

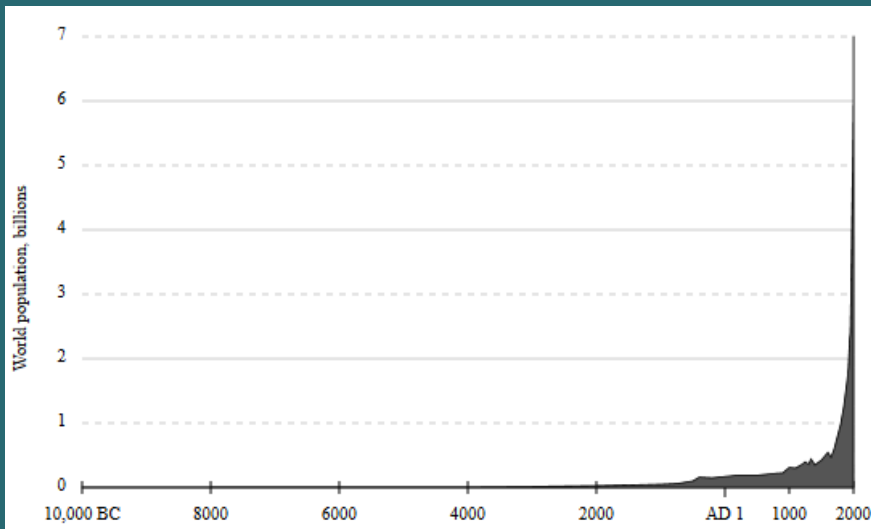


AN NVIDIA POWERED BIOGRAPH
ALIGNMENT AND VISUALIZATION TOOL

G3NA-V

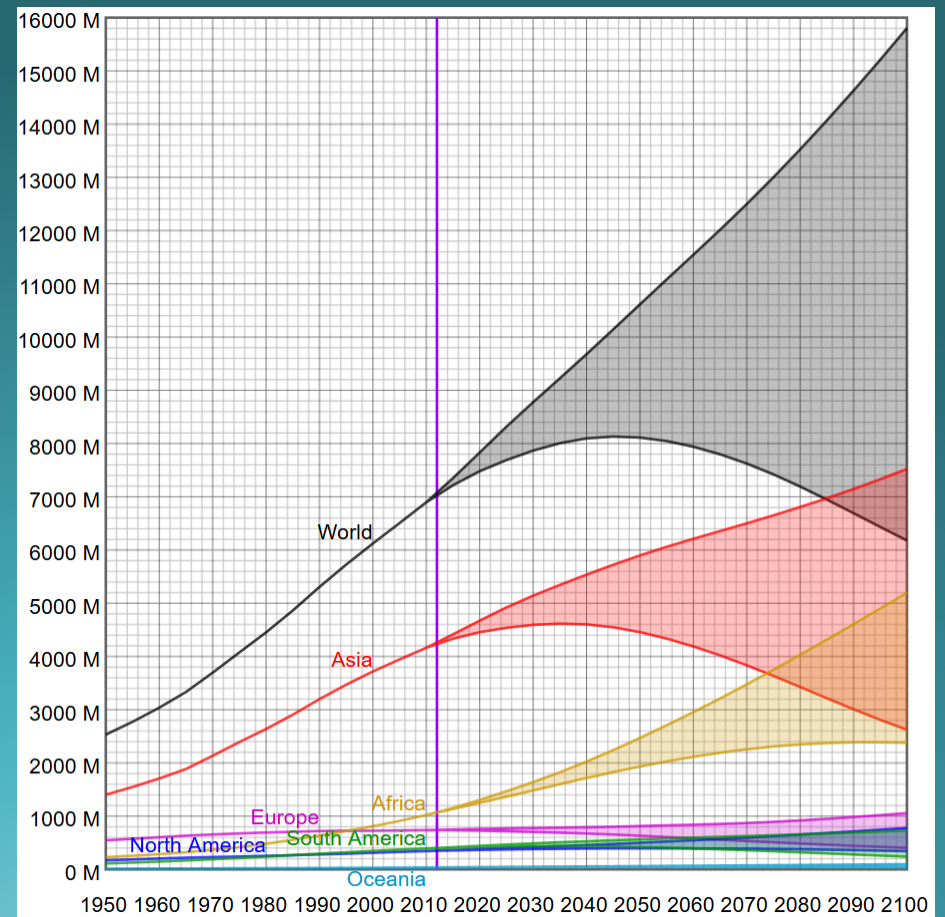
Alex Feltus, Melissa C. Smith, Karan Sapra

The world's population is growing...



1776: New York City (25,000), Boston (15,000).
2014: New York City (8,336,697), Boston (636,479).

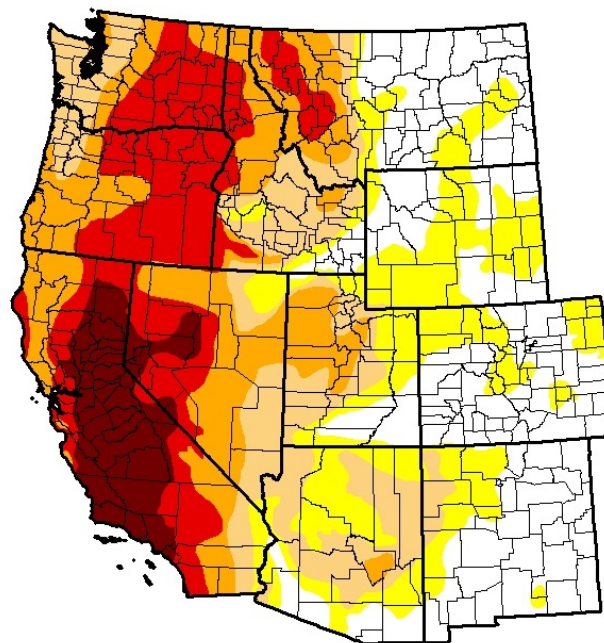
Current World Population
7,379,817,607



The world's climate is changing...



U.S. Drought Monitor West



November 3, 2015

(Released Thursday, Nov. 5, 2015)

Valid 7 a.m. EST

Drought Conditions (Percent Area)

	None	D0-D4	D1-D4	D2-D4	D3-D4	D4
Current	27.09	72.91	54.45	39.19	22.42	6.90
Last Week 10/27/2015	26.79	73.21	55.42	41.21	26.23	7.62
3 Months Ago 8/4/2015	26.53	73.47	60.09	42.99	22.24	7.17
Start of Calendar Year 12/30/2014	34.76	65.24	54.48	33.50	18.68	5.40
Start of Water Year 9/29/2015	22.77	77.23	57.81	42.42	26.50	7.62
One Year Ago 11/4/2014	34.59	65.41	54.48	34.16	18.75	8.45

Intensity:

- D0 Abnormally Dry
- D1 Moderate Drought
- D2 Severe Drought
- D3 Extreme Drought
- D4 Exceptional Drought

The Drought Monitor focuses on broad-scale conditions. Local conditions may vary. See accompanying text summary for forecast statements.

