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Cover Artistic illustration of a heterogeneous interactome module (HIM) in a cell nucleus. Here, the deck represents the cell nucleus. The sailors (representative of transcription factor proteins) and the ropes (representative of chromatin) form a HIM that reflects a “transcriptional niche” in the nucleus. In this issue, a new algorithm, MOCHI, integrates transcription factor binding and 3D genome structure to identify HIMs and finds that they have strong spatial preferences within the nucleus and exhibit distinct functional properties. (Cover illustration by Ella Marushchenko, Ella Maru Studio, <https://scientific-illustrations.com/>. [For details, see Tian et al., pp. 227–238.]