1 - We simulated additional types of relationships (Figure @fig:datasets_rel, second row), including some previously described from gene expression data [@doi:10.1126/science.1205438; @doi:10.3389/fgene.2019.01410; @doi:10.1091/mbc.9.12.3273].

2 - For the random/independent pair of variables, all coefficients correctly agree with a value close to zero.

3 - The non-coexistence pattern, captured by all coefficients, represents a case where one gene (x) might be expressed while the other one (y) is inhibited, highlighting a potentially strong biological relationship (such as a microRNA negatively regulating another gene).

4 - For the other two examples (quadratic and two-lines), Pearson and Spearman do not capture the nonlinear pattern between variables x and y.

5 - These patterns also show how CCC uses different degrees of complexity to capture the relationships.

6 - For the quadratic pattern, for example, CCC separates x into more clusters (four in this case) to reach the maximum ARI.

7 - The two-lines example shows two embedded linear relationships with different slopes, which neither Pearson nor Spearman detect ($p=-0.12$ and $s=0.05$, respectively).

8 - Here, CCC increases the complexity of the model by using eight clusters for x and six for y, resulting in $c=0.31$.

1 + Simulations of additional types of relationships (Figure @fig:datasets_rel, second row), including some previously described from gene expression data [@doi:10.1126/science.1205438; @doi:10.3389/fgene.2019.01410; @doi:10.1091/mbc.9.12.3273], showed that for random/independent variables, all coefficients correctly agreed with a value close to zero.

2 + The non-coexistence pattern, captured by all coefficients, represented a case where one gene (x) is expressed while the other one (y) is inhibited, highlighting a potentially strong biological relationship (such as a microRNA negatively regulating another gene).

3 + Pearson and Spearman did not capture the nonlinear patterns between variables x and y in the quadratic and two-lines examples, while CCC increased the complexity of the model by using different degrees of complexity to capture the relationships.

4 + For the quadratic pattern, CCC used four clusters for x and achieved the maximum ARI.

5 + In the two-lines example, CCC used eight clusters for x and six for y, resulting in $c=0.31$, while Pearson and Spearman gave $p=-0.12$ and $s=0.05$, respectively.