

Geomodels Institute of Research



Surface Extraction from LIDAR

SEFL

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Faculty of Earth Science
Dept. of Earth and Ocean Dynamics
University of Barcelona
C/Martí Franques s/n
08028 Barcelona
Spain

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Introduction

Contents of SEFL Reference Guide

This document contains four sections:

1 Presentation

The aim of this software is to give some process and analysis tools for working with cloud point in a geology environment. We suggest a workflow to detect and isolate geological surfaces in an outcrop. The software is divided in four sections, first section is for create planar regressions, second section to work with the data continuity, third the complementary tools and finally a special module for horizontal works like topographic works with a tool for calculate differences.

2 Software

2.1 Planar Regressions

In this menu are present the tools to create and load files with planar regressions data. These files are shaped by coordinates (X, Y and Z), and his related information, constituted by the three components vector (u, v, w), Dip Direction and Dip from these vectors, parameters of: collinearity index, coplanarity index and the number of points used for each planar regression. Finally, a value relating to the intensity of the signal captured by laser scanner (Reflectivity) or the texture of the object scanned in RGB format or no information about the intensity. This menu is composing by three items.

- *Create Planar Regressions*
- *Load Planar Regressions*
- *Directory Options*

2.2 Continuity Tools

In this menu, we can found tools to classify or filter information contained on the *Planar Regressions* files, in order to his neighbouring point's information and his continuity. .

- *Filter by Attributes*
- *Create Clusters*
- *Autotracking*

2.3 Tools

The menu contains tools to manipulate *Planar Regressions* files, but working point by point.

- *Attributes Classification*
- *Fracture Measures*
- *Measurements*
- *Merge Files*
- *Morphology*
- *Reduced Files*
- *Scan Line*
- *Statistics from Planar Regression Files*
- *Stereoplot*
- *Translate and Rotate Coordinates*
- *Scale*

Related documentation

Contains articles and related information where explain internal functionalities from algorithms or workflow.

- **Dershowitz & Herda.**, (1992). USRM Symp 1992.
- **Fernández, O.**(2004).*Reconstruction of geological structures in 3D: An example from the southern Pyrenees*. Appendices. Phd Thesis.p.p.3-8.
- **Garcia-Sellés, D., Arbués, P., Falivene, O., Gratacos, O., Tavani, S. & Muñoz, J. A.**, (2011). *Supervised identification and reconstruction of near-planar geological surfaces from terrestrial laser scanning*. Computers & Geosciences 37, 1584–1594 (Available online in www.elsevier.com/locate/cageo).
- **Santana, D., Corominas, J., Mavrouli, O. & Garcia-Sellés, D.** (2012). *Magnitude-frequency relation for rockfall scars using a Terrestrial Laser Scanner*. Engineering Geology 145-146, 50–64
- **Allmendinger, R. W.** (1991). Problem solving in structural geology using vectors and tensors. Cornell University. Ithaca, New York 14853-1504
- **Bingham, C.**,(1964). Distributions on the sphere and on the projective plane, PhD Dissertation, Yale University, New Haven, CT

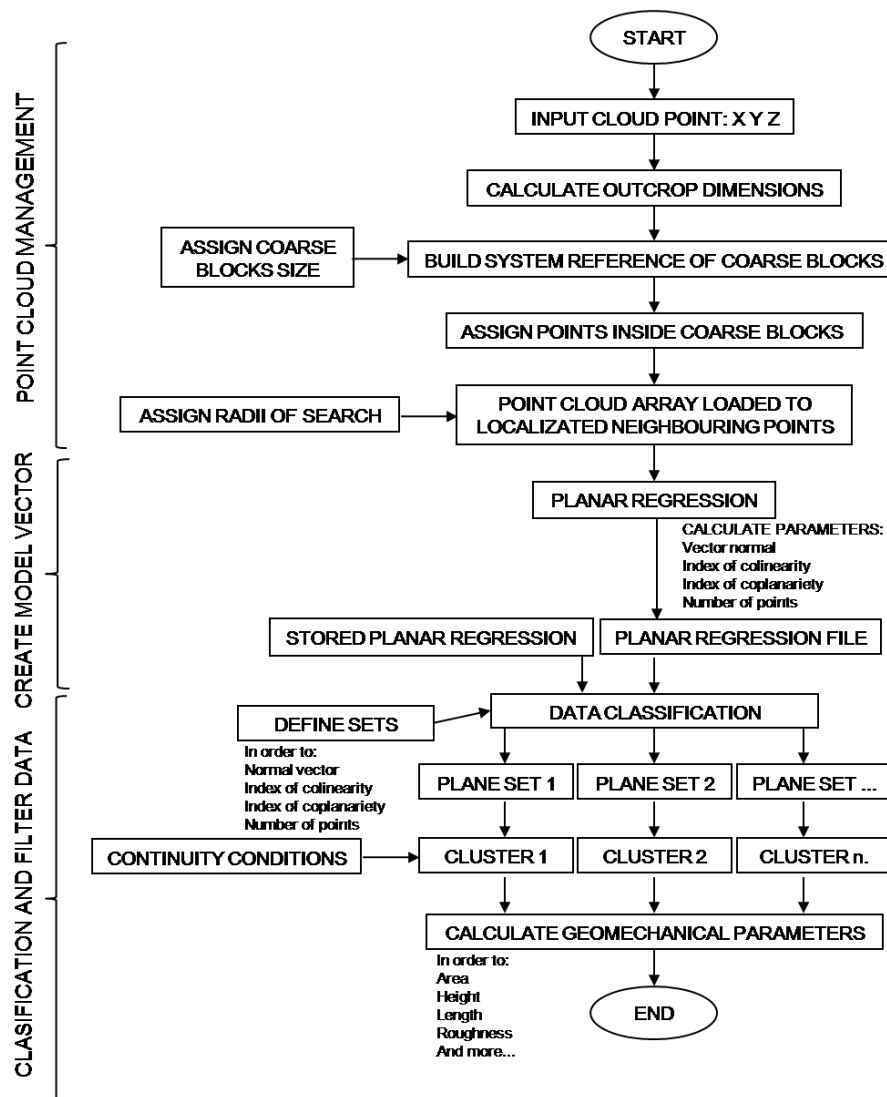
Technical support

Report any problems, or send your suggestions, can be sent to Geomodels Research Institute or directly to software technical team by e-mail at dgarcia@ub.edu

1 Overview

1.1 Workflow

The software has been designed to capture surfaces, surfaces understood as sequence of small planes, from laser scanner data with high resolution. With this aim, the software takes a cloudpoint and generates multievaluate surfaces to recognize planes. In a second step, multievaluate surfaces are classified in order to the orientation to form different families. In the next step, these families form clusters through their continuity attributes, as distance between points and angular difference, and finally clusters can be support a morphologic analysis.



1. SEFL workflow

2 Software

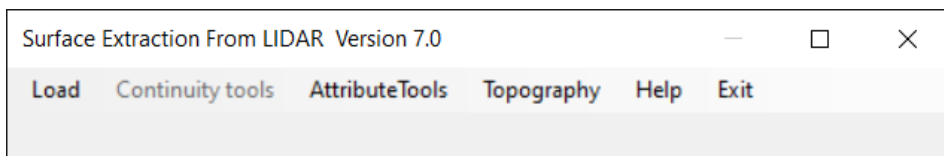


Fig. 1. Main interface of the SEFL

Software is structured in four submenus, where outputs are ASCII files. Output files visualization must be doing with software as Gocad (Paradigm), PolyWorks (Innovmetric) or CloudCompare. Main four submenus are:

- **Planar regressions**, menu to create or load files with planar regressions.
- **Continuity tools**, menu with the algorithms based on continuity attributes.
- **Attribute Tools**, with complementary tools and morphology analysis.
- **Topography**, Specific tools for data processing (reduction and comparison) on the topographic X-Y planes.

2.1 Planar Regressions

2.1.1 Create Planar Regressions

In this option are generate the planar regressions, necessary input file is a file with 3D coordinates(X, Y, Z) without commas. The menu contains three options for input file attributes:

- **No texture**. Only three dimensions coordinates.
- **X Y Z +Reflectivity** (Integer). The three dimensions coordinates and laser scanner reflectivity.
- **X Y Z +R G B** (Integer). The three dimensions coordinates and texture information image for red, green and blue channels.

The dialog box offer **Selected file and load point cloud** button to read and load the selected file, as first action and active the dialog box in **Coarse Grid Definition**.

Coarse Grid Definition options offer how define coarse grid side, this parameter is important to expedite the continuity process. Automatically, the dialog box reports model dimension for each axis in whole cloud point, and the number of points.

In first approach, coarse grid side is 0.1 m, this number are used to calculate the coarse grid number for whole cloud point and for each axis. Number of coarse cells for axis must not be greater to 1000 for normal computers.

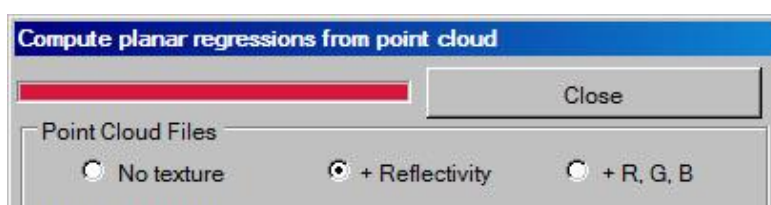


Fig. 2.The regressions planar dialog box.

Coarse grid side variation creates variation over the number of coarse cells for axis. User can enter a different side and visualizes the new solution in **Calculate coarse cells number** button.

Once the size already has been selected, **Generate coarse cells and assign points to cells** button start the process to assign each point into its cells through its space position.

