



iGEM 2008

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Miha Janež in
Miha Moškon**



PREGLED PREDSTAVITVE

- iGEM 2008 Jamboree,
- osnove biokock,
- zanimivi projekti na iGEM-u 2008,
- računalniška orodja za delo z biokockami in sintezno biologijo.



IGEM 2008 JAMBOREE!

- International Genetically Engineered Machine Competition,
- začetek leta 2004 – 5 ekip ,
- 2008 – 84 ekip (tudi Slovenija),
- vsaka ekipa predstavi svoj projekt,
- več področji tekmovanja:
 - environment,
 - food or energy,
 - foundational advance,
 - health or medicine,
 - manufacturing,
 - new application,
 - software.
- <http://2008.igem.org>



iGEM 2008 JAMBOREE!



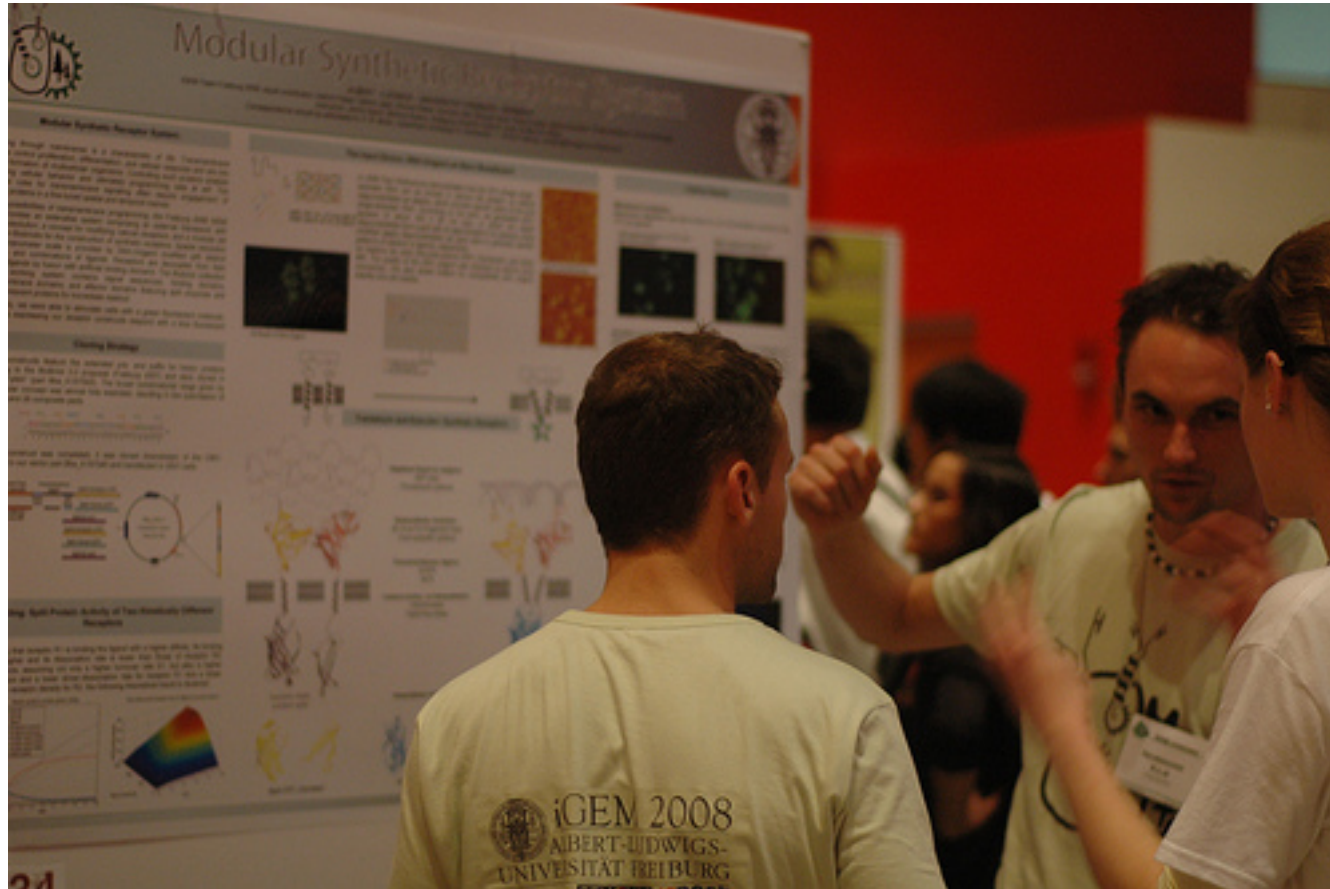
IGEM 2008 JAMBOREE!



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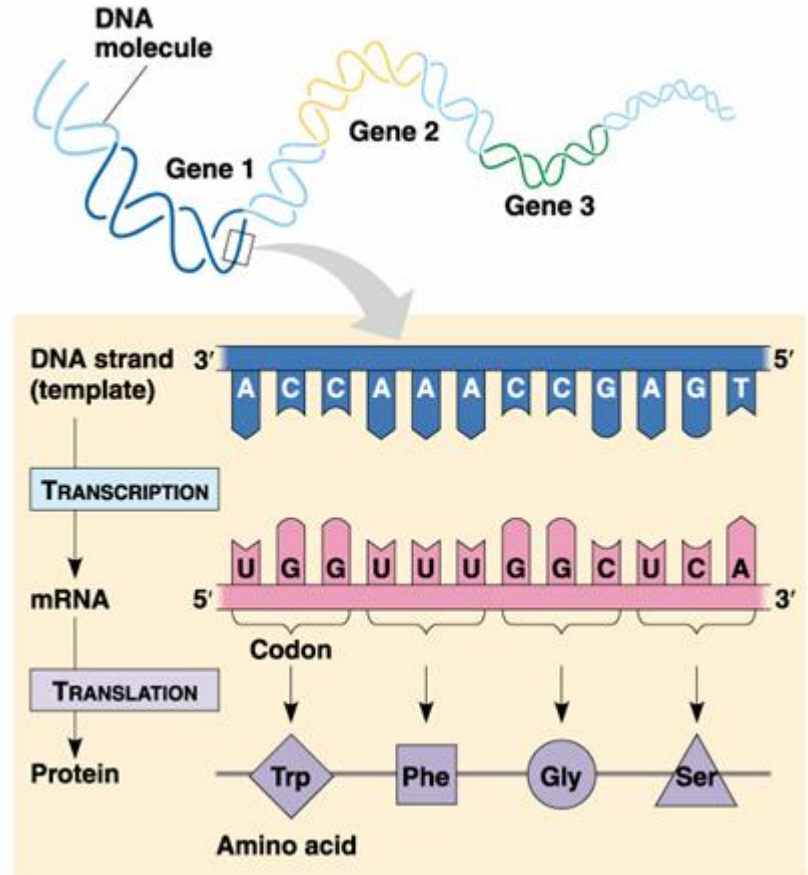


