Miriah Meyer

Postdoctoral Research Fellow
Harvard University

My name is Miriah Meyer and I am currently a postdoc at Harvard University in Cambridge Mass. Before becoming a postdoc I was a grad student at the univ or utah, just down the hill in Salt Lake City.

I did my graduate work in the Scientific Computing and Imaging Institute...

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Graduate Student
University of Utah

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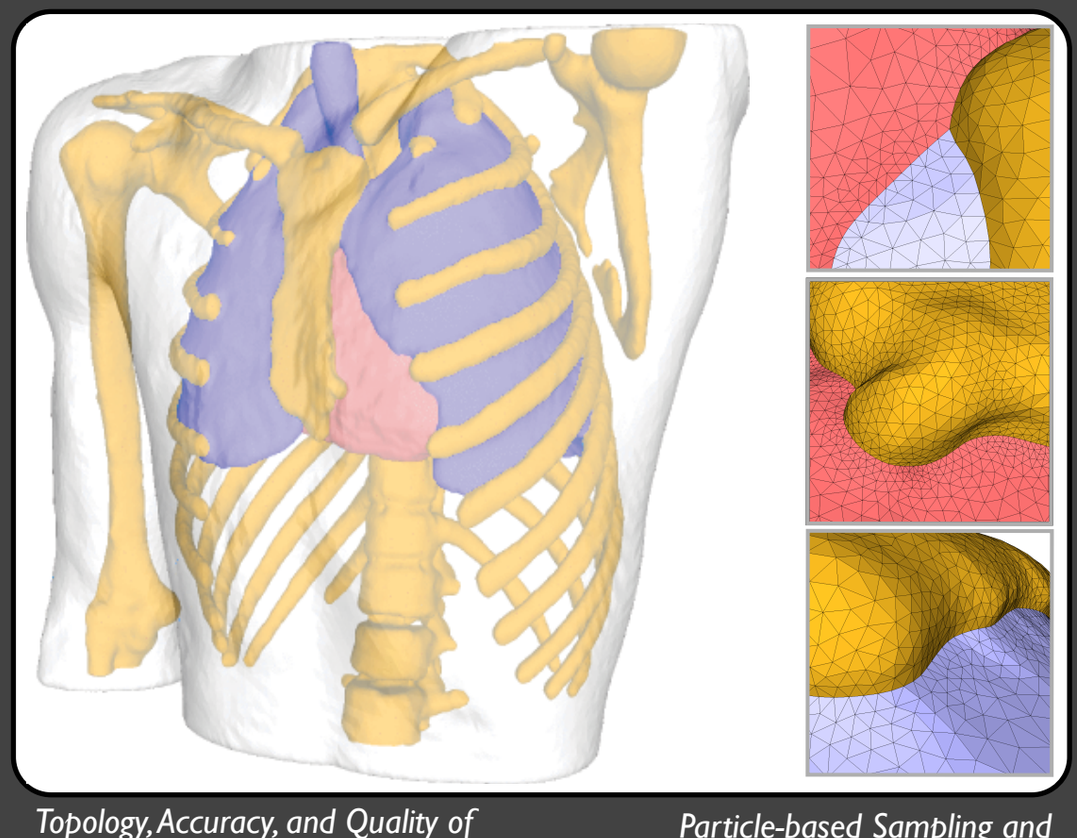
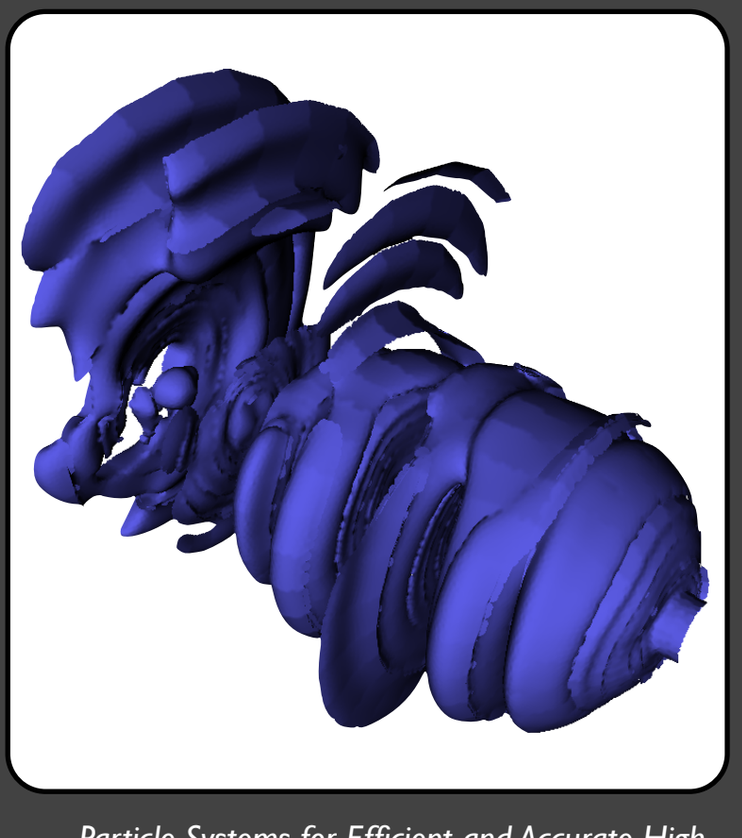
Robust Particle Systems for Curvature Dependent Sampling of Implicit Surfaces.
M. Meyer et al., SMI 2005.



Topology, Accuracy, and Quality of Isosurface Meshes Using Dynamic Particles.
M. Meyer et al., Vis 2007.

Particle-based Sampling and Meshing of Multimaterial Volumes.
M. Meyer et al., Vis 2008.



Particle Systems for Efficient and Accurate High-Order Finite Element Visualization
M. Meyer et al., TVCG 2006.

... and my research centered around a dynamic particle system model we developed to efficiently and accurately sample surfaces. We applied this work to several problems, including the visualization of high-order finite element data sets. We also combined the particle system with level-set methods and computational geometry principles to generate high-quality meshes for medical simulations.

When I finished my PhD I wanted to focus on interdisciplinary research, and I wanted to work very closely with scientists...

Hanspeter Pfister

Harvard Initiative in Innovative Computing

illustration: Bang Wong

Tamara Munzner

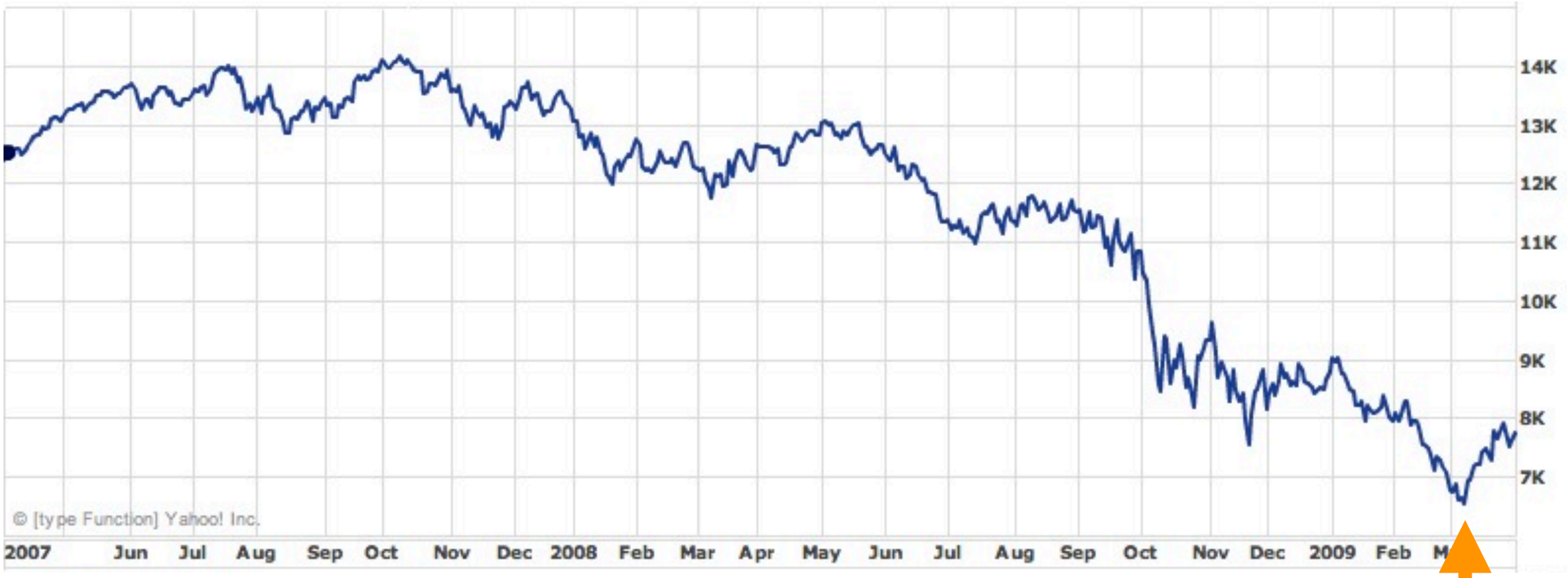
... At the time, my postdoc mentor, Hanspeter Pfister, had just moved to Harvard, and he had a very open-ended visualization postdoc position available in a lab called the Initiative in Innovative Computing. I've known Hanspeter since my pregrad school days and knew that he would be a supportive mentor, and also that he was passionate about interdisciplinary research.

