



General Mills produces healthier crops with greater yields

Bioscientists experience synergies and efficiencies with JMP® Genomics

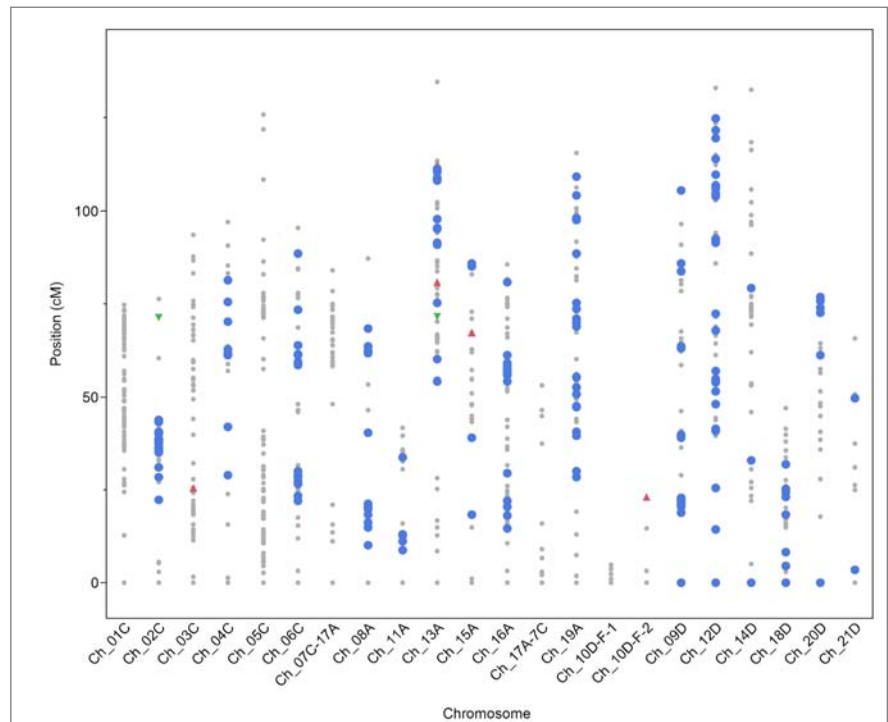
You know that “Heart Healthy” logo on the Cheerios box? It’s the work of bioscientists like Eric Jackson that enables General Mills to make that claim.

Jackson works in crop bioscience research and development, supporting Green Giant, Nature Valley and other General Mills product lines. His job is to help produce healthier crop varieties with higher yields. Oats are among the crops that Jackson most frequently researches.

As the “genomics guy” in the group, Jackson must tackle large data sets every day. JMP® Genomics allows him to do so quickly and effectively by combining point-and-click access, dynamically interactive JMP graphics and robust SAS® Analytics.

Jackson began using JMP statistical discovery software from SAS in 1998 while in graduate school – before JMP developed a customized product specifically for genomics research. “I was attracted to JMP because of its ability to provide accurate and meaningful models that could be run easily on a GUI interface on a desktop,” Jackson says.

“Having the ability to dynamically link by clicking on graphs, the ability to subset things, then drive down for more detail – all of that really attracted me. It allowed for a lot of opportunities.”



Chromosome anchoring of a consensus linkage map. Grey dots indicate positions of non-anchored markers on each linkage group, while colored dots indicate positions of physically anchored SNPs (blue dots), DArTs (red up arrows), and RFLPs (green down arrows).

Once in the workforce, Jackson continued to use JMP, but he needed genomics-specific software as well, and he found the existing offerings cumbersome. Then he discovered JMP Genomics and was hooked.

“It took everything that was arduous and that would give me problems in TASSEL and Structure and allowed me to do those analyses more quickly because of the power of JMP with SAS in the background,” he said.

“And I still could do it all on the desktop.”

Since then, Jackson has been a dedicated JMP Genomics user and even a collaborator in its development. Today, he typically uses JMP Genomics for predictive modeling and linkage mapping – the latter of which he’s been instrumental in developing. It’s a great example of the JMP philosophy of working with the experts in the field to refine and broaden the toolkit.

