Erratum to: CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer

Mark D. M. Leiserson1,2†, Hsin-Ta Wu1,2†, Fabio Vandin1,3 and Benjamin J. Raphael1,2*

We also updated the description of our procedure for assessing the convergence of the MCMC algorithm in Additional file 1, section S2, which should read:

“To assess the convergence of the MCMC algorithm, we ran multiple chains with different initializations. For one of these initializations, we used the collection output by Multi-Dendrix [21] (using the same values of the parameters t and k as in CoMEt). The remaining initializations were random collections. We ran the MCMC algorithm with these initializations, running each chain for a given number of iterations. We consider the chains converged if the mean total variation distance between the chains is smaller than 0.005. Otherwise, we increase the number of iterations by a factor of 1.5. We repeat this process until the chains converge or the total number of iterations per chain reaches a maximum number of iterations, which we set as 1 billion. The output of the MCMC algorithm is the union of the sampling distributions from the different initializations.”

The corrected Additional file 1 is included in this Erratum.

Additional file

Additional file 1: Supplementary information. Supplementary results and figures. (PDF 5528 kb)

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References

1. Leiserson MDM, Wu H, Vandin F, Raphael BJ. CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. Genome Biol. 2015;16:160.