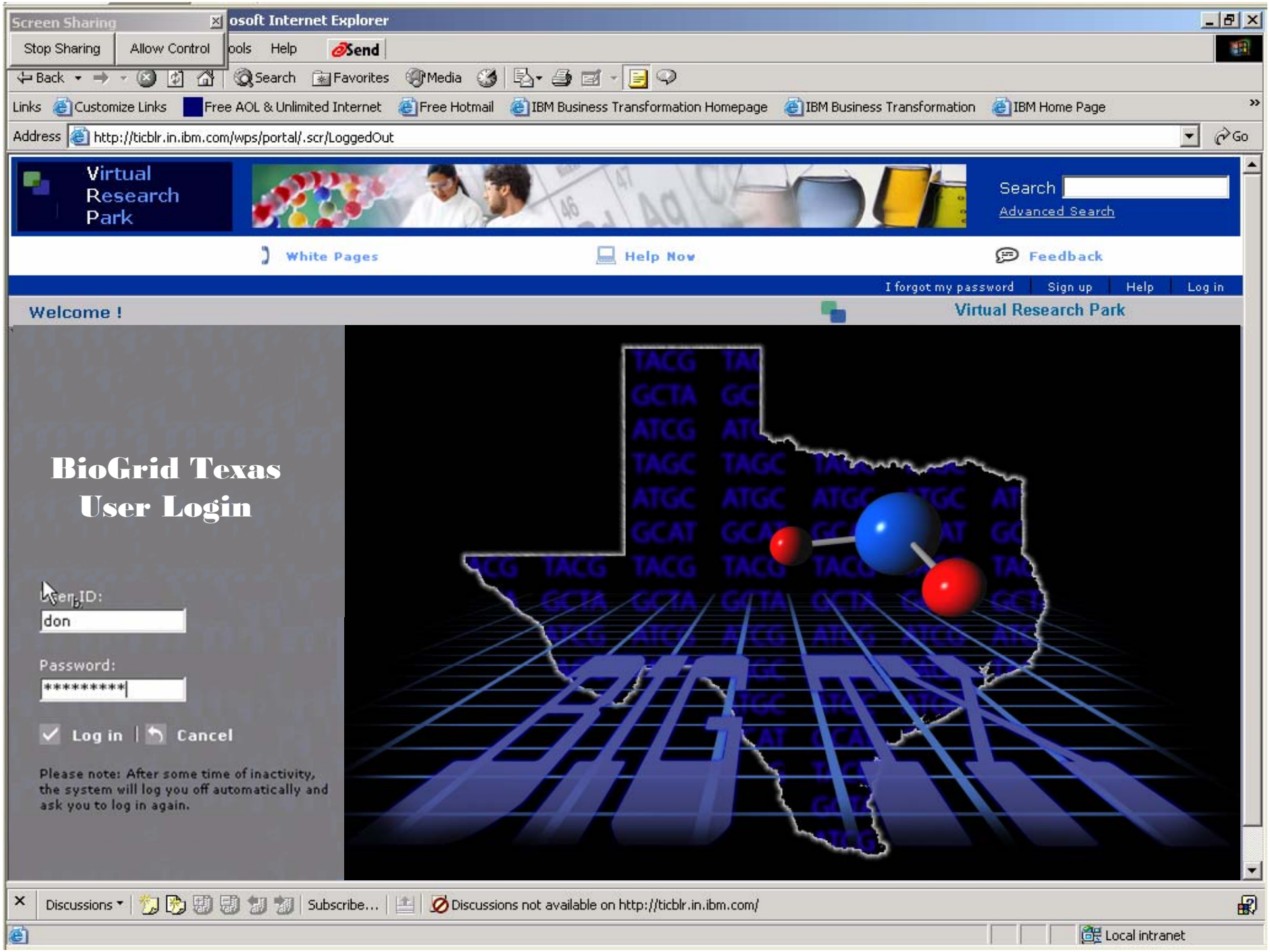
BioGrid Texas

Computer Science and Engineering, Physics, and the College of Science at the University of Texas at Arlington, International Business Machines, and the Texas Workforce Commission

(Presented by: Dave Levine)

BioGrid at UTA

- BioGrid Texas began in the Spring of 2004
- Funded by the State of Texas Workforce Commission and supported by IBM (Health Care and Life Sciences)
- Conceived of and managed initially by Associate Dean of Science, Paul Medley
- Collaboration between Colleges of Science and Engineering at UTA, UT Southwestern Medical School, UNT Health Sciences and IBM (and others)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BioGrid Texas

