PROPHETA: A NEW MORPHOMETRIC ANALYSIS SOFTWARE FOR INDUSTRIAL PRODUCT DESIGN

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ABSTRACT:

This paper introduces ProPheTA (Product Phenetics-based Typology Assessment) as a new morphometric analysis software for industrial, phenetics-based product design (PP). Phenetics is used in Biology to determine similarities between species by comparing their formal external attributes. This way, PP replicates this procedure and, by doing a morphological analysis of different models from the same product family, makes it possible to relate their morphology with the user's emotional, perceptive, hedonic and buying intention response. All this requires working with CAD models, aligning, scaling, selecting them along the X, Y and Z axes, editing images, obtaining dissimilarity indexes, and correlating them with the user's response. Various CAD and morphometric computation tools not explicitly developed for these procedures are used to fulfil these tasks. File compatibility problems and excessive manual work and working time must be circumvented. ProPheTA has been developed in Matlab to solve these problems using a single platform. Its performance in a previous PP study, which related shape to buying intention, has been evaluated to demonstrate its reliability and speed. Results show a ten-time speed improvement in the computation with identical dissimilarity results. In addition, ProPheTA offers several advantages, such as ease of use, robust batch-processing capabilities, multiple output formats and improved compatibility. These functionalities, together with its ability to analyze the outline of 3D shapes without manual selection of landmark points, make it a versatile software application which is flexible, reliable and much faster. Thus, ProPheta is arguably valuable for helping speed up the application of PP in industrial design.

Keywords: phenetics, product design, morphology, computer-based assessment

RESUMEN:

Este trabajo introduce la aplicación ProPheTA (Product Phenetics-based Typology Assessment) como nuevo software de análisis morfométrico para el diseño basado en la Fenética de Producto (FP). La fenética se emplea en biología para establecer similitudes entre especies comparándolas según una serie de características formales externas. Así, la FP reproduce ese procedimiento para, partiendo del análisis morfológico de distintos modelos de una misma familia de productos, relacionar su morfología con la respuesta emocional, perceptiva, hedónica y de intención de compra del usuario. Para ello se requiere tratar con modelos CAD, alinearlos, escalarlos, seccionarlos a lo largo de los ejes X, Y, Z, editar imágenes, obtener índices de disimilitud formal y correlacionarlos con la respuesta del usuario. Actualmente, para esos tratamientos se usan varias herramientas de CAD y de cálculo morfométrico que no han sido concebidas para ese tipo de aplicación. Eso requiere soslayar problemas de compatibilidad de archivos, excesivo trabajo manual y mucho tiempo. ProPheta se ha programado en Matlab para resolver esos problemas trabajando en una plataforma única. Para demostrar su fiabilidad y rapidez se ha comparado su desempeño con el obtenido en una aplicación de la FP que relacionaba forma con intención de compra. Los resultados muestran que con ProPheTA se obtienen los mismos índices de disimilitud y diez veces más rápido. Además, ProPheTA dispone de ventajas adicionales como mayor facilidad de uso, una capacidad de procesamiento en lotes más robusta, varios formatos de salida y una elevada compatibilidad. Estas características, junto con su capacidad para analizar directamente el contorno de formas 3D sin la selección manual de puntos de referencia, la convierten en una plataforma versátil, flexible, fiable y mucho más rápida. Así, se puede afirmar que ProPheTA resulta especialmente útil para agilizar la aplicación de la FP al diseño industrial.

Palabras clave: fenética, diseño de producto, morfología, evaluación computacional

1.- INTRODUCTION

User-oriented design puts users and their needs at the centre of the design process of products and services [1]-[2]. Over time, Product success has become increasingly dependent on intangible qualities communicated through their formal attributes like aesthetics, style, and symbolic and emotional aspects [3]-[4]. In fact, these qualities have even acquired greater importance than functional product characteristics.

Various methodologies, which try to relate shape features of products with users' perceptions, have been put forward in recent years, like Kansei Engineering [5]-[6], Empathic Design [7], Product Semantics [8]-[9]-[10] and Conjoint Analysis [11], to name a few. From a

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shape-focused perspective, both Kansei Engineering and Conjoint Analysis discretize shape, decomposing the product into features and levels, where those features are mathematically related to users' perceptions, but the process is hardly generalizable.

