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► **To cite this version:**

Quentin Royer, Diane Von Gunten, Yann Le Coarer, Nicolas Lamouroux, Hervé Capra, et al..
HABBY : A New Open-Source Software to Estimate Hydraulic Habitat Suitability. IAHR 2022 from
snow to sea, Jun 2022, Granada, Spain. hal-03708269

HAL Id: hal-03708269

<https://hal.science/hal-03708269v1>

Submitted on 29 Jun 2022

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HABBY: A New Open-Source Software to Estimate Hydraulic Habitat Suitability

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Abstract

The life of aquatic fauna in streams and rivers depends on hydrological variability with considerable emphasis on minimum discharge in flow regulated reaches. One of the methods used to define ecologically suitable minimum discharges is the physical habitat simulation method (habitat model) which converts the outputs of a hydrodynamic river model into habitat suitability for different aquatic taxa, based on their estimated hydraulic preferences. The application of this method requires the use of dedicated software. One of the current computer programs for habitat simulations in France (EVHA) is not technically up-to-date and had to be replaced. Much more than an update of existing software, HABBY is a new free and open-source program, which will be very useful to estimate ecological flows through aquatic habitat availability and suitability. Compatible with MS-Windows, macOS, and GNU/Linux, HABBY is developed in Python. It does not contain any internal hydrodynamic model but accepts, as inputs, the output files of several commonly used models. It also incorporates three statistical habitat models, including Estimhab, a popular statistical model in France. Moreover, a system of scripts helps to store past studies and facilitates the implementation of complex case studies.

Keywords: Ecohydraulics, Ecological flow, Habitat modelling, Fish and Invertebrate, Hydraulic models

1. INTRODUCTION

Rivers and streams provide a wide range of ecosystem services such as irrigation, drinking water supply or power generation. The anthropogenic use of freshwater is therefore intensive: most of the world's largest rivers are impacted by human activities, which threaten aquatic biodiversity worldwide.

One of the main stresses on freshwater biodiversity is the degradation of aquatic habitats resulting from major changes in flows due to, among other things, dam regulation, land use changes and water abstraction. Freshwater biological communities depend on the interactions of biological, physical, and chemical characteristics of rivers and streams. These characteristics are strongly impacted by flow regulation, which represents a significant risk to freshwater community and the river ecosystem as a whole. It is therefore sometimes necessary to estimate a suitable basic flow rate and to adapt its variability (i.e. environmental flows) for a more acceptable and efficient management of the water resource.

To determine such environmental flows, several methods are currently used, such as look-up tables, holistic methodologies, habitat simulation or hydraulic rating methods. The habitat simulation method is one of the most widely used (Tharme, 2003; Lamouroux et al., 2017, 2018). It is based on hydraulic models of stream study reaches. Environmental flows are estimated based on hydraulic conditions that meet biological requirements, generally documented for most sensitive (target) species-taxa at different life stages. In most cases, this method uses hydraulic model outputs (i.e. estimations of water depths and mean flow velocities), substrate data in GIS representation and biological models (e.g. preference curves) to estimate the minimum suitable flow and its required variability if needed.

This paper presents HABBY, a new tool^a that overcomes some of the limitations of conventional software implementing the habitat simulation method:

- HABBY can process the outputs of a variety of world-renowned 1D and 2D hydraulic models for shallow waters, as it is crucial to adapt the choice of a hydraulic model to the question addressed and to the local characteristics of the water system;
- HABBY couples the hydraulic model with a variety of univariate and bivariate biological models (e.g. preference curves) and allows users to add their own biological models;
- It has an open-source license allowing users to modify the program for their own research needs or to obtain full information on how the modelling was done.

2. METHODOLOGIES

HABBY is designed to estimate availability of fish and macroinvertebrate suitable habitat respect to flow discharge.

a <https://habby.wiki.inrae.fr/en:habby>

2.1 Microhabitat method

The principle of the method consists in calculating, for a given river reach and a given flow, a suitable habitat availability for target species-taxa. Habitat suitability is based on preferences of life stages of aquatic taxa for water depth, flow velocity and substrate size. Indeed, a given taxonomic life stage can survive in several types of habitats but will mainly select those with the most suitable conditions for its development. The selected hydraulic conditions that characterize a habitat (habitat suitability) are expressed using:

- a Suitability Index (SI) ranging from 0 (worst value) to 1 (best value) depending on whether the conditions are suitable or not for the species in question;
- or a Weighted Usable Area (WUA) ($WUA = SI * \text{Wetted Area}$).

