Implementing Nemo Profile in MASS Bionet

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### Overview

**Problem:** Add Nemo Profile to a MASS implementation of network motif finder.

#### **Challenges:**

- Locating code base
- Running code across clusters
- Learning core concepts
- Deciding between C++ or Java

#### Network Motifs

Statistically significant sub-graphs or patterns



Figure 1

# **Biological Applications**

Protein-protein interactions



# Algorithm: Enumerate Subgraphs (ESU)



# Network Motif

Label	Frequency of Target		
C~	110		
CF	91848		
Cr	1169		
CR	59745		
C^	606		
CN	8148		

### Bionet

Java implementation of ESU algorithm written by former student Matthew Kipps:

- 1. Sequential
- 2. MASS Agent-based
- 3. MASS Places-based
- 4. MPI

# Why parallelize?



Sequential bionet execution time for various

Execution time (milliseconds)

### Sequential Bionet



#### MASS Agent-Based Bionet



#### Nemo Profile

What if we want to know to which motifs each node belongs?

Node	C~	CF	Cr	CR
1	54	2004	2	0
2	74	80	254	95
3	43	1543	84	135
n	105	765	90	437

#### Problem

How to carry node data back to the host in order to implement Nemo Profile?



# Why convert from g6 format?



#### Solution

Convert g6 hash map into a hash map of hash maps



#### Next steps

- 1. Implementation (in process)
- 2. Experiments
- 3. Research paper / Conference: The 6th IEEE International Conference on Big Data and Cloud Computing (BDCloud 2016)

#### Long term

- 1. Reduce agent explosion
- 2. Add the motif-finding portion of the algorithm



### References

- 1. Figure 1: CC BY-SA 3.0, <u>https://en.wikipedia.org/w/index.php?curid=36822143</u>
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- 3. Figure 3: CC BY-SA 3.0, https://en.wikipedia.org/w/index.php?curid=36822191
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