

Introduction to pathways, or - what to do with the gene lists...
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EADGENE **SABRE**
 CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

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

Introduction to pathways
 or - what to do with the gene lists....

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From images to gene lists

"GeneID"	"Gene"	"Accession"	"Ref"	"Species"	"Type"	"Ref"
10	11	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
20	21	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
30	31	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
40	41	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
50	51	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
60	61	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
70	71	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
80	81	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
90	91	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"
100	101	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"

"Gene list"

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From images to gene lists

Weeks/months → Quarters/Years...

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Which genes to include in the list?

- Fold-change
- P-value
- Fold-change+ P-value

Ranking vs cut-off

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The annotation....

"GeneID"	"Gene"	"Accession"	"Ref"	"Species"	"Type"	"Ref"
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100	101	210740	"Homo sapiens"	"Homo sapiens"	"mRNA"	"NM_015176.3"

- Update the annotation?
- Orthologous genes?
- More than one annotation? (different species...)
- The "unknown genes"?

"Gene list"

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Post-analytical work

Pattern discovery

- Supervised
- Unsupervised

Graphical

- Cluster heat maps
- PCA
- SVM
- ...

Network/pathway reconstruction

- Literature Networks
- Gene Ontology
- Pathways (KEGG)
- "Unknown genes"?

"Gene list" + annotation (selection / all)

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Post-analytical work

Feel good ↔ New knowledge

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Comments / coffee

?

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