Product Phenetics (PP) [12] represents a new approach that offers the designer tools to infer cognitive, emotional, hedonic and buying intention responses considering the entire morphology of the product. This methodology uses a high quantity of morphological information and subjective qualities relating to using products already on the market. Its application has helped establish relationships between morphology and emotional response [12], showing a significant correlation between product shapes and users' purchase intention [13], as well as relating shapes to pressure distribution and its influence on perceived comfort [14]. However, the steps required for handling 3D models and subsequent comparison of morphologies are numerous and currently employ a rather heterogeneous set of software tools, some of which have to perform computationally intensive tasks requiring time-consuming manual tasks.

A piece of software called ProPheTA (Product Phenetics-based Typology Assessment) has been developed to overcome the difficulties mentioned above. This application integrates a set of modules that allow dealing with 3D geometries and carrying out the morphology comparison process using the same environment, serving as the basis for a future application that would allow the automation of the conceptual design of products. The comparison of morphologies in PP requires a 3D space common to all models to be analyzed, in which they can be grouped, aligned and scaled with respect to specific reference criteria. In addition, these models must be sectioned into multiple 2D tomograms in which an automatic selection of landmark points can be performed to compute dissimilarity indices between morphologies based on Procrustes analysis [15]-[16].

While there are other commercial and free morphometric analysis applications, such as MorphoJ [17], Morpheus [18] and Morphome3cs II [19], these have been developed for specific applications and domains. Furthermore, they do not implement an automated process for selecting landmark points, nor are they easily integrated with other functionalities already mentioned and required in PP, such as 3D model slicing and two-by-two comparison of resulting tomograms. It was, therefore, necessary to devise a tool such as the one described in this paper, which is structured as follows. Section 2.1 describes the model coordinate adjustment module, section 2.2 describes the scaling module, section 2.3 details the tomogram acquisition module, section 2.4 describes the morphological analysis module and section 3, based on a previous study, compares the results of using ProPheTA with those obtained without the support of the application. Finally, section 4 includes a discussion and section 5 the conclusions.

2.- METHODOLOGY

The following describes the various modules of which ProPheTA is composed to perform the relevant functions in the different phases of the process.

2.1 COORDINATE ADJUSTMENT MODULE

The coordinate adjustment module incorporates functionality to load the geometry of 3D models in STL format into a 3D workspace. The STL format is commonly used in the fields of rapid prototyping, 3D printing and computer-aided manufacturing [20]-[21], ensuring high interoperability with other industrial design tools. Models can be oriented and positioned in 3D space as required by the user since, depending on the source data, the arrangement of the models with respect to the coordinate system can deviate considerably from the desired configuration. The reference system can be configured as right-handed or left-handed. Part of the graphical user interface of this module is shown in Figure 1.

Morphological analysis in PP requires the superposition and alignment of models. The coordinate adjustment module allows this process to be carried out automatically, based on profiles by product type, or manually (partially assisted). For example, in the case of drilling machines, the reference point of the morphologies is often defined as the insertion point of the tooling, and the axes for alignment are determined by considering the models in standard use arrangement [13].

In addition, ProPheTA has an automatic rotation functionality that facilitates the alignment of the models. The module has implemented two different procedures: automatic rotation by area and distance. In the first one, a reference area of the morphology is selected, and the model is rotated along two axes so that the projection of this area on the plane perpendicular to the third axis is minimal (Figure 2). In the second one, the model is iteratively rotated to maximize the dimensions of a model along one of the axes (Figure 2). In both cases, the size of the rotation steps is configurable.

Fig.1. Graphical interface of the Coordinate Adjustment and Scaling module (bottom)

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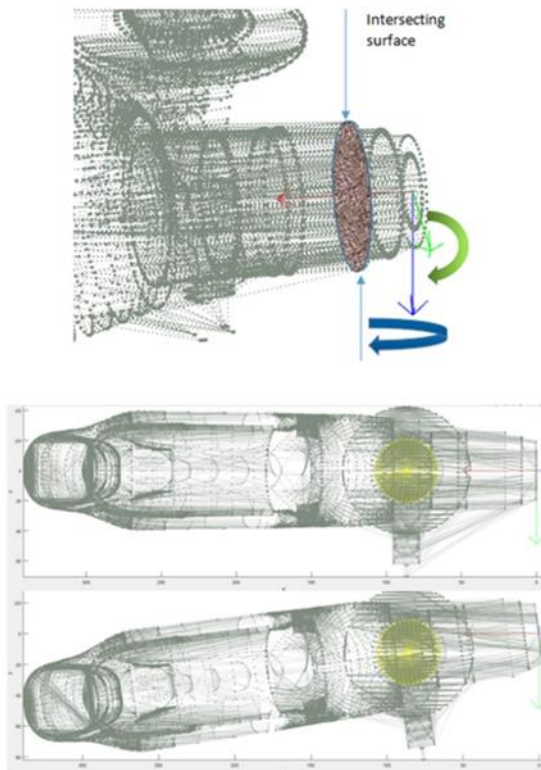
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Fig.2. Automatic rotation by area (top) and by distance (bottom)

