VIZBI 2012

VISUALIZATION PRINCIPLES

Practical Session

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In this session you will work together in teams to critique and redesign a figure from the literature.

BREAKOUT

We will form 6 teams after Cydney's talk and a figure will be assigned to each team. You may begin working on your figure right away, or take a break (11:20–11:30) before starting.

PRESENTATION

Each team will present their figure, critique and redesign to the group. You will have 10 minutes. It is up to the team to select the format and speaker, or speakers, for their presentation.

Your presentation should include

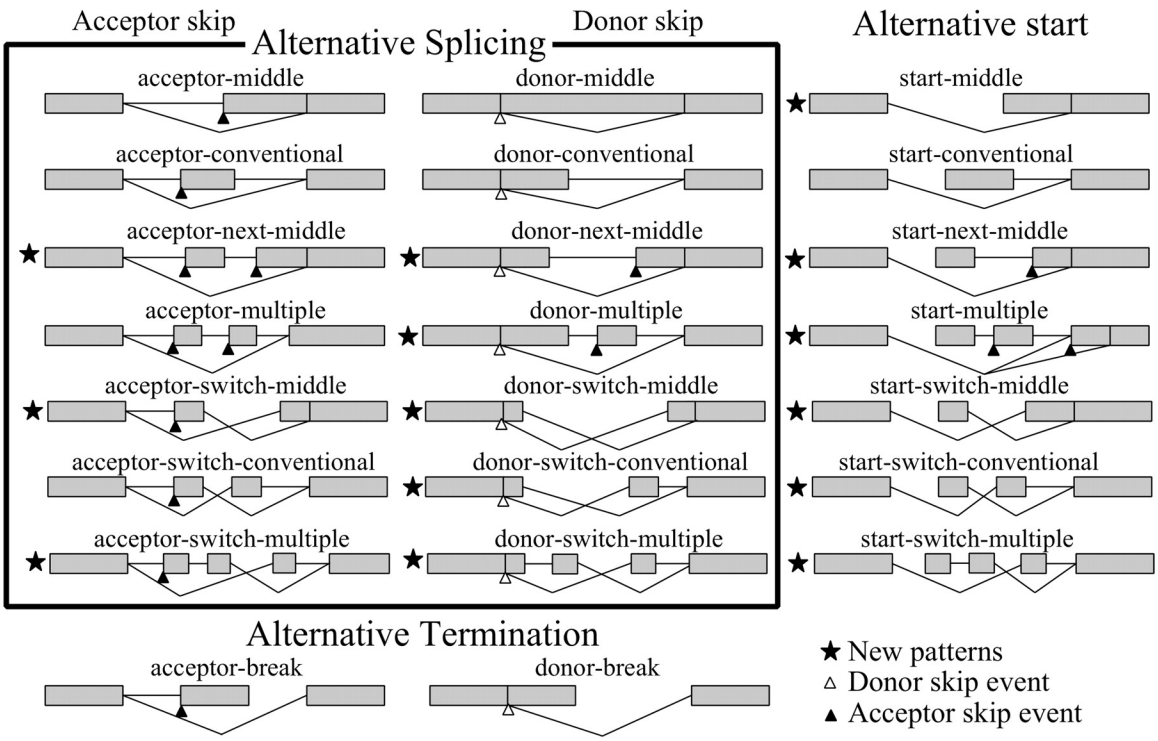
– a brief description of the figure
– an assessment of the figure's strong and weak points
– your redesign of the figure

The figure redesign does not need to be a complete print-ready figure. Create a sketch or mockup. In your presentation, emphasize your improvements

– what requires improvement
– why it requires improvement
– how you plan to improve it

This document is available at
http://mkweb.bcgsc.ca/vizbi/2012/practical.pdf
All papers can be downloaded from
http://mkweb.bcgsc.ca/vizbi/2012/papers/papers.zip

