

A GRIM SCRIPT

Analysing Groyne Impacts on Morphology Script

A Grim Script (Analysing Groyne Impacts on Morphology Script) is a freely available Python plugin for the open source GIS program QGIS, which provides a set of tools for quickly and easily examining the impacts of groynes on beach morphology and sediment transport.

This document is a user guide for the plugin, giving step by step instructions for its use and a high level overview of some of the technical details. The first section gives some background information about the program, and instructions for installing it. The next section deals with using the program itself. First is information on opening the plugin and navigating between screens. Next is information on using the Groyne Elevation Analysis tool within the program, and after that information on using the Beach Profile Generation tool. The third main section gives some details about how to interpret the outputs from these programs, along with some suggestions on how to use them in your own analysis. Finally is a broad overview of how the program automatically constructs groyne cells.

Script Format

Grim is implemented as a Python QGIS plugin. It adds a button to the QGIS interface that can be clicked to bring up a series of screens, which guide you through the analysis process. This format was chosen as it is more user friendly than a simple PYQGIS script, and the complexity of a standalone application was not required.

Installation

To install the script, copy the folder “*Grim*” to your QGIS plugins folder. This will look similar to “*C:\Users\Thomas\.qgis2\python\plugins*”. The plugin will then be loaded the next time you start QGIS.

Using the Plugin

After installation, the icon for the Grim plugin will appear on your QGIS toolbar (Figure 1). Click it to begin the program.

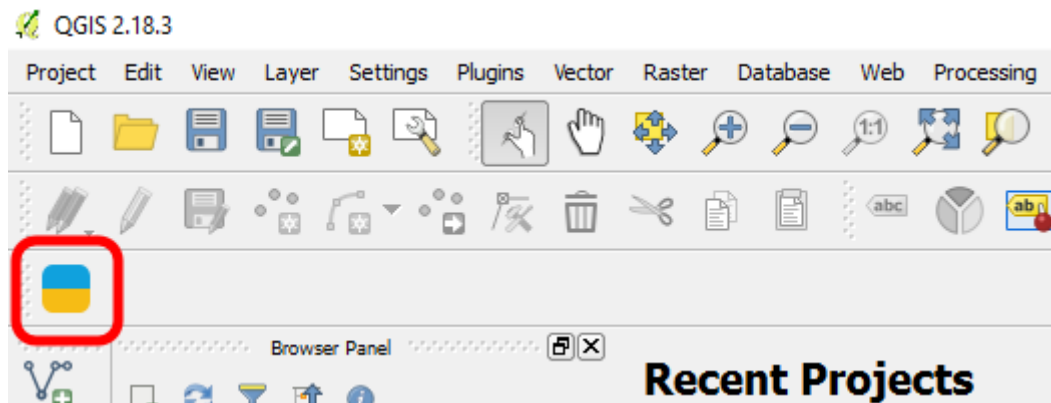


Figure 1: The Grim icon on the QGIS toolbar.

Alternatively, you may start the plugin by navigating to the *Plugin* menu, then the *Grim* submenu, and clicking the *Grim* menu item (Figure 2).

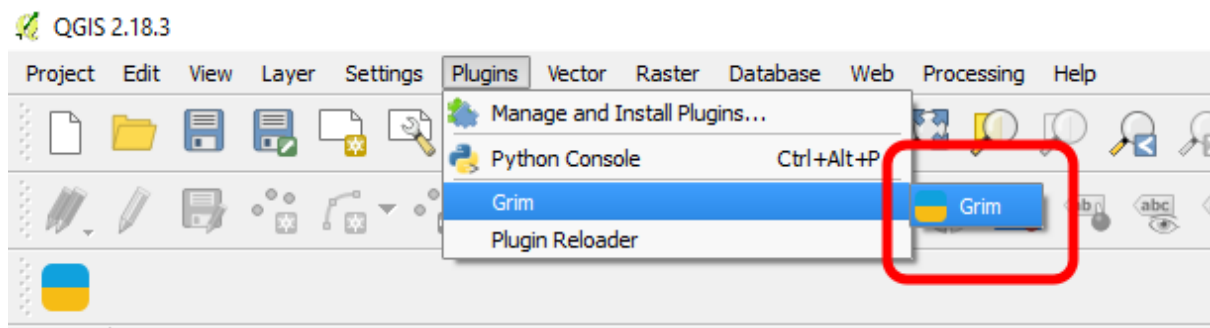


Figure 2: The Grim menu item within the Plugins menu.

Once opened, the first screen displayed is the welcome screen (Figure 3).



Figure 3: The welcome screen, the first screen to be displayed.

Grim includes two tool that are designed to simplify the process of analysing the impacts of groynes on beach morphology and sediment transport. This screen allows you to choose which tool you would like to use.

1. *Groyne Elevation Analysis*: This tool takes one or more elevation rasters covering the same area (normally created from LiDAR data, but DEMs from any source can be used), showing an area of beach at different times, along with the locations of groynes. It then calculates the area of each groyne cell, and the average elevation and volume of beach material within it. This can provide an indicator of the effects of a groyne field on beach morphology, showing spatial, and if multiple rasters are used, temporal variations. For more information, see the section **Groyne Elevation Analysis**.
2. *Beach Profile Generation*: This tool takes one or more elevation rasters covering the same area, and one or more lines along which elevation profiles are created and stored as both a shapefile and CSV spreadsheet file. For more information, view the **Beach Profile Generation** section.

To select a tool, click the appropriate radio button (circle). To navigate between pages in the plugin, use the

3. *Previous button*: Click this to go to the previous page. In this case, as we are on the first page already, the button has been disabled.
4. *Next button*: Click this to go to the next page. In this case, as no tool has been selected, the button has been disabled.

In certain situations such as this, the next button is disabled until an appropriate choice has been made. Along the bottom of the screen, there are two more buttons:

5. *Help button*: This can be clicked at any time to open this help file. The file is opened in a new window, and your progress will not be lost.
6. *Close button*: Click this to close the window. Please note that all progress will be lost if you do this.

The plugin also contains the standard interface elements common to most Windows applications.

7. *What is this? button*: Click this, and then hover over items in the window. If the cursor icon changes from a red circle with a line through it to a pointer with a question mark, the item can be clicked to find out more information (Figure 4).
8. *Exit button*: As with the *Close Button*, this can be clicked to exit the dialogue, but be aware that if you do so all changes will be lost.

Now that you have a basic understanding of how to navigate around the plugin, select the tool that you would like to use. Notice that the *Next button* becomes enabled. Click it to proceed to the next screen.

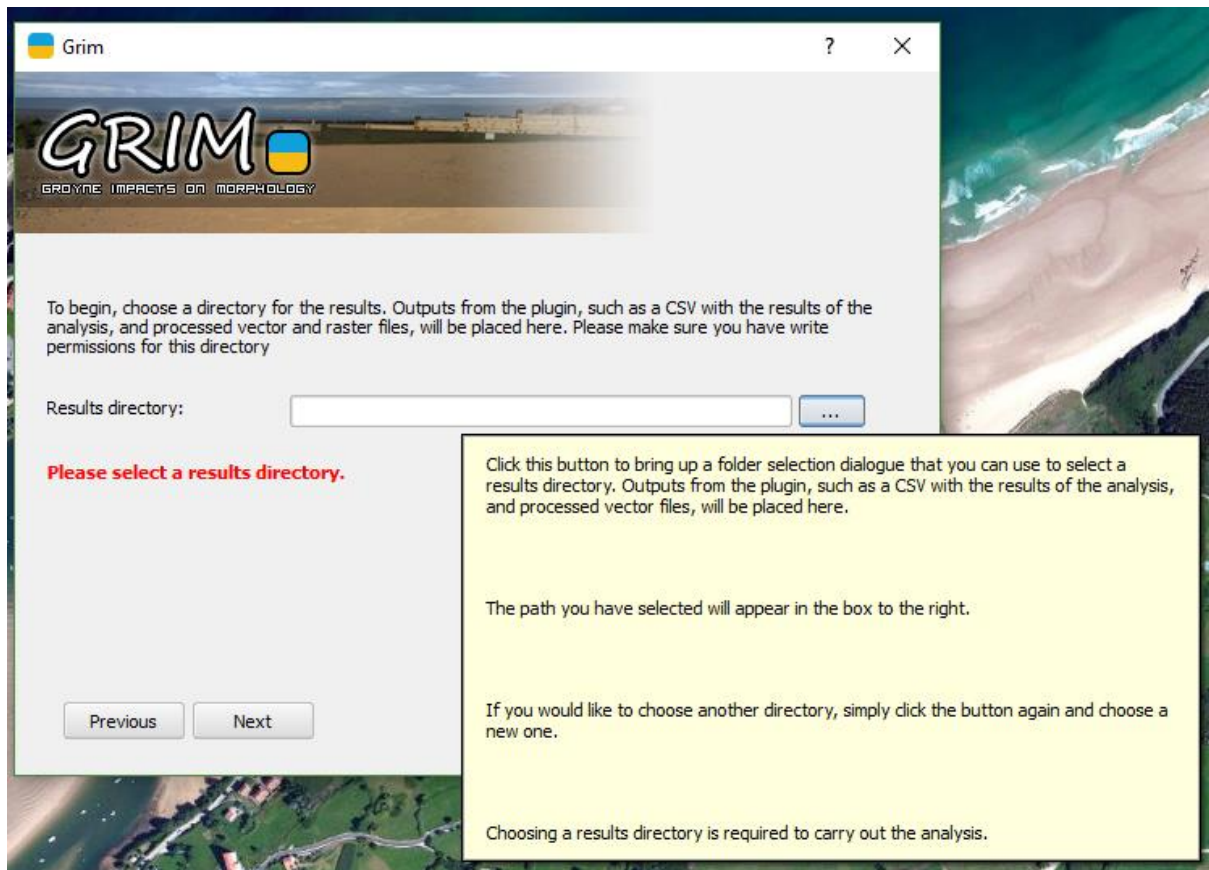


Figure 4: An example of a “What is this?” dialogue.

Groyne Elevation Analysis Tool

This section is concerned with the Groyne Elevation Analysis Tool. For details on the Beach Profile Generation Tool, please see the next section.

Results Directory Selection

The next screen you will be presented with is the results directory selection screen (Figure 5). Grim produces several outputs, including a CSV file with the results in a numeric format, and a shapefile representing groyne cells, with things such as area and volume stored as attributes. This screen allows you to select where Grim places these outputs. **It is highly recommended that you choose an empty directory**, to avoid the chance of any existing files being overwritten. To select a directory, first click the “...” button, and a directory selection window will appear. Select the appropriate directory, and then click “Select Folder” at the bottom right of the screen. The path to this directory will then be displayed in the box.

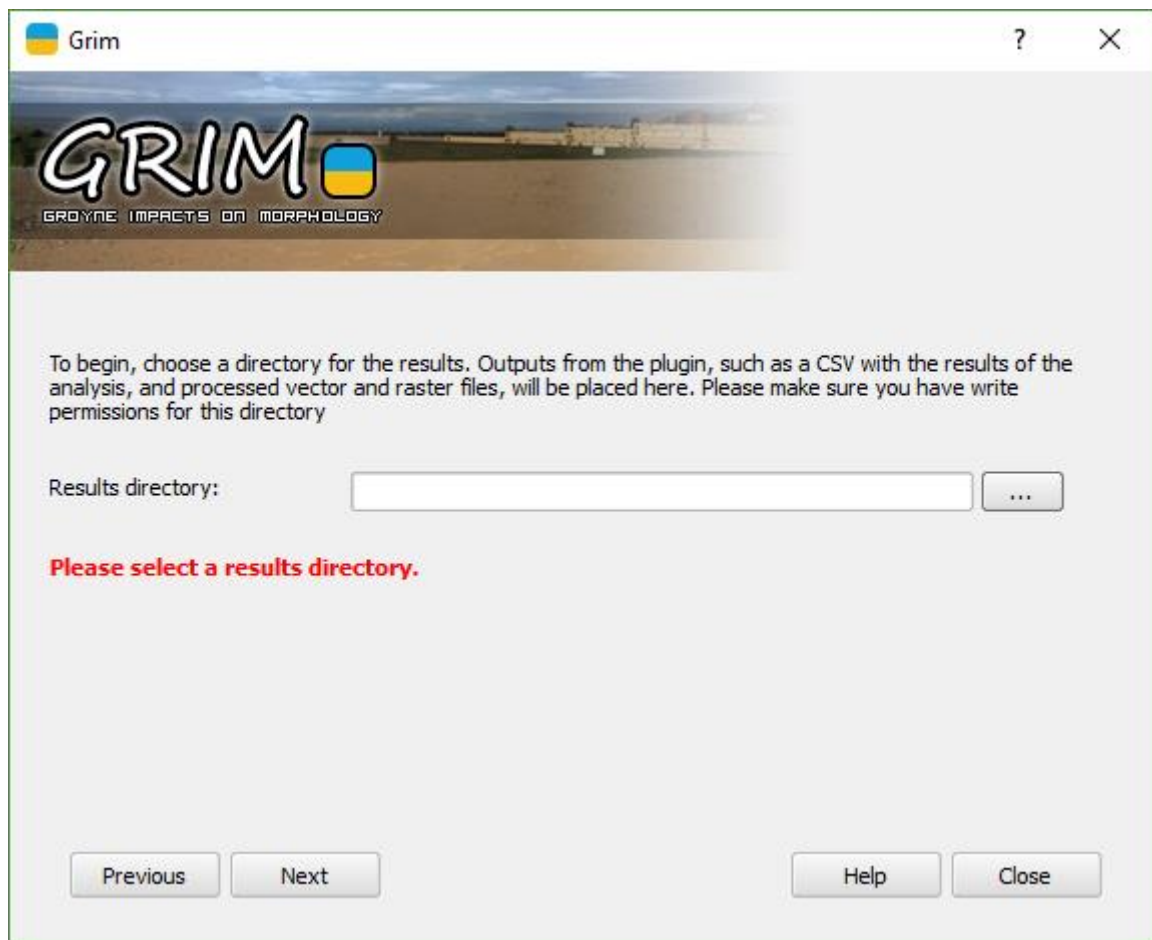


Figure 5: The results directory selection screen.

