

# DOCUMENTATION

## HNAT Habitat Network Analysis Tool v 0.1.3

Developed by the Spatial Morphology Group (SMoG)  
for QGIS  
250225



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**Development of a digital tool for integrated impact assessment of social, economic, ecological and cultural-historical values in transport infrastructure planning in urban environments**  
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([www.formas.se](http://www.formas.se))

# 1. OVERVIEW

## Habitat Network Analysis Tool

Habitat Network Analysis Tool is a plugin for the open-source Geographic Information System QGIS (<https://qgis.org/en/site/>). The tool supports analyses of species habitat networks with the capacity of supporting a multi-species approach. It is developed within the ongoing project 'Development of a digital tool for integrated impact assessment of social, economic, ecological and cultural-historical values in transport infrastructure planning in urban environments' (short name is ILKA 2.0) financed by the Swedish government research funding agency FORMAS (Dnr FR-2021/02438). The project is funded within the Swedish national research framework "From research to implementation for a sustainable society 2021". It aims to create a practical software where socio-economic, ecological and cultural historical analyses can be integrated when exploring effects of urban transformations, with specific focus on different types of alterations of the transport infrastructure.

For the background of the project see:

Berghauser Pont M, Stavroulaki I, Kindvall O, Lanemo E., Levan M. (2022) Integrated Urban Environment Effect Analysis of Infrastructural Transformations. Chalmers and Trafikverket, Gothenburg., DOI: 10.13140/RG.2.2.21118.66885

### ***1.1. Technical details***

Habitat Network Analysis Tool is a plugin for the open-source Geographic Information System QGIS (<https://qgis.org/en/site/>). The plugin is written in Python and uses QGIS GDAL (Geospatial Data Abstraction Library) and GRASS (Geographic Resources Analysis Support System) via the QGIS processing framework for some of its calculations.

The plugin adds a processing algorithm to the QGIS Processing Toolbox, which means it can be used either directly from the QGIS Processing Toolbox or in QGIS Modeler.

### ***1.2. Download and Licence***

The application is available via: <https://github.com/SMoG-Chalmers/hnat>

The code is released under GNU General Public License and is available at <https://github.com/SMoG-Chalmers/hnat/releases/tag/v0.1.3>

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## 2. DESCRIPTION

### 2.1. *INPUT DATA*

#### 1. A Biotope map in raster format GeoTIFF

The pixel values of the biotope map consist of integer numbers (i.e. Biotope codes) corresponding to different Biotopes and types of exploited land. This raster file should cover the whole landscape to be analysed plus a buffer zone big enough to exclude misleading edge effects. The buffer zone must exceed the maximum dispersal distance expected by the organisms included in the analyses.

#### 2. A "Habitat network parameters table" in the format of Excel sheet (fig.1).

The parameter table should be organized so that each species-specific habitat network model to be analysed using the Biotope map is represented by a) three model-specific parameters and b) a set of biotope-specific parameters provided in three separate columns, as shown in fig 1 and explained in detailed below.

To run analysis for several different habitat network models at the same time, one only has to add the 3 corresponding set of three columns for each model (i.e. biotope specific parameters) on the right of the ones shown in fig 1, and provide them with unique network names.

	<b>Network name</b>	Amphibians_S0		
	<b>Average dispersal distance (metres)</b>	600		
	<b>Minimum dispersal probability</b>	0,01		
<b>BiotopeName</b>	<b>BiotopeCode</b>	<b>Quality</b>	<b>Source</b>	<b>Friction</b>
Skyddsvärt träd	100	7	0	1
Pine forest	111	6	0	1
Spruce forest	112	4	0	2
Mixed coniferous forest	113	5	0	1
Mixed forest	114	7	0	1
Deciduous forest	115	9	0	1
Deciduous hardwood forest	116	9	0	1
Mixed deciduous forest	117	9	0	1
Temporarily non forest	118	6	0	1
Wet pine forest	121	7	0	1
Wet spruce forest	122	5	0	2
Wet mixed coniferous forest	123	6	0	1
Wet mixed forest	124	8	0	1
Wet deciduous forest	125	10	0	1
Wet deciduous hardwood forest	126	10	0	1
Wet mixeddeciduous hardwood forest	127	10	0	1
Wet temporarily non forest	128	7	0	1
Non-vegetated other open land	41	3	0	2
Vegetated other open land	42	7	0	1
Shrubland	200	7	0	1
Arable land	3	2	0	2

Figure 1. Example of Habitat Network Parameters table. In this case, parameters are provided for only one “Species” or “Network model”, which was given the Network name “Amphibians\_S0”. All bold strings except “BiotopeName” are mandatory headers referring to the different input parameters. The parameter table may optionally include other headers for extra information like biotope names, which makes the parameter table more readable.