Next dialog box activation is used to define parameters that control the regression planar. These parameters are:

Minimum radius: Is the smallest distance between the seed point and the rest of the points to start the planar regression. When the number of points is reduced, the planar regression can be affected due to one bad distribution or erroneous concentration of points.

Maximum radius: Is the biggest distance between the seed points and the rest of the points to be accepted at the planar regression.

Both parameters are essentials to start the planar regression.

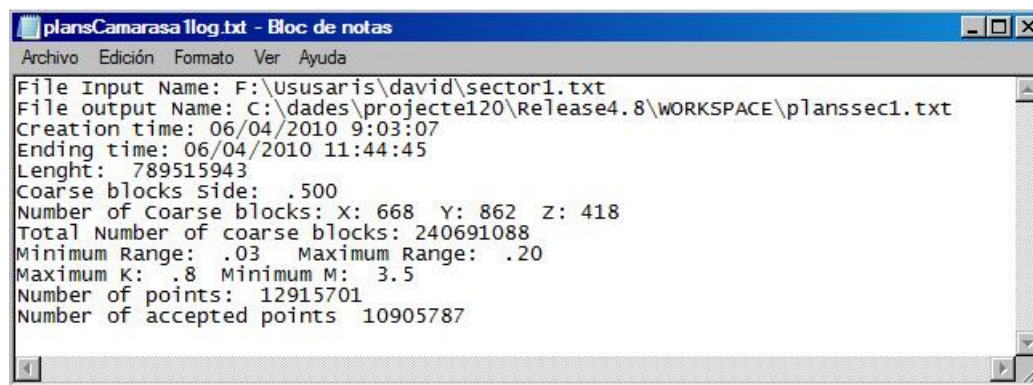
Minimum M: Coplanarity index or degree of fit. Good planes have higher index values. Value 3.2 is an acceptable value for good planes. We must decide cut value to separate accepted planes from rejected planes. If we want keep open the threshold, put zero. Upper accepted limit is 500. We can define the cut value in other process.

Maximum K: Collinearity index. Good planes have lower values. An acceptable threshold may be 0.8 or 1.2. Open value is 100. In this case, value can be defined in other process.

Output file name and output folder can be defined. In **Planar Regression >Options** is possible too.

Activate option **Create statistics file** write a file in the directory predefined with the quantity of values for each dip direction and dip planes. This file can be visualizes in **Tools > Stereoplot**.

With the **Create log** activate, a file with the planar regression creation information history is write.



```

plansCamarasa1log.txt - Bloc de notas
Archivo Edición Formato Ver Ayuda
File Input Name: F:\Ususaris\david\sector1.txt
File output Name: C:\dades\projecte120\Release4.8\WORKSPACE\planssec1.txt
Creation time: 06/04/2010 9:03:07
Ending time: 06/04/2010 11:44:45
Lenght: 789515943
Coarse blocks Side: .500
Number of Coarse blocks: x: 668 Y: 862 Z: 418
Total Number of coarse blocks: 240691088
Minimum Range: .03 Maximum Range: .20
Maximum K: .8 Minimum M: 3.5
Number of points: 12915701
Number of accepted points 10905787
  
```

Fig. 3.Planar regression log example.

Lower value of number of points to calculate a planar regression is 5, because is the minimum value to guaranty the planar regression solution and give sort information with the quality of the planar regression.

Compute planar regressions button start the process. The file result contains the following parameters in ASCII code.

X space Y space Z space i space j space k space Dip Dir space Dip space M space K space n + Intensity / RGB

Where each parameter means:

X Y Z: Coordinates 3D for each point of the pointcloud.

i j k: Normal vector components calculate by the planar regression.

M: Coplanarity index or Degree of fit.

K: Collinearity index.

n: Number of points used to calculate each planar regression.

Options

Reflectivity: 8 bytes values of intensity surveyed by laser scanner.

R G B: Three values in 8 bytes to represent the texture colour of the point cloud

2.1.2 Load Planar Regressions

This dialog box load dates created at the dialog box **planar regressions**, indispensable for execute process of **Continuity tools > Attribute classification, Create Clusters** and **Autotracking**.

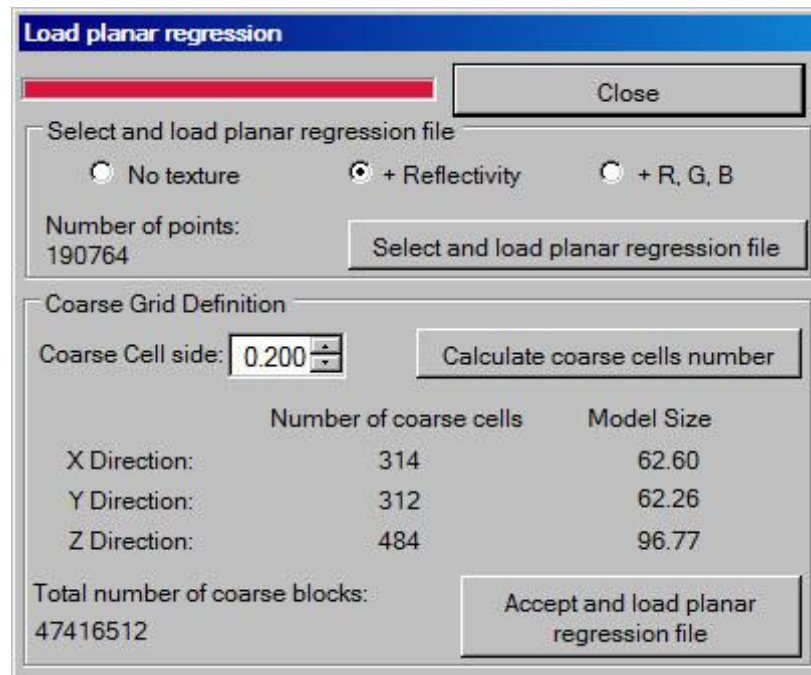


Fig. 4. Dialog box to load file of Planar Regressions, necessary to continuity studies.

Read planar regressions file: This button opens the file created in the dialog box **Planar regression > Create planar regression**, after selecting the correct option about intensities.

Coarse Grid definition: Is necessary defining the coarse block side to allocate the points, in the same process than **Planar regression > Create planar regression**. With button **Calculate number of coarse cells** we can test the total dimensions of the model in order an efficient time consuming process by the computer. When the file is loaded, **Continuity tools** change to active in the main interface.

2.1.3 Directory Options

The software creates a folder denominated *WORKSPACE*, where the output files will be written. In Directory options are the tools to change default folder.

Refresh: Show the path of SEFL v7.exe active folder.

Add folder WORKSPACE: A new folder *WORKSPACE* or another folder name is created in the new path selected by the user. This folder will be used to allocate all output files created by SEFL.

Create directory: Execute the instructions.

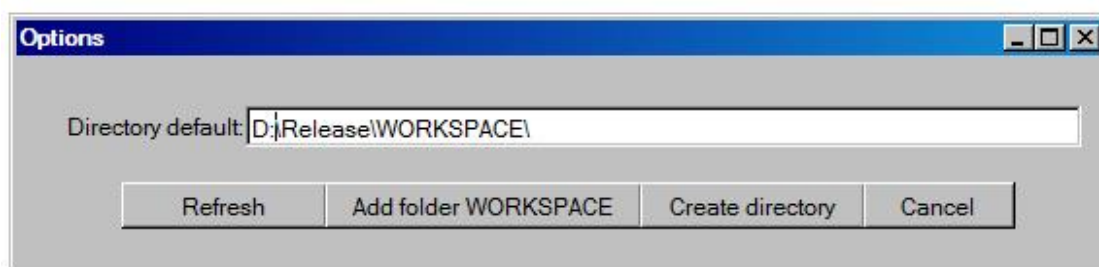


Fig. 5. Dialog Box to define the output files folder.

2.2 Continuity Tools

Tools of this section are used when is necessary know the relations between points and its attributes with neighbour's points and its attributes. The aim is check the grade of his continuity. This relationship can determinate two process, remove points without continuity and create clusters of points. User set up continuity conditions to determinate the process. Execute the functionalities of this section require previously load files create at **Planar regressions > Create Planar Regressions** at main interface **Planar Regressions > Load Planar Regressions**. One time the file is load; user can access to **Continuity Tools**, and select one tool, **Filter By Attributes** or **Create Clusters**. Dialog box contains the parameters to control and execute the process. When the continuity process is over, parameters can be changed successively after each process without be necessary load again the planar regression file.

2.2.1 Filter By Attributes

This functionality tries to remove isolate point. User must set up with the dialog box parameters the isolate terms. Isolate terms are according to the distance between points, minimum number of points to considerate isolation or are not representative of some planar structure and the degree of tolerance between the normal vectors associate to each point. Output files (Filtercontinuity.txt) keep the structure of input.

Maximum radius: Search radii around the each point to establish isolate terms.

Minimum number of points: Minimum number of points to establish isolate terms.

Planar regression vectors tolerance: Degrees of tolerance between the normal vectors of the seed point and each neighbouring point.

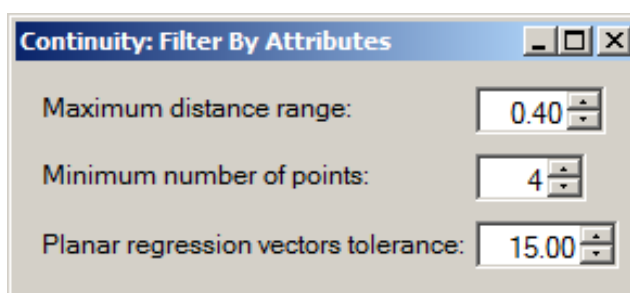


Fig. 6. Dialog box with the parameters to establish continuity terms in **Filter by continuity**.

