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VIRTUAL HERITAGE: HIGH QUALITY ACQUISITION AND PRESENTATION 3D

ViHAP3D

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MeshMerge 1.0

User Manual

Abstract

Post-processing tools are the software instruments needed to transform the raw data produced by 3D scanners (basically, a set of range maps) into optimized and application-oriented representations, which should integrate geometry and appearance and run smoothly in distributed environments.

This document, Deliverable **4.2.2** describes the features and usage of the MeshSimplify tool.

Deliverable **4.2, First Release of Post-Processing Tools** is composed by

- **4.2.1** Alignment Tool: MeshAlign v.2 with User Manual
- **4.2.2** Merge Tool: MeshMerge v.1 with User Manual

MESHMERGE *User Manual*

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System specification

- **OS platform:** Windows 98/NT/2000
- **Hard disk:** per consentire la memorizzazione del file di output
- **Main memory:** minimum 512 MB, recommended 1024 MB or more
- **CPU:** Intel Pentium III 1000 Mhz or more

Software Installation and Registration

Just copy the executables in a directory included in your path.

All software is comman-line and can be executed in any MS-DOS window shell.

After software installation is necessary to register your copy of merge software using the **VcgRegister.exe** program (see next figure):

Figura 1: VcgReg

Select the application Meshmerge Full from the menu and follow the instructions.

MeshMerge Tutorial

1.1. Introduction

Version 1.0 of the MeshMerge package contains only the Plymc tool. Other tools (implementing different reconstruction algorithms) could be added in future release versions.

Plymc program is used to merge toghether (this process is also called fusion) range map obtained during 3D scanning and aligned with the Meshalign program. The final result is a single model (triangle mesh) covering the entire object.

Plymc is based on a volumetric algorithm, the process is divided in three main parts: firstly all range maps are converted into intersections of the surfaces with the grid of a discretized volume (grid size is specified by user); when all range maps have been converted, the program merge together intersection almost coincidental (redundant data) ; finally a surface touching all intersection is reconstructed.

Acquisition of very large object can produce a huge amount of data, merging all the range map in a single step can be impossible even with very much free RAM. For this reason it is possible to perform the merging in separate steps: the user can specify to subdivide the final objects in different pieces to reduce memory occupancy. The partial reconstruction can afterwards be joined in a single model with ease.

1.2. How to choose the right resolution

The choice of the merging resolution it's fundamental to obtain good results. Resolution is expressed as the size of the grid used in the volumetric algorithm: smaller grid size produces more detailed results at the cost of a larger memory occupation.
To better evaluate the cell size is necessary to know:

- Size of the object
- Probing step of the scanner

Using a reconstruction resolution much higher than the scanner probing characteristics is useless, empirically the reconstruction cell size should be around *half* of the probing step of the scanner (but no smaller than this value).
The size of the object is used to evaluate the final size (in triangles) of the model produced: number of cell in the grid is easily found dividing the object bounding box volume by the size of merging cells. As an empiric evaluation, the number of triangles obtained from a grid with size **Nx * Ny * Nz = K^3** cells can expected to be **30 K^2** to **50 K^2.**

1.3. Plymc

The software is command line and can be executed in any MS-DOS window, two different command line can be used. The first possibility is to specify manually all the ply files involved (the ply files should be already aligned in a single coordinate system):

Plymc [options] file1.ply [file2.ply ...]

it is also possible to use directly the alignment obtained by the Meshalign software:

Plymc [options] file.aln

[options]

-o outfile.ply	specify the output file name (default is mcout.ply)
-c n_cells	Set numbers of k cells in the volume (default: 10000)
-V size	Set the required voxel size (override –c)
-S [ ]	Compute all the subvolumes of a partition (specify 3 integers) [*read below*]
-s [ ]	Compute only a subvolume (specify 6 integers) [*read below*]
-w ncell	Set distance field Expansion factor in voxel (default 3) overlapping parts from different range maps nearer than this value are merged toghether.
-W mm	Set distance field Exp. as an absolute dist (override -w)
-a at	Set angle threshold for distance field expansion (default 30)
-f ft	Set the fill threshold (default 12)

-L smp Set Number of smoothing passes to be done after merging of all meshes

-I Make a single smoothing step after each expansion

-G Disable Geodesic Quality

-O off Set an Offset (off < 0!) threshold and build a double surface (the second surface is internal, for rapid prototyping)

-q qt Set Quality threshold for smoothing. Only voxel with quality lower than the spec one are smoothed (default 1)

The Quality threshold is expressed in absolute units and represents the geodetic distance from the mesh border. I.e. -q3 means that all voxels that are within 3mm from the mesh border are smoothed.

To define a subvolume you have to specify six integers; the first three integers specify the subdivision along the three axis and the last three ones what subvolume you desire; examples:

- -s 1 1 1 0 0 0 default no subdivision at all
- -s 1 1 3 0 0 1 make three Z-slices and take the middle one
- -s 2 2 2 1 1 1 the last octant in a octree-like subdivision

To automatically compute all subvolumes of a given subdivision use '-S'

- -S 2 2 2 compute all the octant of a octree-like subdivision
- -S 1 1 4 compute four Z-slices

1.4. Merging of very large objects

When merging bigger objects (or when merging at very high resolution) it is recommended to use the subvolumes options. In this way the merging process is performed on each subvolume separately; this reduce the memory occupancy since only range map contributing the current part are loaded and analyzed

After this step multiple ply files are produced, each one containing a subpart of the object; all meshes are in the same coordinate space, so the final model is just the sum of all its subpart.

It's important to say that Plymc does not provide the joining function to reunite different parts of a sub-block merging; this functionality is implemented in the MeshSimplify package, see the related manual for more info.