

Parallel plug-in for 3D reconstruction of medical images

Abstract

In this paper we present our new parallel plug-in for creating virtual models of human organs and other parts of a human body. The plug-in is incorporated into Blender environment and Python scripts are used for its basic functionality. For more demanding operations parallel implementation in C++ language with hybrid technique combining OpenMP and MPI is used. The implementation can exploit computational power of both non-accelerated as well as Intel Xeon Phi accelerated compute nodes of a cluster. In this paper we describe the plug-in construction and its basic functionality. The figures illustrate the process of the 3D model reconstruction of a mandible.

Keywords: Medical imaging, Blender plug-in, Surface Reconstruction, Metaballs, Python, Intel Xeon Phi

1. Introduction

The rapid development of medical imaging and image processing methods leads to the development of the techniques that can be used to create virtual models of human body. The models of human organs are now widely required by doctors for diagnostic purposes and planning of patient treatments. For surgeons such models can be of high importance when very complicated surgical operations are planned.

In this paper parallel tool for processing of medical images is presented. This tool was developed to create 3D virtual model of human organs from CT (Computed Tomography) and MRI (Magnetic Resonance Imaging) scans. It exploits advanced techniques for model reconstruction, parallel implementation techniques of more demanding methods running on the supercomputer, and processing and rendering of results in the real time.

In our development an open-source software Blender is used. Tool presented in this paper is created as a new internal plug-in of Blender. GUI and basic behaviour of the plug-in are implemented in the Python scripting language. More demanding tools are implemented in C++ using libraries and directives for parallel programming like MPI and OpenMP. The control menu, which has a workflow structure, is placed in Blender's UV/Image Editor. Using this menu a required 3D model can be created in a few easy steps (loading of data, denoising, segmentation, boundary extraction and model reconstruction). The support for auxiliary calculations is performed by our new application called Blender-client.

In Section 2 we describe the creation and control of the internal plug-in and its component Blender-client. In Section 3 the workflow of the 3D model reconstruction and its basic components is outlined. In the final section, methods for surface reconstruction by the Metaballs and Poisson surface reconstruction method are depicted and their advantages and disadvantages are illustrated.

2. Internal plug-in

Our plug-in is based on the Blender version 2.75. To compile it the latest Intel library 2016.01 (MPI compiler) is used in combination with GCC version 4.9.3.

Using Intel compiler gives us the possibility to take all advantages of the Intel libraries such as vectorization, compilation for the Intel Xeon Phi coprocessor (MIC) and the exploitation of the latest standard of OpenMP and MPI for parallelization. It also allows distribution of calculations not only across the nodes, but also to the MIC coprocessors.

Our plug-in is made as a Blender module which is created and registered in the following manner:

```
51 static PyObject *poissonReconstruction_func
52 (PyObject * /*self*/, PyObject *args)
53 {
54     ...
55     if (!PyArg_ParseTuple(args, "Ooff", &pyBoundary,
56                             &pyBoundaryVector, ...))
57     {
58         return NULL;
59     }
60     ...
61     PyObject* vertices = PyList_New(vs.size());
62     PyObject* faces = PyList_New(fs.size());
63     ...
64     return Py_BuildValue("OO", vertices, faces);
65 }
66
67 static PyMethodDef methods[] =
68 {
69     ...
70     {"poissonReconstruction",
71      (PyCFunction)poissonReconstruction_func, METH_VARARGS, "" },
72     ...
73 }
74
75 static struct PyModuleDef module =
76 {
77     PyModuleDef_HEAD_INIT,
78     "_xxx_dicom",
79     ...
80     methods,
81     ...
82 }
83
84 static PyObject *XXX_initPython(void)
85 {
86     PyObject *mod = PyModule_Create(&module);
87     return (void*)mod;
88 }
89
90 static struct _inittab bpy_internal_modules[] =
```

