

# Zonation 5: Hands-on exercises

```

, var d=a.fn.tab; a.fn.tab=b, a.fn.tab.Constructor=c, a.fn.tab.noConflict=function(){return a.fn.t
"show")); a(document).on("click.bs.tab.data-api", "[data-toggle='tab']", e).on("click.bs.tab.data
se strict"; function b(b){return this.each(function(){var d=a(this), e=d.data("bs.affix"), f="ob
typeof b&&e[b]()}}) var c=function(b,d){this.options=a.extend({}, c.DEFAULTS, d), this.$target=a
", a.proxy(this.checkPosition, this)).on("click.bs.affix.data-api", a.proxy(this.checkPositionWi
null, this.pinnedOffset=null, this.checkPosition()); c.VERSION="3.3.7", c.RESET="affix affix-top
State=function(a,b,c,d){var e=this.$target.scrollTop(), f=this.$element.offset(), g=this.$targ
"bottom"==this.affixed) return null!=c?!(e+this.unpin<=f.top)&&"bottom":!(e+g<=a-d)&&"bottom"
l!=c&&e<=c?"top":null!=d&&i+j>=a-d&&"bottom"}, c.prototype.getPinnedOffset=function(){if (c
c.RESET).addClass("affix"); var a=this.$target.scrollTop(), b=this.$element.height(), d=this
WithEventLoop=function(){setTimeout(a.proxy(this.checkPosition, this), 100);}}; a(window).on(
ent.height(), d=this.$element.offset(), e=this.$target.scrollTop(), f=this.$element.height(), g=

```

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- I. Getting started: folder structure
- II. Exercise data: case European tree species
- III. Zonation basics: input and output files

Exercises (slide 26 onwards):

1. Running Zonation 5 + Graphical user interface (GUI)
2. Changing the marginal loss rule
3. Adding more input features
4. Adding weights
5. Adding human impacts as a negatively-weighted feature
6. Adding protected areas as a hierarchic mask

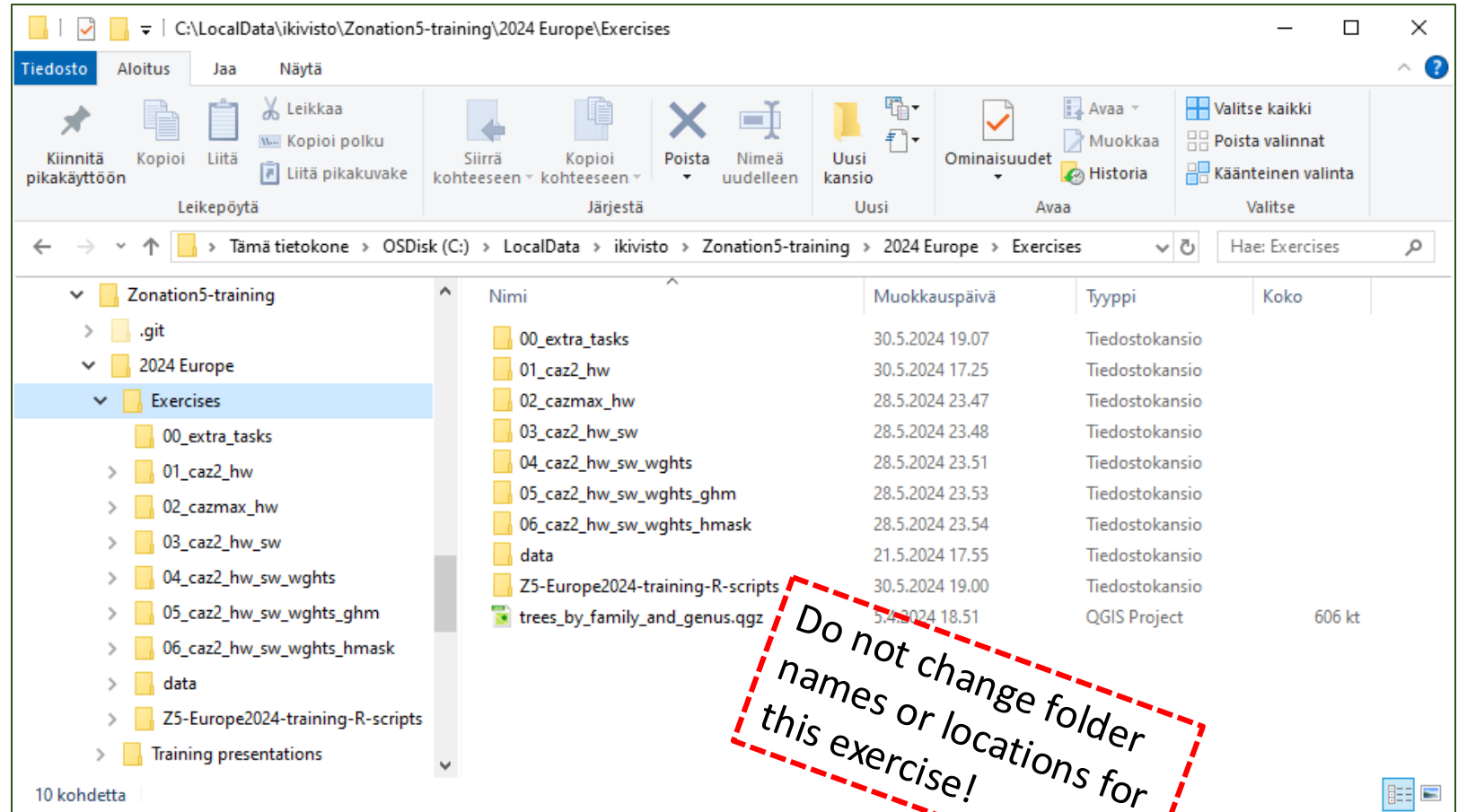
I.

What's in the folders?

# I. Folder structure

Good practice to do analyses in separate versions/variants

- Verification
- Sensitivity analysis, i.e. trace how different settings influence the results





# I. Name your files descriptively

## 01\_caz2\_hw

01 = ID number  
caz2 = Core Area Zonation 2 (Zonation marginal loss rule)  
hw = Hardwoods (type of input biodiversity features)

Code	Description
01	ID number
caz2	Zonation marginal loss rule: CAZ2
cazmax	Zonation marginal loss rule: CAZMAX
hw	Input features: hardwoods
sw	Input features: softwoods
wghts	Varying weights
ghm	Input feature: Layer based on The Global Human Modification dataset
hmask	Protected areas as a hierarchic mask

# I. Inside a Zonation variant folder

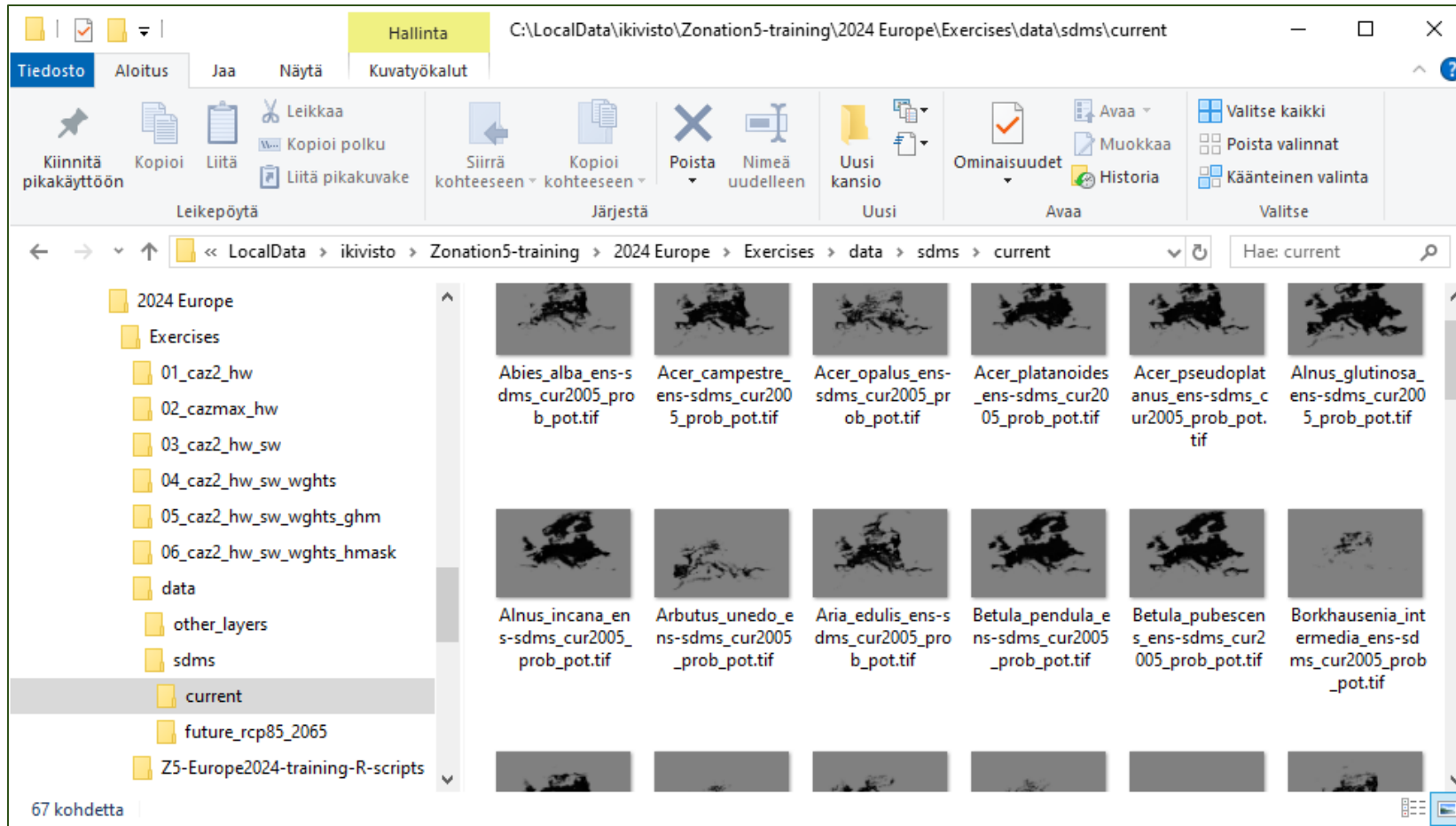
The screenshot shows a Windows File Explorer window with the address bar displaying the path: C:\LocalData\ikivisto\Zonation5-training\2024 Europe\Exercises\01\_caz2\_hw. The left sidebar shows a tree view of the folder structure, with '01\_caz2\_hw' selected. The main pane displays a list of files and folders with columns for Name, Modification Date, Type, and Size.