Notice the red text beneath the directory selection widgets highlighting that a directory has not yet been selected. While you can move to subsequent pages without selecting some inputs, you will not be able to carry out the analysis until all required inputs have been selected. Click the *Next button* to continue.

Elevation Raster Selection

Next is the elevation raster selection screen (Figure 6). Grim analyses elevation data in the form of a raster digital elevation model. Although these are normally produced using LiDAR, DEMs produced by any means may be used. For Grim to work, the rasters must at least cover the area covered by the groyne cells. If the rasters are to be compared with each other, it is also recommended that they have the same resolution and height units.

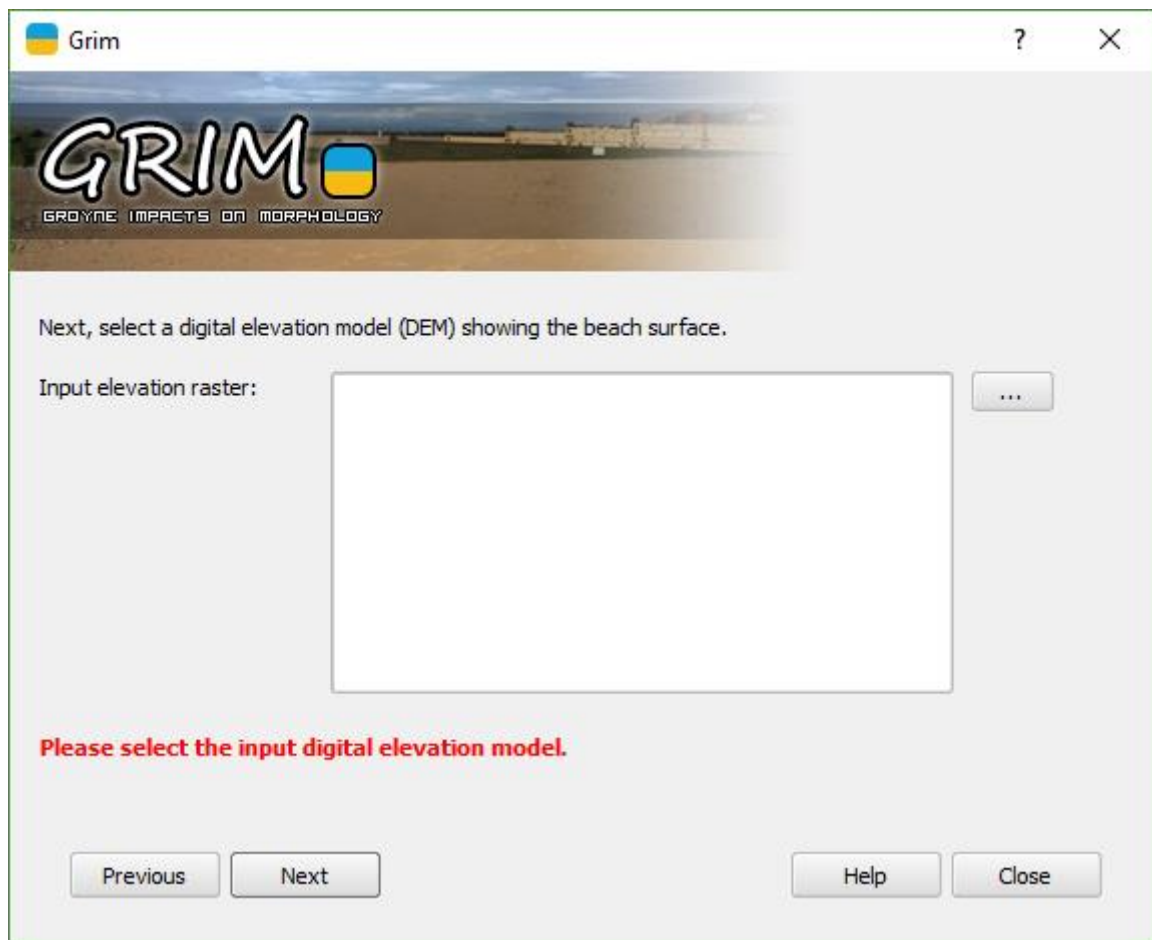


Figure 6: The elevation raster selection screen.

To select one or more rasters, click the “...” button to open the file selection dialogue. To select a single raster, click it and select *Open* at the bottom right of the screen. To select more than one raster, press control while clicking each raster in turn. Alternatively, click and drag your mouse to produce a box highlighting the files you would like to select.

Paths to your selected files will appear in the box. Selected rasters that are valid will appear green, while invalid layers will appear red (Figure 7). You cannot complete the analysis unless all selected files are valid. Once again, hit the *Next button* to continue.

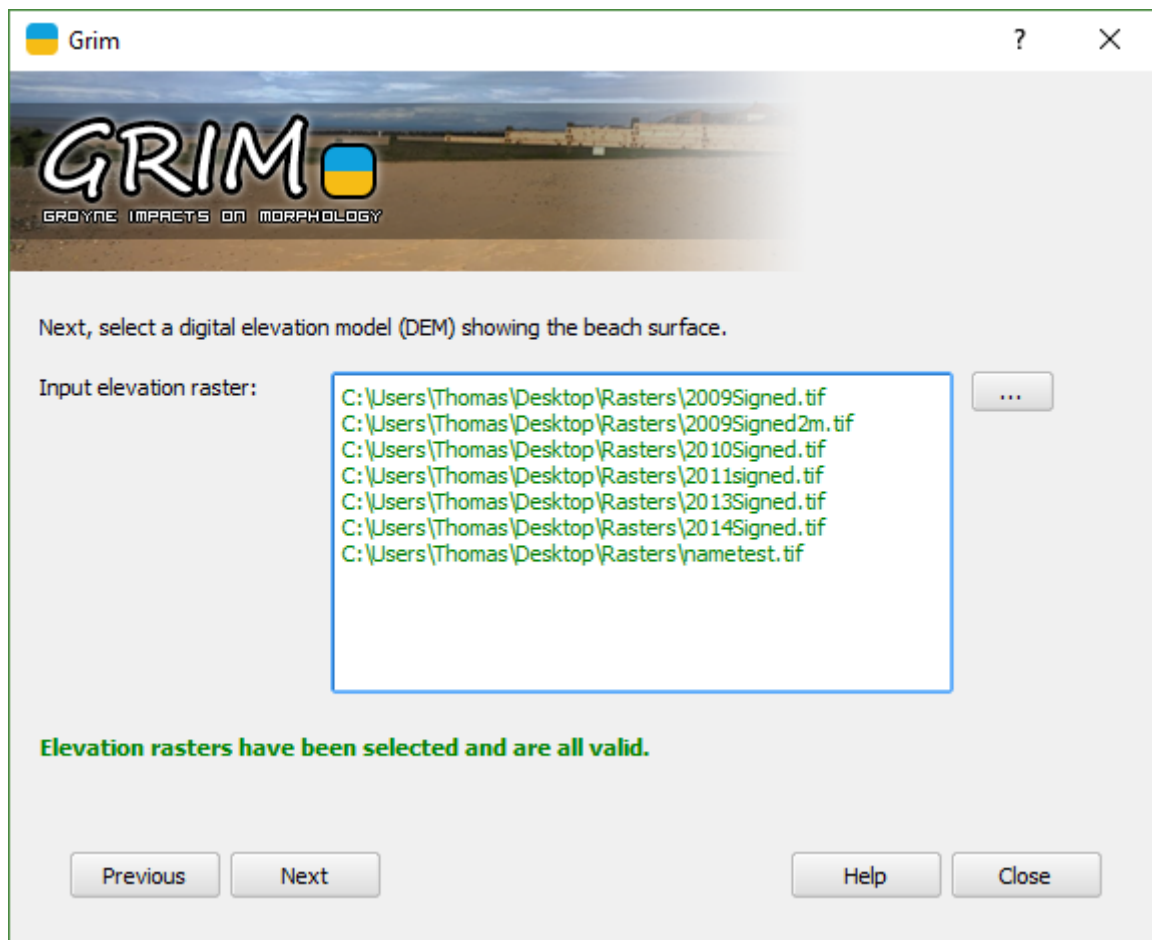


Figure 7: The Elevation Raster Selection Screen, with all selected layers found to be valid.

Groyne Input Method Selection

Grim calculates the average elevation and volume of material within **groyne cells**. This is the name given to the area between two or more groynes. You can either use groyne cells you have created yourself, or upload the locations of the groynes themselves and Grim will delineate the groyne cells for you.

On the groyne input method selection screen (Figure 8), you can select how you would like to input the locations of groyne cells or groynes.

- Single polygon shapefile, with each groyne cell as a separate feature
- Multiple polygon shapefiles, with a single groyne cell in each
- Single line shapefile, with each groyne as a separate feature
- Multiple line shapefiles, with a single groyne in each
- Multiple multipoint shapefiles, with a single groyne in each

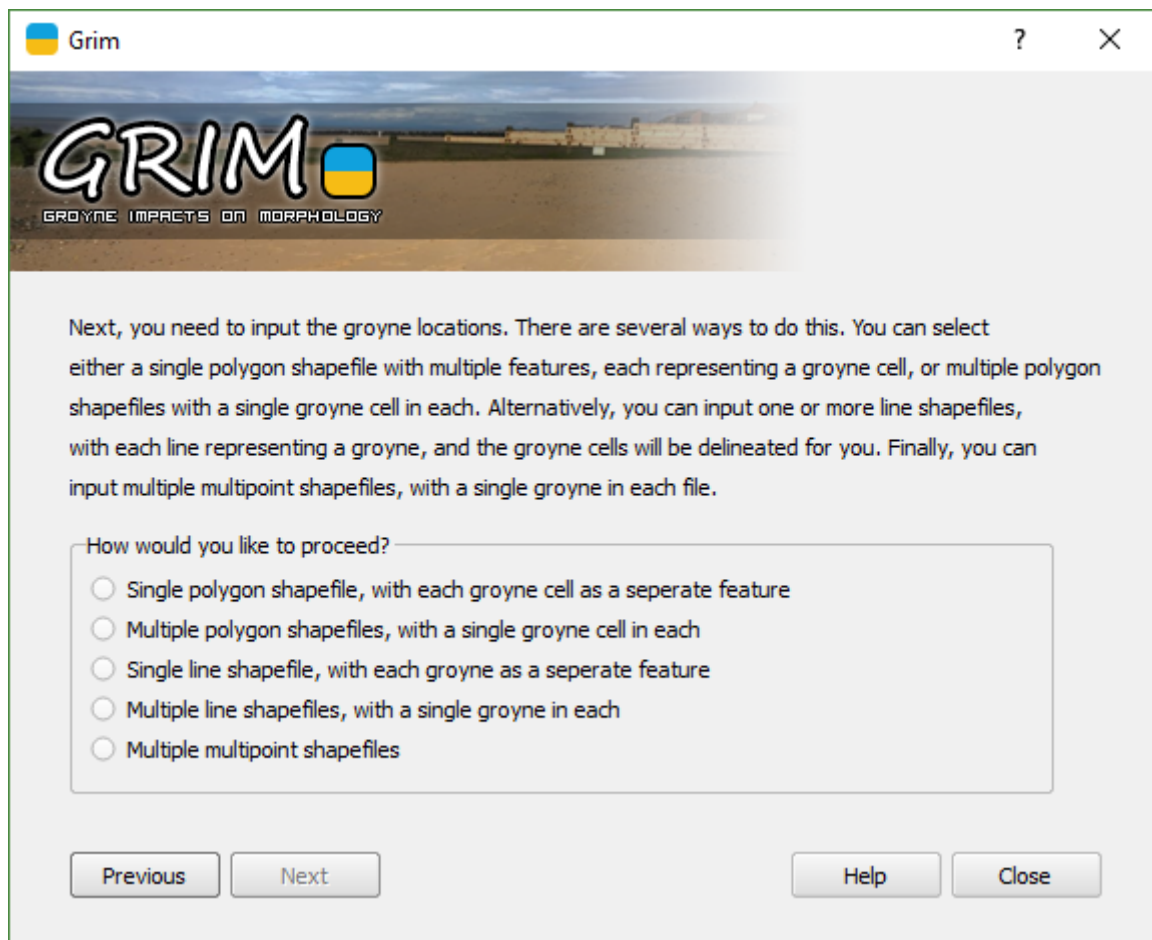


Figure 8: The Groyne Input Method selection screen, with no option selected.

Select which method you would like to use, and hit *Next*. More information about each method can be found in the following sections.

Single polygon shapefile, with each groyne cell as a separate feature

This input takes a single polygon shapefile. It should contain one or more features, with each feature containing a single polygon representing a groyne cell (Figure 9).