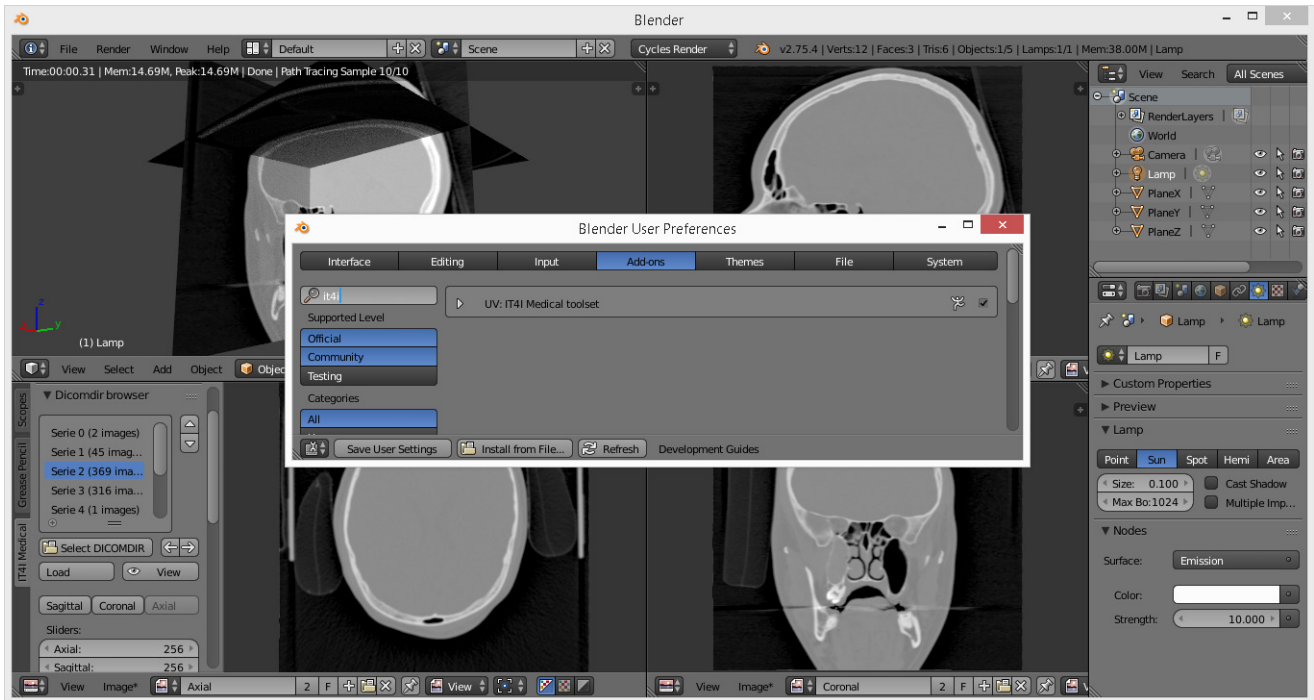


Figure 1: Blender environment with our plug-in

```

91 {
92   ...
93   { "_xxx_dicom", XXX_initPython },
94 };

```

```

139 # Create mesh and object
140 createMesh(verts, faces)
141
142 return {"FINISHED"}

```

95 Then it is enough to create Python script `__init__.py`
 96 and save it to directory `blender/2.75/scripts/addons/xxx`
 97 Example of such file could look like this:

143 Graphical elements were created by above mentioned
 144 script directly in Blender environment as it is depicted in
 145 Figure 1.

```

98 bl_info = {
99   "name": "XXX Medical toolset",
100   "category": "UVV",
101   "author": "",
102   "version": (1,0,0),
103   "description": "XXX Medical toolset"
104 }
105
106 import bpy, _xxx_dicom
107 ...
108 # Draw the panel for poisson method
109 class UIPoisson(Panel):
110   bl_idname = 'Poisson_panel_11'
111   bl_category = "XXX Medical"
112   bl_space_type = 'IMAGE_EDITOR'
113   bl_region_type = 'TOOLS'
114   bl_label = "Perform poisson reconstruction"
115
116   def draw(self, context):
117     layout = self.layout
118     scn = bpy.context.scene
119
120     row = layout.row()
121     row.prop(context.scene, "poisson_depth", slider=False)
122     row.prop(context.scene, "poisson_smooth", slider=False)
123
124     row = layout.row()
125     row.operator("custom.poisson_rec", icon="OBJECT_DATAMODE",
126               text="Make poisson reconstruction")
127
128 # Select Make poisson reconstruction button
129 class UIPoisson_rec(bpy.types.Operator):
130   bl_idname = "custom.poisson_rec"
131   bl_label = "Poisson rec"
132   bl_description = "Create poisson reconstruction from data"
133
134   def execute(self, context):
135     (verts, faces) =
136       _xxx_dicom.poissonReconstruction(boundary,
137     boundaryVector, ...)
138
139

