

Importing and Using the Conda Environment for My Current Project

This document provides clear instructions on how to import the Conda environment using the provided YAML file and how to activate and use it for the Genome Assembly pipeline in my current project. This environment includes essential tools such as FastQC, TRIMMOMATIC, QUAST, SPADES, PROKKA and featureCounts.

Prerequisites

- **Conda Installation:**
Ensure that you have Conda installed on your system (Anaconda or Miniconda is recommended).
 - **Environment YAML File:**
The YAML file (`environment.yml`) is located in the `environment` folder within your project directory.
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Step-by-Step Instructions

1. Navigate to Your Project Directory

Open your terminal and change directory to your project folder. For example:

```
cd /path/to/your/current/project
```

2. Create the Conda Environment from the YAML File

Run the following command to create the new environment using the YAML file:

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

3. Verify Environment Creation

After the environment is created, list your Conda environments to verify:

```
conda env list
```

4. Activate the New Environment

Activate the environment by running:

```
conda activate genome_assembl_env
```

5. Confirm the Environment is Active

Your terminal prompt should now display the active environment name. You can also verify by running:

```
conda info --envs
```

Additional Tips

Updating the Environment

If changes are made to the environment YAML file, update your environment using:

```
conda env update -f environment/environment.yml
```

Deactivating the Environment

When you are finished working, deactivate the environment by executing:

```
conda deactivate
```