So I accepted his offer, moved to Boston, and began searching for collaborations. Right away I started meeting biologists, from Harvard, Harvard Med, and MIT, and realized that the vast amount of genomics data they were collecting made for a killer application domain for visualization research. At that point I made the conscious decision to switch research fields and focus on developing visualization systems for genomics data. As this was a new area for both of us, we started a collaboration with infovis expert Tamara Munzner from UBC, who has since turned into a co-mentor for me.

Then, a few months after I started my postdoc, just as I was getting started on a couple of exciting projects...

Dow Jones Industrial Average

source: finance.yahoo.com



... the economy tanked and Harvard lost a third of its endowment. Along with many other initiatives across campus, the IIC's budget was cut, and I was looking at just a few more months of funding.

Hanspeter and I started looking around for grants we could apply for when we heard about the CIFellows program from a colleague. I only had one week until the deadline, so I worked full-time on my proposal. But, given the short amount of time I had to prepare, and also the sheer number of applications that were submitted to the program, I was not optimistic about my chances...

-------- Original Message --------
Subject: CIFellows notification
Date: Fri, 10 Jul 2009
From: Peter Lee <Peter.Lee@cs.cmu.edu>

Dear Miriah,

On behalf of the Computing Research Association, the Computing Community Consortium, and the CIFellows Steering Committee, I am extremely pleased to tell you that you have been named a 2009 Computing Innovation Fellow.

With this award, we intend to provide funding for your proposed postdoctoral work at Harvard University under the mentorship of Hanspeter Pfister. As soon as we receive confirmation (email is fine) that you accept this award and that your mentor still agrees to host you, CRA will issue the necessary paperwork (technically, a "subaward agreement") to the host institution and to NSF. Depending on how quickly NSF and the host approve the agreement, the fellowship may begin. Please note that the host organization and NSF must provide approvals before the fellowship can begin.

We request that you and your mentor respond to this message as quickly as possible, but in any event no later than July 24, 2009. If you accept, you should

... So when I received this email from Peter stating that I was named Computing Innovation Fellow, you can imagine how happy I was to have the opportunity to continue in my postdoc.

in my proposal,

what made the difference?

- clear, concise, visual, and memorable
- passionate, interdisciplinary research

I have been asked numerous times, what, in my proposal, made the difference? I actually have no idea as we didn't receive feedback from the selection committee, but that does not stop me speculating. First, I was given some very good advice from Hanspeter to make my proposal clear, concise, visual, and memorable.

Readability is important, but I suspect what was more important was that I was passionate about interdisciplinary research. And judging from the research of the other fellows here, I'm guessing this is a dominate trait among the awardees.

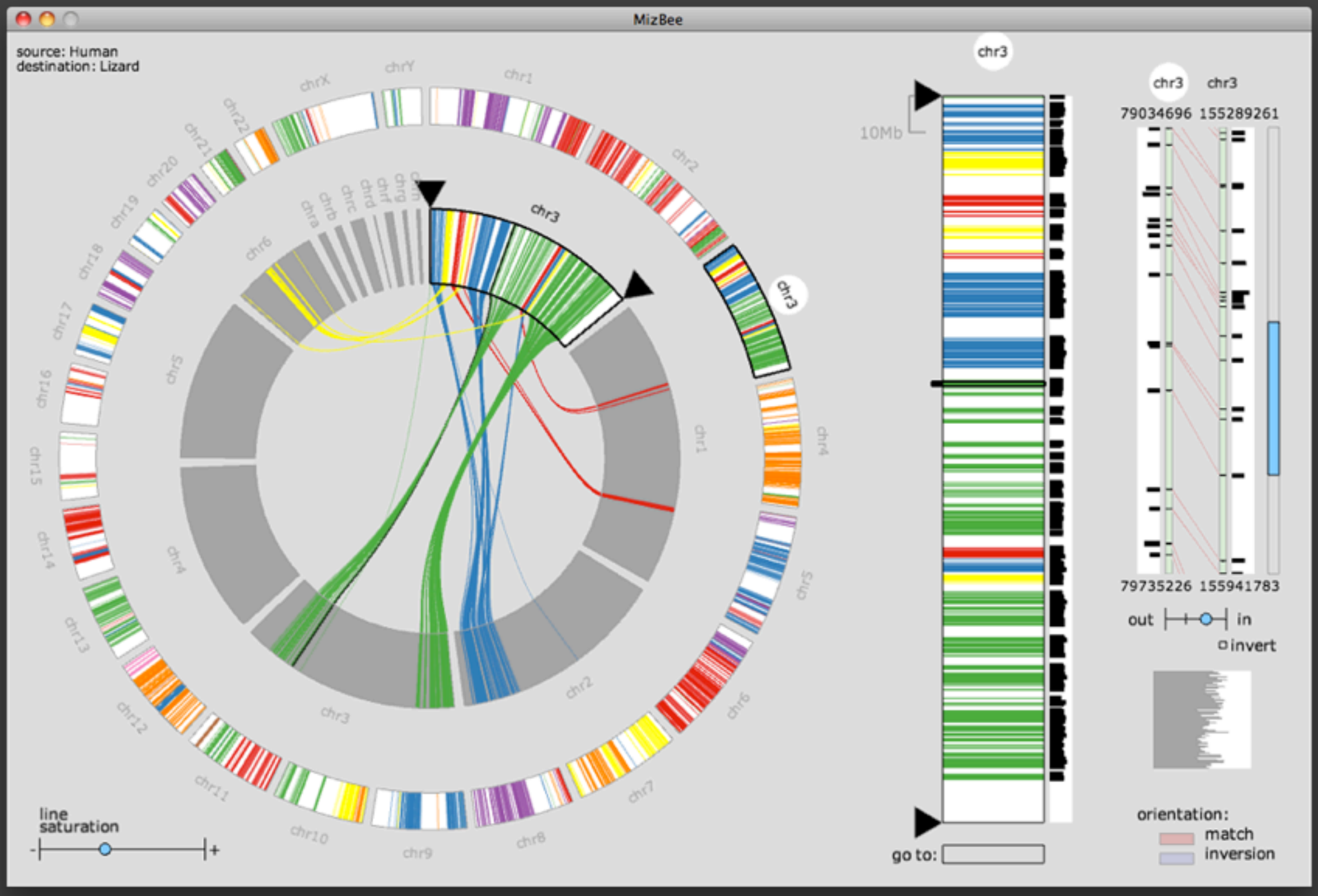
collaboratively design and develop visualization tools for biological data

My own research focuses on collaboratively designing and developing visualization tools for biological data.

In my postdoc, I've worked on several different projects...

MizBee

comparative genomics

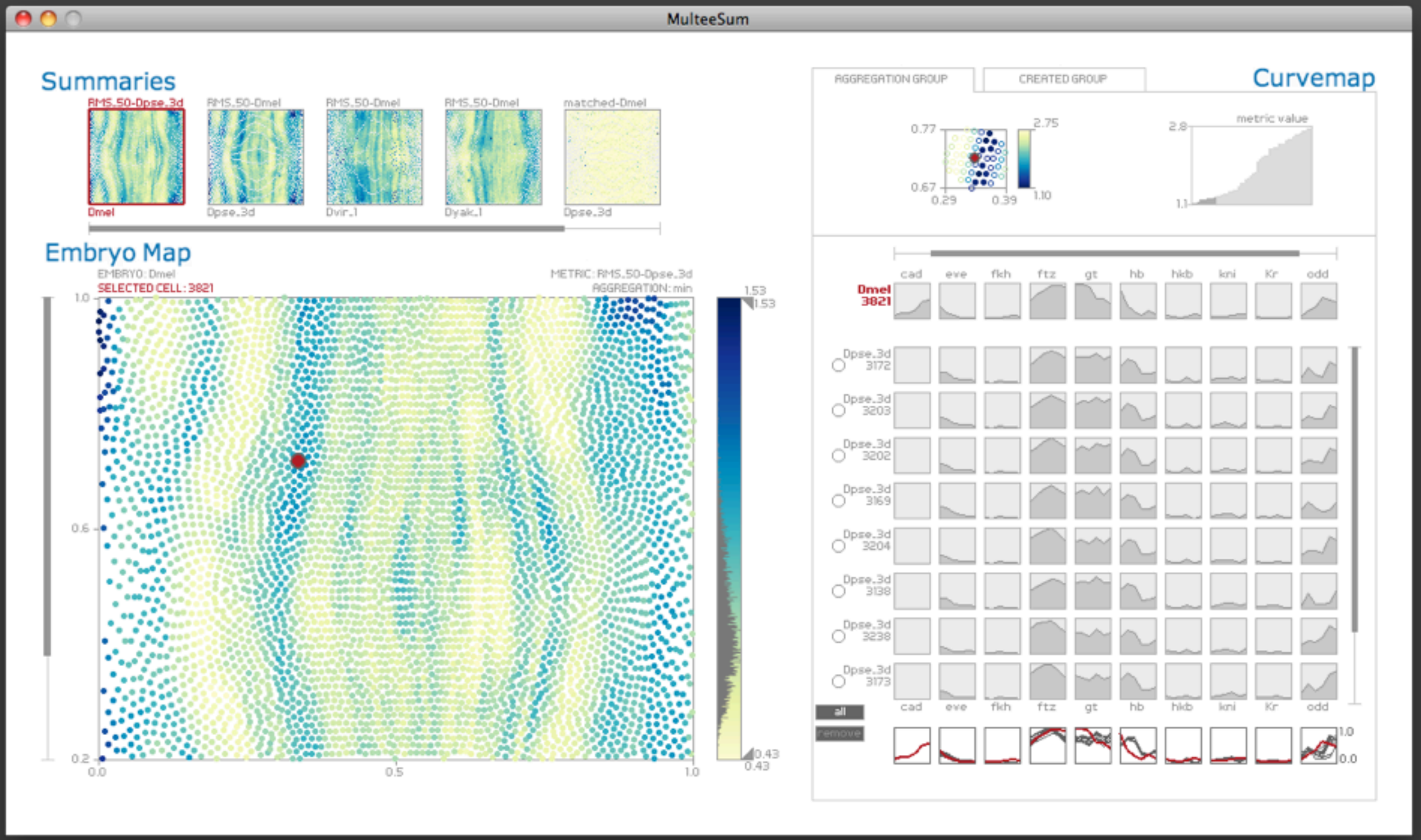


M. Meyer et al., *MizBee: A Multiscale Synteny Browser,* IEEE InfoVis 2009.

... One of them is a tool called MizBee, which we developed in collaboration with several biologists who work in the field of comparative genomics at the Broad Institute, which is a joint MIT/Harvard biology center in Cambridge. MizBee visualizes similarities between genomes at multiple different scales.

