Transatlantic TUmour MOdel Repositories

D4.2.3

Final models wrapped up based on adopted markup languages

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ABSTRACT: This deliverable documents the TumorML wrapped existing cancer models provided by related EC projects (ACGT and ContraCancrum) and US (CViT). The markup acts as a standard format for transmitting models between elements of the TUMOR project infrastructure. A brief introduction to the related completed work in previous deliverables is provided, followed by the TumorML markup code listings of a selection of models taken from a snapshot of the TUMOR model repository. This deliverable should be reviewed in parallel with the deliverables D3.2 that provides the basic science background of each model, and D4.2.2 that describes in detail the TumorML specification.

KEYWORD LIST: markup, XML, cancer modelling, models

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Contents

1 Executive Summary

The TUMOR project aims at developing a European *clinically oriented* semantic-layered cancer digital model repository from existing EC projects that will be interoperable with the US grid-enabled semantic-layered digital model repository platform at CViT.org (Center for the Development of a Virtual Tumor, Massachusetts General Hospital (MGH), Boston, USA) which is NIH/NCI-caBIG compatible. This interoperable, CViT interfaced, environment will offer a range of services to international cancer modellers, bio-researchers and eventually clinicians aimed at supporting both basic cancer quantitative research and individualized optimization of cancer treatment. This 'transatlantic' project will therefore be the starting point for an international validation environment that will support joint applications, verification and validation of the clinical relevance of cancer models.

The purpose of this deliverable is to document the models published to the TUMOR model repository wrapped up in *TumorML*, a markup language to be used by the TUMOR project to enable interoperability between the component parts of the TUMOR infrastructure, described in deliverable D4.2.2. The models here have been published in various papers and the model authors have provided them to the TUMOR project and repository for public access.

In deliverable D4.2.1 a review the state-of-the-art markup languages was carried out to determine what existing vocabularies could be used to wrap up and annotate cancer models that will be stored and made available in the TUMOR digital model repository. The work described in deliverable D4.2.2 used the aforementioned design as a starting point and further refined the design in collaboration with WP3 and WP5 to produce the finalized schema. Deliverable D4.2.3, this document, presents a selection of models published to the TUMOR repository wrapped up in the markup developed in WP4.

2 Introduction

The main aim of the TUMOR project is to create a European-based digital repository for clinically oriented cancer models. The repository will store models provided by other EC projects such as the Advancing Clinico Genomic Trials on Cancer (ACGT) and the Clinically Oriented Translational Cancer Multilevel Modeling (ContraCancrum) projects. Biological model repositories are not novel, as demonstrated by existing services provided by the CellML repository, E-Cell, and biomodels.net to name but a few. However, one of the key aims of the TUMOR project is to enable the European cancer model repository to seamlessly interoperate with its US equivalent service that was developed by the Center for the Development of a Virtual Tumor (CViT) project led by the Massachusetts General Hospital (MGH) in Boston, USA. This 'transatlantic' link may ultimately allow the US and EU cancer research communities to pool their resources through effective model sharing, and act as a bridge between the two communities to foster further research advancements in cancer.

WP4 of the TUMOR project focuses on developing interoperable interfaces between the two repositories. This will be achieved by the development of a set of Web services to allow the two repositories to communicate with each other, a task led by MGH/Infotech. Secondly, and the focus of this deliverable, the TUMOR project is to develop a simulation markup language specifically targeted at the cancer modelling domain that will act as the standard communication format between elements of the TUMOR infrastructure and eventually for exporting models to external services. The success criteria of the new markup language are to achieve the following two goals.

1. Being able to demonstrate the import and export of models between the two repositories preserving as much metadata as possible, and translating between the US and EU schemas where appropriate.
2. Demonstrating a 'transatlantic' compound model linked together via markup describing each component model's interfaces and their couplings.

To address the specific domain of cancer modelling, we have developed a markup language, *TumorML*, to describe computational cancer models within TUMOR. The specification of TumorML is fully described in deliverable D4.2.2. The XML schema has been implemented and the TUMOR infrastructure uses TumorML as the medium for transmitting model descriptions between components of the infrastructure, as described in ID5.1.1.

This deliverable documents a selection of modelds taken from a snapshot of the TUMOR repository, where each of the models is wrapped up in TumorML markup. The models were uploaded and metadata populated by users manually, and the markup is automatically generated by the TUMOR web services.

