What is Systems Biology?

Info flow in cell

1. DNA
2. mRNA
3. Protein

OMICS data

1. DNA
2. mRNA
3. Protein

OMICS networks

1. DNA
2. mRNA
3. Protein

Global networks analysis

1. DNA
2. mRNA
3. Protein

Processes, pathways, maps, outside databases

- Biological process
- Cell growth and/or maintenance
- Transport
- Lipid transport
- Fatty acid transport
- Long-chain fatty acid transport
- Short-chain fatty acid transport
- Medium-chain fatty acid transport
- Phospholipid transport
- Peroxisomal membrane transport
- Sterol transport

GeneGo Copyright GeneGo 2000-2003
Functional prioritization and analysis of HT datasets

“Whole genome” datasets
1 – 10,000 statistically significant datapoints

Ontologies of cellular processes, diseases

Signalizing, metabolic pathways and maps

Biological networks: protein interactions and metabolic transformations

Prioritization of subnetworks:
- Relevance to data
- Relevance to processes
- Relevance to disease, tissue, organelle etc.
- Relevance to pathways
  p-values, z-score, g-score

Small, customized datasets connected via physical and functional interactions; signature networks
### Content: a curated database of human drug metabolism

<table>
<thead>
<tr>
<th>Feature</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>98,000 direct protein interactions</td>
<td></td>
</tr>
<tr>
<td>Over 9,000 human proteins</td>
<td></td>
</tr>
<tr>
<td>&gt;90% known human genes on networks</td>
<td></td>
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<tr>
<td>SNPs for most known genes</td>
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<tr>
<td>700 GPCRs with ligands</td>
<td></td>
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<tr>
<td>1,700 Trans. factors and sites</td>
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<tr>
<td>4,000 diseases and conditions</td>
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</tr>
<tr>
<td>30,000 pathway/disease links</td>
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<tr>
<td>20,000 xenobiotics</td>
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<tr>
<td>21,000 metabolic reactions</td>
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</tr>
<tr>
<td>5,000 endogenous metabolites</td>
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<tr>
<td>&gt;2,000,000 synonyms resolved</td>
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<tr>
<td>7,200 drugs</td>
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<tr>
<td>Human, mouse, rat, fly, worm, dog, chicken, yeast, chimpanzee</td>
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</tbody>
</table>
MetaCore™: Key features

MetaCore™ database content

Over 98,000 curated interactions

425 pathway maps represent well-studied pathways

~100% coverage of functionally characterized human genes

Networks for over 500 diseases

Human, Dog, Chicken, Chimp, Yeast, fly, worm, mouse, rat

~6,000 drugs and their targets

>500,000 synonyms resolved

MetaCore™, data-mining tools, algorithms and visualization

Seven major network-building algorithms

User-specified settings for network building

Networks filters on:
- Tissue specificity
- Type of interactions
- Experimental data
- User-selected objects

Export list of gene from maps/networks

Logical operations on gene lists

Pathway editor
MetaCore™ Platform

- Data Parser
- Pathway Editor
- Networks Building Tools
- Gene Expression Tools: Affy, Agilent, SAGE
- Network comparison
- Visualization Tools

curated pathways from the literature

Novel Database Architecture
Oracle Based
Networks of protein interactions
- Dynamic; built “on-the-fly”
- Exploratory tool
- Build new pathways for genes of interest

Interactive, static maps
- 400 maps
- Signaling, regulation, metabolism, diseases
- Backbone of formalized “state of art” in the field
Concurrent visualization of different data types, experiments

Agilent  Affymetrix  Proteomic  SAGE