MulteeSum

systems biology

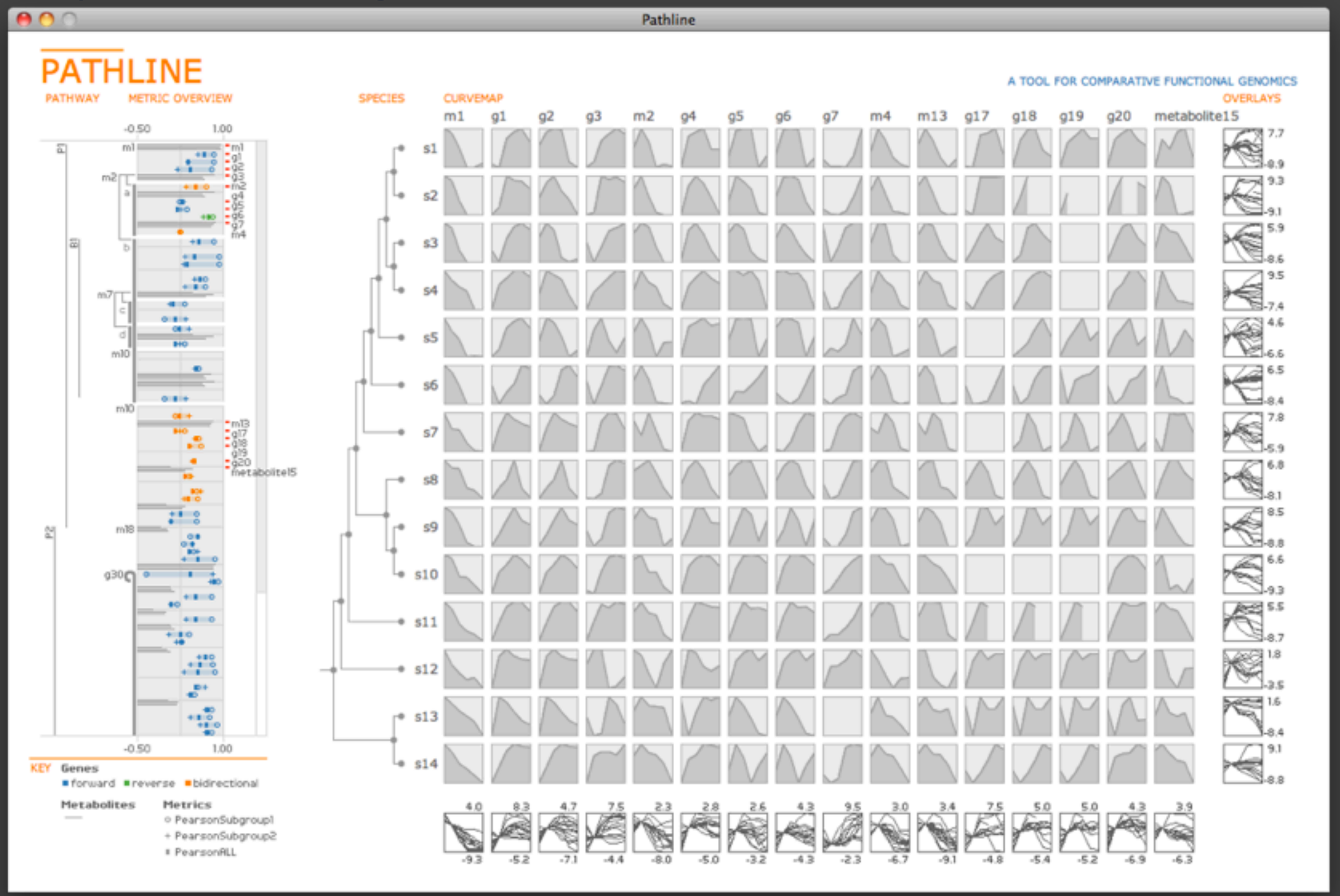


M. Meyer et al., *MulteeSum: A Tool for Comparative Temporal Gene Expression and Spatial Data,* IEEE InfoVis 2010, to appear.

Another project is called MulteeSum, which is work done with a systems biology lab at Harvard Medical School. This group studies gene expression patterns in developing fruit fly embryos, and MulteeSum helps them tease out and understand differences between species of flies.

Pathline

comparative functional genomics



M. Meyer et al., *Pathline: A Tool for Comparative Functional Genomics*, EuroVis 2010.

And a third project is a tool called Pathline, which I'm going to describe in a bit more detail. This tool was developed to answer questions about data from the emerging field of comparative functional genomics.

comparative functional genomics

how do genes work together to perform different functions in a cell?

how do these gene interactions vary across different species?

collaborators: Regev Lab at the Broad Institute

biology: metabolism in yeast

data: multiple genes
multiple time points
multiple related species
many complex gene interactions

problem: *existing tools only look at a subset of this data*

In this emerging field, scientists are asking the high-level questions...

We are working with the a group of biologists at the Broad Institute who are pioneering this new field by studying metabolism in yeast. They are collecting data for multiple genes, at multiple time points, for multiple related species of yeast. And they want to understand all of this data in the context of many complex gene interactions.

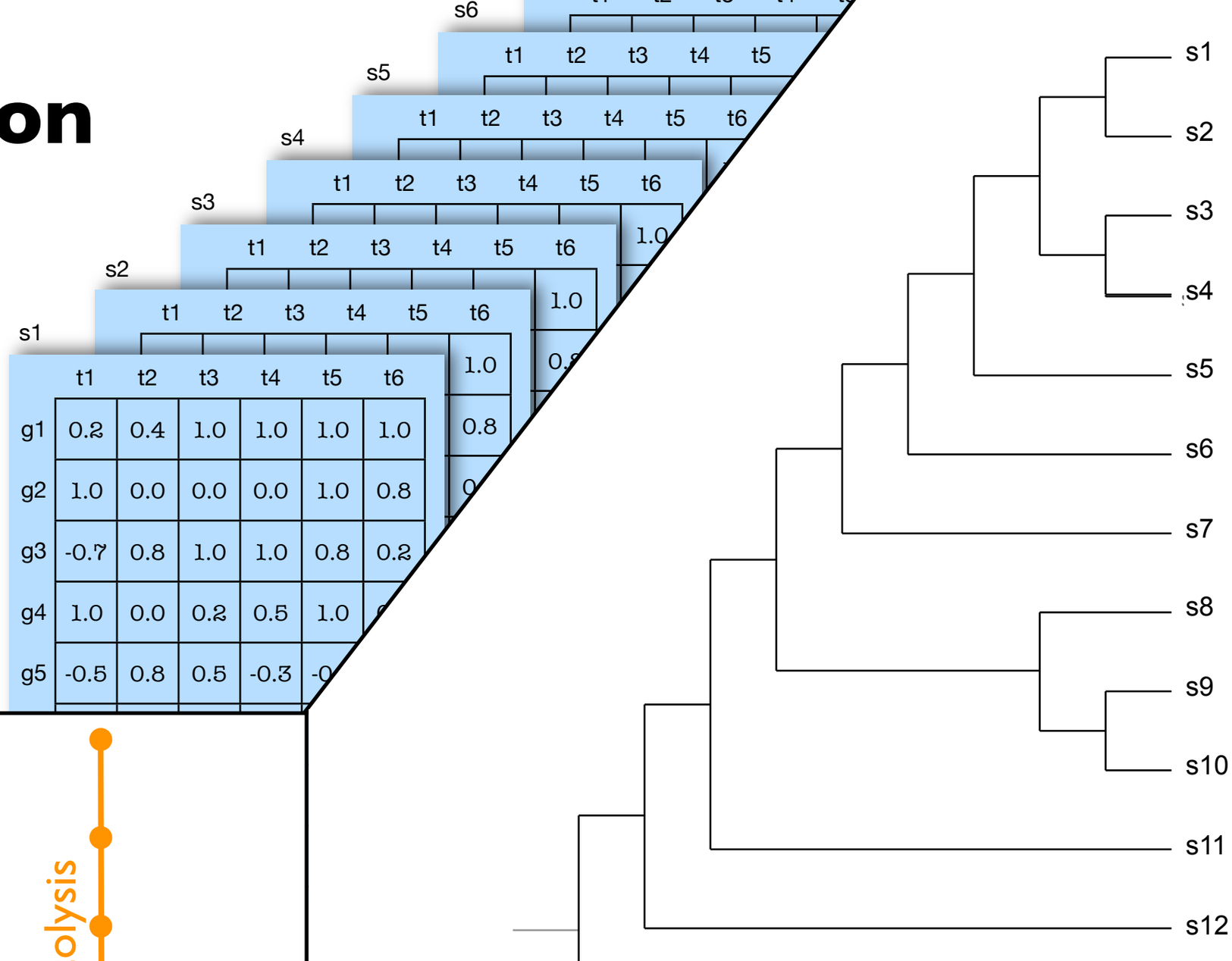
When we started working with this group they had the problem that existing tools only look at a subset of this data. So our goal was develop a single system for this data.

