimum possible step to `min_resource`.

- **reduction_factor** (*int*) – A parameter for specifying reduction factor of promotable trials (in the paper this parameter is referred to as η). At the completion point of each rung, about $\frac{1}{\mathsf{reduction\_factor}}$ trials will be promoted.
- **min_early_stopping_rate** (*int*) – A parameter for specifying the minimum early-stopping rate (in the paper this parameter is referred to as s).
- **bootstrap_count** (*int*) – Minimum number of trials that need to complete a rung before any trial is considered for promotion into the next rung.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns

A boolean value representing whether the trial should be pruned.

Return type

bool

optuna.pruners.HyperbandPruner

`class optuna.pruners.HyperbandPruner`(*min_resource=1*, *max_resource='auto'*, *reduction_factor=3*, *bootstrap_count=0*)

Pruner using Hyperband.

As SuccessiveHalving (SHA) requires the number of configurations n as its hyperparameter. For a given finite budget B, all the configurations have the resources of $\frac{B}{n}$ on average. As you can see, there will be a trade-off of B and $\frac{B}{n}$. Hyperband attacks this trade-off by trying different n values for a fixed budget.

Note

- In the Hyperband paper, the counterpart of *RandomSampler* is used.
- Optuna uses *TPESampler* by default.
- The benchmark result shows that *optuna.pruners.HyperbandPruner* supports both samplers.

Note

If you use `HyperbandPruner` with *TPESampler*, it's recommended to consider setting larger `n_trials` or `timeout` to make full use of the characteristics of *TPESampler* because *TPESampler* uses some (by default, 10) *Trial*s for its startup.

As Hyperband runs multiple *SuccessiveHalvingPruner* and collects trials based on the current *Trial*'s bracket ID, each bracket needs to observe more than 10 *Trial*s for *TPESampler* to adapt its search space.

Thus, for example, if `HyperbandPruner` has 4 pruners in it, at least 4×10 trials are consumed for startup.

Note

Hyperband has several *SuccessiveHalvingPruner*s. Each *SuccessiveHalvingPruner* is referred to as "bracket" in the original paper. The number of brackets is an important factor to control the early stopping behavior of Hyperband and is automatically determined by `min_resource`, `max_resource` and `reduction_factor` as $\mathrm{The\ number\ of\ brackets} = \mathrm{floor}(\log_{\texttt{reduction\_factor}}(\frac{\texttt{max\_resource}}{\texttt{min\_resource}})) + 1$. Please set `reduction_factor` so that the number of brackets is not too large (about 4 – 6 in most use cases). Please see Section 3.6 of the original paper for the detail.

Note

`HyperbandPruner` computes bracket ID for each trial with a function taking `study_name` of *`Study`* and *`number`*. Please specify `study_name` to make the pruning algorithm reproducible.

Example

We minimize an objective function with Hyperband pruning algorithm.

```python
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)
classes = np.unique(y)
n_train_iter = 100


def objective(trial):
    alpha = trial.suggest_float("alpha", 0.0, 1.0)
    clf = SGDClassifier(alpha=alpha)

    for step in range(n_train_iter):
        clf.partial_fit(X_train, y_train, classes=classes)

        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step)

        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(
    direction="maximize",
    pruner=optuna.pruners.HyperbandPruner(
        min_resource=1, max_resource=n_train_iter, reduction_factor=3
    ),
)
study.optimize(objective, n_trials=20)
```

Parameters

- **`min_resource`** (*`int`*) – A parameter for specifying the minimum resource allocated to a trial noted as r in the paper. A smaller r will give a result faster, but a larger r will give a better guarantee of successful judging between configurations. See the details for *`SuccessiveHalvingPruner`*.
- **`max_resource`** (*`str | int`*) – A parameter for specifying the maximum resource allocated

to a trial. R in the paper corresponds to `max_resource / min_resource`. This value represents and should match the maximum iteration steps (e.g., the number of epochs for neural networks). When this argument is "auto", the maximum resource is estimated according to the completed trials. The default value of this argument is "auto".

Note

With "auto", the maximum resource will be the largest step reported by *report()* in the first, or one of the first if trained in parallel, completed trial. No trials will be pruned until the maximum resource is determined.

Note

If the step of the last intermediate value may change with each trial, please manually specify the maximum possible step to `max_resource`.

- **reduction_factor** (*int*) – A parameter for specifying reduction factor of promotable trials noted as η in the paper. See the details for *SuccessiveHalvingPruner*.
- **bootstrap_count** (*int*) – Parameter specifying the number of trials required in a rung before any trial can be promoted. Incompatible with `max_resource` is `"auto"`. See the details for *SuccessiveHalvingPruner*.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns

A boolean value representing whether the trial should be pruned.

Return type

bool

optuna.pruners.ThresholdPruner

class optuna.pruners.**ThresholdPruner**(*lower=None*, *upper=None*, *n_warmup_steps=0*, *interval_steps=1*)

Pruner to detect outlying metrics of the trials.

Prune if a metric exceeds upper threshold, falls behind lower threshold or reaches `nan`.

Example

```python
from optuna import create_study
from optuna.pruners import ThresholdPruner
from optuna import TrialPruned


def objective_for_upper(trial):
    for step, y in enumerate(ys_for_upper):
        trial.report(y, step)

        if trial.should_prune():
            raise TrialPruned()
    return ys_for_upper[-1]


def objective_for_lower(trial):
    for step, y in enumerate(ys_for_lower):
        trial.report(y, step)

        if trial.should_prune():
            raise TrialPruned()
    return ys_for_lower[-1]


ys_for_upper = [0.0, 0.1, 0.2, 0.5, 1.2]
ys_for_lower = [100.0, 90.0, 0.1, 0.0, -1]

study = create_study(pruner=ThresholdPruner(upper=1.0))
study.optimize(objective_for_upper, n_trials=10)

study = create_study(pruner=ThresholdPruner(lower=0.0))
study.optimize(objective_for_lower, n_trials=10)
```

Parameters

- **lower** (*float | None*) – A minimum value which determines whether pruner prunes or not. If an intermediate value is smaller than lower, it prunes.
- **upper** (*float | None*) – A maximum value which determines whether pruner prunes or not. If an intermediate value is larger than upper, it prunes.
- **n_warmup_steps** (*int*) – Pruning is disabled if the step is less than the given number of warmup steps.
- **interval_steps** (*int*) – Interval in number of steps between the pruning checks, offset by the warmup steps. If no value has been reported at the time of a pruning check, that particular check will be postponed until a value is reported. Value must be at least 1.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns

A boolean value representing whether the trial should be pruned.

Return type

bool

optuna.pruners.WilcoxonPruner

class optuna.pruners.**WilcoxonPruner**(**, *p_threshold=0.1*, *n_startup_steps=2*)

Pruner based on the Wilcoxon signed-rank test.

This pruner performs the Wilcoxon signed-rank test between the current trial and the current best trial, and stops whenever the pruner is sure up to a given p-value that the current trial is worse than the best one.

This pruner is effective for optimizing the mean/median of some (costly-to-evaluate) performance scores over a set of problem instances. Example applications include the optimization of:

- the mean performance of a heuristic method (simulated annealing, genetic algorithm, SAT solver, etc.) on a set of problem instances,
- the k-fold cross-validation score of a machine learning model, and
- the accuracy of outputs of a large language model (LLM) on a set of questions.

There can be "easy" or "hard" instances (the pruner handles correspondence of the instances between different trials). In each trial, it is recommended to shuffle the evaluation order, so that the optimization doesn't overfit to the instances in the beginning.

When you use this pruner, you must call `Trial.report(value, step)` method for each step (instance id) with the evaluated value. The instance id may not be in ascending order. This is different from other pruners in that the reported value need not converge to the real value. To use pruners such as *SuccessiveHalvingPruner* in the same setting, you must provide e.g., the historical average of the evaluated values.

See also

Please refer to *report()*.

Example

```python
import optuna
import numpy as np


# We minimize the mean evaluation loss over all the problem instances.
```

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```
def evaluate(param, instance):
    # A toy loss function for demonstrative purpose.
    return (param - instance) ** 2


problem_instances = np.linspace(-1, 1, 100)


def objective(trial):
    # Sample a parameter.
    param = trial.suggest_float("param", -1, 1)

    # Evaluate performance of the parameter.
    results = []

    # For best results, shuffle the evaluation order in each trial.
    instance_ids = np.random.permutation(len(problem_instances))
    for instance_id in instance_ids:
        loss = evaluate(param, problem_instances[instance_id])
        results.append(loss)

        # Report loss together with the instance id.
        # CAVEAT: You need to pass the same id for the same instance,
        # otherwise WilcoxonPruner cannot correctly pair the losses across trials␣
↪and
        # the pruning performance will degrade.
        trial.report(loss, instance_id)

        if trial.should_prune():
            # Return the current predicted value instead of raising `TrialPruned`.
            # This is a workaround to tell the Optuna about the evaluation
            # results in pruned trials. (See the note below.)
            return sum(results) / len(results)

    return sum(results) / len(results)


study = optuna.create_study(pruner=optuna.pruners.WilcoxonPruner(p_threshold=0.1))
study.optimize(objective, n_trials=100)
```

Note

This pruner cannot handle `infinity` or `nan` values. Trials containing those values are never pruned.

Note

If *should_prune()* returns `True`, you can return an estimation of the final value (e.g., the average of all evaluated values) instead of `raise optuna.TrialPruned()`. This is a workaround for the problem that currently there is no way to tell Optuna the predicted objective value for trials raising `optuna.TrialPruned`.

Parameters

- **p_threshold** (*float*) – The p-value threshold for pruning. This value should be between 0 and 1. A trial will be pruned whenever the pruner is sure up to the given p-value that the current trial is worse than the best trial. The larger this value is, the more aggressive pruning will be performed. Defaults to 0.1.

  Note

  This pruner repeatedly performs statistical tests between the current trial and the current best trial with increasing samples. The false-positive rate of such a sequential test is different from performing the test only once. To get the nominal false-positive rate, please specify the Pocock-corrected p-value.

- **n_startup_steps** (*int*) – The number of steps before which no trials are pruned. Pruning starts only after you have `n_startup_steps` steps of available observations for comparison between the current trial and the best trial. Defaults to 2. Note that the trial is not pruned at the first and second steps even if the *n_startup_steps* is set to 0 or 1 due to the lack of enough data for comparison.

Note

Added in v3.6.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.6.0.

Methods

prune(study, trial)	Judge whether the trial should be pruned based on the reported values.

prune(*study*, *trial*)

Judge whether the trial should be pruned based on the reported values.

Note that this method is not supposed to be called by library users. Instead, *optuna.trial.Trial.report()* and *optuna.trial.Trial.should_prune()* provide user interfaces to implement pruning mechanism in an objective function.

Parameters

- **study** (Study) – Study object of the target study.
- **trial** (FrozenTrial) – FrozenTrial object of the target trial. Take a copy before modifying this object.

Returns

A boolean value representing whether the trial should be pruned.

Return type

bool

8.3.10 optuna.samplers

The *samplers* module defines a base class for parameter sampling as described extensively in *BaseSampler*. The remaining classes in this module represent child classes, deriving from *BaseSampler*, which implement different sampling strategies.

See also

pruning tutorial explains the overview of the sampler classes.

See also

user_defined_sampler tutorial could be helpful if you want to implement your own sampler classes.

See also

If you are unsure about which sampler to use, please consider using AutoSampler, which automatically selects a sampler during optimization. For more detail, see the article on AutoSampler.

	RandomSampler	GridSampler	TPESampler	CmaEsSampler	NSGAIISampler	QMCSampler	GPSampler	BoTorchSampler	BruteForceSampler
Float parameters	✓	✓	✓	✓	▲	✓	✓	✓	✓ (× for infinite domain)
Integer parameters	✓	✓	✓	✓	▲	✓	✓	▲	✓
Categorical parameters	✓	✓	✓	▲	✓	▲	✓	▲	✓
Pruning	✓	✓	✓	▲	× (▲ for single-objective)	✓	▲	▲	✓
Multivariate optimization	▲	▲	✓	✓	▲	▲	✓	✓	▲
Conditional search space	✓	▲	✓	▲	▲	▲	▲	▲	✓
Multi-objective optimization	✓	✓	✓	×	✓ (▲ for single-objective)	✓	✓	✓	✓
Batch optimization	✓	✓	✓	✓	✓	✓	▲	✓	✓
Distributed optimization	✓	✓	✓	✓	✓	✓	▲	✓	✓
Constrained optimization	×	×	✓	×	✓	×	✓	✓	×
Time complexity (per trial) (*)	$O(d)$	$O(dn)$	$O(dn$ l	$O(d^3)$	$O(mp^2)$ (***)	$O(dn)$	$O(n^3)$	$O(n^3)$	$O(d)$
Recommended budgets (#trials) (**)	as many as one likes	number of combinations	100 – 1000	1000 – 10000	100 – 10000	as many as one likes	– 500	10 – 100	number of combinations

Note

✓: Supports this feature. ▲: Works, but inefficiently. ×: Causes an error, or has no interface.

(*): We assumes that d is the dimension of the search space, n is the number of finished trials, m is the number of objectives, and p is the population size (algorithm specific parameter). This table shows the time complexity of the sampling algorithms. We may omit other terms that depend on the implementation in Optuna, including $O(d)$ to call the sampling methods and $O(n)$ to collect the completed trials. This means that, for example, the actual time complexity of `RandomSampler` is $O(d+n+d) = O(d+n)$. From another perspective, with the exception of `NSGAIISampler`, all time complexity is written for single-objective optimization.

(**): (1) The budget depends on the number of parameters and the number of objectives. (2) This budget includes `n_startup_trials` if a sampler has `n_startup_trials` as one of its arguments.

(***): This time complexity assumes that the number of population size p and the number of parallelization are regular. This means that the number of parallelization should not exceed the number of population size p.

Note

Samplers initialize their random number generators by specifying `seed` argument at initialization. However, samplers reseed them when `n_jobs!=1` of *optuna.study.Study.optimize()* to avoid sampling duplicated parameters by using the same generator. Thus we can hardly reproduce the optimization results with `n_jobs!=1`. For the same reason, make sure that use either `seed=None` or different `seed` values among processes with distributed optimization explained in distributed tutorial.

Note

For float, integer, or categorical parameters, see configurations tutorial.

For pruning, see pruning tutorial.

For multivariate optimization, see *BaseSampler*. The multivariate optimization is implemented as *sample_relative()* in Optuna. Please check the concrete documents of samplers for more details.

For conditional search space, see configurations tutorial and *TPESampler*. The `group` option of *TPESampler* allows *TPESampler* to handle the conditional search space.

For multi-objective optimization, see multi_objective tutorial.

For batch optimization, see Batch-Optimization tutorial. Note that the `constant_liar` option of *TPESampler* allows *TPESampler* to handle the batch optimization.

For distributed optimization, see distributed tutorial. Note that the `constant_liar` option of *TPESampler* allows *TPESampler* to handle the distributed optimization.

For constrained optimization, see an example.

BaseSampler	Base class for samplers.
GridSampler	Sampler using grid search.
RandomSampler	Sampler using random sampling.
TPESampler	Sampler using TPE (Tree-structured Parzen Estimator) algorithm.
CmaEsSampler	A sampler using cmaes as the backend.
GPSampler	Sampler using Gaussian process-based Bayesian optimization.
PartialFixedSampler	Sampler with partially fixed parameters.
NSGAIISampler	Multi-objective sampler using the NSGA-II algorithm.
NSGAIIISampler	Multi-objective sampler using the NSGA-III algorithm.
QMCSampler	A Quasi Monte Carlo Sampler that generates low-discrepancy sequences.
BruteForceSampler	Sampler using brute force.

optuna.samplers.BaseSampler

class optuna.samplers.**BaseSampler**

Base class for samplers.

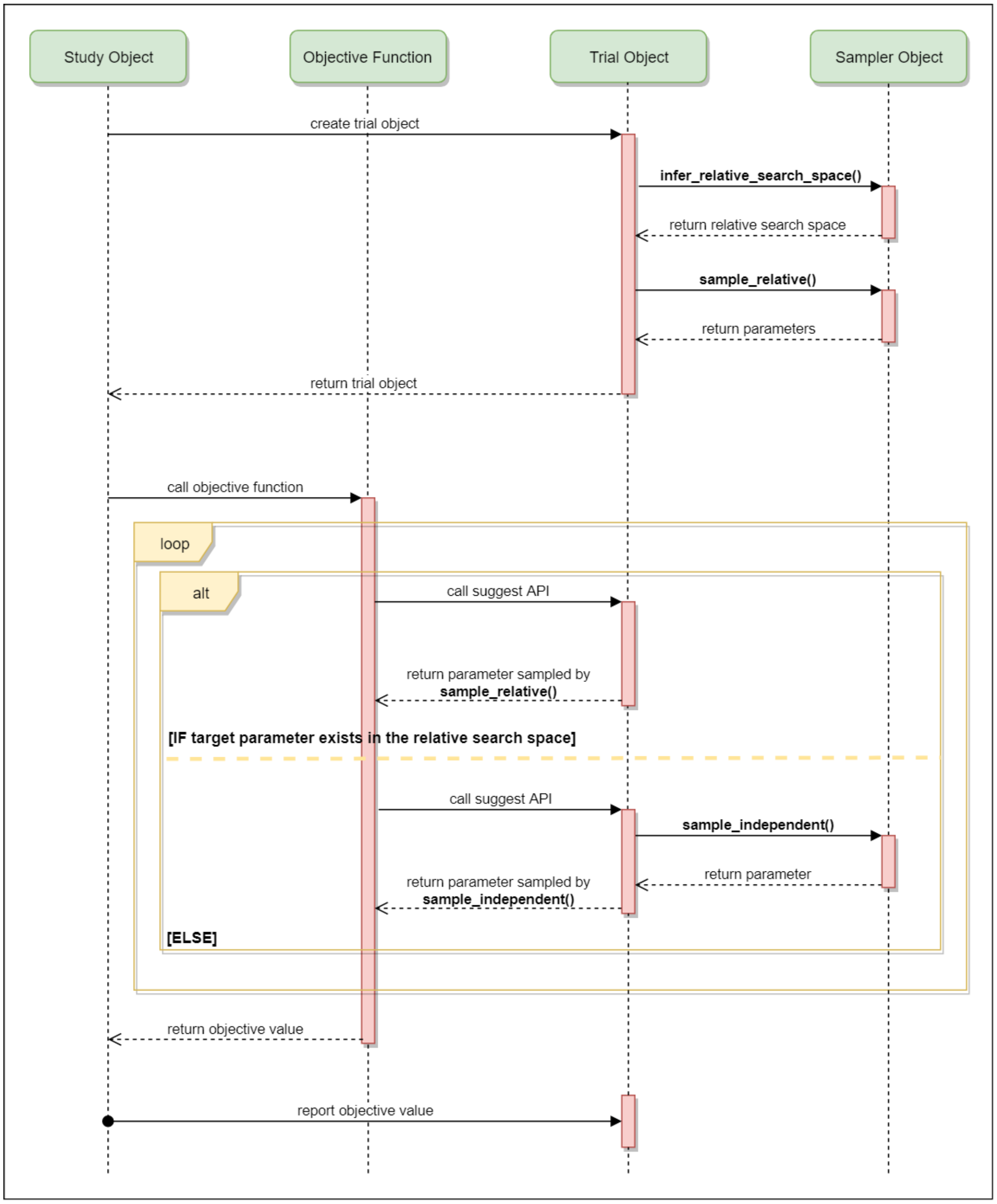
Optuna combines two types of sampling strategies, which are called *relative sampling* and *independent sampling*.

The relative sampling determines values of multiple parameters simultaneously so that sampling algorithms can use relationship between parameters (e.g., correlation). Target parameters of the relative sampling are described in a relative search space, which is determined by `infer_relative_search_space()`.

The independent sampling determines a value of a single parameter without considering any relationship between parameters. Target parameters of the independent sampling are the parameters not described in the relative search space.

More specifically, parameters are sampled by the following procedure. At the beginning of a trial, `infer_relative_search_space()` is called to determine the relative search space for the trial. During the execution of the objective function, `sample_relative()` is called only once when sampling the parameters belonging to the relative search space for the first time. `sample_independent()` is used to sample parameters that don't belong to the relative search space.

The following figure depicts the lifetime of a trial and how the above three methods are called in the trial.


Study Object
Objective Function
Trial Object
Sampler Object
create trial object
infer_relative_search_space()
return relative search space
sample_relative()
return parameters
return trial object
call objective function
loop
alt
call suggest API
return parameter sampled by sample_relative()
[IF target parameter exists in the relative search space]
call suggest API
sample_independent()
return parameter
return parameter sampled by sample_independent()
[ELSE]
return objective value
report objective value

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type
None

abstractmethod infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

abstractmethod sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.

- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

abstractmethod sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns
A dictionary containing the parameter names and the values.

Return type
dict[str, Any]

optuna.samplers.GridSampler

class optuna.samplers.**GridSampler**(*search_space*, *seed=None*)

Sampler using grid search.

With *GridSampler*, the trials suggest all combinations of parameters in the given search space during the study.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_int("y", -100, 100)
    return x**2 + y**2


search_space = {"x": [-50, 0, 50], "y": [-99, 0, 99]}
study = optuna.create_study(sampler=optuna.samplers.GridSampler(search_space))
study.optimize(objective)
```

Note

This sampler with ask_and_tell raises `RuntimeError` just after evaluating the final grid. This is because *GridSampler* automatically stops the optimization if all combinations in the passed `search_space` have already been evaluated, internally invoking the *stop()* method. As a workaround, we need to handle the error manually as in https://github.com/optuna/optuna/issues/4121#issuecomment-1305289910.

Note

GridSampler does not take care of a parameter's quantization specified by discrete suggest methods but just samples one of values specified in the search space. E.g., in the following code snippet, either of `-0.5` or `0.5` is sampled as `x` instead of an integer point.

```python
import optuna


def objective(trial):
    # The following suggest method specifies integer points between -5 and 5.
    x = trial.suggest_float("x", -5, 5, step=1)
    return x**2


# Non-int points are specified in the grid.
search_space = {"x": [-0.5, 0.5]}
study = optuna.create_study(sampler=optuna.samplers.GridSampler(search_space))
study.optimize(objective, n_trials=2)
```

Note

A parameter configuration in the grid is not considered finished until its trial is finished. Therefore, during distributed optimization where trials run concurrently, different workers will occasionally suggest the same parameter configuration. The total number of actual trials may therefore exceed the size of the grid.

Note

All parameters must be specified when using *GridSampler* with *enqueue_trial()*.

Parameters

- **search_space** (*Mapping[str, Sequence[GridValueType]]*) – A dictionary whose key and value are a parameter name and the corresponding candidates of values, respectively.
- **seed** (*int | None*) – A seed to fix the order of trials as the grid is randomly shuffled. This shuffle is beneficial when the number of grids is larger than `n_trials` in `optimize()` to suppress suggesting similar grids. Please note that fixing `seed` for each process is strongly recommended in distributed optimization to avoid duplicated suggestions.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
is_exhausted(study)	Return True if all the possible params are evaluated, otherwise return False.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.

- **trial** (FrozenTrial) – Target trial object.

Return type
None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

> **See also**
>
> Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

is_exhausted(*study*)

Return True if all the possible params are evaluated, otherwise return False.

Parameters
study (Study)

Return type
bool

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

`sample_relative`(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns
A dictionary containing the parameter names and the values.

Return type
dict[str, Any]

optuna.samplers.RandomSampler

`class optuna.samplers.RandomSampler`(*seed=None*)

Sampler using random sampling.

This sampler is based on *independent sampling*. See also *BaseSampler* for more details of 'independent sampling'.

Example

```python
import optuna
from optuna.samplers import RandomSampler


def objective(trial):
    x = trial.suggest_float("x", -5, 5)
    return x**2


study = optuna.create_study(sampler=RandomSampler())
study.optimize(objective, n_trials=10)
```

Parameters
seed (*int* | *None*) – Seed for random number generator.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float]* | *None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type
None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type

None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns

A dictionary containing the parameter names and parameter's distributions.

Return type

dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type

None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*distributions.BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns

A parameter value.

Return type

Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns

A dictionary containing the parameter names and the values.

Return type

dict[str, Any]

optuna.samplers.TPESampler

class optuna.samplers.**TPESampler**(***, *consider_prior=True*, *prior_weight=1.0*, *consider_magic_clip=True*, *consider_endpoints=False*, *n_startup_trials=10*, *n_ei_candidates=24*, *gamma=<function default_gamma>*, *weights=<function default_weights>*, *seed=None*, *multivariate=False*, *group=False*, *warn_independent_sampling=True*, *constant_liar=False*, *constraints_func=None*, *categorical_distance_func=None*)

Sampler using TPE (Tree-structured Parzen Estimator) algorithm.

On each trial, for each parameter, TPE fits one Gaussian Mixture Model (GMM) `l(x)` to the set of parameter values associated with the best objective values, and another GMM `g(x)` to the remaining parameter values. It chooses the parameter value `x` that maximizes the ratio `l(x)/g(x)`.

For further information about TPE algorithm, please refer to the following papers:

- Algorithms for Hyper-Parameter Optimization
- Making a Science of Model Search: Hyperparameter Optimization in Hundreds of Dimensions for Vision Architectures
- Tree-Structured Parzen Estimator: Understanding Its Algorithm Components and Their Roles for Better Empirical Performance

For multi-objective TPE (MOTPE), please refer to the following papers:

- Multiobjective Tree-Structured Parzen Estimator for Computationally Expensive Optimization Problems
- Multiobjective Tree-Structured Parzen Estimator

Please also check our articles:

- Significant Speed Up of Multi-Objective TPESampler in Optuna v4.0.0
- Multivariate TPE Makes Optuna Even More Powerful

Example

An example of a single-objective optimization is as follows:

```python
import optuna
from optuna.samplers import TPESampler


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return x**2


study = optuna.create_study(sampler=TPESampler())
study.optimize(objective, n_trials=10)
```

Note

TPESampler, which became much faster in v4.0.0, c.f. our article, can handle multi-objective optimization with many trials as well. Please note that *NSGAIISampler* will be used by default for multi-objective optimization, so if users would like to use *TPESampler* for multi-objective optimization, `sampler` must be explicitly specified when study is created.

Parameters

- **consider_prior** (*bool*) – Enhance the stability of Parzen estimator by imposing a Gaussian prior when `True`. The prior is only effective if the sampling distribution is either *FloatDistribution*, or *IntDistribution*.

  Warning

  Deprecated in v4.3.0. `consider_prior` argument will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. From v4.3.0 onward, `consider_prior` automatically falls back to `True`. See https://github.com/optuna/optuna/releases/tag/v4.3.0.

- **prior_weight** (*float*) – The weight of the prior. This argument is used in *FloatDistribution*, *IntDistribution*, and *CategoricalDistribution*.
- **consider_magic_clip** (*bool*) – Enable a heuristic to limit the smallest variances of Gaussians used in the Parzen estimator.
- **consider_endpoints** (*bool*) – Take endpoints of domains into account when calculating variances of Gaussians in Parzen estimator. See the original paper for details on the heuristics to calculate the variances.
- **n_startup_trials** (*int*) – The random sampling is used instead of the TPE algorithm until the given number of trials finish in the same study.
- **n_ei_candidates** (*int*) – Number of candidate samples used to calculate the expected improvement.
- **gamma** (*Callable[[int], int]*) – A function that takes the number of finished trials and returns the number of trials to form a density function for samples with low grains. See the original paper for more details.
- **weights** (*Callable[[int], np.ndarray]*) – A function that takes the number of finished trials and returns a weight for them. See Making a Science of Model Search: Hyperparameter Optimization in Hundreds of Dimensions for Vision Architectures for more details.

  Note

  In the multi-objective case, this argument is only used to compute the weights of bad trials, i.e., trials to construct *g(x)* in the paper). The weights of good trials, i.e., trials to construct *l(x)*, are computed by a rule based on the hypervolume contribution proposed in the paper of MOTPE.

- **seed** (*int | None*) – Seed for random number generator.
- **multivariate** (*bool*) – If this is `True`, the multivariate TPE is used when suggesting parameters. The multivariate TPE is reported to outperform the independent TPE. See BOHB: Robust and Efficient Hyperparameter Optimization at Scale and our article for more details.

  Note

  Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

- **group** (*bool*) – If this and multivariate are True, the multivariate TPE with the group decomposed search space is used when suggesting parameters. The sampling algorithm decomposes the search space based on past trials and samples from the joint distribution in each decomposed subspace. The decomposed subspaces are a partition of the whole search space. Each subspace is a maximal subset of the whole search space, which satisfies the following: for a trial in completed trials, the intersection of the subspace and the search space of the trial becomes subspace itself or an empty set. Sampling from the joint distribution on the subspace is realized by multivariate TPE. If group is True, multivariate must be True as well.

  Note

  Added in v2.8.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.8.0.

  Example:

```python
import optuna


def objective(trial):
    x = trial.suggest_categorical("x", ["A", "B"])
    if x == "A":
        return trial.suggest_float("y", -10, 10)
    else:
        return trial.suggest_int("z", -10, 10)


sampler = optuna.samplers.TPESampler(multivariate=True, group=True)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=10)
```

- **warn_independent_sampling** (*bool*) – If this is True and multivariate=True, a warning message is emitted when the value of a parameter is sampled by using an independent sampler. If multivariate=False, this flag has no effect.
- **constant_liar** (*bool*) – If True, penalize running trials to avoid suggesting parameter configurations nearby.

  Note

  Abnormally terminated trials often leave behind a record with a state of RUNNING in the storage. Such “zombie” trial parameters will be avoided by the constant liar algorithm during subsequent sampling. When using an *RDBStorage*, it is possible to enable the heartbeat_interval to change the records for abnormally terminated trials to FAIL.

  Note

  It is recommended to set this value to True during distributed optimization to avoid having multiple workers evaluating similar parameter configurations. In particular, if each objective function evaluation is costly and the durations of the running states are significant, and/or the number of workers is high.

> **Note**
>
> Added in v2.8.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.8.0.

- **constraints_func** (*Callable[[FrozenTrial], Sequence[float]] | None*) – An optional function that computes the objective constraints. It must take a *FrozenTrial* and return the constraints. The return value must be a sequence of `float` s. A value strictly larger than 0 means that a constraints is violated. A value equal to or smaller than 0 is considered feasible. If `constraints_func` returns more than one value for a trial, that trial is considered feasible if and only if all values are equal to 0 or smaller.

  The `constraints_func` will be evaluated after each successful trial. The function won't be called when trials fail or they are pruned, but this behavior is subject to change in the future releases.

  > **Note**
  >
  > Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

- **categorical_distance_func** (*dict[str, Callable[[CategoricalChoiceType, CategoricalChoiceType], float]] | None*) – A dictionary of distance functions for categorical parameters. The key is the name of the categorical parameter and the value is a distance function that takes two `CategoricalChoiceType` s and returns a `float` value. The distance function must return a non-negative value.

  While categorical choices are handled equally by default, this option allows users to specify prior knowledge on the structure of categorical parameters. When specified, categorical choices closer to current best choices are more likely to be sampled.

  > **Note**
  >
  > Added in v3.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.4.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
hyperopt_parameters()	Return the the default parameters of hyperopt (v0.1.2).
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.

continues on next page

Table 33 – continued from previous page

sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type
None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type
None

static hyperopt_parameters()

Return the the default parameters of hyperopt (v0.1.2).

TPESampler can be instantiated with the parameters returned by this method.

Example

Create a *TPESampler* instance with the default parameters of hyperopt.

```
import optuna
from optuna.samplers import TPESampler


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return x**2


sampler = TPESampler(**TPESampler.hyperopt_parameters())
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=10)
```

Returns
A dictionary containing the default parameters of hyperopt.

Return type
dict[str, *Any*]

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns

A parameter value.

Return type

Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns

A dictionary containing the parameter names and the values.

Return type

dict[str, Any]

optuna.samplers.CmaEsSampler

class optuna.samplers.**CmaEsSampler**(*x0=None*, *sigma0=None*, *n_startup_trials=1*, *independent_sampler=None*, *warn_independent_sampling=True*, *seed=None*, ***, *consider_pruned_trials=False*, *restart_strategy=None*, *popsize=None*, *inc_popsize=-1*, *use_separable_cma=False*, *with_margin=False*, *lr_adapt=False*, *source_trials=None*)

A sampler using cmaes as the backend.

Example

Optimize a simple quadratic function by using *CmaEsSampler*.

```
$ pip install cmaes
```

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    y = trial.suggest_int("y", -1, 1)
    return x**2 + y


sampler = optuna.samplers.CmaEsSampler()
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=20)
```

Please note that this sampler does not support CategoricalDistribution. However, *FloatDistribution* with step, (*suggest_float()*) and *IntDistribution* (*suggest_int()*) are supported.

If your search space contains categorical parameters, I recommend you to use *TPESampler* instead. Furthermore, there is room for performance improvements in parallel optimization settings. This sampler cannot use some trials for updating the parameters of multivariate normal distribution.

For further information about CMA-ES algorithm, please refer to the following papers:

- N. Hansen, The CMA Evolution Strategy: A Tutorial. arXiv:1604.00772, 2016.
- A. Auger and N. Hansen. A restart CMA evolution strategy with increasing population size. In Proceedings of the IEEE Congress on Evolutionary Computation (CEC 2005), pages 1769–1776. IEEE Press, 2005.
- N. Hansen. Benchmarking a BI-Population CMA-ES on the BBOB-2009 Function Testbed. GECCO Workshop, 2009.
- Raymond Ros, Nikolaus Hansen. A Simple Modification in CMA-ES Achieving Linear Time and Space Complexity. 10th International Conference on Parallel Problem Solving From Nature, Sep 2008, Dortmund, Germany. inria-00287367.
- Masahiro Nomura, Shuhei Watanabe, Youhei Akimoto, Yoshihiko Ozaki, Masaki Onishi. Warm Starting CMA-ES for Hyperparameter Optimization, AAAI. 2021.
- R. Hamano, S. Saito, M. Nomura, S. Shirakawa. CMA-ES with Margin: Lower-Bounding Marginal Probability for Mixed-Integer Black-Box Optimization, GECCO. 2022.
- M. Nomura, Y. Akimoto, I. Ono. CMA-ES with Learning Rate Adaptation: Can CMA-ES with Default Population Size Solve Multimodal and Noisy Problems?, GECCO. 2023.

See also

You can also use optuna_integration.PyCmaSampler which is a sampler using cma library as the backend.

Parameters

- **x0** (*dict[str, Any] | None*) – A dictionary of an initial parameter values for CMA-ES. By default, the mean of `low` and `high` for each distribution is used. Note that `x0` is sampled uniformly within the search space domain for each restart if you specify `restart_strategy` argument.
- **sigma0** (*float | None*) – Initial standard deviation of CMA-ES. By default, `sigma0` is set to `min_range / 6`, where `min_range` denotes the minimum range of the distributions in the search space.
- **seed** (*int | None*) – A random seed for CMA-ES.
- **n_startup_trials** (*int*) – The independent sampling is used instead of the CMA-ES algorithm until the given number of trials finish in the same study.
- **independent_sampler** (BaseSampler *| None*) – A *BaseSampler* instance that is used for independent sampling. The parameters not contained in the relative search space are sampled by this sampler. The search space for *CmaEsSampler* is determined by *intersection_search_space()*.

  If `None` is specified, *RandomSampler* is used as the default.

  See also

  optuna.samplers module provides built-in independent samplers such as *RandomSampler* and *TPESampler*.

- **warn_independent_sampling** (*bool*) – If this is `True`, a warning message is emitted when the value of a parameter is sampled by using an independent sampler.

  Note that the parameters of the first trial in a study are always sampled via an independent sampler, so no warning messages are emitted in this case.

- **restart_strategy** (*str | None*) – Strategy for restarting CMA-ES optimization when converges to a local minimum. If `None` is given, CMA-ES will not restart (default). If 'ipop' is given, CMA-ES will restart with increasing population size. if 'bipop' is given, CMA-ES will restart with the population size increased or decreased. Please see also `inc_popsize` parameter.

  Warning

  Deprecated in v4.4.0. `restart_strategy` argument will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. From v4.4.0 onward, `restart_strategy` automatically falls back to `None`, and `restart_strategy` will be supported in OptunaHub. See https://github.com/optuna/optuna/releases/tag/v4.4.0.

- **popsize** (*int | None*) – A population size of CMA-ES.

- **inc_popsize** (*int*) – Multiplier for increasing population size before each restart. This argument will be used when `restart_strategy = 'ipop'` or `restart_strategy = 'bipop'` is specified.

  Warning

  Deprecated in v4.4.0. `inc_popsize` argument will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. From v4.4.0 onward, `inc_popsize` is no longer utilized within Optuna, and `inc_popsize` will be supported in OptunaHub. See https://github.com/optuna/optuna/releases/tag/v4.4.0.

- **consider_pruned_trials** (*bool*) – If this is `True`, the PRUNED trials are considered for sampling.

  Note

  Added in v2.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.0.0.

  Note

  It is suggested to set this flag `False` when the *MedianPruner* is used. On the other hand, it is suggested to set this flag `True` when the *HyperbandPruner* is used. Please see the benchmark result for the details.

- **use_separable_cma** (*bool*) – If this is `True`, the covariance matrix is constrained to be diagonal. Due to reduce the model complexity, the learning rate for the covariance matrix is increased. Consequently, this algorithm outperforms CMA-ES on separable functions.

  Note

  Added in v2.6.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.6.0.

- **with_margin** (*bool*) – If this is `True`, CMA-ES with margin is used. This algorithm prevents samples in each discrete distribution (*FloatDistribution* with `step` and *IntDistribution*) from being fixed to a single point. Currently, this option cannot be used with `use_separable_cma=True`.

  Note

  Added in v3.1.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

- **lr_adapt** (*bool*) – If this is `True`, CMA-ES with learning rate adaptation is used. This algorithm focuses on working well on multimodal and/or noisy problems with default settings. Currently, this option cannot be used with `use_separable_cma=True` or `with_margin=True`.

> **Note**
>
> Added in v3.3.0 or later, as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

- **source_trials** (*list*[FrozenTrial] *| None*) – This option is for Warm Starting CMA-ES, a method to transfer prior knowledge on similar HPO tasks through the initialization of CMA-ES. This method estimates a promising distribution from `source_trials` and generates the parameter of multivariate gaussian distribution. Please note that it is prohibited to use `x0`, `sigma0`, or `use_separable_cma` argument together.

> **Note**
>
> Added in v2.6.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.6.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

> **Note**
>
> Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be `None` if trial succeeded.

Return type
None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type
None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, *BaseDistribution*]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns
A dictionary containing the parameter names and the values.

Return type
dict[str, *Any*]

optuna.samplers.GPSampler

class `optuna.samplers.GPSampler`(**, seed=None, independent_sampler=None, n_startup_trials=10, deterministic_objective=False, constraints_func=None, warn_independent_sampling=True*)

Sampler using Gaussian process-based Bayesian optimization.

This sampler fits a Gaussian process (GP) to the objective function and optimizes the acquisition function to suggest the next parameters.

The current implementation uses Matern kernel with nu=2.5 (twice differentiable) with automatic relevance determination (ARD) for the length scale of each parameter. The hyperparameters of the kernel are obtained by maximizing the marginal log-likelihood of the hyperparameters given the past trials. To prevent overfitting, Gamma prior is introduced for kernel scale and noise variance and a hand-crafted prior is introduced for inverse squared lengthscales.

As an acquisition function, we use:

- log expected improvement (logEI) for single-objective optimization,
- log expected hypervolume improvement (logEHVI) for Multi-objective optimization, and
- the summation of logEI and the logarithm of the feasible probability with the independent assumption of each constraint for (black-box inequality) constrained optimization.

For further information about these acquisition functions, please refer to the following papers:

- Unexpected Improvements to Expected Improvement for Bayesian Optimization
- Differentiable Expected Hypervolume Improvement for Parallel Multi-Objective Bayesian Optimization
- Bayesian Optimization with Inequality Constraints

The optimization of the acquisition function is performed via:

1. Collect the best param from the past trials,
2. Collect `n_preliminary_samples` points using Quasi-Monte Carlo (QMC) sampling,
3. Choose the best point from the collected points,
4. Choose `n_local_search - 2` points from the collected points using the roulette selection,
5. Perform a local search for each chosen point as an initial point, and
6. Return the point with the best acquisition function value as the next parameter.

Note that the procedures for non single-objective optimization setups are slightly different from the single-objective version described above, but we omit the descriptions for the others for brevity.

The local search iteratively optimizes the acquisition function by repeating:

1. Gradient ascent using l-BFGS-B for continuous parameters, and
2. Line search or exhaustive search for each discrete parameter independently.

The local search is terminated if the routine stops updating the best parameter set or the maximum number of iterations is reached.

We use line search instead of rounding the results from the continuous optimization since EI typically yields a high value between one grid and its adjacent grid.

Note

This sampler requires `scipy` and `torch`. You can install these dependencies with `pip install scipy torch`.

Parameters

- **seed** (*int | None*) – Random seed to initialize internal random number generator. Defaults to `None` (a seed is picked randomly).
- **independent_sampler** (`BaseSampler` *| None*) – Sampler used for initial sampling (for the first `n_startup_trials` trials) and for conditional parameters. Defaults to `None` (a random sampler with the same `seed` is used).
- **n_startup_trials** (*int*) – Number of initial trials. Defaults to 10.
- **deterministic_objective** (*bool*) – Whether the objective function is deterministic or not. If `True`, the sampler will fix the noise variance of the surrogate model to the minimum value (slightly above 0 to ensure numerical stability). Defaults to `False`. Currently, all the objectives will be assume to be deterministic if `True`.
- **constraints_func** (*Callable[[*`FrozenTrial`*], Sequence[float]] | None*) – An optional function that computes the objective constraints. It must take a *`FrozenTrial`* and return the constraints. The return value must be a sequence of `float` s. A value strictly larger than 0 means that a constraints is violated. A value equal to or smaller than 0 is considered feasible. If `constraints_func` returns more than one value for a trial, that trial is considered feasible if and only if all values are equal to 0 or smaller.

  The `constraints_func` will be evaluated after each successful trial. The function won't be called when trials fail or are pruned, but this behavior is subject to change in future releases. Currently, the `constraints_func` option is not supported for multi-objective optimization.
- **warn_independent_sampling** (*bool*) – If this is `True`, a warning message is emitted when the value of a parameter is sampled by using an independent sampler, meaning that no GP model is used in the sampling. Note that the parameters of the first trial in a study are always sampled via an independent sampler, so no warning messages are emitted in this case.

Note

Added in v3.6.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.6.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type

None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.

- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns
A dictionary containing the parameter names and the values.

Return type
dict[str, Any]

optuna.samplers.PartialFixedSampler

class optuna.samplers.**PartialFixedSampler**(*fixed_params*, *base_sampler*)

Sampler with partially fixed parameters.

Example

After several steps of optimization, you can fix the value of y and re-optimize it.

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    y = trial.suggest_int("y", -1, 1)
    return x**2 + y


study = optuna.create_study()
study.optimize(objective, n_trials=10)

best_params = study.best_params
fixed_params = {"y": best_params["y"]}
partial_sampler = optuna.samplers.PartialFixedSampler(fixed_params, study.sampler)

study.sampler = partial_sampler
study.optimize(objective, n_trials=10)
```

Parameters

- **fixed_params** (*dict[str, Any]*) – A dictionary of parameters to be fixed.

