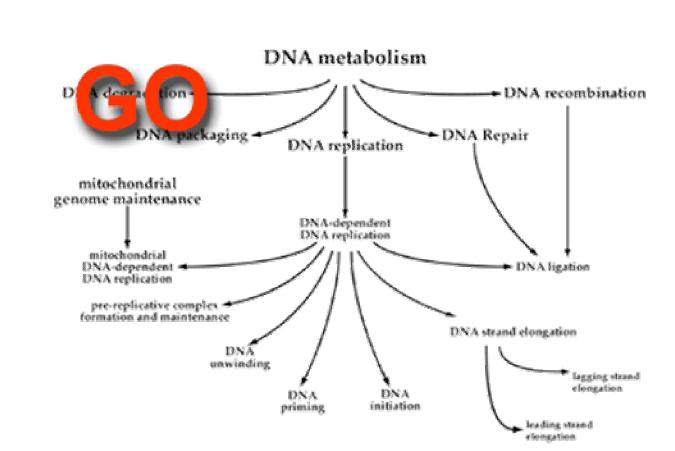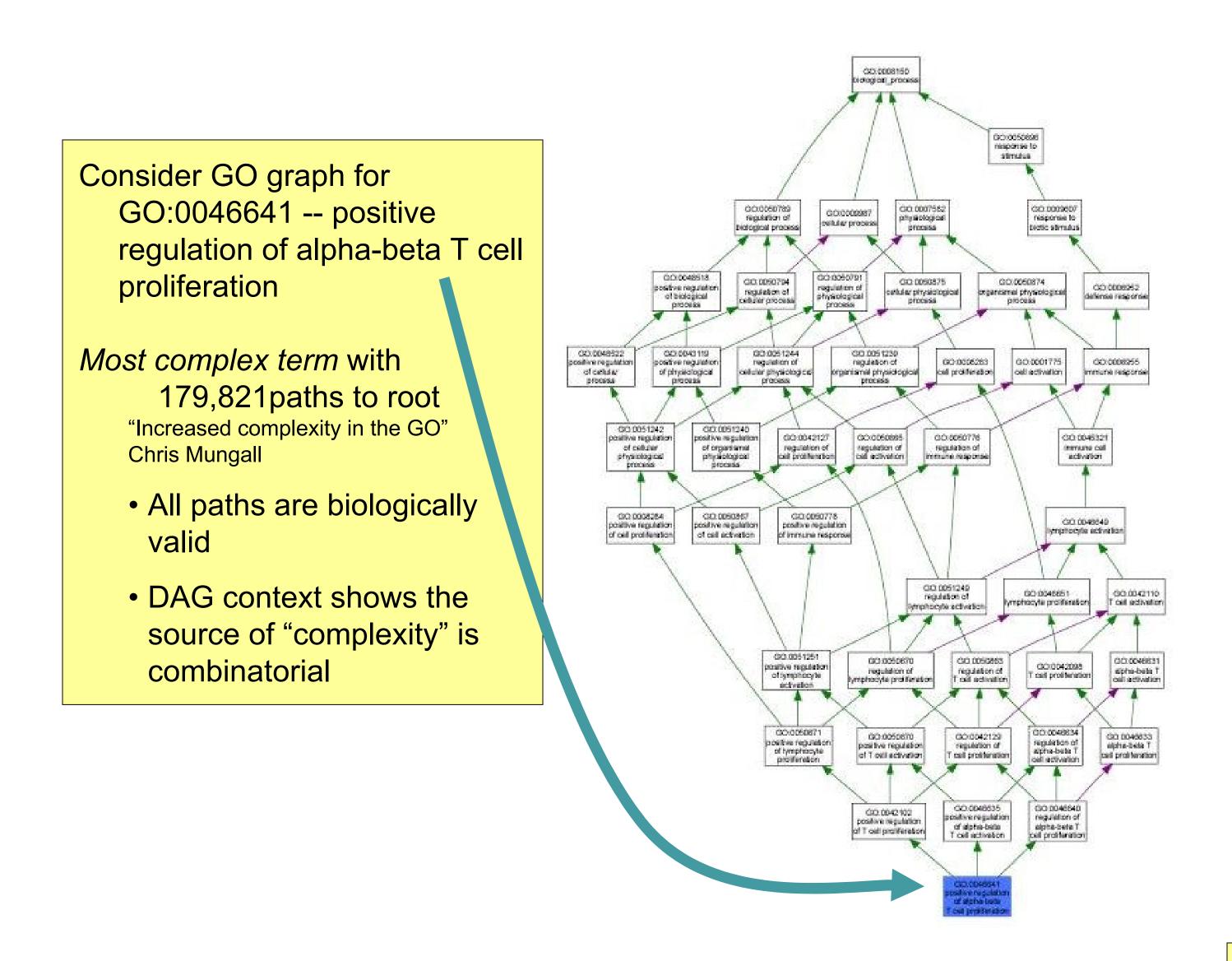# GOgraphEX: GO graphical EXplorer