3 TumorML descriptions of models

Here we provide the TumorML descriptions of a selection of models published to the TUMOR model repository that were made available at the time of publishing this deliverable (13 September 2012). The full description of the markup specification is found in deliverable D4.2.2 and will not be described again here. Detailed model descriptions, highilighting the basic science aspects of the following models, are provided in deliverable D3.2.

EGFR-ERK Pathway module

Note: This model is taken from the CViT DMR, provided by MGH.

```
<t:tumorml xmlns:t=http://www.tumor-project.eu/tumorml/1.0
xmlns:xsi=http://www.w3.org/2001/XMLSchema-instance
xsi:schemaLocation="http://www.tumor-project.eu/tumorml/1.0 http://www.tumor
project.eu/tumorml/1.0/tumorml_latest2.xsd" id="egfr_erk_pathway">
   <t:header>
      <t:title>EGFR-ERK Pathway</t:title>
      <t:description>
          This is a multiscale agent-based model for investigating expansion dynamics
of epithelial cancers (e.g., glioma, NSCLC) within a two-dimensional microenvironment.
At the molecular level, we present a specific EGFR-ERK intracellular signaling
pathway. The goal of this work is to provide useful insights into the quantitative
understanding of the relationship between signaling properties of underlying molecular
changes and the multi-cellular responses they may trigger.

          This particular version of the model has been first applied to non small cell
lung cancer (NSCLC) and has been published in Theoretical Biology and Medical
Modelling 2007, 4:50. (http://www.tbiomed.com/content/4/1/50). A follow-up work on
cross scale sensitivity analysis of this model has been published in BioSystems,
92(3): 249-258, 2008.
      </t:description>
      <t:creator>
         <t:person id="zhiui_wang">
             <t:fullname>Zhihui Wang</t:fullname>
         </t:person>
      </t:creator>
      <t:publisher>
         <t:person id="massachusetts_general_hospital">
            <t:fullname>Complex Biosystems Modeling Laboratory (CBML) Massachusetts
General Hospital</t:fullname>
         </t:person>
      </t:publisher>
      <t:contributor>
          <t:person id="thomas_s_deisboeck">
              <t:fullname>Thomas S. Deisboeck, M.D.</t:fullname>
          </t:person>
      </t:contributor>
      <t:date>2012-06-22T00:00:00+00:00</t:date>
      <t:math>discrete</t:math>
      <t:biocomplexityDirection>bottomUp</t:biocomplexityDirection>
      <t:cancer>Lung Cancer</t:cancer>
      <t:materialization>solid</t:materialization>
      <t:homogeneity>homogeneous</t:homogeneity>
      <t:imageBasedDetectability>imageable</t:imageBasedDetectability>
      <t:freeGrowth>false</t:freeGrowth>
      <t:treatmentIncluded>false</t:treatmentIncluded>
   </t:header>
    <t:model>
       <t:parameters>
          <t:in name="egf" optional="0">
              <t:value type="double"/>
          </t:in>
          <t:out name="cell cycle time" optional="0">
              <t:value type="double"/>
          </t:out>
          <t:out name="PLC_g" optional="0">
```

```
43                <t:value type="double"/>
44             </t:out>
45          </t:parameters>
46          <t:implementation id="urn:lsid:cvit.org:cmef:0.919920521935164">
47             <t:title>EGFR-ODE Model for EC revision #3 (6/25/2012) from Massachusetts
    General Hospital. Calculates Cell Cycle Time for EGF concentration. (Updated for
    command line parameters)</t:title>
48             <t:date>2012-06-25T00:00:00+00:00</t:date>
49             <t:package name="EGFR_ODE_EC" checksum="">
50                <t:file name="EGFR_ODE_EC" source="http://mgh-
    cvit.infotechsoft.com:8080/repository_files/deisboeck/2012/5/25/EGFR_ODE-2012-06-
    25.zip"/>
51          </t:package>
52          <t:command>EGFR_ODE_EC $egf</t:command>
53          <t:requirements>
54             <t:operatingSystem>linux</t:operatingSystem>
55             <t:CPUArchitecture>x86_64</t:CPUArchitecture>
56             <t:language>cpp</t:language>
57          </t:requirements>
58          </t:implementation>
59       </t:model>
60    </t:tumorml>
```

Note: The following 3 models are taken directly from the TUMOR model repository, as output by the repository web service.