data and tasks

In designing a visualization tool to tackle problems like this, the first thing we do is perform an analysis of the data and tasks of our users.

gene expression

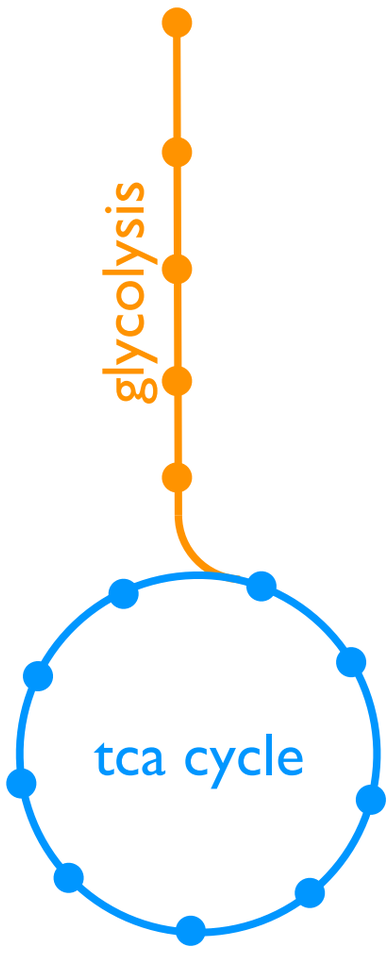
- quantitative value
- thousands of genes
- multiple time points
- many species of yeast
- **3D table**



metabolic pathways

- series of gene interactions

- **directed graph**



phylogeny

- evolutionary relationship of species

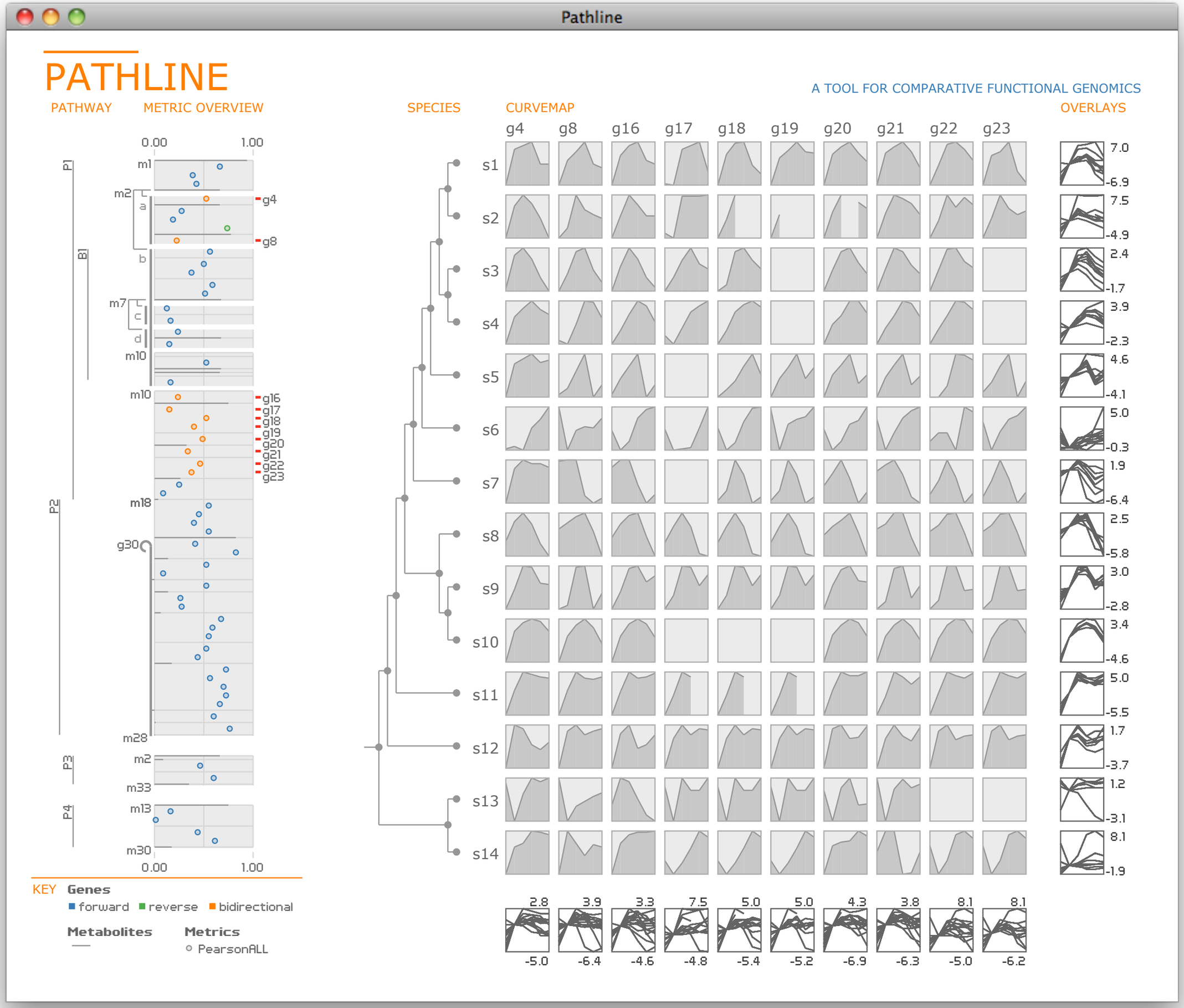
- **binary tree**

In this project, we have three main data sources. The first is gene expression data, which is a quantitative value. They measure the expression levels of thousands genes and at multiple time points. And they do this for many species of yeast. The result is a 3D table of values.

The next data source is metabolic pathways. These pathways describes a series of gene interactions involved with metabolism, and they are represented as a directed graph.

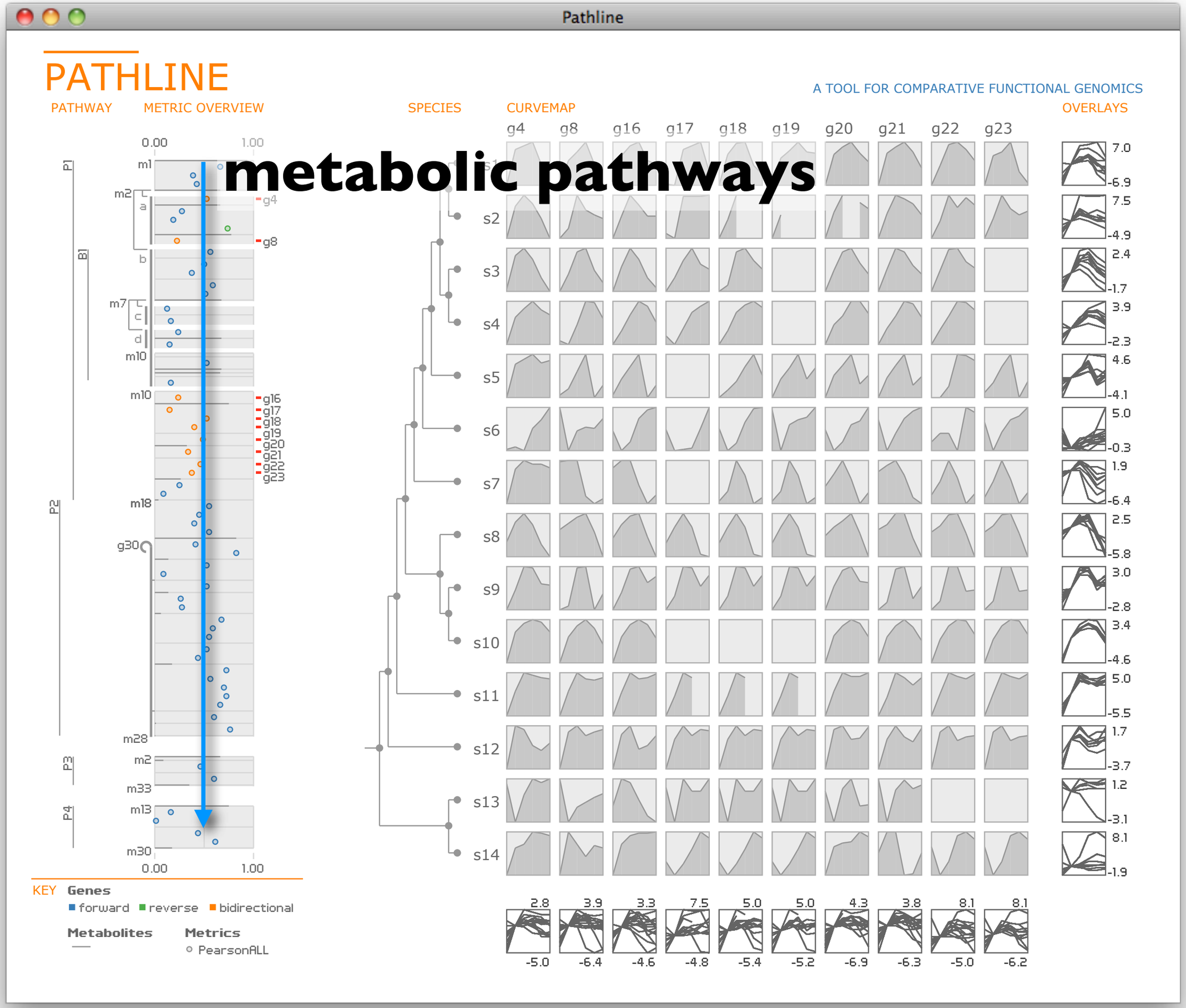
And finally, there is phylogeny, which describes the evolutionary relationship of species. This is represented as a binary tree.