Virtual Research Park for Life Sciences & Health Care

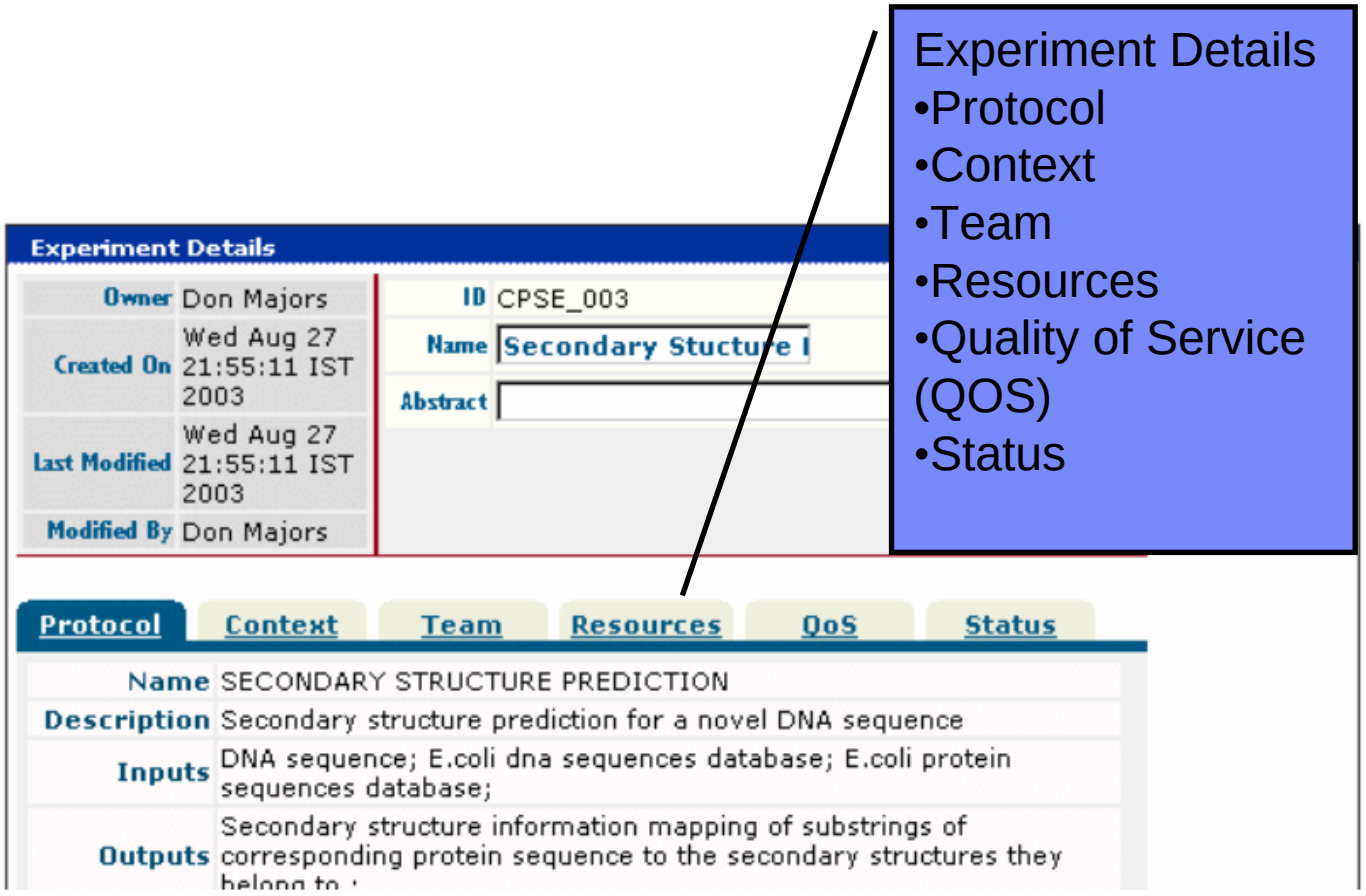
What is BioGrid Texas?

- Collaborative research, development and information-sharing system for Life Sciences and Health Care
  - Virtual Research Park (VRP)
  - Healthcare Collaborative Network (HCN)
- Universal Web interface and open development platform created by IBM Healthcare and Life Sciences
- Very large scale computing network
  - Utilizes high-performance grid computing technology infrastructure at The University of Texas at Arlington
- Allows geographically dispersed R&D teams and health care organizations to collaborate like never before