Mary E. Dolan and Judith A. Blake
Mouse Genome Informatics, The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609 USA
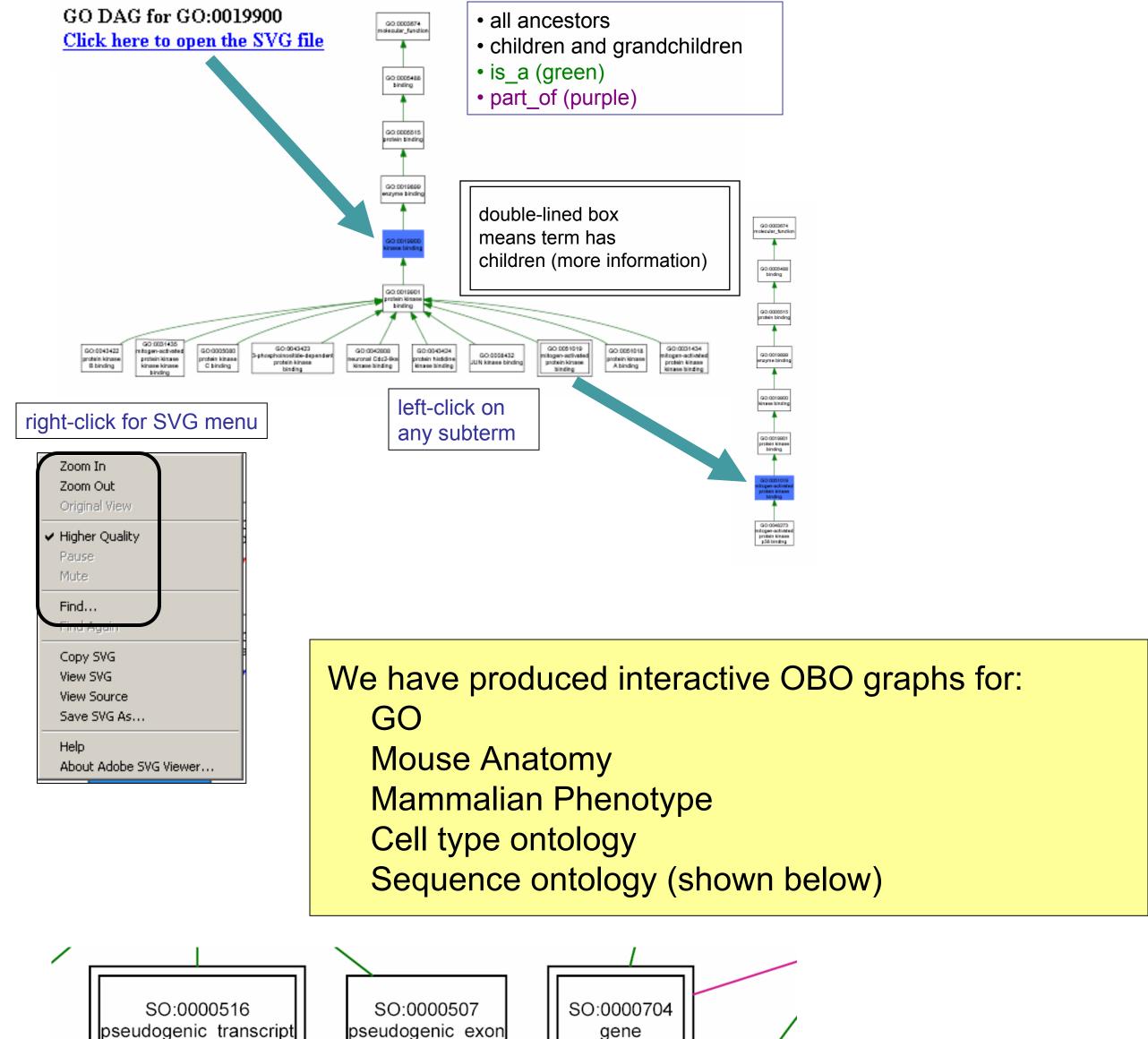
GOgraphEX is a tool for visualization of GO ontology terms and annotations that displays the biological knowledge captured in the DAG structure