```

146 2.1. Blender client

147 For faster execution of most time consuming algorithms,
 148 we have created a client system, which performs the most
 149 demanding tasks such as Marching Cubes method. The
 150 basic principle of the client system is shown in Figure 2.
 151 The Blender plug-in is used in Offload mode for computa-
 152 tion on MIC. The client itself works in symmetric mode. In
 153 this mode MPI programs are executed on both host com-
 154 puter (CPU) and MIC accelerator. Series of such clients
 155 working in symmetric mode can be established. Work di-
 156 vision and collection of results is maintained using MPI.
 157 Since MIC has a different architecture and requires dif-
 158 ferent binary file produced by the Intel compiler, two dif-
 159 ferent files have to be compiled before MPI program is
 160 executed.

161 3. Basic elements of the plug-in

162 The plug-in contains user friendly menu which has a
 163 workflow structure. It is placed in the UV/Image Editor,
 164 see Figure 1. By this menu a required 3D model can be
 165 created in a few easy steps:

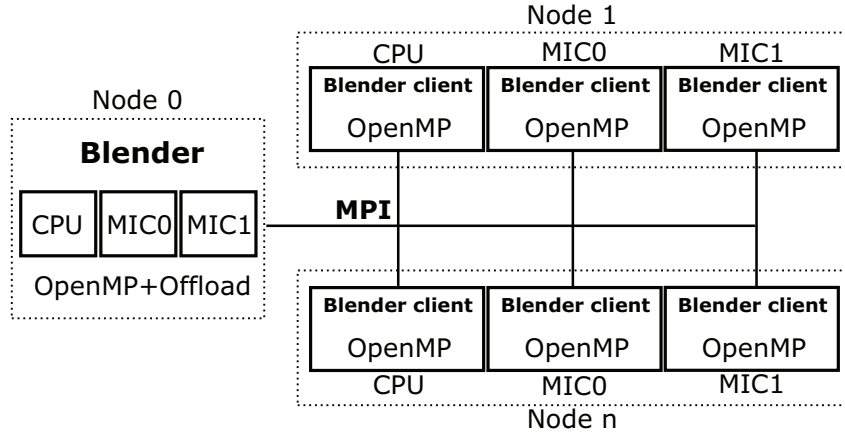


Figure 2: Overview of the communication between Blender and its client

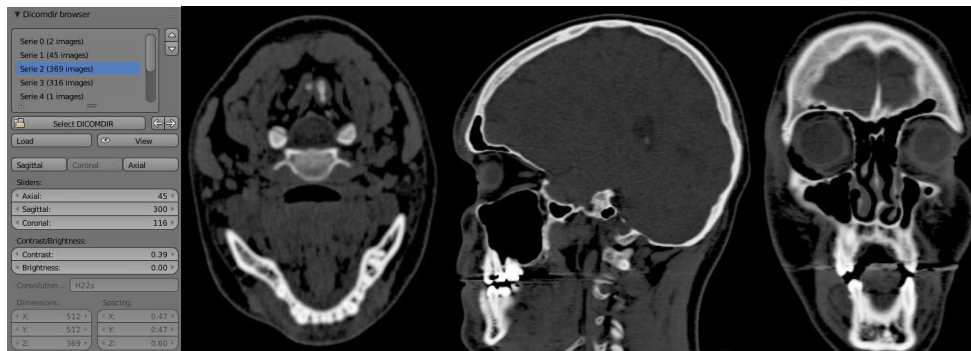


Figure 3: Loaded data

- 176 1. loading data from DICOM format (GDCM libraries
177 are used),
- 178 2. application of a filter to reduce image noise: e.g.,
179 Gaussian blur, BM3D filter, anisotropic filter,
- 180 3. image segmentation (e.g., thresholding, K-means clus-
181 tering),
- 182 4. boundary extraction, computation of normals,
- 183 5. 3D model reconstruction (e.g., Metaballs and Pois-
184 son surface reconstruction method),
- 185 6. visualization

176 3.1. Input data

177 In the first step of the process we have to obtain the
178 image data stored in the DICOM format, see Figure 3. DI-
179 COM (Digital Imaging and Communications in Medicine)
180 is a standard for storing, displaying and distributing med-
181 ical data obtained from CT, MRI or ultrasound. For load-