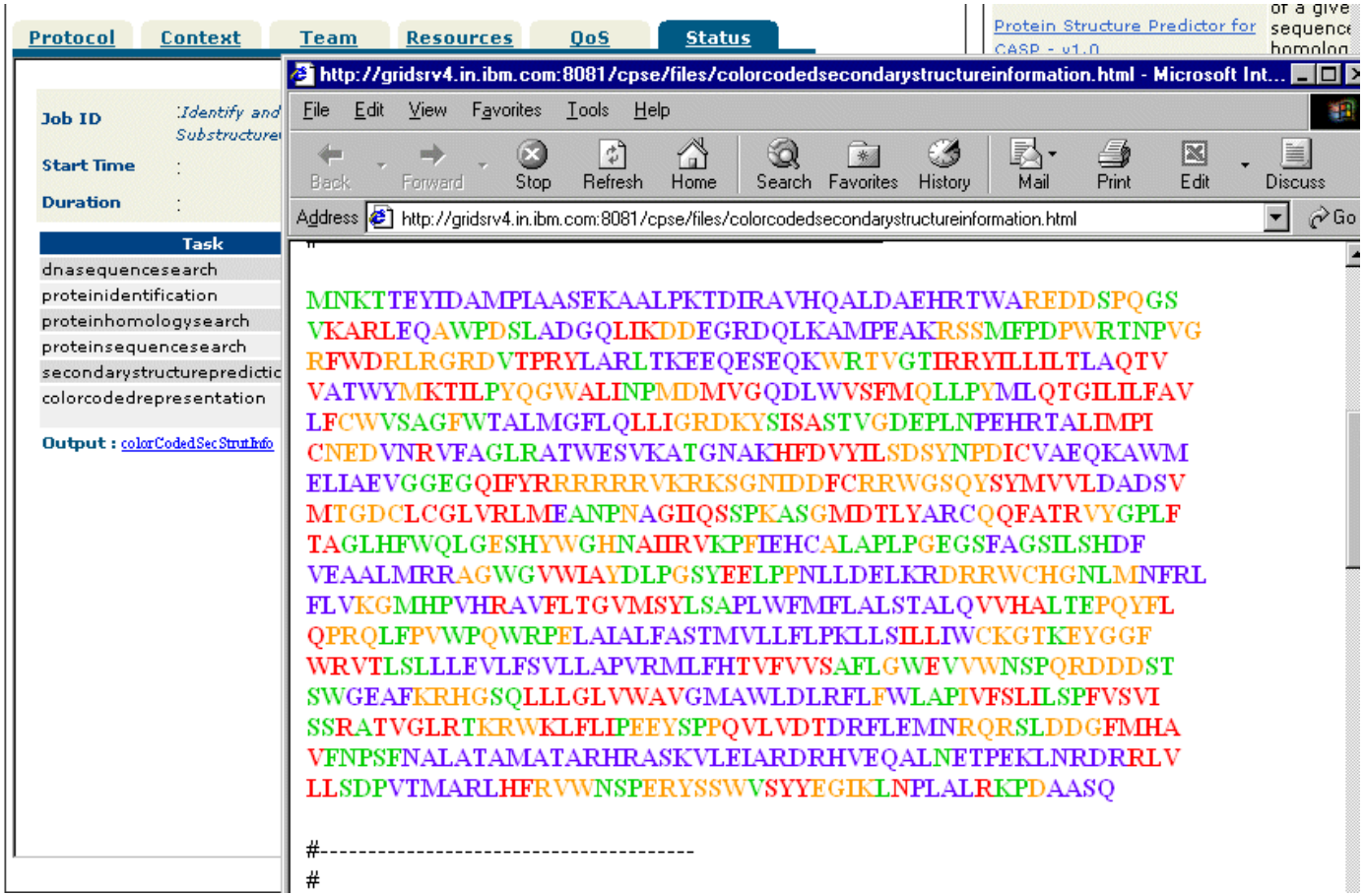
Goal: The Virtual Collaboratory

- IBM Life Sciences Virtual Research Park incorporates a sweeping new concept called the "**Collaboratory**"
  - Allows users to solve problems using community resources and knowledge distributed across a grid computing infrastructure