IMAGE 1

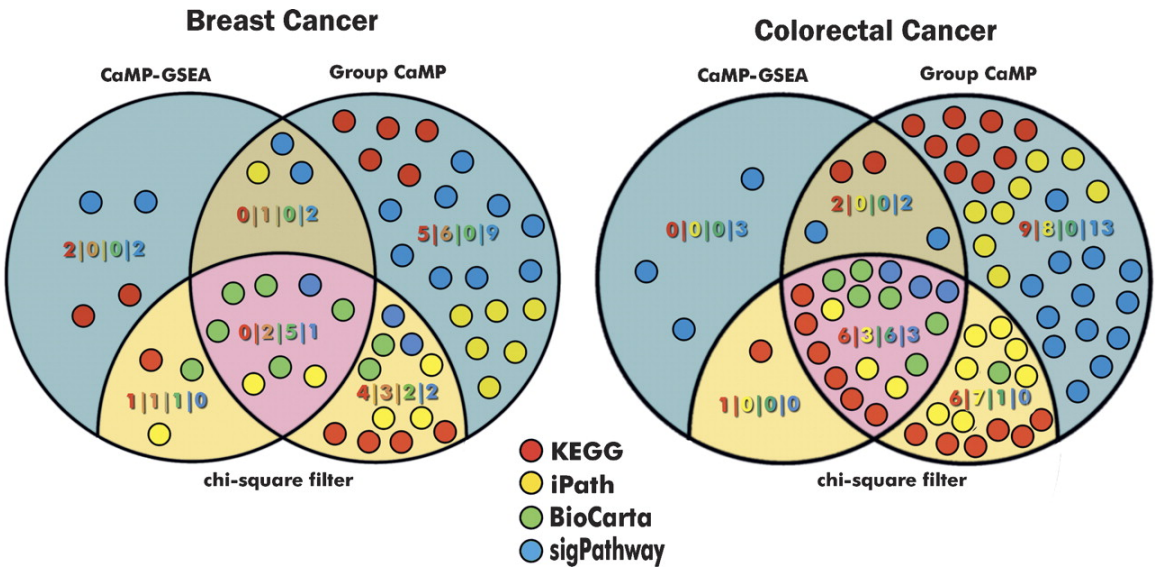


Combinatorial classification of ATS units.

Sharov AA, Dudekula DB, Ko MS (2005). Genome-wide assembly and analysis of alternative transcripts in mouse. Genome Res 15: 748-754.