#### A. Parameters that are specific to each habitat network model to be analysed

##### a. ‘Network name’

A text string that will be used by the tool when naming output data layers. All output data layers generated for each specified network name will automatically be grouped and stored in model-specific folders.

##### b. ‘Average dispersal distance (metres)’ (x)

It indicates the mean migration distance per selected species, meaning how far the selected species can move on average.

##### c. ‘Minimum dispersal probability’ ( $P_{\min}$ )

This value should be a number greater than 0, but less than 1. It defines a limit for the lowest dispersal probability to be calculated for the specific habitat network model.

If the biotope map is analysed for different species/habitats and source biotopes, then the above general network parameters should be specified per species and source biotope.

**B. Parameters that are biotope-specific and have to be specified with an integer value for each Biotope code provided in the Biotope map:**

**a. 'Quality'**

The quality parameter should be an integer value ranging from 0 (biotopes with no value) to some positive value indicating the most valuable biotopes. Quality indicates the expected availability of different food or nutritional resources and different structures used for shelter, hibernation, or reproduction for the selected species.

**b. 'Friction'**

Friction indicates the 'cost' it takes to move to each pixel from the adjacent pixels. It represents the willingness of individuals to move into, or through, the different biotopes existing in the list. Biotopes where the movement is not restricted in any way should have this parameter set to 1. Integers greater than 1 are set to biotopes which the selected species avoid when moving, or biotopes where dispersal becomes reduced due to high mortality risks. Great barriers to dispersal can have values like 100 or even 1000. A friction value of 1000 means that the individuals only reach 0.001 times the distance reached within biotopes where the friction is set to 1.

**c. 'Source'**

Source (or Reproduction) indicates which biotopes the selected species uses for reproduction and will thereby function as a source habitat from which the individuals are expected to disperse from to forage, shelter etc.

It should be set to 1 for the source biotopes

It should be set to zero for the other biotopes

If the biotope map is analysed for different species and source biotopes, then the Quality, Friction and Reproduction parameters should be specified per species and source biotope.

Please note that the parameter names should be written exactly as above.

**The user is advised to look at the excel template provided.**

## **2.2. HABITAT NETWORK ANALYSES**

The following 6 calculation steps are done exporting different raster layers:

### **1. 'Source' raster**

The tool calculates a 'Source' raster based on the 'Source' column of the "Habitat network parameter table".

The 'Source' raster shows the distribution of habitat patches used for reproduction or nesting. These habitat patches are the sources (i.e. origins) from which individuals disperse to the surrounding landscape.

## 2. 'Quality' raster

The tool calculates the 'Habitat Quality' raster based on the 'Quality' column of the "Habitat network parameter table".

The 'Habitat quality' raster shows the relative quality of existing biotopes in terms of habitat used by the focal species.

## 3. 'Friction' raster

The tool calculates the 'Friction' raster based on the 'Friction' column of the "Habitat network parameter table".

The 'Friction' raster shows how resistance to dispersing individuals varies in the landscape due to biotope composition and existence of barriers. High values indicate greater barrier effects compared to low values.

## 4. 'Cost-distance' analysis, 'Cost-distance' raster

The core method of the habitat network analysis is based on a commonly used GIS-algorithm called "Cost-Distance". This method generates the patterns of species dispersing from source habitat patches out over the surrounding landscape, considering the fact that individual species may avoid transporting themselves through certain biotopes (i.e. with high friction). It also includes barrier effects due to increased mortality such as e.g. road kill. Roads and built areas may for example act as barriers for many organisms.

The 'Cost-Distance' algorithm uses the 'Friction' raster and the 'Source' raster as input.

Analysis steps:

- a) First the **maximum Cost-Distance ( $D_{max}$ )** is calculated for the modelled species:

$$D_{max} = Round.Up[-x \ln(P_{min})]$$

Where,  $x$  is the 'Average dispersal distance (meters)' of the modelled species  
and  $P_{min}$  is the 'Minimum dispersal probability'<sup>1</sup>

When  $D_{max}$  is applied to the "Cost-Distance" calculation, only pixels occurring within a maximum cost-distance from the nearest source habitat patch will get a value.

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<sup>1</sup> Note that these are two of the input parameters included in the "Habitat network parameter table".

- b) Second, the tool ‘calls’ the built-in ‘**r.cost**’ algorithm in GRASS (Algorithm ID: ‘grass7:r.cost’ ).