IGEM 2008 JAMBOREE!



BIOKOČKE

- karakterizirana zaporedja DNK,
- postopek generiranja proteina:
 - transkripcija mRNK,
 - translacija mRNK v protein.



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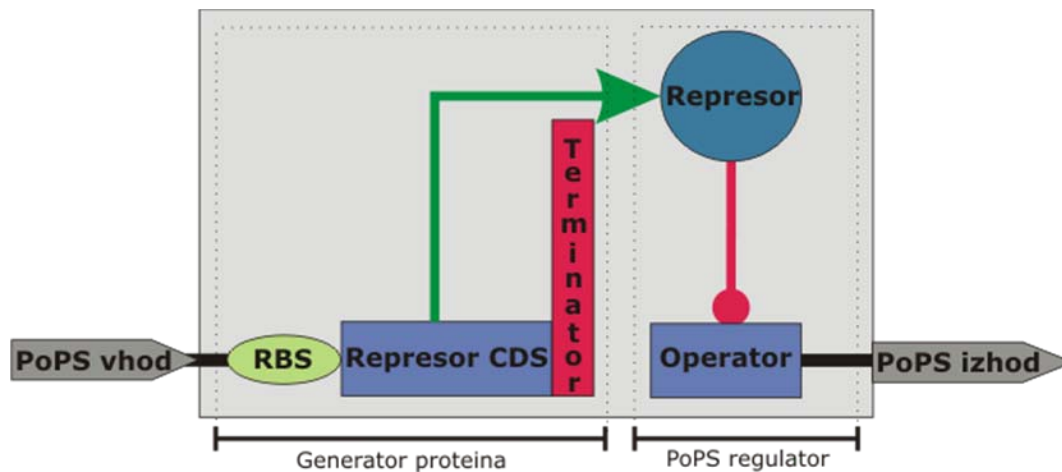
BIOKOCKE

- prednost biokock je karakterizacija DNK zaporedij
 - <http://partsregistry.org/>
- osnovni gradniki (*parts*):
 - regulator,
 - mesto vezave ribosoma,
 - zaporedje kodirajočega proteina,
 - terminator,
 - konjugator,
- osnovne gradnike združujemo v naprave,
- naprave združujemo v sisteme (zaključene projekte).



LOGIČNE NAPRAVE

- vhodno/izhodni signal (PoPS),
- biološka NOT vrata:

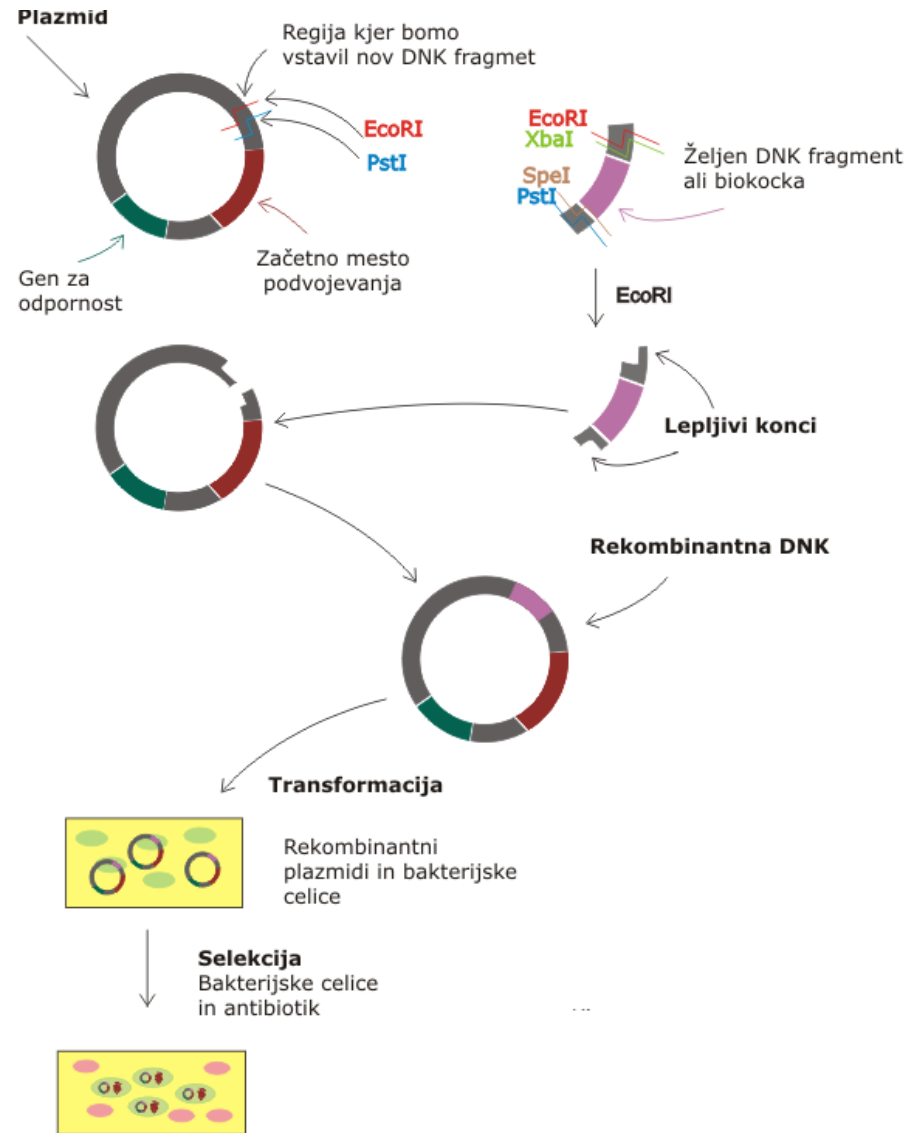


Vhod	R2	Izhod
0	0	1
1	1	0



VSTAVLJANJE BIOKOCKE V ORGANIZEM

- biokocke združujemo s plazmidi,
- plazmid vstavimo v organizem,
- s tem organizmu dodamo nove biološke funkcije,
- vnesemo gen za odpornost na določen antibiotik – postopek selekcije.