Nimi	Muokkauspäivä	Tyyppi	Koko
out	28.5.2024 23.46	Tiedostokansio	
01_caz2_hw.z5	5.4.2024 16.18	Z5-tiedosto	1 kt
features.txt	21.5.2024 18.11	Tekstitiedosto	1 kt
z5_call.cmd	28.5.2024 23.45	Windows-komentosarja	1 kt

Annotations with arrows pointing to the files in the table:

- An arrow points from the 'out' folder to the text box: "Zonation automatically creates a folder for output files (see below)".
- An arrow points from the '01\_caz2\_hw.z5' file to the text box: "Necessary input files (see below)".
- An arrow points from the 'features.txt' file to the text box: "Necessary input files (see below)".
- An arrow points from the 'z5\_call.cmd' file to the text box: "Necessary input files (see below)".

# I. Input GIS layers are in the 'data' folder





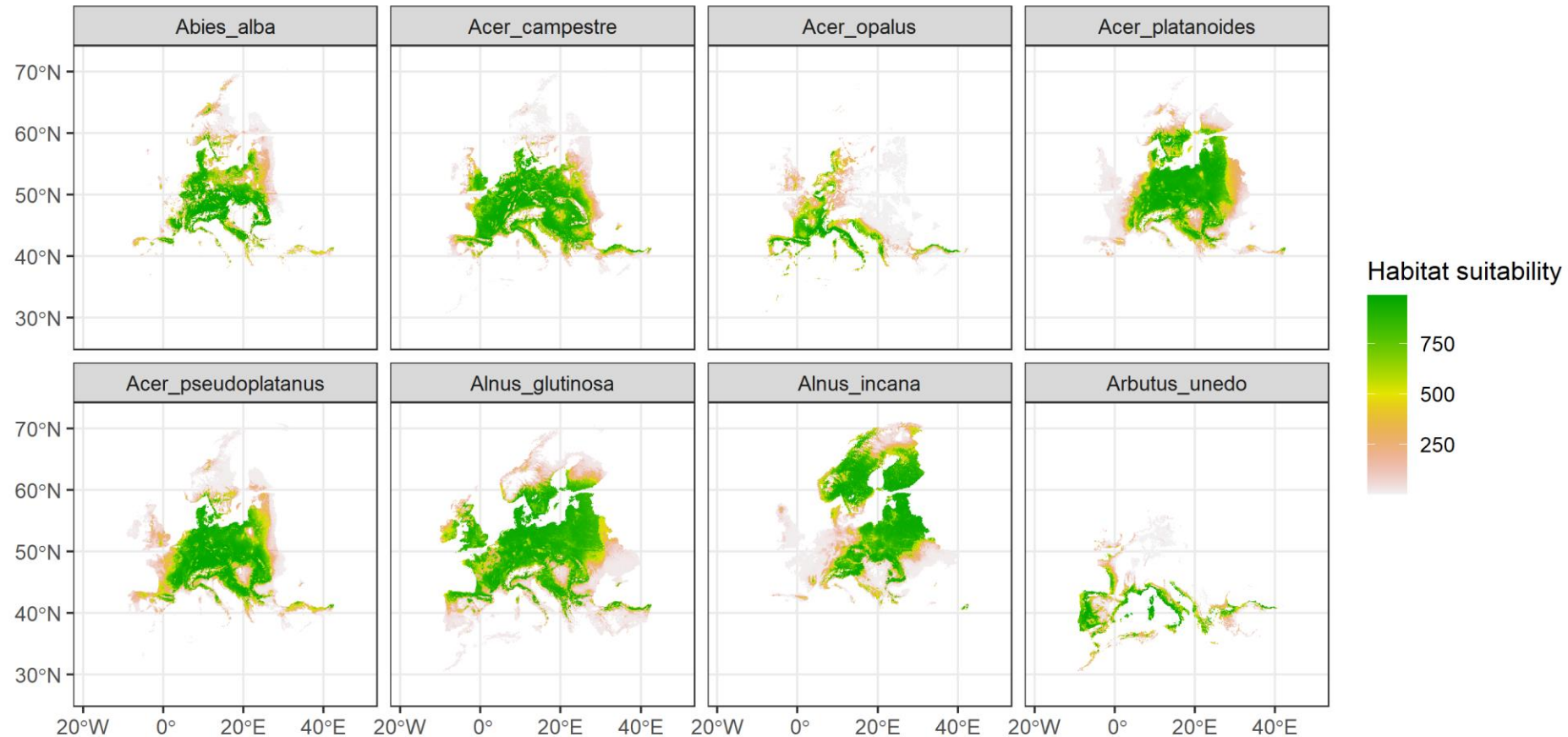
II.

# The European case data

Get familiar with the data used in these exercises

## II. Feature data: European tree species

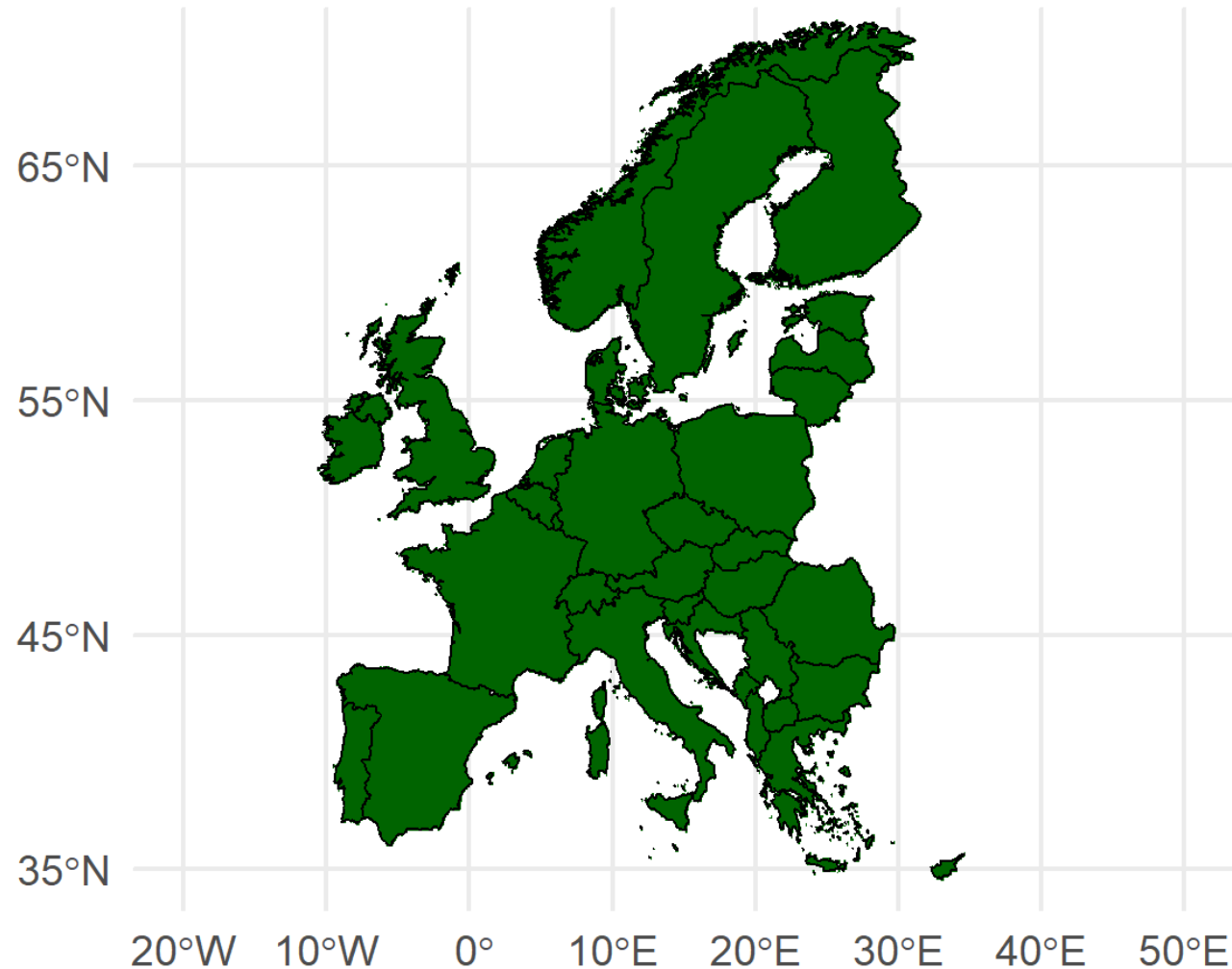
- Species distribution models (SDMs) for European tree species by Mauri et al. (2022)
- Habitat suitability for each spp. at 10 km resolution.
- Current distributions
- If you have QGIS installed, you can examine layers using trees\_by\_family\_and\_genus.qgz file



More information on this [link](#).