JMP Genomics lets Jackson sift through those millions of markers to find a combination that predicts, for example, a better yield or an enhanced resistance to disease.

Dismantling the haystack

The primary objective of Jackson's work is to produce healthier varieties of oats, sweet corn, broccoli and other crops while gaining higher yields. Predictive modeling capabilities in JMP Genomics have played a central role in this research.

"Lately, I've been doing a lot of genomic prediction in breeding, running prediction models in JMP Genomics and then cross-validating those models," he explains.

JMP Genomics provides the most sophisticated predictive modeling tools on the market. It offers eight predictive modeling methods, with integrated predictor filtering, predictor lock-in and cross-validation. These tools are particularly suited to Jackson's work, since he's investigating perhaps several hundred plants at a time, each with columns of variables that may reach into the millions.

JMP Genomics lets Jackson sift through those millions of markers to find a

combination that predicts, for example, a better yield or an enhanced resistance to disease. Without the built-in modeling tools, this work would be like searching for the proverbial needle in a haystack.

"When I began using JMP Genomics, I was really impressed with how easily I could maneuver through and drill down into this data," Jackson says. "Now that we're into predictive modeling, it's even more exciting."

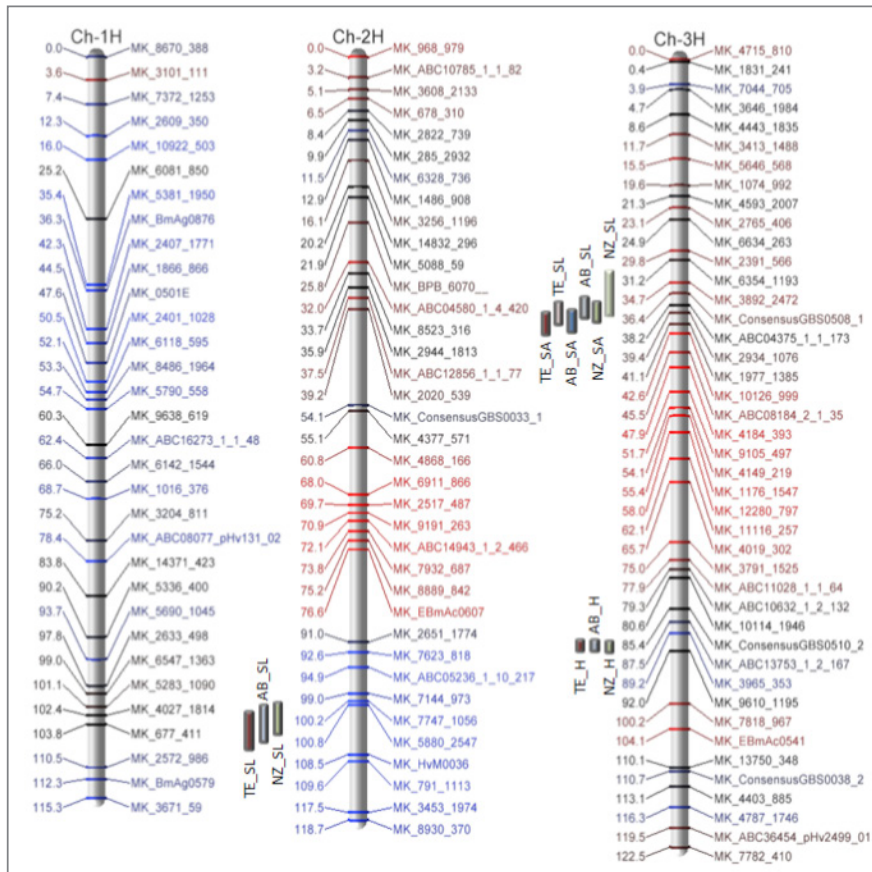
"We currently use JMP Genomics to build robust prediction models for our maize breeding program," he says. Those models have improved the team's selection accuracy and intensity, resulting in more insights than can be gained with classical phenotypic selection.

