Anaqualand 2.0

Modelling connectivity in riverscapes.

Introduction

Anaqualand is a freeware allowing calculations of structural and biological connectivity in riverscapes using ascii raster files. It allows an evaluation of hydrographic and biological distances between points or patches along a river; in upstream, downstream or both directions.

Modelling approaches of the biological connectivity were implemented using the concept of minimal cumulative resistance (MCR) (Knaapen et al., 1992), or more recently the 'least cost' model (Adriaensen et al., 2003), which measure for distance modified with the cost to move between habitat patches based on detailed geographical information on the riverscape as well as behavioural aspects of the organisms studied. For more details about the global approach see (Le Pichon, 2006; Le Pichon et al., 2006).

Anaqualand is available under the [CeCILL](#) user licence and was developed by the research unit HBAN - Cemagref - Antony in 2006.

Céline Le Pichon: project initiator

Guillaume Gorges: user specifications director

Thierry Faure (LISC/CEMAGREF): technical contributor

Hugues Boussard (SAD_PAYSAGE/INRA): designer-developer

Presentation

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[species](#)

[hydrographic distance calculation](#)

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Setup

1. download the Java virtual machine 1.5 (jre-5.0) minimum from :
http://java.sun.com/j2se/1.5.0/download.jsp,

2. click on 'Download JRE 5.0' and get the version according to your operating system,

how to install ?

1. download 'anaqualand2.0.X.zip' from :
http://www.rennes.inra.fr/sad/outils/indexoutil.htm,

2. unzip the file into your system,
--> Be carreful not to use 'PowerArchiver' to unzip. Some problems would occured !!!

3. make sure you have got the following repertories:
--> data
   --> ascii
   --> dbf
   --> project
   --> text
--> doc
   --> help
--> image
--> lib
--> system
   --> file
   --> temp

how to launch ?

--> just a double-click on the file 'anaqualand.bat'

how to uninstall ?

delete the folder named 'anaqualand2.0.X'

Faq

go the Frenquently Asked Question

We ask whoever which uses officially 'Anaqualand 2.0.0' to quote the following sentence:

"Le Pichon C., Gorges G., Faure T., Boussard H. (2006) 'Anaqualand 2.0 : Modelling connectivity in riverscapes '. Cemagref, HBAN."

Riverscape

To create the riverscape, Anaqualand needs different files:

1. an ASCII raster file (.asc) representing the matrix of the physical layer

```
ncols          30
nrows          22
xllcorner      530855.859051
yllcorner      6485991.3
cellsize       2
NODATA_value   0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 9 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 1 1 1 1 1 1 1 1 2 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 1 1 1 1 1 1 1 1 2 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 1 0 0 0 1 1 1 1 2 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 1 1 2 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 1 2 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 1 2 2 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 6 6 6 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 7 7 7 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 0 0 0 0 7 7 7 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
```

The file contains: number of colons, number of rows, coordinates of the low left corner of the map, the pixel size (in meter) and the nodata value (pixels outside the river). Each pixel is represented by an integer code. The code correspond to the elements of the river based on the combination of physical variables mapped by the user. It could be channel units mapped with a GPS following (Hawkins et al., 1993) classification (based on morphological and hydraulic properties of channel geomorphological units) or other classification based on variables such as substrate, temperature or shelters etc...

2. a text file (.txt) describing the datas,


```
databf4sum04t.txt - Bloc-notes
Fichier  Edition  Format  Affichage  ?
Riffle   3
Lateral  1
Run      2
Backwater        4
Mid-channel      5
Eddy     6
unknown  7
```
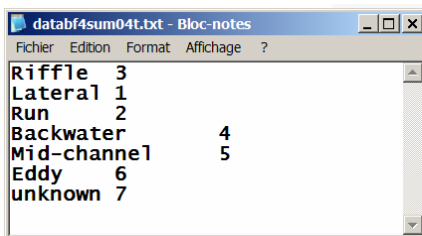
The data file explains the pixel codes of the ascii raster file of the river and give an explicit indication of the units describe in the river. In the example, the codes (from 1 to 7) are channel units types. On each line, use eventually "_" to make the separation between words; codes are separated by tabulation.

3. the coordinates (X et Y) of the upstream pixel of the river and the coordinates (X et Y) of the downstream pixel of the river, in order to fix the orientation of the river (see Annexe 1).
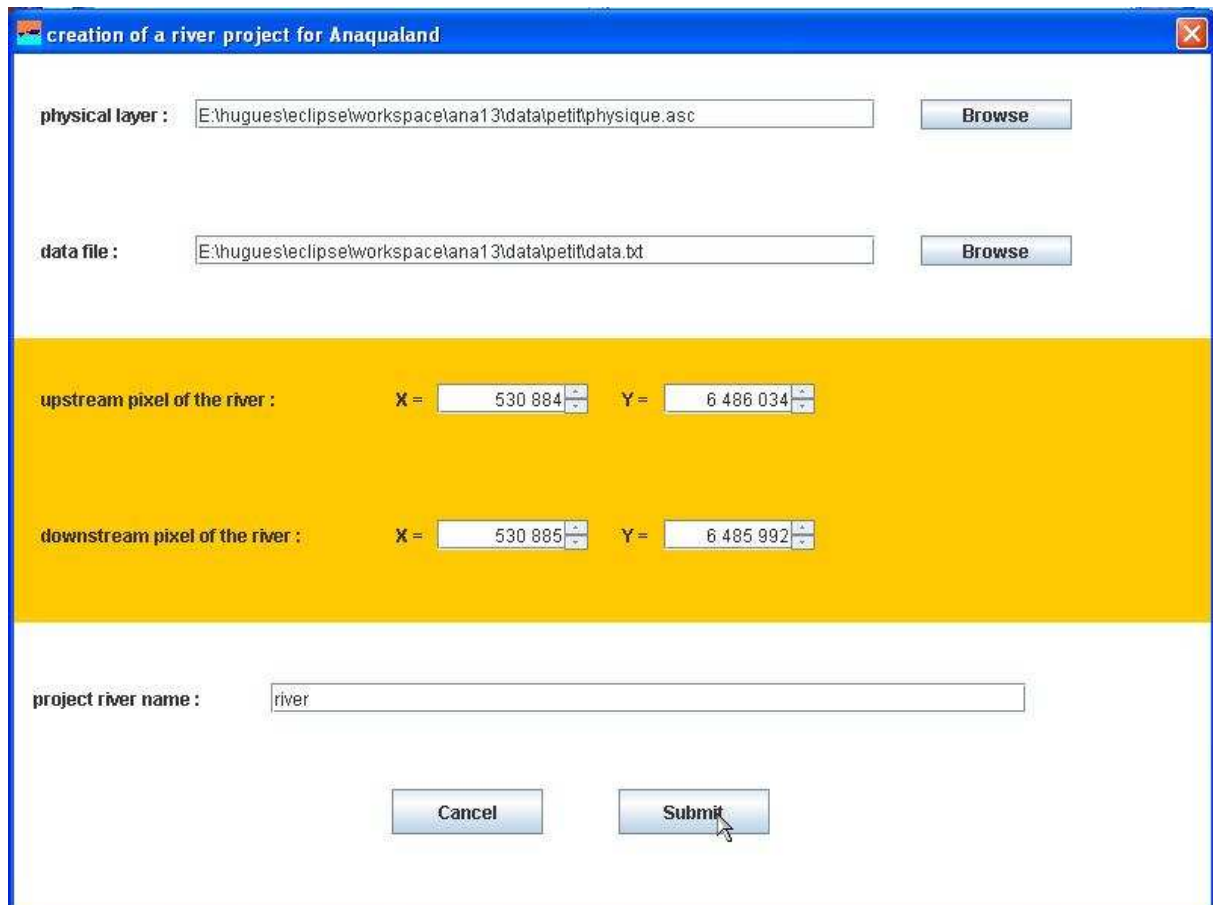
4. and name it...