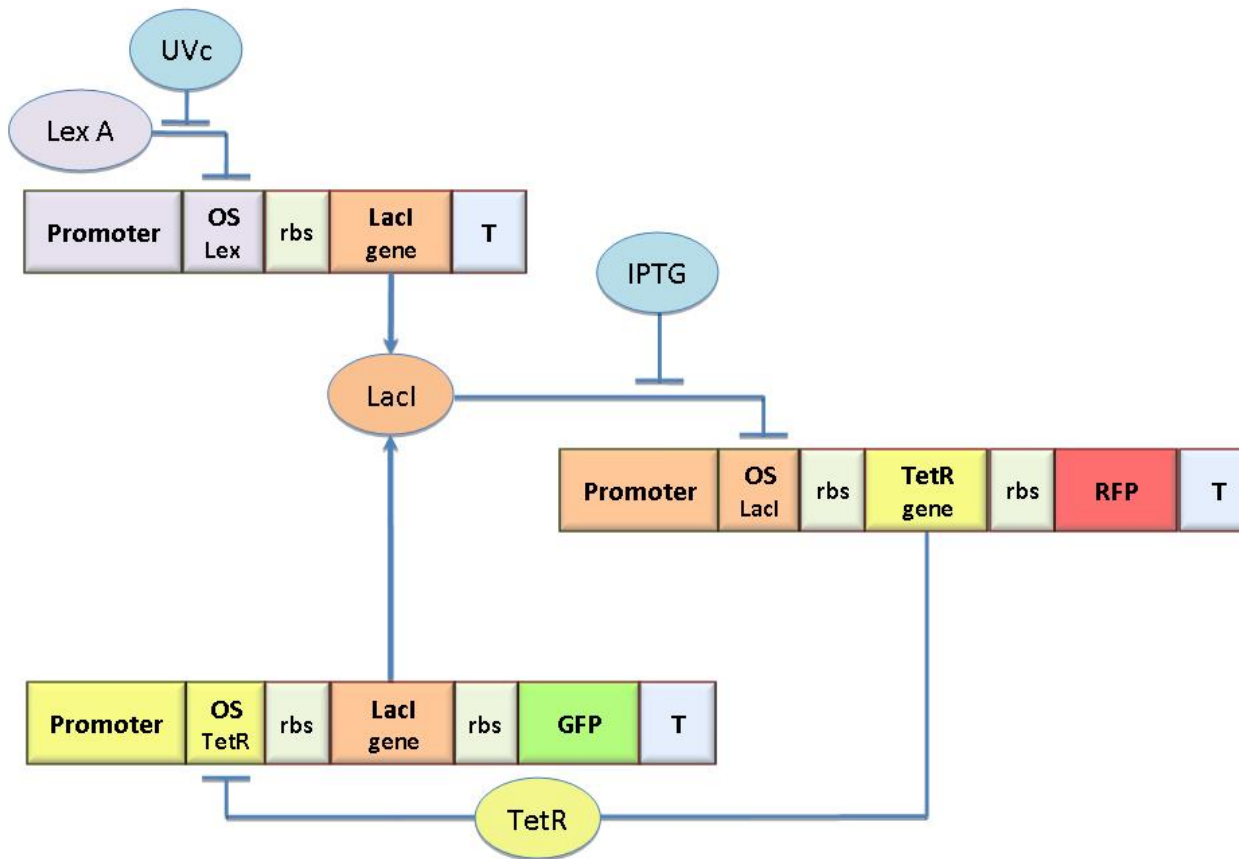
RAČUNALNIŠTVO NA IGEM-U 2008

- Foundational Advance
 - Izboljšanje obstoječih funkcij in struktur
 - Spomin
 - Medcelična komunikacija
- New application
 - Nov pristop, metode, okoliščine
 - Nevronske mreže
 - Kodirne funkcije
 - Uporaba tlaka in električnih impulzov
- Software
 - Orodja za modeliranje in analiziranje



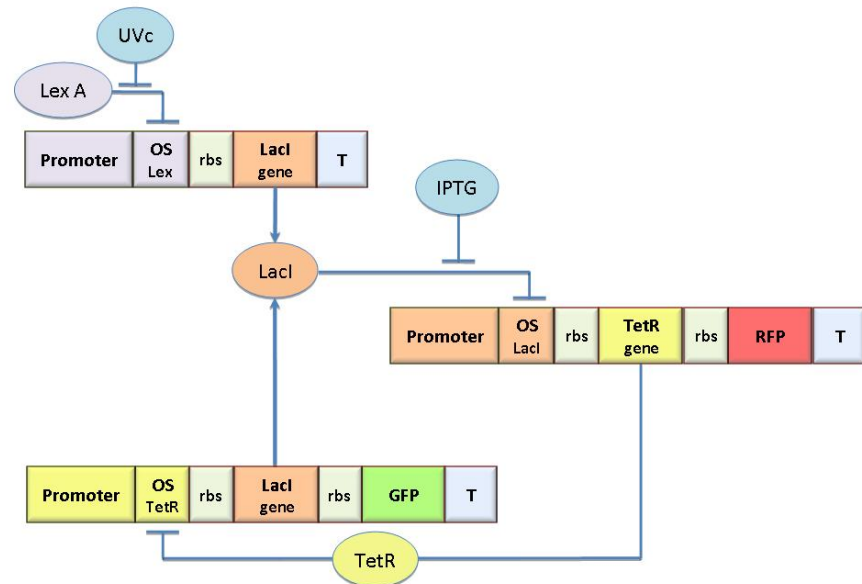
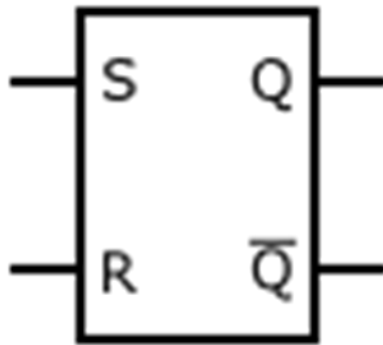
BOLOGNA – ECOLI. PROM