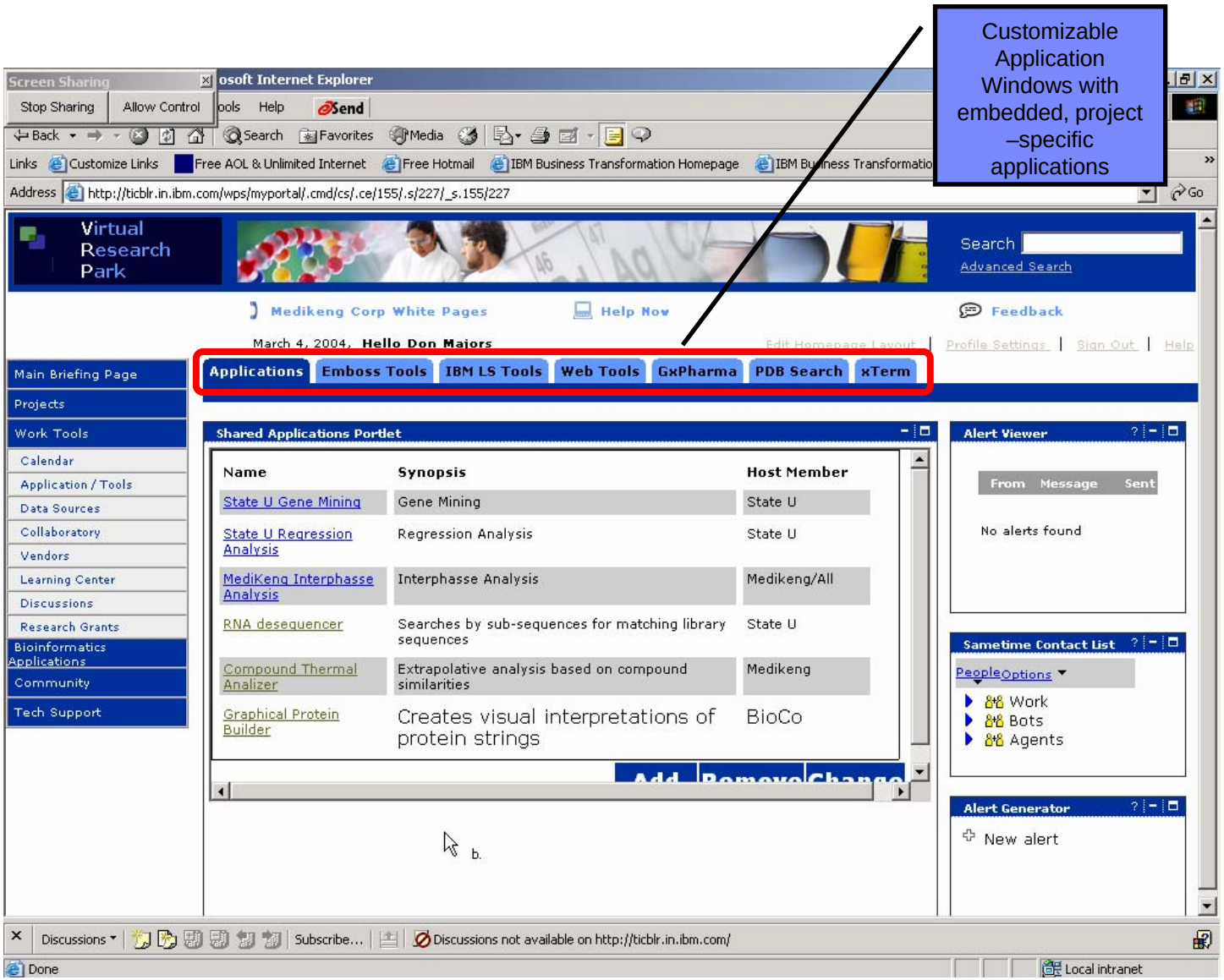
Experiment Details



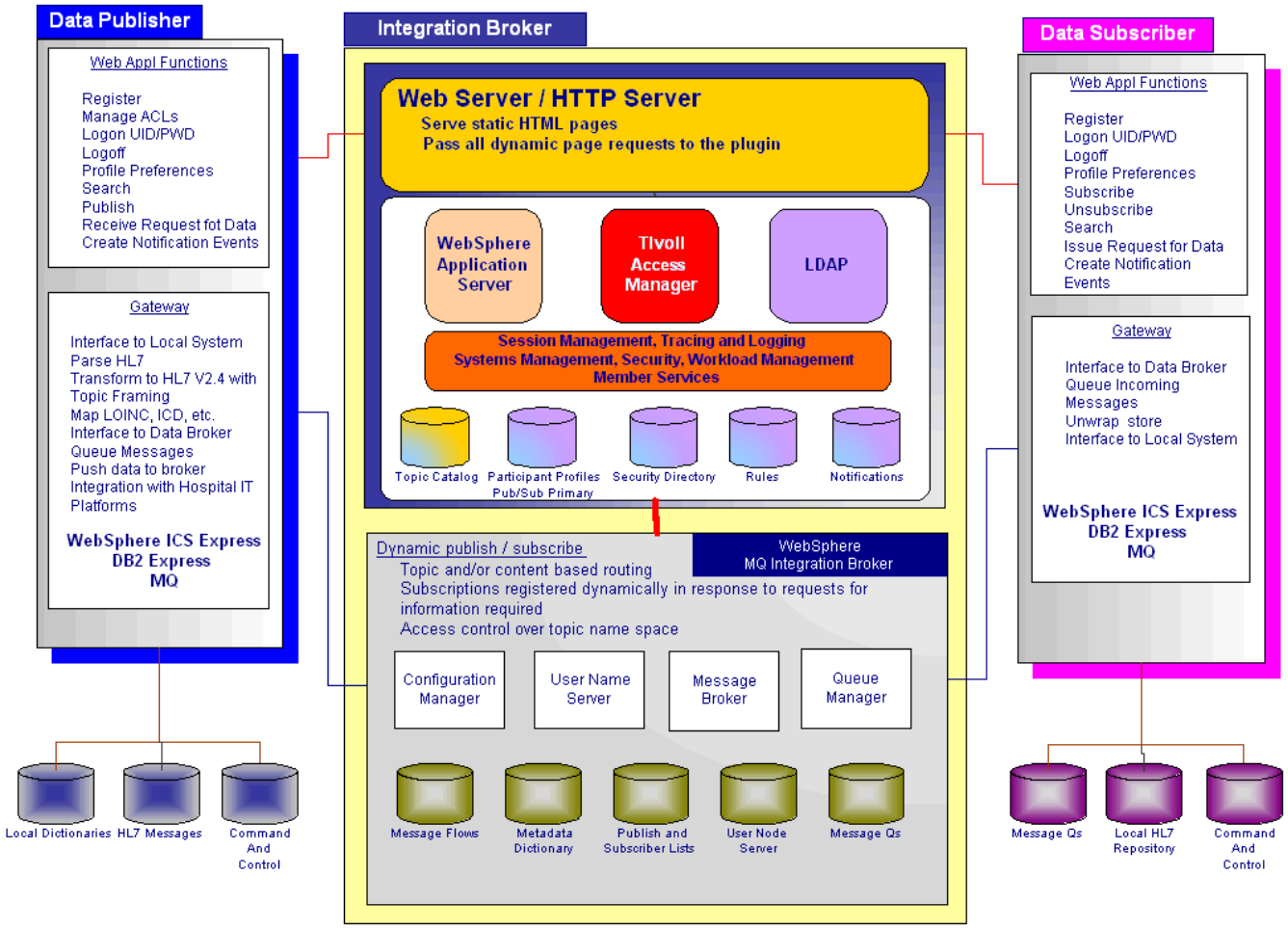
Project Results



Application Sharing



Healthcare Collaborative Network



Focus Groups

- **Bioinformatics, Computational Biology, Cell and Molecular Biology, Genomics and Proteomics**
  - Bioinformatics requires a higher level of competence in math and computer science
  - BioGrid system will bring together people with skills to interface with other life science professionals
    - Communicate with bioinformatics experts and biostatisticians for analysis of genetic and genomic data
    - Help train future generations of bioinformaticians
  - Access to the latest bioinformatics applications