We performed an analysis of all this data, as well as the tasks our collaborators needed to perform to answer there



Here is what pathline looks like. There are two main views, the high level linearized pathway view on the left, and the detailed curvemap view on the right. These views are linked together, which I'll show briefly in a demo later.

We encode the metabolic pathways on the left...



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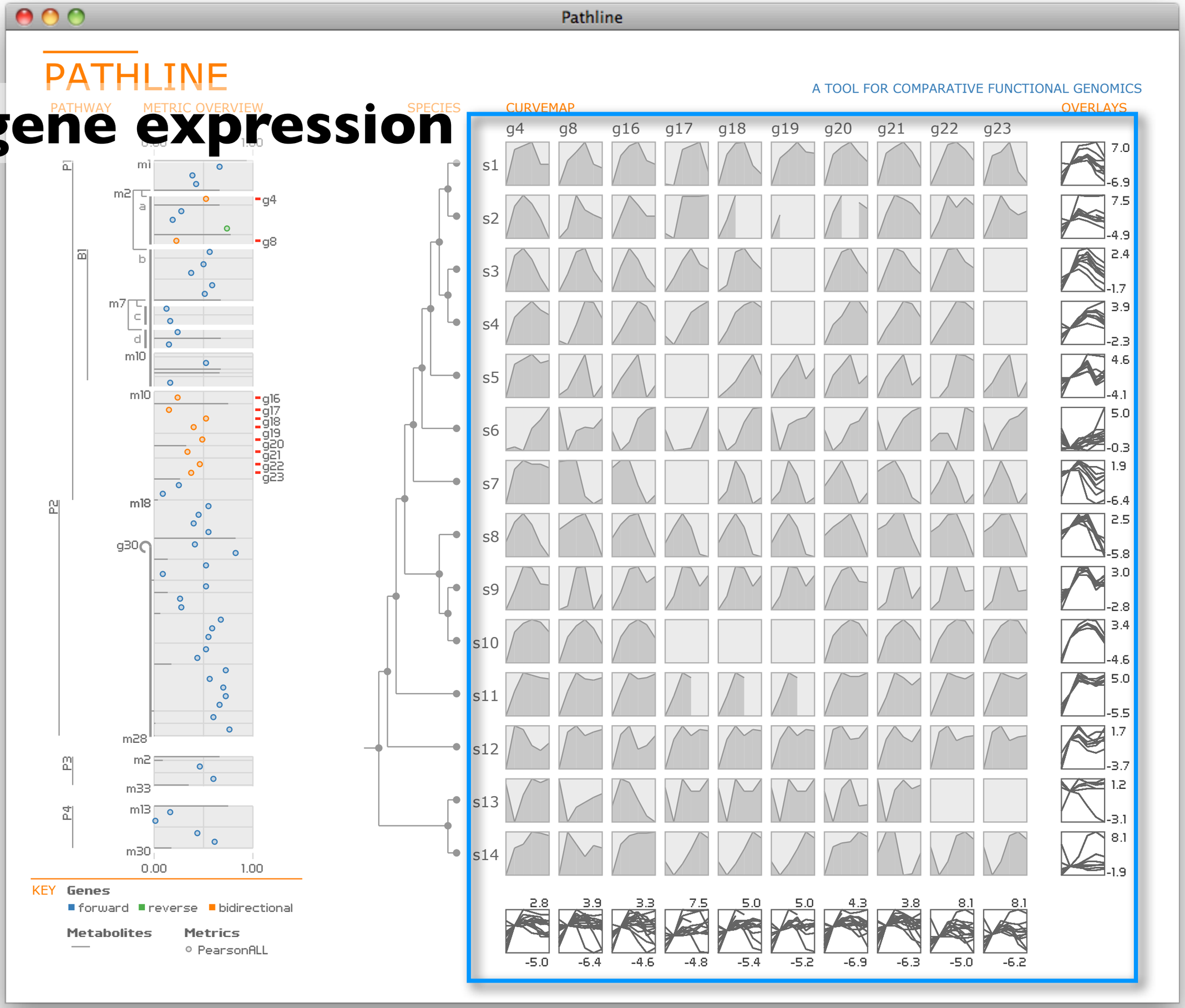
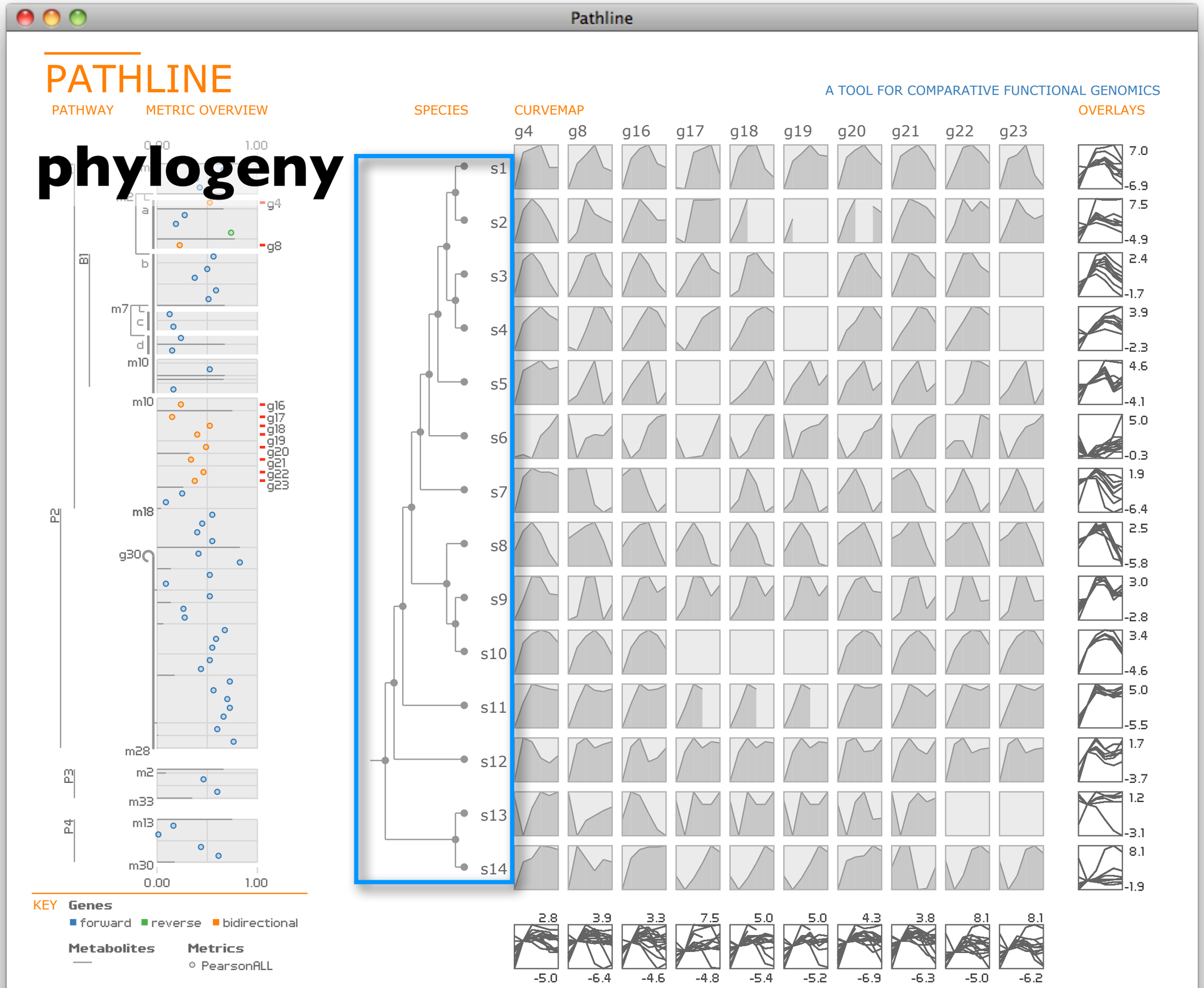


and gene expression values in the curvemap display, which is augmented with a phylogentic tree.