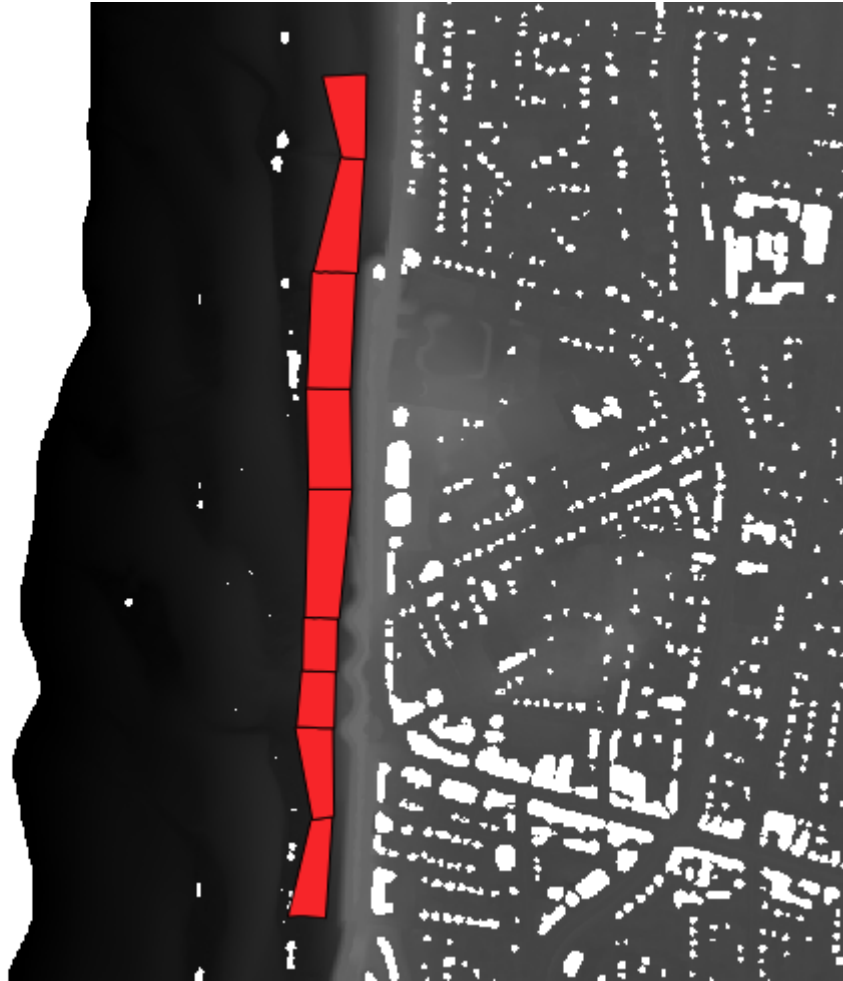


Figure 9: An example of a single shapefile containing multiple features, each representing a groyne cell, overlain over a raster digital elevation model (DEM).

To select the shapefile, click the “...” *button*, navigate to the appropriate file and then click “Open” at the bottom right of the screen. Hit the “Next” button to continue.

Multiple polygon shapefiles, with a single groyne cell in each

This input takes multiple polygon shapefiles. Each shapefile is expected to contain a single feature, which is a polygon representing a single groyne cell. To select the shapefiles, click the “...” *button* and navigate to the appropriate files. To select more than one file, hold control while clicking, or click and drag your mouse to create a rectangle, overlapping with the files you wish to select. It is important to note that Grim processes the files in the order you input them. You can see this order in the box along the bottom of the files selection screen. For example in Figure 10, it can be seen that the files are ordered from *mypoly1.shp* to *mypoly4.shp*. Files are ordered in the order they are shown in the file selection screen. To change this order, *right click* in the file selection screen and select *Sort by*. Available options include *Name* and *Date Modified*.

File name: "mypoly1.shp" "mypoly2.shp" "mypoly3.shp" "mypoly4.shp" ▼

Figure 10: The box at the bottom of the screen will show the order that the shapefiles have been input.

There is currently no facility to sort input files within Grim. If you would like to change the order, a simple method is naming the files in the correct order and selecting the *Sort by* option. Once you have selected your polygons, hit the *Next Button* to continue.

Single line shapefile, with each groyne as a separate feature

This input takes a single line shapefile. It should contain one or more features, with each feature containing a single line representing a single groyne (Figure 11). To select the shapefile, click the *"..." button*, navigate to the appropriate file and then click *"Open"* at the bottom right of the screen. Hit the *Next* button to continue.

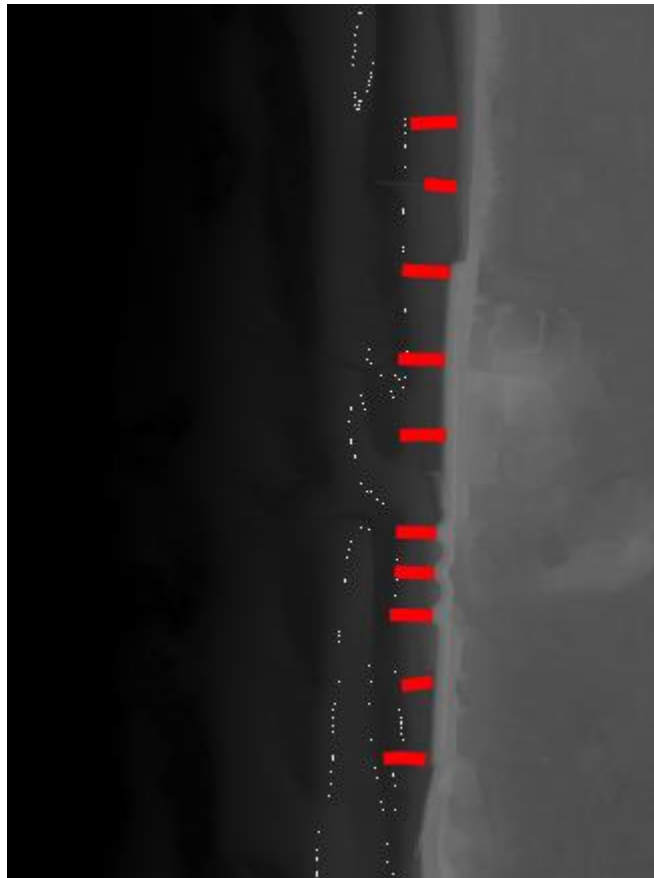


Figure 11: An example of a single line shapefile with multiple features, with each feature containing a single line representing a groyne.

For more details on how Grim creates groyne cells from input groynes, view the **How Grim Creates Groyne Cells** section.

Multiple line shapefiles, with a single groyne in each

This input takes multiple line shapefiles. Each shapefile is expected to contain a single feature, which is a line representing a single groyne (Figure 12). To select the shapefiles, click the “...” *button* and navigate to the appropriate files. To select more than one file, hold control while clicking, or click and drag your mouse to create a rectangle, overlapping with the files you wish to select. It is important to note that Grim processes the files in the order you input them. You can see this order in the box along the bottom of the files selection screen (Figure 13). For example in Figure 11, it can be seen that the files are ordered from *LineGroyne1.shp* to *LineGroyne4.shp*. Files are ordered in the order they are shown in the file selection screen. To change this order, *right click* in the file selection screen and select *Sort by*. Available options include *Name* and *Date Modified*.

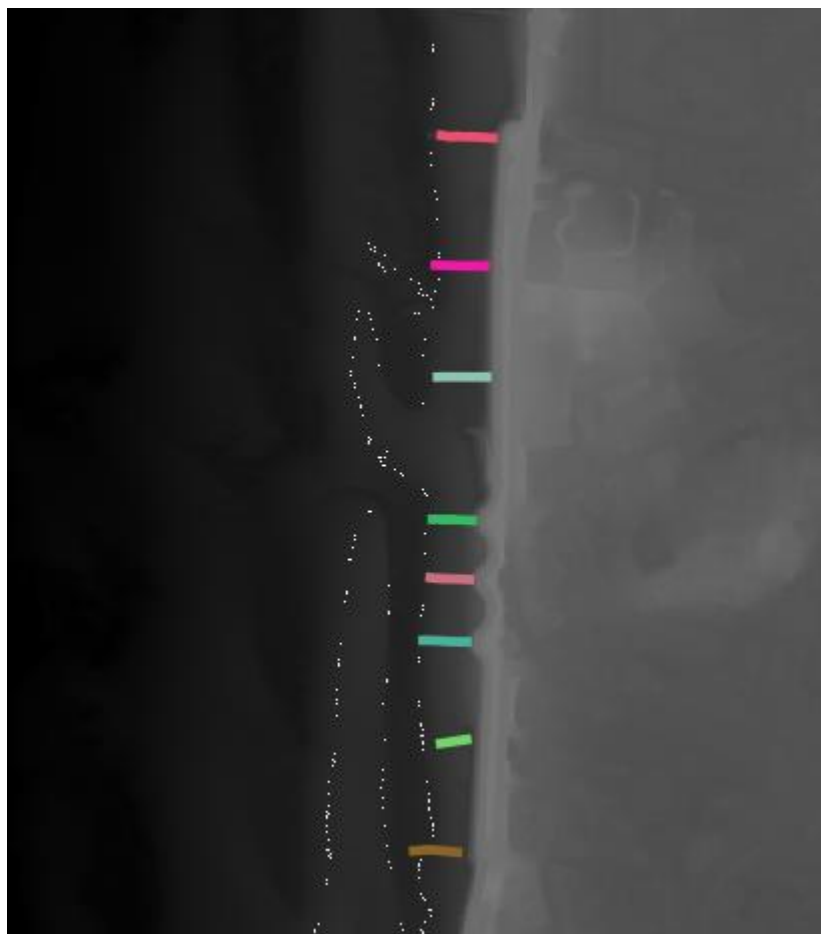


Figure 12: An example of multiple line shapefiles, with each shapefile representing a single groyne.

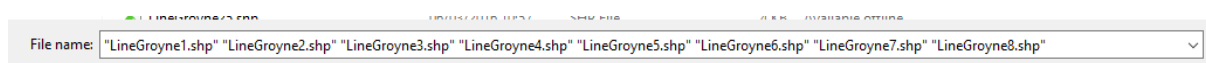


Figure 13: The box at the bottom of the screen will show the order that the shapefiles have been input.

There is currently no facility to sort input files within Grim. If you would like to change the order, a simple method is naming the files in the correct order and selecting the *Sort by* option. Once you have selected your polygons, hit the *Next button* to continue.

For more details on how Grim creates groyne cells from input groynes, view the **How Grim Creates Groyne Cells** section.

Multiple point shapefiles, with a single groyne in each

This input takes multiple multipoint shapefiles. Each shapefile is expected to contain multiple features, with a single point in each feature. The points in each shapefile are expected to run along the length of a single groyne (Figure 16). To generate a groyne cell from these points, each shapefile requires an attribute to order the points by. For example, the point at one end of the groyne may have a value of 1, the next point along 2 and so forth. These are used to create a line from the points. Alternatively, Grim will attempt to order the points using their field ID. This is normally the order in which the features were added to the shapefile. To select which field to order the points in the shapefiles by, use the drop down box (Figure 14). This box will only display attributes present in all uploaded shapefiles.

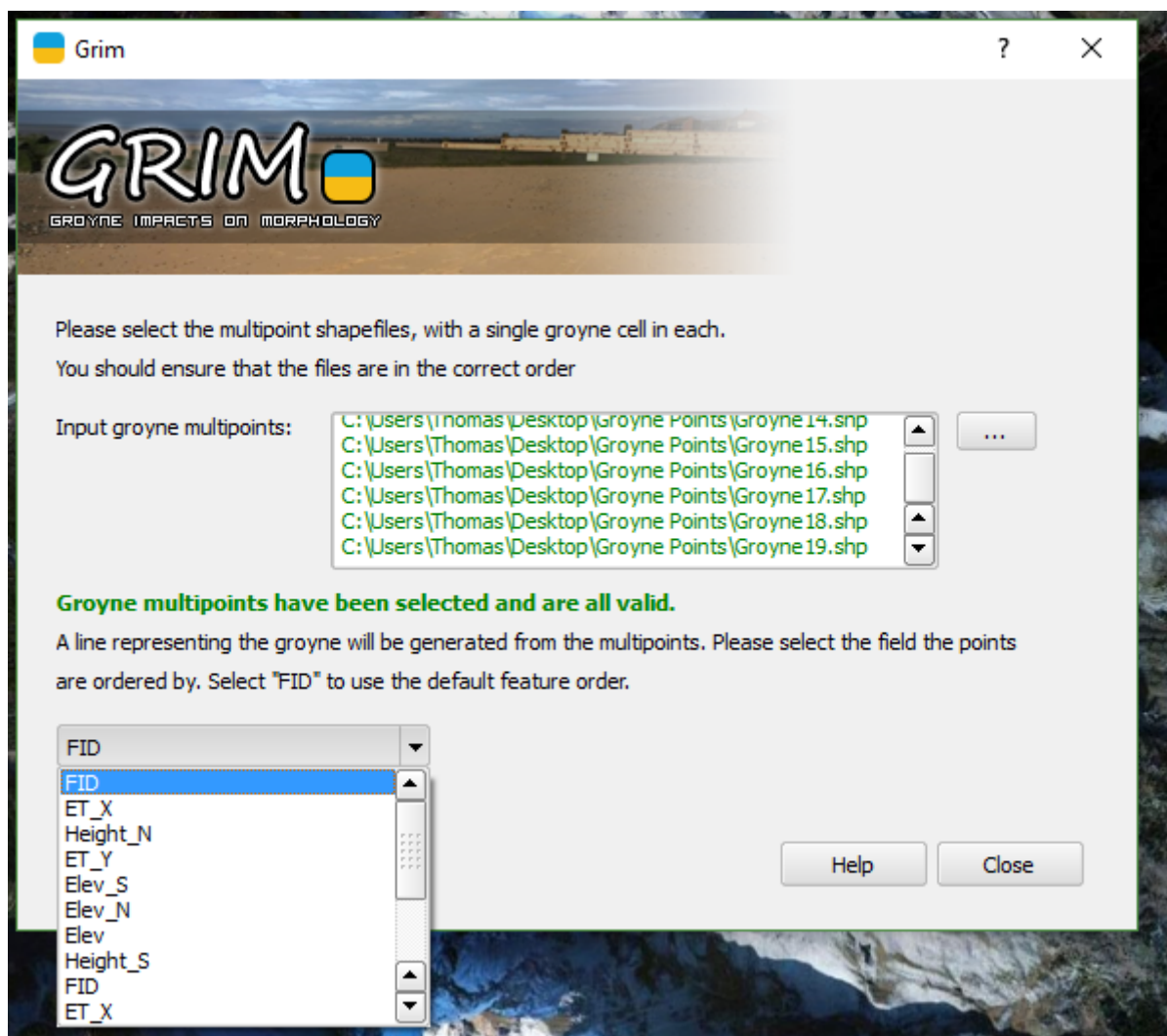


Figure 14: The drop down box you can use to select which field to order the points by. Alternatively, select FID to order the points by their feature ID.