- **base_sampler** (BaseSampler) – A sampler which samples unfixed parameters.

> **Note**
>
> Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

> **Note**
>
> Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type

None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns

A dictionary containing the parameter names and parameter's distributions.

Return type

dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type

None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns

A parameter value.

Return type

Any

`sample_relative`(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns

A dictionary containing the parameter names and the values.

Return type

dict[str, Any]

optuna.samplers.NSGAIISampler

class optuna.samplers.**NSGAIISampler**(***, *population_size=50*, *mutation_prob=None*, *crossover=None*, *crossover_prob=0.9*, *swapping_prob=0.5*, *seed=None*, *constraints_func=None*, *elite_population_selection_strategy=None*, *child_generation_strategy=None*, *after_trial_strategy=None*)

Multi-objective sampler using the NSGA-II algorithm.

NSGA-II stands for "Nondominated Sorting Genetic Algorithm II", which is a well known, fast and elitist multi-objective genetic algorithm.

For further information about NSGA-II, please refer to the following paper:

- A fast and elitist multiobjective genetic algorithm: NSGA-II

Note

TPESampler became much faster in v4.0.0 and supports several features not supported by `NSGAIISampler` such as handling of dynamic search space and categorical distance. To use *TPESampler*, you need to explicitly specify the sampler as follows:

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    f1 = x**2 + y
    f2 = -((x - 2) ** 2 + y)
    return f1, f2


# We minimize the first objective and maximize the second objective.
sampler = optuna.samplers.TPESampler()
study = optuna.create_study(directions=["minimize", "maximize"], sampler=sampler)
study.optimize(objective, n_trials=100)
```

Please also check our article for more details of the speedup in v4.0.0.

Parameters

- **population_size** (*int*) – Number of individuals (trials) in a generation. `population_size` must be greater than or equal to `crossover.n_parents`. For *UNDXCrossover* and *SPXCrossover*, `n_parents=3`, and for the other algorithms, `n_parents=2`.
- **mutation_prob** (*float | None*) – Probability of mutating each parameter when creating a new individual. If `None` is specified, the value `1.0 / len(parent_trial.params)` is used where `parent_trial` is the parent trial of the target individual.
- **crossover** (`BaseCrossover` *| None*) – Crossover to be applied when creating child individuals. The available crossovers are listed here: https://optuna.readthedocs.io/en/stable/reference/samplers/nsgaii.html.

  UniformCrossover is always applied to parameters sampled from *CategoricalDistribution*, and by default for parameters sampled from other distributions unless this argument is specified.

  For more information on each of the crossover method, please refer to specific crossover documentation.
- **crossover_prob** (*float*) – Probability that a crossover (parameters swapping between parents) will occur when creating a new individual.
- **swapping_prob** (*float*) – Probability of swapping each parameter of the parents during crossover.

- **seed** (*int | None*) – Seed for random number generator.
- **constraints_func** (*Callable[[FrozenTrial], Sequence[float]] | None*) – An optional function that computes the objective constraints. It must take a `FrozenTrial` and return the constraints. The return value must be a sequence of `float` s. A value strictly larger than 0 means that a constraints is violated. A value equal to or smaller than 0 is considered feasible. If `constraints_func` returns more than one value for a trial, that trial is considered feasible if and only if all values are equal to 0 or smaller.

  The `constraints_func` will be evaluated after each successful trial. The function won't be called when trials fail or they are pruned, but this behavior is subject to change in the future releases.

  The constraints are handled by the constrained domination. A trial x is said to constrained-dominate a trial y, if any of the following conditions is true:

  1. Trial x is feasible and trial y is not.
  2. Trial x and y are both infeasible, but trial x has a smaller overall violation.
  3. Trial x and y are feasible and trial x dominates trial y.

  Note

  Added in v2.5.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.5.0.

- **elite_population_selection_strategy** (*Callable[[Study, list[FrozenTrial]], list[FrozenTrial]] | None*) – The selection strategy for determining the individuals to survive from the current population pool. Default to `None`.

  Note

  The arguments `elite_population_selection_strategy` was added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

- **child_generation_strategy** (*Callable[[Study, dict[str, BaseDistribution], list[FrozenTrial]], dict[str, Any]] | None*) – The strategy for generating child parameters from parent trials. Defaults to `None`.

  Note

  The arguments `child_generation_strategy` was added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

- **after_trial_strategy** (*Callable[[Study, FrozenTrial, TrialState, Sequence[float] | None], None] | None*) – A set of procedure to be conducted after each trial. Defaults to `None`.

Note

The arguments `after_trial_strategy` was added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
get_parent_population(study, generation)	Get the parent population of the given generation.
get_population(study, generation)	Get the population of the given generation.
get_trial_generation(study, trial)	Get the generation number of the given trial.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.
select_parent(study, generation)	Select parent trials from the population for the given generation.

Attributes

`population_size`

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (`Study`) – Target study object.
- **trial** (`FrozenTrial`) – Target trial object. Take a copy before modifying this object.
- **state** (`TrialState`) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be `None` if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the `infer_relative_search_space()` call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (`Study`) – Target study object.
- **trial** (`FrozenTrial`) – Target trial object.

Return type

None

get_parent_population(*study*, *generation*)

Get the parent population of the given generation.

This method caches the parent population in the study's system attributes.

Parameters

- **study** (`Study`) – Target study object.
- **generation** (*int*) – Target generation number.

Returns

List of parent frozen trials. If *generation == 0*, returns an empty list.

Return type

list[FrozenTrial]

get_population(*study*, *generation*)

Get the population of the given generation.

Parameters

- **study** (`Study`) – Target study object.
- **generation** (*int*) – Target generation number.

Returns

List of frozen trials in the given generation.

Return type

list[FrozenTrial]

get_trial_generation(*study*, *trial*)

Get the generation number of the given trial.

This method returns the generation number of the specified trial. If the generation number is not set in the trial's system attributes, it will calculate and set the generation number.

The current generation number depends on the maximum generation number of all completed trials.

Parameters

- **study** (Study) – Study object which trial belongs to.
- **trial** (FrozenTrial) – Trial object to get the generation number.

Returns
Generation number of the given trial.

Return type
int

`infer_relative_search_space`(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before `sample_relative()` method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using `sample_independent()` method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

See also

Please refer to `intersection_search_space()` as an implementation of `infer_relative_search_space()`.

`reseed_rng`()

Reseed sampler's random number generator.

This method is called by the `Study` instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

`sample_independent`(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by `sample_relative()` method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns
A dictionary containing the parameter names and the values.

Return type
dict[str, Any]

select_parent(*study*, *generation*)

Select parent trials from the population for the given generation.

This method is called once per generation to select parents from the population of the current generation.

Output of this function is cached in the study system attributes.

This method must be implemented in a subclass to define the specific selection strategy.

Parameters

- **study** (Study) – Target study object.
- **generation** (*int*) – Target generation number.

Returns
List of parent frozen trials.

Return type
list[*FrozenTrial*]

optuna.samplers.NSGAIIISampler

`class optuna.samplers.NSGAIIISampler(*, population_size=50, mutation_prob=None, crossover=None, crossover_prob=0.9, swapping_prob=0.5, seed=None, constraints_func=None, reference_points=None, dividing_parameter=3, elite_population_selection_strategy=None, child_generation_strategy=None, after_trial_strategy=None)`

Multi-objective sampler using the NSGA-III algorithm.

NSGA-III stands for "Nondominated Sorting Genetic Algorithm III", which is a modified version of NSGA-II for many objective optimization problem.

For further information about NSGA-III, please refer to the following papers:

- An Evolutionary Many-Objective Optimization Algorithm Using Reference-Point-Based Nondominated Sorting Approach, Part I: Solving Problems With Box Constraints
- An Evolutionary Many-Objective Optimization Algorithm Using Reference-Point-Based Nondominated Sorting Approach, Part II: Handling Constraints and Extending to an Adaptive Approach

Parameters

- **reference_points** (*np.ndarray | None*) – A 2 dimension `numpy.ndarray` with objective dimension columns. Represents a list of reference points which is used to determine who to survive. After non-dominated sort, who out of borderline front are going to survived is determined according to how sparse the closest reference point of each individual is. In the default setting the algorithm uses *uniformly* spread points to diversify the result. It is also possible to reflect your *preferences* by giving an arbitrary set of *target* points since the algorithm prioritizes individuals around reference points.
- **dividing_parameter** (*int*) – A parameter to determine the density of default reference points. This parameter determines how many divisions are made between reference points on each axis. The smaller this value is, the less reference points you have. The default value is 3. Note that this parameter is not used when `reference_points` is not `None`.
- **population_size** (*int*)
- **mutation_prob** (*float | None*)
- **crossover** (*BaseCrossover | None*)
- **crossover_prob** (*float*)
- **swapping_prob** (*float*)
- **seed** (*int | None*)
- **constraints_func** (*Callable[[FrozenTrial], Sequence[float]] | None*)
- **elite_population_selection_strategy** (*Callable[[Study, list[FrozenTrial]], list[FrozenTrial]] | None*)
- **child_generation_strategy** (*Callable[[Study, dict[str, BaseDistribution], list[FrozenTrial]], dict[str, Any]] | None*)
- **after_trial_strategy** (*Callable[[Study, FrozenTrial, TrialState, Sequence[float] | None], None] | None*)

Note

Other parameters than `reference_points` and `dividing_parameter` are the same as *NSGAIISampler*.

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (`Study`) – Target study object.
- **trial** (`FrozenTrial`) – Target trial object. Take a copy before modifying this object.
- **state** (`TrialState`) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be `None` if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type
None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (`Study`) – Target study object.
- **trial** (`FrozenTrial`) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (`Study`) – Target study object.
- **trial** (`FrozenTrial`) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns
A dictionary containing the parameter names and the values.

Return type
dict[str, Any]

optuna.samplers.QMCSampler

class optuna.samplers.**QMCSampler**(*, *qmc_type='sobol'*, *scramble=False*, *seed=None*, *independent_sampler=None*, *warn_asynchronous_seeding=True*, *warn_independent_sampling=True*)

A Quasi Monte Carlo Sampler that generates low-discrepancy sequences.

Quasi Monte Carlo (QMC) sequences are designed to have lower discrepancies than standard random sequences. They are known to perform better than the standard random sequences in hyperparameter optimization.

For further information about the use of QMC sequences for hyperparameter optimization, please refer to the following paper:

- Bergstra, James, and Yoshua Bengio. Random search for hyper-parameter optimization. Journal of machine learning research 13.2, 2012.

We use the QMC implementations in Scipy. For the details of the QMC algorithm, see the Scipy API references on scipy.stats.qmc.

Note

The search space of the sampler is determined by either previous trials in the study or the first trial that this sampler samples.

If there are previous trials in the study, `QMCSampler` infers its search space using the trial which was created first in the study.

Otherwise (if the study has no previous trials), `QMCSampler` samples the first trial using its *independent_sampler* and then infers the search space in the second trial.

As mentioned above, the search space of the `QMCSampler` is determined by the first trial of the study. Once the search space is determined, it cannot be changed afterwards.

Parameters

- **qmc_type** (*str*) – The type of QMC sequence to be sampled. This must be one of *"halton"* and *"sobol"*. Default is *"sobol"*.

  Note

  Sobol' sequence is designed to have low-discrepancy property when the number of samples is $n = 2^m$ for each positive integer m. When it is possible to pre-specify the number of trials suggested by *QMCSampler*, it is recommended that the number of trials should be set as power of two.

- **scramble** (*bool*) – If this option is `True`, scrambling (randomization) is applied to the QMC sequences.
- **seed** (*int | None*) – A seed for `QMCSampler`. This argument is used only when `scramble` is `True`. If this is `None`, the seed is initialized randomly. Default is `None`.

  Note

  When using multiple `QMCSampler`'s in parallel and/or distributed optimization, all the samplers must share the same seed when the *scrambling* is enabled. Otherwise, the low-discrepancy property of the samples will be degraded.

- **independent_sampler** (`BaseSampler` *| None*) – A `BaseSampler` instance that is used for independent sampling. The first trial of the study and the parameters not contained in the relative search space are sampled by this sampler.

  If `None` is specified, `RandomSampler` is used as the default.

See also

samplers module provides built-in independent samplers such as *RandomSampler* and *TPESampler*.

- **warn_independent_sampling** (*bool*) – If this is `True`, a warning message is emitted when the value of a parameter is sampled by using an independent sampler.

  Note that the parameters of the first trial in a study are sampled via an independent sampler in most cases, so no warning messages are emitted in such cases.

- **warn_asynchronous_seeding** (*bool*) – If this is `True`, a warning message is emitted when the scrambling (randomization) is applied to the QMC sequence and the random seed of the sampler is not set manually.

Note

When using parallel and/or distributed optimization without manually setting the seed, the seed is set randomly for each instances of *QMCSampler* for different workers, which ends up asynchronous seeding for multiple samplers used in the optimization.

See also

See parameter `seed` in *QMCSampler*.

Example

Optimize a simple quadratic function by using *QMCSampler*.

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    y = trial.suggest_int("y", -1, 1)
    return x**2 + y


sampler = optuna.samplers.QMCSampler()
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=8)
```

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (optuna.trial.FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type
None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option n_jobs>1. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.

- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns
A dictionary containing the parameter names and the values.

Return type
dict[str, Any]

optuna.samplers.BruteForceSampler

class optuna.samplers.**BruteForceSampler**(*seed=None*, *avoid_premature_stop=False*)

Sampler using brute force.

This sampler performs exhaustive search on the defined search space.

Example

```python
import optuna


def objective(trial):
    c = trial.suggest_categorical("c", ["float", "int"])
    if c == "float":
        return trial.suggest_float("x", 1, 3, step=0.5)
    elif c == "int":
        a = trial.suggest_int("a", 1, 3)
        b = trial.suggest_int("b", a, 3)
        return a + b
```

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```


study = optuna.create_study(sampler=optuna.samplers.BruteForceSampler())
study.optimize(objective)
```

Note

The defined search space must be finite. Therefore, when using *FloatDistribution* or *suggest_float()*, `step=None` is not allowed.

Note

The sampler may fail to try the entire search space in when the suggestion ranges or parameters are changed in the same *Study*.

Parameters

- **seed** (*int | None*) – A seed to fix the order of trials as the search order randomly shuffled. Please note that it is not recommended using this option in distributed optimization settings since this option cannot ensure the order of trials and may increase the number of duplicate suggestions during distributed optimization.
- **avoid_premature_stop** (*bool*) – If `True`, the sampler performs a strict exhaustive search. Please note that enabling this option may increase the likelihood of duplicate sampling. When this option is not enabled (default), the sampler applies a looser criterion for determining when to stop the search, which may result in incomplete coverage of the search space. For more information, see https://github.com/optuna/optuna/issues/5780.

Note

Added in v3.1.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

Methods

after_trial(study, trial, state, values)	Trial post-processing.
before_trial(study, trial)	Trial pre-processing.
infer_relative_search_space(study, trial)	Infer the search space that will be used by relative sampling in the target trial.
reseed_rng()	Reseed sampler's random number generator.
sample_independent(study, trial, param_name, ...)	Sample a parameter for a given distribution.
sample_relative(study, trial, search_space)	Sample parameters in a given search space.

after_trial(*study*, *trial*, *state*, *values*)

Trial post-processing.

This method is called after the objective function returns and right before the trial is finished and its state is stored.

Note

Added in v2.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.4.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **state** (TrialState) – Resulting trial state.
- **values** (*Sequence[float] | None*) – Resulting trial values. Guaranteed to not be None if trial succeeded.

Return type

None

before_trial(*study*, *trial*)

Trial pre-processing.

This method is called before the objective function is called and right after the trial is instantiated. More precisely, this method is called during trial initialization, just before the *infer_relative_search_space()* call. In other words, it is responsible for pre-processing that should be done before inferring the search space.

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object.

Return type

None

infer_relative_search_space(*study*, *trial*)

Infer the search space that will be used by relative sampling in the target trial.

This method is called right before *sample_relative()* method, and the search space returned by this method is passed to it. The parameters not contained in the search space will be sampled by using *sample_independent()* method.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.

Returns
A dictionary containing the parameter names and parameter's distributions.

Return type
dict[str, BaseDistribution]

See also

Please refer to *intersection_search_space()* as an implementation of *infer_relative_search_space()*.

reseed_rng()

Reseed sampler's random number generator.

This method is called by the *Study* instance if trials are executed in parallel with the option `n_jobs>1`. In that case, the sampler instance will be replicated including the state of the random number generator, and they may suggest the same values. To prevent this issue, this method assigns a different seed to each random number generator.

Return type
None

sample_independent(*study*, *trial*, *param_name*, *param_distribution*)

Sample a parameter for a given distribution.

This method is called only for the parameters not contained in the search space returned by *sample_relative()* method. This method is suitable for sampling algorithms that do not use relationship between parameters such as random sampling and TPE.

Note

The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (`Study`) – Target study object.
- **trial** (`FrozenTrial`) – Target trial object. Take a copy before modifying this object.
- **param_name** (*str*) – Name of the sampled parameter.
- **param_distribution** (*BaseDistribution*) – Distribution object that specifies a prior and/or scale of the sampling algorithm.

Returns
A parameter value.

Return type
Any

sample_relative(*study*, *trial*, *search_space*)

Sample parameters in a given search space.

This method is called once at the beginning of each trial, i.e., right before the evaluation of the objective function. This method is suitable for sampling algorithms that use relationship between parameters such as Gaussian Process and CMA-ES.

> **Note**
>
> The failed trials are ignored by any build-in samplers when they sample new parameters. Thus, failed trials are regarded as deleted in the samplers' perspective.

Parameters

- **study** (Study) – Target study object.
- **trial** (FrozenTrial) – Target trial object. Take a copy before modifying this object.
- **search_space** (*dict[str, BaseDistribution]*) – The search space returned by *infer_relative_search_space()*.

Returns

A dictionary containing the parameter names and the values.

Return type

dict[str, Any]

> **Note**
>
> The following *optuna.samplers.nsgaii* module defines crossover operations used by *NSGAIISampler*.

optuna.samplers.nsgaii

The *nsgaii* module defines crossover operations used by *NSGAIISampler*.

BaseCrossover	Base class for crossovers.
UniformCrossover	Uniform Crossover operation used by *NSGAIISampler*.
BLXAlphaCrossover	Blend Crossover operation used by *NSGAIISampler*.
SPXCrossover	Simplex Crossover operation used by *NSGAIISampler*.
SBXCrossover	Simulated Binary Crossover operation used by *NSGAIISampler*.
VSBXCrossover	Modified Simulated Binary Crossover operation used by *NSGAIISampler*.
UNDXCrossover	Unimodal Normal Distribution Crossover used by *NSGAIISampler*.

optuna.samplers.nsgaii.BaseCrossover

class optuna.samplers.nsgaii.**BaseCrossover**

Base class for crossovers.

A crossover operation is used by *NSGAIISampler* to create new parameter combination from parameters of `n` parent individuals.

> **Note**
>
> Concrete implementations of this class are expected to only accept parameters from numerical distributions. At the moment, only crossover operation for categorical parameters (uniform crossover) is built-in into *NSGAIISampler*.

Methods

crossover(parents_params, rng, study, ...)	Perform crossover of selected parent individuals.

Attributes

n_parents	Number of parent individuals required to perform crossover.

abstractmethod crossover(*parents_params*, *rng*, *study*, *search_space_bounds*)

Perform crossover of selected parent individuals.

This method is called in *sample_relative()*.

Parameters

- **parents_params** (*np.ndarray*) – A numpy.ndarray with dimensions num_parents x num_parameters. Represents a parameter space for each parent individual. This space is continuous for numerical parameters.
- **rng** (*np.random.RandomState*) – An instance of numpy.random.RandomState.
- **study** (Study) – Target study object.
- **search_space_bounds** (*np.ndarray*) – A numpy.ndarray with dimensions len_search_space x 2 representing numerical distribution bounds constructed from transformed search space.

Returns

A 1-dimensional numpy.ndarray containing new parameter combination.

Return type

np.ndarray

abstract property n_parents: int

Number of parent individuals required to perform crossover.

optuna.samplers.nsgaii.UniformCrossover

class optuna.samplers.nsgaii.**UniformCrossover**(*swapping_prob=0.5*)

Uniform Crossover operation used by *NSGAIISampler*.

Select each parameter with equal probability from the two parent individuals. For further information about uniform crossover, please refer to the following paper:

- Gilbert Syswerda. 1989. Uniform Crossover in Genetic Algorithms. In Proceedings of the 3rd International Conference on Genetic Algorithms. Morgan Kaufmann Publishers Inc., San Francisco, CA, USA, 2-9.

Parameters

swapping_prob (*float*) – Probability of swapping each parameter of the parents during crossover.

Methods

crossover(parents_params, rng, study, ...)	Perform crossover of selected parent individuals.

Attributes

`n_parents`

crossover(*parents_params*, *rng*, *study*, *search_space_bounds*)

Perform crossover of selected parent individuals.

This method is called in *sample_relative()*.

Parameters

- **parents_params** (*np.ndarray*) – A `numpy.ndarray` with dimensions `num_parents x num_parameters`. Represents a parameter space for each parent individual. This space is continuous for numerical parameters.
- **rng** (*np.random.RandomState*) – An instance of `numpy.random.RandomState`.
- **study** (Study) – Target study object.
- **search_space_bounds** (*np.ndarray*) – A `numpy.ndarray` with dimensions `len_search_space x 2` representing numerical distribution bounds constructed from transformed search space.

Returns

A 1-dimensional `numpy.ndarray` containing new parameter combination.

Return type

np.ndarray

optuna.samplers.nsgaii.BLXAlphaCrossover

class optuna.samplers.nsgaii.**BLXAlphaCrossover**(*alpha=0.5*)

Blend Crossover operation used by *NSGAIISampler*.

Uniformly samples child individuals from the hyper-rectangles created by the two parent individuals. For further information about BLX-alpha crossover, please refer to the following paper:

- Eshelman, L. and J. D. Schaffer. Real-Coded Genetic Algorithms and Interval-Schemata. FOGA (1992).

Parameters

alpha (*float*) – Parametrizes blend operation.

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Methods

crossover(parents_params, rng, study, ...)	Perform crossover of selected parent individuals.

Attributes

`n_parents`

crossover(*parents_params*, *rng*, *study*, *search_space_bounds*)

Perform crossover of selected parent individuals.

This method is called in *sample_relative()*.

Parameters

- **parents_params** (*np.ndarray*) – A `numpy.ndarray` with dimensions `num_parents x num_parameters`. Represents a parameter space for each parent individual. This space is continuous for numerical parameters.
- **rng** (*np.random.RandomState*) – An instance of `numpy.random.RandomState`.
- **study** (Study) – Target study object.
- **search_space_bounds** (*np.ndarray*) – A `numpy.ndarray` with dimensions `len_search_space x 2` representing numerical distribution bounds constructed from transformed search space.

Returns

A 1-dimensional `numpy.ndarray` containing new parameter combination.

Return type

np.ndarray

optuna.samplers.nsgaii.SPXCrossover

class `optuna.samplers.nsgaii.`**SPXCrossover**(*epsilon=None*)

Simplex Crossover operation used by *NSGAIISampler*.

Uniformly samples child individuals from within a single simplex that is similar to the simplex produced by the parent individual. For further information about SPX crossover, please refer to the following paper:

- Shigeyoshi Tsutsui and Shigeyoshi Tsutsui and David E. Goldberg and David E. Goldberg and Kumara Sastry and Kumara Sastry Progress Toward Linkage Learning in Real-Coded GAs with Simplex Crossover. IlliGAL Report. 2000.

Parameters

epsilon (*float | None*) – Expansion rate. If not specified, defaults to `sqrt(len(search_space) + 2)`.

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Methods

`crossover`(parents_params, rng, study, ...)	Perform crossover of selected parent individuals.

Attributes

`n_parents`

crossover(*parents_params*, *rng*, *study*, *search_space_bounds*)

Perform crossover of selected parent individuals.

This method is called in `sample_relative()`.

Parameters

- **parents_params** (*np.ndarray*) – A `numpy.ndarray` with dimensions `num_parents x num_parameters`. Represents a parameter space for each parent individual. This space is continuous for numerical parameters.
- **rng** (*np.random.RandomState*) – An instance of `numpy.random.RandomState`.
- **study** (`Study`) – Target study object.
- **search_space_bounds** (*np.ndarray*) – A `numpy.ndarray` with dimensions `len_search_space x 2` representing numerical distribution bounds constructed from transformed search space.

Returns

A 1-dimensional `numpy.ndarray` containing new parameter combination.

Return type

np.ndarray

optuna.samplers.nsgaii.SBXCrossover

class optuna.samplers.nsgaii.**SBXCrossover**(*eta=None*, *uniform_crossover_prob=0.5*, *use_child_gene_prob=0.5*)

Simulated Binary Crossover operation used by `NSGAIISampler`.

Generates a child from two parent individuals according to the polynomial probability distribution.

In the paper, SBX has only one argument, `eta`, and generate two child individuals. However, Optuna can only return one child individual in one crossover operation, so it uses the `uniform_crossover_prob` and `use_child_gene_prob` arguments to make two individuals into one.

- Deb, K. and R. Agrawal. "Simulated Binary Crossover for Continuous Search Space." Complex Syst. 9 (1995): n. pag.

Parameters

- **eta** (*float | None*) – Distribution index. A small value of `eta` allows distant solutions to be selected as children solutions. If not specified, takes default value of `2` for single objective functions and `20` for multi objective.
- **uniform_crossover_prob** (*float*) – `uniform_crossover_prob` is the probability of uniform crossover between two individuals selected as candidate child individuals.

This argument is whether or not two individuals are crossover to make one child individual. If the `uniform_crossover_prob` exceeds 0.5, the result is equivalent to `1-uniform_crossover_prob`, because it returns one of the two individuals of the crossover result. If not specified, takes default value of `0.5`. The range of values is `[0.0, 1.0]`.

- **`use_child_gene_prob`** (*`float`*) – `use_child_gene_prob` is the probability of using the value of the generated child variable rather than the value of the parent. This probability is applied to each variable individually. where `1-use_chile_gene_prob` is the probability of using the parent's values as it is. If not specified, takes default value of `0.5`. The range of values is `(0.0, 1.0]`.

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Methods

`crossover`(parents_params, rng, study, ...)	Perform crossover of selected parent individuals.

Attributes

`n_parents`

`crossover`(*parents_params*, *rng*, *study*, *search_space_bounds*)

Perform crossover of selected parent individuals.

This method is called in *`sample_relative()`*.

Parameters

- **`parents_params`** (*`np.ndarray`*) – A `numpy.ndarray` with dimensions `num_parents x num_parameters`. Represents a parameter space for each parent individual. This space is continuous for numerical parameters.
- **`rng`** (*`np.random.RandomState`*) – An instance of `numpy.random.RandomState`.
- **`study`** (`Study`) – Target study object.
- **`search_space_bounds`** (*`np.ndarray`*) – A `numpy.ndarray` with dimensions `len_search_space x 2` representing numerical distribution bounds constructed from transformed search space.

Returns

A 1-dimensional `numpy.ndarray` containing new parameter combination.

Return type

np.ndarray

optuna.samplers.nsgaii.VSBXCrossover

class `optuna.samplers.nsgaii.`**`VSBXCrossover`**(*eta=None*, *uniform_crossover_prob=0.5*, *use_child_gene_prob=0.5*)

Modified Simulated Binary Crossover operation used by *`NSGAIISampler`*.

vSBX generates child individuals without excluding any region of the parameter space, while maintaining the excellent properties of SBX.

In the paper, vSBX has only one argument, `eta`, and generate two child individuals. However, Optuna can only return one child individual in one crossover operation, so it uses the `uniform_crossover_prob` and `use_child_gene_prob` arguments to make two individuals into one.

- Pedro J. Ballester, Jonathan N. Carter. Real-Parameter Genetic Algorithms for Finding Multiple Optimal Solutions in Multi-modal Optimization. GECCO 2003: 706-717

Parameters

- **`eta`** (*`float` | `None`*) – Distribution index. A small value of `eta` allows distant solutions to be selected as children solutions. If not specified, takes default value of `2` for single objective functions and `20` for multi objective.
- **`uniform_crossover_prob`** (*`float`*) – `uniform_crossover_prob` is the probability of uniform crossover between two individuals selected as candidate child individuals. This argument is whether or not two individuals are crossover to make one child individual. If the `uniform_crossover_prob` exceeds 0.5, the result is equivalent to `1-uniform_crossover_prob`, because it returns one of the two individuals of the crossover result. If not specified, takes default value of `0.5`. The range of values is `[0.0, 1.0]`.
- **`use_child_gene_prob`** (*`float`*) – `use_child_gene_prob` is the probability of using the value of the generated child variable rather than the value of the parent. This probability is applied to each variable individually. where `1-use_chile_gene_prob` is the probability of using the parent's values as it is. If not specified, takes default value of `0.5`. The range of values is `(0.0, 1.0]`.

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Methods

`crossover`(parents_params, rng, study, ...)	Perform crossover of selected parent individuals.

Attributes

`n_parents`

`crossover`(*parents_params*, *rng*, *study*, *search_space_bounds*)

Perform crossover of selected parent individuals.

This method is called in *`sample_relative()`*.

Parameters

- **parents_params** (*np.ndarray*) – A `numpy.ndarray` with dimensions `num_parents x num_parameters`. Represents a parameter space for each parent individual. This space is continuous for numerical parameters.
- **rng** (*np.random.RandomState*) – An instance of `numpy.random.RandomState`.
- **study** (`Study`) – Target study object.
- **search_space_bounds** (*np.ndarray*) – A `numpy.ndarray` with dimensions `len_search_space x 2` representing numerical distribution bounds constructed from transformed search space.

Returns

A 1-dimensional `numpy.ndarray` containing new parameter combination.

Return type

np.ndarray

optuna.samplers.nsgaii.UNDXCrossover

`class optuna.samplers.nsgaii.UNDXCrossover(`*sigma_xi=0.5*, *sigma_eta=None*`)`

Unimodal Normal Distribution Crossover used by *NSGAIISampler*.

Generates child individuals from the three parents using a multivariate normal distribution.

- H. Kita, I. Ono and S. Kobayashi, Multi-parental extension of the unimodal normal distribution crossover for real-coded genetic algorithms, Proceedings of the 1999 Congress on Evolutionary Computation-CEC99 (Cat. No. 99TH8406), 1999, pp. 1581-1588 Vol. 2

Parameters

- **sigma_xi** (*float*) – Parametrizes normal distribution from which `xi` is drawn.
- **sigma_eta** (*float | None*) – Parametrizes normal distribution from which `etas` are drawn. If not specified, defaults to `0.35 / sqrt(len(search_space))`.

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Methods

crossover(parents_params, rng, study, ...)	Perform crossover of selected parent individuals.

Attributes

`n_parents`

crossover(*parents_params*, *rng*, *study*, *search_space_bounds*)

Perform crossover of selected parent individuals.

This method is called in *sample_relative()*.

Parameters

- **parents_params** (*np.ndarray*) – A `numpy.ndarray` with dimensions `num_parents x num_parameters`. Represents a parameter space for each parent individual. This space is continuous for numerical parameters.
- **rng** (*np.random.RandomState*) – An instance of `numpy.random.RandomState`.
- **study** (Study) – Target study object.
- **search_space_bounds** (*np.ndarray*) – A `numpy.ndarray` with dimensions `len_search_space x 2` representing numerical distribution bounds constructed from transformed search space.

Returns

A 1-dimensional `numpy.ndarray` containing new parameter combination.

Return type

np.ndarray

8.3.11 optuna.search_space

The *search_space* module provides functionality for controlling search space of parameters.

IntersectionSearchSpace	A class to calculate the intersection search space of a *Study*.
intersection_search_space	Return the intersection search space of the given trials.

optuna.search_space.IntersectionSearchSpace

class optuna.search_space.**IntersectionSearchSpace**(*include_pruned=False*)

A class to calculate the intersection search space of a *Study*.

Intersection search space contains the intersection of parameter distributions that have been suggested in the completed trials of the study so far. If there are multiple parameters that have the same name but different distributions, neither is included in the resulting search space (i.e., the parameters with dynamic value ranges are excluded).

Note that an instance of this class is supposed to be used for only one study. If different studies are passed to *calculate()*, a `ValueError` is raised.

Parameters

include_pruned (*bool*) – Whether pruned trials should be included in the search space.

Methods

calculate(study)	Returns the intersection search space of the *Study*.

calculate(*study*)

Returns the intersection search space of the *Study*.

Parameters

study (Study) – A study with completed trials. The same study must be passed for one instance of this class through its lifetime.

Returns

A dictionary containing the parameter names and parameter's distributions sorted by parameter names.

Return type

dict[str, BaseDistribution]

optuna.search_space.intersection_search_space

optuna.search_space.**intersection_search_space**(*trials*, *include_pruned=False*)

Return the intersection search space of the given trials.

Intersection search space contains the intersection of parameter distributions that have been suggested in the completed trials of the study so far. If there are multiple parameters that have the same name but different distributions, neither is included in the resulting search space (i.e., the parameters with dynamic value ranges are excluded).

Note

IntersectionSearchSpace provides the same functionality with a much faster way. Please consider using it if you want to reduce execution time as much as possible.

Parameters

- **trials** (*list[FrozenTrial]*) – A list of trials.
- **include_pruned** (*bool*) – Whether pruned trials should be included in the search space.

Returns

A dictionary containing the parameter names and parameter's distributions sorted by parameter names.

Return type

dict[str, *BaseDistribution*]

8.3.12 optuna.storages

The *storages* module defines a BaseStorage class which abstracts a backend database and provides library-internal interfaces to the read/write histories of the studies and trials. Library users who wish to use storage solutions other than the default *InMemoryStorage* should use one of the child classes of BaseStorage documented below.

RDBStorage	Storage class for RDB backend.
RetryFailedTrialCallback	Retry a failed trial up to a maximum number of times.
fail_stale_trials	Fail stale trials and run their failure callbacks.
JournalStorage	Storage class for Journal storage backend.
InMemoryStorage	Storage class that stores data in memory of the Python process.
run_grpc_proxy_server	Run a gRPC server for the given storage URL, host, and port.
GrpcStorageProxy	gRPC client for *run_grpc_proxy_server()*.

optuna.storages.RDBStorage

class optuna.storages.**RDBStorage**(*url*, *engine_kwargs=None*, *skip_compatibility_check=False*, ***, *heartbeat_interval=None*, *grace_period=None*, *failed_trial_callback=None*, *skip_table_creation=False*)

Storage class for RDB backend.

Note that library users can instantiate this class, but the attributes provided by this class are not supposed to be directly accessed by them.

Example

Create an *RDBStorage* instance with customized `pool_size` and `timeout` settings.

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    return x**2


storage = optuna.storages.RDBStorage(
    url="sqlite:///:memory:",
    engine_kwargs={"pool_size": 20, "connect_args": {"timeout": 10}},
)

study = optuna.create_study(storage=storage)
study.optimize(objective, n_trials=10)
```

Parameters

- **url** (*str*) – URL of the storage.
- **engine_kwargs** (*dict[str, Any] | None*) – A dictionary of keyword arguments that is passed to sqlalchemy.engine.create_engine function.
- **skip_compatibility_check** (*bool*) – Flag to skip schema compatibility check if set to `True`.
- **heartbeat_interval** (*int | None*) – Interval to record the heartbeat. It is recorded every `interval` seconds. `heartbeat_interval` must be `None` or a positive integer.