If the result of the first approach is not satisfactory, is possible change some parameters and continued with other approaches until a satisfactory solution. It is not necessary close the dialog box neither loading the file.

2.2.2 Create Clusters

This algorithm allows create point clusters in order to continuity. The output file name is "Clusters.txt". The dialog box **Create Clusters** contains the followings parameters:

Maximum radius: Searching radius in meters around the seed point.

Planar regression vectors tolerance: Tolerance in degrees between the normal vectors of the seed point and points tested, one by one.

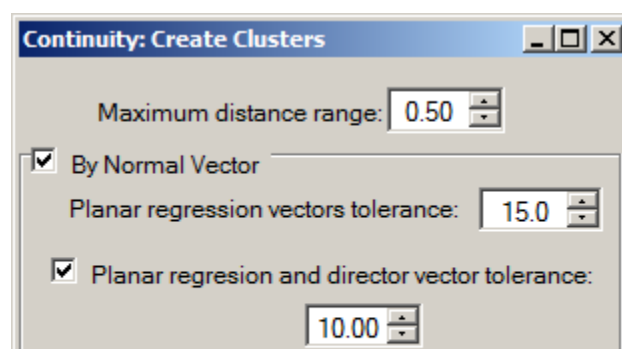


Fig. 7. Dialog box for creation clusters

Planar regression and vector director tolerance: Tolerance in degrees between the normal vector of the seed points and the director vector of the seed point and tested point. The value for points in the same plane is 90° , if points are in different planes, measured angle will be 0° , and distance between points brings influence over the measure. The input values are inverted. Tolerance 0° defines points in a same plane.

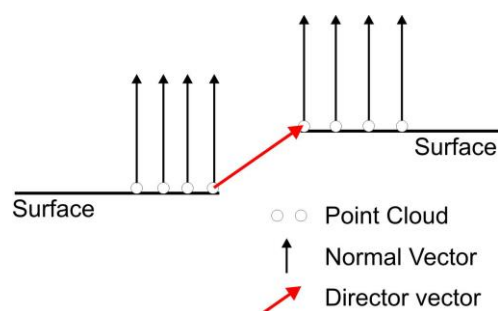


Fig. 8. Similar normal vectors attributes along surfaces cannot be placed in the same surface. Director vector between point clouds can differentiate surfaces.

2.2.3 Autotracking

In construction

2.3 Attribute tools

2.3.1 Attributes Classification

This algorithm classify in order to the attributes the files obtained on the menu **Planar Regressions> Create Planar Regressions**. The attributes are the azimuth

of the Dip Direction and Dip of the normal vector obtained on the planar regression. Dip Directions and Dips limits can be introduced by three different ways. The outputs files names are “Set (+Set number, if there are more of one).txt”

Fig. 9. Dialog box to classify files of the planar regressions.

Box with the number of file whose polygon will be stored, the same file number can be present to different polygons

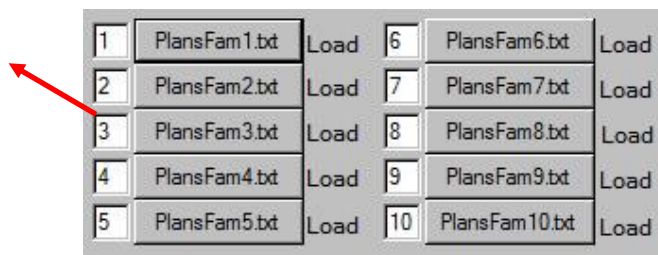


Fig. 9. Detail of the functionality to cluster families in accordance with the assigned polygon.

- **Classification by Dip Dir. and Dip.** This option is for planar regression files where the user wants to introduce the attribute of azimuth and dip through the formats of Dip Direction and Dip, therefore vectors are separate into its constituents parts and only classify will be make.
- **Classification Area by Dip Direction and Dip.** Vector information is separated into its constituent parts, horizontal and vertical, with the format

of Dip Direction and Dip. To separate families are introduced polygons who define areas assigned to each family. These polygons are drawing in **Tools > Stereoplot**. The maximum number of polygons to draw is 24. When the polygon files are loading, user can join different polygons in the same output file, thus must be put the same number into the box number.

- **Classification by Normal Vector.** User can define one vector orientation and delimit one tolerance in degrees to create one classification. Only can be created one classification.

2.3.2 Fracture Measures

Fracture Measures analyse Morphology files to find associate parameters to fracture sets. Input files are Morphology files from Mechanical Units (M. U.) with header. First step for calculate fracture sets parameters is analyse each morphological file individualized by M. U. (Tool **Create M.U. Bounds and Files**).

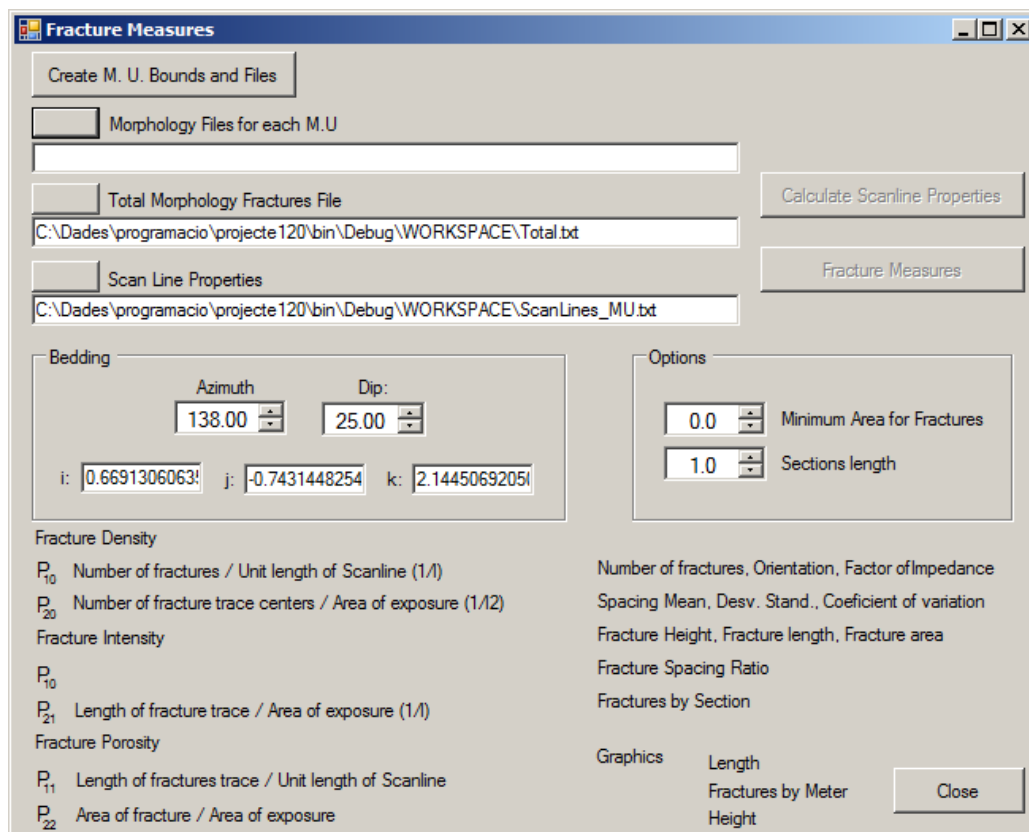


Fig. 10. Interface for Fracture Measures.

Create M. U. Bounds and Files: Is the tool to define the bounds of each M. U.

M.U. Bound number: Number of M.U. Bound. Start with #0

Plane Orientation (Dip Direction and Dip) and Coordinates: M. U. bound is idealized with a plane. To define the plane is necessary one orientation and one position in coordinates X, Y, Z in the center of the extension.

Upper Horizontal Extension and Lower Horizontal Extension: The bounds used to define M. U. can be limited laterally with the parameters *Horizontal Extension* (parallel to the Plane Orientation set for the bound). The parameters define the extension of the upper Unit to the defined bound and the lower Unit. The extensions of the each Unit is repeated in both bounds, the upper and lower with the exception of the first and ultimate bound, defined only one time.

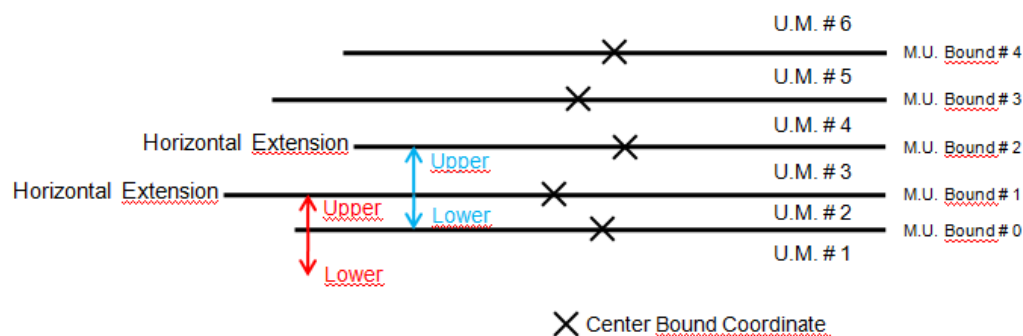


Fig. 11. Graphic concept for M.U. Bounds and their parameters.

Create Bounds for M. U.

Lower Bound is the first

M. U. Bound number: 4

Plane Orientation (Dip Direction, Dip) 138.00 30.00

Coordinates (X, Y, Z) 61436.74 9576.14 925.51

Upper Horizontal Extension 10.00

Lower Horizontal Extension 50.00

<< Save >>

Classify Fractures by M.U.