Presenting terms in DAG context makes the relationships of terms clear

Consider GO graph for GO:0046641 -- positive regulation of alpha-beta T cell proliferation

Most complex term with 179,821 paths to root
"Increased complexity in the GO"
Chris Mungall

- All paths are biologically valid
- DAG context shows the source of "complexity" is combinatorial

Graph provides context for annotations and makes examination of large annotation sets feasible

Consider MGI GO annotations for Pax8

Compare with…

Category	ID	Term	Evidence	Reference
biological_process	GO:0001656	metanephros development	IGI	PMID:12435636
biological_process	GO:0006183	GTP biosynthesis	IEA	MGI:2152098
biological_process	GO:0006228	UTP biosynthesis	IEA	MGI:2152098
biological_process	GO:0006241	CTP biosynthesis	IEA	MGI:2152098
biological_process	GO:0006350	transcription	IEA	MGI:1354194
biological_process	GO:0006355	regulation of transcription, DNA-dependent	TAS	PMID:10197584
biological_process	GO:0007275	development	IEA	MGI:1354194
biological_process	GO:0007275	development	IEA	MGI:2152098
biological_process	GO:0009887	organ morphogenesis	TAS	PMID:10197584
biological_process	GO:0030154	cell differentiation	IEA	MGI:1354194
cellular_component	GO:0005634	nucleus	IEA	MGI:1354194
cellular_component	GO:0005634	nucleus	IEA	MGI:2152098
cellular_component	GO:0005667	transcription factor complex	TAS	PMID:10197584
molecular_function	GO:0003677	DNA binding	IEA	MGI:1354194
molecular_function	GO:0003700	transcription factor activity	TAS	PMID:10197584
molecular_function	GO:0004550	nucleoside diphosphate kinase activity	IEA	MGI:2152098
molecular_function	GO:0005524	ATP binding	IEA	MGI:2152098

Interactive OBO graphs allow curators to explore DAG neighborhood of terms. GO graphs as SVG images allow pan-zoom-search functionality.

Example below GO:0019900

GO DAG for GO:0019900
Click here to open the SVG file

- all ancestors
- children and grandchildren
- is_a (green)
- part_of (purple)

double-lined box means term has children (more information)

right-click for SVG menu

left-click on any subterm

Zoom In
Zoom Out
Original View
✓ Higher Quality
Pause
Mute
Find…

Copy SVG
View SVG
View Source
Save SVG As…

Help
About Adobe SVG Viewer…

We have produced interactive OBO graphs for:
GO
Mouse Anatomy
Mammalian Phenotype
Cell type ontology
Sequence ontology (shown below)

GO Comparative graphs: *"How do GO annotations of different organisms compare?"*

rat: physiology annotations

human: immunology annotations

A2m GO annotations mouse, human, rat
red/green branches show that annotations are complementary

Complementarity of model organism annotations suggests using this approach to coordinate annotations across species and to view these graphs as "summary" graphs rather than as "comparative" graphs

