

# Analysis of structural connectivity between HCV wetlands

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## Script

wetland\_new.py

## Description

The model creates input data to Omniscape for simulating structural connectivity between HCV wetlands in a given study area and post-processes the output from Omniscape into 10 m connectivity maps with value 0-10, indicating the degree of structural connectivity (the higher the stronger).

## Mapset

connectivity\_wetland\_new

## Necessary preparations

1. Update NMD using the script [update\\_NMD.py](#) (see separate documentation)
2. Generate raster data on protected, restricted and continuity forest using the script [HCV\\_kskog.py](#) in mapset *HCV\_kskog*
3. Create continuous input wetness data (see separate documentation)
4. Update HCV wetland data with wetlands in the mountain range (see separate documentation)

## Necessary input data

1. **nmd\_gen\_sv\_updated@update\_NMD**
  - NMD updated with recent fellings and transmission lines, generated using [update\\_NMD.py](#), located in mapset *update\_NMD*
2. **input\_study\_area\_raw\_[region]**
  - vector data representing the study area. There can be multiple study areas. They should have the same name except for [region]
3. **out\_input\_HCV\_kskog\_final@HCV\_kskog**
  - Raster data on protected, restricted and continuity forest. Generated by [HCV\\_forest\\_areas.py](#), located in mapset *HCV\_kskog*
4. **input\_wetness\_nmd**
  - Raster data on wetness index based on NMD. See necessary preparations.
5. **input\_wetlands**
  - Vector data on HCV wetlands. See necessary preparations

## Input parameters in GUI

- **Region**
  - Name of the study area. Should match the input data **input\_study\_area\_raw\_[region]**
- **Buffer**
  - Size of the buffer (m) added to the study area to avoid edge effects.
- **Suffix**
  - Optional suffix to the output file name
- **Natural vegetation**
  - Resistance value for natural vegetation, including land classified as wetlands, HCV forest, continuity forest, or other open land with vegetation. Defaults to 10. HCV wetlands are automatically set to 1, regardless of the value here.
- **Other forest**
  - Resistance value for "other forest", i.e., forests that are not recently harvested and that does not qualify as protected, restricted or continuity forest or wetland forest. In general this means production forest. Defaults to 50
- **Non-natural vegetation**
  - Vegetation that has been substantially modified, i.e., recently harvested forests, agriculture, and vegetation under transmission lines. Defaults to 150.
- **No vegetation**
  - Non-vegetated land. Defaults to 300.

## Output data

- **[region]\_out\_calc\_resistance\_[suffix]**
  - where [region] and [suffix] is specified in the GUI.
  - Resistance layer (raster, 10 m) for the study area, saved as grass raster and exported to geotiff and ascii (input to Omniscape).
- **[region]\_out\_calc\_resistance\_20m\_[suffix]**
  - Same as above but with 20m resolution

## Post-processing

After running the Omniscape simulations using the output data described above, the script can post-process the (normalized) cumulated current maps and generate 10 m connectivity maps with values 0-10. This is the final result of the model.

## Usage

1. Run the script from a GRASS console within the given mapset to open the GUI.
2. Specify the input parameters (important: save buffer and suffix before saving region)
3. Press "Prepare datasets" (this is only necessary once for each region, buffer, and suffix)
4. Press "Compute resistance layer"
5. Use the output data to run Omniscape
6. Press "Run post-processing" and browse to the output data from Omniscape.

## Updating the analysis

### For updates on land-use data (NMD)

Rerun `update_NMD.py` and then run the model

### For updates on protected, restricted and continuity forest

Rerun `HCV_kskog.py` (see separate documentation) and `density_analysis.py` (see separate documentation) and then run the model (the name of input data 3 and 4 may change – update the script if necessary).

### For updates on wetness data

Pre-process according to separate documentation. Then run the model.

### For updates on HCV wetlands

Pre-process according to separate documentation. Then run the model.