To select the shapefiles, click the “...” button and navigate to the appropriate files. To select more than one file, hold control while clicking, or click and drag your mouse to create a rectangle, overlapping with the files you wish to select. It is important to note that Grim processes the files in the order you input them. You can see this order in the box along the bottom of the files selection screen. For example in Figure 15, it can be seen that the files are ordered from *LineGroyne1.shp* to *LineGroyne4.shp*. Files are ordered in the order they are shown in the file selection screen. To change this order, *right click* in the file selection screen and select *Sort by*. Available options include *Name* and *Date Modified*.

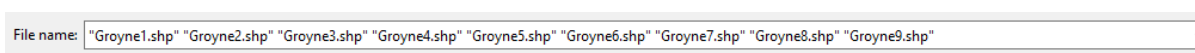


Figure 15: The box at the bottom of the screen will show the order that the shapefiles have been input.

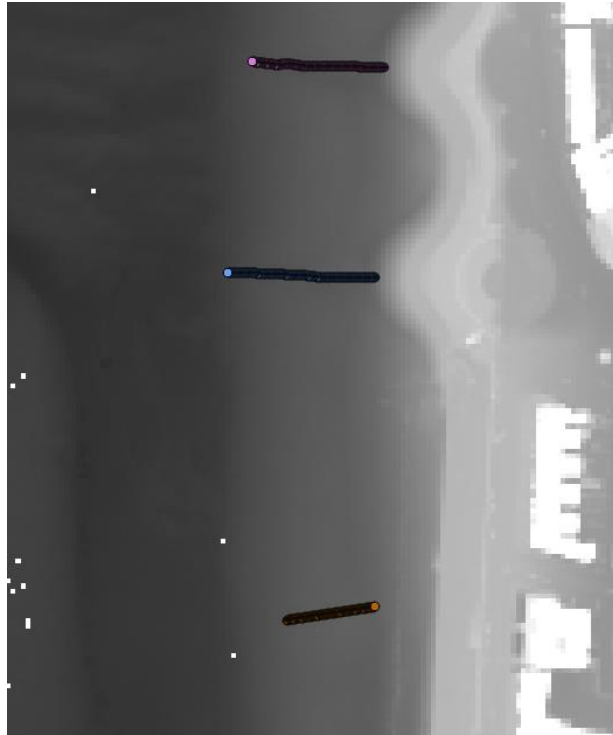


Figure 16: An example of multiple point shapefiles, where each shapefile represents a single groyne. The points are arranged in order along the groyne, running from one end to another.

For more details on how Grim creates groyne cells from input groynes, view the **How Grim Creates Groyne Cells** section.

Advanced Settings

The next screen is advanced settings (Figure 17). Here, you can choose a value to adjust all heights by, and therefore all resulting average height and volume calculations. For example, by entering -10, all elevations in the results will be reduced by 10. This can be useful in calculating elevations relative to a different datum than the one used in the input rasters.

The unit used is the height unit of the input elevation rasters. Use the arrows to increase or decrease the number by 0.1, or click the box and type a number of your choosing. Leaving the number at 0 will result in no changes being made to the results.



Figure 17: The Advanced Settings screen.

Click *Next* to continue to the final screen.

Calculate

The final page is the calculate screen (Figure 18). This contains a single button, *Calculate*, which can be clicked to perform the analysis, creating a results CSV and one or more shapefiles in your selected results directory.

If you have input all the required information, click the button to perform the analysis. If any required information is missing, a red label will be displayed and the button will be greyed out and you will be unable to click it. If this is the case, use the *Previous* button to go back and input the required data, and the *Next* button to return to this screen and click the button.

Please note that depending on the amount of data to be analysed, the analysis may take several minutes or more. During this time, the calculate screen will be displayed but you will be unable to interact with it. You will be notified when the analysis is complete.

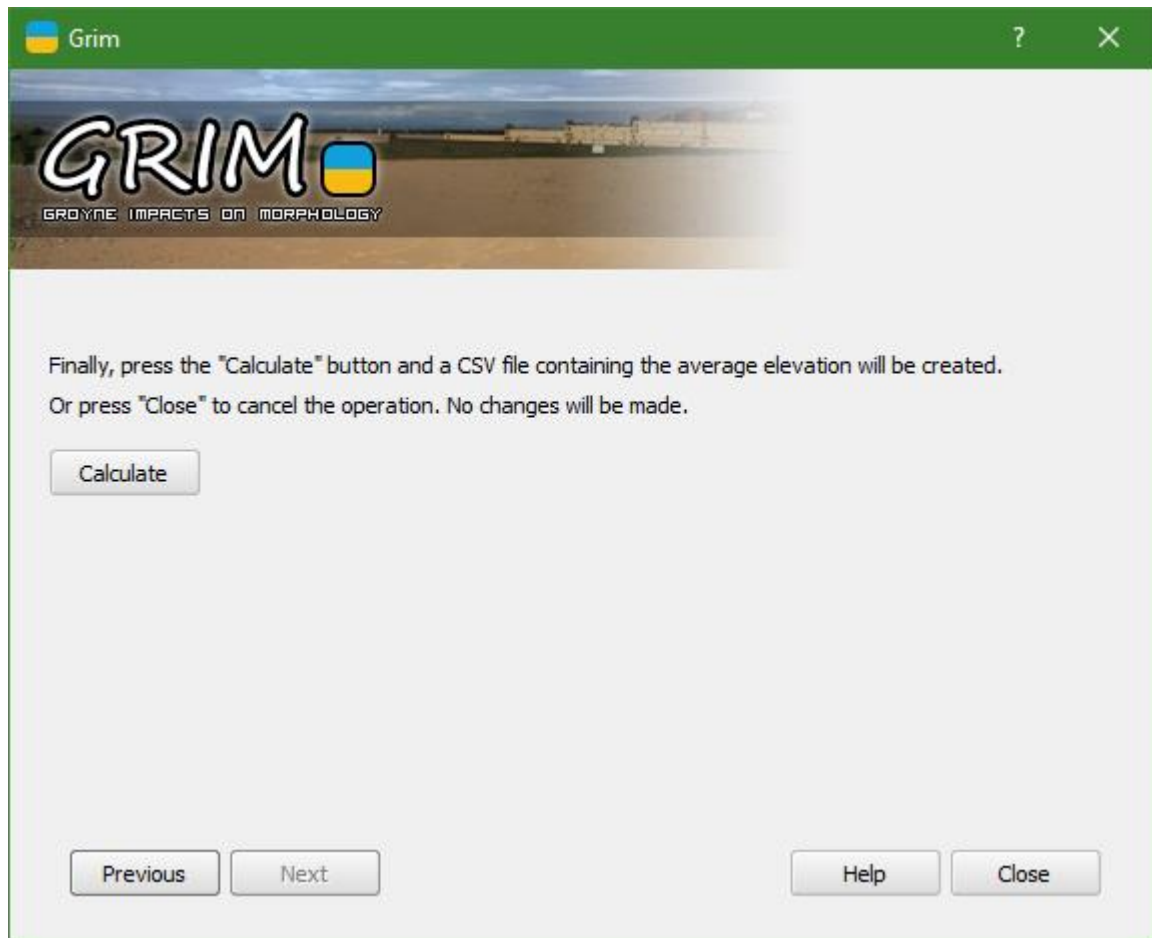


Figure 18: The Calculate screen, with all required information entered.

Analysis Complete

Once the analysis has been carried out, the analysis complete screen will be displayed (Figure 19). This will display some information about the outputs produced, and where to find them. The screen can now be closed.

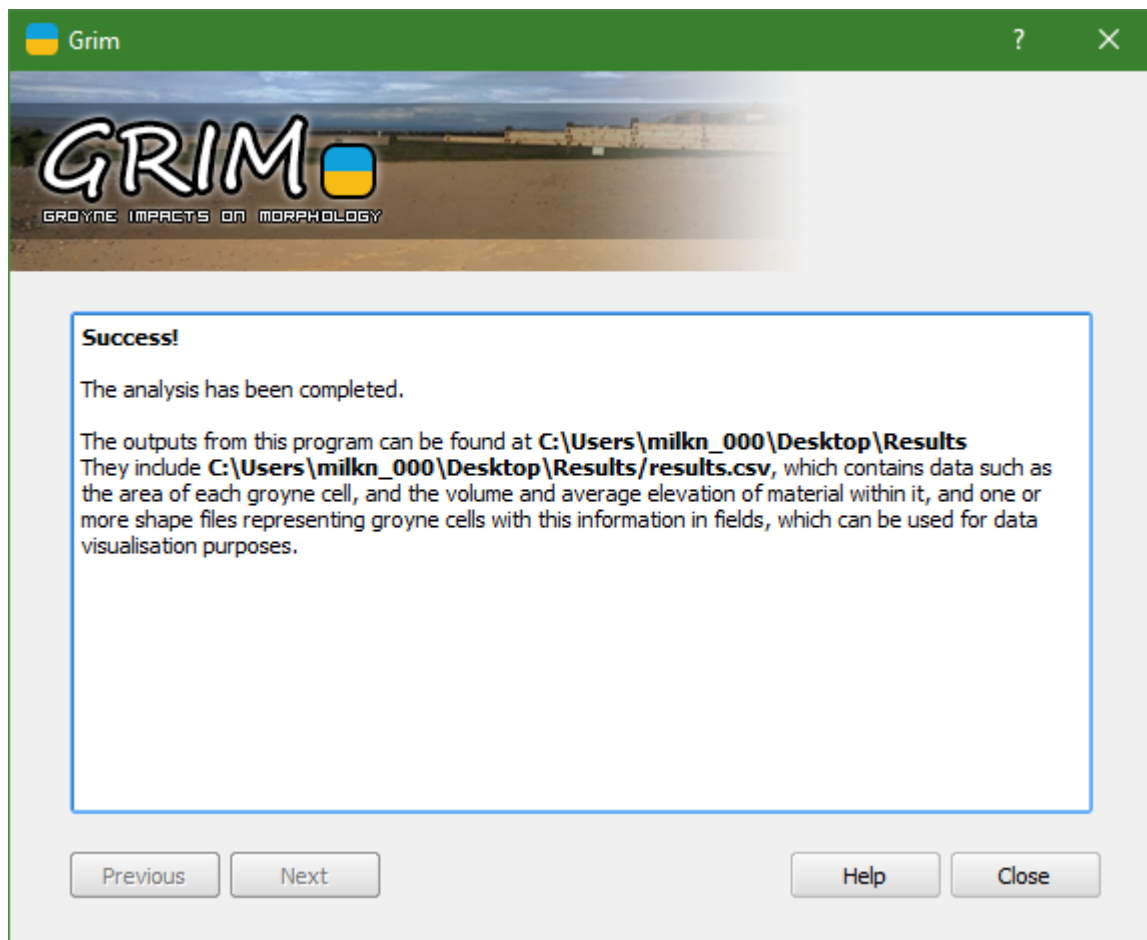


Figure 19: The Analysis Complete screen.

Beach Profile Generation Tool

This section is concerned with the Beach Profile Generation Tool. For details on the Groyne Elevation Analysis Tool, please see the previous section.

Results Directory Selection

The next screen you will be presented with is the results directory selection screen. Grim produces several outputs, including a CSV file with the results in a numeric format, and one or more point shapefiles with the elevation stored as attributes, which can be used for visualisation purposes. This screen allows you to select where Grim places these outputs. **It is highly recommended that you choose an empty directory**, to avoid the chance of any existing files being overwritten. To select a directory, first click the “...” button, and a directory selection window will appear. Select the appropriate directory, and then click “*Select Folder*” at the bottom right of the screen. The path to this directory will then be displayed in the box.

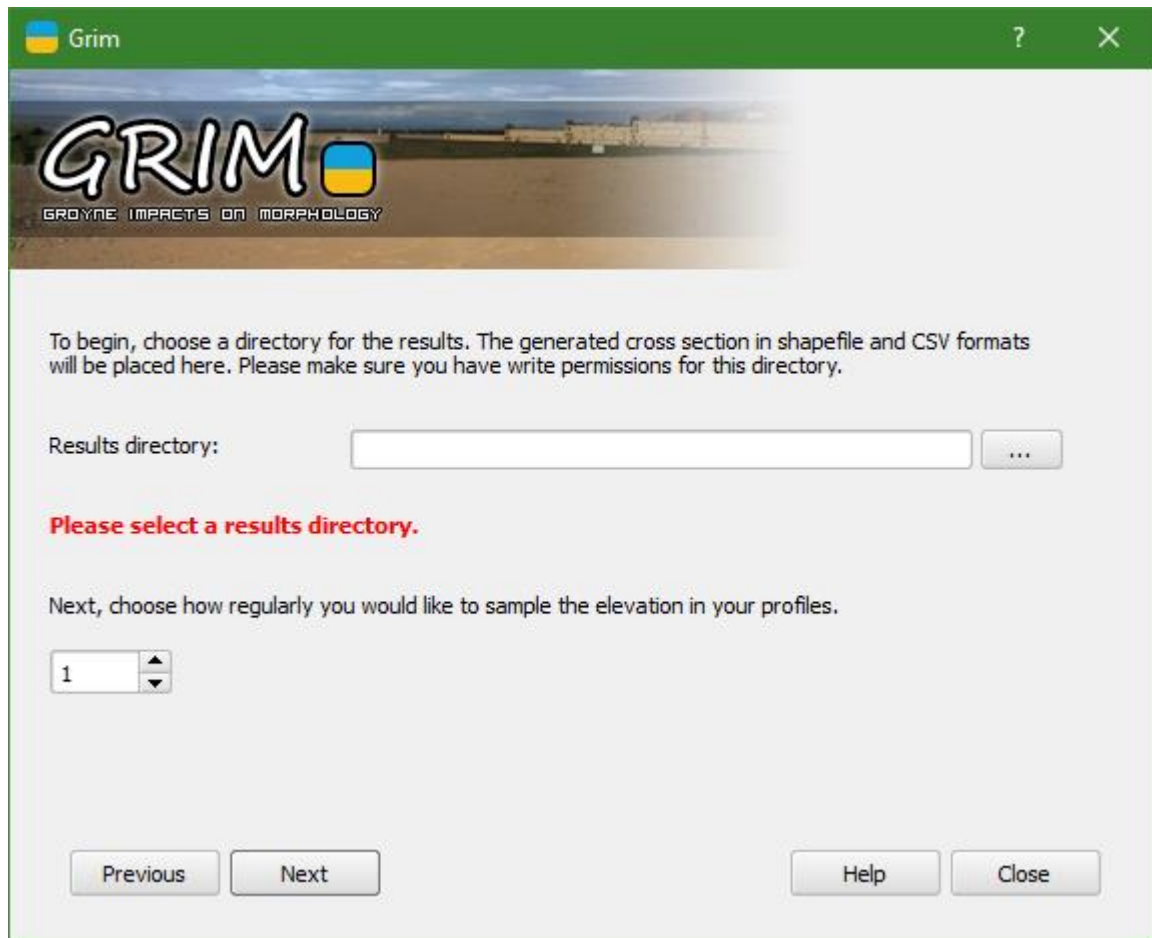


Figure 20: The Results Directory Selection screen.