In addition to these enhanced results, Jackson says, "I can't tell you what a huge timesaver JMP has been."

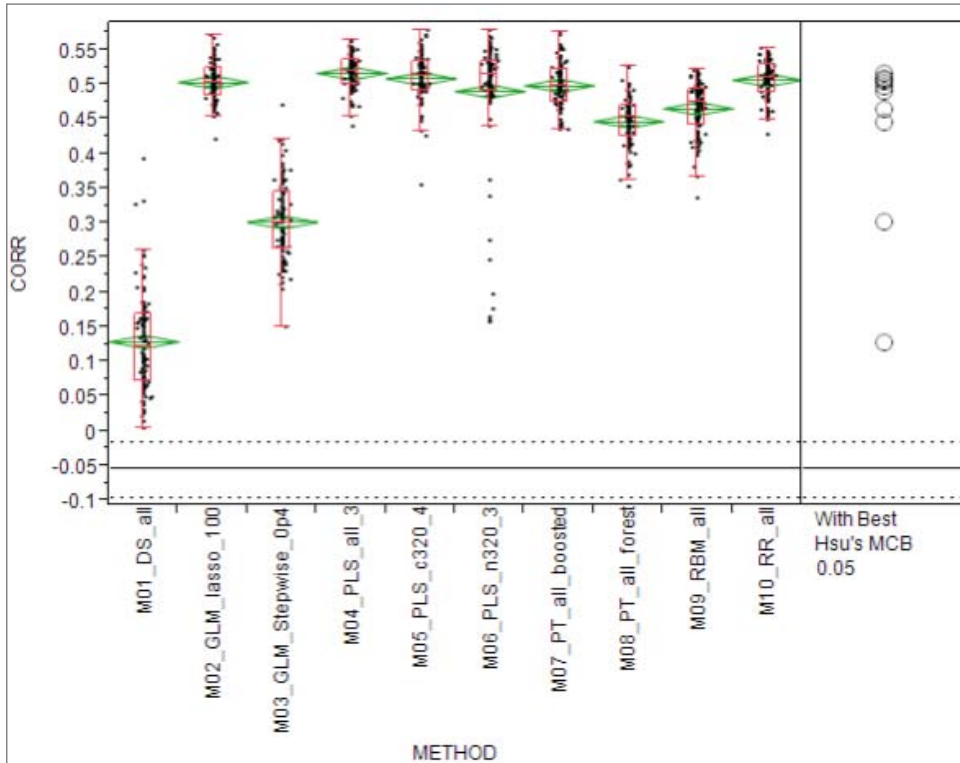
State-of-the-art linkage mapping suite

Jackson's input has played a significant role in the development of another set of JMP Genomics capabilities that have likewise rendered his work much easier and more effective – state-of-the-art linkage mapping tools.

"Linkage mapping is something we didn't do in JMP Genomics before Eric started talking with us about it," explains Jordan Hiller, a JMP Genomics Application Scientist. "He described this great need that he and his colleagues had and made us aware that the other software that was out there was slow and difficult to use."



Genetic marker linkage maps are used to improve various agronomic crops. You can create new linkage groups using genotypes from experimental inbred crosses, order markers within linkage groups using advanced optimization algorithms, and visualize newly created or imported marker maps.



This cross-validation of predictive models for genomic selection is similar to what Jackson and his team use. Each box plot represents the performance of a model for predicting yield from genomic markers.

The Human Genome Project, completed just over 10 years ago, provided geneticists with a comprehensive map of the genetic makeup of human beings. No such vista is available for plants; scientists must gain their insights incrementally.

In the absence of a fully mapped genome, linkage mapping plays a critical role by providing a series of genetic landmarks that allow researchers to learn where individual segments are situated along the double helix.

The JMP Genomics team recognized an opportunity to integrate SAS algorithms for operations research into JMP Genomics, producing a suite of

tools in the software that enables biologists to quickly and effectively build genetic maps in the dynamic, visual environment.

Jackson's knowledge of the biology of linkage mapping was critical in developing the software's linkage mapping capabilities. Using JMP Genomics and other software tools, Jackson and his colleagues constructed and visualized the first complete, physically anchored hexaploid oat map. Their research findings were published in the journal PLOS ONE.