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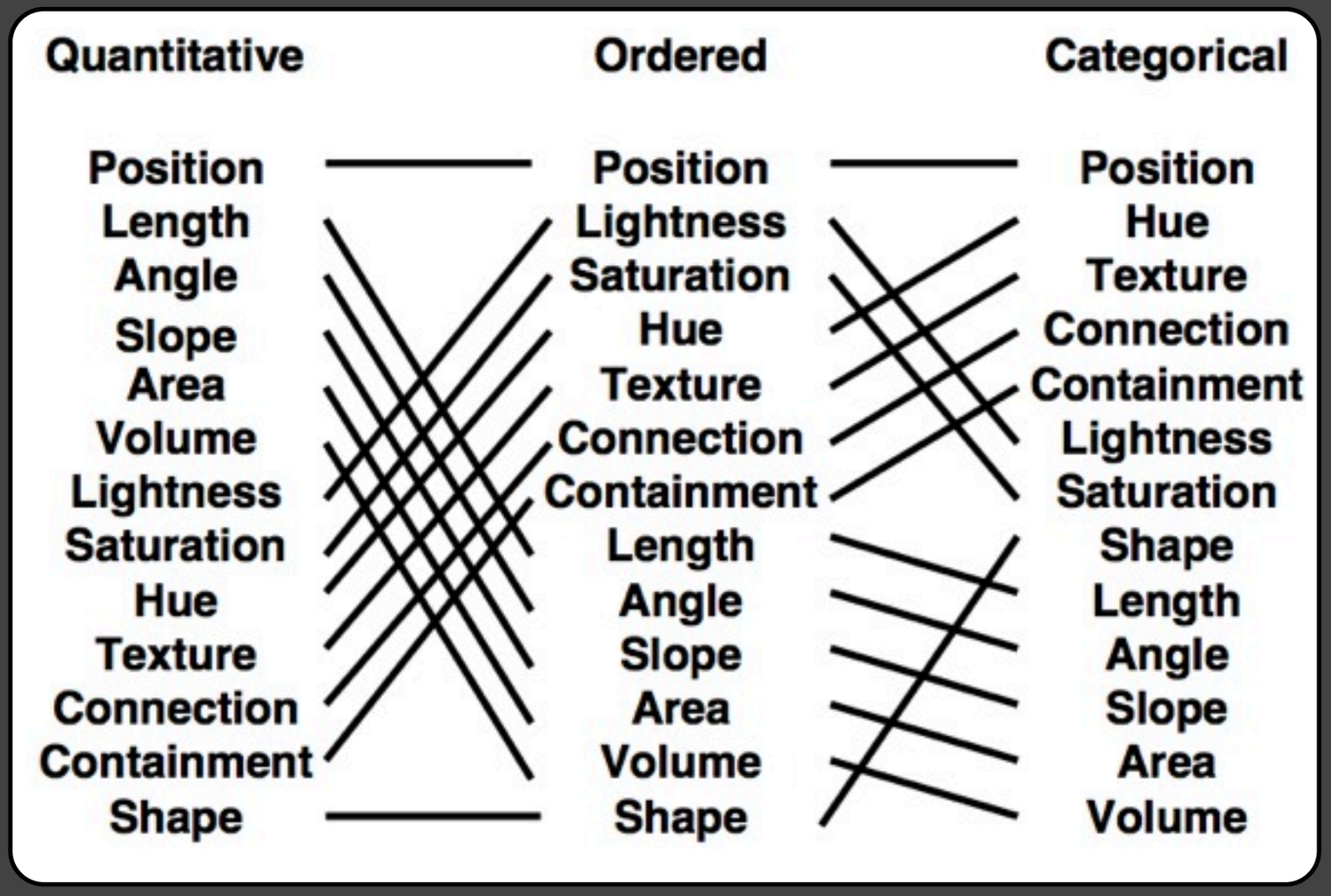
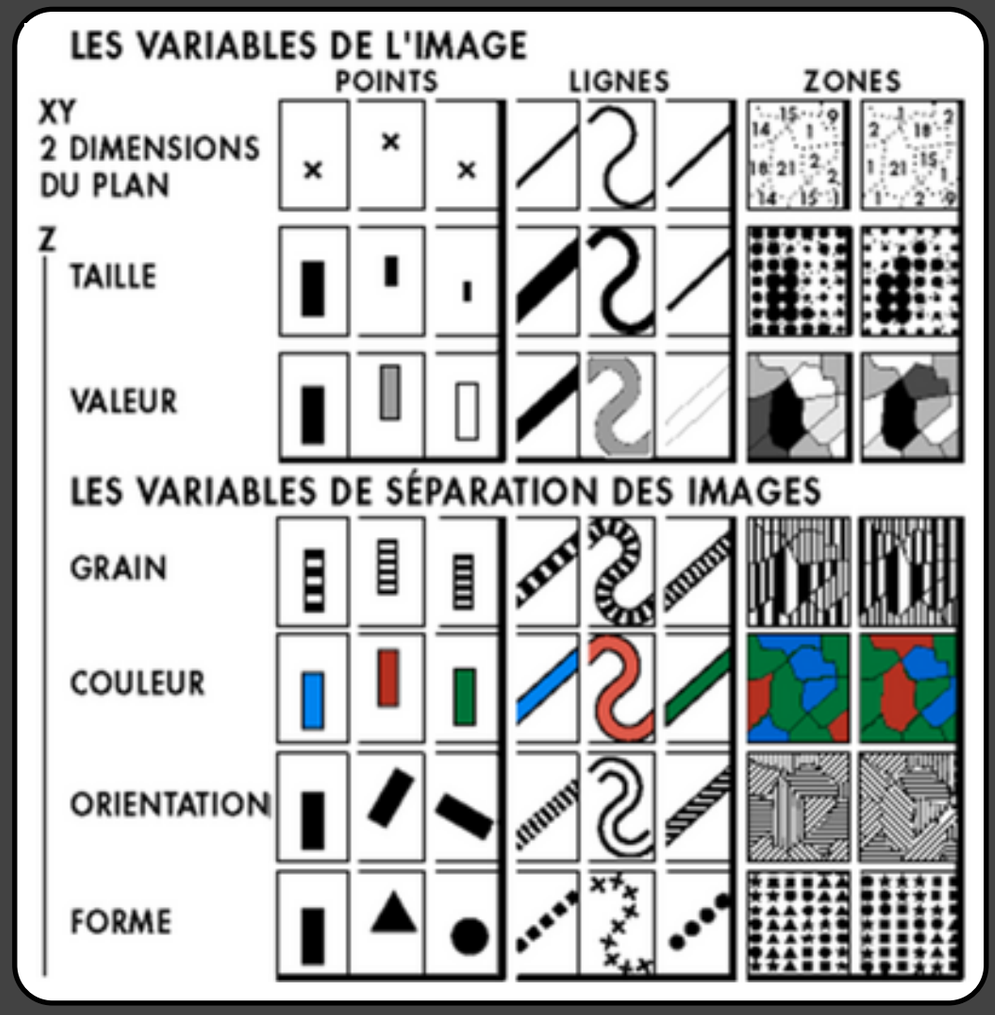
design

In designing a tool like Pathline, we draw on visualization principles to guide the design of visual encodings and interaction mechanisms.



Automating the Design of Graphical Presentations of Relational Information
MacKinlay, 1986



Semiology of Graphics
Bertin, 1967

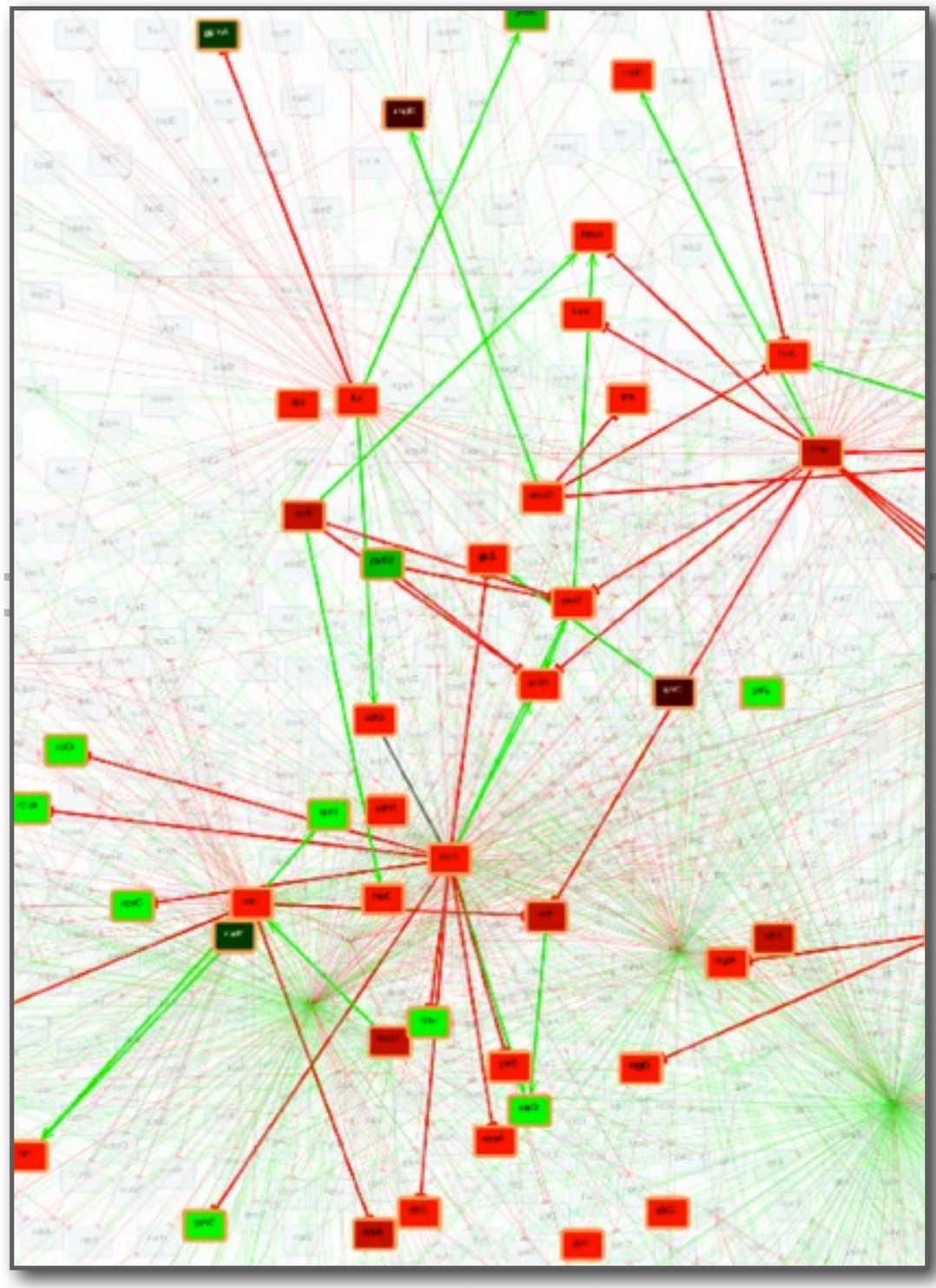
Early work in visualization looked at the different ways to encode information visually, such as using position, color, size, shape, and so on. These researchers conducted user studies to understand what types of encodings are best for different types of data.

encode quantitative values with spatial position

For Pathline, we centered our design around encoding quantitative values with spatial position as it has been shown that we are much more accurate at comparing values using a positional encoding than any other information channel.

