



CHALLENGE

Effectively summarize thousands of variables and analyze them to better understand how various genetic combinations affect physical appearance.

SOLUTION

JMP Genomics from SAS combines sophisticated analysis with graphical data presentation to promote understanding of research results.

RESULTS

The analytic versatility of JMP Genomics lets researchers explore vast data sets from many perspectives. Point-and-click menus make it easy for students to use.

MORE INFORMATION

Learn more about the work of the McIntyre Lab:

http://bioinformatics.ufl.edu/McIntyre_Lab/index_mcintyre_lab.htm

Learn more about SAS: www.sas.com

Superior graphics – and a lasso – foster genetics studies

At the University of Florida, students and researchers see results with JMP® Genomics

Lauren McIntyre loves the lasso.

For McIntyre, a statistical geneticist, it's definitely, first and foremost, about the graphics. It's the visuals of JMP Genomics software from SAS that really do it for her, most particularly that lasso that allows her to corral data points and then highlight them.

"That's my favorite tool. I feel like such a cowgirl: 'I'm going to lasso these points and now I'm going to turn them red.'" The lasso is just one tool within JMP Genomics that McIntyre uses with regularity, and that she finds to be indispensable.

"JMP is just really wonderful at providing a clear look at your data and understanding its structure," she affirms.

McIntyre is Associate Professor in the University of Florida's Department of Molecular Genetics and Microbiology and part of the Genetics Institute. She uses JMP in both her research and teaching.

Clarifying relationships

McIntyre's research focuses on the use of statistical theory to clarify the relationship between genotype (an organism's genetic blueprint) and phenotype (its appearance). She explores new ways of looking at things that help connect the dots between DNA, gene expression, proteins and phenotype.

"We collect a lot of data about the state of the genome, how that expresses itself in RNA and how that translates into protein," she explains. "If you're observing flies, you might be interested in the total body length or the shape of the wings. If you're observing plants, you might look at resistance.

"At every level, you have thousands of data points, so you need to think about ways of effectively understanding what the connections are between the levels and also understanding the structure of your data within the level."

McIntyre's objective is to try to figure out how to effectively summarize this data and better understand what it indicates in order to move on to the next level. Meeting this objective is what led her to JMP Genomics.

**STATISTICAL
DISCOVERY.™
FROM SAS.**

“JMP provides graphical methods for data presentation on very highly complex planes – things like factor analysis, multidimensional scaling and all kinds of plots – and these tools are quite useful now that in genetics we have these issues with dimensionality.”

Lauren McIntyre

A decade ago, McIntyre says, geneticists were measuring hundreds of variables; now it's thousands.

“JMP provides graphical methods for data presentation on very highly complex planes – things like factor analysis, multidimensional scaling and all kinds of plots – and these tools are quite useful now that in genetics we have these issues with dimensionality.”

Shuffling the cards

McIntyre – who says that at 8 years old she was the “baddest card shark in the neighborhood,” in large part due to her ability to count cards – makes an analogy between card playing and genetics.

“You have all these genes, and different alleles [coding sequences] within those genes, and then you shuffle them around and you make different combinations and you see what you get. Then you count them into little bins, and then based on different combinations of outcomes, you can make different inferences.

“One of the big challenges is coming up with experiments that shuffle alleles in particular ways so that the allelic combinations constructed assist in testing your predictions.”

McIntyre began using SAS® software in 1988 and remains a SAS fanatic. She was introduced to JMP about seven years ago.

What initially attracted her to JMP, she says, are its superior graphics – how the plots are interconnected – for example, the ability to circle points on one plot and have them highlighted on another.

McIntyre uses JMP Genomics in teaching graduate-level genomics and bioinformatics and says her department will probably soon begin to use it in introductory statistics classes as well. In addition to a campuswide license for JMP statistical discovery software, the university has a JMP Genomics license that enables all students, professors and researchers in McIntyre's department to take advantage of its sophisticated analysis and data visualization.

JMP is ideal for students, she says, because it offers a good balance between ease of use and flexibility.

Perhaps what McIntyre most particularly likes about JMP Genomics, though, is that it's a SAS product. She knows that it's built on a strong and flexible foundation and appreciates that she can see what's been implemented behind the scenes in SAS code. While others may be turning to open-source software, McIntyre finds the investment in SAS well worth it because she can be assured that the software is well-tested.

Step by step

Dan Ruzicka, a postdoctoral student at the Danforth Plant Science Center in St. Louis with whom McIntyre works, agrees with her about that balance.

Ruzicka is working on a cross-disciplinary project funded by the National Science Foundation that's examining how tomato roots interact with their environment and how that affects nutrient uptake.

“This is a field experiment, it's being conducted in a real agricultural setting, and so there are a lot more variables than in a controlled lab experiment,” Ruzicka explains. “With JMP Genomics, we can upload our array data and do all the quality control to make sure that we don't have samples that are way out there in terms of variability.

“Lauren absolutely recommended JMP and we agreed that it was the way to go for this project.”

Ruzicka says that, in his view, the biggest advantage of JMP Genomics over other platforms is the ability it gives users to control the workflow.

“It allows you to tailor your analysis either to what your needs are in terms of the experiment or what your scientific opinion is regarding what type of normalization or summarization you should perform,” he says. “With a lot of other platforms, their software engineers wrote the software to just do a very simple analysis – so they may be user friendly, but you're stuck. You can't change anything.”

Even given that flexibility, says Ruzicka, JMP Genomics is intuitive to use: “The advantage of it being built on JMP is that it’s all point and click. It walks you through. Everything is tab formatted. You do everything on one tab and then you move to the next tab.”

“I put him on the speakerphone and we can work through things step by step,” says McIntyre of her work with Ruzicka. “We can just progress through the menu and he knows what the next step is going to be because it’s the next step on the menu.”

Ruzicka says that McIntyre has been a great resource in training him, “not so much in how the software runs – because I can get that from JMP; they have great Webinars and things like that – but more in talking me through the options, showing, for example, how you have a choice of subtracting the median signal intensity during normalization, why you would choose this method, the advantages and disadvantages.”

Making life easier

Other postdocs with whom McIntyre works echo Ruzicka’s perspective on JMP Genomics.

“I’d used JMP before and really enjoyed it,” says Marina Telonis-Scott, a postdoc associate, “and the genomics version is especially helpful for the kind of microarray projects I work on, which include Affymetrix and two-color arrays.”

Telonis-Scott says that the distribution and box plots are helpful. “I also do most of my residual diagnostics and plots in JMP. I like the ‘mark by column’ and ‘select by row’ kinds of features when I’m graphing, to look at different levels in my experiments.”

Also: “I really like the graphic outputs from JMP. They just make life a bit easier by having all the scripts ready to run, and I can generate large amounts of info about how my slides look in a relatively fast time.”

“What I like about JMP is the ability to easily connect between visual representations of the data and specific data points,” says another of McIntyre’s postdocs, Rita Graze. “You can subset outliers or other points of interest just by selecting them on a plot. I also use QC analysis to easily and quickly examine my microarray data for any problems prior to analysis.”

“When students start out, they don’t necessarily organize their thoughts in a way that’s conducive to doing a solid statistical analysis,” McIntyre observes. “So what I love about JMP Genomics is that the menus and the tabs force students to organize their thoughts and their workflow. Once they’ve done that a few times, they can really abstract a lot better.

“You can do a lot of things with JMP, but it’s still relatively intuitive. And you get to use the lasso.”

“I really like the graphic outputs from JMP. They just make life a bit easier by having all the scripts ready to run, and I can generate large amounts of info about how my slides look in a relatively fast time.”

Marina Telonis-Scott

Photo of Lauren McIntyre by Sarah Kiewel, UF Health Science Center.



SAS Institute Inc. World Headquarters +1 919 677 8000 To contact your local JMP office, please visit www.jmp.com

SAS and all other SAS Institute Inc. product or service names are registered trademarks or trademarks of SAS Institute Inc. in the USA and other countries. ® indicates USA registration. Other brand and product names are trademarks of their respective companies. Copyright © 2008, SAS Institute Inc. All rights reserved. 103721_521140.1208