METU-BIN

iGEM Software Team

iGEM 2011 World Championship Jamboree, MIT
Team METU-BIN
Main Problem

- Number of teams
- Number of submitted BioBricks
- Large Database

iGEM Competition 2011, World Championship Jamboree, MIT, Boston, USA
Wet-Lab Users Facing Challenges

Searching  Deciding

Constructing  Finding
Goal of METU-BIN

• Provide web based tool
  – Helps synthetic biologists
    • Searching the Part Registry with input and output keywords.
    • Designing the new genetic devices.
M4B: Mining for BioBricks
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INPUT

OUTPUT

Presenting & Scoring All Possible Genetic Devices
Plan
Construction of Relational Database
Algorithm
Scoring
Next Version
Collaboration & Human Practice
Plan

- A network of all bioparts in 2011 distribution which describes the bilateral relations.
- A search algorithm to reveal all possible device combinations.
- Visualization tools for graphical representation of the results.
- A web-based user interface for the developed software.
Extraction of Relations of Bioparts and Construction of Relational Database
Difficulty in going over biobricks and finding the relations ever so growing Parts Registry

Part Connections Database

The complex information in Parts Registry is simplified by translating into input and output relations.
Extraction of Relations of Bioparts and Construction of Relational Database
1. Minimal & Functional Device

2. Inputs according to Promoters

3. Outputs according to Genes

4. Combination between devices: “Output of the first gene will be the input of the following promoters”
5. Simplification to minimal & functional device
   - Inverter
   - Reporter
   - Composite parts
   - Generator
   - Signaling
   - Intermediate
   - Translation Unit
Rules Defined by METU-BIN

Inverters

Q04510

cl lam
B0034 C0051

cl lam
B0010 B0012 R0051
Rules Defined by METU-BIN

Composites

Intermediate Devices

Signalling Devices

Generators

Reporter

Translational Unit
6. Accessories is assigned as a new class

- DNA
- RNA
- Tags
Technologies

• Java Web Technologies
  – Swing
  – Applet
• MySQL Database
• yFiles Graphical Library
Algorithms

• Two main algorithms
  – Searching
    • Going over the parts in 2011 distribution
  – Scoring
    • Ranking of resulting devices based on whole Parts Registry
Search Algorithm

- BioBrick Network Traversal Algorithm
  - DFS (Depth First Search)
Scoring Algorithm

1. BEGIN
2. Get Result List
3. Get a Composite Device from List
4. Get an edge from path
5. Get the score of edge from DB
6. Normalize the score into [0,1]
7. log(score)
8. Sum up final score
9. Summation is OK, for the path?
10. All device scores calculated?
   - NO: Go back to 4
   - YES: Add score to the device info.
11. END
Community Based Ranking of BioBricks
Usage Frequency of BioBricks

Collaborative Filtering
Device & Edge

• Basic Device

• Edge
If a device has **edges** from the devices of Parts Registry that are

- Available
- Partially Confirmed
- Works

its score will be **higher**
Visualization

yFiles graphics library
Advantages of M4B

- Time Saving
- Effort Saving
- Cost Reduction
- Storage & Performance Saving for PCs

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Improvements on our code

• Search options for multiple input and output parameters.
• Including all possible biobrick categories in search algorithm
• Providing link-outs for gene products to external databases such as NCBI, ENSEMBL.
Improvements to the Parts Registry

• Provide SBOL codes to present in M4B results.
• Add safety warnings for the genetic devices with potential threats.
Collaboration

• METU-ANKARA

• Uppsala-Sweden

TEAM
UPPSALA-SWEDEN
Setting the colour

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Human Practice

- Innovative approach - the construction of innovative devices
- Sharing the resulting biobrick constructs
- Sharing the favorite results image
- Availability of ownership information
Human Practice
M4B has an innovative new interface designed by METU-BIN for mining the Parts Registry.

The ”Part Connections Database” that examines the bilateral relations between biobricks is retrieved from the Parts Registry by METU-BIN.

The novel EDGE-SUM Scoring measure is developed by METU-BIN and implemented in M4B. Presenting possible genetic device results by ranking them is a methodology to quantify Biobricks.
THANK YOU! ANY QUESTIONS?