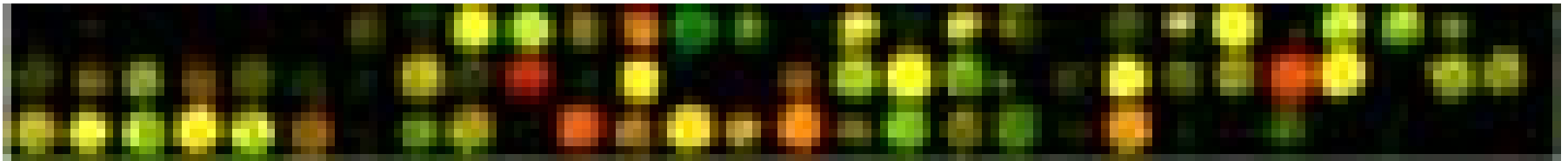


MAGE Jamboree: Introduction to MGED Society



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Thanks...

- NCICB for hosting the jamboree
- Today's speakers
- Jamboree participants
- NHGRI/NIBIB for funding
- **MERVI HEISKANEN**



A few of my favorite acronyms

- Microarray Gene Expression Data Society (MGED)
- Minimum Information Annotating a Microarray Experiment (MIAME)
- MicroArray Gene Expression Object Model (MAGE-OM) and Markup Language (MAGE-ML)
- MGED Ontology (MO)



What is MGED?

- MGED - Microarray Gene Expression Data group
 - Established November, 1999, Cambridge, UK
 - MGED8 met in Bergen, Norway in September 2005
 - Next MGED meeting in Seattle, Washington in September 2006



What does MGED do?

- MGED is a grass-roots organization composed of people who produce, store and analyze microarray data
- The mission of MGED is to produce standards that allow people to share and understand the data produced by microarray experiments



How is MGED supported?

- Most efforts are *volunteered* (such as at the MAGE jamborees)
- MGED has a few corporate sponsors to help offset costs of meetings and communication
- Grant from NHGRI and NIBIB helps with development of MAGEv2 and a set of supporting software



Background : Interpretation and Analysis

- Extremely difficult to either interpret or analyze expression results without being aware of all the variables

Biological characteristics, experimental design, protocol parameters, filtering parameters, etc.

- Typically, these annotations, if they exist at all, are not attached to the data

Perhaps in a lab notebook, eventual publication (if ever published), or in the worst scenario, only in the experimenter's head



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Background : MIAME checklist

- MGED Guide to authors, editors and reviewers of microarray gene expression papers
- In the interests of full disclosure and open research, a checklist of requirements was proposed, aimed at allowing manuscript readers “to understand the experiment, to identify the sequences being assayed, and to interpret the resulting data. ”

http://www.mged.org/Workgroups/MIAME/miame_checklist.html



MIAME checklist

- Six parts
 1. Biological Samples
 2. Hybridizations
 3. Data Normalization and Transformation
 4. Experimental Design and Factors
 5. Array Design
 6. Measurements



MIAME Challenges

- Validating a study as MIAME-compliant is still in the eye of the beholder
- Helping authors, editors and reviewers understand what MIAME is (and what is NOT)
- Extending MIAME concepts to other microarray applications or high-throughput technologies



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MAGE

- An object model : MAGE-OM
- An exchange format : MAGE-ML
- A software toolkit : MAGE-STK



MAGE development

- Software to utilize MAGE is coordinately developed via programming jamborees (such as this one) two or three times a year
- MAGEv2 development occurs at meetings of small working groups an additional 3-4 times a year
- Mailing lists are sources of active discussion and expert opinions



MAGE Challenges

- MAGE-ML documents are not human readable
- Interpretation of MAGE can differ from person to person, therefore data can be encoded in different (and unexpected) ways
- Additional data formats



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MO: MGED Ontology

- Developed to annotate MAGE files
- Will be discussed in detail by Chris Stoeckert



MGED Challenges

- Should we be trying to force researchers to use standards in expected ways?
- Should we concentrate on making it easier for people to use standards in expected ways?
- How active should we be in participating in standards construction in other fields?
- How do we gain greater participation from members of community?



MGED: Future Plans

- Tab-delimited method for communicating data from MAGE-OM
- New version of MAGE-OM (v2) developed in coordination with FUGE
- Further development of MO in coordination with FUGO
- Development of methods to reconcile MAGE-ML documents from different sources
- Collaboration with other high-throughput biomedical communities
- What else (we take suggestions)?



MGED Working Groups

- MIAME: Defining data standards (Brazma)
- MAGE: Establishing data formats (Spellman, Miller)
- Ontologies: Creating ways to describe data (Stoeckert)
- Data Transformation: Describing methods of normalization, quality assessment and analysis (Irizarry, Huber, Quackenbush)
- RSBI: Extending MIAME to other fields (Sansonne)
- MISFISHE: Standards for immunohistochemistry (Deutsch)



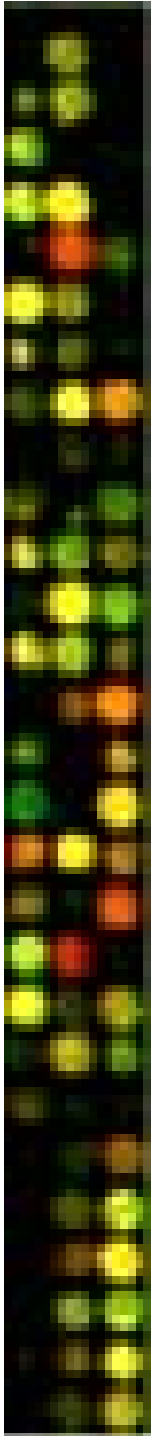
Get Involved with MGED

- Who should participate in MGED?
 - Enthusiasts of standards and object models
 - People who think standards and object models are a pain
- How to get involved?
 - Come to meetings
 - Subscribe to mailing lists



Keeping our eye on the prize

- Standards should help us critically review high-throughput studies
- Standards should help us understand and communicate our high-throughput experiments to others
- Standards should help to validate or contradict results of high-throughput experiments
- Standards should help us make scientific discoveries!



www.mged.org