Habitat Suitability Curves (HSC) are produced for each species-taxa and for each parameter to convert hydraulic conditions into habitat suitability.

2.2 Hydraulic values

Flow velocities and water depths are considered using numerical modelling of shallow water flows. The models can be either 1D or 2D but, in the end, all values will be processed on the nodes of a 2D triangular mesh. The local scale is broken down into each cell discretization of the numerical model allowing the calculation of a cell suitability index (CSI). The CSI indicates whether the local hydraulic conditions meet the biological requirements.

For the 2D modelling, water depths and flow velocities are solutions of the following equation:

$$\partial_t U + \partial_x F(U) + \partial_y G(U) = S(U) \quad [1]$$

where,

$$U = \begin{pmatrix} h \\ hu \\ hv \end{pmatrix}, F(U) = \begin{pmatrix} hu \\ hu^2 + \frac{g}{2}h^2 \\ huv \end{pmatrix}, G(U) = \begin{pmatrix} hv \\ huv \\ hv^2 + \frac{g}{2}h^2 \end{pmatrix}, S(U) = \begin{pmatrix} 0 \\ -gh\partial_x z_b \\ -gh\partial_y z_b \end{pmatrix}$$

The variables (u, v) are the scalar components in the horizontal x and y directions of the depth-averaged velocity ($m \cdot s^{-1}$); h denotes the local water depths (m); g is the constant gravity ($m \cdot s^{-2}$); z_b is the bottom elevation (m).

2.3 Statistical modelling

HABBY also includes statistical habitat models (listed in section 3.1), as a simple alternative to the use of conventional ones (Lamouroux and Capra, 2002). These simplified approaches are based on the observation that the frequency distribution of microhabitat hydraulic variables in stream reaches can be predicted from the average hydraulic geometries of reaches (depth- and width-discharge relationships; Lamouroux et al., 1992; Girard et al., 2014). They provide estimates of statistical distributions of within-reach hydraulics but do not provide spatially-explicit results. They require simple input data but apply only in reaches with morphologies close to natural.

2.4 Substrate

According to the measurement protocol, substrate data can be provided in three different ways with a GIS or a text file giving nodes coordinates (Fig. 1). Regardless of the format of the original substrate values, the tool will automatically interpolate these values onto a 2D triangular mesh.

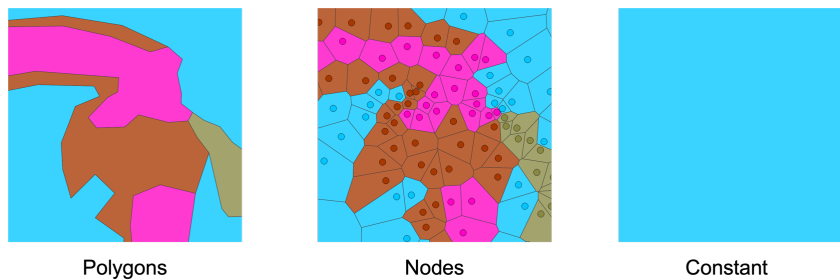


Figure 1. Possible inputs for substrate data

The Wentworth grain size classification (Wentworth, 1922) is used to depict the habitat complexity of the substrate.

2.5 Biological models

Two types of HSC are proposed for fish and invertebrate: univariate and bivariate suitability curves, where the hydraulic variables of interest are water depth, flow velocity, substrate size and bed shear stress. They provide valuable input information regarding the suitability of local hydraulic parameters with the species-taxa requirements. Models available from the literature are progressively implemented in HABBY (e.g., Plichard et al., 2020; Forcellini et al., in press). Adding user-defined external suitability curves is also possible.

Hydrosignatures (Le Coarer, 2007) of hydraulic model data can also be visualized. In a grid of hydraulic classes defined by ranges of water depths and mean flow velocities, a hydrosignature is a table of percentages of area (or volume) distributions of these classes (Fig. 2). Many of the proposed biological models implemented in HABBY are also associated with a hydrosignature for visualizing their domain of validity.