Notice the red text beneath the directory selection widgets highlighting that a directory has not yet been selected. While you can move to subsequent pages without selecting some inputs, you will not be able to carry out the analysis until all required inputs have been selected.

This screen also allows you to input how regularly you would like to sample the elevation of your rasters. For example, if you input 10, the elevation of the raster every 10 map units along your profile line will be sampled. Use the up and down arrows to increase or decrease the value by one, or click in the box and type a number of your choosing. Then, hit *Next* to continue.

Elevation Raster Selection

Next is the elevation raster selection screen (Figure 21). Grim creates profiles by extracting elevation data from a raster digital elevation model. Although these are normally produced using LiDAR, DEMs produced by any means may be used.

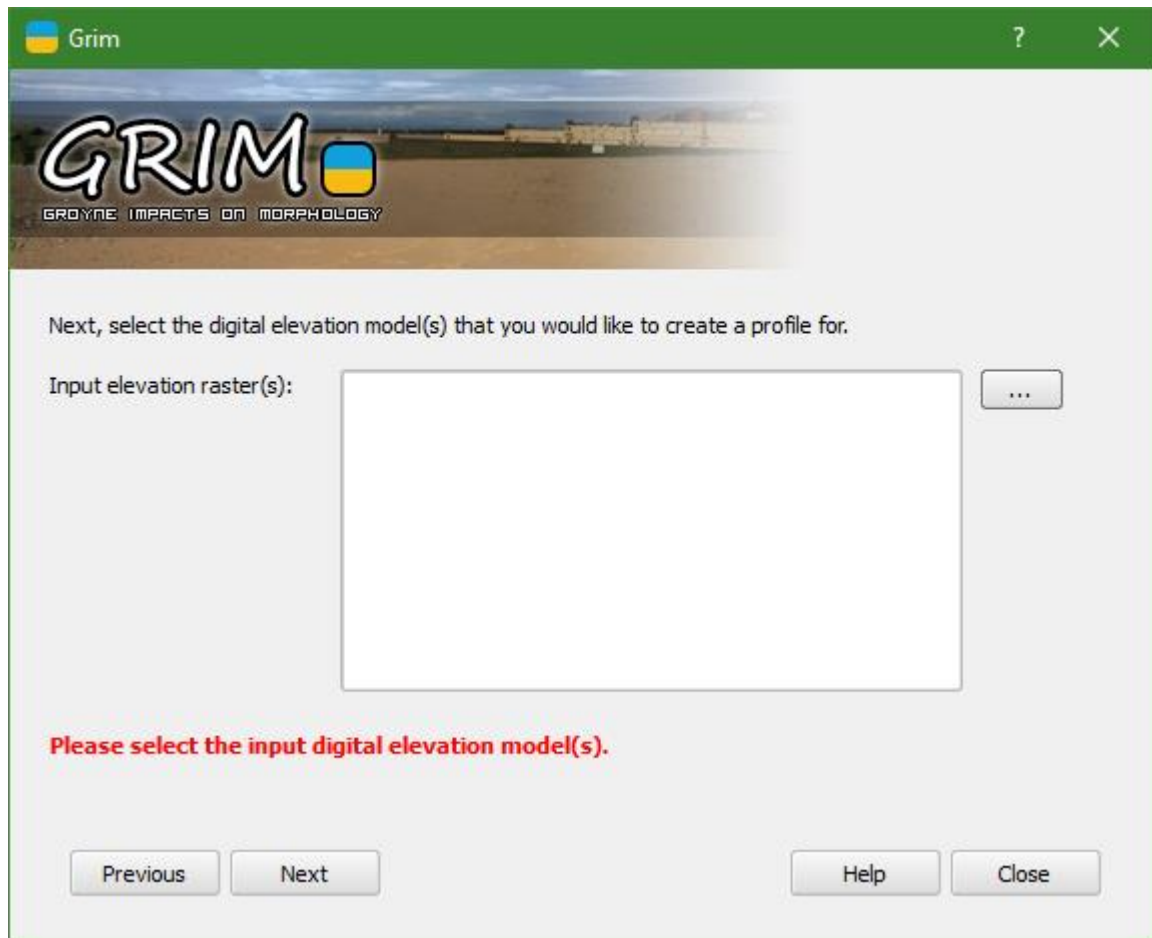


Figure 21: The Elevation Raster Selection screen.

To select one or more rasters, click the “...” button to open the file selection dialogue. To select a single raster, click it and select *Open* at the bottom right of the screen. To select more than one raster, press control while clicking each raster in turn. Alternatively, click and drag your mouse to produce a box highlighting the files you would like to select.

Paths to your selected files will appear in the box. Selected rasters that are valid will appear green, while invalid layers will appear red. You cannot complete the analysis unless all selected files are valid. Once again, hit the *Next button* to continue.

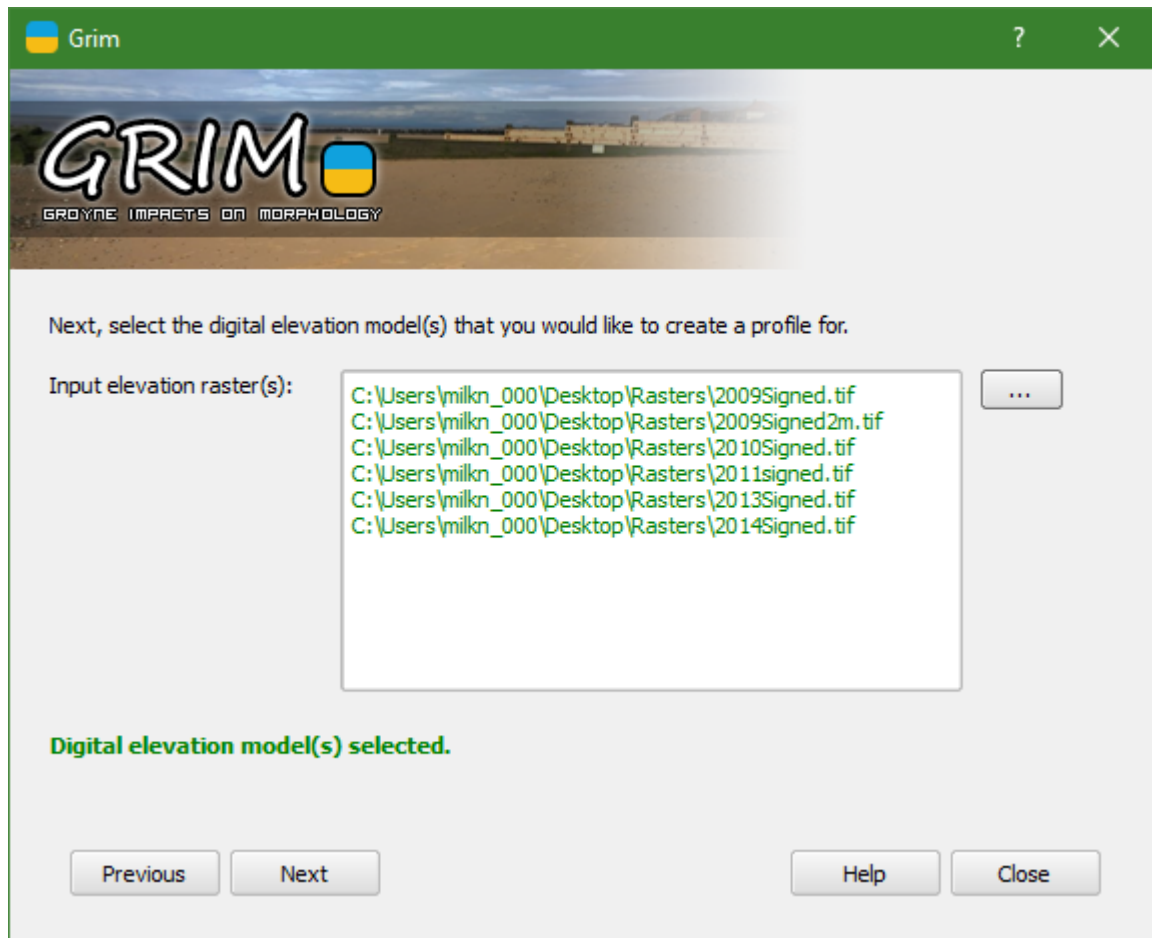


Figure 22: The Elevation Raster Selection Screen, with all selected layers found to be valid.

Profile Line Selection

Next, select the lines along which you would like to create a profile (Figure 23). You should select one or more line shapefiles, with a single profile line in each file.

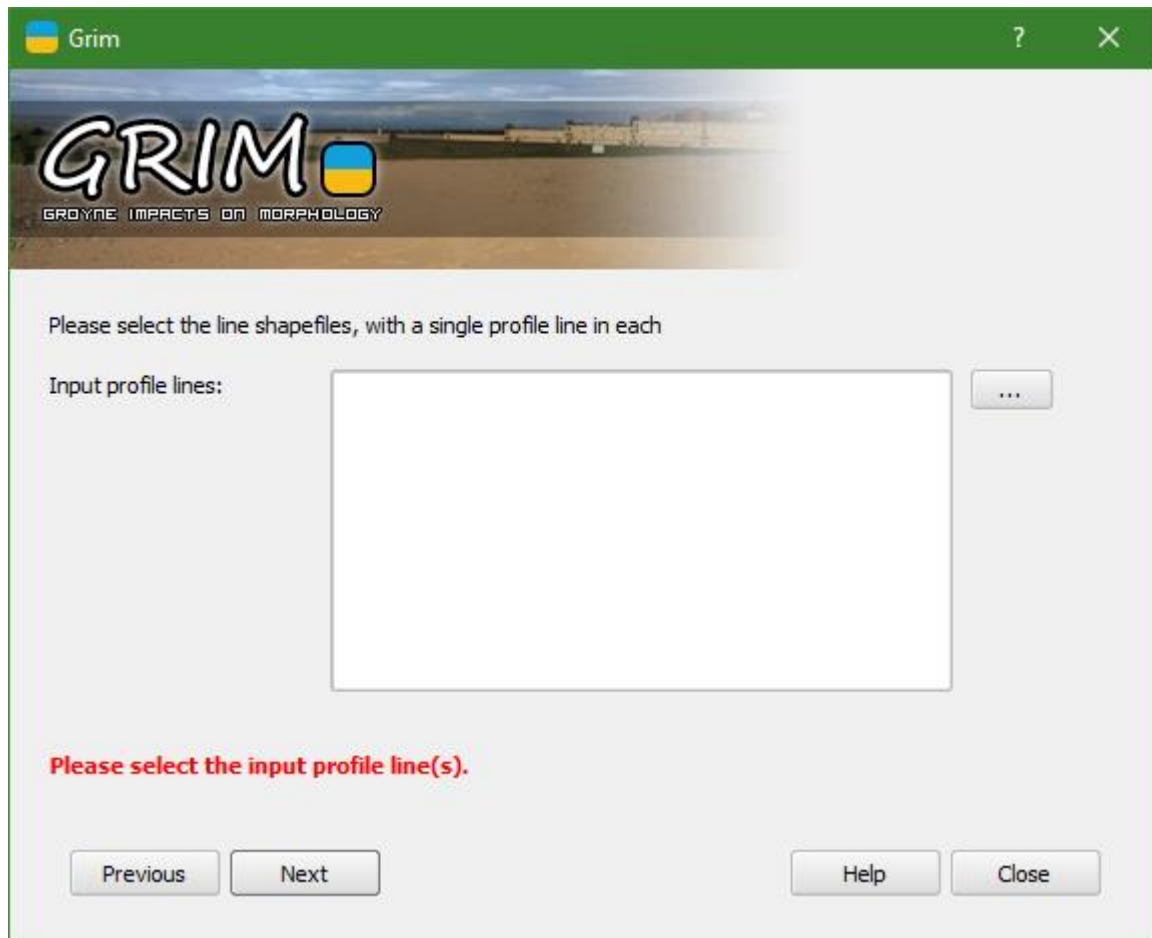


Figure 23: The Input Profile Lines screen.

To select the shapefiles, click the “...” button to open the file selection dialogue. To select a single shapefile, click it and select *Open* at the bottom right of the screen. To select more than one shapefile, press control while clicking each raster in turn. Alternatively, click and drag your mouse to produce a box highlighting the files you would like to select.

Paths to your selected files will appear in the box (Figure 24). Selected shapefiles that are valid will appear green, while invalid layers will appear red. You cannot complete the analysis unless all selected files are valid. Once again, hit the *Next button* to continue.

