

NexGenBiocoder

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NexGenBiocoder is a bioinformatics project repository designed to analyze and interpret biological data using computational methods.

This repository serves as a foundation for learners and researchers interested in genomics, proteomics, and systems biology.

Features

- Sequence data analysis (DNA/RNA/Protein)
- Biological data parsing and visualization
- Integration of tools like Biopython, NumPy, Matplotlib
- Ready-to-run scripts for in silico experiments

Installation

1. Clone the repository:

```
git clone https://github.com/NexGenBiocoder/InSilicoSoul-.git
```

```
cd InSilicoSoul-
```

2. Create a virtual environment and install dependencies:

```
python -m venv venv
```

```
source venv/bin/activate (On Windows: venv\Scripts\activate)
```

```
pip install -r requirements.txt
```

Usage

Update the input file paths and run the script:

```
python analysis_script.py
```

You can modify parameters inside the script as needed.

Folder Structure

InSilicoSoul-/