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INTRODUCING THE DISCUSSION PAPER BY SZÉKELY AND RIZZO

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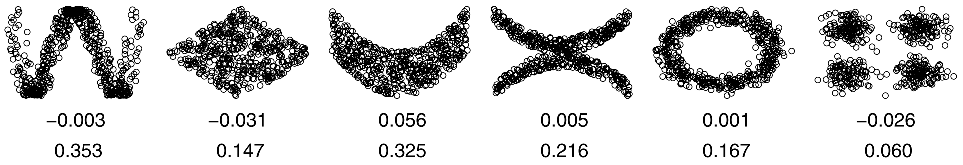
I recall a great sense of excitement in the seminar room in Madison after Professor Székely presented the astonishing findings about distance covariance (in the spring of 2008). It was one of the best statistics seminars I could remember. Since before computers, statisticians have held up Pearson's correlation coefficient as the most essential measure of association between quantitative variables. R. A. Fisher's reputation was sealed, in part, by solving the distribution of this statistic, and so much of linear-model methodology relates to it. And all the time we've had to add the caveat about independence following zero correlation *only if* the data are jointly normal. Spearman's rank correlation has substantial practical utility in cases where normality is unreliable, but the goal to have a *bona fide* dependence measure seemed to have been beyond the scope of ordinary applied statistics. Some valid measures did exist, but being driven by empirical characteristic functions, they were too complicated to enter the toolkit of the applied statistician.

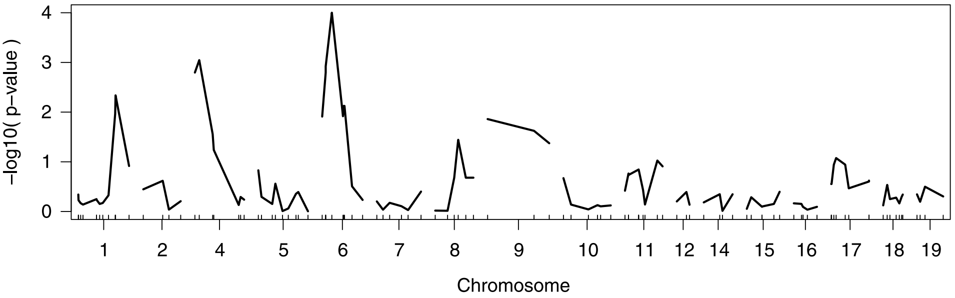
Distance covariance not only provides a *bona fide* dependence measure, but it does so with a simplicity to satisfy Don Geman's *elevator test* (i.e., a method must be sufficiently simple that it can be explained to a colleague in the time it takes to go between floors on an elevator!). You take all pairwise distances between sample values of one variable, and do the same for the second variable. Then center the resulting distance matrices (so each has column and row means equal to zero) and average the entries of the matrix which holds componentwise products of the two centered distance matrices. That's the squared distance covariance between the two variables. The population quantity equals zero if and only if the variables are independent, whatever be the underlying distributions and whatever be the dimension of the two variables. The depth of the finding, the simplicity of the statistic, and the central role of statistical dependence make this an important story for our discipline.

As a numerical entree, consider six simulated examples of unusual joint distributions, mimicking those at the wikipedia.org page on Pearson correlation [R code is available in supplementary files Newton (2009)]. In each case $n = 500$ points are randomly sampled. Although there is dependence between horizontal and vertical components (in all but the case on the far right), the Pearson correlation coefficient is essentially zero (upper row), consistently estimating the underlying zero correlation. The dependence is revealed by the distance correlation (lower row), which is the normalized version of the distance covariance. As expected, p-values from the recommended Monte Carlo test of independence are all small, except in the last case (not shown).



Work has just begun, I think, to explore the utility of distance covariance in applied statistics. In gene mapping, for example, the central statistical problem is to identify dependencies between genetic information (genotype) and other measured characteristics (phenotype) of sampled individuals. Here I describe one way that distance covariance could apply; many versions seem possible. Consider mapping a quantitative trait in the murine physiological response to bacterial infection; 154 mice from a backcross population were typed at 119 genetic markers in a study by Hopkins et al. (2009). A cell-based measure of response-to-infection was also obtained in several tissues from the same animals. At each genetic-marker position (horizontal axis), plotted in the figure below is the p-value (negative log, base ten) from the distance-covariance test of independence between the phenotype (the infection response in bladder tissue) and the genotype (a two-level covariate in this backcross population). The distance between genotypes is the indicator of distinct genotypes at one specific marker location, although extensions could take advantage of various genome metrics.

In several earlier papers Professor Székely and colleagues introduced distance covariance and began to develop its theoretical properties. I invited them to prepare a paper for *AOAS*, considering the potential implications for applied statistics; the following work by Professors Székely and Rizzo is the response to this invitation. It reports further properties of the distance correlation based on a surprising connection to Brownian motion, and it presents some basic computational results from an R software implementation. I am delighted that we have seven contributions to a discussion of the paper which explore the landscape of dependence in great detail.



SUPPLEMENTARY MATERIAL

R code to simulate unusual joint distributions with zero Pearson correlation (DOI: 10.1214/09-AOAS34INTROSUPP; .R).

REFERENCE

HOPKINS, W. J., ELKAHWAJI, J., KENDZIORSKI, C., MOSER, A. R., BRIGGS, P. M. and SUHS, K. A. (2009). Quantitative trait loci associated with susceptibility to *Escherichia coli* bladder and kidney infections in C3H/HeJ female mice. *Journal of Infectious Diseases* **199** 355–361.

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