

Installation and Environment Setup

This document provides step-by-step instructions to install and use the Conda environment for this project. The environment is defined in the `environment.yml` file and includes all necessary dependencies such as Python, NumPy, Pandas, Matplotlib, Seaborn, scikit-learn, and JupyterLab.

Prerequisites

- **Conda Installed:**
Ensure you have [Conda](#) installed. You can use either [Anaconda](#) or [Miniconda](#).

Steps to Install the Environment

1. Create the Conda Environment

Run the following command from the root directory where the `environment.yml` file is located:

```
conda env create -f environment.yml
```

This command creates a new Conda environment named `enzyme_classification` with all the required dependencies.

2. Activate the Environment

Once the environment is created, activate it using:

```
conda activate enzyme_analysis
```

3. Deactivating the Environment

When you are done working, you can deactivate the environment with:

```
conda deactivate
```