

# From Stathab

## Preamble

Using Stathab in HABBY.

## Prerequisites

- Install HABBY.
- Download and extract input files for Stathab:
  - [tuto\\_stathab\\_example\\_data.zip](#)
- A spreadsheet program, such as LibreOffice Calc or Excel (for viewing TXT exports).

## Step by step

### Create a new project

- Launch the software.
- Go to menu **Project - New**.

This opens the **HABBY - New Project** window.

- If necessary, change the **Project directory:**, by clicking .
- Fill in **Project name:** 'Tuto\_Stathab'.
- Choose in **Project type:** 'Statistic'.
- Click on **[Create a project]**.

The project is then created and gives you access to new tabs.

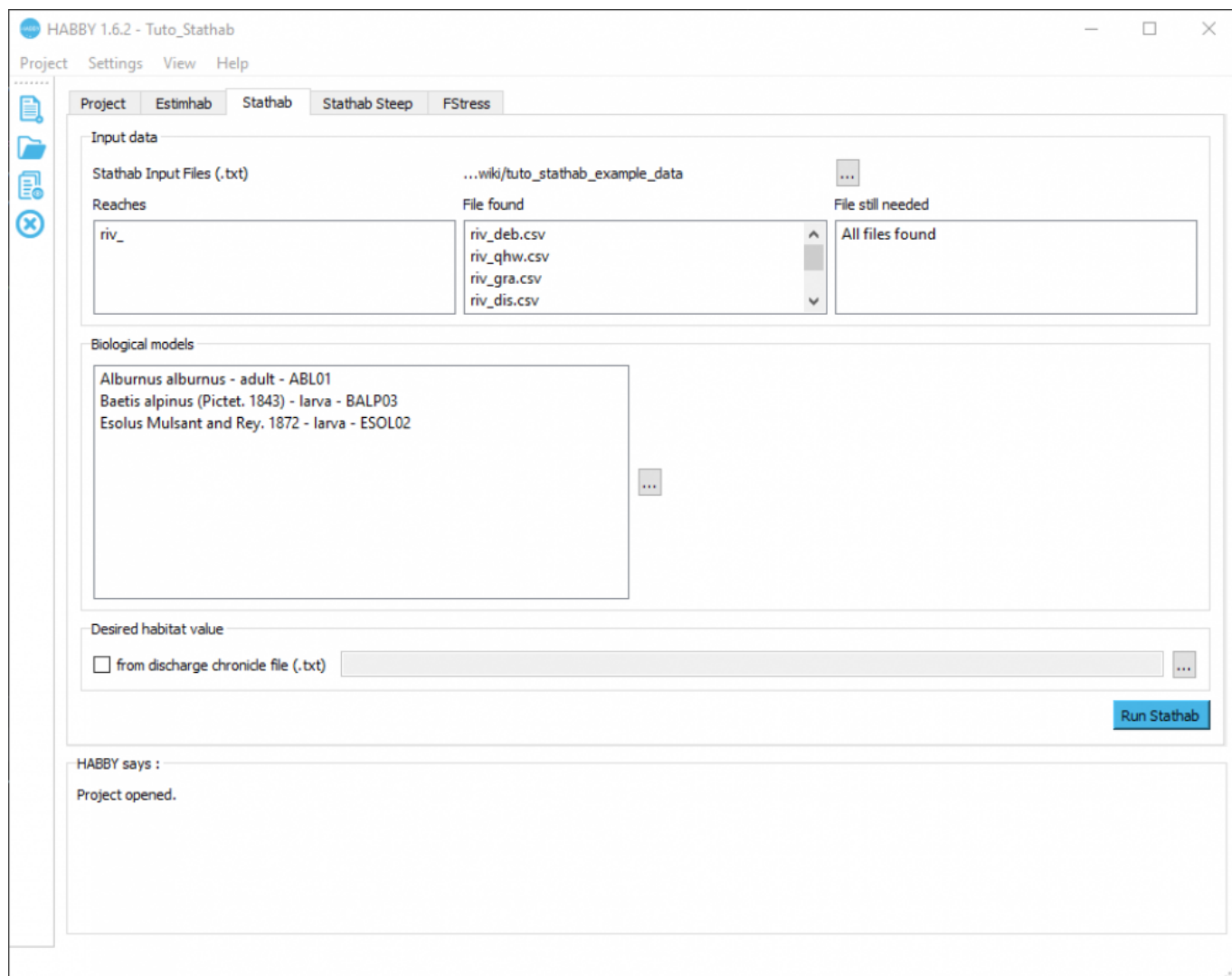
[\\*Guide utilisateur : Création de projet](#)