182 ing DICOM file we have integrated the library Grassroots
183 DICOM (GDCM) directly into Blender. GDCM is a C++
184 library for DICOM medical files.

185 The data from CT are stored as a images, usually as
186 axial slices at mutual axial distance. The distance between
187 two axial slices is mostly in range between 0.6 and 5.0
188 mm. For better accuracy of final model smaller values are
189 preferred.

190 After the data loading, volume of data could be re-
191 stricted to selected area of interest, see Figure 4, by pro-
192 viding tools such as box cutting tool or sphere cutting tool.

193 3.2. Image denoising

194 In present version of the plug-in, three different types of
195 image filters are used for denoising. The Gaussian smooth-
196 ing filter [1], anisotropic diffusion filter [2] and BM3D fil-
197 ter [3]. The results after denoising images by Gaussian
198 smoothing are shown in Figure 4.

199 3.3. Image segmentation

200 After images are pre-processed by denoising, image
201 segmentation is performed. The segmentation simplifies
202 representation of the image so localization of objects and
203 boundaries in the image can be created. We are using two
204 segmentation methods. Simple image thresholding [1] and
205 k-means clustering [4]. They can be used separately or
206 combined together.

207 3.3.1. Thresholding

208 The thresholding method is used to transform the orig-
209 inal image to the reduced version of the image by eliminat-
210 ing selected pixel intensity values [1]. Specifically values
211 grater than T_{max} and lower that T_{min} . The values between
212 T_{min} and T_{max} remain unchanged.

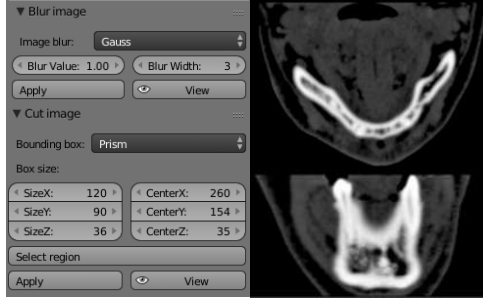


Figure 4: Denoising and cutting image

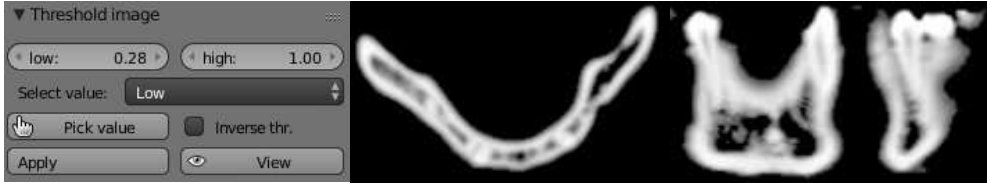


Figure 5: Thresholding

213 We can apply this segmentation technique repeatedly
 214 on the original images with different settings and then
 215 merge the results to provide advanced version of the thresh-
 216 olding method.