FORTH-ICS-CML cancer metabolic model

```
1    <t:tumorml xmlns:t="http://www.tumor-project.eu/tumorml/1.0"
     xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
     xsi:schemaLocation="http://www.tumor-project.eu/tumorml/1.0 http://www.tumor-
     project.eu/tumorml/1.0/tumorml_latest2.xsd" id="3">
2       <t:header>
3          <t:title>FORTH-ICS-CML-Cancer Metabolic Model</t:title>
4          <t:description>
5             The cancer metabolic model as introduced is based on the genome-scale
     computational modeling approaches that have been successfully used in the past to
     predict the metabolic state of fast-growing microorganisms. A genome-scale human
     metabolic network reconstruction accounting for 1496 ORFs, 3742 reactions and 2766
     metabolites is used in order to model the metabolic capabilities of highly
     proliferating cancer human cells. Under the assumption that cancer cells are under a
     selective pressure to increase their proliferation rate.  Shlomi et al. introduce the
     metabolic demands for biomass synthesis required for high proliferation rates while
     they account for cellular capacity for metabolic enzymes. The model has been extended
     here to describe a glioblastoma-specific metabolic model by incorporating metabolic
     gene expression data ] of glioblastoma patients as constraints of the corresponding
     metabolic fluxes.
6          </t:description>
7          <t:date>2012-03-05T18:04:00+0000</t:date>
8          <t:math>continuous</t:math>
9          <t:biocomplexityDirection>bottomUp</t:biocomplexityDirection>
10         <t:cancer>Glioblastoma</t:cancer>
11         <t:materialization/>
12         <t:homogeneity>homogeneous</t:homogeneity>
13         <t:imageBasedDetectability>non-imageable</t:imageBasedDetectability>
14         <t:freeGrowth>1</t:freeGrowth>
15         <t:treatmentIncluded>0</t:treatmentIncluded>
16      </t:header>
17      <t:model>
18         <t:parameters>
19            <t:in name="glucose_uptake_bound" optional="0">
20               <t:value type="double"/>
21            </t:in>
22            <t:in name="glutamine_uptake_bound" optional="1">
23               <t:value type="double"/>
24            </t:in>
25            <t:in name="oxygen_uptake_bound " optional="1">
26               <t:value type="double"/>
27            </t:in>
28            <t:in name="PLCg_flux_lowbound " optional="1">
29               <t:value type="double"/>
30            </t:in>
31            <t:in name="Thres_geneflux_lowbound" optional="1">
32               <t:value type="double"/>
33            </t:in>
```

```
34          <t:out name="growth_rate " optional="0">
35             <t:value type="int"/>
36          </t:out>
37          <t:out name="cell-cycle duration " optional="0">
38             <t:value type="int"/>
39          </t:out>
40          <t:out name="glucose_uptake" optional="0">
41             <t:value type="double"/>
42          </t:out>
43          <t:out name="glutamine_uptake" optional="0">
44             <t:value type="double"/>
45          </t:out>
46          <t:out name="oxygen_uptake " optional="0">
47             <t:value type="double"/>
48          </t:out>
49          <t:out name="lactate_intake" optional="0">
50             <t:value type="double"/>
51          </t:out>
52          <t:out name="hydrogen_intake" optional="0">
53             <t:value type="double"/>
54          </t:out>
55       </t:parameters>
56       <t:implementation id="5">
57          <t:title>metab.zip</t:title>
58          <t:date>2012-06-13T18:55:00+0000</t:date>
59          <t:package name="metab.zip"
   checksum="244E3DBD5CE8FF525EE4A47F23F7D9B1FF084246">
60             <t:file name="metab.zip" source=".../tfiledata/download/45"/>
61          </t:package>
62          <t:command>./run_HomoSap_CancerCellMetab_Brain_Standalone.sh
   /usr/local/MATLAB/R2011a/</t:command>
63          <t:requirements>
64              <t:operatingSystem>linux</t:operatingSystem>
65              <t:CPUArchitecture>x86_64</t:CPUArchitecture>
66              <t:language>matlab</t:language>
67          </t:requirements>
68       </t:implementation>
69    </t:model>
70 </t:tumorml>
```