2.2 SCALING MODULE

Morphological analysis in PP requires scaling the models proportionally to have the same dimension along the axis along which the tomograms are obtained. Thus, this module allows to specify an axis and a target size (Figure 1). The module automatically scales the model proportionally to the requested dimension without distorting its morphology.

The module also allows the computation of the step size between tomograms when scaling operations are not desired. In that case, the number of scans to be performed is entered, and the application computes the necessary step size for each model to be compared.

2.3 MODULE FOR TOMOGRAM ACQUISITION (SLICING)

The fundamental principle of morphological analysis is subdividing the three-dimensional problem into multiple two-dimensional problems. For this purpose, ProPheTA has a sectioning module from which tomograms of the models are obtained along the selected axis (figure 3). The resolution of the tomograms and the slicing interval are configurable depending on the accuracy required by the complexity of the 3D models.

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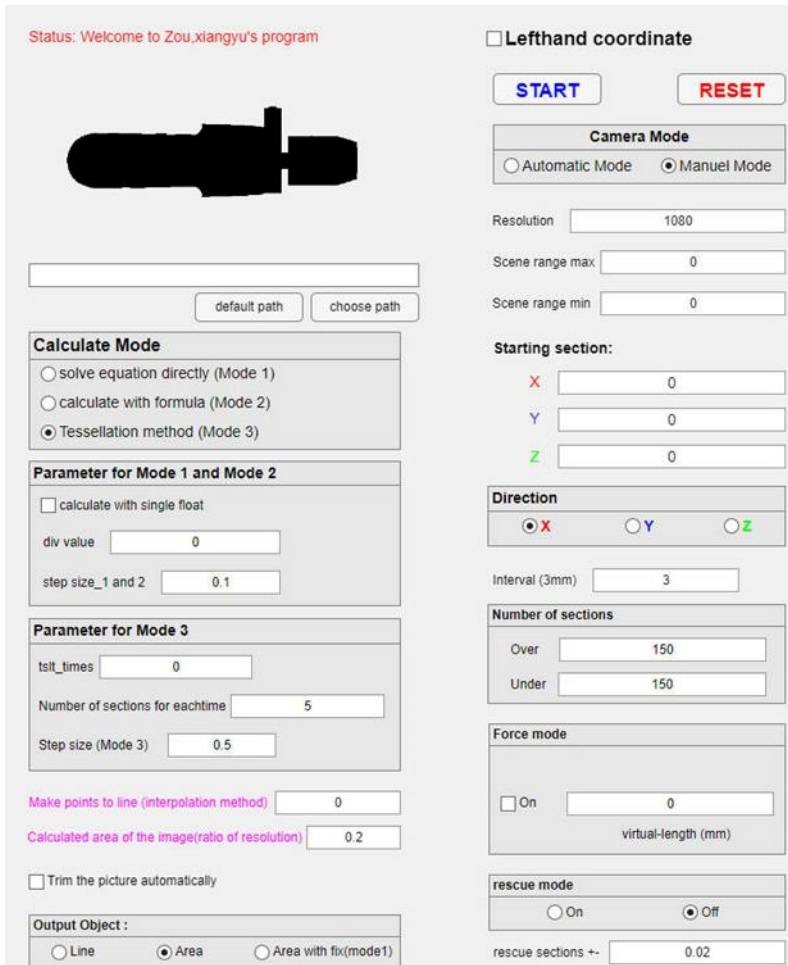
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Fig.3. The tomogram acquisition module interface