All in one

Jackson relies on a variety of other JMP Genomics capabilities as well – cluster

CHALLENGE

To produce healthier varieties of oats, sweet corn, broccoli and other crops.

SOLUTION

JMP® Genomics, which combines dynamically interactive JMP graphics and robust SAS® Analytics.

RESULTS

JMP Genomics has helped General Mills bioscientists improve the accuracy and intensity of gene selection – and save a tremendous amount of time.

analysis and multiple linear regression, among them – and appreciates the comprehensive nature of the software.

“The ability to do it all in one place is a wonderful thing,” he says.

JMP Genomics also helps Jackson communicate his research findings with others. Whether explaining a dendrogram or a cluster analysis, he says, visualization tools in the software promote understanding. “For example, when we’re using hierarchical clustering and building toward an optimal genotype, being able to show how we’re getting there provides great insight.”

Jackson also played a proactive role in the development of action buttons in JMP Genomics that help him save time by eliminating steps when filtering his data.

“In our line of business, as in most others, time is money,” he says.

“If we can find more efficient ways to get this work done, then we can move forward to something else that much more quickly.”

Greater insights and huge time savings make JMP Genomics a healthy choice for General Mills – and Eric Jackson has been instrumental in making it so.



JMP® Genomics

Learn more about the software, which combines JMP and SAS for specialized data analysis and presentation.

jmp.com/genomics

Customer stories

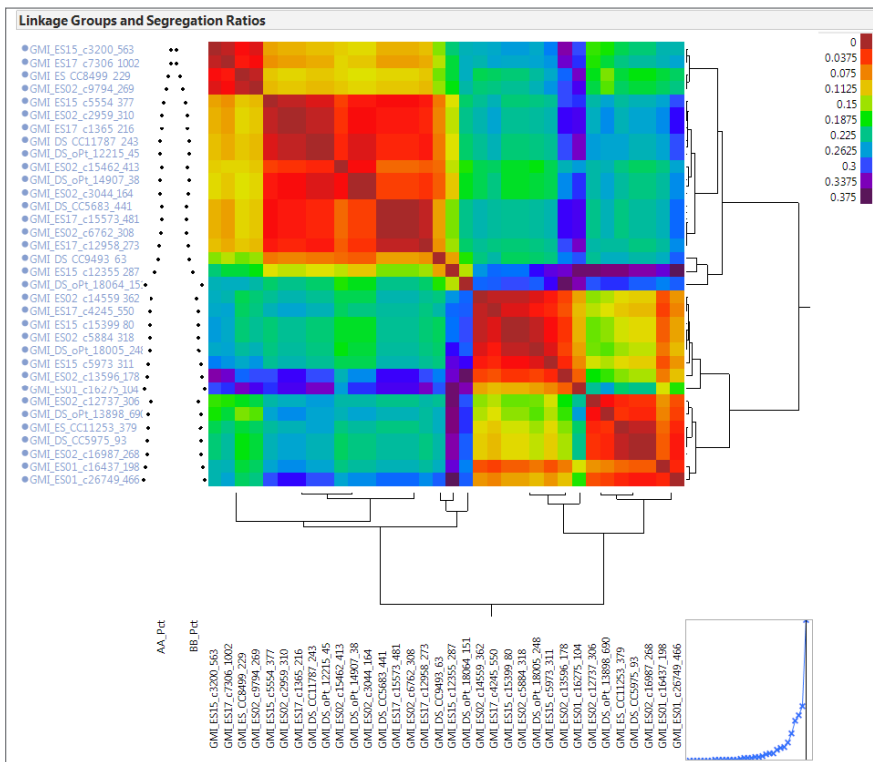
See how other organizations get real work done with JMP.

jmp.com/success

Linkage mapping

Watch the webinar on how the Collaborative Oat Research Enterprise uses JMP Genomics for linkage mapping.

jmp.com/core



JMP Genomics offers automated and interactive options for linkage group identification and marker ordering.



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