Anaqualand interface

Open the freeware and click on "New" ... to see the river window.
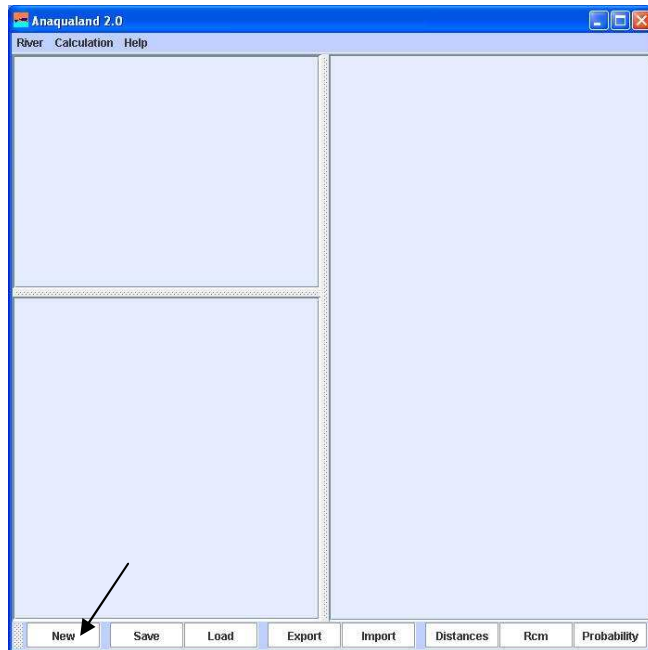
Browse for the ascci raster file (.asc) and the data file (.txt), then enter the X and Y coordinates of downstream and upstream pixel of the river (available with the GIS).

The river project is now created and you have initialized your environment. The right part of the window summarise the initialization of the data and the orientation of the river.

More details about the composition of the physical layer are available when activating the little key and the contextual menu. "View informations" about the composition of the physical layer.
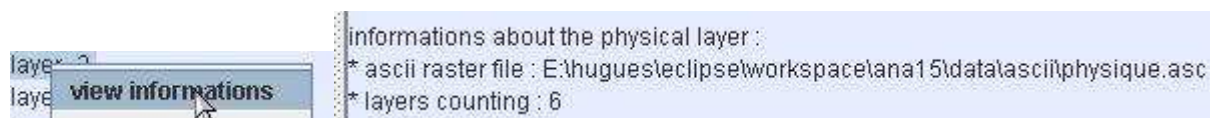
Each code of the physical layer is represented by a layer with its code number. For each layer informations are given; it may be visualize with ImageJ and export in image format (.jpg) and ascii format.
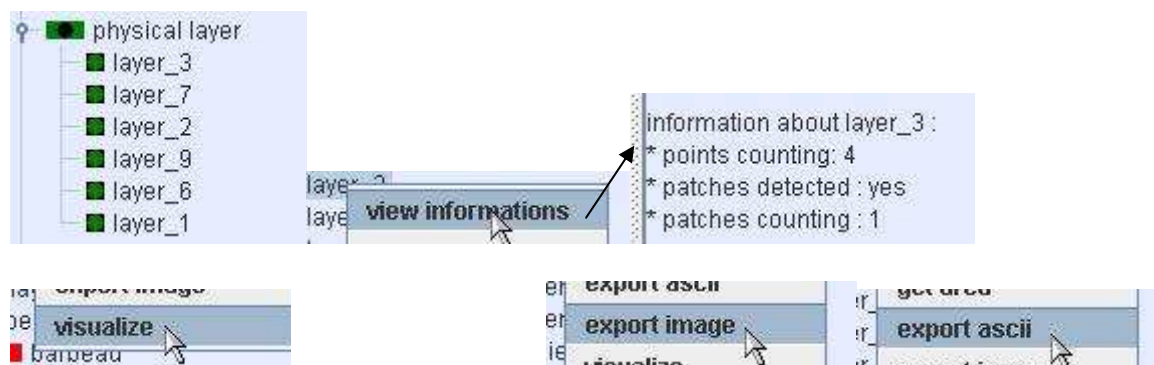
All patches in each layer may be detected using a contextual menu (right click): "detect patches";

Then "get area" allowed to export the area of all patches in a .dbf format. On the right, patches detection is summarized: 11 patches with their size (points=pixels).
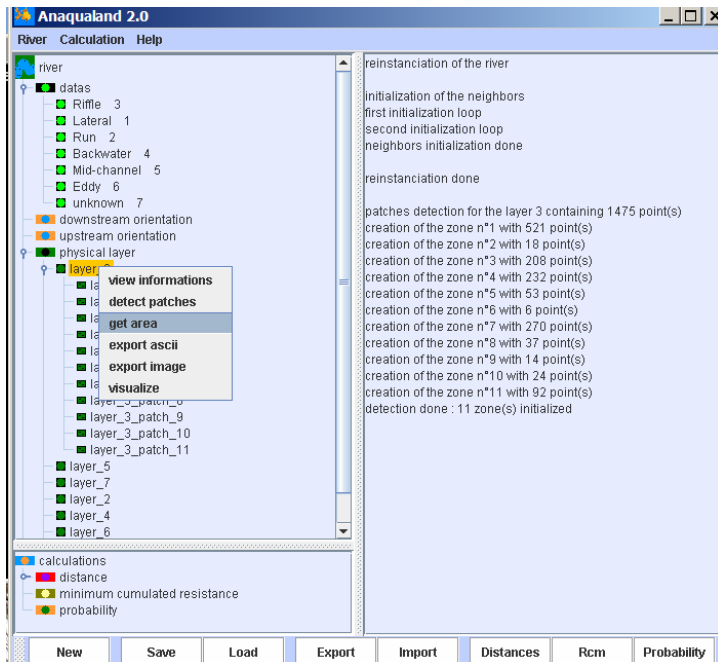
File of patches area in .dbf format:

To view points of a patch: "view points" on the contextual menu of each patch
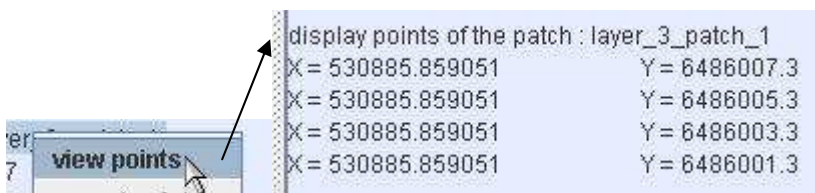
And export their coordinates:
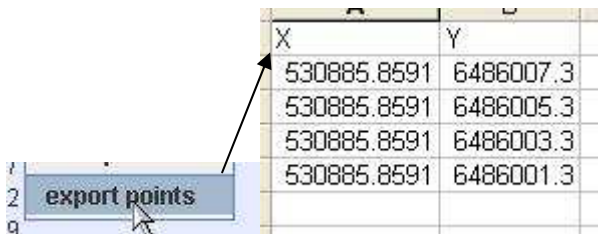
Species

A species is defined by its name.