Cancel

Fig. 12. Interface for Create Bounds for M. U.

When all files belonging to each mechanical unit are loaded in “*Morphology Files for each M.U.*” the process calculate these parameters for each Mechanical Unit.:

| | | | | | |
|--|----------|----------|-----------------------|--------------|--------------|
| Outcrop orientation (Plane) | | | | | |
| - Vector i | Vector j | Vector k | Centroid Coordinate X | Coordinate Y | Coordinate Z |
| ScanLine (line) | | | | | |
| - Vector i | Vector j | Vector k | Centroid Coordinate X | Coordinate Y | Coordinate Z |
| ScanLine (Plane at the Top of the Mechanical Unit) | | | | | |
| - Vector i | Vector j | Vector k | Centroid Coordinate X | Coordinate Y | Coordinate Z |
| ScanLine (Plane at the Bottom of the Mechanical Unit) | | | | | |
| - Vector i | Vector j | Vector k | Centroid Coordinate X | Coordinate Y | Coordinate Z |
| Thickness of Mechanical Unit | | | | | |

h meters, distance between Scanline Top and Scanline Bottom
Extension of Mechanical Unit
 l meters, 2D distance between extreme fractures intersected
Area of Mechanical Unit
 a squared meters. Source $h \times l$
 n **Number of sets**
 Set1 **Name of each Set**
 number of fractures, number of fractures after filter, sum of heights

Bedding orientation must be introduced previously.

Parameters calculated in “*Fracture Measure*” process are:

For each Mechanical Unit (M.U.):

- Height of the M.U. Distance between top and bottom surfaces. From M.U. file.
- Area of the M.U. Sum the whole areas comprise between Top and Bottom scanlines, indifferent from the centroid M.U. position.

For each ScanLine and by Set

- **Scanline length.** Distance between extreme centroids into the M.U along the outcrop orientation.
- **Scanline orientation.** Line of intersection between outcrop plane (plane defined by the centroids of each M.U.) and bedding
- **Number of fractures:** Fractures intersected by Scanline independent of the M.U which belonging.
- **Set orientation:** Mean orientation of the fractures intersected by the Scan line and independent of the M.U. which belonging.
- **Impedance factor:** Number of fractures cutting the scanline in percentage that intersect the top and the bottom plane of the M.U. at the same time.
- **Spacing Mean:** By set, distance between fractures that intersect the scanline, and measured orthogonal at the fracture orientation. Is the mean.
- **Dev. Stand.** Standard deviation of the spacing mean calculate
- **Coef. Variation:** Standard deviation divided by the arithmetic mean, measure used to analyse clustering (Gillespie, 1993). >1 system is clustered, $=1$ balanced and <1 are uniformly spaced.
- **Fracture Height:** Mean of the fracture heights intersected by the Scanline
- **Fracture Length:** Mean of the fracture lengths intersected by the Scanline
- **Fracture Area:** Contribution at the whole M.U. area of each set. Independent of the Scanline
- **P₁₀:** Number of fractures divided by length of Scanline

- **P₁₁**: Length of fractures trace divided by unit length of Scanline
- **P₂₀**: Number of centroids fractures divided by M.U. area
- **P₂₁**: Length of fracture traces divided by area of exposure
- **P₂₂**: Area of fractures per Unit sampling area
- **P₃₂(C₁₃)**: Area of fractures divided by volume of rock mass. Because is very difficult to obtain directly is deduced from the equation $P_{32}=P_{10}C_{13}$
- **P₃₂(C₂₃)**: Area of fractures divided by volume of rock mass. Because is very difficult to obtain directly is deduced from the equation $P_{32}=P_{10}C_{23}$
- **FRS**: Fracture Ratio Space: Spacing divided by Thickness of the M.U.
- **Accumulate fractures**. Along the scanline, plotting the number of fractures of each set by distance, usually 1m.
- **RQD**: Semi-log in each M.U. centroid with the number of fractures, Set and Ratio of fractures distance over 10 cm.

Indirect parameters

- **FRI**: Fracture Ratio Index: Slope of the tendency line between joint spacing and thickness M.U.
- **Fractal Dimension**: The simplest level fractal geometry can be defined as scale independent. (Gillespie, 1993)
- **Plotting Fracture Height/M.U. thickness**.
- **Plotting cumulative frequency of:**

Fracture Length: From the morphology file

Fracture Height: From the morphology file

Fracture Area: From the morphology file

2.3.3 Measurements

Calculate the angle between two angles.

2.3.4 Merge Files

Algorithm merges all type of SEFL files.

- **Source Files**: Output files with the merged files. Is the first input file.
- **Merged Files**: Input files to be merged.

- **Create Merge File:** Start the process.

2.3.5 Morphology

In this section there are tools that works with the cluster morphology created in **Continuity Tools > Create Clusters**. The tools are used to analyze the planes properties along the space.

- **Create Morphology File.** Create a file with morphology information for each point cluster.
 - **Filter Morphology Files.** Select clusters from attributes conditions defined by the user.
 - **From Cluster to Individualize File.** Each cluster present in Cluster.txt is stored in individual files.
 - **From Morphology File to Gocad.ts.** Export morphology files at surface file .ts Gocad.
-
- **Attribute Projected on a Line.** This algorithm project one morphology attribute from "Morphology.txt" along a line, 3D or 2D.
 - **Attribute Projected on a Plane.** In this case, the attributes contained in "morphology.txt", area and long are projected over different planes. Result file can be used in a Fourier analysis in 2D.
-
- **Matching Coordinates-Morphology.** From a list of coordinates X, Y, Z, the algorithm chooses coincident items with items from a Morphology file. Is used to select morphology items by geography criterions.
 - **Spacing and Density.** Functionalities to calculate these parameters from sets of pointcloud surfaces.

2.3.5.1 Create Morphology File

Cluster files creates at **Continuity Tools > Create Clusters** contain a series of points who defines a lot of planes with shapes and characteristic that can be quantify by parameters. First step is calculating a planar regression with all points of each cluster, and the calculate parameters are:

- *Centroid coordinates (X, Y, Z), and if is necessary there are the possibility to add an offset for each axis.*
- *Components of the plane normal vector (i, j, k)*
- *Dip direction and Dip of the plane (Dip Dir, Dip)*
- *Collinearity index (K)*

- *Coplanarity* index (M)
- Roughness index (Roughness)
- Approach to the geometry dimensions of each cluster.
 - Cluster *Length* (Length)
 - Cluster *Height* (Height)
 - *Area* (Area)
- For each cluster is added a numeration (*Number*), the number of points (*Population*) and the *Set* name.

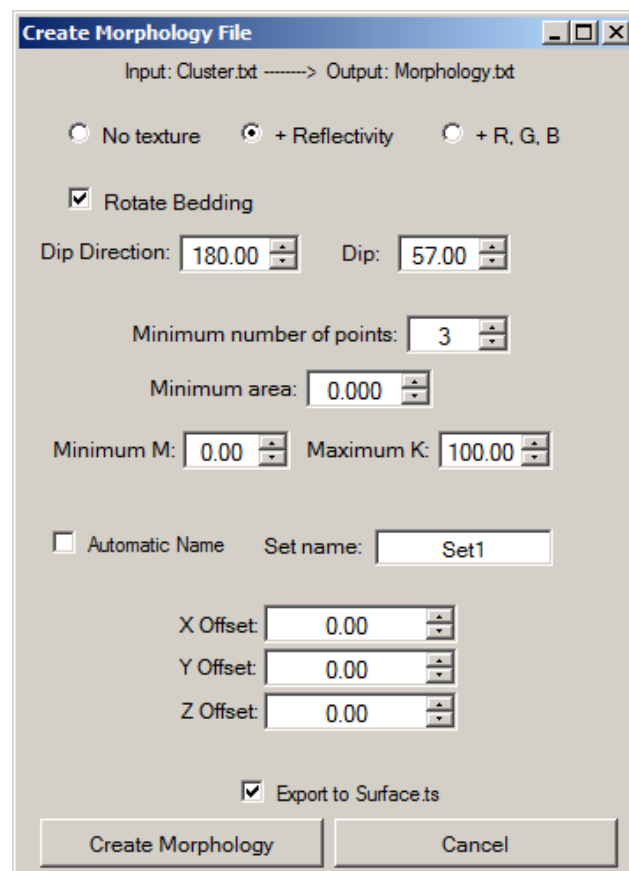


Fig. 13. Dialog box for Create Morphology files.

The output file Morphology.txt is created in the default folder. In the dialog box are the parameters to control the morphologic quality of the adjusted cluster:

- **Rotate Bedding:** Bedding orientation help to adjust de bounders of the plane.
- **Minimum number of points:** Is a number threshold, under this number cluster is not calculate.
- **Minimum area:** Threshold number of square meters of the clusters, cluster with surface under this number is not created.
- **Minimum M:** Limit value for coplanariety index calculates at planar regression.

- **Minimum K:** Limit value for collinearity index calculates at planar regression.

