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Minimal Conflicting Sets in ancestral genome reconstruction

We consider problems of generating minimal obstacles (Conflicting Sets) to the consecutive-ones property for binary matrices used in ancestral genome reconstruction. We show that this problem can be reduced to a joint generation problem for boolean functions, and that this strategy can be helpful in discriminating between true and false positive ancestral syntenies in simulated and real data sets.

This is joint work with Cedric Chauve, Utz-Uwe Haus and Vivija You.