NCSU research: In habitats, houses or tents, lifestyle affects health

CHALLENGE

Two NCSU researchers–one studying red wolves, the other humans–seek to determine what role habitat or lifestyle plays in genetic expression–and thus disease patterns.

SOLUTION

Both Erin Kennerly and Youssef Idaghdour rely on JMP® Genomics to analyze microarray data and find patterns of significant genetic clustering. Both experiments use genotyping and expression results to show the genetic differences between populations.

RESULTS

In both experiments, results of analyses performed with JMP Genomics provide clear indications that environment and/or lifestyle affect expression patterns.

OBSERVATIONS

"It is a great platform for rigorous statistical analysis, including quality control checks of the data and easy transitions to downstream analysis."
– Erin Kennerly

MORE INFORMATION

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Sometimes one good idea leads to another.

That's just what happened in a genetics lab at North Carolina State University in Raleigh. Graduate student Erin Kennerly, a PhD candidate in genetics, was using JMP Genomics to analyze gene expression changes due to habitat differences between wild and captive red wolves. She realized the genes that differed the most between the captive and free-range wolves were involved in pathways also associated with depression or stress.

Kennerly's research led her adviser, Dr. Greg Gibson, to wonder, "Will humans show similar effects due to environmental changes?" And another experiment was launched–this one by Youssef Idaghdour in his native Morocco. Idaghdour, who also is working toward a PhD in genetics at NCSU, led a team that collected blood samples from three Berber populations living in different environments: Bedouin nomads, isolated rural villagers and city dwellers. He then compared the results to determine if lifestyle significantly affects human gene expression–and thus disease patterns.

In both experiments, results of analyses performed with JMP Genomics gave clear indications that environment and/or lifestyle affect expression patterns. In the wolf study, the only significant differences in gene expression were found between the captive and wild wolves. The gene expression profile differences indicated that captive wolves may have a depressed immune system, possibly a response to physiological or dietary stress.

For the human study, Idaghdour analyzed gene expression data, methylation data and some 318,000 SNPs to estimate genetic and epigenetic differences between the three populations. That volume of data might be considered large for most types of statistical studies but is not unusual in genomics. His analysis found that lifestyle, not genetic differences, accounted for approximately one third of the differences in gene expression.

STATISTICAL DISCOVERY.™ FROM SAS.

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>
> **Erin Kennerly**

In samples taken from city dwellers, some of the most highly expressed genes related to respiratory disease, inflammatory disease and cancer. But urban life wasn’t the only source of stress. “Even the Bedouins are stressed, but it’s a different kind of stress,” explained Idaghdour. In the tent-dwelling nomads, stress related to the uncertainty of the food supply for themselves and their flocks of camels, sheep and goats, and also to their exposure to pathogens transmitted by animals. “They move according to how much food is available to the animals for grazing.”

Both Kennerly and Idaghdour relied on JMP Genomics to analyze microarray data and find patterns of significant genetic clustering. Both experiments used genotyping and expression results to show the genetic differences between populations. “That’s where the new JMP Genomics really comes into play,” said Kennerly. “It is a great platform for rigorous statistical analysis, including quality control checks of the data and easy transitions to downstream analysis.”

Kennerly also found the normalization, quality control and pattern discovery tools in JMP Genomics particularly useful. “I like being able to quickly assess the quality of my microarray data and then easily compare several normalization methods side by side,” she explained. “Using the pattern discovery tool, I can quickly look for patterns in my data which may be associated with one of my treatments.”

Idaghdour appreciated the flexibility of JMP Genomics to handle large data sets and its capabilities for both analyzing gene expression and genotyping. “The large choice of all sorts of analysis methods for gene expression data, especially mixed-model analysis, is great, and the fact that I can link my lists to other online databases is very useful,” he said. “The feature I like most is that JMP Genomics is easy to use and saves a lot of time. And I can still view the SAS code from JMP Genomics outputs and learn from it.”

Both researchers have documented their findings in articles published by scientific journals: Kennerly’s by *Molecular Ecology* and Idaghdour’s by *PLoS Genetics*.

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