  Note

  Heartbeat mechanism is experimental. API would change in the future.

  Note

  The heartbeat is supposed to be used with *optimize()*. If you use *ask()* and *tell()* instead, it will not work.

- **grace_period** (*int | None*) – Grace period before a running trial is failed from the last heartbeat. `grace_period` must be `None` or a positive integer. If it is `None`, the grace period will be *2 * heartbeat_interval*.

- **failed_trial_callback** (*Callable[['optuna.study.Study', FrozenTrial], None] | None*) – A callback function that is invoked after failing each stale trial. The function must accept two parameters with the following types in this order: *Study* and *FrozenTrial*.

  Note

  The procedure to fail existing stale trials is called just before asking the study for a new trial.

- **skip_table_creation** (*bool*) – Flag to skip table creation if set to `True`.

Note

If you use MySQL, pool_pre_ping will be set to `True` by default to prevent connection timeout. You can turn it off with `engine_kwargs['pool_pre_ping']=False`, but it is recommended to keep the setting if execution time of your objective function is longer than the *wait_timeout* of your MySQL configuration.

Note

We would never recommend SQLite3 for parallel optimization. Please see the FAQ *How can I solve the error that occurs when performing parallel optimization with SQLite3?* for details.

Note

Mainly in a cluster environment, running trials are often killed unexpectedly. If you want to detect a failure of trials, please use the heartbeat mechanism. Set `heartbeat_interval`, `grace_period`, and `failed_trial_callback` appropriately according to your use case. For more details, please refer to the *tutorial* and Example page.

See also

You can use *RetryFailedTrialCallback* to automatically retry failed trials detected by heartbeat.

Methods

check_trial_is_updatable(trial_id, trial_state)	Check whether a trial state is updatable.
create_new_study(directions[, study_name])	Create a new study from a name.
create_new_trial(study_id[, template_trial])	Create and add a new trial to a study.
delete_study(study_id)	Delete a study.
get_all_studies()	Read a list of `FrozenStudy` objects.
get_all_trials(study_id[, deepcopy, states])	Read all trials in a study.
get_all_versions()	Return the schema version list.
get_best_trial(study_id)	Return the trial with the best value in a study.

continues on next page

Table 60 – continued from previous page

get_current_version()	Return the schema version currently used by this storage.
get_failed_trial_callback()	Get the failed trial callback function.
get_head_version()	Return the latest schema version.
get_heartbeat_interval()	Get the heartbeat interval if it is set.
get_n_trials(study_id[, state])	Count the number of trials in a study.
get_study_directions(study_id)	Read whether a study maximizes or minimizes an objective.
get_study_id_from_name(study_name)	Read the ID of a study.
get_study_name_from_id(study_id)	Read the study name of a study.
get_study_system_attrs(study_id)	Read the optuna-internal attributes of a study.
get_study_user_attrs(study_id)	Read the user-defined attributes of a study.
get_trial(trial_id)	Read a trial.
get_trial_id_from_study_id_trial_number(...	Read the trial ID of a trial.
get_trial_number_from_id(trial_id)	Read the trial number of a trial.
get_trial_param(trial_id, param_name)	Read the parameter of a trial.
get_trial_params(trial_id)	Read the parameter dictionary of a trial.
get_trial_system_attrs(trial_id)	Read the optuna-internal attributes of a trial.
get_trial_user_attrs(trial_id)	Read the user-defined attributes of a trial.
record_heartbeat(trial_id)	Record the heartbeat of the trial.
remove_session()	Removes the current session.
set_study_system_attr(study_id, key, value)	Register an optuna-internal attribute to a study.
set_study_user_attr(study_id, key, value)	Register a user-defined attribute to a study.
set_trial_intermediate_value(trial_id, step, ...)	Report an intermediate value of an objective function.
set_trial_param(trial_id, param_name, ...)	Set a parameter to a trial.
set_trial_state_values(trial_id, state[, values])	Update the state and values of a trial.
set_trial_system_attr(trial_id, key, value)	Set an optuna-internal attribute to a trial.
set_trial_user_attr(trial_id, key, value)	Set a user-defined attribute to a trial.
upgrade()	Upgrade the storage schema.

check_trial_is_updatable(*trial_id*, *trial_state*)

Check whether a trial state is updatable.

Parameters

- **trial_id** (*int*) – ID of the trial. Only used for an error message.
- **trial_state** (TrialState) – Trial state to check.

Raises

UpdateFinishedTrialError – If the trial is already finished.

Return type

None

create_new_study(*directions*, *study_name=None*)

Create a new study from a name.

If no name is specified, the storage class generates a name. The returned study ID is unique among all current and deleted studies.

Parameters

- **directions** (*Sequence*[StudyDirection]) – A sequence of direction whose element is either *MAXIMIZE* or *MINIMIZE*.

- **study_name** (*str | None*) – Name of the new study to create.

Returns
ID of the created study.

Raises
optuna.exceptions.DuplicatedStudyError – If a study with the same `study_name` already exists.

Return type
int

create_new_trial(*study_id*, *template_trial=None*)

Create and add a new trial to a study.

The returned trial ID is unique among all current and deleted trials.

Parameters

- **study_id** (*int*) – ID of the study.
- **template_trial** (FrozenTrial *| None*) – Template *FrozenTrial* with default user-attributes, system-attributes, intermediate-values, and a state.

Returns
ID of the created trial.

Raises
KeyError – If no study with the matching `study_id` exists.

Return type
int

delete_study(*study_id*)

Delete a study.

Parameters
study_id (*int*) – ID of the study.

Raises
KeyError – If no study with the matching `study_id` exists.

Return type
None

get_all_studies()

Read a list of `FrozenStudy` objects.

Returns
A list of `FrozenStudy` objects, sorted by `study_id`.

Return type
list[*FrozenStudy*]

get_all_trials(*study_id*, *deepcopy=True*, *states=None*)

Read all trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.
- **deepcopy** (*bool*) – Whether to copy the list of trials before returning. Set to `True` if you intend to update the list or elements of the list.

- **states** (*Container[TrialState] | None*) – Trial states to filter on. If None, include all states.

Returns
List of trials in the study, sorted by `trial_id`.

Raises
KeyError – If no study with the matching `study_id` exists.

Return type
list[FrozenTrial]

get_all_versions()

Return the schema version list.

Return type
list[str]

get_best_trial(*study_id*)

Return the trial with the best value in a study.

This method is valid only during single-objective optimization.

Parameters
study_id (*int*) – ID of the study.

Returns
The trial with the best objective value among all finished trials in the study.

Raises

- KeyError – If no study with the matching `study_id` exists.
- RuntimeError – If the study has more than one direction.
- ValueError – If no trials have been completed.

Return type
FrozenTrial

get_current_version()

Return the schema version currently used by this storage.

Return type
str

get_failed_trial_callback()

Get the failed trial callback function.

Returns
The failed trial callback function if it is set, otherwise None.

Return type
Callable[[Study, FrozenTrial], None] | None

get_head_version()

Return the latest schema version.

Return type
str

get_heartbeat_interval()

Get the heartbeat interval if it is set.

Returns
The heartbeat interval if it is set, otherwise `None`.

Return type
int | None

get_n_trials(*study_id*, *state=None*)

Count the number of trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.
- **state** (*tuple[TrialState, ...] | TrialState | None*) – Trial states to filter on. If `None`, include all states.

Returns
Number of trials in the study.

Raises
KeyError – If no study with the matching `study_id` exists.

Return type
int

get_study_directions(*study_id*)

Read whether a study maximizes or minimizes an objective.

Parameters
study_id (*int*) – ID of a study.

Returns
Optimization directions list of the study.

Raises
KeyError – If no study with the matching `study_id` exists.

Return type
list[StudyDirection]

get_study_id_from_name(*study_name*)

Read the ID of a study.

Parameters
study_name (*str*) – Name of the study.

Returns
ID of the study.

Raises
KeyError – If no study with the matching `study_name` exists.

Return type
int

get_study_name_from_id(*study_id*)

Read the study name of a study.

Parameters
study_id (*int*) – ID of the study.

Returns
Name of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
str

`get_study_system_attrs`(*study_id*)

Read the optuna-internal attributes of a study.

Parameters
`study_id` (*`int`*) – ID of the study.

Returns
Dictionary with the optuna-internal attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

`get_study_user_attrs`(*study_id*)

Read the user-defined attributes of a study.

Parameters
`study_id` (*`int`*) – ID of the study.

Returns
Dictionary with the user attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

`get_trial`(*trial_id*)

Read a trial.

Parameters
`trial_id` (*`int`*) – ID of the trial.

Returns
Trial with a matching trial ID.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
FrozenTrial

`get_trial_id_from_study_id_trial_number`(*study_id*, *trial_number*)

Read the trial ID of a trial.

Parameters

- **`study_id`** (*`int`*) – ID of the study.
- **`trial_number`** (*`int`*) – Number of the trial.

Returns
ID of the trial.

Raises
`KeyError` – If no trial with the matching `study_id` and `trial_number` exists.

Return type
int

`get_trial_number_from_id`(*trial_id*)

Read the trial number of a trial.

Note

The trial number is only unique within a study, and is sequential.

Parameters
`trial_id` (*`int`*) – ID of the trial.

Returns
Number of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
int

`get_trial_param`(*trial_id*, *param_name*)

Read the parameter of a trial.

Parameters

- **`trial_id`** (*`int`*) – ID of the trial.
- **`param_name`** (*`str`*) – Name of the parameter.

Returns
Internal representation of the parameter.

Raises
`KeyError` – If no trial with the matching `trial_id` exists. If no such parameter exists.

Return type
float

`get_trial_params`(*trial_id*)

Read the parameter dictionary of a trial.

Parameters
`trial_id` (*`int`*) – ID of the trial.

Returns
Dictionary of a parameters. Keys are parameter names and values are external representations of the parameter values.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`get_trial_system_attrs`(*trial_id*)

Read the optuna-internal attributes of a trial.

Parameters
`trial_id` (*int*) – ID of the trial.

Returns
Dictionary with the optuna-internal attributes of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`get_trial_user_attrs`(*trial_id*)

Read the user-defined attributes of a trial.

Parameters
`trial_id` (*int*) – ID of the trial.

Returns
Dictionary with the user-defined attributes of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`record_heartbeat`(*trial_id*)

Record the heartbeat of the trial.

Parameters
`trial_id` (*int*) – ID of the trial.

Return type
None

`remove_session`()

Removes the current session.

A session is stored in SQLAlchemy's ThreadLocalRegistry for each thread. This method closes and removes the session which is associated to the current thread. Particularly, under multi-thread use cases, it is important to call this method *from each thread*. Otherwise, all sessions and their associated DB connections are destructed by a thread that occasionally invoked the garbage collector. By default, it is not allowed to touch a SQLite connection from threads other than the thread that created the connection. Therefore, we need to explicitly close the connection from each thread.

Return type
None

`set_study_system_attr`(*study_id*, *key*, *value*)

Register an optuna-internal attribute to a study.

This method overwrites any existing attribute.

Parameters

- `study_id` (*int*) – ID of the study.
- `key` (*str*) – Attribute key.

- **value** (*Mapping[str, JSONSerializable] | Sequence[JSONSerializable] | str | int | float | bool | None*) – Attribute value. It should be JSON serializable.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

set_study_user_attr(*study_id*, *key*, *value*)

Register a user-defined attribute to a study.

This method overwrites any existing attribute.

Parameters

- **study_id** (*int*) – ID of the study.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

set_trial_intermediate_value(*trial_id*, *step*, *intermediate_value*)

Report an intermediate value of an objective function.

This method overwrites any existing intermediate value associated with the given step.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **step** (*int*) – Step of the trial (e.g., the epoch when training a neural network).
- **intermediate_value** (*float*) – Intermediate value corresponding to the step.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- *`UpdateFinishedTrialError`* – If the trial is already finished.

Return type
None

set_trial_param(*trial_id*, *param_name*, *param_value_internal*, *distribution*)

Set a parameter to a trial.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **param_name** (*str*) – Name of the parameter.
- **param_value_internal** (*float*) – Internal representation of the parameter value.
- **distribution** (*BaseDistribution*) – Sampled distribution of the parameter.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.

- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
None

`set_trial_state_values`(*trial_id*, *state*, *values=None*)

Update the state and values of a trial.

Set return values of an objective function to values argument. If values argument is not `None`, this method overwrites any existing trial values.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **state** (`TrialState`) – New state of the trial.
- **values** (*Sequence[float] | None*) – Values of the objective function.

Returns
`True` if the state is successfully updated. `False` if the state is kept the same. The latter happens when this method tries to update the state of *RUNNING* trial to *RUNNING*.

Raises

- **KeyError** – If no trial with the matching `trial_id` exists.
- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
bool

`set_trial_system_attr`(*trial_id*, *key*, *value*)

Set an optuna-internal attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **key** (*str*) – Attribute key.
- **value** (*Mapping[str, JSONSerializable] | Sequence[JSONSerializable] | str | int | float | bool | None*) – Attribute value. It should be JSON serializable.

Raises

- **KeyError** – If no trial with the matching `trial_id` exists.
- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
None

`set_trial_user_attr`(*trial_id*, *key*, *value*)

Set a user-defined attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **key** (*str*) – Attribute key.

- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
None

upgrade()

Upgrade the storage schema.

Return type
None

optuna.storages.RetryFailedTrialCallback

class optuna.storages.**RetryFailedTrialCallback**(*max_retry=None*, *inherit_intermediate_values=False*)

Retry a failed trial up to a maximum number of times.

When a trial fails, this callback can be used with a class in *optuna.storages* to recreate the trial in `TrialState.WAITING` to queue up the trial to be run again.

The failed trial can be identified by the *retried_trial_number()* function. Even if repetitive failure occurs (a retried trial fails again), this method returns the number of the original trial. To get a full list including the numbers of the retried trials as well as their original trial, call the *retry_history()* function.

This callback is helpful in environments where trials may fail due to external conditions, such as being preempted by other processes.

Usage:

```
import optuna
from optuna.storages import RetryFailedTrialCallback

storage = optuna.storages.RDBStorage(
    url="sqlite:///:memory:",
    heartbeat_interval=60,
    grace_period=120,
    failed_trial_callback=RetryFailedTrialCallback(max_retry=3),
)

study = optuna.create_study(
    storage=storage,
)
```

See also

See *RDBStorage*.

Parameters

- **max_retry** (*int | None*) – The max number of times a trial can be retried. Must be set to `None` or an integer. If set to the default value of `None` will retry indefinitely. If set to an integer, will only retry that many times.

- **inherit_intermediate_values** (*bool*) – Option to inherit *trial.intermediate_values* reported by `optuna.trial.Trial.report()` from the failed trial. Default is `False`.

Note

Added in v2.8.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.8.0.

Methods

`retried_trial_number`(trial)	Return the number of the original trial being retried.
`retry_history`(trial)	Return the list of retried trial numbers with respect to the specified trial.

static retried_trial_number(*trial*)

Return the number of the original trial being retried.

Parameters
trial (`FrozenTrial`) – The trial object.

Returns
The number of the first failed trial. If not retry of a previous trial, returns `None`.

Return type
int | None

Note

Added in v2.8.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.8.0.

static retry_history(*trial*)

Return the list of retried trial numbers with respect to the specified trial.

Parameters
trial (`FrozenTrial`) – The trial object.

Returns
A list of trial numbers in ascending order of the series of retried trials. The first item of the list indicates the original trial which is identical to the `retried_trial_number()`, and the last item is the one right before the specified trial in the retry series. If the specified trial is not a retry of any trial, returns an empty list.

Return type
list[int]

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

optuna.storages.fail_stale_trials

optuna.storages.**fail_stale_trials**(*study*)

Fail stale trials and run their failure callbacks.

The running trials whose heartbeat has not been updated for a long time will be failed, that is, those states will be changed to *FAIL*.

See also

See *RDBStorage*.

Parameters
study (Study) – Study holding the trials to check.

Return type
None

Note

Added in v2.9.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.9.0.

optuna.storages.JournalStorage

class optuna.storages.**JournalStorage**(*log_storage*)

Storage class for Journal storage backend.

Note that library users can instantiate this class, but the attributes provided by this class are not supposed to be directly accessed by them.

Journal storage writes a record of every operation to the database as it is executed and at the same time, keeps a latest snapshot of the database in-memory. If the database crashes for any reason, the storage can re-establish the contents in memory by replaying the operations stored from the beginning.

Journal storage has several benefits over the conventional value logging storages.

1. The number of IOs can be reduced because of larger granularity of logs.
2. Journal storage has simpler backend API than value logging storage.
3. Journal storage keeps a snapshot in-memory so no need to add more cache.

Example

```python
import optuna


def objective(trial): ...


storage = optuna.storages.JournalStorage(
    optuna.storages.journal.JournalFileBackend("./optuna_journal_storage.log")
)

```

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```
study = optuna.create_study(storage=storage)
study.optimize(objective)
```

In a Windows environment, an error message "A required privilege is not held by the client" may appear. In this case, you can solve the problem with creating storage by specifying `JournalFileOpenLock` as follows.

```
file_path = "./optuna_journal_storage.log"
lock_obj = optuna.storages.journal.JournalFileOpenLock(file_path)

storage = optuna.storages.JournalStorage(
    optuna.storages.journal.JournalFileBackend(file_path, lock_obj=lock_obj),
)
```

Methods

`check_trial_is_updatable`(trial_id, trial_state)	Check whether a trial state is updatable.
`create_new_study`(directions[, study_name])	Create a new study from a name.
`create_new_trial`(study_id[, template_trial])	Create and add a new trial to a study.
`delete_study`(study_id)	Delete a study.
`get_all_studies`()	Read a list of `FrozenStudy` objects.
`get_all_trials`(study_id[, deepcopy, states])	Read all trials in a study.
`get_best_trial`(study_id)	Return the trial with the best value in a study.
`get_n_trials`(study_id[, state])	Count the number of trials in a study.
`get_study_directions`(study_id)	Read whether a study maximizes or minimizes an objective.
`get_study_id_from_name`(study_name)	Read the ID of a study.
`get_study_name_from_id`(study_id)	Read the study name of a study.
`get_study_system_attrs`(study_id)	Read the optuna-internal attributes of a study.
`get_study_user_attrs`(study_id)	Read the user-defined attributes of a study.
`get_trial`(trial_id)	Read a trial.
`get_trial_id_from_study_id_trial_number`(...	Read the trial ID of a trial.
`get_trial_number_from_id`(trial_id)	Read the trial number of a trial.
`get_trial_param`(trial_id, param_name)	Read the parameter of a trial.
`get_trial_params`(trial_id)	Read the parameter dictionary of a trial.
`get_trial_system_attrs`(trial_id)	Read the optuna-internal attributes of a trial.
`get_trial_user_attrs`(trial_id)	Read the user-defined attributes of a trial.
`remove_session`()	Clean up all connections to a database.
`restore_replay_result`(snapshot)	
`set_study_system_attr`(study_id, key, value)	Register an optuna-internal attribute to a study.
`set_study_user_attr`(study_id, key, value)	Register a user-defined attribute to a study.
`set_trial_intermediate_value`(trial_id, step, ...)	Report an intermediate value of an objective function.
`set_trial_param`(trial_id, param_name, ...)	Set a parameter to a trial.
`set_trial_state_values`(trial_id, state[, values])	Update the state and values of a trial.
`set_trial_system_attr`(trial_id, key, value)	Set an optuna-internal attribute to a trial.
`set_trial_user_attr`(trial_id, key, value)	Set a user-defined attribute to a trial.

Parameters

`log_storage` (*`BaseJournalBackend`*) `check_trial_is_updatable`(*trial_id*, *trial_state*)

Check whether a trial state is updatable.

Parameters

- **trial_id** (*int*) – ID of the trial. Only used for an error message.
- **trial_state** (TrialState) – Trial state to check.

Raises

UpdateFinishedTrialError – If the trial is already finished.

Return type

None

`create_new_study`(*directions*, *study_name=None*)

Create a new study from a name.

If no name is specified, the storage class generates a name. The returned study ID is unique among all current and deleted studies.

Parameters

- **directions** (*Sequence[*StudyDirection*]*) – A sequence of direction whose element is either *MAXIMIZE* or *MINIMIZE*.
- **study_name** (*str | None*) – Name of the new study to create.

Returns

ID of the created study.

Raises

optuna.exceptions.DuplicatedStudyError – If a study with the same `study_name` already exists.

Return type

int

`create_new_trial`(*study_id*, *template_trial=None*)

Create and add a new trial to a study.

The returned trial ID is unique among all current and deleted trials.

Parameters

- **study_id** (*int*) – ID of the study.
- **template_trial** (FrozenTrial *| None*) – Template *FrozenTrial* with default user-attributes, system-attributes, intermediate-values, and a state.

Returns

ID of the created trial.

Raises

KeyError – If no study with the matching `study_id` exists.

Return type

int

`delete_study`(*study_id*)

Delete a study.

Parameters

study_id (*int*) – ID of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

`get_all_studies()`

Read a list of `FrozenStudy` objects.

Returns
A list of `FrozenStudy` objects, sorted by `study_id`.

Return type
list[*FrozenStudy*]

`get_all_trials`(*study_id*, *deepcopy=True*, *states=None*)

Read all trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.
- **deepcopy** (*bool*) – Whether to copy the list of trials before returning. Set to `True` if you intend to update the list or elements of the list.
- **states** (*Container[TrialState] | None*) – Trial states to filter on. If `None`, include all states.

Returns
List of trials in the study, sorted by `trial_id`.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
list[FrozenTrial]

`get_best_trial`(*study_id*)

Return the trial with the best value in a study.

This method is valid only during single-objective optimization.

Parameters
study_id (*int*) – ID of the study.

Returns
The trial with the best objective value among all finished trials in the study.

Raises

- `KeyError` – If no study with the matching `study_id` exists.
- `RuntimeError` – If the study has more than one direction.
- `ValueError` – If no trials have been completed.

Return type
FrozenTrial

`get_n_trials`(*study_id*, *state=None*)

Count the number of trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.

- **state** (*tuple[TrialState, ...] | TrialState | None*) – Trial states to filter on. If None, include all states.

Returns
Number of trials in the study.

Raises
KeyError – If no study with the matching study_id exists.

Return type
int

get_study_directions(*study_id*)

Read whether a study maximizes or minimizes an objective.

Parameters
study_id (*int*) – ID of a study.

Returns
Optimization directions list of the study.

Raises
KeyError – If no study with the matching study_id exists.

Return type
list[StudyDirection]

get_study_id_from_name(*study_name*)

Read the ID of a study.

Parameters
study_name (*str*) – Name of the study.

Returns
ID of the study.

Raises
KeyError – If no study with the matching study_name exists.

Return type
int

get_study_name_from_id(*study_id*)

Read the study name of a study.

Parameters
study_id (*int*) – ID of the study.

Returns
Name of the study.

Raises
KeyError – If no study with the matching study_id exists.

Return type
str

get_study_system_attrs(*study_id*)

Read the optuna-internal attributes of a study.

Parameters
study_id (*int*) – ID of the study.

Returns
Dictionary with the optuna-internal attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

`get_study_user_attrs`(*study_id*)

Read the user-defined attributes of a study.

Parameters
`study_id` (*`int`*) – ID of the study.

Returns
Dictionary with the user attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

`get_trial`(*trial_id*)

Read a trial.

Parameters
`trial_id` (*`int`*) – ID of the trial.

Returns
Trial with a matching trial ID.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
FrozenTrial

`get_trial_id_from_study_id_trial_number`(*study_id*, *trial_number*)

Read the trial ID of a trial.

Parameters

- **`study_id`** (*`int`*) – ID of the study.
- **`trial_number`** (*`int`*) – Number of the trial.

Returns
ID of the trial.

Raises
`KeyError` – If no trial with the matching `study_id` and `trial_number` exists.

Return type
int

`get_trial_number_from_id`(*trial_id*)

Read the trial number of a trial.

Note

The trial number is only unique within a study, and is sequential.

Parameters
trial_id (*int*) – ID of the trial.

Returns
Number of the trial.

Raises
KeyError – If no trial with the matching `trial_id` exists.

Return type
int

get_trial_param(*trial_id*, *param_name*)

Read the parameter of a trial.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **param_name** (*str*) – Name of the parameter.

Returns
Internal representation of the parameter.

Raises
KeyError – If no trial with the matching `trial_id` exists. If no such parameter exists.

Return type
float

get_trial_params(*trial_id*)

Read the parameter dictionary of a trial.

Parameters
trial_id (*int*) – ID of the trial.

Returns
Dictionary of a parameters. Keys are parameter names and values are external representations of the parameter values.

Raises
KeyError – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

get_trial_system_attrs(*trial_id*)

Read the optuna-internal attributes of a trial.

Parameters
trial_id (*int*) – ID of the trial.

Returns
Dictionary with the optuna-internal attributes of the trial.

Raises
KeyError – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

get_trial_user_attrs(*trial_id*)

Read the user-defined attributes of a trial.

Parameters
trial_id (*int*) – ID of the trial.

Returns
Dictionary with the user-defined attributes of the trial.

Raises
KeyError – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

remove_session()

Clean up all connections to a database.

Return type
None

set_study_system_attr(*study_id*, *key*, *value*)

Register an optuna-internal attribute to a study.

This method overwrites any existing attribute.

Parameters

- **study_id** (*int*) – ID of the study.
- **key** (*str*) – Attribute key.
- **value** (*Mapping[str, JSONSerializable] | Sequence[JSONSerializable] | str | int | float | bool | None*) – Attribute value. It should be JSON serializable.

Raises
KeyError – If no study with the matching `study_id` exists.

Return type
None

set_study_user_attr(*study_id*, *key*, *value*)

Register a user-defined attribute to a study.

This method overwrites any existing attribute.

Parameters

- **study_id** (*int*) – ID of the study.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises
KeyError – If no study with the matching `study_id` exists.

Return type
None

set_trial_intermediate_value(*trial_id*, *step*, *intermediate_value*)

Report an intermediate value of an objective function.

This method overwrites any existing intermediate value associated with the given step.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **step** (*int*) – Step of the trial (e.g., the epoch when training a neural network).
- **intermediate_value** (*float*) – Intermediate value corresponding to the step.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type

None

set_trial_param(*trial_id*, *param_name*, *param_value_internal*, *distribution*)

Set a parameter to a trial.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **param_name** (*str*) – Name of the parameter.
- **param_value_internal** (*float*) – Internal representation of the parameter value.
- **distribution** (*BaseDistribution*) – Sampled distribution of the parameter.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type

None

set_trial_state_values(*trial_id*, *state*, *values=None*)

Update the state and values of a trial.

Set return values of an objective function to values argument. If values argument is not `None`, this method overwrites any existing trial values.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **state** (`TrialState`) – New state of the trial.
- **values** (*Sequence[float] | None*) – Values of the objective function.

Returns

`True` if the state is successfully updated. `False` if the state is kept the same. The latter happens when this method tries to update the state of *RUNNING* trial to *RUNNING*.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type
bool

set_trial_system_attr(*trial_id*, *key*, *value*)

Set an optuna-internal attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **key** (*str*) – Attribute key.
- **value** (*Mapping[str, JSONSerializable] | Sequence[JSONSerializable] | str | int | float | bool | None*) – Attribute value. It should be JSON serializable.

Raises

- KeyError – If no trial with the matching `trial_id` exists.
- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
None

set_trial_user_attr(*trial_id*, *key*, *value*)

Set a user-defined attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises

- KeyError – If no trial with the matching `trial_id` exists.
- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
None

optuna.storages.InMemoryStorage

class optuna.storages.**InMemoryStorage**

Storage class that stores data in memory of the Python process.

Example

Create an *InMemoryStorage* instance.

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
```

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```
    return x**2


storage = optuna.storages.InMemoryStorage()

study = optuna.create_study(storage=storage)
study.optimize(objective, n_trials=10)
```

Methods

`check_trial_is_updatable`(trial_id, trial_state)	Check whether a trial state is updatable.
`create_new_study`(directions[, study_name])	Create a new study from a name.
`create_new_trial`(study_id[, template_trial])	Create and add a new trial to a study.
`delete_study`(study_id)	Delete a study.
`get_all_studies`()	Read a list of `FrozenStudy` objects.
`get_all_trials`(study_id[, deepcopy, states])	Read all trials in a study.
`get_best_trial`(study_id)	Return the trial with the best value in a study.
`get_n_trials`(study_id[, state])	Count the number of trials in a study.
`get_study_directions`(study_id)	Read whether a study maximizes or minimizes an objective.
`get_study_id_from_name`(study_name)	Read the ID of a study.
`get_study_name_from_id`(study_id)	Read the study name of a study.
`get_study_system_attrs`(study_id)	Read the optuna-internal attributes of a study.
`get_study_user_attrs`(study_id)	Read the user-defined attributes of a study.
`get_trial`(trial_id)	Read a trial.
`get_trial_id_from_study_id_trial_number`(...	Read the trial ID of a trial.
`get_trial_number_from_id`(trial_id)	Read the trial number of a trial.
`get_trial_param`(trial_id, param_name)	Read the parameter of a trial.
`get_trial_params`(trial_id)	Read the parameter dictionary of a trial.
`get_trial_system_attrs`(trial_id)	Read the optuna-internal attributes of a trial.
`get_trial_user_attrs`(trial_id)	Read the user-defined attributes of a trial.
`remove_session`()	Clean up all connections to a database.
`set_study_system_attr`(study_id, key, value)	Register an optuna-internal attribute to a study.
`set_study_user_attr`(study_id, key, value)	Register a user-defined attribute to a study.
`set_trial_intermediate_value`(trial_id, step, ...)	Report an intermediate value of an objective function.
`set_trial_param`(trial_id, param_name, ...)	Set a parameter to a trial.
`set_trial_state_values`(trial_id, state[, values])	Update the state and values of a trial.
`set_trial_system_attr`(trial_id, key, value)	Set an optuna-internal attribute to a trial.
`set_trial_user_attr`(trial_id, key, value)	Set a user-defined attribute to a trial.

`check_trial_is_updatable`(*trial_id*, *trial_state*)

Check whether a trial state is updatable.

Parameters

- **`trial_id`** (*`int`*) – ID of the trial. Only used for an error message.
- **`trial_state`** (`TrialState`) – Trial state to check.

Raises
UpdateFinishedTrialError – If the trial is already finished.

Return type
None

`create_new_study`(*directions*, *study_name=None*)

Create a new study from a name.

If no name is specified, the storage class generates a name. The returned study ID is unique among all current and deleted studies.

Parameters

- **directions** (*Sequence[*`StudyDirection`*]*) – A sequence of direction whose element is either *MAXIMIZE* or *MINIMIZE*.
- **study_name** (*str | None*) – Name of the new study to create.

Returns
ID of the created study.

Raises
optuna.exceptions.DuplicatedStudyError – If a study with the same `study_name` already exists.

Return type
int

`create_new_trial`(*study_id*, *template_trial=None*)

Create and add a new trial to a study.

The returned trial ID is unique among all current and deleted trials.

Parameters

- **study_id** (*int*) – ID of the study.
- **template_trial** (`FrozenTrial` *| None*) – Template *FrozenTrial* with default user-attributes, system-attributes, intermediate-values, and a state.

Returns
ID of the created trial.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
int

`delete_study`(*study_id*)

Delete a study.

Parameters
study_id (*int*) – ID of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

get_all_studies()

Read a list of FrozenStudy objects.

Returns
A list of FrozenStudy objects, sorted by study_id.

Return type
list[*FrozenStudy*]

get_all_trials(*study_id*, *deepcopy=True*, *states=None*)

Read all trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.
- **deepcopy** (*bool*) – Whether to copy the list of trials before returning. Set to True if you intend to update the list or elements of the list.
- **states** (*Container[TrialState] | None*) – Trial states to filter on. If None, include all states.

Returns
List of trials in the study, sorted by trial_id.

Raises
KeyError – If no study with the matching study_id exists.

Return type
list[FrozenTrial]

get_best_trial(*study_id*)

Return the trial with the best value in a study.

This method is valid only during single-objective optimization.

Parameters
study_id (*int*) – ID of the study.

Returns
The trial with the best objective value among all finished trials in the study.

Raises

- **KeyError** – If no study with the matching study_id exists.
- **RuntimeError** – If the study has more than one direction.
- **ValueError** – If no trials have been completed.

Return type
FrozenTrial

get_n_trials(*study_id*, *state=None*)

Count the number of trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.
- **state** (*tuple[TrialState, ...] | TrialState | None*) – Trial states to filter on. If None, include all states.

Returns
Number of trials in the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
int

`get_study_directions`(*study_id*)

Read whether a study maximizes or minimizes an objective.

Parameters
`study_id` (*`int`*) – ID of a study.

Returns
Optimization directions list of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
list[StudyDirection]

`get_study_id_from_name`(*study_name*)

Read the ID of a study.

Parameters
`study_name` (*`str`*) – Name of the study.

Returns
ID of the study.

Raises
`KeyError` – If no study with the matching `study_name` exists.

Return type
int

`get_study_name_from_id`(*study_id*)

Read the study name of a study.

Parameters
`study_id` (*`int`*) – ID of the study.

Returns
Name of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
str

`get_study_system_attrs`(*study_id*)

Read the optuna-internal attributes of a study.

Parameters
`study_id` (*`int`*) – ID of the study.

Returns
Dictionary with the optuna-internal attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

`get_study_user_attrs`(*study_id*)

Read the user-defined attributes of a study.

Parameters
`study_id` (*int*) – ID of the study.

Returns
Dictionary with the user attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

`get_trial`(*trial_id*)

Read a trial.

Parameters
`trial_id` (*int*) – ID of the trial.

Returns
Trial with a matching trial ID.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
FrozenTrial

`get_trial_id_from_study_id_trial_number`(*study_id*, *trial_number*)

Read the trial ID of a trial.

Parameters

- `study_id` (*int*) – ID of the study.
- `trial_number` (*int*) – Number of the trial.

Returns
ID of the trial.

Raises
`KeyError` – If no trial with the matching `study_id` and `trial_number` exists.

Return type
int

`get_trial_number_from_id`(*trial_id*)

Read the trial number of a trial.

Note

The trial number is only unique within a study, and is sequential.

Parameters
`trial_id` (*int*) – ID of the trial.

Returns
Number of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
int

`get_trial_param`(*trial_id*, *param_name*)

Read the parameter of a trial.

Parameters

- **`trial_id`** (`int`) – ID of the trial.
- **`param_name`** (`str`) – Name of the parameter.

Returns
Internal representation of the parameter.

Raises
`KeyError` – If no trial with the matching `trial_id` exists. If no such parameter exists.

Return type
float

`get_trial_params`(*trial_id*)

Read the parameter dictionary of a trial.

Parameters
`trial_id` (`int`) – ID of the trial.

Returns
Dictionary of a parameters. Keys are parameter names and values are external representations of the parameter values.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`get_trial_system_attrs`(*trial_id*)

Read the optuna-internal attributes of a trial.

Parameters
`trial_id` (`int`) – ID of the trial.

Returns
Dictionary with the optuna-internal attributes of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`get_trial_user_attrs`(*trial_id*)

Read the user-defined attributes of a trial.

Parameters
`trial_id` (`int`) – ID of the trial.

Returns
Dictionary with the user-defined attributes of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`remove_session()`

Clean up all connections to a database.

Return type
None

`set_study_system_attr`(*study_id*, *key*, *value*)

Register an optuna-internal attribute to a study.

This method overwrites any existing attribute.

Parameters

- **`study_id`** (*`int`*) – ID of the study.
- **`key`** (*`str`*) – Attribute key.
- **`value`** (*`Mapping[str, JSONSerializable] | Sequence[JSONSerializable] | str | int | float | bool | None`*) – Attribute value. It should be JSON serializable.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

`set_study_user_attr`(*study_id*, *key*, *value*)

Register a user-defined attribute to a study.

This method overwrites any existing attribute.

Parameters

- **`study_id`** (*`int`*) – ID of the study.
- **`key`** (*`str`*) – Attribute key.
- **`value`** (*`Any`*) – Attribute value. It should be JSON serializable.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

`set_trial_intermediate_value`(*trial_id*, *step*, *intermediate_value*)

Report an intermediate value of an objective function.

This method overwrites any existing intermediate value associated with the given step.

Parameters

- **`trial_id`** (*`int`*) – ID of the trial.
- **`step`** (*`int`*) – Step of the trial (e.g., the epoch when training a neural network).

- **intermediate_value** (*float*) – Intermediate value corresponding to the step.

Raises

- **KeyError** – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type
None

set_trial_param(*trial_id*, *param_name*, *param_value_internal*, *distribution*)

Set a parameter to a trial.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **param_name** (*str*) – Name of the parameter.
- **param_value_internal** (*float*) – Internal representation of the parameter value.
- **distribution** (*BaseDistribution*) – Sampled distribution of the parameter.

Raises

- **KeyError** – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type
None

set_trial_state_values(*trial_id*, *state*, *values=None*)

Update the state and values of a trial.

Set return values of an objective function to values argument. If values argument is not `None`, this method overwrites any existing trial values.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **state** (`TrialState`) – New state of the trial.
- **values** (*Sequence[float] | None*) – Values of the objective function.

Returns
`True` if the state is successfully updated. `False` if the state is kept the same. The latter happens when this method tries to update the state of *RUNNING* trial to *RUNNING*.

Raises

- **KeyError** – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type
bool

set_trial_system_attr(*trial_id*, *key*, *value*)

Set an optuna-internal attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.

- **key** (*str*) – Attribute key.
- **value** (*Mapping[str, JSONSerializable] | Sequence[JSONSerializable] | str | int | float | bool | None*) – Attribute value. It should be JSON serializable.

Raises

- **KeyError** – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type

None

set_trial_user_attr(*trial_id*, *key*, *value*)

Set a user-defined attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises

- **KeyError** – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type

None

optuna.storages.run_grpc_proxy_server

optuna.storages.**run_grpc_proxy_server**(*storage*, ***, *host='localhost'*, *port=13000*, *thread_pool=None*)

Run a gRPC server for the given storage URL, host, and port.

Example

Run this server with the following way:

```
from optuna.storages import run_grpc_proxy_server
from optuna.storages import get_storage

storage = get_storage("mysql+pymysql://<user>:<pass>@<host>/<dbname>[?<options>]")
run_grpc_proxy_server(storage, host="localhost", port=13000)
```

Please refer to the client class *GrpcStorageProxy* for the client usage. Please use `get_storage()` instead of *RDBStorage* since `RDBStorage` by itself does not use cache in process and it may cause significant slowdown.

Parameters

- **storage** (*BaseStorage*) – A storage object to proxy.
- **host** (*str*) – Hostname to listen on.
- **port** (*int*) – Port to listen on.

- **thread_pool** (*ThreadPoolExecutor | None*) – Thread pool to use for the server. If `None`, a default thread pool with 10 workers will be used.

Return type
None

Warning

Currently, gRPC storage proxy does not support the *JournalStorage*. This issue is tracked in https://github.com/optuna/optuna/issues/6084. Please use *RDBStorage* instead.

Note

Added in v4.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v4.2.0.

optuna.storages.GrpcStorageProxy

class optuna.storages.**GrpcStorageProxy**(**, host='localhost', port=13000*)

gRPC client for *run_grpc_proxy_server()*.

Example

This is a simple example of using *GrpcStorageProxy* with *run_grpc_proxy_server()*.