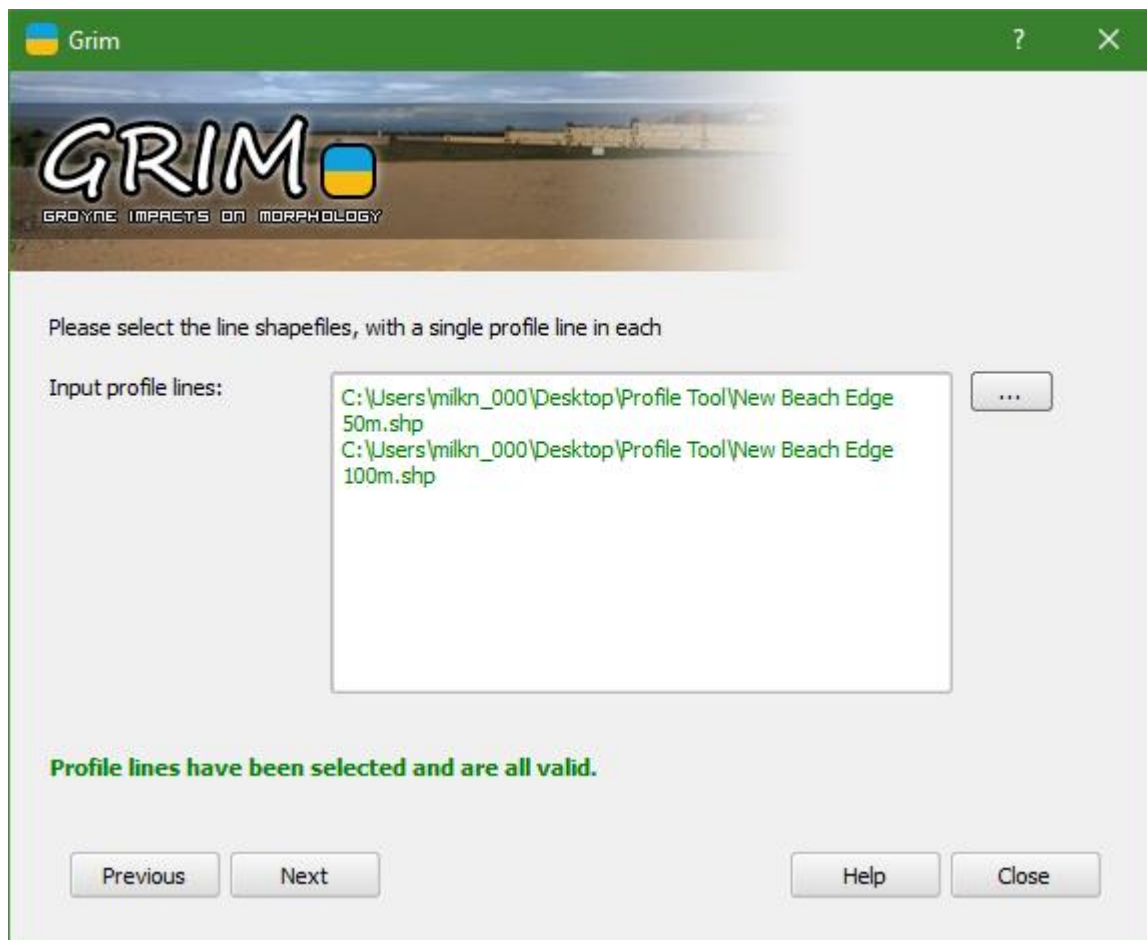


Figure 24: The Profile Line Selection screen, with all shapefiles found to be valid.

Calculate

Finally, you will be taken to the calculate screen (Figure 25). This contains a single button, *Calculate*, which can be clicked to perform the analysis, creating one or more results CSVs and shapefiles in your selected results directory.

If you have input all the required information, click the button to perform the analysis. If any required information is missing, a red label will be displayed and the button will be greyed out and you will be unable to click it. If this is the case, use the *Previous* button to go back and input the required data, and the *Next* button to return to this screen and click the button.

Please note that depending on the amount of data to be analysed, the analysis may take several minutes or more. During this time, the calculate screen will be displayed but you will be unable to interact with it. You will be notified when the analysis is complete.

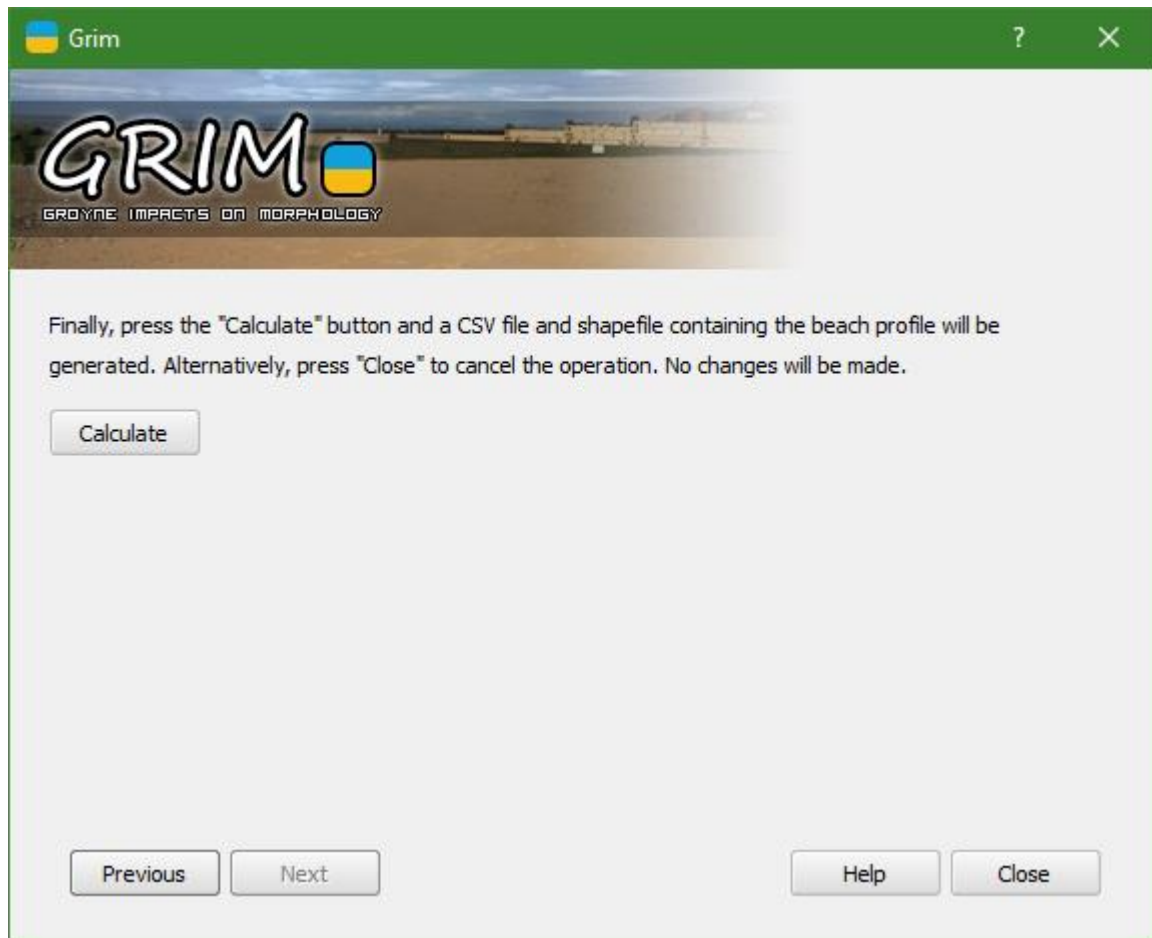


Figure 25: The Calculate screen.

Analysis Complete

Once the analysis has been carried out, the analysis complete screen will be displayed (Figure 26). This will display some information about the outputs produced, and where to find them. The screen can now be closed.

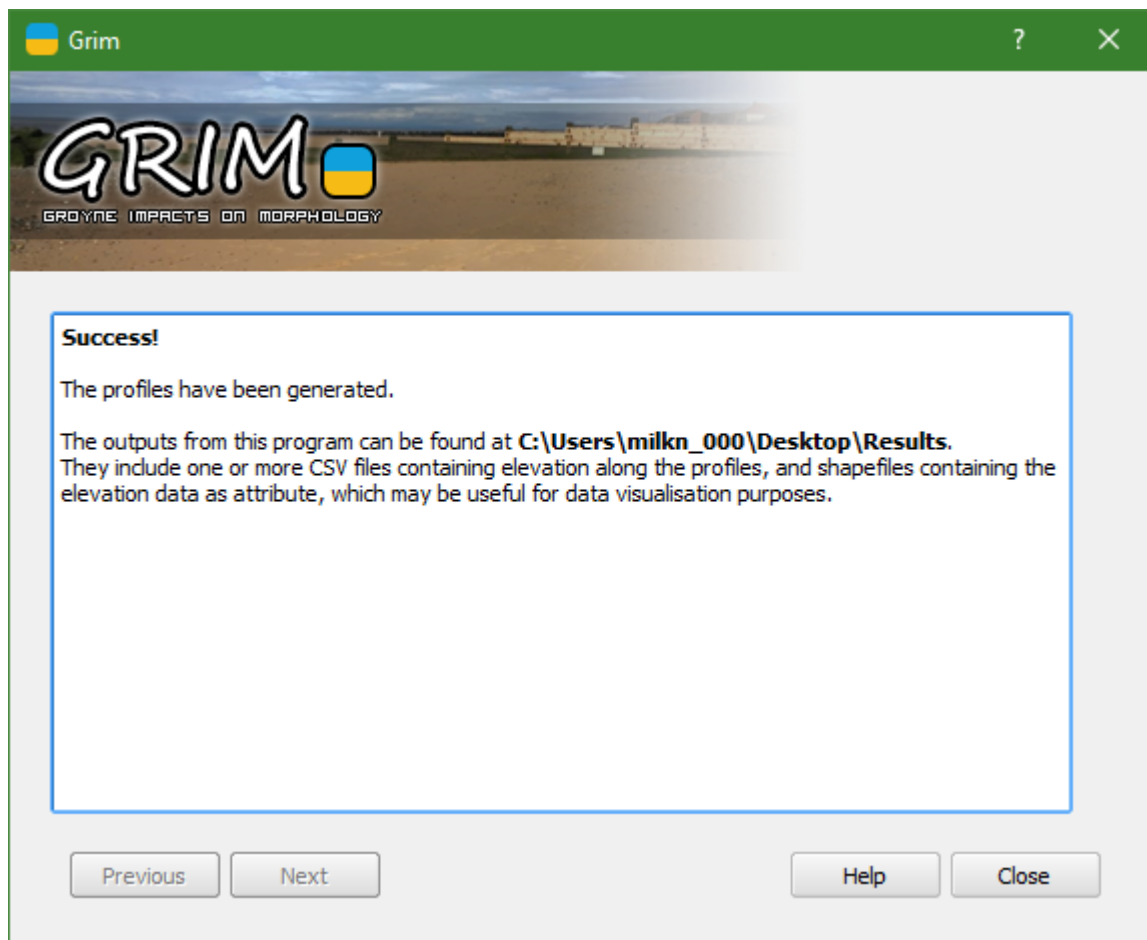


Figure 26: The Analysis Complete Screen.

Understanding the Results

Grim will create one or more CSV and shapefiles in your selected results folder, containing the results of the analysis. The following sections will help you understand and make the most use of these results.

Groyne Elevation Analysis Tool

The Groyne Elevation Analysis tool will create a CSV file name *"results.csv"*, along with one or more shapefiles depending on how you input the groyne cells.

- If you input a single polygon shapefile with each groyne cell as a separate feature, a single shapefile with the name *"originallayername_copy.shp"* will be created. If you input multiple polygon shapefiles, multiple shapefiles will be created following the same naming convention.
- If you input a single line shapefile with each groyne as a separate line, or multiple line shapefiles with a single groyne in each, a single shapefile with the name *"generated_groyne_cells.shp"* will be created.

- If you input multiple point shapefiles, with a single groyne in each, multiple shapefiles with the name “*originalname_copied.shp*” will be created, as well as a shapefile with the name “*generated_groyne_cells.shp*”.

results.csv

results.csv is a standard comma separated values file. It is a plain text file that can be opened in programs like Notepad, but for easier viewing it is recommended you open it in a spreadsheet program such as Microsoft Excel or LibreOffice Calc (Figure 27).

Groyne Cell	Area	2009Signed2m - Volume	2014Signed - Volume	2009Signed2m - Average Elevation	2014Signed - Average Elevation
0	6851.09293	9463462.147	7103372.459	1381.306931	1036.823253
1	6379.058273	10322786.54	12067855.42	1618.230481	1891.79263
2	4712.002916	6934988.292	8389325.192	1471.770798	1780.415959
3	4241.019862	6745212.182	7490096.757	1590.469369	1766.107446
4	11557.91969	19072140.29	18188436.71	1650.13608	1573.677375
5	9961.633679	14776258.67	14325138.15	1483.316808	1438.031011
6	11827.41188	15916238.04	18843520.97	1345.707598	1593.20747
7	9147.025577	15518062.99	18554863.48	1696.514661	2028.513348
8	6527.690166	12638345.93	12957344.69	1936.113022	1984.981572
9	7378.383529	10798496.37	12695861.3	1463.531453	1720.683297
10	20592.73656	29094388.65	24933368.68	1412.847125	1210.784618
11	3672.622349	2821033.546	4670657.473	768.1251372	1271.75
12	9712.359736	3299477.576	4543208.209	339.719457	467.7759405
13	8765.189726	953580.4346	-2280555.41	108.791762	-260.1832341
14	6816.481391	4013135.414	4404505.538	588.7400235	646.1552941
15	6435.826947	3841804.698	3276072.498	596.9403356	509.0367601
16	6454.445127	3722019.367	5651610.226	576.6598513	875.6151946
17	6751.286158	2700325.024	4296879.813	399.9719403	636.4535161
18	9388.634327	188794.061	3650540.549	20.1087884	388.8255119
19	3700.707646	-451264.371	1322170.324	-121.9400218	357.275
20	2915.737553	2760756.409	3430754.919	946.8466757	1176.63365
21	6290.569055	3088255.605	5574092.326	490.9342188	886.1030341
22	1.53955158	1153.389245	782.7965329	749.1722004	508.4574904
23	2369.618496	1229982.129	179552.082	519.0633562	75.77256944
24	10272.19368	2670580.804	-22216.13653	259.9815469	-2.162745098
25	7916.762275	1164226.435	-566503.9271	147.0584053	-71.55752661
26	6595.157169	4913408.128	961481.1393	745.0024316	145.7859327
27	5583.377462	3145207.398	218983.6406	563.3162758	39.22064057
28	6642.389529	4313914.636	1588610.536	649.4522215	239.1625076
29	6387.346689	3434622.725	2760104.243	537.7229219	432.120625
30	6598.272625	3547426.422	3276512.515	537.629562	496.5712546
31	6032.989328	1917770.67	3490646.655	317.8806667	578.5932091
32	6126.799509	2610373.22	3856633.719	426.058208	629.4695481
33	6176.145725	1014070.052	3093888.533	164.1914063	500.9416342
34	4593.202876	1806968.416	4360741.999	393.4005236	949.3902439
35	5009.79006	1941821.976	3205058.46	387.6054591	639.7590361
36	6826.598598	1099626.229	2099470.718	161.0796671	307.5427225
37	7057.83996	-805544.387	1668689.301	-114.1346916	236.4305949

Figure 27: An example results.csv file.