Three BioGrid Projects

- Skin Cancer (lesion) detection (UTSW medical and CSE)
- De novo TE repeat discovery (DNA) (Biology and CSE)
- Mosquito and Malaria gene search (Biology, CSE, Pharmacology)

BioGrid Projects – Skin Cancer

- Skin Cancer (lesion) detection

  Project allowed dermatologists to upload and annotate digital photographs of skin lesions, some cancerous

  A portal into BioGrid allowed a new image to be uploaded and compared to knowledge base

BioGrid Projects – DNA TEs

- New species are being sequenced weekly
- Part of “understanding” the sequence, and indeed finding genes is to compare sequences to other, similar species
- Much of the sequence are the same “strings” appearing over and over again
- These may be within a gene or located between genes (most DNA is “junk”)

Quick Introduction

- Biologists are interested in these long DNA sequences of nucleotides composing genes
- Many of these sequences (a gene, part of a gene, or “junk”) are repetitive, the same sequence (or nearly the same) appearing over and over again in a chromosome or whole genome
- But the genomic data is huge, and genes and TEs don’t stand out

Introduction – Some Results

C. Elegans –

we found 90% of the ones that had been already identified (by other methods), those were almost all correct,(there are 263),

we found 22 previously unidentified TEs (some don't really exist, but some do),

On one processor it took 24 hours, on our

cluster less than 0.5 hour (previously a few days)

Introduction

Humans – (only the X chromosome)

we found 70% of the ones that had been already identified (by other methods), those were all correct,(there are 682),

we found “a few” previously unidentified TEs (some don’t really exist, but some do),

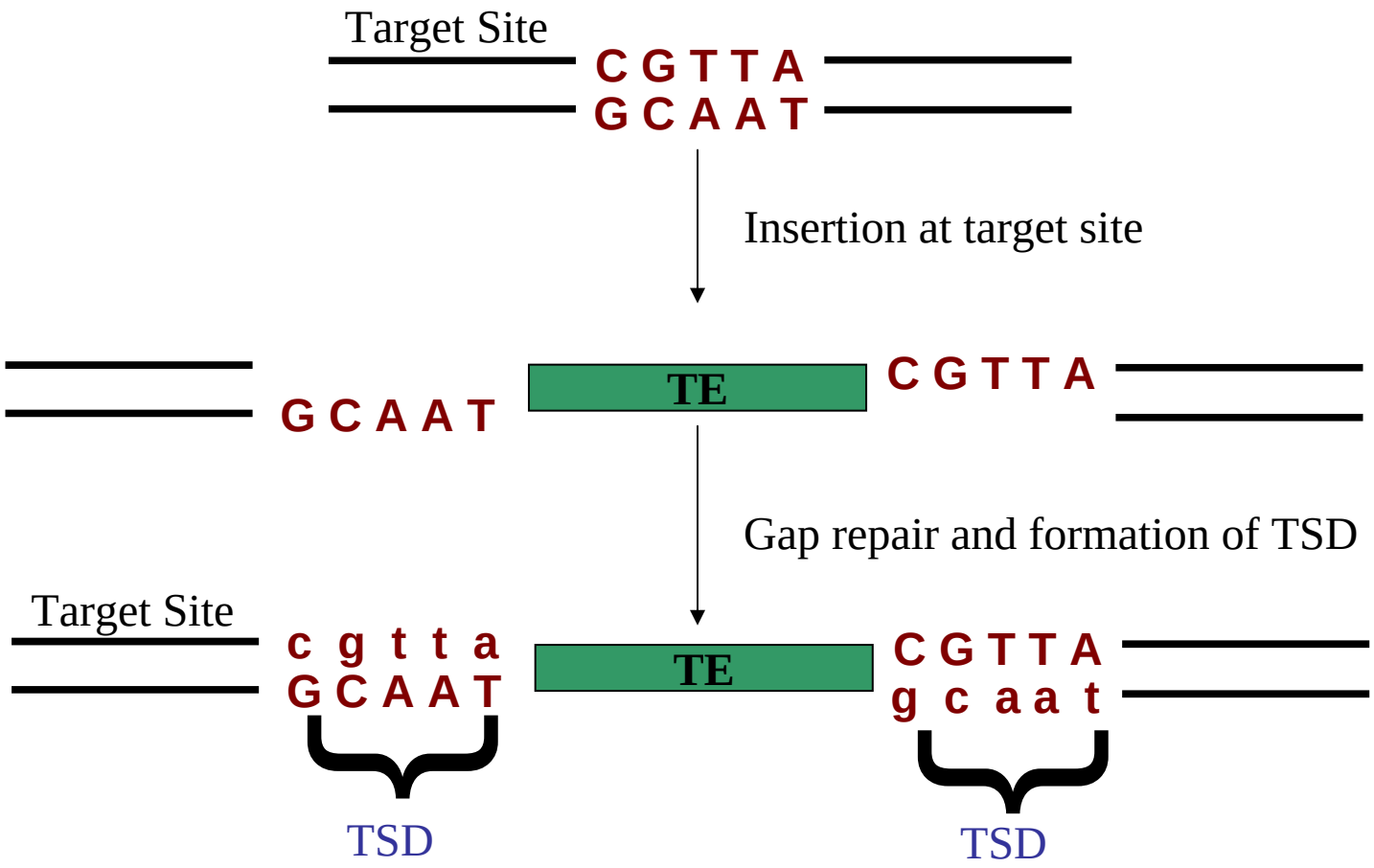
On one processor it took 2 weeks, on our

cluster 10 hours (previously a few months)