```
import optuna
from optuna.storages import GrpcStorageProxy

storage = GrpcStorageProxy(host="localhost", port=13000)
study = optuna.create_study(storage=storage)
```

Please refer to the example in *run_grpc_proxy_server()* for the server side code.

Parameters

- **host** (*str*) – The hostname of the gRPC server.
- **port** (*int*) – The port of the gRPC server.

Warning

Currently, gRPC storage proxy in combination with an SQLite3 database may cause unexpected behaviors when calling *optuna.delete_study()* due to non-invalidated cache.

Note

Added in v4.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v4.2.0.

Methods

check_trial_is_updatable(trial_id, trial_state)	Check whether a trial state is updatable.
close()	Close the gRPC channel.
create_new_study(directions[, study_name])	Create a new study from a name.
create_new_trial(study_id[, template_trial])	Create and add a new trial to a study.
delete_study(study_id)	Delete a study.
get_all_studies()	Read a list of `FrozenStudy` objects.
get_all_trials(study_id[, deepcopy, states])	Read all trials in a study.
get_best_trial(study_id)	Return the trial with the best value in a study.
get_n_trials(study_id[, state])	Count the number of trials in a study.
get_study_directions(study_id)	Read whether a study maximizes or minimizes an objective.
get_study_id_from_name(study_name)	Read the ID of a study.
get_study_name_from_id(study_id)	Read the study name of a study.
get_study_system_attrs(study_id)	Read the optuna-internal attributes of a study.
get_study_user_attrs(study_id)	Read the user-defined attributes of a study.
get_trial(trial_id)	Read a trial.
get_trial_id_from_study_id_trial_number(...	Read the trial ID of a trial.
get_trial_number_from_id(trial_id)	Read the trial number of a trial.
get_trial_param(trial_id, param_name)	Read the parameter of a trial.
get_trial_params(trial_id)	Read the parameter dictionary of a trial.
get_trial_system_attrs(trial_id)	Read the optuna-internal attributes of a trial.
get_trial_user_attrs(trial_id)	Read the user-defined attributes of a trial.
remove_session()	Clean up all connections to a database.
set_study_system_attr(study_id, key, value)	Register an optuna-internal attribute to a study.
set_study_user_attr(study_id, key, value)	Register a user-defined attribute to a study.
set_trial_intermediate_value(trial_id, step, ...)	Report an intermediate value of an objective function.
set_trial_param(trial_id, param_name, ...)	Set a parameter to a trial.
set_trial_state_values(trial_id, state[, values])	Update the state and values of a trial.
set_trial_system_attr(trial_id, key, value)	Set an optuna-internal attribute to a trial.
set_trial_user_attr(trial_id, key, value)	Set a user-defined attribute to a trial.
wait_server_ready([timeout])	Wait until the gRPC server is ready.

check_trial_is_updatable(*trial_id*, *trial_state*)

Check whether a trial state is updatable.

Parameters

- **trial_id** (*int*) – ID of the trial. Only used for an error message.
- **trial_state** (TrialState) – Trial state to check.

Raises

UpdateFinishedTrialError – If the trial is already finished.

Return type

None

close()

Close the gRPC channel.

Return type

None

`create_new_study`(*directions*, *study_name=None*)

Create a new study from a name.

If no name is specified, the storage class generates a name. The returned study ID is unique among all current and deleted studies.

Parameters

- **`directions`** (*`Sequence`*`[StudyDirection]`) – A sequence of direction whose element is either *`MAXIMIZE`* or *`MINIMIZE`*.
- **`study_name`** (*`str | None`*) – Name of the new study to create.

Returns

ID of the created study.

Raises

`optuna.exceptions.DuplicatedStudyError` – If a study with the same `study_name` already exists.

Return type

int

`create_new_trial`(*study_id*, *template_trial=None*)

Create and add a new trial to a study.

The returned trial ID is unique among all current and deleted trials.

Parameters

- **`study_id`** (*`int`*) – ID of the study.
- **`template_trial`** (`FrozenTrial` *`| None`*) – Template *`FrozenTrial`* with default user-attributes, system-attributes, intermediate-values, and a state.

Returns

ID of the created trial.

Raises

`KeyError` – If no study with the matching `study_id` exists.

Return type

int

`delete_study`(*study_id*)

Delete a study.

Parameters

`study_id` (*`int`*) – ID of the study.

Raises

`KeyError` – If no study with the matching `study_id` exists.

Return type

None

`get_all_studies`()

Read a list of `FrozenStudy` objects.

Returns

A list of `FrozenStudy` objects, sorted by `study_id`.

Return type

list[*FrozenStudy*]

get_all_trials(*study_id*, *deepcopy=True*, *states=None*)

Read all trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.
- **deepcopy** (*bool*) – Whether to copy the list of trials before returning. Set to `True` if you intend to update the list or elements of the list.
- **states** (*Container[TrialState] | None*) – Trial states to filter on. If `None`, include all states.

Returns

List of trials in the study, sorted by `trial_id`.

Raises

KeyError – If no study with the matching `study_id` exists.

Return type

list[FrozenTrial]

get_best_trial(*study_id*)

Return the trial with the best value in a study.

This method is valid only during single-objective optimization.

Parameters

study_id (*int*) – ID of the study.

Returns

The trial with the best objective value among all finished trials in the study.

Raises

- **KeyError** – If no study with the matching `study_id` exists.
- **RuntimeError** – If the study has more than one direction.
- **ValueError** – If no trials have been completed.

Return type

FrozenTrial

get_n_trials(*study_id*, *state=None*)

Count the number of trials in a study.

Parameters

- **study_id** (*int*) – ID of the study.
- **state** (*tuple[TrialState, ...] | TrialState | None*) – Trial states to filter on. If `None`, include all states.

Returns

Number of trials in the study.

Raises

KeyError – If no study with the matching `study_id` exists.

Return type

int

`get_study_directions`(*study_id*)

Read whether a study maximizes or minimizes an objective.

Parameters
`study_id` (*int*) – ID of a study.

Returns
Optimization directions list of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
list[StudyDirection]

`get_study_id_from_name`(*study_name*)

Read the ID of a study.

Parameters
`study_name` (*str*) – Name of the study.

Returns
ID of the study.

Raises
`KeyError` – If no study with the matching `study_name` exists.

Return type
int

`get_study_name_from_id`(*study_id*)

Read the study name of a study.

Parameters
`study_id` (*int*) – ID of the study.

Returns
Name of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
str

`get_study_system_attrs`(*study_id*)

Read the optuna-internal attributes of a study.

Parameters
`study_id` (*int*) – ID of the study.

Returns
Dictionary with the optuna-internal attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

`get_study_user_attrs`(*study_id*)

Read the user-defined attributes of a study.

Parameters
`study_id` (*int*) – ID of the study.

Returns
Dictionary with the user attributes of the study.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
dict[str, *Any*]

get_trial(*trial_id*)

Read a trial.

Parameters
`trial_id` (*int*) – ID of the trial.

Returns
Trial with a matching trial ID.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
FrozenTrial

get_trial_id_from_study_id_trial_number(*study_id*, *trial_number*)

Read the trial ID of a trial.

Parameters

- `study_id` (*int*) – ID of the study.
- `trial_number` (*int*) – Number of the trial.

Returns
ID of the trial.

Raises
`KeyError` – If no trial with the matching `study_id` and `trial_number` exists.

Return type
int

get_trial_number_from_id(*trial_id*)

Read the trial number of a trial.

Note

The trial number is only unique within a study, and is sequential.

Parameters
`trial_id` (*int*) – ID of the trial.

Returns
Number of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
int

`get_trial_param`(*trial_id*, *param_name*)

Read the parameter of a trial.

Parameters

- **`trial_id`** (*`int`*) – ID of the trial.
- **`param_name`** (*`str`*) – Name of the parameter.

Returns
Internal representation of the parameter.

Raises
`KeyError` – If no trial with the matching `trial_id` exists. If no such parameter exists.

Return type
float

`get_trial_params`(*trial_id*)

Read the parameter dictionary of a trial.

Parameters
`trial_id` (*`int`*) – ID of the trial.

Returns
Dictionary of a parameters. Keys are parameter names and values are external representations of the parameter values.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`get_trial_system_attrs`(*trial_id*)

Read the optuna-internal attributes of a trial.

Parameters
`trial_id` (*`int`*) – ID of the trial.

Returns
Dictionary with the optuna-internal attributes of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

`get_trial_user_attrs`(*trial_id*)

Read the user-defined attributes of a trial.

Parameters
`trial_id` (*`int`*) – ID of the trial.

Returns
Dictionary with the user-defined attributes of the trial.

Raises
`KeyError` – If no trial with the matching `trial_id` exists.

Return type
dict[str, *Any*]

remove_session()

Clean up all connections to a database.

Return type
None

set_study_system_attr(*study_id*, *key*, *value*)

Register an optuna-internal attribute to a study.

This method overwrites any existing attribute.

Parameters

- **study_id** (*int*) – ID of the study.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

set_study_user_attr(*study_id*, *key*, *value*)

Register a user-defined attribute to a study.

This method overwrites any existing attribute.

Parameters

- **study_id** (*int*) – ID of the study.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises
`KeyError` – If no study with the matching `study_id` exists.

Return type
None

set_trial_intermediate_value(*trial_id*, *step*, *intermediate_value*)

Report an intermediate value of an objective function.

This method overwrites any existing intermediate value associated with the given step.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **step** (*int*) – Step of the trial (e.g., the epoch when training a neural network).
- **intermediate_value** (*float*) – Intermediate value corresponding to the step.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- *`UpdateFinishedTrialError`* – If the trial is already finished.

Return type
None

set_trial_param(*trial_id*, *param_name*, *param_value_internal*, *distribution*)

Set a parameter to a trial.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **param_name** (*str*) – Name of the parameter.
- **param_value_internal** (*float*) – Internal representation of the parameter value.
- **distribution** (*BaseDistribution*) – Sampled distribution of the parameter.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type
None

set_trial_state_values(*trial_id*, *state*, *values=None*)

Update the state and values of a trial.

Set return values of an objective function to values argument. If values argument is not `None`, this method overwrites any existing trial values.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **state** (`TrialState`) – New state of the trial.
- **values** (*Sequence[float] | None*) – Values of the objective function.

Returns
`True` if the state is successfully updated. `False` if the state is kept the same. The latter happens when this method tries to update the state of *RUNNING* trial to *RUNNING*.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.
- ***UpdateFinishedTrialError*** – If the trial is already finished.

Return type
bool

set_trial_system_attr(*trial_id*, *key*, *value*)

Set an optuna-internal attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises

- `KeyError` – If no trial with the matching `trial_id` exists.

- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
None

set_trial_user_attr(*trial_id*, *key*, *value*)

Set a user-defined attribute to a trial.

This method overwrites any existing attribute.

Parameters

- **trial_id** (*int*) – ID of the trial.
- **key** (*str*) – Attribute key.
- **value** (*Any*) – Attribute value. It should be JSON serializable.

Raises

- KeyError – If no trial with the matching `trial_id` exists.
- *UpdateFinishedTrialError* – If the trial is already finished.

Return type
None

wait_server_ready(*timeout=None*)

Wait until the gRPC server is ready.

Parameters
timeout (*float | None*) – The maximum time to wait in seconds. If None, wait indefinitely.

Return type
None

optuna.storages.journal

JournalStorage requires its backend specification and here is the list of the supported backends:

Note

If users would like to use any backends not supported by Optuna, it is possible to do so by creating a customized class by inheriting `optuna.storages.journal.BaseJournalBackend`.

journal.JournalFileBackend	File storage class for Journal log backend.
journal.JournalRedisBackend	Redis storage class for Journal log backend.

optuna.storages.journal.JournalFileBackend

class optuna.storages.journal.**JournalFileBackend**(*file_path*, *lock_obj=None*)

File storage class for Journal log backend.

Compared to SQLite3, the benefit of this backend is that it is more suitable for environments where the file system does not support `fcntl()` file locking. For example, as written in the SQLite3 FAQ, SQLite3 might not work on NFS (Network File System) since `fcntl()` file locking is broken on many NFS implementations. In such scenarios, this backend provides several workarounds for locking files. For more details, refer to the Medium blog post.

It's important to note that, similar to SQLite3, this class doesn't support a high level of write concurrency, as outlined in the SQLAlchemy documentation. However, in typical situations where the objective function is computationally expensive, Optuna users don't need to be concerned about this limitation. The reason being, the write operations are not the bottleneck as long as the objective function doesn't invoke `report()` and `set_user_attr()` excessively.

Parameters

- **`file_path`** (*`str`*) – Path of file to persist the log to.
- **`lock_obj`** (*`BaseJournalFileLock | None`*) – Lock object for process exclusivity. An instance of `JournalFileSymlinkLock` and `JournalFileOpenLock` can be passed.

Methods

`append_logs`(logs)	Append logs to the backend.
`read_logs`(log_number_from)	Read logs with a log number greater than or equal to `log_number_from`.

`append_logs`(*logs*)

Append logs to the backend.

Parameters
`logs` (*`list[dict[str, Any]]`*) – A list that contains json-serializable logs.

Return type
None

`read_logs`(*log_number_from*)

Read logs with a log number greater than or equal to `log_number_from`.

If `log_number_from` is 0, read all the logs.

Parameters
`log_number_from` (*`int`*) – A non-negative integer value indicating which logs to read.

Returns
Logs with log number greater than or equal to `log_number_from`.

Return type
list[dict[str, *Any*]]

optuna.storages.journal.JournalRedisBackend

class `optuna.storages.journal.`**`JournalRedisBackend`**(*url*, *use_cluster=False*, *prefix=''*)

Redis storage class for Journal log backend.

Parameters

- **`url`** (*`str`*) – URL of the redis storage, password and db are optional. (ie: `redis://localhost:6379`)
- **`use_cluster`** (*`bool`*) – Flag whether you use the Redis cluster. If this is `False`, it is assumed that you use the standalone Redis server and ensured that a write operation is atomic. This provides the consistency of the preserved logs. If this is `True`, it is assumed that you use the

Redis cluster and not ensured that a write operation is atomic. This means the preserved logs can be inconsistent due to network errors, and may cause errors.

- **prefix** (*str*) – Prefix of the preserved key of logs. This is useful when multiple users work on one Redis server.

Note

Added in v3.1.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

Methods

append_logs(logs)	Append logs to the backend.
load_snapshot()	Load snapshot from the backend.
read_logs(log_number_from)	Read logs with a log number greater than or equal to `log_number_from`.
save_snapshot(snapshot)	Save snapshot to the backend.

append_logs(*logs*)

Append logs to the backend.

Parameters
logs (*list[dict[str, Any]]*) – A list that contains json-serializable logs.

Return type
None

load_snapshot()

Load snapshot from the backend.

Returns
A serialized snapshot (bytes) if found, otherwise `None`.

Return type
bytes | None

read_logs(*log_number_from*)

Read logs with a log number greater than or equal to `log_number_from`.

If `log_number_from` is 0, read all the logs.

Parameters
log_number_from (*int*) – A non-negative integer value indicating which logs to read.

Returns
Logs with log number greater than or equal to `log_number_from`.

Return type
list[dict[str, *Any*]]

save_snapshot(*snapshot*)

Save snapshot to the backend.

Parameters
snapshot (*bytes*) – A serialized snapshot (bytes)

Return type
None

Users can flexibly choose a lock object for *JournalFileBackend* and here is the list of supported lock objects:

journal.JournalFileSymlinkLock	Lock class for synchronizing processes for NFSv2 or later.
journal.JournalFileOpenLock	Lock class for synchronizing processes for NFSv3 or later.

optuna.storages.journal.JournalFileSymlinkLock

`class optuna.storages.journal.`**`JournalFileSymlinkLock`**`(`*filepath*, *grace_period=30*`)`

Lock class for synchronizing processes for NFSv2 or later.

On acquiring the lock, link system call is called to create an exclusive file. The file is deleted when the lock is released. In NFS environments prior to NFSv3, use this instead of *JournalFileOpenLock*.

Parameters

- **filepath** (*str*) – The path of the file whose race condition must be protected.
- **grace_period** (*int | None*) – Grace period before an existing lock is forcibly released.

Methods

acquire()	Acquire a lock in a blocking way by creating a symbolic link of a file.
release()	Release a lock by removing the symbolic link.

acquire()

Acquire a lock in a blocking way by creating a symbolic link of a file.

Returns
`True` if it succeeded in creating a symbolic link of `self._lock_target_file`.

Return type
bool

release()

Release a lock by removing the symbolic link.

Return type
None

optuna.storages.journal.JournalFileOpenLock

`class optuna.storages.journal.`**`JournalFileOpenLock`**`(`*filepath*, *grace_period=30*`)`

Lock class for synchronizing processes for NFSv3 or later.

On acquiring the lock, open system call is called with the O_EXCL option to create an exclusive file. The file is deleted when the lock is released. This class is only supported when using NFSv3 or later on kernel 2.6 or later. In prior NFS environments, use *JournalFileSymlinkLock*.

Parameters

- **filepath** (*str*) – The path of the file whose race condition must be protected.

- **grace_period** (*int | None*) – Grace period before an existing lock is forcibly released.

Methods

acquire()	Acquire a lock in a blocking way by creating a lock file.
release()	Release a lock by removing the created file.

acquire()

Acquire a lock in a blocking way by creating a lock file.

Returns
`True` if it succeeded in creating a `self._lock_file`.

Return type
bool

release()

Release a lock by removing the created file.

Return type
None

Deprecated Modules

Note

The following modules are deprecated at v4.0.0 and will be removed in the future. Please use the modules defined in `optuna.storages.journal`.

BaseJournalLogStorage	Base class for Journal storages.
JournalFileStorage	
JournalRedisStorage	

optuna.storages.BaseJournalLogStorage

class optuna.storages.**BaseJournalLogStorage**(**args*, ***kwargs*)

Base class for Journal storages.

Storage classes implementing this base class must guarantee process safety. This means, multiple processes might concurrently call `read_logs` and `append_logs`. If the backend storage does not internally support mutual exclusion mechanisms, such as locks, you might want to use *JournalFileSymlinkLock* or *JournalFileOpenLock* for creating a critical section.

Warning

Deprecated in v4.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v4.0.0.

Use `BaseJournalBackend` instead.

Methods

append_logs(logs)	Append logs to the backend.
read_logs(log_number_from)	Read logs with a log number greater than or equal to `log_number_from`.

abstractmethod append_logs(*logs*)

Append logs to the backend.

Parameters

logs (*list[dict[str, Any]]*) – A list that contains json-serializable logs.

Return type

None

abstractmethod read_logs(*log_number_from*)

Read logs with a log number greater than or equal to `log_number_from`.

If `log_number_from` is 0, read all the logs.

Parameters

log_number_from (*int*) – A non-negative integer value indicating which logs to read.

Returns

Logs with log number greater than or equal to `log_number_from`.

Return type

list[dict[str, *Any*]]

optuna.storages.JournalFileStorage

class optuna.storages.**JournalFileStorage**(*file_path*, *lock_obj=None*)

Warning

Deprecated in v4.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v4.0.0.

Use *JournalFileBackend* instead.

Methods

append_logs(logs)	Append logs to the backend.
read_logs(log_number_from)	Read logs with a log number greater than or equal to `log_number_from`.

Parameters

- **file_path** (*str*)
- **lock_obj** (*BaseJournalFileLock | None*)

append_logs(*logs*)

Append logs to the backend.

Parameters
`logs` (*list[dict[str, Any]]*) – A list that contains json-serializable logs.

Return type
None

read_logs(*log_number_from*)

Read logs with a log number greater than or equal to `log_number_from`.

If `log_number_from` is 0, read all the logs.

Parameters
`log_number_from` (*int*) – A non-negative integer value indicating which logs to read.

Returns
Logs with log number greater than or equal to `log_number_from`.

Return type
list[dict[str, *Any*]]

optuna.storages.JournalRedisStorage

class optuna.storages.**JournalRedisStorage**(*url*, *use_cluster=False*, *prefix=''*)

> **Warning**
>
> Deprecated in v4.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v4.0.0.
>
> Use *JournalRedisBackend* instead.

Methods

append_logs(logs)	Append logs to the backend.
load_snapshot()	Load snapshot from the backend.
read_logs(log_number_from)	Read logs with a log number greater than or equal to `log_number_from`.
save_snapshot(snapshot)	Save snapshot to the backend.

Parameters

- **url** (*str*)
- **use_cluster** (*bool*)
- **prefix** (*str*)

append_logs(*logs*)

Append logs to the backend.

Parameters
`logs` (*list[dict[str, Any]]*) – A list that contains json-serializable logs.

Return type
None

`load_snapshot()`

Load snapshot from the backend.

Returns
A serialized snapshot (bytes) if found, otherwise `None`.

Return type
bytes | None

`read_logs`(*log_number_from*)

Read logs with a log number greater than or equal to `log_number_from`.

If `log_number_from` is 0, read all the logs.

Parameters
log_number_from (*int*) – A non-negative integer value indicating which logs to read.

Returns
Logs with log number greater than or equal to `log_number_from`.

Return type
list[dict[str, *Any*]]

`save_snapshot`(*snapshot*)

Save snapshot to the backend.

Parameters
snapshot (*bytes*) – A serialized snapshot (bytes)

Return type
None

8.3.13 optuna.study

The `study` module implements the `Study` object and related functions. A public constructor is available for the `Study` class, but direct use of this constructor is not recommended. Instead, library users should create and load a `Study` using `create_study()` and `load_study()` respectively.

`Study`	A study corresponds to an optimization task, i.e., a set of trials.
`create_study`	Create a new `Study`.
`load_study`	Load the existing `Study` that has the specified name.
`delete_study`	Delete a `Study` object.
`copy_study`	Copy study from one storage to another.
`get_all_study_names`	Get all study names stored in a specified storage.
`get_all_study_summaries`	Get all history of studies stored in a specified storage.
`MaxTrialsCallback`	Set a maximum number of trials before ending the study.
`StudyDirection`	Direction of a `Study`.
`StudySummary`	Basic attributes and aggregated results of a `Study`.

optuna.study.Study

class optuna.study.**Study**(*study_name*, *storage*, *sampler=None*, *pruner=None*)

A study corresponds to an optimization task, i.e., a set of trials.

This object provides interfaces to run a new *Trial*, access trials' history, set/get user-defined attributes of the study itself.

Note that the direct use of this constructor is not recommended. To create and load a study, please refer to the documentation of *create_study()* and *load_study()* respectively.

Methods

add_trial(trial)	Add trial to study.
add_trials(trials)	Add trials to study.
ask([fixed_distributions])	Create a new trial from which hyperparameters can be suggested.
enqueue_trial(params[, user_attrs, ...])	Enqueue a trial with given parameter values.
get_trials([deepcopy, states])	Return all trials in the study.
optimize(func[, n_trials, timeout, n_jobs, ...])	Optimize an objective function.
set_metric_names(metric_names)	Set metric names.
set_system_attr(key, value)	Set a system attribute to the study.
set_user_attr(key, value)	Set a user attribute to the study.
stop()	Exit from the current optimization loop after the running trials finish.
tell(trial[, values, state, skip_if_finished])	Finish a trial created with *ask()*.
trials_dataframe([attrs, multi_index])	Export trials as a pandas DataFrame.

Attributes

best_params	Return parameters of the best trial in the study.
best_trial	Return the best trial in the study.
best_trials	Return trials located at the Pareto front in the study.
best_value	Return the best objective value in the study.
direction	Return the direction of the study.
directions	Return the directions of the study.
metric_names	Return metric names.
system_attrs	Return system attributes.
trials	Return all trials in the study.
user_attrs	Return user attributes.

Parameters

- **study_name** (*str*)
- **storage** (*str | storages.BaseStorage*)
- **sampler** (*'samplers.BaseSampler' | None*)
- **pruner** (pruners.BasePruner | *None*)

add_trial(*trial*)

Add trial to study.

The trial is validated before being added.

Example

```python
import optuna
from optuna.distributions import FloatDistribution


def objective(trial):
    x = trial.suggest_float("x", 0, 10)
    return x**2


study = optuna.create_study()
assert len(study.trials) == 0

trial = optuna.trial.create_trial(
    params={"x": 2.0},
    distributions={"x": FloatDistribution(0, 10)},
    value=4.0,
)

study.add_trial(trial)
assert len(study.trials) == 1

study.optimize(objective, n_trials=3)
assert len(study.trials) == 4

other_study = optuna.create_study()

for trial in study.trials:
    other_study.add_trial(trial)
assert len(other_study.trials) == len(study.trials)

other_study.optimize(objective, n_trials=2)
assert len(other_study.trials) == len(study.trials) + 2
```

See also

This method should in general be used to add already evaluated trials (`trial.state.is_finished() == True`). To queue trials for evaluation, please refer to *`enqueue_trial()`*.

See also

See *`create_trial()`* for how to create trials.

See also

Please refer to add_trial_tutorial for the tutorial of specifying hyperparameters with the evaluated value manually.

Parameters
 trial (FrozenTrial) – Trial to add.

Return type
 None

add_trials(*trials*)

Add trials to study.

The trials are validated before being added.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 10)
    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=3)
assert len(study.trials) == 3

other_study = optuna.create_study()
other_study.add_trials(study.trials)
assert len(other_study.trials) == len(study.trials)

other_study.optimize(objective, n_trials=2)
assert len(other_study.trials) == len(study.trials) + 2
```

See also

See *add_trial()* for addition of each trial.

Parameters
 trials (*Iterable*[FrozenTrial]) – Trials to add.

Return type
 None

ask(*fixed_distributions=None*)

Create a new trial from which hyperparameters can be suggested.

This method is part of an alternative to *optimize()* that allows controlling the lifetime of a trial outside the scope of `func`. Each call to this method should be followed by a call to *tell()* to finish the created trial.

See also

The ask_and_tell tutorial provides use-cases with examples.

Example

Getting the trial object with the *ask()* method.

```
import optuna


study = optuna.create_study()

trial = study.ask()

x = trial.suggest_float("x", -1, 1)

study.tell(trial, x**2)
```

Example

Passing previously defined distributions to the *ask()* method.

```
import optuna


study = optuna.create_study()

distributions = {
    "optimizer": optuna.distributions.CategoricalDistribution(["adam", "sgd"]),
    "lr": optuna.distributions.FloatDistribution(0.0001, 0.1, log=True),
}

# You can pass the distributions previously defined.
trial = study.ask(fixed_distributions=distributions)

# `optimizer` and `lr` are already suggested and accessible with `trial.params`.
assert "optimizer" in trial.params
assert "lr" in trial.params
```

Parameters

fixed_distributions (*dict[str, BaseDistribution] | None*) – A dictionary containing the parameter names and parameter's distributions. Each parameter in this dictionary is automatically suggested for the returned trial, even when the suggest method is not explicitly invoked by the user. If this argument is set to `None`, no parameter is automatically suggested.

Returns

A *Trial*.

Return type

Trial

property best_params: dict[str, Any]

Return parameters of the best trial in the study.

Note

This feature can only be used for single-objective optimization.

Returns

A dictionary containing parameters of the best trial.

property best_trial: *FrozenTrial*

Return the best trial in the study.

Note

This feature can only be used for single-objective optimization. If your study is multi-objective, use *best_trials* instead.

Returns

A *FrozenTrial* object of the best trial.

See also

The reuse_best_trial tutorial provides a detailed example of how to use this method.

property best_trials: list[*FrozenTrial*]

Return trials located at the Pareto front in the study.

A trial is located at the Pareto front if there are no trials that dominate the trial. It's called that a trial `t0` dominates another trial `t1` if `all(v0 <= v1) for v0, v1 in zip(t0.values, t1.values)` and `any(v0 < v1) for v0, v1 in zip(t0.values, t1.values)` are held.

Returns

A list of *FrozenTrial* objects.

property best_value: float

Return the best objective value in the study.

Note

This feature can only be used for single-objective optimization.

Returns

A float representing the best objective value.

property direction: *StudyDirection*

Return the direction of the study.

Note

This feature can only be used for single-objective optimization. If your study is multi-objective, use *directions* instead.

Returns
A *StudyDirection* object.

property directions: list[*StudyDirection*]

Return the directions of the study.

Returns
A list of *StudyDirection* objects.

enqueue_trial(*params*, *user_attrs=None*, *skip_if_exists=False*)

Enqueue a trial with given parameter values.

You can fix the next sampling parameters which will be evaluated in your objective function.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 10)
    return x**2


study = optuna.create_study()
study.enqueue_trial({"x": 5})
study.enqueue_trial({"x": 0}, user_attrs={"memo": "optimal"})
study.optimize(objective, n_trials=2)

assert study.trials[0].params == {"x": 5}
assert study.trials[1].params == {"x": 0}
assert study.trials[1].user_attrs == {"memo": "optimal"}
```

Parameters

- **params** (*dict[str, Any]*) – Parameter values to pass your objective function.
- **user_attrs** (*dict[str, Any] | None*) – A dictionary of user-specific attributes other than `params`.
- **skip_if_exists** (*bool*) – When `True`, prevents duplicate trials from being enqueued again.

Note

This method might produce duplicated trials if called simultaneously by multiple processes at the same time with same `params` dict.

Return type
None

See also

Please refer to enqueue_trial_tutorial for the tutorial of specifying hyperparameters manually.

get_trials(*deepcopy=True*, *states=None*)

Return all trials in the study.

The returned trials are ordered by trial number.

See also

See *trials* for related property.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=3)

trials = study.get_trials()
assert len(trials) == 3
```

Parameters

- **deepcopy** (*bool*) – Flag to control whether to apply `copy.deepcopy()` to the trials. Note that if you set the flag to `False`, you shouldn't mutate any fields of the returned trial. Otherwise the internal state of the study may corrupt and unexpected behavior may happen.
- **states** (*Container[TrialState] | None*) – Trial states to filter on. If `None`, include all states.

Returns
A list of *FrozenTrial* objects.

Return type
list[*FrozenTrial*]

property metric_names: list[str] | None

Return metric names.

Note

Use *set_metric_names()* to set the metric names first.

Returns

A list with names for each dimension of the returned values of the objective function.

optimize(*func*, *n_trials=None*, *timeout=None*, *n_jobs=1*, *catch=()*, *callbacks=None*, *gc_after_trial=False*, *show_progress_bar=False*)

Optimize an objective function.

Optimization is done by choosing a suitable set of hyperparameter values from a given range. Uses a sampler which implements the task of value suggestion based on a specified distribution. The sampler is specified in *create_study()* and the default choice for the sampler is TPE. See also *TPESampler* for more details on 'TPE'.

Optimization will be stopped when receiving a termination signal such as SIGINT and SIGTERM. Unlike other signals, a trial is automatically and cleanly failed when receiving SIGINT (Ctrl+C). If `n_jobs` is greater than one or if another signal than SIGINT is used, the interrupted trial state won't be properly updated.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=3)
```

Parameters

- **func** (*ObjectiveFuncType*) – A callable that implements objective function.
- **n_trials** (*int | None*) – The number of trials for each process. `None` represents no limit in terms of the number of trials. The study continues to create trials until the number of trials reaches `n_trials`, `timeout` period elapses, *stop()* is called, or a termination signal such as SIGTERM or Ctrl+C is received.

  See also

  optuna.study.MaxTrialsCallback can ensure how many times trials will be performed across all processes.

- **timeout** (*float | None*) – Stop study after the given number of second(s). `None` represents no limit in terms of elapsed time. The study continues to create trials until the number of trials reaches `n_trials`, `timeout` period elapses, *stop()* is called or, a termination signal such as SIGTERM or Ctrl+C is received.

- **n_jobs** (*int*) – The number of parallel jobs. If this argument is set to -1, the number is set to CPU count.

  Note

  n_jobs allows parallelization using threading and may suffer from Python's GIL. It is recommended to use process-based parallelization if func is CPU bound.

- **catch** (*Iterable[type[Exception]] | type[Exception]*) – A study continues to run even when a trial raises one of the exceptions specified in this argument. Default is an empty tuple, i.e. the study will stop for any exception except for *TrialPruned*.
- **callbacks** (*Iterable[Callable[[Study, FrozenTrial], None]] | None*) – List of callback functions that are invoked at the end of each trial. Each function must accept two parameters with the following types in this order: *Study* and *FrozenTrial*.

  See also

  See the tutorial of optuna_callback for how to use and implement callback functions.

- **gc_after_trial** (*bool*) – Flag to determine whether to automatically run garbage collection after each trial. Set to True to run the garbage collection, False otherwise. When it runs, it runs a full collection by internally calling gc.collect(). If you see an increase in memory consumption over several trials, try setting this flag to True.

  See also

  How do I avoid running out of memory (OOM) when optimizing studies?

- **show_progress_bar** (*bool*) – Flag to show progress bars or not. To show progress bar, set this True. Note that it is disabled when n_trials is None, timeout is not None, and n_jobs $\neq 1$.

Raises
RuntimeError – If nested invocation of this method occurs.

Return type
None

set_metric_names(*metric_names*)

Set metric names.

This method names each dimension of the returned values of the objective function. It is particularly useful in multi-objective optimization. The metric names are mainly referenced by the visualization functions.

Example

```
import optuna
import pandas


def objective(trial):
```

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```
    x = trial.suggest_float("x", 0, 10)
    return x**2, x + 1


study = optuna.create_study(directions=["minimize", "minimize"])
study.set_metric_names(["x**2", "x+1"])
study.optimize(objective, n_trials=3)

df = study.trials_dataframe(multi_index=True)
assert isinstance(df, pandas.DataFrame)
assert list(df.get("values").keys()) == ["x**2", "x+1"]
```

See also

The names set by this method are used in *trials_dataframe()* and *plot_pareto_front()*.

Parameters
: **metric_names** (*list[str]*) – A list of metric names for the objective function.

Return type
: None

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

set_system_attr(*key*, *value*)

Set a system attribute to the study.

Note that Optuna internally uses this method to save system messages. Please use *set_user_attr()* to set users' attributes.

Parameters

- **key** (*str*) – A key string of the attribute.
- **value** (*Any*) – A value of the attribute. The value should be JSON serializable.

Return type
: None

Warning

Deprecated in v3.1.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

set_user_attr(*key*, *value*)

Set a user attribute to the study.

See also

See *user_attrs* for related attribute.

See also

See the recipe on attributes.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 1)
    y = trial.suggest_float("y", 0, 1)
    return x**2 + y**2


study = optuna.create_study()

study.set_user_attr("objective function", "quadratic function")
study.set_user_attr("dimensions", 2)
study.set_user_attr("contributors", ["Akiba", "Sano"])

assert study.user_attrs == {
    "objective function": "quadratic function",
    "dimensions": 2,
    "contributors": ["Akiba", "Sano"],
}
```

Parameters

- **key** (*str*) – A key string of the attribute.
- **value** (*Any*) – A value of the attribute. The value should be JSON serializable.

Return type

None

stop()

Exit from the current optimization loop after the running trials finish.

This method lets the running *optimize()* method return immediately after all trials which the *optimize()* method spawned finishes. This method does not affect any behaviors of parallel or successive study processes. This method only works when it is called inside an objective function or callback.

Example

```
import optuna
```

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```python
def objective(trial):
    if trial.number == 4:
        trial.study.stop()
    x = trial.suggest_float("x", 0, 10)
    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=10)
assert len(study.trials) == 5
```

Return type
None

property system_attrs: dict[str, Any]

Return system attributes.

Returns
A dictionary containing all system attributes.

> **Warning**
>
> Deprecated in v3.1.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

tell(*trial*, *values=None*, *state=None*, *skip_if_finished=False*)

Finish a trial created with `ask()`.

> **See also**
>
> The ask_and_tell tutorial provides use-cases with examples.

Example

```python
import optuna
from optuna.trial import TrialState


def f(x):
    return (x - 2) ** 2


def df(x):
    return 2 * x - 4


study = optuna.create_study()
```

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```
n_trials = 30

for _ in range(n_trials):
    trial = study.ask()

    lr = trial.suggest_float("lr", 1e-5, 1e-1, log=True)

    # Iterative gradient descent objective function.
    x = 3  # Initial value.
    for step in range(128):
        y = f(x)

        trial.report(y, step=step)

        if trial.should_prune():
            # Finish the trial with the pruned state.
            study.tell(trial, state=TrialState.PRUNED)
            break

        gy = df(x)
        x -= gy * lr
    else:
        # Finish the trial with the final value after all iterations.
        study.tell(trial, y)
```

Parameters

- **trial** (`Trial` | *int*) – A *Trial* object or a trial number.
- **values** (*float* | *Sequence[float]* | *None*) – Optional objective value or a sequence of such values in case the study is used for multi-objective optimization. Argument must be provided if `state` is *COMPLETE* and should be `None` if `state` is *FAIL* or *PRUNED*.
- **state** (`TrialState` | *None*) – State to be reported. Must be `None`, *COMPLETE*, *FAIL* or *PRUNED*. If `state` is `None`, it will be updated to *COMPLETE* or *FAIL* depending on whether validation for `values` reported succeed or not.
- **skip_if_finished** (*bool*) – Flag to control whether exception should be raised when values for already finished trial are told. If `True`, tell is skipped without any error when the trial is already finished.

Returns

A *FrozenTrial* representing the resulting trial. A returned trial is deep copied thus user can modify it as needed.

Return type

FrozenTrial

property trials: list[*FrozenTrial*]

Return all trials in the study.

The returned trials are ordered by trial number.

This is a short form of `self.get_trials(deepcopy=True, states=None)`.

Returns

A list of *FrozenTrial* objects.

See also

See *get_trials()* for related method.

trials_dataframe(*attrs=('number', 'value', 'datetime_start', 'datetime_complete', 'duration', 'params', 'user_attrs', 'system_attrs', 'state')*, *multi_index=False*)

Export trials as a pandas DataFrame.

The DataFrame provides various features to analyze studies. It is also useful to draw a histogram of objective values and to export trials as a CSV file. If there are no trials, an empty DataFrame is returned.

Example

```python
import optuna
import pandas


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=3)

# Create a dataframe from the study.
df = study.trials_dataframe()
assert isinstance(df, pandas.DataFrame)
assert df.shape[0] == 3  # n_trials.
```

Parameters

- **attrs** (*tuple[str, ...]*) – Specifies field names of *FrozenTrial* to include them to a DataFrame of trials.
- **multi_index** (*bool*) – Specifies whether the returned DataFrame employs MultiIndex or not. Columns that are hierarchical by nature such as `(params, x)` will be flattened to `params_x` when set to `False`.

Returns

A pandas DataFrame of trials in the *Study*.

Return type

pd.DataFrame

Note

If `value` is in `attrs` during multi-objective optimization, it is implicitly replaced with `values`.

Note

If *set_metric_names()* is called, the `value` or `values` is implicitly replaced with the dictionary with the objective name as key and the objective value as value.

property user_attrs: dict[str, Any]

Return user attributes.

See also

See *set_user_attr()* for related method.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 1)
    y = trial.suggest_float("y", 0, 1)
    return x**2 + y**2


study = optuna.create_study()

study.set_user_attr("objective function", "quadratic function")
study.set_user_attr("dimensions", 2)
study.set_user_attr("contributors", ["Akiba", "Sano"])

assert study.user_attrs == {
    "objective function": "quadratic function",
    "dimensions": 2,
    "contributors": ["Akiba", "Sano"],
}
```

Returns

A dictionary containing all user attributes.

optuna.study.create_study

`optuna.study.`**`create_study`**`(`*, *storage=None*, *sampler=None*, *pruner=None*, *study_name=None*, *direction=None*, *load_if_exists=False*, *directions=None*`)`

Create a new *Study*.