Utility: Output file can be imported like a table in ARCinfo Workstation. First a table must be created with the necessary items. In the same way, a seed can be created with the denomination "morfologia", and make a copy each time that we need create o load a table. Instructions to create a table:

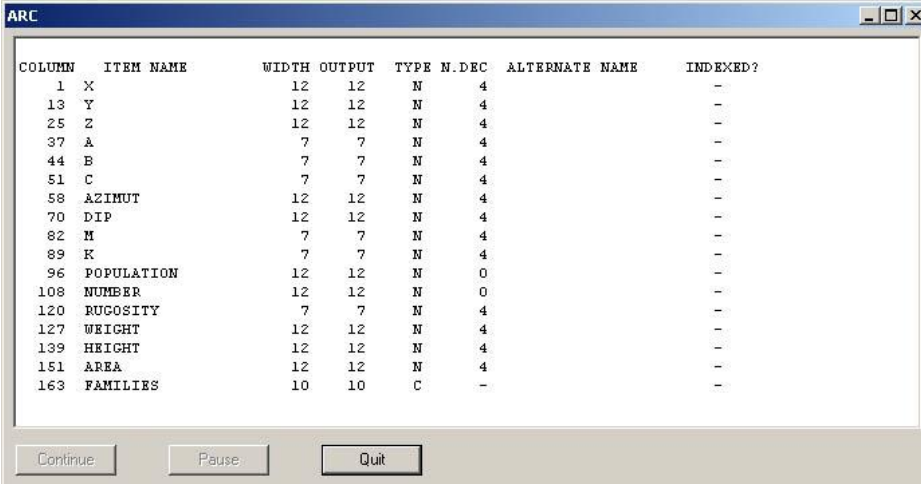
ArcTools > Command Tools > Edit INFO Tables>Define Tables and we define it with items showed in Figure 11.

One time is create the second step is ArcTools > Command Tools>Edit INFO Tables>Add from ASCII and import the file created in SEFL "Morphology.txt".

In Comand Tools>Arc Tools >Manage>Info Tables there are more utilities.

When the new table is created, we can open the table in ArcMap and make a import in ArcMap>Tools>Add xy data. In this dialog box, we select a Coordinate system and open the visualization.

In the last step we must export to .shp format like a points file. In ArcMap extension 3DAnalyst>Convert>Features to 3D and select in Input feature attribute option z. In ArcGis we can query with language SQL, their results can be exported to forma t.dbf to obtain a new "Morphology.txt" file and work in Microstation or grouping o Fourier analysis.



| COLUMN | ITEM NAME | WIDTH | OUTPUT | TYPE | N.DEC | ALTERNATE NAME | INDEXED? |
|--------|------------|-------|--------|------|-------|----------------|----------|
| 1 | X | 12 | 12 | N | 4 | | - |
| 13 | Y | 12 | 12 | N | 4 | | - |
| 25 | Z | 12 | 12 | N | 4 | | - |
| 37 | A | 7 | 7 | N | 4 | | - |
| 44 | B | 7 | 7 | N | 4 | | - |
| 51 | C | 7 | 7 | N | 4 | | - |
| 58 | AZIMUT | 12 | 12 | N | 4 | | - |
| 70 | DIP | 12 | 12 | N | 4 | | - |
| 82 | M | 7 | 7 | N | 4 | | - |
| 89 | K | 7 | 7 | N | 4 | | - |
| 96 | POPULATION | 12 | 12 | N | 0 | | - |
| 108 | NUMBER | 12 | 12 | N | 0 | | - |
| 120 | RUGOSITY | 7 | 7 | N | 4 | | - |
| 127 | WEIGHT | 12 | 12 | N | 4 | | - |
| 139 | HEIGHT | 12 | 12 | N | 4 | | - |
| 151 | AREA | 12 | 12 | N | 4 | | - |
| 163 | FAMILIES | 10 | 10 | C | - | | - |

Fig. 14. Required Items to create a table from "Morphology.txt" file.

Microstation software can import morfology.txt format with the in-house software Morphometry.bas to simplify the morphology planes to show area and orientation, placed the plane in centroid positions. Every family will be drown in different colours

2.3.5.2 Filter Morphology Files

Morphology files create in **Tools > Morphology > Create Morphology File** can be filtered by his attributes.

Vector option: From a vector orientation and a degree tolerance the input file is divided in two new files, accepted orientations and dejected orientations.

Azimuth option: User defines a window orientation to selected data by Dip direction and Dip.

- Coplanarity index (M)
- Collinearity index (K)
- Number of points
- Area
- Length
- Height
- Roughness

2.3.5.3 From Morphology File to Gocad.ts

Planes created at **Tools > Morphology > Create Morphology File** can be exported to Gocad (Paradigm) like surfaces. In Gocad each plane is graphically represented by area, height and length attributes, with the real orientation and the position of the centroid. Input file is "Morphology.txt" and output file is "ExportCluster.ts". According to the Set number to which it belongs is assigned a different color.

Properties attached to the file are:

Set, Height, Length, Area, Azimuth (Dip direction), Dip, M (Coplanarity) and K (Collinearity).

2.3.5.4 From Cluster to Individualized File

All clusters included in cluster.txt can be separated in individual files cluster by cluster. The output files are numerate in order from 1.

2.3.5.5 Attribute Projected on a Line

a) Projection.

This utility allows to project one attribute from morphology file along a line. The attributes to be projected are:

- Roughness
- Dip Direction
- Dip
- Area

The line in which the attributes are projected can be defined by the user through a 3D point and a vector or calculate automatically, then is a perpendicular line at the average orientation planes and pass by the centroids average.

Result is a file planes with the new position centroid, average orientation and particular orientation and the selected attribute. The file name is called "Projection.txt".

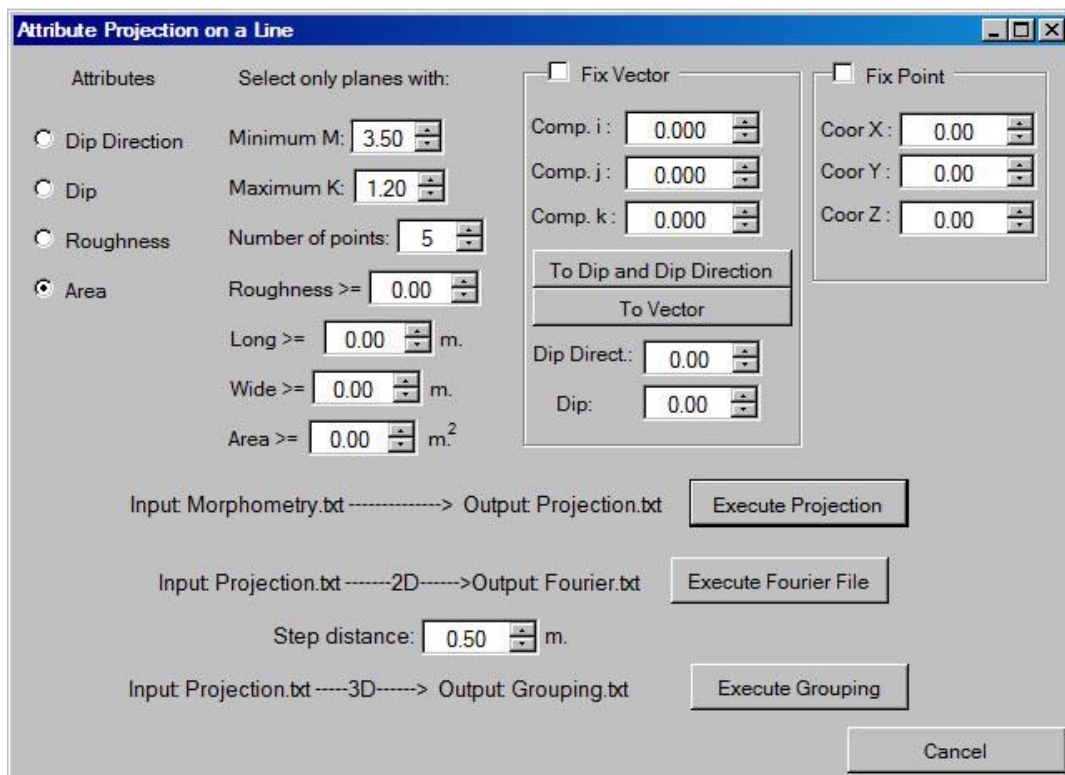


Fig. 15. Dialog box with the utilities to project attribute along a line.

b) Analysis Fourier File

Output file "Projection.txt" can be modified to add area attribute in steps defined by the user. Output file name is "Fourier.txt" and contain two parameters:

- Distance between steps from origin 0.
- Area value added for each step.

Utility: Fourier 2D file can be open en Excel sheet FTT and make analysis to study the planes frequency.

c) Grouping file

Is the same process that in Analysis Fourier File in 3D, with the original coordinates in 3D. Output file is called "Grouping.txt" and the structure is:

Grouping.txt: CoordinateX, CoordinateY, Coordinate Z, Total area step

Utility: Finality is create a file to show lineal graphic along a direction and observe possible tendency with excel or surfer.

2.3.5.6 Attribute Projected on a Plane

This utility allows to project the shape of the cluster over a selected plane. The information contained in the morphology files is projected over a choose plane.

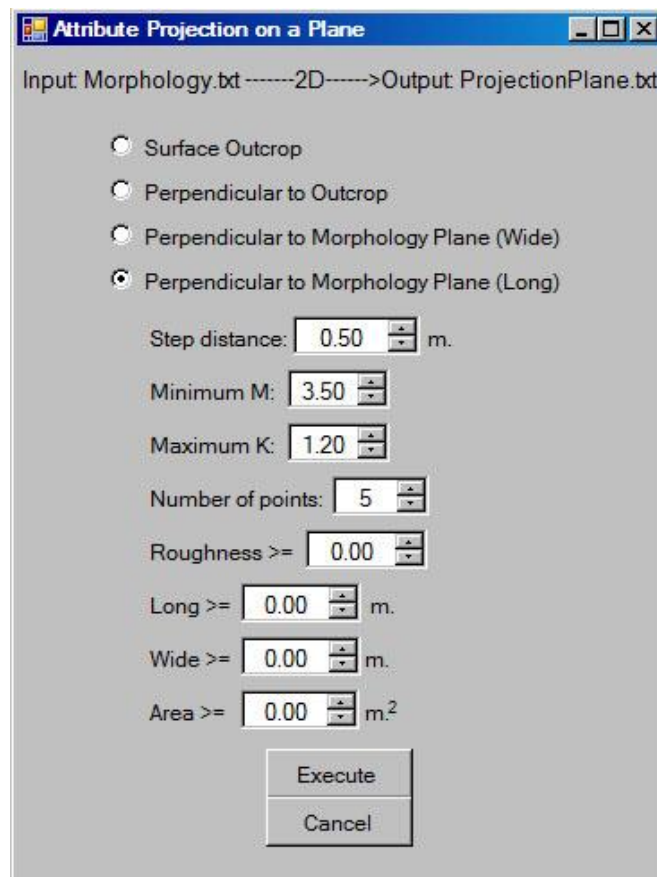


Fig. 16. Dialog box used to project an attribute over a selected plane.