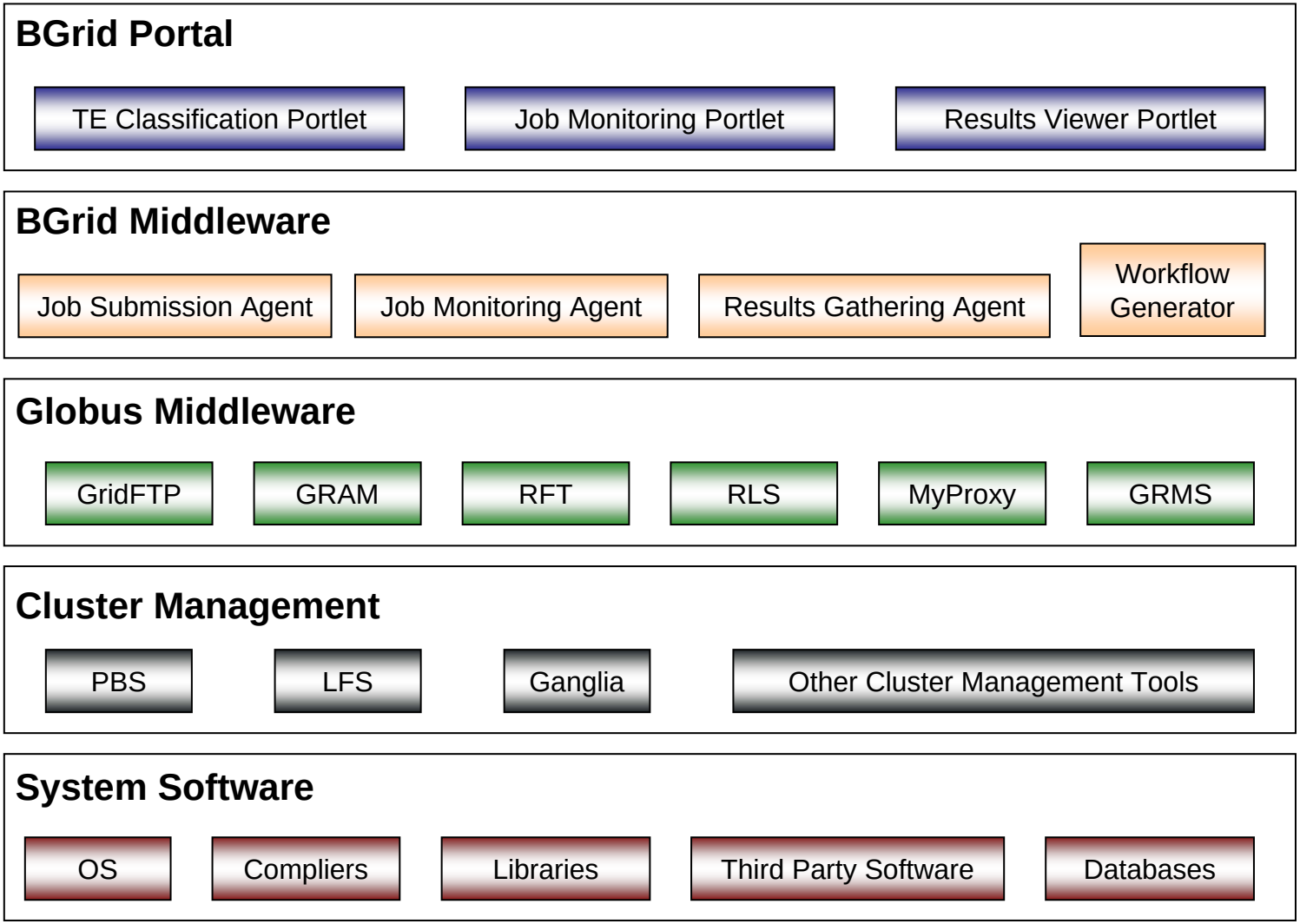
Rationale

- Identifying and classifying TEs can help in genome assembly
- TE annotation is an integral part of genome annotation as they comprise a significant fraction of the genome
- Repbase is a database of annotated repeats
- No tool exists for automatic classification of TEs