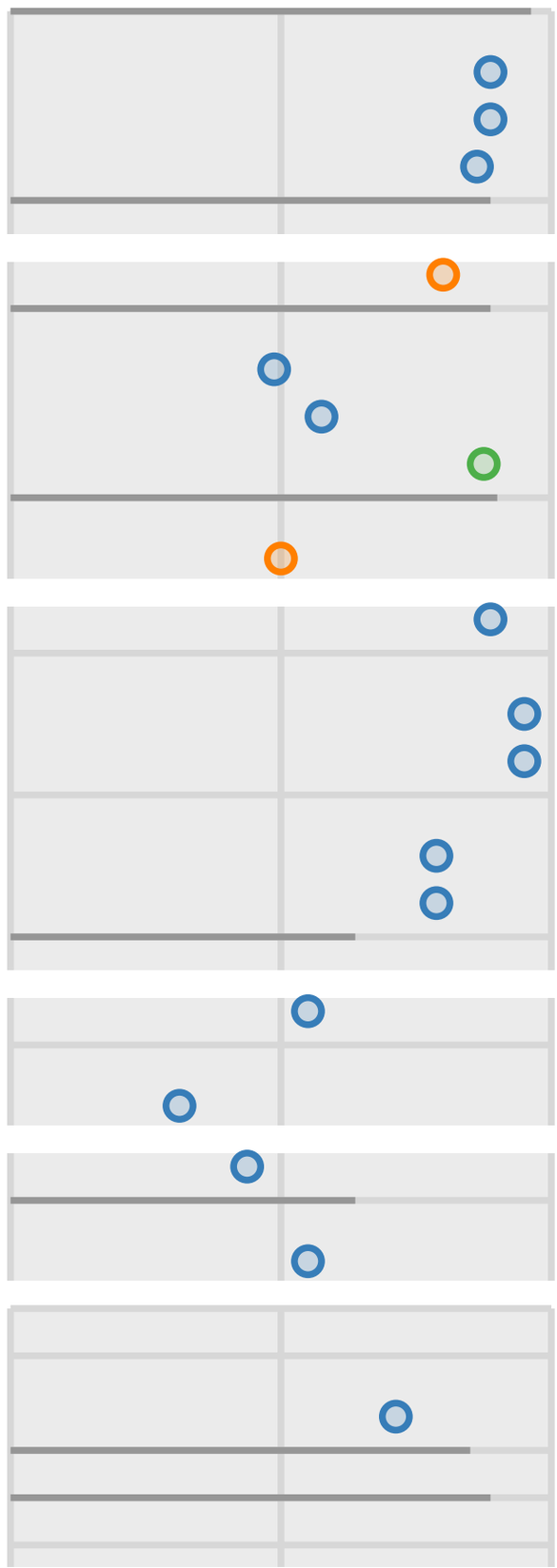
So, instead of using position to show the topology of the pathways and layering values on the nodes with color, we instead linearize the pathways, creating a common coordinate frame to map data using position along the x-axis.

topological layout



www.win.tue.nl/~mwestenb/genevis/

linearized pathway



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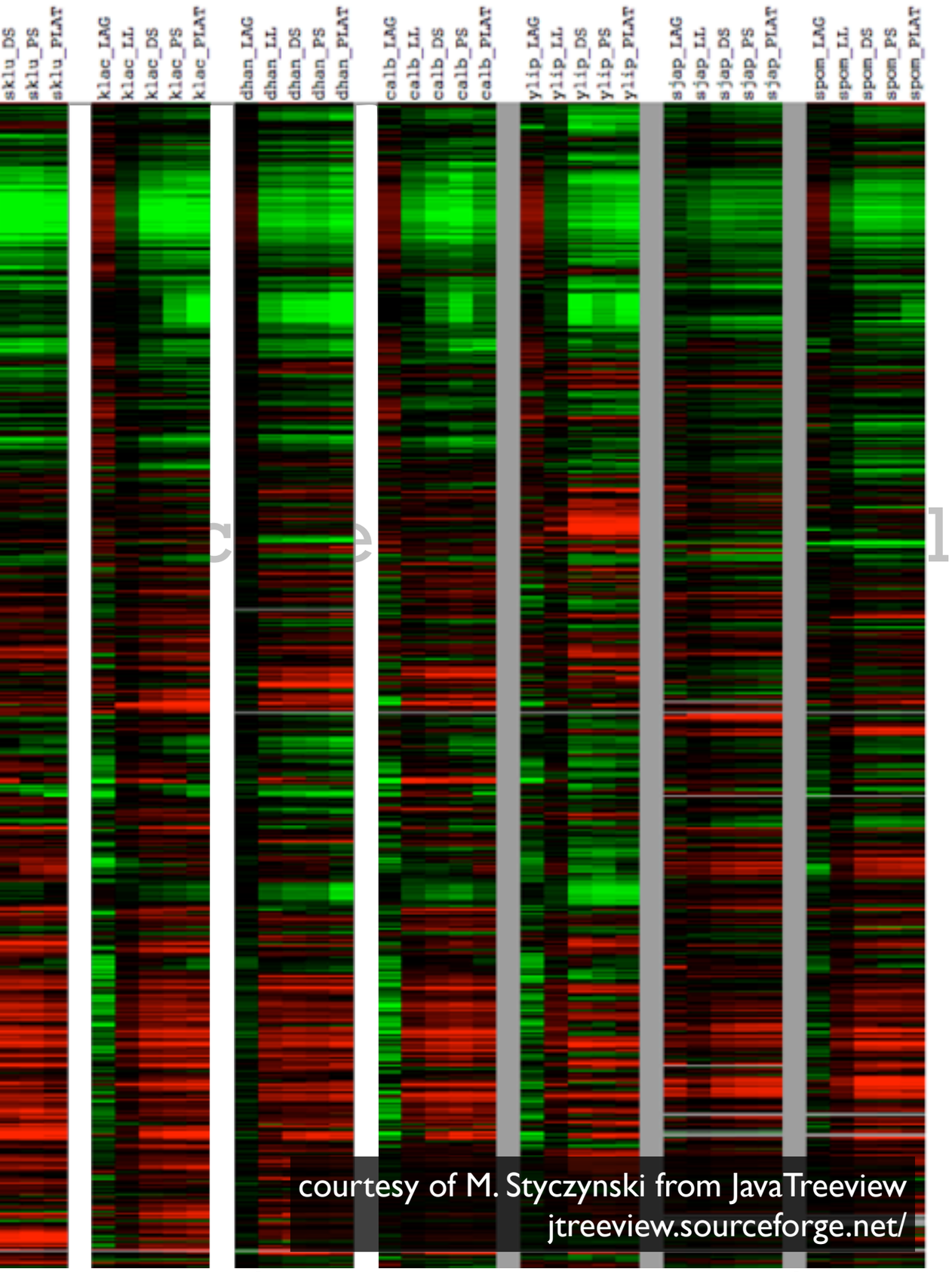
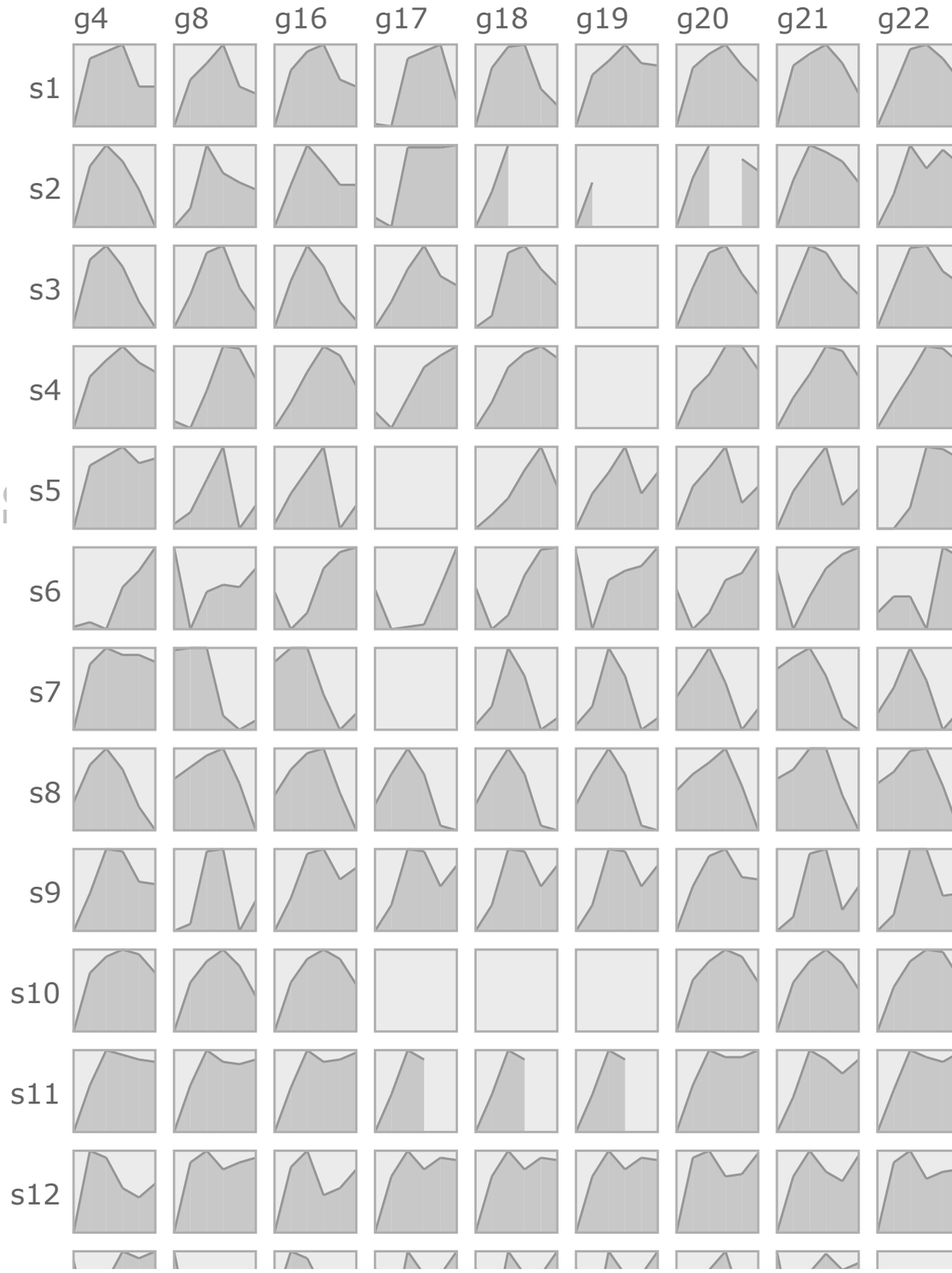
heatmap