The plane to be projected can be chosen between four options:

- **Surface outcrop:** The average plane of the outcrop surface, represented by the clusters centroids.
- **Perpendicular to outcrop:** The perpendicular plane at the average plane of the outcrop surface.
- **Perpendicular to Morphology plane (Wide/Length):** The surface with information is perpendicular at the average orientation of the planes contained in the morphology file and projected along the wide side of the planes.
- **Perpendicular to Morphology plane (Long/Height):** The surface with information is perpendicular at the average orientation of the planes contained in the morphology file and projected along the long side of the planes.

Morphology file can be filtered in order to its attributes:

Collinearity index (K), coplanarity index (M), number of points, roughness, long, wide and area. Output file name is "ProjectionPlane.txt" and the output structure is a codification raster with the size pixel defined by user and a codify of intersection of plane (1) or no (0): position x, position y and projection code (1/0)

2.3.5.7 Matching Coordinates-Morphology

This utility allows selecting items of the file morphology from coordinates centroids. The algorithm is created from the necessity to filter graphically or from SQL language a morphology file in environments as Microstation or Arc Gis.

Morphology files are plotted by its centroids and graphically can be edited (selections or removals of interesting items), the remaining centroids must be exported in a X,Y,Z file (Without commas). Shooting this utility, we can do matching the morphology file and the centroids file. The output file is a new file with the morphology items selected.

Both input files must have the same number of decimals.

2.3.5.8 Spacing and Density

Three utilities are integrated.

- **Calculate Spacing and Density (P20):** The utility calculates the spacing between Fractures/Planes for each Fracture Set and each Mechanical Unit. The morphology file can contain all sets. Unit and Sector define the new nomenclature files. There are two options to calculate the spacing.
 - Plane: Take the orientation of each plane/fracture.
 - Mean Direction: Take the average orientation (Principal or Resultant).

To calculate the spacing between the fractures/planes of the same fracture Set, the algorithm selects items from the morphology file with the same Name Set. Thus the algorithm knows the average orientation, its normal vector and average centroid. Both parameters define a line and this line is used as scanline. Individual items are projected (with each orientation or the average) over this line to calculate the spacing between planes. Output parameters are recorded in a file:

| | |
|--------------------------|--|
| <i>File:</i> | Input file name and path |
| <i>Unit:</i> | Unit nomenclature of the Mechanical Unit |
| <i>Sector:</i> | Sector nomenclature of the Mechanical Unit |
| <i>Set5:</i> | Set Name property |
| -----Spacing----- | |
| <i>Number of Planes:</i> | Number of items used with this Set |
| Name | |

Feature Plane Orientation: Selected option Plane or Average
Bimodal Axial Data distribution: True/False population
Orientation ScanLine Method: Principal Mean Direction or Resultant method
Set Orientation: Dip Direction and Dip orientation of scan line
Eigenvalues: τ_1, τ_2, τ_3
Shape parameter: $\ln(\tau_3/\tau_2)/\ln(\tau_2/\tau_1)$
Strenght parameter: $\ln(\tau_3/\tau_1)$

Coordinates start ScanLine (m)
Coordinates end ScanLine (m)
LengthScanLine (m)
Scanline density (#planes/m)
Scanline orientation (Azimuth-dip)
Mean Spacing (m)
Desv. Standart (m)

Besides, is incorporated a classification by distances to know the most frequent values, showed by the most frequent values, percentages, the mean area of the items and Standard deviation.

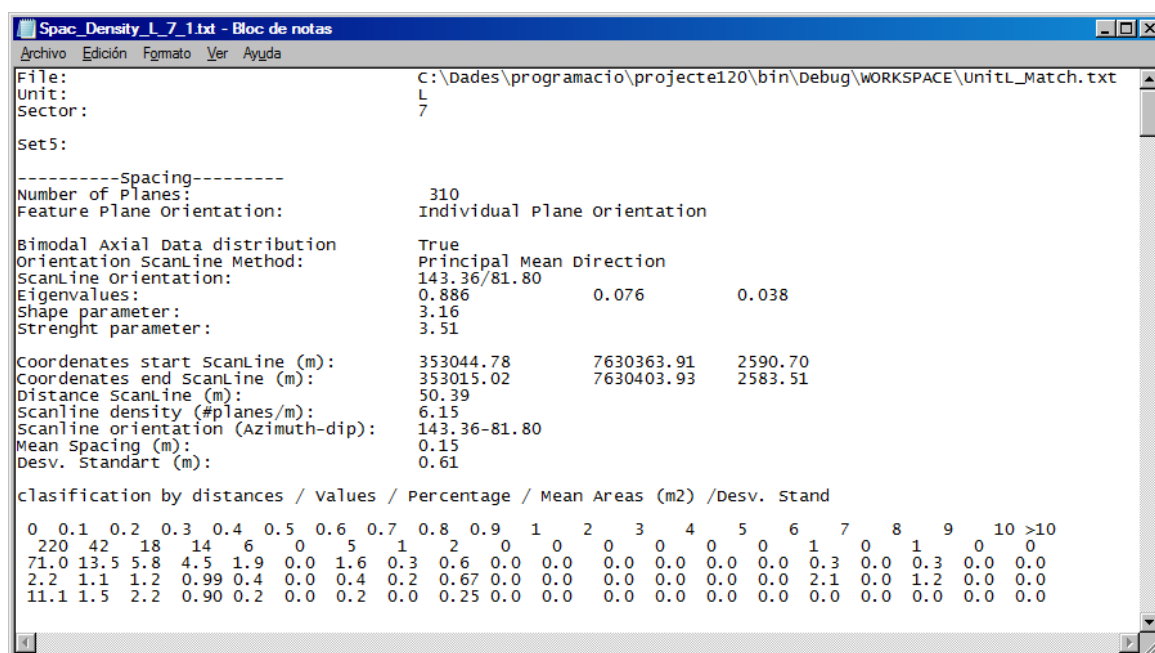


Fig. 17. Spacing output data calculated in Spacing tool.

P20 (Dershowitz & Herda, 1992), for calculate fracture density (number of fractures/planes by mechanical unit surface) is necessary obtain an average plane of the outcrop surface, deduced from the plane/fracture centroids. After, the fracture/planes are intersected by the average outcrop surface plane are used to know the number of fractures. With the addition of the triangles area defined by neighbouring centroids and the centroid of the average plane outcrop surface the total area is calculated. For this reason, the number of fractures used may be less than the mechanical unit of the Set.

Space_Density_Resum_MU_Sector_#.txt is an output file with another presentation of data with abstract in format ASCII code:

| | |
|----------------------------------|---|
| Set Name: | Set fracture Name |
| Number of Planes: | Number of fractures/planes used to calculate the spacing. |
| Fracture/Plane mean orientation: | In Dip Direction and Dip format |
| Mean Spacing: | Number of fracture/planes by scanline length. |
| Spacing by meter | Number of fracture in one meter |
| Scanline length | |
| Fracture/Plane Density: | Number of fractures by area. |
| Frequency: | Spacing between fractures/planes most frequent and in percentage. |

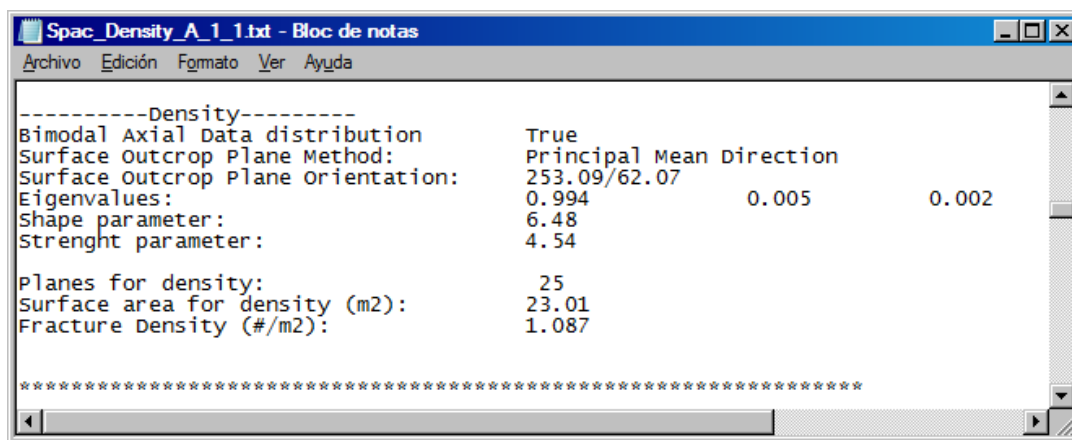


Fig. 18. Density output data calculated in Density tool.

A nomenclature counter is present in the menu in case of divide a mechanical unit and sector.