217 3.3.2. K-means clustering

218 K-means clustering is method originated in signal pro-
 219 cessing and is often used in data mining [4]. Generally this
 220 method can be employed in different areas including image
 221 processing as an image segmentation technique. This
 222 method divides pixels into k clusters according to some
 223 similar features like an intensity of a pixel and distance of
 224 the pixel intensity from a centroid pixel intensity.

225 The parallelization of this method by using Intel Xeon
 226 Phi was introduced in the paper [5].

227 3.4. Finding connected segments, boundary extraction and 228 computation of normals

229 The subsequent task after image segmentation is find-
 230 ing only the connected areas of selected segment and ex-
 231 traction of its boundary, see Figure 6 and Figure 7. Bound-
 232 ary of the segment is represented by a set of pixels obtained
 233 by the flood algorithm. This boundary is used for 3D re-
 234 construction using both methods, Poisson reconstruction
 235 and Metaballs. For application of Poisson method, com-
 236 putation of the normal vector $n_i = (n_x, n_y, n_z)$ in each point
 237 of the boundary is also necessary. The enumeration of the
 238 normal vector is depicted in Figure 8.

239 3.5. Surface reconstruction by Poisson method

240 As mentioned in previous subsection we are using Pois-
 241 son method as a technique for reconstruction of the 3D
 242 surface. Original name is Screened Poisson Surface Recon-
 243 struction [6, 7]. Advantage of this method is that it is not
 244 sensitive to noise, because it uses the whole set of points

245 at once. The basic procedure consists of three steps: com-
 246 putation of gradient $\nabla\chi_M$, computation of indicator func-
 247 tion χ_M and extraction of iso-surface ∂M (using Marching
 248 Cubes method). The gradient is computed from normals
 249 \vec{V} that serve as an input to the method.

250 We need to formulate and solve the Poisson problem.
 251 After supplying a set of vectors \vec{V} we need to find a func-
 252 tion $\tilde{\chi}$ using the equation $\nabla\tilde{\chi} = \vec{V}$. Since the set \vec{V} is not
 253 integrable, we use an operator of divergence and a least
 254 squares method for formulating Poisson equation

$$255 \Delta\tilde{\chi} = \nabla \cdot \vec{V}. \quad (1)$$

256 After discretization we get

$$257 \chi(p) = \sum_{i=1}^N x_i B_i(p), \quad (2)$$

258 where $B_i : \mathbb{R}^3 \rightarrow \mathbb{R}$ is a B-spline basis function.

259 To find the coefficients x_i we have to solve a system of
 260 linear equations $A_{ij}x_j = b_i$ (A is a sparse symmetric matrix)
 261 where

$$262 \begin{aligned} A_{ij} &= \int \langle \nabla B_i(q), \nabla B_j(q) \rangle dq \\ b_i &= \int \langle \nabla B_i(q), \vec{V}(q) \rangle dq \end{aligned} \quad (3)$$

263 In our solution we are using original implementation
 264 from the authors of the method. This version is already
 265 optimized and parallelized. The resulting 3D model com-
 266 ing from the Poisson reconstruction is shown in Figure 9.

267 3.6. Metaballs method

268 The development of a technology for creating realis-
 269 tic and visually interesting images of three-dimensional
 270 shapes goes back to 80's of the 20th century [8]. The



Figure 6: K-means clustering



Figure 7: Boundary extraction

271 method is based on the construction of the iso-surfaces. 293
 272 For each voxel with coordinates (x, y, z) the value of the 294
 273 potential function 295

$$274 \quad g(x, y, z) = \sum_{i=1}^N \begin{cases} f_i(x, y, z) & \text{for } f_i(x, y, z) \leq 1, \\ 0 & \text{other,} \end{cases} \quad (4)$$

275 is computed. In the previous formula N is a total number 296
 276 of the metaballs and $f_i(x, y, z)$ represents a function of the 297
 277 i -th metaball. In our implementation ellipsoidal metaballs 298
 278 with f_i in the form 299

$$279 \quad f_i(x, y, z) = \frac{(x - x_i^0)^2}{(r_i^x)^2} + \frac{(y - y_i^0)^2}{(r_i^y)^2} + \frac{(z - z_i^0)^2}{(r_i^z)^2} \quad (5)$$