The tomogram acquisition module is based on tessellation [22]-[23], in which quadrant operations are performed on the triangles that define the morphology of the model in STL files. It is an iterative process in which the triangles intersected by the slicing plane are subdivided into smaller triangles. Of these smaller triangles, those whose geometric centre is farther away from the slicing plane are discarded. After several iterations, the geometric centres of the remaining triangles define the intersection between the original triangle and the plane (Figure 4).
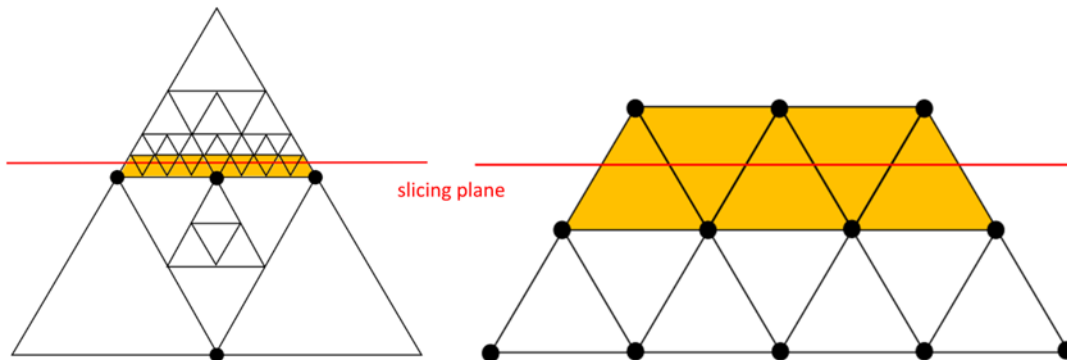

Fig.4. Triangle subdivision process

For complex morphologies, a more robust process is available. An offset is established so that two equidistant tomograms are made, anterior and posterior to the problematic position, and an average tomogram is computed from those.

The module stores each tomogram in a separate uncompressed bitmap image file. It then assigns a name that includes the original file's name containing the model and the position on the axis to which the tomogram corresponds.

2.4 MORPHOLOGICAL ANALYSIS MODULE

This module has a series of functions for the automatic determination of landmark points [24] and an implementation of the Procrustes method algorithm, adapted to process two series of tomograms generated by the previous module. This allows the computation of morphological dissimilarity between two 3D models. It also allows the selection of subsets of tomograms for analysis in certain areas or even to compare a single specific tomogram pair. The results can be exported to a Microsoft Excel spreadsheet. Figure 5 shows the module's graphical user interface.
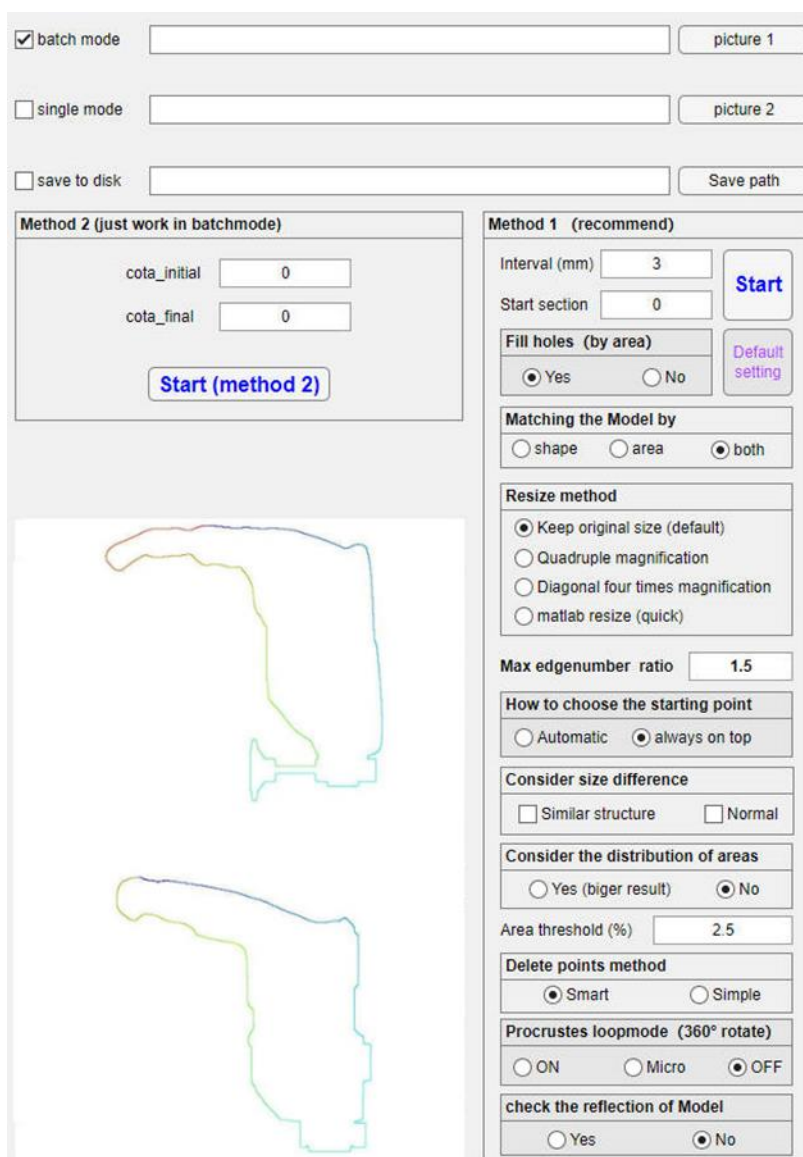