http://mkweb.bcgsc.ca/vizbi/2012/papers/sharov-transcripts.pdf

IMAGE 2

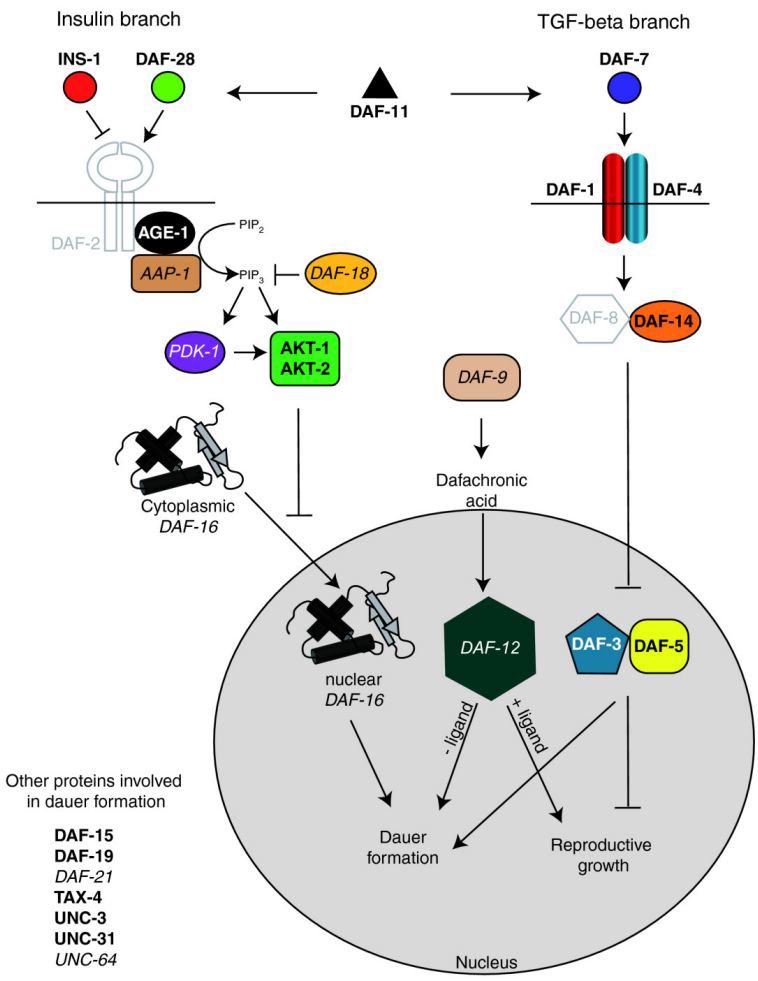


Comparison of mutation enrichment in cellular pathways using complementary statistical approaches. Venn diagrams show the number of pathways identified from four different databases in breast (left) and colorectal cancers (right) using CaMP GSEA and Group CaMP approaches. Each circle represents one pathway and is colored according to the database it belongs to. Pathways that were enriched for mutations and which were filtered for an increase in the number of genes using the $\chi 2$ test are shown in tan or pink. Blue and dark tan areas represent pathways that were excluded using the $\chi 2$ filter (for additional details, see Methods).

Lin J, Gan CM, Zhang X, Jones S, Sjoblom T, Wood LD *et al* (2007). A multidimensional analysis of genes mutated in breast and colorectal cancers. *Genome Res* **17:** 1304-1318.