Author:

David Miskus
NOAA/NWS/NCEP/CPC



<http://droughtmonitor.unl.edu/>

Problem Statement

Current World Population

7,379,817,607

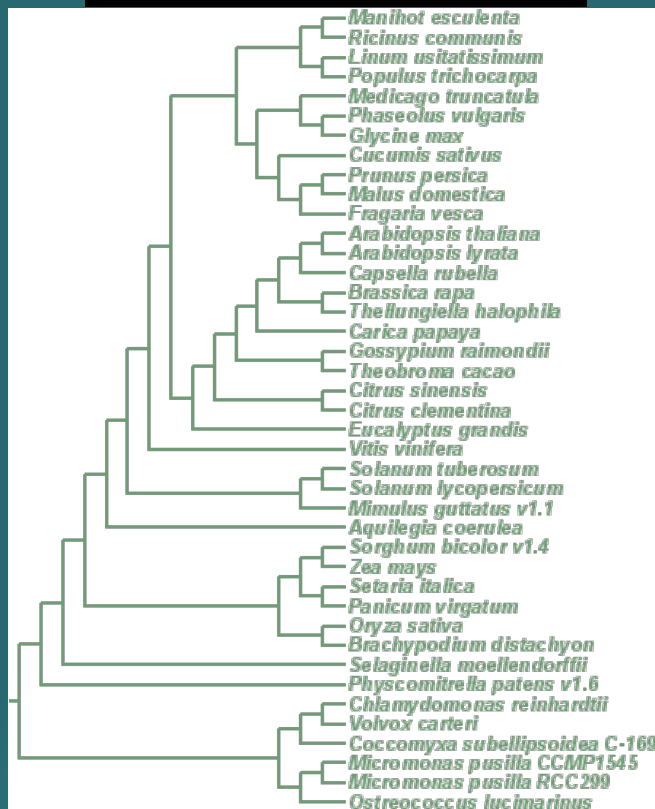
Billions of people need a lot of *Food, Fiber, Fuel, Plastics, Medicines.*

Faster Crop Development required.

Climate history may not predict the future.

Accelerating crop development means understanding genomes...

Sequenced Plant Genomes



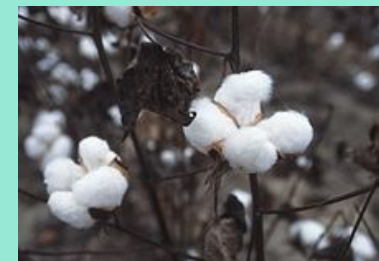
Theobroma cacao
(Cocoa Bean)



Carica papaya
(Papaya)



Sorghum bicolor
(Sorghum)



Gossypium hirsutum
(Cotton)

I Crop Systems Genetics

Genome
Complete



Rice



Sugarcane

Genome
Complete



Sorghum

Genome
Complete

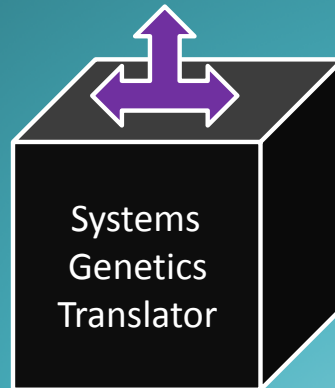


Maize

Genome
Complete



Brachypodium



Genome
Complete



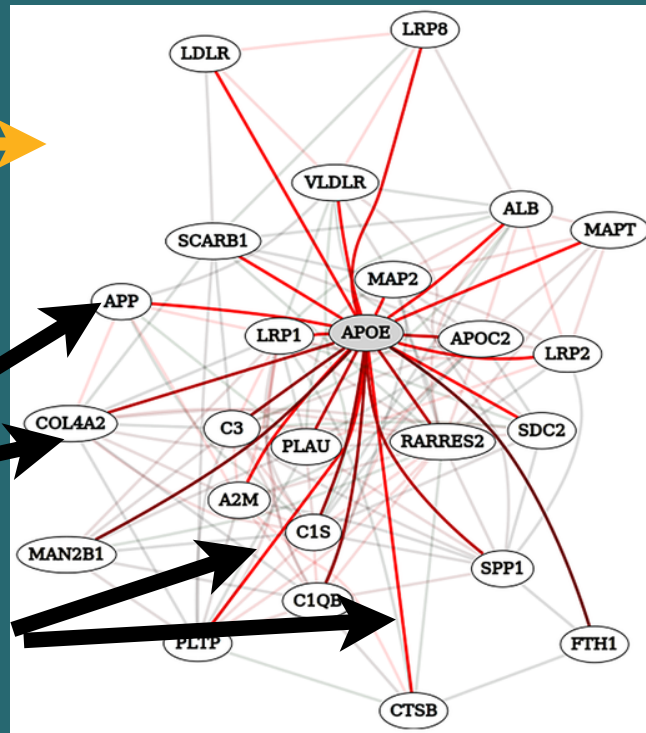
Switch grass



Miscanthus

Complex biological systems can be modeled as graphs...

Alzheimer's (Plaque in Brain)

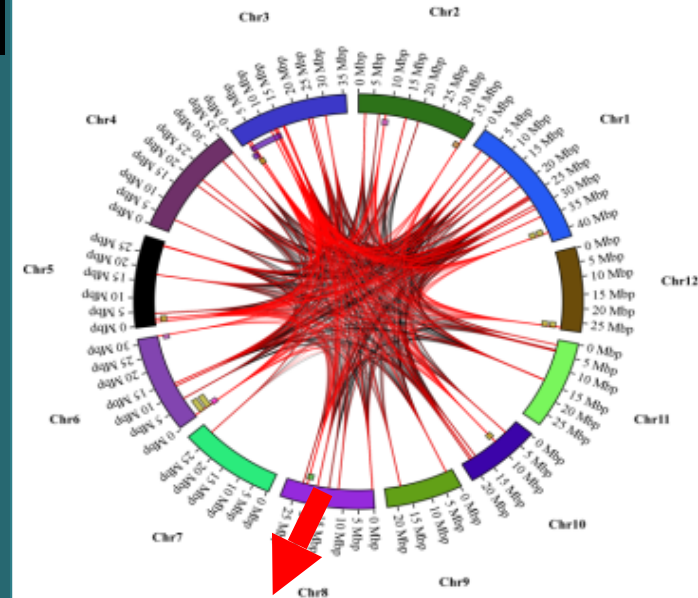


Node
(Gene)

Edge
(Gene Interaction)