Example

```
import optuna


def objective(trial):
```

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```
    x = trial.suggest_float("x", 0, 10)
    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=3)
```

Parameters

- **storage** (*str* | *storages.BaseStorage* | *None*) – Database URL. If this argument is set to None, *InMemoryStorage* is used, and the *Study* will not be persistent.

  Note

  When a database URL is passed, Optuna internally uses SQLAlchemy to handle the database. Please refer to SQLAlchemy's document for further details. If you want to specify non-default options to SQLAlchemy Engine, you can instantiate *RDBStorage* with your desired options and pass it to the `storage` argument instead of a URL.

- **sampler** (*'samplers.BaseSampler'* | *None*) – A sampler object that implements background algorithm for value suggestion. If `None` is specified, *TPESampler* is used during single-objective optimization and *NSGAIISampler* during multi-objective optimization. See also *samplers*.
- **pruner** (pruners.BasePruner | *None*) – A pruner object that decides early stopping of unpromising trials. If `None` is specified, *MedianPruner* is used as the default. See also *pruners*.
- **study_name** (*str* | *None*) – Study's name. If this argument is set to None, a unique name is generated automatically.
- **direction** (*str* | StudyDirection | *None*) – Direction of optimization. Set `minimize` for minimization and `maximize` for maximization. You can also pass the corresponding *StudyDirection* object. `direction` and `directions` must not be specified at the same time.

  Note

  If none of *direction* and *directions* are specified, the direction of the study is set to "minimize".

- **load_if_exists** (*bool*) – Flag to control the behavior to handle a conflict of study names. In the case where a study named `study_name` already exists in the `storage`, a *DuplicatedStudyError* is raised if `load_if_exists` is set to `False`. Otherwise, the creation of the study is skipped, and the existing one is returned.
- **directions** (*Sequence[str* | StudyDirection*]* | *None*) – A sequence of directions during multi-objective optimization. `direction` and `directions` must not be specified at the same time.

Returns

A *Study* object.

Return type
Study

See also

optuna.create_study() is an alias of *optuna.study.create_study()*.

See also

The rdb tutorial provides concrete examples to save and resume optimization using RDB.

optuna.study.load_study

optuna.study.**load_study**(**, study_name, storage, sampler=None, pruner=None*)

Load the existing *Study* that has the specified name.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 10)
    return x**2


study = optuna.create_study(storage="sqlite:///example.db", study_name="my_study")
study.optimize(objective, n_trials=3)

loaded_study = optuna.load_study(study_name="my_study", storage="sqlite:///example.
↪db")
assert len(loaded_study.trials) == len(study.trials)
```

Parameters

- **study_name** (*str | None*) – Study's name. Each study has a unique name as an identifier. If None, checks whether the storage contains a single study, and if so loads that study. study_name is required if there are multiple studies in the storage.
- **storage** (*str | storages.BaseStorage*) – Database URL such as sqlite:///example.db. Please see also the documentation of *create_study()* for further details.
- **sampler** (*'samplers.BaseSampler' | None*) – A sampler object that implements background algorithm for value suggestion. If None is specified, *TPESampler* is used as the default. See also *samplers*.
- **pruner** (pruners.BasePruner *| None*) – A pruner object that decides early stopping of unpromising trials. If None is specified, *MedianPruner* is used as the default. See also *pruners*.

Returns
A *Study* object.

Return type
Study

See also

optuna.load_study() is an alias of *optuna.study.load_study()*.

optuna.study.delete_study

optuna.study.**delete_study**(*, *study_name*, *storage*)

Delete a *Study* object.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2


study = optuna.create_study(study_name="example-study", storage="sqlite:///example.
↪db")
study.optimize(objective, n_trials=3)

optuna.delete_study(study_name="example-study", storage="sqlite:///example.db")
```

Parameters

- **study_name** (*str*) – Study's name.
- **storage** (*str | BaseStorage*) – Database URL such as sqlite:///example.db. Please see also the documentation of *create_study()* for further details.

Return type
None

See also

optuna.delete_study() is an alias of *optuna.study.delete_study()*.

optuna.study.copy_study

optuna.study.**copy_study**(*, *from_study_name*, *from_storage*, *to_storage*, *to_study_name=None*)

Copy study from one storage to another.

The direction(s) of the objective(s) in the study, trials, user attributes and system attributes are copied.

Note

copy_study() copies a study even if the optimization is working on. It means users will get a copied study that contains a trial that is not finished.

Example

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2


study = optuna.create_study(
    study_name="example-study",
    storage="sqlite:///example.db",
)
study.optimize(objective, n_trials=3)

optuna.copy_study(
    from_study_name="example-study",
    from_storage="sqlite:///example.db",
    to_storage="sqlite:///example_copy.db",
)

study = optuna.load_study(
    study_name=None,
    storage="sqlite:///example_copy.db",
)
```

Parameters

- **from_study_name** (*str*) – Name of study.
- **from_storage** (*str | BaseStorage*) – Source database URL such as `sqlite:///example.db`. Please see also the documentation of *create_study()* for further details.
- **to_storage** (*str | BaseStorage*) – Destination database URL.
- **to_study_name** (*str | None*) – Name of the created study. If omitted, `from_study_name` is used.

Raises

DuplicatedStudyError – If a study with a conflicting name already exists in the destination storage.

Return type

None

optuna.study.get_all_study_names

optuna.study.**get_all_study_names**(*storage*)

Get all study names stored in a specified storage.

Example

```python
import optuna


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2


study = optuna.create_study(study_name="example-study", storage="sqlite:///example.
↪db")
study.optimize(objective, n_trials=3)

study_names = optuna.study.get_all_study_names(storage="sqlite:///example.db")
assert len(study_names) == 1

assert study_names[0] == "example-study"
```

Parameters

storage (*str | BaseStorage*) – Database URL such as `sqlite:///example.db`. Please see also the documentation of *create_study()* for further details.

Returns

List of all study names in the storage.

Return type

list[str]

See also

optuna.get_all_study_names() is an alias of *optuna.study.get_all_study_names()*.

optuna.study.get_all_study_summaries

optuna.study.**get_all_study_summaries**(*storage*, *include_best_trial=True*)

Get all history of studies stored in a specified storage.

Example

```python
import optuna


def objective(trial):
    x = trial.suggest_float("x", -10, 10)
    return (x - 2) ** 2

```

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```
study = optuna.create_study(study_name="example-study", storage="sqlite:///example.
↪db")
study.optimize(objective, n_trials=3)

study_summaries = optuna.study.get_all_study_summaries(storage="sqlite:///example.db
↪")
assert len(study_summaries) == 1

study_summary = study_summaries[0]
assert study_summary.study_name == "example-study"
```

Parameters

- **storage** (*str | BaseStorage*) – Database URL such as `sqlite:///example.db`. Please see also the documentation of *create_study()* for further details.
- **include_best_trial** (*bool*) – Include the best trials if exist. It potentially increases the number of queries and may take longer to fetch summaries depending on the storage.

Returns
List of study history summarized as *StudySummary* objects.

Return type
list[StudySummary]

See also

optuna.get_all_study_summaries() is an alias of *optuna.study.get_all_study_summaries()*.

optuna.study.MaxTrialsCallback

class optuna.study.**MaxTrialsCallback**(*n_trials*, *states=(1,)*)

Set a maximum number of trials before ending the study.

While the `n_trials` argument of *optuna.study.Study.optimize()* sets the number of trials that will be run, you may want to continue running until you have a certain number of successfully completed trials or stop the study when you have a certain number of trials that fail. This `MaxTrialsCallback` class allows you to set a maximum number of trials for a particular *TrialState* before stopping the study.

Example

```
import optuna
from optuna.study import MaxTrialsCallback
from optuna.trial import TrialState


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    return x**2
```

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```
study = optuna.create_study()
study.optimize(
    objective,
    callbacks=[MaxTrialsCallback(10, states=(TrialState.COMPLETE,))],
)
```

Parameters

- **n_trials** (*int*) – The max number of trials. Must be set to an integer.
- **states** (*Container[TrialState] | None*) – Tuple of the *TrialState* to be counted towards the max trials limit. Default value is `(TrialState.COMPLETE,)`. If `None`, count all states.

optuna.study.StudyDirection

class optuna.study.**StudyDirection**(**values*)

Direction of a *Study*.

NOT_SET

Direction has not been set.

MINIMIZE

Study minimizes the objective function.

MAXIMIZE

Study maximizes the objective function.

Methods

`conjugate`	Returns self, the complex conjugate of any int.
`bit_length()`	Number of bits necessary to represent self in binary.
`bit_count()`	Number of ones in the binary representation of the absolute value of self.
`to_bytes([length, byteorder, signed])`	Return an array of bytes representing an integer.
`from_bytes(bytes[, byteorder, signed])`	Return the integer represented by the given array of bytes.
`as_integer_ratio()`	Return a pair of integers, whose ratio is equal to the original int.
`is_integer()`	Returns True.

Attributes

`real`	the real part of a complex number
`imag`	the imaginary part of a complex number
`numerator`	the numerator of a rational number in lowest terms
`denominator`	the denominator of a rational number in lowest terms
NOT_SET	
MINIMIZE	

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MAXIMIZE

optuna.study.StudySummary

class optuna.study.**StudySummary**(*study_name*, *direction*, *best_trial*, *user_attrs*, *system_attrs*, *n_trials*, *datetime_start*, *study_id*, ***, *directions=None*)

Basic attributes and aggregated results of a *Study*.

See also *optuna.study.get_all_study_summaries()*.

Parameters

- **study_name** (*str*)
- **direction** (StudyDirection *| None*)
- **best_trial** (trial.FrozenTrial *| None*)
- **user_attrs** (*dict[str, Any]*)
- **system_attrs** (*dict[str, Any]*)
- **n_trials** (*int*)
- **datetime_start** (*datetime.datetime | None*)
- **study_id** (*int*)
- **directions** (*Sequence[*StudyDirection*] | None*)

study_name

Name of the *Study*.

direction

StudyDirection of the *Study*.

Note

This attribute is only available during single-objective optimization.

directions

A sequence of *StudyDirection* objects.

best_trial

optuna.trial.FrozenTrial with best objective value in the *Study*.

user_attrs

Dictionary that contains the attributes of the *Study* set with *optuna.study.Study.set_user_attr()*.

system_attrs

Dictionary that contains the attributes of the *Study* internally set by Optuna.

Warning

Deprecated in v3.1.0. `system_attrs` argument will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

n_trials

The number of trials ran in the *Study*.

datetime_start

Datetime where the *Study* started.

Attributes

direction
directions
system_attrs

8.3.14 optuna.terminator

The *terminator* module implements a mechanism for automatically terminating the optimization process, accompanied by a callback class for the termination and evaluators for the estimated room for improvement in the optimization and statistical error of the objective function. The terminator stops the optimization process when the estimated potential improvement is smaller than the statistical error.

BaseTerminator	Base class for terminators.
Terminator	Automatic stopping mechanism for Optuna studies.
BaseImprovementEvaluator	Base class for improvement evaluators.
RegretBoundEvaluator	An error evaluator for upper bound on the regret with high-probability confidence.
BestValueStagnationEvaluator	Evaluates the stagnation period of the best value in an optimization process.
EMMREvaluator	Evaluates a kind of regrets, called the Expected Minimum Model Regret(EMMR).
BaseErrorEvaluator	Base class for error evaluators.
CrossValidationErrorEvaluator	An error evaluator for objective functions based on cross-validation.
StaticErrorEvaluator	An error evaluator that always returns a constant value.
MedianErrorEvaluator	An error evaluator that returns the ratio to initial median.
TerminatorCallback	A callback that terminates the optimization using Terminator.
report_cross_validation_scores	A function to report cross-validation scores of a trial.

optuna.terminator.BaseTerminator

class optuna.terminator.**BaseTerminator**

Base class for terminators.

Methods

`should_terminate(study)`

optuna.terminator.Terminator

class optuna.terminator.**Terminator**(*improvement_evaluator=None*, *error_evaluator=None*, *min_n_trials=20*)

Automatic stopping mechanism for Optuna studies.

This class implements an automatic stopping mechanism for Optuna studies, aiming to prevent unnecessary computation. The study is terminated when the statistical error, e.g. cross-validation error, exceeds the room left for optimization.

For further information about the algorithm, please refer to the following paper:

- A. Makarova et al. Automatic termination for hyperparameter optimization.

Parameters

- **improvement_evaluator** (BaseImprovementEvaluator | *None*) – An evaluator object for assessing the room left for optimization. Defaults to a *RegretBoundEvaluator* object.
- **error_evaluator** (BaseErrorEvaluator | *None*) – An evaluator for calculating the statistical error, e.g. cross-validation error. Defaults to a *CrossValidationErrorEvaluator* object.
- **min_n_trials** (*int*) – The minimum number of trials before termination is considered. Defaults to `20`.

Raises

ValueError – If `min_n_trials` is not a positive integer.

Example

```
import logging
import sys

from sklearn.datasets import load_wine
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import KFold

import optuna
from optuna.terminator import Terminator
from optuna.terminator import report_cross_validation_scores

```

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```python
study = optuna.create_study(direction="maximize")
terminator = Terminator()
min_n_trials = 20

while True:
    trial = study.ask()

    X, y = load_wine(return_X_y=True)

    clf = RandomForestClassifier(
        max_depth=trial.suggest_int("max_depth", 2, 32),
        min_samples_split=trial.suggest_float("min_samples_split", 0, 1),
        criterion=trial.suggest_categorical("criterion", ("gini", "entropy")),
    )

    scores = cross_val_score(clf, X, y, cv=KFold(n_splits=5, shuffle=True))
    report_cross_validation_scores(trial, scores)

    value = scores.mean()
    logging.info(f"Trial #{trial.number} finished with value {value}.")
    study.tell(trial, value)

    if trial.number > min_n_trials and terminator.should_terminate(study):
        logging.info("Terminated by Optuna Terminator!")
        break
```

See also

Please refer to *TerminatorCallback* for how to use the terminator mechanism with the *optimize()* method.

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

Methods

should_terminate(study)	Judge whether the study should be terminated based on the reported values.

should_terminate(*study*)

Judge whether the study should be terminated based on the reported values.

Parameters

study (Study)

Return type

bool

optuna.terminator.BaseImprovementEvaluator

class optuna.terminator.**BaseImprovementEvaluator**(**args*, ***kwargs*)

Base class for improvement evaluators.

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

Methods

evaluate(trials, study_direction)

optuna.terminator.RegretBoundEvaluator

class optuna.terminator.**RegretBoundEvaluator**(*top_trials_ratio=0.5*, *min_n_trials=20*, *seed=None*)

An error evaluator for upper bound on the regret with high-probability confidence.

This evaluator evaluates the regret of current best solution, which defined as the difference between the objective value of the best solution and of the global optimum. To be specific, this evaluator calculates the upper bound on the regret based on the fact that empirical estimator of the objective function is bounded by lower and upper confidence bounds with high probability under the Gaussian process model assumption.

Parameters

- **top_trials_ratio** (*float*) – A ratio of top trials to be considered when estimating the regret. Default to 0.5.
- **min_n_trials** (*int*) – A minimum number of complete trials to estimate the regret. Default to 20.
- **seed** (*int | None*) – Seed for random number generator.

For further information about this evaluator, please refer to the following paper:

- Automatic Termination for Hyperparameter Optimization

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

Methods

evaluate(trials, study_direction)

optuna.terminator.BestValueStagnationEvaluator

class `optuna.terminator.`**`BestValueStagnationEvaluator`**(*max_stagnation_trials=30*)

Evaluates the stagnation period of the best value in an optimization process.

This class is initialized with a maximum stagnation period (`max_stagnation_trials`) and is designed to evaluate the remaining trials before reaching this maximum period of allowed stagnation. If this remaining trials reach zero, the trial terminates. Therefore, the default error evaluator is instantiated by `StaticErrorEvaluator(const=0)`.

Parameters

`max_stagnation_trials` (*int*) – The maximum number of trials allowed for stagnation.

Note

Added in v3.4.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.4.0.

Methods

`evaluate`(trials, study_direction)

optuna.terminator.EMMREvaluator

class `optuna.terminator.`**`EMMREvaluator`**(*deterministic_objective=False*, *delta=0.1*, *min_n_trials=2*, *seed=None*)

Evaluates a kind of regrets, called the Expected Minimum Model Regret(EMMR).

EMMR is an upper bound of "expected minimum simple regret" in the optimization process.

Expected minimum simple regret is a quantity that converges to zero only if the optimization process has found the global optima.

For further information about expected minimum simple regret and the algorithm, please refer to the following paper:

- A stopping criterion for Bayesian optimization by the gap of expected minimum simple regrets

Also, there is our blog post explaining this evaluator:

- Introducing A New Terminator: Early Termination of Black-box Optimization Based on Expected Minimum Model Regret

Parameters

- **`deterministic_objective`** (*bool*) – A boolean value which indicates whether the objective function is deterministic. Default is `False`.
- **`delta`** (*float*) – A float number related to the criterion for termination. Default to 0.1. For further information about this parameter, please see the aforementioned paper.
- **`min_n_trials`** (*int*) – A minimum number of complete trials to compute the criterion. Default to 2.
- **`seed`** (*int | None*) – A random seed for EMMREvaluator.

Example

```
import optuna
from optuna.terminator import EMMREvaluator
from optuna.terminator import MedianErrorEvaluator
from optuna.terminator import Terminator

sampler = optuna.samplers.TPESampler(seed=0)
study = optuna.create_study(sampler=sampler, direction="minimize")
emmr_improvement_evaluator = EMMREvaluator()
median_error_evaluator = MedianErrorEvaluator(emmr_improvement_evaluator)
terminator = Terminator(
    improvement_evaluator=emmr_improvement_evaluator,
    error_evaluator=median_error_evaluator,
)


for i in range(1000):
    trial = study.ask()

    ys = [trial.suggest_float(f"x{i}", -10.0, 10.0) for i in range(5)]
    value = sum(ys[i] ** 2 for i in range(5))

    study.tell(trial, value)

    if terminator.should_terminate(study):
        # Terminated by Optuna Terminator!
        break
```

Note

Added in v4.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v4.0.0.

Methods

evaluate(trials, study_direction)	

optuna.terminator.BaseErrorEvaluator

class optuna.terminator.**BaseErrorEvaluator**

Base class for error evaluators.

Methods

evaluate(trials, study_direction)	

optuna.terminator.CrossValidationErrorEvaluator

class optuna.terminator.**CrossValidationErrorEvaluator**(**args*, ***kwargs*)

An error evaluator for objective functions based on cross-validation.

This evaluator evaluates the objective function's statistical error, which comes from the randomness of dataset. This evaluator assumes that the objective function is the average of the cross-validation and uses the scaled variance of the cross-validation scores in the best trial at the moment as the statistical error.

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

Methods

evaluate(trials, study_direction)	Evaluate the statistical error of the objective function based on cross-validation.

evaluate(*trials*, *study_direction*)

Evaluate the statistical error of the objective function based on cross-validation.

Parameters

- **trials** (*list[FrozenTrial]*) – A list of trials to consider. The best trial in `trials` is used to compute the statistical error.
- **study_direction** (StudyDirection) – The direction of the study.

Returns

A float representing the statistical error of the objective function.

Return type

float

optuna.terminator.StaticErrorEvaluator

class optuna.terminator.**StaticErrorEvaluator**(*constant*)

An error evaluator that always returns a constant value.

This evaluator can be used to terminate the optimization when the evaluated improvement potential is below the fixed threshold.

Parameters

constant (*float*) – A user-specified constant value to always return as an error estimate.

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

Methods

`evaluate`(trials, study_direction)	

optuna.terminator.MedianErrorEvaluator

class `optuna.terminator.`**`MedianErrorEvaluator`**(*paired_improvement_evaluator*, *warm_up_trials=10*, *n_initial_trials=20*, *threshold_ratio=0.01*)

An error evaluator that returns the ratio to initial median.

This error evaluator is introduced as a heuristics in the following paper:

- A stopping criterion for Bayesian optimization by the gap of expected minimum simple regrets

Parameters

- **`paired_improvement_evaluator`** (`BaseImprovementEvaluator`) – The `improvement_evaluator` instance which is set with this `error_evaluator`.
- **`warm_up_trials`** (*`int`*) – A parameter specifies the number of initial trials to be discarded before the calculation of median. Default to 10. In optuna, the first 10 trials are often random sampling. The `warm_up_trials` can exclude them from the calculation.
- **`n_initial_trials`** (*`int`*) – A parameter specifies the number of initial trials considered in the calculation of median after `warm_up_trials`. Default to 20.
- **`threshold_ratio`** (*`float`*) – A parameter specifies the ratio between the threshold and initial median. Default to 0.01.

Note

Added in v4.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v4.0.0.

Methods

`evaluate`(trials, study_direction)	

optuna.terminator.TerminatorCallback

class `optuna.terminator.`**`TerminatorCallback`**(*terminator=None*)

A callback that terminates the optimization using Terminator.

This class implements a callback which wraps *`Terminator`* so that it can be used with the *`optimize()`* method.

Parameters

`terminator` (`BaseTerminator` | *`None`*) – A terminator object which determines whether to terminate the optimization by assessing the room for optimization and statistical error. Defaults to a *`Terminator`* object with default `improvement_evaluator` and `error_evaluator`.

Example

```
from sklearn.datasets import load_wine
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import KFold

import optuna
from optuna.terminator import TerminatorCallback
from optuna.terminator import report_cross_validation_scores


def objective(trial):
    X, y = load_wine(return_X_y=True)

    clf = RandomForestClassifier(
        max_depth=trial.suggest_int("max_depth", 2, 32),
        min_samples_split=trial.suggest_float("min_samples_split", 0, 1),
        criterion=trial.suggest_categorical("criterion", ("gini", "entropy")),
    )

    scores = cross_val_score(clf, X, y, cv=KFold(n_splits=5, shuffle=True))
    report_cross_validation_scores(trial, scores)
    return scores.mean()


study = optuna.create_study(direction="maximize")
terminator = TerminatorCallback()
study.optimize(objective, n_trials=50, callbacks=[terminator])
```

See also

Please refer to *Terminator* for the details of the terminator mechanism.

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

optuna.terminator.report_cross_validation_scores

optuna.terminator.**report_cross_validation_scores**(*trial*, *scores*)

A function to report cross-validation scores of a trial.

This function should be called within the objective function to report the cross-validation scores. The reported scores are used to evaluate the statistical error for termination judgement.

Parameters

- **trial** (Trial) – A *Trial* object to report the cross-validation scores.
- **scores** (*list[float]*) – The cross-validation scores of the trial.

Return type
None

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

For an example of using this module, please refer to this example.

8.3.15 optuna.trial

The *trial* module contains *Trial* related classes and functions.

A *Trial* instance represents a process of evaluating an objective function. This instance is passed to an objective function and provides interfaces to get parameter suggestion, manage the trial's state, and set/get user-defined attributes of the trial, so that Optuna users can define a custom objective function through the interfaces. Basically, Optuna users only use it in their custom objective functions.

Trial	A trial is a process of evaluating an objective function.
FixedTrial	A trial class which suggests a fixed value for each parameter.
FrozenTrial	Status and results of a *Trial*.
TrialState	State of a *Trial*.
create_trial	Create a new *FrozenTrial*.

optuna.trial.Trial

class optuna.trial.**Trial**(*study*, *trial_id*)

A trial is a process of evaluating an objective function.

This object is passed to an objective function and provides interfaces to get parameter suggestion, manage the trial's state, and set/get user-defined attributes of the trial.

Note that the direct use of this constructor is not recommended. This object is seamlessly instantiated and passed to the objective function behind the *optuna.study.Study.optimize()* method; hence library users do not care about instantiation of this object.

Parameters

- **study** (optuna.study.Study) – A *Study* object.
- **trial_id** (*int*) – A trial ID that is automatically generated.

Methods

report(value, step)	Report an objective function value for a given step.
set_system_attr(key, value)	Set system attributes to the trial.
set_user_attr(key, value)	Set user attributes to the trial.
should_prune()	Suggest whether the trial should be pruned or not.
suggest_categorical()	Suggest a value for the categorical parameter.
suggest_discrete_uniform(name, low, high, q)	Suggest a value for the discrete parameter.
suggest_float(name, low, high, *[, step, log])	Suggest a value for the floating point parameter.

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suggest_int(name, low, high, *[, step, log])	Suggest a value for the integer parameter.
suggest_loguniform(name, low, high)	Suggest a value for the continuous parameter.
suggest_uniform(name, low, high)	Suggest a value for the continuous parameter.

Attributes

datetime_start	Return start datetime.
distributions	Return distributions of parameters to be optimized.
number	Return trial's number which is consecutive and unique in a study.
params	Return parameters to be optimized.
relative_params	
system_attrs	Return system attributes.
user_attrs	Return user attributes.

property datetime_start: datetime | None

Return start datetime.

Returns

Datetime where the *Trial* started.

property distributions: dict[str, BaseDistribution]

Return distributions of parameters to be optimized.

Returns

A dictionary containing all distributions.

property number: int

Return trial's number which is consecutive and unique in a study.

Returns

A trial number.

property params: dict[str, Any]

Return parameters to be optimized.

Returns

A dictionary containing all parameters.

report(*value*, *step*)

Report an objective function value for a given step.

The reported values are used by the pruners to determine whether this trial should be pruned.

See also

Please refer to *BasePruner*.

Note

The reported value is converted to `float` type by applying `float()` function internally. Thus, it accepts all float-like types (e.g., `numpy.float32`). If the conversion fails, a `TypeError` is raised.

Note

If this method is called multiple times at the same `step` in a trial, the reported `value` only the first time is stored and the reported values from the second time are ignored.

Note

`report()` does not support multi-objective optimization.

Example

Report intermediate scores of SGDClassifier training.

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.linear_model import SGDClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)


def objective(trial):
    clf = SGDClassifier(random_state=0)
    for step in range(100):
        clf.partial_fit(X_train, y_train, np.unique(y))
        intermediate_value = clf.score(X_valid, y_valid)
        trial.report(intermediate_value, step=step)
        if trial.should_prune():
            raise optuna.TrialPruned()

    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=3)
```

Parameters

- **`value`** (*`float`*) – A value returned from the objective function.
- **`step`** (*`int`*) – Step of the trial (e.g., Epoch of neural network training). Note that pruners assume that `step` starts at zero. For example, *`MedianPruner`* simply checks if `step` is less than `n_warmup_steps` as the warmup mechanism. `step` must be a positive integer.

Return type
None

set_system_attr(*key*, *value*)

Set system attributes to the trial.

Note that Optuna internally uses this method to save system messages such as failure reason of trials. Please use *set_user_attr()* to set users' attributes.

Parameters

- **key** (*str*) – A key string of the attribute.
- **value** (*Any*) – A value of the attribute. The value should be JSON serializable.

Return type
None

Warning

Deprecated in v3.1.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

set_user_attr(*key*, *value*)

Set user attributes to the trial.

The user attributes in the trial can be access via *optuna.trial.Trial.user_attrs()*.

See also

See the recipe on attributes.

Example

Save fixed hyperparameters of neural network training.

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
from sklearn.neural_network import MLPClassifier

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y, random_state=0)


def objective(trial):
    trial.set_user_attr("BATCHSIZE", 128)
    momentum = trial.suggest_float("momentum", 0, 1.0)
    clf = MLPClassifier(
        hidden_layer_sizes=(100, 50),
        batch_size=trial.user_attrs["BATCHSIZE"],
```

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```
        momentum=momentum,
        solver="sgd",
        random_state=0,
    )
    clf.fit(X_train, y_train)

    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=3)
assert "BATCHSIZE" in study.best_trial.user_attrs.keys()
assert study.best_trial.user_attrs["BATCHSIZE"] == 128
```

Parameters

- **key** (*str*) – A key string of the attribute.
- **value** (*Any*) – A value of the attribute. The value should be JSON serializable.

Return type
None

should_prune()

Suggest whether the trial should be pruned or not.

The suggestion is made by a pruning algorithm associated with the trial and is based on previously reported values. The algorithm can be specified when constructing a `Study`.

Note

If no values have been reported, the algorithm cannot make meaningful suggestions. Similarly, if this method is called multiple times with the exact same set of reported values, the suggestions will be the same.

See also

Please refer to the example code in `optuna.trial.Trial.report()`.

Note

`should_prune()` does not support multi-objective optimization.

Returns
A boolean value. If `True`, the trial should be pruned according to the configured pruning algorithm. Otherwise, the trial should continue.

Return type
bool

suggest_categorical(*name: str*, *choices: Sequence[None]*) → None

suggest_categorical(*name: str*, *choices: Sequence[bool]*) → bool

suggest_categorical(*name: str*, *choices: Sequence[int]*) → int

suggest_categorical(*name: str*, *choices: Sequence[float]*) → float

suggest_categorical(*name: str*, *choices: Sequence[str]*) → str

suggest_categorical(*name: str*, *choices: Sequence[None | bool | int | float | str]*) → None | bool | int | float | str

Suggest a value for the categorical parameter.

The value is sampled from `choices`.

Example

Suggest a kernel function of SVC.

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)


def objective(trial):
    kernel = trial.suggest_categorical("kernel", ["linear", "poly", "rbf"])
    clf = SVC(kernel=kernel, gamma="scale", random_state=0)
    clf.fit(X_train, y_train)
    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=3)
```

Parameters

- **name** – A parameter name.
- **choices** – Parameter value candidates.

See also

CategoricalDistribution.

Returns

A suggested value.

See also

configurations tutorial describes more details and flexible usages.

`suggest_discrete_uniform`(*name*, *low*, *high*, *q*)

Suggest a value for the discrete parameter.

The value is sampled from the range $[\mathsf{low}, \mathsf{high}]$, and the step of discretization is q. More specifically, this method returns one of the values in the sequence $\mathsf{low}, \mathsf{low} + q, \mathsf{low} + 2q, \ldots, \mathsf{low} + kq \le \mathsf{high}$, where k denotes an integer. Note that $high$ may be changed due to round-off errors if q is not an integer. Please check warning messages to find the changed values.

Parameters

- **name** (*str*) – A parameter name.
- **low** (*float*) – Lower endpoint of the range of suggested values. `low` is included in the range.
- **high** (*float*) – Upper endpoint of the range of suggested values. `high` is included in the range.
- **q** (*float*) – A step of discretization.

Returns

A suggested float value.

Return type

float

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use suggest_float(..., step=...) instead.

`suggest_float`(*name*, *low*, *high*, ***, *step=None*, *log=False*)

Suggest a value for the floating point parameter.

Example

Suggest a momentum, learning rate and scaling factor of learning rate for neural network training.

```python
import numpy as np
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
from sklearn.neural_network import MLPClassifier

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y, random_state=0)


def objective(trial):
    momentum = trial.suggest_float("momentum", 0.0, 1.0)
    learning_rate_init = trial.suggest_float(
        "learning_rate_init", 1e-5, 1e-3, log=True
    )
```

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```
    power_t = trial.suggest_float("power_t", 0.2, 0.8, step=0.1)
    clf = MLPClassifier(
        hidden_layer_sizes=(100, 50),
        momentum=momentum,
        learning_rate_init=learning_rate_init,
        solver="sgd",
        random_state=0,
        power_t=power_t,
    )
    clf.fit(X_train, y_train)

    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=3)
```

Parameters

- **name** (*str*) – A parameter name.
- **low** (*float*) – Lower endpoint of the range of suggested values. low is included in the range. low must be less than or equal to high. If log is True, low must be larger than 0.
- **high** (*float*) – Upper endpoint of the range of suggested values. high is included in the range. high must be greater than or equal to low.
- **step** (*float | None*) – A step of discretization.

  Note

  The step and log arguments cannot be used at the same time. To set the step argument to a float number, set the log argument to False.

- **log** (*bool*) – A flag to sample the value from the log domain or not. If log is true, the value is sampled from the range in the log domain. Otherwise, the value is sampled from the range in the linear domain.

  Note

  The step and log arguments cannot be used at the same time. To set the log argument to True, set the step argument to None.

Returns

A suggested float value.

Return type

float

See also

configurations tutorial describes more details and flexible usages.

suggest_int(*name*, *low*, *high*, ***, *step=1*, *log=False*)

Suggest a value for the integer parameter.

The value is sampled from the integers in $[\text{low}, \text{high}]$.

Example

Suggest the number of trees in RandomForestClassifier.

```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split

import optuna

X, y = load_iris(return_X_y=True)
X_train, X_valid, y_train, y_valid = train_test_split(X, y)


def objective(trial):
    n_estimators = trial.suggest_int("n_estimators", 50, 400)
    clf = RandomForestClassifier(n_estimators=n_estimators, random_state=0)
    clf.fit(X_train, y_train)
    return clf.score(X_valid, y_valid)


study = optuna.create_study(direction="maximize")
study.optimize(objective, n_trials=3)
```

Parameters

- **name** (*str*) – A parameter name.
- **low** (*int*) – Lower endpoint of the range of suggested values. `low` is included in the range. `low` must be less than or equal to `high`. If `log` is `True`, `low` must be larger than 0.
- **high** (*int*) – Upper endpoint of the range of suggested values. `high` is included in the range. `high` must be greater than or equal to `low`.
- **step** (*int*) – A step of discretization.

Note

Note that high is modified if the range is not divisible by step. Please check the warning messages to find the changed values.

Note

The method returns one of the values in the sequence $\text{low}, \text{low} + \text{step}, \text{low} + 2 * \text{step}, \dots, \text{low} + k * \text{step} \leq \text{high}$, where k denotes an integer.

Note

The `step != 1` and `log` arguments cannot be used at the same time. To set the `step` argument step ≥ 2, set the `log` argument to `False`.

- **log** (*bool*) – A flag to sample the value from the log domain or not.

Note

If `log` is true, at first, the range of suggested values is divided into grid points of width 1. The range of suggested values is then converted to a log domain, from which a value is sampled. The uniformly sampled value is re-converted to the original domain and rounded to the nearest grid point that we just split, and the suggested value is determined. For example, if *low = 2* and *high = 8*, then the range of suggested values is *[2, 3, 4, 5, 6, 7, 8]* and lower values tend to be more sampled than higher values.

Note

The `step != 1` and `log` arguments cannot be used at the same time. To set the `log` argument to `True`, set the `step` argument to 1.

Return type
int

See also

configurations tutorial describes more details and flexible usages.

suggest_loguniform(*name*, *low*, *high*)

Suggest a value for the continuous parameter.

The value is sampled from the range $[\mathsf{low}, \mathsf{high})$ in the log domain. When $\mathsf{low} = \mathsf{high}$, the value of low will be returned.

Parameters

- **name** (*str*) – A parameter name.
- **low** (*float*) – Lower endpoint of the range of suggested values. `low` is included in the range.
- **high** (*float*) – Upper endpoint of the range of suggested values. `high` is included in the range.

Returns
A suggested float value.

Return type
float

> **Warning**
>
> Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.
>
> Use suggest_float(. . . , log=True) instead.

suggest_uniform(*name*, *low*, *high*)

Suggest a value for the continuous parameter.

The value is sampled from the range $[\mathsf{low}, \mathsf{high})$ in the linear domain. When $\mathsf{low} = \mathsf{high}$, the value of low will be returned.

Parameters

- **name** (*str*) – A parameter name.
- **low** (*float*) – Lower endpoint of the range of suggested values. `low` is included in the range.
- **high** (*float*) – Upper endpoint of the range of suggested values. `high` is included in the range.

Returns

A suggested float value.

Return type

float

> **Warning**
>
> Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.
>
> Use suggest_float instead.

property system_attrs: dict[str, Any]

Return system attributes.

Returns

A dictionary containing all system attributes.

> **Warning**
>
> Deprecated in v3.1.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

property user_attrs: dict[str, Any]

Return user attributes.

Returns

A dictionary containing all user attributes.

optuna.trial.FixedTrial

class optuna.trial.**FixedTrial**(*params*, *number=0*)

A trial class which suggests a fixed value for each parameter.

This object has the same methods as *Trial*, and it suggests pre-defined parameter values. The parameter values can be determined at the construction of the *FixedTrial* object. In contrast to *Trial*, *FixedTrial* does not depend on *Study*, and it is useful for deploying optimization results.

Example

Evaluate an objective function with parameter values given by a user.