## II. Other layers: Analysis area mask

- Includes a sample of EU member states and neighboring countries
- Excludes overseas territories
- Focused on mainland
- 10 km resolution



III.

# The basics: input and output files, Zonation 5 GUI

The format of input and output files; get familiar with the GUI

# III. The Zonation 5 call file (.cmd/executable text file)

- Script file that runs Zonation
- Sets basic settings
- Activates settings from the settings file

01_caz2_hw.z5	5.4.2024 16.18	Z5-tiedosto
features.txt	21.5.2024 18.11	Tekstitiedosto
z5_call.cmd	28.5.2024 23.45	Windows-komentosarja

## Windows: .cmd

```
z5_call.cmd - Muistio
Tiedosto Muokkaa Muotoile Näytä Ohje
@setlocal
@PATH=C:/Program Files/Zonation5/v2.0.2;%PATH%

z5 -awh --gui --mode=CAZ2 06_caz2_hw_sw_wghts_hmask.z5 out
@pause
```

Specify the filepath for z5.exe

Settings for the run, separator: space

“Flags”: Activate different settings

Open GUI

Set balancing method

Name of the settings file

Name of the output folder

## Linux: text file with execute permission

```
GNU nano 7.2 New Buffer Modified
#!/bin/sh
export PATH=$HOME/Zonation/Zonation5/v2.0.2:$PATH

zonation5 -awh --gui --mode=CAZ2 06_caz2_hw_sw_wghts_hmask.z5 out|

^G Help      ^O Write Out  ^W Where Is   ^K Cut        ^T Execute    ^C Location
^X Exit      ^R Read File  ^\ Replace    ^U Paste      ^J Justify    ^_ Go To Line
```

# III. Flag options in the call file

Flag letter	Explanation
a	use analysis area mask
w	use weights (lower case w)
W	use weights and weight groups (upper case W)
g	use output groups
c	use condition
h	use hierarchic analysis
r	use retention
x	use cost (lower case x)
X	use cost in prioritization (upper case X)
t	use thresholding
d	use single-feature connectivity transform
i	use interaction connectivity transform 1 (lower case i)
I	use interaction connectivity transform 2 (upper case I)
m	use matrix connectivity transform
p	run post-processing analyses after prioritization
b	run pre-processing analyses before prioritization
f	output transformed layers
s	run source-based impact assessment before prioritization
e	run cumulative impact assessment before prioritization

- Flags are activated with “-” and correct letter in the call file
- Flags can be combined in a string:
  - ‘-whma’ would include weights, hierarchic mask, matrix connectivity and analysis area mask
  - can be written separately as well

```
@setlocal
@PATH=C:/Program Files/Zonation5/v2.0.
z5 -awh --gui --mode=CAZ2 06_caz2_hw_s
z5 -wh -a --gui --mode=CAZ2 06_caz2_hw
@pause
```



# III. Settings file (.z5)

- Major settings + filepaths needed for connectivity, costs, etc.
- At minimum, sets the filepath for input feature list file

Obs! Filepaths can be relative or absolute

*Absolute path:*

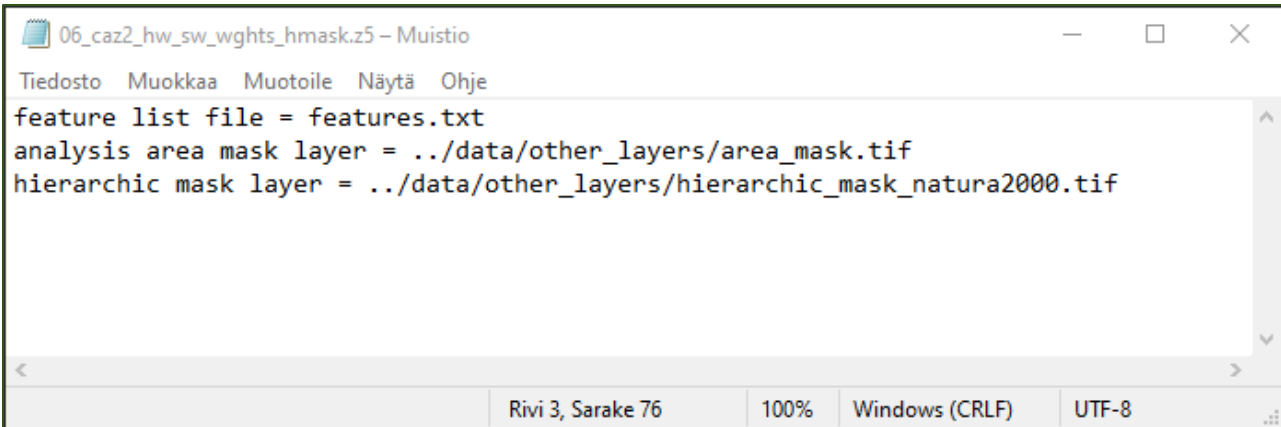
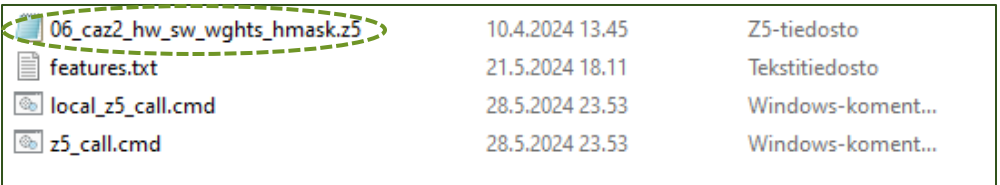
C:/Z5-training/data/other\_layers/area\_mask.tif

*Relative path:*

../data/other\_layers/area\_mask.tif

(i.e. "one folder up from the given file, then to 'data' folder, etc.")

06_caz2_hw_sw_wghts_hmask.z5	10.4.2024 13.45	Z5-tiedosto
features.txt	21.5.2024 18.11	Tekstitiedosto
local_z5_call.cmd	28.5.2024 23.53	Windows-koment...
z5_call.cmd	28.5.2024 23.53	Windows-koment...



```
06_caz2_hw_sw_wghts_hmask.z5 - Muistio
Tiedosto Muokkaa Muotoile Näytä Ohje
feature list file = features.txt
analysis area mask layer = ../data/other_layers/area_mask.tif
hierarchic mask layer = ../data/other_layers/hierarchic_mask_natura2000.tif
Rivi 3, Sarake 76 100% Windows (CRLF) UTF-8
```

### III.

## Setting options affecting the run

Parameter identifier	Explanation
curves output interval	Interval with which to sample points from the performance curves and output into the curves file, given as a fraction (0 to 1) of the number of cells in the feature data. The number of samples is automatically limited to a maximum of 100000.
max iterations	Maximum number of iterations to run during optimization.
mean rank change threshold	Stops iteration when mean rank change goes below the specified threshold
smoothing factor	The memory parameter q
stop on plateau	Whether to stop iteration once the mean rank change is the same or bigger than in the previous iteration. Value 1 means true, 0 means false.
zero mode	How to treat zero values in input layers. Value “none” means treat all zeros as no data. Value “all” means keep all zeros. Value “dynamic” means that the column “keepzeros” in the feature list file determines what to do with zeros. The default is “none”; zeros are not retained.
stop after preprocessing	Determines whether to continue to prioritization after doing all preprocessing steps.

# III. External files that can be specified in the settings file

File parameter identifier	Flag letter in the call file	Additional raster or special .txt file required
feature list file	always required, compulsory	text file (see below)
external solution	--mode=LOAD	the external solution raster (float) to load
analysis area mask layer	a	raster (int)
weight groups file	W	special text file
condition link file	c	special text file
hierarchic mask layer	h	raster (int)
cost layer	x	raster (float)
retention link file	r	special text file
single-feature connectivity link file	d	special text file
interaction connectivity link file	i, I	special text file
matrix connectivity link file	m	special text file
post-processing file	p	special text file
impact assessment scenario file	s	special text file
cumulative impact assessment scenario file	e	special text file
impact buffers file	s	special text file
binning link file	s	special text file

# III. Feature list file (.txt)

- Lists all input feature layers, i.e. distribution maps of
  - species
  - habitats
  - ecosystem services
  - etc.
- Defines some feature-specific options such as weights
- Columns can be in any order. Separated by “white space” (spaces, tabulators) but at least one space is required

06_caz2_hw_sw_wghts_hmask.z5	10.4.2024 13.45	Z5-tiedosto
features.txt	21.5.2024 18.11	Tekstitiedosto
local_z5_call.cmd	28.5.2024 23.53	Windows-koment...
z5_call.cmd	28.5.2024 23.53	Windows-koment...

```
features.txt - Muistio
Tiedosto Muokkaa Muotoile Näytä Ohje
"weight" "filename"
3.1 "../data/sdms/current/Acer_platanoides_ens-sdms_cur2005_prob_pot.tif"
2.1 "../data/sdms/current/Betula_pubescens_ens-sdms_cur2005_prob_pot.tif"
1.5 "../data/sdms/current/Fraxinus_angustifolia_ens-sdms_cur2005_prob_pot.tif"
1.3 "../data/sdms/current/Malus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
3.2 "../data/sdms/current/Populus_tremula_ens-sdms_cur2005_prob_pot.tif"
0.5 "../data/sdms/current/Quercus_frainetto_ens-sdms_cur2005_prob_pot.tif"
2.7 "../data/sdms/current/Sorbus_aucuparia_ens-sdms_cur2005_prob_pot.tif"
3.9 "../data/sdms/current/Tilia_cordata_ens-sdms_cur2005_prob_pot.tif"
4.1 "../data/sdms/current/Abies_alba_ens-sdms_cur2005_prob_pot.tif"
1.3 "../data/sdms/current/Juniperus_thurifera_ens-sdms_cur2005_prob_pot.tif"
3.7 "../data/sdms/current/Pinus_brutia_ens-sdms_cur2005_prob_pot.tif"
4 "../data/sdms/current/Pinus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
Rivi 14, Sarake 1 100% Windows (CRLF) UTF-8
```