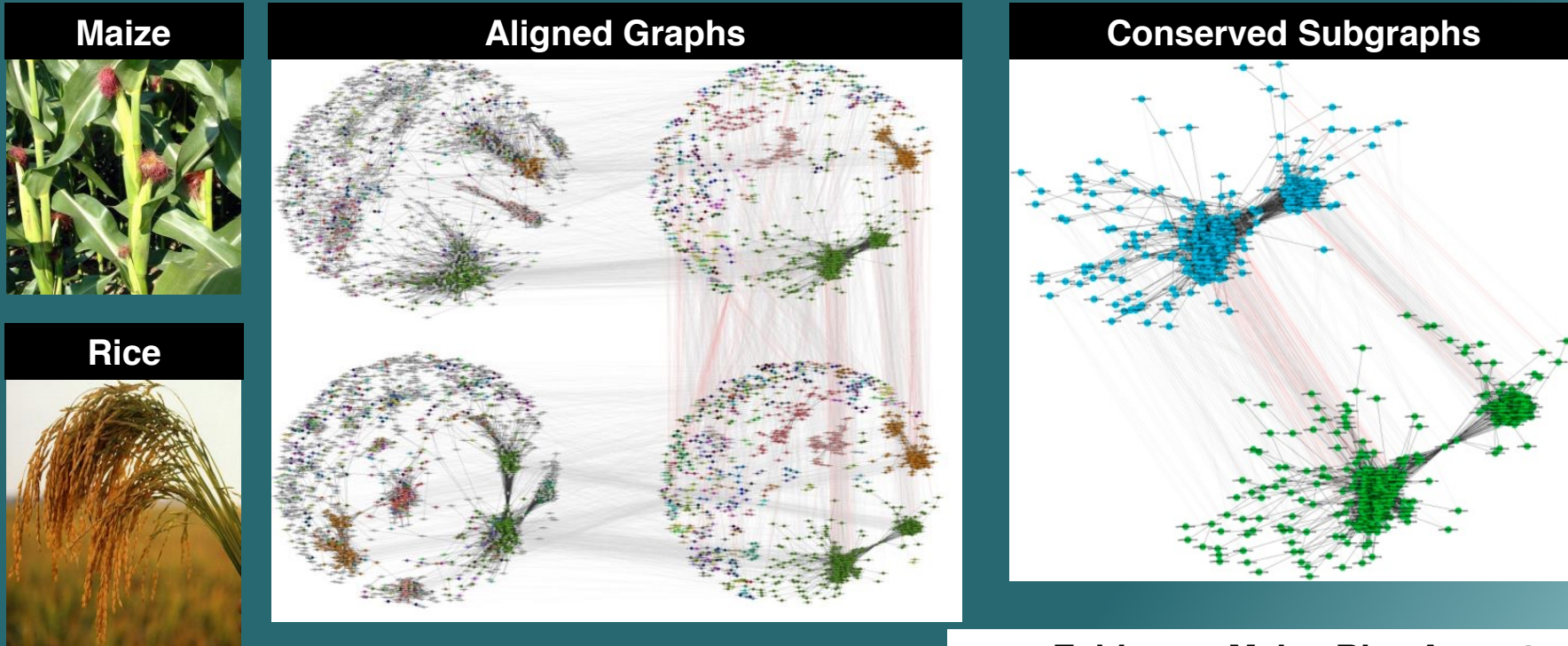
Genenet Engine:
sysbio.genome.clemson.edu

Rice graph mapped to genome



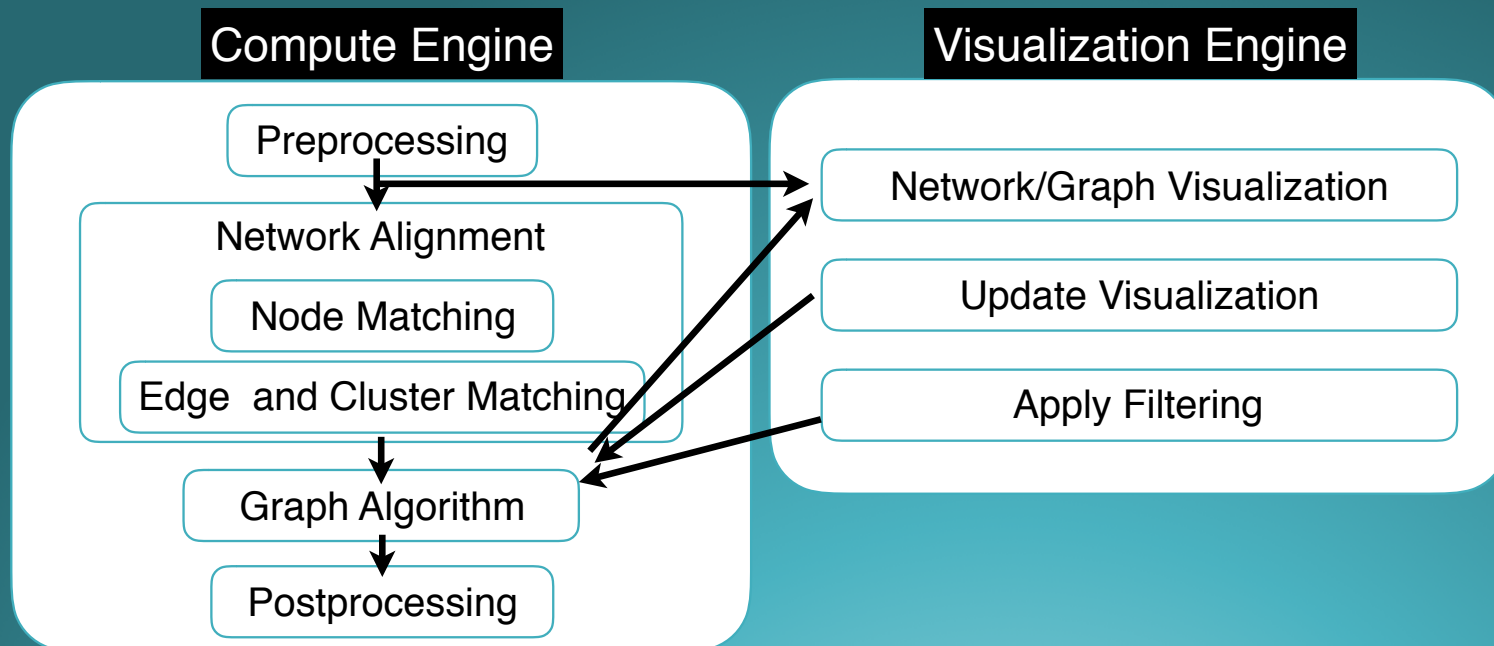
Higher
Yield!!!!

Paleogenomics: Conserved subgraphs can be detected by graph alignment...