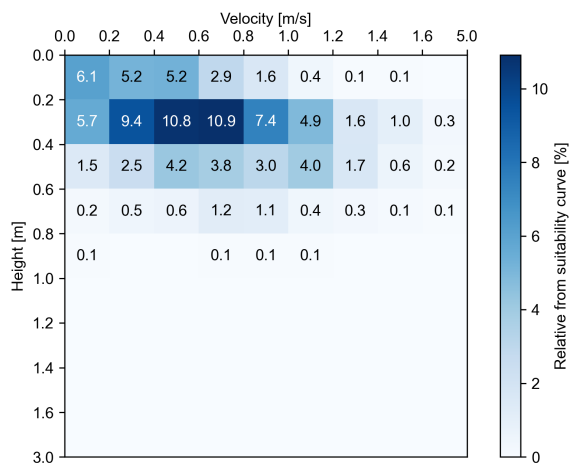


Figure 2. Example of a hydrosignature for an invertebrate model (Baetis Leach, 1815)

3. SOFTWARE DESCRIPTION

HABBY is entirely written in Python language, with the use of the PyQt package for the GUI part (Fig. 3). It is distributed under the open-source CeCILL license. It is freely available on GitHub^b and translated in different languages.

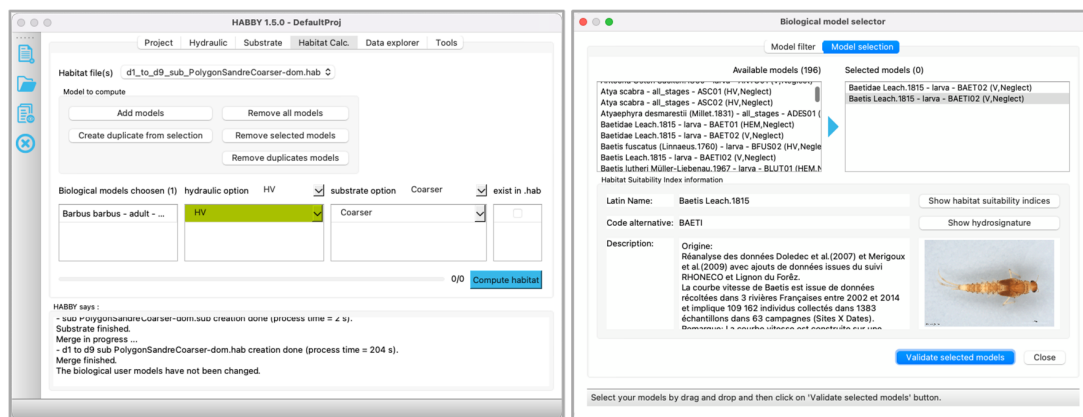


Figure 3. Cross-platform and multi-languages application with the choice of options for the habitat calculation (left) and of the biological models (right)

3.1 Modelling tools

In the current version v1.5 (November 2021), the results of the following hydraulic models can be used as hydraulic inputs for the habitat estimation:

- Mascaret 1D/Telemac 2D (Hervouet, 2007)
- HEC-RAS 1D/2D (2008)
- Basement 2D (Vanzo *et al.*, 2021)
- Rubar20 2D (Paquier, 2011)
- Lammi (Sabaton, 1993)

Other models are still under consideration for a future integration, namely:

- EVHA 1D (Ginot, 1995)
- Iber 2D (Bladé *et al.*, 2014)

^b <https://github.com/Yannlrstea/habby>

- SW2D (Guinot *et al.*, 2018)
- River2D (Steffler *et al.*, 2002)
- FullSWOF (Delestre *et al.*, 2017)
- Flood Modeller (Lin *et al.*, 2006)
- Mike 21 (Warren *et al.*, 1992)

Models outputs can concern an unsteady flow and it is possible to import several files at once.

The hydrosignatures of the hydraulic input data can be performed, and the original Triangulated Irregular Network can be partitioned into cells belonging to a single hydraulic class.

Three statistical models are also implemented:

- STATHAB (Girard *et al.* 2014) and FSTRESS models (Lamouroux *et al.*, 1992) are statistical hydraulic models that can be coupled with many available biological models implemented in HABBY. Stathab considers depth and velocity as local hydraulic variables, whereas FSTRESS is based on bed shear stress and is particularly appropriate for invertebrate taxa (Forcellini *et al.*, in press);
- ESTIMHAB (Lamouroux *et al.* 2002) is a statistical habitat model based on similar statistical principles, but whose output are directly habitat parameters (SI, WUA) for a limited number of pre-selected biological models.

3.2 Workflow

HABBY first reads the output files of hydraulic models and cut all the dry cells from the original mesh. To avoid overestimating the habitat of young fish stages living at the river's edge, the dry parts of the semi-wet cells are also cut out. This process is repeated for all time steps. All new meshes and associated hydraulic parameters values are then saved in a NetCDF file. Data from this file are then merged with substrate values by georeferencing. Finally, by using HSC corresponding to the studied species-taxa preferences, a map of suitability indices is produced (Fig. 4).