http://mkweb.bcgsc.ca/vizbi/2012/papers/lin-mutations.pdf

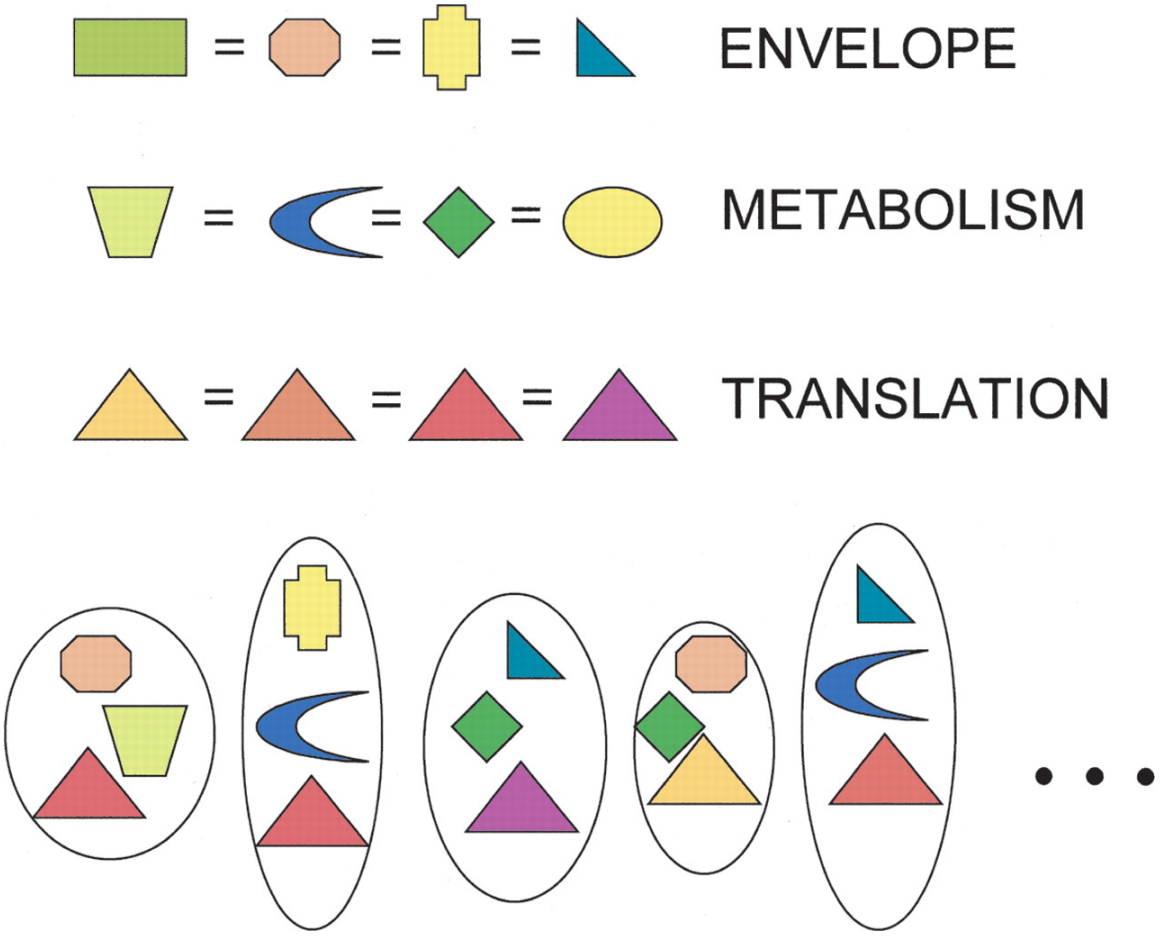
IMAGE 3



A majority of dauer pathway genes are enriched in either the larval pan-neural (LP) or embryonic pan-neural (EP) datasets. Two neuronal pathways influence the decision to dauer, an alternative developmental pathway adopted in unfavorable conditions [49-54]. During normal growth, the DAF-28 insulin-like molecule activates the DAF-2 insulin receptor to initiate a signal transduction pathway that prevents the translocation of the DAF-16 Forkhead transcription factor into the nucleus, thus blocking dauer formation. In a parallel pathway, DAF-7/TGF-beta activates receptors DAF-1 and DAF-4 to inhibit the Smad/Sno complex DAF-3/DAF-5, thereby promoting reproductive growth. The guanylyl cyclase DAF-11 drives expression of DAF-28 and DAF-7. During reproductive growth, the CYP2 cytochrome P450 enzyme DAF-9 is active and produces the DAF-12 ligand dafachronic acid. In the presence of its ligand, the nuclear hormone receptor DAF-12 promotes normal development. In the absence of its ligand, DAF-12 instead promotes dauer formation. Other proteins function independently of these pathways (for example, the DAF-19 transcription factor specifies ciliated neurons that detect exogenous dauer-inducing signals). Bold lettering denotes enriched transcripts and italics marks EGs detected in at least one of the pan-neural datasets. Gray letters refer to transcripts not found in either EP or LP datasets. See Additional data file 18 for a complete description of these genes.

Von Stetina SE, Watson JD, Fox RM, Olszewski KL, Spencer WC, Roy PJ *et al* (2007). Cell-specific microarray profiling experiments reveal a comprehensive picture of gene expression in the C. elegans nervous system. *Genome Biol* **8**: R135.
http://mkweb.bcgsc.ca/vizbi/2012/papers/stetina-celegans.pdf