The results file will contain several columns of data. The first column, titled *Groyne Cell*, will contain the number of the groyne cell being referred to. If you input multiple shapefiles (either groyne cell polygons, or groyne lines or points) the groynes are ordered as they appeared in the shapefiles paths box on the input screen. If you input a single shapefile with multiple features (either groyne cell polygons, or groyne lines) then the groynes are ordered according to their feature ID. This is normally, but not guaranteed to be, the order in which they were created.

The next column, titled *Area*, is the area in map units of the groyne cells, which were either input directly, or delineated by Grim.

The next column(s) will show the volume of material within each groyne cell. They will be named according to the convention “[Name of raster elevation was taken from] – Volume”, and there will be one for each raster you input in the elevation raster selection screen. This volume is calculated by multiplying the average elevation in each groyne cell, by the area of the groyne cell.

The final column(s) will show the average elevation in each groyne cell, using the same height units as the input DEMs. They will be named according to the convention “[Name of raster elevation was taken from] – Average Elevation”, and again there will be one for each raster you input.

This information can be used for example to show how the average elevation of sediment within groyne cells changes along the groyne field (Figure 28), which can be useful in seeing whether groynes downcoast are trapping sediment, preventing longshore drift and starving groynes further up the coast of sediment.

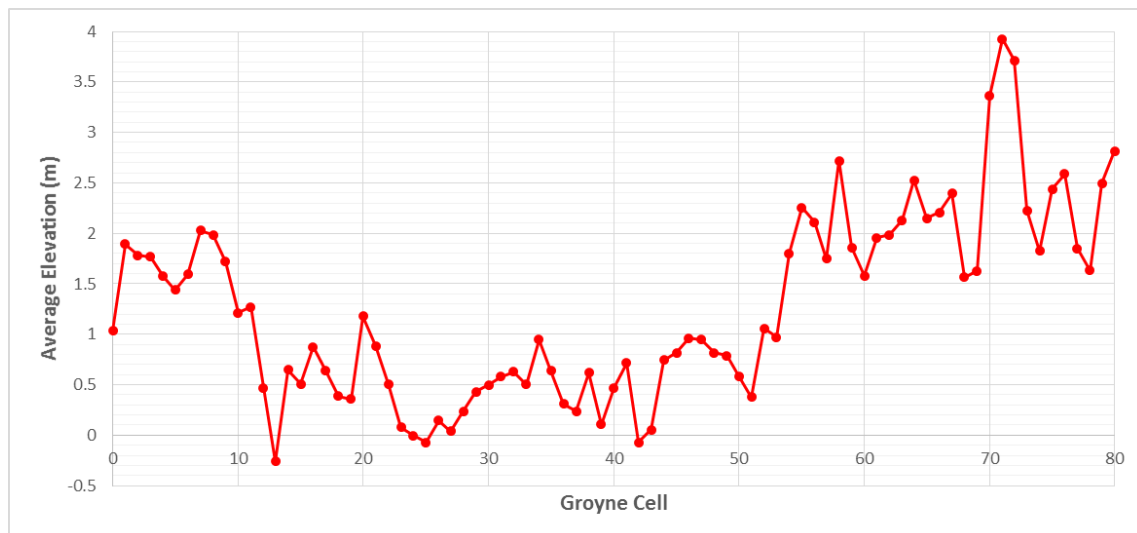


Figure 28: Average elevation within groyne cells at a groyne field at Fleetwood, UK, calculated using Grim.

It can also be used to observe how elevation within groyne cells is changing over time, and whether the groynes are trapping material, losing material, or are in equilibrium (Figure 29).

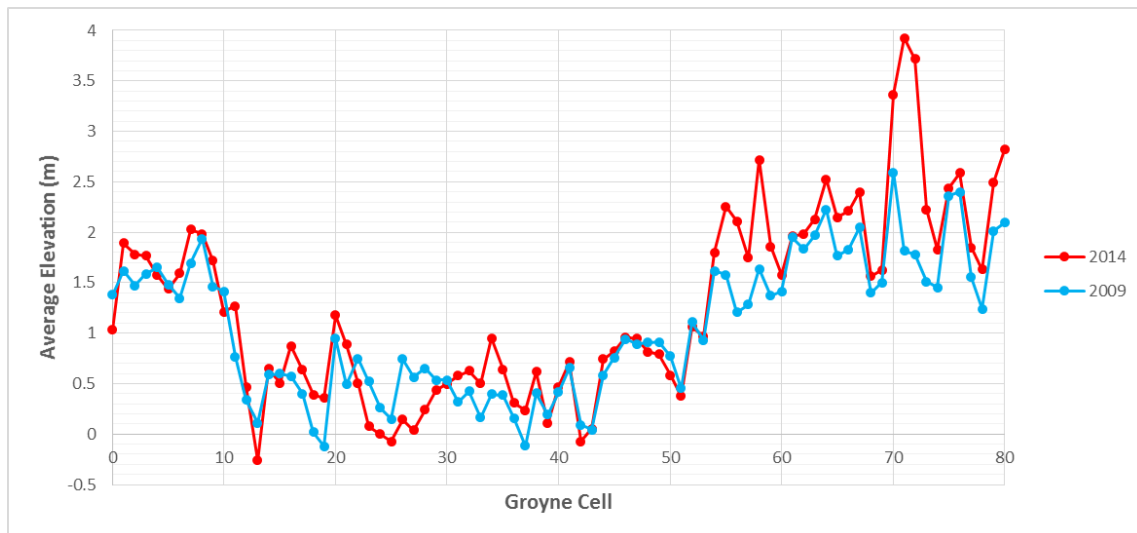


Figure 29: Average elevation within groyne cells at a groyne field at Fleetwood, UK, during two different years, calculated using Grim.

Of course, the data can be used for a variety of other purposes too.

Shapefile(s)

Along with the CSV, Grim will also produce one or more shapefiles showing the locations of groyne cells. Depending on the groyne input method you selected, there will be either multiple shapefiles with a single groyne cell in each, or a single shapefile with each groyne cell as a separate feature. Either way, the attributes the shapefiles contain will be the same. An example attribute table from a shapefile containing multiple groynes is shown in Figure 30.

Groyne Cells :: Features total: 14, filtered: 14, selected: 0

	GR_1_mean	GR_2_mean	GR_Area	GR_1_Vol	GR_2_Vol
1	1381.306930693...	1036.823253082...	6851.092930171...	9463462.147268...	7103372.459033...
2	1618.230480949...	1891.7926296065	6379.058272617...	10322786.53650...	12067855.42396...
3	1471.770797962...	1780.415959252...	4712.002916364...	6934988.292219...	8389325.192341...
4	1590.469368520...	1766.107445805...	4241.019862431...	6745212.182483...	7490096.756850...
5	1650.136080332...	1573.677374784...	11557.9196865502	19072140.28836...	18188436.710296
6	1483.316807738...	1438.031010873...	9961.633679327...	14776258.66908...	14325138.14983...
7	1345.707598371...	1593.207470288...	11827.4118843804	15916238.04188...	18843520.96837...
8	1696.514660831...	2028.513347921...	9147.02557673719	15518062.99393...	18554863.47618...
9	1936.113022113...	1984.981572481...	6527.69016595838	12638345.93463...	12957344.69029...
10	1463.531453362...	1720.683297180...	7378.383529306...	10798496.37010...	12695861.29906...
11	1412.847125097...	1210.7846183725	20592.73656248...	29094388.65018...	24933368.680051
12	768.1251372118...	1271.75	3672.6223492422	2821033.545938...	4670657.47264877
13	339.7194570135...	467.775940471269	9712.359735554...	3299477.57568293	4543208.209494...
14	108.79176201373	-260.183234081...	8765.189725514...	953580.4346233...	-2280555.41012...

Show All Features

Figure 30: Example of an attribute table for a shapefile produced by Grim.

Each shapefile will contain at least three fields. The field *GR_Area* is the area of the groyne cell in map units. The other fields are named with the format *GR_X_mean* and *GR_X_vol* where *X* is a number referencing a raster file in the order they were added. For example, if two DEMs were input, with the DEM from 2009 being first, and the DEM from 2014 being second, the field *GR_1_mean* would refer to the average elevation within the groyne cell in 2009, and *GR_1_Vol* the volume of material in the groyne cell in 2009. If you cannot remember what order the rasters were input, simply check the headers in the accompanying CSV file, as the same order is used there. All height and volume calculation use the same height units as the input raster files.

These shapefiles can be used for data visualisation purposes (Figure 31), or viewing the results more visually.

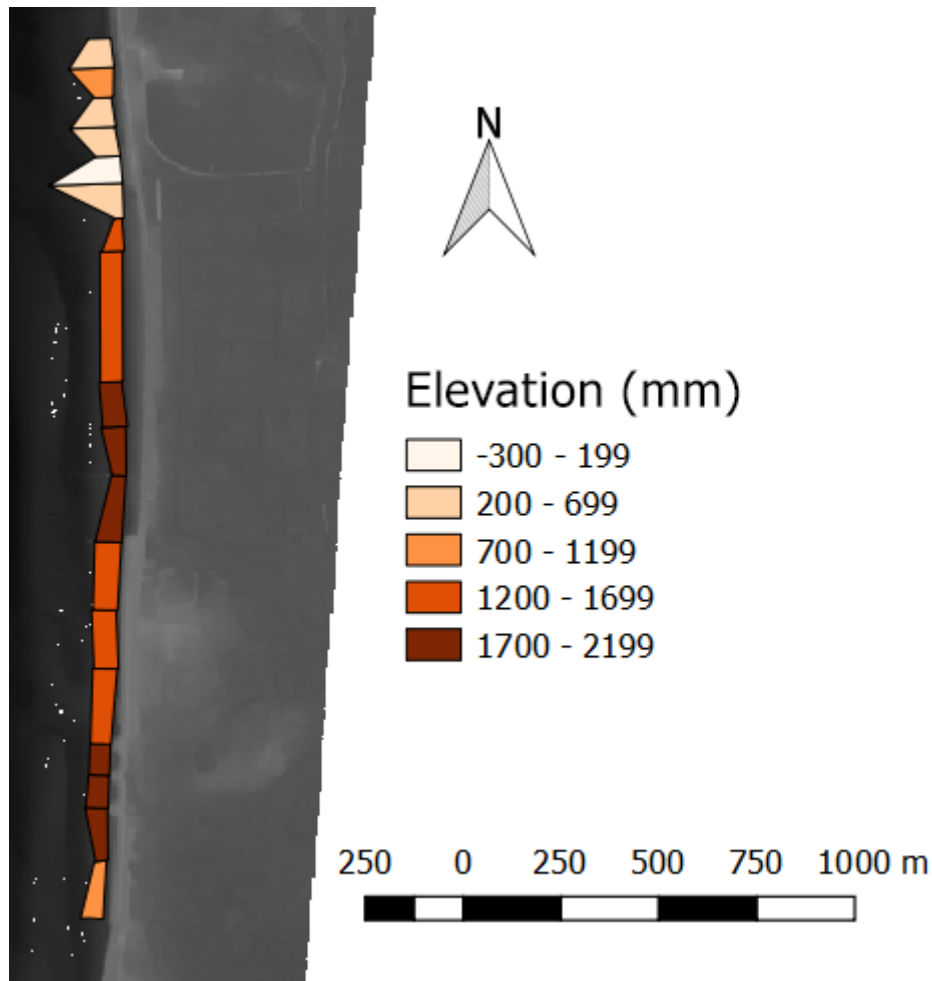


Figure 31: A visualisation created using the shapefile output by Grim, showing average elevation.

Beach Profile Generation Tool

The Beach Profile Generation Tool creates one CSV file and one shapefile for each DEM / profile line combination, with the naming conventions “[profilelinename]_[rastername].csv” and “[profilelinename]_[rastername].shp” respectively. These files contain the elevation data along the line, extracted from the DEM.

CSV

This is a standard comma separated values file. It is a plain text file that can be opened in programs like Notepad, but for easier viewing it is recommended you open it in a spreadsheet program such as Microsoft Excel or LibreOffice Calc (Figure 32).

Distance along profile	Elevation
30	580
60	600
90	560
120	550
150	340
180	220
210	280
240	300
270	280
300	290
330	340
360	250
390	250
420	300
450	450
480	360
510	330
540	330
570	340
600	210
630	120
660	80
690	-170
720	-640
750	-530
780	-530
810	-470
840	-300
870	-130
900	-30
930	-30
960	-20
990	-10

Figure 32: An example results CSV file.

The file is simple and contains two columns. The first column, titled *Distance along profile*, is the distance along the line that elevation was sampled. To check which end of the line measurements were taken from, you can inspect the accompanying shapefile (more details in the next section). The second column, titled *Elevation*, contains the elevation at the given distance along the profile. It uses the same height units as the DEM sampled.

Shapefile

Accompanying the CSV is a point shapefile. Each point represents a location where elevation was sampled. It contains the same distance and elevation data as the CSV file, and such can be used to see where different distances correlate to on the DEM.

The Profile Generation Tool can be useful for quickly creating beach profiles. For example, cross shore profiles could be taken to examine the spatial and temporal variability of the beach slope (Figure 33, Figure 34).