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y


assert objective(optuna.trial.FixedTrial({"x": 1, "y": 0})) == 1
```

Note

Please refer to *Trial* for details of methods and properties.

Parameters

- **params** (*dict[str, Any]*) – A dictionary containing all parameters.
- **number** (*int*) – A trial number. Defaults to 0.

Methods

report(value, step)
set_system_attr(key, value)
set_user_attr(key, value)
should_prune()
suggest_categorical()
suggest_discrete_uniform(name, low, high, q)
suggest_float(name, low, high, *[, step, log])
suggest_int(name, low, high, *[, step, log])

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suggest_loguniform(name, low, high)	
suggest_uniform(name, low, high)	

Attributes

`datetime_start`
`distributions`
`number`
`params`
`system_attrs`
`user_attrs`

set_system_attr(*key*, *value*)

> **Warning**
>
> Deprecated in v3.1.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

Parameters

- **key** (*str*)
- **value** (*Any*)

Return type
None

suggest_discrete_uniform(*name*, *low*, *high*, *q*)

> **Warning**
>
> Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.
>
> Use suggest_float(…, step=…) instead.

Parameters

- **name** (*str*)

- **low** (*float*)
- **high** (*float*)
- **q** (*float*)

Return type
float

suggest_loguniform(*name*, *low*, *high*)

> **Warning**
>
> Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.
>
> Use suggest_float(…, log=True) instead.

Parameters

- **name** (*str*)
- **low** (*float*)
- **high** (*float*)

Return type
float

suggest_uniform(*name*, *low*, *high*)

> **Warning**
>
> Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.
>
> Use suggest_float instead.

Parameters

- **name** (*str*)
- **low** (*float*)
- **high** (*float*)

Return type
float

optuna.trial.FrozenTrial

class optuna.trial.**FrozenTrial**(*number*, *state*, *value*, *datetime_start*, *datetime_complete*, *params*, *distributions*, *user_attrs*, *system_attrs*, *intermediate_values*, *trial_id*, ***, *values=None*)

Status and results of a *Trial*.

An object of this class has the same methods as *Trial*, but is not associated with, nor has any references to a *Study*.

It is therefore not possible to make persistent changes to a storage from this object by itself, for instance by using `set_user_attr()`.

It will suggest the parameter values stored in *params* and will not sample values from any distributions.

It can be passed to objective functions (see *optimize()*) and is useful for deploying optimization results.

Example

Re-evaluate an objective function with parameter values optimized study.

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -1, 1)
    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=3)

assert objective(study.best_trial) == study.best_value
```

Note

Instances are mutable, despite the name. For instance, `set_user_attr()` will update user attributes of objects in-place.

Example:

Overwritten attributes.

```
import copy
import datetime

import optuna


def objective(trial):
    x = trial.suggest_float("x", -1, 1)

    # this user attribute always differs
    trial.set_user_attr("evaluation time", datetime.datetime.now())

    return x**2


study = optuna.create_study()
study.optimize(objective, n_trials=3)
```

```
best_trial = study.best_trial
best_trial_copy = copy.deepcopy(best_trial)

# re-evaluate
objective(best_trial)

# the user attribute is overwritten by re-evaluation
assert best_trial.user_attrs != best_trial_copy.user_attrs
```

Note

Please refer to *Trial* for details of methods and properties.

Parameters

- **number** (*int*)
- **state** (TrialState)
- **value** (*float | None*)
- **datetime_start** (*datetime.datetime | None*)
- **datetime_complete** (*datetime.datetime | None*)
- **params** (*dict[str, Any]*)
- **distributions** (*dict[str, BaseDistribution]*)
- **user_attrs** (*dict[str, Any]*)
- **system_attrs** (*dict[str, Any]*)
- **intermediate_values** (*dict[int, float]*)
- **trial_id** (*int*)
- **values** (*Sequence[float] | None*)

number

Unique and consecutive number of *Trial* for each *Study*. Note that this field uses zero-based numbering.

state

TrialState of the *Trial*.

value

Objective value of the *Trial*. `value` and `values` must not be specified at the same time.

values

Sequence of objective values of the *Trial*. The length is greater than 1 if the problem is multi-objective optimization. `value` and `values` must not be specified at the same time.

datetime_start

Datetime where the *Trial* started.

datetime_complete

Datetime where the *Trial* finished.

`params`

Dictionary that contains suggested parameters.

`distributions`

Dictionary that contains the distributions of *params*.

`user_attrs`

Dictionary that contains the attributes of the *Trial* set with *optuna.trial.Trial.set_user_attr()*.

`system_attrs`

Dictionary that contains the attributes of the *Trial* set with *optuna.trial.Trial.set_system_attr()*.

`intermediate_values`

Intermediate objective values set with *optuna.trial.Trial.report()*.

Methods

report(value, step)	Interface of report function.
set_system_attr(key, value)	
set_user_attr(key, value)	
should_prune()	Suggest whether the trial should be pruned or not.
suggest_categorical()	
suggest_discrete_uniform(name, low, high, q)	
suggest_float(name, low, high, *[, step, log])	
suggest_int(name, low, high, *[, step, log])	
suggest_loguniform(name, low, high)	
suggest_uniform(name, low, high)	

Attributes

datetime_start	
distributions	
duration	Return the elapsed time taken to complete the trial.
last_step	Return the maximum step of *intermediate_values* in the trial.
number	
params	

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system_attrs
user_attrs
value
values

property duration: timedelta | None

Return the elapsed time taken to complete the trial.

Returns
The duration.

property last_step: int | None

Return the maximum step of *intermediate_values* in the trial.

Returns
The maximum step of intermediates.

report(*value*, *step*)

Interface of report function.

Since *FrozenTrial* is not pruned, this report function does nothing.

See also

Please refer to *should_prune()*.

Parameters

- **value** (*float*) – A value returned from the objective function.
- **step** (*int*) – Step of the trial (e.g., Epoch of neural network training). Note that pruners assume that `step` starts at zero. For example, *MedianPruner* simply checks if `step` is less than `n_warmup_steps` as the warmup mechanism.

Return type
None

set_system_attr(*key*, *value*)

Warning

Deprecated in v3.1.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.1.0.

Parameters

- **key** (*str*)
- **value** (*Any*)

Return type
None

should_prune()

Suggest whether the trial should be pruned or not.

The suggestion is always `False` regardless of a pruning algorithm.

Note

FrozenTrial only samples one combination of parameters.

Returns
`False`.

Return type
bool

suggest_discrete_uniform(*name*, *low*, *high*, *q*)

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use suggest_float(…, step=…) instead.

Parameters

- **name** (*str*)
- **low** (*float*)
- **high** (*float*)
- **q** (*float*)

Return type
float

suggest_loguniform(*name*, *low*, *high*)

Warning

Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Use suggest_float(…, log=True) instead.

Parameters

- **name** (*str*)

- **low** (*float*)
- **high** (*float*)

Return type
float

suggest_uniform(*name*, *low*, *high*)

> **Warning**
>
> Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.
>
> Use suggest_float instead.

Parameters

- **name** (*str*)
- **low** (*float*)
- **high** (*float*)

Return type
float

optuna.trial.TrialState

class optuna.trial.**TrialState**(**values*)

State of a *Trial*.

RUNNING
The *Trial* is running.

WAITING
The *Trial* is waiting and unfinished.

COMPLETE
The *Trial* has been finished without any error.

PRUNED
The *Trial* has been pruned with *TrialPruned*.

FAIL
The *Trial* has failed due to an uncaught error.

Methods

`conjugate`	Returns self, the complex conjugate of any int.
`bit_length`()	Number of bits necessary to represent self in binary.
`bit_count`()	Number of ones in the binary representation of the absolute value of self.
`to_bytes`([length, byteorder, signed])	Return an array of bytes representing an integer.

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`from_bytes`(bytes[, byteorder, signed])	Return the integer represented by the given array of bytes.
`as_integer_ratio`()	Return a pair of integers, whose ratio is equal to the original int.
`is_integer`()	Returns True.
`is_finished`()	Return a bool value to represent whether the trial state is unfinished or not.

Attributes

`real`	the real part of a complex number
`imag`	the imaginary part of a complex number
`numerator`	the numerator of a rational number in lowest terms
`denominator`	the denominator of a rational number in lowest terms
`RUNNING`	
`COMPLETE`	
`PRUNED`	
`FAIL`	
`WAITING`	

`is_finished`()

Return a bool value to represent whether the trial state is unfinished or not.

The unfinished state is either `RUNNING` or `WAITING`.

Return type

bool

optuna.trial.create_trial

`optuna.trial.`**`create_trial`**(*, *state=1*, *value=None*, *values=None*, *params=None*, *distributions=None*, *user_attrs=None*, *system_attrs=None*, *intermediate_values=None*)

Create a new *`FrozenTrial`*.

Example

```
import optuna
from optuna.distributions import CategoricalDistribution
from optuna.distributions import FloatDistribution

trial = optuna.trial.create_trial(
    params={"x": 1.0, "y": 0},
    distributions={
        "x": FloatDistribution(0, 10),
        "y": CategoricalDistribution([-1, 0, 1]),
    },
```

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```
    value=5.0,
)

assert isinstance(trial, optuna.trial.FrozenTrial)
assert trial.value == 5.0
assert trial.params == {"x": 1.0, "y": 0}
```

See also

See *add_trial()* for how this function can be used to create a study from existing trials.

Note

Please note that this is a low-level API. In general, trials that are passed to objective functions are created inside *optimize()*.

Note

When `state` is *TrialState.COMPLETE*, the following parameters are required:

- `params`
- `distributions`
- `value` or `values`

Parameters

- **state** (`TrialState`) – Trial state.
- **value** (*float* | *None*) – Trial objective value. Must be specified if `state` is *TrialState.COMPLETE*. `value` and `values` must not be specified at the same time.
- **values** (*Sequence*[*float*] | *None*) – Sequence of the trial objective values. The length is greater than 1 if the problem is multi-objective optimization. Must be specified if `state` is *TrialState.COMPLETE*. `value` and `values` must not be specified at the same time.
- **params** (*dict*[*str*, *Any*] | *None*) – Dictionary with suggested parameters of the trial.
- **distributions** (*dict*[*str*, *BaseDistribution*] | *None*) – Dictionary with parameter distributions of the trial.
- **user_attrs** (*dict*[*str*, *Any*] | *None*) – Dictionary with user attributes.
- **system_attrs** (*dict*[*str*, *Any*] | *None*) – Dictionary with system attributes. Should not have to be used for most users.
- **intermediate_values** (*dict*[*int*, *float*] | *None*) – Dictionary with intermediate objective values of the trial.

Returns

Created trial.

Return type

FrozenTrial

8.3.16 optuna.visualization

The `visualization` module provides utility functions for plotting the optimization process using plotly and matplotlib. Plotting functions generally take a *Study* object and optional parameters are passed as a list to the `params` argument.

Note

In the `optuna.visualization` module, the following functions use plotly to create figures, but JupyterLab cannot render them by default. Please follow this installation guide to show figures in JupyterLab.

Note

The *plot_param_importances()* requires the Python package of scikit-learn.

plot_contour

`optuna.visualization.plot_contour`(*study*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot the parameter relationship as contour plot in a study.

Note that, if a parameter contains missing values, a trial with missing values is not plotted.

Parameters

- **study** (`Study`) – A *Study* object whose trials are plotted for their target values.
- **params** (*list[str] | None*) – Parameter list to visualize. The default is all parameters.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is `None` and `study` is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if `study` is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the color bar.

Returns

A `plotly.graph_objects.Figure` object.

Return type

Figure

Note

The colormap is reversed when the `target` argument isn't `None` or `direction` of *Study* is `minimize`.

The following code snippet shows how to plot the parameter relationship as contour plot.

```python
import optuna
from plotly.io import show

```

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```
def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=30)

fig = optuna.visualization.plot_contour(study, params=["x", "y"])
show(fig)
```

Total running time of the script: (0 minutes 2.061 seconds)

plot_edf

`optuna.visualization.`**`plot_edf`**(*study*, ***, *target=None*, *target_name='Objective Value'*)

Plot the objective value EDF (empirical distribution function) of a study.

Note that only the complete trials are considered when plotting the EDF.

Note

EDF is useful to analyze and improve search spaces. For instance, you can see a practical use case of EDF in the paper Designing Network Design Spaces.

Note

The plotted EDF assumes that the value of the objective function is in accordance with the uniform distribution over the objective space.

Parameters

- **`study`** (`Study` | *`Sequence`*`[Study]`) – A target *`Study`* object. You can pass multiple studies if you want to compare those EDFs.
- **`target`** (*`Callable`*`[[FrozenTrial],` *`float`*`]` | *`None`*) – A function to specify the value to display. If it is `None` and `study` is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if `study` is being used for multi-objective optimization.

- **`target_name`** (*`str`*) – Target's name to display on the axis label.

Returns

A `plotly.graph_objects.Figure` object.

Return type
Figure

The following code snippet shows how to plot EDF.

```
import math

import optuna
from plotly.io import show


def ackley(x, y):
    a = 20 * math.exp(-0.2 * math.sqrt(0.5 * (x**2 + y**2)))
    b = math.exp(0.5 * (math.cos(2 * math.pi * x) + math.cos(2 * math.pi * y)))
    return -a - b + math.e + 20


def objective(trial, low, high):
    x = trial.suggest_float("x", low, high)
    y = trial.suggest_float("y", low, high)
    return ackley(x, y)


sampler = optuna.samplers.RandomSampler(seed=10)

# Widest search space.
study0 = optuna.create_study(study_name="x=[0,5), y=[0,5)", sampler=sampler)
study0.optimize(lambda t: objective(t, 0, 5), n_trials=500)

# Narrower search space.
study1 = optuna.create_study(study_name="x=[0,4), y=[0,4)", sampler=sampler)
study1.optimize(lambda t: objective(t, 0, 4), n_trials=500)

# Narrowest search space but it doesn't include the global optimum point.
study2 = optuna.create_study(study_name="x=[1,3), y=[1,3)", sampler=sampler)
study2.optimize(lambda t: objective(t, 1, 3), n_trials=500)

fig = optuna.visualization.plot_edf([study0, study1, study2])
show(fig)
```

Total running time of the script: (0 minutes 0.439 seconds)

plot_hypervolume_history

`optuna.visualization.`**`plot_hypervolume_history`**(*study*, *reference_point*)

Plot hypervolume history of all trials in a study.

Parameters

- **study** (`Study`) – A *Study* object whose trials are plotted for their hypervolumes. The number of objectives must be 2 or more.
- **reference_point** (*Sequence[float]*) – A reference point to use for hypervolume computation. The dimension of the reference point must be the same as the number of objectives.

Returns
A `plotly.graph_objects.Figure` object.

Return type
Figure

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

The following code snippet shows how to plot optimization history.

```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_examples/optuna.visualization.plot_hypervolume_history.py:29:␣
↪ExperimentalWarning:

optuna.visualization._hypervolume_history.plot_hypervolume_history is experimental␣
↪(supported from v3.3.0). The interface can change in the future.
```

```
import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_float("x", 0, 5)
    y = trial.suggest_float("y", 0, 3)

    v0 = 4 * x**2 + 4 * y**2
    v1 = (x - 5) ** 2 + (y - 5) ** 2
    return v0, v1


study = optuna.create_study(directions=["minimize", "minimize"])
study.optimize(objective, n_trials=50)

reference_point = [100.0, 50.0]
fig = optuna.visualization.plot_hypervolume_history(study, reference_point)
show(fig)
```

Total running time of the script: (0 minutes 0.111 seconds)

plot_intermediate_values

`optuna.visualization.`**`plot_intermediate_values`**`(`*study*`)`

Plot intermediate values of all trials in a study.

Parameters
study (`Study`) – A *`Study`* object whose trials are plotted for their intermediate values.

Returns
A `plotly.graph_objects.Figure` object.

Return type
Figure

The following code snippet shows how to plot intermediate values.

```
import optuna
from plotly.io import show


def f(x):
    return (x - 2) ** 2


def df(x):
    return 2 * x - 4


def objective(trial):
    lr = trial.suggest_float("lr", 1e-5, 1e-1, log=True)

    x = 3
    for step in range(128):
        y = f(x)

        trial.report(y, step=step)
        if trial.should_prune():
            raise optuna.TrialPruned()

        gy = df(x)
        x -= gy * lr

    return y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=16)

fig = optuna.visualization.plot_intermediate_values(study)
show(fig)
```

Total running time of the script: (0 minutes 0.225 seconds)

plot_optimization_history

`optuna.visualization.`**`plot_optimization_history`**(*study*, ***, *target=None*, *target_name='Objective Value'*, *error_bar=False*)

Plot optimization history of all trials in a study.

Parameters

- **study** (`Study` | *Sequence*[`Study`]) – A *Study* object whose trials are plotted for their target values. You can pass multiple studies if you want to compare those optimization histories.

- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is None and study is being used for single-objective optimization, the objective values are plotted.

> **Note**
>
> Specify this argument if study is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the axis label and the legend.
- **error_bar** (*bool*) – A flag to show the error bar.

Returns
A plotly.graph_objects.Figure object.

Return type
Figure

The following code snippet shows how to plot optimization history.

```
import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=10)

fig = optuna.visualization.plot_optimization_history(study)
show(fig)
```

Total running time of the script: (0 minutes 0.097 seconds)

plot_parallel_coordinate

optuna.visualization.**plot_parallel_coordinate**(*study*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot the high-dimensional parameter relationships in a study.

Note that, if a parameter contains missing values, a trial with missing values is not plotted.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted for their target values.
- **params** (*list[str] | None*) – Parameter list to visualize. The default is all parameters.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is None and study is being used for single-objective optimization, the objective values are plotted.

Note

Specify this argument if `study` is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the axis label and the legend.

Returns
A `plotly.graph_objects.Figure` object.

Return type
Figure

Note

The colormap is reversed when the `target` argument isn't `None` or `direction` of *Study* is `minimize`.

The following code snippet shows how to plot the high-dimensional parameter relationships.

```python
import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=10)

fig = optuna.visualization.plot_parallel_coordinate(study, params=["x", "y"])
show(fig)
```

Total running time of the script: (0 minutes 0.866 seconds)

plot_param_importances

`optuna.visualization.`**`plot_param_importances`**(*study*, *evaluator=None*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot hyperparameter importances.

See also

This function visualizes the results of *optuna.importance.get_param_importances()*.

Parameters

- **study** (Study) – An optimized study.
- **evaluator** (*BaseImportanceEvaluator | None*) – An importance evaluator object that specifies which algorithm to base the importance assessment on. Defaults to

FanovaImportanceEvaluator.

- **params** (*list[str] | None*) – A list of names of parameters to assess. If None, all parameters that are present in all of the completed trials are assessed.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is None and study is being used for single-objective optimization, the objective values are plotted. For multi-objective optimization, all objectives will be plotted if target is None.

  Note

  This argument can be used to specify which objective to plot if study is being used for multi-objective optimization. For example, to get only the hyperparameter importance of the first objective, use `target=lambda t:  t.values[0]` for the target parameter.

- **target_name** (*str*) – Target's name to display on the legend. Names set via *set_metric_names()* will be used if target is None, overriding this argument.

Returns

A plotly.graph_objects.Figure object.

Return type

Figure

The following code snippet shows how to plot hyperparameter importances.

```
import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_int("x", 0, 2)
    y = trial.suggest_float("y", -1.0, 1.0)
    z = trial.suggest_float("z", 0.0, 1.5)
    return x**2 + y**3 - z**4


sampler = optuna.samplers.RandomSampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=100)

fig = optuna.visualization.plot_param_importances(study)
show(fig)
```

Total running time of the script: (0 minutes 0.705 seconds)

plot_pareto_front

`optuna.visualization.`**`plot_pareto_front`**(*study*, ***, *target_names=None*, *include_dominated_trials=True*, *axis_order=None*, *constraints_func=None*, *targets=None*)

Plot the Pareto front of a study.

See also

Please refer to multi_objective for the tutorial of the Pareto front visualization.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted for their objective values. The number of objectives must be either 2 or 3 when `targets` is `None`.
- **target_names** (*list[str] | None*) – Objective name list used as the axis titles. If `None` is specified, "Objective {objective_index}" is used instead. If `targets` is specified for a study that does not contain any completed trial, `target_name` must be specified.
- **include_dominated_trials** (*bool*) – A flag to include all dominated trial's objective values.
- **axis_order** (*list[int] | None*) – A list of indices indicating the axis order. If `None` is specified, default order is used. `axis_order` and `targets` cannot be used at the same time.

  Warning

  Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

- **constraints_func** (*Callable[[FrozenTrial], Sequence[float]] | None*) – An optional function that computes the objective constraints. It must take a *FrozenTrial* and return the constraints. The return value must be a sequence of `float` s. A value strictly larger than 0 means that a constraint is violated. A value equal to or smaller than 0 is considered feasible. This specification is the same as in, for example, *NSGAIISampler*.

  If given, trials are classified into three categories: feasible and best, feasible but non-best, and infeasible. Categories are shown in different colors. Here, whether a trial is best (on Pareto front) or not is determined ignoring all infeasible trials.

  Warning

  Deprecated in v4.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v4.0.0.

- **targets** (*Callable[[FrozenTrial], Sequence[float]] | None*) – A function that returns targets values to display. The argument to this function is *FrozenTrial*. `axis_order` and `targets` cannot be used at the same time. If `study.n_objectives` is neither 2 nor 3, `targets` must be specified.

  Note

  Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Returns
A `plotly.graph_objects.Figure` object.

Return type
Figure

The following code snippet shows how to plot the Pareto front of a study.

```
import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_float("x", 0, 5)
    y = trial.suggest_float("y", 0, 3)

    v0 = 4 * x**2 + 4 * y**2
    v1 = (x - 5) ** 2 + (y - 5) ** 2
    return v0, v1


study = optuna.create_study(directions=["minimize", "minimize"])
study.optimize(objective, n_trials=50)

fig = optuna.visualization.plot_pareto_front(study)
show(fig)
```

The following code snippet shows how to plot a 2-dimensional Pareto front of a 3-dimensional study. This example is scalable, e.g., for plotting a 2- or 3-dimensional Pareto front of a 4-dimensional study and so on.

```
import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_float("x", 0, 5)
    y = trial.suggest_float("y", 0, 3)
    v0 = 5 * x**2 + 3 * y**2
    v1 = (x - 10) ** 2 + (y - 10) ** 2
    v2 = x + y

    return v0, v1, v2


study = optuna.create_study(directions=["minimize", "minimize", "minimize"])

study.optimize(objective, n_trials=100)

fig = optuna.visualization.plot_pareto_front(
    study,
    targets=lambda t: (t.values[0], t.values[1]),
    target_names=["Objective 0", "Objective 1"],
)
```

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```
show(fig)
```

Total running time of the script: (0 minutes 0.296 seconds)

plot_rank

optuna.visualization.**plot_rank**(*study*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot parameter relations as scatter plots with colors indicating ranks of target value.

Note that trials missing the specified parameters will not be plotted.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted for their target values.
- **params** (*list[str] | None*) – Parameter list to visualize. The default is all parameters.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is None and **study** is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if study is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the color bar.

Returns

A plotly.graph_objects.Figure object.

Return type

Figure

Note

This function requires plotly >= 5.0.0.

The following code snippet shows how to plot the parameter relationship as a rank plot.

```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/optuna/_experimental.py:32: ExperimentalWarning:

Argument ``constraints_func`` is an experimental feature. The interface can change in␣
↪the future.
```

```
import optuna
from plotly.io import show
```

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```
def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])

    c0 = 400 - (x + y) ** 2
    trial.set_user_attr("constraint", [c0])

    return x**2 + y


def constraints(trial):
    return trial.user_attrs["constraint"]


sampler = optuna.samplers.TPESampler(seed=10, constraints_func=constraints)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=30)

fig = optuna.visualization.plot_rank(study, params=["x", "y"])
show(fig)
```

Total running time of the script: (0 minutes 0.162 seconds)

plot_slice

`optuna.visualization.`**`plot_slice`**(*study*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot the parameter relationship as slice plot in a study.

Note that, if a parameter contains missing values, a trial with missing values is not plotted.

Parameters

- **`study`** (`Study`) – A *`Study`* object whose trials are plotted for their target values.
- **`params`** (*`list[str] | None`*) – Parameter list to visualize. The default is all parameters.
- **`target`** (*`Callable[[FrozenTrial], float] | None`*) – A function to specify the value to display. If it is `None` and `study` is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if `study` is being used for multi-objective optimization.

- **`target_name`** (*`str`*) – Target's name to display on the axis label.

Returns

A `plotly.graph_objects.Figure` object.

Return type

Figure

The following code snippet shows how to plot the parameter relationship as slice plot.

```python
import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=10)

fig = optuna.visualization.plot_slice(study, params=["x", "y"])
show(fig)
```

Total running time of the script: (0 minutes 0.129 seconds)

plot_terminator_improvement

`optuna.visualization.`**`plot_terminator_improvement`**(*study*, *plot_error=False*, *improvement_evaluator=None*, *error_evaluator=None*, *min_n_trials=20*)

Plot the potentials for future objective improvement.

This function visualizes the objective improvement potentials, evaluated with `improvement_evaluator`. It helps to determine whether we should continue the optimization or not. You can also plot the error evaluated with `error_evaluator` if the `plot_error` argument is set to `True`. Note that this function may take some time to compute the improvement potentials.

Parameters

- **study** (`Study`) – A *`Study`* object whose trials are plotted for their improvement.
- **plot_error** (*`bool`*) – A flag to show the error. If it is set to `True`, errors evaluated by `error_evaluator` are also plotted as line graph. Defaults to `False`.
- **improvement_evaluator** (`BaseImprovementEvaluator` *|* *None*) – An object that evaluates the improvement of the objective function. Defaults to *`RegretBoundEvaluator`*.
- **error_evaluator** (`BaseErrorEvaluator` *|* *None*) – An object that evaluates the error inherent in the objective function. Defaults to *`CrossValidationErrorEvaluator`*.
- **min_n_trials** (*`int`*) – The minimum number of trials before termination is considered. Terminator improvements for trials below this value are shown in a lighter color. Defaults to `20`.

Returns

A `plotly.graph_objects.Figure` object.

Return type

Figure

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

The following code snippet shows how to plot improvement potentials, together with cross-validation errors.

```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/sklearn/utils/validation.py:2749: UserWarning:

X does not have valid feature names, but LGBMClassifier was fitted with feature names

/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/sklearn/utils/validation.py:2749: UserWarning:

X does not have valid feature names, but LGBMClassifier was fitted with feature names

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↪packages/sklearn/utils/validation.py:2749: UserWarning:
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/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
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↪packages/sklearn/utils/validation.py:2749: UserWarning:

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/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/sklearn/utils/validation.py:2749: UserWarning:

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↪packages/sklearn/utils/validation.py:2749: UserWarning:
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/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_examples/optuna.visualization.plot_terminator_improvement.py:42:␣
↪ExperimentalWarning:

optuna.visualization._terminator_improvement.plot_terminator_improvement is experimental␣
↪(supported from v3.2.0). The interface can change in the future.

/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/optuna/visualization/_terminator_improvement.py:93: ExperimentalWarning:

RegretBoundEvaluator is experimental (supported from v3.2.0). The interface can change␣
↪in the future.

/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/optuna/visualization/_terminator_improvement.py:98: ExperimentalWarning:

CrossValidationErrorEvaluator is experimental (supported from v3.2.0). The interface can␣
↪change in the future.


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```python
from lightgbm import LGBMClassifier
from sklearn.datasets import load_wine
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import KFold
import optuna
from plotly.io import show
from optuna.terminator import report_cross_validation_scores
from optuna.visualization import plot_terminator_improvement


def objective(trial):
    X, y = load_wine(return_X_y=True)
    clf = LGBMClassifier(
        reg_alpha=trial.suggest_float("reg_alpha", 1e-8, 10.0, log=True),
        reg_lambda=trial.suggest_float("reg_lambda", 1e-8, 10.0, log=True),
        num_leaves=trial.suggest_int("num_leaves", 2, 256),
        colsample_bytree=trial.suggest_float("colsample_bytree", 0.4, 1.0),
        subsample=trial.suggest_float("subsample", 0.4, 1.0),
        subsample_freq=trial.suggest_int("subsample_freq", 1, 7),
        min_child_samples=trial.suggest_int("min_child_samples", 5, 100),
    )
    scores = cross_val_score(clf, X, y, cv=KFold(n_splits=5, shuffle=True))
    report_cross_validation_scores(trial, scores)
    return scores.mean()


study = optuna.create_study()
study.optimize(objective, n_trials=30)

fig = plot_terminator_improvement(study, plot_error=True)
show(fig)
```

Total running time of the script: (0 minutes 1.920 seconds)

plot_timeline

optuna.visualization.**plot_timeline**(*study*, *n_recent_trials=None*)

Plot the timeline of a study.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted with their lifetime.
- **n_recent_trials** (*int | None*) – The number of recent trials to plot. If None, all trials are plotted. If specified, only the most recent n_recent_trials will be displayed. Must be a positive integer.

Returns
A plotly.graph_objects.Figure object.

Raises
ValueError – if n_recent_trials is 0 or negative.

Return type
Figure

The following code snippet shows how to plot the timeline of a study. Timeline plot can visualize trials with overlapping execution time (e.g., in distributed environments).

```
import time

import optuna
from plotly.io import show


def objective(trial):
    x = trial.suggest_float("x", 0, 1)
    time.sleep(x * 0.1)
    if x > 0.8:
        raise ValueError()
    if x > 0.4:
        raise optuna.TrialPruned()
    return x ** 2


study = optuna.create_study(direction="minimize")
study.optimize(
    objective, n_trials=50, n_jobs=2, catch=(ValueError,)
)

fig = optuna.visualization.plot_timeline(study)
show(fig)
```

Total running time of the script: (0 minutes 1.923 seconds)

Note

The following *optuna.visualization.matplotlib* module uses Matplotlib as a backend.

matplotlib

Note

The following functions use Matplotlib as a backend.

plot_contour

optuna.visualization.matplotlib.**plot_contour**(*study*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot the parameter relationship as contour plot in a study with Matplotlib.

Note that, if a parameter contains missing values, a trial with missing values is not plotted.

See also

Please refer to *optuna.visualization.plot_contour()* for an example.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted for their target values.
- **params** (*list[str] | None*) – Parameter list to visualize. The default is all parameters.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is None and study is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if study is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the color bar.

Returns

A matplotlib.axes.Axes object.

Return type

Axes

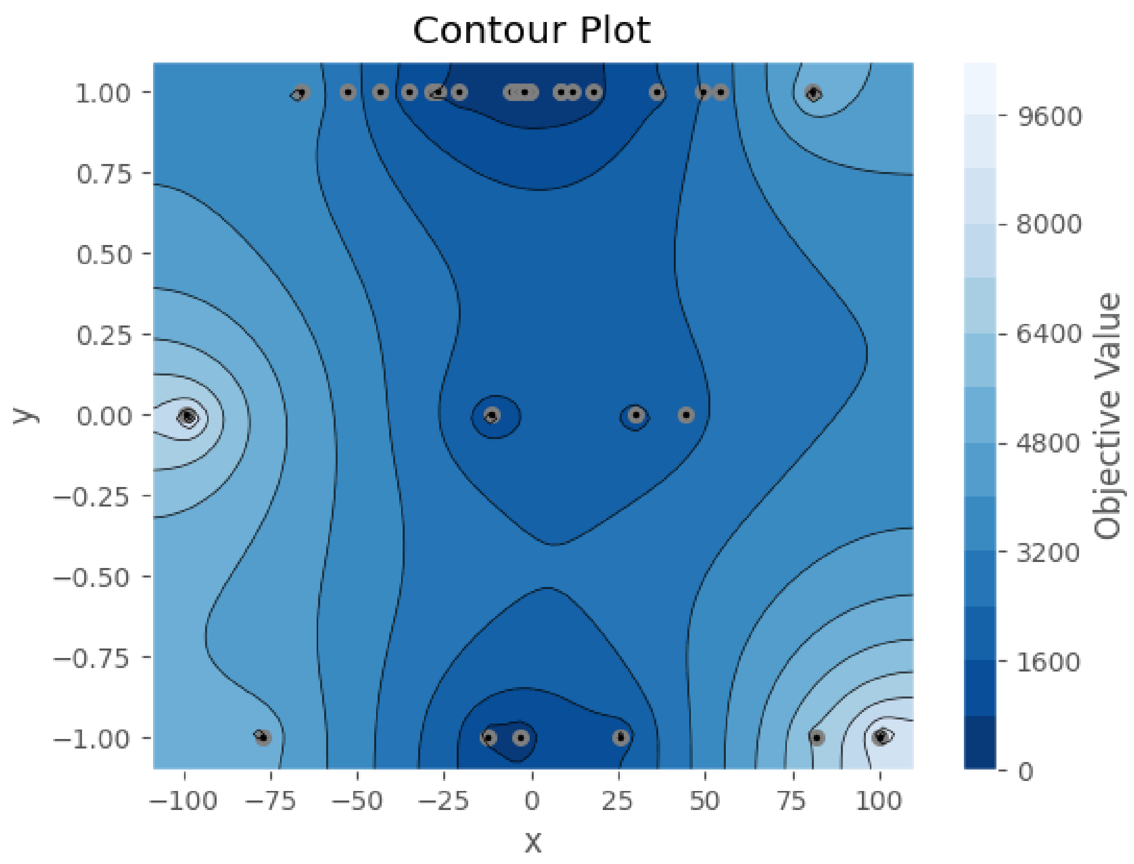
Note

The colormap is reversed when the target argument isn't None or direction of *Study* is minimize.

Note

Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

The following code snippet shows how to plot the parameter relationship as contour plot.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.contour.py:25:␣
↪ExperimentalWarning:

optuna.visualization.matplotlib._contour.plot_contour is experimental (supported from v2.
↪2.0). The interface can change in the future.


<Axes: title={'center': 'Contour Plot'}, xlabel='x', ylabel='y'>
```

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y

```

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```
sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=30)

optuna.visualization.matplotlib.plot_contour(study, params=["x", "y"])
```

Total running time of the script: (0 minutes 0.484 seconds)

plot_edf

`optuna.visualization.matplotlib.plot_edf`(*study*, ***, *target=None*, *target_name='Objective Value'*)

Plot the objective value EDF (empirical distribution function) of a study with Matplotlib.

Note that only the complete trials are considered when plotting the EDF.

See also

Please refer to *optuna.visualization.plot_edf()* for an example, where this function can be replaced with it.

Note

Please refer to matplotlib.pyplot.legend to adjust the style of the generated legend.

Parameters

- **study** (Study | *Sequence*[Study]) – A target *Study* object. You can pass multiple studies if you want to compare those EDFs.
- **target** (*Callable*[[FrozenTrial], *float*] | *None*) – A function to specify the value to display. If it is None and study is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if study is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the axis label.

Returns

A matplotlib.axes.Axes object.

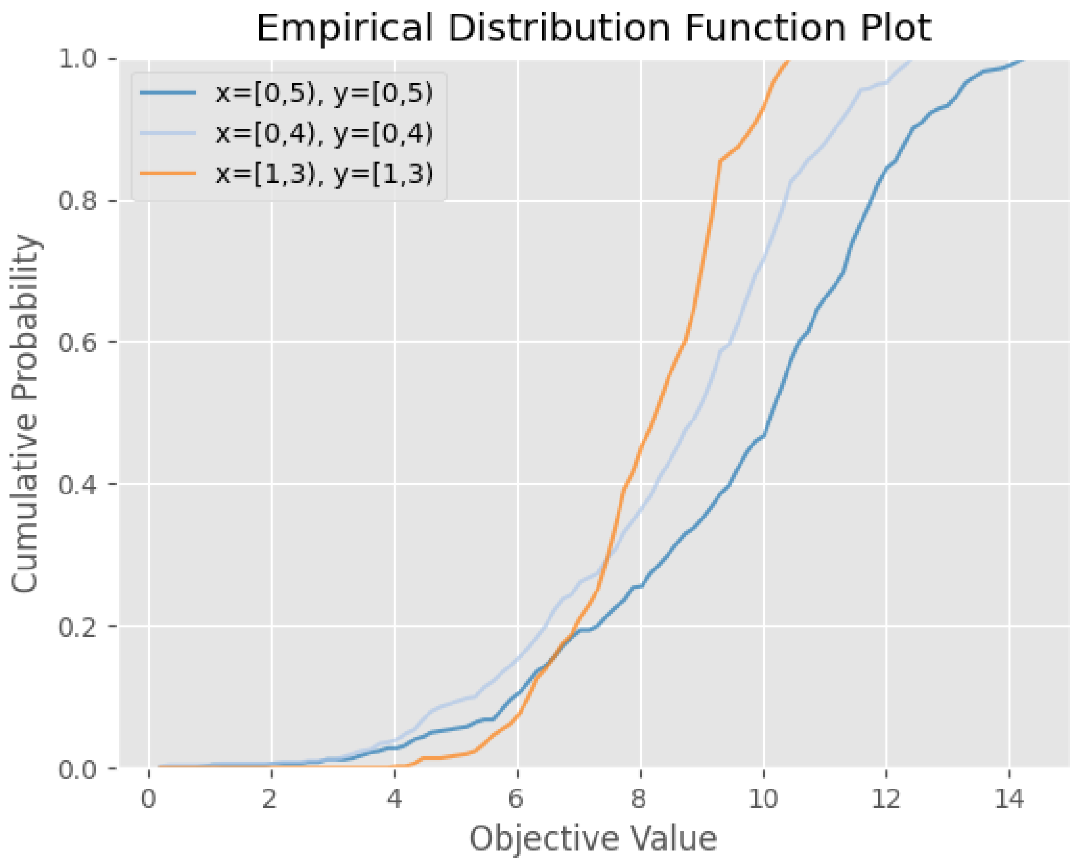
Return type

Axes

Note

Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

The following code snippet shows how to plot EDF.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.edf.py:43:␣
↪ExperimentalWarning:

optuna.visualization.matplotlib._edf.plot_edf is experimental (supported from v2.2.0).␣
↪The interface can change in the future.


<Axes: title={'center': 'Empirical Distribution Function Plot'}, xlabel='Objective Value
↪', ylabel='Cumulative Probability'>
```

```
import math

import optuna


def ackley(x, y):
```

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```python
    a = 20 * math.exp(-0.2 * math.sqrt(0.5 * (x**2 + y**2)))
    b = math.exp(0.5 * (math.cos(2 * math.pi * x) + math.cos(2 * math.pi * y)))
    return -a - b + math.e + 20


def objective(trial, low, high):
    x = trial.suggest_float("x", low, high)
    y = trial.suggest_float("y", low, high)
    return ackley(x, y)


sampler = optuna.samplers.RandomSampler(seed=10)

# Widest search space.
study0 = optuna.create_study(study_name="x=[0,5), y=[0,5)", sampler=sampler)
study0.optimize(lambda t: objective(t, 0, 5), n_trials=500)

# Narrower search space.
study1 = optuna.create_study(study_name="x=[0,4), y=[0,4)", sampler=sampler)
study1.optimize(lambda t: objective(t, 0, 4), n_trials=500)