**Evidence: Maize-Rice Ancestor
Shared Similar Gene Interaction Patterns
50-70 Millions of Years Ago**

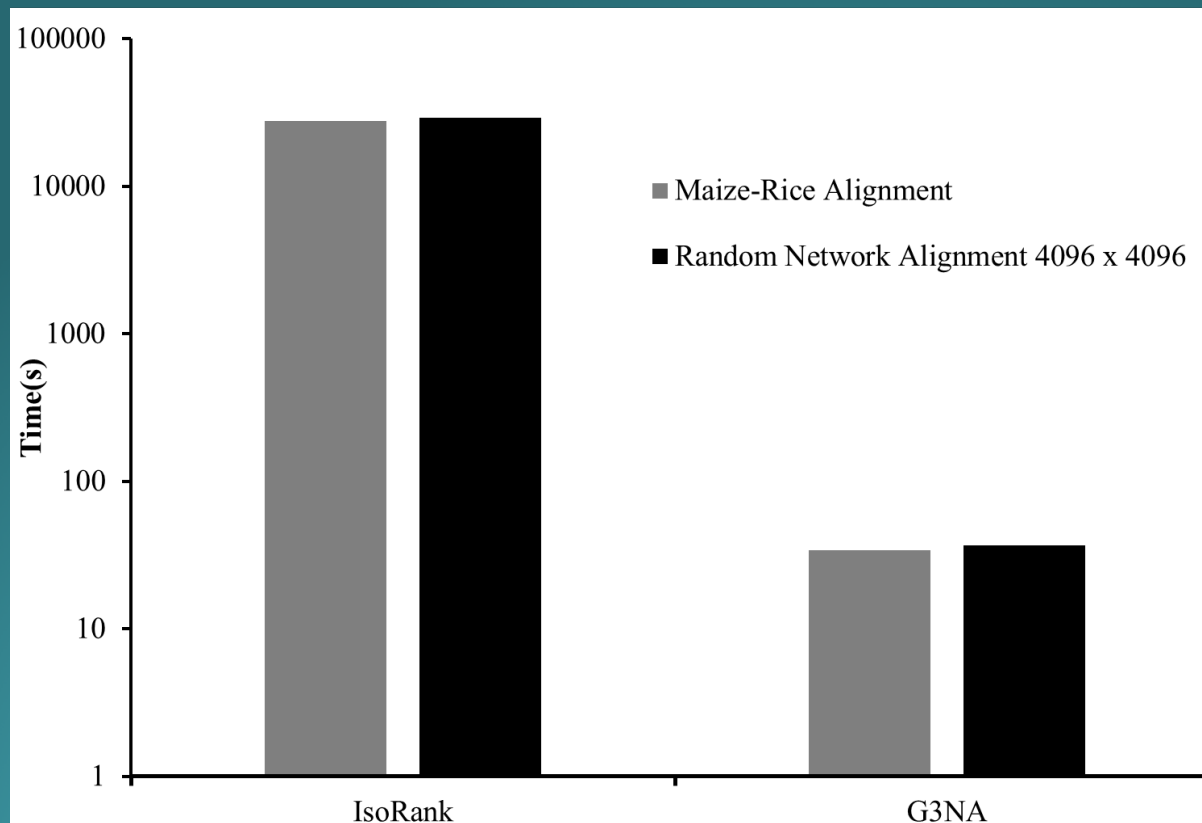
G3NA-V Overview



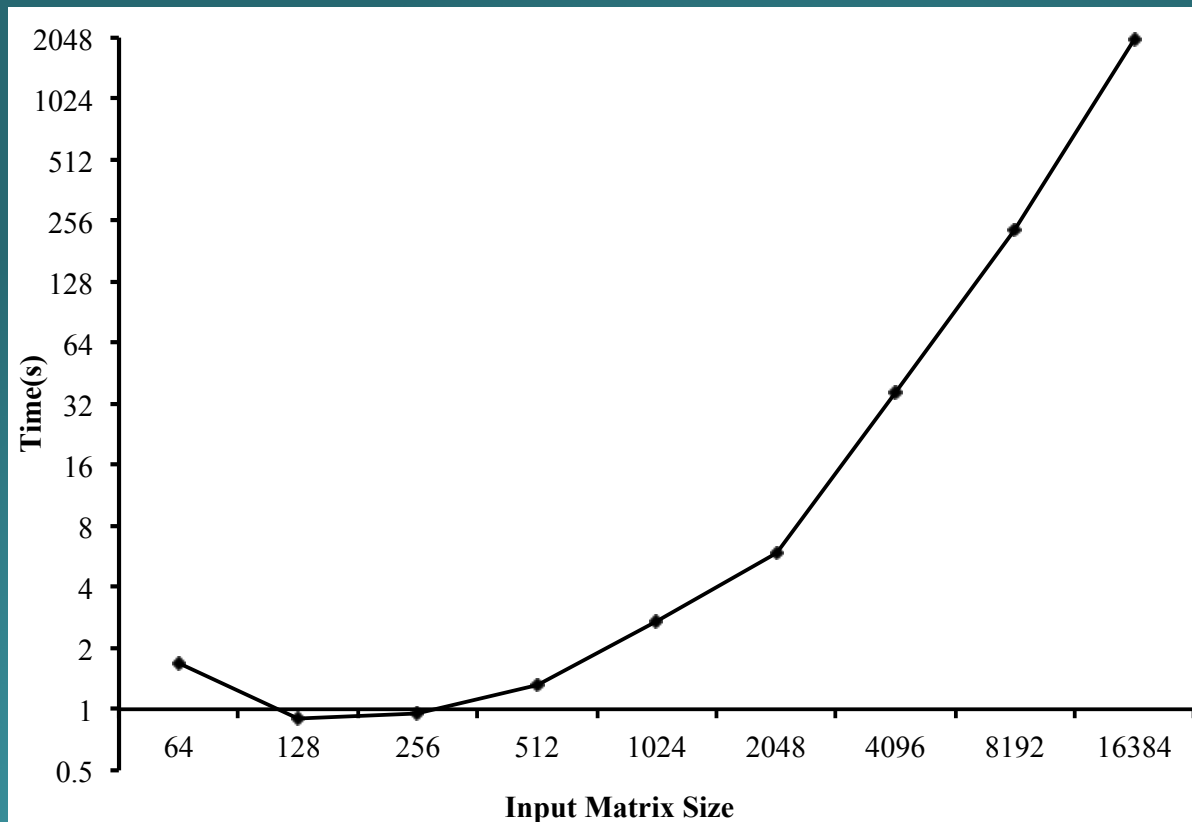
Compute Engine

- **CUDA7 enabled global pairwise aligner GPU-enabled Global Gene Network Aligner (G3NA)**
- **CUDA enabled graph processing libraries**
 - Thrust, Map-graph, etc.
- **Use Multiple GPUs for alignment of multiple graph**
- **Utilize various graph algorithms**
 - Clustering, Page Ranking, Filtering, Max-flow min-cut, etc.

