

# Project Structure

This project is based on a legacy codebase that was originally derived from a GeneWeb system written in OCaml. The folder structure has been carefully designed to ensure the code is both maintainable and scalable, while also preserving compatibility with the original system.

Each folder in the repository **must contain a `README.md` file** describing its purpose, usage, and relevant notes. This helps new contributor and maintainers to quickly understand the role of each module.

Each module should contains `tests` folder to assure that all function work properly

## Directory Tree example

```
python/  
  README.md      → Main project documentation  
  lib/           → Main lib directory for all tools  
    db/          → Database tools for geneweb  
    gedcom/      → Simple gedcom parser for gedcom 5.5.1 and upper  
  
scripts/  
  README.md      → Scripts project documentation  
  
consang/  
  README.md      → Docs for consanguinity calculation module  
  tests/         → All tests for consang (unit, integration etc...)  
  Makefile       → Main makefile for all tests  
  
gwb2ged/  
  README.md      → Docs for GeneWeb → GEDCOM converter  
  tests/         → All tests for gwb2ged (unit, integration etc...)  
  Makefile       → Main makefile for all tests  
  
ged2gwb/  
  README.md      → Docs for GEDCOM → GeneWeb converter
```

tests/ → All tests for ged2gwb (unit, integration etc...)  
Makefile → Main makefile for all tests

gwc/  
README.md → Docs for GeneWeb db creator  
tests/ → All tests for gwc (unit, integration etc...)  
...

## Directory Details

### python/

- **Integration root** containing the GeneWeb binaries, test infrastructure, and utility scripts.
- Contains:
  - **scripts/** → Build, cleanup, and migration utilities.
  - **Binaries** → Core GeneWeb tools.

### lib/

- Core of Geneweb system:
  - **db/** → Geneweb database tools using msgpack
  - **gedcom/** → Gedcom parser tools

### scripts/

- General-purpose scripts for maintenance, data generation, and deployment.
- Includes both Python and shell scripts.

### consang/

- Calculates the consanguinity level of individuals and synchronizes it with the base

### gwb2ged/

- Converts **GeneWeb** → **GEDCOM**.
- Useful for exporting genealogical data into standard GEDCOM format.

### ged2gwb/

- Converts **GEDCOM** → **GeneWeb**.
- Essential for importing genealogical data from external sources.

### gwd/

- The main web server for Geneweb

### gwc/

- **GeneWeb Compiler**: manages and creates the genealogical databases.