

Evoland-HPC

Carlson Büth and Benjamin Black

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Preface

This is a guide and reference book for the Evoland-HPC pipeline. Evoland-HPC models future changes in the provision of ecosystem services under scenarios of climatic, socio-economic, land use change and alternative area-based conservation strategies. Evoland-HPC couples a [land use land cover change \(LULCC\) model for Switzerland](#) (Black et al. 2023, n.d.), state-of-the-art [species distribution modelling \(N-SDM\)](#) (Adde et al. 2023), and ecosystem service models (Kuelling and Adde, n.d.).

1 Introduction

This is a book created from markdown and executable code.

- Mayer, Rabe, and Grêt-Regamey (2023), Black et al. (2023), Adde et al. (2023)

2 Overview

Coupling the three models, we need to define how they depend on each other. Figure 2.1 shows the dependencies between the models.

From this structure, a clear order of execution can be derived. For each of them there is a short description of the model.

2.1 LULCC: Land Use Simulation

The [land use land cover change \(LULCC\) model for Switzerland](#) (Black et al. 2023, n.d.) simulates the land use change in Switzerland from 2010 to 2060...

LULCC depends on [R](#), CRAN packages and [Dinamica EGO](#).

2.2 N-SDM: Species Distribution Modelling

The [species distribution modelling \(N-SDM\)](#) (Adde et al. 2023) uses multiple approaches to determine species distribution maps for Switzerland...

It mainly uses `Base-R`. As N-SDM is built to be used with HPCs (high performance computers), with `bash` scripts SLURM is used to submit jobs.

2.3 NCPs: Nature Contributions to People

A range of NCPs are then estimated from the previous models outputs (Kuelling and Adde, n.d.)... Find a description of the NCP scripts in the [NCPs folder](#).

Additionally to `R` and CRAN packages, [InVEST](#) is used via the `Python` modules [natcap.invest](#).

Focal...

The job of the Future-EI pipeline is to glue all pieces together for use on HPCs. For this, a batch job written in `bash` manages multiple climate scenarios and other parameters, while keeping track of the intermediate results. Such big batch job can be broken down onto steps

