

Integration of biological knowledge related to gene co-expression

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<Experiment>

Chickens (x27): physiological state

- N: fed (ad libitum access to food) (x6)

J16: 16-hour fasting (x5)

J16R5: 16-hour fasting + 5-hour renutrition phase (x7)

The data

J16R16: 16-hour fasting + 16-hour renutrition phase (x9)

- gene expressions (selection)
- fatty acid concentrations (hepatic and plasmatic)

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The data

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What are the mechanisms implemented in reply to fasting?

The data, the expectations

<Merged data tables>



The data, the expectations

<Merged data tables>



<expectations>

To provide an help on the functional interpretation in an exploratory multivariate analysis framework

Exploratory multivariate analysis framework



Dim 1 (33.66 %)

Exploratory multivariate analysis framework

The multitude of gene expressions is projected onto the the correlation circle <u>uninterpretable</u>



Exploratory multivariate analysis framework



Modular approach

Modules



Modular approach

Modules



Modular approach

Modules





Modules



 $< Z_2, Z_2 >$

Modular approach



 $< Z_1, Z_1 >$



Modules

_ Modules

<MODULES of GENES>

Modular approach



Modules

<MODULES of GENES>

Modular approach



Modules

<MODULES of GENES>

Modular approach



Modular approach

Modules







Description of genes and genes products

Gene Ontology

- Cellular Component

- Molecular Function

L Biological Process (BP)

Genes could be grouped by GO BP terms

GO:0006928, cell motility	GO:0009966, regulation of signal transduction	GO:0051276, chromosome organization and biogenesis
CALD1 EGFR ENPP2 FN1 FPRL2 LSP1 MSN PDPN PLAUR PRSS3 SAA2 SPINT2 TNFRSF12A VEGF WASF1 YARS	CASP1 EDG2 F2R HCLS1 HMOX1 IGFBP3 IQSEC1 LYN MALT1 TCF7L1 TNFAIP3 TRIO VEGF YWHAG YWHAH	CBX6 NUSAP1 PCOLN3 PTTG1 SUV39H1 TCF7L1 TSPYL1





I <th

M: Quantitative data frame

Transpose of the table microarrays x genes, the data being centered by row

<u>G: Contingency table</u>

gij = 1 if the gene i belongs to the process j 0 if not



Construction of a space with a new distance between the genes:

Two genes are close in this space if:

1- They are involved in the same biological processes

2- They are co-expressed

3- They are situated at a similar level of the regulatory network



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 → Matrix of the terms

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- → The number of processes the gene is involved in could determine its level in the network
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Canonical Correspondence Analysis

Our Approach ____

Representation of the genes onto the canonical variables



Our Approach _

Representation of the genes onto the canonical variables



Our Approach.

Representation of the genes onto the canonical variables





Objective: to constitute groups of genes. Classification of the genes according to their coordinates on the canonical variables (150 groups).

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Projection onto the groups' representation



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Neighboring terms

- regulation of catabolic processregulation of actin cytoskeleton organization
- histone modification
- regulation of translationregulation of cell growth

•covalent chromatin modification



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- regulation of catabolic processregulation of actin cytoskeleton organization
- •histone modification

0.0

0.2

regulation of translationregulation of cell growth

•covalent chromatin modification



0.6

0.8

1.0

0.4



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0.6

Gene functions

0.0

Calpain-1-cata-protease: <u>Proteolysis</u>
Fructose 1,6 biphosphatase: <u>Neoglucogenesis</u>
UDP glucusyltransferease: <u>Lactose synthesis</u>
3 ketoacyl-coA: <u>Fatty acid oxidation</u>

0.2

0.4

0.6