courtesy of M. Styczynski from JavaTreeview
jtreeview.sourceforge.net/

curvemap

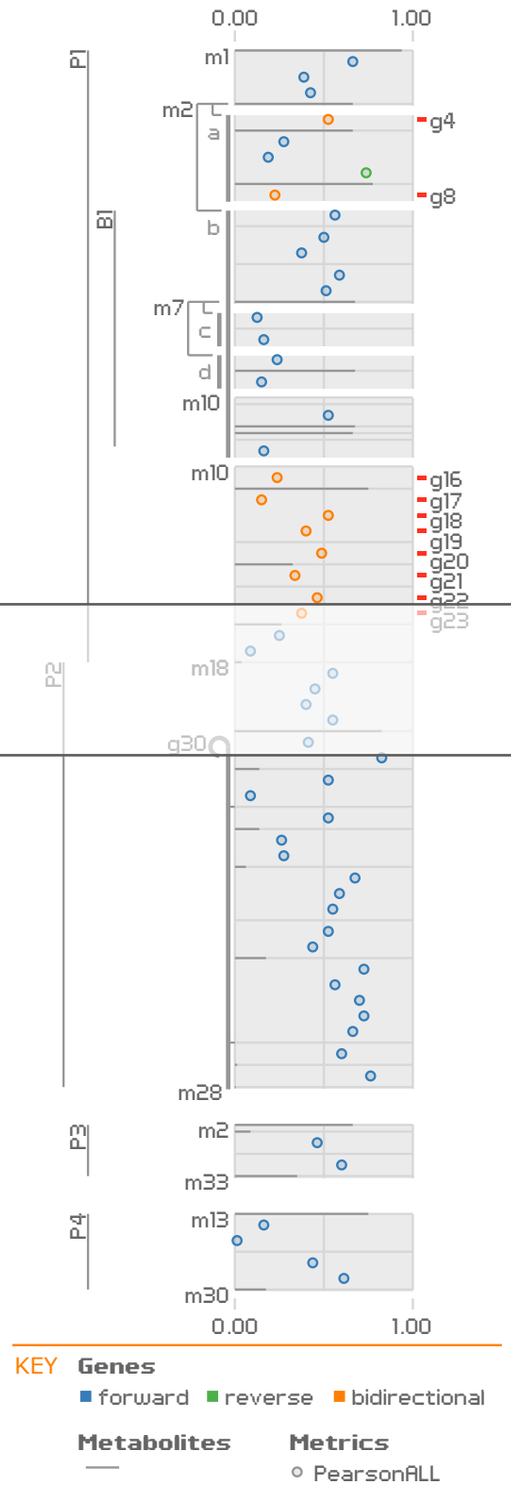


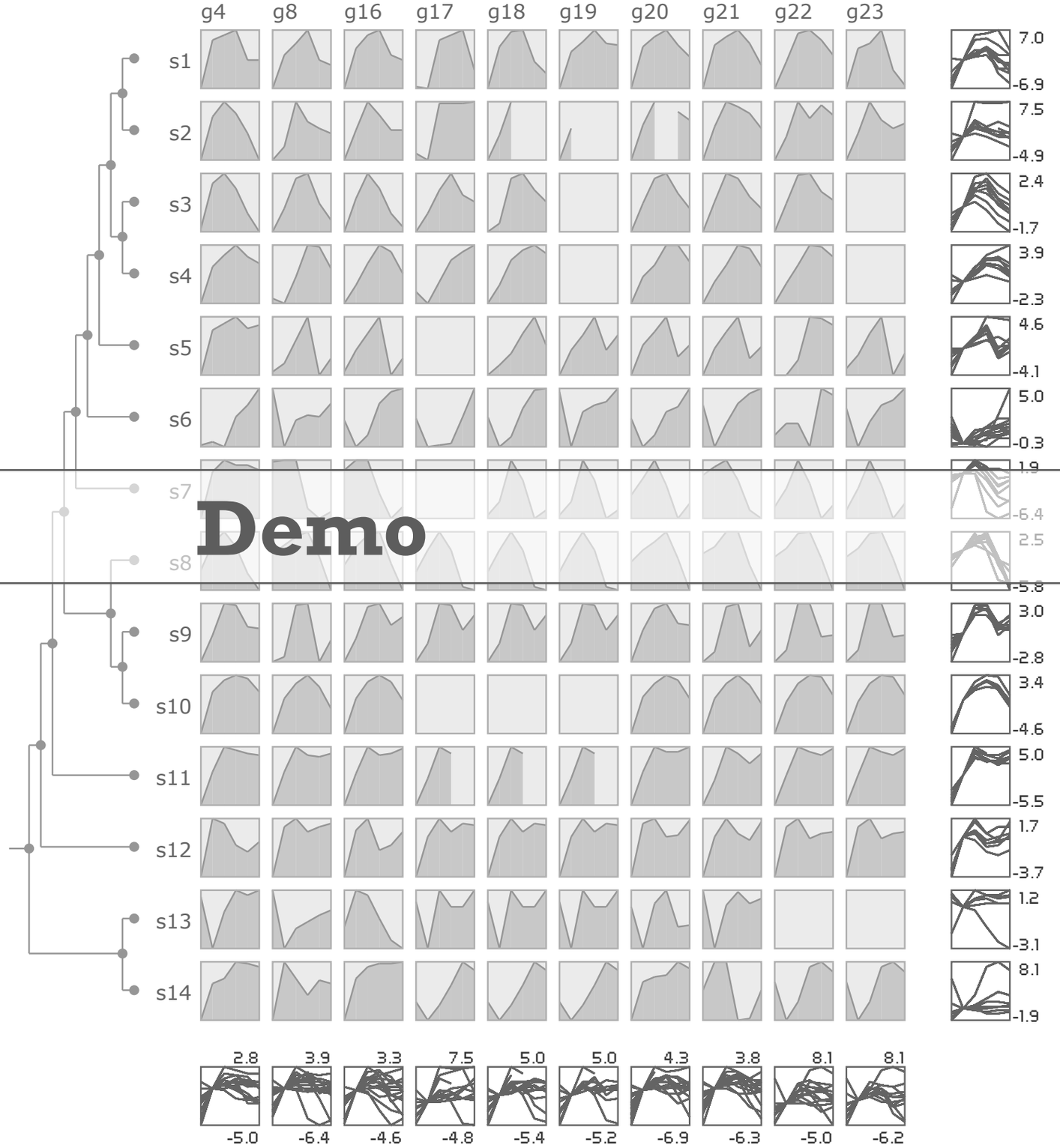
And instead of a traditional heatmap display of gene expression data where the values are encoded using color in a matrix layout, we instead developed the curvemap display, which encodes the expression values as time series curves.

Pathline

PATHLINE

A TOOL FOR COMPARATIVE FUNCTIONAL GENOMICS





Demo

final points

- targeted, focused problems lead to (effective) generalizable solutions
- the CIFellows program fosters focused interdisciplinary research

-I ♥ my postdoc

shameless plug: I am on the job market!

A few final points... What I have found in my own research is that working on targeted, focused problems like the Pathline project can lead to effective generalizable solutions. And I think this holds true beyond the field of visualization. Having support through programs like the CIFellows fosters this type of focused interdisciplinary research by providing junior researchers the time and resources to acquire new domain knowledge and to build lasting collaborations. Personally, I've been able use the generous CIFellows funds to attend numerous biology workshops and to visit different labs, which has not only led to new collaborations, but it has been invaluable for providing insight into the research culture of biology. And finally, while postdoc-ing in computer science is still the exception rather than the norm, my postdoc experience is one i wish every new phd could have. I have had absolute freedom to explore new ideas and directions which has completely reshaped my research and my career aspirations. It makes me even a little sad that it has to end next summer. But not so sad that i won't end this talk with a completely shameless plug...