CORRECTION

EFFICIENT REGULARIZED ISOTONIC REGRESSION WITH APPLICATION TO GENE–GENE INTERACTION SEARCH

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The authors of Hochbaum and Queyranne (2003), henceforth HQ, have brought to our attention that, for the global isotonic regression problem we pose in our paper Luss, Rosset and Shahar (2012), equation (1), the solution of HQ is more computationally efficient than our IRP algorithm and the other similar algorithms we mention [Maxwell and Muckstadt (1985), Spouge, Wan and Wilbur (2003)] in deriving the continuous solution (and not only for integers as we erroneously noted in our original paper). The worst case complexity cited by HQ for solving this problem is $O(mn\log(n^2/m))$, compared to $O(\min(mn^2\log(n), n^4))$ derived for IRP in our paper, where n is the number of observations, and m is the number of isotonicity constraints.

An important feature of the IRP algorithm is that it generates a "regularization path" of partial solutions which greedily maximize between-group differences in every iteration, and in this respect it differs from HQ. The main focus of our paper is on demonstrating the range of applications of efficient isotonic regression solutions (in particular in genetics), and the importance of regularization as the dimension increases, as implemented through our regularization path. These aspects of our contribution are unchanged.

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