### SUPPLEMENTARY INFORMATION

**Supplementary Table S3 (table) | Generic open source platforms for individual-based modelling in microbial ecology**

<table>
<thead>
<tr>
<th>Availability</th>
<th>CellModeller</th>
<th>CHASTE (Cancer, Heart And Soft Tissue Environment)</th>
<th>CompuCell3D</th>
<th>FLAME (Flexible Large-scale Agent Modelling Environment)</th>
<th>iDynoMiCS (individual-based Dynamics of Microbial Communities Simulator)</th>
<th>NetLogo</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Characteristics</strong></td>
<td>Plant tissue growth, Bacterial colonies</td>
<td>Tissue development, Cardiac electrophysiology</td>
<td>Tissue development, Biofilms</td>
<td>Tissue development, Economics</td>
<td>Microbes, Biofilms, Chemostats</td>
<td>Ecology, Sociology, Economics, Teaching, others</td>
</tr>
<tr>
<td><strong>Users can</strong></td>
<td>Specify model and control simulations by programming. Initialize simulations with location data from microscopic images</td>
<td>Build code from source; specify cell-based models and control simulations by programming; use CHASTE as library for own development</td>
<td>Specify model with tool-specific XML file or Python script, helped by Wizard, GUI to run simulation</td>
<td>Specify model with tool-specific XML file combined with specifying agent transition functions by programming in C; all inputs are converted into C source code which the user compiles and runs</td>
<td>Specify model with tool-specific XML file, which requires no programming skills; GUI helps user generate XML file; further customization or extension does require programming skills</td>
<td>Rapidly develop model by programming agent behaviour and using a GUI to control the simulation and view output</td>
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<tr>
<td><strong>Input and output formats</strong></td>
<td>Models loaded/saved as Python scripts; simulation states loaded/saved as Pickles (Python object serialization)</td>
<td>Non cardiac models are specified by C++ code input; many standard text file formats for cell, mesh and other data output, suitable for VTK and meshing software</td>
<td>Models specified as tool-specific XML or Python scripts and lattice and concentration field text files; data output as VTK and other text files</td>
<td>Output of simulation data in tool-specific XML format</td>
<td>Models specified and simulation data saved/loaded as tool-specific XML files; can also read in previous simulation state and random number generator state to continue simulation with same or altered conditions/agents</td>
<td>Models are specified in Scala, simulation state or time series data can be saved/loaded as CSV files</td>
</tr>
</tbody>
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<td>Stable release</td>
<td>4.2.1 (07/2015)</td>
<td>3.3 (01/2015)</td>
<td>3.7.4 (08/2015)</td>
<td>0.17.0 (07/2012)</td>
<td>1.3 (06/2015)</td>
</tr>
<tr>
<td>Programming language</td>
<td>Python</td>
<td>C++</td>
<td>C++, user specifies models in XML or Python</td>
<td>C, model specified with XML files and C functions</td>
<td>Java (simulation output analysis in Matlab, R, Python)</td>
</tr>
<tr>
<td>Influenced by</td>
<td>Engineering tissue shapes, synthetic biology</td>
<td>Systems biology, software engineering</td>
<td>Cellular Potts Model, Complexity science</td>
<td>State machines, Parallel computing</td>
<td>Swarm, Gecko, BacSim, Framework, Biofilm models, Complexity science</td>
</tr>
<tr>
<td>OS</td>
<td>Any with Python</td>
<td>Linux, OS X, (Win)</td>
<td>Windows, OS X, Linux</td>
<td>Any with C compiler</td>
<td>Any with Java</td>
</tr>
<tr>
<td>Example applications</td>
<td>Plant meristem growth(^1), Rod-shaped bacteria generating fractal patterns(^2)</td>
<td>Intestinal crypts(^1) / colorectal cancer(^3), Heart electromechanics(^3)</td>
<td>Tissue morphogenesis (limb(^4) and somite(^5) formation, tumour growth(^6), angiogenesis(^7)), biofilm development(^10)</td>
<td>Skin(^8), NF-κB signalling cascade(^12), <em>E. coli</em> interacting with oxygen(^13), Market economy(^14)</td>
<td>Metabolic switching aerobic/anaerobic(^15), Plasmid transfer in biofilms(^16), Metabolic cooperation(^17), Aging in chemostats(^18)</td>
</tr>
</tbody>
</table>

**Abbreviations:**

CA: Cellular Automaton  
CSV: Comma Separated Value text file  
GIS: Geographical Information System (for spatial or geographical data)  
GUI: Graphical User Interface  
OS: Operating System  
PDE: Partial Differential Equations  
VTK: Visualization Tool Kit  
XML: Extensible Markup Language
References:


