



CHALLENGE

Identify and characterize genes underlying variation in stress tolerance in *Arabidopsis thaliana* to better understand how climate and habitat variation influence the evolution of plant physiology and, ultimately, to improve crop production under stressful growing conditions.

SOLUTION

JMP® Genomics from SAS dynamically links powerful statistical analysis with sophisticated graphics to provide a comprehensive picture of collected results.

RESULTS

Plant researcher Tom Juenger, Associate Professor at the University of Texas, likes the flexible analysis options and the comprehensive functionality of JMP Genomics. He has contributed ideas for two new features that SAS® developers have incorporated into the latest version of the software.

Study of drought stress yields ideas for hardy plants, software features

A University of Texas researcher's recommendations are put into practice in his statistical discovery tool of choice

Tom Juenger, an Associate Professor in the Section of Integrative Biology at the University of Texas at Austin, feels a certain sense of ownership in JMP Genomics – as well he should. After all, he has contributed to its design, as have quite a few other dedicated users of this customized statistical discovery software from SAS.

“I have to say that it’s been really impressive how open to suggestions and comments, and how helpful, the JMP and SAS people have been,” says Juenger, “to the extent that they e-mail out questions about potential experimental designs and analyses, bouncing ideas off of people.”

JMP Genomics provides Juenger with flexible, menu-driven platforms to access, evaluate, analyze and explore data interactively, and it’s designed in an interactive spirit, with an open ear to end-user input.

“Users are encouraged to provide suggestions,” Juenger continues. “I might say, ‘If you could do this in your next release, I think people would really appreciate it. It would save us headaches and would allow us to do certain analyses we can’t currently do.’ And they certainly respond to these suggestions.

“It’s impressed me, and it’s been so helpful to my research.”

Climbing under the hood

Juenger’s research focuses on plant ecological and evolutionary genetics. Currently, he and his team are seeking to identify and characterize genes underlying variation in stress tolerance in *Arabidopsis thaliana*, a small plant native to Europe, Asia and Africa, and the first plant genome ever sequenced. The purpose of this work is to better understand how climate and habitat variation influence the evolution of plant physiology and, ultimately, to improve crop production under stressful growing conditions.

In particular, Juenger is attempting to identify genes associated with drought tolerance using genomewide molecular techniques.

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**STATISTICAL
DISCOVERY.™
FROM SAS.**

“When you’re going from looking at 10 genes to looking at thousands of genes, making biological sense of the results isn’t easy – it’s impossible to do if you don’t have the tools that help you easily visualize and explore the annotation of the results. JMP is great for that.”

Tom Juenger

“A traditional molecular approach would be to overexpress, or knock out, a gene,” says Juenger. The analogy, he says, would be if you were examining a car engine to try to figure out how it works, and you do so by pulling out individual parts, observing and tinkering with them.

“But what we do,” Juenger says, “is look at natural genes from different populations that have experienced natural selection in response to stressful environmental conditions.

“So to continue the analogy, it would be like figuring out how the engine works by comparing different cars.”

Juenger is interested in how plants have evolved solutions to cope with drought.

Molecular geneticists attempt to improve plant performance in adverse conditions using traditional toolkits – breaking a gene, or overexpressing it. But those tools don’t always work so well, says Juenger.

“In contrast, what we’re doing is looking at plants that have evolved to perform well in dry and wet or hot and cold environments. We use genetic mapping and a variety of tools to find the important genes that have allowed plants to survive and thrive under especially stressful conditions. Ultimately, we hope these genes can be used to improve crops.”

JMP Genomics is Juenger’s toolkit of choice.



Tom Juenger, Associate Professor,
University of Texas

A powerful front end for SAS®

Juenger says that he “grew up on SAS.” Then, when he began working in genomics, he turned to JMP.

“It was JMP Genomics that brought me to JMP [software] in general. For me, JMP has been fantastic as a front end to SAS.” When working with data sets with 20,000 or more rows and complex experimental designs, “JMP Genomics really facilitates using the power of SAS.”

Juenger points to three tools within JMP Genomics that are critical to his research:

“We’ve been using Affymetrix microarrays, and JMP Genomics has a very nice procedure for importing and manipulating large microarray data sets and then utilizing a really great

SAS procedure (PROC MIXED) for statistical testing with gene expression data.

“We also use a variety of genetic mapping tools, especially linkage disequilibrium mapping, again with the JMP Genomics front end.


“The third tool – something that when I was first using JMP Genomics I didn’t fully appreciate, but now really see the value in – is that JMP allows easy graphical exploration of the data.

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For Juenger, an important differentiator of JMP Genomics over competitive products is the fact that it is “built on the long history and power of SAS” and that it provides so many tools in one.

“We do quantitative trait locus mapping, association mapping, microarray analysis, and we can now do all these things in JMP Genomics. You do not have to buy this piece of software for that application and another piece of software for this other application.”

The superior graphics that Juenger describes as vital to his work also distinguish JMP Genomics from similar tools. Not only does JMP Genomics



offer sophisticated graphical exploration capabilities, but the clarity with which results can be displayed is unmatched. Juenger uses those graphics to present his research findings to audiences.

Ease of use for new users is yet another differentiator: Novices don't have to write code. Pull-down menus, dialog boxes and a point-and-click environment are other reasons that first-time users find JMP Genomics extremely intuitive, says Juenger.

Juenger will use JMP Genomics for an upcoming class in evolutionary and ecological genetics.

Well-received input

And of course, yet another distinguishing characteristic of JMP Genomics is that openness to input on the part of the development team responsible for the software's evolution.

Juenger says that two suggestions he made for JMP Genomics have been incorporated into the latest release.

One is the ability, when importing microarray data, to filter out which parts of the microarray are actually used to determine gene expression values. Juenger says this tool allows his lab to do analyses that they otherwise couldn't easily perform.

Another is related to association mapping analyses.

"Researchers want to control for population structure and the relatedness of individuals within the analysis," Juenger explains, "and in the past there was really no simple way to do that. With JMP Genomics, there's a procedure for uploading a matrix of that data and using it in association mapping analysis."

Of the JMP Genomics developers, Juenger says, "I think it's great that they listen to people and what we want to be doing and, in a timely fashion, have implemented much of what we're asking for."



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