# Narrowest search space but it doesn't include the global optimum point.
study2 = optuna.create_study(study_name="x=[1,3), y=[1,3)", sampler=sampler)
study2.optimize(lambda t: objective(t, 1, 3), n_trials=500)

optuna.visualization.matplotlib.plot_edf([study0, study1, study2])
```

Total running time of the script: (0 minutes 0.634 seconds)

plot_hypervolume_history

`optuna.visualization.matplotlib.`**`plot_hypervolume_history`**(*study*, *reference_point*)

Plot hypervolume history of all trials in a study with Matplotlib.

Note

You need to adjust the size of the plot by yourself using `plt.tight_layout()` or `plt.savefig(IMAGE_NAME, bbox_inches='tight')`.

Parameters

- **study** (`Study`) – A *Study* object whose trials are plotted for their hypervolumes. The number of objectives must be 2 or more.
- **reference_point** (*Sequence[float]*) – A reference point to use for hypervolume computation. The dimension of the reference point must be the same as the number of objectives.

Returns

A `matplotlib.axes.Axes` object.

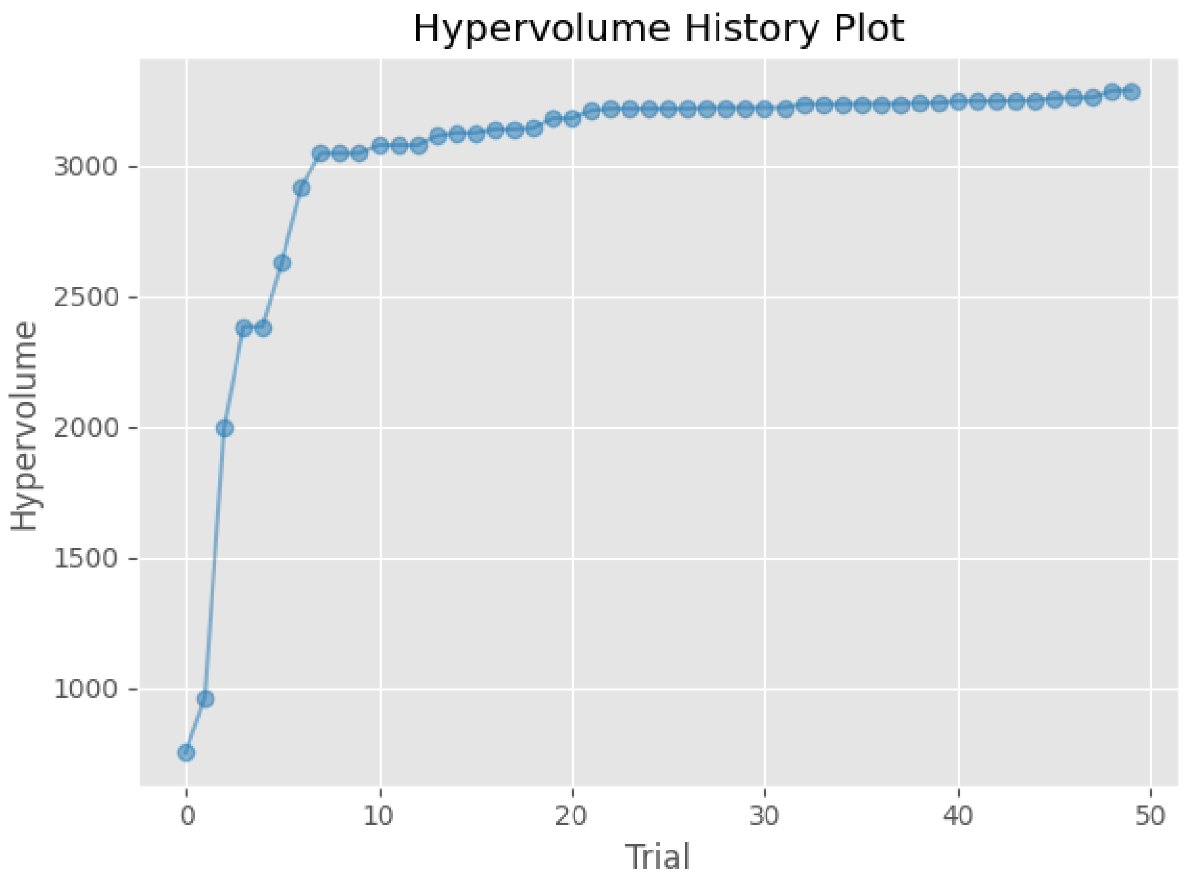
Return type

Axes

Note

Added in v3.3.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.3.0.

The following code snippet shows how to plot optimization history.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.hypervolume_history.
↪py:29: ExperimentalWarning:

optuna.visualization.matplotlib._hypervolume_history.plot_hypervolume_history is␣
↪experimental (supported from v3.3.0). The interface can change in the future.
```

```python
import optuna
import matplotlib.pyplot as plt
```

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```python
def objective(trial):
    x = trial.suggest_float("x", 0, 5)
    y = trial.suggest_float("y", 0, 3)

    v0 = 4 * x ** 2 + 4 * y ** 2
    v1 = (x - 5) ** 2 + (y - 5) ** 2
    return v0, v1


study = optuna.create_study(directions=["minimize", "minimize"])
study.optimize(objective, n_trials=50)

reference_point=[100, 50]
optuna.visualization.matplotlib.plot_hypervolume_history(study, reference_point)
plt.tight_layout()
```

Total running time of the script: (0 minutes 0.247 seconds)

plot_intermediate_values

`optuna.visualization.matplotlib.`**`plot_intermediate_values`**`(`*study*`)`

Plot intermediate values of all trials in a study with Matplotlib.

See also

Please refer to *`optuna.visualization.plot_intermediate_values()`* for an example.

Note

Please refer to matplotlib.pyplot.legend to adjust the style of the generated legend.

Parameters

study (`Study`) – A *`Study`* object whose trials are plotted for their intermediate values.

Returns

A `matplotlib.axes.Axes` object.

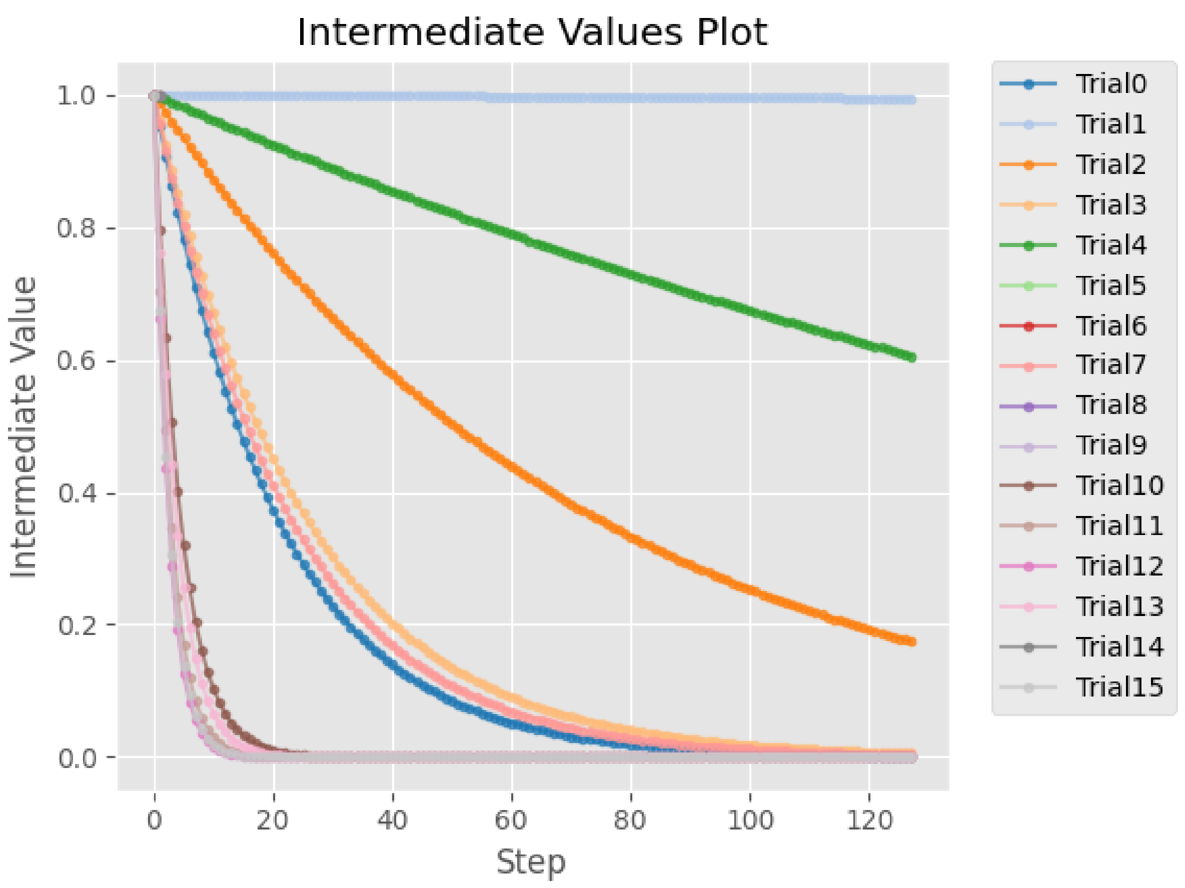
Return type

Axes

Note

Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

The following code snippet shows how to plot intermediate values.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.intermediate_values.
↪py:44: ExperimentalWarning:

optuna.visualization.matplotlib._intermediate_values.plot_intermediate_values is␣
↪experimental (supported from v2.2.0). The interface can change in the future.


<Axes: title={'center': 'Intermediate Values Plot'}, xlabel='Step', ylabel='Intermediate␣
↪Value'>
```

```
import optuna


def f(x):
    return (x - 2) ** 2


def df(x):
```

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```
    return 2 * x - 4


def objective(trial):
    lr = trial.suggest_float("lr", 1e-5, 1e-1, log=True)

    x = 3
    for step in range(128):
        y = f(x)

        trial.report(y, step=step)
        if trial.should_prune():
            raise optuna.TrialPruned()

        gy = df(x)
        x -= gy * lr

    return y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=16)

optuna.visualization.matplotlib.plot_intermediate_values(study)
```

Total running time of the script: (0 minutes 0.483 seconds)

plot_optimization_history

`optuna.visualization.matplotlib.`**`plot_optimization_history`**(*study*, ***, *target=None*, *target_name='Objective Value'*, *error_bar=False*)

Plot optimization history of all trials in a study with Matplotlib.

See also

Please refer to *`optuna.visualization.plot_optimization_history()`* for an example.

Note

You need to adjust the size of the plot by yourself using `plt.tight_layout()` or `plt.savefig(IMAGE_NAME, bbox_inches='tight')`.

Parameters

- **study** (`Study` | *`Sequence`*`[Study]`) – A *`Study`* object whose trials are plotted for their target values. You can pass multiple studies if you want to compare those optimization histories.

- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is `None` and `study` is being used for single-objective optimization, the objective values are plotted.

  > **Note**
  >
  > Specify this argument if `study` is being used for multi-objective optimization.

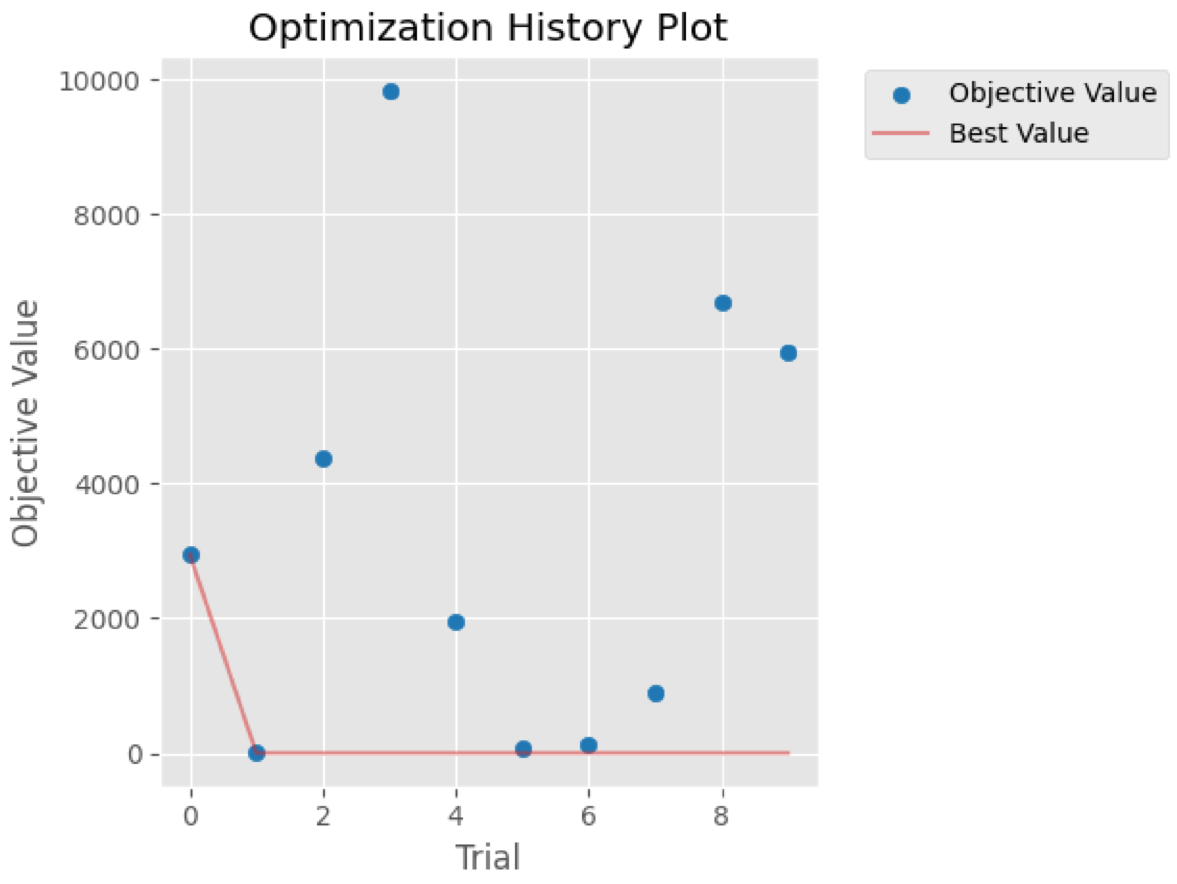
- **target_name** (*str*) – Target's name to display on the axis label and the legend.
- **error_bar** (*bool*) – A flag to show the error bar.

Returns
A `matplotlib.axes.Axes` object.

Return type
Axes

> **Note**
>
> Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

The following code snippet shows how to plot optimization history.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.optimization_history.
↪py:26: ExperimentalWarning:

optuna.visualization.matplotlib._optimization_history.plot_optimization_history is␣
↪experimental (supported from v2.2.0). The interface can change in the future.
```

```
import optuna
import matplotlib.pyplot as plt


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
```

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```
study.optimize(objective, n_trials=10)

optuna.visualization.matplotlib.plot_optimization_history(study)
plt.tight_layout()
```

Total running time of the script: (0 minutes 0.289 seconds)

plot_parallel_coordinate

optuna.visualization.matplotlib.**plot_parallel_coordinate**(*study*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot the high-dimensional parameter relationships in a study with Matplotlib.

Note that, if a parameter contains missing values, a trial with missing values is not plotted.

See also

Please refer to *optuna.visualization.plot_parallel_coordinate()* for an example.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted for their target values.
- **params** (*list[str] | None*) – Parameter list to visualize. The default is all parameters.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is None and study is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if study is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the axis label and the legend.

Returns

A matplotlib.axes.Axes object.

Return type

Axes

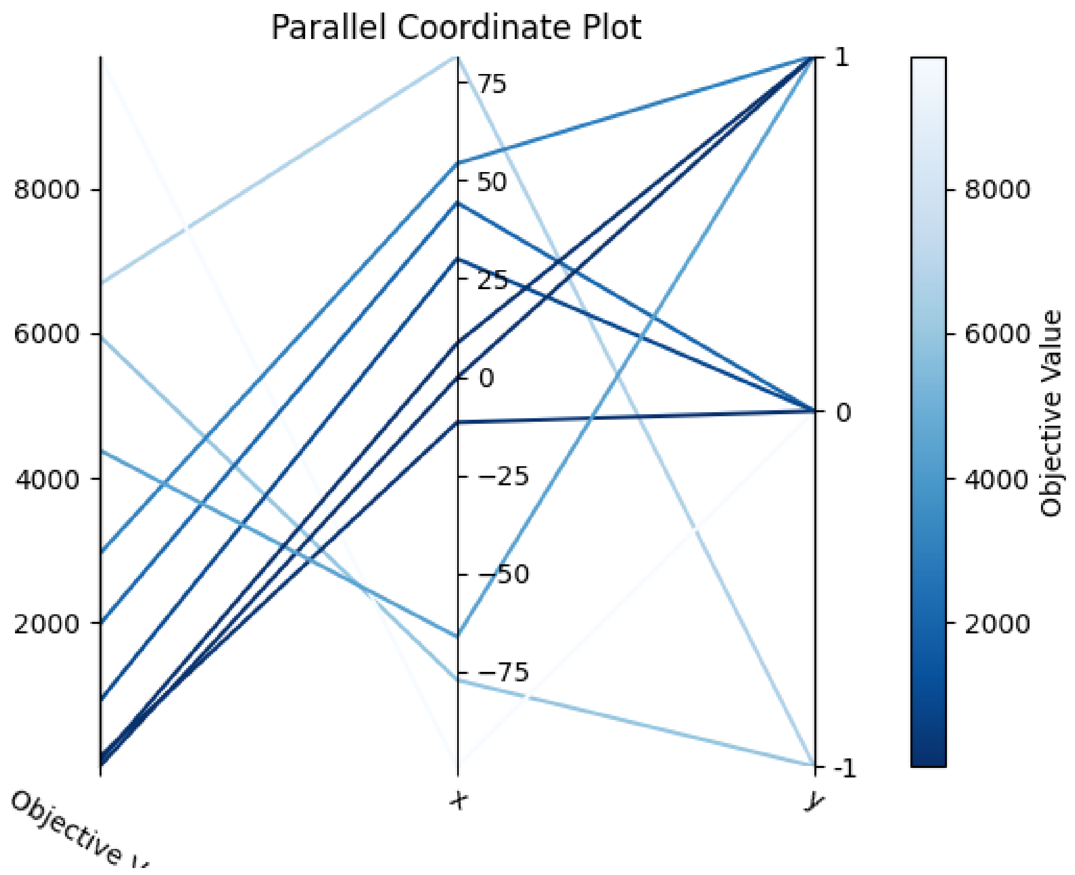
Note

The colormap is reversed when the target argument isn't None or direction of *Study* is minimize.

Note

Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

The following code snippet shows how to plot the high-dimensional parameter relationships.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.parallel_coordinate.
↪py:25: ExperimentalWarning:

optuna.visualization.matplotlib._parallel_coordinate.plot_parallel_coordinate is␣
↪experimental (supported from v2.2.0). The interface can change in the future.


<Axes: title={'center': 'Parallel Coordinate Plot'}>
```

```python
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y
```

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```
sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=10)

optuna.visualization.matplotlib.plot_parallel_coordinate(study, params=["x", "y"])
```

Total running time of the script: (0 minutes 0.390 seconds)

plot_param_importances

`optuna.visualization.matplotlib.plot_param_importances`(*study*, *evaluator=None*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot hyperparameter importances with Matplotlib.

See also

Please refer to *optuna.visualization.plot_param_importances()* for an example.

Parameters

- **study** (Study) – An optimized study.
- **evaluator** (*BaseImportanceEvaluator | None*) – An importance evaluator object that specifies which algorithm to base the importance assessment on. Defaults to *FanovaImportanceEvaluator*.
- **params** (*list[str] | None*) – A list of names of parameters to assess. If None, all parameters that are present in all of the completed trials are assessed.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is None and study is being used for single-objective optimization, the objective values are plotted. For multi-objective optimization, all objectives will be plotted if target is None.

  Note

  This argument can be used to specify which objective to plot if study is being used for multi-objective optimization. For example, to get only the hyperparameter importance of the first objective, use target=lambda t: t.values[0] for the target parameter.

- **target_name** (*str*) – Target's name to display on the axis label. Names set via *set_metric_names()* will be used if target is None, overriding this argument.

Returns

A matplotlib.axes.Axes object.

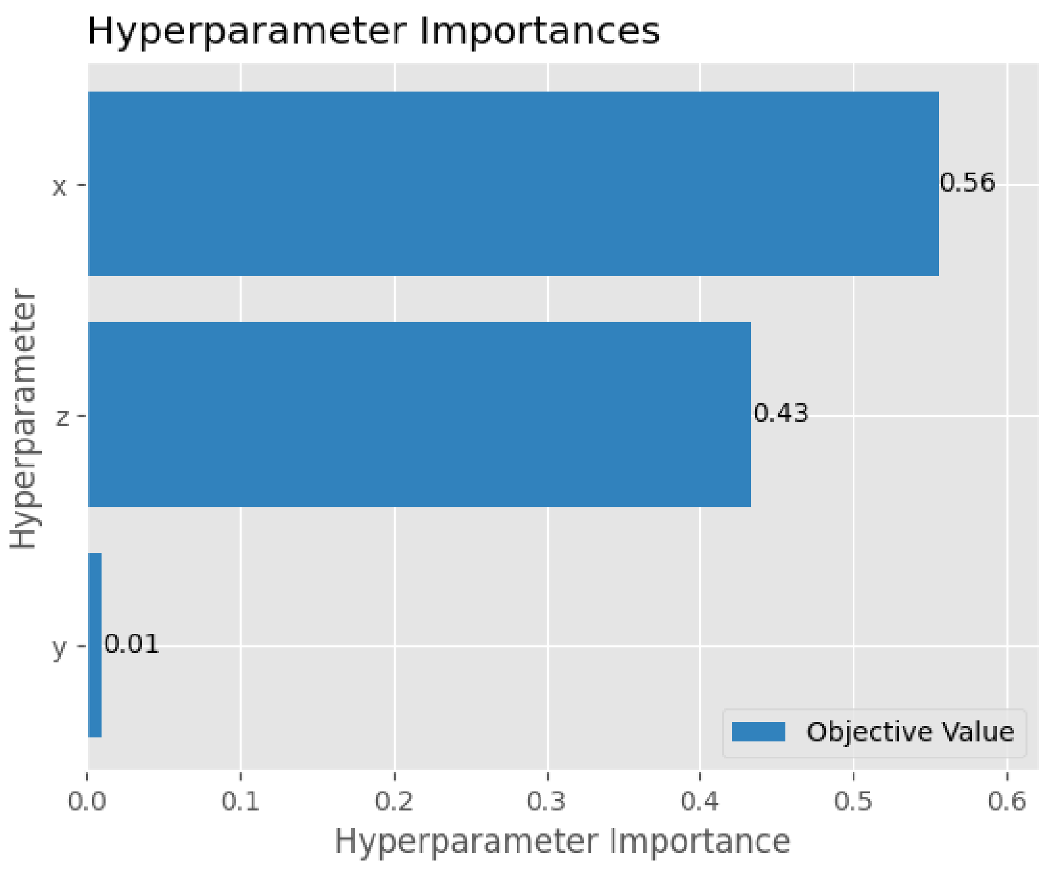
Return type

Axes

Note

Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

The following code snippet shows how to plot hyperparameter importances.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.param_importances.
↪py:26: ExperimentalWarning:

optuna.visualization.matplotlib._param_importances.plot_param_importances is␣
↪experimental (supported from v2.2.0). The interface can change in the future.


<Axes: title={'left': 'Hyperparameter Importances'}, xlabel='Hyperparameter Importance',␣
↪ylabel='Hyperparameter'>
```

```
import optuna


def objective(trial):
    x = trial.suggest_int("x", 0, 2)
    y = trial.suggest_float("y", -1.0, 1.0)
    z = trial.suggest_float("z", 0.0, 1.5)
    return x**2 + y**3 - z**4


sampler = optuna.samplers.RandomSampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=100)

optuna.visualization.matplotlib.plot_param_importances(study)
```

Total running time of the script: (0 minutes 0.827 seconds)

plot_pareto_front

`optuna.visualization.matplotlib.`**`plot_pareto_front`**`(`*study*, ***, *target_names=None*, *include_dominated_trials=True*, *axis_order=None*, *constraints_func=None*, *targets=None*`)`

Plot the Pareto front of a study.

See also

Please refer to *`optuna.visualization.plot_pareto_front()`* for an example.

Parameters

- **`study`** (`Study`) – A *`Study`* object whose trials are plotted for their objective values. `study.n_objectives` must be either 2 or 3 when `targets` is `None`.
- **`target_names`** (*`list[str] | None`*) – Objective name list used as the axis titles. If `None` is specified, "Objective {objective_index}" is used instead. If `targets` is specified for a study that does not contain any completed trial, `target_name` must be specified.
- **`include_dominated_trials`** (*`bool`*) – A flag to include all dominated trial's objective values.
- **`axis_order`** (*`list[int] | None`*) – A list of indices indicating the axis order. If `None` is specified, default order is used. `axis_order` and `targets` cannot be used at the same time.

  Warning

  Deprecated in v3.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v5.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

- **`constraints_func`** (*`Callable[[FrozenTrial], Sequence[float]] | None`*) – An optional function that computes the objective constraints. It must take a *`FrozenTrial`* and return the constraints. The return value must be a sequence of `float` s. A value strictly larger than 0 means that a constraint is violated. A value equal to or smaller than 0 is considered feasible. This specification is the same as in, for example, *NSGAIISampler*.

If given, trials are classified into three categories: feasible and best, feasible but non-best, and infeasible. Categories are shown in different colors. Here, whether a trial is best (on Pareto front) or not is determined ignoring all infeasible trials.

Warning

Deprecated in v4.0.0. This feature will be removed in the future. The removal of this feature is currently scheduled for v6.0.0, but this schedule is subject to change. See https://github.com/optuna/optuna/releases/tag/v4.0.0.

- **targets** (*Callable[[FrozenTrial], Sequence[float]] | None*) – A function that returns a tuple of target values to display. The argument to this function is *FrozenTrial*. `targets` must be `None` or return 2 or 3 values. `axis_order` and `targets` cannot be used at the same time. If the number of objectives is neither 2 nor 3, `targets` must be specified.

Note

Added in v3.0.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.0.0.

Returns

A `matplotlib.axes.Axes` object.

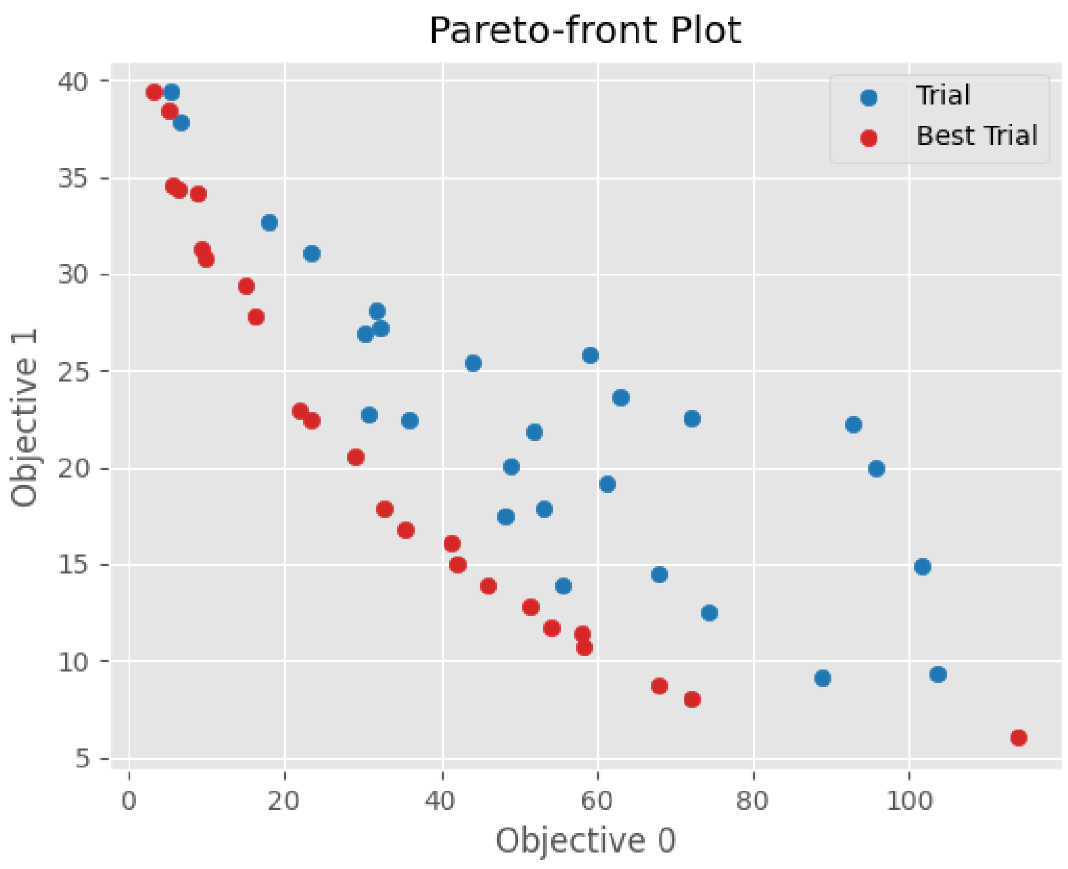
Return type

Axes

Note

Added in v2.8.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.8.0.

The following code snippet shows how to plot the Pareto front of a study.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.pareto_front.py:27:␣
↪ExperimentalWarning:

optuna.visualization.matplotlib._pareto_front.plot_pareto_front is experimental␣
↪(supported from v2.8.0). The interface can change in the future.


<Axes: title={'center': 'Pareto-front Plot'}, xlabel='Objective 0', ylabel='Objective 1'>
```

```
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 5)
    y = trial.suggest_float("y", 0, 3)

    v0 = 4 * x**2 + 4 * y**2
    v1 = (x - 5) ** 2 + (y - 5) ** 2
```

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```
    return v0, v1


study = optuna.create_study(directions=["minimize", "minimize"])
study.optimize(objective, n_trials=50)

optuna.visualization.matplotlib.plot_pareto_front(study)
```

Total running time of the script: (0 minutes 0.272 seconds)

plot_rank

`optuna.visualization.matplotlib.`**`plot_rank`**(*study*, *params=None*, *, *target=None*, *target_name='Objective Value'*)

Plot parameter relations as scatter plots with colors indicating ranks of target value.

Note that trials missing the specified parameters will not be plotted.

See also

Please refer to *`optuna.visualization.plot_rank()`* for an example.

Parameters

- **`study`** (`Study`) – A *`Study`* object whose trials are plotted for their target values.
- **`params`** (*`list[str] | None`*) – Parameter list to visualize. The default is all parameters.
- **`target`** (*`Callable[[FrozenTrial], float] | None`*) – A function to specify the value to display. If it is `None` and **`study`** is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if `study` is being used for multi-objective optimization.

- **`target_name`** (*`str`*) – Target's name to display on the color bar.

Returns

A `matplotlib.axes.Axes` object.

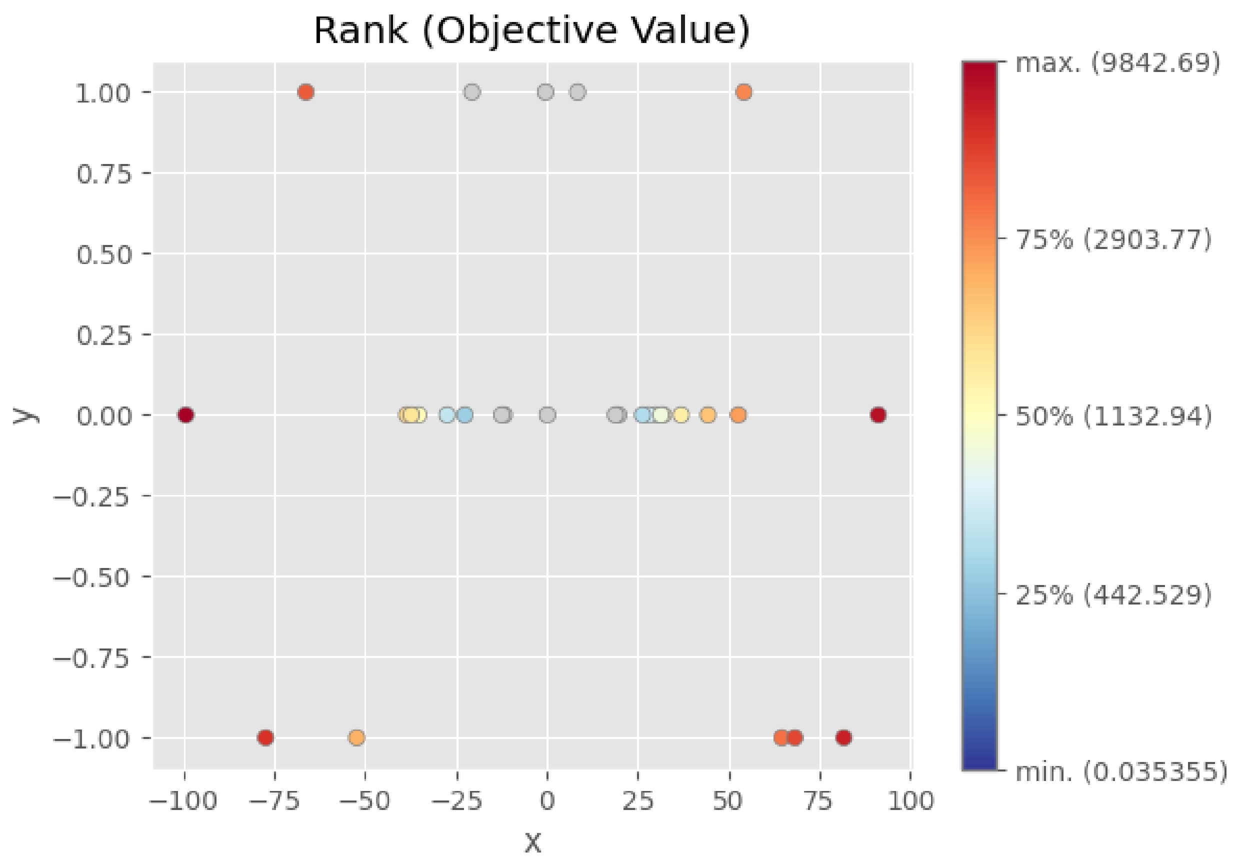
Return type

Axes

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

The following code snippet shows how to plot the parameter relationship as a rank plot.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/optuna/_experimental.py:32: ExperimentalWarning:

Argument ``constraints_func`` is an experimental feature. The interface can change in␣
↪the future.

/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.rank.py:33:␣
↪ExperimentalWarning:

optuna.visualization.matplotlib._rank.plot_rank is experimental (supported from v3.2.0).␣
↪The interface can change in the future.


<Axes: title={'center': 'Rank (Objective Value)'}, xlabel='x', ylabel='y'>
```

```
import optuna
```

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```python
def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])

    c0 = 400 - (x + y) ** 2
    trial.set_user_attr("constraint", [c0])

    return x**2 + y


def constraints(trial):
    return trial.user_attrs["constraint"]


sampler = optuna.samplers.TPESampler(seed=10, constraints_func=constraints)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=30)

optuna.visualization.matplotlib.plot_rank(study, params=["x", "y"])
```

Total running time of the script: (0 minutes 0.336 seconds)

plot_slice

`optuna.visualization.matplotlib.plot_slice`(*study*, *params=None*, ***, *target=None*, *target_name='Objective Value'*)

Plot the parameter relationship as slice plot in a study with Matplotlib.

See also

Please refer to *optuna.visualization.plot_slice()* for an example.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted for their target values.
- **params** (*list[str] | None*) – Parameter list to visualize. The default is all parameters.
- **target** (*Callable[[FrozenTrial], float] | None*) – A function to specify the value to display. If it is `None` and `study` is being used for single-objective optimization, the objective values are plotted.

  Note

  Specify this argument if `study` is being used for multi-objective optimization.

- **target_name** (*str*) – Target's name to display on the axis label.

Returns

A `matplotlib.axes.Axes` object.

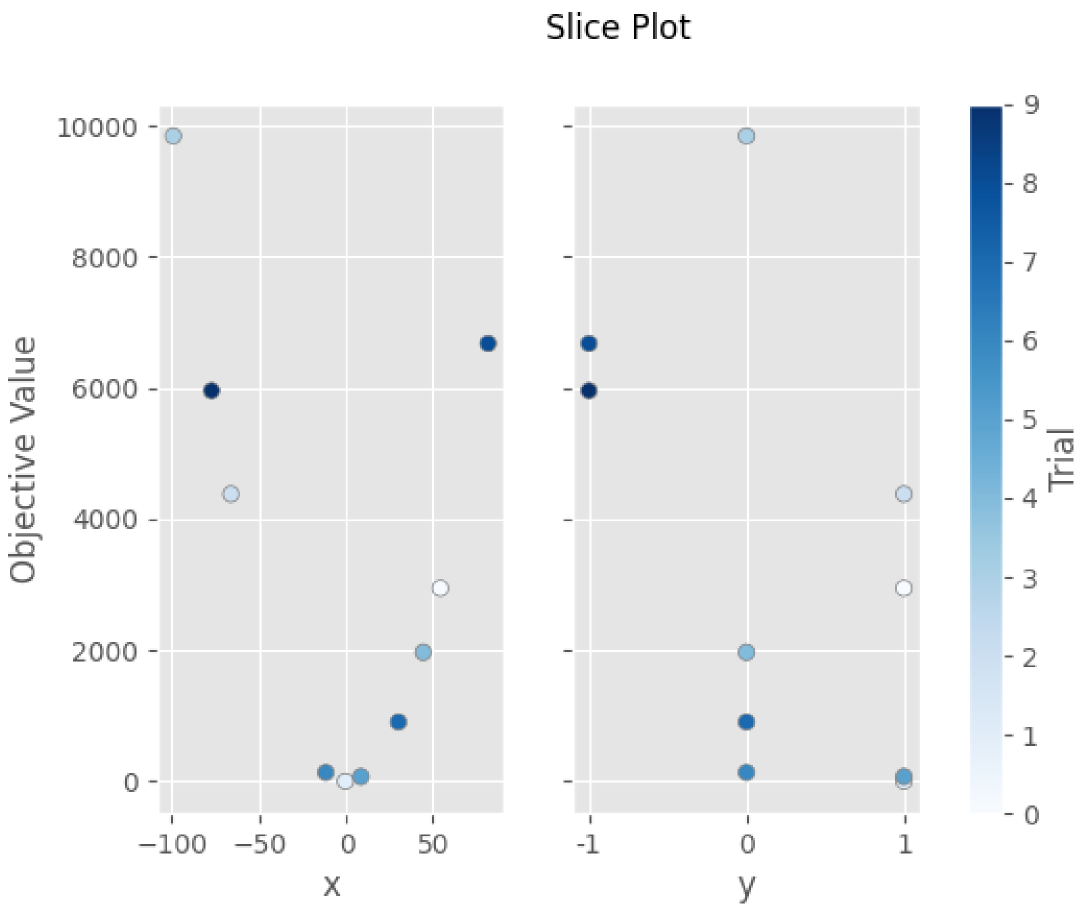
Return type

Axes

Note

Added in v2.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v2.2.0.

