# phylogenetics Documentation

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Phylogenetics is a minimal Python API for doing phylogenetics. It manages the annoying aspects of phylogenetics (i.e. file conversion) for you and lets you focus on exploring and interpreting the data.

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### Basic Example

The main object in phylogenetics is the PhylogeneticsProject. Start by initializing the PhylogeneticsProject object, pointing to a directory where you'd like to store all the phylogenetic data/output.

```
# Imports
from phylogenetics import PhylogeneticsProject

# Initialize a project class
project = PhylogeneticsProject(project_dir='project')
```

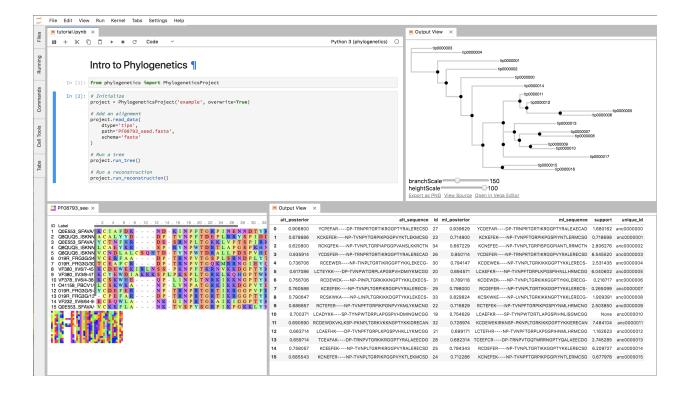
Then, add an alignment (using any file schema you'd like). These sequences will be the tips of your tree. You can now begin building trees and reconstructing ancestral sequences.

```
project.read_data(dtype='tips', path='alignment.fasta', schema='fasta')

# Run PhyML to construct a phylogenetic

# tree by maximum likelihood.
project.run_tree()

# Reconstruct ancestral sequences using default settings.
project.run_reconstruction()
```



Installation

#### Install from PyPi:

pip install phylogenetics

#### To install a development version:

git clone https://github.com/Zsailer/phylogenetics
cd phylogenetics
pip install -e .

### Dependencies

*phylogenetics* manages phylogenetics data. Currently, it doesn't do any of the phylogenetic calculations itself. For this, use external tools like:

- 1. PhyML: building maximum likelihood trees.
- 2. PAML: reconstructing ancestors.

phylogenetics is built on top of following python stack:

- 1. DendroPy: A Python library for phylogenetic scripting, simulation, data processing and manipulation.
- 2. ToyTree: A minimalist tree plotting library using toyplot graphs
- 3. PhyloPandas: Pandas for phylogenetics
- 4. PyASR: Ancestral Sequence Reconstruction in Python

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### 4.1 Installing PhyML and PAML

It's important that the following executables are callable from any location for phylogenetics to work properly with external tools:

- 1. **PhyML**: building maximum likelihood trees.
- 2. PAML: reconstructing ancestors.

#### 4.1.1 PhyML

Get the latest, stable release of 'PhyML'\_

Download, unpack, and install Phyml. Export path to the src file in bashrc file.

### 4.2 TreeProject API

The following pages is the TreeProject API documentation. The TreeProject is the main class you'll use in the phylogenetics package.

### 4.2.1 TreeProject Class