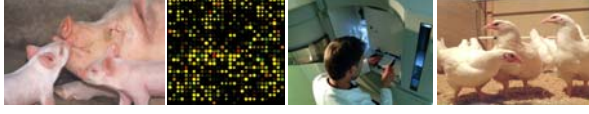


GenMAPP  
 A Software Tool for Analyzing Microarray Data in the Context of Biological Pathways  
 Dennis Prickett  
 Institute for Animal Health, UK

**EADGENE and SABRE Post-Analyses Workshop**  
 12-14th November 2008, Animal Sciences Group, Wageningen UR, Lelystad



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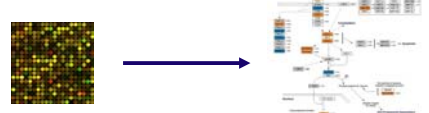
**Overview**

1. Introduction to pathway analysis using GenMAPP
2. GenMAPP analysis of Eimeria array data

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**Why Pathway Analysis?**

- **Intuitive to Biologists**
  - Provide a biological context for results
  - More efficient than searching databases gene-by-gene
  - Intuitive data display for sharing data
- **Computation on Pathway Content**
  - Analyze over-representation of changed genes on pathways and ontologies
  - Generate and compare pathway signatures between models



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**GenMapp**  
 Gene Map Annotator and Pathway Profiler

- Visualize gene expression and other genomic data on biological pathways and other groupings of genes
- Global analysis identifies significantly changed processes and functional groups

[www.GenMAPP.org](http://www.GenMAPP.org)

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**GenMAPP**

- Developed as an internal tool for microarray data
- > 17,000 registrations to download GenMAPP
- Free
- > 300 publications
- Open source

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**GenMAPP Mapp Archive Descriptions**

- Chicken and Bovine MAPPs have been inferred from human MAPPs, using orthology information
- 85 Mapps – Chicken
- 87 Mapps - Bovine

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**GenMAPP Database**

**Pathways**

**Experimental Data**

← →

**Gene Database**

- Genes and annotation
- Relational information
- Assembled from Ensembl and GO
- Distributed by GenMAPP

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**MAPPFinder**

- Enrichment analysis of “changed” genes
- INPUT: Experimental data
- OUTPUT: List of Pathways with associated statistics
- View results in spreadsheet or in GenMAPP
- Originally developed as a separate application

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**Part 2**

**GenMAPP analysis of Eimeria data**

- The average of the M.all.cor values were used where there were significant values for 3/5 probes
- Probes with less than 3 significant values were given a value of 0
- The cutoff value used was +/- 1.5

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**GenMAPP Workflow**

```

  graph TD
    A[Formatted Data] --> B[Import Data]
    B --> C[Set Color Criteria]
    C --> D[Display Data on Pathways]
    D --> E[MappFinder]
    F[Create/Edit Pathways] --> D
    G[MappBuilder] --> D
  
```

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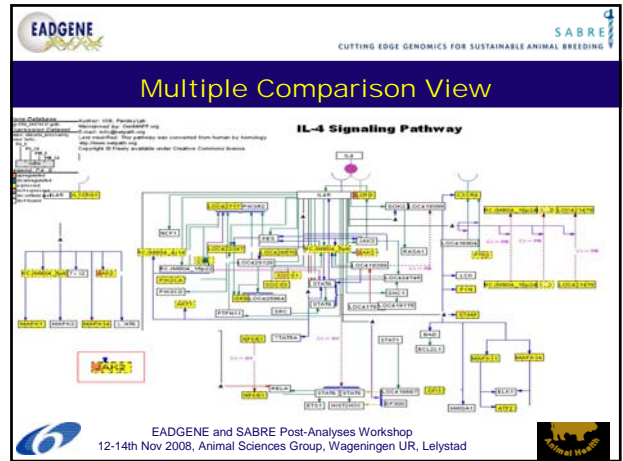
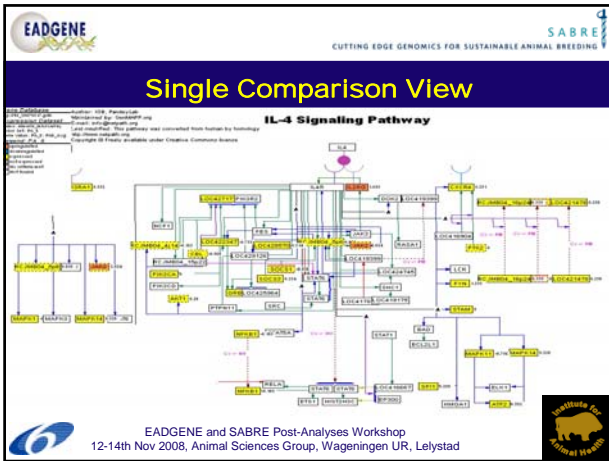
**Analysis Overview**