FORTH-ICS-CML tumor evolution to png: living cells vs time (h) model

```
1  <t:tumorml xmlns:t="http://www.tumor-project.eu/tumorml/1.0"
   xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
   xsi:schemaLocation="http://www.tumor-project.eu/tumorml/1.0 http://www.tumor-
   project.eu/tumorml/1.0/tumorml_latest2.xsd" id="4">
2     <t:header>
3        <t:title>FORTH-ICS-CML-Tumor Evolution to png: Living Cells vs Time (h)</t:title>
4        <t:description>
5            This tool transforms the tumor evolution data of Oncosimulator into a PNG
   formatted image for display
6        </t:description>
7        <t:date>2012-03-06T17:58:00+0000</t:date>
8        <t:math/>
9        <t:biocomplexityDirection/>
10       <t:cancer/>
11       <t:materialization/>
12       <t:homogeneity/>
13       <t:imageBasedDetectability/>
14       <t:freeGrowth>0</t:freeGrowth>
15       <t:treatmentIncluded>0</t:treatmentIncluded>
16    </t:header>
17    <t:model>
18       <t:parameters>
19          <t:in name="tumor_evolution.dat" optional="0">
20             <t:value type="filename"/>
21          </t:in>
22          <t:out name="tumor_evolution.png" optional="1">
23             <t:value type="filename"/>
24          </t:out>
25       </t:parameters>
26       <t:implementation id="6">
27          <t:title>tumor_evol.sh.zip</t:title>
28          <t:date>2012-06-18T18:00:00+0000</t:date>
29          <t:package name="tumor_evol.sh.zip"
   checksum="5A96C761821926CB614A631EAC7C76EB4476D10C">
30             <t:file name="tumor_evol.sh.zip" source=".../tfiledata/download/8"/>
```

```
          </t:package>
          <t:command>sh tumor_evol.sh $tumor_evolution.dat</t:command>
          <t:requirements>
             <t:operatingSystem>linux</t:operatingSystem>
             <t:CPUArchitecture/>
             <t:language>burne shell</t:language>
          </t:requirements>
       </t:implementation>
    </t:model>
</t:tumorml>
```