To add a new species, right click on "species" and on "add new species"; enter the name.
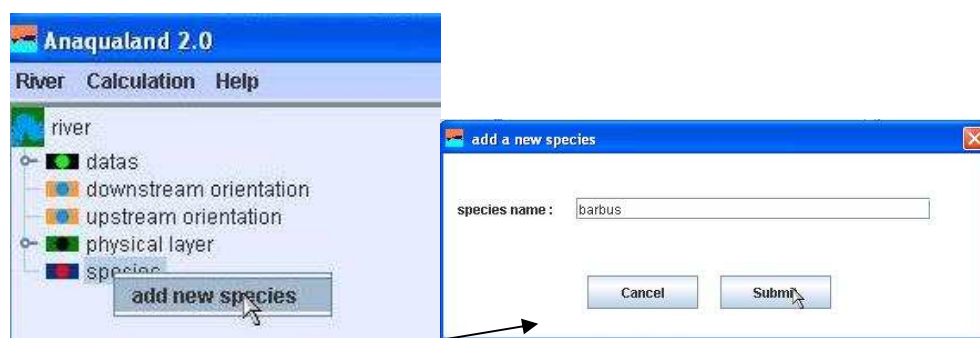
Then a life stage may be added:

Life stage

The life stage could be defined by a body length, an age or a cohort. example: if the species is named "barbus", and the life stage is defined by a body length so the name of the life stage is "barbus_30cm". Just enter "30cm" which is added to the species name. It could be also "0+", so the name will be "barbus_0+".
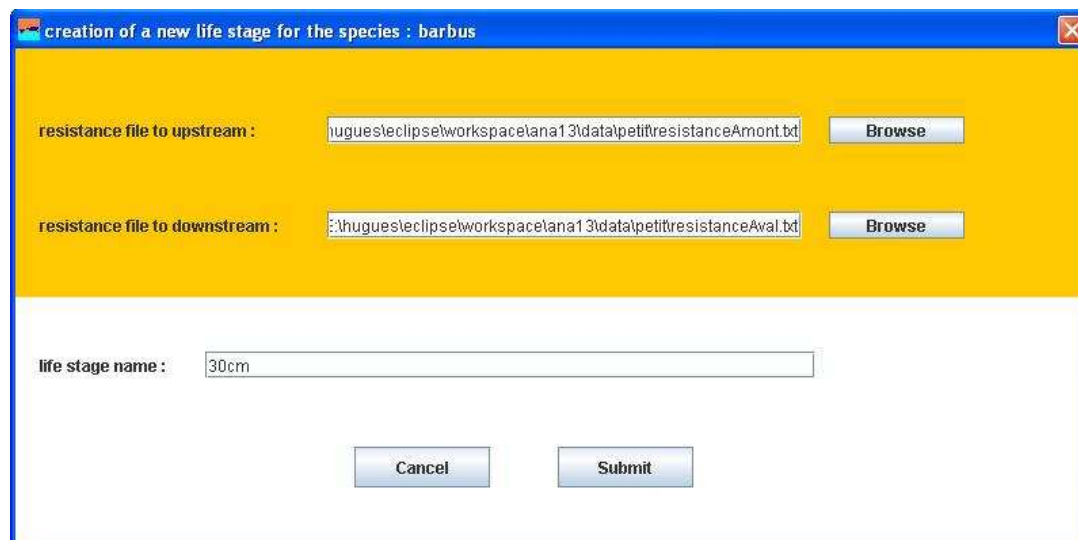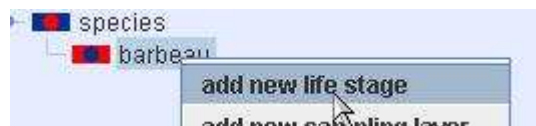
Two resistance files are associated with a life stage, one to upstream and the other to downstream. In other case, it could be the same resistance file for both orientations or if no resistance file is available, create a file with "1" for each code of the physical layer. Resistance values are assigned to each code of the physical layer using a text file.

Resistance file format :

* The first line does not have importance but it must be present.
* The first column contains the codes of the physical layer.
* The second column contains the different values of resistance attributed to the corresponding codes of the physical layer.
* The format of values of resistance is "real".
* The two columns must be delimited by tabulation.
* The resistance could be oriented, to upstream or to downstream.
The resistance may be visualize using the contextual menu:
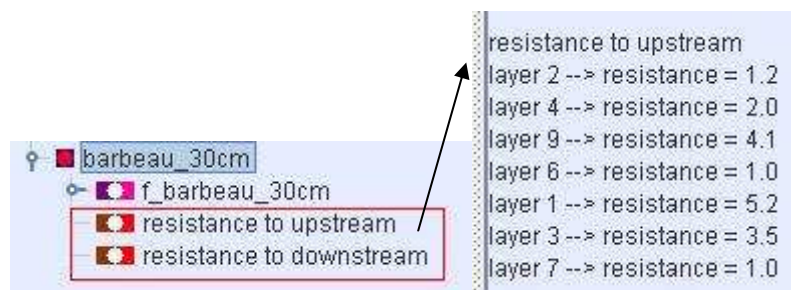
Functional habitat layer

For each life stage, one or more habitat layers may be defined; representing functional patches for the species such as feeding habitat patches, spawning habitat patches, nursery habitat patches etc…

Four ways are proposed to create a new functional habitat layer:

1. Through an ascii raster file containing the functional patches;
2. Through a combination of 1. and the selection of a pre-existent habitat layer;

3. Through the selection of a pre-existent habitat layer;
4. Through the combination of elements of the physical layer per union or intersection.