GO Summary graphs: *"Tell me everything known about this gene"*

SO:0000516
pseudogenic_transcript

SO:0000507
pseudogenic_exon

SO:0000704
gene

SO:0000336
pseudogene

SO:0000673
transcript

SO:0000183
non_transcribed_region

```
id: SO:0000336
name: pseudogene
is_a: SO:0000462 ! pseudogenic_region
relationship: non_functional_homolog_of SO:0000704 ! gene

id: SO:0000673
name: transcript
relationship: member_of SO:0000704 ! gene

id: SO:0000183
name: non_transcribed_region
is_a: SO:0000001 ! region
relationship: part_of SO:0000704 ! gene
```
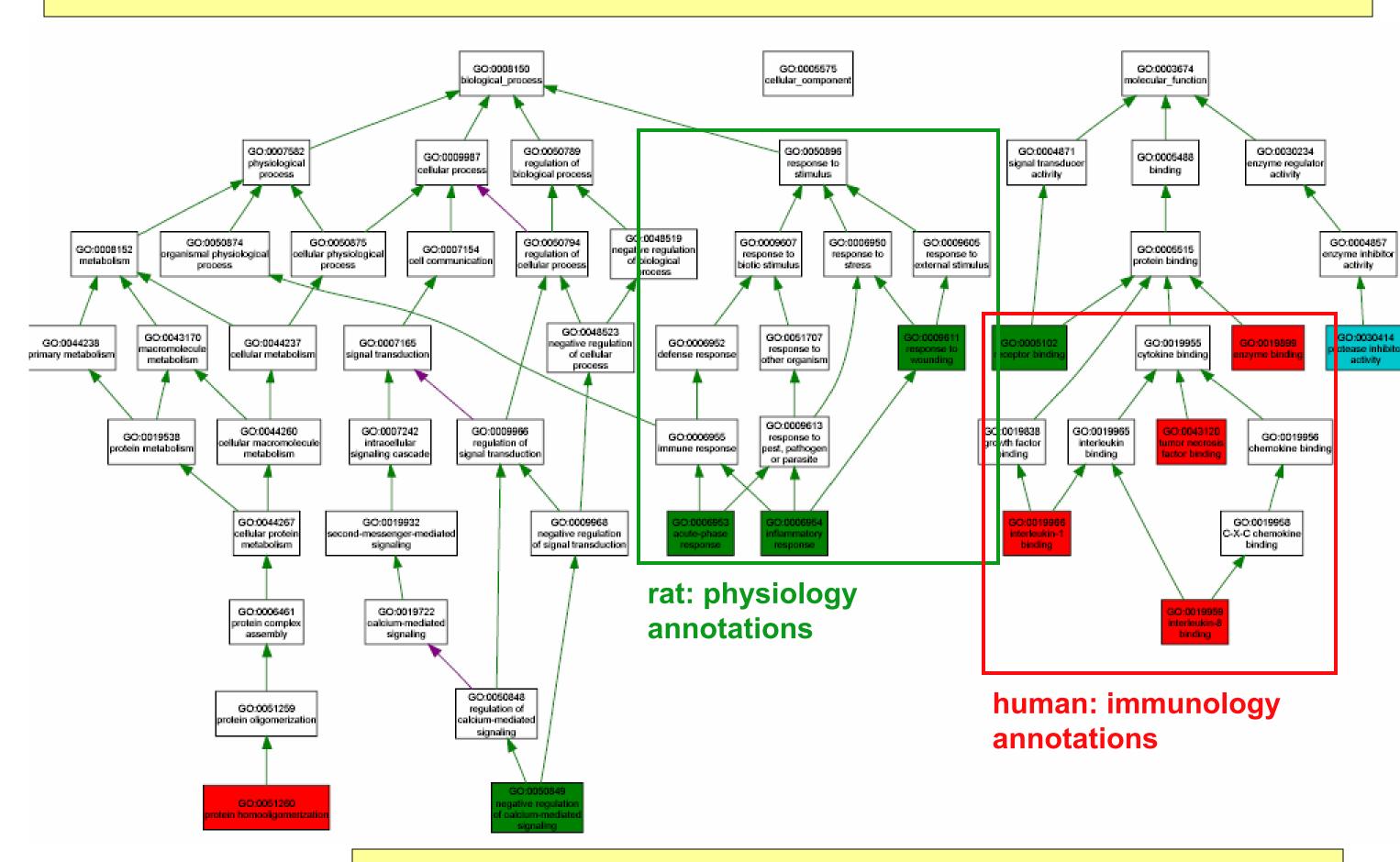
All ontology and annotation graphs are available at: http://proto.informatics.jax.org/prototypes/gograph/

Pax6 HomoloGene cluster: mouse, human, rat, fly, chicken, multiple