Fig.5. Morphological analysis module's graphical user interface

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Procrustes analysis is a shape analysis method that uses isomorphic scaling, translations and rotations to find the best fit between two or more geometrically referenced shapes [15]. The geometric dissimilarity index between two shapes is given by:

$$d = \frac{\sum_{i=1}^{n}\sum_{j=1}^{p}(x_{ij}-z_{ij})^2}{\sum_{i=1}^{n}\sum_{j=1}^{p}(x_{ij}-\overline{x}_i)^2}; \quad X = \begin{bmatrix} x_{11} & x_{12} \\ x_{21} & x_{22} \\ ... & ... \\ x_{n1} & x_{n2} \end{bmatrix}; \text{ and } Z = \begin{bmatrix} z_{11} & z_{12} \\ z_{21} & z_{22} \\ ... & ... \\ z_{n1} & z_{n2} \end{bmatrix}; \quad (1)$$

In equation (1), X and Z are matrices containing the landmark points of the two shapes to be compared. These points usually have a given geometrical meaning and are equivalent in both shapes, such as the vertices of a rectangle [15]-[24]. This module compares points of identical geometric meaning two by two.

The landmark points are determined using a self-developed selection and sequencing algorithm. In order to do this, all the points belonging to the shape perimeter are selected and ordered according to their location, the first being located at one of its ends determined by the user. This process is done clockwise around the perimeter. The number of points extracted from each perimeter will typically differ, so an interpolation algorithm is used to add points to the perimeter with the fewest number of points. The interpolation process is configurable to adapt to situations where the size difference between the two shapes to be compared is significant.

The slicing plane can generate tomograms with more than one shape. We will refer to these as geometric entities (Figure 6). For this case, the authors organize the calculation of the dissimilarity index in several steps. Each geometric entity is assigned a rank according to its size relative to the other geometric entities in its tomography. Once this has been done on the two tomograms to be compared, the entities of identical rank are paired two by two in order from highest to lowest rank. Once matched, the application will perform the Procrustes analysis of each pair according to expression 1, computing a dissimilarity index for each rank (d_1, d_2, d_3, ...). The module incorporates an alternative way of matching entities, in which the dissimilarity index of all entities in the first tomogram is computed with those in the second, with those with the lowest dissimilarity being assigned the same rank. In any case, once paired, the dissimilarities will be given by equations (2) and (3). In these expressions, d is the dissimilarity index between the two tomograms, w_i are the weight coefficients, and A_{1i} y A_{2i} are the areas of the two i-th rank geometric entities of tomograms 1 and 2.
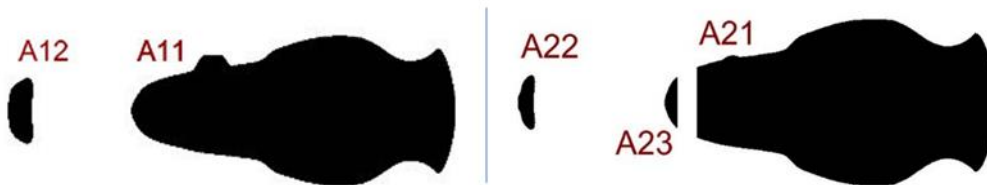