### Using the Stathab tab

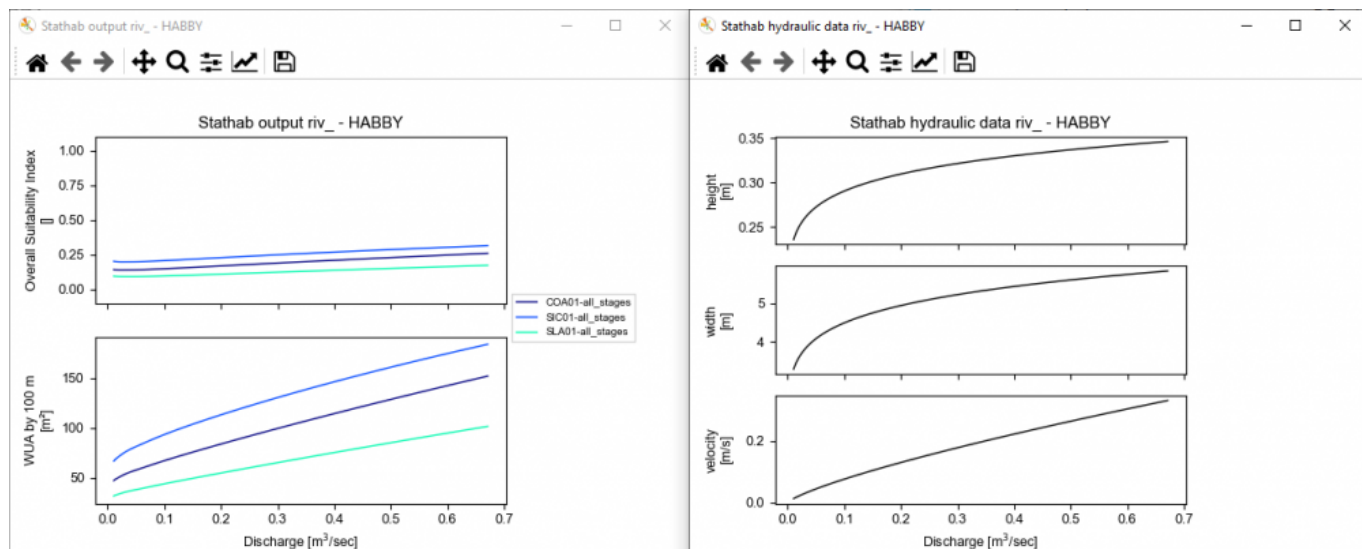
- Click on the **Stathab** tab.
- Click on the **[...]** button to select the directory containing the input files.
- In the selection window, choose the 'tuto\_stathab\_example\_data\input\_stathab' directory.
- Click on the **[Select a folder]** button.
  - The list of **Rivers**, **File found** and **Files not found**, is then displayed.
  - If the directory is valid, **All files found** should be displayed in the **Files not found** list.
- In the 'biological model' group, click on **[...]** to choose a biological model using the **Biological model explorer**.



\*Guide utilisateur : Explorateur de modèle biologique.

- Once you've added the biological model to the list on the **Stathab** tab, click on the **[Launch Stathab]** button.



- The calculation is performed:
  - Interactive figures are then opened



- These same figures are produced as image files in the “Tuto\_Stathaboutput\figures” directory, accessible via the  button in the main window's quick menu.
- Result .txt files produced in the “Tuto\_Stathab\output\text” directory, accessible via the  button in the main window's quick menu.

## Using older Stathab biological models

Biological models from older versions of Stathab are available from this

link

. These are to be added to the HABBY software in the directory of user biological models. Please refer to the reference manual, section [Add additional models](#).

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<https://habby.wiki.inrae.fr/lib/tpl/bootstrap3-multilang/> - **HABBY**

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