- Kolonija bakterij z vgrajenim flip-flopom



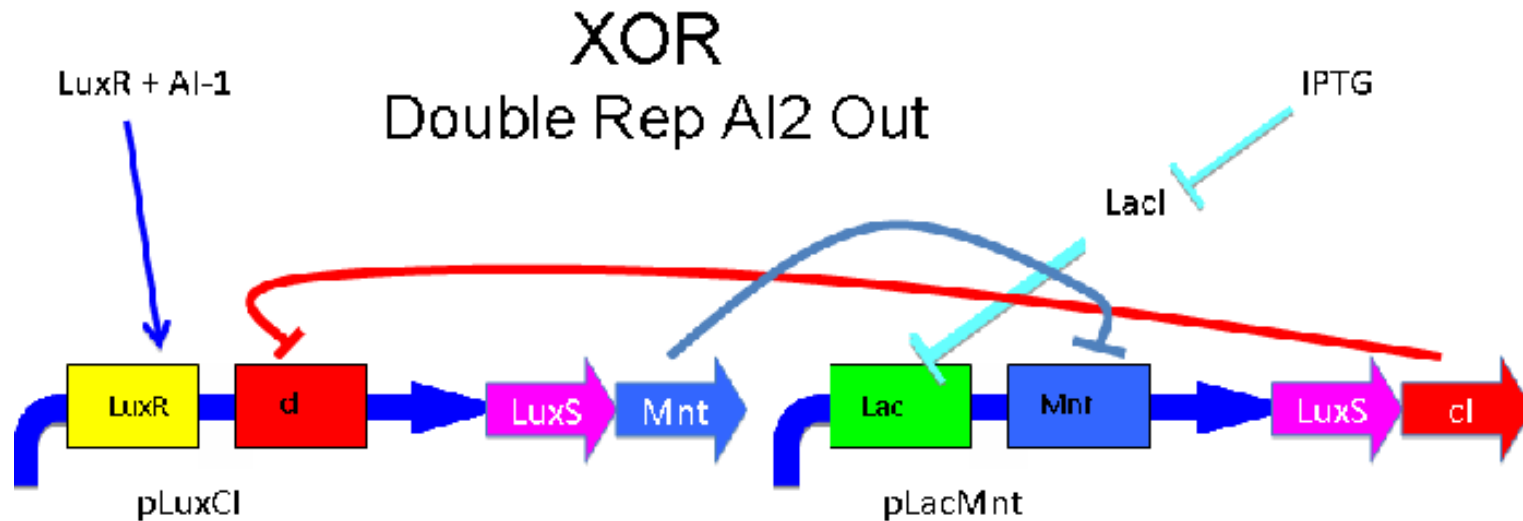
BOLOGNA – ECOLI. PROM

- Flip-flop deluje kot RS pomnilna celica
- LacI in TetR stanji predstavljata izhod
- Uvc je signal SET
- IPTG signal RESET