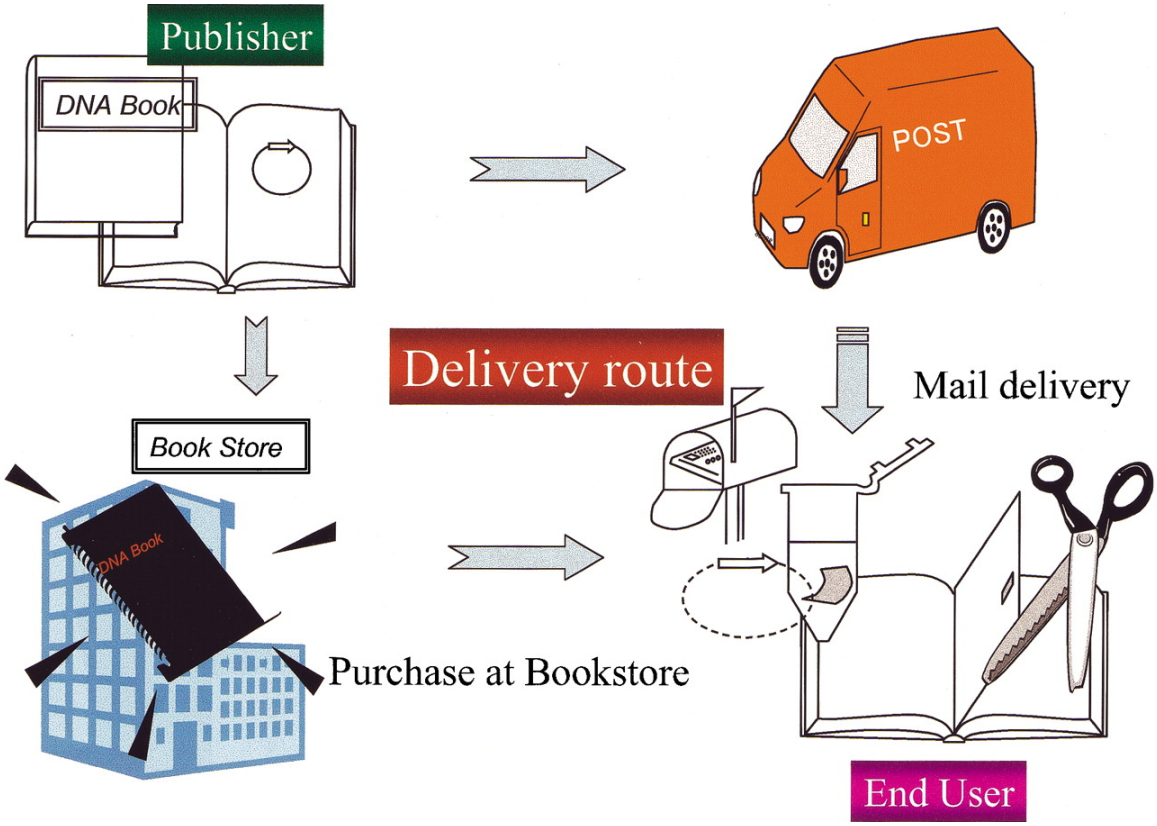
IMAGE 4



A mix-and-match model for prokaryotic genome evolution. Every cell needs genes for multiple functions, and new genomic lineages arise in evolution through mixing and matching of genes performing these different functions, by processes of replacement, including nonorthologous displacement (Koonin et al. 1996). The simplest hypothesis would be that all functions are equally subject to such exchange processes. For many functions, available genes include nonhomologs and even null entries (gene and function loss), indicated here by different shapes. Thus, for these functions, no genes or even gene families will likely appear to be shared among all genomes. For some informational functions especially (such as translation), displacement most often involves genes that, although evolutionarily distinct (as indicated by colors), are homologous (as shown by shape). Such genes will appear among those of the ubiquitous core.

Charlebois RL, Doolittle WF (2004). Computing prokaryotic gene ubiquity: rescuing the core from extinction. *Genome Res* **14:** 2469-2477.
http://mkweb.bcgsc.ca/vizbi/2012/papers/charlebois-evolution.pdf