280 are used. $r_i^x, r_i^y, r_i^z > 0$ determine the length of the semi- 300
 281 axes and (x_i^0, y_i^0, z_i^0) are coordinates of the centre of the i -th 301
 282 metaball. The choice of the ellipsoids is rational, since the 302
 283 distance between two neighbouring slices of CT is much 303
 284 bigger than the size of the pixels in one image. 304

285 The metaballs were originally introduced for a visual- 305
 286 ization of the objects without necessity of the surface mesh 306
 287 generation. This save both the computational time and 307
 288 the memory requirements, since such meshes could have 308
 289 several millions of triangles. However, our plug-in should 309
 290 have a possibility to generate high quality polygonal mesh 310
 291 for post-processing purposes such as generation of the STL 311
 292 file for a 3D print of the model. 312

293 To create a polygonal mesh from voxels the Marching 313
 294 Cubes method is used [9]. This method passes through the 314
 295 input scalar field and from the eight neighbouring points 315
 296 simultaneously (imaginary cube) computes the polygons 316
 297 which represents a corresponding part of the iso-surface.
 298 This method is time demanding and so the efficient parallel
 299 implementation is necessary. The results are depicted in
 300 Figure 9.

301 3.7. Visualization

302 For visualization, Blender Cycles engine is used, see
 303 Figure 9. Although the GPU acceleration is already im-
 304 plemented in Cycles, its functionality is limited. To accel-
 305 erate it, we use Intel Many Integrated Core architecture
 306 (MIC).

307 4. Drawbacks in using Poisson reconstruction and possible 308 solution

309 In terms of surface reconstruction quality, there is a
 310 significant drawback hidden in the principle of the Poisson
 311 method. The method provides satisfactory results, when
 312 reconstructing surfaces of thick objects, see Figure 10. In
 313 specific medical data, we are dealing with objects with
 314 walls as thin as 1 pixel. It is for example reconstruction of
 315 very thin bones, e.g. bones which create the orbital floor.
 316 In such cases the method can not resolve the enveloping

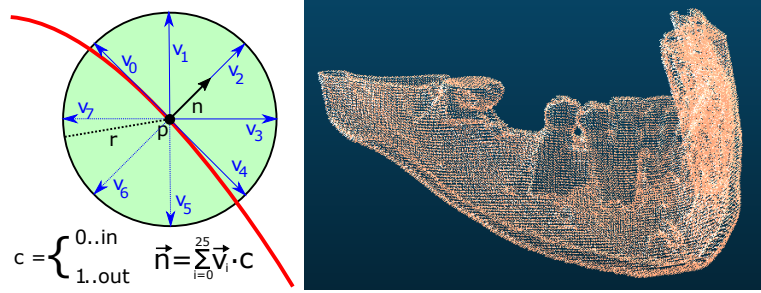


Figure 8: The enumeration of the normal $n_i = (n_x, n_y, n_z)$ from $26 \times$ vectors v_i in selected point of the boundary (left) and the result in all points of the boundary (right).

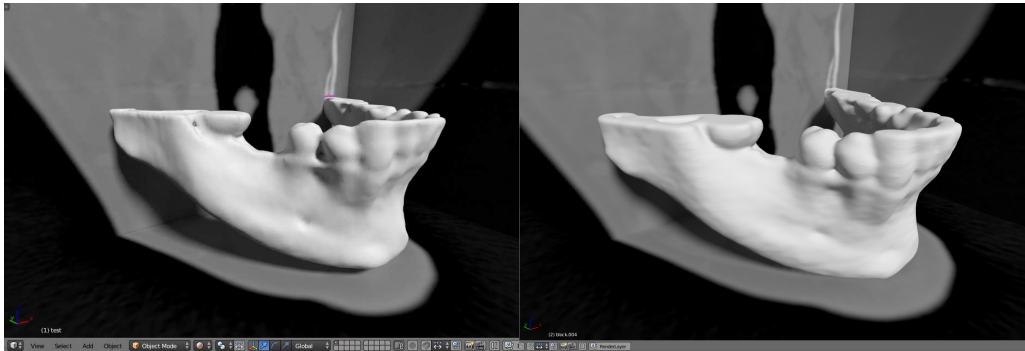


Figure 9: Comparison Poisson method (left) with Metaballs (right)