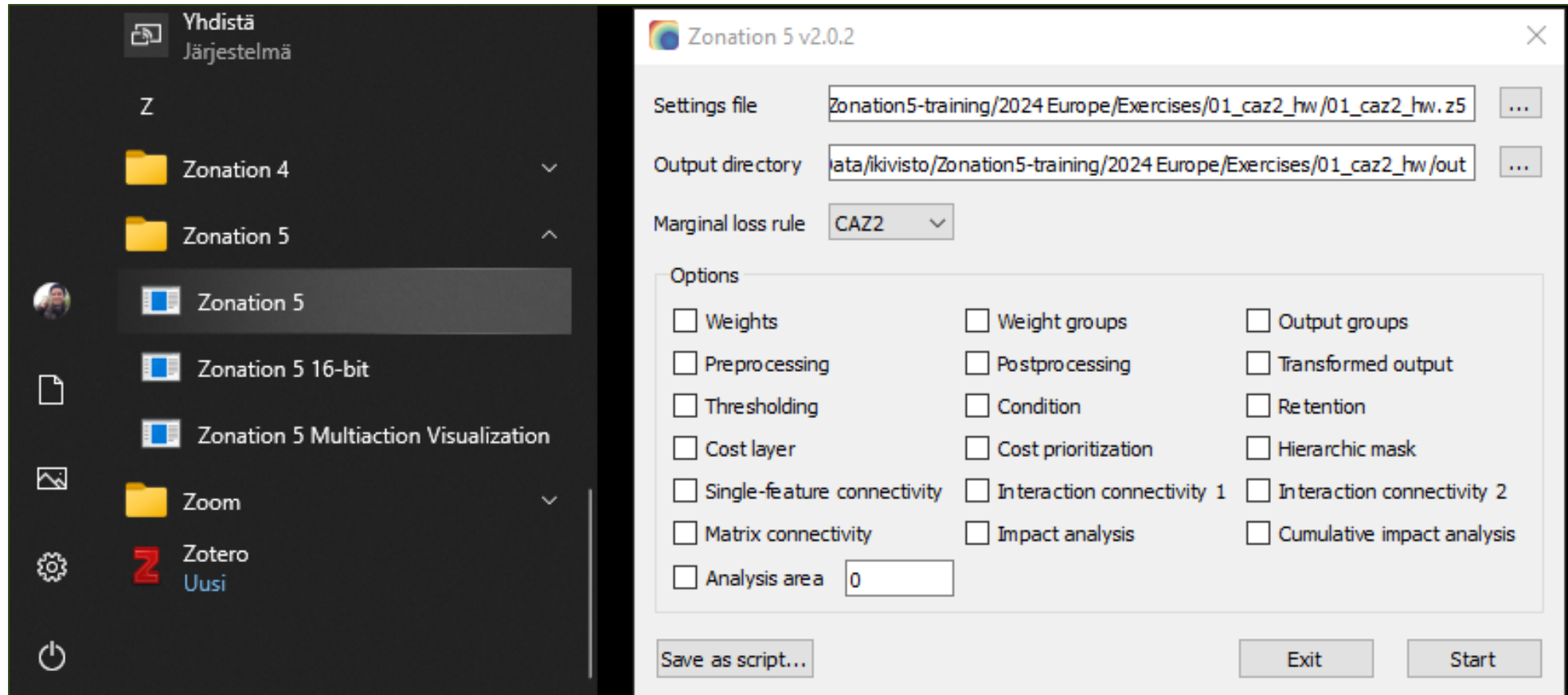
### III.

## Possible columns in the features list

Column identifier (case sensitive)	Explanation
"weight"	feature weight
"wgrp"	weight group
"filename"	feature distribution file name
"condition"	condition transform number
"group"	output group number
"retention"	retention transform number
"threshold"	numeric threshold below which input file is cut to zero = no effect on analysis
"sf_conn"	single-feature connectivity transform number
"iaconn1"	interaction transform 1 number
"iaconn2"	interaction transform 2 number
"matrix_conn"	part in matrix connectivity transform number
"abfz"	parameter of feature-specific power function
"tr_out"	output transformed layer yes (1) /no
"name"	short name for feature (in quotes); if given, used to clarify certain outputs
"keepzeros"	if project setting "zero mode" has the value "dynamic", this determines whether to keep (1) zeros of the layer during processing or treat them as no data (0)
"impact_grp"	impact group number in impact assessment analysis
"impact_bins"	bins used in impact assessment analysis

# III. Graphical User Interface

- For initial scrutinization and visualization of the results & simple post-processing
- Allows creation of new Z5 call files (but settings and feature list files must exist beforehand)

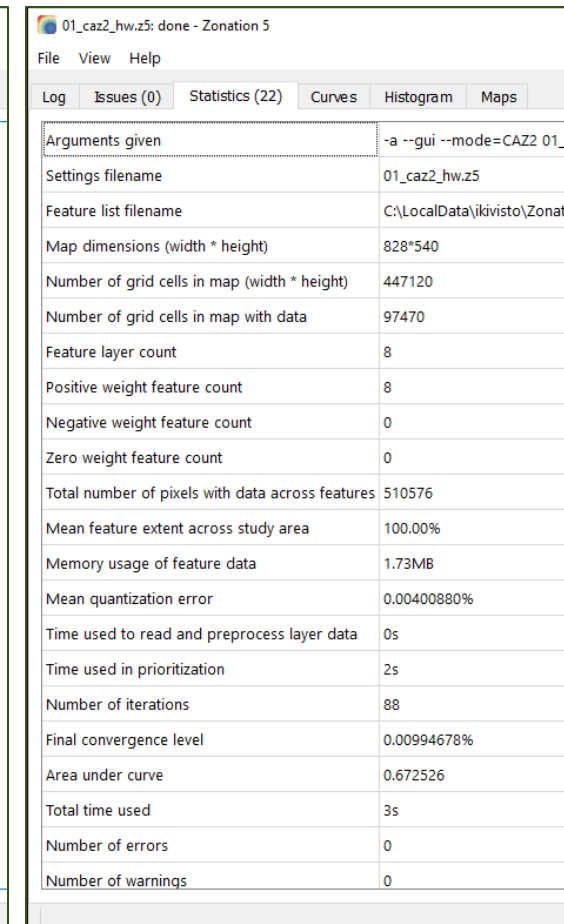




# III.

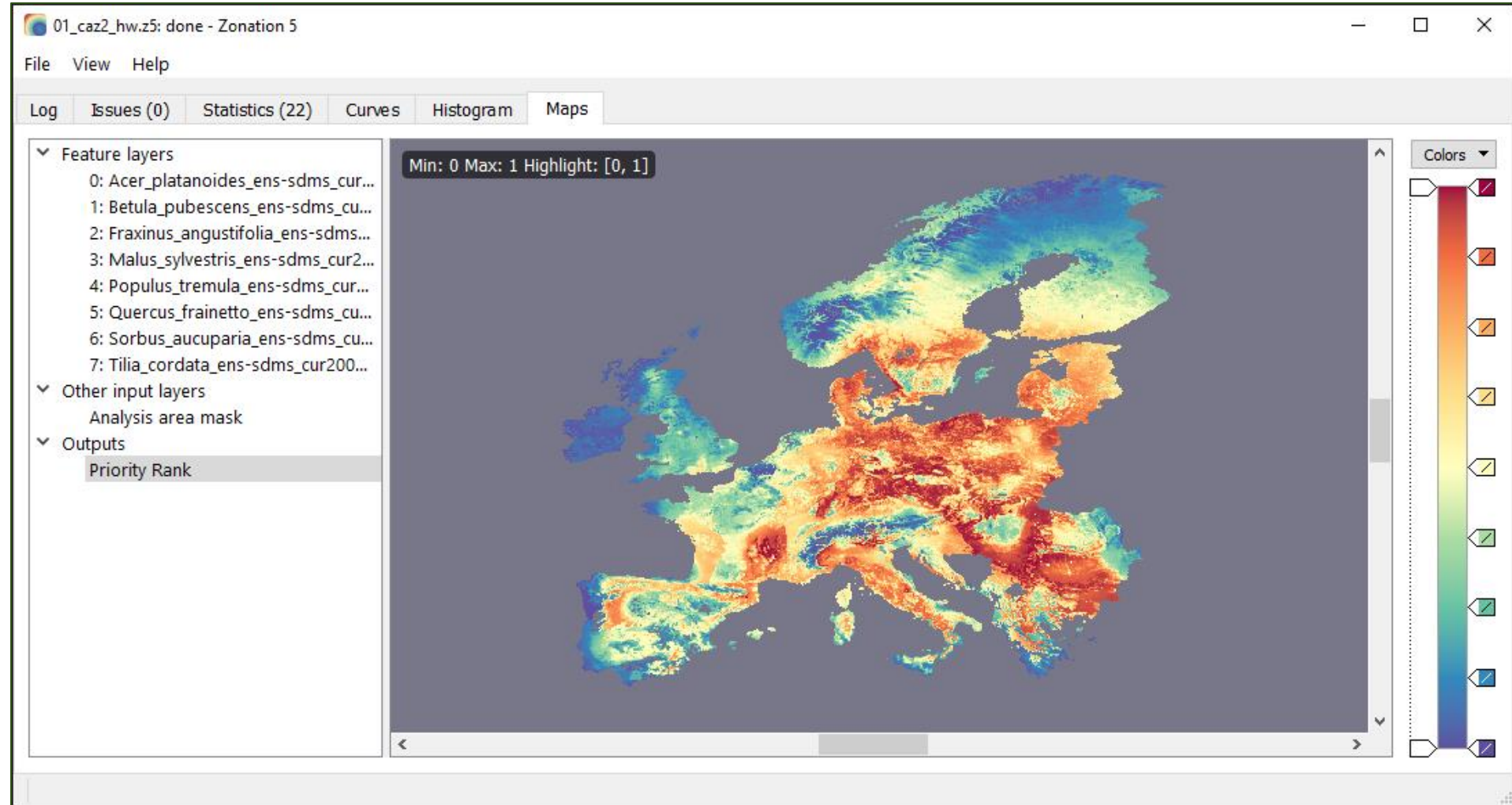
## GUI: 'Log', 'Issues' & 'Stats' tabs

Basic information about the run. 'Issues' tab shows all warnings and errors if any.