1. First way: the ascii raster file containing the patches of habitat (must be the same size, coordinates and pixel size as the physical layer).

```
ncols        30
nrows        22
xllcorner    530855.859051
yllcorner    6485991.3
cellsize     2
NODATA_value 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 5 5 5 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 5 5 5 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
```

Select the file and then the value in the ascii raster file representing the functional habitat:
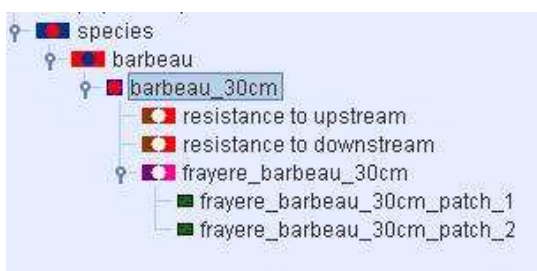

choose a name such as spawning habitat, wintering refugia or other functional habitat useful for the species of interest

The environment is now updated :

2. Second way is to concatenate an ascii raster file containing new patches and a pre-existent layer:

Select a new name and see your updated environment:

3. The third way is to use a pre-existing layer and rename it:

4. The fourth way is a combination of elements of the physical layer per union or intersection.

Sampling layer

Sampling layer is an ascii raster file that contains the spatial location of sampling units. It could be points (one pixel) with a unique code for each point or patches (several pixel with the same code). The other pixels have got the "nodata value". As for the habitat layer, the sampling layer must be the same size, coordinates and pixel size as the physical layer.

The environment is updated:
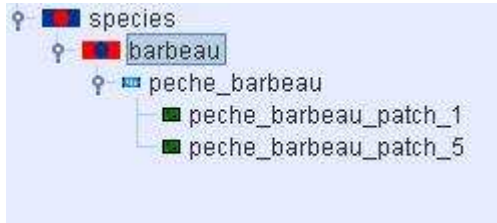
Densities of the species and life stage

If available, densities can be integrated for a life stage and will be used to calculate accessibility. They are integrated according to (1) the physical layer or (2) the functional habitat layer.
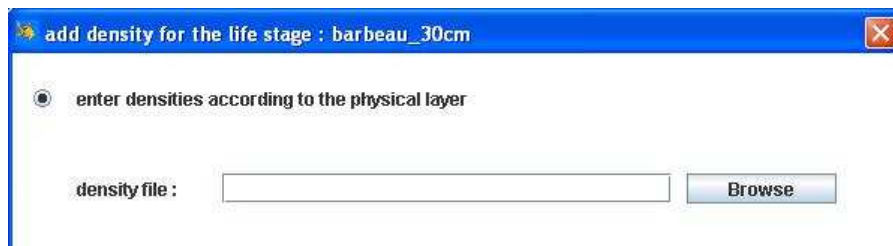
The density file has the same format as the resistances files making the relation between the code of the physical layer and the density affected to each code:

```
type     density
1        1.2
2        2.4
3        5.5
4        10
6        1
7        1
9        0
```

Note : as density values are affected to pixels, the values must be defined according to the cell size. Here, pixel size is 1 m, so values are in individuals/m². The format of the value is "real".

The second option is to enter densities according to the patches of a functional habitat layer. In that case, densities in the habitat and outside the habitat are fixed values.
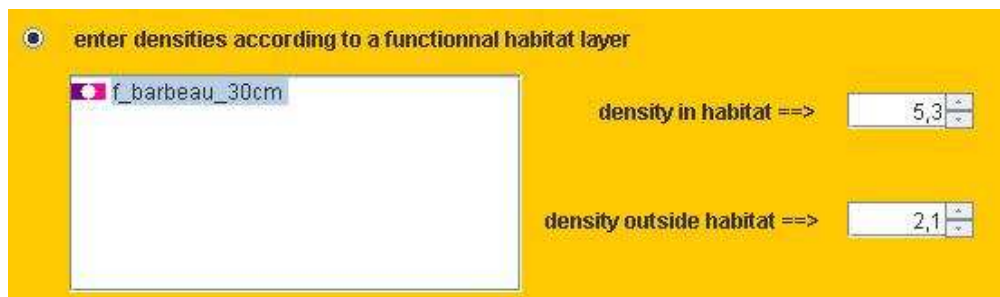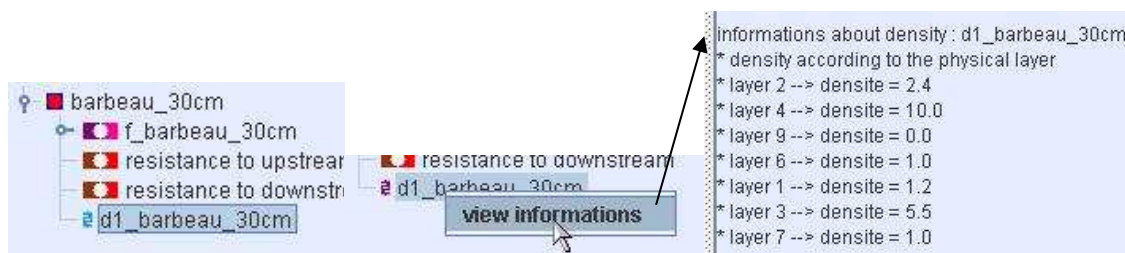

Then name it and click on the "submit" button:

And see the updated environment:

Calculation of hydrographic distances

The hydrographic distance is the shorter distance between a source and a target following the riverscape. Sources and targets may be points (pixels) or patches available in the physical layer, the functional habitat layers or the sampling layers.
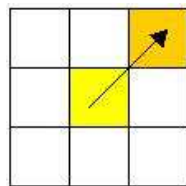
The distance calculation is based on an eight-neighbour-cell algorithm which also allows for movements along the diagonals. In case of diagonal directions, the cell size is multiplied by the square root of two to compensate for the longer distance.
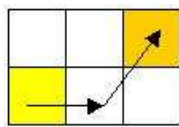
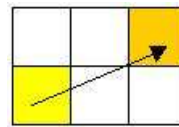The distance between 2 neighbouring pixels is:
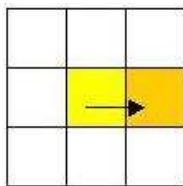
1 * pixel size $\sqrt{2}$ * pixel size

Note that the distance between the two coloured pixels is calculated by this way:

        and not by this way:

Select "distances"in the low part of the menu:

The following window is then available:

The source could be:

1. Pixel

It is defined by the X and Y values. These coordinates (in the same coordinate system as the ascii raster files) are manually enter.

2. Patch

◉ **minimal**

"minimal" means that only the nearest distance from the patch to the target entity is calculated.

◉ **all the pixels**

"all the pixels" means that distances from all pixels of the patch to the target entity are calculated.

3. Layer

◉ **minimal**

"minimal" means that only the nearest distance from the nearest patch of the layer to the target entity is calculated.

◉ **all the pixels (points)**

"all the points" means that distances from all pixels of every patch of the layer to the target are calculated.

◉ **all minimal patches**

"all minimal patches" means that only the nearest distance from every patch to the target are calculated.

The target could be:

1. Pixels

"all the pixels" means that distances to the whole pixels of the map are calculated.