Fig.6. Tomographs that consist of more than one geometrical entity

$$d = w_1 \times d_1 + w_2 \times d_2 + d_3; \quad (2)$$

$$w_i = \frac{A_{1i}+A_{2i}}{A_{11}+A_{12}+A_{21}+A_{22}+A_{23}}; \quad (3)$$

The number of geometric entities in the two tomograms is often different. In Figure 6, the tomography on the right contains an entity that cannot be matched (A_{23}). In that case, the authors decided to calculate a penalty index that depends on the ratio of its area to the sum of all the areas of the two scans (*Equation 4*).

$$d_3 = \frac{A_{23}}{A_{11}+A_{12}+A_{21}+A_{22}+A_{23}}; \quad (4)$$

To calculate the total dissimilarity index along an axis from the dissimilarities of each pair of tomograms, the authors propose the formula described in expression 5. The values dz1, dz2, ..., dzθ are the dissimilarity indices obtained along the z-axis ($d_{z\,total}$), and θ is the total number of scans performed in each model. The total dissimilarities of the X and Y axes ($d_{x\,total}$ y $d_{y\,total}$) are calculated in the same way.

$$d_{z\,total} = \frac{\sqrt{d_{z1}^2+d_{z2}^2+\cdots+d_{z\theta}^2}}{\theta}; \quad (5)$$

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The authors also decided to calculate the global dissimilarity index, which reflects how different two 3D morphologies are, according to expression 6.

$$d_{global} = \sqrt{d_{x\,total}{}^2 + d_{y\,total}{}^2 + d_{z\,total}{}^2}; (6)$$

3.- RESULTS

In the case study below, the ProPheTA tool was used on data that was processed using a heterogeneous toolkit in a previous PP work [13]. The object of the study consisted of six domestic electric drills whose morphology needed to be compared with the model with the highest number of sales in order to check whether the sales ranking of the models was related to the formal similarities between the different products and the best-selling one.

3.1. DATA SETS

The test carried out with ProPheTA sought to confirm the validity and correct execution of the program based on the dissimilarity indices obtained in comparison with those obtained initially without the application's support, as well as to compare computation time differences between the two alternatives.

Originally there were six 3D models of drilling machines obtained using a Microscribe 3DX digitizing arm and the Rhinoceros application. With the original study tools, the models had to be exported to Solidworks, as the process of sectioning the models was done manually using that software. Using ProPheTA, the models were directly imported from the STL format.

The study used the model with the highest sales volume as the reference morphology. The remaining models were compared with this one, so five comparisons were made.

3.2. COORDINATE ADJUSTMENT AND ALIGNMENT

Before morphological comparisons were made, the two models were imported into a common 3D space, where they were overlaid and aligned using the point of attachment of the drill bit to the machine as a reference (Figure 7). Automatic adjustment algorithms were used for alignment. In some cases, a small manual adjustment had to be made with the controls described in section 2.1.

3.3. SCALING

For this study, the models were sliced along the vertical Z axis only, which is marked with the green colour in Figure 7. It was required to obtain the same number of scans in both models, so the non-reference model was scaled proportionally to the same size as the reference model on that axis. The process was carried out automatically by taking advantage of ProPheTA's automatic scaling capabilities. This was done for all pairs of models to be compared (1-2, 1-3, 1-4, 1-5 and 1-6, always keeping the reference model at its original size and scaling the others).

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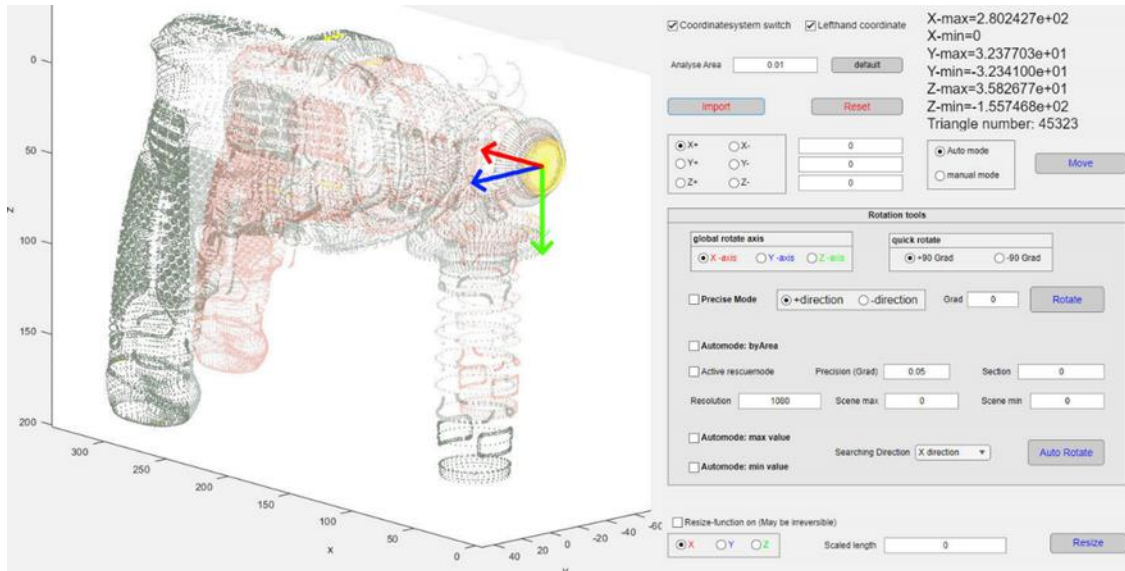Pag. 8 / 12