DAVIDSON – MISSOURI WESTEREN – E.NIGMA

- Prva delujoča XOR vrata in HASH funkcija

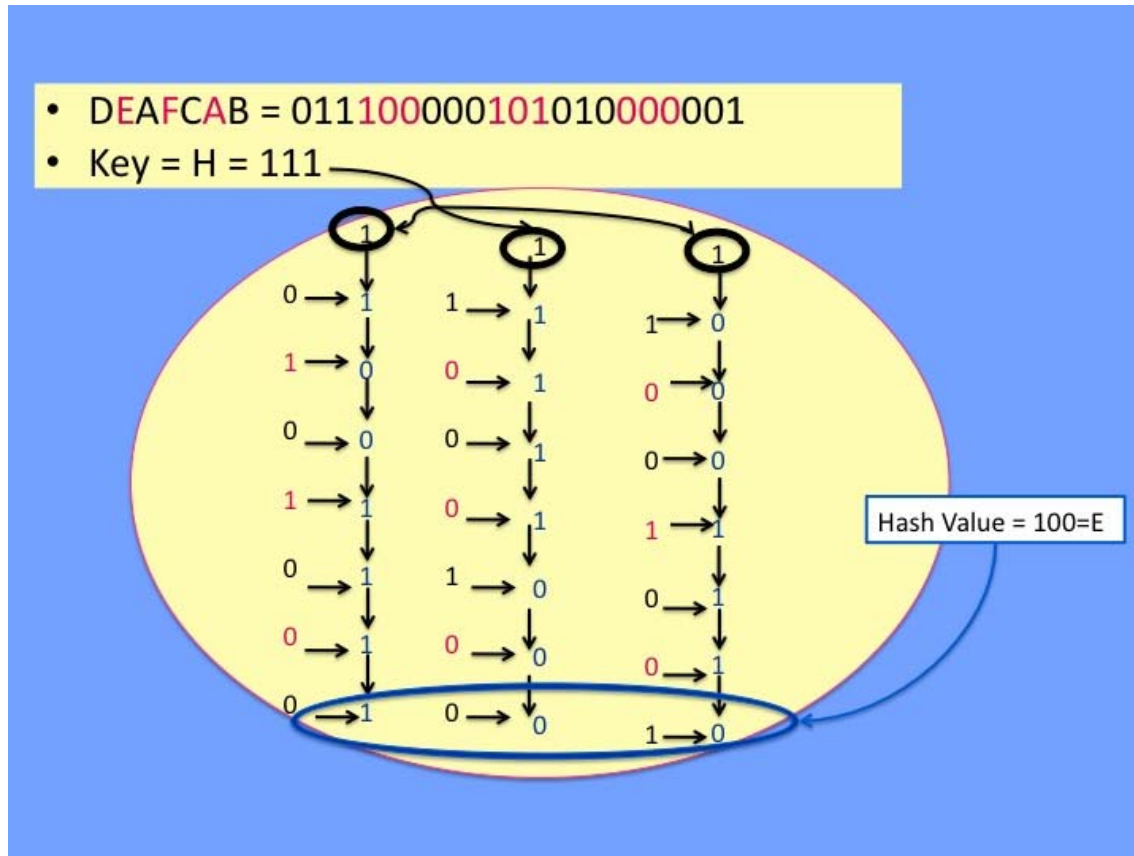


AI-1	IPTG	AI-2
0	0	0
1	0	1
0	1	1
1	1	0



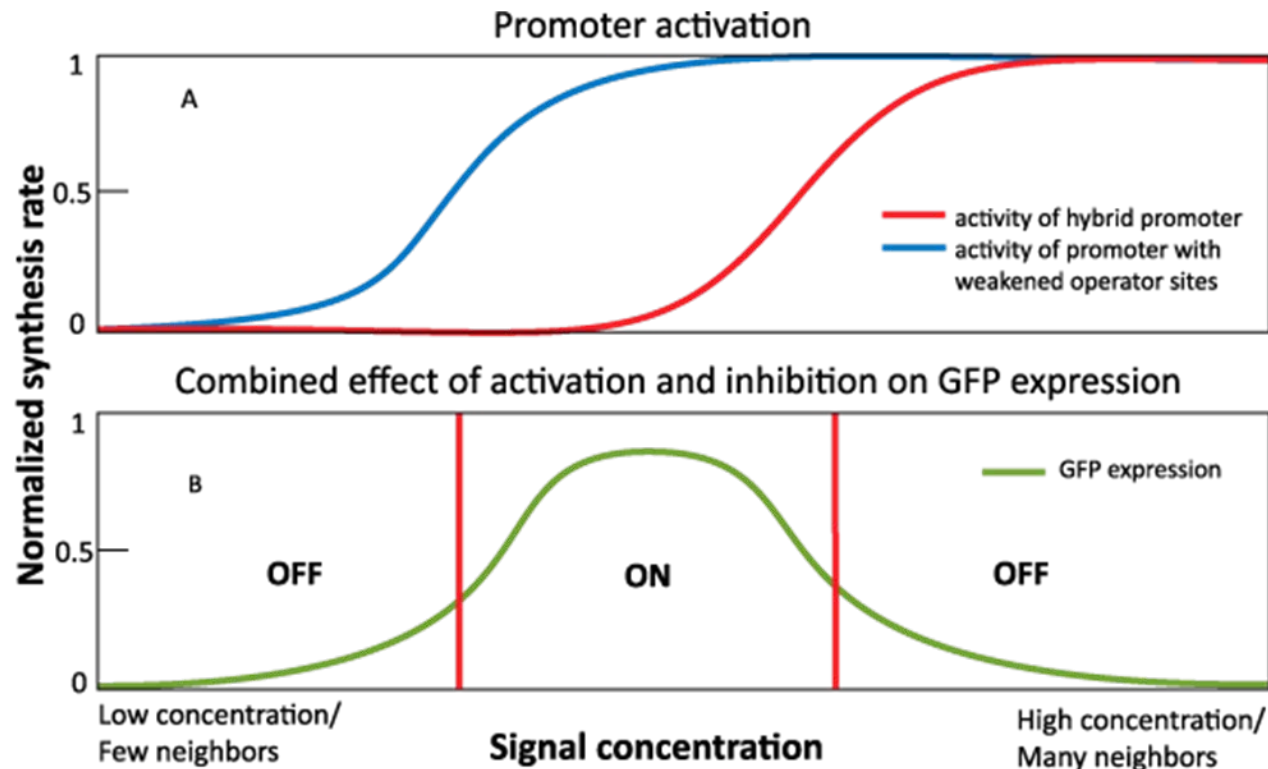
DAVIDSON – MISSOURI WESTEREN – E.NIGMA

- HASH funkcija, SPLIT model



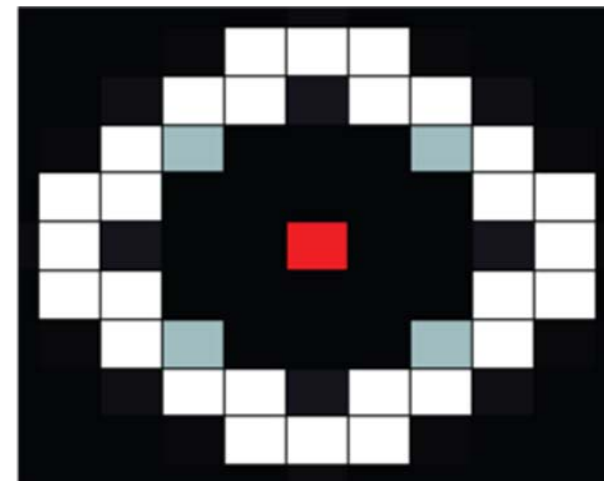
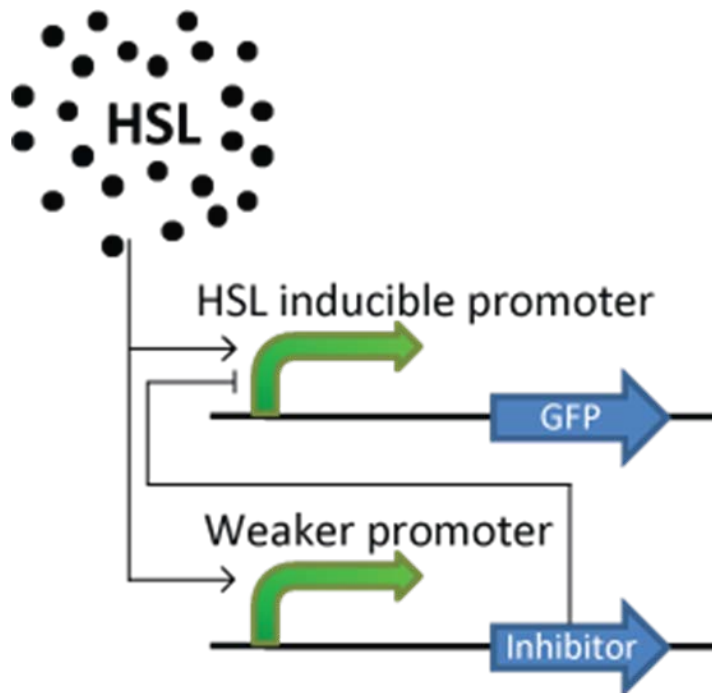
GRONINGEN – GAME OF LIFE

