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# Biodiversity Metric 2.0 – Connectivity Tool Guidance



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## **Further information**

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#### The Biodiversity Metric 2.0 – Connectivity Tool Guidance

This guide shows you how to use the Biodiversity Metric 2.0 'Connectivity Tool' in a few simple steps.

It is important to note that the Connectivity Calculation Tool is to be used only to calculate ecological connectivity for habitats with a 'high' or 'very high' distinctiveness value. For all other distinctiveness categories continue to apply the interim approach set out in the 'User Guide'.

The connectivity tool is also not intended for use with Intertidal Habitats. The approach to be used here is described in the 'Intertidal Habitats addendum'. Connectivity is also not currently applied within the Rivers and Streams component of the Metric.

The output from the Connectivity Tool (a value of H/M/L for each habitat) should be entered manually into the appropriate 'Ecological Connectivity' column in the Biodiversity Metric 2.0 Calculation Tool. The Biodiversity Metric Calculation Tool will then generate a figure for equivalent biodiversity units based on the connectivity score of each habitat alongside the rest of the inputted data.

# Before using the Connectivity Tool you will need to ensure you have the correct data files downloaded/installed to your PC. These are:

<u>Site Extent</u>: A shapefile containing the boundary of your site. This will either be i) the development boundary for calculations of connectivity of existing or proposed 'on-site' habitats or linear features or ii) the boundary of the 'off-site' area where net gain delivery is proposed.

<u>Area Habitat Layer/Linear Habitat Layer:</u> A shapefile containing either the results of your habitat survey or proposed enhancement/creation. The data MUST include a UKHAB habitat classification code or other habitat code used by the metric for each polygon/polyline in order for the tool to work. (For full list see 'All Area Habitats' tab within 'Technical Data' tab of Metric Calculator.)

<u>Reference Habitat Folder:</u> A national dataset of UK BAP Priority Habitat is supplied with the tool however this can be replaced with higher quality local habitat datasets if these are available.

#### Installing/Downloading the Connectivity Tool

We have provided the Connectivity Tool for downloading in 2 formats:

BMCT 2.0 Auto Installer has a built in installation 'wizard' which simply requires you to click 'Next' when prompted in order to download it to your desktop. It will then appear as a program icon accessible from the taskbar of your computer:

We recommend that you use this option if possible.

If that does not work for any reason see the end of this guidance for details of how to install the Connectivity Tool manually using the BMCT 2.0 Manual Installer option.

USING THE CONNECTIVITY TOOL		
The tool requires you	El Biodiversity Metric 2.0 Connectivity Tool (BETA 1.1.0.8)	
to load the 3 datasets	_ Input data	Welcome to the Biodiversity Metric 2.0
previously described	Area Habitat Layer	Connectivity Tool.
into the appropriate	UKHab code field	To run the tool you must provide the following:
boxes:	Linear Habitat Layer	- A Shapefile containing either site
	UKHab code field	habitat polygons or polylines (or both) - A Shapefile containing a polygon of the extent of the site
First, select the <b>'Area</b>	Site Extent	<ul> <li>A folder of regional habitat grids (a national set is supplied with the tool)</li> </ul>
Habitat Layer' drop	Reference habitat folder	The tool will search the site habitat
down menu by clicking	Contract Con	polygons, extracting those that are appropriate to model.lt will then calculate the connectivity metric for
the tab to the right of	Working folder	each habitat identified and summarise the results.
the box and enter your		The results will indicate H M or L respectively For High, Medium And Low
, habitat survey or	Run	connectivity based on the applicable connectivity score range.
proposed habitat		
enhancement/creation		
shapefile		
Then chose the drop		
down menu on the		
'UKHab code' field and		
click 'HabCode'		
Now choose the drop		
down menu next to		
'Linear Habitat Layer'		
to enter your linear		
(hedgerows and lines		
of trees) shapefile.		
Then for the linear		
'UKHAB code field'		
again click 'HabCode'		
For 'Site Extent' you		
should add your site		
boundary shapefile		
boundary snaperne		
Then in <b>'Reference</b>		
Habitat Folder' enter		
the link to the	7	
Reference Habitat		
Folder supplied <b>OR</b> the		
link to your own		
local/regional Priority		
Habitat data and		
select 'OK'		
JEIELL UN		
Then chose the Output		
'Working folder', and		
specify a folder in		
which to store the		
Connectivity Tool		
outputs OR click the		
'Make new folder' Tab		

in the pop-up to create a new folder. (N.B. If an existing folder is specified its contents will be replaced by the model outputs.)	
Then click the 'Run' tab.	Samela output connectivity score:
The Connectivity Tool will generate a score of 'Low, Medium or High' connectivity for each habitat type in an excel file format.	Sample output connectivity score: Statistics [Read-Only]-Excel New Al Al Al Al Al Al Al Al
This will then need to be inputted into the	A-1 Site Habitat Baseline Condense / Show Columns Condense / Show Rows Main Menu Instructions
appropriate "Ecological Connectivity" column within the Metric Calculator.	Habitat sand areas         Habitat distinctiveness         Habitat condition         Ecological           Ref         Broad Habitat         Habitat type         Area (hectares)         Distinctiveness         Score         Condition         Score         Condition         Connectivity         Connectivity
8	