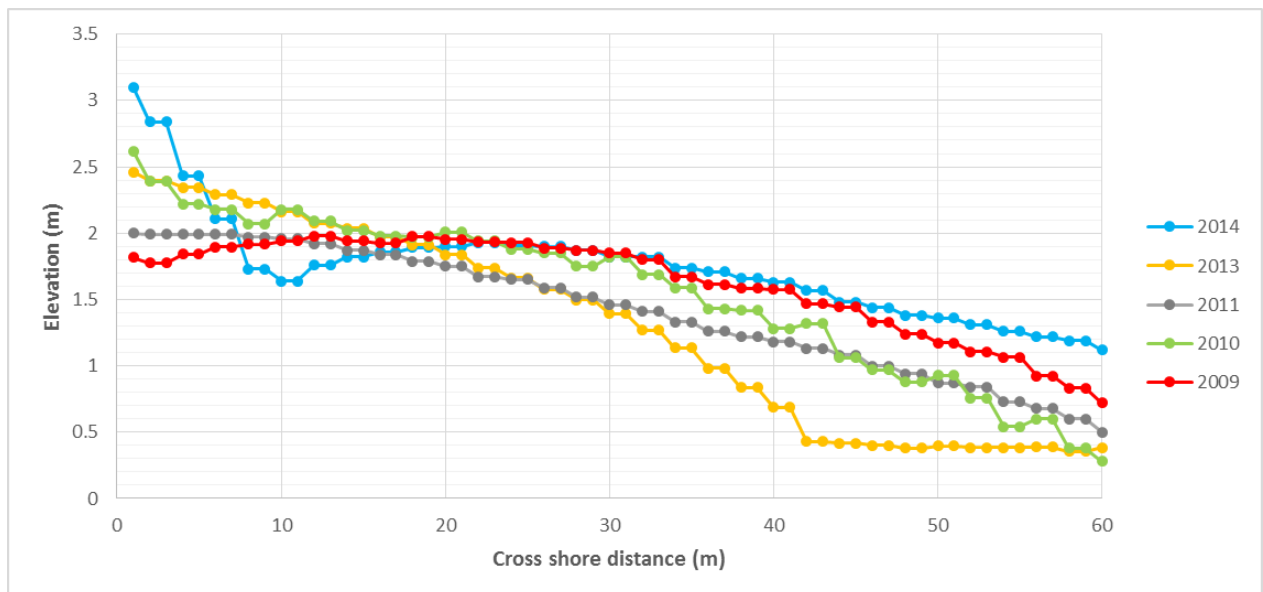


Figure 33: Cross shore profiles taken down the centre of a groyne cell, created using Grim.

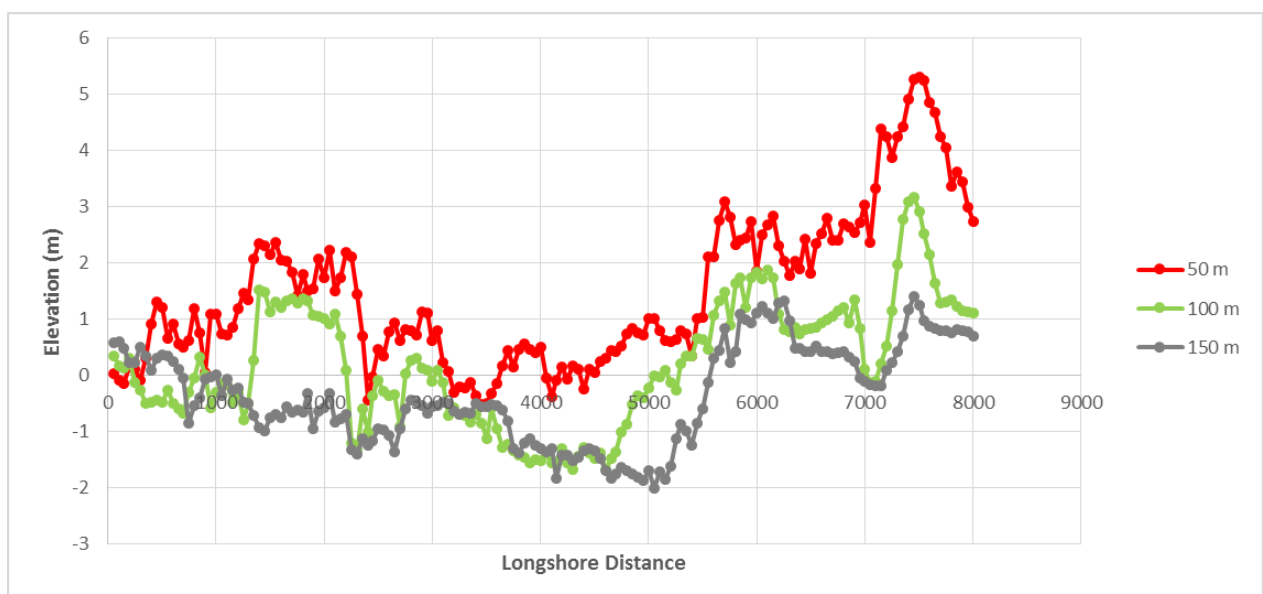


Figure 34: Beach elevation at three different cross shore distances, created using Grim.

How Grim Creates Groyne Cells

The main purpose of the Groyne Elevation Analysis Tool is to calculate the volume and average elevation of material within groyne cells – the space between two groynes (Figure 35).



Figure 35: Two groynes, with the groyne cell highlighted in red.

The tool has several methods for finding the locations of groyne cells. You can input polygons outlining the locations of groyne cells directly. This can be useful if for example you have digitised them from aerial imagery, or if you have your own method of finding their location.

Alternatively, you can input the locations of just the groynes as either lines or points, and Grim will automatically find the locations of groyne cells for you.

If you have input points showing the locations of groynes, Grim will first convert these to lines (Figure 36) by joining them up in an order specified by either a field of your choosing, or their feature ID. This is normally, but not guaranteed to be, the order in which the points were created.

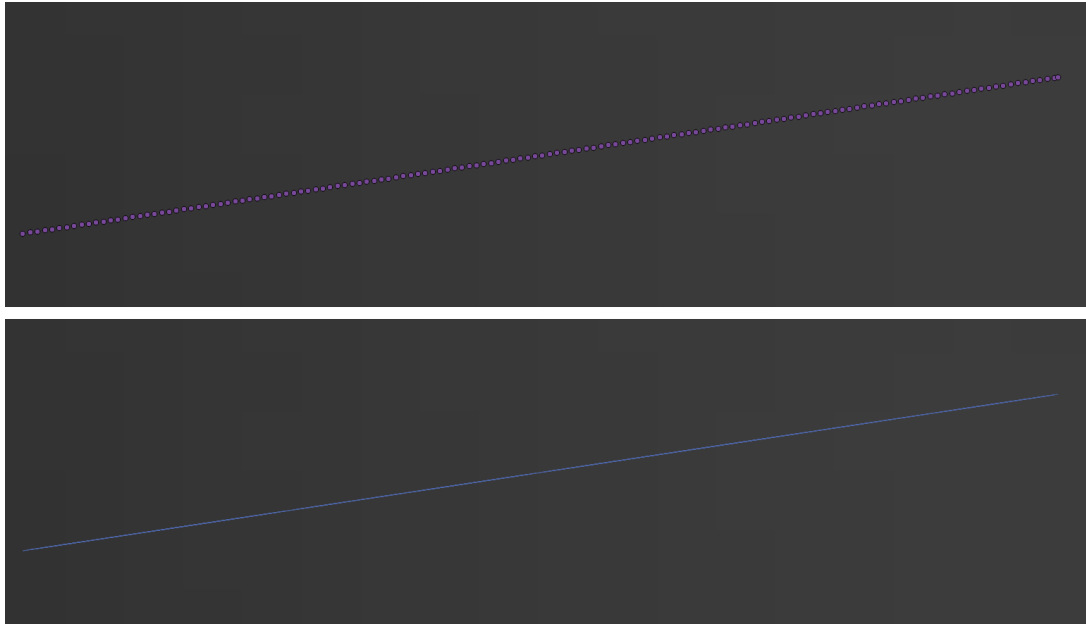


Figure 36: (Above): Point representing a groyne. (Below) Points after being converted to a line.

Next, two adjacent groynes are taken and their end points identified (Figure 37).



Figure 37: Two groynes, with the end of each groyne highlighted.

Lines are then drawn between these end points. It is ensured that these lines do not cross, so that the outline of the groyne is produced correctly (Figure 38).

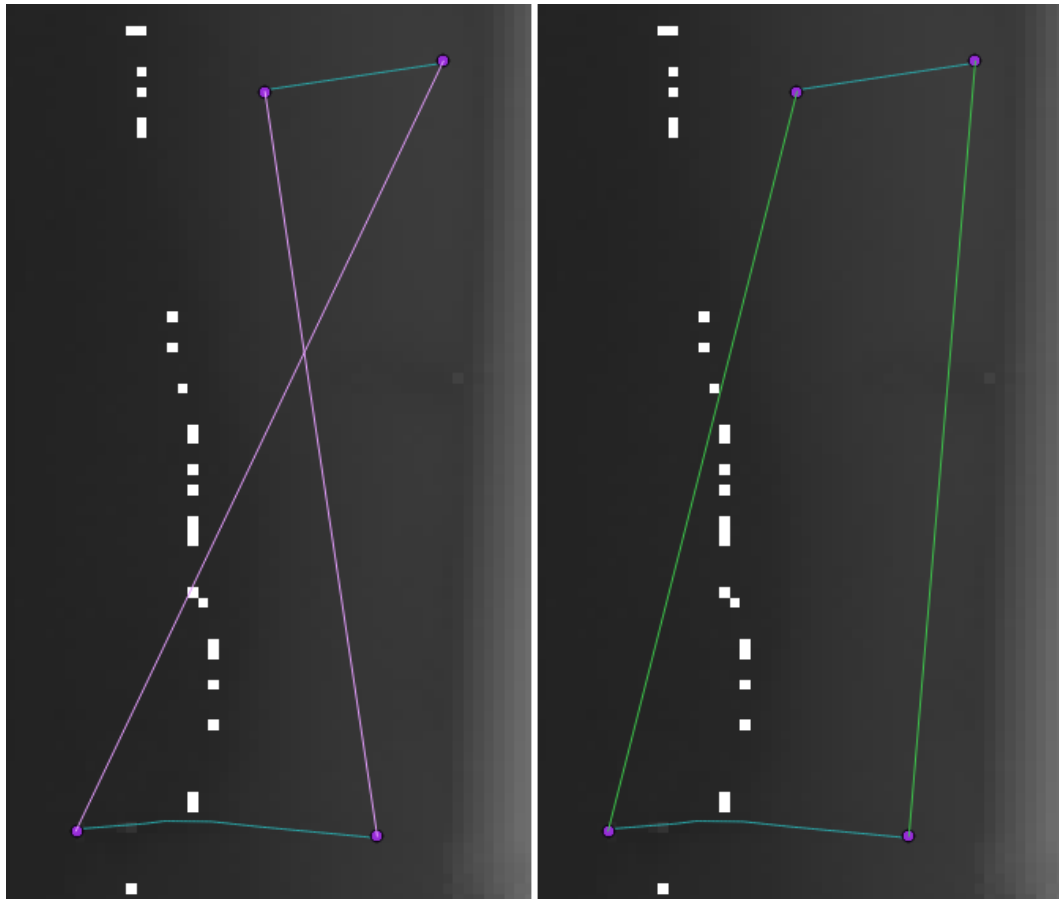


Figure 38: (Left) The end points of each groyne joined together with the lines crossing, with a groyne cell not formed. (Right) The end points joined together with the lines not crossing, the groyne cell is correctly outlined.

Finally, the lines forming the outline of the groyne cell are converted to a polygon (Figure 39).

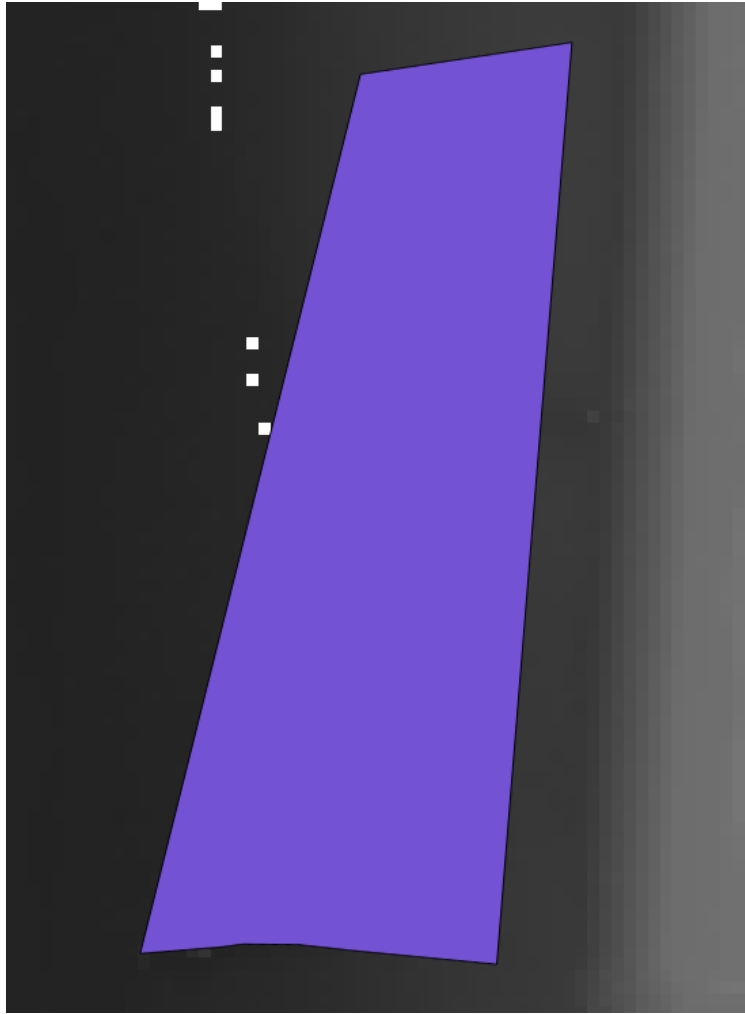


Figure 39: A completed groyne cell polygon.