2. Patch

◉ **minimal**

"minimal" means that one distance from the source to the nearest pixel of the patch is calculated.
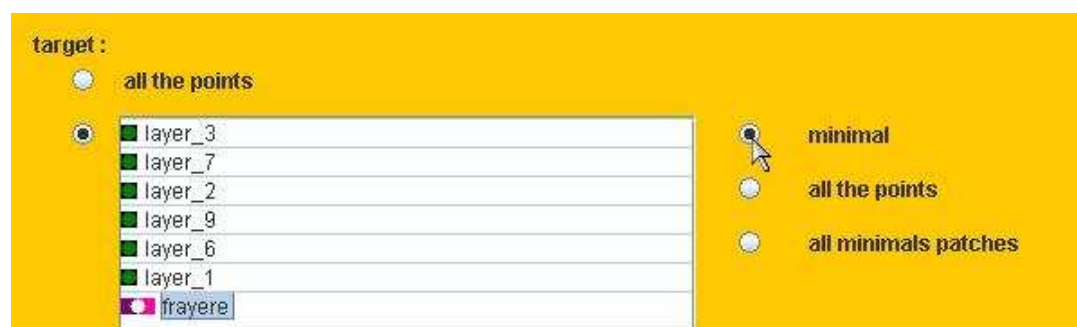
⊙ all the pixels

"all the pixels" means that every distance from the source entity to all pixels of the patch are calculated.

3. Layer

⊙ minimal

"minimal" means that only one distance from the source entity to the nearest pixel of the nearest patch of the layer is calculated.

⊙ all the pixels

"all the pixels" means that distances from the source entity to all pixels of every patch of the layer are calculated.

⊙ all minimal patches

"all minimal patches" means that distances from the source entity to the nearest pixel of each patch of the layer are calculated.

The calculation way:

⊙ both

This option means that no particular direction is specified. The diffusion is made both upstream and downstream on the river.
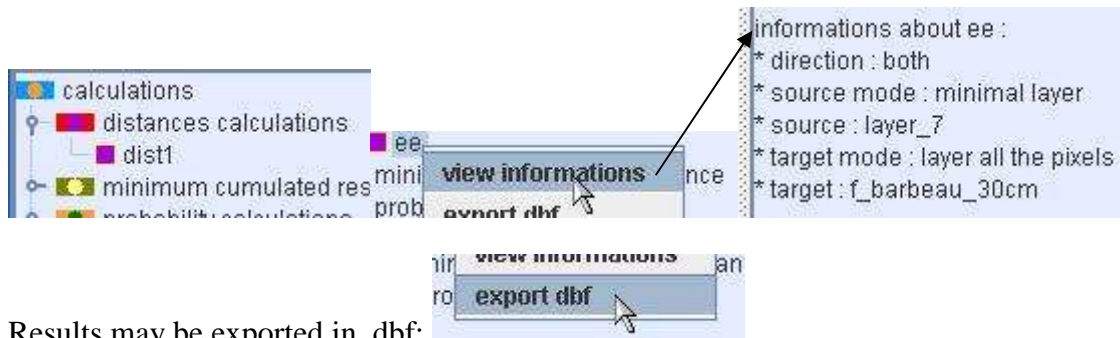
⊙ to upstream

This option means that the searching target is upstream the source.

⊙ to downstream

This option means that the searching target is downstream the source.

Cancel   Submit

informations about ee :
* direction : both
* source mode : minimal layer
* source : layer_7
* target mode : layer all the pixels
* target : f_barbeau_30cm

calculations
  distances calculations
    dist1   ee
  minimum cumulated res   mini   **view informations**   nce
                          prob   **export dbf**

        view informations   an
   ro   **export dbf**

Results may be exported in .dbf:

Calculation of biological ("effective") distances using the Minimal Cumulative Resistance

The biological distance calculation (RCM) is based on an eight-neighbour-cell algorithm which also allows for movements along the diagonals. The source of a RCM calculation are the whole points of the map and the target(s) are the patch(es) available in the functional habitat layers.
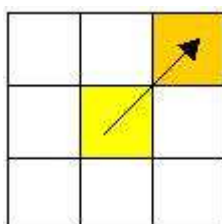
Considering the following resistance map:

4	2	4
4	2	4
2	2	4

The RCM distance between the two coloured pixels is 6 with a cell size of 2
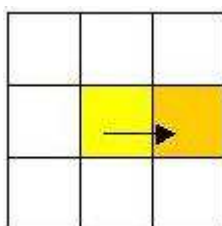
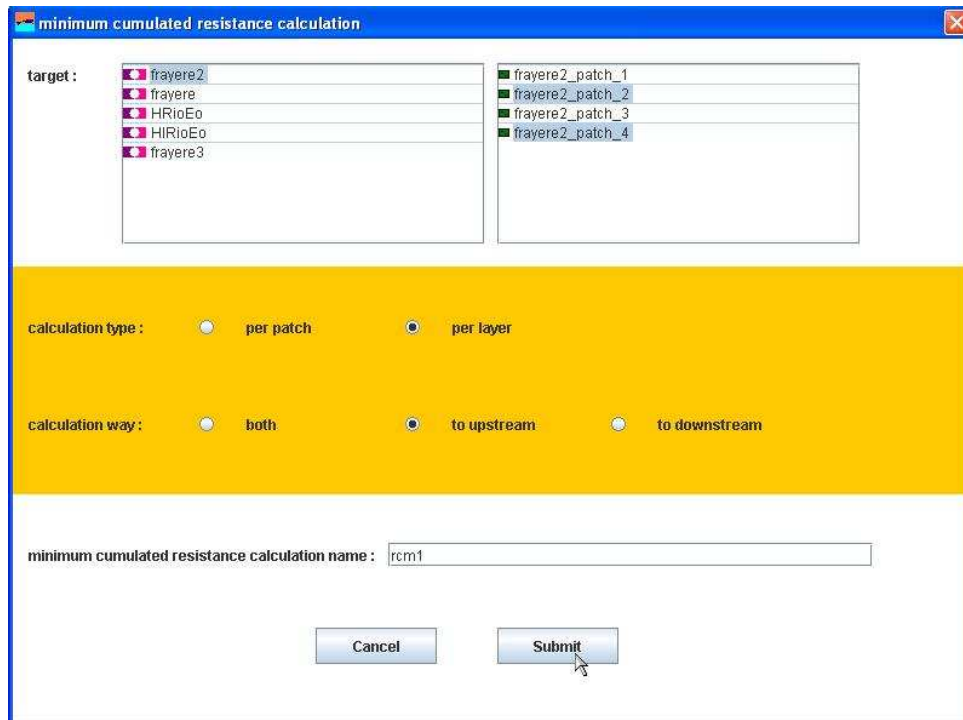$\frac{1}{2}$ * (resistance(source pixel) + resistance(target pixel)) * cellsize

The RCM distance between the two coloured pixels is 8.49 with a cell size of 2

$\sqrt{2}/2$ * (resistance(source pixel) + resistance(target pixel)) * cellsize

Select "RCM" in the low
part of the menu:

The calculation type

per patch

This option means that the calculation is made for each patch of the layer (if the layer is selected in the left part of the window) or for only selected patch (if patches are previously selected on the right part of the window). The result is as many maps as the number of patches, representing the minimal cumulative resistance to attain the patch.

per layer

This option means that the calculation is made simultaneously for all patches of a layer or selected patches. The result is one map, representing the minimal cumulative resistance to reach the nearest patch.