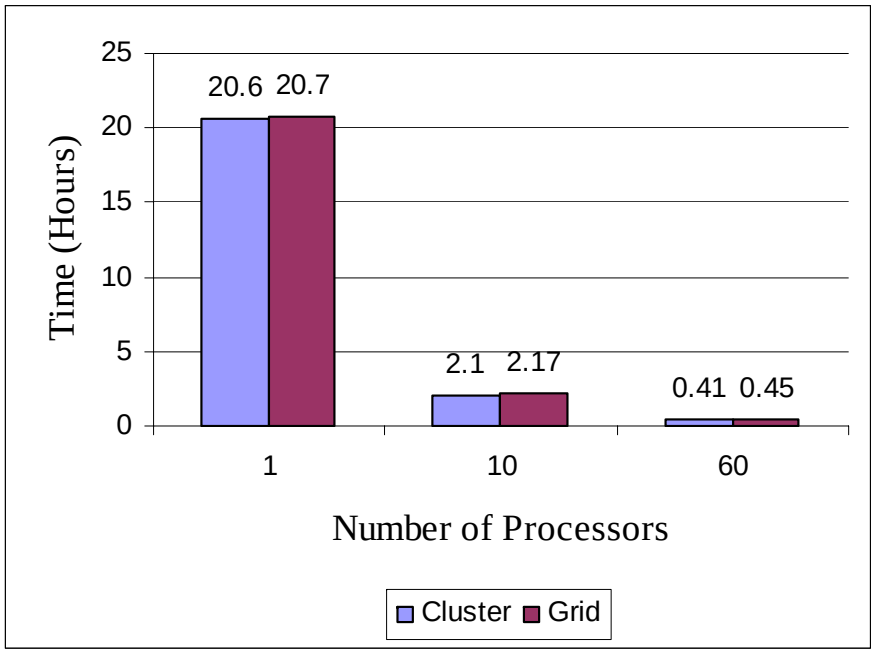
Formation of TSDs



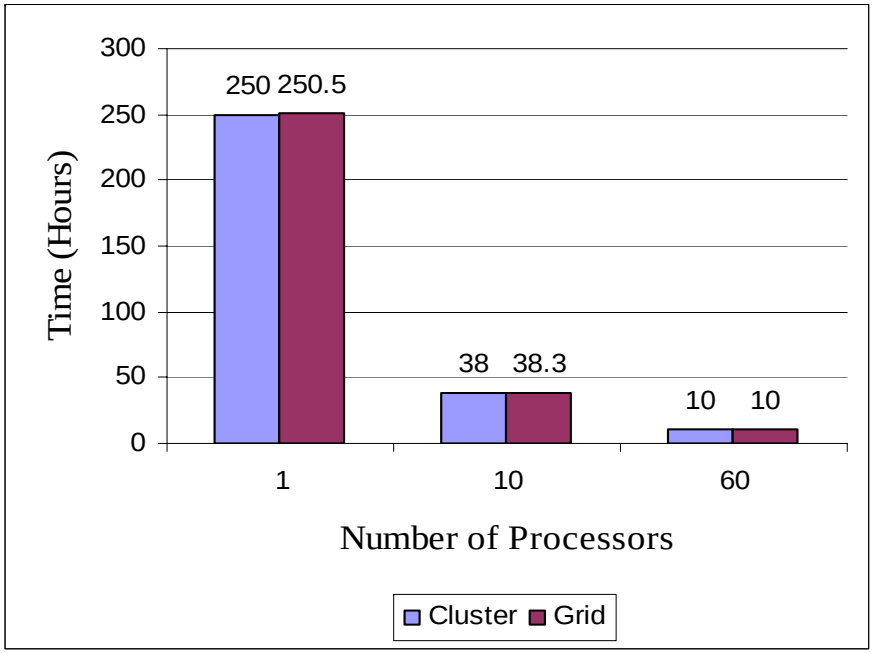
TE Classification on a Grid



Results – Turnaround Time



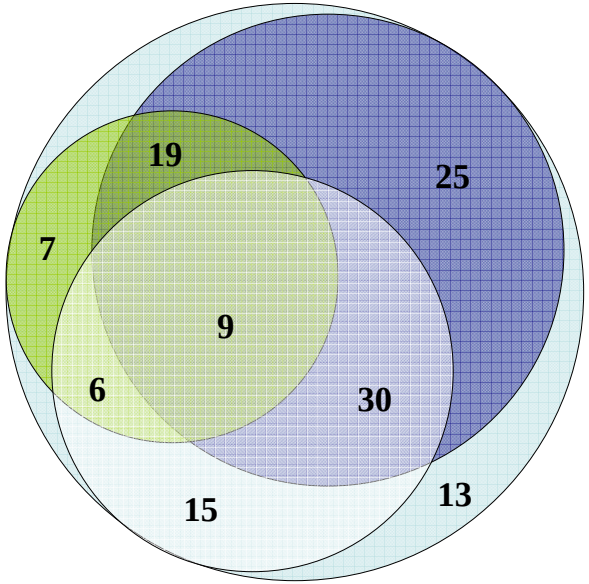
C. Elegans Genome



Human X Chromosome

Comparison of REPCLASS classification with those of Repbase

Caenorhabditis elegans (worm)