ICCS-NTUA-ISOG glioma therapy temozolomide & radiation model

```
<t:tumorml xmlns:t="http://www.tumor-project.eu/tumorml/1.0"
xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:schemaLocation="http://www.tumor-project.eu/tumorml/1.0 http://www.tumor-
project.eu/tumorml/1.0/tumorml_latest2.xsd" id="5">
   <t:header>
      <t:title>ICCS-NTUA-ISOG-Glioma Therapy Temozolomide &amp;amp; Radiation</t:title>
      <t:description>
         The model simulates the spatiotemporal response of glioblastoma multiforme to
combined modality treatment using radiation and chemotherapy with temozolomide agent.
It is based on the consideration of a discrete time and space stochastic cellular
automaton.
      </t:description>
      <t:date>2012-03-09T10:15:00+0000</t:date>
      <t:math>hybrid</t:math>
      <t:biocomplexityDirection>topDown</t:biocomplexityDirection>
      <t:cancer>Glioblastoma</t:cancer>
      <t:materialization>solid</t:materialization>
      <t:homogeneity>homogeneous</t:homogeneity>
      <t:imageBasedDetectability>imageable</t:imageBasedDetectability>
      <t:freeGrowth>0</t:freeGrowth>
      <t:treatmentIncluded>1</t:treatmentIncluded>
   </t:header>
   <t:model>
      <t:parameters>
         <t:in name="stem_cell_cycle_duration" optional="1">
            <t:value type="int"/>
         </t:in>
         <t:in name="limp_cell_cycle_duration" optional="1">
            <t:value type="int"/>
         </t:in>
         <t:in name="stem_max_g0_time" optional="1">
            <t:value type="int"/>
         </t:in>
         <t:in name="limp_max_g0_time" optional="1">
            <t:value type="int"/>
         </t:in>
         <t:in name="necrosis_time" optional="1">
            <t:value type="int"/>
         </t:in>
         <t:in name="apoptosis_time" optional="1">
            <t:value type="int"/>
         </t:in>
         <t:in name="diff_apopt_rate" optional="1">
            <t:value type="double"/>
         </t:in>
         <t:in name="diff_nec_rate" optional="1">
            <t:value type="double"/>
         </t:in>
         <t:in name="stem_g0_to_g1_fraction" optional="1">
            <t:value type="double"/>
         </t:in>
         <t:in name="limp_g0_to_g1_fraction" optional="1">
            <t:value type="double"/>
         </t:in>
         <t:in name="sleep_fraction" optional="1">
            <t:value type="double"/>
         </t:in>
         <t:in name="sym_fraction" optional="1">
            <t:value type="double"/>
         </t:in>
         <t:in name="stem_cell_kill_factor" optional="1">
            <t:value type="int"/>
         </t:in>
```

```
58          <t:in name="limp_cell_kill_factor" optional="1">
59             <t:value type="double"/>
60          </t:in>
61          <t:in name="limp_stages_number" optional="1">
62             <t:value type="int"/>
63          </t:in>
64          <t:in name="Voxel_dimension" optional="1">
65             <t:value type="int"/>
66          </t:in>
67          <t:in name="cell_density" optional="1">
68             <t:value type="int"/>
69          </t:in>
70          <t:in name="Image_width" optional="1">
71             <t:value type="int"/>
72          </t:in>
73          <t:in name="Image_depth" optional="1">
74             <t:value type="int"/>
75          </t:in>
76          <t:in name="Image_height" optional="1">
77             <t:value type="int"/>
78          </t:in>
79          <t:in name="tumor_length" optional="1">
80             <t:value type="int"/>
81          </t:in>
82          <t:in name="tumor_breadth" optional="1">
83             <t:value type="int"/>
84          </t:in>
85          <t:in name="tumor_width" optional="1">
86             <t:value type="int"/>
87          </t:in>
88          <t:in name="reconstruction" optional="1">
89             <t:value type="bool"/>
90          </t:in>
91          <t:in name="in_img" optional="1">
92             <t:value type="bool"/>
93          </t:in>
94          <t:in name="Image_filename" optional="1">
95             <t:value type="filename"/>
96          </t:in>
97          <t:in name="output_dir" optional="1">
98             <t:value type="filename"/>
99          </t:in>
100         <t:in name="execution_stop_time" optional="1">
101            <t:value type="int"/>
102         </t:in>
103         <t:in name="first_chemo_adm_time" optional="1">
104            <t:value type="int"/>
105         </t:in>
106         <t:in name="second_chemo_adm_time" optional="1">
107            <t:value type="int"/>
108         </t:in>
109         <t:in name="third_chemo_adm_time" optional="1">
110            <t:value type="int"/>
111         </t:in>
112         <t:in name="fourth_chemo_adm_time" optional="1">
113            <t:value type="int"/>
114         </t:in>
115         <t:in name="fifth_chemo_adm_time" optional="1">
116            <t:value type="int"/>
117         </t:in>
118         <t:in name="sixth_chemo_adm_time" optional="1">
119            <t:value type="int"/>
120         </t:in>
121         <t:in name="seventh_chemo_adm_time" optional="1">
122            <t:value type="int"/>
123         </t:in>
124         <t:in name="eighth_chemo_adm_time" optional="1">
125            <t:value type="int"/>
126         </t:in>
127         <t:in name="ninth_chemo_adm_time" optional="1">
128            <t:value type="int"/>
129         </t:in>
130         <t:in name="tenth_chemo_adm_time" optional="1">
131            <t:value type="int"/>
132         </t:in>
133         <t:in name="volume_of_distribution" optional="1">
134            <t:value type="double"/>
135         </t:in>
