READ\_ME – EuropaBon D5.3 Macrophyte EBV

02.April.2024

< FULL TITLE AND DOI TO BE INSERTED AS SOON AS KNOWN >

**Data owner and provider :** Benoît O.L. Demars (NIVA), Marit Mjelde (NIVA), Benno Dillinger (NIVA), Seppo Hellsten (SYKE), Minna Kuoppala (SYKE), Juha Riihimäki (SYKE), Richard Johnson (SLU), Jens Fölster (SLU)

**Contact:** [benoit.demars@niva.no](mailto:benoit.demars@niva.no); [benoit.demars@outlook.com](mailto:benoit.demars@outlook.com)

The data are made public prior to publication in a peer reviewed journal for the sake of openness and promote work on species biodiversity. The authors would still appreciate to be contacted, at least until their own work has been published.

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

**Note:** .txt file saved as UTF8 to keep the lake names in different languages in a good format in R

**\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\***

The **EuropaBon** folder host two sub-folders: **Fennoscandia** and **Model scripts**. Fennoscandia hold the data you need to run the species distribution models saved in **Model scripts**.

**Fennoscandia**

The original ‘clean’ dataset was saved as species\_climate\_nosefi\_v3.txt (2079 lakes).

The R script Fennoscandia\_2079\_2059\_1081\_lakes.R provides the details to obtain the subsets of lakes without replicate spatial coordinates (2059 lakes) and with a complete set of co-variates (1081 lakes).

Another R script TP\_reference\_GAM.R details how the TP concentration at reference lakes was modelled and reference TP derived for all lakes

Three country contour shape files are needed for the production of maps:

gadm41\_FIN.gpkg, gadm41\_NOR.gpkg, gadm41\_SWE.gpkg

**Model scripts**

There are three R scripts to run the species distribution models with gam (mgcv), glm and ensemble models (biomod2). This is an example with Isoëtes lacustris. Simply find and replace ISOE\_LAC by another species code (see Appendix 1 of EuropaBon deliverable T5.3) throughout the script allows to run the script for any other species.

There are three R scripts to produce the maps, one for each type of modelling approach.

*\*\*\* All scripts should run, provided the directory paths are adapted \*\*\**