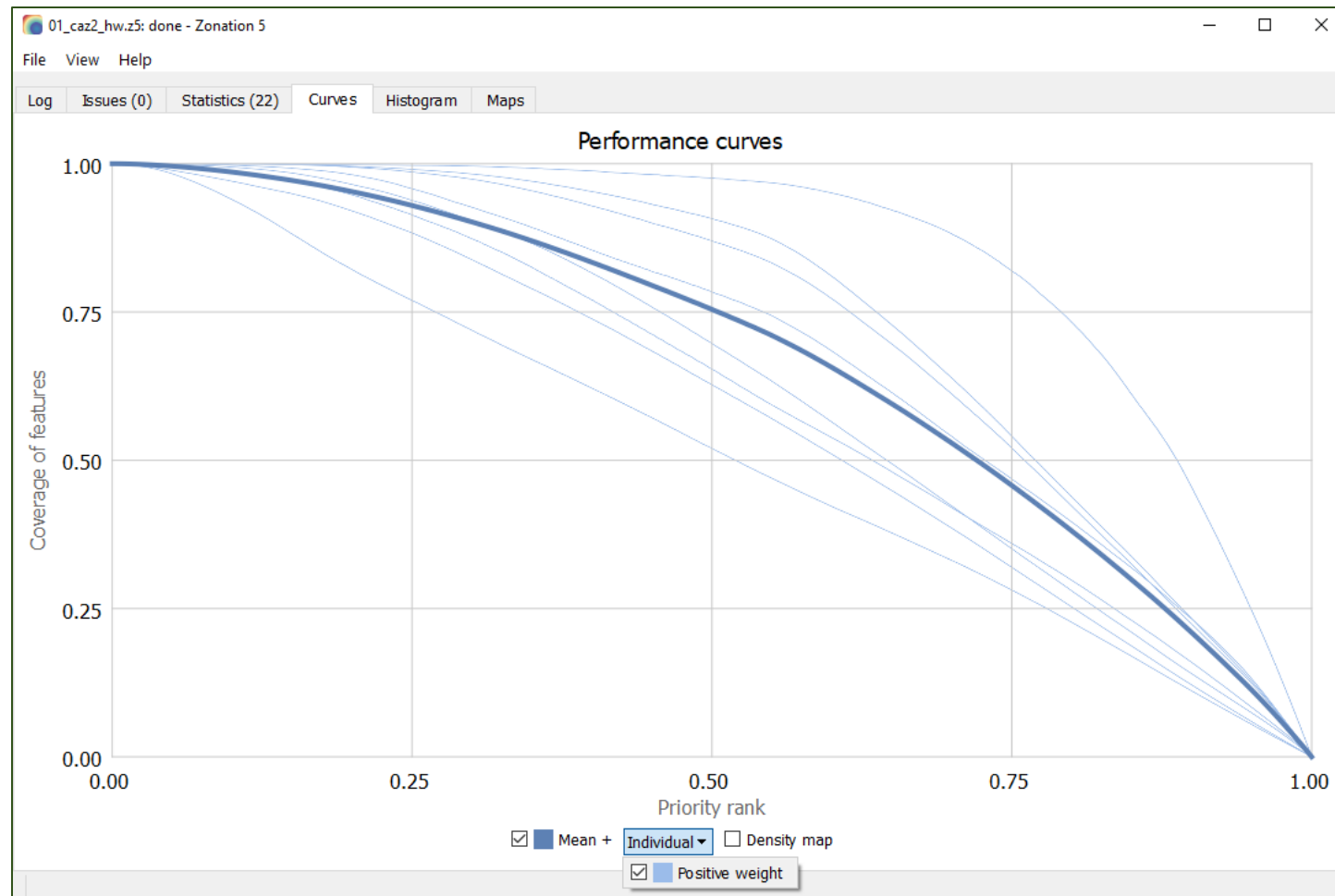
# III. GUI: Maps

- Basic: Priority levels
  - Higher the priority, more important for conservation
- You can modify the colour scale as you wish & save as image
- File > 'Open map' to compare with other maps, e.g. different variants



# III. GUI: Curves

Performance curves: How great proportion of features' distributions is retained within different priority levels (from the map)?



# III. GUI: Histograms

Count of features inside different coverage ranges at a certain priority level

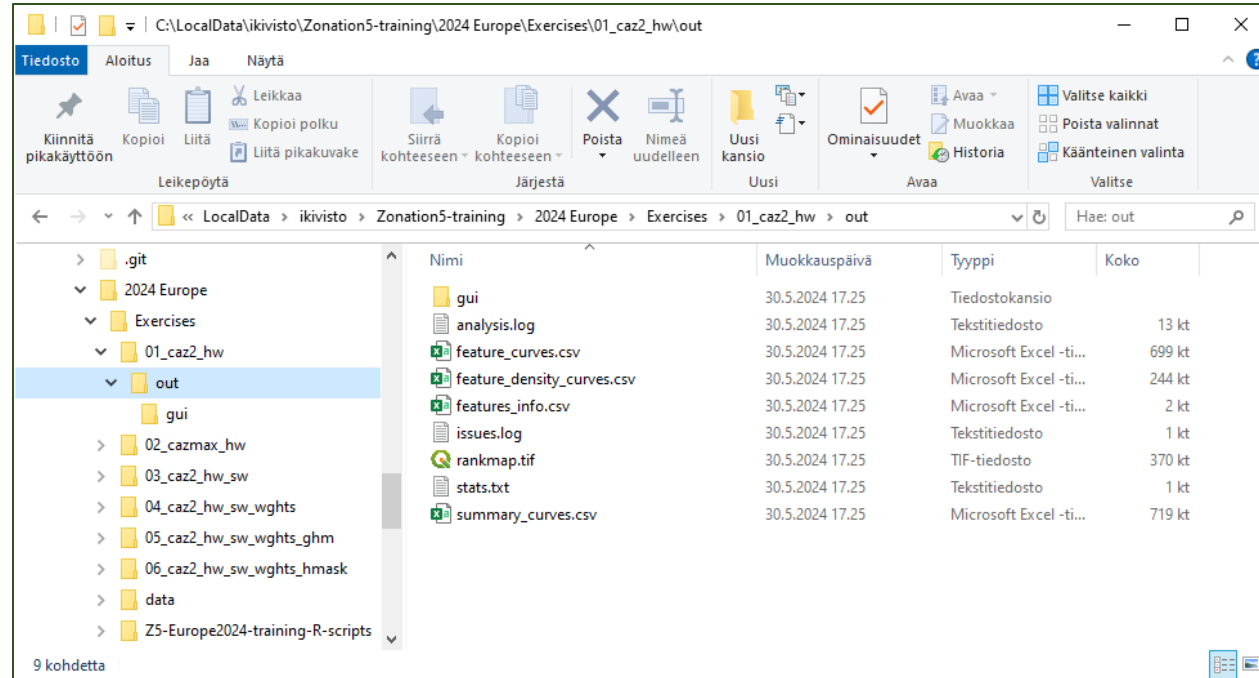
“The top-20% priority areas include:

- 20-30% of four features’,
- 30-40% of one feature’s,
- 40-50% of two features’,
- and 70-80% of one feature’s distributions”



# III. Output files

- Zonation outputs can be explored in the GUI. Files can also be opened and processed in R, Excel, GIS software, etc.
- analysis.log = 'Log' tab in GUI
- feature\_curves.csv = Individual performance curves as a table
- feature\_density\_curves.csv = contains feature density curves, feature density is the range-size rarity score of an area divided by the mean range-size rarity across the whole study area
- features\_info.csv = Standard numeric information of input features
- issues.log = 'Issues' tab in GUI
- rankmap.tif = priority rank map as a GEOTIFF file
- stats.txt = 'Stats' tab in GUI
- summary\_curves.csv = mean, max, min, etc. performance curves as a table
- (empty) gui folder is also created automatically for post-processing analyses done in GUI



# Exercises

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01

# Basic run

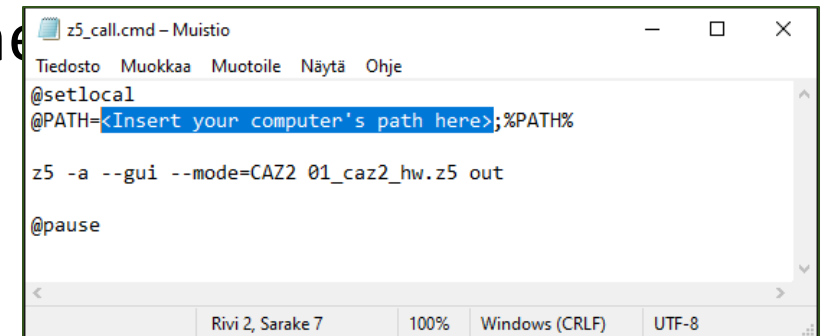
Get basic setup running

Explore the GUI

# 01

## Get Zonation running

1. Edit the `z5_call` file (open in Notepad).
2. Replace `<Insert your computer's path here>` with the path to `z5.exe` in your computer (e.g. something like `'C:/Program Files (x86)/Zonation5'`) & save. Note that the replacement should be made without the brackets.
3. Double-click the `z5_call` file. Zonation 5 GUI should open and run the analysis.
4. Once this succeeds, copy the correct filepath to every exercise variants' `z5_call` files. (Do not make any other



```
z5_call.cmd - Muistio
Tiedosto Muokkaa Muotoile Näytä Ohje
@setlocal
@PATH=<Insert your computer's path here>;%PATH%

z5 -a --gui --mode=CAZ2 01_caz2_hw.z5 out

@pause
```

