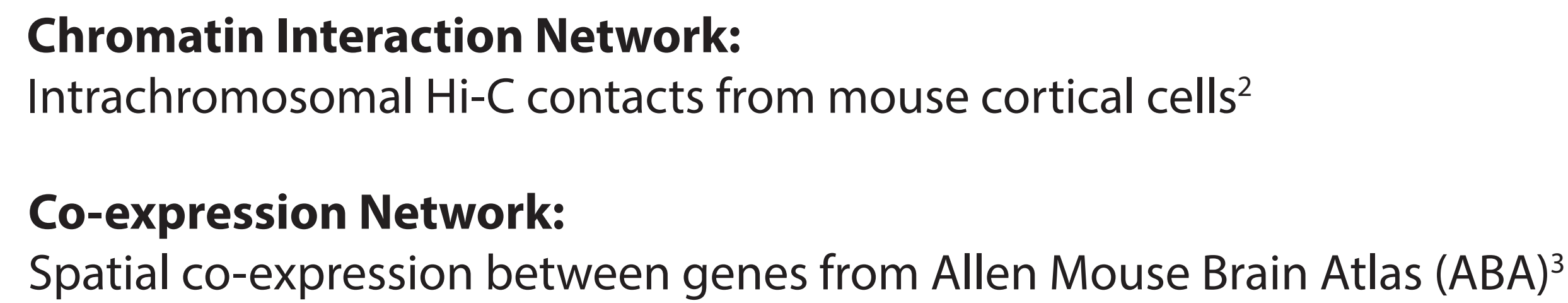


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The 3D conformation of the genome in the cell nucleus influences important biological processes such as gene expression. Predicting gene co-expression from frequent long-range chromatin interactions is a challenging task. We address this by characterizing the topology of the cortical chromatin interaction network using scale-aware topological measures¹. We demonstrate that based on these characterizations it is possible to accurately predict spatial co-expression between genes in the mouse cortex.

Using interaction profile between a gene-pair encoded in interaction network

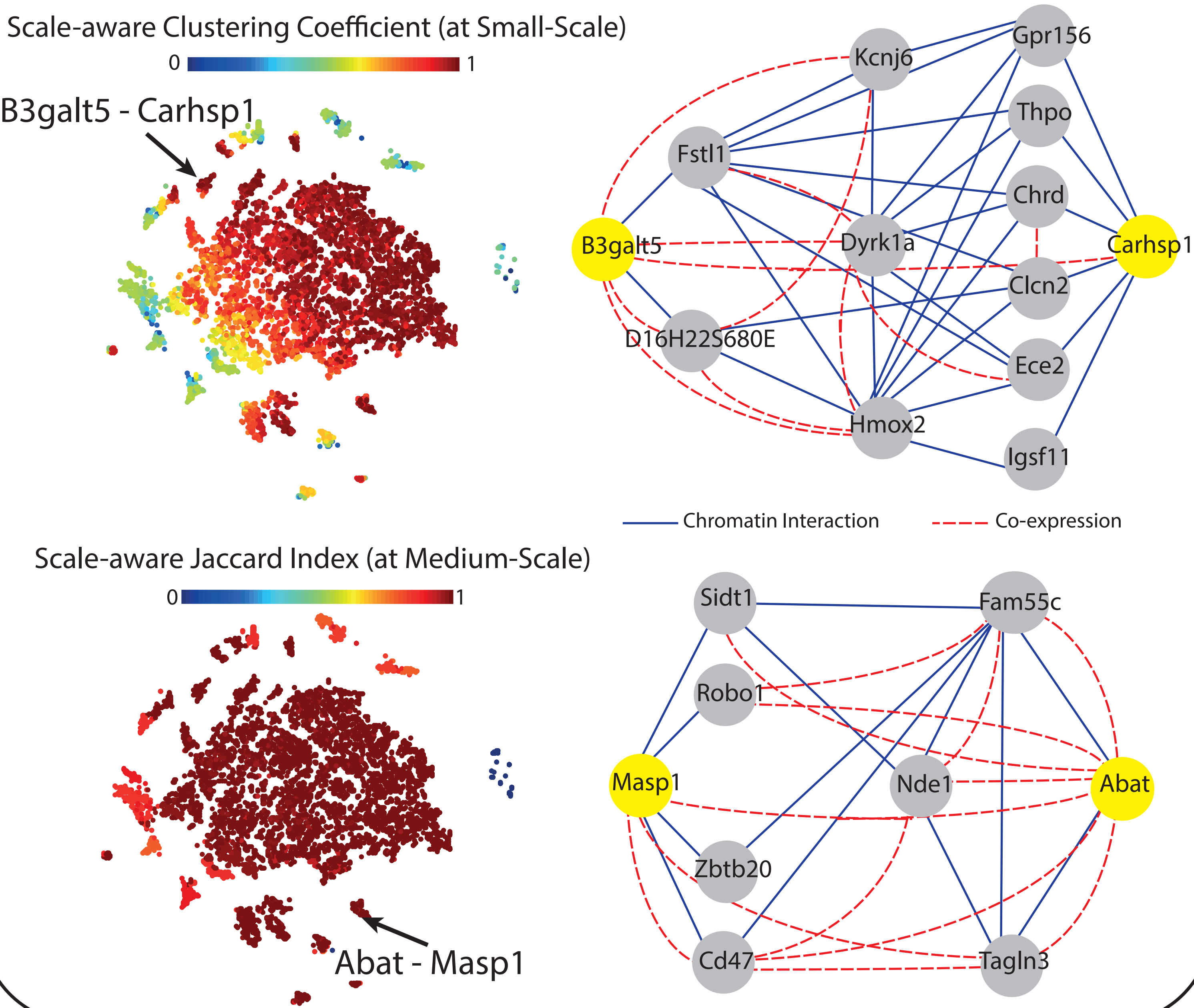


Scale-aware topological measures are calculated based on diffusion kernels

RNN classifier is trained on topological measures



of Chromatin Interaction Network of Chromosome 16



We find that the chromatin interaction profile of a gene-pair is a good predictor of their spatial co-expression. The accuracy of the prediction substantially improves when chromatin interactions are described by scale-aware topological measures of the multi-resolution chromatin interaction network. For co-expression prediction, it is necessary to take into account different levels of chromatin interactions from direct interaction between genes (i.e. small-scale) to chromatin compartment interactions (i.e. large-scale).

Reference

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