- Intervalno stikalo, ki se odziva glede na koncentracijo “prižganih” sosednjih celic.



GRONINGEN – GAME OF LIFE

- Za odziv so uporabili Quorum sensing z 3-hexanoyl homoserine lactone (3OC6-HSL)



OSTALI ZANIMIVI PROJEKTI

- Formiranje vzorcev v prostoru - Laussane
- Raise the Titanic - Kyoto
- Bacterio'clock – Pariz
- Nevronske mreže – Princeton
- Samo organizacija v večceličnem sistemu – USTC
- iBrain – Cambridge

- ImmunoBricks – Slovenia
- Biogurt - MIT



RAČUNALNIŠKA ORODJA ZA NAČRTOVANJE IN SIMULACIJO DELOVANJA BIOLOŠKIH SISTEMOV

- več tisoč gradnikov v MIT repozitoriju
- pri modeliranju kompleksnih bioloških vezij je potrebno računalniško podprto načrtovanje
- za testiranje modela se uporablja računalniška simulacija dinamike vezja



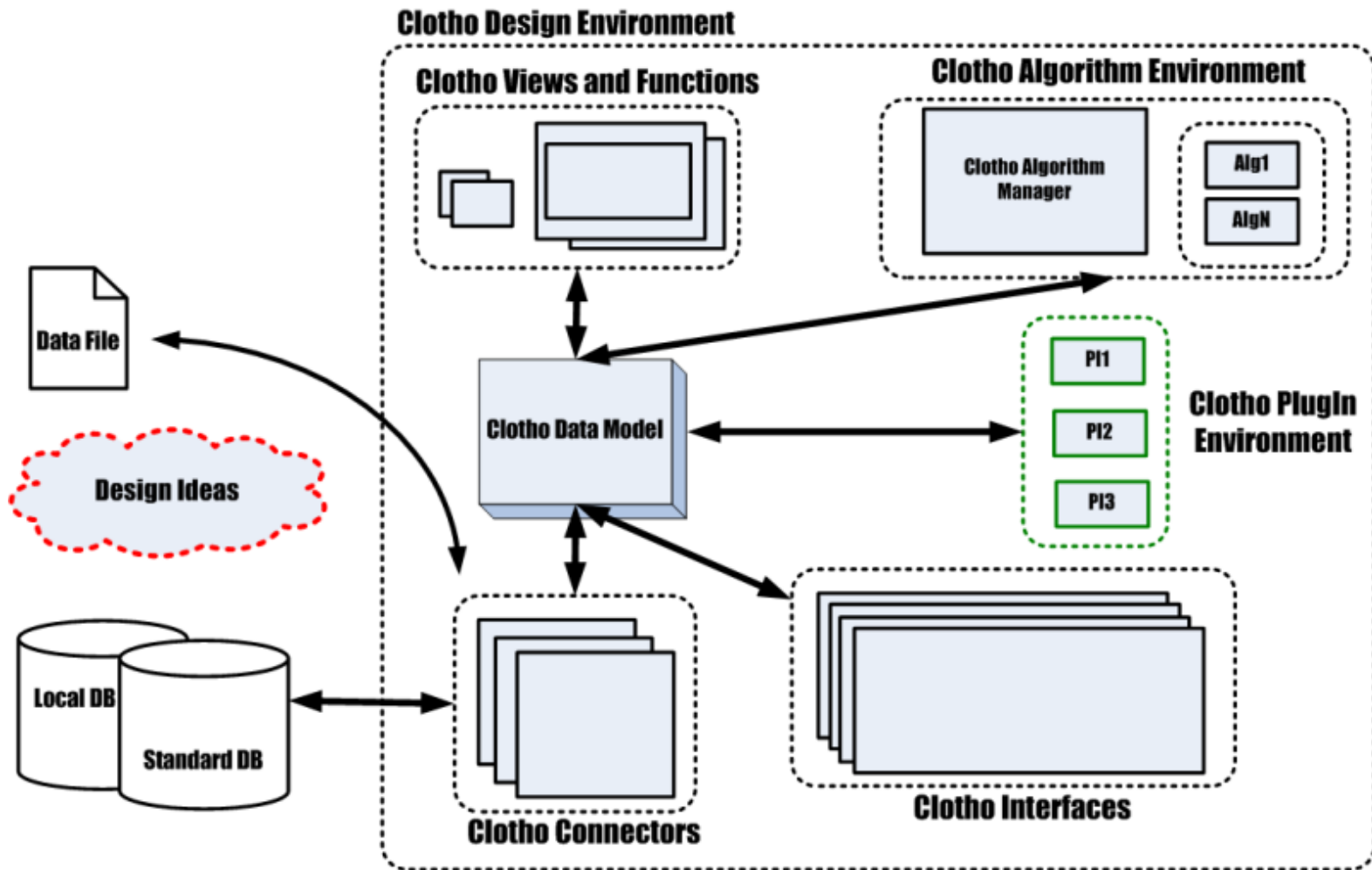
SIMULACIJA DINAMIKE BIOLOŠKEGA VEZJA

- Booleanov model
- modeli z diferencialnimi enačbami
- stohastični modeli
 - skriti Markovski model