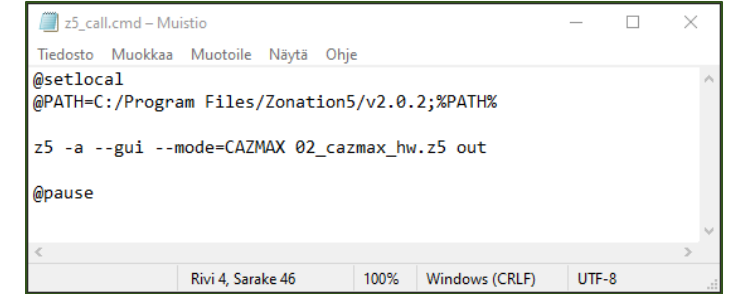
1. Change the rank map's color scale to 'Viridis' and save the map as an image
2. How much input feature's known (=initial) distributions would be preserved on average, if highest 25% of Europe would be protected?
3. How great proportion of Europe would be needed to ensure at least 50% of every features' distributions? (Hint: display the 'Min' curve)

02

# Change the marginal loss rule

See how the marginal loss rule affects prioritization outcomes

1. Edit the marginal loss rule (mode) in `z5_call` file to read 'CAZMAX' (all upper case) & save.
2. Run the analysis.
3. In the Map tab, click 'File' > 'Open map' and open the rankmap from the previous analysis. Compare the results. Why are they different?



```
z5_call.cmd - Muistio
Tiedosto Muokkaa Muotoile Näytä Ohje
@setlocal
@PATH=C:/Program Files/Zonation5/v2.0.2;%PATH%

z5 -a --gui --mode=CAZMAX 02_cazmax_hw.z5 out

@pause

Rivi 4, Sarake 46 100% Windows (CRLF) UTF-8
```

The answer: because the two methods base on completely different types of algorithms. CAZ2 emphasizes a bit more the richness of features, whereas CAZMAX emphasizes more the rare features.

03

# Add more features

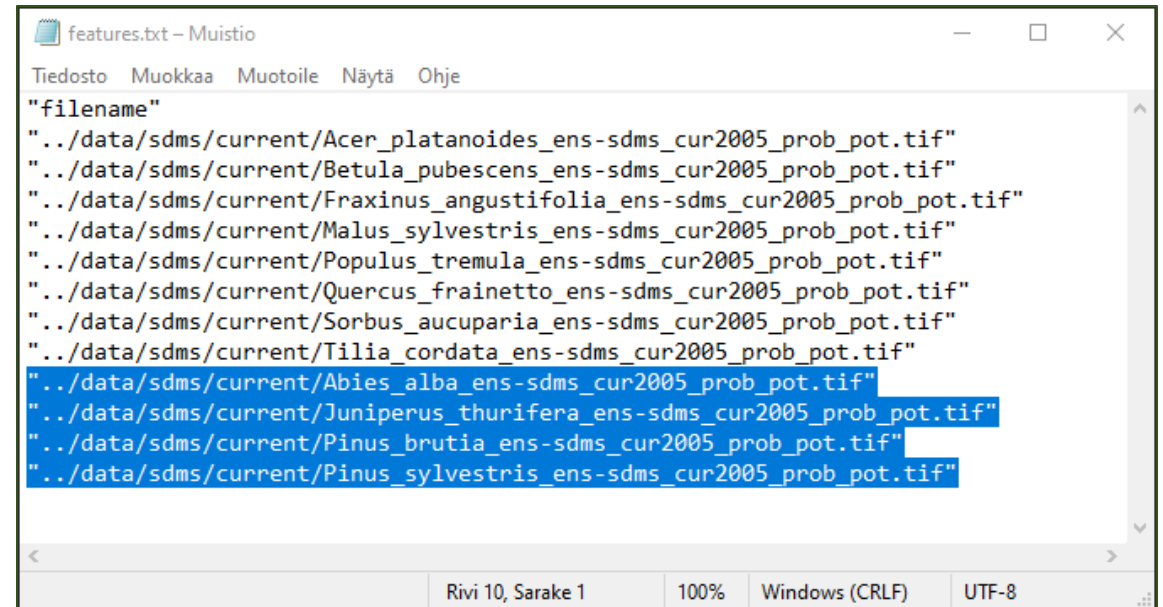
Add species distributions to the analysis



# 03

## Add more features

1. Open the 'features.txt' file.
2. Fill the last four rows to include some softwood species layers to the analysis. Save edits.
3. Explore the outputs & compare them to the 01 variant. What has changed?



```
features.txt - Muistio
Tiedosto Muokkaa Muotoile Näytä Ohje
"filename"
"./data/sdms/current/Acer_platanoides_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Betula_pubescens_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Fraxinus_angustifolia_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Malus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Populus_tremula_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Quercus_frainetto_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Sorbus_aucuparia_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Tilia_cordata_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Abies_alba_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Juniperus_thurifera_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Pinus_brutia_ens-sdms_cur2005_prob_pot.tif"
"./data/sdms/current/Pinus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
```

04

# Weighting features

Give features unique weights

- Weighting should be based on higher-level considerations of conservation planning:
  - Red-list status
  - Endemicity
  - Quality of the data
  - Economic value
  - Preferences
- Note: rarity **not** a reason for higher weights

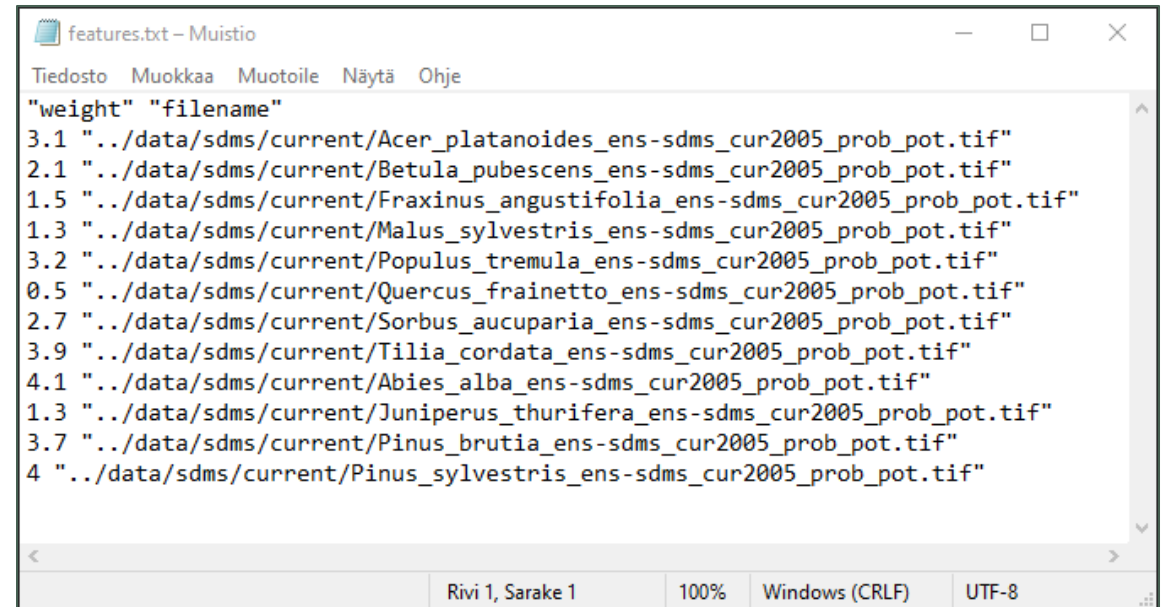
Note that Zonation treats weights as relative!

1.0 Species1.tif		10 Species1.tif
2.0 Species2.tif	=	20 Species2.tif
4.0 Species3.tif		40 Species3.tif

# 04

## Set weights

1. Open the `features.txt` file of the 04 variant.
2. Come up with suitable weights for each feature. What would be the most important to conserve?
3. Compare results with the previous variant.
4. Finally, copy your `features.txt` file to every following variants' folders.



A screenshot of a text editor window titled "features.txt - Muistio". The window has a menu bar with "Tiedosto", "Muokkaa", "Muotoile", "Näytä", and "Ohje". The main text area contains a list of features with their weights and filenames. The status bar at the bottom shows "Rivi 1, Sarake 1", "100%", "Windows (CRLF)", and "UTF-8".