The calculation way

both

This option means that no particular direction is specified. The diffusion is made both upstream and downstream on the river. The result is a map, representing the minimal cumulative resistance to reach the nearest patch from downstream or upstream the patch.

to upstream

This option means that the calculation is made only for pixels downstream the patch(es). If there is more than one patch with a "per layer" calculation, the result is one map, representing the minimal cumulative resistance to reach the nearest upstream patch.

to downstream

This option means that the calculation is made only for pixels upstream the patch(es). If there is more than one patch with a "per layer" calculation, the result is one map, representing the minimal cumulative resistance to reach the nearest downstream patch.

The calculation is integrated into your RCM calculations environment:
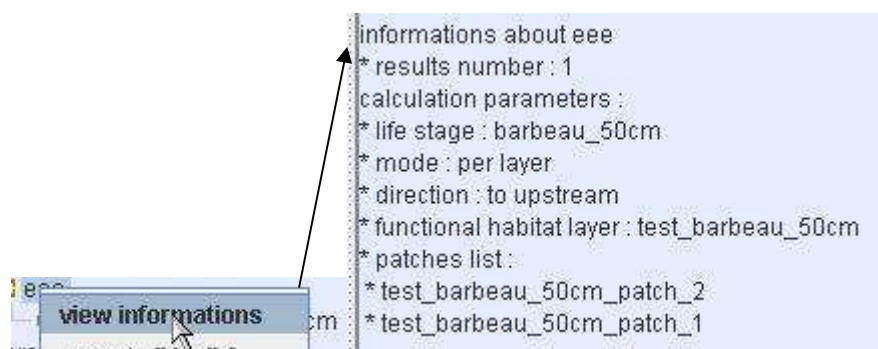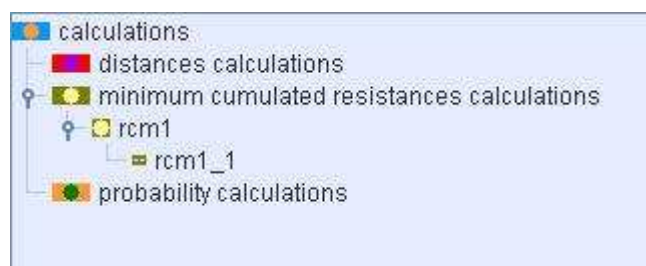
Then you can visualize and export the results:

Before the exportation in .dbf format, RCM may be filter using patches of the physical layer or the functional habitat layer. Only the values of RCM in these selected patches are exported.

The probability of reaching the nearest patch

The probability of reaching a patch is a decreasing function of the minimal cumulative resistance (RCM) and α, in which α is the potential distance covered by a fish during the movement or the migration under consideration. α is documented using literature data or experimental data on movements.

Select "Probability" in the low part of the menu:
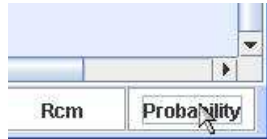
The form of the decreasing function is chosen among the fourth proposed functions:

$$f = e^{-RCM/\alpha}$$

Exponential negative

$$f = \min(\alpha/RCM, 1)$$

Opposite

$$f = e^{-\left(\frac{RCM}{\alpha}\right)^2}$$

Gaussian

$$f = 1 \quad si\ RCM \le \alpha$$
$$f = 0 \quad si\ RCM > \alpha$$

Threshold
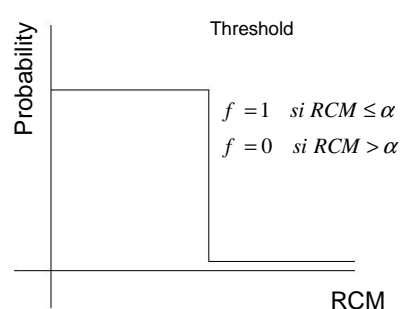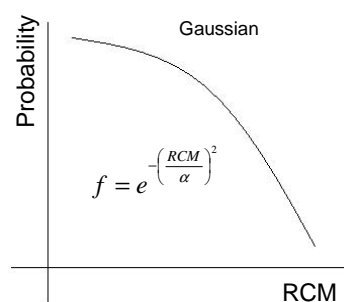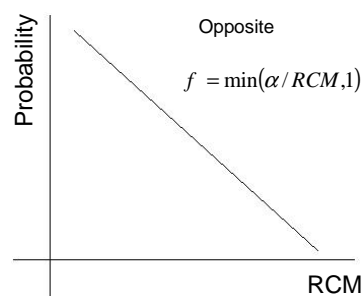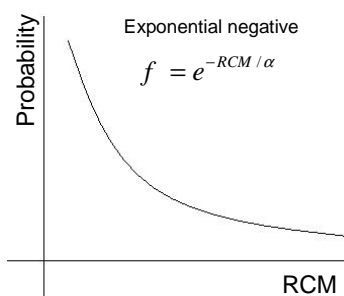
Then, two ways are available to integrate the α parameter into the probability calculation:

--> If the parameter include the resistance of the environment, set it by the first way:

--> If the parameter do not include the resistance of the environment, set it by the second way, the freeware will calculate the resistance of the environment (RMedian) using the resistance values of the physical layer.

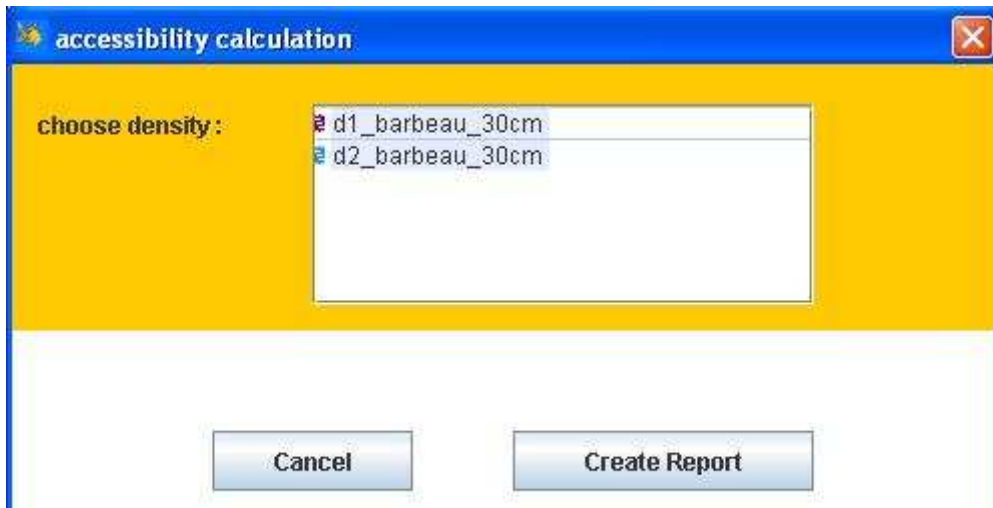The calculation is integrated into your RCM calculations environment:
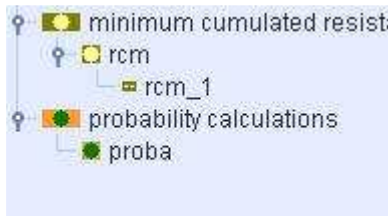
Then you can visualize and export the results:

Using the probability map, click on "run accessibility" to calculate for each patch the sum of the probability to reach this patch multiply by the fish densities in the different elements of the physical layer.

