

ViSeq: Sequence Visualization, Reimagined

ViSeq is a lightweight, high-performance bioinformatics tool for DNA sequence alignment, manual editing, primer design, and phylogenetic analysis. Built with Python and PyQt6, it offers a fast native interface for Windows.

Key Features

- **High-Performance Viewer:** Smoothly handles large datasets using optimized rendering.
- **Smart Primer Design:** Automated thermodynamic analysis to find optimal Forward/Reverse primer pairs with amplicon size control.
- **Sequence Alignment:** Built-in integration with **MUSCLE** for accurate multiple sequence alignments.
- **Phylogenetics:** Generate trees using Neighbor-Joining or **FastTree**, with graphical visualization and Newick export.
- **Editor:** Drag-and-drop sequence reordering, column/row deletion, and gap filling.
- **Search & Navigation:** Regex-based motif search, visual rulers, and synchronized list navigation.

Installation & Running

Option 1: Run the Portable Executable (No Python required)

1. Download the latest release from the

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page.

2. Extract the zip file.
3. Ensure `muscle.exe` and `FastTree.exe` are in the same folder as `ViSeq.exe`.
4. Double-click `ViSeq.exe`.

Option 2: Run from Source Code

If you want to modify the code, you need Python 3.8+ installed.

1. Clone this repository:

```
git clone https://github.com/Kroniqe/ViSeq.git
cd ViSeq
```

2. Install dependencies:

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

3. Run the application:

```
python aliview_clone.py
```

External Tools (Dependencies)

To use Alignment and Phylogenetic features, you must download these external tools and place them in the application folder:

- **MUSCLE** (for Alignment): [Download Here](#) -> Rename to `muscle.exe`
- **FastTree** (for Trees): [Download Here](#) -> Rename to `FastTree.exe`

Building the EXE

To build the executable yourself using PyInstaller:

```
pyinstaller --noconsole --onefile --name="ViSeq" --collect-all Bio aliview_clone.
```

License

This project is licensed under the **GNU General Public License v3.0 (GPLv3)**.

This choice is mandated by the project's dependency on **PyQt6**, which is distributed under GPLv3.

- **PyQt6**: GPLv3
- **Biopython**: Biopython License (Permissive)
- **NumPy/Matplotlib**: BSD/PSF (Permissive)

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