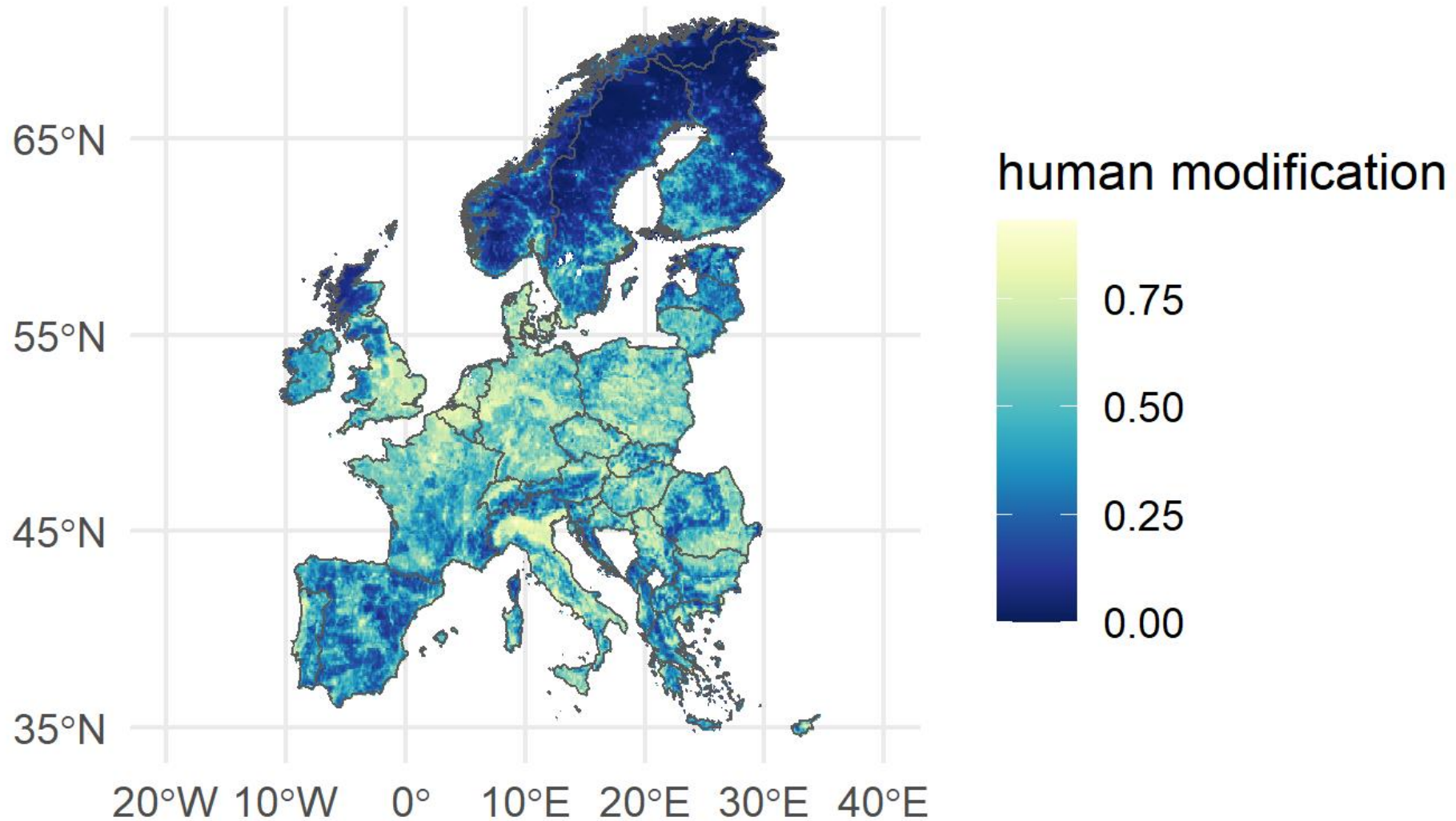
```
"weight" "filename"
3.1 "../data/sdms/current/Acer_platanoides_ens-sdms_cur2005_prob_pot.tif"
2.1 "../data/sdms/current/Betula_pubescens_ens-sdms_cur2005_prob_pot.tif"
1.5 "../data/sdms/current/Fraxinus_angustifolia_ens-sdms_cur2005_prob_pot.tif"
1.3 "../data/sdms/current/Malus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
3.2 "../data/sdms/current/Populus_tremula_ens-sdms_cur2005_prob_pot.tif"
0.5 "../data/sdms/current/Quercus_frainetto_ens-sdms_cur2005_prob_pot.tif"
2.7 "../data/sdms/current/Sorbus_aucuparia_ens-sdms_cur2005_prob_pot.tif"
3.9 "../data/sdms/current/Tilia_cordata_ens-sdms_cur2005_prob_pot.tif"
4.1 "../data/sdms/current/Abies_alba_ens-sdms_cur2005_prob_pot.tif"
1.3 "../data/sdms/current/Juniperus_thurifera_ens-sdms_cur2005_prob_pot.tif"
3.7 "../data/sdms/current/Pinus_brutia_ens-sdms_cur2005_prob_pot.tif"
4 "../data/sdms/current/Pinus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
```

05

# Add a negatively-weighted feature

Add human impact as a negatively-weighted feature

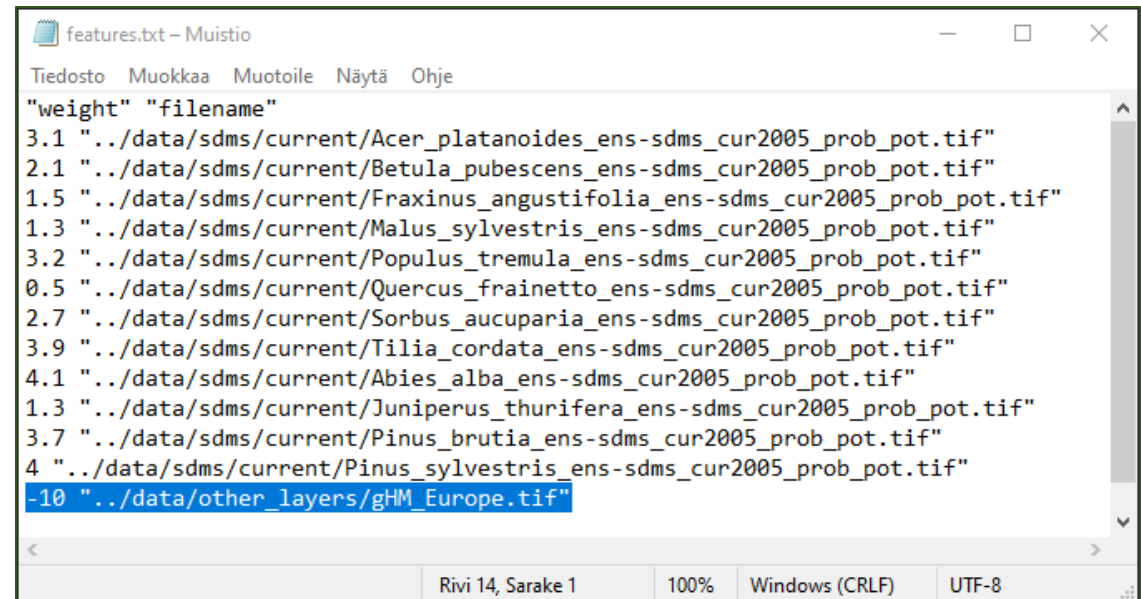
- Positive weight = You want to retain the feature in top-priority levels
- Negative weight = You want to avoid the feature in top-priority levels
- Examples of negatively-weighted features:
  - Invasive species
  - Costs (=avoid expensive places)
  - Competing land-uses, e.g. urban expansion



## 05

# Add gHM as a negatively-weighted feature

- Open the features.txt file of variant 05.
- Add the human modification layer ('gHM\_europe.tif') as a new feature and give it a sufficiently high negative weight.
- Run the analysis and compare the results with the previous variant.



```
features.txt - Muistio
Tiedosto Muokkaa Muotoile Näytä Ohje
"weight" "filename"
3.1 "../data/sdms/current/Acer_platanoides_ens-sdms_cur2005_prob_pot.tif"
2.1 "../data/sdms/current/Betula_pubescens_ens-sdms_cur2005_prob_pot.tif"
1.5 "../data/sdms/current/Fraxinus_angustifolia_ens-sdms_cur2005_prob_pot.tif"
1.3 "../data/sdms/current/Malus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
3.2 "../data/sdms/current/Populus_tremula_ens-sdms_cur2005_prob_pot.tif"
0.5 "../data/sdms/current/Quercus_frainetto_ens-sdms_cur2005_prob_pot.tif"
2.7 "../data/sdms/current/Sorbus_aucuparia_ens-sdms_cur2005_prob_pot.tif"
3.9 "../data/sdms/current/Tilia_cordata_ens-sdms_cur2005_prob_pot.tif"
4.1 "../data/sdms/current/Abies_alba_ens-sdms_cur2005_prob_pot.tif"
1.3 "../data/sdms/current/Juniperus_thurifera_ens-sdms_cur2005_prob_pot.tif"
3.7 "../data/sdms/current/Pinus_brutia_ens-sdms_cur2005_prob_pot.tif"
4 "../data/sdms/current/Pinus_sylvestris_ens-sdms_cur2005_prob_pot.tif"
-10 "../data/other_layers/gHM_Europe.tif"
```



- Different ways for including 'undesired' features (things we don't want to conserve) in the prioritization analyses:
  - Negative weight: "avoid these features"
  - Cost layer: "avoid expensive areas"
  - Condition layer: decrease the biodiversity features' occurrence values in areas of poor condition (e.g. heavy pollution, human footprint)
- Cost and condition layers affect many other features at once → single layer can have a great impact to the prioritization outcome
- General recommendation: cost layer for direct land-acquisition costs (if data exists), negative weighted layers for opportunity costs