317 surface correctly and provides misleading or totally incor- 342
 318 rect results. For this reason different approach capable to 343
 319 overcome such problem have been searched and found in 344
 320 application of Metaballs. 345

321 5. Comparison of Poisson reconstruction and Metaballs 346
 322 method 347

323 We provide qualitative comparison of Poisson and Meta- 348
 324 balls method on two examples. First example is illustra- 349
 325 tive and describes the problem of the Poisson method while 350
 326 reconstructing the thin wall, see Figure 10. Effective so- 351
 327 lution to this problem is shown by Metaballs method also 352
 328 in Figure 10. Second example provides possible detailed 353
 329 reconstruction of mandible by both methods, see Figure 9. 354

330 6. Conclusion 355

331 In the paper we have introduced plug-in for Blender 356
 332 software. Plug-in is using powerful methods for medical 357
 333 image processing and 3D reconstruction of selected ob- 358
 334 jects. Metaballs method has been presented as a suitable 359
 335 solution for 3D reconstruction of problematic parts of hu- 360
 336 man body. As a show case we have provided comparison 361
 337 of the previously used Poisson method and Metaballs 362
 338 method. We have also shown possible advantages of Meta- 363
 339 balls method over Poisson method. Due to high compu- 364
 340 tational demands of selected methods extension to utiliza- 365
 341 tion of HPC resources is also effectively solved within the 366

342 plug-in. User have several options. Use multi-core option, 343
 344 one node solution for the calculations or extend his work 344
 345 by using our Blender-client to large number of computing 345
 346 nodes with plenty of processing cores including Xeon Phi 346
 accelerators. 347

347 7. Future work 348

349 Our goal is to prepare an application, which can create 349
 350 a 3D model in real-time. To accelerate all used methods 350
 351 necessary to complete this task we develop the parallel 351
 352 version of the code. 352

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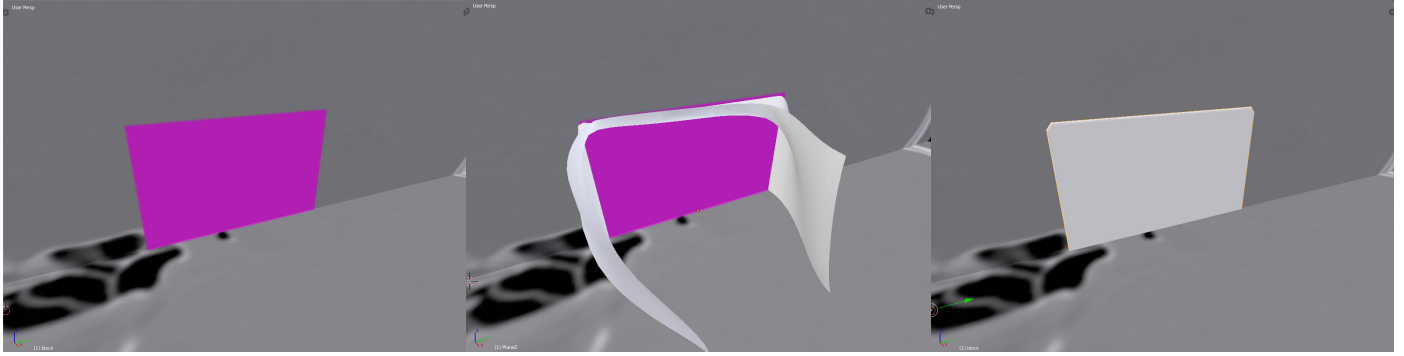


Figure 10: The reconstruction of thin surface: the segmented area (left), the reconstruction by poisson (middle), the reconstruction by metaballs

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