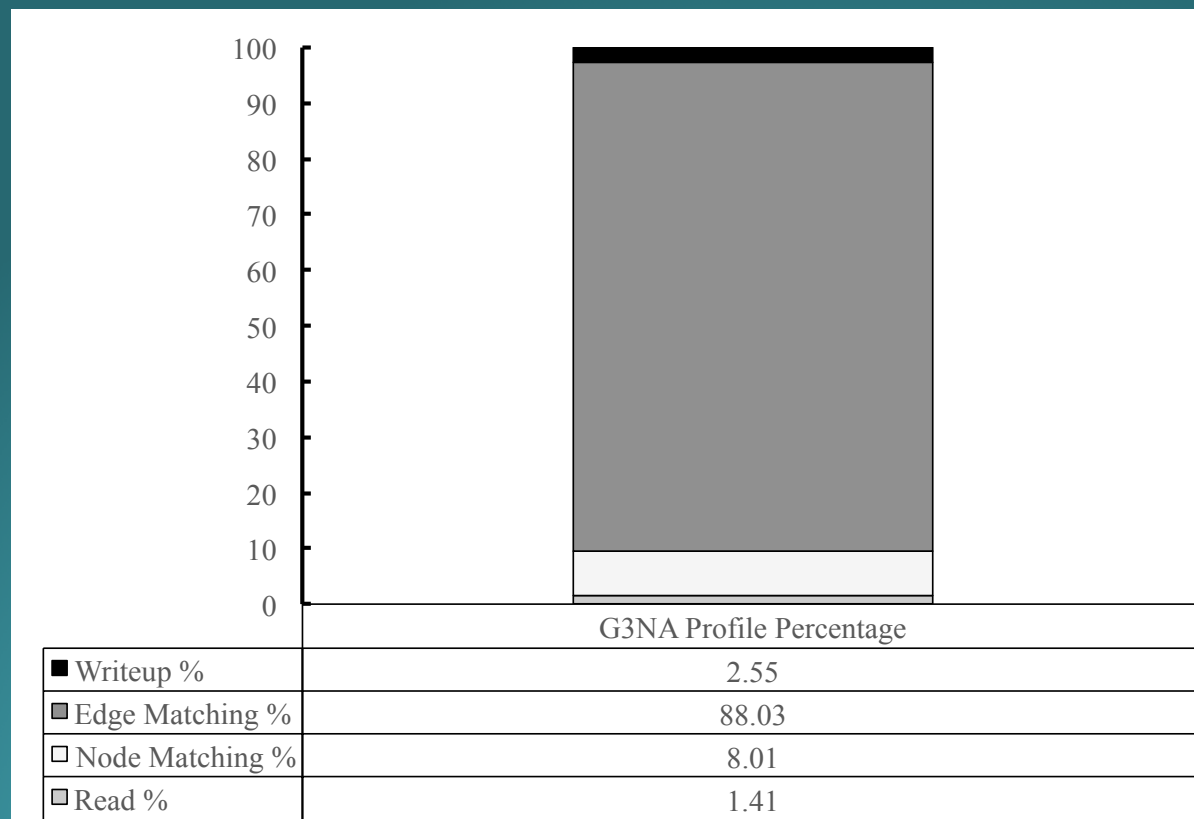
G3NA Comparative Result



G₃NA Scaling Result



G3NA Profiling Overview



Visualization Engine

- **Orientation and Visual Flexibility**
- **GPU enabled OpenGL and GLUT based visualization**
- **Support for Multiple View ports and File formats**
- **CUDA-based Layout algorithms for Graphs and Trees**
- **Dual GPU Support for Compute and Visualization**

Enabling Systems Genetics using HPC



- Enabling anonymous pairwise alignment using Palmetto Supercomputer at Clemson University
- Snappy overview visualization of alignment using WebGL

A screenshot of the web interface for the GPU-enabled Global Gene Network Aligner. The interface is titled "GPU-enabled Global Gene Network Aligner" and shows a sample run with "Sample Maize - Rice Input Data Set" and "G3NA_x64_CUDA_ENABLED". It features an "Upload System" section with three file upload fields: "Network A", "Network B", and "Homology score file". Each field has a "Choose File" button and a "No file chosen" message. Below the upload fields are four input fields for "Topology Threshold" (0.000005), "Homology Threshold" (10), "Clustering Threshold" (0.6), and "Output Filename" (output.gna). There is also an "Email" input field and a green "Submit" button. A network visualization is shown in the center, consisting of blue and green nodes connected by lines, with some nodes highlighted in red and green.

Palmetto Cluster

721.9 Teraflops

2021 Compute
Nodes and 22,336
cores

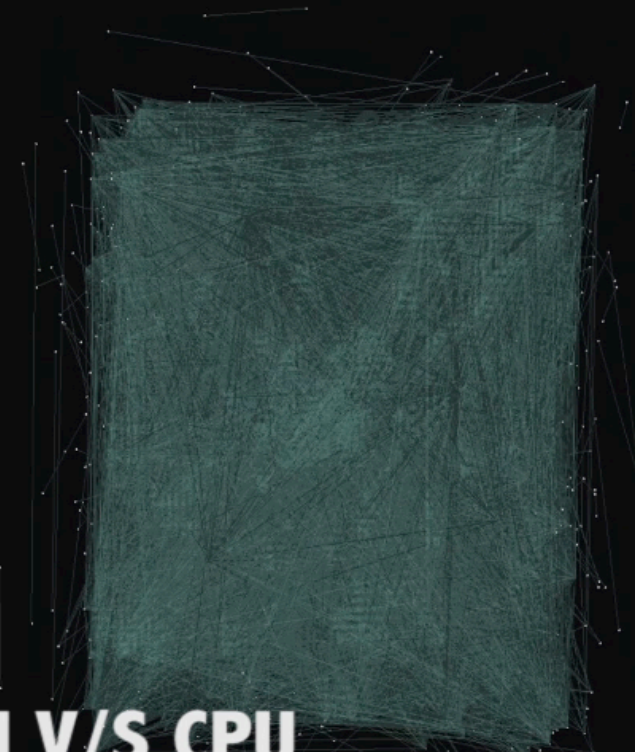
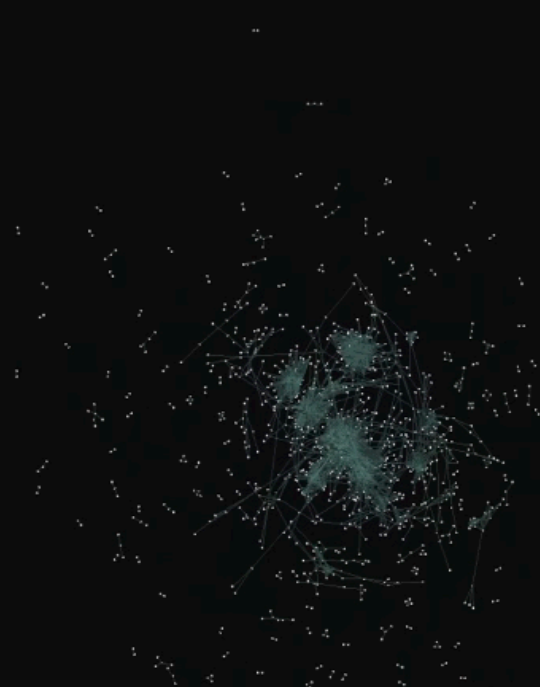
374 nodes with
dual K20/K40 for
acceleration and
visualization