The following code snippet shows how to plot the parameter relationship as slice plot.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.slice.py:25:␣
↪ExperimentalWarning:

optuna.visualization.matplotlib._slice.plot_slice is experimental (supported from v2.2.
↪0). The interface can change in the future.


array([<Axes: xlabel='x', ylabel='Objective Value'>, <Axes: xlabel='y'>],
      dtype=object)
```

```python
import optuna


def objective(trial):
    x = trial.suggest_float("x", -100, 100)
    y = trial.suggest_categorical("y", [-1, 0, 1])
    return x**2 + y


sampler = optuna.samplers.TPESampler(seed=10)
study = optuna.create_study(sampler=sampler)
study.optimize(objective, n_trials=10)

optuna.visualization.matplotlib.plot_slice(study, params=["x", "y"])
```

Total running time of the script: (0 minutes 0.292 seconds)

plot_terminator_improvement

`optuna.visualization.matplotlib.`**`plot_terminator_improvement`**(*study*, *plot_error=False*, *improvement_evaluator=None*, *error_evaluator=None*, *min_n_trials=20*)

Plot the potentials for future objective improvement.

This function visualizes the objective improvement potentials, evaluated with `improvement_evaluator`. It helps to determine whether we should continue the optimization or not. You can also plot the error evaluated with `error_evaluator` if the `plot_error` argument is set to `True`. Note that this function may take some time to compute the improvement potentials.

See also

Please refer to *`optuna.visualization.plot_terminator_improvement()`*.

Parameters

- **`study`** (`Study`) – A *`Study`* object whose trials are plotted for their improvement.
- **`plot_error`** (*`bool`*) – A flag to show the error. If it is set to `True`, errors evaluated by `error_evaluator` are also plotted as line graph. Defaults to `False`.
- **`improvement_evaluator`** (`BaseImprovementEvaluator` | *`None`*) – An object that evaluates the improvement of the objective function. Default to *`RegretBoundEvaluator`*.
- **`error_evaluator`** (`BaseErrorEvaluator` | *`None`*) – An object that evaluates the error inherent in the objective function. Default to *`CrossValidationErrorEvaluator`*.
- **`min_n_trials`** (*`int`*) – The minimum number of trials before termination is considered. Terminator improvements for trials below this value are shown in a lighter color. Defaults to `20`.

Returns

A `matplotlib.axes.Axes` object.

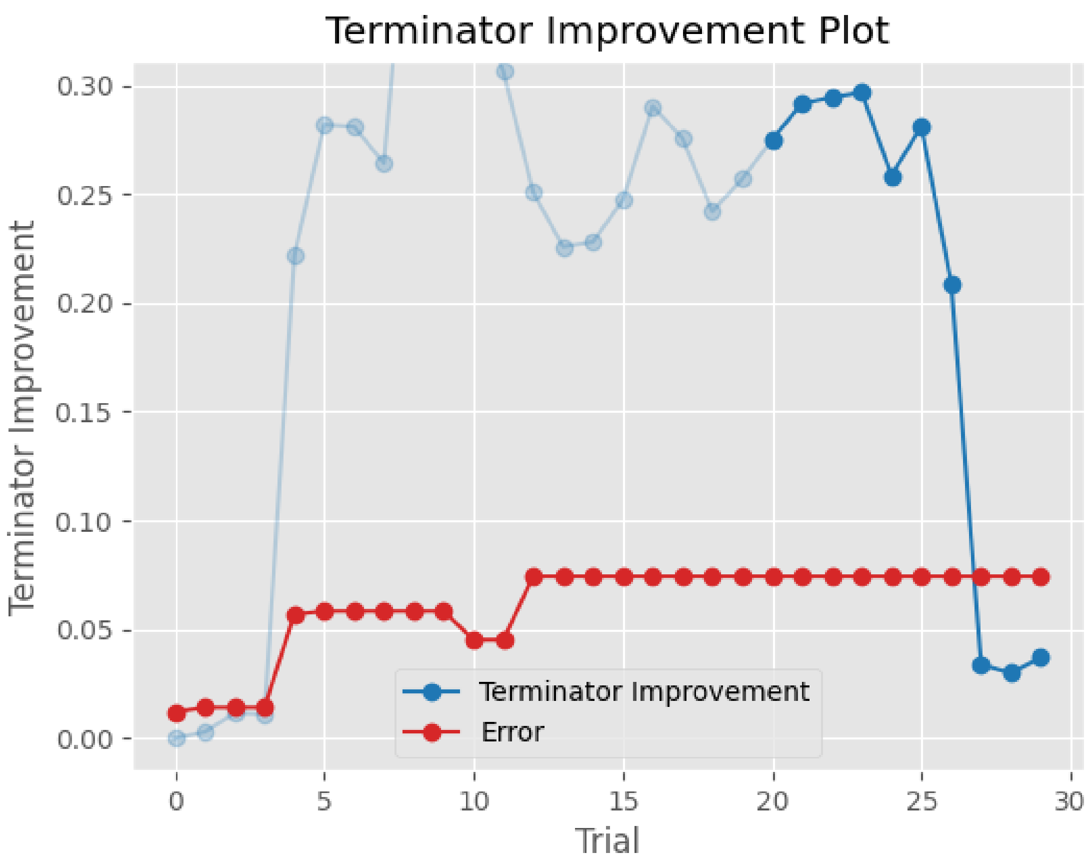
Return type

Axes

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

The following code snippet shows how to plot improvement potentials, together with cross-validation errors.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/sklearn/utils/validation.py:2749: UserWarning:

X does not have valid feature names, but LGBMClassifier was fitted with feature names

/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/sklearn/utils/validation.py:2749: UserWarning:

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/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
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↪packages/sklearn/utils/validation.py:2749: UserWarning:

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↪packages/sklearn/utils/validation.py:2749: UserWarning:
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/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
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↪packages/sklearn/utils/validation.py:2749: UserWarning:

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/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
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/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.terminator_
↪improvement.py:41: ExperimentalWarning:

optuna.visualization.matplotlib._terminator_improvement.plot_terminator_improvement is␣
↪experimental (supported from v3.2.0). The interface can change in the future.

/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/optuna/visualization/_terminator_improvement.py:93: ExperimentalWarning:

RegretBoundEvaluator is experimental (supported from v3.2.0). The interface can change␣
↪in the future.

/home/docs/checkouts/readthedocs.org/user_builds/optuna/envs/latest/lib/python3.12/site-
↪packages/optuna/visualization/_terminator_improvement.py:98: ExperimentalWarning:

CrossValidationErrorEvaluator is experimental (supported from v3.2.0). The interface can␣
↪change in the future.


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 30%|       | 9/30 [00:00<00:00, 85.24it/s]
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<Axes: title={'center': 'Terminator Improvement Plot'}, xlabel='Trial', ylabel=
↪'Terminator Improvement'>
```

```python
from lightgbm import LGBMClassifier
from sklearn.datasets import load_wine
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import KFold
import optuna
from optuna.terminator import report_cross_validation_scores
from optuna.visualization.matplotlib import plot_terminator_improvement


def objective(trial):
    X, y = load_wine(return_X_y=True)
    clf = LGBMClassifier(
```

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```
        reg_alpha=trial.suggest_float("reg_alpha", 1e-8, 10.0, log=True),
        reg_lambda=trial.suggest_float("reg_lambda", 1e-8, 10.0, log=True),
        num_leaves=trial.suggest_int("num_leaves", 2, 256),
        colsample_bytree=trial.suggest_float("colsample_bytree", 0.4, 1.0),
        subsample=trial.suggest_float("subsample", 0.4, 1.0),
        subsample_freq=trial.suggest_int("subsample_freq", 1, 7),
        min_child_samples=trial.suggest_int("min_child_samples", 5, 100),
    )
    scores = cross_val_score(clf, X, y, cv=KFold(n_splits=5, shuffle=True))
    report_cross_validation_scores(trial, scores)
    return scores.mean()


study = optuna.create_study()
study.optimize(objective, n_trials=30)

plot_terminator_improvement(study, plot_error=True)
```

Total running time of the script: (0 minutes 2.067 seconds)

plot_timeline

optuna.visualization.matplotlib.**plot_timeline**(*study*, *n_recent_trials=None*)

Plot the timeline of a study.

See also

Please refer to *optuna.visualization.plot_timeline()* for an example.

Parameters

- **study** (Study) – A *Study* object whose trials are plotted with their lifetime.
- **n_recent_trials** (*int | None*) – The number of recent trials to plot. If None, all trials are plotted. If specified, only the most recent n_recent_trials will be displayed. Must be a positive integer.

Returns

A plotly.graph_objects.Figure object.

Raises

ValueError – if n_recent_trials is 0 or negative.

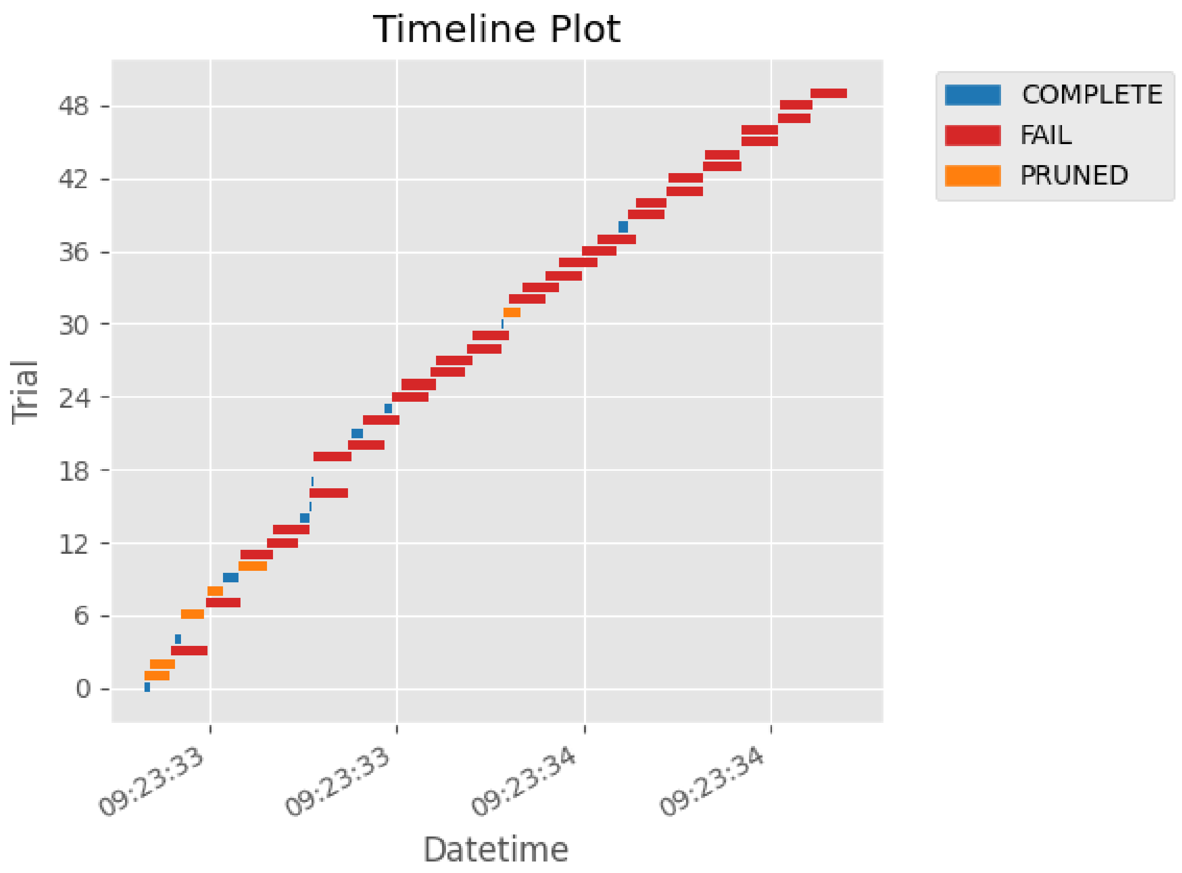
Return type

Axes

Note

Added in v3.2.0 as an experimental feature. The interface may change in newer versions without prior notice. See https://github.com/optuna/optuna/releases/tag/v3.2.0.

The following code snippet shows how to plot the timeline of a study.



```
/home/docs/checkouts/readthedocs.org/user_builds/optuna/checkouts/latest/docs/
↪visualization_matplotlib_examples/optuna.visualization.matplotlib.timeline.py:29:␣
↪ExperimentalWarning:

optuna.visualization.matplotlib._timeline.plot_timeline is experimental (supported from␣
↪v3.2.0). The interface can change in the future.


<Axes: title={'center': 'Timeline Plot'}, xlabel='Datetime', ylabel='Trial'>
```

```
import time
import optuna


def objective(trial):
    x = trial.suggest_float("x", 0, 1)
    time.sleep(x * 0.1)
    if x > 0.8:
        raise ValueError()
```

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```
    if x > 0.4:
        raise optuna.TrialPruned()
    return x**2


study = optuna.create_study(direction="minimize")
study.optimize(objective, n_trials=50, n_jobs=2, catch=(ValueError,))

optuna.visualization.matplotlib.plot_timeline(study)
```

Total running time of the script: (0 minutes 2.158 seconds)

See also

The visualization tutorial provides use-cases with examples.

8.4 FAQ

8.4.1 Can I use Optuna with X? (where X is your favorite ML library)

Optuna is compatible with most ML libraries, and it's easy to use Optuna with those. Please refer to examples.

8.4.2 How to define objective functions that have own arguments?

There are two ways to realize it.

First, callable classes can be used for that purpose as follows:

```python
import optuna


class Objective:
    def __init__(self, min_x, max_x):
        # Hold this implementation specific arguments as the fields of the class.
        self.min_x = min_x
        self.max_x = max_x

    def __call__(self, trial):
        # Calculate an objective value by using the extra arguments.
        x = trial.suggest_float("x", self.min_x, self.max_x)
        return (x - 2) ** 2


# Execute an optimization by using an `Objective` instance.
study = optuna.create_study()
study.optimize(Objective(-100, 100), n_trials=100)
```

Second, you can use `lambda` or `functools.partial` for creating functions (closures) that hold extra arguments. Below is an example that uses `lambda`:

```python
import optuna

# Objective function that takes three arguments.
def objective(trial, min_x, max_x):
    x = trial.suggest_float("x", min_x, max_x)
    return (x - 2) ** 2


# Extra arguments.
```

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```
min_x = -100
max_x = 100

# Execute an optimization by using the above objective function wrapped by `lambda`.
study = optuna.create_study()
study.optimize(lambda trial: objective(trial, min_x, max_x), n_trials=100)
```

Please also refer to sklearn_additional_args.py example, which reuses the dataset instead of loading it in each trial execution.

8.4.3 Can I use Optuna without remote RDB servers?

Yes, it's possible.

In the simplest form, Optuna works with *InMemoryStorage*:

```
study = optuna.create_study()
study.optimize(objective)
```

If you want to save and resume studies, it's handy to use SQLite as the local storage:

```
study = optuna.create_study(study_name="foo_study", storage="sqlite:///example.db")
study.optimize(objective)  # The state of `study` will be persisted to the local SQLite␣
↪file.
```

Please see rdb for more details.

8.4.4 How can I save and resume studies?

There are two ways of persisting studies, which depend if you are using *InMemoryStorage* (default) or remote databases (RDB). In-memory studies can be saved and loaded like usual Python objects using `pickle` or `joblib`. For example, using `joblib`:

```
study = optuna.create_study()
joblib.dump(study, "study.pkl")
```

And to resume the study:

```
study = joblib.load("study.pkl")
print("Best trial until now:")
print(" Value: ", study.best_trial.value)
print(" Params: ")
for key, value in study.best_trial.params.items():
    print(f"    {key}: {value}")
```

Note that Optuna does not support saving/reloading across different Optuna versions with `pickle`. To save/reload a study across different Optuna versions, please use RDBs and upgrade storage schema if necessary. If you are using RDBs, see rdb for more details.

8.4.5 How to suppress log messages of Optuna?

By default, Optuna shows log messages at the `optuna.logging.INFO` level. You can change logging levels by using *optuna.logging.set_verbosity()*.

For instance, you can stop showing each trial result as follows:

```
optuna.logging.set_verbosity(optuna.logging.WARNING)

study = optuna.create_study()
study.optimize(objective)
# Logs like '[I 2020-07-21 13:41:45,627] Trial 0 finished with value:...' are disabled.
```

Please refer to *optuna.logging* for further details.

8.4.6 How to save machine learning models trained in objective functions?

Optuna saves hyperparameter values with their corresponding objective values to storage, but it discards intermediate objects such as machine learning models and neural network weights.

To save models or weights, we recommend utilizing Optuna's built-in `ArtifactStore`. For example, you can use the *upload_artifact()* as follows:

```
base_path = "./artifacts"
os.makedirs(base_path, exist_ok=True)
artifact_store = optuna.artifacts.FileSystemArtifactStore(base_path=base_path)

def objective(trial):
    svc_c = trial.suggest_float("svc_c", 1e-10, 1e10, log=True)
    clf = sklearn.svm.SVC(C=svc_c)
    clf.fit(X_train, y_train)

    # Save the model using ArtifactStore
    with open("model.pickle", "wb") as fout:
        pickle.dump(clf, fout)
    artifact_id = optuna.artifacts.upload_artifact(
        artifact_store=artifact_store,
        file_path="model.pickle",
        study_or_trial=trial.study,
    )
    trial.set_user_attr("artifact_id", artifact_id)
    return 1.0 - accuracy_score(y_valid, clf.predict(X_valid))

study = optuna.create_study()
study.optimize(objective, n_trials=100)
```

To retrieve models or weights, you can list and download them using *get_all_artifact_meta()* and *download_artifact()* as shown below:

```
# List all models
for artifact_meta in optuna.artifacts.get_all_artifact_meta(study_or_trial=study):
    print(artifact_meta)
# Download the best model
trial = study.best_trial
best_artifact_id = trial.user_attrs["artifact_id"]
optuna.artifacts.download_artifact(
    artifact_store=artifact_store,
    file_path='best_model.pickle',
    artifact_id=best_artifact_id,
)
```

For a more comprehensive guide, refer to the ArtifactStore tutorial.

8.4.7 How can I obtain reproducible optimization results?

To make the parameters suggested by Optuna reproducible, you can specify a fixed random seed via `seed` argument of an instance of *`samplers`* as follows:

```
sampler = TPESampler(seed=10)  # Make the sampler behave in a deterministic way.
study = optuna.create_study(sampler=sampler)
study.optimize(objective)
```

To make the pruning by *`HyperbandPruner`* reproducible, please specify a fixed `study_name` of *`Study`* in addition to the `seed` argument.

However, there are two caveats.

First, when optimizing a study in distributed or parallel mode, there is inherent non-determinism. Thus it is very difficult to reproduce the same results in such condition. We recommend executing optimization of a study sequentially if you would like to reproduce the result.

Second, if your objective function behaves in a non-deterministic way (i.e., it does not return the same value even if the same parameters were suggested), you cannot reproduce an optimization. To deal with this problem, please set an option (e.g., random seed) to make the behavior deterministic if your optimization target (e.g., an ML library) provides it.

8.4.8 How are exceptions from trials handled?

Trials that raise exceptions without catching them will be treated as failures, i.e. with the *`FAIL`* status.

By default, all exceptions except *`TrialPruned`* raised in objective functions are propagated to the caller of *`optimize()`*. In other words, studies are aborted when such exceptions are raised. It might be desirable to continue a study with the remaining trials. To do so, you can specify in *`optimize()`* which exception types to catch using the `catch` argument. Exceptions of these types are caught inside the study and will not propagate further.

You can find the failed trials in log messages.

```
[W 2018-12-07 16:38:36,889] Setting status of trial#0 as TrialState.FAIL because of \
the following error: ValueError('A sample error in objective.')
```

You can also find the failed trials by checking the trial states as follows:

```
study.trials_dataframe()
```

number	state	value	…	param	system_attrs
0	TrialState.FAIL		…	0	Setting status of trial#0 as TrialState.FAIL because of the following error: ValueError('A test error in objective.')
1	TrialState.COMPLE'	1269	…	1	

See also

The `catch` argument in *`optimize()`*.

8.4.9 How are NaNs returned by trials handled?

Trials that return NaN (`float('nan')`) are treated as failures, but they will not abort studies.

Trials which return NaN are shown as follows:

```
[W 2018-12-07 16:41:59,000] Setting status of trial#2 as TrialState.FAIL because the \
objective function returned nan.
```

8.4.10 What happens when I dynamically alter a search space?

Since parameters search spaces are specified in each call to the suggestion API, e.g. *`suggest_float()`* and *`suggest_int()`*, it is possible to, in a single study, alter the range by sampling parameters from different search spaces in different trials. The behavior when altered is defined by each sampler individually.

Note

Discussion about the TPE sampler. https://github.com/optuna/optuna/issues/822

8.4.11 How can I use two GPUs for evaluating two trials simultaneously?

If your optimization target supports GPU (CUDA) acceleration and you want to specify which GPU is used in your script, `main.py`, the easiest way is to set `CUDA_VISIBLE_DEVICES` environment variable:

```
# On a terminal.
#
# Specify to use the first GPU, and run an optimization.
$ export CUDA_VISIBLE_DEVICES=0
$ python main.py

# On another terminal.
#
# Specify to use the second GPU, and run another optimization.
$ export CUDA_VISIBLE_DEVICES=1
$ python main.py
```

Please refer to CUDA C Programming Guide for further details.

8.4.12 How can I test my objective functions?

When you test objective functions, you may prefer fixed parameter values to sampled ones. In that case, you can use *`FixedTrial`*, which suggests fixed parameter values based on a given dictionary of parameters. For instance, you can input arbitrary values of x and y to the objective function $x + y$ as follows:

```
def objective(trial):
    x = trial.suggest_float("x", -1.0, 1.0)
    y = trial.suggest_int("y", -5, 5)
    return x + y


objective(FixedTrial({"x": 1.0, "y": -1}))  # 0.0
objective(FixedTrial({"x": -1.0, "y": -4}))  # -5.0
```

Using *`FixedTrial`*, you can write unit tests as follows:

```
# A test function of pytest
def test_objective():
    assert 1.0 == objective(FixedTrial({"x": 1.0, "y": 0}))
    assert -1.0 == objective(FixedTrial({"x": 0.0, "y": -1}))
    assert 0.0 == objective(FixedTrial({"x": -1.0, "y": 1}))
```

8.4.13 How do I avoid running out of memory (OOM) when optimizing studies?

If the memory footprint increases as you run more trials, try to periodically run the garbage collector. Specify `gc_after_trial` to `True` when calling *`optimize()`* or call `gc.collect()` inside a callback.

```
def objective(trial):
    x = trial.suggest_float("x", -1.0, 1.0)
    y = trial.suggest_int("y", -5, 5)
    return x + y


study = optuna.create_study()
study.optimize(objective, n_trials=10, gc_after_trial=True)

# `gc_after_trial=True` is more or less identical to the following.
study.optimize(objective, n_trials=10, callbacks=[lambda study, trial: gc.collect()])
```

There is a performance trade-off for running the garbage collector, which could be non-negligible depending on how fast your objective function otherwise is. Therefore, `gc_after_trial` is `False` by default. Note that the above examples are similar to running the garbage collector inside the objective function, except for the fact that `gc.collect()` is called even when errors, including *`TrialPruned`* are raised.

Note

`ChainerMNStudy` does currently not provide `gc_after_trial` nor callbacks for `optimize()`. When using this class, you will have to call the garbage collector inside the objective function.

8.4.14 How can I output a log only when the best value is updated?

Here's how to replace the logging feature of optuna with your own logging callback function. The implemented callback can be passed to *`optimize()`*. Here's an example:

```
import optuna


# Turn off optuna log notes.
optuna.logging.set_verbosity(optuna.logging.WARN)


def objective(trial):
    x = trial.suggest_float("x", 0, 1)
    return x ** 2


def logging_callback(study, frozen_trial):
    previous_best_value = study.user_attrs.get("previous_best_value", None)
```

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```
    if previous_best_value != study.best_value:
        study.set_user_attr("previous_best_value", study.best_value)
        print(
            "Trial {} finished with best value: {} and parameters: {}. ".format(
            frozen_trial.number,
            frozen_trial.value,
            frozen_trial.params,
            )
        )


study = optuna.create_study()
study.optimize(objective, n_trials=100, callbacks=[logging_callback])
```

Note that this callback may show incorrect values when you try to optimize an objective function with `n_jobs!=1` (or other forms of distributed optimization) due to its reads and writes to storage that are prone to race conditions.

8.4.15 How do I suggest variables which represent the proportion, that is, are in accordance with Dirichlet distribution?

When you want to suggest n variables which represent the proportion, that is, $p[0], p[1], ..., p[n-1]$ which satisfy $0 \le p[k] \le 1$ for any k and $p[0] + p[1] + ... + p[n-1] = 1$, try the below. For example, these variables can be used as weights when interpolating the loss functions. These variables are in accordance with the flat Dirichlet distribution.

```
import numpy as np
import matplotlib.pyplot as plt
import optuna


def objective(trial):
    n = 5
    x = []
    for i in range(n):
        x.append(- np.log(trial.suggest_float(f"x_{i}", 0, 1)))

    p = []
    for i in range(n):
        p.append(x[i] / sum(x))

    for i in range(n):
        trial.set_user_attr(f"p_{i}", p[i])

    return 0

study = optuna.create_study(sampler=optuna.samplers.RandomSampler())
study.optimize(objective, n_trials=1000)

n = 5
p = []
for i in range(n):
    p.append([trial.user_attrs[f"p_{i}"] for trial in study.trials])
axes = plt.subplots(n, n, figsize=(20, 20))[1]
```

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```
for i in range(n):
    for j in range(n):
        axes[j][i].scatter(p[i], p[j], marker=".")
        axes[j][i].set_xlim(0, 1)
        axes[j][i].set_ylim(0, 1)
        axes[j][i].set_xlabel(f"p_{i}")
        axes[j][i].set_ylabel(f"p_{j}")

plt.savefig("sampled_ps.png")
```

This method is justified in the following way: First, if we apply the transformation $x = -\log(u)$ to the variable u sampled from the uniform distribution $Uni(0,1)$ in the interval $[0,1]$, the variable x will follow the exponential distribution $Exp(1)$ with scale parameter 1. Furthermore, for n variables $x[0],...,x[n-1]$ that follow the exponential distribution of scale parameter 1 independently, normalizing them with $p[i] = x[i]/\sum_i x[i]$, the vector p follows the Dirichlet distribution $Dir(\alpha)$ of scale parameter $\alpha = (1,...,1)$. You can verify the transformation by calculating the elements of the Jacobian.

8.4.16 How can I optimize a model with some constraints?

When you want to optimize a model with constraints, you can use the following classes: *TPESampler*, *NSGAIISampler*, *GPSampler* or BoTorchSampler. The following example is a benchmark of Binh and Korn function, a multi-objective optimization, with constraints using *NSGAIISampler*. This one has two constraints $c_0 = (x-5)^2 + y^2 - 25 \le 0$ and $c_1 = -(x-8)^2 - (y+3)^2 + 7.7 \le 0$ and finds the optimal solution satisfying these constraints.

```
import optuna


def objective(trial):
    # Binh and Korn function with constraints.
    x = trial.suggest_float("x", -15, 30)
    y = trial.suggest_float("y", -15, 30)

    # Constraints which are considered feasible if less than or equal to zero.
    # The feasible region is basically the intersection of a circle centered at (x=5,␣
↪y=0)
    # and the complement to a circle centered at (x=8, y=-3).
    c0 = (x - 5) ** 2 + y ** 2 - 25
    c1 = -((x - 8) ** 2) - (y + 3) ** 2 + 7.7

    # Store the constraints as user attributes so that they can be restored after␣
↪optimization.
    trial.set_user_attr("constraint", (c0, c1))

    v0 = 4 * x ** 2 + 4 * y ** 2
    v1 = (x - 5) ** 2 + (y - 5) ** 2

    return v0, v1


def constraints(trial):
```

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```
    return trial.user_attrs["constraint"]


sampler = optuna.samplers.NSGAIISampler(constraints_func=constraints)
study = optuna.create_study(
    directions=["minimize", "minimize"],
    sampler=sampler,
)
study.optimize(objective, n_trials=32, timeout=600)

print("Number of finished trials: ", len(study.trials))

print("Pareto front:")

trials = sorted(study.best_trials, key=lambda t: t.values)

for trial in trials:
    print("  Trial#{}".format(trial.number))
    print(
        "    Values: Values={}, Constraint={}".format(
            trial.values, trial.user_attrs["constraint"][0]
        )
    )
    print("    Params: {}".format(trial.params))
```

If you are interested in an example for BoTorchSampler, please refer to this sample code.

There are two kinds of constrained optimizations, one with soft constraints and the other with hard constraints. Soft constraints do not have to be satisfied, but an objective function is penalized if they are unsatisfied. On the other hand, hard constraints must be satisfied.

Optuna is adopting the soft one and **DOES NOT** support the hard one. In other words, Optuna **DOES NOT** have built-in samplers for the hard constraints.

8.4.17 How can I parallelize optimization?

The variations of parallelization are in the following three cases.

1. Multi-threading parallelization with single node
2. Multi-processing parallelization with single node
3. Multi-processing parallelization with multiple nodes

1. Multi-threading parallelization with a single node

Parallelization can be achieved by setting the argument `n_jobs` in *`optuna.study.Study.optimize()`*. However, the python code will not be faster due to GIL because *`optuna.study.Study.optimize()`* with `n_jobs!=1` uses multi-threading.

While optimizing, it will be faster in limited situations, such as waiting for other server requests or C/C++ processing with numpy, etc., but it will not be faster in other cases.

For more information about 1., see APIReference.

2. Multi-processing parallelization with single node

This can be achieved by using `JournalFileBackend` or client/server RDBs (such as PostgreSQL and MySQL).

For more information about 2., see TutorialEasyParallelization.

3. Multi-processing parallelization with multiple nodes

This can be achieved by using client/server RDBs (such as PostgreSQL and MySQL). However, if you are in the environment where you can not install a client/server RDB, you can not run multi-processing parallelization with multiple nodes.

For more information about 3., see TutorialEasyParallelization.

8.4.18 How can I solve the error that occurs when performing parallel optimization with SQLite3?

We would never recommend SQLite3 for parallel optimization in the following reasons.

- To concurrently evaluate trials enqueued by `enqueue_trial()`, `RDBStorage` uses *SELECT ... FOR UPDATE* syntax, which is unsupported in SQLite3.
- As described in the SQLAlchemy's documentation, SQLite3 (and pysqlite driver) does not support a high level of concurrency. You may get a "database is locked" error, which occurs when one thread or process has an exclusive lock on a database connection (in reality a file handle) and another thread times out waiting for the lock to be released. You can increase the default timeout value like *optuna.storages.RDBStorage("sqlite:///example.db", engine_kwargs={"connect_args": {"timeout": 20.0}})* though.
- For distributed optimization via NFS, SQLite3 does not work as described at FAQ section of sqlite.org.

If you want to use a file-based Optuna storage for these scenarios, please consider using `JournalFileBackend` instead.

```python
import optuna
from optuna.storages import JournalStorage
from optuna.storages.journal import JournalFileBackend

storage = JournalStorage(JournalFileBackend("optuna_journal_storage.log"))

study = optuna.create_study(storage=storage)
...
```

See the Medium blog post for details.

8.4.19 Can I monitor trials and make them failed automatically when they are killed unexpectedly?

Note

Heartbeat mechanism is experimental. API would change in the future.

A process running a trial could be killed unexpectedly, typically by a job scheduler in a cluster environment. If trials are killed unexpectedly, they will be left on the storage with their states *RUNNING* until we remove them or update their state manually. For such a case, Optuna supports monitoring trials using heartbeat mechanism. Using heartbeat, if a process running a trial is killed unexpectedly, Optuna will automatically change the state of the trial that was running on that process to `FAIL` from `RUNNING`.

```
import optuna

def objective(trial):
    (Very time-consuming computation)

# Recording heartbeats every 60 seconds.
# Other processes' trials where more than 120 seconds have passed
# since the last heartbeat was recorded will be automatically failed.
storage = optuna.storages.RDBStorage(url="sqlite:///:memory:", heartbeat_interval=60,␣
↪grace_period=120)
study = optuna.create_study(storage=storage)
study.optimize(objective, n_trials=100)
```

Note

The heartbeat is supposed to be used with `optimize()`. If you use `ask()` and `tell()`, please change the state of the killed trials by calling `tell()` explicitly.

You can also execute a callback function to process the failed trial. Optuna provides a callback to retry failed trials as `RetryFailedTrialCallback`. Note that a callback is invoked at a beginning of each trial, which means `RetryFailedTrialCallback` will retry failed trials when a new trial starts to evaluate.

```
import optuna
from optuna.storages import RetryFailedTrialCallback

storage = optuna.storages.RDBStorage(
    url="sqlite:///:memory:",
    heartbeat_interval=60,
    grace_period=120,
    failed_trial_callback=RetryFailedTrialCallback(max_retry=3),
)

study = optuna.create_study(storage=storage)
```

8.4.20 How can I deal with permutation as a parameter?

Although it is not straightforward to deal with combinatorial search spaces like permutations with existing API, there exists a convenient technique for handling them. It involves re-parametrization of permutation search space of n items as an independent n-dimensional integer search space. This technique is based on the concept of Lehmer code.

A Lehmer code of a sequence is the sequence of integers in the same size, whose i-th entry denotes how many inversions the i-th entry of the permutation has after itself. In other words, the i-th entry of the Lehmer code represents the number of entries that are located after and are smaller than the i-th entry of the original sequence. For instance, the Lehmer code of the permutation $(3, 1, 4, 2, 0)$ is $(3, 1, 2, 1, 0)$.

Not only does the Lehmer code provide a unique encoding of permutations into an integer space, but it also has some desirable properties. For example, the sum of Lehmer code entries is equal to the minimum number of adjacent transpositions necessary to transform the corresponding permutation into the identity permutation. Additionally, the lexicographical order of the encodings of two permutations is the same as that of the original sequence. Therefore, Lehmer code preserves “closeness” among permutations in some sense, which is important for the optimization algorithm. An Optuna implementation example to solve Euclid TSP is as follows:

```python
import numpy as np

import optuna


def decode(lehmer_code: list[int]) -> list[int]:
    """Decode Lehmer code to permutation.

    This function decodes Lehmer code represented as a list of integers to a permutation.
    """
    all_indices = list(range(n))
    output = []
    for k in lehmer_code:
        value = all_indices[k]
        output.append(value)
        all_indices.remove(value)
    return output


# Euclidean coordinates of cities for TSP.
city_coordinates = np.array(
    [[0.0, 0.0], [1.0, 0.0], [0.0, 1.0], [1.0, 1.0], [2.0, 2.0], [-1.0, -1.0]]
)
n = len(city_coordinates)


def objective(trial: optuna.Trial) -> float:
    # Suggest a permutation in the Lehmer code representation.
    lehmer_code = [trial.suggest_int(f"x{i}", 0, n - i - 1) for i in range(n)]
    permutation = decode(lehmer_code)

    # Calculate the total distance of the suggested path.
    total_distance = 0.0
    for i in range(n):
        total_distance += np.linalg.norm(
            city_coordinates[permutation[i]] - city_coordinates[np.roll(permutation,␣
↪1)[i]]
        )
    return total_distance


study = optuna.create_study()
study.optimize(objective, n_trials=10)
lehmer_code = study.best_params.values()
print(decode(lehmer_code))
```

8.4.21 How can I ignore duplicated samples?

Optuna may sometimes suggest parameters evaluated in the past and if you would like to avoid this problem, you can try out the following workaround:

```python
import optuna
from optuna.trial import TrialState


def objective(trial):
    # Sample parameters.
    x = trial.suggest_int("x", -5, 5)
    y = trial.suggest_int("y", -5, 5)
    # Fetch all the trials to consider.
    # In this example, we use only completed trials, but users can specify other states
    # such as TrialState.PRUNED and TrialState.FAIL.
    states_to_consider = (TrialState.COMPLETE,)
    trials_to_consider = trial.study.get_trials(deepcopy=False, states=states_to_
↪consider)
    # Check whether we already evaluated the sampled `(x, y)`.
    for t in reversed(trials_to_consider):
        if trial.params == t.params:
            # Use the existing value as trial duplicated the parameters.
            return t.value

    # Compute the objective function if the parameters are not duplicated.
    # We use the 2D sphere function in this example.
    return x ** 2 + y ** 2


study = optuna.create_study()
study.optimize(objective, n_trials=100)
```

8.4.22 How can I delete all the artifacts uploaded to a study?

Optuna supports *artifacts* for large data storage during an optimization. After you conduct enormous amount of experiments, you may want to remove the artifacts stored during optimizations.

We strongly recommend to create a new directory or bucket for each study so that all the artifacts linked to a study can be entirely removed by deleting the directory or the bucket.

However, if it is necessary to remove artifacts from a Python script, users can use the following code:

Warning

add_trial() and *copy_study()* do not copy artifact files linked to *Study* or *Trial*. Please make sure **NOT** to delete the artifacts from the source study or trial. Failing to do so may lead to unexpected behaviors as Optuna does not guarantee expected behaviors when users call `remove()` externally. Due to the Optuna software design, it is hard to officially support the delete feature and we are not planning to support this feature in the future either.

```python
from optuna.artifacts import get_all_artifact_meta


def remove_artifacts(study, artifact_store):
    # NOTE: ``artifact_store.remove`` is discouraged to use because it is an internal␣
↪feature.
    storage = study._storage
```

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```
    for trial in study.trials:
        for artifact_meta in get_all_artifact_meta(trial, storage=storage):
            # For each trial, remove the artifacts uploaded to ``base_path``.
            artifact_store.remove(artifact_meta.artifact_id)

    for artifact_meta in get_all_artifact_meta(study):
        # Remove the artifacts uploaded to ``base_path``.
        artifact_store.remove(artifact_meta.artifact_id)
```

8.4.23 Can I specify parameter starting points before optimization?

Yes, it's possible.

For a more comprehensive guide, refer to the Specify Hyperparameters Manually.

8.4.24 How can I resolve case sensitivity issues with MySQL?

By default, MySQL performs case-insensitive string comparisons. However, Optuna treats strings in a case-sensitive manner, leading to conflicts in MySQL if parameter names differ only by case.

For example,

```
def objective(trial):
    a = trial.suggest_int("a", 0, 10)
    A = trial.suggest_int("A", 0, 10)
    return a + A
```

In this case, Optuna treats *a* and *A* distinctively while MySQL does not due to its default collation settings. As a result, only one of the parameters will be registered in MySQL.

The following workarounds should be considered:

1. **Use a different storage backend.**
   Please consider using PostgreSQL or SQLite, which supports case-sensitive handling.
2. **Rename the parameters to avoid case conflicts.**
   For example, use *a* and *b* instead of *a* and *A*.
3. **Change MySQL's collation settings to be case-sensitive.**
   You can configure case sensitivity at the database, table, or column level. We defer to the MySQL documentation for more details.

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INDICES AND TABLES

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