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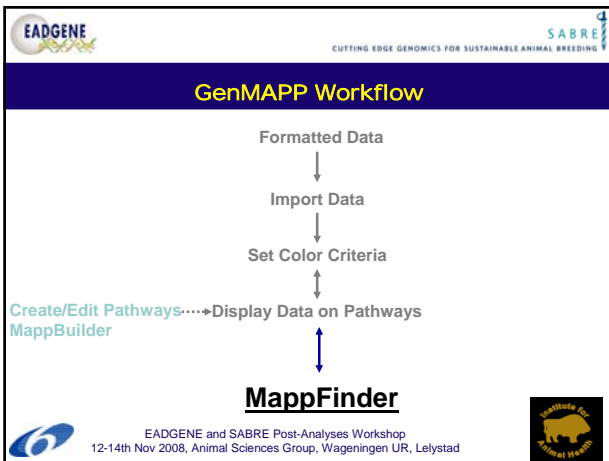
**Analysis Overview**

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- Some Pathways affected**
- Complement activation
  - Ribosomal proteins
  - Nucleotide metabolism
  - TGF- beta signalling pathway
  - Translation factors
  - IL-4 Signalling pathway



**MAPPFinder Analysis**

The screenshot shows the MAPPFinder software interface. It includes a "Select Color Set" dropdown menu, a "Species Selected" field, and a "Run MAPPFinder" button. To the right of the screenshot, a list of instructions is provided:

1. Select any collections of pathways for analysis
2. Select Color Sets and criterion to analyze
3. Run analysis

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**MAPPFinder Browser**

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**MAPPFinder Results**

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**MAPPFinder Results PA\_8 upregulated**

1	2	3	4	5	6	7	8	9	10	11	12
1	MAPPFinder 2.0 Results for the Local MAPPs										
2	File: N:\Bioinformatics\Public\Pathways\GenMAPP 2 Data\Gene Databases\microarray.gene										
3	Table: egenes_2008_05_08_12_00_00										
4	Database: N:\Bioinformatics\Public\Pathways\GenMAPP 2 Data\Gene Databases\microarray.gene										
5	Version: 2.0										
6	Database: gabs										
7	Proteins: none										
8	Calculation Summary										
9	200 probes meet the (FDR) Aug = 1.5 criteria										
10	200 probes meeting the criteria linked to a MAPP system										
11	42 genes linked to a MAPP										
12	18262 probes linked to an ID on a MAPP system										
13	14283 probes linked to an ID on a MAPP system										
14	1175 Genes are linked to the Local MAPPs										
15	The Z score is based on an n of 1175 and a R of 42 distinct genes in the GO										
16	MAPP System	Number Changed	Number Matched	Number On MAPP	Percent Of Percent PZ Score	Permutat	Adjusted				
17	GO:biological_process	4	27	30	18.66667	0.03646	0.494	0			
18	GO:cellular_component	4	27	42	14.81481	0.420671	0.161	0			
19	GO:anatomical_entity	4	40	60	12	0.171022	0.062	0			
20	GO:ribosome	6	42	56	11.90476	0.75	2.36	0			
21	GO:ribosome_biogenesis	1	1	13	10.00000	0.4621	0				
22	GO:translation	2	26	32	10.71429	0.7	2.069	0			
23	GO:ribosomal_gene	1	1	11	10.00000	0.4621	0				
24	GO:ribosomal_protein	1	1	10	10.00000	0.4621	0				
25	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
26	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
27	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
28	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
29	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
30	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
31	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
32	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
33	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
34	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
35	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
36	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
37	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
38	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
39	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
40	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
41	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
42	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
43	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
44	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
45	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
46	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
47	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				
48	GO:ribosome_function	1	1	10	10.00000	0.4621	0				
49	GO:ribosome_organization	1	1	10	10.00000	0.4621	0				
50	GO:ribosome_structure	1	1	10	10.00000	0.4621	0				

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**GenMAPP Workflow**

```

    Formatted Data
    ↓
    Import Data
    ↓
    Set Color Criteria
    ↓
    Create/Edit Pathways → Display Data on Pathways
    MappBuilder
    ↓
    MappFinder
  
```

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**Building a Pathway with MappBuilder**

Test a hypothesis  
Use literature and/or previous knowledge to create a list of candidates



- ✓ Collect a list of gene IDs
- ✓ Import using MappBuilder
- ✓ Organize into biological pathway
- ✓ Add predictions of expected changes

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**Building a Pathway: MappBuilder**

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CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

### GO-ELITE

- A new method for identifying redundant annotations from gene expression data
- From the same group as GenMapp  
[www.genmapp.org/go\\_elite](http://www.genmapp.org/go_elite)
- Designed to identify a minimum non-redundant set of Gene Ontology terms or pathways (using MappFinder GO results) for a set of genes.



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