56Gbit
interconnect

<http://network.genome.clemson.edu>

Maize

Maize



GPU

PERFORMANCE GAIN V/S CPU

CPU

RICE

MAIZE



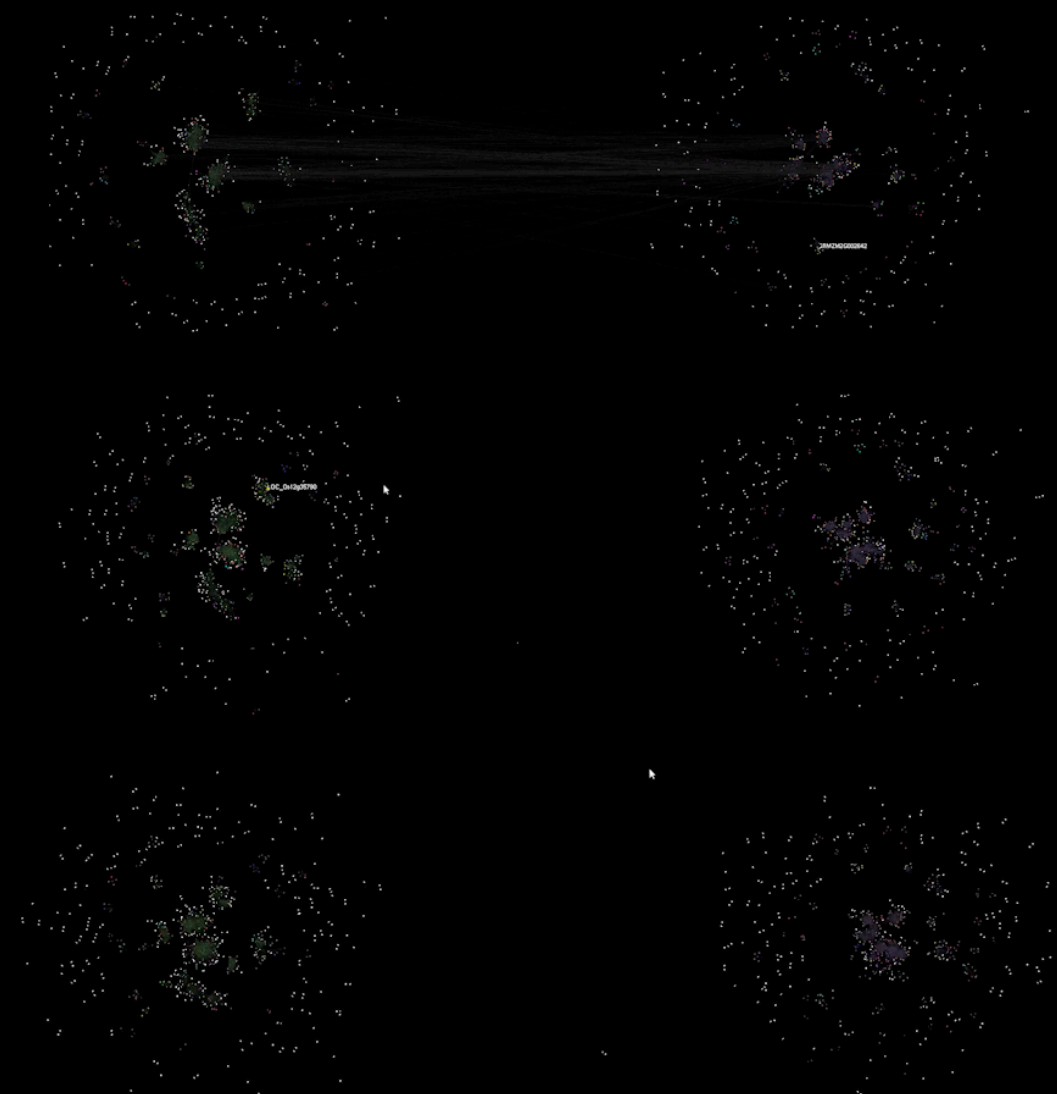
G3NA-V

00:32

MAGNA

20:00

IsoRank-N



GUI

Selected Results

LOC_Os03g25050

Description

LOC_Os03g25050

Go:Term List

- GO:0009628
- GO:0005488
- GO:0009987
- GO:0019538
- GO:0005515**
- GO:0005739
- GO:0006956
- GO:0006457

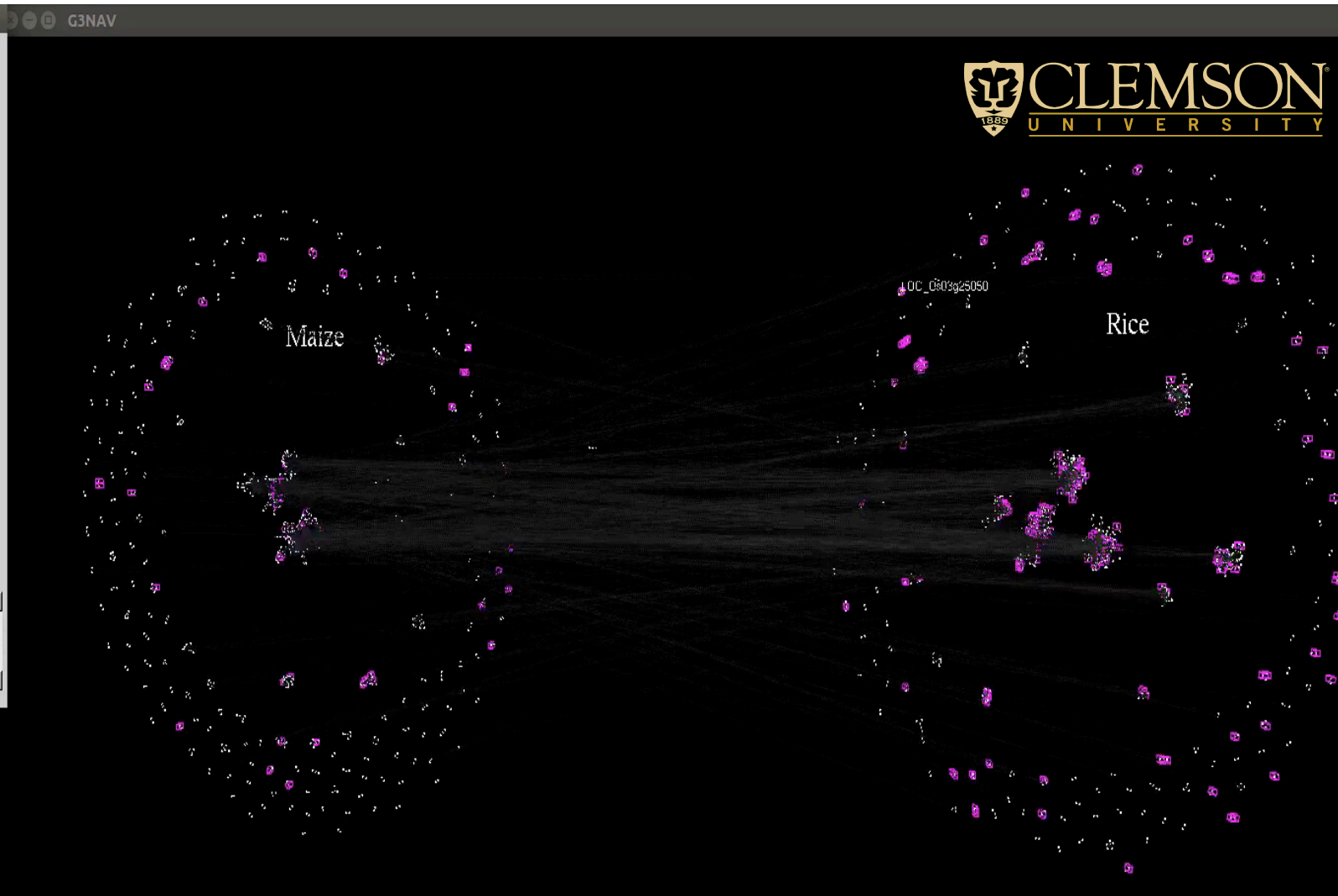
Name : protein binding
"Interacting selectively and non-covalently with any protein or protein complex (a complex of two or more proteins that may include other nonprotein molecules)." [GOC:go_curators]