This algorithm creates a raster where each pixel gives the estimated cost-weighted distance from the source pixels, measured as number of pixels crossed. For this the ‘Source’ raster and the ‘Friction’ raster as used as inputs, together with the parameter ‘Maximum Cumulative Cost’ which delimits the maximum number of pixel steps to be calculated.

The ‘Maximum Cumulative Cost’ parameter is here set to  $D_{\max}$  divided by the pixel size of input rasters.

The resulting raster layer named ‘cost\_distance\_intermediate.tif’ is only stored temporally in the back end of HNAT.

- c) Finally, the tool uses the built in algorithm ‘Raster Calculator’ in GDAL (‘gdal.rastercalculator’) to generate a Cost-distance raster measured in metres. This is done by multiplying the pixel values of ‘cost\_distance\_intermediate.tif’ with the pixel size of the input raster layers.
- d) The final ‘**Cost-Distance raster**’ is created and exported with the pixel values of *D measured in metres*.

Note that the final output raster layer name has a suffix with the *\_Dmax* e.g. ‘Cost-Distance Raster\_max 2023m’, when the *Dmax* is 2023m

In a nutshell, the final ‘**Cost-Distance**’ raster shows the cost-weighted distances to the nearest available source patches, which has been modelled based on the Friction Raster.

## 5. ‘Dispersal probability’ calculation, ‘Dispersal’ raster

The Cost-distance (*D*) values are recalculated to the probability (*P*) that dispersing individuals of the modelled species will cross a pixel. This is done using the negative exponential function:

$$P = e^{-\frac{D}{x}}$$

where,

*x* is the ‘Average dispersal distance (meters)’ of the modelled species

*e* is the Euler's number and

*D* is the Cost-distance, i.e. the cost weighted distance to the nearest source habitat pixel

The ‘Dispersal raster’ with pixel values of *P* is exported.

In a nutshell, the exported ‘**Dispersal**’ raster shows the habitat connectivity in terms of cost-weighted dispersal probabilities, which has been calculated based on the Cost-distance

Raster in combination with the Average dispersal distance(x) specified in the Habitat Network Parameter table.

## 6. 'Habitat functionality' calculation, 'Functionality' raster

Functionality is calculated by multiplying the pixel values in the **Quality raster** and the **Dispersal** raster. The pixels with null values are converted to zero.

By multiplying the pixel values representing the Quality and the likelihood that individuals reach the pixel (i.e. the Dispersal probability), one gets map where habitat quality is weighted by the habitat connectivity. A high value of functionality is only achieved if the habitat is both of good quality and highly reachable from the habitat types needed for e.g. reproduction or nesting.

### 2.3. OUTPUT LAYERS

- Source raster
- Quality raster
- Friction raster
- Cost-distance raster\_Dmax
- Dispersal raster
- Functionality raster

**Table 1: List of data layers generated by HNAT.**

Raster name	Description
Source raster	A map showing the distribution of habitat patches used for reproduction or nesting. These patches are sources of dispersing individuals.
Friction Raster	A raster map showing the how resistance to dispersing individuals varies in the landscape due to biotope composition and existence of barriers. High values indicate greater barrier effects compared to low values
Cost-Distance Raster	A map showing the cost-weighted distances to the nearest available source patches which as been modelled based on the Friction Raster
Dispersal Raster	A map showing habitat connectivity in terms of cost-weighted dispersal probabilities which has been calculated based on the Cost-distance Raster in combination with the average dispersal distance specified in the parameter file.
Quality Raster	A map showing the relative quality of existing biotopes in terms of habitat used by the focal species
Functionality Raster	A map showing the spatial variation in habitat functionality within the studied landscape. This map has been generated by multiplying the Quality Raster with the Dispersal Raster. By doing this one get a map where habitat quality is weighted by the habitat connectivity. A high value of functionality is only achieved if the habitat is both of good quality and highly reachable from the habitat types needed for e.g. reproduction or nesting.]



### 3. REFERENCES

Berghauser Pont, M., Stavroulaki, I., Kindvall, O., Lanemo, E., Levan, M. (2022) Integrated Urban Environment Effect Analysis of Infrastructural Transformations. Chalmers and Trafikverket, Gothenburg., DOI: 10.13140/RG.2.2.21118.66885

Kindvall, O., Berghauser Pont, M., Stavroulaki, I., Lanemo, E., Wigren, L. & Levan, M. (2024). Predicting habitat functionality using habitat network models in urban planning. Environment and Planning B: Urban Analytics and City Science. <https://doi.org/10.1177/23998083241299165>

Kindvall, O. (2024). Input data files for habitat network analyses of amphibians in the Gothenburg region (Version 1) [Data set]. Chalmers University of Technology. Available at: <https://doi.org/10.5878/dn29-z128>