Environment

With Anaqualand 2.0, you can save and load your environment. Note: when you save your project, everything is save except the neighbours, so when you load a project, Anaqualand 2.0 needs to recompute the neighbours...
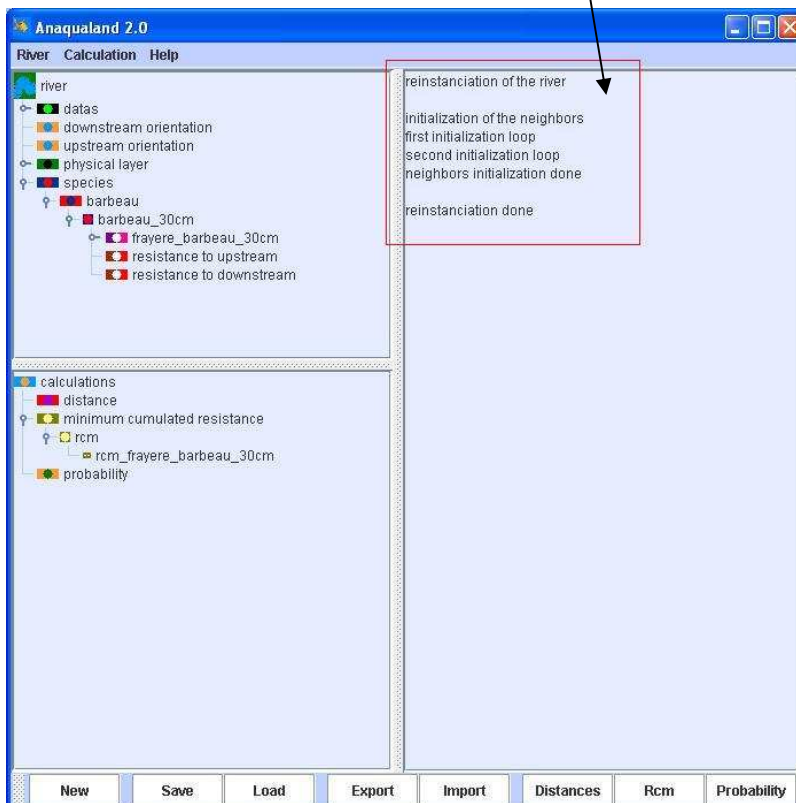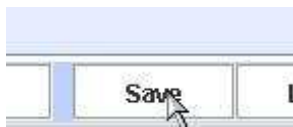
Xml project

With Anaqualand 2.0, you can export and import xml projects. You can consider that the .xml project is a file describing the parameters for creating your river environment and running calculations.

Exportation
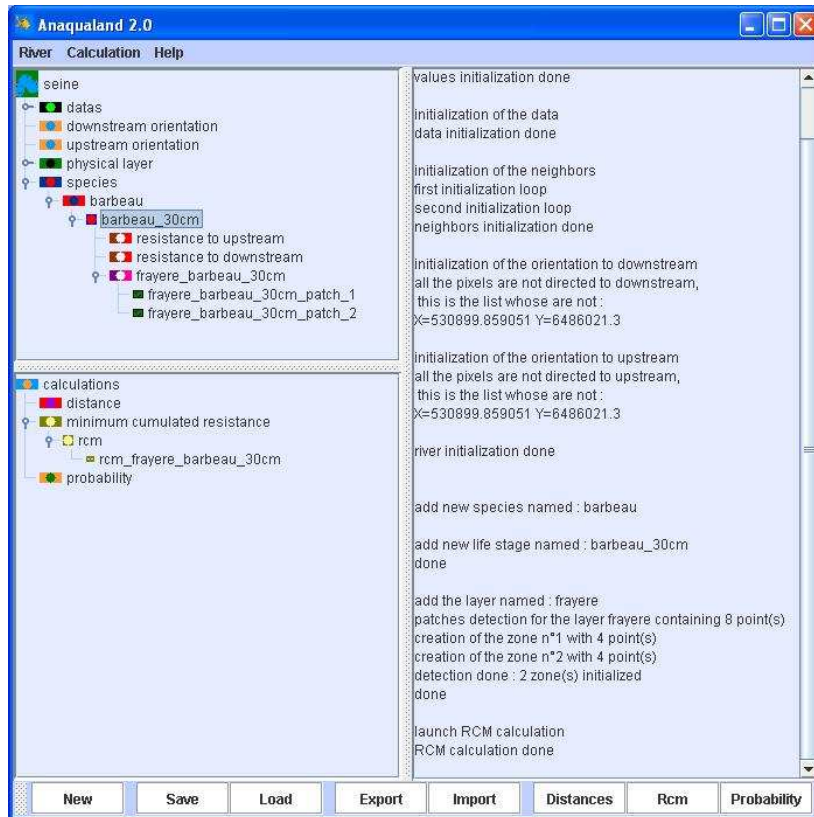
Select "export" in the low part of the menu:

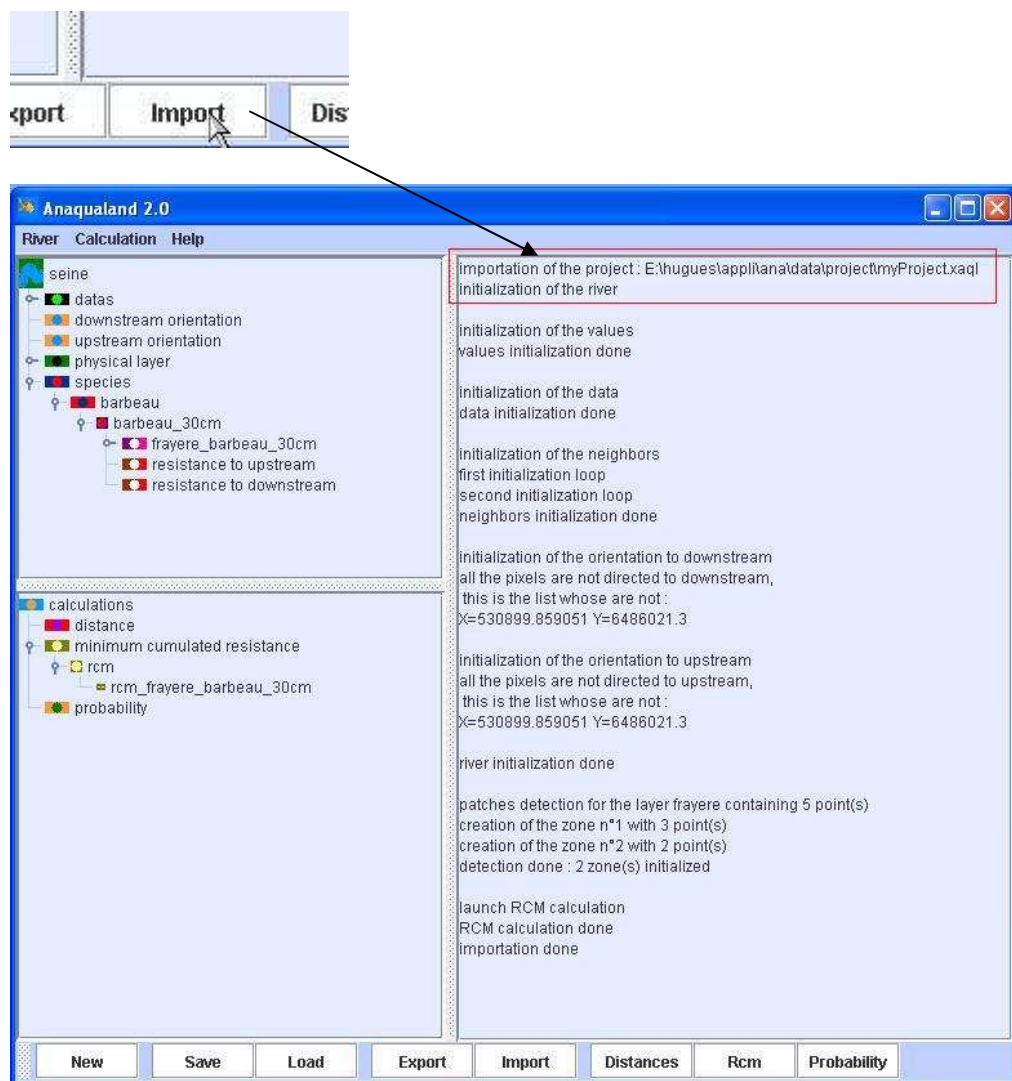Some parameters can be changed directly when opening the xml file (here the file name of the habitat layer)

```xml
<?xml version="1.0" encoding="UTF-8"?>
<river name="seine">
    <data>E:\hugues\appli\ana\data\text\data.txt</data>
    <physical_layer>E:\hugues\appli\ana\data\ascii\physique.asc</physical_layer>
    <upstream_X>530884.0</upstream_X>
    <upstream_Y>6486034.0</upstream_Y>
    <downstream_X>530885.0</downstream_X>
    <downstream_Y>6485992.0</downstream_Y>
    <species name="barbeau">
        <stage characteristic="30cm">
            <upstream_resistance>E:\hugues\appli\ana\data\text\resistance1.txt</upstream_resistance>
            <downstream_resistance>E:\hugues\appli\ana\data\text\resistance1.txt</downstream_resistance>
            <habitat_layer name="frayere" type="1" order="1">
                <file value="5">E:\hugues\appli\ana\data\ascii\frayere2.asc</file>
            </habitat_layer>
        </stage>
    </species>
    <calculation>
        <rcm name="rcm" direction="both" mode="per layer">
            <layer>frayere_barbeau_30cm</layer>
            <patch>frayere_barbeau_30cm_patch_1</patch>
            <patch>frayere_barbeau_30cm_patch_2</patch>
        </rcm>
    </calculation>
</river>
```

"Import" to create the modified environment.

Importation

References

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Knaapen, J. P., Scheffer, M. et Harms, B. (1992). Estimating habitat isolation in landscape planning. *Landscape and Urban Planning*, **23**(1), 1-16.

Le Pichon, C. (2006). Une approche "paysage aquatique" pour une meilleure connaissance du fonctionnement des écosystèmes fluviaux et l'amélioration de la conservation des peuplements de poissons. Thèse de Doctorat, Spécialité écologie, Université Pierre et Marie Curie - Paris VI, Paris, 323 p.

Le Pichon, C., Gorges, G., Boët, P., Baudry, J., Goreaud, F. et Faure, T. (2006). A spatially explicit resource-based approach for managing stream fishes in riverscapes. *Environmental management*, **37**(3), 322 - 335.

Annexe 1

Le principe d'orientation est le suivant :

Orientation Amont

```
                    2   1   0   1
                    2   1   1   1
                    2   2   2   2
        Cas 1       3   3   3   3
                    4   4   4   4
                    5   5   5   5
                    6   6   6   6
                    7   7   7   7
10  10  10  10  10   9   8   8   8   8   8
10  10  10  10  10   9   9   9   9   9   9
10                  10  10  10  10  10  10  10
                    11  11  11  11  11
       Cas 2        12  12  12  12
                    13  13  13  13
                    14  14  14  14
                    15  15  15  15
                    16  16  16  16
                    17  17  17  17
                    18  18  18  18
                    19  19  19  19
                    20  20  20  20
                    21  21  21  21
```

Orientation Aval

```
                    21  21  21  21
                    20  20  20  20
                    19  19  19  19
                    18  18  18  18
                    17  17  17  17
                    16  16  16  16
                    15  15  15  15
                    14  14  14  14
13  13  13  13  13  13  13  13  13  13  13
13  13  13  13  12  12  12  12  12  12  12
13                  12  11  11  11  11  11  11
                    10  10  10  10  10
       Cas 2         9   9   9   9
                     8   8   8   8
                     7   7   7   7
                     6   6   6   6
                     5   5   5   5
                     4   4   4   4
                     3   3   3   3
                     2   2   2   2
                     2   1   1   1
                     2   1   0   1
```

1. l'utilisateur défini le pixel le plus aval de la carte et le pixel le plus amont.

2. l'Orientation Aval s'initialise en deux boucles :
La première part du pixel le plus aval, on lui affecte la valeur 0 et on met en liste d'attente tous ses voisins.
On reprend ensuite la liste et on leur met la valeur 1, on place également leurs voisins dans une liste d'attente à qui on posera la valeur 2 et ainsi de suite jusqu'à ce que tous les pixels atteignables soient orientés.
La deuxième boucle part du pixel le plus en amont et vérifie que tous ses voisins ont une valeur inférieure ou égale.
Si la valeur est supérieure, on change la valeur pour lui mettre la valeur du pixel courant. On repart avec la liste des voisins et ainsi de suite.

3. l'Orientation Amont se fait à l'identique mais on part du pixel le plus amont.

4. Pour définir si un pixel est plus en amont qu'un autre, on regarde sa valeur d'orientation Amont.
pixelA plus en amont que pixelB si :
valeurOrientationAmont(pixelA) < valeurOrientationAmont(pixelB) (cas 1)

et si valeurOrientationAmont(pixelA) = valeurOrientationAmont(pixelB) (cas 2), alors il faut regarder leur valeur d'Orientation Aval

si valeurOrientationAval(pixelA) < valeurOrientationAval(pixelB) alors le pixel A est plus en aval que la pixel B, et inversement.