Left (original):

1 - Not-only-linear correlation coefficients might also be helpful in the field of genetic studies.

2 - In this context, genome-wide association studies (GWAS) have been successful in understanding the molecular basis of common diseases by estimating the association between genotype and phenotype [@doi:10.1016/j.ajhg.2017.06.005].

3 - However, the estimated effect sizes of genes identified with GWAS are generally modest, and they explain only a fraction of the phenotype variance, hampering the clinical translation of these findings [@doi:10.1038/s41576-019-0127-1].

4 - Recent theories, like the omnigenic model for complex traits [@pmid:28622505; @pmid:31051098], argue that these observations are explained by highly-interconnected gene regulatory networks, with some core genes having a more direct effect on the phenotype than others.

5 - Using this omnigenic perspective, we and others [@doi:10.1101/2021.07.05.450786; @doi:10.1186/s13040-020-00216-9; @doi:10.1101/2021.10.21.21265342] have shown that integrating gene co-expression networks in genetic studies could potentially identify core genes that are missed by linear-only models alone like GWAS.

6 - Our results suggest that building these networks with more advanced and efficient correlation coefficients could better estimate gene co-expression profiles and thus more accurately identify these core genes.

7 - Approaches like CCC could play a significant role in the precision medicine field by providing the computational tools to focus on more promising genes representing potentially better candidate drug targets.

Right (revised):

1 + Not-only-linear correlation coefficients may be useful in genetic studies.

2 + Genome-wide association studies (GWAS) have been successful in understanding the connection between genotype and phenotype, but the estimated effect sizes of the identified genes are usually small, and they explain only a small part of the phenotype variance [@doi:10.1016/j.ajhg.2017.06.005; @doi:10.1038/s41576-019-0127-1].

3 + This has hindered the clinical translation of these findings.

4 + The omnigenic model for complex traits [@pmid:28622505; @pmid:31051098] suggests that highly-interconnected gene regulatory networks could explain this, with some core genes having a more direct effect on the phenotype than others.

5 + We and others [@doi:10.1101/2021.07.05.450786; @doi:10.1186/s13040-020-00216-9; @doi:10.1101/2021.10.21.21265342] have demonstrated that integrating gene co-expression networks in genetic studies could potentially identify core genes that are not found with linear-only models such as GWAS.

6 + Our results indicate that using more advanced and efficient correlation coefficients to build these networks could better estimate gene co-expression profiles and thus more accurately identify these core genes.

7 + Approaches like CCC could have a significant role in precision medicine by providing the computational tools to focus on more promising genes, which may represent better candidate drug targets.