E-Cell 3D

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Virtual Cell
W/ 127 genes

The E-CELL Project

Erythrocyte
Mitochondria
Chemotaxis
E-Cell Project

- **Technology project** aiming for dynamic whole-cell simulation
  - development of
    - simulator
    - simulation methods
    - quantitative measurement technologies (ex. metabolomics)
    - modeling methods

- **E-Cell 3 (current version)**
  - coherent system (no spatial information)
  - programmable with Python API
  - multi-algorithm/multi-timescale simulation with DEVS (discrete event systems)

- **E-Cell 4 (under development)**
  - handles spatial information
Quartz Composer

- **Development API shipped with MacOS X 10.4 or above**
  - Graphical programming environment
  - OpenGL + Shading Language + AppKit data types + javascript
  - Easy integration with Cocoa GUI

- **Custom patch development**
  - Objective-C (or other languages supporting Cocoa, such as RubyCocoa)
  - OpenGL for better performance
A macro patch renders its subpatches an image.

A macro basically creates a new string destination in the form of an IE. The subpatches of this macro then render to that new destination 2D output of the original one. The resulting string can be used as any regular image, for example, it can be passed to Core Image filters or used as a mask.

Dimensions of the image can be set by the patch’s settings. If set to (0,0), the image dimensions will automatically use the dimensions of the original string.
What’s new in 2008? (I)

- **Rewrite for MacOS X 10.5 (Leopard)**
  - Previous version was based on *unofficial API* (reverse-engineering...) on MacOS X 10.4 (Tiger)
  - **Objective-C 2.0** in new Xcode
  - We had to **rewrite** most of the OpenGL part of Quartz Composer Custom Patch.
  - Now completely ported and optimized.
  - Obviously a drawback of using non open-source framework...
  - but, Quartz Composer in MacOS X 10.6 (Snow Leopard) drastically improved its performance with OpenCL.
What’s new in 2008? (2)

- **Eliminating E-Cell dependence**
  - The system is now based on SBML models (not EML anymore)
  - Simulation engine can be any simulator supporting SBML
  - Systems Biology Workbench (SBW) bridge is under development, but currently takes intermediate file.
  - 3D layout is based on Graph::Layout::Aesthetic (CPAN)
Demo
E-Cell Simulation Environment 3D

Make your cell simulation come to Life.

ecell3d.iab.keio.ac.jp

promo @ VRS
オープンバイオ
Open Bio Japan
Open Bio Japan meetings

3 meetings in the past 12 months.

2007.10  7th meeting focus on visualization
          Odaiba, Tokyo

2007.12  8th meeting no talks, open-space discussions
          Ginza, Tokyo

2008.03  9th annual meeting
          JAIST, Ishikawa

2008.02  BioHackathon for Web Services
          Odaiba, Tokyo
CABINを用いたバーチャルリアリティ

K. Nishimura
K. Nishiyama
T. Itoh

1.

2.

New Interfaces and Scientific Visualization.
Mizutani
Gene Ontology Browser

Nakao
AJAX Codon Table Viewer

Nakamura
eXpanda PPI Visualizer

Katayama
KEGG Global map
Learning Bioinformatics with Open Source Software

- BioRuby
- KEGG API
- G-language System
- ChemRuby
- Bioconductor
- BioPerl
- EMBOSS
- BLAST/clustalw/BLAT ...

about $40
accompanied with KNOB (Knoppix for Bio) DVD
including more than the above list of software

Tokyo-Denki University Press (March 2008)
thank you