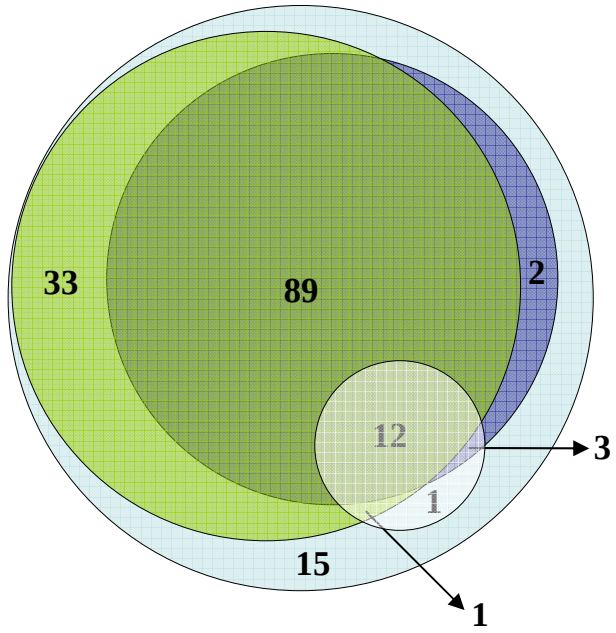


Percentage classified	89.5%
Accuracy of classification	100%

Repbase

REPCLASS
- Structural
- Homology
- TSD

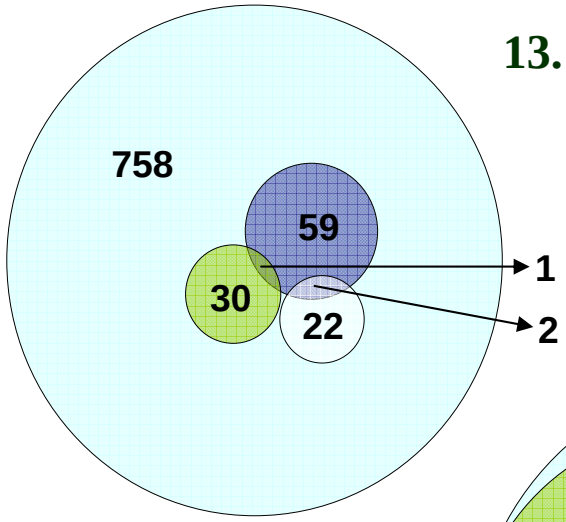
Drosophila Melanogaster (fruit fly)



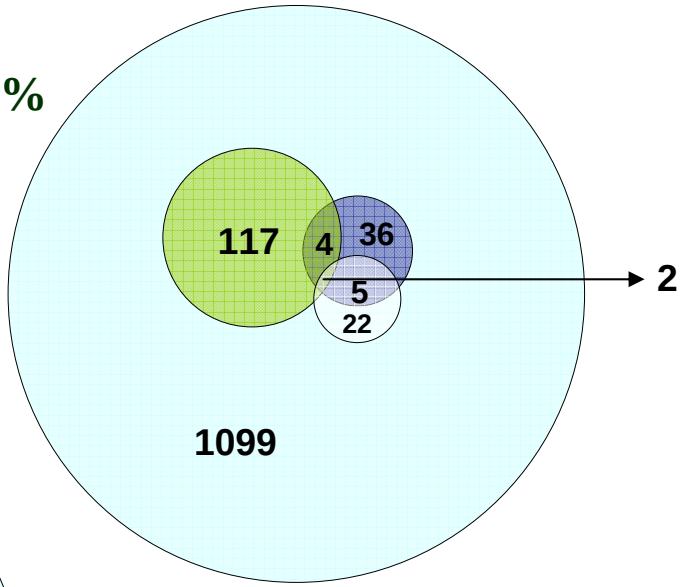
Percentage classified	90.38%
Accuracy of classification	100%

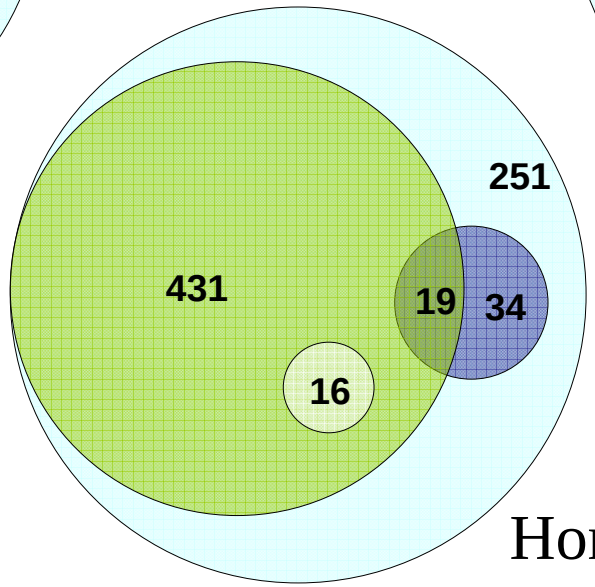
Classification of new genomes

S. purpuratus (sea urchin)



Ciona intestinalis (sea squirt)





Unclassified

REPCLASS

- Structural
- Homology
- TSD

Homo sapiens X Chromosome

Malaria and Mosquitoes

- Malaria is a really nasty disease
- 300 to 500 million people/year get it,
  more than one million/year die from it
- Anopheles Gambiae (and similar) carry it
- Many efforts are based on vaccine, killing mosquitoes, treatment
- We don’t want a better mosquito trap,
  we want a better mosquito

Mosquitoes (Anopheles)

- There are about 15,000 genes predicted on 5 chromosomes
- Some areas on chromosomes poorly covered (mapped)
- Looking for a gene or a few genes that can be engineered so that Anopheles can’t carry malaria

Mosquitoes (Anopheles)

- May have found some (so far) yet-undiscovered genes
- Currently verifying some results in lab with actual mosquitoes
- (Very creepy)

Discoveries

- Biologists love talking about their science – in detail
- Like physicists they are very computer knowledgeable
- They will explain biology/genetics in as much detail as one needs or wants
- Some parallel applications exist, most very rudimentary

Thank You

Thank You for your time

I’ll be happy to answer questions now

or later, off-line