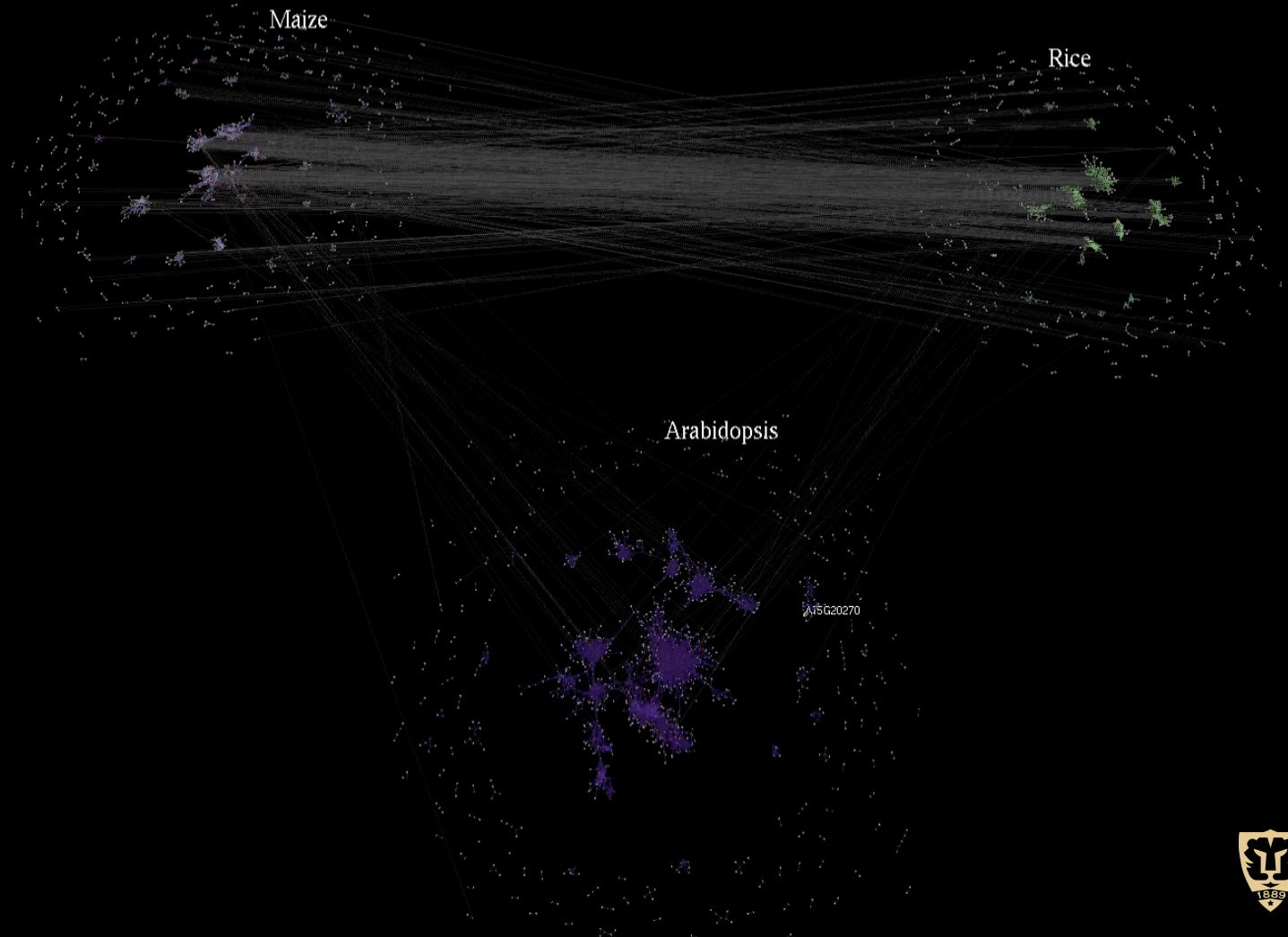
Search Window

Search Term

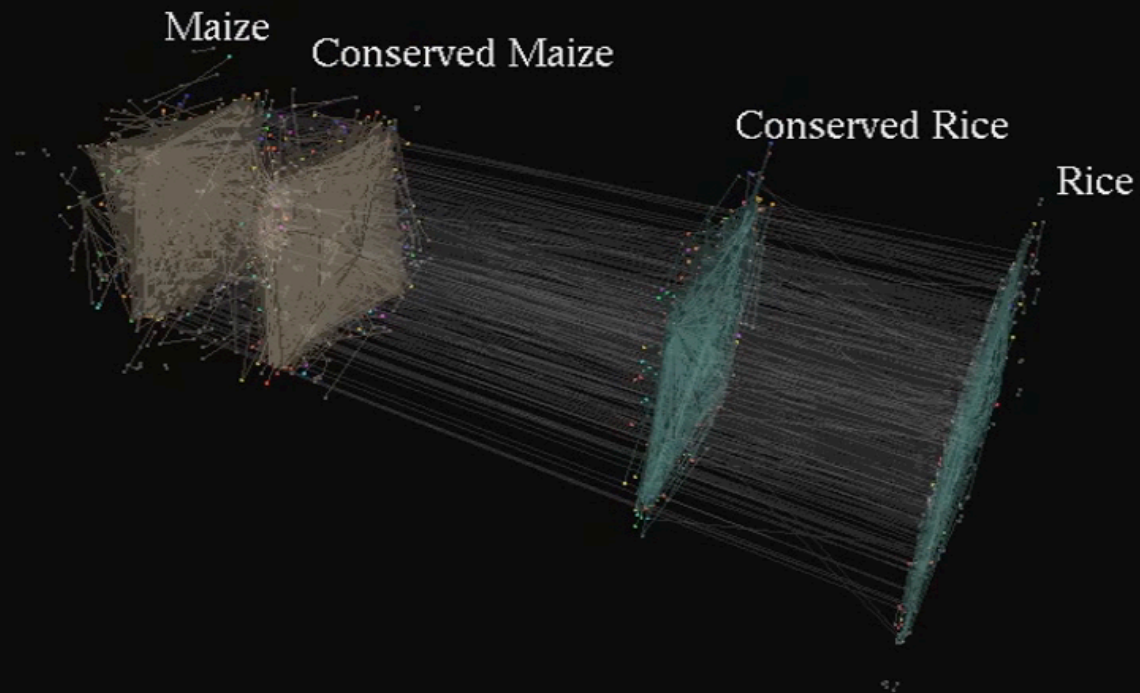
Search

Clear

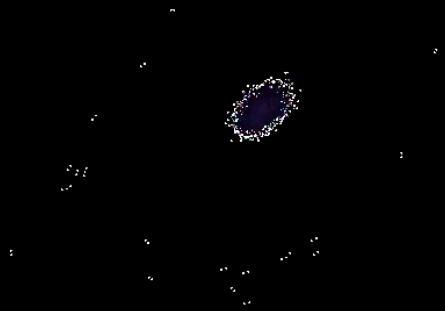




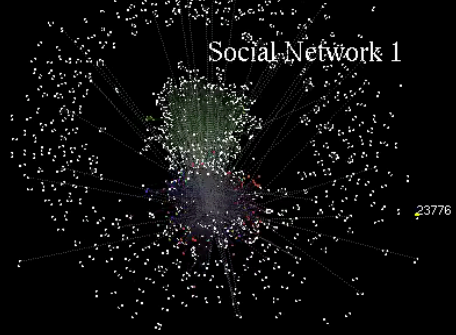
STACKED CONSERVED SUB GRAPHS



Social Network 3

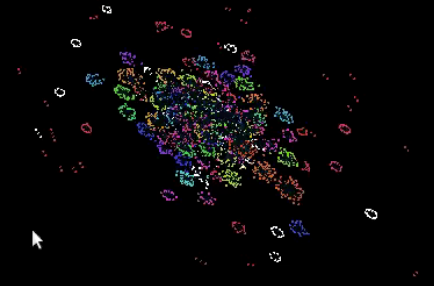


Social Network 2



Social Network 1

Social Network 4



Conclusion

- NVIDIA powered tool for alignment and visualizations of graphs and networks
- Support for ontologies and supporting information regarding graph and networks
- Supports various file formats
- Multi-view port based visualization

Future Work

- Support for other visualization methods such as matrix layout, etc
- Support for multiple ontology formats
- Auto layout mechanism
- Port to QT for alignment and visualization on mobile devices

It takes a Village...



Feltus Lab

- Will Poehlman (<PhD, G&B)
- Calvin Cox (<BSc, G&B)
- Zach Gerstner (<BSc, Microbiology)
- Leland Dunwoodie (<BSc, G&B)
- Brittany Rosener (<BSc, G&B)
- Nick Watts (Programmer, CCIT)

@Clemson

- Karan Sapra (ECE)
- Melissa Smith (ECE)
- KC Wang (ECE/CCIT)
- Ryan Izard (ECE)
- Juan Deng (ECE)
- Walt Ligon (ECE)
- Nick Mills (ECE)
- Brian Atkinson (ECE)
- Stephen Kresovich (G&B)
- Zach Brenton (G&B)
- Julia Frugoli (G&B)
- Josh Levine (CS)
- Chris Konger & Clemson Networking(CCIT)
- Becky Ligon (CCIT)
- Randy Martin (CCIT)
- Jim Bottum (CCIT)

- Stephen Ficklin Lab (WSU)
- Don Preuss & NLM Networking (NCBI)