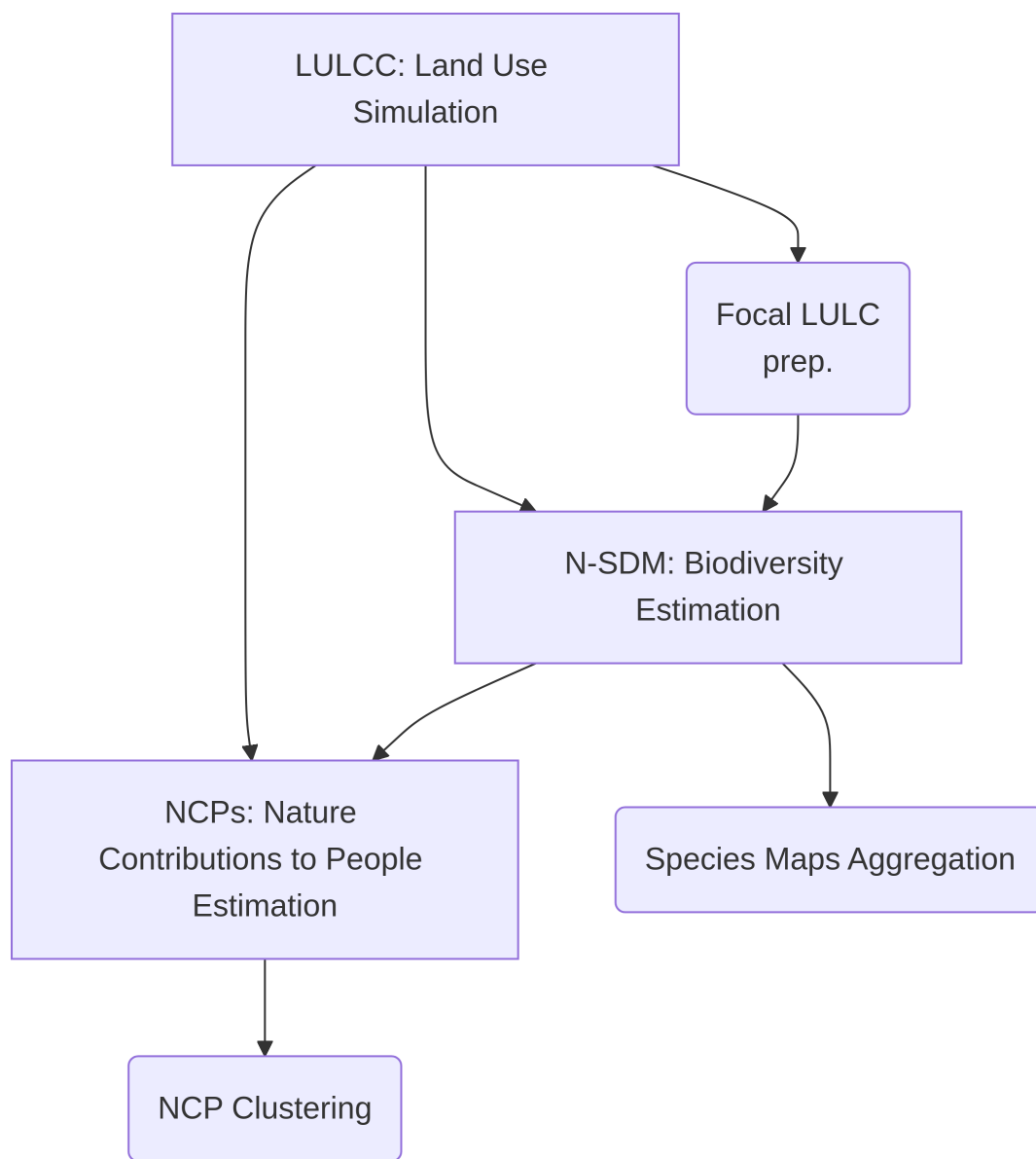


Figure 2.1: Pipeline Overview

from the diagram above, and parallelization through tasks with several cpus. As each step is different in requirements and execution, resources must be allocated accordingly. The most computationally expensive step is the N-SDM model. Further details will be given in the following sections.

3 Pipeline

The pipeline consists out of a SLURM batch job as structured in Figure [2.1](#). To refresh: a SLURM *batch job* consists out of one or more *steps*, each consisting out of one or more *tasks*, which of each can use one or more CPU cores.

4 Setup

To set up Future-EI for usage, you need to clone this repository, install the models used in Figure 2.1, and configure the local paths for inputs and parameters. For the `bash` script, environment variables are set in the `src/config.yml` file.

4.1 Micromamba/Conda

For some pipeline steps, we use conda environments. For this, we recommend using `micromamba`, it does the same thing as `conda`, but resolves dependencies much faster, with the flexibility of `miniconda` (only command line interface, no GUI). Find the installation instructions [here](#). Using `conda`, the commands work the same, only `micromamba` needs to be replaced by `conda`. The given scripts identify the installed package manager, as can be found in `src/bash_functions.sh`.

4.2 Dinamica EGO

Dinamica EGO is available on [the project website](#), but will be shipped in the LULCC docker image for simplicity. It can be automatically installed or built using the `src/steps/10_LULCC/docker_setup.sh` script, which uses variables from the `src/config.yml` file, and depends on the `dinamica-ego-docker` container. The script is compatible with `docker` and `apptainer`.

For a full description of the environments, see the environments:

4.3 Environments

For the steps in the pipeline, different environments and modules are required. These are collected in each step folder. For each, there are scripts to reproduce our used environment. To make all bash scripts in the source executable, give them the permission as follows:

```
# possibly activate globstar: shopt -s globstar
chmod +x src/**/*.sh
```

Attention: When you set up the environments, make sure to use compatible versions of the same packages between the different steps, to ensure upward compatibility.

4.4 Yaml Parser yq

For the `bash` scripts, we use `yq` to parse the `yaml` configuration file. `yq` needs to be available in the `PATH` variable of the shell. To install the latest version, run the following command:

```
bin_dir=/usr/bin &&\
wget https://github.com/mikefarah/yq/releases/latest/download/yq_linux_amd64 -O $bin_dir/yq
chmod +x $bin_dir/yq
```

Other [installation options](#) and binaries can be found on the repository's README. To make `yq` available in the `PATH` variable, make sure the `$bin_dir` is in the `PATH` variable. To check the parser is installed correctly, run `yq --version` in the shell. And to print contents of `config.yml` as idiomatic YAML to stdout, run `yq -P -oy src/config.yml`.

5 Summary

In summary, this book has no content whatsoever.

References

- Adde, Antoine, Pierre-Louis Rey, Philipp Brun, Nathan Külling, Fabian Fopp, Florian Altermatt, Olivier Broennimann, et al. 2023. “*N-SDM* : A High-Performance Computing Pipeline for Nested Species Distribution Modelling.” *Ecography* 2023 (6): e06540. <https://doi.org/10.1111/ecog.06540>.
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