Finally for each Mechanical Unit and set name is creates a Gocad surface file in .ts format (2.3.4 **From Morphology File to Gocad.ts**)

- **Calculate P10 (Set/distance).** This utility make a counting of Set Name fractures properties along the Scanline by meter, is the parameter P10 (Dershowitz & Herda, 1992).

Utility:

Mean Resultant Direction: The selected features are grouped in a set and are calculated the Resultant of vector data, is an appropriate statistical method if polar data have a fisher distribution (with a single polarity).

Preferred Mean Orientation. It is an eigenvector method based in matrices (Bingham statistics) and on the concept of moments of inertia. The minimum moment of inertia is obtained for an axis passing through the "average" orientation and the maximum moment is obtained 90° away from the minimum, along an axis corresponding to the pole of the best-fit girdle. In the matrix of sums directions cosine products are obtained these axes, mutually with perpendicular directions, the eigenvectors, these eigenvalues are properties of the matrix. Eigenvector1 is the largest moment of inertia, and Eigenvector3 is the smallest moment of inertia, and estimates the centre of the densest cluster, similar

to a mean direction. Eigenvector2 is the emptiest part. They give as indication of the type of concentration in the distribution. $E1 < E2 < E3$. If $E1 = E2 < E3$ is a pure cluster. If $E1 < E2 = E3$ pure girdle. This method is the better to a Bingham distribution (bi-modal) or poles to folded surfaces. The process produces more information:

Normalized Eigenvalues. (Related documents, Allmendinger 1991). The best result for a bipolar distribution set is two short values and one very long and two values of equal length and one much shorter will define a girdle distribution. Three values of nearly equal result define a random distribution.

Shape parameter. $\ln(T3/T2)/\ln(T2/T1)$

Strength parameter: $\ln(T3/T1)$

Utility:

PolyWorks/Inspect/Cross-Sections/Create: With Method: Anchor on Model and options of Max point-to-plane distance +/- 0.2 and sampling step +/- 0.3. A cross section as a way of scanline can be drawn. On a second step an exportation is executed like Export Cross-Section to DXF (Microstation environment to be edited and reduced like vegetation) individually or multiple. Another way is export to Export Cross-Section Points to Text File... Can be present a problem with the order of the points, necessary to create the P10 and must be corrected (See: **Sorting Coordinates list**).

One time the Scanline points are correct, from Gocad must be imported the Gocad .ts surface of fractures/planes and must be imported the scanlines from File/import objects/Cultural Data/Column-based File as curve. The third step is activate Gocad in module Point Set and in File New choose From Curves and Surface Intersection, the resultant Point Set file is a file with the coordinates and is heir to the properties. After, these files must be exported like Custom ASCII or Excel.

Finally in Project 120 must be executed the tool Gocad Pointset X, Y, Z-----> set/m in steps defined by the user. Output is the number of fractures/planes for each fracture set along the scanline.

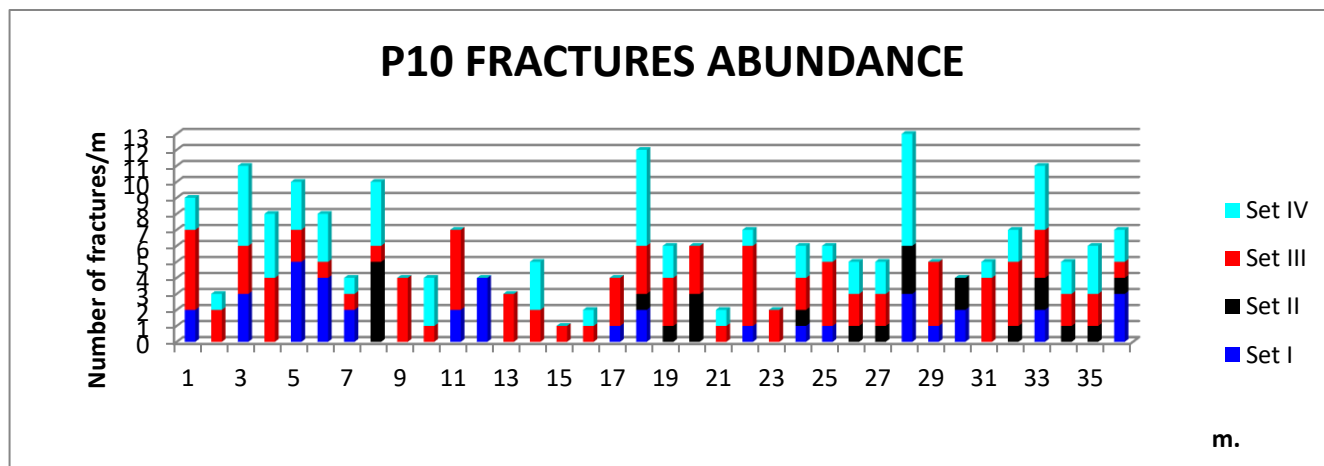


Fig. 19. Excel template to display data processed for SEFL and for each Mechanical Unit along the Scanline.

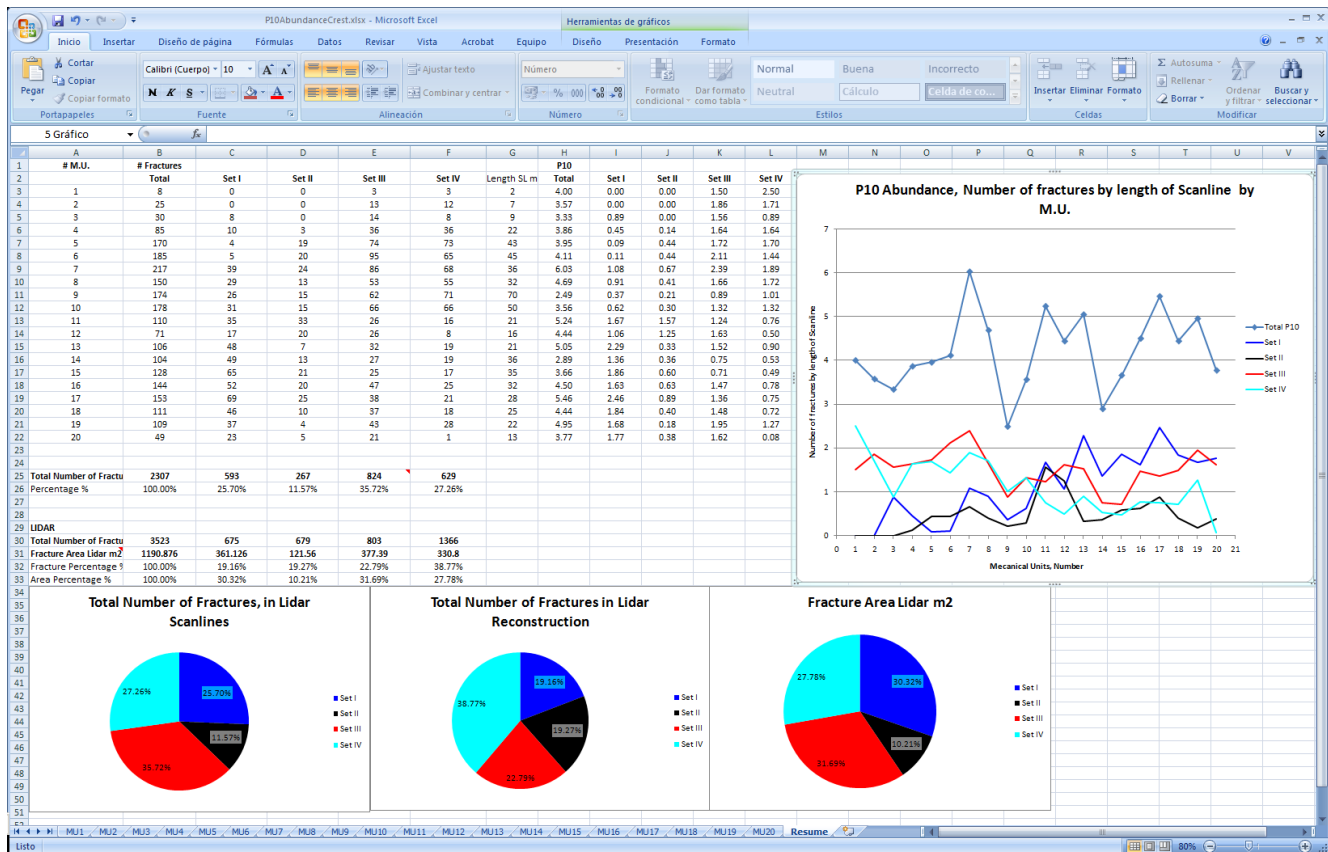


Fig. 20. Excel Template to display the resume data for all Mechanical Units.

- **Sorting Coordinates list.** In the preceding section it is necessary to obtain a sorted scanline. First option is a simple sorting for coordinates, searching the closest point, and the second is with a set properties and maximum distances to avoid gaps.

2.3.6 Reduce Files

The different SEFL files can be reduced in size with this tool. The output files get the name "Reduce.txt", with the same structure than the input file. Files from Planar Regression or point cloud files can be reduced of three different ways:

- **Reduce:** Select one item from each *Factor to reduce* from the file. The final number of points is showed.
- **Segmentation:** This option breaks the input file in a number of files determined by the quantity of points contained in the new files. New files will be created to contain all points in necessary number of files.

Subset: User introduces the two coordinates corners of a box and all points and attributes placed into the box are included in a new file. First coordinate point, Upper Right Front and second coordinate point Lower Left Bottom are the coordinates of the box.