CLOTHO

DIAGRAM TOKA PODATKOV



CLOTHO

PREGLED NUKLEOTIDNEGA ZAPOREDJA

Clotho: Sequence View (Address: 1) New Sequence

File Edit Tools ORFs Highlighting Windows

Tools

Features Restriction Sites

Locked Allow Degeneracy Dam/Dcm Circular

Sequence	Location	Start	Length	End	%GC	Tm
2072	0	440 < 1 > 21 < 0 > 460 < 0 > 61 (61)			76.0	107

```
1 GATCCtaaCTCCAGctgcagttgcaggcttctcgcctcactgactcgcctgcctcgggtcgttcgggtgcggcgagcggatcacgctcactcaaaaggcggtaaatcagg
108 ttatccacagaatcaggggat aacgcaggaagaacatgtgagcaaaaaggccagcaaaaaggccaggaaccgt aaaaaggccgcggttgcctggcgtttttccataggct
215 ccgccccctgacgagcatcacaaaaatcgacgctcaagtcagaggtggcgaaaccgacaggactataaagat accaggcgtttccccctggaagctccctcgtgc
322 gctctcctgttccgacctgcccgttaccggat acctgtccgcctttctcccttcgggaagcgtggcgtttctcatagctcacgctgtaggatctcagttcgggtg
429 taggtcgttcgctccaagctgggctgtgtgcacgaacccccctcagcccgaccgctgcgccttaccggtaactatcgtcttgagtccaaccggtaagacacga
536 ettatcgccactggcagcagccactggtaacaggattagcagagcgaggatgtaggcgggtgctacagagttcttgaagtggtggcctaaactacggctacactagaa
643 ggacagtatctgggtatctgcgctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatccggcaaacaaaccaccgctggtagcgggtggtttttt
750 gtttcaagcagcagattaccgcagaaaaaaaggatctcaagaagatctttgatctttctacggggctcagcgtcagtggaacgaaaactcacgttaagggat
857 tttggctatgagatatacaaaaaggatctcacctagatctttt aaattaaaaatgaagttttaaataaatctaaagtataatagagt aaacttggtctgacagtt
964 accaatgcttaatacagtgagccactatctcagcagatctgtctatttcggttcaatcaatagttgcctgactccccgctcgtgtagataactacgataccggagggett a
1071 ccatctggccccagtgctgcaatgataccgcgagacccacgctcacggctccagattatcagcaataaacagccagccggaagggccgagcgcagaagtggtcc
1178 tgc aaactttaccgctccatccagctctatt aattggtgcgggaagct agagt aagt agttcgcagtt aat agtttgcgcaacggtt gttgccattgctacagca
1285 tcgtggtgtcacgctcgtcgtttggtatggcttcattcagctccgggtcccaacgatcaaggcgagttacatgatccccatgttgtcaaaaaagcgggttagctcc
1392 ttcggtcctccgatcgttgccagaagt aagttggccgcagtggtatcactc atggttatggcagcactgcataatctcttactgtc atgccatccgt aagatgctt
1499 ttctgtgactggtgagtagtcaacc aagtcattctgagaat agtgtatgcggcgaccgagttgctcttgcccggcgtcaat accgggat aat accgcgccacatagca
1606 gaactttaaaagtgctcatcattggaaaacggttctcggggcgaaaactctcaaggatcttaccgctggtgagatccagttcgatgt aacccactcgtgcacccaac
1713 t gatcttcagcatctttactttcaccagcgtttctgggtgagcaaaaaacaggaagc aaaaatgccgcaaaaaagggaataaggggcagacaggaataatgttgaatact
1820 catactcttctttttcaatattattgaagcatttatcagggttattgtctc atgagcggat acatatttgaatgtataggaaaaat aaacaaatagggggtccgc
1927 gcacatttccccaaaaagtgccacctgacgtctaaagaaaccattattatcatgacattaacctataaaaaataggcgtatcacgagggcagaatttcagat aaaaaaa
2034 tcttagcttctcgtcaaggatgatttctggaattc atga
```

Sequence Comments

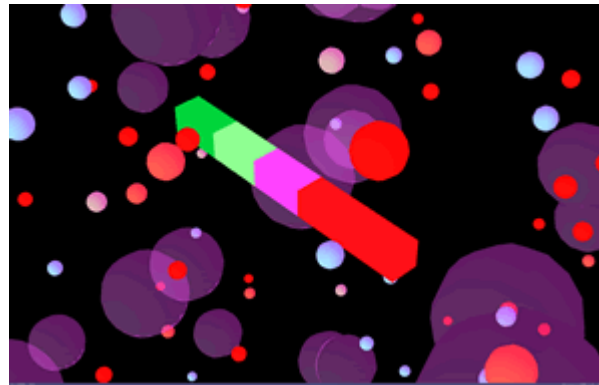
Output Data

Leu-Gln-Ala-Gly-Leu-Cys-Ala



EVOGEM

- simulacija delovanja biološke vezja z uporabo evolucijskega programiranja
- vizualizacija delovanja



ATHENA

The screenshot displays the ATHENA software interface, which is used for modeling and simulating biological systems. The main window shows a network diagram with two modules, M0 and M1.

Module M0: Contains Gene₂, Promoter₂, Promoter₀, and Gene₀. Gene₂ is transcribed into S₂, which is then translated into J₅. Promoter₂ and Promoter₀ are transcribed into S₀, which is then translated into J₁. Gene₀ is transcribed into S₁, which is then translated into J₃. J₅ and J₁ are shown as inhibited species.

Module M1: Contains Promoter₁ and Gene₁. Promoter₁ is transcribed into S₁, which is then translated into J₃.