- Joe Breen & Utah Networking (Utah)
- Jill Wegrzyn (UCONN)
- Meg Staton (UT-Knoxville)
- Dorrie Main (WSU)
- Tim Gilmanov (IU)
- Maciej Brodowicz (IU)
- Daniel Kogler (IU)
- Alireza Kheirhahan (LSU)
- Adrian Serio (LSU)
- Hartmut Kaiser (LSU)
- Chris Branton (LSU)
- Florence Hudson (Internet2)

And it takes money...



- **“CAREER: Harnessing Hybrid Computing Resources in PetaScale Computing and Beyond”**
Source: National Science Foundation [1149644] (M Smith, PI)
- ***Genomic and Breeding Foundations for Bioenergy Sorghum Hybrids.***
Source: Plant Feedstock Genomics for Bioenergy [DE-FOA-000041] (S Kresovich, PI)
- ***MRI: Acquisition of a High Performance Computing Instrument for Collaborative Data-Enabled Science.***
Source: National Science Foundation [1228312] (A Apon, PI)
- ***“CC-NIE Integration: Clemson-NextNet”***
Source: National Science Foundation [1245936] (KC Wang, PI)
- **“Big Data Visualization REU”**
Source: National Science Foundation [1359223](V Byrd, PI)
- ***“Tripal Gateway: Platform for Next-Generation Data Analysis and Sharing”***
Source: NSF-DIBBS [1443040] (S. Ficklin, PI)
- ***“BIGDATA: F: DKM: Collaborative Research: PXFS: ParalleX Based Transformative I/O System for Big Data”***
Source: NSF-BIGDATA [1447771] (W. Ligon PI)
- ***“Big Data Analysis Tools for Agricultural Genomics”***
Source: Clemson University Experiment Station (USDA Hatch Project) [SC-1700492] (Feltus, PI)



Clemson Collaborators