136         <t:in name="bioavailability" optional="1">
```

```
137             <t:value type="double"/>
138          </t:in>
139          <t:in name="absorption_rate" optional="1">
140             <t:value type="double"/>
141          </t:in>
142          <t:in name="elimination_rate" optional="1">
143             <t:value type="double"/>
144          </t:in>
145          <t:in name="survival_fraction" optional="1">
146             <t:value type="double"/>
147          </t:in>
148          <t:in name="chemo_dose" optional="1">
149             <t:value type="double"/>
150          </t:in>
151          <t:in name="first_radio_adm_time" optional="1">
152             <t:value type="int"/>
153          </t:in>
154          <t:in name="second_radio_adm_time" optional="1">
155             <t:value type="int"/>
156          </t:in>
157          <t:in name="third_radio_adm_time" optional="1">
158             <t:value type="int"/>
159          </t:in>
160          <t:in name="fourth_radio_adm_time" optional="1">
161             <t:value type="int"/>
162          </t:in>
163          <t:in name="fifth_radio_adm_time" optional="1">
164             <t:value type="int"/>
165          </t:in>
166          <t:in name="sixth_radio_adm_time" optional="1">
167             <t:value type="int"/>
168          </t:in>
169          <t:in name="seventh_radio_adm_time" optional="1">
170             <t:value type="int"/>
171          </t:in>
172          <t:in name="eighth_radio_adm_time" optional="1">
173             <t:value type="int"/>
174          </t:in>
175          <t:in name="ninth_radio_adm_time" optional="1">
176             <t:value type="int"/>
177          </t:in>
178          <t:in name="tenth_radio_adm_time" optional="1">
179             <t:value type="int"/>
180          </t:in>
181          <t:in name="alpha" optional="1">
182             <t:value type="double"/>
183          </t:in>
184          <t:in name="beta" optional="1">
185             <t:value type="double"/>
186          </t:in>
187          <t:in name="OER" optional="1">
188             <t:value type="double"/>
189          </t:in>
190          <t:in name="radio_dose" optional="1">
191             <t:value type="double"/>
192          </t:in>
193          <t:in name="apoptosis_rate" optional="1">
194             <t:value type="double"/>
195          </t:in>
196          <t:out name="Volume_reduction" optional="0">
197             <t:value type="string"/>
198          </t:out>
             <t:out name="Final_tumor_raw_image" optional="0">
199             <t:value type="filename"/>
200          </t:out>
201          <t:out name="Final_tumor_occupied_voxels" optional="0">
202             <t:value type="filename"/>
203          </t:out>
204          <t:out name="Initial_tumor_occupied_voxels" optional="0">
205             <t:value type="filename"/>
206          </t:out>
207          <t:out name="Parameters_log_file" optional="0">
208             <t:value type="filename"/>
209          </t:out>
210          <t:out name="Cell_composition_and_Td" optional="0">
211             <t:value type="filename"/>
212          </t:out>
213          <t:out name="Tumor_temporal_evolution" optional="0">
214             <t:value type="filename"/>
```

```
215          </t:out>
216       </t:parameters>
217       <t:implementation id="22">
218          <t:title>ICCS-NTUA-ISOG-glioma.zip</t:title>
219          <t:date>2012-06-21T19:42:00+0000</t:date>
220          <t:package name="ICCS-NTUA-ISOG-glioma.zip"
    checksum="F3B064FB9D901AB1A2EF440C0CA2F3839B957392">
221             <t:file name="ICCS-NTUA-ISOG-glioma.zip"
    source=".../tfiledata/download/33"/>
222          </t:package>
223          <t:command>./ICCS-NTUA-ISOG-glioma input.xml</t:command>
224          <t:requirements>
225             <t:operatingSystem>linux</t:operatingSystem>
226             <t:CPUArchitecture>x86_64</t:CPUArchitecture>
227             <t:language>cpp</t:language>
228          </t:requirements>
229       </t:implementation>
230       <t:implementation id="23">
231          <t:title>ICCS-NTUA-ISOG-GliomaTherapyTemozolomide&amp;amp;Radiation.zip</t:title>
232          <t:date>2012-06-21T19:48:00+0000</t:date>
233          <t:package name="ICCS-NTUA-ISOG-GliomaTherapyTemozolomide&amp;amp;Radiation.zip"
    checksum="7A45302A813E90F5B5FF5911D4253B9AFBDBF1FA">
234             <t:file name="ICCS-NTUA-ISOG-GliomaTherapyTemozolomide&amp;amp;Radiation.zip"
    source=".../tfiledata/download/144"/>
235          </t:package>
236          <t:command>ICCS-NTUA-ISOG-glioma.exe input.xml</t:command>
237          <t:requirements>
238             <t:operatingSystem>win7</t:operatingSystem>
239             <t:CPUArchitecture>x86_64</t:CPUArchitecture>
240             <t:language>cpp</t:language>
241          </t:requirements>
242       </t:implementation>
243    </t:model>
244 </t:tumorml>
```

4 Appendix I - Abbreviations and acronyms

ACGT – Advancing Clinico Genomic Trials on Cancer

caBIG – cancer Biomedical Informatics Grid

ContraCancrum - Clinically Oriented Translational Cancer Multilevel Modelling

CViT – Center for the Development of a Virtual Tumor

FORTH – Foundation for Research and Technology – Hellas

ICS – Institute of Computer Science

ICCS – Institute of Communications and Computer Systems

DMR – Digital Model Repository

MGH – Massachusetts General Hospital

NCI – National Cancer Institute

NIH – National Institute of Health

TUMOR – Transatlantic Tumor Model Repositories

TumorML – The TUMOR Markup Language

XML – Extensible Markup Language