06

# Account for existing protected areas

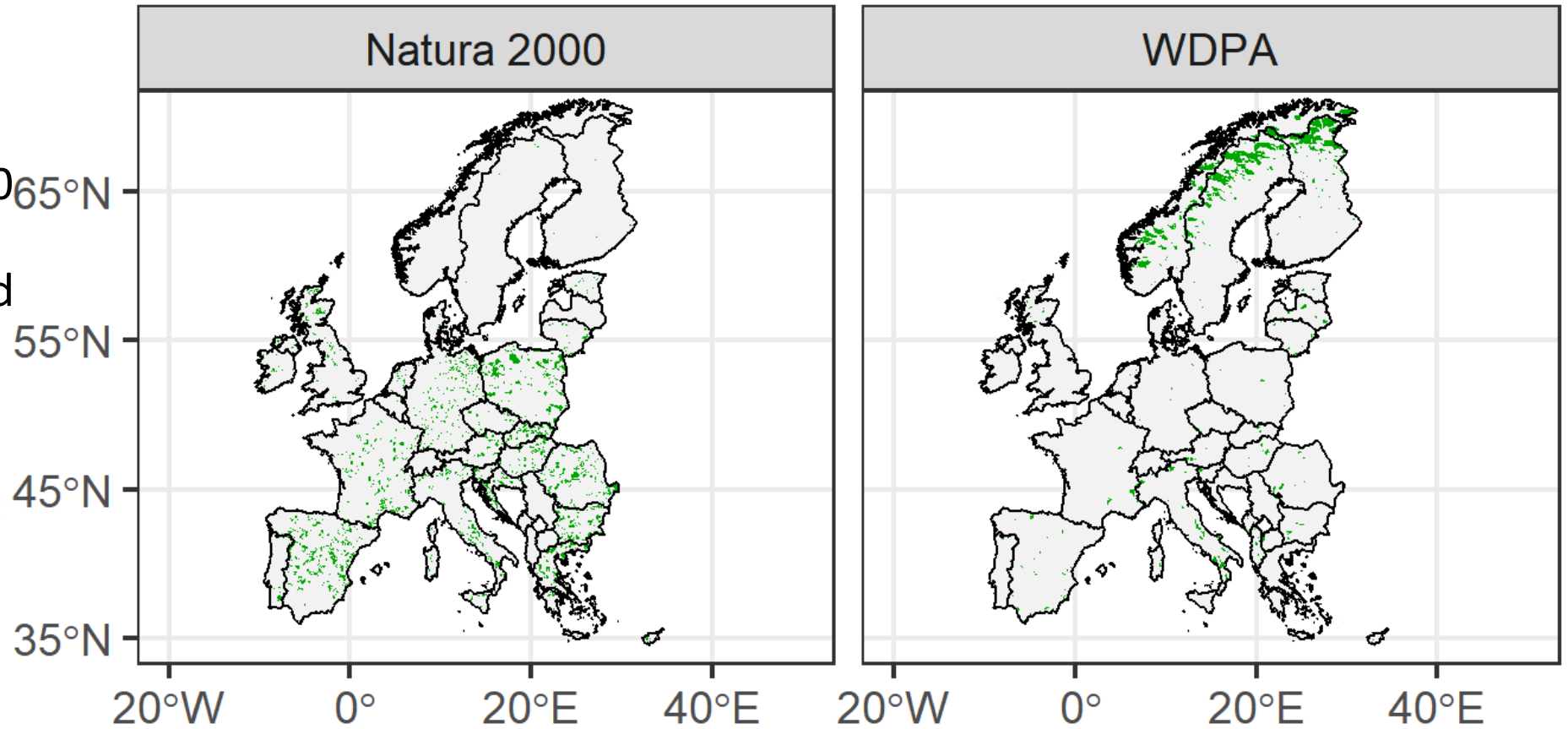
Add existing PAs as a hierarchic mask

- Often, one desires to account for the current PAs
  - evaluation of existing network
  - cost-efficient expansion of the current network
- In Zonation, this is achieved using ‘hierarchic mask’
  - top-priorities become forced in the mask (e.g. PAs)
  - allows identification of the “next-best” areas that would best complement the network

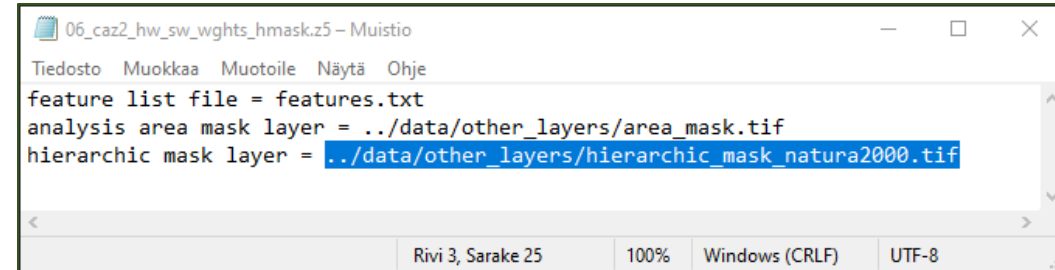
# 06

## Protected areas across Europe

- Protected areas (dark green) receive automatically the highest priorities
- Two sets: Natura 2000 areas & World Database of Protected Areas (IUCN categories 1a, 1b, 2)
  - Here we test the Natura 2000 dataset



1. Specify the hierarchic mask layer (current PAs) in the settings.z5 file. Save edits & run the analysis.
2. Explore curves. Using hierarchic mask creates a “kink” in the curve. Why?
3. Explore the rank map. Now the highest priorities are in the current PAs.
4. Adjust the colour scheme of the rank map to represent existing PAs with black. (Hint: use output curves to find the percentage coverage of protected areas.)

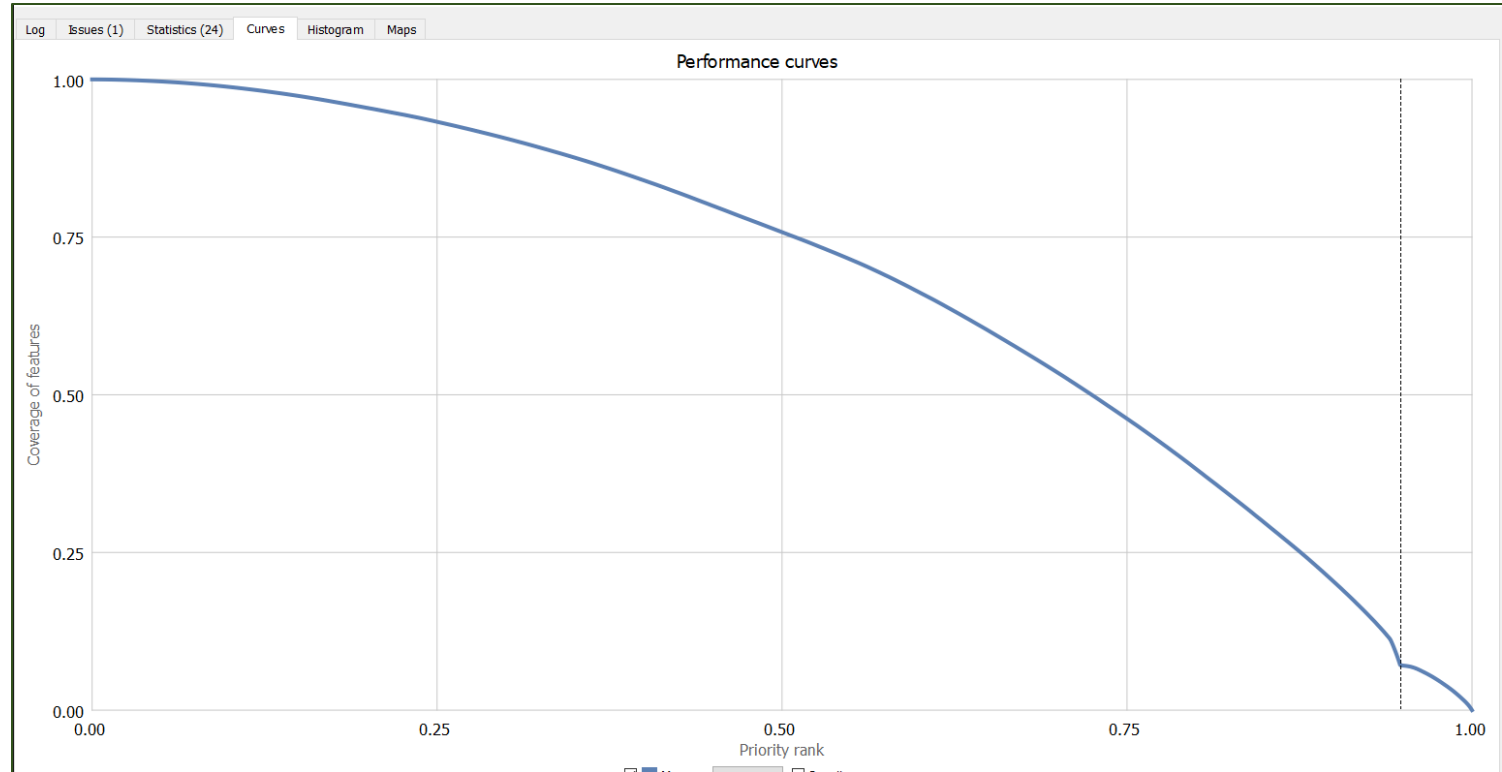


A screenshot of a text editor window titled "06\_caz2\_hw\_sw\_wghts\_hmask.z5 - Muistio". The window contains the following text:

```
Tiedosto Muokkaa Muotoile Näytä Ohje
feature list file = features.txt
analysis area mask layer = ../data/other_layers/area_mask.tif
hierarchic mask layer = ../data/other_layers/hierarchic_mask_natura2000.tif
```

The text is displayed in a monospaced font. The status bar at the bottom shows "Rivi 3, Sarake 25", "100%", "Windows (CRLF)", and "UTF-8".

1. How many features have over 10% of their distributions within the current PA network? (Hint: take your mouse in the “kink” and click – you should move in the histogram tab)
2. Go back to curves. How much more land needs to be protected so that at least 25% of every features’ distributions would be covered? Based on your analysis, is the current PA network sufficient?



- Add all the species to the analysis & test all marginal loss rules. Explore the curves and histograms.
  - features.txt file for this can be found from folder 00\_extra\_tasks
  - How do the options differ?
- Change the hierarchic mask to the World Database of Protected Areas map (WDPA) and compare its effectiveness to the Natura 2000 network.

Well done! Now to save the  
world 😊

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