Fig.7. Location and alignment of two drilling machine models with detail of the Coordinate Adjustment and Alignment Module's graphical user interface.

3.4. SLICING

The slicing process along the Z-axis was set up in 3-mm steps to replicate previous work [13]. All machines were sectioned, and a total of 414 tomograms were obtained in bitmap image files (BMP). The application detected four sections with possible inconsistencies in two of the models, one of them being the reference model. By taking advantage of the manual slicing functionality and applying an offset at the problematic slicing point (see section 2.3), valid tomograms were obtained at the affected points. It should be noted that inconsistencies also appeared in the manual slicing process due to a failure in the modelling of the products. In that case, however, these positions were omitted from the morphological analysis, as no thought had yet been given to how to deal with this eventuality.

The task of sectioning the six models with PropheTA took one hour and 35 minutes, to which an additional 25 minutes had to be added to revise and correct the four problematic sections. In the original study, this task was carried out entirely manually using the Solidworks application and obtaining, step by step, intersections between a plane perpendicular to the slicing axis and the model itself. These intersections were then captured at identical scales and digitally edited, as they had to be black-and-white bitmaps to be processed by the morphological analysis algorithm used in the study. The time spent on the original work for the slicing phase was 21 hours.

3.5. MORPHOLOGICAL ANALYSIS

The ProPheTA morphological analysis engine is an evolution of the application used in [13], which was implemented as a Matlab script. The image files containing the tomograms, which the slicing module had generated, had their names coded with the model number, the perpendicular axis along which the slicing was performed and the position. Therefore, the module could select two by two scans to be compared to compute the dissimilarity index (Figure 5).

Table 1 contains the total dissimilarity indices along the Z-axis (d_z) obtained with ProPheTA, as well as those obtained with the heterogeneous set of tools used in [13] and the percentage variation obtained with respect to these.

Models being compared	dz obtained by ProPheTA	dz obtained using a heterogeneous set of tools	Variation from the value obtained with the heterogeneous set of tools
2 y 1	0,031927	0,032050	-0,384%
3 y 1	0,034950	0,035082	-0,376%
4 y 1	0,042312	0,042506	-0,456%
5 y 1	0,029943	0,029774	+0,568%
6 y 1	0,038628	0,038499	+0,335%

Table 1. Total dissimilarity indices obtained using ProPheTA and using a heterogeneous toolbox

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To verify that the use of ProPheTA did not alter the data distribution obtained by the heterogeneous toolkit, a two-sample Kolgomorov-Smirnov test was performed, with the null hypothesis being that both data sets belonged to the same distribution. The test was performed under MATLAB, in which a value for the Kolgomorov D statistic of 0.20 and a p-value of 0.9996 were obtained. With five samples per distribution (n = 5 and m = 5), the region of rejection of the hypothesis with a statistical significance of 0.05 would be given by [25]:

$$nmD \geq 20$$

In this case, nmD = 5, so the null hypothesis that both samples belonged to the same distribution of values could not be rejected. In fact, using the indices obtained with ProPheTA did not alter the results obtained in [13], allowing the same conclusions to be reached: the greater the formal dissimilarity with respect to the best-selling model, the lower the sales volume.

4.- DISCUSSION

In this paper, we have presented ProPheTA, an application that integrates a set of tools that allow to perform the necessary operations for the calculation of morphological dissimilarities in the context of PP. The application, developed in MATLAB, allows the positioning, aligning and scaling of the models to be compared in a common 3D space. It also allows the shapes to be sliced along an axis to obtain tomograms that are compared two by two, obtaining a formal dissimilarity index for each one of them. It then calculates a total dissimilarity per axis from the set of indices obtained along each axis, and finally obtains a global dissimilarity index from the total dissimilarity indices of the X, Y and Z axes, quantifying how morphologically different two products are.