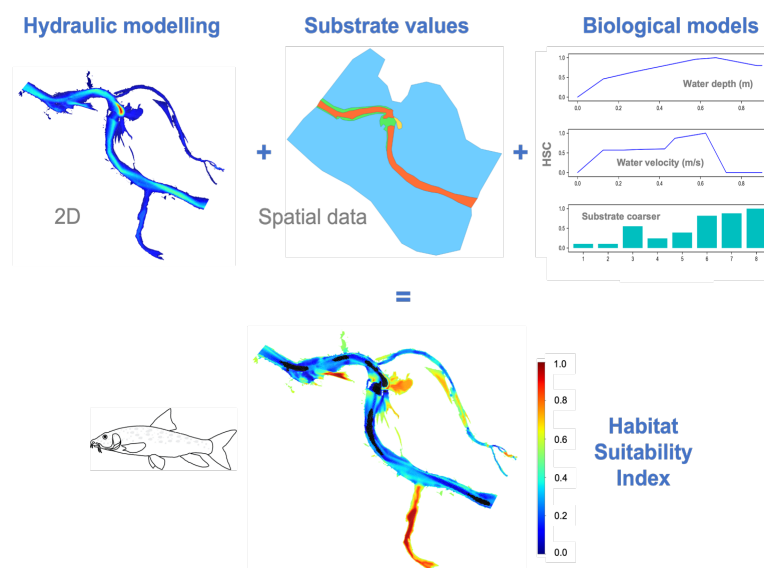


Figure 4. The different modelling steps leading to habitat suitability estimation

The workflow is clearly identified by the graphical interface of the software (GUI). All calculations are performed in parallel when possible, using QThread. HABBY also offers a TUI mode (console) for experts, allowing to perform more advanced studies (uncertainty quantification, global sensitivity analysis, optimization...). To this end, a Python script is automatically written when using the GUI, allowing a project to be restarted more directly, with or without modifications.

3.3 Post-processing

The results of habitat calculations can be exported in different open and standard-based data formats:

- Delimited text files (.txt) where each line is a record of the values at the nodes of the mesh;
- Portable network graphics (.png) to visualize the map of habitat results in 2D;
- GeoPackage (.gpkg) to save the habitat results as a SQLite database container. This file can be easily imported with a geographic information system application like QGIS;
- Stereolithography (.stl) to store the digital terrain model;
- Paraview (.pvd, .vtu) to visualize the habitat evolution using 2D and 3D animations (see an example in Fig. 5).

Habitat evolution in relation to river flows, hydrological record or design scenario can be easily visualized with HABBY to help finding the most suitable conditions for the species.

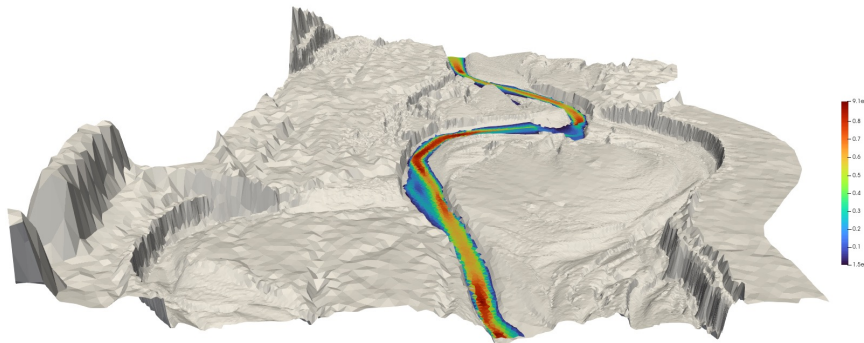


Figure 5. Example of a Suitability Index (SI) visualization with Paraview, from Telemac 2D results (for *Barbus barbus*, in a reach of the Durance River, France)

4. CONCLUSIONS AND PERSPECTIVES

The HABBY software can contribute to define ecological flows for all water stakeholders from end users to researchers. This multilingual and open-source project is open to international collaboration.

Work is underway to improve the transition from finite volumes to finite elements, and to enable the automatic removal of hydraulic aberrations at the edge of the wetted bed. In 2022, two features will be added:

- A curvilinear axis system will allow to split the stretch of river, allowing to make analyses according to an upstream-downstream gradient;
- Based on 2D hydraulic outputs, the lateral ramping velocity calculated through horizontal ramping rate will be provided to assess risks of fish stranding during hydropeaking events.

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