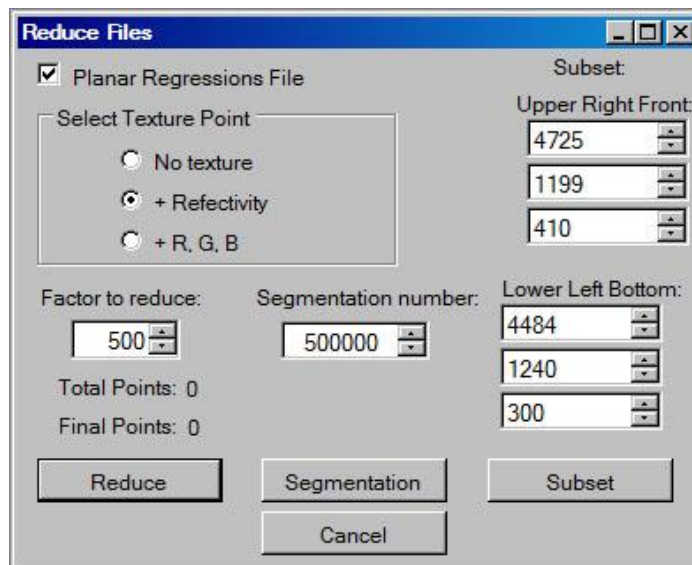


Fig. 21. Menu Dialog box to reduce the size of files.

2.3.7 Scan Line

In construction

2.3.8 Statistics from Planar Regressions File

Algorithm read files to create a statistic file from Dip direction and Dip attributes that can be visualized in **Tools > Stereoplot**. Input files are files from **Create Planar Regression**.

2.3.9 Stereoplot

This tool can visualize the stereographic density diagram of Dip directions and dips calculate in **Planar Regression > Create Planar Regressions** or **Tools > Stereoplot**. User can draw to 24 polygons to classify "families" of orientations and dips in files separated at **Attributes Tools > Attributes Classification**. These polygons are editable to be able to modify their shapes o delete nodes. The values of Dip Direction and Dip are shown in the dialog box in pole notation or planar.

Load statistic file: Read and load statistical files created in **Planar Regression > Create Planar Regressions** with activate option **Create statistics file** or **Tools > Stereoplot**. The algorithm segments the density of values between a maximum and a minimum in a scale of ten colours.

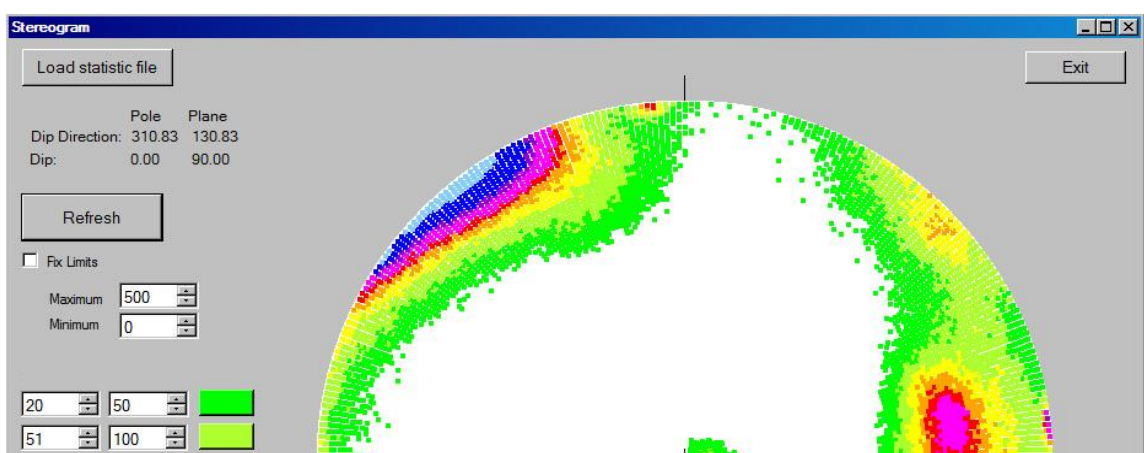


Fig. 22. Stereographic with a file statistic example loaded.

Refresh: The button visualizes the changes or the loss vision in the stereographic.

Fix limits: Activated this option, the maximum values and minimum can be changed to automatically visualize different intervals of density

Polygons: The function of the polygons is delimited the orientation families. Stereographic is used to observe the possible picks of density and observe the family limits. The maximum number of polygons is 24.

Draw polygon: Action of draw a polygon start when the user select the number of polygon option and select the button **Draw polygon**. With the mouse over the stereographic, click creates a node and double click close the polygon. Automatically, the following polygon number is active and the user can continue creating a new polygon after select button **Draw polygon** again.

Edit polygon: Edit polygon action, allow change node positions or delete nodes. To activate edit polygon, user must select the number of polygon option to be edited and press button **Edit polygon**, polygon lines selection will change of colour to be active. One click over the node, active the node, and one click over the new position define the change. Double click over a node delete the node. When all actions are ending **Refresh** button allow visualize the new edition results.

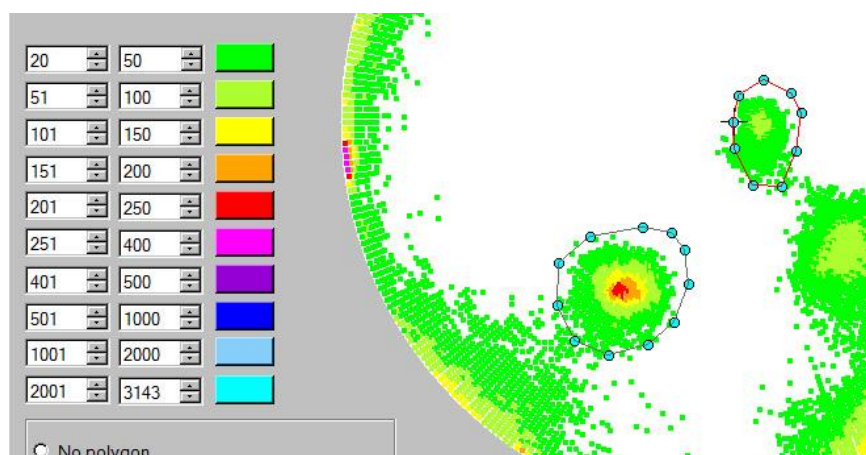


Fig. 23. Polygons example to define two new families

2.3.10 Translate and Rotate Coordinates

SEFL offers one dialog box to translate and rotate coordinates of a file. Output file name is "Coordinate.txt". Label offsets are the value of the coordinates to translate, and Rotation Angle the labels to rotate points around axes X (omega), Y (Phi) and Z (Kappa) and the point of rotation. The process only can rotate one angle value each time.

Utility: Is necessary make the rotation step by step, first one angle and after another. Kappa controls the rotation around axis Z. To place a horizontal plane, we need unrotate the dip (Kappa) and after the Dip direction (Omega & Phi).

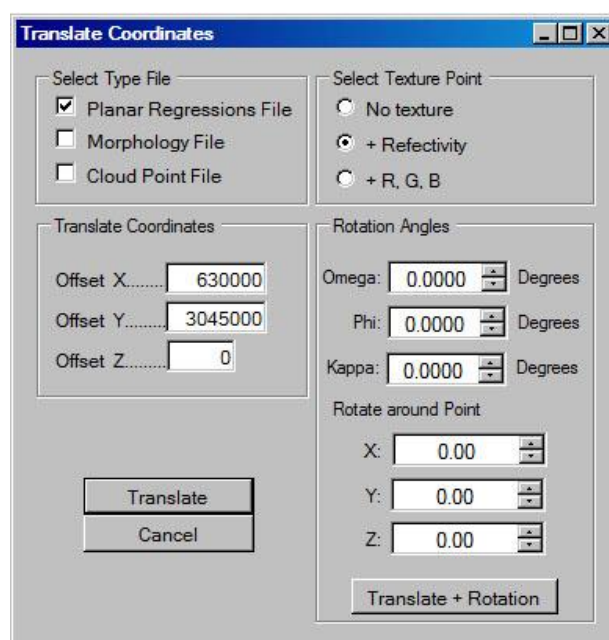


Fig. 24. Dialog box to translate and rotate points.

2.3.11 Scale

Project120 offers one dialog box to translate and rotate

2.4 Topography

This module has tools for manipulate cloudpoints with topographical purposes, such as reducing the number of points, or smooth reduction in topographic cloud point. The second tool elaborates comparisons in the Z axis.

2.4.1 Topography Module

The module can reduce the pointcloud density through the cells. Reducing the number of points is in agreement with the point number by cell or the cell size. The reduction is performed when the number of points contained in the cell is reduced to a single point. The user can choose whether the ending point is simplified by the arithmetic mean of the Z values or the ending point is the lowest Z value.

In the first menu, **Point Cloud Files**, the user load the point cloud with coordinates X, Y, Z or texture colour (R, G, B) or without texture or a Differences model.

In **Coarse Grid Definition** the user specifies the grid cell, this value is important because it is the minimum size where the point reduction occurs by cell size. The shape of the cell is completely rectangular. The population of this rectangle is reduced a one point in the next step.

Reduction by cell, the reduction to a single point by rectangle is executed according to selected values, for the lowest Z value or an average of Z.

Reduction by Slope, by rectangle with more than 5 points, a slope between points is calculated and the point exceeding the maximum slope is deleted or by distances or ranges.

The last option, **Differences along Z axis** is a comparative between models, the comparison is executed at Z coordinates, and point by point. The user can define a maximum range between points in a X-Y plane. In **threshold** we can adjust a window of differences in Z coordinate.

2.4.2 Filter Differences File

Output file differences model can be filtered by exclusion between maximum and minimum or filtered of reflectivity or RGB texture.