Simulation Window: Shows a graph of Concentration (Y-axis, 0 to 12) versus Time (X-axis, 0 to 5). The graph displays the concentration of various species over time. The legend indicates the following species and their corresponding colors:

- S₁ (Blue)
- S₀ (Cyan)
- S₂ (Purple)
- M_{1_k0} (Light Blue)
- M_{1_k2} (Light Green)
- J₀ (Pink)
- J₅ (Light Purple)
- J₁ (Light Green)
- M_{1_k1} (Yellow)

Module Viewer: Shows the properties of the main module. The Module ID is "Main". The Reactions table is as follows:

ID	Rate
J0	Gene_0
J1	M0_k0*S0
J4	Gene_2
J5	M0_k0*S2

The Molecular Species table is as follows:

ID	Concentration	Constant
S0	5	
S1	0	
S2	4	

The DNA Parts table is as follows:

ID	PoP5
Gene_0	$10/(1+S2^2)$
Gene_1	10
Gene_2	$10/(1+S0^2)$
Promoter_0	$10/(1+S2^2)$

The Parameters table is as follows:

ID	Value
M0_k0	1
M1_k0	1

The Simulation Window shows the "Simulation" tab selected. The "Reset" and "Simulate" buttons are visible. The "Start Time" is 0, "End Time" is 5, and "Num Points" is 1000. The "X-axis" is set to "Time". The "select/deselect" button is also visible.

The status bar at the bottom left indicates "initializing simulator..."



SIMBIOLOGY

- deluje v MATLAB-u
- omogoča modeliranje, simulacijo in analizo bioloških procesov
- omogoča dodajanje lastnih algoritmov



SIMBIOLOGY

```

M-Code Capture Tool
File Edit Find Diagram BlockLibrary Analysis PlotTypes Desktop Window Help
Save Edit Capture the Simbiology Desktop actions as M-code.

504 Configure the output factors.
505 output1 = m2.Compartments[1].Species[2];
506 set(cs.SensitivityAnalysisOptions, 'SpeciesOutputs', [output1]);
507
508 Run simulation.
509 data = sbiosimulate(m2, cs);
510
511 Turn off sensitivity analysis.
512 set(cs.SolverOptions, 'SensitivityAnalysis', false);
513 set(cs.SensitivityAnalysisOptions, 'SpeciesInputFactors', []);
514 set(cs.SensitivityAnalysisOptions, 'ParameterInputFactors', []);
515
516 Get the active configuration set.
517 cs = getConfigset(m2, 'default');
518
519 Configure the configuration set for sensitivity analysis.
520 set(cs.SolverOptions, 'SensitivityAnalysis', true);
521
522 Configure Normalization.
523 set(cs.SensitivityAnalysisOptions, 'Normalization', 'none');
524
525 Configure the species input factors.
526 set(cs.SensitivityAnalysisOptions, 'SpeciesInputFactors', []);
527
528 Configure the parameter input factors.
529 parameterInput1 = m2.Parameters(1);
530 parameterInput2 = m2.Parameters(7);
  
```

Model Session - apoptosis

Overview

Type	Count
Compartments	2
Species	9
Reactions	6
Parameters	7
Initials	0
Events	0

Configuration Settings

Item	Value	Step From
1 default	default	11800.0 seconds (simulation time)

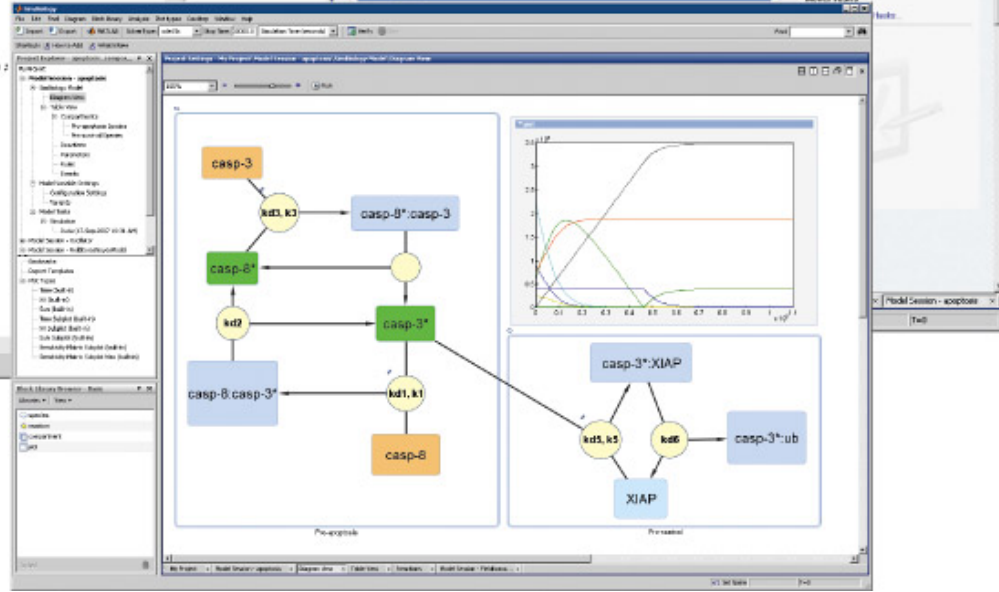
Task Manager

Built-in Model Tasks

- Simulate
- Calculate conserved cycles
- Calculate stoichiometry
- Run parameter scan
- Run parameter scan with sensitivities
- Run ensemble simulation
- Create custom analysis

User Defined Model Tasks

- Import custom task...
- Delete custom task...



SYNBIOSS

- tri komponente:

- Wiki
- Designer
- Desktop Simulator

- spletni vmesnik SynBioSS Designer

INPUT BIOBRICKS

Create a BioBrick construct by entering the Bricks IN ORDER. (e.g. Promoter→RBS→DNA→Terminator)

BioBrick ID: Type:

INPUT BIOBRICKS

Create a BioBrick construct by entering the Bricks IN ORDER. (e.g. Promoter→RBS→DNA→Terminator)

BioBrick ID: Type:



POVEZAVE

- Clotho

http://2008.igem.org/Team:UC_Berkeley_Tools

- evoGEM

http://parts.mit.edu/igem07/index.php/Calgary/evoGEM_introduction

- Athena

<http://staff.washington.edu//deepakc/downloads.html>

- SimBiology

<http://www.mathworks.com/products/simbiology>

- SynBioSS

<http://synbioSS.sourceforge.net/>