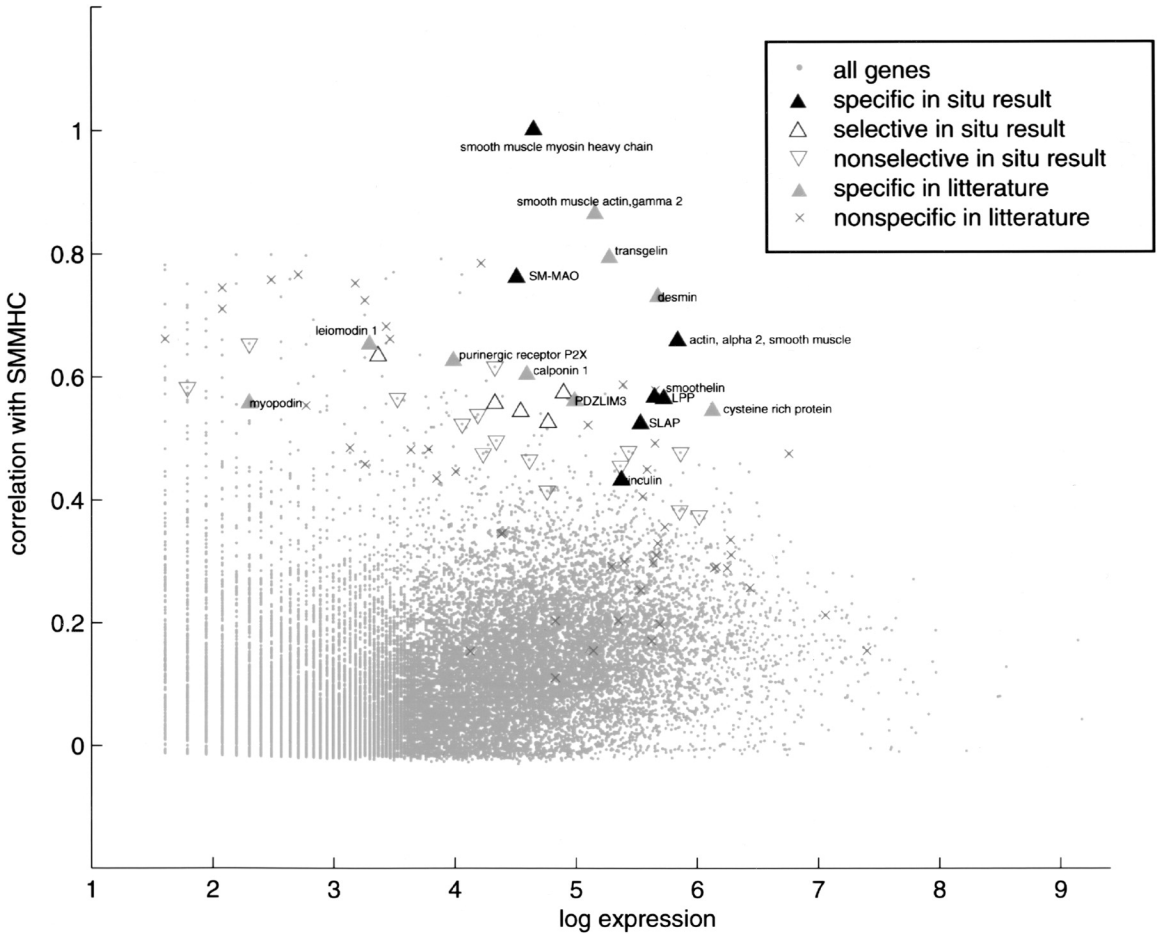
IMAGE 5



Concept of the “DNA Book.” DNA of genes are attached to pages of the DNA Book, and delivered to readers through conventional distribution channels, such as couriers and bookstores. Readers can extract and amplify DNA from the pages.

Kawai J, Hayashizaki Y (2003). DNA book. *Genome Res* **13:** 1488-1495.
http://mkweb.bcgsc.ca/vizbi/2012/papers/kawai-dna-book.pdf

IMAGE 6



ISH results in relation to profile similarity to SM-MHC (Y-axis) and to expression level (X-axis). Expression level is defined as the logarithm of the number of UniGene detections for a gene, and profile similarity is defined as Pearson's correlation in theraw data set. Gray dots, All 29,812 genes with at least five UniGene detections; dark upward-pointing triangles, ISH-detected SMC markers; open upward-pointing triangles, ISH-detected SMC marker-related genes; downward-pointing triangles, genes with a nonselective expression pattern in the ISH experiment; grey upward-pointing triangles, SMC markers from the literature; crosses, nonselective genes from the literature.

Nelander S, Mostad P, Lindahl P (2003). Prediction of cell type-specific gene modules: identification and initial characterization of a core set of smooth muscle-specific genes. *Genome Res* **13:** 1838-1854.

http://mkweb.bcgsc.ca/vizbi/2012/papers/nelander-genes.pdf