To illustrate a use case of the application, a study in the field of PP using a heterogeneous set of tools has been used. The data set from comparing five drilling machine models with a sixth reference model was recalculated using ProPheTA. The Kolgomorov-Smirnov test applied to the two data sets showed that the null hypothesis that the dissimilarity indices follow the same distribution could not be ruled out, thus validating ProPheTA as a tool for morphological analysis in the field of PP. It also eliminated cumbersome work and yielded results ten times faster.

Other morphological analysis applications have been discarded because of the difficulty of integrating them with other modules or programmes to compute the dissimilarity indices provided and required for the application of PP. In this line, MorphoJ is a software that has been developed for morphometric computations [17]. It can work with both 2D and 3D information and has a considerable amount of functionalities implemented. For example, it can detect outliers in data sets, perform linear discriminant analyses, and even perform canonical correlation analyses. It can also perform Procrustes analysis. However, as it is a purely morphometric application, it does not have automatic routines for manipulating and slicing 3D models or batch processing capabilities to analyze sets of shapes. In fact, it cannot work directly with STL files and relies on external applications to select landmark points.

On the other hand, Morpheus allows the import of 3D models from PLY and OBJ files [18]. The format of its document files is very flexible, including metadata and other non-application-specific information. Simultaneous loading of several models is allowed, where one can be set as a reference. However, the application has no slicing routines or statistical functions implemented. For example, Procrustes analysis only performs the adjustment of the shapes to be compared, storing the information in a data file designed to be processed by routines implemented in the R language that are not included in the application. Finally, Morphome3cs is based on the R programming language and the .NET 4.5 architecture [19]. It has a graphical user interface with very powerful visualization capabilities. Some of its algorithms leverage the computational power of the GPU through Nvidia's CUDA API, substantially reducing computational time. Like MorphoJ, it has a large number of data analysis functions, which can be extended with scripts implemented in R or Python. Even more interesting are the morphological analysis capabilities for dense meshes not based on landmark selection. However, the application lacks the capabilities to slice the models automatically and to batch process large numbers of morphological comparisons. Likewise, there is no possibility of aligning the shapes from within the software, so external applications must be used in this case.

ProPheTA is still under development, and several actions are planned to broaden its scope and improve other minor aspects. The main lines of action include the following points:

- Adding functions: a module will be implemented to interpret the results of finite element analyses applied to the shapes and relate them to the results of morphological analyses. The module's core is already developed, but the interface and data comparison functions are still preliminary. Additional modules are also being planned, such as statistical procedures that allow the grouping of shapes and the analysis of significant differences in dependent variables such as perception, emotion, hedonic component or purchase intention.

- Improving the computational performance of the application: work is underway to improve and refactor the ProPheTA source code, and it is being adapted to parallel processing architectures to profit from today's multi-core processors. The code migration to C++ and Java is also planned to improve efficiency and reduce computational requirements.

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- Improvement of the graphical user interface: due to restrictions of the development platform used, how the 3D models are displayed and manipulated, although it does not affect the use of the application, can be improved. The aim is to provide the application with a clearer and more orderly interface and an integrated help and information query system.

Beyond these improvements, ProPheTA is, in its current state, a very relevant tool for morphological analysis by eliminating manual and tedious tasks, increasing versatility and reliability, and reducing computational times, acting as a single repository for 3D model processing and morphological analysis.

5.- CONCLUSIONS

The ProPheTA application has been developed to assist in the implementation of PP to relate industrial product morphology to associated product perception, emotional response, hedonic response and purchase intention. It solves the problem of computing dissimilarity between 3D models by splitting the problem into several computationally more manageable 2D problems, in which Procrustes analysis is used to calculate the geometric dissimilarity between tomograms of different products obtained at intervals along Cartesian axes. The application automates many tasks that previously had to be done by hand using a heterogeneous set of tools, resulting in considerable time and labour savings. The analysis of the application results with respect to those obtained with the previous tools shows no significant differences in the dissimilarities computed, thus confirming its reliability. The application is still under development, with some improvements to be implemented, especially regarding computational performance and the graphical user interface.

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